

Supporting Information

Chemoproteomics-Enabled Covalent Ligand Screen Reveals a Cysteine Hotspot in Reticulon 4 that Impairs ER Morphology and Cancer Pathogenicity

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Supplemental Methods

Materials. IAYne was obtained from CHESS GmbH. Heavy and light TEV-biotin tags were synthesized per previously described methods^{5,21}.

Cell Culture. SW620 cells were purchased from ATCC. SW620 cells were grown in L-15 media with 10% fetal bovine serum (FBS) in ambient CO₂. U2OS cells were grown in DMEM media supplemented with 10% FBS at 37°C with 5% CO₂.

Survival and Proliferation Assays. Cells were plated the evening before the experiment, and allowed to adhere overnight. For serum-free cell survival assays, cells were plated in media not containing FBS. For cell proliferation assays, cells were plated in regular media. For the chemical genetics screen, cells were treated with either DMSO or the cysteine-reactive fragment for 48 h and cell viability was assessed by Hoescht stain using our previously described methods²².

Tumor Xenograft Growth Studies. C.B17 SCID male mice (6-8 weeks old) were injected subcutaneously into the flank with 2,000,000 cells in serum-free media. For pharmacological treatments, mice were exposed by intraperitoneal (ip) injection with either vehicle (18:1:1 PBS/ethanol/PEG40) or 50 mg/kg DKM 3-30 once per day starting ten days after the initiation of the xenograft experiment and until the completion of the study. Tumors were measured every 7 days by caliper measurements. Animal experiments were conducted in accordance with the guidelines of the Institutional Animal Care and Use Committee of the University of California, Berkeley.

IsoTOP-ABPP Analysis. IsoTOP-ABPP analyses were performed as previously described⁵⁻⁷. For competitive IsoTOP-ABPP, SW620 cell lysates were pre-incubated with DMSO vehicle or DKM 3-30 (50 µM) for 30 min at 37°C in phosphate-buffered saline (PBS), and then labeled with IAYne (100 µM) for 1 h at room temperature. They were subsequently treated with isotopically light (control) or heavy (treated) TEV-biotin (100 µM) and CuAAC was performed as previously described^{5,6}. For analysis of cysteine reactivity in primary colorectal tumor tissue, tumors were pooled and incubated with either 100 µM IAYne and isotopically heavy TEV-biotin or 10 µM IAYne and isotopically light TEV-biotin followed by CuAAC. Proteins were precipitated over one hour and pelleted by centrifugation at 6500 x g. Proteins were washed 3 times with cold methanol then denatured and resolubilized by heating in 1.2% SDS/PBS to 85° C for 5 min. Insoluble components were precipitated by centrifugation at 6500 x g and soluble proteome was diluted in 5 ml PBS, for a final concentration of 0.2% SDS. Labeled proteins were bound to avidin-agarose beads (170 µL resuspended beads/sample, Thermo Pierce) while rotating overnight at 4°C. Bead-linked proteins were enriched by washing three times each in PBS and water, then resuspended in 6 M urea/PBS (Sigma-Aldrich) and reduced in dithiothreitol (1 mM, Sigma-Aldrich), alkylated with iodoacetamide (18 mM, Sigma-Aldrich), then washed and resuspended in 2 M urea/PBS with 1 mM calcium chloride and trypsinized overnight with 0.5 µg/µl sequencing grade trypsin (Promega). Tryptic peptides were discarded and beads were washed three times each in PBS and water, then washed with one wash of TEV buffer containing 1 µM DTT. TEV-biotin tag was digested overnight in TEV buffer containing 1 µM DTT and 5 µL Ac-TEV protease at 29°C. Peptides were diluted in water and acidified with final concentration of 5% formic acid (1.2 M, Spectrum).

Peptides from all proteomic experiments were pressure-loaded onto a 250 mm inner diameter fused silica capillary tubing packed with 4 cm of Aqua C18 reverse-phase

resin (Phenomenex # 04A-4299) which was previously equilibrated on an Agilent 600 series HPLC using gradient from 100% buffer A to 100% buffer B over 10 min, followed by a 5 min wash with 100% buffer B and a 5 min wash with 100% buffer A. The samples were then attached using a MicroTee PEEK 360 μ m fitting (Thermo Fisher Scientific #p-888) to a 13 cm laser pulled column packed with 10 cm Aqua C18 reverse-phase resin and 3 cm of strong-cation exchange resin for isoTOP-ABPP studies. Samples were analyzed using an Q Exactive Plus mass spectrometer (Thermo Fisher Scientific) using a 5-step Multidimensional Protein Identification Technology (MudPIT) program, using 0 %, 25 %, 50 %, 80 %, and 100 % salt bumps of 500 mM aqueous ammonium acetate and using a gradient of 5-55 % buffer B in buffer A (buffer A: 95:5 water:acetonitrile, 0.1 % formic acid; buffer B 80:20 acetonitrile:water, 0.1 % formic acid). Data was collected in data-dependent acquisition mode with dynamic exclusion enabled (60 s). One full MS (MS1) scan (400-1800 m/z) was followed by 15 MS2 scans (ITMS) of the nth most abundant ions. Heated capillary temperature was set to 200° C and the nanospray voltage was set to 2.75 kV.

Data was extracted in the form of MS1 and MS2 files using Raw Extractor 1.9.9.2 (Scripps Research Institute) and searched against the Uniprot mouse database using ProLuCID search methodology in IP2 v.3 (Integrated Proteomics Applications, Inc)²³. Cysteine residues were searched with a static modification for carboxyamino-methylation (+57.02146) and up to two differential modifications for methionine oxidation and either the light or heavy TEV tags (+464.28596 or +470.29977, respectively). Peptides were required to have at least one tryptic end and to contain the TEV modification. ProLUCID data was filtered through DTASelect to achieve a peptide false-positive rate below 1%.

Gel-Based ABPP. Gel-based ABPP methods were performed as previously described²⁴. Recombinant RTN4 (0.06 μ g) protein (RTN4-Fisher Scientific) were pre-treated with DMSO or DKM 3-30, respectively, for 1 h at 37°C in an incubation volume of 50 μ L PBS, and were subsequently treated with IAYne (10 μ M final concentration) for 30 min at 37°C. CuAAC was performed to append rhodamine-azide onto IAYne probe-labeled proteins. The samples were separated by SDS/PAGE and scanned using a ChemiDoc MP (Bio-Rad Laboratories, Inc). Inhibition of target labeling was assessed by densitometry using ImageStudio Light software.

RTN4 Knockdown. Targets were knocked down transiently with siRNA or stably with shRNA as previously described^{22,25}. For siRNA studies, SW620 cells (200,000 cells/well) were seeded overnight after which siControl (non-targeting siRNA) or siRTN4 oligonucleotides (5 pooled siRNAs targeting each target purchased from Dharmacon) were transfected into cells using Dharmafect 1. Cells were harvested after 48 h for qPCR and for seeding for cell viability assays.

For shRNA studies, shControl (targeting GFP) or shRTN4 constructs (purchased from Sigma) were transfected into HEK293T cells alongside lentiviral vectors using FuGENE. Lentivirus was collected from filtered cultured medium 48 h post-transfection and used to infect the target cancer cell line with Polybrene (0.01 mg/ml). Target cells were selected over 3 days with 1 mg/ml puromycin. The short hairpin sequences for the generation of RTN4 knockdown lines were:
CCGGGCAGTGTTGATGTGGGTATTTCTCGAGAAATACCCACATCAACACTGCTTTTT
TG and
CCGGGCTATATCTGAGGAGTTGGTTCTCGAGAACCAACTCCTCAGATATAGCTTTTT
TG. The control shRNA was targeted against GFP with the target sequence
GCAAGCTGACCCTGAAGTTCAT. Knockdown was confirmed by qPCR.

qPCR. qPCR was performed using the manufacturer's protocol for Fisher Maxima SYBR Green with 10 mM primer concentrations or for Bio-Rad SsoAdvanced Universal Probes Supermix. Primer sequences for Fisher Maxima SYBR Green were derived from Harvard Primer Bank. Primer sequences for Bio-Rad SsoAdvanced Universal Probes Supermix were designed with Primer 3 Plus.

Fluorescence microscopy. SW620 and U2OS cells were transiently transfected with a plasmid encoding GFP-tagged Sec61 β (kindly provided by Gia Voeltz, University of Colorado Boulder) using fuGENE6 (Roche) according to the manufacturer's instructions. Transfected cells plated on poly-L-lysine treated coverslips were treated, washed in PBS, and fixed by incubation in 4% paraformaldehyde in PBS for 10 min. Fixed cells were washed extensively in PBS and nuclei stained by addition of 4',6-diamidino-2-phenylindole (DAPI) (Thermo Fisher Scientific) for 10 min. Coverslips were mounted using Fluoromount-G (SouthernBiotech) and visualized using a DeltaVision Elite microscope outfitted with a 60x oil immersion objective. Acquired stacks of images of fixed cells were deconvolved and analyzed using SoftWoRx and ImageJ. For time-lapse imaging of live cells, transfected cells were plated on poly-L-lysine treated glass-bottom 4-well imaging chambers (Lab-Tek II; Thermo Fisher Scientific). Imaging was performed using a DeltaVision Elite microscope encased in a chamber that was maintained at 37°C and was continuously perfused with humidified 5% CO₂. Acquired images were analyzed using SoftWoRx and ImageJ.

Homology modeling and multiple sequence alignments. The threaded homology model of the human Rtn4 (amino acids 1054-1120 of Rtn4a) on the NMR solution structure of the corresponding region of mouse Rtn4 (PDB 2KO2) was generated using Protein Homology/analogY Recognition Engine V 2.0 (Phyre2). Figures were made using PyMOL. Multiple sequence alignments were generated using Clustal Omega and figures were made using BoxShade.

Primary Human Colorectal Tumors. Eligible patients completed written consent for our tissue banking protocol that is approved by the University of Alabama at Birmingham Institutional Review Board. During the colorectal tumor resection, a 1 cm³ portion of the tumor was dissected free of the fresh resection specimen, divided into 4-5 aliquots, placed into 1.5 mL cryovials, flash frozen, and stored at -80°C. Adjacent non-tumor bearing colorectal tissue was also collected and banked in a similar manner.

Flow cytometry analysis of apoptosis. For the measurement of apoptosis, cells were isolated and stained as described in the manufacturer's instructions. In brief, trypsinized cells and cells present in the media were pelleted by centrifugation at 500x g for 5 min, washed in PBS, and then resuspended in the supplied Binding Buffer (10 mM HEPES/NaOH pH 7.4, 140 mM NaCl, 2.5 mM CaCl₂) containing propidium iodide (BD Biosciences) and Alexa Fluor™ 647 annexin V conjugate (Thermo Fisher Scientific). Cells were incubated for 15 min and then diluted with Binding Buffer to a final volume of 0.5 mL. Fluorescence was measured using a BD Biosciences LSR Fortessa cytometer. FlowJo Software was used to quantify the percentage of apoptotic (Annexin V positive and propidium iodide positive) transfected (GFP-positive) cells (n=3). T-test was employed for all statistical analyses.

Synthesis of Cysteine-Reactive Library

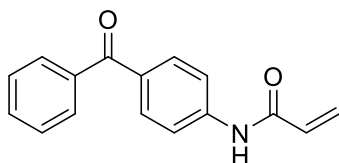
Chemicals and reagents were purchased from major commercial suppliers and used without further purification. Reactions were performed under a nitrogen atmosphere unless otherwise noted. Silica gel flash column chromatography was performed using EMD or Sigma Aldrich silica gel 60 (230-400 mesh). Proton and carbon nuclear magnetic resonance (^1H NMR and ^{13}C NMR) data was acquired on a Bruker AVB 400, AVQ 400, or AV 600 spectrometer at the University of California, Berkeley. High resolution mass spectrum were obtained from the QB3 mass spectrometry facility at the University of California, Berkeley using positive or negative electrospray ionization (+ESI or -ESI). Yields are reported as a single run.

General Procedure A

The amine (1 eq.) was dissolved in DCM (5 mL/mmol) and cooled to 0°C . To the solution was added acryloyl chloride (1.2 eq.) followed by triethylamine (1.2 eq.). The solution was warmed to room temperature and stirred overnight. The solution was then washed with brine and the crude product was purified by silica gel chromatography (and recrystallization if necessary) to afford the corresponding acrylamide.

General Procedure B

The amine (1 eq.) was dissolved in DCM (5 mL/mmol) and cooled to 0°C . To the solution was added chloroacetyl chloride (1.2 eq.) followed by triethylamine (1.2 eq.). The solution was warmed to room temperature and stirred overnight. The solution was then washed with brine and the crude product was purified by silica gel chromatography (and recrystallization if necessary) to afford the corresponding chloroacetamide.



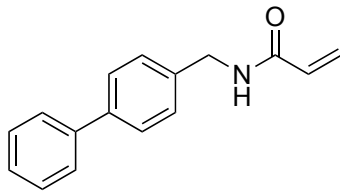
N-(4-benzoylphenyl)acrylamide (DKM 2-117)

Following **General Procedure A** starting from 4-aminobenzophenone (587 mg, 3.0 mmol), product was obtained after silica gel chromatography (10% to 30% ethyl acetate in hexanes) in 37% yield as a yellow solid (275 mg).

^1H NMR (400MHz, CDCl_3): δ 8.77 (s, 1H), 7.80-7.73 (m, 6H), 7.57 (tt, J = 1.5, 7.4 Hz, 1H), 7.46 (t, J = 7.6 Hz, 2H), 6.46 (dd, J = 1.6 16.9 Hz, 1H), 6.37 (dd, J = 9.9, 16.9 Hz, 1H), 5.75 (dd, J = 1.6, 9.9 Hz, 1H).

^{13}C NMR (100MHz, CDCl_3): δ 196.3, 164.4, 142.3, 137.8, 133.0, 132.5, 131.7, 131.0, 130.0, 128.8, 128.4, 119.3.

HRMS (+ESI): Calculated: 252.1019 ($\text{C}_{16}\text{H}_{14}\text{NO}_2$). Observed: 252.1014.



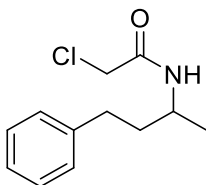
N-([1,1'-biphenyl]-4-ylmethyl)acrylamide (DKM 2-37)

Following **General Procedure A** starting from 4-phenylbenzylamine (552 mg, 3.0 mmol), product was obtained after silica gel chromatography (0% to 80% ethyl acetate in hexanes) in 10% yield as an off-white solid (73 mg).

¹H NMR (400MHz, CDCl₃): δ 7.58-7.55 (m, 4H), 7.44 (t, *J* = 7.5 Hz, 2H), 7.38-7.33 (m, 3H), 6.35 (dd, *J* = 1.3, 17.0 Hz, 1H), 6.13 (dd, *J* = 10.3, 17.0 Hz, 1H), 6.01 (s, 1H), 5.68 (dd, *J* = 1.3, 10.3 Hz, 1H), 4.56 (d, *J* = 5.8 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.5, 140.77, 140.73, 137.2, 130.7, 128.9, 128.5, 127.6, 127.5, 127.2, 127.1, 43.5.

HRMS (+ESI): Calculated: 238.1226 (C₁₆H₁₆NO). Observed: 238.1224.



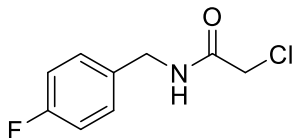
2-Chloro-N-(4-phenylbutan-2-yl)acetamide (DKM 2-76)

Following **General Procedure B** starting from 1-methyl-3-phenylpropylamine (614 mg, 4.1 mmol) product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 81% yield as a white solid (662 mg).

¹H NMR (400MHz, CDCl₃): δ 7.34-7.31 (m, 2H), 7.24-7.21 (m, 3H), 6.55 (d, *J* = 7.4 Hz, 1H), 4.15-4.07 (m, 1H), 4.04 (s, 2H), 2.70 (t, *J* = 8.2 Hz, 2H), 1.89-1.83 (m, 2H), 1.26 (d, *J* = 6.4 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.1, 141.3, 128.4, 128.2, 125.9, 45.7, 42.7, 38.1, 32.3, 20.7.

HRMS (+ESI): Calculated: 226.0993 (C₁₂H₁₇ClNO). Observed: 226.0992.



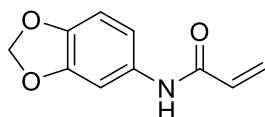
2-chloro-N-(4-fluorobenzyl)acetamide (DKM 2-80)

Following **General Procedure B** starting from 4-fluorobenzylamine (369 mg, 2.9 mmol) product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 77% yield as a white solid (452 mg).

¹H NMR (400MHz, CDCl₃): δ 7.28-7.24 (m, 2H), 7.05-7.01 (m, 2H), 6.97 (s, 1H), 4.45 (d, *J* = 5.6 Hz, 2H), 4.09 (s, 2H).

¹³C NMR (100MHz, CDCl₃): δ 166.1, 163.6, 161.2, 133.20, 133.17, 129.64, 129.56, 115.9, 115.7, 43.2, 42.7.

HRMS (-ESI): Calculated: 200.0284 (C₉H₈NOCIF). Observed: 200.0284.



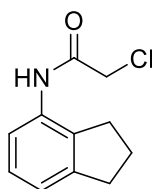
N-(benzo[d][1,3]dioxol-5-yl)acrylamide (DKM 2-86)

Following **General Procedure A** starting from 3,4-(methylenedioxy)aniline (486 mg, 2.9 mmol), product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 68% yield as a white solid (438 mg).

¹H NMR (400MHz, (CD₃)₂SO): δ 10.05 (s, 1H), 7.39 (d, *J* = 2.0 Hz, 1H), 7.02 (dd, *J* = 2.0, 8.4 Hz, 1H), 6.87 (d, *J* = 8.4 Hz, 1H), 6.38 (dd, *J* = 10.1, 17.0 Hz, 1H), 6.22 (dd, *J* = 2.1, 17.0 Hz, 1H), 5.99 (s, 2H), 5.72 (dd, *J* = 2.1, 10.1 Hz, 1H).

¹³C NMR (100MHz, (CD₃)₂SO): δ 162.8, 147.0, 143.1, 133.4, 131.8, 126.5, 112.1, 108.1, 101.4, 101.0.

HRMS (+ESI): Calculated: 192.0655 (C₁₀H₁₀NO₃). Observed: 192.0651.



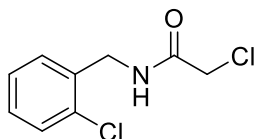
2-chloro-N-(2,3-dihydro-1H-inden-4-yl)acetamide (DKM 2-91)

Following **General Procedure B** starting from 4-aminoindan (372 mg, 2.8 mmol) product was obtained after silica gel chromatography (0% to 40% ethyl acetate in hexanes) in 49% yield as an off-white solid (289 mg).

¹H NMR (400MHz, CDCl₃): δ 8.19 (s, 1H), 7.74 (d, *J* = 8.4 Hz, 1H), 7.15 (t, *J* = 7.8 Hz, 1H), 7.05 (d, *J* = 7.6 Hz, 1H), 4.16 (s, 2H), 2.94 (t, *J* = 7.6 Hz, 2H), 2.82 (t, *J* = 7.4 Hz, 2H), 2.10 (quint, *J* = 7.5 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 163.8, 145.5, 134.5, 132.8, 127.3, 121.6, 118.5, 43.1, 33.2, 29.8, 24.8.

HRMS (+ESI): Calculated: 210.0680 (C₁₁H₁₃ClNO). Observed: 210.0680.



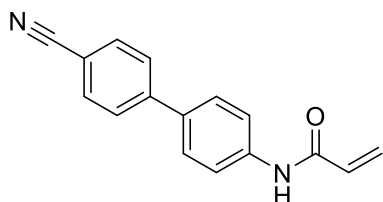
2-Chloro-N-(2-chlorobenzyl)acetamide (DKM 2-94)

Following **General Procedure B** starting from 2-chlorobenzylamine (432 mg, 3.1 mmol) product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 67% yield as a white solid (443 mg).

¹H NMR (400MHz, CDCl₃): δ 7.36-7.18 (m, 5H), 4.51 (d, *J* = 6.4 Hz, 2H), 4.01 (s, 2H).

¹³C NMR (100MHz, CDCl₃): δ 166.1, 134.7, 133.5, 129.8, 129.5, 129.1, 127.1, 42.5, 41.6.

HRMS (-ESI): Calculated: 215.9988 (C₉H₈NOCl₂). Observed: 215.9988.



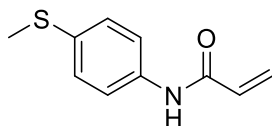
N-(4'-cyano-[1,1'-biphenyl]-4-yl)acrylamide (DKM 2-98)

Following **General Procedure A** starting from 4-(4-aminophenyl)benzonitrile (387 mg, 2.0 mmol), product was obtained after silica gel chromatography (1% to 2% ethyl methanol in DCM) in 70% yield as a yellow solid (348 mg).

¹H NMR (600MHz, (D₃C)₂CO): 9.52 (s, 1H), 7.90-7.89 (m, 2H), 7.87-7.86 (m, 2H), 7.84-7.82 (m, 2H), 7.73-7.71 (m, 2H), 6.49 (dd, *J* = 10.0, 16.9 Hz, 1H), 6.39 (dd, *J* = 2.0, 16.9 Hz, 1H), 5.76 (dd, *J* = 2.0, 10.0 Hz, 1H).

¹³C NMR (150MHz, (D₃C)₂CO): δ 164.3, 145.7, 140.9, 134.8, 133.6, 132.7, 128.5, 128.2, 127.6, 120.8, 119.5, 111.3.

HRMS (-ESI): Calculated: 247.0877 (C₁₆H₁₁N₂O). Observed: 247.0875.



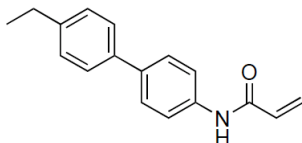
N-(4-(methylthio)phenyl)acrylamide (DKM 3-10)

Following **General Procedure A** starting from 4-(methylthio)aniline (405 mg, 2.9 mmol), product was obtained after silica gel chromatography (10% to 40% ethyl acetate in hexanes) in 64% yield as a clear oil (362 mg).

¹H NMR (400MHz, MeOD): δ 7.59-7.56 (m, 2H), 7.26-7.22 (m, 2H), 6.42 (dd, *J* = 9.6, 17.0 Hz, 1H), 6.34 (dd, *J* = 2.3, 17.0 Hz, 1H), 5.75 (dd, *J* = 2.3, 9.6 Hz, 1H), 2.45 (s, 3H).

^{13}C NMR (100MHz, MeOD): δ 166.0, 137.2, 135.4, 132.4, 128.6, 127.7, 121.9, 16.4.

HRMS (+ESI): Calculated: 194.0634 ($\text{C}_{10}\text{H}_{12}\text{NOS}$). Observed: 194.0631.



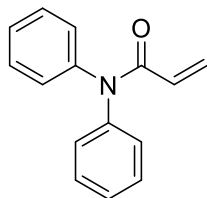
N-(4'-ethyl-[1,1'-biphenyl]-4-yl)acrylamide (DKM 3-16)

Following **General Procedure A** starting from 4-amino-4-ethylbiphenyl (386 mg, 2.0 mmol), product was obtained after silica gel chromatography (10% to 70% ethyl acetate in hexanes) in 65% yield as a white solid (164 mg).

^1H NMR (400MHz, $(\text{CD}_3)_2\text{CO}$): δ 7.82 (d, J = 8.2 Hz, 2H), 7.62-7.59 (m, 2H), 7.58-7.54 (m, 2H), 7.29 (d, J = 8.2 Hz, 2H), 6.47 (dd, J = 9.9, 16.9 Hz, 1H), 6.36 (dd, J = 2.2, 16.9 Hz, 1H), 5.72 (dd, J = 2.2, 9.9 Hz, 1H), 2.67 (q, J = 7.6 Hz, 2H), 1.24 (t, J = 7.6 Hz, 3H).

^{13}C NMR (100MHz, $(\text{CD}_3)_2\text{CO}$): δ 164.1, 144.0, 139.5, 13.9, 137.1, 132.9, 129.3, 127.9, 127.4, 127.2, 120.7, 29.2, 16.2.

HRMS (+ESI): Calculated: 252.1383 ($\text{C}_{17}\text{H}_{18}\text{NO}$). Observed: 252.1379.



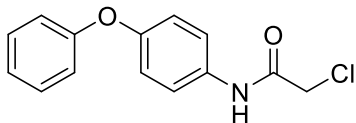
N,N-diphenylacrylamide (DKM 3-70)

A solution of diphenylamine (347 mg, 2.1 mmol) in DCM (10 mL) was cooled to 0 °C. To the solution was added acryloyl chloride (222 mg, 2.5 mmol) followed by triethylamine (279 mg, 2.8 mmol). The solution was allowed to warm to room temperature and stirred overnight. The solution was washed with brine and citric acid and the crude product was purified via silica gel chromatography (20% to 60% ethyl acetate in hexanes) to afford the product in 24% yield as a dark yellow oil (112 mg).

^1H NMR (400MHz, CDCl_3): δ 7.43-7.28 (m, 10H), 6.52 (dd, J = 2.0, 16.8 Hz, 1H), 6.25 (dd, J = 10.2, 16.8 Hz, 1H), 5.67 (dd, J = 1.8, 10.2 Hz, 1H).

^{13}C NMR (100MHz, CDCl_3): δ 165.8, 142.6, 129.7, 129.3, 128.5, 127.0.

HRMS (+ESI): Calculated: 246.0889 ($\text{C}_{15}\text{H}_{13}\text{NONa}$). Observed: 246.0887.



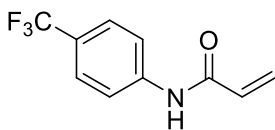
2-Chloro-*N*-(4-phenoxyphenyl)acetamide (TRH 1-23)

Following **General Procedure B** starting from 4-phenoxyaniline (370 mg, 2.0 mmol) product was obtained after silica gel chromatography (10% to 30% ethyl acetate in hexanes) in 46% yield as a white solid (315 mg).

¹H NMR (400MHz, CDCl₃): δ 8.42 (s, 1H), 7.52-7.48 (m, 2H), 7.35-7.31 (m, 2H), 7.10 (t, *J* = 7.3 Hz, 1H), 7.01-6.98 (m, 4H), 4.17 (s, 2H).

¹³C NMR (100MHz, CDCl₃): δ 164.2, 157.2, 154.4, 132.1, 129.8, 123.4, 122.2, 119.4, 118.7, 42.9.

HRMS (-ESI): Calculated: 260.0484 (C₁₄H₁₁NO₂Cl). Observed: 260.0482.



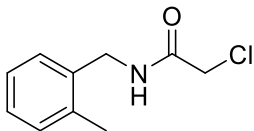
N-(4-(trifluoromethyl)phenyl)acrylamide (TRH 1-50)

Following **General Procedure A** starting from 4-(trifluoromethyl)aniline (328 mg, 2.0 mmol), product was obtained after silica gel chromatography (10% to 30% ethyl acetate in hexanes) in 55% yield as a white solid (239 mg).

¹H NMR (400MHz, MeOD): δ 7.78 (d, *J* = 8.3 Hz, 2H), 7.55 (d, *J* = 8.6 Hz, 2H), 6.44-6.32 (m, 2H), 5.75 (dd, *J* = 8.4, 2.8 Hz, 1H).

¹³C NMR (100MHz, MeOD): δ 166.3, 143.3, 132.1, 128.6, 127.04, 127.00, 126.97, 126.93, 126.6, 124.3, 120.9.

HRMS (-ESI): Calculated: 214.0485 (C₁₀H₇NOF₃). Observed: 214.0484.



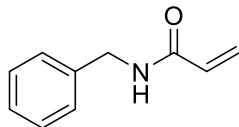
2-Chloro-*N*-(2-methylbenzyl)acetamide (TRH 1-55)

Following **General Procedure B** starting from 2-methylbenzylamine (239 mg, 2.0 mmol) product was obtained after silica gel chromatography (30% ethyl acetate in hexanes) and recrystallization from 5% ethyl acetate in hexanes in 64% yield as a white solid (191 mg).

¹H NMR (400 MHz, CDCl₃): δ 7.25-7.19 (m, 4H), 6.85 (s, 1H), 4.46 (d, *J* = 5.6 Hz, 2H), 4.04 (s, 2H), 2.33 (s, 3H).

^{13}C NMR (100 MHz, CDCl_3): δ 165.8, 136.4, 135.0, 130.6, 128.4, 128.0, 126.3, 42.6, 42.0, 19.0.

HRMS (-ESI): Calculated: 196.0535 ($\text{C}_{10}\text{H}_{11}\text{NOCl}$). Observed: 196.0534.



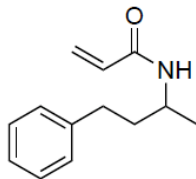
N-benzylacrylamide (DKM 2-31)

Following **General Procedure A** starting from benzylamine (334 mg, 3.1 mmol), product was obtained after silica gel chromatography (0% to 50% ethyl acetate in hexanes) in 75% yield as a white solid (376 mg).

^1H NMR (400MHz, CDCl_3): δ 7.28-7.18 (m, 6H), 6.19-6.16 (m, 2H), 5.53 (dd, J = 4.6, 7.3 Hz, 1H), 4.36 (d, J = 5.9 Hz, 2H).

^{13}C NMR (100MHz, CDCl_3): δ 165.8, 138.1, 130.8, 128.6, 127.7, 127.3, 126.5, 43.5.

HRMS (+ESI): Calculated: 162.0913 ($\text{C}_{10}\text{H}_{12}\text{NO}$). Observed: 162.0912.



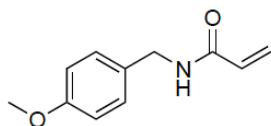
N-(4-phenylbutan-2-yl)acrylamide (DKM 2-32)

Following **General Procedure A** starting from 1-methyl-3-phenylpropylamine (606 mg, 4.0 mmol), product was obtained after silica gel chromatography (0% to 50% ethyl acetate in hexanes) in 89% yield as a clear oil (735 mg).

^1H NMR (400MHz, CDCl_3): δ 7.32-7.29 (m, 2H), 7.23-7.20 (m, 3H), 6.84 (d, J = 8.4 Hz, 1H), 6.36-6.24 (m, 2H), 5.64 (dd, J = 2.8, 9.2 Hz, 1H), 4.21-4.14 (m, 1H), 2.70 (t, J = 7.8 Hz, 2H), 1.93-1.77 (m, 2H), 1.24 (d, J = 6.4 Hz, 3H).

^{13}C NMR (100MHz, CDCl_3): δ 165.1, 141.7, 131.3, 128.3, 128.2, 125.80, 125.77, 45.1, 38.4, 32.5, 20.8.

HRMS (+ESI): Calculated: 204.1383 ($\text{C}_{13}\text{H}_{18}\text{NO}$). Observed: 204.1380.



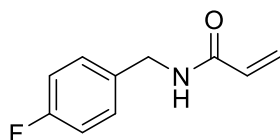
N-(4-methoxybenzyl)acrylamide (DKM 2-33)

Following **General Procedure A** starting from 4-methoxybenzylamine (424 mg, 3.1 mmol), product was obtained after silica gel chromatography (0% to 50% ethyl acetate in hexanes) in 60% yield as a clear oil (343 mg).

¹H NMR (400MHz, CDCl₃): δ 7.14 (d, *J* = 8.8 Hz, 2H), 6.85 (s, 1H), 6.79 (d, *J* = 8.4 Hz, 2H), 6.24-6.14 (m, 2H), 5.56 (dd, *J* = 2.0, 9.6 Hz, 1H), 4.33 (d, *J* = 5.6 Hz, 2H), 3.73 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.6, 158.9, 130.9, 130.3, 129.1, 126.4, 113.9, 55.2, 42.9.

HRMS (+ESI): Calculated: 192.1019 (C₁₁H₁₄NO₂). Observed: 192.1017.



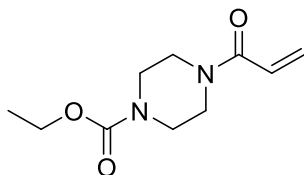
N-(4-fluorobenzyl)acrylamide (DKM 2-34)

Following **General Procedure A** starting from 4-fluorobenzylamine (368 mg, 2.9 mmol), product was obtained after silica gel chromatography (0% to 60% ethyl acetate in hexanes) in 52% yield as an off-white solid (276 mg).

¹H NMR (400MHz, CDCl₃): δ 7.24-7.19 (m, 2H), 6.97 (t, *J* = 8.5 Hz, 2H), 6.42 (s, 1H), 6.27 (d, *J* = 17.0 Hz, 1H), 6.12 (dd, *J* = 17.0, 10.2 Hz, 1H), 5.63 (d, *J* = 10.2 Hz, 1H), 4.42 (d, *J* = 5.8 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.7, 163.5, 134.0, 130.6, 129.6, 129.5, 127.0, 115.7, 115.5, 43.0.

HRMS (+ESI): Calculated: 180.0819 (C₁₀H₁₁NOF). Observed: 180.0818.



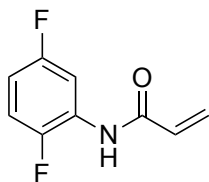
Ethyl 4-acryloylpiperazine-1-carboxylate (DKM 2-39)

Following **General Procedure A** starting from ethyl 1-piperazinecarboxylate (477 mg, 3.0 mmol), product was obtained after silica gel chromatography (0% to 70% ethyl acetate in hexanes) in 58% yield as a yellow oil (372 mg).

¹H NMR (400MHz, CDCl₃): δ 6.46 (dd, *J* = 10.5, 16.8 Hz, 1H), 6.18 (dd, *J* = 1.9, 16.8 Hz), 5.60 (dd, *J* = 1.9, 10.5 Hz), 4.03 (q, *J* = 7.1 Hz, 2H), 3.54 (s, 2H), 3.44 (s, 2H), 3.39-3.36 (m, 4H), 1.15 (t, *J* = 7.1 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.3, 155.1, 128.2, 127.1, 61.5, 45.4, 43.6, 43.3, 41.5, 14.5.

HRMS (+ESI): Calculated: 213.1234 (C₁₀H₁₇N₂O₃). Observed: 213.1232.



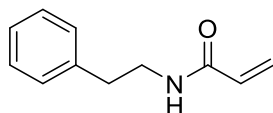
N-(2,5-difluorophenyl)acrylamide (DKM 2-40)

Following **General Procedure A** starting from 2,5-difluoroaniline (369 mg, 2.9 mmol), product was obtained after silica gel chromatography (0% to 15% ethyl acetate in hexanes) in 27% yield as a white solid (141 mg).

¹H NMR (400MHz, (CD₃)₂CO): δ 9.26 (s, 1H), 8.29-8.24 (m, 1H), 7.24-7.18 (m, 1H), 6.90-6.84 (m, 1H), 6.67 (dd, *J* = 10.2, 16.9 Hz, 1H), 6.41 (dd, *J* = 1.9, 16.9 Hz, 1H), 5.79 (dd, *J* = 1.9, 10.2 Hz, 1H).

¹³C NMR (100MHz, (CD₃)₂CO): δ 164.6, 160.4, 151.0, 148.7, 132.0, 128.9, 128.8, 128.5, 116.7, 116.6, 116.5, 116.4, 111.1, 111.0, 110.8, 110.7, 110.0, 109.7.

HRMS (+ESI): Calculated: 184.0568 (C₉H₈ F₂NO). Observed: 184.0567.



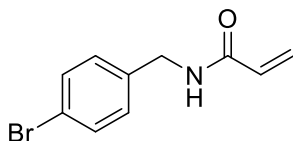
N-phenethylacrylamide (DKM 2-42)

Following **General Procedure A** starting from phenylethylamine (367 mg, 3.0 mmol), product was obtained after silica gel chromatography (0% to 50% ethyl acetate in hexanes) in 85% yield as a yellow oil (450 mg).

¹H NMR (400MHz, CDCl₃): δ 7.30-7.18 (m, 5H), 6.63 (s, 1H), 6.25 (dd, *J* = 1.8, 17.0 Hz, 1H), 6.13 (dd, *J* = 10.0, 17.0 Hz 1H), 5.59 (dd, *J* = 1.6, 10.0 Hz, 1H), 3.56 (q, *J* = 6.8 Hz, 2H), 2.85 (t, *J* = 7.3 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.8, 138.8, 131.0, 128.7, 128.6, 126.4, 126.1, 40.8, 35.6.

HRMS (+ESI): Calculated: 176.1070 (C₁₁H₁₄NO). Observed: 176.1068.



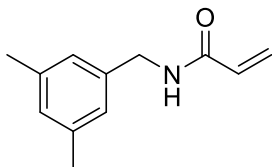
N-(4-bromobenzyl)acrylamide (DKM 2-43)

Following **General Procedure A** starting from 4-bromobenzylamine (535 mg, 2.9 mmol), product was obtained after silica gel chromatography (0% to 50% ethyl acetate in hexanes) in 59% yield as a white solid (407 mg).

¹H NMR (400MHz, CDCl₃): δ 7.37 (d, *J* = 8.4 Hz, 2H), 7.07 (d, *J* = 8.4 Hz, 2H), 7.00 (s, 1H), 6.24-6.10 (m, 2H), 5.59 (dd, *J* = 2.0, 9.7 Hz, 1H), 4.32 (d, *J* = 6.0 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.9, 137.2, 131.7, 130.6, 129.4, 126.9, 121.2, 42.8.

HRMS (+ESI): Calculated: 240.0019 (C₁₀H₁₁BrNO). Observed: 240.0016.



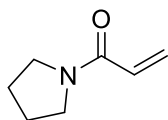
N-(3,5-dimethylbenzyl)acrylamide (DKM 2-47)

Following **General Procedure A** starting from 3,5-dimethylbenzylamine (257 mg, 1.9 mmol), product was obtained after silica gel chromatography (0% to 40% ethyl acetate in hexanes) in 77% yield as a white solid (276 mg).

¹H NMR (400MHz, CDCl₃): δ 6.89-6.87 (m, 4H), 6.26 (dd, *J* = 2.1, 17.0 Hz, 1H), 6.18 (dd, *J* = 9.7, 17.0 Hz, 1H), 5.59 (dd, *J* = 2.1, 9.7 Hz, 1H), 4.35 (d, *J* = 6.0 Hz, 2H), 2.28 (s, 6H).

¹³C NMR (100MHz, CDCl₃): δ 165.6, 138.1, 138.0, 130.9, 129.0, 126.3, 125.6, 43.4, 12.2.

HRMS (+ESI): Calculated: 190.1226 (C₁₂H₁₆NO). Observed: 190.1225.



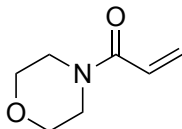
1-(pyrrolidin-1-yl)prop-2-en-1-one (DKM 2-48)

Following **General Procedure A** starting from pyrrolidine (223 mg, 3.1 mmol), product was obtained after silica gel chromatography (0% to 80% ethyl acetate in hexanes) in 38% yield as a pale yellow oil (148 mg).

¹H NMR (400MHz, CDCl₃): δ 6.40 (dd, *J* = 10.0, 16.8 Hz, 1H), 6.29 (dd, *J* = 2.4, 16.8 Hz, 1H), 5.60 (dd, *J* = 2.4, 10.0 Hz, 1H), 3.48 (t, *J* = 6.8 Hz, 4H), 1.91 (quint, *J* = 6.7 Hz, 2H), 1.82 (quint, *J* = 6.7 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 164.4, 128.8, 127.2, 46.6, 45.9, 26.1, 24.3.

HRMS (+ESI): Calculated: 126.0913 (C₇H₁₂NO). Observed: 126.0912.



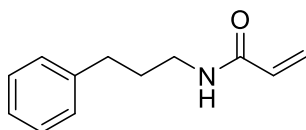
1-morpholinoprop-2-en-1-one (DKM 2-49)

Following **General Procedure A** starting from morpholine (273 mg, 3.1 mmol), product was obtained after silica gel chromatography (0% to 80% ethyl acetate in hexanes) in 46% yield as a yellow oil (205 mg).

¹H NMR (400MHz, CDCl₃): δ 6.45 (dd, *J* = 10.5, 16.8 Hz, 1H), 6.20 (dd, *J* = 1.9, 16.8 Hz, 1H), 5.61 (dd, *J* = 1.9, 10.5 Hz, 1H), 5.38 (s, 6H), 3.46 (s, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.3, 128.1, 126.9, 66.6, 46.0, 42.1.

HRMS (+ESI): Calculated: 142.0863 (C₇H₁₂NO₂). Observed: 142.0861.



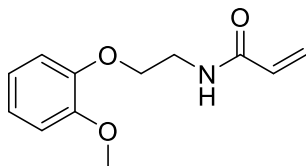
N-(3-phenylpropyl)acrylamide (DKM 2-50)

Following **General Procedure A** starting from 3-phenyl-1-propylamine (275 mg, 2.0 mmol), product was obtained after silica gel chromatography (0% to 60% ethyl acetate in hexanes) in 58% yield as a yellow oil (223 mg).

¹H NMR (400MHz, CDCl₃): δ 7.29-7.25 (m, 2H), 7.20-7.16 (m, 3H), 6.99 (s, 1H), 6.29-6.17 (m, 2H), 5.59 (dd, *J* = 2.6, 9.0 Hz, 1H), 3.34 (q, *J* = 6.7 Hz, 2H), 2.65 (t, *J* = 7.6 Hz, 2H), 1.87 (quint, *J* = 7.4 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 166.0, 141.4, 131.1, 128.33, 128.26, 125.9, 39.2, 33.2, 31.0.

HRMS (+ESI): Calculated: 190.1226 (C₁₂H₁₆NO). Observed: 190.1225.



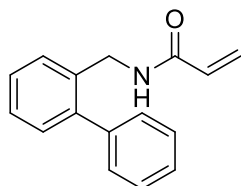
N-(2-(2-methoxyphenoxy)ethyl)acrylamide (DKM 2-58)

Following **General Procedure A** starting from 2-(2-methoxyphenoxy)ethanamine (509 mg, 3.0 mmol), product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 70% yield as a yellow oil (470 mg).

¹H NMR (400MHz, CDCl₃): δ 6.95-6.84 (m, 4H), 6.77 (s, 1H), 6.26 (d, *J* = 17.1 Hz, 1H), 6.11 (dd, *J* = 10.2, 17.1 Hz, 1H), 5.59 (d, *J* = 10.2 Hz, 1H), 4.07 (t, *J* = 5.2 Hz, 2H), 3.79 (s, 3H), 3.69 (q, *J* = 5.4 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.7, 149.6, 147.7, 130.8, 126.4, 122.1, 121.0, 114.8, 111.8, 68.5, 55.7, 38.9.

HRMS (+ESI): Calculated: 244.0944 (C₁₂H₁₅NO₃Na). Observed: 244.0940.



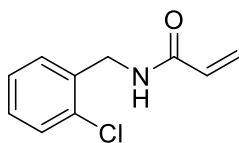
N-([1,1'-biphenyl]-2-ylmethyl)acrylamide (DKM 2-59)

Following **General Procedure A** starting from 2-phenylbenzylamine (202 mg, 1.1 mmol), product was obtained after silica gel chromatography (0% to 40% ethyl acetate in hexanes) in 70% yield as a yellow oil (184 mg).

¹H NMR (400MHz, CDCl₃): δ 7.41-7.22 (m, 9H), 6.16 (dd, *J* = 1.2, 17.2 Hz, 1H), 6.03-5.97 (m, 2H), 5.55 (dd, *J* = 1.2, 10.0 Hz, 1H), 4.44 (d, *J* = 5.6 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.3, 141.6, 140.6, 135.2, 130.6, 130.2, 129.0, 128.7, 128.4, 127.8, 127.4, 127.3, 126.4, 41.4.

HRMS (+ESI): Calculated: 238.1226 (C₁₆H₁₆NO). Observed: 238.1223.



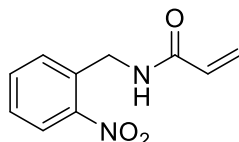
N-(2-chlorobenzyl)acrylamide (DKM 2-60)

Following **General Procedure A** starting from 2-chlorobenzylamine (406 mg, 2.9 mmol), product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 34% yield as a white solid (162 mg).

¹H NMR (400MHz, CDCl₃): δ 7.34-7.30 (m, 2H), 7.20-7.16 (m, 2H), 6.84 (s, 1H), 6.25 (dd, *J* = 2.0, 17.0 Hz, 1H), 6.16 (dd, *J* = 9.7, 17.0 Hz, 2H), 5.60 (dd, *J* = 2.0, 9.7 Hz, 1H), 4.52 (d, *J* = 6.1 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.9, 135.5, 133.5, 130.6, 129.8, 129.5, 128.8, 127.1, 126.8, 41.4.

HRMS (+ESI): Calculated: 196.0524 (C₁₀H₁₁ClNO). Observed: 196.0521



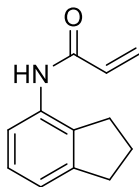
N-(2-nitrobenzyl)acrylamide (DKM 2-62)

Following **General Procedure A** starting from 2-nitrobenzylamine hydrochloride (406 mg, 2.9 mmol) with an extra equivalent of triethylamine, product was obtained after silica gel chromatography (50% ethyl acetate in hexanes) in 42% yield as a yellow solid (255 mg).

¹H NMR (400MHz, CDCl₃): δ 7.98 (dd, *J* = 1.1, 8.2 Hz, 1H), 7.58-7.52 (m, 2H), 7.41-7.37 (m, 1H), 7.03 (s, 1H), 6.22 (dd, *J* = 2.0, 17.0 Hz, 1H), 6.14 (dd, *J* = 9.7, 17.0 Hz, 1H), 5.59 (dd, *J* = 2.0, 9.7 Hz, 1H), 4.68 (d, *J* = 6.4 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.8, 148.2, 134.1, 133.6, 131.9, 130.4, 128.7, 127.1, 125.1, 41.2.

HRMS (+ESI): Calculated: 207.0764 (C₁₀H₁₁N₂O₃). Observed: 207.0760.



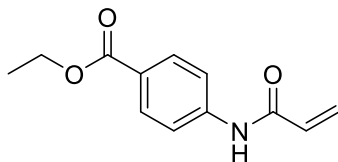
N-(2,3-dihydro-1H-inden-4-yl)acrylamide (DKM 2-84)

Following **General Procedure A** starting from 4-aminoindan (402 mg, 3.0 mmol), product was obtained after silica gel chromatography (30% ethyl acetate in hexanes) in 59% yield as a white solid (332 mg).

¹H NMR (400MHz, CDCl₃): δ 7.72 (d, *J* = 7.5 Hz, 1H), 7.54 (s, 1H), 7.10 (t, *J* = 7.7 Hz, 1H), 7.01 (d, *J* = 7.2 Hz, 1H), 6.40-6.26 (m, 2H), 5.69 (dd, *J* = 1.9, 9.7 Hz, 1H), 2.91 (t, *J* = 7.4 Hz, 2H), 2.78 (t, *J* = 7.4 Hz, 2H), 2.05 (quint, *J* = 7.4 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): 163.5, 145.3, 134.4, 133.6, 131.2, 127.5, 127.2, 12.0, 19.2, 33.2, 30.1, 24.8.

HRMS (+ESI): Calculated: 188.1070 (C₁₂H₁₄NO). Observed: 188.1069.



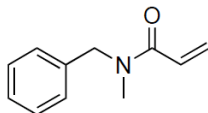
Ethyl 4-acrylamidobenzoate (DKM 2-85)

Following **General Procedure A** starting from benzocaine (486 mg, 2.9 mmol), product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 68% yield as a white solid (438 mg).

¹H NMR (400MHz, CDCl₃): δ 9.39 (s, 1H), 7.95 (d, *J* = 8.7 Hz, 2H), 7.74 (d, *J* = 8.7 Hz, 2H), 6.43-6.41 (m, 2H), 5.71 (dd, *J* = 4.7, 6.9 Hz, 2H), 4.31 (q, *J* = 7.1 Hz, 2H), 1.33 (s, *J* = 7.1 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 166.5, 164.6, 142.5, 131.0, 130.6, 128.4, 125.7, 119.4, 61.0, 14.2.

HRMS (-ESI): Calculated: 218.0823 (C₁₂H₁₂NO₃). Observed: 218.0822



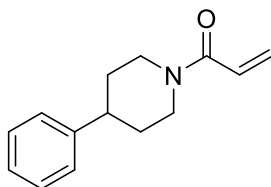
N-benzyl-N-methylacrylamide (DKM 2-95)

Following **General Procedure A** starting from *N*-methylbenzylamine (350 mg, 2.9 mmol), product was obtained after silica gel chromatography (20% ethyl acetate in hexanes) in 60% yield as a clear oil (304 mg).

¹H NMR (~48:52 rotamer ratio, asterisks denote minor peaks, 400MHz, CDCl₃): δ 7.34-7.23 (m, 4H), 7.16 (s, 1H), 7.14* (s, 1H), 6.61 (dd, *J* = 10.4, 16.8 Hz, 1H), 6.57* (dd, *J* = 10.4, 16.8 Hz, 1H), 6.38 (dd, *J* = 1.9, 16.8 Hz, 1H), 6.36* (dd, *J* = 1.9, 16.8 Hz, 1H), 5.71 (dd, *J* = 1.9, 10.4 Hz, 1H), 5.64* (dd, *J* = 1.9, 10.4 Hz), 4.63 (s, 2H), 4.56* (s, 2H), 2.98* (s, 3H), 2.96 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 167.0, 166.4, 137.1, 136.5, 128.8, 128.5, 128.2, 128.0, 17.62, 127.59, 127.3, 126.3, 53.3, 51.0, 34.8, 34.0.

HRMS (+ESI): Calculated: 176.1070 (C₁₁H₁₄NO). Observed: 176.1070.



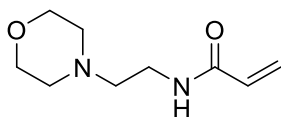
1-(4-phenylpiperidin-1-yl)prop-2-en-1-one (DKM 2-97)

Following **General Procedure A** starting from 4-phenylpiperidine (331 mg, 2.1 mmol), product was obtained after silica gel chromatography (0% to 50% ethyl acetate in hexanes) in 86% yield as a yellow oil (379 mg).

¹H NMR (400MHz, CDCl₃): δ 7.32-7.28 (m, 2H), 7.22-7.17 (m, 3H), 6.62 (dd, *J* = 10.6, 16.8 Hz, 1H), 6.30 (dd, *J* = 1.9, 16.8 Hz, 1H), 5.68 (dd, *J* = 1.9, 10.6 Hz, 1H), 4.82 (d, *J* = 12.9 Hz, 1H), 4.11 (d, *J* = 13.2 Hz, 1H), 3.15 (t, *J* = 8.5 Hz, 1H), 2.78-2.67 (m, 2H), 1.90 (d, *J* = 12.9 Hz, 2H), 1.64 (quint, *J* = 12.3 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): 165.3, 145.0, 128.5, 127.8, 127.4, 126.6, 126.4, 46.4, 42.7, 33.9, 32.7.

HRMS (+ESI): Calculated: 216.1383 (C₁₄H₁₈NO). Observed: 216.1383.



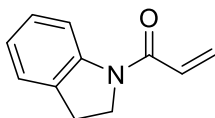
N-(2-morpholinoethyl)acrylamide (DKM 2-100)

Following **General Procedure A** starting from 2-morpholinoethylamine (580 mg, 3.0 mmol), product was obtained after silica gel chromatography (2% to 6% methanol in dichloromethane) in 33% yield as a white solid (184 mg).

¹H NMR (400MHz, CDCl₃): δ 6.39 (s, 1H), 6.21 (dd, *J* = 1.7, 17.0 Hz, 1H), 6.08 (dd, *J* = 10.1, 17.0 Hz, 1H), 5.56 (dd, *J* = 1.7, 10.1 Hz, 1H), 3.63 (t, *J* = 4.6 Hz, 4H), 3.36 (q, *J* = 6.2 Hz, 2H), 2.45 (t, *J* = 6.2 Hz, 2H), 2.40-2.38 (m, 4H).

¹³C NMR (100MHz, CDCl₃): δ 165.5, 130.9, 126.2, 66.9, 57.0, 53.3, 35.7.

HRMS (+ESI): Calculated: 185.1285 (C₉H₁₇N₂O₂). Observed: 185.1280.



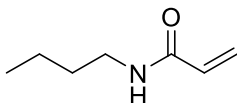
1-(indolin-1-yl)prop-2-en-1-one (DKM 2-101)

Following **General Procedure A** starting from indoline (580 mg, 3.0 mmol), product was obtained after silica gel chromatography (0% to 20% ethyl acetate in hexanes) in 56% yield as a green solid (285 mg).

¹H NMR (400MHz, CDCl₃): δ 8.30 (d, *J* = 7.7 Hz, 1H), 7.22-7.17 (m, 2H), 7.03 (t, *J* = 7.9 Hz, 1H), 6.60-6.48 (m, 2H), 5.79 (dd, *J* = 2.6, 9.5 Hz, 1H), 4.15 (t, *J* = 8.5 Hz, 2H), 3.20 (t, *J* = 8.1, 2H).

¹³C NMR (100MHz, CDCl₃): δ 163.6, 142.6, 131.5, 129.0, 128.6, 127.2, 124.4, 123.8, 117.2, 47.8, 27.7.

HRMS (+ESI): Calculated: 174.0913 (C₁₁H₁₂NO). Observed: 174.0911.



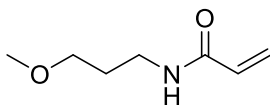
N-butylacrylamide (DKM 2-102)

Following **General Procedure A** starting from butylamine (223 mg, 3.0 mmol), product was obtained after silica gel chromatography (20% ethyl acetate in hexanes) in 61% yield as a clear oil (237 mg).

¹H NMR (400MHz, CDCl₃): δ 6.81 (s, 1H), 6.21-6.10 (m, 2H), 5.52 (dd, *J* = 3.6, 8.3 Hz, 1H), 3.26-3.21 (m, 2H), 1.48-1.41 (m, 2H), 1.33-1.23 (m, 2H), 0.84 (t, *J* = 7.3 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 166.0, 131.2, 125.6, 39.3, 31.5, 20.1, 13.7.

HRMS (+ESI): Calculated: 128.1070 (C₇H₁₄NO). Observed: 128.1068.



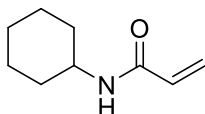
N-(3-methoxypropyl)acrylamide (DKM 2-103)

Following **General Procedure A** starting from 3-methoxypropylamine (274 mg, 3.1 mmol), product was obtained after silica gel chromatography (35% to 60% ethyl acetate in hexanes) in 54% yield as a clear oil (236 mg).

¹H NMR (400MHz, CDCl₃): δ 6.84 (s, 1H), 6.15 (dd, *J* = 2.0, 17.0 Hz, 1H), 6.07 (dd, *J* = 9.8, 17.0 Hz, 1H), 5.51 (dd, *J* = 2.0, 9.8 Hz, 1H), 3.39 (t, *J* = 5.9 Hz, 2H), 3.33 (q, *J* = 6.3 Hz, 2H), 3.25 (s, 3H), 1.72 (quint, *J* = 6.3 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.8, 131.2, 125.7, 71.3, 58.7, 37.7, 29.0.

HRMS (+ESI): Calculated: 144.1019 (C₇H₁₄NO₂). Observed: 144.1017.



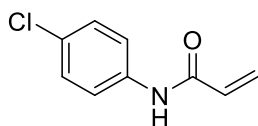
N-cyclohexylacrylamide (DKM 2-106)

Following **General Procedure A** starting from cyclohexylamine (292 mg, 2.9 mmol), product was obtained after silica gel chromatography (20% to 30% ethyl acetate in hexanes) in 86% yield as a white solid (313 mg).

¹H NMR (400MHz, (CDCl₃): δ 6.55 (d, *J* = 6.7 Hz, 1H), 6.21-6.09 (m, 2H), 5.51 (dd, *J* = 2.5, 9.1 Hz, 1H), 3.79-3.70 (m, 1H), 1.86-1.82 (m, 2H), 1.67-1.63 (m, 2H), 1.56-1.52 (m, 1H), 1.28-1.21 (m, 2H), 1.16-1.05 (m, 3H).

¹³C NMR (100MHz, CDCl₃): δ 164.8, 131.5, 125.7, 48.3, 32.9, 25.5, 24.9.

HRMS (+ESI): Calculated: 154.1226 (C₉H₁₆NO). Observed: 154.1224.



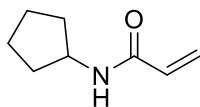
N-(4-chlorophenyl)acrylamide (DKM 2-107)

Following **General Procedure A** starting from 4-chloroaniline (386 mg, 3.0 mmol), product was obtained after silica gel chromatography (0% to 40% ethyl acetate in hexanes) followed by recrystallization from toluene in 31% yield as a white solid (168 mg).

¹H NMR (400MHz, (CD₃)₂CO): δ 9.47 (s, 1H), 7.77-7.74 (m, 2H), 7.35-7.31 (m, 2H), 6.43 (dd, *J* = 9.6, 16.9 Hz, 1H), 6.35 (dd, *J* = 2.5, 16.9 Hz, 1H), 5.73 (dd, *J* = 2.5, 9.6 Hz, 1H).

¹³C NMR (100MHz, (CD₃)₂CO): δ 164.1, 139.0, 132.5, 129.5, 128., 127.5, 121.7.

HRMS (-ESI): Calculated: 180.0222 (C₉H₇NOCl). Observed: 180.0221.



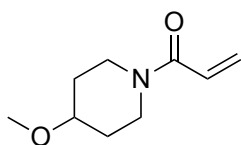
N-cyclopentylacrylamide (DKM 2-108)

Following **General Procedure A** starting from cyclopentylamine (257 mg, 3.0 mmol), product was obtained after silica gel chromatography (20% to 30% ethyl acetate in hexanes) in 55% yield as a colorless oil (229 mg).

¹H NMR (400MHz, (CDCl₃): δ 6.70 (s, 1H), 6.21-6.10 (m, 2H), 5.51 (dd, *J* = 3.5, 8.5 Hz, 1H), 5.53-5.50 (sex, *J* = 7.1 Hz, 1H), 1.94-1.86 (m, 2H), 1.65-1.46 (m, 4H), 1.41-1.32 (m, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.4, 131.3, 125.7, 51.1, 32.9, 23.8.

HRMS (+ESI): Calculated: 140.1070 (C₈H₁₄NO). Observed: 140.1067.



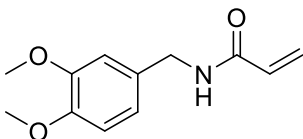
1-(4-methoxypiperidin-1-yl)prop-2-en-1-one (DKM 2-109)

Following **General Procedure A** starting from 4-methoxypiperidine (461 mg, 3.0 mmol), product was obtained after silica gel chromatography (40% to 60% ethyl acetate in hexanes) in 75% yield as a pale yellow oil (386 mg).

¹H NMR (400MHz, CDCl₃): δ 6.45 (dd, *J* = 10.6, 16.8 Hz, 1H), 6.09 (dd, *J* = 2.0, 16.8 Hz, 1H), 5.51 (dd, *J* = 2.0, 10.6 Hz, 1H), 3.80-3.74 (m, 1H), 3.65-3.58 (m, 1H), 3.33-3.17 (m, 6H), 1.74-1.67 (m, 2H), 1.47-1.39 (m, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.1, 127.6, 127.2, 75.0, 55.5, 42.7, 38.9, 31.1, 29.9.

HRMS (+ESI): Calculated: 170.1176 (C₉H₁₆NO₂). Observed: 170.1176.



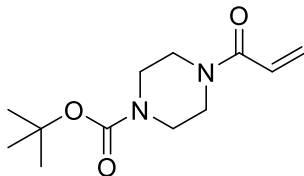
N-(3,4-dimethoxybenzyl)acrylamide (DKM 2-110)

Following **General Procedure A** starting from 3,4-dimethoxybenzylamine (497 mg, 3.0 mmol), product was obtained after silica gel chromatography (30% to 40% ethyl acetate in hexanes) in 65% yield as a white solid (425 mg).

¹H NMR (400MHz, CDCl₃): δ 7.07 (s, 1H), 6.70-6.64 (m, 3H), 6.18-6.08 (m, 2H), 5.50 (dd, *J* = 3.1, 8.8 Hz, 1H), 4.26 (d, *J* = 5.8 Hz, 2H), 3.70 (d, *J* = 7.8 Hz, 6H).

¹³C NMR (400MHz, CDCl₃): δ 165.5, 148.7, 148.0, 130.73, 130.67, 126.2, 119.9, 110.98, 110.96, 55.64, 55.55, 43.12.

HRMS (+ESI): Calculated: 222.1125 (C₁₂H₁₆NO₃). Observed: 222.1121.



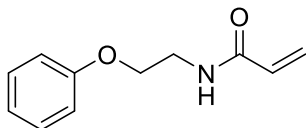
tert-butyl 4-acryloylpiperazine-1-carboxylate (DKM 2-111)

Following **General Procedure A** starting from 1-boc-piperazine (552 mg, 3.0 mmol), product was obtained after silica gel chromatography (50% to 70% ethyl acetate in hexanes) in 75% yield as a pale yellow oil (534 mg).

¹H NMR (400MHz, CDCl₃): δ 6.48 (dd, *J* = 10.5, 16.8 Hz, 1H), 6.20 (dd, *J* = 1.8, 16.8 Hz, 1H), 5.60 (dd, *J* = 1.8, 10.5 Hz, 1H), 3.55 (s, 2H), 3.44 (s, 2H), 3.36-3.34 (m, 4H), 1.37 (s, 9H).

¹³C NMR (100MHz, CDCl₃): δ 165.4, 154.4, 128.2, 127.2, 80.2, 45.5, 41.7, 28.3.

HRMS (+ESI): Calculated: 241.1547 (C₁₂H₂₁N₂O₃). Observed: 241.1543.



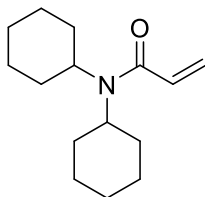
N-(2-phenoxyethyl)acrylamide (DKM 2-113)

Following **General Procedure A** starting from 2-phenoxyethylamine (279 mg, 2.0 mmol), product was obtained after silica gel chromatography (30% to 70% ethyl acetate in hexanes) in 61% yield as a white solid (239 mg).

¹H NMR (400MHz, CDCl₃): δ 7.31-7.25 (m, 2H), 6.98-6.94 (m, 1H), 6.90-6.87 (m, 2H), 6.58 (s, 1H), 6.31 (dd, *J* = 1.6, 17.0 Hz, 1H), 6.17 (dd, *J* = 10.2, 17.0 Hz, 1H), 5.64 (dd, *J* = 1.6, 10.2 Hz, 1H), 4.05 (t, *J* = 5.2 Hz, 2H), 3.73 (q, *J* = 5.4 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.9, 158.4, 130.7, 129.6, 126.7, 121.2, 114.4, 66.5, 39.1.

HRMS (+ESI): Calculated: 192.1019 (C₁₁H₁₄NO₂). Observed: 192.1016.



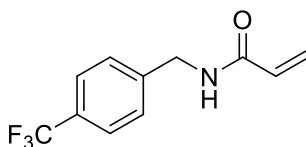
N,N-dicyclohexylacrylamide (DKM 2-114)

Following **General Procedure A** starting from dicyclohexylamine (537 mg, 3.0 mmol), product was obtained after silica gel chromatography (20% to 40% ethyl acetate in hexanes) in 55% yield as a white solid (382 mg).

¹H NMR (400MHz, CDCl₃): δ 6.49 (dd, *J* = 10.6, 16.8 Hz, 1H), 6.11 (dd, *J* = 1.9, 16.8 Hz, 1H), 5.49 (dd, *J* = 2.0, 10.6 Hz, 1H), 3.45 (s, 1H), 3.22 (s, 1H), 2.22 (s, 2H), 1.74-1.49 (m, 12H), 1.22-1.07 (m, 6H).

¹³C NMR (100MHz, CDCl₃): δ 166.2, 130.9, 125.5, 57.5, 55.6, 31.6, 30.1, 26.4, 26.0, 25.3.

HRMS (+ESI): Calculated: 236.2009 (C₁₅H₂₆NO). Observed: 236.2004.



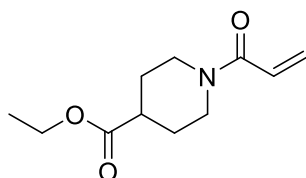
N-(4-(trifluoromethyl)benzyl)acrylamide (DKM 2-116)

Following **General Procedure A** starting from 4-(trifluoromethyl)benzylamine (516 mg, 2.9 mmol), product was obtained after silica gel chromatography (20% to 30% ethyl acetate in hexanes) in 24% yield as a white solid (165 mg).

¹H NMR (600MHz, CDCl₃): δ 7.53 (d, *J* = 8.0 Hz, 2H), 7.35 (d, *J* = 8.0 Hz, 2H), 6.58 (s, 1H), 6.28 (dd, *J* = 1.5, 17.0 Hz, 1H), 6.14 (dd, *J* = 10.1, 17.0 Hz, 1H), 5.64 (dd, *J* = 1.5, 10.1 Hz, 1H), 4.50 (d, *J* = 6.0 Hz, 2H).

¹³C NMR (150MHz, CDCl₃): δ 165.9, 142.3, 130.5, 130.0, 129.7, 128.0, 127.3, 125.73, 125.69, 125.66, 125.62, 43.1.

HRMS (-ESI): Calculated: 228.0642 (C₁₁H₉NOF₃). Observed: 228.0641.



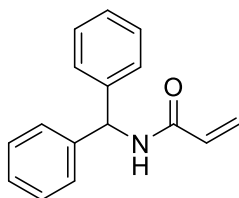
Ethyl 1-acryloylpiperidine-4-carboxylate (DKM 2-120)

Following **General Procedure A** starting from ethyl isonipecotate (459 mg, 2.9 mmol), product was obtained after silica gel chromatography (20% to 45% ethyl acetate in hexanes) in 71% yield as a pale yellow liquid (440 mg).

¹H NMR (400MHz, CDCl₃): δ 6.40 (dd, *J* = 10.6, 16.8 Hz, 1H), 6.04 (dd, *J* = 2.0, 16.8 Hz, 1H), 5.47 (dd, *J* = 2.0, 10.6 Hz, 1H), 4.23 (d, *J* = 13.2 Hz, 1H), 3.93 (q, *J* = 7.1 Hz, 2H), 3.76 (d, *J* = 14.0 Hz, 1H), 2.99 (t, *J* = 11.8 Hz, 1H), 2.70 (t, *J* = 11.5 Hz, 1H), 2.37 (tt, *J* = 4.1, 10.7 Hz, 1H), 1.77-1.73 (m, 2H), 1.51-1.42 (m, 2H), 1.05 (t, *J* = 7.1 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 173.7, 165.0, 127.5, 127.2, 60., 44.7, 41.0, 40.5, 28.2, 27.4, 13.8.

HRMS (+ESI): Calculated: 212.1281 (C₁₁H₁₈NO₃). Observed: 212.1276.



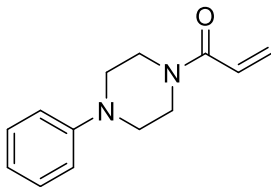
N-benzhydrylacrylamide (DKM 3-4)

Following **General Procedure A** starting from benzhydrylamine (459 mg, 3.0 mmol), product was obtained after silica gel chromatography (0% to 20% ethyl acetate in hexanes) and recrystallization from toluene in 15% yield as a white solid (110 mg).

¹H NMR (400MHz, (CD₃)₂CO): δ 7.35-7.23 (m, 10H), 6.45 (dd, *J* = 10.2, 17.0 Hz, 1H), 6.36-6.34 (m, 1H), 6.25 (dd, *J* = 2.2, 17.0 Hz, 1H), 5.61 (dd, *J* = 2.2, 10.2 Hz, 1H).

¹³C NMR (100MHz, (CD₃)₂CO): δ 164.84, 164.76, 143.51, 143.48, 132.51, 132.47, 129.4, 128.5, 128.0, 126.3, 57.5, 57.4.

HRMS (+ESI): Calculated: 238.1226 (C₁₆H₁₆NO). Observed: 238.1222.



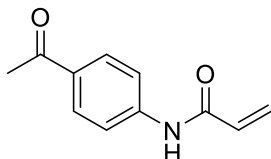
1-(4-phenylpiperazin-1-yl)prop-2-en-1-one (DKM 3-5)

Following **General Procedure A** starting from 1-phenylpiperazine (479 mg, 3.0 mmol), product was obtained after silica gel chromatography (30% to 70% ethyl acetate in hexanes) in 87% yield as a yellow oil (555 mg).

¹H NMR (400MHz, CDCl₃): 7.30-7.25 (m, 2H), 6.92-6.87 (m, 3H), 6.60 (dd, *J* = 10.5, 16.8 Hz, 1H), 6.33 (dd, *J* = 2.0, 16.8 Hz, 1H), 5.72 (dd, *J* = 2.0, 10.5 Hz, 1H), 3.81 (s, 2H), 3.66 (s, 2H), 3.14 (t, *J* = 5.2 Hz, 4H).

¹³C NMR (100MHz, CDCl₃): δ 165.0, 150.6, 18.9, 127.8, 127.1, 120.2, 116.3, 49.4, 48.9, 45.3, 41.5.

HRMS (+ESI): Calculated: 217.1335 (C₁₃H₁₇N₂O). Observed: 217.1332.



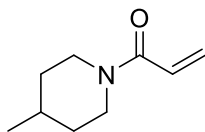
N-(4-acetylphenyl)acrylamide (DKM 3-7)

Following **General Procedure A** starting from 4-aminoacetophenone (398 mg, 2.9 mmol), product was obtained after silica gel chromatography (20% to 50% ethyl acetate in hexanes) in 45% yield as a white solid (253 mg).

¹H NMR (400MHz, CDCl₃): δ 8.40 (s, 1H), 7.92 (d, *J* = 8.7 Hz, 2H), 7.73 (d, *J* = 8.7 Hz, 2H), 6.46 (dd, *J* = 1.3, 16.9 Hz, 1H), 6.34 (dd, *J* = 10.1, 16.9 Hz, 1H), 5.79 (dd, *J* = 1.3, 10.1 Hz, 1H), 2.57 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 197.5, 164.1, 142.5, 133.0, 130.9, 129.9, 128.9, 119.4, 26.6.

HRMS (+ESI): Calculated: 190.0863 (C₁₁H₁₂NO₂). Observed: 190.0858.



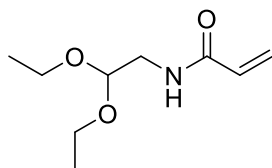
1-(4-methylpiperidin-1-yl)prop-2-en-1-one (DKM 3-8)

Following **General Procedure A** starting from 4-methylpiperidine (295 mg, 3.0 mmol), product was obtained after silica gel chromatography (10% to 30% ethyl acetate in hexanes) in 84% yield as a yellow oil (385 mg).

¹H NMR (400MHz, CDCl₃): δ 6.51 (dd, *J* = 10.6, 16.5 Hz, 1H), 6.16 (dd, *J* = 2.0, 16.5 Hz, 1H), 5.57 (dd, *J* = 2.0, 10.6 Hz, 1H), 4.53 (d, *J* = 13.1 Hz, 1H), 3.88 (d, *J* = 13.3 Hz, 1H), 2.99-2.92 (m, 1H), 2.55 (td, *J* = 2.1, 12.8 Hz, 1H), 1.62 (d, *J* = 13.1 Hz, 2H), 1.57-1.49 (m, 1H), 1.10-0.98 (m, 2H), 0.87 (d, *J* = 6.5 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.2, 128.0, 127.0, 46.2, 42.4, 34.7, 33.7, 31.1, 21.7.

HRMS (+ESI): Calculated: 154.1226 (C₉H₁₆NO). Observed: 154.1224.



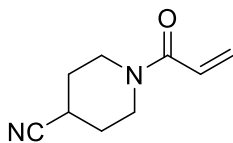
N-(2,2-diethoxyethyl)acrylamide (DKM 3-9)

Following **General Procedure A** starting from aminoacetaldehyde diethyl acetal (402 mg, 3.0 mmol), product was obtained after silica gel chromatography (10% to 40% ethyl acetate in hexanes) in 75% yield as a clear oil (313 mg).

¹H NMR (400MHz, CDCl₃): 6.25-6.19 (m, 2H), 6.09 (dd, *J* = 10.1, 17.0 Hz, 1H), 5.56 (dd, *J* = 1.7, 10.1 Hz, 1H), 4.48 (t, *J* = 5.3 Hz, 1H), 3.64 (dq, *J* = 7.1, 9.4 Hz, 2H), 3.47 (dq, *J* = 7.1, 9.4 Hz, 2H), 3.38 (t, *J* = 5.6 Hz, 2H), 1.13 (t, *J* = 7.1 Hz, 6H).

¹³C NMR (100MHz, CDCl₃): δ 165.7, 130.6, 126.4, 100.6, 62.8, 42.0, 15.2.

HRMS (+ESI): Calculated: 188.1281 (C₉H₁₈NO₃). Observed: 188.1278.



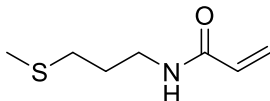
1-acryloylpiperidine-4-carbonitrile (DKM 3-11)

Following **General Procedure A** starting from piperidine-4-carbonitrile (329 mg, 3.0 mmol), product was obtained after silica gel chromatography (30% to 70% ethyl acetate in hexanes) in 48% yield as a colorless oil (234 mg).

¹H NMR (400MHz, CDCl₃): 6.49 (dd, *J* = 10.6, 16.8 Hz, 1H), 6.19 (d, *J* = 1.9, 16.8 Hz, 1H), 5.64 (dd, *J* = 1.9, 10.6 Hz, 1H), 3.77-3.46 (m, 4H), 2.88-2.82 (sept, *J* = 3.9 Hz, 1H), 1.90-1.73 (m, 4H).

¹³C NMR (100MHz, CDCl₃): δ 165.4, 128.3, 127.3, 120.8, 43.8, 39.9, 29.1, 28.1, 26.3.

HRMS (+ESI): Calculated: 165.1022 (C₉H₁₃N₂O). Observed: 165.1020.



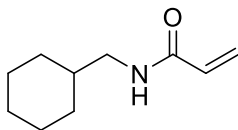
N-(3-(methylthio)propyl)acrylamide (DKM 3-12)

Following **General Procedure A** starting from 3-(methylthio)propylamine (313 mg, 3.0 mmol), product was obtained after silica gel chromatography (20% to 60% ethyl acetate in hexanes) in 69% yield as a colorless oil (328 mg).

¹H NMR (400MHz, CDCl₃): δ 6.79 (s, 1H), 6.19 (dd, *J* = 2.2, 17.0 Hz, 1H), 6.11 (dd, *J* = 9.6, 17.0 Hz, 1H), 5.55 (dd, *J* = 2.2, 9.6 Hz, 1H), 3.35 (q, *J* = 6.5 Hz, 2H), 2.47 (t, *J* = 7.2 Hz, 2H), 2.02 (s, 3H), 1.78 (quint, *J* = 7.0 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.9, 131.0, 126.1, 38.6, 31.6, 28.6, 15.4.

HRMS (+ESI): Calculated: 160.0791 (C₇H₁₄NOS). Observed: 160.0788.



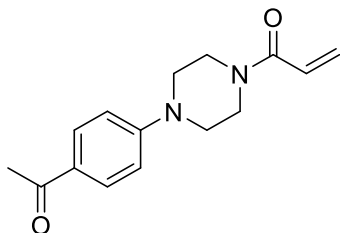
N-(cyclohexylmethyl)acrylamide (DKM 3-13)

Following **General Procedure A** starting from cyclohexanemethylamine (331 mg, 2.9 mmol), product was obtained after silica gel chromatography (10% to 50% ethyl acetate in hexanes) in 67% yield as a pale yellow solid (330 mg).

¹H NMR (400MHz, CDCl₃): 6.51 (s, 1H), 6.22 (dd, *J* = 2.5, 17.0 Hz, 1H), 6.15 (dd, *J* = 9.3, 17.0 Hz, 1H), 5.55 (dd, *J* = 2.5, 9.3 Hz, 1H), 3.11 (t, *J* = 6.5 Hz, 2H), 1.70-1.58 (m, 5H), 1.51-1.40 (m, 1H), 1.22-1.04 (m, 3H), 0.93-0.83 (m, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.9, 131.2, 125.9, 45.9, 38.0, 30.9, 26.4, 25.8.

HRMS (+ESI): Calculated: 168.1383 (C₁₀H₁₈NO). Observed: 168.1380.



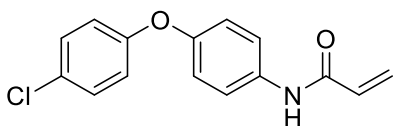
1-(4-(4-acetylphenyl)piperazin-1-yl)prop-2-en-1-one (DKM 3-29)

Following **General Procedure A** starting from 4'-piperazinoacetophenone (607 mg, 3.0 mmol), product was obtained after silica gel chromatography (50% to 85% ethyl acetate in hexanes) in 65% yield as a yellow solid (496 mg).

¹H NMR (400MHz, CDCl₃): δ 7.79 (d, *J* = 9.0 Hz, 2H), 6.78 (d, *J* = 9.0 Hz, 2H), 6.54 (dd, *J* = 10.5, 16.8 Hz, 1H), 6.25 (dd, *J* = 1.9, 16.8 Hz, 1H), 5.66 (dd, *J* = 1.9, 10.5 Hz, 1H), 3.75 (s, 2H), 3.66 (s, 2H), 3.31-3.29 (m, 4H), 2.42 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 196.3, 165.2, 153.4, 130.2, 128.3, 127.9, 127.0, 113.5, 47.3, 47.0, 45.0, 41.2, 26.0.

HRMS (+ESI): Calculated: 259.1441(C₁₅H₁₉N₂O₂). Observed: 259.1436.



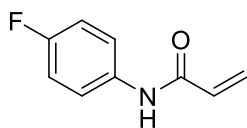
N-(4-(4-chlorophenoxy)phenyl)acrylamide (DKM 3-30)

Following **General Procedure A** starting from 4-(4-chlorophenoxy)aniline (440 mg, 2.0 mmol), product was obtained after silica gel chromatography (10% to 30% ethyl acetate in hexanes) in 33% yield as a white solid (180 mg).

¹H NMR (400MHz, CDCl₃): δ 8.00 (s, 1H), 7.56 (d, *J* = 8.9 Hz, 2H), 7.29-7.25 (m, 2H), 6.96-6.88 (m, 4H), 6.43 (dd, *J* = 1.4, 16.9 Hz, 1H), 6.30 (dd, *J* = 10.1, 16.9 Hz, 1H), 5.75 (dd, *J* = 1.4, 10.1 Hz, 1H).

¹³C NMR (100MHz, CDCl₃): δ 163.9, 156.2, 153.4, 133.7, 131.2, 129.8, 128.2, 128.0, 122.1, 119.8, 119.7.

HRMS (+ESI): Calculated: 272.0484 (C₁₅H₁₁NO₂Cl). Observed: 272.0479.



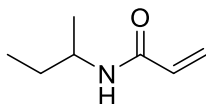
N-(4-fluorophenyl)acrylamide (DKM 3-31)

Following **General Procedure A** starting from 4-fluoroaniline (239 mg, 2.2 mmol), product was obtained after silica gel chromatography (20% to 30% ethyl acetate in hexanes) in 16% yield as a white solid (56 mg).

¹H NMR (600MHz, MeOD): δ 7.64-7.60 (m, 2H), 7.07-7.03 (m, 2H), 6.41 (dd, *J* = 9.8, 17.0 Hz, 1H), 6.35 (dd, *J* = 2.1, 17.0 Hz, 1H), 5.76 (dd, *J* = 2.1, 9.8 Hz, 1H).

¹³C NMR (150MHz, MeOD): δ 166.0, 161.56, 160.0, 135.93, 135.91, 132.3, 127.8, 123.2, 123.1, 116.4, 116.2.

HRMS (-ESI): Calculated: 164.0517 (C₉H₇NOC). Observed: 164.0517.



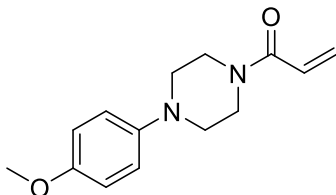
N-(sec-butyl)acrylamide (DKM 3-32)

Following **General Procedure A** starting from sec-butylamine (222 mg, 3.0 mmol), product was obtained after silica gel chromatography (10% to 40% ethyl acetate in hexanes) in 74% yield as a yellow oil (287 mg).

¹H NMR (400MHz, CDCl₃): δ 6.56 (d, *J* = 5.6 Hz, 1H), 6.17 (s, 1H), 6.16 (d, *J* = 3.5 Hz, 1H), 5.51 (dd, *J* = 4.3, 7.6 Hz, 1H), 3.93-3.83 (m, 1H), 1.47-1.36 (m, 2H), 1.06 (d, *J* = 6.6 Hz, 3H), 0.82 (t, *J* = 7.5 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.2, 131.4, 125.6, 46.6, 29.5, 20.2, 10.4.

HRMS (+ESI): Calculated: 128.1070 (C₇H₁₄NO). Observed: 128.1069.



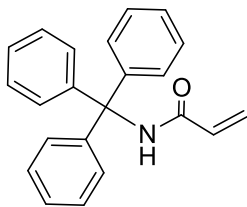
1-(4-(4-methoxyphenyl)piperazin-1-yl)prop-2-en-1-one (DKM 3-36)

Following **General Procedure A** starting from 1-(4-methoxyphenyl)piperazine (388 mg, 2.0 mmol), product was obtained after silica gel chromatography (20% to 80% ethyl acetate in hexanes) in 29% yield as a white solid (143 mg).

¹H NMR (400MHz, CDCl₃): δ 6.87-6.79 (m, 4H), 6.57 (dd, *J* = 10.5, 16.8 Hz, 1H), 6.28 (dd, *J* = 1.9, 16.8 Hz, 1H), 5.68 (dd, *J* = 1.9, 10.5 Hz, 1H), 3.79 (s, 2H), 3.72 (s, 3H), 3.66 (s, 2H), 3.01 (t, *J* = 5.1 Hz, 4H).

¹³C NMR (100MHz, CDCl₃): δ 165.2, 154.3, 145.1, 128.0, 127.3, 118.8, 114.4, 55.4, 51.3, 50.7, 45.8, 41.9.

HRMS (+ESI): Calculated: 247.1441 (C₁₄H₁₉N₂O₂). Observed: 247.1443.



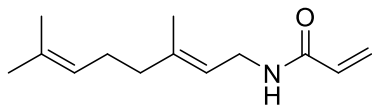
N-tritylacrylamide (DKM 3-41)

Following **General Procedure A** starting from triphenylmethylaniline (386 mg, 1.5 mmol), product was obtained after silica gel chromatography (5% to 30% ethyl acetate in hexanes) in 74% yield as a white solid (346 mg).

¹H NMR (400MHz, CDCl₃): δ 7.38-7.27 (m, 15H), 6.83 (s, 1H), 6.28-6.26 (m, 2H), 5.66 (dd, *J* = 3.9, 7.2 Hz, 1H).

¹³C NMR (100MHz, CDCl₃): δ 164.6, 144.6, 131.5, 128.8, 128.1, 127.2, 127.1, 70.7.

HRMS (+ESI): Calculated: 314.1539 (C₂₂H₂₀NO). Observed: 314.1542.



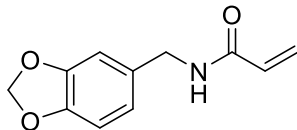
(E)-N-(3,7-dimethylocta-2,6-dien-1-yl)acrylamide (DKM 3-42)

Following **General Procedure A** starting from geranylamine (462 mg, 3.0 mmol), product was obtained after silica gel chromatography (10% to 40% ethyl acetate in hexanes) in 23% yield as a colorless oil (141 mg).

¹H NMR (400MHz, CDCl₃): δ 6.25 (dd, *J* = 1.5, 17.0 Hz, 1H), 6.09 (dd, *J* = 10.2, 17.0 Hz, 1H), 5.83 (s, 1H), 5.59 (dd, *J* = 1.5, 10.2 Hz), 5.22-5.18 (m, 1H), 5.07-5.03 (m, 1H), 3.90 (t, *J* = 6.2 Hz, 2H), 2.09-2.03 (m, 2H), 2.00-1.97 (m, 2H), 1.65 (s, 6H), 1.57 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.5, 140.2, 131.8, 131.0, 126.2, 123.9, 119.7, 39.6, 37.6, 26.5, 25.8, 17.8, 16.4.

HRMS (+ESI): Calculated: 208.1696 (C₁₃H₂₂NO). Observed: 208.1697.



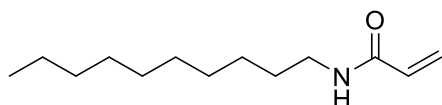
N-(benzo[d][1,3]dioxol-5-ylmethyl)acrylamide (DKM 3-43)

Following **General Procedure A** starting from piperonylamine (312 mg, 2.1 mmol), product was obtained after silica gel chromatography (20% to 50% ethyl acetate in hexanes) in 74% yield as a white solid (315 mg).

¹H NMR (400MHz, CDCl₃): δ 6.78 (s, 1H), 6.71 (s, 1H), 6.68 (s, 2H), 6.22 (dd, *J* = 1.9, 17.0 Hz, 1H), 6.13 (dd, *J* = 9.9, 17.0 Hz, 1H), 5.87 (s, 2H), 5.58 (dd, *J* = 1.9, 9.9 Hz, 1H), 4.30 (d, *J* = 5.8 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 165.7, 147.8, 146.9, 132.0, 130.8, 126.6, 121.1, 108.4, 108.2, 101.0, 43.4.

HRMS (+ESI): Calculated: 206.0812 (C₁₁H₁₂NO₃). Observed: 206.0808.



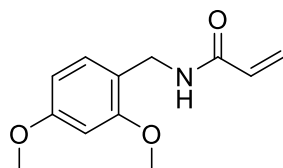
N-decylacrylamide (TRH 1-12)

Following **General Procedure A** starting from decylamine (479 mg, 3.0 mmol), product was obtained after silica gel chromatography (20% to 40% ethyl acetate in hexanes) in 26% yield as a white solid (163 mg).

¹H NMR (400MHz, CDCl₃): δ 6.54 (s, 1H), 6.21 (dd, *J* = 2.0, 16.9 Hz, 1H) 6.13 (dd, *J* = 9.7, 16.9 Hz, 1H), 5.55 (dd, *J* = 2.0, 9.7 Hz, 1H), 3.25 (q, *J* = 6.7 Hz, 2H), 1.50-1.45 (m, 2H), 1.29-1.20 (m, 14H), 0.83 (t, *J* = 6.7 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.8, 131.2, 125.9, 71.9, 39.7, 31.9, 29.6, 29.6, 29.38, 29.35, 27.0, 22.7, 14.1.

HRMS (+ESI): Calculated: 212.2009 (C₁₃H₂₆NO). Observed: 212.2009.



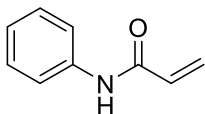
N-(2,4-dimethoxybenzyl)acrylamide (TRH 1-13)

Following **General Procedure A** starting from 2,4-dimethoxybenzylamine (514 mg, 3.0 mmol), product was obtained after silica gel chromatography (20% to 60% ethyl acetate in hexanes) in 11% yield as a white solid (73 mg).

¹H NMR (400MHz, CDCl₃): δ 7.17 (d, *J* = 8.1 Hz, 1H), 6.43-6.39 (m, 2H), 6.26-6.22 (m, 2H), 6.07 (dd, *J* = 10.7, 17.0 Hz, 1H), 5.57 (dd, *J* = 1.4, 10.7 Hz, 1H), 4.41 (d, *J* = 5.8 Hz, 2H), 3.79 (s, 3H), 3.77 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.2, 160.6, 158.6, 131.1, 130.7, 126.2, 118.7, 104.0, 98.6, 55.5, 55.4, 39.0.

HRMS (+ESI): Calculated: 222.1125 (C₁₂H₁₆NO₃). Observed: 222.1124.



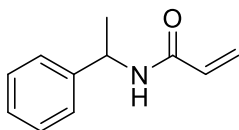
N-Phenylacrylamide (TRH 1-19)

Following **General Procedure A** starting from aniline (277 mg, 3.0 mmol), product was obtained after recrystallization from a 1:20 ethyl acetate:hexanes mixture in 46% yield as a white solid (200 mg).

¹H NMR (400MHz, CDCl₃): δ 8.59 (s, 1H), 7.63 (d, *J* = 7.9 Hz, 2H), 7.30 (t, *J* = 7.9 Hz, 2H), 7.11 (t, *J* = 7.4 Hz, 1H), 6.44-6.33 (m, 2H), 5.70 (dd, *J* = 2.8, 8.9 Hz, 1H).

¹³C NMR (100MHz, CDCl₃): δ 164.3, 138.0, 131.4, 129.0, 127.7, 124.6, 120.5.

HRMS (+ESI): Calculated: 148.0757 (C₉H₁₀NO). Observed: 148.0754.



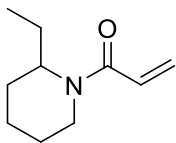
N-(1-phenylethyl)acrylamide (TRH 1-20)

Following **General Procedure A** starting from 1-phenylethan-1-amine (387 mg, 3.0 mmol), product was obtained after silica gel chromatography (5% to 20% ethyl acetate in hexanes) in 46% yield as a white solid (315 mg).

¹H NMR (400MHz, CDCl₃): δ 7.61 (d, *J* = 7.8 Hz, 1H) 7.37-7.24 (m, 5H), 6.33-6.24 (m, 2H), 5.57 (dd, *J* = 4.8, 7.9 Hz, 1H), 5.20 (quint, *J* = 7.2 Hz, 1H), 1.49 (d, *J* = 7.0 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.0, 143.4, 131.1, 128.4, 126.9, 126.0, 126.0, 48.7, 21.8.

HRMS (+ESI): Calculated: 176.1070 (C₁₁H₁₄NO). Observed: 176.1067.



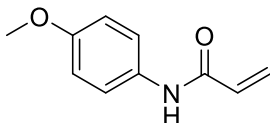
1-(2-ethylpiperidin-1-yl)prop-2-en-1-one (TRH 1-27)

Following **General Procedure A** starting from 2-ethylpiperidine (238 mg, 2.0 mmol), product was obtained after silica gel chromatography (5% to 30% ethyl acetate in hexanes) in 72% yield as a white solid (253 mg).

¹H NMR (400MHz, CDCl₃): δ 6.41 (dd, *J* = 10.6, 16.7 Hz, 1H), 6.03 (d, *J* = 16.4 Hz, 1H), 5.43 (dd, *J* = 2.0, 10.6 Hz, 1H), 4.54-4.34 (m, 1H), 3.77-3.58 (m, 1H), 2.93-2.42 (m, 1H), 1.61-1.06 (m, 8H), 0.66 (t, *J* = 7.5 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.9, 130.0, 129.1, 128.4, 126.6, 54.4, 49.6, 41.1, 36.5, 28.8, 27.5, 26.2, 25.2, 23.0, 22.1, 18.8, 10.4.

HRMS (+ESI): Calculated: 168.1383 (C₁₀H₁₈NO). Observed: 168.1380.



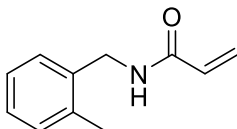
N-(4-methoxyphenyl)acrylamide (TRH 1-32)

Following **General Procedure A** starting from p-anisidine (258 mg, 2.0 mmol), product was obtained after silica gel chromatography (10% to 50% ethyl acetate in hexanes) in 58% yield as a white solid (216 mg).

¹H NMR (400MHz, CDCl₃): δ 8.94 (s, 1H), 7.48 (d, *J* = 9.1 Hz, 2H), 6.78 (d, *J* = 9.1 Hz, 2H), 6.34 (d, *J* = 5.6 Hz, 2H), 5.61 (t, *J* = 5.9 Hz, 1H), 3.73 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 164.3, 156.4, 131.4, 131.1, 127., 122.3, 114.0, 55.4.

HRMS (+ESI): Calculated: 178.0863 (C₁₀H₁₂O₂N). Observed: 178.0859.



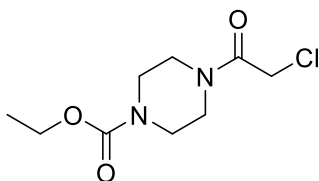
N-(2-methylbenzyl)acrylamide (TRH 1-54)

Following **General Procedure A** starting from 2-methylbenzylamine (240 mg, 2.0 mmol), product was obtained after silica gel chromatography (30% to 40% ethyl acetate in hexanes) in 73% yield as a white solid (257 mg).

¹H NMR (400MHz, CDCl₃): δ 7.26-7.12 (m, 4H), 6.66 (s, 1H), 6.24-6.12 (m, 2H), 5.57 (dd, *J* = 9.5, 2.2 Hz, 1H), 4.39 (d, *J* = 5.4 Hz, 2H), 2.27 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.6, 136.3, 135.7, 130.7, 130.4, 128.4, 127.6, 126.4, 126.1, 41.6, 19.0.

HRMS (+ESI): Calculated: 176.1070 (C₁₁H₁₄NO). Observed: 176.1067.



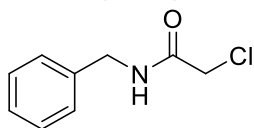
Ethyl 4-(2-chloroacetyl)piperazine-1-carboxylate (DKM 2-52)

Following **General Procedure B** starting from ethyl 1-piperazinecarboxylate (477 mg, 3.0 mmol) product was obtained after silica gel chromatography (0% to 80% ethyl acetate in hexanes) in 80% yield as a pale yellow oil (569 mg).

¹H NMR (400MHz, CDCl₃): δ 4.04-3.99 (m, 4H), 3.48-3.34 (m, 8H), 1.14 (t, *J* = 7.1 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.1, 155.0, 61.5, 45.8, 43.3, 43.0, 41.7, 40.7, 14.4.

HRMS (+ESI): Calculated: 235.0844 (C₉H₁₆ClN₂O₃). Observed: 235.0842.



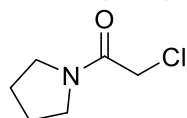
N-benzyl-2-chloroacetamide (DKM 2-67)

Following **General Procedure B** starting from benzylamine (430 mg, 3.1 mmol) product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 70% yield as a white solid (416 mg).

¹H NMR (400MHz, CDCl₃): δ 7.40-7.31 (m, 5H), 7.08 (s, 1s), 4.50 (d, *J* = 5.8 Hz, 2H), 4.09 (s, 2H).

¹³C NMR (100MHz, CDCl₃): δ 166.0, 137.4, 128.8, 127.8, 43.8, 42.6

HRMS (-ESI): Calculated: 182.0378 (C₉H₉NOCl). Observed: 182.0378.



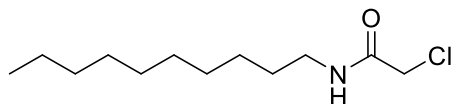
2-Chloro-1-(pyrrolidin-1-yl)ethan-1-one (DKM 2-71)

Following **General Procedure B** starting from pyrrolidine (511 mg, 3.0 mmol) product was obtained after silica gel chromatography (0% to 30% ethyl acetate in hexanes) in 83% yield as a clear oil (368 mg).

¹H NMR (400MHz, CDCl₃): δ 3.94 (s, 2H), 3.41 (quint, *J* = 7.2 Hz, 4H), 1.91 (quint, *J* = 6.3 Hz, 2H), 1.80 (quint, *J* = 6.6 Hz, 2H).

¹³C NMR (100MHz, CDCl₃): δ 164.7, 46.5, 46.3, 42.1, 26.1, 24.1.

HRMS (+ESI): Calculated: 170.0343 (C₆H₁₀ClNNaO). Observed: 170.0343.



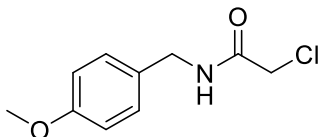
2-Chloro-N-decylacetamide (DKM 2-72)

Following **General Procedure B** starting from decylamine (472 mg, 3.0 mmol) product was obtained after silica gel chromatography (0% to 40% ethyl acetate in hexanes) in 81% yield as a white solid (555 mg).

¹H NMR (400MHz, CDCl₃): δ 6.71 (s, 1H), 3.97 (s, 2H), 3.22 (q, *J* = 6.8 Hz, 2H), 1.51-1.44 (m, 2H), 1.24-1.19 (m, 14 H), 0.81 (t, *J* = 6.8 Hz, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.8, 42.7, 39.9, 31.9, 29.5, 29.29, 29.27, 29.22, 26.8, 22.6, 14.1.

HRMS (+ESI): Calculated: 234.1619 (C₁₂H₂₅ClNO). Observed: 234.1618.



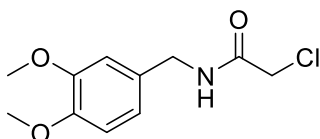
2-chloro-N-(4-methoxybenzyl)acetamide (DKM 2-83)

Following **General Procedure B** starting from 4-methoxybenzylamine (430 mg, 3.1 mmol) product was obtained after silica gel chromatography (0% to 40% ethyl acetate in hexanes) in 55% yield as an off-white solid (369 mg).

¹H NMR (400MHz, CDCl₃): δ 7.20 (d, *J* = 8.6 Hz, 2H), 6.91 (s, 1H), 6.86 (d, *J* = 8.6 Hz, 2H), 4.40 (d, *J* = 5.7 Hz, 2H), 4.05 (s, 2H), 3.78 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.9, 159.2, 129.4, 129.2, 114.2, 55.3, 43.4, 42.7

HRMS (+ESI): Calculated: 214.0629 (C₁₀H₁₃ClNO₂). Observed: 214.0627.



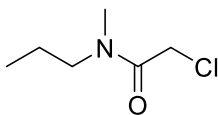
2-chloro-N-(3,4-dimethoxybenzyl)acetamide (DKM 2-93)

Following **General Procedure B** starting from 3,4-dimethoxybenzylamine (517 mg, 3.1 mmol) product was obtained after silica gel chromatography (0% to 50% ethyl acetate in hexanes) in 55% yield as an off-white solid (416 mg).

¹H NMR (400MHz, CDCl₃): δ 6.97 (s, 1H), 6.77 (m, 3H), 4.35 (d, *J* = 5.8 Hz, 2H), 4.01 (s, 2H), 3.81 (s, 3H), 3.80 (s, 3H).

¹³C NMR (100MHz, CDCl₃): δ 165.8, 149.0, 148.5, 129.8, 120.1, 111.13, 111.07, 55.83, 55.79, 43.6, 42.5.

HRMS (+ESI): Calculated: 266.0554 (C₁₁H₁₄NO₃ClNa). Observed: 266.0553.



2-Chloro-N-methyl-N-propylacetamide (TRH 1-53)

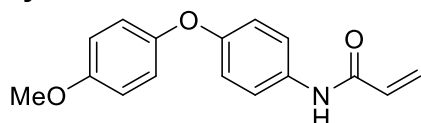
Following **General Procedure B** starting from *N*-methylpropylamine (147 mg, 2.0 mmol) product was obtained after silica gel chromatography (30% to 40% ethyl acetate in hexanes) in 64% yield as a white solid (191 mg).

¹H NMR (~46:54 rotamer ratio, asterisks denote minor peaks, 400 MHz, CDCl₃): δ 4.03* (s, 2H), 4.02 (s, 2H), 3.28* (t, *J* = 7.4 Hz, 2H), 3.23 (t, *J* = 7.5 Hz, 2H), 3.00 (s, 3H), 2.88* (s, 3H), 1.64-1.56* (m, 2H), 1.53-1.46 (m, 2H), 0.87* (t, *J* = 7.5 Hz, 3H), 0.83 (t, *J* = 7.5 Hz, 3H).

^{13}C NMR (asterisks denote minor rotamer peaks, 100 MHz, CDCl_3): δ 166.4, 166.3*, 51.9*, 49.8, 41.5, 40.9*, 35.6, 33.6*, 21.6*, 20.1, 11.1, 11.0*.

HRMS (+ESI): Calculated: 150.0680 ($\text{C}_6\text{H}_{13}\text{NOCl}$). Observed: 150.0678.

Synthesis and Characterization of YP 1-46



N-(4-(4-methoxyphenoxy)phenyl)acrylamide (YP-1-46)

To a solution of 4-methoxyphenol (622 mg, 5 mmol) in DMF (2 mL) was added potassium carbonate (1.38 g, 10 mmol). After 10 minutes of stirring, 1-fluoro-4-nitrobenzene (0.43 mL, 4 mmol) was added and the reaction was stirred overnight. As the reaction was not complete by TLC after 21 hours, the reaction was heated to 90 degrees for 1 hour at which point the reaction was found to be complete. The reaction was then diluted with water and extracted three times with ethyl acetate. The combined organics were dried with magnesium sulfate and concentrated to give 1.07 g of crude 1-methoxy-4-(nitrophenoxy)benzene as a yellow solid that was used without further purification.

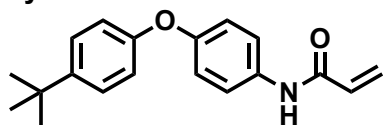
To a stirring solution of the resulting crude (490 mg, ~2 mmol) and 10% palladium on activated charcoal (49 mg) in methanol (4 mL) was added triethylsilane (2.33 g, 20 mmol) dropwise through an addition funnel under a nitrogen-filled balloon. After 30 min, the mixture was filtered through celite and the solvent was removed in vacuo. Without further purification, the obtained crude product was dissolved in DCM (10 mL) and the resultant solution was cooled to 0 °C. To the solution was added acryloyl chloride (217 mg, 2.4 mmol) followed by triethylamine (243 mg, 2.4 mmol). The solution was allowed to warm to room temperature after 20 min and stirred overnight. The solution was washed two times with brine and the crude product was purified via silica gel chromatography (30% to 70% ethyl acetate in hexanes) to afford 161 mg of the product as a white solid (33% yield over 3 steps).

^1H NMR (400MHz, CDCl_3): δ 7.94 (s, 1H), 7.50-7.48 (m, 2H), 6.96-6.92 (m, 2H), 6.90-6.84 (m, 4H), 6.40 (dd, J = 1.6, 16.8 Hz, 1H), 6.27 (dd, J = 10.1, 16.8 Hz, 1H), (dd, J = 1.6, 10.1 Hz, 1H), 3.79 (s, 3H).

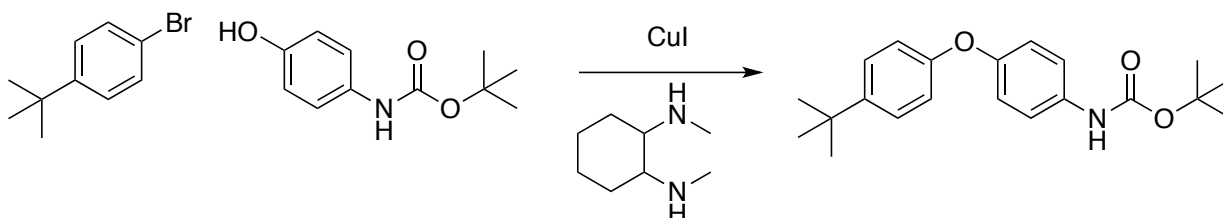
^{13}C NMR (100MHz, CDCl_3): δ 163.8, 155.8, 155.1, 150.4, 132.6, 131.1, 127.6, 121.9, 120.5, 118.2, 114.9, 55.7.

HRMS (+ESI): Calculated: 270.1125 ($\text{C}_{16}\text{H}_{16}\text{NO}_3$). Observed: 270.1125.

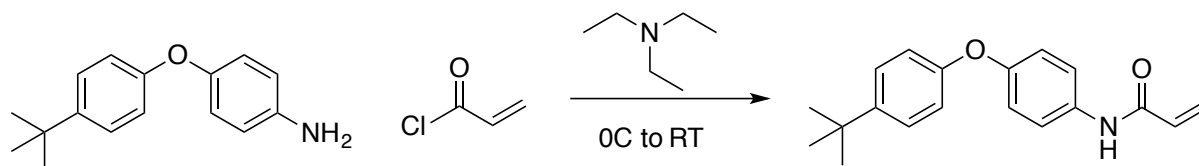
Synthesis and Characterization of AMR 1-125



N-(4-(4-(*tert*-butyl)phenoxy)phenyl)acrylamide (AMR 1-125)



An oven dried round bottom flask was charged with a magnetic stir bar, copper (I) iodide (38mg, 0.2 mmol), N-Boc-4-hydroxyaniline (502mg, 2.4 mmol), potassium carbonate (552.8mg, 2 mmol), and crushed 4 angstrom sieves (~200mg). The flask was evacuated and filled with nitrogen twice. Under nitrogen, 1-Bromo-4-*tert*-butylbenzene (346uL, 2 mmol) and *N,N'*-Dimethyl-1,2-cyclohexanediamine (62uL, 0.2 mmol) were added along with 2mL of butyronitrile. The flask was allowed to react at 70C for 24 hours. At the end of the reaction, the mixture was diluted with CH₂Cl₂ and rinsed through Celite to remove inorganic salts and other solids. The crude reaction mixture was purified using column chromatograph (10% ethyl acetate in hexanes). The product was a yellow oil (yield 31%).



An oven dried round bottom flask was charged with the amine starting material (154.2mg, 0.6mmol) along with dry CH₂Cl₂ and allowed to cool to 0C. Acryloyl chloride (69.4mg, 0.8mmol) was then added to the flask, followed by triethylamine (196uL, 1.4mmol), and the reaction was allowed to come to room temperature overnight. At the end of the reaction, the mixture was washed with brine and then purified using column chromatography (10% ethyl acetate in hexanes). The product was a waxy, white solid (yield <10%).

¹H NMR (900MHz, CDCl₃): δ 7.51 (d, 2H, J=8.5Hz), δ 7.31 (d, 2H, J=8.5Hz), δ 6.97 (m, 2H,), δ 6.90 (m, 2H,), δ 6.42 (d, 1H, J=16.8Hz), δ 6.22 (dd, 1H, J=16.8, 10.3 Hz), δ 5.75 (m, 1H,), δ 1.3 (s, 9H).

¹³C NMR (900MHz, CDCl₃): δ 163.4, 155.1, 154.2, 146.3, 133.0, 131.2, 127.9, 126.7, 121.7, 119.5, 118.3, 34.5, 31.7, 29.9

HRMS (+ESI): Calculated: 296.1645 (C₁₉H₂₁NO₂) Observed: 296.1643.

Supplemental Table Legends

Table S1. Covalent ligand screening data. SW620 cells were treated with either DMSO or cysteine-reactive fragment (50 μ M) for 48 h after which serum-free cell survival or proliferation were assessed by Hoescht staining. Shown are average and sem values from n=3/group.

Table S2. IsoTOP-ABPP analyses of DKM 3-5 and DKM 3-30 in SW620 cells. SW620 cell proteomes were pre-treated with DMSO or DKM 3-5 (50 μ M) or DKM 3-30 (50 μ M) for 30 min at 37°C prior to labeling of proteomes with IAYne (100 μ M) for 1h at room temperature. Proteomes were then subjected to copper-catalyzed azide-alkyne cycloaddition with a biotin-azide tag bearing an isotopically light (for DMSO-treated) versus heavy (for ligand-treated) valine and a TEV protease recognition site. Proteomes were then mixed in a 1:1 ratio and probe-modified peptides were enriched and released by TEV protease for subsequent quantitative proteomic analysis. The data was filtered for only those probe-modified peptides that were identified in at least 2 out of 3 runs. Ratios for the same redundant probe-modified peptides and peptides across runs were averaged. Top hits of covalent ligands were confirmed to have more than one light to heavy ratio greater than 2. Shown in Tabs 1 and 3 are the final consolidated and averaged light to heavy ratios for those peptides only observed in at least 2 out of 3 biological replicates for isoTOP-ABPP studies with DKM 3-5 and DKM 3-30, respectively. Shown in Tabs 2 and 4 are the raw data and ratios for the total peptides identified across all 3 biological replicates for isoTOP-ABPP studies with DKM 3-5 and DKM 3-30, respectively.

Supplemental Figures

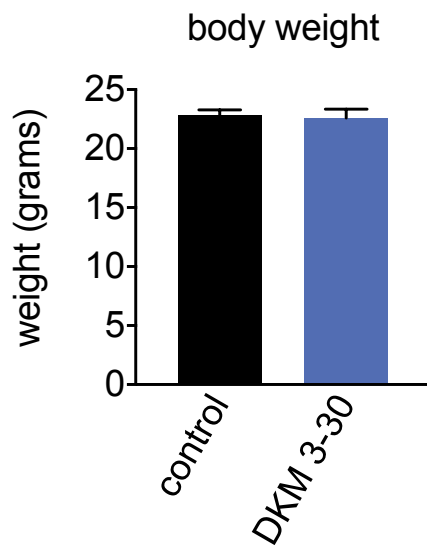


Figure S1. Body weight of mice treated with DKM 3-30 in tumor xenograft studies. Mice from tumor xenograft studies shown in **Fig. 1E** were weighed at the end of the study. The mice treated with DKM 3-30 did not show any significant changes in body weight compared to vehicle-treated control mice. Data are presented as mean $\pm$ sem, n=8 mice/group.

cell viability effects of DKM 3-30
upon expression of human RTN4 in MEF cells

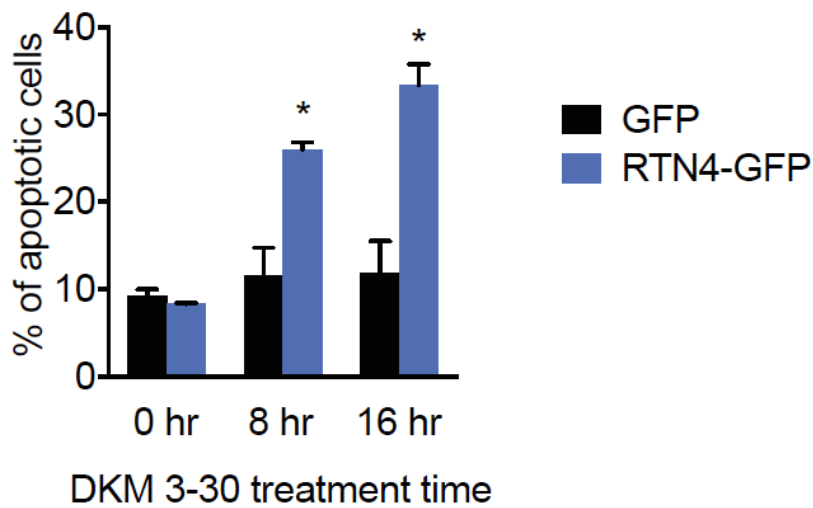


Figure S2. Effect of DKM 3-30 in Mouse Embryonic Fibroblast (MEF) cells expressing human RTN4. C1101 in human RTN4 is instead a serine in mouse RTN4. DKM 3-30 does not induce apoptosis in GFP-expressing MEF cells, but induces apoptosis in MEF cells expressing human RTN4-GFP. GFP or RTN4-GFP expressing MEF cells were treated with DKM 3-30 (50 μ M) for 0, 8, or 16 h and apoptotic cells (propidium iodine positive and Annexin-V positive) were assessed by flow cytometry. Data are presented as mean $\pm$ sem. Significance is expressed as * $p < 0.05$ compared to 0 h time-point.

Q9NQC3	RTN4_HU	1	MEDLDQSP	LVSSSD	SPRPQPAFKYQFVREPEDEEEEEEEEEDE	EDLEELVLERKPA
Q6JRV0	RNT4_XE	1	--MDEQSP	DISSSH	-----GDERREPAQPGERKFW	
Q9NQC3	RTN4_HU	61	AGTSAAPVPTA	PAGAPLMDFG	NDVFPPAPRGPLPAAPFVAPERQPSWDPSVVSSTVPAP	
Q6JRV0	RNT4_XE	30	DDLDDVLDL-T	--GG--AGQFSQ	FFSGSHPARDIEEEEEDEEERGAWKDSLSPVVEE-	
Q9NQC3	RTN4_HU	121	SPLSAAAVSP	SKLPEDDEPPAR	PPPPPPASVSPQAEPVWTFAPAPAAPSTFAAPKRRG	
Q6JRV0	RNT4_XE	84	EGSGIDSI	S-----P-----	VSPHSPAVPSAEMEEP-----ERFPA-CTA	
Q9NQC3	RTN4_HU	181	SGSVDET	LFAAPAEFVIR	SSAENMDLKEQFGNTISAGQEDFP	SVLLETAASLPSLSP
Q6JRV0	RNT4_XE	119	PSGSVDEN	LFTLPAASAH	LMHASADK---IMEFYSTVSTGQEEFASVLLQSTASLSLPS	
Q9NQC3	RTN4_HU	241	LSAASFKE	HEYLGNLSVLP	TETGLQENVSEASKVSEKAKTLLIDRDLTFSELEYSEM	
Q6JRV0	RNT4_XE	176	LSTDSSKE	HAETVAFPTGLA	AATEALQEP	TDNMY-SVSR-----I
Q9NQC3	RTN4_HU	301	GSSFSVSP	KAESAVIVAN	PREETIVKNDDEERLVSNNILHNQOELPTALTKLVKEDEVV	
Q6JRV0	RNT4_XE	214	TSHLP	SDNLESKAL-DQV	KEEVIFSEKRG-----YVVDHPTSQOETI-----SEHAKL	
Q9NQC3	RTN4_HU	361	SSEKAKDS	FNEKRVAV-----	EAPMREEVADFKPFERVWEVKDSKEDSDMLAAGGK	
Q6JRV0	RNT4_XE	262	YSQSAKEM	FSGMLQSVAPP	HEEFTDIKEVYDPYVDFKPFMSKSGDVGYEVSDV-----	
Q9NQC3	RTN4_HU	412	FESNLESK	VDKKCFADSL	---QTNHKKDSESSNDTSFSPSTPEGIKDRSGAVITCAPFN	
Q6JRV0	RNT4_XE	316	-AEKFQVD	VGRNLNESA	VKHEEKSSSEMEIDS-ISDISPLTPELLPDST-DVDMFAT--	
Q9NQC3	RTN4_HU	469	PAATESIATNI	PLLGDP	TSENKTDEKKIEKKAOIVTEK-NTSTKTSNPFVLAQDSET	
Q6JRV0	RNT4_XE	371	-----VEQNIP	PSFGGCHVAG	NKTDEKKIEDIEAQKTSVGFGLKVAIVNPFYNE-SAQES	
Q9NQC3	RTN4_HU	528	DYVTTDN	LTKVTEEVVAN	MPCELTTPDLVQEACESELNEVTGTRIAVETKMDLVQTSSE-VM	
Q6JRV0	RNT4_XE	425	EYVTT	THV-----ATHV	STKPECFTPDLVQEAYESEAYDTGIPKQKYESNIDLVTAAANSV	
Q9NQC3	RTN4_HU	587	QESLYFA	AQLCPFSFESE	ATPSPVLPDIVMEAPLNSAVPSAGASVIOFSSSPLEA-SSVN	
Q6JRV0	RNT4_XE	480	QEKVSPTA	QAPARLEE	DSVSPVLPDIVMEAPLASALETVA---LKPDISEVGIKPPAR	
Q9NQC3	RTN4_HU	646	YSIKHEP	ENPPFYEEAM	SVSKKVSIGIKKEPENINAAALQETEAPYISACDLIKET	
Q6JRV0	RNT4_XE	537	VSKTKAE	PEKPPSYEEAV	TEVQONQDLA-A-ALGGSKQGAVVEETEPPYISACDLIKGT	
Q9NQC3	RTN4_HU	706	KLSAEPAP	DFSDYSEMA	KVEQPVPDHSLEVEDSSPDSEPVDLFSDDSIDPVPKODETVM	
Q6JRV0	RNT4_XE	595	ESVAGS	TEFSKLKQNE	FESQ-----FMESPDESPPDSECEPSYKQWDSVQK--EAFS	
Q9NQC3	RTN4_HU	766	LVKESL	TETSFESMIE	YENKEKLS--ALPPEGGKPYLESFKLSLDNTRK--DTLPLDEVST	
Q6JRV0	RNT4_XE	649	IKTESV	NA---QSII	IPEQKQVFDQKSEESSPSKSYLDSFQPEICVSKATSDLFAGKLT	
Q9NQC3	RTN4_HU	822	LSRKEKI	PLQMEELST	AVSYNDDLFISKEAQIRETETFS	SDSSPIEIIDFPTLISSKTDS
Q6JRV0	RNT4_XE	706	L--LQEK	PLQMEELDE	GLSLEKI-PCTRKYS	PVSES---PEPRFS---PVPEDLSSKLG
Q9NQC3	RTN4_HU	882	FSK--L	AREYTDLEV	SHKSEIANAPDGAGSLFCTELPHDLSLKNIQPKVEEKISFSDDF	
Q6JRV0	RNT4_XE	756	IQKEVL	LAKQPEDK	VQKNRSNLD	FVPEENIEFTFAVQKEDDSG----KAVSDTFGGLDTT
Q9NQC3	RTN4_HU	939	SKNGSAT	SKVL	LLPPDV	SALATQAEIESIVKPKVLVKE-AENKLPSDTEKEDRSPSAIFS
Q6JRV0	RNT4_XE	811	TKGGS	AVHEVK-----	VDPKPPSKEDDGSKLPKES-----KASTVS	
Q9NQC3	RTN4_HU	998	AELSKT	SVVDLLYWR	DIKKTGVVFGASL	FLLSLVFSIVSVTAAYIALALLSVTISFRIY
Q6JRV0	RNT4_XE	849	SSDFMN	SVVDLLYWR	DIKRS	GVVFGASLFLLSLVFSIVSVLAAYIALALLSVTISFRIY
Q9NQC3	RTN4_HU	1058	KGVIQAI	QKSD	EGHPFRAYLESE	VaiseELVQKYSNSALGHVNCTIKELRRFLVDDLVD
Q6JRV0	RNT4_XE	909	KGILQAI	QKSE	EGHPFRSILE	SNLAVPEDLVQKYCNVALNHVNCTIKELRRFLVDDLVD
Q9NQC3	RTN4_HU	1118	SLKFAV	LMWVFTYV	GALFNGLTLLI	ALISLFSVPVIYERHQAQIDHYLGANKNVKDAM

Figure S3. Sequence alignment of human and xenopus laevis RTN4. The position of the shared cysteine in human RTN4 (C1101) and xenopus laevis RTN4 (C952) is indicated by the red arrow. The shaded amino acids indicate shared sequence identity (*black*) or similarity (*gray*).

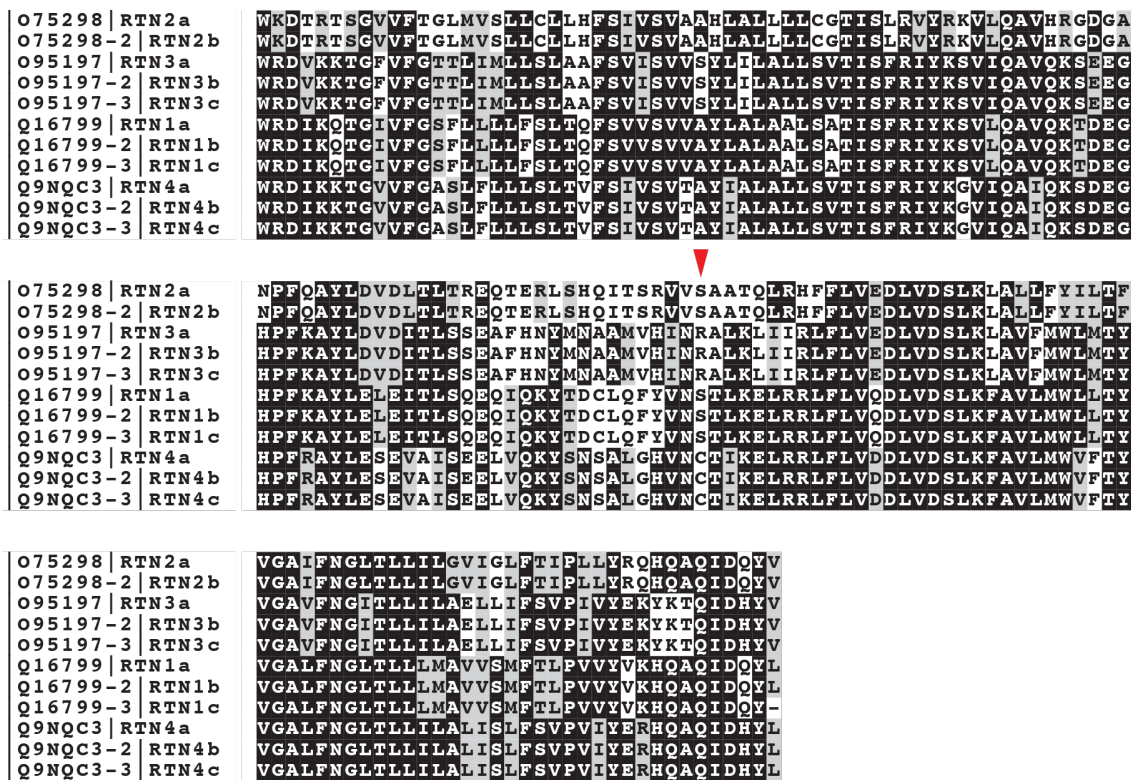


Figure S4. Sequence alignment of the reticulon homology domain from human reticulon proteins. The reticulon homology domain consists of the tandem hydrophobic regions and the intervening linker region. C1101 of RTN4 is indicated by the red arrow. The shaded amino acids indicate shared sequence identity (*black*) or similarity (*gray*).

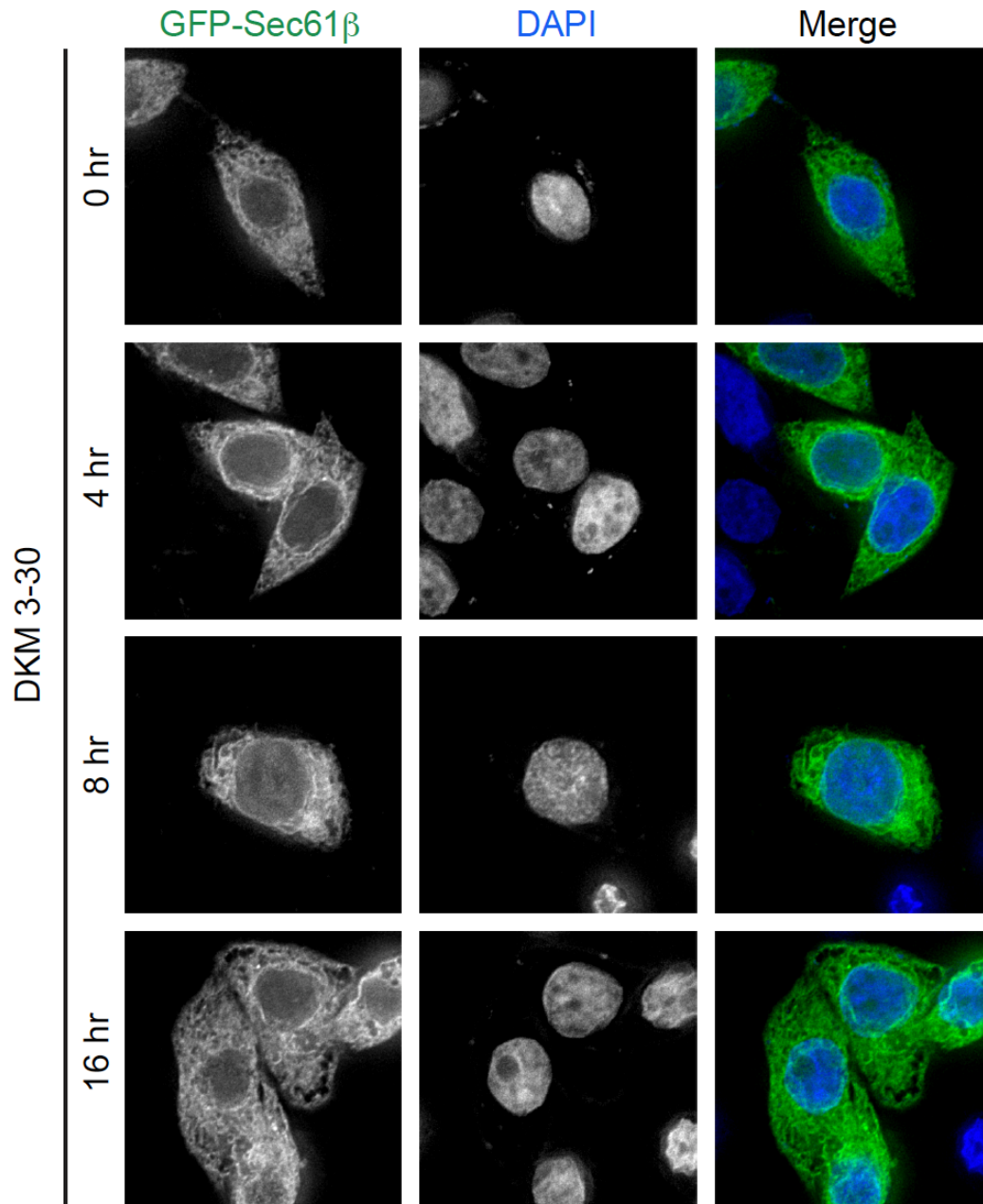
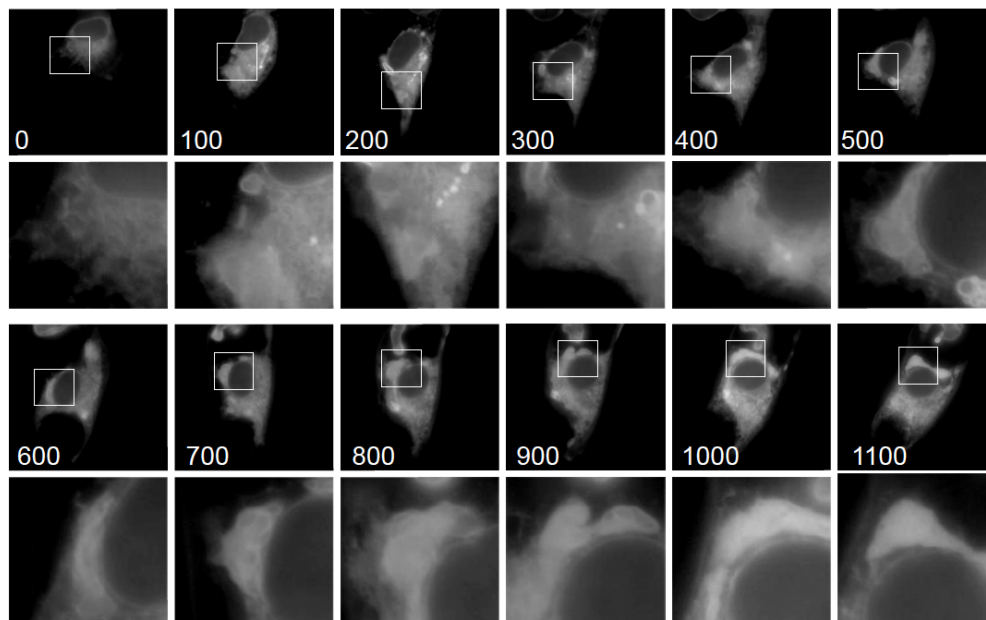


Figure S5. ER Morphology in SW620 Colorectal Cancer Cells. SW620 cells expressing GFP-tagged Sec61 β were treated with DKM 3-30 (50 μ M) for the indicated times and the ER (*green*) and nuclear (*blue*) morphology visualized by fluorescence microscopy.

A DKM 3-30



B DKM 3-30

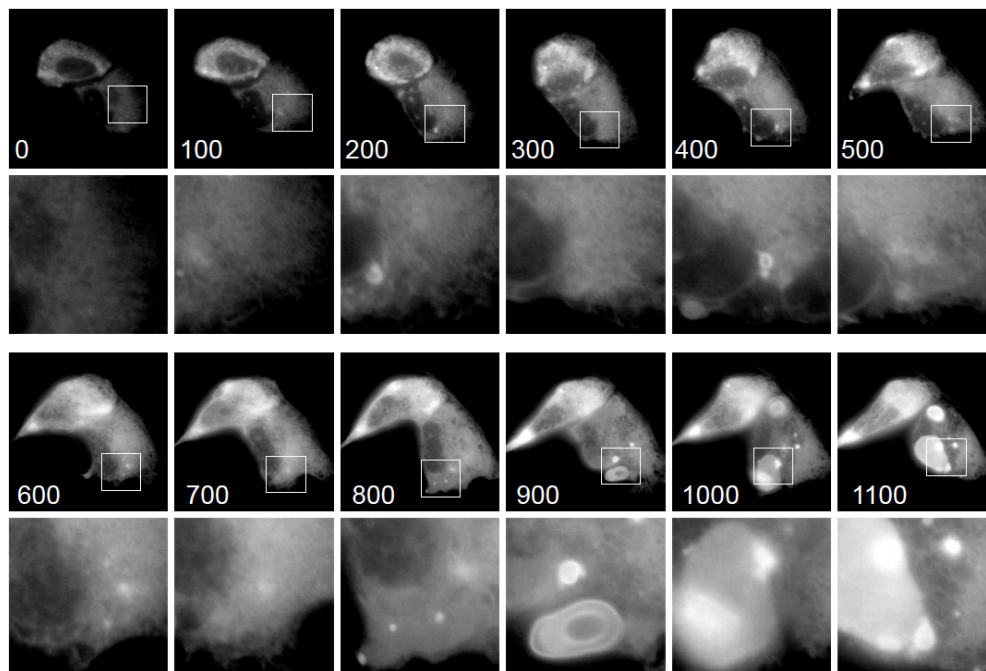
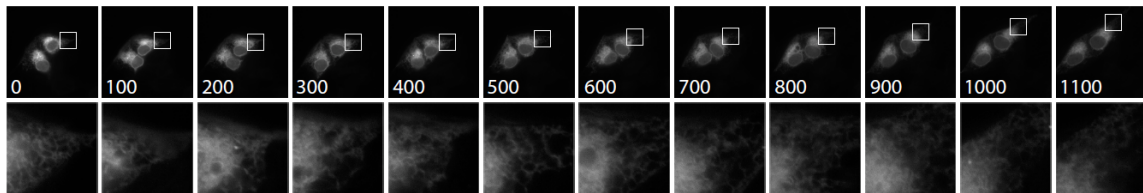
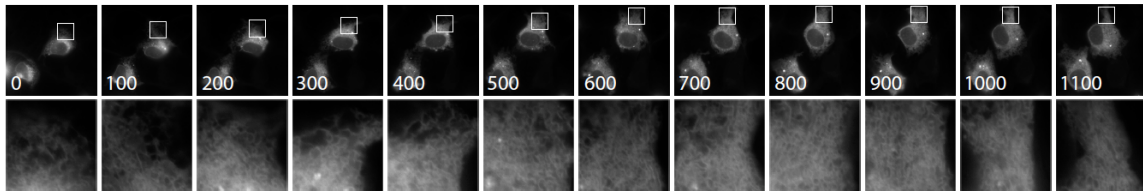


Figure S6. DKM 3-30 alters ER morphology. (A,B) U2OS cells expressing GFP-tagged Sec61 β were treated with DKM 3-30 (50 μ M) and ER morphology visualized by time-lapse fluorescence microscopy. Time (min) is indicated on each panel. Bottom panels indicate boxed region.

Control



50 μ M YP 1-49



1 μ M AMR 1-125

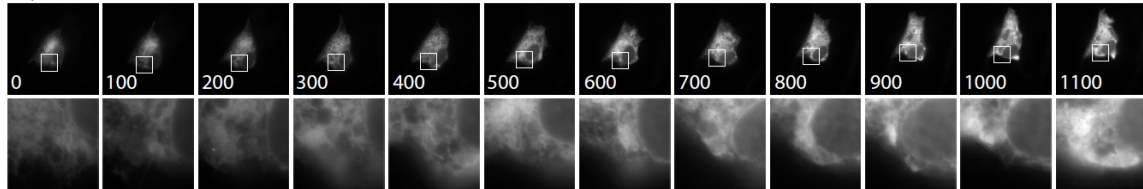


Figure S7. AMR 1-125, but not YP 146, alters ER morphology. U2OS cells expressing GFP-tagged Sec61 β were incubated with control, 1 μ M AMR 1-125, or 50 μ M YP 146 and the ER morphology was visualized by time-lapse fluorescence microscopy. Time (min) is indicated on each panel. Bottom panels indicate boxed region.

Table S1: Screen

SW620 survival	Avg	sem	p value		SW620 proliferation	Avg	sem	p value
DKM 3-30	0.30660 6886	0.05698 9117	0.02213 4468		DKM 2-94	0.32328 6425	0.02918 1847	0.00026 9142
DKM 3-16	0.33790 081	0.04113 0092	0.02280 4386		DKM 2-71	0.41465 8775	0.01301 6339	4.05508E -06
DKM 2-40	0.35511 3663	0.03203 7012	0.00311 3124		DKM 2-98	0.41667 7045	0.01635 6386	6.50504E -06
DKM 2-91	0.38206 2732	0.03332 7139	0.00089 675		DKM 2-83	0.47779 1761	0.03313 836	0.00093 3188
DKM 2-101	0.39229 6911	0.06433 0275	0.00756 8126		DKM 2-80	0.47822 9212	0.02259 2141	0.00050 2012
DKM 3-10	0.41110 4436	0.05713 7278	0.00704 7036		DKM 2-76	0.49649 0029	0.03229 1156	0.00102 0204
DKM 2-94	0.43095 6498	0.04836 4539	0.00238 5156		DKM 3-70	0.53049 0697	0.01587 6322	2.15237E -05
DKM 2-76	0.44237 5493	0.07362 6826	0.00708 115		DKM 2-52	0.53235 2055	0.02014 819	5.62731E -05
DKM 2-80	0.46927 6425	0.07656 8906	0.00935 3129		TRH 1-55	0.53251 5006	0.08581 5137	0.01678 7282
TRH 1-55	0.47494 7026	0.04131 2053	0.00236 5117		DKM 3-30	0.53990 8512	0.02591 5439	0.01502 823
TRH 1-12	0.48750 3533	0.03290 2278	0.00723 549		DKM 2-93	0.57063 1878	0.03836 6743	0.00265 7648
DKM 3-7	0.50754 5355	0.03809 2157	0.05455 0853		DKM 2-91	0.59467 2452	0.03124 9574	0.00218 281
DKM 2-95	0.51717 9832	0.10242 2848	0.03890 3195		DKM 3-16	0.60203 2918	0.03279 4068	0.02620 2588
DKM 3-43	0.51963 7287	0.08047 7391	0.07865 9349		TRH 1-53	0.72104 6149	0.05960 07	0.03315 8233
DKM 2-98	0.52414 1209	0.12682 9983	0.03640 0057		DKM 2-67	0.73111 4338	0.00563 7245	3.21269E -06
DKM 3-36	0.53806 8365	0.09230 7252	0.09564 4106		DKM 2-37	0.73382 8089	0.02195 611	0.00145 3964
TRH 1-32	0.55000 1217	0.09885 5746	0.10045 3518		DKM 2-59	0.73900 5512	0.03132 4617	0.00305 7884
DKM 3-41	0.55029 8638	0.08826 4813	0.09874 7793		TRH 1-50	0.76461 37	0.03806 1476	0.00870 9497
DKM 3-70	0.57438 6956	0.11063 8221	0.12641 1699		DKM 3-10	0.78768 1886	0.10219 31	0.21231 0226
DKM 2-37	0.57479 4017	0.18340 2421	0.10919 892		DKM 3-5	0.81528 7886	0.02722 0639	0.00303 3719
TRH 1-50	0.57691 9713	0.07154 1268	0.09260 6859		DKM 2-84	0.83596 8439	0.04977 2152	0.03171 5111
DKM 3-5	0.58623 0751	0.03821 9248	0.01208 3118		DKM 2-48	0.84689 5918	0.04314 9557	0.03854 5247
DKM 2-108	0.61258 2703	0.01780 652	0.01364 4465		DKM 2-95	0.85489 2548	0.01121 1287	0.06522 3892
DKM 3-31	0.64899 5421	0.08309 4332	0.16406 7696		TRH 1-12	0.88798 5921	0.06521 6595	0.18601 5736
DKM 2-83	0.65735 6274	0.07013 3936	0.03179 8652		DKM 2-116	0.89659 7875	0.02643 5811	0.02108 8225
DKM 2-59	0.66294 045	0.07318 367	0.04922 0124		DKM 3-41	0.93370 6644	0.04617 0689	0.61834 4482

TRH 1-53	0.69292 6974	0.06758 3873	0.04079 0567		DKM 3-13	0.93616 9984	0.02625 4095	0.60153 639
DKM 3-32	0.69621 0673	0.07332 5842	0.20344 0957		DKM 3-43	0.93883 509	0.01349 1316	0.60441 2802
DKM 2-93	0.73723 5579	0.05838 9236	0.04794 3135		DKM 3-32	0.94553 4216	0.02731 7623	0.65544 2364
DKM 2-84	0.73741 0851	0.06853 3742	0.07662 3617		DKM 2-62	0.95190 0478	0.01546 6708	0.05644 7858
DKM 2-113	0.74586 5144	0.03172 8278	0.06078 064		DKM 2-110	0.95368 8738	0.06380 2492	0.51238 4909
DKM 3-9	0.75463 2372	0.02831 5416	0.24442 9691		DKM 2-108	0.95425 0983	0.11077 7759	0.78047 6206
DKM 2-114	0.75997 8853	0.03482 671	0.07417 2629		DKM 2-120	0.95835 1408	0.01152 5941	0.04868 4322
DKM 3-13	0.76747 2891	0.05602 7814	0.28920 8997		DKM 2-109	0.95884 5586	0.02306 0043	0.17365 1039
DKM 2-34	0.78050 4195	0.01710 4938	0.08759 8447		DKM 2-97	0.96082 9971	0.05221 1902	0.50125 6229
DKM 2-47	0.78362 133	0.04985 2169	0.11612 0806		DKM 2-101	0.96202 6335	0.05225 9147	0.68661 8609
DKM 3-29	0.79233 9259	0.04701 4126	0.31105 6364		DKM 3-36	0.97337 2248	0.03512 338	0.83069 5652
DKM 2-49	0.80085 4309	0.06436 6289	0.16003 7749		DKM 2-40	0.97712 2752	0.00894 8405	0.45355 1197
DKM 2-71	0.81490 8894	0.07556 0073	0.39587 0089		DKM 2-107	0.98543 9364	0.08674 7763	0.91293 2595
DKM 2-43	0.84212 5151	0.05519 9293	0.22716 9421		DKM 3-31	0.99426 023	0.03504 8143	0.96311 7369
DKM 2-107	0.85735 495	0.04878 5475	0.26156 5517		DKM 2-100	0.99665 4157	0.03505 2907	0.93096 7387
DKM 2-67	0.86712 7976	0.14078 0933	0.62042 4476		DKM 3-7	0.99749 4674	0.01237 8724	0.98271 6965
DKM 2-50	0.88561 6685	0.01550 3525	0.30480 7542		TRH 1-32	0.99789 9182	0.03050 6964	0.96001 8493
DKM 2-31	0.89422 5624	0.04129 1365	0.36879 1517		DKM 2-72	1.00111 0514	0.02527 3175	0.97447 9914
DKM 2-48	0.89844 8559	0.04925 2692	0.39997 4076		DKM 3-9	1.00203 2785	0.09648 5633	0.99073 525
DKM 2-32	0.90654 1965	0.10892 3829	0.55486 1497		DKM 2-106	1.00247 8305	0.01641 5116	0.90203 8636
DKM 2-33	0.91609 6991	0.07868 706	0.53619 3984		DKM 2-60	1.00395 6785	0.04779 3568	0.96431 2632
DKM 2-52	0.92037 9497	0.09768 5065	0.72455 8091		DKM 2-86	1.02374 3856	0.12583 6909	0.89671 661
DKM 2-39	0.93287 4836	0.05142 6657	0.57107 2022		DKM 3-8	1.04572 2076	0.00332 4928	0.69278 2302
TRH 1-13	0.94234 7437	0.04823 2721	0.62004 1946		DKM 2-34	1.04997 4155	0.07209 6622	0.55009 8033
DKM 2-72	0.96260 9864	0.05614 8195	0.84853 0624		DKM 2-111	1.05643 9945	0.01321 4812	0.02529 0247
DKM 2-58	0.97779 4494	0.05369 744	0.84989 1842		DKM 3-12	1.06474 6877	0.05610 5628	0.64370 9823
TRH 1-19	1.01324 4669	0.06027 1908	0.91631 1935		DKM 2-49	1.08827 7372	0.02328 1555	0.06505 5747
DKM 2-	1.01641	0.05788	0.88273		DKM 2-39	1.10101	0.02928	0.06161

120	2308	762	2253			6012	0834	5115
DKM 3-42	1.03885 691	0.20886 1512	0.90864 8774		DKM 2-114	1.10550 4011	0.07824 3449	0.41211 0965
DKM 2-42	1.04079 3076	0.03568 6065	0.71080 6957		DKM 2-47	1.11678 3781	0.02001 4825	0.02377 4054
DKM 2-97	1.06304 0937	0.26712 1694	0.83342 8521		DKM 2-103	1.11962 8221	0.10985 5657	0.47626 4358
DKM 2-60	1.07722 4637	0.16163 3463	0.75076 4514		DKM 3-42	1.12430 4818	0.07494 3108	0.26822 1309
DKM 2-86	1.09220 3543	0.12606 4713	0.64540 8347		DKM 2-32	1.14469 0474	0.12272 4503	0.31304 632
DKM 2-110	1.12078 6999	0.16590 9839	0.55412 2348		DKM 2-33	1.15008 3978	0.10690 3117	0.24431 0787
TRH 1-20	1.13791 9573	0.04524 4288	0.26555 2223		DKM 2-58	1.15698 1213	0.03543 2672	0.02343 0164
DKM 2-62	1.15356 846	0.08535 5078	0.27596 9491		DKM 2-31	1.15728 3342	0.09198 4333	0.17531 8508
DKM 3-11	1.19885 9218	0.17913 7907	0.53156 5459		DKM 3-11	1.17976 5812	0.01971 9218	0.17909 4699
DKM 3-4	1.22189 6476	0.03054 3898	0.08528 6158		TRH 1-19	1.18944 2589	0.06932 2145	0.14670 5213
DKM 2-116	1.22727 7893	0.20125 0014	0.35840 3678		DKM 3-4	1.19715 4652	0.09542 4614	0.21850 8161
DKM 2-102	1.24378 8835	0.05239 661	0.09503 1156		DKM 3-29	1.21070 1961	0.04190 22	0.01761 6555
DKM 3-12	1.28819 4484	0.09417 9417	0.24947 4195		TRH 1-20	1.21463 0286	0.11475 0335	0.24655 0361
DKM 2-111	1.33289 746	0.22527 8366	0.24008 0854		TRH 1-27	1.25415 4222	0.07997 6644	0.06957 5542
DKM 2-103	1.35050 1637	0.05989 8758	0.04120 4031		DKM 2-43	1.27597 5496	0.02939 1836	0.00216 6962
DKM 2-100	1.37624 6154	0.03252 2242	0.01542 1639		TRH 1-13	1.27912 0775	0.03962 9877	0.00417 3915
DKM 2-109	1.39726 0387	0.02466 1634	0.01171 8831		DKM 2-50	1.30404 3479	0.01041 7594	0.00041 3725
TRH 1-27	1.43849 6026	0.23790 4295	0.27895 4818		DKM 2-102	1.32743 2615	0.04704 1006	0.01648 5849
DKM 2-106	1.44066 2577	0.25283 5971	0.17465 5498		DKM 2-42	1.36650 0508	0.00245 6401	0.00015 1716
DKM 3-8	1.51946 0533	0.08821 1957	0.06850 898		TRH 1-54	1.39356 2473	0.00680 8191	1.49026E -06
TRH 1-54	1.75382 2295	0.24154 7841	0.10061 9546		DKM 2-113	1.47354 594	0.07287 8537	0.01233 7171

Table S2 (i) isoTOP-ABPP data: DKM 3-30 final average ratios

Peptide	PTM index from ip2	average area ratio	uniprot	protein	# of runs
YSNSALGHVNC*TIK	C1101	3.03808665	Q9NQC3 F8W914	Q9NQC3-1 Isoform 1 of Reticulon-4 OS=Homo sapiens GN=RTN4 # F8W914 Reticulon OS=Homo sapiens GN=RTN4 PE=1 SV=1 #	3
AYEYVEC*PIR		2.53694826	P53701	P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 #	2
APPWVPAMGFTLAPSLGC*FVGSR	C19	2.51111954	B1AH87 P30536	B1AH87 Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=1 SV=1 # P30536 Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 #	2
YYGGAENVDEIELLC*QR		2.42664368	G3V5L0	G3V5L0 Serine hydroxymethyltransferase# mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 #	2
KVIGIEC*SSISDYAVK	C101	2.39921406	Q99873	Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 #	2
TYDPSGDSTLPTC*SK		2.34664	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #	2
FTTSC*MTGYSPQLQLSSGGSGSYSPGVTYSPVSGYNK	C158 C157	2.30655747	Q96SK2 Q96SK2	Q96SK2-2 Isoform 2 of Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 # Q96SK2 Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 #	2

SLVQNNCLSRPNIFLC*PEIEPK	C145	2.27943299	Q8TAQ2 Q8TAQ2 Q8TAQ2 F8VXC8	Q8TAQ2-2 Isoform 2 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 # Q8TAQ2 SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 # Q8TAQ2-3 Isoform 3 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 # F8VXC8 SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 #	2
LWNTLGVC*K		2.21603058	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #	2
SLPSAVYC*IEDK	C674	2.20207684	O43290	O43290 U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 #	2
EGGQYGLVAAC*AAGGQGHAMIVEAYPK	C436	2.14166255	P55084 P55084	P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 # P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB #	2
AAIGC*GIVESILNWVK	C486 C431	2.1371498	P11388 P11388 P11388 P11388	P11388-3 Isoform 3 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A # P11388-2 Isoform 2 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A # P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 # P11388-4 Isoform 4 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A #	2

LC*PLKDEPWPIHPWEPGSFR	C105 C78	2.11255406	E7ETU7 H0Y9G6 E9PF06 P09001	E7ETU7 39S ribosomal protein L3# mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # H0Y9G6 39S ribosomal protein L3# mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # E9PF06 39S ribosomal protein L3# mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # P09001 39S ribosomal protein L3# mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 #	2
VIEASDVVLEVLDARDPLGC*R	C144	2.08317503	Q9BVP2 Q9BVP2	Q9BVP2 Guanine nucleotide- binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 # Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 #	2
YVAAAFPSAC*GK	C172	2.07373933	B4DW73 Q16822	B4DW73 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 # Q16822 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 #	3
VC*TLAIIDPGDSDIIR	C92	2.06285771	P62888 E5RI99	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 # E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 #	2
STPYEC*GFDPMSPAR	C39	2.01022356	P03897	P03897 NADH-ubiquinone oxidoreductase chain 3 OS=Homo sapiens GN=MT-ND3 PE=1 SV=1 #	2
VALEGLRPTIPPGISPHVC*K	C361	2.00435826	Q13418	Q13418-2 Isoform 2 of Integrin-	2

	C453		Q13418 A0A0A0MTH3 Q13418	linked protein kinase OS=Homo sapiens GN=ILK # Q13418 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 # A0A0A0MTH3 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1 # Q13418-3 Isoform 3 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK #	
LLEETGIC*VVPGSFGQQR	C477	1.94223026	Q8TD30	Q8TD30 Alanine aminotransferase 2 OS=Homo sapiens GN=GPT2 PE=1 SV=1 #	2
FGVIC*LEDLIHEIAFPGK		1.91829421	Q6DKI1	Q6DKI1 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 #	2
ASC*LYGQLPK		1.88797486	P09211	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 #	3
ATGHSGGGC*ISQGR		1.8399368	I3L407 I3L139 Q9HA64 I3L3W5	I3L407 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=1 # I3L139 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=1 # Q9HA64 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 # I3L3W5 Ketosamine-3-kinase (Fragment) OS=Homo sapiens GN=FN3KRP PE=1 SV=1 #	3
HVVC*AAETGSGK		1.81784259	Q9NUL7	Q9NUL7 Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=1 SV=2 #	3
STFFNVLTNSQASAENFPFC*TIDPNESRVVPDER		1.77596442	J3KQ32 Q9NTK5	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 # Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 #	2

VDDEILGFISEATPLGGIQAASTESC*NQQLDLALCR		1.77564439	P42166	P42166 Lamina-associated polypeptide 2# isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 #	2
IDRYTQQGFGNLPIC*MAK	C841 C906 C907	1.77468753	A0A087WVM4 Q6UB35 B7ZM99	A0A087WVM4 Monofunctional C1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # Q6UB35 Monofunctional C1-tetrahydrofolate synthase# mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 # B7ZM99 MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 #	2
AVC*MLSNTTAIAEAWAR	C376	1.77339068	P68366 Q13748 Q9NY65 C9J2C0 Q71U36 Q9NY65 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #	3
LC*YVALDFENEMATAASSSSLEK	C219	1.74230926	P68133 P68032	P68133 Actin# alpha skeletal muscle OS=Homo sapiens	3

				GN=ACTA1 PE=1 SV=1 # P68032 Actin# alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 #	
YATSCYSCC*PR	C173	1.71077036	Q13057 Q13057	Q13057-2 Isoform 2 of Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY # Q13057 Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4 #	2
VIGSGC*NLDSAR	C192	1.71070171	P00338 P07195 P00338	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA # P07195 L- lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 # P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 #	2
VLPMTGVEAGETAC*K		1.70882272	P04181	P04181 Ornithine aminotransferase# mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 #	2
AVLLVGLC*DSGK	C73	1.69690794	Q9Y5M8	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 #	3
VTDDLVC*LVYK		1.69629998	P49458	P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 #	2
VC*EEIAIIPSKK	C35	1.6864058	H0YN88 A0A075B716 P08708	H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 # P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 #	2
VQENSAYIC*SR	C585	1.67485543	Q9Y3T9	Q9Y3T9 Nucleolar complex protein	2

				2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 #	
NCAVSC*AGEK	C141	1.66567494	Q15813 Q15813	Q15813 Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 # Q15813-2 Isoform 2 of Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE #	2
GC*STVLSPEGSAQFAAQIFGLSNHLVWSK	C374	1.66214235	P22234	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 #	2
TIQFVDWC*PTGFK	C347	1.65831063	Q13748 Q9BQE3 Q9NY65 C9J2C0 Q71U36 Q9NY65	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q9NY65- 2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 # C9J2C0 Tubulin alpha- 8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 #	2
AGQPHSSSDAAQAPAEQPHSSSDAAQAPC*PR	C51	1.65703433	P29372 P29372 A2IDA3 P29372 P29372	P29372-4 Isoform 3 of DNA-3- methyladenine glycosylase OS=Homo sapiens GN=MPG # P29372 DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 # A2IDA3 DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 # P29372-5 Isoform 4 of DNA-3-methyladenine glycosylase OS=Homo sapiens	2

				GN=MPG # P29372-2 Isoform 2 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG #	
LALFNPDC*WDRNNPEPWNK	C44	1.65313053	O00483	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 #	2
AVASQLDC*NFLK		1.65174024	A0A087X2I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #	2
C*SGIGDNPGSETAAPR	C1317	1.64434432	H0YAC6 P50851	H0YAC6 Lipopolysaccharide-responsive and beige-like anchor protein (Fragment) OS=Homo sapiens GN=LRBA PE=1 SV=1 # P50851 Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4 #	2
QPAIMPGQSYGLEDGSC*SYK		1.64035256	M0QXS5 P14866	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #	2
GNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDC*HTAHIAK		1.64031665	P68104 A0A087WVQ9	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 #	2
YWLC*AATGPSIK		1.63971656	P63244	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 #	2

LQSGIC*HLFR		1.63952553	P14868	P14868 Aspartate--tRNA ligase# cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 #	2
TIYAGNALC*TVK	C155	1.6292925	P13804	P13804 Electron transfer flavoprotein subunit alpha# mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 #	3
TSC*GSPNYAAPEVISGR	C200	1.62716973	Q13131 Q13131	Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 # Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 #	2
TFC*GTPEYLAPEVLEDNDYGR	C310	1.62402515	P31749 P31751 Q9Y243 Q9Y243 M0R0P9	P31749 RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2 # P31751 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 # Q9Y243-2 Isoform 2 of RAC- gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 # Q9Y243 RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 PE=1 SV=1 # M0R0P9 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=1 #	2
ISC*MSKPPAPNPTPPR		1.61979545	P46734 P46734	P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 # P46734 Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo	2

				sapiens GN=MAP2K3 PE=1 SV=2 #	
RPYGVGLLIAGYDDMGPHIFQTC*PSANYFDCR	C123 C154	1.59521485	P25786 P25786 F5GX11	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 # P25786 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 # F5GX11 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 #	3
LADQC*TGLQGFLVFHSGGGTSGGFTSLLMER	C129 C199	1.58924159	Q9BQE3 P68363 F5H5D3 Q71U36	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P68363 Tubulin alpha- 1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 #	2
LNLSC*IHSPVVNELMR		1.58552316	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #	2
LVVPATQC*GSLIGK	C109	1.58233902	Q15365	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #	2
NLSDLIDLVPSLC*EDLLSSVDQPLK	C65 C24	1.57747364	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87	2

				Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #	
SVHYC*PATK	C193	1.57226553	P25205 P25205	P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 # P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 #	2
NFYGGNGIVGAQVPLGAGIALAC*K	C188 C219	1.5670335	P08559 P08559 P08559	P08559 Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 # P08559-4 Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 # P08559-2 Isoform 2 of Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Homo sapiens GN=PDHA1 #	2
HISPTAPDTLGC*YPFYK	C384 C419	1.56371201	A0A087WWF6 P49005	A0A087WWF6 DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1 # P49005 DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1 #	2
QGEYGLASIC*NGGGGASAMLIQKL		1.56272382	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1	3

				SV=1 #	
HSMNPFC*EIAVEEAVR	C133	1.56257621	P38117 P38117	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB #	2
LGMLSPEGTC*K	C212	1.560251	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #	2
GLC*GAIHSSIAK	C103	1.55686303	P36542 P36542	P36542 ATP synthase subunit gamma# mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 # P36542-2 Isoform Heart of ATP synthase subunit gamma# mitochondrial OS=Homo sapiens GN=ATP5C1 #	2
LVAFC*PFASSQVALENANAVSEGVVHEDLR		1.55421672	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #	2
GSDC*GIVNVNIPTSGAEIGGAFGGEK	C450	1.54895211	P49419 P49419	P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 # P49419 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 #	2
LNQQQHPPDC*K	C239	1.54715283	Q5T280	Q5T280 Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 #	3
C*LHNFLTDGVPAEGAFTEDFQGLR	C268 C316	1.54437278	G3V1A6 P57764	G3V1A6 Gasdermin domain containing 1# isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 # P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD	2

				PE=1 SV=1 #	
TPC*NAGTFSQPEK	C129	1.54426894	O43684 J3QT28 O43684	O43684 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 # J3QT28 Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=1 SV=1 # O43684-2 Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 #	2
CPEALFQPSFLGMESC*GIHETTFNSIMK		1.54002639	P63261 P60709	P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 #	2
SWC*PDCVQAEPVVR		1.53956959	Q9BRA2	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 #	2
KLDTNSDGGQLDFSEFLNLIGGLAMAC*HDSFLK		1.53289223		Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 #	2
SIQFVDWC*PTGFK	C347	1.53230482	P68366 P68363 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #	2
SGGSGGC*SGAGGASNCGTGSGR		1.53170311	E9PI68 A0A087WUC6 Q15005	E9PI68 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=1 # A0A087WUC6 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=1 # Q15005 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3 #	3

FTLDC*THPVEDGIMDAANFEQLQER		1.53027608	P35268	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 #	2
DLNYC*FSGMSDHR	C267	1.52971496	P31943 G8JLB6 P55795	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 # G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 # P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 #	3
C*EFEEVQGFLDQVAHK		1.52800408	E9PI14 Q9NX20	E9PI14 39S ribosomal protein L16# mitochondrial (Fragment) OS=Homo sapiens GN=MRPL16 PE=1 SV=1 # Q9NX20 39S ribosomal protein L16# mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1 #	2
NLPFPTYFPDGDDEELPEDLYDENVC*QPGAPSITFA	C365 C338	1.5266735	E7ETU7 H0Y9G6 P09001	E7ETU7 39S ribosomal protein L3# mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # H0Y9G6 39S ribosomal protein L3# mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 # P09001 39S ribosomal protein L3# mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 #	2
GQVC*LPVISAENWKPATK	C144	1.52311035	P68036 P68036 P68036	P68036 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 # P68036-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 # P68036-3 Isoform 3 of Ubiquitin-conjugating enzyme E2	2

				L3 OS=Homo sapiens GN=UBE2L3 #	
C*FGTGAAGNR		1.52274032	P78527	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 #	3
ADPDGPEAQAEAC*SGER	C18	1.51985182	Q9NX24	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 #	2
VHPAMATAAGGC*R		1.51526714	H7C0N4 H7C561	H7C0N4 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 # H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 #	3
EMFPYEASTPTGISASC*R	C323	1.50909917	G5E972 P42167 P42167	G5E972 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 # P42167 Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 # P42167-2 Isoform Gamma of Lamina-associated polypeptide 2# isoforms beta/gamma OS=Homo sapiens GN=TMPO #	2
LNIISNLDC*VNEVIGIR	C357 C402 C390	1.50907123	P30154 P30154 P30154 P30153	P30154-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B # P30154-4 Isoform 4 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B # P30154 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo	2

				sapiens GN=PPP2R1B PE=1 SV=3 # P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 #	
YMACC*LLYR	C386 C316	1.50831702	P68366 Q9BQE3 P68363 F5H5D3 Q71U36 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #	2
SC*SGVEFSTSGSSNTDTGK	C36	1.50674267	A0A0A0MR02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #	3
AGSDGESIGNC*PFSQR	C35	1.50630488	Q9Y696	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 #	3
GC*EVVVSGK		1.50195918	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #	2
NILGGTVFREPIIC*K	C154	1.50153146	P48735 P48735	P48735 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 # P48735-2 Isoform 2 of Isocitrate	3

				dehydrogenase [NADP]# mitochondrial OS=Homo sapiens GN=IDH2 #	
AGAIAPC*EVTVPAQNTGLGPEK		1.49987947	P05388	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 #	3
TIGGGDDSFITFFC*ETGAGK		1.4949216	P68366 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #	2
FNNWGGSLSLGHPFGATGC*R	C413	1.49470358	P55084 P55084	P55084 Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 # P55084-2 Isoform 2 of Trifunctional enzyme subunit beta# mitochondrial OS=Homo sapiens GN=HADHB #	2
NWYVQPSC*ATSGDGLYGLTWLTSNYKS	C155	1.49359999	P62330	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 #	2
APC*QAGDLR		1.49218986	P48431	P48431 Transcription factor SOX-2 OS=Homo sapiens GN=SOX2 PE=1 SV=1 #	2
QVLMGPYNPDTC*PEVGFFDVLGNDR		1.49027316	Q9H3P7	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 #	3
VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGAC*GLR	C39	1.4894993	A0A087X260 A0A087WYY0 B1AKP7 Q13148 G3V162	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-	2

				binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #	
IQCTLQDVGSALATPC*SSAR	C80	1.48650918	Q96EY8 S4R3P5	Q96EY8 Cob(I)yrinic acid a#c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 # S4R3P5 Cob(I)yrinic acid a#c-diamide adenosyltransferase# mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 #	2
NLSFFLTTPC*AR	C492	1.48475541	P42224 P42224 J3KPM9	P42224-2 Isoform Beta of Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 # P42224 Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 # J3KPM9 Signal transducer and activator of transcription OS=Homo sapiens GN=STAT1 PE=1 SV=1 #	2
LLACIASRPGQC*GR		1.48225437	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #	2
C*SDNSSYEELSPISASSSTR	C205 C711 C346	1.48132186	Q8IXK0 A0A0A0MSI2 Q8IXK0 Q8IXK0 Q8IXK0 B3KPJ4 Q8IXK0	Q8IXK0-2 Isoform 2 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 # A0A0A0MSI2 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 # Q8IXK0 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 # Q8IXK0-3 Isoform 3 of	2

				Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 # Q8IXK0-4 Isoform 4 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 # B3KJP4 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 # Q8IXK0-5 Isoform 5 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 #	
C*LAQEVNIPDWIVDLR		1.48059607	Q9Y4W2 Q9Y4W2	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 # Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L #	2
HEEFEEGC*K	C41 C245	1.48052364	I3L3Q4 Q9HC38 Q9HC38 F6TLX2	I3L3Q4 Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=1 SV=1 # Q9HC38-2 Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 # Q9HC38-3 Isoform 3 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 # F6TLX2 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 #	2
GLDYEGGGC*R	C691	1.47961922	O60568	O60568 Procollagen-lysine#2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 #	2
LLQC*DPSSASQF		1.47292198	P37235	P37235 Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3 #	3

TVPFLPLLGGC*IDDTILSR	C180	1.46871284	Q7Z7H8 Q7Z7H8	Q7Z7H8 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 # Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10# mitochondrial OS=Homo sapiens GN=MRPL10 #	3
IINDNATYC*R		1.46850625	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #	2
SLLINAVEASC*IR	C262 C188	1.46835531	E2QRB3 P32322 P32322 A0A087WTV6 P32322 J3KR12 Q96C36	E2QRB3 Pyrroline-5-carboxylate reductase 1# isoform CRA_c OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322 Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # A0A087WTV6 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 # P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # J3KR12 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 # Q96C36 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 #	2
PPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIAC*K		1.4672988	P68104 A0A087WVQ9	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # A0A087WVQ9 Elongation factor 1-alpha 1	2

				OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 #	
HPLTQELKEC*EGIVPVPLAEK		1.46330944	P82932	P82932 28S ribosomal protein S6# mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 #	2
HTGPGILSMANAGPNTNGSQFFIC*TAK	C115	1.4619617	P62937	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 #	2
IISDNLYC*K		1.46057834	Q9Y2X3	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 #	3
LIDFLEC*GK	C234	1.45204378	P17844 J3KTA4	P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 # J3KTA4 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 #	2
KAVVVC*PK	C588	1.44929906	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #	2
LTTPTYGDLNHLVSATMSGVTTC*LR	C239 C221	1.4470993	Q13885 P68371 Q9BVA1 P04350 Q5JP53	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # P68371 Tubulin beta- 4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 #	3

VCETDGC*SSEAK	C10 C14	1.44699753	D6RF24 H0Y9L0 P53582	D6RF24 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=1 # H0Y9L0 Methionine aminopeptidase 1 (Fragment) OS=Homo sapiens GN=METAP1 PE=1 SV=1 # P53582 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=2 #	3
VC*PPHMLPEDGANLSSAR	C29	1.44174648	Q9GZY8 A0A0A0MS29 Q9GZY8 H7C433 E9PQX8	Q9GZY8-2 Isoform 2 of Mitochondrial fission factor OS=Homo sapiens GN=MFF # A0A0A0MS29 Mitochondrial fission factor OS=Homo sapiens GN=MFF PE=1 SV=1 # Q9GZY8 Mitochondrial fission factor OS=Homo sapiens GN=MFF PE=1 SV=1 # H7C433 Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=1 SV=1 # E9PQX8 Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=1 SV=1 #	2
TFVDFSQC*LHEEYR		1.4412551	Q53GQ0	Q53GQ0 Very-long-chain 3- oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 #	2
FALAC*NASDKIIEPIQSR		1.43956572	P35250 P35250	P35250-2 Isoform 2 of Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 # P35250 Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3 #	2
TIAEC*LADELINAAK	C172	1.43784341	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal	3

				protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #	
FMTPIQDNPSGWGPC*AVPEQFR	C19	1.43774291	O15371 O15371 O15371	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D # O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 # O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D #	3
SVLLCGIEAQAC*ILNTTLDLLDR	C114	1.43694517	K7ENV7 K7EKW4 Q96AB3	K7ENV7 Isochorismatase domain- containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=7 # K7EKW4 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=1 # Q96AB3 Isochorismatase domain-containing protein 2 OS=Homo sapiens GN=ISOC2 PE=1 SV=1 #	2
AVAILC*NHQR		1.43665633	P11387	P11387 DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 #	3
GNFTLPEVAEC*FDEITYVELQKEEAQK	C629	1.43590192	Q00839 Q00839	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 # Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU #	2
TIIP LISQC*TPK	C212	1.43560215	P40926	P40926 Malate dehydrogenase#	3

				mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 #	
DVQIGDIVTVGEC*RPLSK	C131	1.43545724	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #	2
LLDLVQQSC*NYK	C30	1.43434873	B1AHD1 P55769	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 # P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 #	3
C*MTNTPVVVR	C120	1.43349655	P32322 P32322 P32322	P32322 Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 # P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 # P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1# mitochondrial OS=Homo sapiens GN=PYCR1 #	2
VLGLGLGC*LR		1.43161418	Q9BRJ7 K7EIN2	Q9BRJ7 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 # K7EIN2 Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 #	3
VC*ISILHAPGDDPMGYESSAER		1.42896783	P60604 P60604	P60604-2 Isoform 2 of Ubiquitin- conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 # P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 #	2
AYHEQLSVAEITNAC*FEPANQMVK		1.4272155	P68366 Q13748 Q71U36 P68366	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A # Q13748 Tubulin alpha-3C/D chain OS=Homo	3

				sapiens GN=TUBA3C PE=1 SV=3 # Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 # Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 # P68366 Tubulin alpha- 4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 #	
AGQC*VIGLQMGTNK	C153 C155 C164	1.42679269	Q99439 B4DDF4 B4DUT8 A0A087X271	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #	3
SGDAAIVDMVPGKPMC*VESFSDYPPLGR		1.42177167	P68104 A0A087WVQ9	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 #	2
VSDTVVEPYNATLSVHQLVENTDETYC*IDNEALYDICFR	C201 C183	1.42171818	P68371 Q9BVA1 P04350 Q5JP53 Q9BUF5	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # Q9BVA1 Tubulin beta- 2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #	2
C*EFQDAYVLLSEKK		1.42052504	P10809	P10809 60 kDa heat shock protein#	2

				mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #	
SSQC*HTGSSPR	C439	1.41912782	O15226 O15226	O15226-2 Isoform 2 of NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF # O15226 NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF PE=1 SV=2 #	2
LNISFPATGC*QK		1.41849224	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #	3
FHADSVK*K		1.41740571	Q9BW61	Q9BW61 DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1 #	2
C*MQLTDFILK	C54	1.41733212	E7EPB3 P50914	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 # P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 #	2
ELEVLLMC*NK	C91 C109	1.41557263	P62910 F8W727 D3YTB1	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #	2
NHLLPDIVTC*VQSSR	C184	1.41539307	Q9BSD7	Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 #	2
VNGTTPC*AFPTHYEEALKDEEK		1.41354821	O15479	O15479 Melanoma-associated antigen B2 OS=Homo sapiens GN=MAGEB2 PE=1 SV=3 #	2
LTEGC*SFR	C93 C77	1.41326939	H0YMV8 Q71UM5 P42677	H0YMV8 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=1 SV=1 # Q71UM5 40S ribosomal protein S27-like	2

				OS=Homo sapiens GN=RPS27L PE=1 SV=3 # P42677 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 #	
C*ALSSPSLAFTPIK	C120	1.41160582	Q8NFH5 Q8NFH5 Q8NFH5	Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 # Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 #	2
SSVQEEC*VSTISSKDEDPLAATR		1.41017814	Q7L0Y3	Q7L0Y3 Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2 #	3
TQNLPMC*QLISR		1.40932098	P37268	P37268 Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 #	2
C*SEGSFLLTTFPRPVTVEPMDQLDDEEGLPEK	C119	1.40677481	Q15233 Q15233	Q15233-2 Isoform 2 of Non-POU domain-containing octamer- binding protein OS=Homo sapiens GN=NONO # Q15233 Non-POU domain-containing octamer- binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 #	3
SMVSPVPSPTGTISVPNSC*PASPR		1.40503239	P85037	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 #	2
EITSLDTENIDEILNNADVALVNFYADWC*R	C58	1.40392083	Q9BS26	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 #	2
GHSSDSNPAIC*R	C31	1.40183653	Q5JTH9	Q5JTH9 RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 #	2
FC*IWTESAFR	C250	1.40168032	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1	2

				SV=5 #	
SLC*NLEESITSAGRDDLESFQLEISGFLK		1.40151676	Q52LJ0 Q52LJ0	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #	2
IDC*FSEVPTSVFGEK		1.40149614	O00567	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 #	2
NMSVHLSPC*FR	C116	1.40075094	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #	3
GLPC*TELFVAPVGVASKR	C79 C428	1.40056743	H0Y901 E9PDI4 O00515	H0Y901 Ladinin-1 (Fragment) OS=Homo sapiens GN=LAD1 PE=1 SV=1 # E9PDI4 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=1 # O00515 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 #	3
VAC*ITEQVLTLVNKR		1.39946392	P04843	P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 #	3
NSQWVPTLPNSSHHLDAVPC*STTINR	C138	1.39926383	Q12824 Q12824 G5E975	Q12824 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 PE=1 SV=2 # Q12824-2 Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 # G5E975 SWI/SNF related# matrix associated# actin dependent regulator of chromatin# subfamily	2

				b# member 1# isoform CRA_c OS=Homo sapiens GN=SMARCB1 PE=1 SV=1 #	
NVQLLSQFVSPFTGC*YGR		1.39741717	Q9Y3D5	Q9Y3D5 28S ribosomal protein S18c# mitochondrial OS=Homo sapiens GN=MRPS18C PE=1 SV=1 #	2
LC*SSSSDTSSR	C385	1.39636437	Q86WB0 Q86WB0 C9J0I9	Q86WB0 Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 # Q86WB0- 2 Isoform 2 of Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 # C9J0I9 Nuclear- interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 #	2
LVVPASQC*GSLIGK	C109	1.39621638	Q15366 Q15366 Q15366 Q15366	Q15366-3 Isoform 3 of Poly(rC)- binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #	3
VNAAGTDPSSPVGFVLGVDLLHIFLEGATFLC*PADVTDP		1.39467126	Q9UI43	Q9UI43 rRNA methyltransferase 2# mitochondrial OS=Homo sapiens GN=FTSJ2 PE=1 SV=1 #	2
C*PFTGNVSIR	C60	1.39362413	P62280	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 #	2
LTALDYHNPAGFNC*KDETEFR	C19	1.39356072	Q9Y224	Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 #	3
VPTANVSVDLTC*R	C247	1.39080843	P04406	P04406 Glyceraldehyde-3-	2

				phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #	
DSGYGDIWC*PERGEFLAPPR	C176 C228 C213	1.38828888	J3KP06 F8WD26 Q8WWI1 Q8WWI1 Q8WWI1 Q8WWI1	J3KP06 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 # F8WD26 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 # Q8WWI1-4 Isoform 4 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # Q8WWI1 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 # Q8WWI1-3 Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 # Q8WWI1-2 Isoform 2 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 #	2
NFNYHILSPC*DLSNYTDLAMSTVK	C461	1.3870117	G5E9W3 Q9UKF6	G5E9W3 Cleavage and polyadenylation specific factor 3# 73kDa# isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 # Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 #	3
AC*QSIYPLHDVFVR	C201	1.38604365	D6RB09 D6RAT0 P61247 D6RG13	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 # P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens	3

				GN=RPS3A PE=1 SV=1 #	
WC*EYGLTFTEK	C65	1.38499888	A0A0A0MR02 P45880	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 # P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 #	2
KTPC*GEGSK	C70	1.38447633	P60866 P60866	P60866 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 # P60866-2 Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 #	2
NC*LTNFHGMDLTR	C96	1.38422694	D6RB09 D6RAT0 P61247 D6RG13	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 # D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 # P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 # D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 #	2
YGIIC*MEDLIHEIYTVGKR	C186	1.38026781	P18124 A8MUD9	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 # A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 #	3
C*ASQAGMTAYGTR	C127 C132	1.3800695	E9PDU6 Q15417 Q15417	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 # Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 #	2

KAQC*PIVER	C66	1.3793522	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #	2
NGDIC*ETSGKPK	C60	1.37918018	Q16637 E7EQZ4 Q16637 Q16637 Q16637 B4DP61	Q16637 Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1 # E7EQZ4 Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1 # Q16637-3 Isoform SMN- delta7 of Survival motor neuron protein OS=Homo sapiens GN=SMN1 # Q16637-2 Isoform SMN-delta5 of Survival motor neuron protein OS=Homo sapiens GN=SMN1 # Q16637-4 Isoform SMN-delta57 of Survival motor neuron protein OS=Homo sapiens GN=SMN1 # B4DP61 Survival motor neuron protein OS=Homo sapiens GN=SMN2 PE=1 SV=1 #	2
KGAGNPQASTLALQSNITQC*LLGQPWPLNEAQVQASVVK	C1261 C1260 C1299	1.37575576	E7ETY2 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 Q13428 J3KQ96	E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 # Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-6 Isoform 6 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 #	3

				Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 # Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 # J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 #	
FCSFSPC*IEQVQR	C209	1.37450881	Q96FX7	Q96FX7 tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens GN=TRMT61A PE=1 SV=1 #	2
IHMGSC*AENTAK		1.37318588	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #	3
GC*IVDANLSVLNLVIVK		1.37277071	P62753	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 #	3
IAILTC*PFEPPKPK	C253	1.37174437	E9PCA1 B7ZAR1 P48643	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 # P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 #	2
TLTSC*FLSCVVCVEGIVTK	C164	1.37168402	P25205 P25205	P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 # P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 #	2
LGYILTC*PSNLGTGLR	C347	1.371464	P12532	P12532-2 Isoform 2 of Creatine	2

			P12532	kinase U-type# mitochondrial OS=Homo sapiens GN=CKMT1A # P12532 Creatine kinase U-type# mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 #	
LMWLFGC*PLLLDDVAR		1.37108127	O15067	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 #	2
INISEGNC*PER	C54	1.37066894	Q15366 Q15366 Q15366 Q15366 Q15365	Q15366-3 Isoform 3 of Poly(rC)- binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 # Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 #	3
SGQGAFGNMC*R	C96	1.37027949	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #	3
GLC*AIAQAESLR		1.37005231	P23396	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 #	3
IIPLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK		1.36969252	P61978 P61978	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 # P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK #	3
C*PEALFQPSFLGMESCGIHETTFNSIMK		1.36914664	P60709	P60709 Actin# cytoplasmic 1	2

			P63261	OS=Homo sapiens GN=ACTB PE=1 SV=1 # P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 #	
LC*FSTAQHAS		1.36866528	M0QXS5 P14866	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 # P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 #	2
LGTLAPFC*CPWEQLTQDWESR	C705	1.36836374	Q99575	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 #	2
AAVEEGIVLGGGC*ALLR		1.36556159	P10809	P10809 60 kDa heat shock protein# mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 #	3
LDLGLCSVSC*ALEFIPNSK	C256	1.36498549	Q9BSH4	Q9BSH4 Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1 #	2
VC*NFLASQVPFPSR	C205	1.36390593	Q99714	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 #	3
VTDGALVVDCVSGVC*VQTETVLR	C136	1.36256773	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #	2
YAIC*SALAASALPALVMSK	C125	1.36224975	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #	3
TATAVAHC*K	C25	1.36125171	M0R210 P62249	M0R210 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 # P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 #	3
GC*TATLGNTAK		1.36119434	P15880	P15880 40S ribosomal protein S2	2

				OS=Homo sapiens GN=RPS2 PE=1 SV=2 #	
VC*NYGLTFTQK	C66	1.36015171	Q9Y277 Q9Y277	Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 # Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 #	2
SLHDALC*VLAQTVK	C348	1.35987264	P78371	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 #	2
AWVWNTHADFADEC*PKPELLAIR	C209 C132	1.35932263	C9JXG8 P43487 C9JJ34 F6WQW2 C9JGV6 P43487	C9JXG8 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=2 # P43487 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # C9JJ34 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # F6WQW2 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 # C9JGV6 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=7 # P43487-2 Isoform 2 of Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 #	2
C*HTPPLYR		1.35753021	M0R117 Q02543	M0R117 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 # Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A	2

				PE=1 SV=2 #	
YIGENLQLLVDRPDGTYC*FR		1.35717729	Q9Y221	Q9Y221 60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens GN=NIP7 PE=1 SV=1 #	2
ALANVNIGSLIC*NVGAGGPAPAAGAAPAGGPAPSTAAAPAEK		1.35554343	P05386	P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 #	2
ANC*IDSTASAEAVFASEVKK	C268 C183	1.35552489	M0QXL5 M0R299 P22087 M0R2Q4	M0QXL5 rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 # M0R299 rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 # P22087 rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2 # M0R2Q4 rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 #	2
NC*IVLIDSTPYR		1.3538717	P62241	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 #	2
YSTGSDSASFHTTPSMC*LNPDLGGPPLEAYTIQGQY	C217	1.35384729	Q15366 Q15366	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 # Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 #	2
LGEWVGLC*K		1.35382857	P25398	P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 #	2
C*ASQVGMTAPGTR	C215 C204	1.35264814	Q99439 B4DDF4 B4DUT8	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo	2

				sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 #	
TTSSANNPNLMYQDEC*DR	C586 C507 C505	1.35035001	Q92841 H3BLZ8 Q92841 Q92841 Q92841	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 # Q92841-2 Isoform 3 of Probable ATP- dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 # Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 # Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 #	2
ISLGLPVGAVINC*ADNTGAK		1.34593607	P62829	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 #	2
AYGGSMC*AK		1.34565126	P49207	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 #	2
VVNSETPVVVDFHAQWC*GPCK	C90	1.34546552	Q99757 F8WDN2	Q99757 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 # F8WDN2 Thioredoxin# mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 #	2
GVPGAIVNVSSQC*SQR	C137	1.34471115	Q7Z4W1 J3QS36 J3KS22	Q7Z4W1 L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 # J3QS36 L-xylulose reductase (Fragment) OS=Homo sapiens	2

				GN=DCXR PE=1 SV=1 # J3KS22 L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=1 SV=7 #	
GC*LWALNPAKIDK		1.34453256	O15353	O15353 Forkhead box protein N1 OS=Homo sapiens GN=FOXN1 PE=2 SV=1 #	2
DLC*FSPGLMEASHVVNDVNEAVQLVFR	C362	1.3424977	Q9BXW7 Q9BXW7	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 # Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 #	2
HGFC*GIPITDTGR		1.33773601	P12268	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 #	3
ASDHGWVC*DQR	C309	1.33684927	Q9HC36	Q9HC36 rRNA methyltransferase 3# mitochondrial OS=Homo sapiens GN=RNMTL1 PE=1 SV=2 #	2
AVC*MLSNTTAVAEAWAR	C376	1.33065439	Q9BQE3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #	3
HIGDGC*CLTR	C202	1.32887276	A0A087WZT2 Q6UX53	A0A087WZT2 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=1 # Q6UX53 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=2 #	3
SDLGPC*EK		1.32842532	D6RDI2 J3KPP4 O95232	D6RDI2 Luc7-like protein 3 (Fragment) OS=Homo sapiens GN=LUC7L3 PE=1 SV=1 # J3KPP4 Cisplatin resistance-associated overexpressed protein# isoform CRA_b OS=Homo sapiens GN=LUC7L3 PE=1 SV=1 # O95232 Luc7-like protein 3 OS=Homo	2

				sapiens GN=LUC7L3 PE=1 SV=2 #	
LPITVLNGAPGFINLC*DALNAWQLVK	C240	1.32837373	P31939 P31939	P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 # P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC #	2
VDEFPLC*GHMVSDEYEQLSSEALEAAR	C49	1.32795576	X1WI28 P27635	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 # P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 #	3
IISNASC*TTNCLAPLAK	C152	1.32735267	P04406	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 #	3
DLTTAGAVTQC*YR		1.32663642	Q02543	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 #	2
SAC*SLESNLEGLAGVLEADLPNYK	C44	1.32282302	Q09161	Q09161 Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 #	2
KITAFVPNDGC*LNFIEENDEVLVAGFGR		1.32248898	P62266	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 #	2
TGC*TFPEKPDFH	C318 C336	1.3221859	P55263 P55263 P55263	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK # P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 # P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK #	3
NQSFC*PTVNLDKLWTLVSEQTR	C70	1.32205485	P46776 E9PLL6 E9PJD9	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 # E9PLL6 60S ribosomal	3

				protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 # E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 #	
SGEEDFESLASQFSDC*SSAK	C113	1.32123313	K7EN45 K7EMU7 Q13526	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 # K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 # Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 #	2
SPWLAGNELTVADVVLWSVLQQIGGC*SVTPANVQR		1.32023056	Q13155	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 #	2
VNQAIWLLC*TGAR	C155	1.31946636	P46782 M0R0R2 M0R0F0	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 # M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 # M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 #	3
AC*DLPAAVHFPDTER		1.31869299	H7BXI1	H7BXI1 Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 #	2
YYALCGFGGVLSC*GLTHTAVVPLDLVK		1.31406687	Q00325	Q00325-2 Isoform B of Phosphate carrier protein# mitochondrial OS=Homo sapiens GN=SLC25A3 #	2
EC*LPLIIFLR		1.31288878	P62701	P62701 40S ribosomal protein S4# X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 #	3
VLVTTNVC*AR	C392	1.31162782	Q9UMR2	Q9UMR2-3 Isoform 3 of ATP-	2

	C393 C367 C310		Q9UMR2 Q9NUU7 Q9NUU7 H3BQK0 F6QDS0 I3L352	dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B # Q9UMR2 ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 # Q9NUU7- 2 Isoform 2 of ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A # Q9NUU7 ATP- dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 # H3BQK0 ATP- dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 # F6QDS0 HCG2043426# isoform CRA_b OS=Homo sapiens GN=hCG_2043426 PE=1 SV=1 # I3L352 ATP-dependent RNA helicase DDX19A (Fragment) OS=Homo sapiens GN=DDX19A PE=1 SV=1 #	
SYC*AEIAHNVSSK	C114 C96	1.31029315	P62910 F8W727 D3YTB1	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 # F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 # D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 #	2
TAFQEALDAAGDKLVVDFSATWC*GPCK		1.30833711	P10599	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 #	2
LC*YVALDFEQEMATAASSSSLEK		1.30393158	P60709 P63261 Q6S8J3	P60709 Actin# cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 # P63261 Actin# cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 # Q6S8J3 POTE ankyrin domain family member E	3

				OS=Homo sapiens GN=POTEE PE=1 SV=3 #	
VRPSTGNSASTPQSQC*LPSEIEVK	C131	1.30323394	Q9UJX3 Q9UJX3	Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 # Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 #	2
AATGEEVSAEDLGGADLHC*R		1.30276264	Q9HCC0	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain# mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 #	2
PGHLQEGFGC*VVTNRFDQLFDDSDPFEVLK	C11	1.29912919	Q8NC51 Q8NC51 Q8NC51 Q8NC51	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 # Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 # Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 #	3
C*ASQSGMTAYGTR	C166 C164 C175	1.29891305	Q99439 B4DDF4 B4DUT8 A0A087X271	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 # B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 # A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 #	3
LC*VQNSPQEAR	C150	1.29620031	P33240	P33240-2 Isoform 2 of Cleavage	3

			P33240 E7EWR4 E9PID8 A0A0A0MT56	stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 # P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 # A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 #	
PC*SEETPAISPSKR	C3	1.29615867	P33316 H0YNJ9	P33316-2 Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase# mitochondrial OS=Homo sapiens GN=DUT # H0YNJ9 Deoxyuridine 5'- triphosphate nucleotidohydrolase# mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=1 #	2
LDINLLDNVVNC*LYHGEGAQQR		1.29506246	O14980	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 #	2
NMMAAC*DPR	C285 C650 C303 C266	1.29454224	Q13509 Q13885 P68371 A6NNZ2 A0A0B4J269 Q9BVA1 Q3ZCM7 P04350 K7ESM5 Q5JP53 Q9BUF5	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 # Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 # P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 # A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 # A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 # Q9BVA1	3

				Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 # Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 # P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 # K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 # Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 # Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 #	
IAVHC*TVR	C72	1.29366889	P62913 Q5VVC8 P62913	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 # Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 # P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 #	2
C*PQVEEAIVQSGQKK	C146	1.29209712	Q9BVP2 Q9BVP2	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 # Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 #	2
SQAPC*ANKDEADLSSK	C300	1.2914237	Q96SK2 Q96SK2	Q96SK2-2 Isoform 2 of Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 # Q96SK2 Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 #	2
C*LGHPPEEFYNLVR		1.29111679	P37268	P37268 Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1	2

				SV=1 #	
NTVLC*NVVEQLQADLAR	C70	1.2908252	Q14258	Q14258 E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 #	2
AFQYVETHGEVC*PANWTPDSPTIKPSAASK		1.28901553	P30048	P30048 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 #	3
QAVLGAGLPSTPC*TTINK	C119	1.28885679	P24752	P24752 Acetyl-CoA acetyltransferase# mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 #	3
GTPEQPQC*GFSNAVQILR	C67	1.2866097	Q86SX6	Q86SX6 Glutaredoxin-related protein 5# mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 #	3
ADHQPLTEASYVNLPTIALC*NTDSPLR	C148	1.28569661	A0A0C4DG17 C9J9K3 P08865	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 # C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 # P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 #	3
GSDELFSTC*VTNGPFIMSSNSASAANGNDSKK	C23	1.28503662	A0A0U1RRM4 P26599 P26599 P26599	A0A0U1RRM4 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 # P26599-3 Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 # P26599-2 Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 # P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 #	3

AYHEQLTVAEITNAC*FEPANQMVK	C295 C365	1.28267065	Q9BQE3 F5H5D3	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 # F5H5D3 Tubulin alpha- 1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 #	2
INPYMSSPC*HIEMILTEK	C106 C144	1.28196342	J3KRX5 J3QLC8 A0A087WXM6 P18621 A0A0A6YYL6 J3QQT2 P18621	J3KRX5 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # J3QLC8 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=1 # A0A087WXM6 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 # A0A0A6YYL6 Protein RPL17- C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 # J3QQT2 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 # P18621-3 Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 #	2
YIYDQC*PAVAGYGPIELPDYNR	C453	1.28086198	P31930	P31930 Cytochrome b-c1 complex subunit 1# mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 #	2
C*ELSSSVQTDINLPYLTMDSGPK		1.27796511	P38646	P38646 Stress-70 protein# mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 #	3
GC*LLYGPPGTGK		1.27436825	A0A087X2I1 P62333	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 # P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 #	3

ALNALC*DGLIDELNQALK		1.27434754	P30084	P30084 Enoyl-CoA hydratase# mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 #	3
NTPSFLIAC*NK	C179	1.27116999	Q9Y5M8	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 #	2
C*MPTFQFFK		1.27070282	P10599	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 #	3
TGNGPMSVC*GR	C493	1.27005913	O95793 O95793 O95793 A0A087X1A5 Q5JW30	O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 # O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 # O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 # A0A087X1A5 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 # Q5JW30 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 #	2
HELQANC*YEEVKDR	C139 C177	1.26932573	E9PK25 G3V1A4 P23528	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 # G3V1A4 Cofilin 1 (Non-muscle)# isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 # P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 #	3
AFAFVTFADDQIAQSLC*GEDLIK	C244	1.26849554	A0A087X260 A0A087WYY0 B1AKP7	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 #	2

			Q13148 G3V162	A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 # G3V162 TAR DNA binding protein# isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 #	
LTPGC*EAEAETEAICFFVQQFTDMEHNR	C2359	1.26429021	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #	2
LECVEPNC*R		1.26300307	Q969Q0	Q969Q0 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 #	2
SYC*NDQSTGDIK	C106	1.26284516	P00492	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 #	2
ATC*APQHGAPGPGPADASK	C2516 C2535	1.26183717	P21333 A0A087WWY3 Q60FE5 P21333	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA # A0A087WWY3 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 # Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 # P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 #	2
ATYDKLC*K		1.26161979	P62851	P62851 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 #	2
GSC*STEVEKETQEK	C69	1.26098754	O75348	O75348 V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 #	2
TVDSQGPTPVC*TPTFLER		1.25809516	Q9BYG3	Q9BYG3 MKI67 FHA domain-	2

				interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 #	
LC*YVALDFEQEMAMVASSSSLEK	C880	1.25597356	P0CG39	P0CG39 POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 #	3
VFIMDSC*DELIPEYLNfir	C366	1.25136211	P08238	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 #	3
HC*SQVDSVR	C112	1.24909716	Q14247 Q14247 Q14247	Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN # Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 # Q14247-2 Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN #	2
AAAPAPEEEMDEC*EQALAAEPK	C266	1.24801537	P26641 P26641	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 # P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G #	2
EKTAC*AINK	C293	1.2460795	Q8NCA5 E9PH82 Q52LJ0 Q8NCA5 Q52LJ0	Q8NCA5-2 Isoform 2 of Protein FAM98A OS=Homo sapiens GN=FAM98A # E9PH82 Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1 # Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 # Q8NCA5 Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1 # Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B #	2
SGTIC*SSELPGAFAAGFHLNEHLYNMIIR	C200	1.24306972	A0A0C4DGQ5 P04632 K7ELJ7	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # P04632 Calpain small	2

				subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 # K7ELJ7 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 #	
TASISSSPSEGTPTVGSYGC*TPQSLPK	C787	1.24042598	Q6PKG0 Q6PKG0	Q6PKG0-3 Isoform 2 of La-related protein 1 OS=Homo sapiens GN=LARP1 # Q6PKG0 La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 #	3
EVIAVSCGPAQC*QETIR	C162	1.23744029	P38117 P38117	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 # P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB #	2
NC*PHVVVGTPGR	C164	1.23698375	O00148	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 #	3
SC*PSFSASSEGR	C9	1.2364364	D6RCP9 P27707 D6RFG8 D6RG38	D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 # D6RG38 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 #	2
GLIAAIC*AGPTALLAHEIGFGSK	C86	1.23001091	Q99497 K7ELW0 K7EN27	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 # K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 # K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 #	2

LYYFQYPC*YQEGLR		1.22870856	Q9NRW3	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 #	3
GC*WDSIHVVEVQEK	C135 C176	1.22164672	P47756 P47756 B1AK88 B1AK87 B1AK85	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 # P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB # B1AK88 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK87 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 # B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 #	2
SCYDLSC*HAR		1.21645888	P41250	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 #	2
VGSFC*LSEAGAGSDSFALK	C73	1.21430515	P45954 P45954	P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB # P45954 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 #	2
AINC*ATSGVVGLVNCLR	C1448	1.21332206	P49327	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 #	2

TSAVPSPC*GK	C260	1.21330821	P49748 P49748 P49748	P49748-3 Isoform 3 of Very long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADVL # P49748 Very long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 # P49748-2 Isoform 2 of Very long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Homo sapiens GN=ACADVL #	2
INEIVYFLPFC*HSELIQLVNK	C513 C371 C572	1.21132483	Q9H078 Q9H078 Q9H078 Q9H078 Q9H078 H0YGM0	Q9H078 Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1 # Q9H078-4 Isoform 4 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-2 Isoform 2 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-5 Isoform 5 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # Q9H078-3 Isoform 3 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB # H0YGM0 Caseinolytic peptidase B protein homolog (Fragment) OS=Homo sapiens GN=CLPB PE=1 SV=1 #	2
IGFPETEEEEIEIASNSDC*IFPSAPDVK	C353	1.2085197	Q9Y3F4 Q9Y3F4	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP # Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo	2

				sapiens GN=STRAP PE=1 SV=1 #	
IVGYFVSGC*DPSIMGIGPVP AISGALK	C287	1.20678041	A0A0B4J2A4 P42765	A0A0B4J2A4 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 # P42765 3-ketoacyl-CoA thiolase# mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 #	2
RGPC*IIYNEDNGIIK	C208	1.20670047	P36578	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 #	2
AALVTSFC*MFKYMALYSMIQR	C542	1.20030456	H0Y4Z2	H0Y4Z2 Cation-transporting ATPase (Fragment) OS=Homo sapiens GN=ATP13A4 PE=1 SV=1 #	2
ESLNASIVDAINQAADC*WGIR	C167	1.20004754	Q9UJZ1	Q9UJZ1 Stomatin-like protein 2# mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 #	2
EEHLC*TQR		1.19846195	J3KN67	J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 #	2
GC*GVVKFESPEVAER		1.19669217	P52272 P52272 A0A087X0X3	P52272 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 # P52272-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM # A0A087X0X3 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=1 #	3
KC*SASNR	C17	1.18869135	Q8WVC2 Q9BYK1 P63220	Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # Q9BYK1 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 # P63220 40S ribosomal protein S21 OS=Homo	2

				sapiens GN=RPS21 PE=1 SV=1 #	
TPC*SSLLPLLNAHAATSGK	C307 C367 C397	1.17507629	B8ZZZ7 Q9NUQ6 A0A0A0MSG5 Q9NUQ6 Q9NUQ6 Q9NUQ6	B8ZZZ7 DNA polymerase-transactivated protein 6# isoform CRA_b OS=Homo sapiens GN=SPATS2L PE=1 SV=1 # Q9NUQ6-4 Isoform 4 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L # A0A0A0MSG5 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=1 # Q9NUQ6 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 # Q9NUQ6-2 Isoform 2 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L # Q9NUQ6-3 Isoform 3 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L #	2
VSLDPELEEALTSASDTELC*DLAAILGMHNLITNTK	C132	1.17069609	Q9NYL9	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 #	3
FDPTQFQDC*IIQGLTETGTDLEAVAK	C35 C39	1.16681369	Q7L1Q6 C9IZ80 Q7L1Q6 Q7L1Q6 Q7L1Q6	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 # C9IZ80 Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=1 # Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 # Q7L1Q6-2 Isoform 2 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 #	2

LGGS LIVAFEGC*PV	C146	1.15762988	P60981 P60981	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN # P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 #	2
TQYSCYC*CK	C229	1.15467068	Q9UGI8 Q9UGI8	Q9UGI8 Testin OS=Homo sapiens GN=TES PE=1 SV=1 # Q9UGI8-2 Isoform 2 of Testin OS=Homo sapiens GN=TES #	2
IC*PVEFNPNFVAR		1.15353869	Q9UI30 F5GX77	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 # F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 #	2
TPSYSISSTLNPQAPEFILGC*TASK	C142	1.14619275	Q14694 H3BQC6 Q14694 Q14694	Q14694-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 # H3BQC6 Ubiquitin carboxyl- terminal hydrolase 10 (Fragment) OS=Homo sapiens GN=USP10 PE=1 SV=1 # Q14694 Ubiquitin carboxyl- terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 # Q14694-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 #	2
ASVGFGGSC*FQK	C209	1.14288174	O60701 O60701	O60701 UDP-glucose 6- dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 # O60701-2 Isoform 2 of UDP-glucose 6- dehydrogenase OS=Homo sapiens GN=UGDH #	2
NTGQTC*VCSNQFLVQR		1.13090774	C9J8Q5 P01763	C9J8Q5 Succinate-semialdehyde dehydrogenase# mitochondrial	2

			P51649 P51649	OS=Homo sapiens GN=ALDH5A1 PE=1 SV=1 # P01763 Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1 # P51649 Succinate- semialdehyde dehydrogenase# mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 # P51649- 2 Isoform 2 of Succinate- semialdehyde dehydrogenase# mitochondrial OS=Homo sapiens GN=ALDH5A1 #	
FQSSAVMALQEASEAYLVGLFEDTNLC*AIHAK		1.12440124	Q71DI3	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 #	2
AGAVVAVPTDTLYGLACAASC*SAALR	C99	1.11060194	Q86U90	Q86U90 YrdC domain-containing protein# mitochondrial OS=Homo sapiens GN=YRDC PE=1 SV=1 #	3
AVLLASDAQEC*TLEEVVER	C332	1.10310789	Q27J81 Q27J81	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 # Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 #	2
FQSSAVMALQEACEAYLVGLFEDTNLC*AIHAK	C111	1.07958576	P68431	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 #	2
NMITGTSQADC*AVLIVAAGVGEFEAGISK		1.07883348	P68104 Q05639 A0A087WVQ9	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 # Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 # A0A087WVQ9 Elongation factor 1- alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 #	2
GNHEC*ASINR	C83 C126	1.04910159	P62136 P62140 P62136	P62136-2 Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA # P62140	3

				Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 # P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 #	
LC*DFGVSGQLIDSMANSFVGTR	C207 C211 C114	1.0352245	G5E9C7 Q02750 P36507 Q02750	G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 # P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 # Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 #	2
SC*GSSTPDEFPTDIPGK		1.0186588	P41091	P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 #	2
GTLTLC*PYHSDR	C620	0.9961605	Q13200 Q13200 Q13200	Q13200-2 Isoform 2 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 # Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 # Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 #	2

LSLDGQNIYNAC*CTLR	C250 C281	0.94660721	A0A0U1RRM4 P26599 P26599 P26599	A0A0U1RRM4 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 # P26599-3 Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 # P26599-2 Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 # P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 #	2
ADASSTPSFQQAFASSC*TISSNGPGQR	C688	0.9392041	Q68CZ2 Q68CZ2	Q68CZ2-2 Isoform 2 of Tensin-3 OS=Homo sapiens GN=TNS3 # Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 #	2
STLTDSLVC*K	C41	0.93733209	P13639	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 #	3
SDITKLEVDAIVNAANSSLLGGGGVDGC*IHR	C186	0.90524177	Q9BQ69	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 #	2
LC*EPEVLNSLEETYSPPFR	C261 C177 C224	0.9025738	H0YJA2 Q6PJT7 Q6PJT7 G3V5I6 Q6PJT7 G3V256 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7 Q6PJT7	H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo	2

				sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 # Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 # Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 #	
C*PAPPRGPPAPAPEVEELAR	C161	0.80715207	P48681	P48681 Nestin OS=Homo sapiens GN=NES PE=1 SV=2 #	2
AAC*LESAQEPAGAWGNK	C53	0.75933034	A0A024R4E5	A0A024R4E5 High density lipoprotein binding protein (Vigilin)# isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1 #	2
LHTGPLPEQC*R	C163	0.68394162	A0JLT2 J3KR33 A0JLT2	A0JLT2-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 # J3KR33 Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 PE=1 SV=1 # A0JLT2 Mediator of RNA polymerase II	2

				transcription subunit 19 OS=Homo sapiens GN=MED19 PE=1 SV=2 #	
FQSAAGALQEASEAYLVGLFEDTNLC*A		0.66202651	K7EK07 P84243	K7EK07 Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1 # P84243 Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 #	2
FQSSAVMALQEAREAYLVGLFEDTNLC*AIHAK	C111	0.64596116	Q5TEC6	Q5TEC6 Histone H3 OS=Homo sapiens GN=HIST2H3PS2 PE=1 SV=1 #	2
HLNEIDLFHC*IDPNDSK	C62 C58	0.59088167	A0A087WYT3 Q15185 Q15185	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 # Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 #	2
QC*PIMDPAWEAPEGVPIDAIIFGGR	C297	0.28659591	B4DW73 Q16822	B4DW73 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 # Q16822 Phosphoenolpyruvate carboxykinase [GTP]# mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 #	3
SEC*DQDYIPETDQDC*SMSPCPQRTPDSGLAQHPFQNEDYR	C1290 C1250 C1278 C1262	0.11891909	Q9P2N4 Q9P2N4 H0Y859 Q9P2N4	Q9P2N4 A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 PE=1 SV=4 # Q9P2N4-1 Isoform 2 of A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 # H0Y859 A disintegrin and	2

				metalloproteinase with thrombospondin motifs 9 (Fragment) OS=Homo sapiens GN=ADAMTS9 PE=4 SV=1 # Q9P2N4-4 Isoform 4 of A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 #	
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Table S2 (ii) isoTOP-ABPP data: DKM 3-30 total raw data

peptide	PTM index	run information	ratios	average area ratios	protein
LQDAFSSIGQSC(464.28596)HLDLPQIAVVGGQSAGK	C27,NA,NA,C27,NA,NA	;;X;X;	1.20216;;X;X;	1.20216	P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 , P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 ,
LVVPASQC(464.28596)GSLIGK	NA,C109,C109,C109,NA	;;;;;	1.38602;;1.41174;;1.27579;;	1.38602	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,
LQDAFSSIGQSC(464.28596)HLDLPQIAVVGGQSAGK	C27,NA,NA,C27,NA,NA	;;X;X;	1.423;;X;X;	1.423	P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 , P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 ,
QAVLGAGLPSTPC(470.29977)TTINK	C119,NA,NA	;;;;;;;	1.40775,1.52669;;1.04798,1.38136;;1.18532,1.30164;;	1.3415	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
QAVLGAGLPSTPC(470.29977)TTINK	C119,NA,NA	;;X;X;	2.04699;;X;X;	2.04699	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
TC(464.28596)YPLESRPSLS LGTITDEEM(15.994915)K	C1921,M1940,NA	;;X;X;	1.66816;;X;X;	1.66816	A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 ,
LHYGTDPC(464.28596)TGQPFRLFVSVR	C137,NA,C139,NA	;;X;X;	1.43996;;X;X;	1.43996	Q8NFF5 FAD synthase OS=Homo sapiens GN=FLAD1 PE=1 SV=1 , Q8NFF5-3 Isoform 3 of FAD synthase OS=Homo sapiens GN=FLAD1 , Q8NFF5-2 Isoform 2 of FAD synthase OS=Homo sapiens GN=FLAD1 ,
M(15.994915)VAAVAC(464.28596)AQVPK	NA,NA,NA	;;X;X;	1.27213;;X;X;	1.27213	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
STC(470.29977)SLTPALAA HFSENLIK	NA,NA,NA,NA,NA	;;X;X;	0.9379;;X;X;	0.9379	Q9BTA9 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=3 , Q9BTA9-

					5 Isoform 4 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC , Q9BTA9-2 Isoform 2 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC , A0A0A0MRT2 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=1 ,
C(470.29977)PGGRNPWT GVSQFLQTSQK	C198,NA	,,X;X;	1.51195,,X;X;	1.51195	Q99447-3 Isoform 3 of Ethanolamine-phosphate cytidyltransferase OS=Homo sapiens GN=PCYT2 ,
IPDIVLWPTC(470.29977)H DDVVK	NA,NA,NA	U,,X;X;	1.01328,,X;X;	1.01328	O00116 Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1 ,
ENFDEVVNDADIILVEFYAP WC(464.28596)GHCKK	C206,NA	U,,X;X;	1.37444,,X;X;	1.37444	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 ,
THPSAAVPVC(470.29977) PR	C361,NA,NA	,,X;X;	1.38398,,X;X;	1.38398	Q3KQU3 MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1 , Q3KQU3-2 Isoform 2 of MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 ,
M(15.994915)IC(470.2997 7)QEFWLDYPKSNQFFVEP FDSNMNR	M1,C3,NA,NA	U,,X;X;	1.86571,,X;X;	1.86571	Q12887-2 Isoform 2 of Protoheme IX farnesyltransferase, mitochondrial OS=Homo sapiens GN=COX10 ,
ADPDGPEAQAEAC(470.29 977)SGER	C18,NA	,,X;X;	1.62312,,X;X;	1.62312	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
SLHDALC(464.28596)VVK	NA,NA	,,X;X;	1.53352,,X;X;	1.53352	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 ,
M(15.994915)ETYC(470.2 9977)SSGSTDTSPVIDAVTH ALTATTPYTR	M284,C288,NA,NA	,,X;X;	1.43555,,X;X;	1.43555	Q02338 D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 ,
TGNGPM(15.994915)SVC(464.28596)GR	NA,M490,C493,NA,NA,NA ,NA	,,,,X;	1.11663,,1.44457,, X;	1.2806	O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 , O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , A0A087X1A5 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 , Q5JW30 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 ,

AVC(464.28596)M(15.994915)LSNTTAVAEAWAR	C376,M377,NA	,,,,;	1.52612,1.0769,,1.64111,,1.16241,,	1.344265	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
AVC(464.28596)M(15.994915)LSNTTAVAEAWAR	C376,M377,NA	,,;X;X;	2.30873,2.06293,,X;X;	2.18583	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
VIEASDVVLEVL DARDPLGC (470.29977)R	C144,C144,NA	,,;X;X;	2.14806,,;X;X;	2.14806	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
KLDTNSDGQLDFSEFLNLIG GLAM(15.994915)AC(470.29977)HDSFLK	M89,C91,NA	U,,;X;X;	1.63894,,;X;X;	1.63894	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
KLDTNSDGQLDFSEFLNLIG GLAM(15.994915)AC(470.29977)HDSFLK	M89,C91,NA	U,,;X;X;	1.64969,,;X;X;	1.64969	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
KLDTNSDGQLDFSEFLNLIG GLAM(15.994915)AC(470.29977)HDSFLK	M89,C91,NA	U,U,,;X;X;	1.99796,1.96508,,X;X;	1.98152	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
FQSSAVM(15.994915)ALQ EACEAYLVGLFEDTNLC(464.28596)AIHAK	M91,C111,NA	U,U,U,,;X;X;	1.43218,1.30674,1.42897,,1.20565,,X;	1.367855	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
YGAVDPLLALLAVPDMSSLA C(464.28596)GYLR	C223,NA	U,,;X;X;	1.48056,,;X;X;	1.48056	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 ,
SLEIC(464.28596)HPQER	C308,NA,NA,NA,C308,NA, C266,NA,NA	,,;X;X;	1.02646,,;X;X;	1.02646	Q9Y305 Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2 , Q9Y305-3 Isoform 3 of Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 , Q9Y305-4 Isoform 4 of Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 , Q9Y305-2 Isoform 2 of Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 ,
NMMAAC(464.28596)DPR	C303,NA,C303,C303,C650, C303,C303,NA,C266,C285, C303,NA	,,,,,;	3.34569,1.53692,0.07077,3.34569,1.53692,,1.1315,1.1315,;1.18433,1.18433,,	1.18433	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 , P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , A0A0B4J269 Uncharacterized protein

					OS=Homo sapiens PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
LAPILC(464.28596)DGTAT FVDLVPGR	NA,NA	,,X;X;	1.18474,,X;X;	1.18474	O43264 Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 ,
SDLGPC(464.28596)EK	NA,NA,NA,NA,NA	,,,X;	1.31351,,1.34351,; X;	1.32851	D6RDI2 Luc7-like protein 3 (Fragment) OS=Homo sapiens GN=LUC7L3 PE=1 SV=1 , J3KPP4 Cisplatin resistance-associated overexpressed protein, isoform CRA_b OS=Homo sapiens GN=LUC7L3 PE=1 SV=1 , O95232 Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 ,
HLFC(464.28596)PDLLR	NA,NA,C22,NA,NA,NA,NA, NA,NA,NA,NA,NA,C22,NA, C22,NA,NA	,,X;X;	1.06335,,X;X;	1.06335	Q9NUI1 Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 , Q4VXZ8 Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 , G3V0I9 2,4-dienoyl CoA reductase 2, peroxisomal, isoform CRA_a OS=Homo sapiens GN=DECR2 PE=1 SV=1 , A0A0J9YWI0 Peroxisomal 2,4-dienoyl-CoA reductase (Fragment) OS=Homo sapiens GN=DECR2 PE=1 SV=1 , A0A0J9YXZ6 Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 , Q9NUI1-2 Isoform 2 of Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 , A0A0J9YY83 Peroxisomal 2,4-dienoyl-CoA reductase (Fragment) OS=Homo sapiens GN=DECR2 PE=1 SV=1 ,
DYPLELFM(15.994915)AQ C(464.28596)YGNISDLGK	M146,C149,NA,M153,C15 6,NA,M175,C178,NA,NA, NA,NA,M153,C156,NA,NA	,,,X;X;	1.14713,1.35203,,X ;X;	1.24958	F5GXU9 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=BCKDHA PE=4 SV=1 , P12694-2 Isoform 2 of 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA , M0R0C8 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=4 SV=1 , H0YH31 2-oxoisovalerate

					dehydrogenase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=BCKDHA PE=4 SV=1 , F5H5P2 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 , P12694 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 ,
NM(15.994915)GLSPPASS TSTSSTC(464.28596)R	NA,NA	;;X;X;	1.0418;;X;X;	1.0418	Q9HC52 Chromobox protein homolog 8 OS=Homo sapiens GN=CBX8 PE=1 SV=3 ,
C(464.28596)PIIASLSFGAT R	C200,NA,NA,NA	;;X;X;	3.64848;;X;X;	3.64848	E9PSA5 Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3 (Fragment) OS=Homo sapiens GN=ALKBH3 PE=1 SV=1 , Q96Q83 Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3 OS=Homo sapiens GN=ALKBH3 PE=1 SV=1 , H0YDH4 Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3 (Fragment) OS=Homo sapiens GN=ALKBH3 PE=1 SV=1 ,
NISFPATGC(464.28596)QK	NA,NA	;;X;X;	1.17173;;X;X;	1.17173	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
QMAGC(470.29977)LEDCT R	C174,NA,NA	;;X;X;	1.54572;;X;X;	1.54572	O00411 DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 ,
NC(464.28596)IVLIDSTPYR QWYESHYALPLGR	NA,NA	;;X;X;	1.46061;;X;X;	1.46061	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
NC(464.28596)IVLIDSTPYR QWYESHYALPLGR	NA,NA	;;X;X;	1.37206;;X;X;	1.37206	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
VITVDGNIC(470.29977)TG K	NA,NA,NA	;;X;X;	1.41443;;X;X;	1.41443	E7ESZ7 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1 ,
SKDGVC(470.29977)VR	C185,NA,C185,NA	;;X;X;	1.73849;;X;X;	1.73849	P55786 Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 , E9PLK3 Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=1 , P55786-2 Isoform 2 of Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS ,
LQHINPLLPAC(464.28596) LNKEESK	NA,C325,NA	;;X;X;	1.77734;;X;X;	1.77734	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 , Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP ,
VDEFPLC(464.28596)GHM VSDEYEQLSSEALEAAR	C49,NA	;;X;X;	1.3691,1.4171;;X;X;	1.3931	P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,

LNQQQHPDC(470.29977)K	C239,NA	,,;,;	1.31155,,2.03605,,1.38684,;	1.38684	Q5T280 Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 ,
NLLC(464.28596)GFYGR	C247,NA,NA	,,;X;X;	0.9972,1.47833,,X;X;	1.237765	B0QYD3 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 , Q9UH17 DNA dC- dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=1 SV=1 ,
EGGQYGLVAAC(464.28596)AAGGQGHAMIVEAYPK	C436,NA,C436,NA,NA	,,;X;X;	1.8092,1.91428,,X;X;	1.86174	P55084 Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 , P55084-2 Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB ,
NTVLC(464.28596)NVVEQFLQADLAR	C70,NA	U,U,,;X;X;	1.37991,1.50733,,X;X;	1.44362	Q14258 E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 ,
SLVQNNCLSRPNIFLC(470.29977)PEIEPK	NA,NA,C145,NA,NA	,,;X;X;	1.77474,,X;X;	1.77474	Q8TAQ2-2 Isoform 2 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 , Q8TAQ2 SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 , Q8TAQ2-3 Isoform 3 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 , F8VXC8 SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 ,
AIYDTPC(470.29977)IQAESEKWQQALK	NA,NA	,,;X;X;	1.24735,,X;X;	1.24735	O00232 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 ,
SGEEDFESLASQFSDC(470.29977)SSAK	NA,C113,NA,NA	,,;,X;,;	1.4338,1.87857,1.4263,,X;1.16743,,;	1.43005	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 , K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 , Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 ,
GM(15.994915)YGIENEVFLSLPC(464.28596)ILNAR	NA,NA	U,U,,;X;X;	1.41691,1.49701,,X;X;	1.45696	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 ,
C(470.29977)PEALFQPSFLGMESCGIHETTFNSIM(15.994915)K	NA,NA,NA	,,;X;X;	1.45252,1.50897,,X;X;	1.480745	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
C(470.29977)PEALFQPSFLGMESCGIHETTFNSIM(15.994915)K	NA,NA,NA,NA,NA	,,;,X;,;	1.51924,1.75542,,X;1.019,,;	1.51924	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ,
C(464.28596)QGDGVSYEETTIPRPSAYHNLFLPLISR	C226,NA,C226,NA,NA	,,;X;X;	1.60598,,X;X;	1.60598	Q96RR1 Twinkle protein, mitochondrial OS=Homo sapiens GN=PEO1 PE=1 SV=1 , Q96RR1-2 Isoform 2 of Twinkle

					protein, mitochondrial OS=Homo sapiens GN=PEO1 ,
DLTTAGAVTQC(464.28596)YR	NA,NA	,,;,X;	1.17363,1.66503,,1.19482,,X;	1.19482	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 ,
TFVPAM(15.994915)TAIH GPPITAPVVC(470.29977)T R	M535,C549,NA,M646,C660,M580,C594,NA	,,;X;X;	1.62595,1.47068,,X;X;	1.548315	Q96RN5-3 Isoform 3 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 , Q96RN5-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 , Q96RN5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=2 , G3V1P5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=1 ,
GLPC(464.28596)TELFVAP VGASKR	C79,NA,C428,NA	,,;,;	1.51685,,1.68568,,1.07447,,	1.51685	H0Y901 Ladinin-1 (Fragment) OS=Homo sapiens GN=LAD1 PE=1 SV=1 , E9PDI4 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=1 , O00515 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 ,
ATDSKEPPGELC(470.29977)PDVLYR	NA,C46,NA,NA,NA	,;X;X;	0.71166,,X;X;	0.71166	Q9BUK6 Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 PE=1 SV=1 , Q9BUK6-2 Isoform 2 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 , Q9BUK6-3 Isoform 3 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 , Q9BUK6-7 Isoform 7 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 ,
ISLGLPVGAVINC(464.28596)ADNTGAK	NA,NA	,;X;,;	1.53064,,X;1.32304,,	1.42684	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 ,
C(470.29977)M(15.994915)PTFQFFKK	NA,NA	,;X;X;	1.32321,,X;X;	1.32321	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,
ISLGLPVGAVINC(464.28596)ADNTGAK	NA,NA	,,;,X;	1.42294,,1.13138,,X;	1.27716	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 ,
ISLGLPVGAVINC(464.28596)ADNTGAK	NA,NA	,;X;X;	1.49434,,X;X;	1.49434	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 ,
GLHDSC(464.28596)PGQAR	NA,NA	,;X;X;	1.98689,,X;X;	1.98689	Q32NC0 UPF0711 protein C18orf21 OS=Homo sapiens GN=C18orf21 PE=1 SV=1 ,
VPAFEGDDGFC(470.29977)VFESNAIYYVSNEELR	C68,NA,NA	,;X;X;	1.76908,,X;X;	1.76908	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
VQVM(15.994915)DAC(464.28596)LR	NA,NA	U,,X;X;	1.71623,,X;X;	1.71623	Q9UBF6 RING-box protein 2 OS=Homo sapiens GN=RN7 PE=1 SV=1 ,

AAVPLGGFLC(470.29977) NVADK	NA,NA,NA	U,,X;X;	1.21321,,X;X;	1.21321	Q7L8L6 FAST kinase domain-containing protein 5, mitochondrial OS=Homo sapiens GN=FASTKD5 PE=1 SV=1 ,
SLITSDKGFTVM(15.994915)TLESLEEIQDVSC(464.28596)AWK	M590,C603,NA	U,,X;X;	1.19925,,X;X;	1.19925	Q9BQ39 ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1 ,
GYWASLDASTQTTHLTPN NLIGC(464.28596)IIGR	C293,NA	U,,X;X;	1.66653,,X;X;	1.66653	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
SC(464.28596)PETLTHAVGM(15.994915)SESPIGPK	NA,NA	,,X;X;	4.88693,,X;X;	4.88693	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
ISGPNPLSC(470.29977)LK	NA,NA	U,,X;X;	1.83722,,X;X;	1.83722	Q9BRU9 rRNA-processing protein UTP23 homolog OS=Homo sapiens GN=UTP23 PE=1 SV=2 ,
KNM(15.994915)QITILTC(470.29977)R	M141,C148,M141,C148,NA	,,X;X;	2.55236,,X;X;	2.55236	O95456 Proteasome assembly chaperone 1 OS=Homo sapiens GN=PSMG1 PE=1 SV=1 , O95456-2 Isoform 2 of Proteasome assembly chaperone 1 OS=Homo sapiens GN=PSMG1 ,
VGLSGAPADAC(470.29977)JSTAQK	C394,NA	U,,X;X;	1.39474,,X;X;	1.39474	Q8NFW8 N-acylneuraminate cytidyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 ,
IHM(15.994915)GSC(470.29977)AENTAK	NA,NA,NA	U,,U,,U,,	1.50317,,1.39854,,1.26521,,	1.39854	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
TVDSQGPTPVC(464.28596)TPTFLER	NA,NA	,,,X;	1.29567,,1.22161,,X;	1.25864	Q9BYG3 MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 ,
ITSNC(470.29977)TIGLR	NA,C171,NA	,,X;X;	1.65814,,X;X;	1.65814	Q9UPT9-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 22 OS=Homo sapiens GN=USP22 , Q9UPT9 Ubiquitin carboxyl-terminal hydrolase 22 OS=Homo sapiens GN=USP22 PE=1 SV=2 ,
CC(470.29977)LTTCFNKPE DK	C145,NA	U,,X;X;	2.78417,,X;X;	2.78417	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
LC(470.29977)SSSSSDTSSR	NA,C385,NA,NA	,,X,,;	1.43558,,X;1.35822,,	1.3969	Q86WB0 Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 , Q86WB0-2 Isoform 2 of Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 , C9J0I9 Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 ,
EADQKEQFSQGSPSNC(464.28596)LETSIAEIFPLGK	C161,NA,C102,NA,NA	,,X;X;	1.61153,,X;X;	1.61153	Q9NQ88 Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 , A0A0U1RQD1 Chromosome 12 open reading frame 5, isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 ,

C(464.28596)PEALFQPCFL GMESCGIHETTFNSIM(15.9 94915)K	C957,M983,NA	,,X;X;	1000.0,,X;X;	1000	P0CG38 POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 ,
TWYVQATC(464.28596)AT QGTGLYEGLDWLSNELSKR	NA,NA	,,,X;X;	1.41838,1.54075,,X ;X;	1.479565	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
IDC(464.28596)FSEVPTSV FGEK	NA,NA	,,X;X;	1.47239,,X;X;	1.47239	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
TWYVQATC(464.28596)AT QGTGLYEGLDWLSNELSKR	NA,NA	,,X;X;	2.35394,,X;X;	2.35394	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
EM(15.994915)FPYEASTP TGISASC(464.28596)R	M308,C323,NA,NA,NA,NA ,NA,NA	,,,X;	1.5275,,1.49092,,X;	1.50921	G5E972 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 , P42167 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 , P42167-2 Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO ,
FTTSC(464.28596)M(15.9 94915)TGYSPLQLGLSSGG SGSYSPGVTYSPVSGYNK	C157,M158,C158,M159,N A	,,X;;	1.38633,,X;1.54421 ,,	1.46527	Q96SK2-2 Isoform 2 of Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 , Q96SK2 Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 ,
FTTSC(464.28596)M(15.9 94915)TGYSPLQLGLSSGG SGSYSPGVTYSPVSGYNK	C157,M158,C158,M159,N A	,,,X;	2.49273,,3.96536,, X;	3.229045	Q96SK2-2 Isoform 2 of Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 , Q96SK2 Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 ,
GRDDC(470.29977)GTFED TGPLLQFDYK	C268,NA,NA	,,X;X;	1.25016,,X;X;	1.25016	Q14684-2 Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B , Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 ,
SC(470.29977)PETLTHAVG M(15.994915)SESPIGPK	NA,NA	,,X;X;	5.87789,,X;X;	5.87789	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
VVNEINIEDLC(470.29977) LTK	NA,NA	,,X;X;	1.77807,,X;X;	1.77807	Q8N5K1 CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 ,
FHINWDNNM(15.994915) DRLEAIETQDPSLGC(470.2 9977)GLPLNCTPIK	NA,NA	,,X;X;	1.49789,,X;X;	1.49789	Q9NVP2 Histone chaperone ASF1B OS=Homo sapiens GN=ASF1B PE=1 SV=1 ,
NAGNC(464.28596)LSPAV IVGLLK	NA,NA,NA	,,X;X;	1.60848,,X;X;	1.60848	O43175 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 , Q5SZU1 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 ,

C(464.28596)ASQAGM(15.994915)TAYGTR	C132,M138,C127,M133,NA,NA	;;X;;	1.43834;;X;1.21765;;	1.327995	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 ,
NAGNC(464.28596)LSPAV IVGLLK	NA,NA,NA	;;X;X;	1.59068;;X;X;	1.59068	O43175 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 , Q5SZU1 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 ,
C(464.28596)ASQAGM(15.994915)TAYGTR	C132,M138,C127,M133,NA,NA	;;;X;	1.4204;;1.37162;;X;	1.39601	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 ,
HLYTLDGGDIINALC(470.29977)FSPNR	NA,NA	;;X;X;	1.0515;;X;X;	1.0515	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
LIDFLEC(464.28596)GK	C234,NA,NA	;;;X;	1.42229;;1.48242;;X;	1.452355	P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 , J3KTA4 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 ,
HLYTLDGGDIINALC(470.29977)FSPNR	NA,NA	;;;X;X;	1.40133,1.30863;;X;X;	1.35498	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
TC(470.29977)ATDLQTK	NA,NA,NA,NA,NA,NA,NA	;;X;X;	1.14738;;X;X;	1.14738	O95861-4 Isoform 4 of 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 , O95861 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1 , O95861-2 Isoform 2 of 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 ,
SLC(470.29977)NLEESITSA GR	NA,NA,NA	;;X;X;	3.26882;;X;X;	3.26882	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
LVILANNC(464.28596)PAL R	C52,C52,NA	;;X;X;	0.89752;;X;X;	0.89752	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 , E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 ,
YYDAIAC(464.28596)LK	NA,NA	;;X;X;	1.71926;;X;X;	1.71926	O00170 AH receptor-interacting protein OS=Homo sapiens GN=AIP PE=1 SV=2 ,
YGIIC(470.29977)MEDLIH EIYTVGKR	C186,NA,NA	;;;;	1.45835;;1.32431;;1.23287;;	1.32431	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,

FGVIC(470.29977)LEDLIE IAFPGK	NA,NA	U,U;;U;;X;	1.8804,1.89888;;1.9 7696;;X;	1.89888	Q6DKI1 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 ,
EITSLDTENIDEILNNADVAL VNFYADWC(464.28596)R	C58,NA	U,U;;X;X;	1.46801,1.37845;;X ;X;	1.42323	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 ,
EITSLDTENIDEILNNADVAL VNFYADWC(464.28596)R	C58,NA	U,U,U;;U;;X;	1.3721,1.43423,1.3 3471;;1.45585;;X;	1.403165	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 ,
YGIIC(470.29977)MEDLIH EIYTVGKR	C186,NA,NA	;;X;;	1.42511;;X;1.29311 ;;	1.35911	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
KESESC(464.28596)DC(46 4.28596)LQGFQLTHSLGG GTGSGMGTLISK	C127,C129,NA	;;X;X;	42.38156;;X;X;	42.38156	Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 ,
GLTDLSAC(470.29977)K	NA,NA	;;X;X;	1.38969;;X;X;	1.38969	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
GSDELFSTC(464.28596)VT NGPFIM(15.994915)SSNS ASAANGNDSKK	C23,M31,NA,C23,M31,NA ,NA	;;;;;	1.19968;;1.15851;;1 .30729;;	1.19968	A0A0U1RRM4 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 , P26599-3 Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 , P26599-2 Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 , P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
GSDELFSTC(464.28596)VT NGPFIM(15.994915)SSNS ASAANGNDSKK	NA,NA	;;X;X;	1.64832;;X;X;	1.64832	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
LLDLVQQSC(464.28596)N YK	NA,C30,NA	;;;;;	1.50427,0.98881;;1. 6128;;1.19104;;	1.347655	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 , P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 ,
VGIGRPAHPEAVQAHVLGC (470.29977)FSPAQELLPL LLDR	NA,NA	U;;X;X;	1.6685;;X;X;	1.6685	Q86Y79 Probable peptidyl-tRNA hydrolase OS=Homo sapiens GN=PTRH1 PE=1 SV=1 ,
VGLNAQAAC(464.28596)A PR	C157,NA	U;;X;X;	1.32042;;X;X;	1.32042	P48681 Nestin OS=Homo sapiens GN=NES PE=1 SV=2 ,
ECEHCDC(464.28596)LQG FQLTHSLGGGTGSGM(15.9 94915)GTLLISK	C129,M147,NA	;;X;X;	1.53157;;X;X;	1.53157	Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
SC(464.28596)SGVEFSTSG	C36,NA	;;X;X;	1.35017,1.99625;;X	1.67321	P45880 Voltage-dependent anion-selective channel protein

SSNTDTGKVTGTLETK			;X;		2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
STSTSEPTTGC(470.29977) SLK	C734,NA	U,,X;X;	1.54777,,X;X;	1.54777	Q8ND82 Zinc finger protein 280C OS=Homo sapiens GN=ZNF280C PE=1 SV=1 ,
GSDELFTSC(464.28596)VT NGPFIM(15.994915)SSNS ASAANGNSDK	NA,NA	,,,X;X;	1.43058,1.18751,,X ;X;	1.309045	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
AVC(470.29977)MLSNTTA IAEAWAR	NA,NA,NA,NA,NA,NA,C37 6,NA,NA	,,,,,;	1.56869,2.15152,,1. 48551,,1.34186,;	1.5271	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
AVC(470.29977)MLSNTTA IAEAWAR	NA,C376,NA,NA,NA,C376, NA,NA	,,,,,X;	1.91209,1.84488,,2. 04237,,X;	1.91209	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
LALNC(470.29977)VGGK	C187,NA,C187,NA,NA	,,X;X;	1.0803,,X;X;	1.0803	Q9BV79 Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR PE=1 SV=2 , Q9BV79-2 Isoform 2 of Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR ,
LC(470.29977)PGGQLPFL YGTEVHTDTNKIEEFLEAVL CPPR	NA,NA	U,,X;X;	1.38518,,X;X;	1.38518	O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 ,
C(470.29977)EFDSQASAP R	NA,NA	,,X;X;	1.34396,,X;X;	1.34396	O43542 DNA repair protein XRCC3 OS=Homo sapiens GN=XRCC3 PE=1 SV=1 ,

GPAVGIDLGTTYSC(464.28596)VGVFQHGK	C17,NA,NA,NA	;;X;X;	1.00551,0.64444,;X;X;	0.824975	P11142 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 , P11142-2 Isoform 2 of Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 , E9PKE3 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 ,
IIAVSFPAAGC(464.28596)SEESYLHNLQEVTR	NA,NA	;;X;X;	0.89495,;X;X;	0.89495	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
HFLIEC(470.29977)TPK	NA,NA	;;X;X;	1.41061,;X;X;	1.41061	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
IIAVSFPAAGC(464.28596)SEESYLHNLQEVTR	NA,NA	;;X;X;	1.34171,;X;X;	1.34171	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
VRNC(470.29977)SSPEFSK	C58,NA,C53,NA	;;X;X;	1.27564,;X;X;	1.27564	B0QZ18 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 , Q99829 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 , A6PVH9 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 ,
VLELVSITANKNTC(470.29977)PGDR	NA,NA,C391,NA,NA	;;X;X;	1.39405,;X;X;	1.39405	P34897 Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 , P34897-3 Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 ,
KM(15.994915)C(470.29977)LFAGFQR	NA,M574,C575,NA	;;X;X;	1.58339,;X;X;	1.58339	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
ADASSTPSFQQAFASSC(470.29977)TISSNGPGQR	C688,NA,NA	;;;X;	0.66619,;1.30468,;X;	0.985435	Q68CZ2-2 Isoform 2 of Tensin-3 OS=Homo sapiens GN=TNS3 , Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
SEHGPISFPESGQPEC(464.28596)LK	C295,NA,NA,C323,NA	;;X;X;	1.09398,;X;X;	1.09398	Q96ME7-3 Isoform 3 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 , Q96ME7 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=2 , Q96ME7-2 Isoform 2 of Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 , G3XAG1 Zinc finger protein 512 OS=Homo sapiens GN=ZNF512 PE=1 SV=1 ,
AVASQLDC(470.29977)NFLK	NA,NA,NA	;;X;;;	1.49482,;X;1.7003,;	1.59756	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 , P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 ,
AQLSGLQLQPC(470.29977)LYK	NA,NA	;;X;X;	1.17235,;X;X;	1.17235	O43159 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 ,

TILTLGVSTLGDVKNNQES DC(470.29977)VSK	NA,NA,NA	,,X;X;	1.61031,,X;X;	1.61031	A6NDG6 Glycerol-3-phosphate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 , H3BV17 Glycerol-3-phosphate phosphatase (Fragment) OS=Homo sapiens GN=PGP PE=1 SV=1 ,
IYLCDIGIPQQVFQEVGINYH SPFGC(464.28596)K	C499,NA	U,,X;X;	1.42885,,X;X;	1.42885	Q96F86 Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1 ,
YKWC(464.28596)EYGLTF TEK	C65,NA	,,X;X;	1.51329,,X;X;	1.51329	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
SWC(464.28596)PDCVQA EPVVR	NA,NA	,,,X;X;	1.45861,1.43251,,X; X;	1.44556	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 ,
SWC(464.28596)PDCVQA EPVVR	NA,NA	,,,,X;	1.42576,1.70616,,1. 50014,,X;	1.50014	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 ,
TASISSPSEGTPTVGSYGC(470.29977)TPQSLPK	C787,C787,NA	,,,,,;	1.30137,,1.22523,,1. .197,,;	1.22523	Q6PKG0-3 Isoform 2 of La-related protein 1 OS=Homo sapiens GN=LARP1 , Q6PKG0 La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 ,
LCLNIC(470.29977)VGESG DR	C25,NA,NA	,,X;X;	1.55575,,X;X;	1.55575	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 , P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 ,
KVAEPELM(15.994915)GT PDGTC(470.29977)YPPPP VPR	NA,M1882,C1889,NA	,,X;X;	0.91065,,X;X;	0.91065	F8VPD4 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 , P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 ,
PLCTKMAFLCAAC(464.285 96)GEIQSFPLPDGK	NA,C245,NA,C245,NA	,,X;X;	1.19725,,X;X;	1.19725	Q9UJA3-3 Isoform 3 of DNA helicase MCM8 OS=Homo sapiens GN=MCM8 , Q9UJA3-4 Isoform 4 of DNA helicase MCM8 OS=Homo sapiens GN=MCM8 , Q9UJA3 DNA helicase MCM8 OS=Homo sapiens GN=MCM8 PE=1 SV=2 , Q9UJA3-2 Isoform 2 of DNA helicase MCM8 OS=Homo sapiens GN=MCM8 ,
SDPSIVLLQC(470.29977) DIQK	C187,NA	U,,X;X;	1.69509,,X;X;	1.69509	P62760 Visinin-like protein 1 OS=Homo sapiens GN=VSNL1 PE=1 SV=2 ,
C(470.29977)ASQSGMTAY GTR	C175,C164,NA,NA	,,X;X;	1.54838,,X;X;	1.54838	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
SDPSIVLLQC(470.29977) DIQK	C187,NA	U,U,U,,X;X;	2.40427,3.47833,3. 11318,,X;X;	3.11318	P62760 Visinin-like protein 1 OS=Homo sapiens GN=VSNL1 PE=1 SV=2 ,
C(470.29977)ASQSGMTAY GTR	C175,C164,NA,C166,NA	,,,,;	1.3711,,1.64964,,1. 1507,,;	1.3711	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,

					B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
IYDPEIPTDEVENEFQSQQN ISASVPNPVIC(470.29977) NSM(15.994915)FPVEDV FR	C259,M262,NA,NA,NA	,;X;X;	1.09239,,X;X;	1.09239	Q14966-3 Isoform 3 of Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 , Q14966-4 Isoform 4 of Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 , Q14966 Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 PE=1 SV=2 ,
VLLSICSLLC(464.28596)DP NPDDPLVPEIAR	C113,NA,NA	,;X;X;	1.52543,,X;X;	1.52543	P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 , P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 ,
NFNYHILSPC(464.28596)D LSNYTDLAM(15.994915)S TVK	C461,M471,NA,NA,NA,NA	,,;,;	1.35086,,1.67422,,1.16471,;	1.35086	G5E9W3 Cleavage and polyadenylation specific factor 3, 73kDa, isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 , Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 ,
ATVAPEDVSEVIFGHVLAAG C(464.28596)GQNPVR	NA,NA,NA	,;X;X;	1.40645,,X;X;	1.40645	Q9BWD1 Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 ,
PEALFQPC(470.29977)FLG MESCGIHETTFNSIM(15.99 4915)K	C965,M983,NA	,;X;X;	0.03138,,X;X;	0.03138	P0CG38 POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 ,
KC(470.29977)STPEEIK	C6,NA,NA	,;X;X;	1.58861,,X;X;	1.58861	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN , P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 ,
M(15.994915)WQALTLLFS LLPC(470.29977)ALVQLTL LFVHRDLR	M35,C48,NA	U,,X;X;	0.33671,,X;X;	0.33671	P51811 Membrane transport protein XK OS=Homo sapiens GN=XK PE=1 SV=5 ,
FNNWGGSLSLGHPFGATG C(464.28596)R	C413,NA,C413,NA,NA	,,;,X;	1.53599,,1.46614,,X;	1.501065	P55084 Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 , P55084-2 Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB ,
FNNWGGSLSLGHPFGATG C(464.28596)R	C413,NA,C413,NA,NA	,;X;X;	2.81227,,X;X;	2.81227	P55084 Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 , P55084-2 Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB ,
AAGPLLTDEC(470.29977)R	C199,NA	U,,X;X;	0.85042,,X;X;	0.85042	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,

M(15.994915)KLNISFPAT GC(470.29977)QK	NA,NA	,,X;X;	1.46045,,X;X;	1.46045	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
NLAVAM(15.994915)C(47 0.29977)SR	NA,NA,M54,C55,M54,C55 ,NA	,,X;X;	1.15576,,X;X;	1.15576	Q5JS54-3 Isoform 3 of Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 , Q5JS54 Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 PE=2 SV=2 , Q5JS54-2 Isoform 2 of Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 , D6RB92 Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 PE=1 SV=1 ,
SAC(470.29977)SLESNLEG LAGVLEADLPNYK	C44,NA	,,X;;	1.46423,,X;1.19017 ,,	1.3272	Q09161 Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 ,
LC(464.28596)DFGSATTIS HYPDYSWSAQR	NA,C111,NA	,,X;X;	2.22798,,X;X;	2.22798	O14976 Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=1 SV=2 , O14976-2 Isoform 2 of Cyclin-G- associated kinase OS=Homo sapiens GN=GAK ,
GEAYNLFEHNC(464.28596)NTFSNEVAQFLTGR	C108,NA	U,,X;X;	1.58602,,X;X;	1.58602	Q6ICB0 Desumoylating isopeptidase 1 OS=Homo sapiens GN=DESI1 PE=1 SV=1 ,
ASVGFGGSC(470.29977)F QK	NA,C209,NA	,,X;X;	1.23765,,X;X;	1.23765	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 , O60701-2 Isoform 2 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH ,
GEAYNLFEHNC(464.28596)NTFSNEVAQFLTGR	C108,NA	U,,X;X;	1.60821,,X;X;	1.60821	Q6ICB0 Desumoylating isopeptidase 1 OS=Homo sapiens GN=DESI1 PE=1 SV=1 ,
LLQC(464.28596)DPSSASQ F	NA,NA	,,X;X;	1.61386,,X;X;	1.61386	P37235 Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3 ,
VASGSTATAAAGPSC(470.2 9977)ALK	NA,NA,NA	,,X;X;	1.64845,,X;X;	1.64845	P41134-2 Isoform ID-B of DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 , P41134 DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 PE=1 SV=3 ,
FDTGNLC(470.29977)M(1 5.994915)VTGGANLGR	NA,NA,NA	U,,X;X;	1.56678,,X;X;	1.56678	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
NLSDLIDLVPSC(470.2997 7)EDLLSSVDQPLK	NA,NA,C65,NA,NA,C24,NA ,NA,NA,NA	,,,X;	1.53749,1.39868,,1. 82539,,X;	1.53749	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 , P47756-2 Isoform 2 of F- actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB , B1AK88 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK87 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK85 F-actin-capping

					protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 ,
TIPLISQC(464.28596)TPK	C212,NA,NA	,,;,;	1.56383,,1.57005,,1.23338,,	1.56383	P40926 Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 ,
GPC(470.29977)IIYNEDNG IIK	C208,NA	,,X;X;	1.20724,,X;X;	1.20724	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
VPTANVSVVDLTC(464.28596)R	C247,NA	,,X;,;	1.20602,1.53508,,X;1.45317,,	1.45317	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
FIC(464.28596)TTS AIQNR	NA,NA,NA	,,X;X;	1.46686,,X;X;	1.46686	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 , P53396-2 Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY ,
DLNYC(464.28596)FSGM(15.994915)SDHR	C267,M271,C267,M271,C267,M271,NA	,,;,;	1.57267,1.94646,,1.34098,1.37072,,1.48867,,	1.48867	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 , P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 ,
LAEQC(464.28596)GGLQG FLIFRSFGGGTGS GFTSLLM(15.994915)ER	C96,M121,NA,NA	,,X;X;	4.27259,4.54578,,X;X;	4.409185	A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 , A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 ,
CPEALFQPSFLGMESC(470.29977)GIHETTFNSIMK	NA,NA,NA	,,X;X;	1.74815,,X;X;	1.74815	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
GLFGAGGAAGGC(470.29977)GVAGAGADGYGYLAPP K	NA,NA	U,,X;X;	1.84528,,X;X;	1.84528	P58012 Forkhead box protein L2 OS=Homo sapiens GN=FOX L2 PE=1 SV=1 ,
LC(464.28596)YVALDFEQE MAM(15.994915)AASSSSEK	C917,M929,NA	U,,X;X;	1000.0,,X;X;	1000	P0CG38 POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 ,
TLETANC(464.28596)MSS QTK	C96,NA,NA,NA,NA	,,X;X;	1.44613,,X;X;	1.44613	P50416-2 Isoform 2 of Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A , P50416 Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 ,
VSDTVVEPYNATLSVHQLVE NTDETYC(470.29977)IDNE ALYDIC(470.29977)FR	C201,C211,C201,C211,NA,C183,C193,C201,C211,NA	,,X;X;	1.67199,1.53251,1.82714,,X;X;	1.67199	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 ,

					Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
C(464.28596)ALLASEVPQL ALQLLDPESYVR	NA,NA	U,,X;X;	1.30735,,X;X;	1.30735	Q6PJG6 BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 ,
HSM(15.994915)NPFC(47 0.29977)EIAVEEAVR	M129,C133,M129,C133,NA	,,,X,,,;	1.31876,1.5253,,X; 1.44423,,;	1.44423	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
AAAPAPEEEM(15.994915) DEC(470.29977)EQALAAE PK	M263,C266,NA,NA	,,X,,,;	1.20379,,X;1.15203 ,,;	1.17791	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
HSM(15.994915)NPFC(47 0.29977)EIAVEEAVR	M129,C133,M129,C133,NA	,,,,X;	1.5504,2.07132,,2.0 5828,,X;	2.05828	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
AAAPAPEEEM(15.994915) DEC(470.29977)EQALAAE PK	M263,C266,NA,NA	,,X;X;	1.28734,,X;X;	1.28734	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
INDALSC(470.29977)EYEC R	NA,NA,NA	,,X;X;	0.87187,,X;X;	0.87187	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
AGQC(464.28596)VIGLQM (15.994915)GTNK	C164,M170,C153,M159,NA, C155,M161,NA	,,,,;	1.47991,1.49033,,1. 42005,,1.25542,,;	1.44998	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
IAVAAQNC(470.29977)YK	C67,NA,NA	,,X;X;	1.767,,X;X;	1.767	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 , P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 ,
ITLIIGGSYGAGNYGM(15.9 94915)C(464.28596)GR	NA,NA,NA	,,X;X;	2.11197,,X;X;	2.11197	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
YGIIC(470.29977)MEDLIH EIYTVGK	C186,NA	,,,X;X;	1.45447,1.41031,,X ;X;	1.43239	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
YGIIC(470.29977)MEDLIH EIYTVGK	C186,NA,NA	,,,,;	1.44899,1.50487,1. 47894,,1.50643,,1.2	1.47894	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7

			8875,;		OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
SC(464.28596)FPSLFQAEQ THR	C183,NA	U,;X;X;	1.76775,;X;X;	1.76775	P50336 Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1 ,
AC(470.29977)PRPEGLNF QDLK	NA,C227,NA,NA	,;X;X;	1.74753,;X;X;	1.74753	P15927-3 Isoform 3 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 , P15927-2 Isoform 2 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 , P15927 Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1 ,
STLTDSLVC(464.28596)K	C41,NA	U,;U,;U,;	0.8949,;0.9338,;0.9 5641,;	0.9338	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
LTPGC(470.29977)EAEAET EAICFFVQQFTDM(15.9949 15)EHNR	C2359,M2378,NA	,,;X;	1.27407,1.38654,;1. 14397,;X;	1.27407	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
AHTVLAASC(470.29977)A R	NA,NA	U,;X;X;	1.43737,;X;X;	1.43737	Q8WUY1 Protein THEM6 OS=Homo sapiens GN=THEM6 PE=1 SV=2 ,
FQSSAVM(15.994915)ALQ EAREAYLVGLFEDTNLC(470 .29977)AIHAK	M91,C111,NA	U,;U,;X;	0.71742,;0.58162,; X;	0.64952	Q5TEC6 Histone H3 OS=Homo sapiens GN=HIST2H3PS2 PE=1 SV=1 ,
C(464.28596)GFLPGNEK	C106,NA,NA	,;X;X;	1.30439,;X;X;	1.30439	A0A087X1Z3 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1 , Q9UL46 Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 ,
ALNALC(464.28596)DGLID ELNQALK	NA,NA,NA	U,;U,;U,;	1.30236,;1.24613,;1 .27017,;	1.27017	P30084 Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 ,
TDVLVLSC(464.28596)DLI TDVALHEVVDLFR	C106,NA,C106,NA	,;X;X;	1.40457,;X;X;	1.40457	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 , Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 , Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 ,
AEPPQC(464.28596)TSLA WSADGQTLFAGYTDNLVR	NA,NA	,,;X;X;	1.43612,1.60011,;X ;X;	1.518115	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
TIYAGNALC(464.28596)TV K	C155,NA,NA	,,;X;	1.43769,;1.69875,;1 .81445,;	1.69875	P13804 Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 ,
AIYDTPC(464.28596)IQAE SEKWQQALK	NA,NA	,;X;X;	1.25887,;X;X;	1.25887	O00232 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 ,

YC(464.28596)PNSVLVIID VKPK	NA,NA	;;X;X;	1.21822;;X;X;	1.21822	P51665 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2 ,
VIGIEC(464.28596)SSISDY AVK	NA,C119,C101,C95,C95,NA,NA	;;;X;X;	1.80169,1.71978,1.12524;;X;X;	1.71978	E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 , H7C211 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 , Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 , Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 , Q99873-2 Isoform 2 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 , Q99873-3 Isoform 3 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 ,
SIHLAC(470.29977)TAGIF DAYVPPEGDAR	C80,NA,NA,NA,NA	;;X;X;	1.76395;;X;X;	1.76395	A0A087X2D5 39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=1 , Q9BRJ2 39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=2 ,
TPSYSISSTLNPQAEFILGC(470.29977)TASK	C142,C142,NA,NA	;;X;X;	1.04414;;X;X;	1.04414	Q14694-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 , Q14694 Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 , Q14694-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 ,
LC(464.28596)SGVLGTVV HGK	NA,NA	;;X;X;	1.16404;;X;X;	1.16404	Q9Y6C9 Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 ,
LC(464.28596)SGVLGTVV HGK	NA,NA	;;X;X;	1.39226;;X;X;	1.39226	Q9Y6C9 Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 ,
TTSSANNPNLM(15.994915)YQDEC(464.28596)DR	M502,C507,M581,C586,NA,NA,M500,C505,NA	;;;X;	1.25176;;1.25971;;X;	1.255735	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 , Q92841-2 Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 , Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 ,
EVLRCFTVLAC(470.29977)	NA,NA,NA,C344,NA	;;X;X;	1.36308;;X;X;	1.36308	Q8NDA8 Maestro heat-like repeat-containing protein family

SSPDR					member 1 OS=Homo sapiens GN=MROH1 PE=2 SV=3 , E9PHY8 Maestro heat-like repeat-containing protein family member 1 OS=Homo sapiens GN=MROH1 PE=1 SV=1 , Q8NDA8-7 Isoform 7 of Maestro heat-like repeat-containing protein family member 1 OS=Homo sapiens GN=MROH1 , Q8NDA8-2 Isoform 2 of Maestro heat-like repeat-containing protein family member 1 OS=Homo sapiens GN=MROH1 ,
VQENSAYIC(470.29977)SR	C585,NA	U,,U,,X;	1.75121,,1.60183,,X;	1.67652	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 ,
QNEEIEAMAAIYGEEWC(470.29977)VIDDC(464.28596)AK	NA,NA,NA	,,X;X;	2.87567,,X;X;	2.87567	J3QRS6 Protein IMPACT (Fragment) OS=Homo sapiens GN=IMPACT PE=1 SV=1 , Q9P2X3 Protein IMPACT OS=Homo sapiens GN=IMPACT PE=1 SV=2 ,
AAGELGIAVCNIPSAAVEETADSTIC(470.29977)HILNLYR	NA,C140,C208,NA	,,X;X;	1.28559,,X;X;	1.28559	P56545-2 Isoform 2 of C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 , P56545 C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 , Q5SQP8 C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 ,
FC(464.28596)AFGGNPPVTGPR	NA,C150,NA	,,X;X;	1.07452,,X;X;	1.07452	O15446-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP , O15446 DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP PE=1 SV=1 ,
EGYTSFWNDC(464.28596)ISSGLR	NA,C70,NA	,,,X;X;	1.58994,1.58994,,X;X;	1.58994	Q9H4A6 Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 , Q9H4A5 Golgi phosphoprotein 3-like OS=Homo sapiens GN=GOLPH3L PE=1 SV=1 ,
LSLDGQNIYNAC(464.28596)CTLR	C281,NA,C250,NA,NA	,,X,,,;	1.54983,,X;0.57817,,;	1.064	A0A0U1RRM4 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 , P26599-3 Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 , P26599-2 Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 , P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
LSLDGQNIYNAC(464.28596)CTLR	NA,NA	,,X;X;	4.49739,,X;X;	4.49739	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
GC(470.29977)EVVVS GK	NA,NA	,,,X;	1.50767,,1.49627,,X;	1.50197	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 ,
IC(464.28596)SIYTQSGEN	NA,NA,NA	,,X;X;	2.36997,,X;X;	2.36997	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo

SLVQEGSEASPIGK					sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
VPQC(470.29977)PSGR	C88,NA	U,,X;X;	1.34819,,X;X;	1.34819	Q16186 Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 ,
SC(464.28596)PETLTHAVG MSESPIGPK	NA,NA	,,X;X;	1.18105,,X;X;	1.18105	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
SIEIPRPVDGVEVPGC(470.2 9977)GK	NA,NA,NA,NA	,,X;X;	1.74383,,X;X;	1.74383	K7ENG2 Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=1 , P26368 Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 , P26368-2 Isoform 2 of Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 ,
C(464.28596)PFTGNVSIR	C60,NA	,,,X;	1.54042,1.50494,,1.41776,1.05614,,X;	1.46135	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
C(464.28596)LNNLAASQL K	NA,NA,NA	,,X;X;	1.3011,,X;X;	1.3011	Q14318 Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2 , Q14318-2 Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 ,
TVPFLPLLGGC(464.28596) IDDTILSR	C180,NA,NA,NA,NA	,,,;	1.50618,,1.62971,,1.31619,,	1.50618	Q7Z7H8 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 , Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 ,
THPSAAVPVC(464.28596) PR	C361,NA,NA	,,X;X;	1.38398,,X;X;	1.38398	Q3KQU3 MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1 , Q3KQU3-2 Isoform 2 of MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 ,
SLTGC(470.29977)WSAGT ISK	NA,NA,C49,NA,NA	,,X;X;	1.50575,,X;X;	1.50575	Q6KB66-2 Isoform 2 of Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 , Q6KB66 Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2 ,
VNC(464.28596)LAPGLIK	NA,NA,NA,NA,NA,NA	,,X;X;	1.42854,,X;X;	1.42854	H0YNP7 Dehydrogenase/reductase SDR family member 4 (Fragment) OS=Homo sapiens GN=DHRS4 PE=4 SV=1 , Q9BTZ2-8 Isoform 8 of Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens GN=DHRS4 , Q9BTZ2-4 Isoform 4 of Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens GN=DHRS4 , P0CG22 Putative dehydrogenase/reductase SDR family member 4-like 1

					OS=Homo sapiens GN=DHRS4L1 PE=5 SV=1 , Q9BTZ2 Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens GN=DHRS4 PE=1 SV=3 ,
LSNVAPPC(470.29977)ILR	NA,NA,NA,NA	;;X;X;	1.50382;;X;X;	1.50382	C9JB30 Microtubule-associated protein RP/EB family member 3 (Fragment) OS=Homo sapiens GN=MAPRE3 PE=1 SV=1 , Q9UPY8 Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens GN=MAPRE3 PE=1 SV=1 , Q9UPY8-2 Isoform 2 of Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens GN=MAPRE3 ,
VRPSTGNSASTPQSQC(464.28596)LPSEIEVK	C131,NA,NA	;;X;;;	1.38813;;X;1.22353;;	1.30583	Q9UIX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 , Q9UIX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 ,
FQLTDC(464.28596)QIYEV LSVIR	C143,C143,NA	;;X;X;	1.3018,1.2666;;X;X;	1.2842	Q16555-2 Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 , Q16555 Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 ,
VRNC(464.28596)SSPEFSK	C58,NA,C53,NA	;;X;X;	1.27564;;X;X;	1.27564	B0QZ18 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 , Q99829 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 , A6PVH9 Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 ,
TAVC(464.28596)DIPPRGL K	C354,C354,C354,NA,C336,NA	;;X;X;	1.68832;;X;X;	1.68832	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
LDVGNFSWGSEC(464.28596)CTR	NA,NA	U;;X;X;	1.61444;;X;X;	1.61444	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
LDVGNFSWGSEC(464.28596)CTR	NA,NA	U;;X;X;	1.5987;;X;X;	1.5987	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
AQC(470.29977)PIVER	C66,NA,C66,NA	;;X;X;	1.4705;;X;X;	1.4705	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,

YINENLIVNTDELGRDC(464.28596)LINAAK	NA,NA	,,X;X;	1.31507,,X;X;	1.31507	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 ,
FCSFSPC(470.29977)IEQV QR	C209,NA	,,X;X;	1.7066,,X;X;	1.7066	Q96FX7 tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens GN=TRMT61A PE=1 SV=1 ,
AENGLLM(15.994915)TPC (470.29977)YTANFVAPEVL KR	NA,NA,M561,C564,M576,C579,M480,C483,NA,NA	,,X;X;	1.45856,,X;X;	1.45856	Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 , P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 , Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 ,
ECISIHVGQAGVQIGNAC(470.29977)WELCYCLEHGIQPDGQM(15.994915)PSDK	C20,M36,NA,NA,NA	,,X;X;	1.97218,,X;X;	1.97218	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
AVQDLC(464.28596)GWR	C428,NA	U,,X;X;	1.44191,,X;X;	1.44191	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 ,
QGEYGLASIC(470.29977)N GGGGASAMLIQK	NA,NA,NA	U,,X;X;	1.69198,,X;X;	1.69198	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
IC(470.29977)NAVSPDKD VDGFBHVINVGR	C145,NA,NA,NA,NA	,,X;X;	2.00284,,X;X;	2.00284	P13995 Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 PE=1 SV=2 , P13995-2 Isoform 2 of Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 ,
AASQINVC(464.28596)GVR	C159,NA,NA	,,X;X;	1.60897,,X;X;	1.60897	Q14678-2 Isoform 2 of KN motif and ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=KANK1 , Q14678 KN motif and ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=KANK1 PE=1 SV=3 ,
LHTAANAATATETTC(470.29977)QDVAATPVAR	C33,NA,NA	U,,X;X;	1.27997,,X;X;	1.27997	Q9NP92 28S ribosomal protein S30, mitochondrial OS=Homo sapiens GN=MRPS30 PE=1 SV=2 ,
C(464.28596)PEALFQPSFL	NA,NA,NA,NA,NA	,,X,,,;	1.52566,,X;1.18186	1.35376	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB

GM(15.994915)ESCGIHET TFNSIMK			;;		PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ,
LHHPMAVDLGELDSLVASI M(15.994915)DAPTIC(470 .29977)PDCGESFSPGAFL QHQRHR	M185,C191,NA	U,,X;X;	2.5151,,X;X;	2.5151	Q5TEC3 Zinc finger protein 697 OS=Homo sapiens GN=ZNF697 PE=2 SV=2 ,
FQSSAVM(15.994915)ALQ EACEAYLVGLFEDTNLC(470 .29977)A	M91,C111,NA	U,U,,X;U,;	0.53786,0.53877,,X ;0.6139,,	0.53877	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
SLTSC(470.29977)SSDITLR	C246,C209,C261,C261,NA	;;X;X;	1.49461,,X;X;	1.49461	J3KP06 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , F8WD26 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , Q8WWI1 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 , Q8WWI1-3 Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 ,
C(470.29977)NGQPVPFQ QPK	C205,NA,NA,NA,NA,NA,C6 7,NA,NA,C205,NA,NA,NA, NA	;;X;X;	0.93668,,X;X;	0.93668	Q9NRZ9-3 Isoform 3 of Lymphoid-specific helicase OS=Homo sapiens GN=HELLS , Q9NRZ9-4 Isoform 4 of Lymphoid-specific helicase OS=Homo sapiens GN=HELLS , Q9NRZ9-2 Isoform 2 of Lymphoid-specific helicase OS=Homo sapiens GN=HELLS , F6XU50 Helicase, lymphoid- specific, isoform CRA_l OS=Homo sapiens GN=HELLS PE=1 SV=1 , A0A087WSW7 Helicase, lymphoid-specific, isoform CRA_d OS=Homo sapiens GN=HELLS PE=1 SV=1 , Q9NRZ9 Lymphoid-specific helicase OS=Homo sapiens GN=HELLS PE=1 SV=1 , A0A0B4J1V9 Helicase, lymphoid-specific, isoform CRA_b OS=Homo sapiens GN=HELLS PE=1 SV=1 ,
AAC(464.28596)LESAQEP AGAWGNK	C53,NA,NA	;;X;;;	1.1422,,X;0.5048,,	0.8235	A0A024R4E5 High density lipoprotein binding protein (Vigilin), isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1 ,
AAC(464.28596)LESAQEP AGAWGNK	NA,NA,NA,NA,NA,NA,C53, NA,NA,C53,NA,C53,C53,N A,NA	;;X;X;	1.53846,,X;X;	1.53846	C9JT62 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JES8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JBS3 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JEJ8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JK79 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JHZ8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP

					PE=1 SV=2 , C9JIZ1 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JZI8 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , A0A0U1RVI6 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=1 , A0A024R4E5 High density lipoprotein binding protein (Vigilin), isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1 , C9J5E5 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JHS7 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=2 , C9JHN6 Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=1 SV=7 ,
KGTVLLADNVIC(464.28596)PGAPDFLAHVR	C173,NA	;;X;X;	1.14552;;X;X;	1.14552	P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 ,
GC(470.29977)SNEPYFGSLTALVCQHSITPLALPCK	NA,NA	;;X;X;	1.57806;;X;X;	1.57806	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
M(15.994915)FPNAPYLPS C(470.29977)LESQPAIR	M195,C205,M200,C210,NA,NA,M195,C205,NA,NA,M127,C137,NA,M127,C137,NA	;;X;X;	1.94501;;X;X;	1.94501	J3KNN9 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , P19544-7 Isoform 7 of Wilms tumor protein OS=Homo sapiens GN=WT1 , P19544-8 Isoform 8 of Wilms tumor protein OS=Homo sapiens GN=WT1 , H0Y7K5 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , A0A0A0MT54 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , P19544 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=2 , P19544-3 Isoform 3 of Wilms tumor protein OS=Homo sapiens GN=WT1 , P19544-2 Isoform 2 of Wilms tumor protein OS=Homo sapiens GN=WT1 , H0Y3F0 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , P19544-4 Isoform 4 of Wilms tumor protein OS=Homo sapiens GN=WT1 ,
VYQPVSC(470.29977)PLSDLSENVESVVNEEK	C251,NA,C251,NA,NA	;;X;X;	1.57747;;X;X;	1.57747	Q99590 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 , A0A0A0MTP7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 , Q99590-2 Isoform 2 of Protein SCAF11 OS=Homo sapiens GN=SCAF11 , F8VXG7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 ,
NM(15.994915)SVHLSPC(470.29977)FR	M109,C116,NA	;;;;;	1.49971;;1.41034;;1.31273;;	1.41034	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
LTTPTYGDLNHLVSATMSG VTTC(470.29977)LR	NA,C239,C239,NA,C221,NA	;;;;;	1.5365,1.57108;;1.46067;;1.3179;;	1.498585	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 , P68371 Tubulin beta-4B chain

					OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
YYALCGFGVLSC(464.28596)GLTHTAVVPLDLVK	NA,NA,NA	;;;X;	1.40757;;1.24625;;X;	1.32691	Q00325-2 Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 ,
YYALCGFGVLSC(464.28596)GLTHTAVVPLDLVK	NA,NA,NA	;;X;X;	1.4855;;X;X;	1.4855	Q00325-2 Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 ,
SPQPVC(470.29977)SPAG SEGTPK	C279,NA	;;X;X;	1.71048;;X;X;	1.71048	Q6KC79 Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2 ,
TFVPAM(15.994915)TAIH GPPIAPVVC(464.28596)TR	M535,C549,NA,M646,C660,M580,C594,NA	;;;X;X;	1.55003,1.47068;;X;X;	1.510355	Q96RN5-3 Isoform 3 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 , Q96RN5-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 , Q96RN5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=2 , G3V1P5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=1 ,
HFC(464.28596)PNVPIILV GNKK	NA,NA,C107,NA	;;X;X;	1.34432;;X;X;	1.34432	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 , P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 , E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 ,
TWYVQATC(470.29977)AT QGTGLYEGLDWLSNELSK	NA,NA	;;X;X;	1.4976;;X;X;	1.4976	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
SEGGSGGGAAGGGAGGAG AGAGC(464.28596)GSGGS SVGVR	NA,C32,NA,C32,NA	;;X;X;	1.22914;;X;X;	1.22914	Q9NSY1-3 Isoform 3 of BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K , Q9NSY1-2 Isoform 2 of BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K , K4DI97 BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=1 , Q9NSY1 BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=2 ,
LGHAGGNQSDASHLLNQS GGAGEDC(464.28596)QIF	C721,NA,NA	;;X;X;	1.36301;;X;X;	1.36301	U3KPZ7 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 , Q9P2N5 RNA-binding protein 27 OS=Homo sapiens

STPGHPK					GN=RBM27 PE=1 SV=2 ,
C(464.28596)ASQSGM(15.994915)TAYGTR	C175,M181,C164,M170,NA,NA	,,,X;	1.39396,,1.25121,,X;	1.322585	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
INPYM(15.994915)SSPC(464.28596)HIEMILTEK	NA,NA,M140,C144,M102,C106,NA,NA,NA,NA	,,,X;	1.41419,,1.1621,,X;	1.288145	J3KRX5 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 , J3QLC8 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=1 , A0A087WXM6 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 , P18621 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3 , A0A0A6YYL6 Protein RPL17-C18orf32 OS=Homo sapiens GN=RPL17-C18orf32 PE=3 SV=1 , J3QQT2 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 , P18621-3 Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 ,
HFVLDEC(464.28596)DK	C197,NA	,,X;X;	1.00987,,X;X;	1.00987	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 ,
SCYDLSC(464.28596)HAR	NA,NA	U,,X;U,,	1.27713,,X;1.15867,,	1.2179	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 ,
QC(470.29977)PIMDPAW EAPGVPIIDAIIFGGR	C297,NA,NA,NA,NA	,,,,,;	0.01022,,1.63393,,1.49798,1.5837,,	1.54084	B4DW73 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 , Q16822 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 ,
FTSGAFLSPSVSQEC(470.29977)R	NA,NA,C1068,NA,NA	,,X;X;	0.89214,,X;X;	0.89214	P52948-5 Isoform 5 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 , P52948 Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4 , P52948-6 Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 , H7C3P6 Nuclear pore complex protein Nup98-Nup96 (Fragment) OS=Homo sapiens GN=NUP98 PE=1 SV=1 ,
QC(470.29977)PIMDPAW EAPGVPIIDAIIFGGR	NA,NA,NA	,,X;X;	0.00585,,X;X;	0.00585	Q16822 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 ,
VSC(464.28596)SPVSAQLL SVLQGLLHLEPTLR	C284,NA,NA	,,X;X;	1.48774,,X;X;	1.48774	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 , Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 ,

IDC(470.29977)FSEVPTSV FGEK	NA,NA	,,,X;	1.49147,,;1.31695,, X;	1.40421	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
DAGGKSWC(464.28596)P DCVQAEPVVR	NA,NA	,;X;X;	1.37357,,;X;X;	1.37357	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 ,
AHGISSYFPVQAAVIPALLES AAC(464.28596)GFLVGR	NA,NA	U,,X;X;	1.59004,,;X;X;	1.59004	Q8N8A6 ATP-dependent RNA helicase DDX51 OS=Homo sapiens GN=DDX51 PE=1 SV=3 ,
AHGISSYFPVQAAVIPALLES AAC(464.28596)GFLVGR	NA,NA	U,,X;X;	1.96022,,;X;X;	1.96022	Q8N8A6 ATP-dependent RNA helicase DDX51 OS=Homo sapiens GN=DDX51 PE=1 SV=3 ,
ALIVGHC(470.29977)MPG PR	NA,NA,NA	U,,X;X;	1.46406,,;X;X;	1.46406	Q6P1L8 39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 ,
AYSFAM(15.994915)GC(4 64.28596)WPK	NA,M150,C152,M168,C17 0,NA,NA,NA	,;X;X;	1.33769,,;X;X;	1.33769	O43414-3 Isoform 3 of ERI1 exoribonuclease 3 OS=Homo sapiens GN=ERI3 , HOY4B0 ERI1 exoribonuclease 3 (Fragment) OS=Homo sapiens GN=ERI3 PE=1 SV=1 , O43414-2 Isoform 2 of ERI1 exoribonuclease 3 OS=Homo sapiens GN=ERI3 , F6QUN3 ERI1 exoribonuclease 3 (Fragment) OS=Homo sapiens GN=ERI3 PE=1 SV=1 , O43414 ERI1 exoribonuclease 3 OS=Homo sapiens GN=ERI3 PE=1 SV=2 ,
LC(464.28596)FSTAQHAS	NA,NA,NA	,;X;;	1.32858,,;X;1.40996 ,,	1.36927	MOQXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
C(470.29977)C(470.29977)LTYCFNKPEDK	C144,NA	U,,X;X;	1.656,,;X;X;	1.656	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
ISAFGYLEC(470.29977)SA K	NA,NA,C159,NA	,;X;X;	1.61801,,;X;X;	1.61801	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 , P08134 Rho- related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 , E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 ,
SGQGAFGNM(15.994915) C(464.28596)R	M95,C96,NA	,,,,,;	1.74614,,;1.33633,,;1 .26759,,	1.33633	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
EGGQYGLVAAC(464.2859 6)AAGGQGHAM(15.99491 5)IVEAYPK	C436,M445,NA,C436,M44 5,NA,NA	,,,;X;	1.58671,,;2.89071,, X;	2.23871	P55084 Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 , P55084-2 Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB ,

C(470.29977)VQSNIVLLTQ AFR	NA,NA,NA,NA,NA	,,X;X;	0.76325,,X;X;	0.76325	O94925-3 Isoform 3 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS , O94925 Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1 ,
NMAC(470.29977)VQR	C124,NA,NA,NA	,,X;X;	1.36427,,X;X;	1.36427	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 , P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 , X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 ,
AVLLASDAQEC(470.29977) TLEEVVER	C332,NA,NA	,,,X;X;	0.78963,1.71712,,X; X;	1.253375	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 , Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 ,
C(470.29977)ALSSPSLAFT PPIK	C120,NA,NA,NA	,,,,X;	1.45708,,1.43304,, X;	1.44506	Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 ,
VDEFPLC(470.29977)GHM (15.994915)VSDEYEQLSSE ALEAAR	C49,M52,C49,M52,NA	,,,,,;	1.28595,,1.3067,,1. 27252,,	1.28595	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
NTGIIC(464.28596)TIGPAS R	NA,NA	,,X;X;	1.42685,,X;X;	1.42685	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 ,
VDEFPLC(470.29977)GHM (15.994915)VSDEYEQLSSE ALEAAR	C49,M52,NA	,,,,X;X;	1.4259,1.45679,1.4 3534,,X;X;	1.43534	P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
TDC(470.29977)SPIQFESA WALTNIASGTSEQTK	C133,NA	U,U,,X;X;	1.14875,0.82461,,X; X;	0.98668	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 ,
GFTDADNTWEPEENLDC(4 64.28596)PELIEAFLNSQK	C69,NA	,,X;X;	1.03041,,X;X;	1.03041	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 ,
VHPAM(15.994915)ATAA GGC(464.28596)R	NA,NA,NA	,,,,,;	1.68748,,1.67358,,1. .23192,,	1.67358	H7C0N4 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 , H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 ,
SGDLFNC(464.28596)GSLT IR	NA,NA,NA	,,X;X;	1.31418,,X;X;	1.31418	P21953 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Homo sapiens GN=BCKDHB PE=1 SV=2 ,
AC(470.29977)SVGAVPGIT K	C278,NA	U,,X;X;	1.49906,,X;X;	1.49906	Q9NVN8 Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens GN=GNL3L PE=1 SV=1 ,
SSLSC(464.28596)SLQEGLI PGSQFWDASK	C485,NA	,,X;X;	1.41653,,X;X;	1.41653	P52701 DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2 ,

LALEQQQLIC(464.28596)K	C69,NA	;;X;X;	1.27591;;X;X;	1.27591	Q8IWX8 Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=3 ,
IIDLEEADEIEDIQQEITVLS QC(470.29977)DSSYVTK	C77,NA,NA,NA	;;X;X;	0.75475;;X;X;	0.75475	B4E0Y9 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 , Q9P289-3 Isoform 3 of Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 , Q9P289 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=2 ,
LWNTLGVC(470.29977)K	NA,NA	;;X;X;	1.58344;;X;X;	1.58344	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
C(464.28596)SVPVDQASE SLLK	C213,NA	U;;X;X;	1.83791;;X;X;	1.83791	Q9NVN8 Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens GN=GNL3L PE=1 SV=1 ,
TTSFAESC(470.29977)KPV QQPSAFGSM(15.994915) K	NA,C14,M26,NA	;;X;X;	1.6861;;X;X;	1.6861	P49841-2 Isoform 2 of Glycogen synthase kinase-3 beta OS=Homo sapiens GN=GSK3B , P49841 Glycogen synthase kinase-3 beta OS=Homo sapiens GN=GSK3B PE=1 SV=2 ,
C(470.29977)M(15.99491 5)QLTDFILK	NA,C54,M55,NA	;;;X;	1.50052;;1.34414;; X;	1.42233	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 , P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 ,
LVIYGGM(15.994915)SGC(470.29977)R	M224,C227,M224,C227,M 224,C227,NA,NA	;;X;X;	1.52018;;X;X;	1.52018	P51610-2 Isoform 2 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 , P51610 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 , P51610-4 Isoform 4 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 , A6NEM2 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 ,
VILITPTPLC(470.29977)ET AWEEQCIIQGCK	C137,C117,NA	;;X;X;	1.43113;;X;X;	1.43113	Q2TAA2 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 , H7C5G1 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 ,
VCETDGC(470.29977)SSE AK	C14,C10,C14,NA	;;;;;	1.64221;;1.45853;;1 .25411;;	1.45853	D6RF24 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=1 , H0Y9L0 Methionine aminopeptidase 1 (Fragment) OS=Homo sapiens GN=METAP1 PE=1 SV=1 , P53582 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=2 ,
AEPPQC(470.29977)TSLA WSADGQTLFAGYTDNLVR	NA,NA	;;;X;X;	1.43612,1.96038;;X ;X;	1.69825	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
PDGPEAQAEAC(464.2859 6)SGER	C18,NA	;;X;X;	1.61674;;X;X;	1.61674	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,

ECISIHVGQAGVQIGNACW ELYC(464.28596)LEHGIQP DGQM(15.994915)PSDK	C25,M36,NA,NA,NA	;;X;X;	1.83488;;X;X;	1.83488	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha- 1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
SGGLQTPEC(464.28596)LS R	NA,NA	;;X;X;	1.44395;;X;X;	1.44395	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 ,
SPAGLQVCVNVSVSLAGM(15.994915)C(464.28596)H HKQMWQYLK	NA,NA	U;;X;X;	1.6374;;X;X;	1.6374	F8WFC9 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=1 ,
DLC(470.29977)FSPGLM(1 5.994915)EASHVVNDVNE AVQLVFR	NA,C362,M368,NA	;;;X;	1.48296,1.38206;;1. 36608;;X;	1.38206	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 , Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 ,
AC(464.28596)FEPANQM VK	C295,NA	;;X;X;	2.74577;;X;X;	2.74577	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
DLC(470.29977)FSPGLM(1 5.994915)EASHVVNDVNE AVQLVFR	NA,NA	;;;X;X;	2.12781,1.74039;;X ;X;	1.9341	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 ,
LLAC(464.28596)IASR	NA,NA	;;X;X;	1.49617;;X;X;	1.49617	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
KIWC(470.29977)FGPDGT GPNILTDITK	C651,NA	U;;X;X;	0.96806;;X;X;	0.96806	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
AATMSAVEAATC(470.299 77)R	NA,C266,NA,C129,NA	;;X;X;	0.90415;;X;X;	0.90415	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 , Q53H96 Pyrroline-5- carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 , Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL , B5MD87 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2 ,
GLTLLFASGDSGAGC(464.2 8596)WSVSGR	NA,NA,NA	;;X;X;	1.63488;;X;X;	1.63488	O14773 Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 , O14773-2 Isoform 2 of Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 ,
C(464.28596)IPALDSLTPA NEDQK	NA,NA,NA	U;;X;X;	1.2888;;X;X;	1.2888	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
VTDDLVC(470.29977)LVYK	NA,NA	U;;X;X;	2.04695;;X;X;	2.04695	P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 ,

PPM(15.994915)EAAGFTA QVIILNHPGQISAGYAPVLD CHTAHIAC(470.29977)K	NA,NA,NA	,,,X;	1.53428,,1.4028,,X;	1.46854	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , A0A087WVQ9 Elongation factor 1- alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
IAVHC(470.29977)TVR	C72,NA,NA,NA	,,,X;	1.27799,,1.34411,, X;	1.31105	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 , Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 , P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 ,
TAVC(464.28596)DIPPR	C354,NA	,,X;X;	0.09045,,X;X;	0.09045	Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 ,
M(15.994915)SDSADKPID NDAEGVWSPDIEQSFQEAL AIYPPC(470.29977)GR	NA,NA,NA	,,X;X;	1.54556,,X;X;	1.54556	P28347 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=2 , HOYE88 Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=1 SV=1 ,
AGGPPQVAGAQAAC(464. 28596)SEDR	NA,C35,NA	,,X;X;	1.32572,,X;X;	1.32572	B3KVZ3 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 , Q9H3R5 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 ,
ISPVDVNSRPSSC(464.2859 6)LTNFLNLR	C248,NA	,,X;X;	1.46581,,X;X;	1.46581	Q9NVM9 Protein asunder homolog OS=Homo sapiens GN=ASUN PE=1 SV=2 ,
ISPVDVNSRPSSC(464.2859 6)LTNFLNLR	C248,NA	,,X;X;	1.43372,,X;X;	1.43372	Q9NVM9 Protein asunder homolog OS=Homo sapiens GN=ASUN PE=1 SV=2 ,
NC(464.28596)IVLIDSTPYR	NA,NA	,,,X;X;	1.47765,1.53275,1. 52229,,X;X;	1.52229	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
NC(464.28596)IVLIDSTPYR	NA,NA	,,,,X;	1.39566,1.47945,,1. 56403,,X;	1.47945	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
YGIIC(464.28596)M(15.99 4915)EDLIHEIYTVGKR	C186,M187,NA,NA	,,,,,;	1.44381,,1.43778,,1 .27639,,	1.43778	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
LAPILC(470.29977)DGTAT FVDLVPGR	NA,NA	,,X;X;	1.18474,,X;X;	1.18474	O43264 Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 ,
YGIIC(464.28596)M(15.99 4915)EDLIHEIYTVGKR	C186,M187,NA,NA	,,X,,;	1.49595,,X;1.35972 ,,	1.427835	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
LPC(464.28596)EMDAQG PK	NA,C187,NA	,,X;X;	1.34134,,X;X;	1.34134	Q9UGI8 Testin OS=Homo sapiens GN=TES PE=1 SV=1 , Q9UGI8-2 Isoform 2 of Testin OS=Homo sapiens GN=TES ,
YGIIC(464.28596)M(15.99	C186,M187,NA	,,X;X;	1.43317,,X;X;	1.43317	P18124 60S ribosomal protein L7 OS=Homo sapiens

4915)EDLIHEIYTVGKR					GN=RPL7 PE=1 SV=1 ,
WTQTLSELDLAVPFC(464.28596)VNFR	C188,NA	U,U,;X;X;	1.14014,1.01672,;X;X;	1.07843	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 ,
SLRLSC(464.28596)TASGF TFGDYAM(15.994915)SW VR	NA,NA,NA	,;X;X;	112.63245,;X;X;	112.63245	A0A087WU91 Protein IGHV3-49 OS=Homo sapiens GN=IGHV3-49 PE=1 SV=1 , A0A0A0MS15 Protein IGHV3-49 (Fragment) OS=Homo sapiens GN=IGHV3-49 PE=1 SV=1 ,
SSVQEEC(464.28596)VSTI SSSKDEDPLAATR	NA,NA	,,;,;,;	1.24413,1.29639,;2.06672,;1.18635,;	1.27026	Q7L0Y3 Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2 ,
LPHC(464.28596)ASM(15.994915)TPDGWSFALK	NA,NA,NA,C1718,M1721,NA,NA	,;X;X;	1.1181,;X;X;	1.1181	G5E9E7 Tight junction protein 1 (Zona occludens 1), isoform CRA_e OS=Homo sapiens GN=TJP1 PE=1 SV=1 , A0A087X0K9 Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=1 , G3V1L9 Tight junction protein 1 (Zona occludens 1), isoform CRA_a OS=Homo sapiens GN=TJP1 PE=1 SV=1 ,
LYYFQYPC(464.28596)YQEGLR	NA,NA	U,U,;X;X;	1.53273,1.52156,;X;X;	1.527145	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 ,
NHLLPDIVTC(470.29977)VQSSR	C184,NA	U,U,;X;U,;	1.47138,1.48499,;X;1.36385,;	1.47138	Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 ,
YKVC(470.29977)NYGLTFTQK	NA,NA	,;X;X;	1.22171,;X;X;	1.22171	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 ,
C(464.28596)ASQVGM(15.994915)TAPGTR	C215,M221,C204,M210,NA,NA	,,;,;X;	1.46505,;1.24887,;X;	1.35696	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
TGNGPMSVC(470.29977)GR	NA,C493,NA,NA,NA,NA	,;X;X;	1.41359,;X;X;	1.41359	O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 , O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , A0A087X1A5 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 , Q5JW30 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 ,
YKVC(470.29977)NYGLTFTQK	NA,NA	,;X;X;	1.65324,;X;X;	1.65324	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 ,

TFC(470.29977)GTPEYLAP EVLEDNDYGR	C310,NA,NA,NA,NA,NA	,,,X;	1.8352,,1.43715,,X;	1.636175	P31749 RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2 , P31751 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 , Q9Y243-2 Isoform 2 of RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 , Q9Y243 RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 PE=1 SV=1 , M0R0P9 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=1 ,
LQHINPLLPAC(464.28596) LNK	NA,C325,NA	,,X;X;	1.64397,,X;X;	1.64397	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 , Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP ,
VC(470.29977)GYDTPFPHI FEPFYIPDKWK	NA,NA,NA	U,,X;X;	1.59779,,X;X;	1.59779	P21953 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Homo sapiens GN=BCKDHB PE=1 SV=2 ,
VC(470.29977)GYDTPFPHI FEPFYIPDKWK	NA,NA,NA	U,,X;X;	1.54377,,X;X;	1.54377	P21953 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Homo sapiens GN=BCKDHB PE=1 SV=2 ,
SC(470.29977)GHQTSASSL K	NA,NA	U,,X;X;	1.4563,,X;X;	1.4563	Q9HB90 Ras-related GTP-binding protein C OS=Homo sapiens GN=RRAGC PE=1 SV=1 ,
ITSC(470.29977)IFQLLQEA GIK	C63,NA	,,X;X;	1.50261,,X;X;	1.50261	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
DGTVLC(464.28596)ELINA LYPEGQAPVKK	C63,NA,NA,NA	,,X;X;	1.37489,,X;X;	1.37489	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 , P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 , X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 ,
YMACC(464.28596)LLYR	NA,C316,C283,NA,NA,NA, NA,NA	,,X;X;	1.43056,,X;X;	1.43056	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
ALANVNIGSLIC(464.28596)	NA,NA	,,,X;	1.29285,1.29285,,1.	1.29285	P05386 60S acidic ribosomal protein P1 OS=Homo sapiens

)NVGAGGPAPAAGAAPAG GPAPSTAAAPAEK			57611,;X;		GN=RPLP1 PE=1 SV=1 ,
ALANVNIGSLIC(464.28596)NVGAGGPAPAAGAAPAG GPAPSTAAAPAEK	NA,NA,NA	,,,;X;,,,;	1.29102,1.33587,1. 29102,1.33587,;X;1 .29358,1.34567,1.2 9358,1.34567,;	1.314725	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 , P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 ,
ALANVNIGSLIC(464.28596)NVGAGGPAPAAGAAPAG GPAPSTAAAPAEK	NA,NA	,,,;X;	1.33949,1.30666,1. 33949,1.30666,;1.4 1942,;X;	1.33949	P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 ,
VVMALGDYM(15.994915) GASCHAC(470.29977)IGG TNVR	NA,NA	,;X;X;	1.36007,;X;X;	1.36007	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 ,
IKSGEEDFESLASQFSDC(46 4.28596)SSAK	NA,C113,NA,NA	,;X,;;	1.40128,;X;1.04706 ,;	1.22417	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 , K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 , Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 ,
LALFNPDC(464.28596)W DR	C44,NA	U,;X;X;	1.68703,;X;X;	1.68703	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 ,
LTEGC(470.29977)SFR	C93,C77,NA,NA	,;X;	1.41458,;1.41196,; X;	1.41327	H0YMV8 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=1 SV=1 , Q71UM5 40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3 , P42677 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 ,
IKSGEEDFESLASQFSDC(46 4.28596)SSAK	NA,C113,NA,NA	,,,;X;	1.43882,1.46656,1. 37611,;1.31223,;1.1 0802,;	1.37611	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 , K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 , Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 ,
VANVVDHSLQDC(470.299 77)VFSK	C90,C90,C49,NA,C49,NA, NA,NA,C90,NA	,;X;X;	1.60003,;X;X;	1.60003	A9UHW6-3 Isoform 3 of MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD , J3KSU6 MIF4G domain- containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=1 , J3QLJ5 MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD PE=1 SV=1 , J3QLD1 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=1 , J3KSB8 MIF4G domain

					containing isoform 4 OS=Homo sapiens GN=MIF4GD PE=1 SV=1 , J3QRZ6 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=7 , A9UHW6-2 Isoform 2 of MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD , J3QKW3 MIF4G domain-containing protein (Fragment) OS=Homo sapiens GN=MIF4GD PE=1 SV=7 , A9UHW6 MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD PE=1 SV=1 ,
NHLLPDIVTC(464.28596)VQSSRK	C184,NA	U,,X;X;	1.17335,,X;X;	1.17335	Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 ,
VNSDC(464.28596)DSVLP SNFLLGGNIFDPLNLSLLDE EVSR	NA,NA	U,,X;X;	1.47205,,X;X;	1.47205	Q7L2J0 7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1 ,
SILSPGGSC(464.28596)GPIK	NA,NA,C215,NA,NA	,,X;X;	1.2502,,X;X;	1.2502	P78347 General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 , P78347-4 Isoform 4 of General transcription factor II-I OS=Homo sapiens GN=GTF2I , P78347-3 Isoform 3 of General transcription factor II-I OS=Homo sapiens GN=GTF2I , P78347-2 Isoform 2 of General transcription factor II-I OS=Homo sapiens GN=GTF2I ,
C(464.28596)PGGRNPWT GVSQFLQTSQK	C198,NA	,,X;X;	1.51195,,X;X;	1.51195	Q99447-3 Isoform 3 of Ethanolamine-phosphate cytidyltransferase OS=Homo sapiens GN=PCYT2 ,
NVVAC(464.28596)ESIGR	C125,NA,NA	U,,X;X;	1.04158,,X;X;	1.04158	Q9H0U6 39S ribosomal protein L18, mitochondrial OS=Homo sapiens GN=MRPL18 PE=1 SV=1 ,
GLPC(470.29977)TELFVAP VGVASKR	C79,NA,C428,NA	,,X;X;	1.54602,,X;X;	1.54602	H0Y901 Ladinin-1 (Fragment) OS=Homo sapiens GN=LAD1 PE=1 SV=1 , E9PDI4 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=1 , O00515 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 ,
TPTSGQSVSTC(464.28596)SSK	NA,NA	,,X;X;	1.34983,,X;X;	1.34983	Q32NC0 UPF0711 protein C18orf21 OS=Homo sapiens GN=C18orf21 PE=1 SV=1 ,
LMHLFTSGDC(470.29977)K	C91,NA	U,,X;X;	1.45958,,X;X;	1.45958	Q8WXD5 Gem-associated protein 6 OS=Homo sapiens GN=GEMIN6 PE=1 SV=1 ,
M(15.994915)KLNISFPAT GC(464.28596)QK	NA,NA	,,X;X;	1.46045,,X;X;	1.46045	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
M(15.994915)YGISLC(470.29977)QAILDETKGDYEK	NA,NA	U,,X;X;	1.38367,,X;X;	1.38367	P04083 Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 ,

LDTNSDGQLDFSEFLNLIGGLAM(15.994915)AC(470.29977)HDSFLK	M89,C91,NA	U,,X;X;	1.43359,,X;X;	1.43359	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
NLAVAM(15.994915)C(464.28596)SR	NA,NA,M54,C55,M54,C55,NA	,,X;X;	1.15576,,X;X;	1.15576	Q5JS54-3 Isoform 3 of Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 , Q5JS54 Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 PE=2 SV=2 , Q5JS54-2 Isoform 2 of Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 , D6RB92 Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 PE=1 SV=1 ,
IIC(470.29977)QGFTGK	C58,NA,C60,NA,NA	,,X;X;	1.28712,,X;X;	1.28712	H7C233 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=SUCLG1 PE=1 SV=1 , P53597 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4 ,
AHGC(464.28596)FPEGR	NA,NA,NA	,,X;X;	1.42916,,X;X;	1.42916	Q7Z5L9-2 Isoform 2 of Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 , Q7Z5L9 Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2 ,
C(464.28596)LAQEVNIPDWIVDLR	NA,NA,NA	,,X;;	1.51709,,X;1.44498,,	1.481035	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
AFLDNPGILSELC(470.29977)GTLSR	NA,C272,C272,NA	,,X;X;	1.1001,,X;X;	1.1001	B4E1N1 Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=1 , Q6NXE6 Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=2 , Q6NXE6-2 Isoform 2 of Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 ,
YAIC(464.28596)SALAASALPALVM(15.994915)SK	C125,M138,NA	,,,,,	1.50007,1.4424,,1.28463,1.33735,,1.22696,1.28915,,	1.31325	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
YAIC(464.28596)SALAASALPALVM(15.994915)SK	C125,M138,NA	,,X;X;	1.65944,,X;X;	1.65944	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
LC(464.28596)YVALDFEQEM(15.994915)ATAASSSSEK	NA,NA,NA,NA,NA,NA	,,,,,	1.2684,1.3396,1.31463,,1.40584,1.21258,,1.14382,,	1.291515	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 , Q6S8J3 POTE ankyrin domain family

					member E OS=Homo sapiens GN=POTEE PE=1 SV=3 ,
ISSTLKVEPC(470.29977)SL TPGYTK	C219,NA,NA,NA,NA,NA	;;X;X;	2.37473;;X;X;	2.37473	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1-2 Isoform 2 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 , G5E9D4 Elongation protein 4 homolog (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=ELP4 PE=1 SV=1 ,
LFNTAVC(464.28596)ESK	NA,NA,NA	U;;X;X;	1.70597;;X;X;	1.70597	Q9BXJ9 N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1 ,
LTAC(464.28596)QVATAF NLSR	NA,C425,C425,NA	;;X;X;	1.86785;;X;X;	1.86785	O95671-3 Isoform 3 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671-2 Isoform 2 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671 N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3 ,
YC(464.28596)DHENAAFK DVALVLTVLLEETLEASVGP R	C382,NA	U;;X;X;	8.28156;;X;X;	8.28156	Q8NFQ8 Torsin-1A-interacting protein 2 OS=Homo sapiens GN=TOR1AIP2 PE=1 SV=1 ,
LPPIYPNAPC(464.28596) FNNVAEYESFLR	NA,NA	U;;X;X;	1.49729;;X;X;	1.49729	P83369 U7 snRNA-associated Sm-like protein LSM11 OS=Homo sapiens GN=LSM11 PE=1 SV=2 ,
VTHLVANC(470.29977)TQ GEK	NA,C221,NA,C221,NA	;;X;X;	1.78571;;X;X;	1.78571	Q9H8V3-4 Isoform 4 of Protein ECT2 OS=Homo sapiens GN=ECT2 , Q9H8V3-3 Isoform 3 of Protein ECT2 OS=Homo sapiens GN=ECT2 , Q9H8V3-2 Isoform 2 of Protein ECT2 OS=Homo sapiens GN=ECT2 , Q9H8V3 Protein ECT2 OS=Homo sapiens GN=ECT2 PE=1 SV=4 ,
SC(470.29977)FPSLFQAEQ THR	C183,NA	U;;X;X;	1.76775;;X;X;	1.76775	P50336 Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1 ,
VSC(470.29977)SPVSAQLL SVLQGLLHLEPTLR	C284,NA,NA	;;X;X;	1.48774;;X;X;	1.48774	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 , Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 ,
C(464.28596)SEGSFLLTTF PRPVTVEPMDQLDDEEGLP EK	NA,NA	;;X;X;	1.34684;;X;X;	1.34684	Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 ,

VSC(470.29977)SPVSAQLL SVLQGLLHLEPTLR	C284,NA,NA	,,X;X;	1.8592,,X;X;	1.8592	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 , Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 ,
YSTGSDSASFHTTPSM(15. 994915)C(470.29977)LNP DLEGPPLEAYTIQGQY	M216,C217,NA,NA	,,,,X;	1.36614,,1.35427,, X;	1.360205	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,
FQGIKHEC(470.29977)QA NGPEDLNR	C118,NA,NA	,,X;X;	1.0944,,X;X;	1.0944	P60981-2 Isoform 2 of Dextrin OS=Homo sapiens GN=DSTN , P60981 Dextrin OS=Homo sapiens GN=DSTN PE=1 SV=3 ,
LM(15.994915)DL DVEQLG IPEQEYSC(470.29977)VVK	NA,NA	U,,X;X;	1.21151,,X;X;	1.21151	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 ,
C(470.29977)PAPPRGPPA PAPEVEELAR	C161,NA	U,,X;X;	1.29196,,X;X;	1.29196	P48681 Nestin OS=Homo sapiens GN=NES PE=1 SV=2 ,
C(470.29977)M(15.99491 5)PTFQFFK	NA,NA	,,,,;	1.29825,,1.30454,,1 .21148,;	1.29825	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,
IAVAAQNC(464.28596)YK	C67,NA,NA	,,X;X;	1.78804,,X;X;	1.78804	P60174-1 Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 , P60174 Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 ,
ALNALC(470.29977)DGLID ELNQALK	NA,NA,NA	U,,U,,U,;	1.30236,,1.24613,,1 .28019,;	1.28019	P30084 Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 ,
AFDTAGNGYC(470.29977) R	C223,NA	,,X;X;	1.43855,,X;X;	1.43855	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
TIQFVDWC(464.28596)PT GFK	NA,C347,NA,NA,NA,C347, NA	,,,X,,,;	1.62533,1.83993,,X ;1.43818,;	1.62533	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 , Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 ,
AGSDGESIGNC(464.28596)PFSQR	C35,NA	U,,X;X;	1.61325,,X;X;	1.61325	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 ,
AGSDGESIGNC(464.28596)PFSQR	C35,NA	U,,U,,U,;	1.55027,,1.54588,,1 .17539,;	1.54588	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 ,
C(470.29977)ILTTVPDGTG VM(15.994915)SR	NA,C188,M200,C199,M21 1,NA,NA	,,X;X;	1.67266,,X;X;	1.67266	Q5VT66-2 Isoform 2 of Mitochondrial amidoxime-reducing component 1 OS=Homo sapiens GN=MARC1 , Q5VT66-3

					Isoform 3 of Mitochondrial amidoxime-reducing component 1 OS=Homo sapiens GN=MARC1 , H7BYZ9 Mitochondrial amidoxime-reducing component 1 (Fragment) OS=Homo sapiens GN=MARC1 PE=1 SV=1 , Q5VT66 Mitochondrial amidoxime-reducing component 1 OS=Homo sapiens GN=MARC1 PE=1 SV=1 ,
AVC(470.29977)M(15.994915)LSNTTAVAEAWAR	C376,M377,NA	;;X;X;	1.64507,1.0769;;X;X;	1.360985	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
M(15.994915)SSYAFFVQTC(464.28596)R	NA,M13,C23,M13,C23,NA,M13,C23,NA	;;X;X;	1.54545;;X;X;	1.54545	P26583 High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 , Q5T7C4 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=1 , B2RPK0 Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 , D6R9A6 High mobility group protein B2 (Fragment) OS=Homo sapiens GN=HMGB2 PE=1 SV=1 , P09429 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 ,
AVC(470.29977)M(15.994915)LSNTTAVAEAWAR	C376,M377,NA	;;X;X;	2.06293;;X;X;	2.06293	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
YM(15.994915)ACC(464.28596)LLYR	NA,M313,C316,M313,C316,M383,C386,NA,NA,NA	;;;X;	1.57467;;1.44476;;X;	1.509715	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
TYDPSGDSTLPTC(470.29977)SK	NA,NA	U;;X;U;;	1.36969;;X;5.00278;;	3.186235	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
DILKEM(15.994915)FPYEA STPTGISASC(464.28596)R	M308,C323,NA,NA,NA,NA,NA,NA	;;X;X;	1.13741;;X;X;	1.13741	G5E972 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 , P42167 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 , P42167-2 Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO ,
M(15.994915)AVGPPDC(464.28596)PVGGLTFPGR	M155,C162,NA,NA,NA	;;X;X;	1.21211;;X;X;	1.21211	H3BNM4 INO80 complex subunit E OS=Homo sapiens GN=INO80E PE=1 SV=1 , Q8NBZ0 INO80 complex subunit E

					OS=Homo sapiens GN=INO80E PE=1 SV=1 , J3KNE2 INO80 complex subunit E OS=Homo sapiens GN=INO80E PE=1 SV=1 ,
NQSFC(464.28596)PTVNL DKLWTLVSEQTR	NA,C70,NA,NA	,,;,;,;	1.40474,1.4252,,1.28818,,1.20483,;	1.34646	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 , E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 , E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 ,
NQSFC(464.28596)PTVNL DKLWTLVSEQTR	NA,C70,NA,NA	,,;,;,;	1.33165,1.40022,,1.09153,,1.22858,;	1.280115	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 , E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 , E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 ,
GC(464.28596)QDFGWDP CFQPDGYEQTYAEMPK	C129,NA	,,;X;X;	1.6092,,;X;X;	1.6092	Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 ,
IIDLEEADEIEDIQEITVLS QC(464.28596)DSSVYVK	C77,NA,NA,NA	,,;X;X;	0.75475,,;X;X;	0.75475	B4E0Y9 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1 , Q9P289-3 Isoform 3 of Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 , Q9P289 Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=2 ,
TTC(464.28596)SSGSALGP GAGAAQPSASPLEGLDLSY PR	C12,C12,NA,NA	,,;X;X;	2.27556,,;X;X;	2.27556	Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=2 SV=1 , F8WDZ3 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 , Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 ,
VFIM(15.994915)DNC(470 .29977)EELIPEYLNFR	NA,M371,C374,NA	,,;X;X;	1.10461,,;X;X;	1.10461	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 , P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 ,
SC(470.29977)TAPTAQPH DRPLTASSSLAPGQR	C239,C239,NA	,,;X;X;	1.92489,,;X;X;	1.92489	Q7Z5J4 Retinoic acid-induced protein 1 OS=Homo sapiens GN=RAI1 PE=1 SV=2 , Q7Z5J4-3 Isoform 3 of Retinoic acid-induced protein 1 OS=Homo sapiens GN=RAI1 ,
TFDLYANVRPC(470.29977)VSIEGYK	C49,NA,C49,NA,NA	,,;X;X;	1.16271,,;X;X;	1.16271	P50213-2 Isoform 2 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A ,

					P50213 Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 ,
VQENSAYIC(464.28596)SR	C585,NA	U,,X;X;	1.75937,,X;X;	1.75937	Q9Y3T9 Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 ,
C(464.28596)EGINISGNFY R	NA,NA	,,X;X;	1.50692,,X;X;	1.50692	M0QYS1 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=1 SV=2 ,
VALEGLRPTIPPGISPHVC(464.28596)K	C361,NA,C453,NA,NA	,,,,X;	1.61321,,2.70016,,X;	2.156685	Q13418-2 Isoform 2 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK , Q13418 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 , A0A0A0MTH3 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1 , Q13418-3 Isoform 3 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK ,
LSDFGLC(464.28596)TGLK	C142,NA,C194,NA	,,X;X;	1.63213,,X;X;	1.63213	Q9Y2H1-2 Isoform 2 of Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L , Q9Y2H1 Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3 , F5H277 Serine/threonine-protein kinase 38-like (Fragment) OS=Homo sapiens GN=STK38L PE=1 SV=7 ,
KC(470.29977)GETAFIAPQ CEM(15.994915)IPIEWVCR	C81,M93,NA	,,X;X;	1.3368,,X;X;	1.3368	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
KC(470.29977)GETAFIAPQ CEM(15.994915)IPIEWVCR	C81,M93,NA	,,X;X;	1.25979,,X;X;	1.25979	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
SIEIPRPVDGVEVPGC(464.28596)GK	NA,NA,NA,NA	,,X;X;	1.78902,,X;X;	1.78902	K7ENG2 Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=1 , P26368 Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 , P26368-2 Isoform 2 of Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 ,
AC(464.28596)QSIYPLHDV FVR	NA,NA,C201,NA,NA	,,,,;	1.30263,,1.4925,,1.42456,,	1.42456	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
LC(464.28596)VQNSPQEA	C150,C150,NA,NA,NA,NA	,,,,;	1.38061,,1.47074,,1	1.38061	P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2

R			.07253,;		OS=Homo sapiens GN=CSTF2 , P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 , E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 , E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 , A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 ,
AC(464.28596)QSIYPLHDV FVR	NA,NA,C201,NA,NA	,,;,;	1.41052,;1.34029,;1.39623,;	1.39623	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
AC(464.28596)QSIYPLHDV FVR	C201,NA	,;X;X;	2.26968,;X;X;	2.26968	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 ,
LDLGLCSVSC(470.29977) ALEFIPNSK	C256,NA	U,;X;X;	1.20895,;X;X;	1.20895	Q9BSH4 Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1 ,
HTGPGILSM(15.994915)A NAGPNTNGSQFFIC(470.29 977)TAK	M100,C115,NA	,,;X,;	1.11732,1.1937,;X; 2.3428,;	1.1937	P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
SGQGAFGNMC(470.29977) JR	C96,NA	,;X,;	1.50215,;X;1.0792,;	1.290675	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
FM(15.994915)TPVIQDNP SGWGPC(464.28596)AVPE QFR	M5,C19,NA,NA,NA	,,;,;	1.3775,;1.42958,;1.28268,;	1.3775	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D , O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 , O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D ,
C(470.29977)QDSMINNSQ C(464.28596)HKQGDFPYQ VGTELSIQISEDENYIVNK	NA,NA	,;X;X;	0.69509,;X;X;	0.69509	Q9NYT6 Zinc finger protein 226 OS=Homo sapiens GN=ZNF226 PE=2 SV=2 ,
GVAQTPGSVEEDALLC(464 .28596)GPVSK	C79,NA	,;X;X;	1.52133,;X;X;	1.52133	Q9BQP7 Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens GN=MGME1 PE=1 SV=1 ,
ALIVGHC(470.29977)M(15 .994915)PGPR	NA,NA,NA	U,;X;X;	1.30918,;X;X;	1.30918	Q6P1L8 39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 ,
C(470.29977)VYTYIQEFYR	NA,NA,C948,C892,NA	,;X;X;	1.67809,;X;X;	1.67809	B5MCI0 Smoothelin OS=Homo sapiens GN=SMTN PE=1

					SV=1 , A0A096LNK9 Smoothelin (Fragment) OS=Homo sapiens GN=SMTN PE=1 SV=1 , A0A087WVP4 Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=1 , P53814-5 Isoform B2 of Smoothelin OS=Homo sapiens GN=SMTN ,
VHPAMATAAGGC(470.29 977)R	NA,NA	;;X;X;	1.64504;;X;X;	1.64504	H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 ,
C(464.28596)VQSNIVLLTQ AFR	NA,NA,NA,NA,NA	;;X;X;	0.76325;;X;X;	0.76325	O94925-3 Isoform 3 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS , O94925 Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1 ,
SQSPAASDC(470.29977)SS SSSASLPSSGR	NA,C121,NA	;;X;X;	2.25954;;X;X;	2.25954	O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 , C9JFK9 BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=1 SV=1 ,
FTLDC(464.28596)THPVED GIM(15.994915)DAANFEQ FLQER	NA,NA	U;;X;X;	1.60025;;X;X;	1.60025	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 ,
VLLSICSLLC(470.29977)DP NPDDPLVPEIAR	C113,NA,NA	;;X;X;	1.52543;;X;X;	1.52543	P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 , P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 ,
GRDDC(464.28596)GTFED TGPLLQFDYK	C268,NA,NA	;;X;X;	1.30396;;X;X;	1.30396	Q14684-2 Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B , Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 ,
M(15.994915)AGIFDVNTC (464.28596)YGSPQSPQLIR	NA,NA,NA,M419,C428,NA ,NA	;;X;X;	1.25471;;X;X;	1.25471	Q9BTX1-2 Isoform 2 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1 Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 PE=1 SV=2 , Q9BTX1-4 Isoform 4 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1-5 Isoform 5 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1-6 Isoform 6 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 ,
LNPAVTC(464.28596)AGK	NA,NA	U;;X;X;	1.19592;;X;X;	1.19592	Q8TD19 Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2 ,
AYHEQLSVAEITNAC(464.2 8596)FEPANQM(15.99491	NA,NA,NA,NA,NA,NA	,,,,;	1.37927,1.43927,1.46053;;1.39099;;1.2	1.39099	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q13748 Tubulin alpha-3C/D chain

5)VK			774,;		OS=Homo sapiens GN=TUBA3C PE=1 SV=3 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
AYHEQLSVAEITNAC(464.28596)FEPANQM(15.994915)VK	NA,C295,M302,NA,NA,NA	,,;,X;	1.50452,1.52033,;1.40535,1.43854,;X;	1.47153	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
SLC(464.28596)NLEESITSA GRDDLESFQLEISGFLK	NA,NA,NA	,,;,X;	1.27122,1.41719,;1.52808,;X;	1.41719	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
SLC(464.28596)NLEESITSA GRDDLESFQLEISGFLK	NA,NA,NA	,;X;X;	1.54847,;X;X;	1.54847	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
VC(464.28596)ENIPIVLCK NK	NA,NA,NA,NA,NA	,;X;X;	11.46042,;X;X;	11.46042	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 , J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 , B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 , F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 ,
M(15.994915)HSVGIC(464.28596)GSDVHYWEYGR	M39,C45,NA	,;X;X;	1.98182,;X;X;	1.98182	Q00796 Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 ,
KLPLTALAQNMQEASTQLE DSLLGC(470.29977)WR	NA,NA	U,;X;X;	0.68808,;X;X;	0.68808	I3L1S9 Rho GTPase-activating protein 17 OS=Homo sapiens GN=ARHGAP17 PE=1 SV=1 ,
VLGAHILGPGAGEM(15.994915)VNEAALALEYGASC(464.28596)EDIAR	M440,C454,M463,C477,NA,NA,NA,M415,C429,NA,NA	,;X;X;	1.22996,;X;X;	1.22996	E9PEX6 Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=1 SV=1 , P09622 Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 , P09622-2 Isoform 2 of Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD , P09622-3 Isoform 3 of Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD ,
SELLAEFPGFLEGEDGDT AKIC(464.28596)QADIVEA	C172,NA	,;X;X;	1.32798,;X;X;	1.32798	O15213 WD repeat-containing protein 46 OS=Homo sapiens GN=WDR46 PE=1 SV=3 ,

VDIASAAK					
GSSPTPPC(470.29977)SPV QPSK	NA,NA,NA,C459,NA	;;X;X;	1.44639;;X;X;	1.44639	F8VPI7 Double-stranded RNA-binding protein Stauf en homolog 2 OS=Homo sapiens GN=STAU2 PE=1 SV=1 , Q9NUL3-3 Isoform 3 of Double-stranded RNA-binding protein Stauf en homolog 2 OS=Homo sapiens GN=STAU2 , E9PH62 Double-stranded RNA-binding protein Stauf en homolog 2 OS=Homo sapiens GN=STAU2 PE=1 SV=1 , Q9NUL3-2 Isoform 2 of Double-stranded RNA-binding protein Stauf en homolog 2 OS=Homo sapiens GN=STAU2 ,
VVMALGDYM(15.994915) GASCHAC(464.28596)IGG TNVR	NA,NA	;;X;X;	1.36007;;X;X;	1.36007	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 ,
ALVDGPC(470.29977)TQV R	NA,C42,NA	;;X;X;	1.48985;;X;X;	1.48985	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 , P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 ,
QEPLGSDSEGVNC(470.299 77)LAYDEAIM(15.994915) AQQDR	C23,M31,C23,M31,NA	;;X;X;	1.51276;;X;X;	1.51276	J3KR44 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 , Q96FW1 Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2 ,
GEAYNLFEHNC(470.29977)NTFSNEVAQFLTGR	C108,NA	U;;X;X;	1.85077;;X;X;	1.85077	Q6ICB0 Desumoylating isopeptidase 1 OS=Homo sapiens GN=DESI1 PE=1 SV=1 ,
QGEYGLASIC(464.28596)N GGGGASAM(15.994915)LI QKL	NA,NA,NA	U;;U;;U;;	1.47039;;1.65935;;1 .21095;;	1.47039	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
VQTLLEEELGKEEC(464.28 596)FQNK	C354,C354,NA,NA	;;X;X;	1.59014;;X;X;	1.59014	Q9BVJ6-2 Isoform 2 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A , Q9BVJ6 U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1 , Q9BVJ6-3 Isoform 3 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A ,
HFC(470.29977)PNVPIILV GNKK	NA,NA,C107,NA	;;X;X;	1.34432;;X;X;	1.34432	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 , P08134 Rho- related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 , E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 ,

NQSFC(464.28596)PTVNL DK	NA,C70,NA,NA	,,;,;	1.41138,,1.35699,,1 .34187,;	1.35699	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 , E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 , E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 ,
TLTSC(464.28596)FLSCVV CVEGIVTK	NA,NA	U,,X;X;	1.60224,1.63966,,X ;X;	1.62095	J3KQ69 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=2 ,
QSVVVPYEPQVGTEFTIL YNFMC(464.28596)NSSCV GGM(15.994915)NRR	NA,C258,M266,C258,M26 6,NA,NA,C258,M266,NA,C 258,M266,C258,M266,C1 87,M195,NA,C209,M217, NA,NA	,;X;X;	2.76869,,X;X;	2.76869	O15350-12 Isoform 11 of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-6 Isoform Zeta of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350 Tumor protein p73 OS=Homo sapiens GN=TP73 PE=1 SV=1 , O15350-8 Isoform dN-Alpha of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-5 Isoform Epsilon of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-13 Isoform 12 of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-10 Isoform dN-Gamma of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-4 Isoform Delta of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-2 Isoform Beta of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-11 Isoform 10 of Tumor protein p73 OS=Homo sapiens GN=TP73 , A0A0C4DFW9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP73 PE=1 SV=1 , O15350-9 Isoform dN-Beta of Tumor protein p73 OS=Homo sapiens GN=TP73 , O15350-3 Isoform Gamma of Tumor protein p73 OS=Homo sapiens GN=TP73 ,
NM(15.994915)SVHLSPC(464.28596)FR	M109,C116,NA	,,;,;	1.49789,,1.37939,,1 .31667,;	1.37939	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
NIC(464.28596)FTVWDVG GQDR	NA,NA	,;X;X;	1.39071,,X;X;	1.39071	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
NIC(464.28596)FTVWDVG GQDR	NA,NA	,,,X;X;	1.43451,0.87388,0. 97432,,X;X;	0.97432	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
LTTPTYGDLNHLVSATMSG VTTC(464.28596)LR	NA,C239,C239,NA,C221,N A	,,;,;	1.5365,1.56607,,1.4 6262,,1.3179,;	1.49956	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 , P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens

					GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
TTGLVGLAVC(464.28596) NTPHER	NA,C13,C17,C17,NA,NA	,,X;X;	1.32546,,X;X;	1.32546	Q16718-2 Isoform 2 of NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 , H7BYD0 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (Fragment) OS=Homo sapiens GN=NDUFA5 PE=1 SV=1 , F8WAS3 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=1 , Q16718 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3 , C9IZN5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (Fragment) OS=Homo sapiens GN=NDUFA5 PE=1 SV=1 ,
RPLNPLASGQGTSEENTFYS WLEGLC(464.28596)VEK	C241,NA	U,,X;X;	1.35972,,X;X;	1.35972	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 ,
AGIDGESIGNC(470.29977) PFSQR	NA,NA,C32,NA	,,X;X;	2.07907,,X;X;	2.07907	Q9NZA1 Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3 , Q9NZA1-3 Isoform 3 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 , Q9NZA1-2 Isoform 1 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 ,
YGAVDPLLALLAVPDM(15.994915)SSLAC(470.29977) GYLR	M218,C223,NA	U,,X;X;	1.48326,,X;X;	1.48326	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 ,
IYFGSNIPNM(15.994915)F VDSSC(470.29977)ALK	NA,NA	U,,X;X;	1.43788,,X;X;	1.43788	O75477 Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 ,
LLM(15.994915)EQESSAC(470.29977)SR	NA,NA,NA	,,X;X;	2.71999,,X;X;	2.71999	O96011 Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B PE=1 SV=1 , O96011-2 Isoform 2 of Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B ,
METYC(464.28596)SSGST DTSPVIDAVTHALTATPYT R	C288,NA,NA	,,X;X;	8.73647,,X;X;	8.73647	Q02338 D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 ,
C(470.29977)LTQQAVALQ R	NA,C1138,NA,NA	,,X;X;	1.7736,,X;X;	1.7736	O75153 Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2 , K7EIG1 Clustered mitochondria protein homolog (Fragment) OS=Homo sapiens GN=CLUH PE=1 SV=2 , I3L2B0 Clustered

					mitochondria protein homolog (Fragment) OS=Homo sapiens GN=CLUH PE=1 SV=2 ,
NMM(15.994915)AAC(464.28596)DPR	M300,C303,NA,M300,C303,M300,C303,M647,C650,M300,C303,M300,C303,NA,M263,C266,M282,C285,M300,C303,NA	,,,,,,,,,,,,;	1.52615,1.30379,1.52615,1.30379,0.81059,0.81059,;1.3967,1.22285,1.3967,1.22285,;1.27483,1.27483,;	1.28931	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 , P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
GILLYGPPGC(470.29977)GK	C259,NA,NA	,;X;X;	1.87302,;X;X;	1.87302	I3L0N3 Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=1 , P46459 Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3 ,
PGHLQEGFGC(470.29977)VVTNRFDQLFDDSDPFVLEK	C11,C11,C11,NA,NA	,,,,,;	1.24185,1.24991,;1.17798,;1.20633,;	1.22409	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 , Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 , Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 , Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 ,
PGHLQEGFGC(470.29977)VVTNRFDQLFDDSDPFVLEK	C11,C11,C11,NA,NA	,;X;X;	1.34894,;X;X;	1.34894	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 , Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 , Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 , Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 ,

M(15.994915)KVELC(464.28596)SFSGYK	NA,M1,C6,M1,C6,NA	;;X;X;	1.50957;;X;X;	1.50957	C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 ,
LVAFC(464.28596)PFASSQ VALENANAVSEGVVHEDLR	NA,NA	,,,,;X;	1.41541,1.42711,1.58939;;1.33758;;X;	1.42126	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
SVANVIQQAGC(464.28596)PVPEYIK	C536,NA	;;X;X;	1.48942;;X;X;	1.48942	Q9Y2R4 Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3 ,
LVAFC(464.28596)PFASSQ VALENANAVSEGVVHEDLR	NA,NA	,,,X;;;	1.52453,1.77806,1.77478;;X;1.60636;;	1.69057	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
AYSPLHGGSGSYSVC(470.29977)SNSDTK	NA,NA,C190,NA,NA	;;X;X;	1.66792;;X;X;	1.66792	H0YAZ1 Store-operated calcium entry-associated regulatory factor (Fragment) OS=Homo sapiens GN=SARAF PE=1 SV=1 , Q96BY9 Store-operated calcium entry-associated regulatory factor OS=Homo sapiens GN=SARAF PE=1 SV=1 , H0YAN9 Store-operated calcium entry-associated regulatory factor (Fragment) OS=Homo sapiens GN=SARAF PE=1 SV=1 , Q96BY9-2 Isoform 2 of Store-operated calcium entry-associated regulatory factor OS=Homo sapiens GN=SARAF ,
LREC(470.29977)LPLIIFLR	NA,NA,NA	U;;X;X;	1.39278;;X;X;	1.39278	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
NYLPAINGIVFLVDC(464.28596)ADHSR	C102,C102,NA	;;X;X;	1.34967;;X;X;	1.34967	Q5SQT8 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 , Q9NR31 GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1 ,
AGAVVAVPTDTLYGLACAA SC(470.29977)SAALR	C99,NA,NA	U;;U;;U;;	1.42567;;1.08425;;0.88619;;	1.08425	Q86U90 YrdC domain-containing protein, mitochondrial OS=Homo sapiens GN=YRDC PE=1 SV=1 ,
NIAQIAVVMGSC(464.28596)TAGGAYVPAM(15.994915)ADENIIVR	NA,NA,NA	;;X;X;	1.68742;;X;X;	1.68742	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
HGFC(470.29977)GIPITDT GR	NA,NA	,,,,;	1.44026;;1.52221;;1.20142;;	1.44026	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 ,
NLSLDLIDLVPSLC(464.28596)EDLLSSVDQPLK	NA,NA,C65,NA,NA,C24,NA,NA,NA,NA	;;X;X;	1.22745;;X;X;	1.22745	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 , P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB , B1AK88 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_d OS=Homo sapiens

					GN=CAPZB PE=1 SV=1 , B1AK87 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 ,
NLSDLIDLVPSTLC(464.28596)EDLLSSVDQPLK	NA,NA,C65,NA,NA,C24,NA,NA,NA,NA	,,X;X;	1.32774,,X;X;	1.32774	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 , P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB , B1AK88 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK87 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 ,
C(470.29977)IPALDSLTPA NEDQK	NA,NA,NA	U,,X;X;	1.28444,,X;X;	1.28444	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
C(470.29977)IPALDSLTPA NEDQK	NA,NA,NA	U,,X;X;	1.32693,,X;X;	1.32693	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
TFM(15.994915)C(464.28596)TGRPGWLTSLR	M49,C50,M49,C50,NA	,,X;X;	1.61032,,X;X;	1.61032	Q15392-2 Isoform 2 of Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 , Q15392 Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2 ,
VLPMNTGVEAGETAC(464.28596)K	NA,NA,NA	U,,X;X;	1.80484,,X;X;	1.80484	P04181 Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 ,
ECENC(470.29977)DCLQG FQLTHSLGGGTGSGM(15.994915)GTLLISK	C474,M494,NA	,,,X;X;	0.00392,0.0,,X;X;	0.00196	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
IQFNDLQSLLC(470.29977)ATLQNVLR	C440,C440,NA	,,X;X;	1.31441,,X;X;	1.31441	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 , Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 ,
DTQTSITDSC(464.28596)A VYR	C100,NA	U,U,U,,X;X;	2.11136,1.65951,2.11303,,X;X;	2.11136	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
GQKC(464.28596)EFQDAY VLLSEK	NA,NA,NA	U,,X;X;	1.29697,,X;X;	1.29697	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
TNHIGHTGYLNTVTVPDGS LC(464.28596)ASGGKDGQ	NA,NA	,,X;X;	1.39525,,X;X;	1.39525	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,

AM(15.994915)LWDLNEG K					
IAPC(464.28596)PSQDSLY SDPLDSTSAQAGEGVQR	C308,NA	,;X;X;	2.14918,,X;X;	2.14918	Q99704 Docking protein 1 OS=Homo sapiens GN=DOK1 PE=1 SV=1 ,
SLGTPEDGMAVC(464.285 96)MFMQNTLTRFM(15.99 4915)SR	NA,NA	U,,X;X;	1.22264,,X;X;	1.22264	H0Y525 Ethylmalonyl-CoA decarboxylase (Fragment) OS=Homo sapiens GN=ECHDC1 PE=1 SV=1 ,
SIQFVDWC(470.29977)PT GFK	NA,C347,NA,NA	,,,;,,;X;	1.49499,1.88157,1. 70328,,1.41343,1.6 0335,,X;	1.60335	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
VMTIPYQPM(15.994915)P ASSPVIC(464.28596)AGG QDR	M186,C194,NA	U,,X;X;	1.5316,,X;X;	1.5316	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
LVVPASQC(470.29977)GS LIGK	C109,C109,NA	,;X;X;	1.35657,,X;X;	1.35657	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,
LVVPASQC(470.29977)GS LIGK	NA,C109,C109,C109,NA	,,,;,,;	1.38602,1.72502,,1. 3936,,1.27579,,	1.38981	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,
ALADAQIPYSAVDQACVGY VFGDSTC(464.28596)GQR	NA,NA	,;X;X;	2.04658,,X;X;	2.04658	P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 ,
VAC(464.28596)IGAWHPA R	C253,NA	,;X;X;	1.43958,,X;X;	1.43958	P39023 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 ,
NSQWVPTLPNSSHHLDAVP C(464.28596)STTINR	C138,C138,C138,NA,NA,N A,NA,NA,NA	,;X;,,;	1.40338,,X;1.36319 ,,	1.383285	Q12824 SWI/SNF-related matrix-associated actin- dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 PE=1 SV=2 , Q12824-2 Isoform B of SWI/SNF-related matrix-associated actin- dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 , G5E975 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, isoform CRA_c OS=Homo sapiens GN=SMARCB1 PE=1 SV=1 ,

FEQSDLEAFYNVITVC(464.28596)GTNEVR	NA,C308,NA	;;X;X;	1.25896;;X;X;	1.25896	Q5JPI3-2 Isoform 2 of Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 , Q5JPI3 Uncharacterized protein C3orf38 OS=Homo sapiens GN=C3orf38 PE=1 SV=1 ,
CPEALFQPSFLGMESC(470.29977)GIHETTFNSIM(15.994915)K	NA,NA,NA,NA,NA	;;;X;	1.51924;;1.94828;;X;	1.73376	P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 , P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
GNHEC(470.29977)ASINR	NA,C126,C83,NA	;;X;X;	1.33499;;X;X;	1.33499	P62136-2 Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA , P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 , P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 ,
SLHDALC(470.29977)VLAQTVK	C348,NA	;;X;;;	1.45772;;X;1.04717;;	1.252445	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 ,
C(470.29977)SWLVPSPK	NA,C210,NA	;;X;X;	1.97275;;X;X;	1.97275	Q3SXM5 Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens GN=HSDL1 PE=1 SV=3 , Q3SXM5-2 Isoform 2 of Inactive hydroxysteroid dehydrogenase-like protein 1 OS=Homo sapiens GN=HSDL1 ,
SLHDALC(470.29977)VLAQTVK	C348,NA	;;;;	1.69006;;1.58481;;1.44074;;	1.58481	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 ,
SLHDALC(470.29977)VLAQTVK	C348,NA	;;X;X;	1.63008;;X;X;	1.63008	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 ,
TSLDLYANVIHC(470.29977)K	NA,NA,NA	;;X;X;	1.649;;X;X;	1.649	P51553 Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 ,
GPAVGIDLGTYSYC(470.29977)VGVFQHGK	C17,NA,NA,NA	;;X;X;	0.95246;;X;X;	0.95246	P11142 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 , P11142-2 Isoform 2 of Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 , E9PKE3 Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 ,
LICC(470.29977)DILDVLDKHLIPAANTGESK	C98,NA,NA	;;X;X;	0.97936;;X;X;	0.97936	P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 , P62258-2 Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE ,
DSGAALGLGIALHSPC(470.29977)YAQVR	NA,C269,NA	;;X;X;	2.14375;;X;X;	2.14375	K7ESE6 Glucose-6-phosphatase 3 (Fragment) OS=Homo sapiens GN=G6PC3 PE=1 SV=1 , Q9BUM1 Glucose-6-

					phosphatase 3 OS=Homo sapiens GN=G6PC3 PE=1 SV=2 ,
GSSVDAPPRPC(464.28596))HTTPDSQFGTEHVLR	NA,C635,NA	,;X;X;	1.65609,,X;X;	1.65609	Q9BSJ8-2 Isoform 2 of Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 , Q9BSJ8 Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 ,
C(464.28596)SEGSFLLTTF PRPVTVEPM(15.994915)D QLDDEEGLPEK	C119,M138,NA,NA	,,;,;	1.58199,,2.0305,,1.31178,;	1.58199	Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO , Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 ,
GISEFIVM(15.994915)AAD AEPLIILHLPLLC(470.2997 7)EDKNVPYVFVR	NA,M56,C73,NA	,;X;X;	1.31738,,X;X;	1.31738	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 , P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 ,
GISEFIVM(15.994915)AAD AEPLIILHLPLLC(470.2997 7)EDKNVPYVFVR	NA,M56,C73,NA	,;X;X;	1.39899,,X;X;	1.39899	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 , P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 ,
VNSDC(470.29977)DSVLP SNFLLGGNIFDPLNLNLLDE EVS	NA,NA	U,,X;X;	1.47205,,X;X;	1.47205	Q7L2J0 7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1 ,
VVVAENFDEIVNNENKDVLI EFYAPWC(470.29977)GHC K	NA,NA	U,,X;X;	2.67839,,X;X;	2.67839	P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 ,
SC(470.29977)PSFSASSE GTR	C9,C9,C9,NA	,;X;X;	1.38594,,X;X;	1.38594	D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 , P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 , D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 ,
VSVHC(464.28596)PVFDY VPPELITLFIISNIGGNAPSYI YR	C310,NA	U,,X;X;	1.48492,,X;X;	1.48492	P49770 Translation initiation factor eIF-2B subunit beta OS=Homo sapiens GN=EIF2B2 PE=1 SV=3 ,
VILITPTPLC(464.28596)ET AWEEQCIHQGCK	C137,C117,NA	,;X;X;	1.46129,,X;X;	1.46129	Q2TAA2 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Homo sapiens GN=IAH1 PE=1 SV=1 , H7C5G1 Isoamyl acetate-hydrolyzing esterase 1 homolog (Fragment) OS=Homo sapiens GN=IAH1 PE=1 SV=1 ,
VNAAGTDPSSPVGFVLGVD LLHIFPLEGATFLC(464.285 96)PADVTDPR	NA,NA,NA	U,,U;X;	1.51342,,1.28524,,X;	1.39933	Q9UI43 rRNA methyltransferase 2, mitochondrial OS=Homo sapiens GN=FTSJ2 PE=1 SV=1 ,
AC(464.28596)FQVGTSEE M(15.994915)K	NA,C157,M166,C729,M73 8,NA,C729,M738,C717,M	,;X;X;	1.99475,,X;X;	1.99475	P35658-4 Isoform 4 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 , A0A0A0MSW3

	726,NA				Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=1 , P35658 Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 , P35658-2 Isoform 2 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 , P35658-3 Isoform 3 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 , P35658-5 Isoform 5 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 ,
C(470.29977)VLPEEDSGEL AKPK	C318,NA,NA	;;X;X;	2.46056;;X;X;	2.46056	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP , Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 ,
LPITVLNGAPGFINLC(470.2 9977)DALNAWQLVK	NA,C240,NA	;;X;X;	1.37765;;X;X;	1.37765	P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 , P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC ,
TFDLYANVRPC(464.28596)VSIEGYK	C49,NA,C49,NA,NA	;;X;X;	1.16271;;X;X;	1.16271	P50213-2 Isoform 2 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A , P50213 Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 ,
C(464.28596)FLAQPVTLTD IYTHWQQTSELGR	NA,NA,NA,NA,NA,NA,C38, C38,C38,NA	;;X;X;	1.20364;;X;X;	1.20364	E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 , Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-6 Isoform 6 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 , Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 , J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 ,
C(464.28596)FLAQPVTLTD IYTHWQQTSELGR	NA,NA,NA,NA,NA,NA,C38, C38,C38,NA	;;X;X;	0.69653;;X;X;	0.69653	E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 , Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-6 Isoform 6 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-4 Isoform 4 of

					Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 , Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 , J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 ,
FILSLASC(470.29977)KK	C194,NA,NA	;;X;X;	1.55471;;X;X;	1.55471	E9PMU0 RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=1 , Q9H0A0 RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=2 ,
SSHAPATC(464.28596)K	C655,NA,NA	;;X;X;	1.41656;;X;X;	1.41656	Q8ND24 RING finger protein 214 OS=Homo sapiens GN=RNF214 PE=1 SV=2 , Q8ND24-2 Isoform 2 of RING finger protein 214 OS=Homo sapiens GN=RNF214 ,
C(470.29977)DLSPWAVSR	NA,NA	;;X;X;	1.87015;;X;X;	1.87015	O14966 Ras-related protein Rab-7L1 OS=Homo sapiens GN=RAB29 PE=1 SV=1 ,
YIYDQC(464.28596)PAVA GYGPIELPDYNR	C453,NA,NA	U;;U;X;	1.1609;;1.39748;;X;	1.27919	P31930 Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 ,
IISDNLYC(464.28596)K	NA,NA	;;;;;	1.55473;;1.42448;;1 .4069;;	1.42448	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
ADASSTPSFQQAFASSC(47 0.29977)TISSNGPGQRR	NA,NA	;;X;X;	7.07549;;X;X;	7.07549	Q68C22 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
LTTPTYGDLNHLVSATM(15 .994915)SGVTTC(470.299 77)LR	NA,M233,C239,M233,C23 9,NA,M215,C221,NA	;;;;;	1.38656,1.41473,1. 67709;;1.34864;;1.2 0745;;	1.38656	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 , P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
QNSDFLC(470.29977)QM DLLQEFYETTLEALKDAK	C130,NA	U;;X;X;	1.47163;;X;X;	1.47163	P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 ,
GC(470.29977)LWALNPAK IDK	NA,NA	U;;X;U;;	1.43599;;X;1.2589;;	1.347445	O15353 Forkhead box protein N1 OS=Homo sapiens GN=FOXN1 PE=2 SV=1 ,
LLQC(470.29977)DPSSASQ F	NA,NA	;;;;;	1.61386;;1.47356;;1 .34371;;	1.47356	P37235 Hippocalcin-like protein 1 OS=Homo sapiens GN=HPCAL1 PE=1 SV=3 ,
DLNYC(464.28596)FSGMS	C267,C267,C267,NA	;;X;X;	1.44591,1.86585;;X	1.65588	P31943 Heterogeneous nuclear ribonucleoprotein H

DHR			;X;		OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 , P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 ,
STFFNVLTSQASAENFPFC (470.29977)TIDPNESRVPV PDER	NA,NA,NA	,,;,X;	1.57621,2.35277,,1. 51046,,X;	1.57621	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 , Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 ,
DLNYC(464.28596)FSGMS DHR	C267,C267,C267,NA	,;X;X;	1.57618,,X;X;	1.57618	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 , P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 ,
SDITKLEVDIVNAANSSLLG GGGVVGGC(464.28596)IHR	C186,NA	U,U,,X;U,;	1.43444,1.72543,,X ;1.32481,,	1.43444	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
GFGFVC(464.28596)FSSPE EATK	NA,NA,C339,NA,NA,NA,N A,C339,NA	,;X;X;	0.94684,,X;X;	0.94684	B1ANR0 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC4 PE=1 SV=1 , Q13310 Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1 , Q13310-2 Isoform 2 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 , P11940 Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 , A0A087WTT1 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 , Q13310-3 Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 , P11940-2 Isoform 2 of Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 , Q9H361 Polyadenylate-binding protein 3 OS=Homo sapiens GN=PABPC3 PE=1 SV=2 ,
TFVDFFSQC(464.28596)LH EEYR	NA,NA	U,,U,,X;	1.39305,,1.50388,, X;	1.448465	Q53GQ0 Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 ,
TPESTKPGPVC(470.29977) QPPVSQSR	C209,NA	U,,X;X;	1.80372,,X;X;	1.80372	Q6AI12 Ankyrin repeat domain-containing protein 40 OS=Homo sapiens GN=ANKRD40 PE=1 SV=2 ,
SDLYEVIQSTLDGLLC(464.2 8596)TSLPVWLENHTALT VM(15.994915)ASK	NA,NA	,;X;X;	1.548,,X;X;	1.548	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 ,

TNHIGHTGYLNTVTVSPDGS LC(464.28596)ASGGK	NA,NA	,,X;X;	0.17551,,X;X;	0.17551	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
TNHIGHTGYLNTVTVSPDGS LC(464.28596)ASGGK	NA,NA	,,X;X;	1.543,,X;X;	1.543	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
VCNALALLQC(464.28596) VASHPETR	NA,NA,C99,NA	,,X;X;	1.47626,,X;X;	1.47626	Q92600-2 Isoform 2 of Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 , Q92600 Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 PE=1 SV=1 , Q92600-3 Isoform 3 of Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 ,
GTEAGQVGEPGIPTGEAGP SC(470.29977)SSASDKLPR	C241,NA	U,,X;X;	0.64909,,X;X;	0.64909	O15355 Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 ,
GLIAAIC(464.28596)AGPT ALLAHEIGFGSK	NA,C86,NA,NA	,,,X,,,;	1.26856,1.23897,,X ;1.26402,,;	1.26402	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
GLIAAIC(464.28596)AGPT ALLAHEIGFGSK	NA,C86,NA,NA	,,X,,,;	1.23904,,X;1.23,,;	1.23452	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
LLEETGIC(464.28596)VVP GSGFGQR	C477,NA	,,,X;	1.92471,,1.95991,, X;	1.94231	Q8TD30 Alanine aminotransferase 2 OS=Homo sapiens GN=GPT2 PE=1 SV=1 ,
TGNGPMSVC(464.28596) GR	NA,C493,NA,NA,NA,NA	,,X;X;	1.41359,,X;X;	1.41359	O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 , O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , A0A087X1A5 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 , Q5JW30 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 ,
VLPM(15.994915)NTGVEA GETAC(464.28596)K	NA,NA,NA	U,,U,,X;	1.41973,,2.06714,, X;	1.743435	P04181 Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 ,

SSIINSLKQEQM(15.994915)C(464.28596)NVGVSMGLTR	M267,C268,M267,C268,NA	;;X;X;	1.68925;;X;X;	1.68925	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
LAEQC(464.28596)GGLQGFLIFRSFGGGTSGFTSLLMER	C96,NA,NA	;;X;X;	3.32944;;X;X;	3.32944	A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 , A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 ,
YDNSLKIISNASC(464.28596)TTNCLAPLAK	C152,NA	;;X;X;	1.40689;;X;X;	1.40689	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
LNIIISNLDC(470.29977)VNEVIGIR	C402,C357,NA,C390,NA	;;;X;	1.40721,1.5481,,1.57852;;X;	1.5481	P30154-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B , P30154-4 Isoform 4 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B , P30154 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3 , P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 ,
YYALCGFGGVLSC(470.29977)GLTHTAVVPLDLVK	NA,NA,NA	;;;X;	1.36624,,1.24398,,X;	1.30511	Q00325-2 Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 ,
YYALCGFGGVLSC(470.29977)GLTHTAVVPLDLVK	NA,NA,NA	;;X;X;	1.4855;;X;X;	1.4855	Q00325-2 Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 ,
VSLDPELEEALTSASDTELC(464.28596)DLAAILGM(15.994915)HNLITNTK	C132,M140,NA	U;;U;;U;;	1.2115,,1.13134,,1.17062;;	1.17062	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 ,
IDRYTQQGFGNLPIC(464.28596)M(15.994915)AK	C841,M842,NA,C906,M907,NA,C907,M908,NA	;;X;;	2.10763;;X;1.49434;;	1.800985	A0A087WVM4 Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 , Q6UB35 Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 , B7ZM99 MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 ,
C(464.28596)YEMASHLR	NA,NA	;;X;X;	0.80932;;X;X;	0.80932	P07737 Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 ,
GSSPQNNTTPKPSVEGQQPAAAAAC(470.29977)EPVDHAQSESILK	C394,NA,NA	;;X;X;	0.8598;;X;X;	0.8598	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 , Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 ,

LVTSPCC(464.28596)IVTST YGTANM(15.994915)ER	NA,C598,M610,NA	,,;X;X;	1.21743,1.28203,,;X; ;X;	1.24973	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 , P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 ,
HIQNPSAAELVHFLGPLDLI VNTC(470.29977)SGPDIA R	NA,NA,NA	,;X;X;	1.42255,,;X;X;	1.42255	Q9H6S3-3 Isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 , Q9H6S3 Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2 ,
HIQNPSAAELVHFLGPLDLI VNTC(470.29977)SGPDIA R	NA,NA,NA	,;X;X;	1.25313,,;X;X;	1.25313	Q9H6S3-3 Isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 , Q9H6S3 Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2 ,
STPYEC(464.28596)GFDP M(15.994915)SPAR	C39,M44,NA	U,,;U;X;	2.15327,,;1.87668,,; X;	2.014975	P03897 NADH-ubiquinone oxidoreductase chain 3 OS=Homo sapiens GN=MT-ND3 PE=1 SV=1 ,
LGVHPLSC(470.29977)HG WVLGEHGDSSVPVWSGM NVAGVSLK	C214,NA,NA	,;X;X;	1.2692,,;X;X;	1.2692	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA , P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 ,
YSTGSDSASFPHTPSMC(4 70.29977)LNPDLEGPPLEA YTIQGQY	C217,NA	,;X;X;	1.36945,,;X;X;	1.36945	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 ,
LGTLPFCC(470.29977)P WEQLTQDWESR	C706,NA	U,,;X;X;	1.43308,,;X;X;	1.43308	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 ,
VFDPSC(464.28596)GLPYY WNADTDLVSWLSPHDPNS VVTK	NA,C60,C49,C60,C60,C60, NA,NA,NA	,;X;X;	1.2401,,;X;X;	1.2401	O60828-2 Isoform 2 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 , O60828 Polyglutamine- binding protein 1 OS=Homo sapiens GN=PQBP1 PE=1 SV=1 , H7C053 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 , O60828-3 Isoform 3 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 , C9JQA1 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 , O60828-7 Isoform 7 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 , O60828-6 Isoform 6 of Polyglutamine-binding protein 1 OS=Homo sapiens

					GN=PQBP1 , O60828-4 Isoform 4 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 ,
VFDPS(464.28596)GLPYY WNADTLVSWLSPHDPNS VVTK	NA,C60,C49,C60,C60,C60, NA,NA,NA	,;X;X;	1.3718,;X;X;	1.3718	O60828-2 Isoform 2 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 , O60828 Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 PE=1 SV=1 , H7C053 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 , O60828-3 Isoform 3 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 , C9JQA1 Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=1 SV=1 , O60828-7 Isoform 7 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 , O60828-6 Isoform 6 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 , O60828-4 Isoform 4 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 ,
GC(470.29977)STVLSPEGS AQFAAQIFGLSNHLVWSK	C374,NA	,,,;X;	1.40825,1.82021,1. 80761,;2.78731,;X;	1.81391	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
C(464.28596)YQLPPGAR	C223,NA,NA	,;X;X;	1.14763,;X;X;	1.14763	P13716 Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1 , P13716-2 Isoform 2 of Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD ,
VGLTNYAAAYC(470.29977))TGILLAR	C100,NA	,;X;X;	2.02664,;X;X;	2.02664	P46777 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 ,
IHMGSC(464.28596)AENT AK	NA,NA,NA	U,;U,;U,;	1.43424,;1.30399,;1 .23214,;	1.30399	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
LVTSPC(464.28596)CIVTST YGTANM(15.994915)ER	NA,C597,M610,NA	,;X;X;	1.21743,;X;X;	1.21743	P07900-2 Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 , P07900 Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 ,
IINDNATYC(464.28596)R	NA,NA	,;X;X;	1.6454,;X;X;	1.6454	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
AKVDEFPLC(470.29977)G HM(15.994915)VSDEYEQL SSEALEAAR	C49,M52,C49,M52,NA	,,,;	1.43674,;1.32644,;1 .22167,;	1.32644	X1W128 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
LTESPC(470.29977)ALVAS QYGWSGNM(15.994915)E	C645,M658,NA	U,;X;X;	1.49078,;X;X;	1.49078	P14625 Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 ,

R					
AKVDEFPLC(470.29977)G HM(15.994915)VSDEYEQL SSEALEAAR	C49,M52,C49,M52,NA	,,;X,;	1.42011,1.47207,,;X ;1.1993,;	1.42011	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
AKVDEFPLC(470.29977)G HM(15.994915)VSDEYEQL SSEALEAAR	C49,M52,C49,M52,NA	,,;,;	1.44465,,1.23527,,1 .25214,;	1.25214	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
KITAFVPNDGC(470.29977) LNFIEENDEVLVAGFGR	NA,NA	,,;X;	1.4709,,1.07634,,X;	1.27362	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
KITAFVPNDGC(470.29977) LNFIEENDEVLVAGFGR	NA,NA	,;X;X;	1.62603,,;X;X;	1.62603	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
YFAGNLASGGAAGATSLC(4 70.29977)FVYPLDFAR	NA,C129,C129,C129,NA	,,,,X;X;	1.49001,1.45912,1. 49001,1.45912,,;X;X ;	1.474565	P12236 ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 , P12235 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 , P05141 ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 , V9GYG0 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=1 ,
IC(464.28596)NAVSPDKD VDGFHVINVGR	C145,NA,NA,NA,NA	,;X;X;	2.00284,,;X;X;	2.00284	P13995 Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 PE=1 SV=2 , P13995-2 Isoform 2 of Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 ,
GSDELFSTC(470.29977)VT NGPFIM(15.994915)SSNS ASAANGNDSKK	NA,NA	,,;X;X;	1.37033,1.20204,,;X ;X;	1.286185	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
GSDELFSTC(470.29977)VT NGPFIM(15.994915)SSNS ASAANGNDSKK	NA,NA	,,;X;X;	1.64832,,1.0485,,;X;	1.34841	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
VIEINPYLLGTMSGC(470.2 9977)AADCQYWER	NA,NA,NA,NA	,;X;X;	2.45569,,;X;X;	2.45569	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 , X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 , P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 ,
NNLLC(470.29977)NGLSLK	NA,NA,C77,NA	,;X;X;	1.41332,,;X;X;	1.41332	Q9NVH0-2 Isoform 2 of Exonuclease 3'-5' domain- containing protein 2 OS=Homo sapiens GN=EXD2 , Q9NVH0

					Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2 , C9JLF4 Exonuclease 3'-5' domain-containing protein 2 (Fragment) OS=Homo sapiens GN=EXD2 PE=1 SV=1 ,
FLVPDM(15.994915)MDDI C(470.29977)QEQFLELSYL NGVPEPSR	M259,C264,NA,NA,M220, C225,NA,NA,NA,NA,NA,N A	;;X;X;	1.52594;;X;X;	1.52594	Q07666 KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 , Q07666-3 Isoform 3 of KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 , Q07666-2 Isoform 2 of KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 ,
GQVC(464.28596)LPVISAE NWKPATK	C144,NA,C144,NA	;;;X;	1.22441;;1.89468;; X;	1.559545	P68036 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 , P68036-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 , P68036-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 ,
TPSQLSDNNC(470.29977) RQ	C334,NA	U;;X;X;	1.13852;;X;X;	1.13852	Q4G0F5 Vacuolar protein sorting-associated protein 26B OS=Homo sapiens GN=VPS26B PE=1 SV=2 ,
NWYVQPSC(470.29977)A TSGDGLYEGLTWLTSNYKS	C155,NA	U,U,U;;U;;X;	1.5728,1.23783,1.5 4909;;1.65016;;X;	1.560945	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 ,
C(464.28596)HIISQFNQGF YDCVIATDAEVLGAPVK	NA,NA,NA	;;X;X;	2.29855;;X;X;	2.29855	Q9NY93 Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens GN=DDX56 PE=1 SV=1 , H7C3E9 Probable ATP-dependent RNA helicase DDX56 (Fragment) OS=Homo sapiens GN=DDX56 PE=1 SV=1 ,
LEKPNEGYLEFFVDC(470.2 9977)SASATPEFEGR	C85,NA	U;;X;X;	1.48526;;X;X;	1.48526	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 ,
HGSPTAPIC(464.28596)LG SPEFTDQGR	C173,C542,C542,NA,NA,N A	;;X;X;	1.55177;;X;X;	1.55177	H0YDE2 Pleckstrin homology domain-containing family A member 7 (Fragment) OS=Homo sapiens GN=PLEKHA7 PE=1 SV=1 , Q6IQ23-2 Isoform 2 of Pleckstrin homology domain-containing family A member 7 OS=Homo sapiens GN=PLEKHA7 , Q6IQ23 Pleckstrin homology domain-containing family A member 7 OS=Homo sapiens GN=PLEKHA7 PE=1 SV=2 , Q6IQ23-3 Isoform 3 of Pleckstrin homology domain-containing family A member 7 OS=Homo sapiens GN=PLEKHA7 , E9PKC0 Pleckstrin homology domain-

					containing family A member 7 OS=Homo sapiens GN=PLEKHA7 PE=1 SV=1 ,
EFHQAGKPIGLCC(470.29977)IAPVLA AK	C188,NA	;;X;X;	2.14522;;X;X;	2.14522	A0A096LP16 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
EFHQAGKPIGLCC(470.29977)IAPVLA AK	C188,NA	;;X;X;	1.64295;;X;X;	1.64295	A0A096LP16 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
SELLLAEEPGFLEGEDGDT AKIC(470.29977)QADIVEA VDIASAAK	C172,NA	;;X;X;	1.32798;;X;X;	1.32798	O15213 WD repeat-containing protein 46 OS=Homo sapiens GN=WDR46 PE=1 SV=3 ,
TLIQNC(464.28596)GASTI R	NA,C410,NA,NA	;;X;X;	1.73519;;X;X;	1.73519	P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 , B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 , P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 ,
TYDPSGDSTLPTC(464.28596)SK	NA,NA	U;;U;;U;;	1.36969;;1.37945;;4.73262;;	1.37945	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
SLHDALC(464.28596)VLA QTVK	C348,NA	;;X;;;	1.55385;;X;1.04717;;	1.30051	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 ,
SLHDALC(464.28596)VLA QTVK	C348,NA	;;X;X;	1.53;;X;X;	1.53	P78371 T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 ,
IC(470.29977)SHSAPEQQ AR	C19,NA	U;;X;X;	1.95764;;X;X;	1.95764	O75683 Surfeit locus protein 6 OS=Homo sapiens GN=SURF6 PE=1 SV=3 ,
AC(470.29977)QSIYPLHDV FVR	NA,NA,C201,NA,NA	;;;;;	1.38544;;1.33447;;1.39623;;	1.38544	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
AC(470.29977)QSIYPLHDV FVR	C201,NA	;;X;X;	2.17455;;X;X;	2.17455	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 ,
ESM(15.994915)C(470.29977)STPAFPVSPETPYVK	NA,NA	;;X;X;	1.60349;;X;X;	1.60349	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
GLC(464.28596)GAIHSSIA K	C103,NA,NA,NA,NA	;;X;;;	1.48551;;X;1.64605;;	1.56578	P36542 ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 , P36542-2 Isoform Heart of ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 ,

LPACVVDC(464.28596)GT GYTK	C12,NA	,,X;X;	1.34281,,X;X;	1.34281	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 ,
AAREEC(464.28596)PVFTP PGGETLDQVK	C114,NA,C55,NA,NA	,,X;X;	1.08639,,X;X;	1.08639	Q9NQ88 Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 , A0A0U1RQD1 Chromosome 12 open reading frame 5, isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 ,
C(464.28596)ELSSSVQTDI NLPYLTM(15.994915)DSS GPK	NA,NA,NA	,,,;	1.16981,,1.14243,1. 48086,,1.12314,,	1.15612	P38646 Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 ,
TATAVAHC(464.28596)K	C25,C25,NA	,,,;	1.39699,1.47278,,1. 34633,,1.23957,,	1.37166	M0R210 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 , P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 ,
VLQSEFC(464.28596)NAV R	NA,C47,NA,NA	,,X;X;	1.34335,,X;X;	1.34335	Q9NUP9 Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1 , G3V1D4 Lin-7 homolog C (C. elegans), isoform CRA_b OS=Homo sapiens GN=LIN7C PE=1 SV=1 ,
VLLISGFPVQVC(470.29977)K	NA,C109,C109,NA,NA,NA	,,X;X;	3.4001,,X;X;	3.4001	E9PKN8 Tudor and KH domain-containing protein (Fragment) OS=Homo sapiens GN=TDRKH PE=1 SV=1 , F6TB26 Tudor and KH domain-containing protein OS=Homo sapiens GN=TDRKH PE=1 SV=1 , Q9Y2W6 Tudor and KH domain-containing protein OS=Homo sapiens GN=TDRKH PE=1 SV=2 , Q5SZR4 Tudor and KH domain containing, isoform CRA_a OS=Homo sapiens GN=TDRKH PE=1 SV=1 ,
SGANVLICGPNGC(464.285 96)GK	C367,NA	,,X;X;	1.60904,,X;X;	1.60904	P28288 ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1 ,
ADQQYEC(464.28596)VAE IGEGAYGK	C15,NA	U,,X;X;	1.59012,,X;X;	1.59012	Q00534 Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1 ,
M(15.994915)VYSTC(464. 28596)SLNPIEDEAVIASLLE K	M80,C85,NA,NA	,,X;X;	1.57084,,X;X;	1.57084	Q08J23 tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 , Q08J23-2 Isoform 2 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 ,
LC(470.29977)TQLEGLQST VTGHVER	C976,NA	,,X;X;	1.54769,,X;X;	1.54769	Q6P2E9 Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1 ,
GC(464.28596)TATLGNFA K	NA,NA	,,,X;	1.38442,,1.33812,, X;	1.36127	P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 ,
RTIQFVDWC(464.28596)P	C347,NA,NA,NA,C347,NA	,,X;X;	1.81384,,X;X;	1.81384	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens

TGFK					GN=TUBA1C PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 ,
NTPSFLIAC(470.29977)NK QDIAM(15.994915)AK	C179,M186,NA	;;X;X;	1.51356;;X;X;	1.51356	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
ALAPLLAFVTKPNSALESC(470.29977)SFAR	NA,NA	U;;X;X;	1.33086;;X;X;	1.33086	P46060 Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 ,
FVQC(470.29977)PDGELQ K	NA,C182,NA,NA	;;X;X;	1.9833;;X;X;	1.9833	Q9Y230 RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 , Q9Y230-2 Isoform 2 of RuvB-like 2 OS=Homo sapiens GN=RUVBL2 , M0R0Y3 RuvB-like helicase OS=Homo sapiens GN=RUVBL2 PE=1 SV=1 ,
IFGSIPM(15.994915)QAC(470.29977)QQK	M152,C155,M152,C155,M 152,C155,M152,C155,NA	;;X;X;	1.64141;;X;X;	1.64141	F5H6J5 Zinc finger CCHC domain-containing protein 8 (Fragment) OS=Homo sapiens GN=ZCCHC8 PE=1 SV=1 , Q6NZY4-2 Isoform 2 of Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 , Q6NZY4 Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2 , F5GX80 Zinc finger CCHC domain-containing protein 8 (Fragment) OS=Homo sapiens GN=ZCCHC8 PE=1 SV=1 ,
RGSDELFSTC(464.28596)V TNGPFIM(15.994915)SSN SASAANGNSK	NA,NA	;;X;X;	8.35577;;X;X;	8.35577	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
VLVVGAGGIGC(464.28596)ELLK	C30,NA	;;X;X;	1.44551;;X;X;	1.44551	Q9UBT2 SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2 ,
QVQSLTC(464.28596)EVD ALKGTNESLER	C328,C328,NA	;;X;X;	1.74595;;X;X;	1.74595	B0YJC4 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=1 , P08670 Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 ,
AIVDC(464.28596)GFEHPS EVQHECIPQAILGM(15.994 915)DVLCQAK	NA,C62,M82,NA,NA	;;X;X;	1.21304;;X;X;	1.21304	Q13838-2 Isoform 2 of Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B , O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 , Q13838 Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1 ,
LVNIVTENC(464.28596)S	C322,NA,C191,NA	;;X;X;	1.82905;;X;X;	1.82905	A0A087X0W9 OTU domain containing 6B, isoform CRA_b OS=Homo sapiens GN=OTUD6B PE=1 SV=1 , Q8N6M0 OTU

					domain-containing protein 6B OS=Homo sapiens GN=OTUD6B PE=1 SV=1 ,
NAIQLLASFLANNPFSC(464.28596)K	NA,NA	,;X;X;	0.91225,;X;X;	0.91225	Q15021 Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 ,
ADDTFEALC(464.28596)IE PFSSPPELPDVM(15.994915)KPQDSGSSANEQAVQ	NA,NA,C84,M98,NA,NA,NA,NA	,;X;X;	1.29754,;X;X;	1.29754	I3L0M9 Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1 , Q15370 Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1 , B8ZZU8 Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 ,
LM(15.994915)AVTEYIPPK PAIHPSC(464.28596)LPSP PSPPQEEIGLIR	M48,C64,NA,NA,NA,NA	,;X;X;	1.38406,;X;X;	1.38406	Q7Z7H8 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 , Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 ,
WPETPPFSYTC(470.29977))GDPSTYRVTFVCPQK	NA,NA,NA,C1201,NA	,;X;X;	0.7707,;X;X;	0.7707	A6NJZ7 RIMS-binding protein 3C OS=Homo sapiens GN=RIMBP3C PE=1 SV=3 , J3KP16 RIMS-binding protein 3C OS=Homo sapiens GN=RIMBP3C PE=4 SV=1 , A6NNM3 RIMS-binding protein 3B OS=Homo sapiens GN=RIMBP3B PE=3 SV=3 , Q9UFD9 RIMS-binding protein 3A OS=Homo sapiens GN=RIMBP3 PE=1 SV=4 ,
TGC(464.28596)TFPEKPDF H	C318,C336,C336,NA	,;,,,;	1.38665,;1.44073,;1.18273,;	1.38665	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK , P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 , P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK ,
M(15.994915)MYPIC(470.29977)LTQDEFHPFIEALLP HVR	M1,C7,M1,C7,M1,C7,M1,C7,M1,C7,M1,C7,NA,M1,C7,NA	,;X;X;	1.9554,;X;X;	1.9554	O00712-5 Isoform 5 of Nuclear factor 1 B-type OS=Homo sapiens GN=NFIB , Q5VW26 Nuclear factor 1 OS=Homo sapiens GN=NFIB PE=1 SV=1 , Q5VW27 Nuclear factor 1 OS=Homo sapiens GN=NFIB PE=1 SV=1 , Q5VW30 Nuclear factor 1 OS=Homo sapiens GN=NFIB PE=1 SV=1 , Q5W0Y9 Nuclear factor 1 B-type OS=Homo sapiens GN=NFIB PE=1 SV=1 , O00712-2 Isoform 3 of Nuclear factor 1 B-type OS=Homo sapiens GN=NFIB , A0A087WXP2 Nuclear factor 1 B-type OS=Homo sapiens GN=NFIB PE=1 SV=1 , O00712 Nuclear factor 1 B-type OS=Homo sapiens GN=NFIB PE=1 SV=2 ,

ETTEAAC(470.29977)R	C164,NA,NA,NA	;;X;X;	1.67841;;X;X;	1.67841	Q9Y2Q3-3 Isoform 3 of Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 , Q9Y2Q3 Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3 , Q9Y2Q3-2 Isoform 2 of Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 ,
C(470.29977)YVQPQWVF DSVNAR	NA,C386,C374,NA	;;X;X;	1.59759;;X;X;	1.59759	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 , O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 , B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 ,
GSDC(470.29977)GIVNVNI PTSGAEIGGAFGGEK	C450,NA,NA	;;;X;	1.53374;;1.53907;; X;	1.536405	P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 , P49419 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 ,
FRCPEALFQPSFLGMESC(4 64.28596)GIHETTFNSIM(1 5.994915)K	NA,NA,NA,NA,NA	;;X;;;	1.40076;;X;1.25085 ;;	1.325805	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ,
FRCPEALFQPSFLGMESC(4 64.28596)GIHETTFNSIM(1 5.994915)K	NA,NA,NA,NA,NA	;;X;;;	1.38399;;X;1.28523 ;;	1.33461	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ,
FRCPEALFQPSFLGMESC(4 64.28596)GIHETTFNSIM(1 5.994915)K	NA,NA,NA	;;X;X;	1.56682;;X;X;	1.56682	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
EGIC(464.28596)ALGGTSE LSSEGTQHSYSEEEKYAFVN WINK	NA,NA	;;X;X;	1.28912;;X;X;	1.28912	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 ,
SQSPAASDC(464.28596)SS SSSSASLPSSGR	NA,C121,NA	;;X;X;	2.25954;;X;X;	2.25954	O95817 BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 , C9JFK9 BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=1 SV=1 ,
C(464.28596)TKEEHLCTQR	NA,C226,C205,C201,C210, NA	;;X;X;	1.11254;;X;X;	1.11254	J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , P06753-2 Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 , A0A087WWU8 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , Q5VU61 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 , Q5HYB6 Epididymis luminal protein 189 OS=Homo sapiens GN=DKFZp686J1372 PE=1

					SV=1 ,
LQAQQDAVNIVC(464.28596)HSK	NA,C37,C22,C37,NA	,,X;X;	2.23621,,X;X;	2.23621	P55036-2 Isoform Rpn10E of 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 , Q5VWC4 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 , A6PVX3 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=1 SV=1 , P55036 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 ,
APPWVPAM(15.994915)GFTLAPSLGC(464.28596)FVGSR	M9,C19,NA,NA	,,X;;	2.44152,,X;2.59581,,	2.518665	B1AH87 Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=1 SV=1 , P30536 Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 ,
DVQIGDIVTVGEC(464.28596)RPLSK	C131,NA	,,,X;;	1.44872,1.51448,,X;1.32372,,	1.44872	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
VDDEILGFISEATPLGGIQAASTESC(470.29977)NQQLDLALCR	NA,NA,NA	U,,X;X;	1.90829,,X;X;	1.90829	P42166 Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 ,
C(464.28596)TGGEVGATSALAPK	NA,NA	,,X;X;	1.30077,,X;X;	1.30077	P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 ,
DVQIGDIVTVGEC(464.28596)RPLSK	C131,NA	,,X;X;	1.55729,,X;X;	1.55729	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
VDDEILGFISEATPLGGIQAASTESC(470.29977)NQQLDLALCR	NA,NA,NA	U,,X;X;	3.5268,,X;X;	3.5268	P42166 Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 ,
VC(464.28596)NYGLTFTQK	C66,NA,NA	,,,X;	1.38918,,1.33173,,X;	1.360455	Q9Y277-2 Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 , Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 ,
SGAAWTC(464.28596)QQLR	C87,NA,NA,NA,NA	,,X;X;	0.50715,,X;X;	0.50715	Q9HD33 39S ribosomal protein L47, mitochondrial OS=Homo sapiens GN=MRPL47 PE=1 SV=2 , Q9HD33-2 Isoform 2 of 39S ribosomal protein L47, mitochondrial OS=Homo sapiens GN=MRPL47 ,
M(15.994915)ININILSVC(470.29977)K	NA,NA	,,X;X;	1.7941,,X;X;	1.7941	Q53GQ0 Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 ,

NLVQC(464.28596)GDFPH LLVYGPSGAGKK	NA,C32,NA	,,X;X;	2.08313,,X;X;	2.08313	P40938 Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2 , P40938-2 Isoform 2 of Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 ,
VGLPIGQGGFGC(464.2859 6)IYLADM(15.994915)NSS ESVGSDAPCVVK	NA,NA	U,,X;X;	0.61206,,X;X;	0.61206	Q99986 Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 ,
LEVDAIVNAANSSLLGGGG VDGC(470.29977)IHR	C186,NA	U,,X;U,,	1.53991,,X;0.58547 ,,	1.06269	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
LEVDAIVNAANSSLLGGGG VDGC(470.29977)IHR	C186,NA	U,,X;U,,	1.55897,,X;0.22829 ,,	0.89363	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
ASC(464.28596)LYGQLPK	NA,NA	,,,;	2.08892,,1.89369,,1 .70121,,	1.89369	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 ,
TFVPAMTAIHGPPITAPVVC (464.28596)TR	C549,NA,C660,C594,NA	,,X;X;	1.9859,,X;X;	1.9859	Q96RN5-3 Isoform 3 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 , Q96RN5-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 , Q96RN5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=2 , G3V1P5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=1 ,
TLETANC(470.29977)MSS QTK	C96,NA,NA,NA,NA	,,X;X;	1.44613,,X;X;	1.44613	P50416-2 Isoform 2 of Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A , P50416 Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 ,
EVIQSDSLWLVEFYAPWC(4 70.29977)GHCQR	C107,C60,NA,NA,NA,NA	,,X;X;	2.18493,,X;X;	2.18493	Q15084-2 Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 , Q15084-4 Isoform 4 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 , Q15084-5 Isoform 5 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 , Q15084 Protein disulfide- isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 , Q15084-3 Isoform 3 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 ,
IAALVVDNGSGM(15.9949 15)C(464.28596)K	NA,NA,NA	,,X;X;	1.03124,,X;X;	1.03124	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
FLC(470.29977)ESVFSYQV ASTLK	NA,NA	U,,X;X;	1.24251,,X;X;	1.24251	Q96DE5 Anaphase-promoting complex subunit 16 OS=Homo sapiens GN=ANAPC16 PE=1 SV=1 ,

TAFQEALDAAGDKLVVDF SATWC(470.29977)GPCK	NA,NA	;;X;;	1.3542,1.31473;;X; 1.2093,;	1.31473	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,
C(470.29977)SVPVDQASE SLLK	C213,NA	U;;X;X;	1.83791;;X;X;	1.83791	Q9NVN8 Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens GN=GNL3L PE=1 SV=1 ,
LC(470.29977)FSTAQHAS	NA,NA,NA	;;X;X;	1.33065;;X;X;	1.33065	MOQXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
TAFQEALDAAGDKLVVDF SATWC(470.29977)GPCK	NA,NA	;;X;;	1.33649,1.28045;;X; ;1.36055,;	1.33649	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,
EKTAC(464.28596)AINK	NA,NA,NA,C293,NA,NA	;;X;;	1.2847;;X;1.20862,;	1.24666	Q8NCA5-2 Isoform 2 of Protein FAM98A OS=Homo sapiens GN=FAM98A , E9PH82 Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1 , Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q8NCA5 Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
FSPNSSNPIIVSC(470.2997 7)GWDK	NA,NA	;;X;X;	1.60031;;X;X;	1.60031	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
APEILLGC(470.29977)K	NA,C177,NA	;;X;X;	1.66929;;X;X;	1.66929	P24941 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2 , G3V5T9 Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=1 ,
ANC(464.28596)IDSTASAE AVFASEVKK	NA,C183,C268,NA,NA	;;;X;	1.35499,;1.35606,; X;	1.355525	MOQXL5 rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 , M0R299 rRNA 2'-O- methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 , P22087 rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2 , M0R2Q4 rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1 ,
GSSVDAPPRPC(470.29977)HTTPDSQFGTEHVLR	NA,C635,NA	;;X;X;	1.65609;;X;X;	1.65609	Q9BSJ8-2 Isoform 2 of Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 , Q9BSJ8 Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 ,
LALFNPDVC(470.29977)W DRNNPEPWNK	C44,NA	U;;X;U,;	1.6207;;X;1.68621,;	1.653455	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 ,
LM(15.994915)WLFGC(46 4.28596)PLLLDDVAR	NA,NA	;;X;;	1.48211;;X;1.26837 ,;	1.37524	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 ,

CPEALFQPSFLGM(15.994915)ESC(470.29977)GIHETT FNSIMK	NA,NA,NA	,,X;X;	1.40696,,X;X;	1.40696	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
PSSHKDLTQCVTC(464.28596)QEK	NA,NA	U,,X;X;	3.15163,,X;X;	3.15163	Q8N448 Ligand of Numb protein X 2 OS=Homo sapiens GN=LN2 PE=1 SV=1 ,
VM(15.994915)TIPYQPM ASSPVIC(464.28596)AGG QDR	M179,C194,NA	U,U,,X;X;	1.36647,1.05351,,X;X;	1.20999	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
NIC(464.28596)FTVWDVG GQDK	NA,NA	,,X;X;	1.46749,,X;X;	1.46749	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 ,
LHDAIVEVTC(464.28596)LLR	NA,C470,C470,NA,C470,NA,NA,NA,NA	,,X;X;	1.32073,,X;X;	1.32073	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 , O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 , O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L ,
VVNSETPVVDFHAQWC(470.29977)GPCK	C90,NA,C90,NA,NA	,,,X;	1.44923,1.25175,,1.24887,,X;	1.25175	Q99757 Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 , F8WDN2 Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 ,
M(15.994915)LQPC(464.28596)GPPADKPEEN	NA,NA	U,,X;X;	1.44556,,X;X;	1.44556	Q9BWJ5 Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1 ,
LSC(464.28596)QPM(15.994915)LSLDDFQLQPPVTFR	NA,NA	U,,X;X;	1.18952,,X;X;	1.18952	O75607 Nucleoplasmin-3 OS=Homo sapiens GN=NPM3 PE=1 SV=3 ,
AATGEEVSAEDLGGADLHC(470.29977)R	NA,NA,NA	,,X;;	1.54064,,X;1.17146,,	1.35605	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
GC(470.29977)LLYGPPGT GK	NA,NA,NA	,,,;	1.3841,,1.42087,,1.12243,,	1.3841	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 , P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 ,
VITVDGNIC(464.28596)TG K	NA,NA,NA	,,X;X;	1.41443,,X;X;	1.41443	E7ESZ7 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens

					GN=NDUFA10 PE=1 SV=1 ,
LLM(15.994915)EQESSAC(464.28596)SR	NA,NA,NA	;;X;X;	2.72724;;X;X;	2.72724	O96011 Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B PE=1 SV=1 , O96011-2 Isoform 2 of Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B ,
HVVC(470.29977)AAETGS GK	NA,NA	U;;U;U;;	1.83762;;1.79242;;1.80842;;	1.80842	Q9NUL7 Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=1 SV=2 ,
TFM(15.994915)C(470.29977)TGRPGWLTSLR	M49,C50,M49,C50,NA	;;X;X;	1.61032;;X;X;	1.61032	Q15392-2 Isoform 2 of Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 , Q15392 Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2 ,
YVEPIEDVPC(464.28596)GNIVGLVGVDQFLVK	C466,NA	U;;X;X;	0.74081;;X;X;	0.74081	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
HIQNPSAAELVHFLFGPLDLI VNTC(464.28596)SGPDIA R	NA,NA,NA	;;X;X;	1.4124;;X;X;	1.4124	Q9H6S3-3 Isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 , Q9H6S3 Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2 ,
C(464.28596)PGPLAVANG VVK	NA,NA,NA	;;X;X;	1.63826;;X;X;	1.63826	Q9Y6Y8 SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1 , Q9Y6Y8-2 Isoform 2 of SEC23-interacting protein OS=Homo sapiens GN=SEC23IP ,
YHPTFFNDVFSTLFLDQPGG C(464.28596)HVTCLV	C638,NA	;;X;X;	1.3677;;X;X;	1.3677	Q14166 Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2 ,
HIQNPSAAELVHFLFGPLDLI VNTC(464.28596)SGPDIA R	NA,NA,NA	;;X;X;	1.2211;;X;X;	1.2211	Q9H6S3-3 Isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 , Q9H6S3 Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2 ,
IISNASC(464.28596)TTNCL APLAK	C152,NA	iiiiiii	1.40638;;1.39311,1.31594,1.37926;;1.22123,1.13228;;	1.3476	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
AATM(15.994915)SAVEAATC(470.29977)R	NA,M258,C266,NA,M121,C129,NA	;;X;X;	1.42483;;X;X;	1.42483	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 , Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 , Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL , B5MD87 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens

					GN=PYCRL PE=1 SV=2 ,
IISNASC(464.28596)TTNCL APLAK	C152,NA	,,,,,,;	1.33176,1.41671,1.43758,1.49107,,1.37203,1.38967,,1.22197,1.17545,;	1.38085	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
LLSNM(15.994915)MC(47 0.29977)QYR	NA,NA,NA,NA	,,X;X;	1.42524,X;X;	1.42524	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 , X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 , P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 ,
FDPTQFQDC(470.29977)II QGLTETGTDLEAVAK	C35,NA,NA,C39,C35,NA	,,,,X;	1.22516,1.42651,,1.0779,,X;	1.22516	Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 , C9IZ80 Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=1 , Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 , Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 , Q7L1Q6-2 Isoform 2 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 ,
TPC(464.28596)NAGTFSQ PEK	C129,C129,NA,NA	,,,,X;	1.3387,,1.7753,,X;	1.557	O43684 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 , J3QT28 Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=1 SV=1 , O43684-2 Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 ,
GILLYGPPGC(464.28596)G K	C259,NA,NA	,,X;X;	1.87302,,X;X;	1.87302	I3L0N3 Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=1 , P46459 Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3 ,
TLSFYFPPC(470.29977)GK	C388,NA,NA	,,X;X;	1.4898,,X;X;	1.4898	Q9UG63-2 Isoform 2 of ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 , Q9UG63 ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2 ,
NC(470.29977)SETQYESK	C112,NA	U,,X;X;	1.36461,,X;X;	1.36461	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 ,
SGRYEAAFPFLSPC(470.299 77)GR	NA,NA,NA	,,X;X;	1.35378,,X;X;	1.35378	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 , Q6P1X6 UPF0598 protein

					C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 ,
IQESC(470.29977)QSGTK	NA,C104,NA,C104,NA	,,;X;X;	1.7687,,;X;X;	1.7687	I3L419 Protein FAM64A OS=Homo sapiens GN=FAM64A PE=1 SV=1 , Q9BSJ6 Protein FAM64A OS=Homo sapiens GN=FAM64A PE=1 SV=1 , I3L156 Protein FAM64A OS=Homo sapiens GN=FAM64A PE=1 SV=2 , Q9BSJ6-2 Isoform 2 of Protein FAM64A OS=Homo sapiens GN=FAM64A ,
GNFTLPEVAEC(470.29977) FDEITYVELQKEEAQK	NA,C629,NA	,,,X,,,;	1.30919,1.29889,,;X ;1.27178,,;	1.29889	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
GNFTLPEVAEC(470.29977) FDEITYVELQKEEAQK	NA,C629,NA	,,,X,,,;	1.36304,1.56229,,;X ;1.59141,,;	1.56229	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
ISSVLAGGSC(470.29977)R	C40,NA,NA	,;X;X;	2.43153,,;X;X;	2.43153	P08779 Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 ,
LLAPDC(470.29977)EIIQEV GKLYPLEIVFGM(15.99491 5)NGR	C215,M233,NA	U,,;X;X;	1.53163,,;X;X;	1.53163	Q9NQT5 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 ,
GTPEQPQC(464.28596)GF SNAVQILR	C67,NA,NA	U,,;U,,;U,U,,;	1.35305,,;1.3254,,;1. 23264,1.24329,,;	1.284345	Q86SX6 Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 ,
NTPSFLIAC(470.29977)NK	C179,NA	,;X;X;	1.33562,,;X;X;	1.33562	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
GTPEQPQC(464.28596)GF SNAVQILR	C67,NA,NA	U,,;X;X;	1.62561,,;X;X;	1.62561	Q86SX6 Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 ,
EGYTSFWNDC(470.29977) ISSGLR	NA,C70,NA	,,,X;X;	2.09317,2.09317,,;X ;X;	2.09317	Q9H4A6 Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 , Q9H4A5 Golgi phosphoprotein 3-like OS=Homo sapiens GN=GOLPH3L PE=1 SV=1 ,
HFLSDTGM(15.994915)AC (464.28596)R	NA,NA	,;X;X;	1.72796,,;X;X;	1.72796	Q5TFE4 5'-nucleotidase domain-containing protein 1 OS=Homo sapiens GN=NT5DC1 PE=1 SV=1 ,
C(470.29977)FGTGAAGNR	NA,NA	,,,,,;	1.47201,,;1.55616,,;1 .54139,,;	1.54139	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 ,
LGEWVGLC(470.29977)K	NA,NA	U,,;U,,;X;	1.39248,,;1.31625,,; X;	1.354365	P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 ,
HEEFEEGC(464.28596)K	NA,NA,C41,C245,NA	,;X,,,;	1.54138,,;X;1.42207 ,,;	1.481725	I3L3Q4 Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=1 SV=1 , Q9HC38-2

					Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 , Q9HC38-3 Isoform 3 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 , F6TLX2 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 ,
M(15.994915)ALDALLQEIALSEPQLC(470.29977)EVLQVAGPDR	NA,NA,NA	,,X;X;	1.30002,,X;X;	1.30002	C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 , Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 ,
LNLPINIIIGLAPLC(470.29977)ENM(15.994915)PSGK	C335,M338,NA,NA	,,X;X;	1.34922,,X;X;	1.34922	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 , P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 ,
EVC(464.28596)PVLQDQFLCHVAK	C22,NA,NA	,,X;X;	0.3576,,X;X;	0.3576	C9IZ04 Serine/threonine-protein phosphatase 4 regulatory subunit 2 (Fragment) OS=Homo sapiens GN=PPP4R2 PE=1 SV=1 , Q9NY27 Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Homo sapiens GN=PPP4R2 PE=1 SV=3 ,
ILQDDIESLM(15.994915)PIVYTPTVGLAC(464.28596)SQYGHIFR	M108,C120,NA,NA	,,X;X;	1.84654,,X;X;	1.84654	P23368 NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1 ,
LVSSPC(464.28596)CIVTSTYGTANM(15.994915)ERC(470.29977)LSEQSVAISR	C589,M602,NA	U,U,,X;X;	1.38037,1.41354,,X;X;	1.396955	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 ,
	NA,NA,NA	,,X;X;	1.1593,,X;X;	1.1593	P41134-2 Isoform ID-B of DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 , P41134 DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 PE=1 SV=3 ,
NMSVHLSPC(464.28596)FR	C116,NA	,,X;X;	1.3596,,X;X;	1.3596	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
LPLC(464.28596)SLPGEPGNGPDQQLQR	C75,NA	U,,X;X;	1.30388,,X;X;	1.30388	Q96GX2 Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 ,
TC(464.28596)ATDLQTK	NA,NA,NA,NA,NA,NA,NA	,,X;X;	1.14738,,X;X;	1.14738	O95861-4 Isoform 4 of 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 , O95861 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1 , O95861-2 Isoform 2 of 3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 ,
SRPNASGGAAC(464.28596)SGPGPEPAVFCEPVVK	C108,NA,NA,NA,NA	,,X;X;	1.94577,,X;X;	1.94577	Q6L8Q7 2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=2 , Q6L8Q7-2 Isoform 2 of 2',5'-

					phosphodiesterase 12 OS=Homo sapiens GN=PDE12 ,
LNNLIC(470.29977)DESDV KDIAFK	C362,NA,NA,NA,NA,NA	;;X;X;	1.50436;;X;X;	1.50436	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1-2 Isoform 2 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 , G5E9D4 Elongation protein 4 homolog (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=ELP4 PE=1 SV=1 ,
GSSPQNTTTPKPSVEGQQP AAAAAC(464.28596)EPVD HAQSESILK	C394,NA,NA	;;X;X;	0.8598;;X;X;	0.8598	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 , Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 ,
SPWLAGNELTVADVVLWS VLQQIGGC(464.28596)SV TVPANVQR	NA,NA	;;X;X;	1.41438;;X;X;	1.41438	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 ,
SPWLAGNELTVADVVLWS VLQQIGGC(464.28596)SV TVPANVQR	NA,NA	;;X;X;	1.35051;;X;X;	1.35051	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 ,
SPWLAGNELTVADVVLWS VLQQIGGC(464.28596)SV TVPANVQR	NA,NA	;;X;X;	1.56906;;X;X;	1.56906	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 ,
LQSGIC(470.29977)HLFR	NA,NA,NA	;;;X;	1.59877;;1.68132;; X;	1.640045	P14868 Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 ,
YINENLIVNTDELGRDC(470 .29977)LINAAK	NA,NA	;;X;X;	1.31507;;X;X;	1.31507	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 ,
INISEGNC(464.28596)PER	NA,C54,C54,C54,C54,NA	,,,,,;	1.37591,1.45394,1. 61773;;1.33466,1.3 5835;;1.24054,;	1.36713	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 , Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
VNQAIWLLC(470.29977)T GAR	C155,NA,C155,NA	;;X;X;	1.32766;;X;X;	1.32766	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,

VIEASDVVLEVL DARDPLGC (464.28596)R	C144,C144,NA	,,,X;	2.14806,,;2.02025,, X;	2.084155	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
C(464.28596)PAPPRGPPA PAPEVEELAR	C161,NA	U,,X;U,,	1.22328,,X;0.53258 ,,	0.87793	P48681 Nestin OS=Homo sapiens GN=NES PE=1 SV=2 ,
VNQAIWLLC(470.29977)T GAR	C155,NA,C155,NA	,,,,,;	1.39978,1.36989,,1. 42863,,1.27043,,	1.384835	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
WSAAC(464.28596)AYLHP ALSR	C242,NA,NA	U,,X;X;	1.67312,,X;X;	1.67312	Q8NE62 Choline dehydrogenase, mitochondrial OS=Homo sapiens GN=CHDH PE=1 SV=2 ,
RSIQFVDWC(470.29977)P TGFK	NA,NA,NA,NA	,,X;X;	1.67116,,X;X;	1.67116	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
ENDC(470.29977)SSVQA MR	NA,NA,NA	,,X;X;	1.60741,,X;X;	1.60741	Q494V2-2 Isoform 2 of Cilia- and flagella-associated protein 100 OS=Homo sapiens GN=CFAP100 , Q494V2 Cilia- and flagella-associated protein 100 OS=Homo sapiens GN=CFAP100 PE=2 SV=1 ,
ATC(464.28596)APQHGAP GPGPADASK	C2535,C2516,C2535,C250 3,NA	,,X;X;	1.59462,,X;X;	1.59462	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA , Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 , P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 , Q5HY54 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 ,
GTSQADC(470.29977)AVLI VAAGVGEFEAGISKNGQTR	NA,NA	,,X;X;	4.35482,,X;X;	4.35482	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
IVPVDIYIPGC(464.28596)P PTAEALLYGILQLQR	NA,NA,NA	U,,X;X;	1.9456,,X;X;	1.9456	O75251 NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDUFS7 PE=1 SV=3 ,
TQNL PNC(470.29977)QLIS R	NA,NA	,,,X;	1.33646,,1.48397,, X;	1.410215	P37268 Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 ,
ADHQPLTEASYVNLPTIALC(470.29977)NTDSPLR	NA,C148,NA,NA	,,,,,;	1.41518,,1.37929,,1. .09356,,	1.37929	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 , C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 , P08865

					40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 ,
GTLTLC(464.28596)PYHSD R	C620,NA,NA,NA	,,,X;	1.21756,,0.81502,,X;	1.01629	Q13200-2 Isoform 2 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 , Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 , Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 ,
ADHQPLTEASYVNLPTIALC(470.29977)NTDSPLR	NA,C148,NA,NA	,,,,;	1.387,,1.28097,,1.06501,,	1.28097	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 , C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 , P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 ,
VWAVLPSSPEAC(470.29977)GAASLQER	C170,NA,NA	U,,X;X;	1.63584,,X;X;	1.63584	Q5T440 Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 ,
DNLTWTSDSAGEEC(470.29977)DAAEGAEN	C237,NA	U,,X;X;	1.17879,,X;X;	1.17879	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 ,
LTTPYGDNLHLVSATM(15.994915)SGVTTC(464.28596)LR	M233,C239,M233,C239,NA,M215,C221,NA	,,,,X;	1.54216,1.67709,,1.18788,,X;	1.54216	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
TTSSANNPNLM(15.994915)YQDEC(464.28596)DRR	M502,C507,M581,C586,NA,NA,M500,C505,NA	,,X,,,;	1.63919,,X;1.22355,,	1.43137	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 , Q92841-2 Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 , Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 ,
DVPLADPGLDNDVGVEVG GSGGC(464.28596)LEER	NA,NA	U,,X;X;	1.47177,,X;X;	1.47177	Q9NPA3 Mid1-interacting protein 1 OS=Homo sapiens GN=MID1IP1 PE=1 SV=1 ,
RNHDGEC(470.29977)TAA PTNR	NA,NA	,,X;X;	1.76807,,X;X;	1.76807	Q12769 Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3 ,

STSTSEPTTGC(464.28596)SLK	C734,NA	U,,X;X;	1.54777,,X;X;	1.54777	Q8ND82 Zinc finger protein 280C OS=Homo sapiens GN=ZNF280C PE=1 SV=1 ,
NLSFFLTTPPC(470.29977)AR	C492,NA,NA,NA	,,X;;	1.68843,,X;1.30565,,	1.49704	P42224-2 Isoform Beta of Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 , P42224 Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 , J3KPM9 Signal transducer and activator of transcription OS=Homo sapiens GN=STAT1 PE=1 SV=1 ,
CHEFVTFSC(470.29977)PGADKGPDTDLFSPVLLVCLYLLR	C84,NA	U,,X;X;	1.66527,,X;X;	1.66527	J3KN97 Protein kinase C alpha type (Fragment) OS=Homo sapiens GN=PRKCA PE=1 SV=1 ,
TLLLC(470.29977)GYPNVGK	NA,NA	,,X;X;	1.39459,,X;X;	1.39459	Q9BZE4 Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 ,
KM(15.994915)C(464.28596)LFAGFQR	NA,M574,C575,NA	,,X;X;	1.58339,,X;X;	1.58339	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
FLTFKDC(464.28596)DPGEVNK	NA,NA,C133,NA,NA	,,X;X;	1.91724,,X;X;	1.91724	Q9NYK5 39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3 , Q9NYK5-2 Isoform 2 of 39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 ,
TASISSPSEGTPTVGSYGC(464.28596)TPQSLPK	C787,C787,NA	,,,;	1.30137,,1.22523,,1.197,,	1.22523	Q6PKG0-3 Isoform 2 of La-related protein 1 OS=Homo sapiens GN=LARP1 , Q6PKG0 La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 ,
GIFPVLC(464.28596)KDPVQEAWAEDVDLR	NA,NA	,,X;X;	1.46856,,X;X;	1.46856	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 ,
VGLPIGQGGFGC(464.28596)IYLADM(15.994915)NSSESVGSAPCVVKVEPSDNGPLFTELK	NA,NA	U,,X;X;	2.58229,,X;X;	2.58229	Q99986 Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1 ,
LNQQQHPDC(464.28596)K	C239,NA	,,,;	1.31155,,2.03605,,1.38684,,	1.38684	Q5T280 Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3 ,
LC(464.28596)CPATAPQEAPAEGR	C114,NA,NA	,,X;X;	0.70308,,X;X;	0.70308	Q96B54 Zinc finger protein 428 OS=Homo sapiens GN=ZNF428 PE=1 SV=2 , M0QXZ5 Zinc finger protein 428 (Fragment) OS=Homo sapiens GN=ZNF428 PE=1 SV=1 ,
LIC(470.29977)CDILDVLDK	C97,NA,NA	,,X;X;	1.29871,,X;X;	1.29871	P62258 14-3-3 protein epsilon OS=Homo sapiens

HLIPAANTGESK					GN=YWHAE PE=1 SV=1 , P62258-2 Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE ,
TATAVAHC(470.29977)KR	C25,NA	,;X;X;	1.55007,,;X;X;	1.55007	P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 ,
AQLVEIVGC(470.29977)HFR	NA,NA	U,,;X;X;	1.50562,,;X;X;	1.50562	O75446 Histone deacetylase complex subunit SAP30 OS=Homo sapiens GN=SAP30 PE=1 SV=1 ,
AVAILC(464.28596)NHQR	NA,NA	U,,;U,,;U,,;	1.42276,,;1.38026,,;1.50588,,;	1.42276	P11387 DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 ,
AQLNIGNVLPVGT(15.994915)PEGTIVCC(470.29977)LEEKPGDR	M107,C115,M107,C115,M107,C115,NA	,;X;X;	1.28846,,;X;X;	1.28846	E9PKU4 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 , E9PKZ0 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=1 SV=1 , P62917 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2 ,
IIPGFM(15.994915)C(470.29977)QGGDFTR	M61,C62,M61,C62,M61,C62,NA	,;X;X;	1.44701,,;X;X;	1.44701	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
EVIASVCGPAQC(464.28596)QETIR	C162,C162,NA	,,,;X;	1.38425,1.063,1.29845,,;1.26134,,;X;	1.279895	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
TLTSC(470.29977)FLSCVV CVEGIVTK	NA,C164,NA	,,,;X;	1.62162,,;1.16027,,;X;	1.390945	P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 , P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 ,
EVIASVCGPAQC(464.28596)QETIR	C162,C162,NA	,;X;X;	1.59723,,;X;X;	1.59723	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
AQLSGLQLQPC(464.28596)LYK	NA,NA	,;X;X;	0.59698,,;X;X;	0.59698	O43159 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 ,
AVSPAIPSAPLYEEITYSGISD GLSQASC(470.29977)PLA AIDHILDSSR	NA,C406,C406,NA,NA,NA	,;X;X;	0.91642,,;X;X;	0.91642	O60291-4 Isoform 4 of E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 , O60291-3 Isoform 3 of E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 , O60291 E3 ubiquitin-protein ligase MGRN1

					OS=Homo sapiens GN=MGRN1 PE=1 SV=2 , O60291-2 Isoform 2 of E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 , K7EPJ5 E3 ubiquitin-protein ligase MGRN1 (Fragment) OS=Homo sapiens GN=MGRN1 PE=1 SV=1 ,
TILTLTGVSTLGDVKNNQES DC(464.28596)VSK	NA,NA,NA	;;X;X;	1.61031;;X;X;	1.61031	A6NDG6 Glycerol-3-phosphate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 , H3BV17 Glycerol-3-phosphate phosphatase (Fragment) OS=Homo sapiens GN=PGP PE=1 SV=1 ,
IC(464.28596)SWM(15.99 4915)GTGLCPGPLSPR	C570,M573,C616,M619,NA	;;X;X;	1.33365;;X;X;	1.33365	Q5T9A4-3 Isoform 3 of ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B , Q5T9A4 ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1 ,
SLWSSLC(470.29977)LGPA PAPPGPVSPEGR	C40,NA,NA,NA	;;X;X;	1.88769;;X;X;	1.88769	Q9BRR6-2 Isoform 2 of ADP-dependent glucokinase OS=Homo sapiens GN=ADPGK , H3BRS6 ADP-dependent glucokinase (Fragment) OS=Homo sapiens GN=ADPGK PE=1 SV=1 , Q9BRR6 ADP-dependent glucokinase OS=Homo sapiens GN=ADPGK PE=1 SV=1 ,
NNTQVLINC(470.29977)R	C36,C36,C46,NA	;;X;X;	1.31902;;X;X;	1.31902	P62316 Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 , P62316-2 Isoform 2 of Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 , K7ERG4 Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 ,
VAAALENTHLLEVNNQC(470.29977)LSAR	C158,NA	U;;X;X;	3.44874;;X;X;	3.44874	Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 ,
IQCTLQDVGSALATPC(464.28596)SSAR	NA,NA,NA,C80,NA,NA,NA	;;;X;	1.33835;;1.65107;;X;	1.49471	Q96EY8 Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 , S4R3P5 Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 ,
KC(464.28596)STPEEIK	C6,NA,NA	;;X;X;	1.58861;;X;X;	1.58861	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN , P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 ,
AGAIAPC(470.29977)EVTV PAQNTGLGPEK	NA,NA	;;;;	1.74262;;1.45942;;1.31211;;	1.45942	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 ,
SAQPSPHYM(15.994915)A APSSGQIYGSGPQGYNTQP VPVSGQC(470.29977)PPP	NA,NA,M235,C262,NA,NA ,NA	;;X;X;	1.39316;;X;X;	1.39316	A0A087WZF1 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 , C9JXK9 Lipoma-preferred partner (Fragment) OS=Homo sapiens GN=LPP PE=1 SV=1 , C9JUT4

STR					LIM domain containing preferred translocation partner in lipoma, isoform CRA_e OS=Homo sapiens GN=LPP PE=1 SV=1 , Q93052 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 ,
AHGISSYFPVQAAVIPALLES AAC(470.29977)GFLVGR	NA,NA	U,,X;X;	1.7259,,X;X;	1.7259	Q8N8A6 ATP-dependent RNA helicase DDX51 OS=Homo sapiens GN=DDX51 PE=1 SV=3 ,
SAC(464.28596)SLESNLEG LAGVLEADLPNYK	C44,NA	,,;,;	1.46423,,1.33647,,1 .19017,,	1.33647	Q09161 Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 ,
C(464.28596)ESAFLSK	NA,C36,C36,NA	,,X;X;	1.53517,,X;X;	1.53517	C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 ,
FVIHCNSPVWGADKC(464. 28596)EELLEK	C285,NA,NA	,,X;X;	1.96509,,X;X;	1.96509	O75367-3 Isoform 3 of Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY , O75367 Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4 ,
LVFLAC(464.28596)C(464. 28596)VAPTNP	C301,C301,NA	U,,X;X;	1.51726,,X;X;	1.51726	Q14566 DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 ,
KEC(470.29977)ENCDCLQ GFQLTHSLGGGTGSGMGTL LISK	C471,NA	,,X;X;	0.08288,,X;X;	0.08288	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
KEC(470.29977)ENCDCLQ GFQLTHSLGGGTGSGMGTL LISK	C471,NA	,,X;X;	0.02697,,X;X;	0.02697	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
FDTGNLC(464.28596)M(1 5.994915)VTGGANLGR	NA,NA,NA	U,,X;X;	1.56678,,X;X;	1.56678	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
RGPC(470.29977)IYNEDN GIK	C208,NA	,,;,X;	1.39084,,1.04694,, X;	1.21889	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
RGPC(470.29977)IYNEDN GIK	C208,NA	,,X;X;	1.40422,,X;X;	1.40422	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
KNM(15.994915)QITILTC(464.28596)R	M141,C148,M141,C148,N A	,,X;X;	2.55236,,X;X;	2.55236	O95456 Proteasome assembly chaperone 1 OS=Homo sapiens GN=PSMG1 PE=1 SV=1 , O95456-2 Isoform 2 of Proteasome assembly chaperone 1 OS=Homo sapiens GN=PSMG1 ,
NVQLLSQFVSPFTGC(464.2 8596)IYGR	NA,NA,NA	U,,U,,X;	1.42143,,1.37381,, X;	1.39762	Q9Y3D5 28S ribosomal protein S18c, mitochondrial OS=Homo sapiens GN=MRPS18C PE=1 SV=1 ,

RVPTANVSVDLTC(464.28596)R	C247,NA	,,X;X;	1.45882,,X;X;	1.45882	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
TIGGGDSFTTFFC(464.28596)ETGAGK	NA,NA,NA	,,,,,,X;	1.52163,1.61386,1.5058,1.58852,,1.1681,,X;	1.52163	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
YYGGAENVDEIELLC(464.28596)QR	NA,NA,NA	,,,X;	1.54526,,3.81075,,X;	2.678005	G3V5L0 Serine hydroxymethyltransferase, mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 ,
AAREEC(470.29977)PVFTP PGGETLDQVK	C114,NA,C55,NA,NA	,,X;X;	1.08639,,X;X;	1.08639	Q9NQ88 Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 , A0A0U1RQD1 Chromosome 12 open reading frame 5, isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 ,
WLSDEC(464.28596)TNAV VNFLSR	C345,NA,NA,NA,C345,NA,NA	,,X;X;	1.37694,,X;X;	1.37694	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 , A0A0C4DGA2 Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 , O75521 Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 ,
IC(470.29977)PVEFNPV AR	NA,NA,NA	,,,X;	1.28091,,1.06059,,X;	1.17075	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 , F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 ,
SHHLEMVIQLLAIMCVSCIC(470.29977)WSPFLTHWGK	NA,NA	U,,X;X;	0.74582,,X;X;	0.74582	P43088-7 Isoform 7 of Prostaglandin F2-alpha receptor OS=Homo sapiens GN=PTGFR ,
LPHC(470.29977)ASM(15.994915)TPDGWSFALK	NA,NA,NA,C1718,M1721,NA,NA	,,X;X;	1.1181,,X;X;	1.1181	G5E9E7 Tight junction protein 1 (Zona occludens 1), isoform CRA_e OS=Homo sapiens GN=TJP1 PE=1 SV=1 , A0A087X0K9 Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=1 , G3V1L9 Tight junction protein 1 (Zona occludens 1), isoform CRA_a OS=Homo sapiens GN=TJP1 PE=1 SV=1 ,
SGDLFNC(470.29977)GSLT IR	NA,NA,NA	,,X;X;	1.31418,,X;X;	1.31418	P21953 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Homo sapiens GN=BCKDHB PE=1 SV=2 ,
ASVGFGGSC(464.28596)F QK	NA,C209,NA	,,X;;	1.23765,,X;1.05537,,	1.14651	O60701 UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 , O60701-2 Isoform 2 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH ,
YGAVDPLLALLAVPDMSSLA C(470.29977)GYLR	C223,NA	U,,X;X;	1.48056,,X;X;	1.48056	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 ,

LGYLTC(464.28596)PSNL GTGLR	C347,NA,C347,NA,NA	,,X;;	1.30666,,X;1.17936 ,,	1.24301	P12532-2 Isoform 2 of Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A , P12532 Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 ,
LGYLTC(464.28596)PSNL GTGLR	C347,NA,C347,NA,NA	,,,X;	1.31162,,1.71898,, X;	1.5153	P12532-2 Isoform 2 of Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A , P12532 Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 ,
C(470.29977)YGLHAFIVPI R	NA,NA	,,X;X;	2.23614,,X;X;	2.23614	Q15067-2 Isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 ,
C(470.29977)HIDLSGIVEE VKAQYDAVAAR	NA,NA,C244,NA,NA	,,X;X;	1.29085,,X;X;	1.29085	Q6KB66-2 Isoform 2 of Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 , Q6KB66 Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2 ,
SGVIVLPC(464.28596)GAG K	NA,NA	U,,X;X;	2.96294,,X;X;	2.96294	P19447 TFIIF basal transcription factor complex helicase XPB subunit OS=Homo sapiens GN=ERCC3 PE=1 SV=1 ,
YIGENLQLLVDRPDGTYC(4 64.28596)FR	NA,NA	,,,X;	1.57109,,1.17239,, X;	1.37174	Q9Y221 60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens GN=NIP7 PE=1 SV=1 ,
ISEVFDC(464.28596)WFES GSM(15.994915)PYAQVH YPFENKR	NA,NA,NA	,,X;X;	1.57729,,X;X;	1.57729	P41252 Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 ,
ISEVFDC(464.28596)WFES GSM(15.994915)PYAQVH YPFENKR	NA,NA,NA	,,X;X;	1.29103,,X;X;	1.29103	P41252 Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 ,
ISEVFDC(464.28596)WFES GSM(15.994915)PYAQVH YPFENKR	NA,NA,NA	,,X;X;	2.3621,,X;X;	2.3621	P41252 Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 ,
ITAFVPNDGC(464.28596)L NFIEENDEVLVAGFGR	NA,NA	,,,X;X;	1.4549,1.32625,1.2 4082,,X;X;	1.32625	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
APPWVPAMGFTLAPSLGC(464.28596)FVGSR	C19,NA,NA	,,X;X;	2.4501,,X;X;	2.4501	B1AH87 Putative peripheral benzodiazepine receptor- related protein (Fragment) OS=Homo sapiens GN=TSPO PE=1 SV=1 , P30536 Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 ,
ITAFVPNDGC(464.28596)L NFIEENDEVLVAGFGR	NA,NA	,,,,,	1.46128,1.44654,,1. 23461,,1.23372,,	1.340575	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
TPSQLSDNNC(464.28596) RQ	C334,NA	U,,X;X;	1.13852,,X;X;	1.13852	Q4G0F5 Vacuolar protein sorting-associated protein 26B OS=Homo sapiens GN=VPS26B PE=1 SV=2 ,

AC(464.28596)FCIDNEALY DICFR	NA,NA	U,,X;X;	35.2566,,X;X;	35.2566	Q9H4B7 Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 ,
LLPAITILGC(470.29977)R	NA,NA,NA	,,X;X;	1.55101,,X;X;	1.55101	Q96IJ6 Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 , Q96IJ6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA ,
LADQC(464.28596)TGLQG FLVFHSFGGGTGSFTSLLM (15.994915)ER	C129,M154,C129,M154,C199,M224,NA,NA	,,,X;	1.43974,1.38135,,1.44547,,X;	1.43974	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 ,
LADQC(464.28596)TGLQG FLVFHSFGGGTGSFTSLLM (15.994915)ER	C129,M154,NA,NA,NA	,,X;X;	1.58311,1.53944,,X;X;	1.561275	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
LNLPINIIGLAPLC(464.28596)ENM(15.994915)PSGK	C335,M338,NA,NA	,,X;X;	1.34922,,X;X;	1.34922	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 , P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 ,
VSDDVPDC(464.28596)K	C578,NA,NA	,,X;X;	1.27334,,X;X;	1.27334	Q9NV88 Integrator complex subunit 9 OS=Homo sapiens GN=INTS9 PE=1 SV=2 , Q9NV88-2 Isoform 2 of Integrator complex subunit 9 OS=Homo sapiens GN=INTS9 ,
KC(470.29977)SASNR	C17,C17,C17,NA	,,X,,,;	1.13586,,X;1.24398,,;	1.18992	Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 , Q9BYK1 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 , P63220 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 ,
GLTLLFASGDSGAGC(470.29977)WSVSGR	NA,NA,NA	,,X;X;	1.63488,,X;X;	1.63488	O14773 Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 , O14773-2 Isoform 2 of Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 ,
FLC(464.28596)ESVFSYQV ASTLK	NA,NA	U,,X;X;	1.24251,,X;X;	1.24251	Q96DE5 Anaphase-promoting complex subunit 16 OS=Homo sapiens GN=ANAPC16 PE=1 SV=1 ,
LC(470.29977)PLKDEPWPI HPWEPGSFR	C105,NA,NA,NA,C78,NA,NA	,,X;X;	1.48385,,X;X;	1.48385	E7ETU7 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , H0Y9G6 39S ribosomal protein L3, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , P09001 39S ribosomal protein L3,

					mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 ,
LC(470.29977)PLKDEPWPI HPWEPGSFR	C105,NA,NA,NA,C78,NA,C 78,NA,NA	,,,X;	1.72741,,2.58357,, X;	2.15549	E7ETU7 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , H0Y9G6 39S ribosomal protein L3, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , E9PF06 39S ribosomal protein L3, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , P09001 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 ,
TC(470.29977)PVQLWVDS TPPPGTR	NA,C141,NA,C102,C141,C 102,NA,NA,NA	,,X;X;	1.14094,,X;X;	1.14094	P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 , P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 ,
LGGTC(464.28596)VNVGC VPK	NA,NA,NA,NA,C102,NA,N A	,,X;X;	1.24596,,X;X;	1.24596	P00390-2 Isoform Cytoplasmic of Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR , P00390 Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 , P00390-3 Isoform 2 of Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR ,
VGTAKVNC(470.29977)M VMADQNQVWVGSEDSVIY IINVHSMSCNK	C950,NA,C955,NA,NA	,,X;X;	0.65386,,X;X;	0.65386	A2RUS2 DENN domain-containing protein 3 OS=Homo sapiens GN=DENND3 PE=1 SV=2 , A2RUS2-2 Isoform 2 of DENN domain-containing protein 3 OS=Homo sapiens GN=DENND3 , H0YAY3 DENN domain-containing protein 3 (Fragment) OS=Homo sapiens GN=DENND3 PE=1 SV=1 , E9PF32 DENN domain-containing protein 3 OS=Homo sapiens GN=DENND3 PE=1 SV=1 ,
LLEQFVC(470.29977)AHT GIIFYAPYTGVCVK	NA,NA,NA	U,,X;X;	1.89407,,X;X;	1.89407	Q9Y676 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=1 SV=1 ,
LYYFQYPC(470.29977)YQE GLR	NA,NA	U,,U,,U,,	1.05654,,1.3361,,1. 20257,,	1.20257	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 ,
LYYFQYPC(470.29977)YQE	NA,NA	U,U,,X;X;	1.54411,1.52156,,X	1.532835	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo

GLR			;X;		sapiens GN=APOBEC3C PE=1 SV=2 ,
STFFNVLTSQASAENFPFC (464.28596)TIDPNESR	NA,NA,NA	;;X;X;	1.51864,1.48753;;X; ;X;	1.503085	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 , Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 ,
EGGQYGLVAAC(470.2997 7)AAGGQGHAMIVEAYPK	C436,NA,C436,NA,NA	;;X;X;	1.8092;;X;X;	1.8092	P55084 Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 , P55084-2 Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB ,
SVNSLDGLASVLYPGC(464. 28596)DTLDKVFTYAK	C85,NA	U;;X;X;	1.32684;;X;X;	1.32684	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 ,
AAGELGIAVCNIPSAAVEET ADSTIC(464.28596)HILNLY R	NA,C140,C208,NA	;;X;X;	1.28559;;X;X;	1.28559	P56545-2 Isoform 2 of C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 , P56545 C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 , Q5SQP8 C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 ,
MPC(464.28596)QLHQVIV AR	C640,NA	;;X;X;	1.63487;;X;X;	1.63487	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 ,
SM(15.994915)VSPVPSPT GTISVPNSC(470.29977)PA SPR	NA,NA	;;;X;	1.54942;;1.2741;;X;	1.41176	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 ,
VC(470.29977)ISILHAPGD DPM(15.994915)GYESSAE R	NA,NA,NA	;;X;;;	1.4698;;X;1.38927;;	1.429535	P60604-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 , P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 ,
VQPQWSPPAGTQPC(470. 29977)R	C110,NA,NA	;;X;X;	1.35872;;X;X;	1.35872	P49589-3 Isoform 3 of Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS ,
IGNC(464.28596)PFSQR	NA,NA,C35,NA,C32,NA	;;X;X;	1.40031,1.40031;;X; ;X;	1.40031	Q9NZA1 Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3 , Q9NZA1-3 Isoform 3 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 , Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 , O00299 Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 , Q9NZA1-2 Isoform 1 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 ,
DLSYC(464.28596)LSGMY DHR	NA,NA	U;;X;X;	1.50674;;X;X;	1.50674	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 ,

DLSYC(464.28596)LSGMY DHR	NA,NA	U,,X;X;	1.39411,,X;X;	1.39411	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 ,
ASFENNCEIGC(470.29977) FAK	C15,NA	,,X;X;	0.78764,,X;X;	0.78764	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 ,
NHLLPDIVTC(470.29977)V QSSRK	C184,NA	U,,X;X;	1.17335,,X;X;	1.17335	Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 ,
C(464.28596)SGIGDNPGS ETAAPR	C1317,NA,NA	,,X;;;	1.93691,,X;1.39597 ,;	1.66644	H0YAC6 Lipopolysaccharide-responsive and beige-like anchor protein (Fragment) OS=Homo sapiens GN=LRBA PE=1 SV=1 , P50851 Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4 ,
ELVNAQC(470.29977)AK	C93,C19,NA	,,X;X;	1.45911,,X;X;	1.45911	Q9Y3C7 Mediator of RNA polymerase II transcription subunit 31 OS=Homo sapiens GN=MED31 PE=1 SV=1 , I3L2J1 Mediator of RNA polymerase II transcription subunit 31 OS=Homo sapiens GN=MED31 PE=1 SV=1 ,
VTEDENDEPIEIPSEDDGTVL LSTVTAQFPGAC(464.2859 6)GLR	NA,C39,C39,C39,NA,NA,NA	,,,X;	1.44424,1.55525,1.41083,,1.55327,,X;	1.498755	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
VTEDENDEPIEIPSEDDGTVL LSTVTAQFPGAC(464.2859 6)GLR	NA,C39,C39,C39,NA,NA,NA	,,,X;X;	1.67148,2.1752,,X; X;	1.92334	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
YQEAAPNVANNTGPHAAS C(464.28596)FGAK	C517,NA,C517,NA,NA,NA, NA,NA,NA,C295,C564,NA, NA,C295,NA,C618,NA,C56 4,C564,C618,NA,C295,C51 7,NA,C295,C295,NA,C564,	,,X;X;	1.27632,,X;X;	1.27632	O60716-23 Isoform 3C of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-30 Isoform 4B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-19 Isoform 3AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-2 Isoform 1AB of Catenin delta-1 OS=Homo sapiens

	NA,C517,NA,NA,NA,NA				GN=CTNND1 , O60716-4 Isoform 1BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , C9JZR2 Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=2 , O60716-32 Isoform 4 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-10 Isoform 2AB of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-18 Isoform 3AB of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-3 Isoform 1AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-15 Isoform 2C of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-16 Isoform 2 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-24 Isoform 3 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-29 Isoform 4A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-8 Isoform 1 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-5 Isoform 1A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-26 Isoform 4AB of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-11 Isoform 2AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-9 Isoform 2ABC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-7 Isoform 1C of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-28 Isoform 4BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-25 Isoform 4ABC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-21 Isoform 3A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-6 Isoform 1B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-27 Isoform 4AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-31 Isoform 4C of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716 Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 , O60716-13 Isoform 2A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-12 Isoform 2BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-17 Isoform 3ABC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-14 Isoform 2B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-22 Isoform
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					3B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-20 Isoform 3BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 ,
ADHQPLTEASYVNLPTIALC(464.28596)NTDSPLR	NA,C148,NA,NA	,,;,;	1.41427,,1.37929,,1.0888,,	1.37929	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 , C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 , P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 ,
ADHQPLTEASYVNLPTIALC(464.28596)NTDSPLR	NA,C148,NA,NA	,,;,X;	1.387,,1.28097,,X;	1.333985	A0A0C4DG17 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1 , C9J9K3 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=7 , P08865 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 ,
FYTDPEAVKDIPDGATVLVGGFGLC(470.29977)GIPE NLIDALLK	NA,NA,NA	U,,X;X;	0.84025,,X;X;	0.84025	P55809 Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 ,
LNILQEGHAQC(464.28596)LEAVR	C146,NA,NA,NA,NA,NA,NA,NA	,,X;X;	1.52819,,X;X;	1.52819	H7C3L3 Ankyrin repeat domain-containing protein 54 (Fragment) OS=Homo sapiens GN=ANKRD54 PE=1 SV=1 , D3YTC9 Ankyrin repeat domain-containing protein 54 OS=Homo sapiens GN=ANKRD54 PE=1 SV=1 , Q6NXT1 Ankyrin repeat domain-containing protein 54 OS=Homo sapiens GN=ANKRD54 PE=1 SV=2 , F8WB76 Ankyrin repeat domain-containing protein 54 (Fragment) OS=Homo sapiens GN=ANKRD54 PE=1 SV=1 , Q6NXT1-2 Isoform 2 of Ankyrin repeat domain-containing protein 54 OS=Homo sapiens GN=ANKRD54 , B5MCX7 Ankyrin repeat domain-containing protein 54 OS=Homo sapiens GN=ANKRD54 PE=1 SV=1 ,
AAVEEGIVLGGGC(464.28596)ALLR	NA,NA,NA	U,U,,U,U,,U,;	1.39896,1.38758,,1.36544,1.39223,,1.21556,,	1.38758	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
AAVEEGIVLGGGC(464.28596)ALLR	NA,NA,NA	U,U,,U,,U,;	1.37479,1.41909,,1.42282,,1.26818,,	1.39694	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
C(464.28596)YVQPQWVF DSVNAR	NA,C386,C374,NA	,,X;X;	1.56403,,X;X;	1.56403	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 , O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 , B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 ,

ITAFVPNDGC(470.29977)LNFIEENDEVLVAGFGRK	NA,NA	,,X;X;	1.79115,,X;X;	1.79115	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
C(464.28596)VGLSAPQLGVPR	C108,NA,NA	U,,X;X;	0.8782,,X;X;	0.8782	Q9HBH1 Peptide deformylase, mitochondrial OS=Homo sapiens GN=PDF PE=1 SV=1 ,
SGAELALDYLC(470.29977)R	C75,NA,C107,C92,NA	,,X;X;	1.40379,,X;X;	1.40379	H7C0T1 Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=1 SV=1 , Q9BRJ6 Uncharacterized protein C7orf50 OS=Homo sapiens GN=C7orf50 PE=1 SV=1 , C9JQV0 Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=1 SV=1 , H7C2R9 Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=1 SV=1 ,
LIC(464.28596)CDILDVLDKHLIPAANTGESK	C97,NA,NA	,,X;X;	1.29871,,X;X;	1.29871	P62258 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1 , P62258-2 Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE ,
YC(464.28596)FPNYVGRPK	C34,C34,NA	,,X;X;	1.08758,,X;X;	1.08758	P61163 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 , R4GMT0 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 ,
VC(464.28596)EEIAIIPSKK	NA,C35,C35,NA	,,,X;;	1.72644,1.43535,,X; ;1.36076,,	1.43535	H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 , A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 , P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 ,
C(470.29977)PADNPGLVQAQPR	NA,NA	,,X;X;	1.24322,,X;X;	1.24322	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
YYRPTEVDFLQGDC(470.29977)TK	NA,NA,NA	,,X;X;	1.64741,,X;X;	1.64741	O60547 GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS PE=1 SV=1 ,
VC(464.28596)EEIAIIPSKK	NA,C35,C35,NA	,,,;;	1.99418,1.61388,,2.52843,,1.52138,;	1.80403	H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 , A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 , P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 ,
C(470.29977)PADNPGLVQAQPR	NA,NA	,,X;X;	1.45076,,X;X;	1.45076	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
M(15.994915)LVPLAKLSCLDGLQLLLC(470.29977)LELLPIILFIPGIR	M1,C19,NA,NA	U,,X;X;	0.32054,,X;X;	0.32054	D6RJF8 Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (Fragment) OS=Homo sapiens GN=ETFDH PE=4 SV=1 ,

YVENPSQVLNC(464.28596)ER	NA,C1344,NA	;;X;X;	2.4497;;X;X;	2.4497	O75694-2 Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 , O75694 Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 ,
RPYGVGLLIAGYDDM(15.994915)GPHIFQTC(470.29977)PSANYFDCR	M146,C154,NA,NA	;;X;X;	1.29784;;X;X;	1.29784	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 , P25786 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 ,
AAGPLLTDEC(464.28596)R	C199,NA	U;;X;X;	0.85042;;X;X;	0.85042	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
RPYGVGLLIAGYDDM(15.994915)GPHIFQTC(470.29977)PSANYFDCR	M146,C154,NA,M115,C123,NA	;;;;;	1.34343;;2.36239;;1.27906;;	1.34343	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 , P25786 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 , F5GX11 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 ,
HISPTAPDTLGC(470.29977)YPFYK	C419,C384,NA	;;X;;;	1.64865;;X;1.48315;;	1.5659	A0A087WWF6 DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1 , P49005 DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1 ,
LSNVAPPC(464.28596)ILR	NA,NA,NA,NA	;;X;X;	1.50382;;X;X;	1.50382	C9JB30 Microtubule-associated protein RP/EB family member 3 (Fragment) OS=Homo sapiens GN=MAPRE3 PE=1 SV=1 , Q9UPY8 Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens GN=MAPRE3 PE=1 SV=1 , Q9UPY8-2 Isoform 2 of Microtubule-associated protein RP/EB family member 3 OS=Homo sapiens GN=MAPRE3 ,
ASKDLAQTSYFMATNSLHLT TFSLQYTPPVVAC(464.28596)VCIHLAC(470.29977)K	NA,NA	U;;X;X;	4.02811;;X;X;	4.02811	O60563 Cyclin-T1 OS=Homo sapiens GN=CCNT1 PE=1 SV=1 ,
FGEVVDC(470.29977)TLKL DPITGR	NA,C126,NA,NA,NA,NA,NA A	;;X;X;	0.83165;;X;X;	0.83165	Q14103-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD , Q14103-3 Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD , H0Y8G5 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=7 , H0YA96 Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=1 , Q14103 Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 , Q14103-2

					Isoform 2 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD ,
NQC(464.28596)LFTNTQCK	NA,NA,C68,NA,NA,C68,NA	;;X;X;	1.49358;;X;X;	1.49358	B7Z6B6 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , Q9UL40 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , B7Z6Q2 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , Q9UL40-2 Isoform 2 of Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 , D6RJ07 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , Q9UL40-3 Isoform 3 of Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 ,
IDRYTQQGFGNLPIC(470.29977)M(15.994915)AK	C841,M842,NA,C906,M907,NA,C907,M908,NA	;;X;X;	1.80013;;X;X;	1.80013	A0A087WVM4 Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 , Q6UB35 Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 , B7ZM99 MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 ,
LC(464.28596)EPEVLNSLEETYSPPFR	C177,C261,C261,NA,C224,NA,NA,NA,NA,NA,NA	;;X;;;;	1.01486;;X;0.81591;;	0.915385	H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7-11 Isoform 11 of Zinc finger CCCH

					domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 ,
GSC(470.29977)STEVEKET QEK	C69,NA	U,,X;X;	1.2671,,X;X;	1.2671	O75348 V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 ,
TLKLTPTYGDLNHLVSATM SGVTTC(464.28596)LR	C239,C239,NA,C221,NA	,,X;X;	1.51768,,X;X;	1.51768	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
SC(470.29977)TDESELLHP ELLSQEFLLLTLEQK	C10,C48,C48,NA	,,X;X;	1.41981,,X;X;	1.41981	C9J4K0 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 , Q9BVC5 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 , Q9BVC5-2 Isoform 2 of Ashwin OS=Homo sapiens GN=C2orf49 ,
GSC(470.29977)STEVEKET QEK	C69,NA	U,,X;U,,	1.31165,,X;1.2538,,	1.282725	O75348 V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 ,
ALANSLAC(470.29977)QG K	NA,C393,NA,NA	,,X;X;	1.24823,,X;X;	1.24823	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 , P04075-2 Isoform 2 of Fructose- bisphosphate aldolase A OS=Homo sapiens GN=ALDOA , J3KPS3 Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=1 SV=1 ,
TQLAVC(470.29977)QQR	C396,NA,NA	,,X;X;	1.42599,,X;X;	1.42599	Q02790 Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 , H0YFG2 Peptidyl-prolyl cis- trans isomerase FKBP4 (Fragment) OS=Homo sapiens GN=FKBP4 PE=1 SV=1 ,
KAQC(470.29977)PIVER	C66,NA,C66,NA	,,,X;	1.4838,,1.3333,,X;	1.40855	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
C(464.28596)LHNFLTDGV PAEGAFTEDFQGLR	C316,NA,C268,NA	,,X;X;	1.44679,,X;X;	1.44679	G3V1A6 Gasdermin domain containing 1, isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 , P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 ,
EC(464.28596)LPLIIFLR	NA,NA,NA	U,U,U,,U,,U,,	1.34481,1.3007,1.3 8873,,1.3392,,1.212 69,,	1.3392	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,

GEPGLEQPFWISSVAALLNT DLVATGSHSSC(464.28596 JVR	NA,NA	U,,X;X;	0.63486,,X;X;	0.63486	O43818 U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens GN=RRP9 PE=1 SV=1 ,
C(464.28596)LHNFLTDGV PAEGAFTEDFQGLR	C316,NA,C268,NA	,,X;,,	1.45946,,X;1.68464 ,,	1.57205	G3V1A6 Gasdermin domain containing 1, isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 , P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 ,
LC(470.29977)DFGVSGQLI DSM(15.994915)ANSFVGT R	C207,M219,NA,NA	,,X;X;	1.3458,,X;X;	1.3458	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 , Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 ,
VEPC(464.28596)SLTPGYT K	C219,NA,NA,NA,NA,NA	,,X;X;	1.9037,,X;X;	1.9037	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1-2 Isoform 2 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 , G5E9D4 Elongation protein 4 homolog (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=ELP4 PE=1 SV=1 ,
CC(464.28596)LTYCFNKPE DK	C145,NA	U,,X;X;	2.78417,,X;X;	2.78417	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
LTTPTYGDLNHLVSATM(15 .994915)SGVTTC(464.285 96)LRFPQQLNADLR	M233,C239,M233,C239,N A,M215,C221,NA	,,X;X;	1.41499,,X;X;	1.41499	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
SPAGLQVLNDYLADKSYIEG YVPSQADVAVFEAVSSPPP ADLC(470.29977)HALR	NA,NA	,,X;X;	1.04275,,X;X;	1.04275	P24534 Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 ,
EITAIESSVPC(464.28596)Q LLESVLQELK	NA,C704,NA	,,X;X;	1.13845,,X;X;	1.13845	O75694-2 Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 , O75694 Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 ,
DSEDNPQTLFSATC(470.2 9977)PHWVFNVAK	C310,C310,NA	,,X;X;	1.13159,,X;X;	1.13159	Q9NR30 Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 , Q9NR30-2 Isoform 2 of Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 ,
SSGEIVYC(464.28596)GQV	NA,NA	,,X;X;	1.35843,,X;X;	1.35843	Q02543 60S ribosomal protein L18a OS=Homo sapiens

FEK					GN=RPL18A PE=1 SV=2 ,
SSGEIVYC(464.28596)GQV FEK	NA,NA	,;X;X;	1.72031,;X;X;	1.72031	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 ,
LEGDLTGPSVGVEVPDVELE C(464.28596)PDAK	NA,NA	U,;X;X;	1.47944,;X;X;	1.47944	Q09666 Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 ,
VLQNMEQC(470.29977)Q K	NA,NA	,;X;X;	2.21672,;X;X;	2.21672	Q96ER3 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=2 ,
TLSFYFPPC(464.28596)GK	C388,NA,NA	,;X;X;	1.42926,;X;X;	1.42926	Q9UG63-2 Isoform 2 of ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 , Q9UG63 ATP- binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2 ,
YPNC(464.28596)PTDVR	C347,NA,NA,NA	,;X;X;	0.04041,;X;X;	0.04041	O43929-3 Isoform 3 of Origin recognition complex subunit 4 OS=Homo sapiens GN=ORC4 , O43929 Origin recognition complex subunit 4 OS=Homo sapiens GN=ORC4 PE=1 SV=2 , O43929-2 Isoform 2 of Origin recognition complex subunit 4 OS=Homo sapiens GN=ORC4 ,
DLC(464.28596)FSPGLM(1 5.994915)EASHVVNDVNE AVQLVFR	NA,C362,M368,NA	,,;X;	1.34133,1.48296,;1. 36608,;X;	1.36608	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 , Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 ,
DLC(464.28596)FSPGLM(1 5.994915)EASHVVNDVNE AVQLVFR	NA,C362,M368,NA	,,;X;	1.21449,;1.4906,;X;	1.352545	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 , Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 ,
LDVGNSWGSECC(470.29 977)TR	NA,NA	U,;X;X;	1.65599,;X;X;	1.65599	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
THC(464.28596)PYAVALPE VAPAQLTEALR	C143,NA	,;X;X;	1.91925,;X;X;	1.91925	Q6PJG6 BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 ,
GQVC(470.29977)LPVISAE NWKPATK	C144,NA,C144,NA	,;X;X;	1.26738,;X;X;	1.26738	P68036 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 , P68036-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 , P68036-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 ,
GQVC(470.29977)LPVISAE NWKPATK	C144,NA,C144,NA	,;X;X;	1.24643,;X;X;	1.24643	P68036 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 , P68036-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens

					GN=UBE2L3 , P68036-3 Isoform 3 of Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 ,
STFFNVLTSQASAENFPFC (464.28596)TIDPNESRPV PDER	NA,NA,NA	,,X;X;	1.54991,,X;X;	1.54991	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 , Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 ,
YGINTTDIFQTVDLWEGKN M(15.994915)AC(470.299 77)VQR	M122,C124,NA,NA,NA	,,X;X;	1.56243,,X;X;	1.56243	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 , P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 , X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 ,
SGRYEAAFPFLSPC(464.285 96)GR	NA,NA,NA	,,X;X;	1.39037,,X;X;	1.39037	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 , Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 ,
DEAVKEC(470.29977)GK	NA,NA,NA	,,X;X;	0.22861,,X;X;	0.22861	Q9NRE2-2 Isoform 2 of Teashirt homolog 2 OS=Homo sapiens GN=TSHZ2 , Q9NRE2 Teashirt homolog 2 OS=Homo sapiens GN=TSHZ2 PE=1 SV=3 ,
VC(464.28596)NFLASQVP FPSR	C205,NA	,,,;,,;	1.19981,1.35481,1.33365,,1.37556,,1.26328,,	1.33365	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
VC(464.28596)NFLASQVP FPSR	C205,NA	,,,;,,;	1.38393,,1.39189,,1.31166,,	1.38393	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
DAALLC(464.28596)VR	NA,NA	U,,X;X;	1.31434,,X;X;	1.31434	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 ,
SLAPPDASILISNVC(470.29 977)SIGDHVAQELFQGSDL GM(15.994915)AEEAERPG EK	NA,C274,M292,NA	,,X;X;	1.52069,,X;X;	1.52069	A0A087X0R7 Protein SENP3-EIF4A1 (Fragment) OS=Homo sapiens GN=SENP3-EIF4A1 PE=4 SV=1 , Q9H4L4 Sentrin-specific protease 3 OS=Homo sapiens GN=SENP3 PE=1 SV=2 ,
AFAFVTFADDQIAQSLC(47 0.29977)GEDLIK	NA,C244,C244,C244,NA,NA,NA	,,,;X;	1.34503,,1.22802,,X;	1.286525	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
IAVYSC(470.29977)PFDG MITETK	C225,NA	,,X;X;	0.99789,,X;X;	0.99789	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 ,

LDINLLDNVVNC(464.28596)LYHGEQAQQR	NA,NA	,,,X;	1.42966,,1.43083,,X;	1.430245	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 ,
NTPSFLIAC(464.28596)NK	C179,NA	,,,X;	1.33562,,1.20983,,X;	1.272725	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
LDINLLDNVVNC(464.28596)LYHGEQAQQR	NA,NA	,,X,;	1.4297,,X;1.05775,,	1.243725	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 ,
IIC(464.28596)SAGLSLLAE ERQENLPDEIYHVYSFALR	NA,NA,NA	,,X;X;	1.74238,,X;X;	1.74238	Q9BV86 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 , S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 ,
LGSVVTRGDEC(470.29977)GLALGR	C88,NA,NA	,,X;X;	1.39407,,X;X;	1.39407	P54886 Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 , P54886-2 Isoform Short of Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 ,
AYHEQLTVAEITNAC(470.29977)FEPANQM(15.994915)VK	C295,M302,C365,M372,NA	,,,X;	1.33151,,0.96404,,X;	1.147775	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
AYHEQLTVAEITNAC(470.29977)FEPANQM(15.994915)VK	C295,M302,NA	,,,,,;	1.22817,1.55396,1.41467,,1.41364,,1.27693,,	1.41364	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
NC(470.29977)PHVVVGTPGR	C164,NA	,,,,,;	1.17757,1.4128,,1.38356,,1.19485,,	1.289205	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 ,
FRC(464.28596)PEALFQPS FLGM(15.994915)ESCGIH ETTFNSIMK	NA,NA,NA	,,X;X;	1.39953,,X;X;	1.39953	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
FRC(464.28596)PEALFQPS FLGM(15.994915)ESCGIH ETTFNSIMK	NA,NA,NA	,,X;X;	1.94863,,X;X;	1.94863	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
TWYVQATC(464.28596)ATQGTGLYEGLDWLSNELSK	NA,NA	,,X;X;	1.4976,,X;X;	1.4976	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
GIFPVLC(470.29977)KDPVQEAWAEDVDLR	NA,NA	,,X;X;	1.46856,,X;X;	1.46856	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 ,
ASPLPPPPPPGAEPAC(470.29977)PGSSAAAPYK	C128,NA	U,,X;X;	1.91955,,X;X;	1.91955	Q8NDT2 Putative RNA-binding protein 15B OS=Homo sapiens GN=RBM15B PE=1 SV=3 ,
AVSPAIPSAPLYEITYSGISD GLSQASC(464.28596)PLA	NA,C406,C406,NA,NA,NA	,,X;X;	0.91642,,X;X;	0.91642	O60291-4 Isoform 4 of E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 , O60291-3 Isoform 3 of E3

AIDHILDSSR					ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 , O60291 E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 PE=1 SV=2 , O60291-2 Isoform 2 of E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 , K7EPJ5 E3 ubiquitin-protein ligase MGRN1 (Fragment) OS=Homo sapiens GN=MGRN1 PE=1 SV=1 ,
ESLNASIVDAINQAADC(470.29977)WGIR	C167,NA,NA	;;X;X;	1.30366;;X;X;	1.30366	Q9UJZ1 Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 ,
YSTGSDSASFHTTSMC(464.28596)LNPDLEGPPLEAYTIQGQY	C217,NA	;;X;X;	1.39672;;X;X;	1.39672	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 ,
LM(15.994915)HLFTSGDC(470.29977)K	M83,C91,NA	U;;X;X;	1.19938;;X;X;	1.19938	Q8WXD5 Gem-associated protein 6 OS=Homo sapiens GN=GEMIN6 PE=1 SV=1 ,
ISAFGYLEC(464.28596)SAK	NA,NA,C159,NA	;;X;X;	1.6441;;X;X;	1.6441	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 , P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 , E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 ,
YVC(464.28596)EGPSHGG LPGASSEK	C62,NA,NA	;;X;X;	1.14338;;X;X;	1.14338	P19838-2 Isoform 2 of Nuclear factor NF-kappa-B p105 subunit OS=Homo sapiens GN=NFKB1 , P19838 Nuclear factor NF-kappa-B p105 subunit OS=Homo sapiens GN=NFKB1 PE=1 SV=2 ,
ISPVDVNSRPSSC(470.29977)LTNFLNNGR	C248,NA	;;X;X;	1.46581;;X;X;	1.46581	Q9NVM9 Protein asunder homolog OS=Homo sapiens GN=ASUN PE=1 SV=2 ,
IYHPNINSNGSIC(470.29977)LDILR	C87,NA,NA	;;;X;X;	1.39556,1.44051;;X;X;	1.418035	P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 , P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 ,
SVHYC(470.29977)PATK	NA,C193,NA	;;X;;;	1.49922;;X;1.64887;;	1.574045	P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 , P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 ,
ISPVDVNSRPSSC(470.29977)LTNFLNNGR	C248,NA	;;X;X;	1.43372;;X;X;	1.43372	Q9NVM9 Protein asunder homolog OS=Homo sapiens GN=ASUN PE=1 SV=2 ,

LDEC(464.28596)EEAFQG TK	C103,NA,NA,NA,NA,NA	;;X;X;	1.00679;;X;X;	1.00679	P61289-3 Isoform 3 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 , B3KQ25 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , K7ESG5 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289-2 Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 ,
GC(470.29977)QDFGWDP CFQPDGYEQTYAEMPK	C129,NA	;;X;X;	1.6092;;X;X;	1.6092	Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 ,
SC(464.28596)SGVEFSTSG SSNTDTGK	NA,C36,NA	;;;;;	1.25184;;1.52091;;1.35337;;	1.35337	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 , P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
SC(464.28596)SGVEFSTSG SSNTDTGK	NA,C36,NA	;;;;X;	1.3231;;1.87394,1.91718;;X;	1.87394	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 , P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
NC(464.28596)GC(464.28596)LGASPNLEQLQEENLK	C32,C34,NA,NA	;;X;X;	1.4082;;X;X;	1.4082	P54136 Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 ,
VGSFC(470.29977)LSEAGA GSDSFALK	C73,NA,NA,NA,NA	;;X;;;	1.06149;;X;1.38912;;	1.225305	P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB , P45954 Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 ,
NCAVSC(470.29977)AGEK	C141,NA,NA	;;X;X;	1.81503;;X;X;	1.81503	Q15813 Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 , Q15813-2 Isoform 2 of Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE ,
AAQGPPAPAVPPNTDVM(15.994915)AC(464.28596) TQTALLQK	M144,C146,M150,C152,M113,C115,NA	;;X;X;	1.63246;;X;X;	1.63246	H0YEB6 Sjogren syndrome/scleroderma autoantigen 1 (Fragment) OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 , O60232 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 , G3V1B8 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 ,
VPPFPLPLEPC(470.29977)	C42,NA,NA	;;X;X;	1.45143;;X;X;	1.45143	Q12789 General transcription factor 3C polypeptide 1

TQEFLWR					OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 , Q12789-3 Isoform 2 of General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 ,
PC(464.28596)GEDWLSHP LGIVQGFFAQNGVNPDWE K	NA,C3,NA	;;X;X;	1.72321,1.57578;;X ;X;	1.649495	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 , Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP ,
PC(464.28596)GEDWLSHP LGIVQGFFAQNGVNPDWE K	NA,C3,NA	;;X;X;	1.27913;;X;X;	1.27913	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 , Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP ,
SC(464.28596)TDESELLHP ELLSQEFLLLTLEQK	C10,C48,C48,NA	;;X;X;	1.55522,1.69409;;X ;X;	1.624655	C9J4K0 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 , Q9BVC5 Ashwin OS=Homo sapiens GN=C2orf49 PE=1 SV=1 , Q9BVC5-2 Isoform 2 of Ashwin OS=Homo sapiens GN=C2orf49 ,
VLGLGLGC(470.29977)LR	NA,NA,NA	;;;;;	1.53266;;1.49726;;1 .27468;;	1.49726	Q9BRJ7 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 , K7EIN2 Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 ,
YEAAPFLSPC(470.29977) GR	NA,NA,NA	;;X;X;	0.84485;;X;X;	0.84485	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 , Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 ,
GC(464.28596)IGTFSAM(1 5.994915)NLHSGLR	NA,NA,NA,NA	;;X;X;	1.04425;;X;X;	1.04425	Q9Y4X0-4 Isoform 4 of AMME syndrome candidate gene 1 protein OS=Homo sapiens GN=AMMECR1 , Q9Y4X0 AMME syndrome candidate gene 1 protein OS=Homo sapiens GN=AMMECR1 PE=1 SV=1 , Q6DCA0 AMMECR1-like protein OS=Homo sapiens GN=AMMECR1L PE=1 SV=1 ,
YEAAPFLSPC(470.29977) GR	NA,NA,NA	;;X;X;	1.60977;;X;X;	1.60977	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 , Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 ,
VC(470.29977)NVAPIAGE TK	C188,C336,NA	;;X;X;	0.85928;;X;X;	0.85928	H0YG10 Nucleolar GTP-binding protein 2 (Fragment) OS=Homo sapiens GN=GNL2 PE=1 SV=2 , Q13823 Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 ,
IVQTLC(470.29977)TVR	C147,NA	;;X;X;	2.1562;;X;X;	2.1562	Q96D53 AarF domain-containing protein kinase 4 OS=Homo sapiens GN=ADCK4 PE=1 SV=2 ,
C(464.28596)CFLCM(15.9	NA,C33,M38,C33,M38,NA	;;X;X;	1.47075;;X;X;	1.47075	Q16527 Cysteine and glycine-rich protein 2 OS=Homo

94915)VCR					sapiens GN=CSRP2 PE=1 SV=3 , F8VQR7 Cysteine and glycine-rich protein 2 OS=Homo sapiens GN=CSRP2 PE=1 SV=1 , F8VW96 Cysteine and glycine-rich protein 2 OS=Homo sapiens GN=CSRP2 PE=1 SV=1 ,
SEC(470.29977)DQDYIPET DQDC(464.28596)SMSPCP QRTPDSGLAQHPFQNYR	C1250,C1262,C1278,C129 0,NA,C1250,C1262,NA	;;;X;;	0.13819,0.12166;;X ;0.10003,;	0.12166	Q9P2N4 A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 PE=1 SV=4 , Q9P2N4-1 Isoform 2 of A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 , HOY859 A disintegrin and metalloproteinase with thrombospondin motifs 9 (Fragment) OS=Homo sapiens GN=ADAMTS9 PE=4 SV=1 , Q9P2N4-4 Isoform 4 of A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 ,
HSSSC(464.28596)LPLPEF VDNTQVPSYCLNAR	NA,C89,C89,NA,NA	;;X;X;	1.55069;;X;X;	1.55069	A0A0D9SFR5 TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 PE=4 SV=1 , Q9ULP9-2 Isoform 2 of TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 , Q9ULP9 TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 PE=1 SV=2 , H3BQ06 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 ,
IAPC(470.29977)PSQDSLY SDPLDSTSAQAGEGVQR	C308,NA	;;X;X;	2.14918;;X;X;	2.14918	Q99704 Docking protein 1 OS=Homo sapiens GN=DOK1 PE=1 SV=1 ,
AAAPAPEEEMDEC(464.28 596)EQALAAEPK	C266,NA,NA	,,,,,;	1.23303,1.68438,1. 73174;;1.29569,1.2 9578;;1.18026,;	1.295735	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
TELQGLIGQLDEVSLKNPC(464.28596)IR	NA,C327,NA	;;X;X;	1.3059;;X;X;	1.3059	Q9UL15-2 Isoform 2 of BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 , Q9UL15 BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 PE=1 SV=1 ,
LQC(470.29977)FGDVIPN PLDTFGNVQM(15.994915)ASSTDQTEALPLVVR	C411,M429,NA	U;;X;X;	2.3189;;X;X;	2.3189	Q92786 Prospero homeobox protein 1 OS=Homo sapiens GN=PROX1 PE=1 SV=2 ,
GSDELFSTC(470.29977)VT NGPFIM(15.994915)SSNS ASAANGNSK	NA,NA	;;;X;	1.47331,1.18751;;1. 31529;;X;	1.31529	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
ADPDGPEAQAEAC(464.28	C18,NA	;;;X;	1.56519;;1.54545,;	1.55532	Q9NX24 H/ACA ribonucleoprotein complex subunit 2

596)SGER			X;		OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
TPGAATASASGAAEDGAC(470.29977)GCLPNPGTFEECHR	C74,NA	;;X;X;	1.72726;;X;X;	1.72726	O96008 Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1 ,
GLGC(470.29977)QTLGPHNPTPPSLDM(15.994915)FAEELAEETPTPTQR	C234,M250,NA	U;;X;X;	1.26837;;X;X;	1.26837	O95400 CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens GN=CD2BP2 PE=1 SV=1 ,
TIAEC(464.28596)LADELINAAK	C172,NA,C172,NA	,,,,,;	1.55341,1.37174,1.40092;;1.58992,1.59002;;1.26777;;	1.477165	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
TIAEC(464.28596)LADELINAAK	C172,NA,C172,NA	;;;;;	1.35399;;1.59154;;1.4236;;	1.4236	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
ELEAVC(464.28596)QDVLSLLDNYLIK	C97,NA	U;;X;X;	1.24273;;X;X;	1.24273	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 ,
M(15.994915)VAAVAC(470.29977)AQVPK	NA,NA,NA	;;X;X;	1.27213;;X;X;	1.27213	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
C(470.29977)TGGEVGATSALAPK	NA,NA	;;X;X;	1.30077;;X;X;	1.30077	P30050 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 ,
AFQYVETHGEVC(470.29977)PANWTPDSPTIKPSPAASK	NA,NA,NA	;;X;X;	1.60816;;X;X;	1.60816	P30048 Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 ,
AFQYVETHGEVC(470.29977)PANWTPDSPTIKPSPAASK	NA,NA,NA	,,,,,;	1.22274,1.47484;;1.31817;;1.12761;;	1.270455	P30048 Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 ,
AFQYVETHGEVC(470.29977)PANWTPDSPTIKPSPAASK	NA,NA,NA	;;X;X;	1.29018;;X;X;	1.29018	P30048 Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 ,
ECENC(470.29977)DCLQGFQLTHSLGGGTSGMGMTLLISK	C474,NA	;;X;X;	0.01041;;X;X;	0.01041	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,

ENFDEVVNDADIILVEFYAP WC(470.29977)GHCKK	C206,NA	U,,X;X;	1.37444,,X;X;	1.37444	P13667 Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 ,
DGLTDVYNKIHM(15.9949 15)GSC(470.29977)AENTA K	NA,NA,NA	U,,X;X;	1.71581,,X;X;	1.71581	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
LLHVFACACPGC(470.2997 7)STGGAR	NA,NA,NA	,,X;X;	1.27522,,X;X;	1.27522	Q9BRP1 Programmed cell death protein 2-like OS=Homo sapiens GN=PDCD2L PE=1 SV=1 , K7ESF4 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 ,
GPC(464.28596)IYNEDNG IIK	C208,NA	,,X;X;	1.20724,,X;X;	1.20724	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
EEHLC(470.29977)TQR	NA,NA	,,X,,;	1.36004,,X;1.05608 ,,	1.20806	J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 ,
M(15.994915)KVELC(470. 29977)SFSGYK	NA,M1,C6,M1,C6,NA	,,X;X;	1.50957,,X;X;	1.50957	C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 ,
TATAVAHC(464.28596)KR	C25,NA	,,X;X;	1.55007,,X;X;	1.55007	P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 ,
FQSSAVM(15.994915)ALQ EACEAYLVGLFEDTNLC(470 .29977)AIHAK	M91,C111,NA	U,U,,U;X;	1.38516,1.42897,,1. 20565,,X;	1.38516	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
NGYDYGQC(470.29977)R	C80,NA,NA	,,X;X;	1.22786,,X;X;	1.22786	S4R3G0 Serine/arginine-rich-splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 , Q13242 Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 ,
VFIM(15.994915)DSC(470 .29977)DELIPEYLNfir	M363,C366,NA	U,,U;U,,;	1.15171,,1.31604,,1 .29357,,;	1.29357	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 ,
C(464.28596)MQLTDFILK	NA,C54,NA	,,X;X;	1.52197,,X;X;	1.52197	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 , P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 ,
IGIASQALGIAQTALDC(464. 28596)AVNYAENR	NA,NA,C285,NA,NA	,,X;X;	1.68236,,X;X;	1.68236	P16219 Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 , E9PE82 Short-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 ,
LGNNC(470.29977)VFAPA DVTSEKDVQTALALAK	C58,NA	,,X;X;	1.36665,,X;X;	1.36665	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,

LGNNC(470.29977)VFAPA DVTSEKDVQTALALAK	C58,NA	,,X;X;	1.09079,,X;X;	1.09079	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
SVVC(464.28596)QESDLP DELLYGR	NA,NA	U,,X;X;	0.49789,,X;X;	0.49789	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 ,
C(464.28596)IAMMCNEFF EGFPDKQPR	C81,NA	U,,X;X;	16.44201,,X;X;	16.44201	P26447 Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 ,
AAGTDSFNGHPPQGC(470. 29977)ASTPVAR	C553,C517,NA,C553,NA,N A,NA	,,X;X;	1.68642,,X;X;	1.68642	Q9NVU0 DNA-directed RNA polymerase III subunit RPC5 OS=Homo sapiens GN=POLR3E PE=1 SV=1 , Q9NVU0-5 Isoform 5 of DNA-directed RNA polymerase III subunit RPC5 OS=Homo sapiens GN=POLR3E , Q9NVU0-2 Isoform 2 of DNA-directed RNA polymerase III subunit RPC5 OS=Homo sapiens GN=POLR3E , Q9NVU0-3 Isoform 3 of DNA-directed RNA polymerase III subunit RPC5 OS=Homo sapiens GN=POLR3E , A0A0C4DH01 DNA-directed RNA polymerase III subunit RPC5 OS=Homo sapiens GN=POLR3E PE=1 SV=1 , Q9NVU0-4 Isoform 4 of DNA-directed RNA polymerase III subunit RPC5 OS=Homo sapiens GN=POLR3E ,
TDVLVLS(470.29977)DLI TDVALHEVVDLFR	C106,NA,C106,NA	,,X;X;	1.40457,,X;X;	1.40457	Q9NR50-3 Isoform 3 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 , Q9NR50-2 Isoform 2 of Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 , Q9NR50 Translation initiation factor eIF-2B subunit gamma OS=Homo sapiens GN=EIF2B3 PE=1 SV=1 ,
LFDVC(470.29977)TVSR	C83,NA	U,,X;X;	1.09746,,X;X;	1.09746	Q00534 Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1 ,
YSDVEVPASVTGYSFASDG DSGTC(464.28596)SPLR	NA,NA,C430,NA,C430,C43 0,C430,C430,NA	,,,X;X;	1.69851,2.67574,,X ;X;	2.187125	P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 , P35611-5 Isoform 5 of Alpha-adducin OS=Homo sapiens GN=ADD1 , P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 , E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 , P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 , E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 , P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 , P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 ,
GHSAC(464.28596)EPENL	C147,M158,NA	U,,X;X;	1.61382,,X;X;	1.61382	Q9ULX3 RNA-binding protein NOB1 OS=Homo sapiens

EFSSFM(15.994915)FWR					GN=NOB1 PE=1 SV=1 ,
VMTIPYQPM(15.994915)P ASSPVIC(470.29977)AGG QDR	M186,C194,NA	U,,X;X;	1.52219,,X;X;	1.52219	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
SGEEDFESLASQFSDC(464. 28596)SSAK	NA,C113,NA,NA	,,,,,	1.4338,1.4263,,1.13 355,1.34637,,1.140 09,;	1.34637	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 , K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 , Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 ,
SRPNASGGAAC(470.2997 7)SGPGPEPAVFCEPVVK	C108,NA,NA,NA,NA	,,X;X;	1.94577,,X;X;	1.94577	Q6L8Q7 2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=2 , Q6L8Q7-2 Isoform 2 of 2',5'- phosphodiesterase 12 OS=Homo sapiens GN=PDE12 ,
AINC(470.29977)ATSGVV GLVNCLR	C1448,NA	,,,X;	1.33972,,1.0669,,X;	1.20331	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
AINC(470.29977)ATSGVV GLVNCLR	C1448,NA	,,X;X;	2.8313,,X;X;	2.8313	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
GLEPEKIIGATDSC(470.299 77)GDLMFLM(15.994915) K	NA,NA	U,,X;X;	1.43553,,X;X;	1.43553	P45973 Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1 SV=1 ,
LNQVC(470.29977)FDDDG TSSPQDR	NA,NA	,,X;X;	0.82111,,X;X;	0.82111	Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 ,
VC(464.28596)GYDTPFPHI FEPFYIPDKWK	NA,NA,NA	U,,X;X;	1.54377,,X;X;	1.54377	P21953 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Homo sapiens GN=BCKDHB PE=1 SV=2 ,
CPEALFQPSFLGM(15.9949 15)ESC(464.28596)GIHETT FNSIMK	NA,NA,NA	,,X;X;	1.45964,,X;X;	1.45964	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
GM(15.994915)YGIENEVF LSLPC(470.29977)ILNAR	NA,NA	U,,X;X;	1.42208,,X;X;	1.42208	P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 ,
GQVLSTINTNQM(15.9949 15)NNTHAAVSPC(470.299 77)GR	M230,C240,M230,C240,M 194,C204,NA	,,X;X;	1.34971,,X;X;	1.34971	Q9Y4P3 Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1 , Q96E41 TBL2 protein OS=Homo sapiens GN=TBL2 PE=1 SV=1 , E9PF19 Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1 ,
GISC(464.28596)MNTTSE SPFK	NA,NA	U,,X;X;	0.98665,,X;X;	0.98665	Q15181 Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 ,
SC(470.29977)SGVEFSTSG SSNTDTGKVTGTLETK	C36,NA	,,,X;X;	1.35017,1.99625,,X ;X;	1.67321	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,

C(470.29977)SGIGDNPGS ETAAPR	NA,NA	;;X;X;	1.93691;;X;X;	1.93691	P50851 Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4 ,
FQSSAVM(15.994915)ALQ EASEAYLVGLFEDTNLC(464 .28596)AIHAK	NA,NA	U,U;;U;;X;	1.38652,1.41774;;1. 42413;;X;	1.41774	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 ,
LFNC(464.28596)SASLDW PR	NA,NA,NA	;;X;X;	0.05459;;X;X;	0.05459	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
LFNC(464.28596)SASLDW PR	NA,NA,NA	;;X;X;	4.34945;;X;X;	4.34945	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
GLHDSC(470.29977)PGQA R	NA,NA	;;X;X;	1.98689;;X;X;	1.98689	Q32NC0 UPF0711 protein C18orf21 OS=Homo sapiens GN=C18orf21 PE=1 SV=1 ,
VC(470.29977)VETVESGA M(15.994915)TK	C402,M411,NA,NA,NA,NA	;;X;X;	2.32104;;X;X;	2.32104	P48735 Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 , P48735-2 Isoform 2 of Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 ,
ATC(470.29977)APQHGAP GPGPADASK	C2535,C2516,C2535,C250 3,NA	;;X;X;	1.59462;;X;X;	1.59462	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA , Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 , P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 , Q5HY54 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 ,
SGDAAIVEMVPGKPM(15.9 94915)C(464.28596)VESFS QYPPLGR	NA,NA	U;;X;X;	1.47289;;X;X;	1.47289	Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 ,
WHC(464.28596)TVCEDY DLCITCYNTKNHDK	C1683,NA	U;;X;X;	3.02499;;X;X;	3.02499	Q09472 Histone acetyltransferase p300 OS=Homo sapiens GN=EP300 PE=1 SV=2 ,
LWNTLGVC(464.28596)K	NA,NA	;;X;;;	1.58344,4.24921;;X ;1.6174;;	1.6174	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
C(464.28596)PADNPGLVQ AQPR	NA,NA	;;X;X;	1.24322;;X;X;	1.24322	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
C(464.28596)PADNPGLVQ AQPR	NA,NA	;;X;X;	1.45076;;X;X;	1.45076	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
AC(464.28596)VGNAHYHK	C123,C123,NA	;;X;X;	1.29206;;X;X;	1.29206	Q9UKX7-2 Isoform 2 of Nuclear pore complex protein

					Nup50 OS=Homo sapiens GN=NUP50 , Q9UKX7 Nuclear pore complex protein Nup50 OS=Homo sapiens GN=NUP50 PE=1 SV=2 ,
LVIYGGM(15.994915)SGC(464.28596)R	M224,C227,M224,C227,M224,C227,NA,NA	,;X;X;	1.52018,,;X;X;	1.52018	P51610-2 Isoform 2 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 , P51610 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 , P51610-4 Isoform 4 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 , A6NEM2 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 ,
ALIHSAC(470.29977)VK	NA,C145,NA	,;X;X;	1.0037,,;X;X;	1.0037	Q08257 Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 , A6NP24 Quinone oxidoreductase (Fragment) OS=Homo sapiens GN=CRYZ PE=1 SV=1 ,
AVC(464.28596)M(15.994915)LSNTTAIAEAWAR	NA,C376,M377,NA,NA,NA,C376,M377,NA,NA	,,;,;,;X;	1.98594,1.73716,,;1.38571,1.38025,,;X;	1.561435	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
AVC(464.28596)M(15.994915)LSNTTAIAEAWAR	NA,NA,NA,NA,NA,NA,C376,M377,NA,NA	,,;,;,;	2.16376,1.71874,,;1.73851,,;3.56339,,;	1.951135	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
NMSVHLSPC(470.29977)FR	C116,NA	,;X;X;	1.3596,,;X;X;	1.3596	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
LM(15.994915)DLDVEQLG IPEQEYSC(464.28596)VVK	NA,NA	U,,;X;X;	1.20763,,;X;X;	1.20763	P12004 Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 ,

LVYSTCSLC(470.29977)QE ENEDVVRDALQQNPGAFR	NA,NA	,,X;X;	1.42414,,X;X;	1.42414	Q96P11-2 Isoform 2 of Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens GN=NSUN5 ,
LC(470.29977)VQNSPQEA R	C150,C150,NA,NA,NA,NA	,,;,;	1.38061,,1.47074,,1.07253,;	1.38061	P33240-2 Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 , P33240 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 , E7EWR4 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 , E9PID8 Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 , A0A0A0MT56 Cleavage stimulation factor subunit 2 (Fragment) OS=Homo sapiens GN=CSTF2 PE=1 SV=1 ,
NGDIC(464.28596)ETSGKP K	C60,C60,NA,C60,C60,NA,NA	,,;,X;	1.38748,,1.37093,;X;	1.379205	Q16637 Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1 , E7EQZ4 Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1 , Q16637-3 Isoform SMN-delta7 of Survival motor neuron protein OS=Homo sapiens GN=SMN1 , Q16637-2 Isoform SMN-delta5 of Survival motor neuron protein OS=Homo sapiens GN=SMN1 , Q16637-4 Isoform SMN-delta57 of Survival motor neuron protein OS=Homo sapiens GN=SMN1 , B4DP61 Survival motor neuron protein OS=Homo sapiens GN=SMN2 PE=1 SV=1 ,
ICDEC(464.28596)NYGSYQ GR	C49,NA	U,,X;X;	1.57454,,X;X;	1.57454	Q7RTV0 PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1 ,
PC(470.29977)SEETPAISPS KR	C3,NA,C3,NA,NA	,,X;,;	1.50935,,X;1.11308,;	1.311215	P33316-2 Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT , H0YNJ9 Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=1 ,
VIGSGC(464.28596)NLDSA R	C192,NA,NA,NA	,,;,X;	1.64993,,1.61878,;X;	1.634355	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA , P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 , P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 ,
IGFPETEEEEEEIASNSDC(464.28596)IFPSAPDVKA	C353,NA,NA	,,;X;X;	1.22599,1.14008,,X;X;	1.183035	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP , Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 ,

LPSLPLVQGELVGLTC(464.28596)LTATHTSLQHQPLQLTTLDDQYIR	C213,NA,NA,NA,NA	;;X;X;	1.30269;;X;X;	1.30269	Q7Z7H8 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 , Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 ,
AVC(464.28596)MLSNTTAVAEAWAR	C376,NA	;;;X;X;	1.61987,1.45736;;X;X;	1.538615	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
TC(464.28596)LSQLLDIMK	C244,NA	;;X;X;	1.46382;;X;X;	1.46382	P51946 Cyclin-H OS=Homo sapiens GN=CCNH PE=1 SV=1 ,
NFNYHILSPC(470.29977)DLSNYTDLAM(15.994915)S TVK	C461,M471,NA,NA,NA,NA	;;;;;	1.36537;;1.67663;;1.18067;;	1.36537	G5E9W3 Cleavage and polyadenylation specific factor 3, 73kDa, isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=1 SV=1 , Q9UKF6 Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 ,
LC(464.28596)YVALDFENEM(15.994915)ATAASSSSEK	NA,NA,C219,M229,NA,NA	;;;;;	1.78271;;1.69903;;1.7462;;	1.7462	P68133 Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 , P68032 Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 ,
C(464.28596)EFQDAYVLLSEKK	NA,NA,NA	U;;X;X;	1.37365;;X;X;	1.37365	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
C(464.28596)EFQDAYVLLSEKK	NA,NA,NA	U,U;;X;U;;	1.4393,1.41374;;X;1.21009;;	1.41374	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
PPM(15.994915)EAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIAC(464.28596)K	NA,NA,NA	;;;X;	1.45544;;1.47972;;X;	1.46758	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
YAGLSTC(470.29977)FR	NA,NA,NA,NA,NA	;;X;X;	1.28197;;X;X;	1.28197	Q5T5C7 Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 , P49591 Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 ,
GC(464.28596)LELIKETGVPIAGR	NA,NA,NA,NA,NA	;;X;X;	1.48666;;X;X;	1.48666	P11586 C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 , F5H2F4 C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=1 ,
WC(464.28596)EYGLTFTEK	C65,NA	;;X;X;	1.2707;;X;X;	1.2707	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
GVSASAVPFTPSSPLLSC(464.28596)SQEGSR	NA,NA,NA,NA	;;X;X;	0.98527;;X;X;	0.98527	Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 , J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 , Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 ,

VMALQEAC(464.28596)EAYLVGLFEDTNLCAIHAKR	C97,NA	U,,X;X;	4.4252,,X;X;	4.4252	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
FASYC(464.28596)LTEPGSGSDAASLLTSAK	NA,NA,NA,NA,NA	,,X;X;	1.47919,,X;X;	1.47919	Q9UKU7 Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACAD8 PE=1 SV=1 , Q9UKU7-3 Isoform 3 of Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACAD8 ,
YSNSALGHVNC(470.29977)TIK	NA,C1101,NA	,,;,;	2.9645,,2.9748,,2.57898,,	2.9645	Q9NQC3-1 Isoform 1 of Reticulon-4 OS=Homo sapiens GN=RTN4 # F8W914 Reticulon OS=Homo sapiens GN=RTN4 PE=1 SV=1 #
EENVGLHQTLDTLNLNC(470.29977)I	C283,NA,NA	,,X;X;	1.07486,,X;X;	1.07486	P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 , P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 ,
LKGC(470.29977)SNEPYFGLTALVCQHSITPLALPCK	NA,NA	,,X;X;	1.41578,,X;X;	1.41578	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
GSDC(464.28596)GIVNVNIPITSGAEIGGAFGGEK	C450,NA,NA	,,;,X;	1.58426,,1.53907,,X;	1.561665	P49419-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 , P49419 Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 ,
GLPWSC(470.29977)SADEVQR	C22,C22,NA	,,X;X;	1.43795,,X;X;	1.43795	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 ,
C(464.28596)NGQPVPFQQPK	C205,NA,NA,NA,NA,NA,C67,NA,NA,C205,NA,NA,NA,NA	,,X;X;	0.93668,,X;X;	0.93668	Q9NRZ9-3 Isoform 3 of Lymphoid-specific helicase OS=Homo sapiens GN=HELLS , Q9NRZ9-4 Isoform 4 of Lymphoid-specific helicase OS=Homo sapiens GN=HELLS , Q9NRZ9-2 Isoform 2 of Lymphoid-specific helicase OS=Homo sapiens GN=HELLS , F6XU50 Helicase, lymphoid-specific, isoform CRA_l OS=Homo sapiens GN=HELLS PE=1 SV=1 , A0A087WSW7 Helicase, lymphoid-specific, isoform CRA_d OS=Homo sapiens GN=HELLS PE=1 SV=1 , Q9NRZ9 Lymphoid-specific helicase OS=Homo sapiens GN=HELLS PE=1 SV=1 , A0A0B4J1V9 Helicase, lymphoid-specific, isoform CRA_b OS=Homo sapiens GN=HELLS PE=1 SV=1 ,
ELVNAQC(464.28596)AK	C93,C19,NA	,,X;X;	1.45911,,X;X;	1.45911	Q9Y3C7 Mediator of RNA polymerase II transcription subunit 31 OS=Homo sapiens GN=MED31 PE=1 SV=1 , I3L2J1 Mediator of RNA polymerase II transcription subunit 31

					OS=Homo sapiens GN=MED31 PE=1 SV=1 ,
YVAAAFPSAC(470.29977)GK	C172,NA,NA,NA,NA	,,;,;	2.05376,,1.78985,,2.42603,,	2.05376	B4DW73 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 , Q16822 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 ,
LALNC(464.28596)VGGK	C187,NA,C187,NA,NA	,,X;X;	1.0803,,X;X;	1.0803	Q9BV79 Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR PE=1 SV=2 , Q9BV79-2 Isoform 2 of Trans-2-enoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=MECR ,
KAAAPAPEEEMDEC(464.28596)EQALAAEPK	C266,NA,NA	,,;,;	1.19001,,1.49754,,1.16536,,	1.19001	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
YSYVC(464.28596)PDLVK	C235,NA	,,X;X;	1.49891,,X;X;	1.49891	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 ,
TVEIC(470.29977)PFSFDSR	C572,C572,NA	,,X;X;	1.93282,,X;X;	1.93282	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 , Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 ,
LGM(15.994915)LSPEGTC(470.29977)K	M205,C212,NA	,,;,X;	1.40654,,1.73076,,X;	1.56865	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
SEGGFIWAC(464.28596)K	NA,NA	U,,X;X;	1.40372,,X;X;	1.40372	O75874 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 ,
SSQC(470.29977)HTGSSPR	C439,NA,NA	,,X;,;	1.41462,,X;1.42365,,	1.419135	O15226-2 Isoform 2 of NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF , O15226 NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF PE=1 SV=2 ,
EKLNLSC(470.29977)IHSPVVNELM(15.994915)R	NA,NA	U,,X;X;	1.43222,,X;X;	1.43222	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
GAVEC(464.28596)CPNCR	NA,NA	,,X;X;	1.33714,,X;X;	1.33714	P31689 DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 ,
C(470.29977)IPYAVLLEALALR	NA,NA,NA,C110,NA,NA	,,X;X;	1.43202,,X;X;	1.43202	F5H248 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 , Q9UBW8 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 , F5H4U8 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 , F5GYF7 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=7 , F5H7C6 COP9 signalosome

					complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 ,
GLPC(470.29977)TELFVAP VGVASK	C79,NA,C428,NA	;;X;X;	1.44615;;X;X;	1.44615	H0Y901 Ladinin-1 (Fragment) OS=Homo sapiens GN=LAD1 PE=1 SV=1 , E9PDI4 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=1 , O00515 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 ,
HTGPGILSM(15.994915)A NAGPNTNGSQFFIC(464.28 596)TAK	M100,C115,M100,C115,M 100,C115,NA	;;X;X;	1.16392;;X;X;	1.16392	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
C(464.28596)PEALFQPSFL GMESCGIHETTFNSIM(15.9 94915)K	NA,NA,NA	;;X;X;	1.75542;;X;X;	1.75542	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
HTGPGILSM(15.994915)A NAGPNTNGSQFFIC(464.28 596)TAK	M100,C115,M100,C115,M 100,C115,NA	;;X;X;	1.1971;;X;X;	1.1971	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
VLELVSITANKNTC(464.285 96)PGDR	NA,NA,C391,NA,NA	;;X;X;	1.39405;;X;X;	1.39405	P34897 Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 , P34897-3 Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 ,
FLENTPSSLNIEDLFLSLAQ YYC(470.29977)SK	C283,C146,NA,NA	;;X;X;	1.74128;;X;X;	1.74128	Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 , E9PGE5 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=1 , Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 ,
VC(464.28596)PPHM(15.9 94915)LPEDGANLSSAR	NA,NA,NA,NA,C29,M33,N A	;;X;;;	1.46849;;X;1.41549 ;;	1.44199	Q9GZY8-2 Isoform 2 of Mitochondrial fission factor OS=Homo sapiens GN=MFF , A0A0A0MS29 Mitochondrial fission factor OS=Homo sapiens GN=MFF PE=1 SV=1 , Q9GZY8 Mitochondrial fission factor OS=Homo sapiens GN=MFF PE=1 SV=1 , H7C433 Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=1 SV=1 , E9PQX8 Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=1 SV=1 ,

C(464.28596)MTNTPVVVR	C120,NA,C120,NA,NA,NA,NA	;;;X;	1.51475;;0.93541;;X;	1.22508	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 ,
GC(464.28596)AFVTFTTR	C176,C177,NA,NA,NA	;;X;X;	1.60728;;X;X;	1.60728	Q92879-4 Isoform 4 of CUGBP Elav-like family member 1 OS=Homo sapiens GN=CELF1 , G5EA30 CUG triplet repeat, RNA binding protein 1, isoform CRA_c OS=Homo sapiens GN=CELF1 PE=1 SV=1 ,
AVASQLDC(464.28596)NFLK	NA,NA,NA	;;;;;	1.49482;;1.96465;;1.7003;;	1.7003	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 , P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 ,
QSELEPVVSLVDVLEEDEELENEAC(464.28596)AVLGGS DSEK	NA,NA,NA,NA,C35,NA	;;X;X;	1.17156;;X;X;	1.17156	H0YJAO Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 , G3V2G3 Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 , G3V253 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=1 , G3V336 Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 , Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 ,
LMHLFTSGDC(464.28596)K	C91,NA	U;;X;X;	1.45958;;X;X;	1.45958	Q8WXD5 Gem-associated protein 6 OS=Homo sapiens GN=GEMIN6 PE=1 SV=1 ,
NC(470.29977)IVLIDSTPYR QWYESHYALPLGR	NA,NA	;;X;X;	1.46158;;X;X;	1.46158	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
C(470.29977)YSTPSGYLEL PDLGQPYRSAYVSLEEYLG LALDVDR	C639,NA,NA,C985,C714,NA,C985,C639,C368,NA,NA,NA,NA	;;X;X;	0.72173;;X;X;	0.72173	A0A087WTH4 Neuroblastoma breakpoint family member 11 (Fragment) OS=Homo sapiens GN=NBPF11 PE=4 SV=1 , A0A087WUF1 Neuroblastoma breakpoint family member 12 OS=Homo sapiens GN=NBPF12 PE=4 SV=1 , Q5TAG4 Neuroblastoma breakpoint family member 12 OS=Homo sapiens GN=NBPF12 PE=2 SV=2 , Q3BBV0 Neuroblastoma breakpoint family member 1 OS=Homo sapiens GN=NBPF1 PE=2 SV=1 , A0A087WUW2 Neuroblastoma breakpoint family member 12 OS=Homo sapiens GN=NBPF12 PE=4

					SV=1 , Q86T75 Neuroblastoma breakpoint family member 11 OS=Homo sapiens GN=NBPF11 PE=2 SV=3 , A0A087WY24 Neuroblastoma breakpoint family member 12 OS=Homo sapiens GN=NBPF12 PE=4 SV=1 , A0A087WW93 Neuroblastoma breakpoint family member 12 OS=Homo sapiens GN=NBPF12 PE=4 SV=1 , H7BZX4 Neuroblastoma breakpoint family member 12 OS=Homo sapiens GN=NBPF12 PE=4 SV=2 , A0A075B758 Neuroblastoma breakpoint family member 11 OS=Homo sapiens GN=NBPF11 PE=4 SV=2 , A0A087WVG8 Neuroblastoma breakpoint family member 11 OS=Homo sapiens GN=NBPF11 PE=4 SV=1 , A0A075B764 Neuroblastoma breakpoint family member 12 OS=Homo sapiens GN=NBPF12 PE=4 SV=1 ,
NC(470.29977)IVLIDSTPYR QWYESHYALPLGR	NA,NA	;;X;;	1.37941;;X;1.09611;;	1.23776	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
NC(470.29977)IVLIDSTPYR QWYESHYALPLGR	NA,NA	;;X;X;	1.34575;;X;X;	1.34575	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
LTTPTYGDLNHLVSATM(15.994915)SGVTTC(470.29977)LRFPGQLNADLR	M233,C239,M233,C239,NA,M215,C221,NA	;;X;X;	1.54783;;X;X;	1.54783	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
C(470.29977)LGPPTTPGPY R	C56,C56,NA,NA,NA,NA	;;X;X;	0.76069;;X;X;	0.76069	P29372-4 Isoform 3 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372 DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 , A2IDA3 DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 , P29372-5 Isoform 4 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372-2 Isoform 2 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG ,
SDPSIVLLLC(464.28596)DIQK	C187,NA	U,U,U;;X;X;	2.41009,3.47833,3.11318;;X;X;	3.11318	P62760 Visinin-like protein 1 OS=Homo sapiens GN=VSNL1 PE=1 SV=2 ,
TYGGC(470.29977)EGPDAM(15.994915)YVK	NA,NA,NA	;;X;X;	1.97203;;X;X;	1.97203	E5RHG8 Transcription elongation factor B polypeptide 1 (Fragment) OS=Homo sapiens GN=TCEB1 PE=1 SV=1 ,

					Q15369 Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1 ,
IFVGNVSAAC(464.28596)T SQELR	C90,NA	;;X;X;	1.02501;;X;X;	1.02501	Q96PK6-5 Isoform 5 of RNA-binding protein 14 OS=Homo sapiens GN=RBM14 ,
KECENCDC(470.29977)LQ GFQLTHSLGGGTGSGM(15. 994915)GTLISK	C476,M494,NA	;;X;X;	0.01143;;X;X;	0.01143	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
GSSPTPPC(464.28596)SPV QPSK	NA,NA,NA,C459,NA	;;X;X;	1.49756;;X;X;	1.49756	F8VPI7 Double-stranded RNA-binding protein Stauf homolog 2 OS=Homo sapiens GN=STAU2 PE=1 SV=1 , Q9NUL3-3 Isoform 3 of Double-stranded RNA-binding protein Stauf homolog 2 OS=Homo sapiens GN=STAU2 , E9PH62 Double-stranded RNA-binding protein Stauf homolog 2 OS=Homo sapiens GN=STAU2 PE=1 SV=1 , Q9NUL3-2 Isoform 2 of Double-stranded RNA-binding protein Stauf homolog 2 OS=Homo sapiens GN=STAU2 ,
C(464.28596)LAQEVNIPD WIVDLRHELTHK	NA,NA,NA	;;X;X;	0.2331;;X;X;	0.2331	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
SLHDALC(470.29977)VVK	NA,NA	;;X;X;	1.53352;;X;X;	1.53352	P17987 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 ,
GLAAALLLC(464.28596)Q NK	C645,NA	U;;X;X;	1.56477;;X;X;	1.56477	O43290 U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 ,
GLYGIKDDVFLSVPC(470.2 9977)ILGQNGISDLVK	C322,NA,NA	;;X;X;	1.23445;;X;X;	1.23445	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA , P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 ,
GLYGIKDDVFLSVPC(470.2 9977)ILGQNGISDLVK	C322,NA,NA	;;X;X;	1.29183;;X;X;	1.29183	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA , P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 ,
PGHLQEGFGC(464.28596) VVTNRFDQLFDDSDPFV LK	C11,C11,C11,NA,NA	;;;X;	1.23741,1.24288;;1. 17794;;X;	1.23741	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERP1 PE=1 SV=2 , Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERP1 , Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding

					protein OS=Homo sapiens GN=SERBP1 , Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 ,
PGHLQEGFGC(464.28596) VVTNRFDQLFDDSDPFV LK	C11,C11,C11,NA,NA	;;X;;	1.34894;;X;1.57947 ;;	1.464205	Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 , Q8NC51-4 Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 , Q8NC51-2 Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 , Q8NC51-3 Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 ,
VC(470.29977)NFLASQVP FPSR	C205,NA	;;;X;	1.38393;;1.37907;;X;	1.3815	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
AGGPPQVAGAQAAC(470.29977)SEDR	NA,C35,NA	;;X;X;	1.32572;;X;X;	1.32572	B3KVZ3 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 , Q9H3R5 Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 ,
HGELWC(470.29977)AVSK	C913,NA	;;X;X;	1.5709;;X;X;	1.5709	O94906 Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 ,
SQEATEAAPSC(464.28596)VGDMADTPR	C84,C241,NA,NA,NA,NA	;;X;X;	0.89978;;X;X;	0.89978	Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 , Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 , Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 , Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 , Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 ,
SSVNC(464.28596)PFSSQ DM(15.994915)KYPSPFFV FGEK	NA,NA	U;;X;X;	2.09726;;X;X;	2.09726	Q08211 ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 ,
SGTIC(470.29977)SSELPG AFEAAGFHLNEHLYNM(15.994915)IIR	NA,NA,C200,M222,NA	;;;X;;	1.26079,1.06805;;X ;1.2634;;	1.26079	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , K7ELJ7 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 ,
SGTIC(470.29977)SSELPG AFEAAGFHLNEHLYNM(15.994915)IIR	NA,NA,NA	;;X;X;	1.44918;;X;X;	1.44918	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 ,
VLQNMEQC(464.28596)Q K	NA,NA	;;X;X;	2.21672;;X;X;	2.21672	Q96ER3 Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=2 ,

AVLLVGLC(470.29977)DS GK	C73,NA	;;;;;	1.36563;;1.81145;;1.41215,2.37352;;	1.6118	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
KLFAPQQILQC(470.29977)SPAN	C230,NA,NA,NA	;;X;X;	1.50865;;X;X;	1.50865	P04183 Thymidine kinase, cytosolic OS=Homo sapiens GN=TK1 PE=1 SV=2 , K7ERV3 Thymidine kinase OS=Homo sapiens GN=TK1 PE=1 SV=1 ,
TLIQNC(470.29977)GASTIR	NA,C410,NA,NA	;;X;X;	1.73519;;X;X;	1.73519	P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 , B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 , P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 ,
LETPPPWLAM(15.994915)FTDQPALPNPC(464.28596)SPASVAPAPDWTPLPWGRPR	NA,NA,M472,C483,NA	;;X;X;	1.64087;;X;X;	1.64087	Q9BST9 Rhotekin OS=Homo sapiens GN=RTKN PE=1 SV=2 , Q9BST9-3 Isoform 3 of Rhotekin OS=Homo sapiens GN=RTKN , Q9BST9-2 Isoform 2 of Rhotekin OS=Homo sapiens GN=RTKN ,
YIGENLQLLVDRPDGTYC(470.29977)FR	NA,NA	;;X;X;	1.57109;;X;X;	1.57109	Q9Y221 60S ribosome subunit biogenesis protein NIP7 homolog OS=Homo sapiens GN=NIP7 PE=1 SV=1 ,
LNPQC(470.29977)IPYTLQNHYYR	NA,C497,NA,NA	;;X;X;	1.58898;;X;X;	1.58898	O95453-2 Isoform 2 of Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN , O95453-3 Isoform 3 of Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN , O95453 Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN PE=1 SV=1 ,
IYFGSNIPNM(15.994915)FVDSSC(464.28596)ALK	NA,NA	U;;X;X;	1.43788;;X;X;	1.43788	O75477 Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1 ,
AFDTAGNGYC(464.28596)R	C223,NA	;;X;X;	1.43855;;X;X;	1.43855	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
SYC(464.28596)AEIAHNVS SK	C96,C114,C96,NA	;;X;X;	1.41557;;X;X;	1.41557	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
AVILGPPGSGKGTVC(470.29977)QR	C22,NA,NA	U;;X;X;	1.76181;;X;X;	1.76181	P27144 Adenylate kinase 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 ,
LVSSPC(464.28596)CIVTSTYGTANMER	C589,NA	U;;X;X;	1.17926;;X;X;	1.17926	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 ,
TTSILC(470.29977)LAR	NA,NA,NA	;;X;X;	1.44563;;X;X;	1.44563	P35250-2 Isoform 2 of Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 , P35250 Replication factor C

					subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3 ,
VLDALFPCVQGGTTAIPGAF GC(470.29977)GK	C221,C221,NA	;;X;X;	2.01666;;X;X;	2.01666	P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A , P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 ,
ECISIHVGQAGVQIGNACW ELYC(470.29977)LEHGIQP DGQM(15.994915)PSDK	C25,M36,NA,NA,NA	;;X;X;	1.39966;;X;X;	1.39966	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
ECISIHVGQAGVQIGNACW ELYC(470.29977)LEHGIQP DGQM(15.994915)PSDK	C25,M36,NA,NA,NA	;;X;X;	1.80204;;X;X;	1.80204	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
SLGTPEDGM(15.994915)A VC(470.29977)MFMQNTL TR	NA,M124,C127,NA,NA	;;X;X;	1.35986;;X;X;	1.35986	Q9NTX5 Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 PE=1 SV=2 , Q9NTX5-2 Isoform 2 of Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1 , H0Y525 Ethylmalonyl-CoA decarboxylase (Fragment) OS=Homo sapiens GN=ECHDC1 PE=1 SV=1 ,
YAIC(464.28596)SALAASA LPALVMSK	C125,NA	;;X;X;	1.39344;;X;X;	1.39344	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
C(470.29977)ELSSSVQTDI NLPYLTM(15.994915)DSS GPK	NA,NA,NA	;;;X;	1.19621;;1.48969;; X;	1.34295	P38646 Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 ,
LPACVVDC(470.29977)GT GYTK	C12,NA	;;X;X;	1.34281;;X;X;	1.34281	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 ,
GVQDIVVGEGTHFLIPWVQ KPIIFDC(464.28596)R	NA,C69,NA,C69,C69,NA,N A	;;X;X;	1.0729;;X;X;	1.0729	E7ESE2 Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=1 SV=2 , C9JW96 Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=1 SV=2 , C9JZ20 Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=1 SV=1 , P35232 Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1 , P35232-2 Isoform 2 of Prohibitin OS=Homo sapiens GN=PHB , E9PCW0 Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=1 SV=2 ,
PVIYLSAAARPGLGQYLC(47 0.29977)NQLGLPFPCLC(47 0.29977)R	NA,NA,NA,C209,C220,NA, C163,C174,NA,NA,NA	;;X;X;	1.53511;;X;X;	1.53511	Q6P474 Putative pyridoxal-dependent decarboxylase domain-containing protein 2 OS=Homo sapiens GN=PDXDC2P PE=5 SV=3 , Q6P996-3 Isoform 3 of Pyridoxal-

					dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 , Q86XE2 PDXDC1 protein OS=Homo sapiens GN=PDXDC1 PE=1 SV=2 , H3BND4 Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1 SV=1 , Q6P996-5 Isoform 5 of Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 , Q6P996-4 Isoform 4 of Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 , J3KNK7 Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1 SV=2 , Q6P996 Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1 SV=2 ,
C(464.28596)HSLTPNFLQ M(15.994915)QLQK	C273,M283,NA	U,,X;X;	1.36931,,X;X;	1.36931	Q14145 Kelch-like ECH-associated protein 1 OS=Homo sapiens GN=KEAP1 PE=1 SV=2 ,
IIFVVGGPGSGKGTQC(470.29977)EK	C41,NA,NA	,,X;X;	1.31455,,X;X;	1.31455	Q5T9B7 Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=1 , P00568 Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 ,
NM(15.994915)MAAC(470.29977)DPR	M299,C303,M299,C303,M646,C650,M299,C303,NA,M281,C285,M299,C303,NA	,,,,,,X;	1.6589,1.6589,0.81059,0.81059,,1.48069,1.48069,,X;	1.48069	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
HIGDGC(470.29977)CLTR	NA,C202,NA	,,X;X;	1.43892,,X;X;	1.43892	A0A087WZT2 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=1 , Q6UX53 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=2 ,
C(470.29977)ASQAGM(15.994915)TAYGTR	C132,M138,C127,M133,NA,NA	,,,X;	1.40123,,1.37162,,X;	1.386425	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417-2 Isoform 2 of Calponin-3

					OS=Homo sapiens GN=CNN3 ,
AGAIAPC(464.28596)EVTV PAQNTGLGPEK	NA,NA	,,;,;	1.74262,,1.45942,,1 .34148,;	1.45942	P05388 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1 ,
VRPSTGNSASTPQSQC(470 .29977)LPSEIEVK	C131,NA,NA	,,X,;	1.38813,,X;1.22353 ,,	1.30583	Q9UJX3-2 Isoform 2 of Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 , Q9UJX3 Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4 ,
ECENCDC(470.29977)LQG FQLTHSLGGGTGSGMGTLI SK	C476,NA	,,X;X;	0.04815,,X;X;	0.04815	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
ECENCDC(470.29977)LQG FQLTHSLGGGTGSGMGTLI SK	C476,NA	,,X;X;	0.01646,,X;X;	0.01646	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
ASFENNC(464.28596)EIGC FAK	C11,NA	,,X;X;	0.70186,,X;X;	0.70186	P56537 Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 ,
KVIGIEC(464.28596)SSISD YAVK	C101,NA	,,X,;	1.62241,,X;2.61227 ,,	2.11734	Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 ,
DGTVLC(470.29977)ELINA LYPEGQAPVKK	C63,NA,NA,NA	,,X;X;	1.18242,,X;X;	1.18242	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 , P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 , X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 ,
DGTVLC(470.29977)ELINA LYPEGQAPVKK	C63,NA,NA,NA	,,X;X;	1.18304,,X;X;	1.18304	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 , P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 , X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 ,
ASC(464.28596)TTNCLAPL AK	C152,NA	,,X;X;	1.37001,,X;X;	1.37001	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
SSVQEEC(470.29977)VSTI SSSKDEDPLAATR	NA,NA	,,X;X;	1.31721,1.29639,,X ;X;	1.3068	Q7L0Y3 Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2 ,
AINC(464.28596)ATSGVV GLVNCLR	C1448,NA	,,;,X;	1.33972,,1.13127,, X;	1.235495	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
AINC(464.28596)ATSGVV GLVNCLR	C1448,NA	,,X;X;	2.8313,,X;X;	2.8313	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
LLDIAC(464.28596)WIHHK	C117,C102,NA,C82,NA	,,X;X;	2.9885,,X;X;	2.9885	F8WD96 Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 , C9JH19 Cathepsin D (Fragment) OS=Homo sapiens GN=CTSD PE=1 SV=1 , P07339 Cathepsin D OS=Homo

					sapiens GN=CTSD PE=1 SV=1 , F8W787 Cathepsin D (Fragment) OS=Homo sapiens GN=CTSD PE=1 SV=1 ,
VGSFC(464.28596)LSEAGA GSDSFALK	C73,NA,NA,NA,NA	,;X;X;	1.06149,,X;X;	1.06149	P45954-2 Isoform 2 of Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB , P45954 Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 ,
SGQGAFGNMC(464.28596) JR	C96,NA	,;X;;	1.50215,,X;1.0792,;	1.290675	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
LPEGSPTWLGISC(464.28596) SSYER	C111,C111,C111,NA,NA,NA,NA,NA	,;X;X;	1.5015,,X;X;	1.5015	Q13506 NGFI-A-binding protein 1 OS=Homo sapiens GN=NAB1 PE=1 SV=2 , C9JID4 NGFI-A-binding protein 1 (Fragment) OS=Homo sapiens GN=NAB1 PE=1 SV=1 , C9JL92 NGFI-A-binding protein 1 (Fragment) OS=Homo sapiens GN=NAB1 PE=1 SV=1 , B8ZZS2 NGFI-A binding protein 1 (EGR1 binding protein 1), isoform CRA_b OS=Homo sapiens GN=NAB1 PE=1 SV=1 , Q13506-2 Isoform Short of NGFI-A-binding protein 1 OS=Homo sapiens GN=NAB1 , C9JJ42 NGFI-A-binding protein 1 (Fragment) OS=Homo sapiens GN=NAB1 PE=1 SV=1 ,
IIPGLEGLQLPSPTATSQLPL ESDAVEC(470.29977)LNY QHYK	NA,NA,NA	,,;,;	1.37831,,1.32337,,1.35426,;	1.35426	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
IIPGLEGLQLPSPTATSQLPL ESDAVEC(470.29977)LNY QHYK	NA,NA,NA	,,;,;X;	1.3729,1.74211,,1.35799,1.26803,,X;	1.365445	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
IIPGLEGLQLPSPTATSQLPL ESDAVEC(470.29977)LNY QHYK	NA,NA,NA	,;X;X;	1.54062,,X;X;	1.54062	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
VLGLGLGC(464.28596)LR	NA,NA,NA	,,;,;	1.53266,,1.50648,,1.27468,;	1.50648	Q9BRJ7 Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 , K7EIN2 Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1 ,
YEAAPFLSPC(464.28596) GR	NA,NA,NA	,;X;X;	0.84485,,X;X;	0.84485	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 , Q6P1X6 UPF0598 protein

					C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 ,
YEAAPFLSPC(464.28596)GR	NA,NA,NA	;;X;X;	1.542;;X;X;	1.542	H0YF29 UPF0598 protein C8orf82 (Fragment) OS=Homo sapiens GN=C8orf82 PE=1 SV=1 , Q6P1X6 UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=1 SV=2 ,
TPSYSISSTLNQPAPEFILGC(464.28596)TASK	C142,NA,C142,NA,NA	;;X;;	1.04414;;X;1.25822;;	1.15118	Q14694-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 , H3BQC6 Ubiquitin carboxyl-terminal hydrolase 10 (Fragment) OS=Homo sapiens GN=USP10 PE=1 SV=1 , Q14694 Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 , Q14694-3 Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 ,
VHPAMATAAGGC(464.28596)R	NA,NA	;;X;X;	1.64504;;X;X;	1.64504	H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 ,
VSVGQSC(470.29977)GFS GK	NA,NA,NA,C1075,C878,NA,C535,NA	;;X;X;	1.73543;;X;X;	1.73543	O75128-7 Isoform 7 of Protein cordon-bleu OS=Homo sapiens GN=COBL , H7C1N2 Protein cordon-bleu (Fragment) OS=Homo sapiens GN=COBL PE=1 SV=1 , O75128 Protein cordon-bleu OS=Homo sapiens GN=COBL PE=1 SV=2 , O75128-2 Isoform 2 of Protein cordon-bleu OS=Homo sapiens GN=COBL , J3KR05 Protein cordon-bleu (Fragment) OS=Homo sapiens GN=COBL PE=1 SV=1 , O75128-3 Isoform 3 of Protein cordon-bleu OS=Homo sapiens GN=COBL , O75128-6 Isoform 6 of Protein cordon-bleu OS=Homo sapiens GN=COBL ,
ITSC(464.28596)IFQLQEA GIK	C63,NA	;;X;X;	1.50261;;X;X;	1.50261	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
C(464.28596)ASQAGMTA YGTR	C132,C127,NA,NA	;;;X;	1.39661;;1.43309;;X;	1.41485	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 ,
AGLSPANC(464.28596)QSDR	NA,NA	U;;X;X;	0.53857;;X;X;	0.53857	Q14692 Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1 ,
SSSVTTSETQPC(464.28596)TPSSSDYSDLQR	NA,NA	;;X;X;	1.29245;;X;X;	1.29245	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 ,
ALIIVAVQCGCDGTFLTQS GKVLAC(470.29977)GLNE	NA,NA	U;;X;X;	0.5945;;X;X;	0.5945	Q8TD19 Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2 ,

FNK					
IIVFSAC(464.28596)R	NA,NA	;;X;X;	1.83321;;X;X;	1.83321	Q07960 Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 ,
KTPC(470.29977)GEGSK	NA,C70,NA	;;;X;	1.40658;;1.36272;;X;	1.38465	P60866 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 , P60866-2 Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 ,
VM(15.994915)TIPYQMP ASSPVIC(470.29977)AGG QDR	M179,C194,NA	U,U,U;;X;X;	1.37893,1.21387,1.71619;;X;X;	1.37893	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
VIIVQAC(470.29977)R	C173,C258,NA,C328,NA,C258,NA,C202,C211,NA	;;X;X;	1.18397;;X;X;	1.18397	P51878-3 Isoform 3 of Caspase-5 OS=Homo sapiens GN=CASP5 , P49662-4 Isoform 4 of Caspase-4 OS=Homo sapiens GN=CASP4 , P51878-6 Isoform 6 of Caspase-5 OS=Homo sapiens GN=CASP5 , P51878-5 Isoform 5 of Caspase-5 OS=Homo sapiens GN=CASP5 , P51878-2 Isoform 2 of Caspase-5 OS=Homo sapiens GN=CASP5 , P49662 Caspase-4 OS=Homo sapiens GN=CASP4 PE=1 SV=1 , P51878 Caspase-5 OS=Homo sapiens GN=CASP5 PE=1 SV=3 , P49662-2 Isoform 2 of Caspase-4 OS=Homo sapiens GN=CASP4 , A0A087WZP8 Caspase OS=Homo sapiens GN=CASP4 PE=1 SV=1 ,
SC(464.28596)SGVEFSTSG HAYTDTGK	NA,NA	;;X;X;	0.9672;;X;X;	0.9672	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 ,
FRCPEALFQPSFLGMESC(470.29977)GIHETTFNSIM(15.994915)K	NA,NA,NA,NA,NA	;;;;	1.38559;;1.59017;;1.26756;;	1.38559	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ,
FRCPEALFQPSFLGMESC(470.29977)GIHETTFNSIM(15.994915)K	NA,NA,NA	;;X;X;	1.5645;;X;X;	1.5645	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
FYTDPEAVKDIPDGATVLV GGFGLC(464.28596)GIPE NLIDALLK	NA,NA,NA	U;;X;X;	0.84025;;X;X;	0.84025	P55809 Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 ,
MPC(464.28596)QSLQPEP INTPTHTK	C1006,NA,NA	;;X;X;	1.05887;;X;X;	1.05887	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 , P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 ,
C(464.28596)LLSDELSNIA M(15.994915)QVR	C71,M82,NA,NA	;;X;X;	0.78526;;X;X;	0.78526	Q86YH6-2 Isoform 2 of Decaprenyl-diphosphate synthase subunit 2 OS=Homo sapiens GN=PDSS2 , Q86YH6

					Decaprenyl-diphosphate synthase subunit 2 OS=Homo sapiens GN=PDSS2 PE=1 SV=2 ,
TVEIC(464.28596)PFSFDS R	C572,C572,NA	;;X;X;	1.47087;;X;X;	1.47087	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 , Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 ,
YVENPSQVLNC(470.29977) JER	NA,C1344,NA	;;X;X;	1.61581;;X;X;	1.61581	O75694-2 Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 , O75694 Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 ,
LC(464.28596)VPAM(15.9 94915)NVNDSVTK	NA,NA,NA,NA,NA,C250,M 254,C352,M356,NA	;;X;X;	1.25816;;X;X;	1.25816	O43865-2 Isoform 2 of Adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 , O43865 Adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2 , Q96HN2-3 Isoform 3 of Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 , H0Y8B3 Adenosylhomocysteinase (Fragment) OS=Homo sapiens GN=AHCYL2 PE=1 SV=1 , Q96HN2 Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 PE=1 SV=1 , Q96HN2-4 Isoform 4 of Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 , Q96HN2-2 Isoform 2 of Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 ,
LC(464.28596)VPAM(15.9 94915)NVNDSVTK	NA,NA,NA,NA,NA,C250,M 254,C352,M356,NA	;;X;X;	0.98792;;X;X;	0.98792	O43865-2 Isoform 2 of Adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 , O43865 Adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2 , Q96HN2-3 Isoform 3 of Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 , H0Y8B3 Adenosylhomocysteinase (Fragment) OS=Homo sapiens GN=AHCYL2 PE=1 SV=1 , Q96HN2 Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 PE=1 SV=1 , Q96HN2-4 Isoform 4 of Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 , Q96HN2-2 Isoform 2 of Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 ,
LVMSYVAAVC(470.29977) GK	C129,NA,C129,NA	;;X;X;	2.04469;;X;X;	2.04469	O43795 Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3 , E9PDF6 Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=1 , O43795-2

					Isoform 2 of Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B ,
LVFLAC(464.28596)CVAPT NPR	C301,NA	U,,X;X;	1.66726,,X;X;	1.66726	Q14566 DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 ,
LVFLAC(464.28596)CVAPT NPR	C301,NA	U,,X;X;	2.01896,,X;X;	2.01896	Q14566 DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 ,
ATGHSGGGC(464.28596)I SQGR	NA,NA,NA,NA,NA	,,;,;	1.64923,,2.23242,,1.69181,,	1.69181	I3L407 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=1 , I3L139 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=1 , Q9HA64 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 , I3L3W5 Ketosamine-3-kinase (Fragment) OS=Homo sapiens GN=FN3KRP PE=1 SV=1 ,
DSGYGDIWC(470.29977)P ERGEFLAPPR	C213,C176,NA,C228,C228,NA,NA	,,X;,;	1.51569,,X;1.2798,,	1.397745	J3KP06 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , F8WD26 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , Q8WWI1-4 Isoform 4 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 , Q8WWI1 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 , Q8WWI1-3 Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 , Q8WWI1-2 Isoform 2 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 ,
DLGGIVLANACGPC(464.28596)IGQWDRK	C451,NA,C476,NA,NA	,,X;X;	1.37554,,X;X;	1.37554	Q99798 Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 , A2A274 Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=1 ,
GHSSDSNPAIC(470.29977)R	C31,NA	,,;,X;	1.58715,,1.23816,,X;	1.412655	Q5JTH9 RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 ,
PGQISAGYAPVLDCHTAHIA C(464.28596)K	NA,NA	,,X;X;	3.47852,,X;X;	3.47852	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
NCGC(464.28596)LGASPN LEQLQEENLK	C34,NA,NA	,,X;X;	0.53395,,X;X;	0.53395	P54136 Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 ,
VLRHEEFEEGC(464.28596)K	NA,NA,C41,C245,NA	,,X;X;	1.86263,,X;X;	1.86263	I3L3Q4 Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=1 SV=1 , Q9HC38-2 Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 , Q9HC38-3 Isoform 3 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 , F6TLX2 Glyoxalase domain-containing protein

					4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 ,
VM(15.994915)QPQILEVN FNPDC(464.28596)ER	M599,C612,NA	;;X;X;	1.37084;;X;X;	1.37084	Q14166 Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTL12 PE=1 SV=2 ,
VC(470.29977)EDLDTSVN LAWTSGTNCTR	C199,NA	;;X;X;	1.88096;;X;X;	1.88096	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
SEFYANEAC(470.29977)K	NA,NA,C381,NA,C219,NA, NA	;;X;X;	0.92079;;X;X;	0.92079	A0A087X0W7 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 , A0A087WT95 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 , P49753 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 ,
PTPWGPEKEGGPLGHGIC(470.29977)SAHPTGPGHPL	NA,NA,NA	U;;X;X;	0.73208;;X;X;	0.73208	H7BZW4 Phospholipase B1, membrane-associated (Fragment) OS=Homo sapiens GN=PLB1 PE=4 SV=1 ,
SAGDLGIAVCNPAASVEET ADSTLC(464.28596)HILNL YR	C123,C123,NA	;;X;X;	0.49011;;X;X;	0.49011	Q13363-2 Isoform 2 of C-terminal-binding protein 1 OS=Homo sapiens GN=CTBP1 , Q13363 C-terminal-binding protein 1 OS=Homo sapiens GN=CTBP1 PE=1 SV=2 ,
KAVVVC(470.29977)PK	NA,C588,NA	;;;X;	1.50809;;1.3928;;X;	1.450445	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
IPGGIIEDSC(470.29977)VL R	NA,C168,NA,NA	;;X;X;	1.7146;;X;X;	1.7146	P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 , B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 , P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 ,
VTDGALVVVDCVSGVC(46 4.28596)VQTETVLR	C136,NA	U;;X;X;	0.95577;;X;X;	0.95577	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
VTDGALVVVDCVSGVC(46 4.28596)VQTETVLR	C136,NA	U;;X;U;;	1.45957;;X;1.32284 ;;	1.391205	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
NFEATLGWLQEAC(464.2 8596)SR	NA,NA,NA	;;X;X;	1.65597;;X;X;	1.65597	Q9P2J5 Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2 ,
AAQVALLYLQELAEELSTAL PAPVSC(464.28596)PEGP K	NA,NA	;;X;X;	1.09309;;X;X;	1.09309	Q8WUA4 General transcription factor 3C polypeptide 2 OS=Homo sapiens GN=GTF3C2 PE=1 SV=2 ,
AWVWNTHADFADEC(464. 28596)PKPELLAIR	NA,C132,C132,C209,NA,C 132,NA	;;;X;	1.25395;;1.47355;; X;	1.36375	C9JXG8 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=2 , P43487 Ran-

					specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 , C9JJ34 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=1 , F6WQW2 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 , C9JGV6 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=7 , P43487-2 Isoform 2 of Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 ,
ISDTGSAGLM(15.994915)LVEFFAPWC(470.29977)GHCKR	NA,NA	;;X;X;	2.22751;;X;X;	2.22751	P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 ,
ARDC(464.28596)LIPM(15.994915)GITSENVAR	NA,NA,NA	;;X;X;	1.3196;;X;X;	1.3196	P09110 3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 ,
NQSFC(470.29977)PTVNLDKLWTLVSEQTR	NA,C70,NA,NA	;;X;;	1.40577;;X;1.21647;;	1.31112	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 , E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 , E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 ,
GQVLSTINTNQM(15.994915)NNTHAAVSPC(464.28596)GR	M230,C240,M230,C240,M194,C204,NA	;;X;X;	1.34971;;X;X;	1.34971	Q9Y4P3 Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1 , Q96E41 TBL2 protein OS=Homo sapiens GN=TBL2 PE=1 SV=1 , E9PF19 Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1 ,
NQSFC(470.29977)PTVNLDKLWTLVSEQTR	NA,C70,NA,NA	;;;;	1.41104,1.38974;;1.11387;;1.25129;;	1.320515	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 , E9PLL6 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 , E9PJD9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 ,
VVM(15.994915)ALGDYMGASCHAC(470.29977)IGGTNVR	NA,NA	;;X;X;	1.58713;;X;X;	1.58713	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 ,
C(470.29977)ALLASEVPQLALQLLDPESYVR	NA,NA	U;;X;X;	1.30735;;X;X;	1.30735	Q6PJG6 BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 ,
FQSAAIGALQEASEAYLVGLFEDTNLC(470.29977)A	NA,NA,NA	;;X;;	0.61868;;X;0.70841;;	0.663545	K7EK07 Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=1 SV=1 , P84243 Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 ,

VGVGTC(470.29977)GIAD KPMTQYQDTSK	C214,NA	U,,X;X;	1.12495,,X;X;	1.12495	O75940 Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 ,
STFFNVLTNSQASAENFPFC (470.29977)TIDPNESR	NA,NA,NA	,,,X;X;	1.46097,1.33152,,X ;X;	1.396245	J3KQ32 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1 , Q9NTK5 Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 ,
YIELFLNSC(470.29977)PK	NA,NA,NA,NA,NA,NA	,,,X;X;	1.56887,1.18665,,X ;X;	1.37776	F5H5I6 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=2 , H0YAK1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 , H0Y8R1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 , Q12849-5 Isoform 2 of G- rich sequence factor 1 OS=Homo sapiens GN=GRSF1 , Q12849 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=3 ,
C(464.28596)IPYAVLLEAL ALR	NA,NA,NA,C110,NA,NA	,,X;X;	1.43202,,X;X;	1.43202	F5H248 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 , Q9UBW8 COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1 , F5H4U8 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 , F5GYF7 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=7 , F5H7C6 COP9 signalosome complex subunit 7a (Fragment) OS=Homo sapiens GN=COPS7A PE=1 SV=1 ,
GLPC(464.28596)TELFVAP VGVASK	C79,NA,C428,NA	,,X;X;	1.45318,,X;X;	1.45318	H0Y901 Ladinin-1 (Fragment) OS=Homo sapiens GN=LAD1 PE=1 SV=1 , E9PDI4 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=1 , O00515 Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 ,
TSLDLYANVIHC(464.28596)K	NA,NA,NA	,,X;X;	1.649,,X;X;	1.649	P51553 Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1 ,
LDVGNFSWGSEC(470.299 77)C(470.29977)TRK	NA,NA	U,,X;X;	1.57656,,X;X;	1.57656	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
SEGGSGGGAAGGGAGGAG AGAGC(470.29977)GSGGS SVGVR	NA,C32,NA,C32,NA	,,X;X;	1.22914,,X;X;	1.22914	Q9NSY1-3 Isoform 3 of BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K , Q9NSY1-2 Isoform 2 of BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K , K4DI97 BMP-2-inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=1 , Q9NSY1 BMP-2-

					inducible protein kinase OS=Homo sapiens GN=BMP2K PE=1 SV=2 ,
EC(464.28596)EGIVPVPLA EK	NA,NA,NA	U,,X;X;	1.26522,,X;X;	1.26522	P82932 28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 ,
LGHAGGNQSDASHLLNQS GGAGEDC(470.29977)QIF STPGHPK	C721,NA,NA	,,X;X;	1.36301,,X;X;	1.36301	U3KPZ7 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 , Q9P2N5 RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=1 SV=2 ,
EC(464.28596)EGIVPVPLA EK	NA,NA,NA	U,,X;X;	1.68947,,X;X;	1.68947	P82932 28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 ,
AC(470.29977)FEPANQM(15.994915)VK	NA,C295,M302,NA,NA,NA ,NA	,,X;X;	1.44989,,X;X;	1.44989	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
GLC(470.29977)GAIHSSIA K	C103,NA,NA,NA,NA	,,X;;	1.48551,,X;1.6173,,	1.551405	P36542 ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 , P36542-2 Isoform Heart of ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 ,
GLEC(464.28596)SPSTPT M(15.994915)NSYFYK	NA,NA	,,X;X;	2.39938,,X;X;	2.39938	Q08AM6 Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=1 SV=1 ,
YGIIC(470.29977)M(15.994915)EDLIHEIYTVGKR	C186,M187,NA	,,X;X;	1.44381,,X;X;	1.44381	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
NC(470.29977)GC(470.29977)LGASPNLEQLQEENLK	C32,C34,NA,NA	,,X;X;	1.4082,,X;X;	1.4082	P54136 Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 ,
YGIIC(470.29977)M(15.994915)EDLIHEIYTVGKR	C186,M187,NA	,,X;X;	1.46365,,X;X;	1.46365	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
YGIIC(470.29977)M(15.994915)EDLIHEIYTVGKR	C186,M187,NA	,,X;X;	1.43317,,X;X;	1.43317	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
C(464.28596)ATPVIIDEILP SKK	C145,C145,NA	,,X;X;	1.37874,,X;X;	1.37874	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 , Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 ,
HFLSDTGMAC(470.29977) R	NA,NA	,,X;X;	1.9503,,X;X;	1.9503	Q5TFE4 5'-nucleotidase domain-containing protein 1 OS=Homo sapiens GN=NT5DC1 PE=1 SV=1 ,
LC(464.28596)SAHGVLVP	C362,NA	,,X;X;	1.21384,,X;X;	1.21384	P17812 CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1

GGFGVR					SV=2 ,
THTYEC(470.29977)R	NA,NA,C1137,NA	;;X;X;	2.24216;;X;X;	2.24216	C9J4M6 DNA-directed RNA polymerase subunit beta OS=Homo sapiens GN=POLR2B PE=1 SV=2 , C9J2Y9 DNA-directed RNA polymerase subunit beta OS=Homo sapiens GN=POLR2B PE=1 SV=2 , P30876 DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1 ,
GTLTLC(470.29977)PYHSD R	NA,NA,NA	;;X;X;	1.21756;;X;X;	1.21756	Q13200 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 , Q13200-3 Isoform 3 of 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 ,
YNPTWHC(464.28596)IVG R	NA,NA,NA	;;X;X;	1.2373;;X;X;	1.2373	P63167 Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 ,
C(464.28596)AIQNAPNPG GGD LQK	NA,C137,NA	;;X;X;	1.60069;;X;X;	1.60069	P48200 Iron-responsive element-binding protein 2 OS=Homo sapiens GN=IREB2 PE=1 SV=3 , A0A0A6YY96 Iron-responsive element-binding protein 2 OS=Homo sapiens GN=IREB2 PE=1 SV=1 ,
C(464.28596)TLPLTGK	C59,NA,NA	;;X;X;	1.26893;;X;X;	1.26893	P55809 Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 ,
NTLANSC(464.28596)GTGI R	NA,NA	;;X;X;	1.25491;;X;X;	1.25491	Q96RE7 Nucleus accumbens-associated protein 1 OS=Homo sapiens GN=NACC1 PE=1 SV=1 ,
HLYTLDGGDIINALC(470.29977)F	NA,NA	;;X;X;	0.06087;;X;X;	0.06087	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
TIC(464.28596)SHVQNMI K	NA,C74,NA	;;X;X;	0.93134;;X;X;	0.93134	D6RAN4 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=7 , P32969 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 ,
LGVHPLSC(470.29977)HG WVLGEHGDSSVPVWSGM(15.994915)NVAGVSLK	C214,M233,NA,NA	;;X;X;	1.34194;;X;X;	1.34194	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA , P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 ,
LLEGDGGPNTGGM(15.994915)GAYC(470.29977)PAP QVSN D L L L K	NA,NA	;;X;X;	1.06841;;X;X;	1.06841	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 ,
YSTGSDSASFHTTPSM(15.994915)C(464.28596)LNP DLEGPPLEAYTIQGQY	M216,C217,NA,NA	;;;X;	1.3518;;1.29556;;X;	1.32368	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,

YSTGSDSASFPHTTSPM(15.994915)C(464.28596)LNP DLEGPPL EAYTIQGQY	M216,C217,NA,NA	,,,X;	1.36614,,1.35427,,X;	1.360205	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,
YKWC(470.29977)EYGLTF TEK	C65,NA	,,X;X;	1.51329,,X;X;	1.51329	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
NWYVQPSC(464.28596)A TSGDGLYEGLTWLTSNYKS	C155,NA	U,U,U,,X;X;	1.5728,1.23783,1.54909,,X;X;	1.54909	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 ,
QSLFC(470.29977)PK	C27,NA	,,X;X;	1.52722,,X;X;	1.52722	Q56VL3 OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 ,
VM(15.994915)ALQEAC(464.28596)EAYLVGLFEDTN LCAIHAK	M91,C97,NA	U,U,,U,,X;	10.44979,16.07032,,14.04641,,X;	14.04641	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
SGGSGGC(464.28596)SGA GGASNCGTGSGR	NA,NA,NA,NA	,,,;	1.60024,,1.47136,,1.51804,,	1.51804	E9PI68 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=1 , A0A087WUC6 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=1 , Q15005 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3 ,
YAGLSTC(464.28596)FR	NA,NA,NA,NA,NA	,,X;X;	1.28197,,X;X;	1.28197	Q5T5C7 Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1 , P49591 Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3 ,
SLC(470.29977)NLEESITSA GRDDLESFQLEISGFLK	NA,NA,NA	,,,X;	1.27122,1.41719,,1.52808,,X;	1.41719	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
IC(470.29977)SIYTQSGEN SLVQEGSEASPIGK	NA,NA,NA	,,X;X;	2.36997,,X;X;	2.36997	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
SLC(470.29977)NLEESITSA GRDDLESFQLEISGFLK	NA,NA,NA	,,X;X;	1.54847,,X;X;	1.54847	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
NQC(470.29977)LFTNTQCK	NA,NA,C68,NA,NA,C68,NA	,,X;X;	1.49358,,X;X;	1.49358	B7Z6B6 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , Q9UL40 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , B7Z6Q2 Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , Q9UL40-2 Isoform 2 of Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 , D6RJ07 Zinc finger protein 346

					OS=Homo sapiens GN=ZNF346 PE=1 SV=1 , Q9UL40-3 Isoform 3 of Zinc finger protein 346 OS=Homo sapiens GN=ZNF346 ,
IIPGLEGLQLPSPTATSQLPL ESDAVEC(464.28596) LNY QHYK	NA,NA,NA	;;X;;	1.38145;;X;1.37303 ;;	1.37724	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
IIPGLEGLQLPSPTATSQLPL ESDAVEC(464.28596) LNY QHYK	NA,NA,NA	;;;;	1.37592;;1.12282,1. 27521;;1.21485;;	1.24503	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
IIPGLEGLQLPSPTATSQLPL ESDAVEC(464.28596) LNY QHYK	NA,NA,NA	;;;;	1.52775;;1.36865;;1 .4612;;	1.4612	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
VC(470.29977) NYGLTFTQ K	NA,NA	;;X;X;	1.38918;;X;X;	1.38918	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 ,
DLAGAPPGEVVG(464.28 596) FTPQSR	C584,NA,NA	;;X;X;	1.56857;;X;X;	1.56857	Q9Y446-2 Isoform PKP3b of Plakophilin-3 OS=Homo sapiens GN=PKP3 , Q9Y446 Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1 ,
IGAAIQEELGYNC(464.285 96) QTGGVIAEILR	NA,NA	;;X;X;	1.59092;;X;X;	1.59092	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
TTTPNM(15.994915) NPAI NYQPQSSSVPC(470.2997 7) QR	M292,C308,NA	U;;X;X;	1.66243;;X;X;	1.66243	Q8WXI9 Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1 ,
SHSDNDRPNC(464.28596) SWNTQYSSAYTSR	C167,NA,NA	;;X;X;	1.80058;;X;X;	1.80058	O75494-3 Isoform 3 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10 , O75494-6 Isoform 6 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10 ,
SLVQNNCLSRPNIFLC(464. 28596) PEIEPK	NA,NA,C145,NA,NA	;;X;;	1.81465;;X;2.86326 ;;	2.338955	Q8TAQ2-2 Isoform 2 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 , Q8TAQ2 SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 , Q8TAQ2-3 Isoform 3 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 , F8VXC8 SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1 ,

YVAAAFPSAC(464.28596) GK	C172,NA,NA,NA,NA	;;;;;	2.05376;;1.78985;;2.42603,;	2.05376	B4DW73 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 , Q16822 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 ,
FC(464.28596)IWTESAFR	C250,NA	;;X;X;	1.49277;;X;X;	1.49277	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
APC(470.29977)QAGDLR	NA,NA	U;;U;;X;	1.6427;;1.35547;;X;	1.499085	P48431 Transcription factor SOX-2 OS=Homo sapiens GN=SOX2 PE=1 SV=1 ,
VICAEOPYIC(470.29977)K DFPETNNILK	C456,NA	;;X;X;	1.65825;;X;X;	1.65825	P49915 GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 ,
VTDDLVC(464.28596)LVYK	NA,NA	U,U;;U;;X;	2.05585,2.04695;;1.15987;;X;	2.04695	P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 ,
WEALHAAECPC(464.28596)GPSLIR	NA,NA	U;;X;X;	1.15651;;X;X;	1.15651	P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 ,
C(464.28596)WDPSPQAYF TLPR	NA,C354,C348,NA	;;X;X;	1.23062;;X;X;	1.23062	I3L0Z8 Segment polarity protein dishevelled homolog DVL-2 (Fragment) OS=Homo sapiens GN=DVL2 PE=1 SV=1 , O14641 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 , I3L2N2 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 ,
GC(464.28596)GVVKFESP EVAER	NA,NA,NA,NA	;;;;;	1.30419;;1.45377;;0.90388,;	1.30419	P52272 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 , P52272-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM , A0A087X0X3 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=1 ,
YGIIC(470.29977)M(15.994915)EDLIHEIYTVGK	C186,M187,NA	;;X;X;	1.51788;;X;X;	1.51788	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
YGIIC(470.29977)M(15.994915)EDLIHEIYTVGK	C186,M187,NA,NA	;;;;;	1.64698,1.63021,1.53503;;1.36804;;1.38246,;	1.53503	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
APC(464.28596)QAGDLRD M(15.994915)ISMYLPGAE VPEPAAPSR	NA,NA	U;;X;X;	2.28893;;X;X;	2.28893	P48431 Transcription factor SOX-2 OS=Homo sapiens GN=SOX2 PE=1 SV=1 ,
FLENTPSSLNIEDIEFLSLAQ YYC(464.28596)SK	C283,C146,NA,NA	;;X;X;	1.74128;;X;X;	1.74128	Q9NUY8 TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=3 , E9PGE5 TBC1 domain family

					member 23 OS=Homo sapiens GN=TBC1D23 PE=1 SV=1 , Q9NUY8-2 Isoform 2 of TBC1 domain family member 23 OS=Homo sapiens GN=TBC1D23 ,
SVLLCGIEAQAC(470.29977)ILNTTDLDDR	C114,NA,NA,NA	,,,X;	1.5395,1.43807,1.27022,,1.51608,,X;	1.477075	K7ENV7 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=7 , K7EKW4 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=1 , Q96AB3 Isochorismatase domain-containing protein 2 OS=Homo sapiens GN=ISOC2 PE=1 SV=1 ,
HFLIEC(464.28596)TPK	NA,NA	,;X;X;	1.41255,,X;X;	1.41255	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
SPHSPSPATPPSQSSSC(470.29977)SDAPM(15.994915)LSTVHSAK	C240,M245,NA,NA,C242,M247,NA,C242,M247,NA,C240,M245,NA,NA	,;X;X;	1.30652,,X;X;	1.30652	E9PQN2 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=1 , E9PK91 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=1 , Q9NYF8 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 , Q9NYF8-4 Isoform 4 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 , E9PKI6 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=1 , E9PK09 Bcl-2-associated transcription factor 1 (Fragment) OS=Homo sapiens GN=BCLAF1 PE=1 SV=7 , Q9NYF8-3 Isoform 3 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 , Q9NYF8-2 Isoform 2 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 , E9PJA7 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=1 ,
TIGGGDSFTTFFC(470.29977)ETGAGK	NA,NA,NA	,,,X;	1.52163,1.61386,1.5058,1.58852,,1.3811,,X;	1.52163	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
NWYVQPSC(470.29977)ATSGDGLYGLTWLTSNYK	C155,NA	U,U,,X;X;	1.78391,1.8128,,X;X;	1.798355	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 ,
C(464.28596)EFQDAYVLLSEK	NA,NA,NA	U,U,,X;X;	1.35424,1.38966,,X;X;	1.37195	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
QAVLGAGLPSTPC(464.28596)TTINK	C119,NA,NA	,,,X;	1.40775,,1.04798,1.37964,,1.31436,,	1.347	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
C(464.28596)EFQDAYVLLSEK	NA,NA,NA	U,U,U,,X;X;	1.57782,1.45763,1.37683,,1.54467,,X;	1.50115	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,

QAVLGAGLPSTPC(464.28596)TTINK	C119,NA,NA	,,X;X;	2.04699,,X;X;	2.04699	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
EDPTVSALLTSEKDWQGFLE LYLQNSPEAC(470.29977) DYGL	NA,NA	,,X;X;	1.34144,,X;X;	1.34144	P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 ,
EDPTVSALLTSEKDWQGFLE LYLQNSPEAC(470.29977) DYGL	NA,NA	,,X;X;	2.04714,,X;X;	2.04714	P78417 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 ,
NC(470.29977)IVLIDSTPYR	NA,NA	,,X;X;	1.53275,,X;X;	1.53275	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
NC(470.29977)IVLIDSTPYR	NA,NA	,,,X;X;	1.39566,1.47945,,X; ;X;	1.437555	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
IHM(15.994915)GSC(464.28596)AENTAK	NA,NA,NA	U,,U;U,;	1.49542,,1.39854,,1. .2753,;	1.39854	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
VTQNLPM(15.994915)KEG C(464.28596)TEVSLLR	M304,C308,NA,NA	,,X;X;	1.54687,,X;X;	1.54687	H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1 , Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 ,
ELEVLLMC(470.29977)NK	C91,C109,C91,NA	,,,,,X;	1.24938,1.82129,1. 62302,,1.7186,,X;	1.67081	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
QPAIM(15.994915)PGQSY GLEDGSC(464.28596)SYK DFSESER	NA,NA,NA	,,X;X;	1.19115,,X;X;	1.19115	MOQXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
VFIM(15.994915)DSC(464.28596)DELIPEYLNfir	M363,C366,NA	U,,U;U,;	1.14625,,1.31934,,1. .29497,;	1.29497	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 ,
AGVSGC(470.29977)FSTF QPTTGHR	NA,NA	U,,X;X;	1.67958,,X;X;	1.67958	Q96EK4 THAP domain-containing protein 11 OS=Homo sapiens GN=THAP11 PE=1 SV=2 ,
KC(470.29977)PFTGNVSIR	C60,NA	,,X;X;	1.53591,,X;X;	1.53591	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
GLC(464.28596)AIAQAESL R	NA,NA	,,,,,,;	1.55248,1.57528,1. 59847,,1.14136,1.3 7922,,1.14783,;	1.46585	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 ,

LEVDAIVNAANSSLLGGGG VDGC(464.28596)IHR	C186,NA	U,U,,X;X;	1.56156,0.95847,,X; X;	1.260015	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
LEVDAIVNAANSSLLGGGG VDGC(464.28596)IHR	C186,NA	U,,X;U,;	1.5995,,X;0.21708,,	0.90829	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
SSGGFWWAC(464.28596)K	C308,NA,NA,NA,NA	,,X;X;	1.6534,,X;X;	1.6534	P48735 Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 , P48735-2 Isoform 2 of Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 ,
TSSVSNPQDSVGSPC(470.2 9977)SR	NA,NA,C108,NA,NA	,,X;X;	1.79288,,X;X;	1.79288	P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 , F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 , P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN , P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN ,
TSSVSNPQDSVGSPC(470.2 9977)SR	NA,NA,C108,NA,NA	,,X;X;	1.74934,,X;X;	1.74934	P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 , F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 , P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN , P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN ,
C(470.29977)ASQSGM(15. 994915)TAYGTR	C175,M181,C164,M170,N A,NA	,,,X;	1.39248,,1.25121,, X;	1.321845	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
ISNITC(470.29977)DSFK	NA,NA	,,X;X;	1.26305,,X;X;	1.26305	Q96FC7 Phytanoyl-CoA hydroxylase-interacting protein-like OS=Homo sapiens GN=PHYHIPL PE=1 SV=3 ,
NVVAC(470.29977)ESIGR	C125,NA,NA	U,,X;X;	1.04158,,X;X;	1.04158	Q9H0U6 39S ribosomal protein L18, mitochondrial OS=Homo sapiens GN=MRPL18 PE=1 SV=1 ,
VASGSTATAAAGPSC(464.2 8596)ALK	NA,NA,NA	,,X;X;	0.97168,,X;X;	0.97168	P41134-2 Isoform ID-B of DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 , P41134 DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 PE=1 SV=3 ,
AVQDLC(470.29977)GWR	C428,NA	U,,X;X;	1.44191,,X;X;	1.44191	Q9P258 Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 ,
VASGSTATAAAGPSC(464.2 8596)ALK	NA,NA,NA	,,X;X;	1.64845,,X;X;	1.64845	P41134-2 Isoform ID-B of DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 , P41134 DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 PE=1 SV=3 ,
AASQINVC(470.29977)GV R	C159,NA,NA	,,X;X;	1.60897,,X;X;	1.60897	Q14678-2 Isoform 2 of KN motif and ankyrin repeat domain- containing protein 1 OS=Homo sapiens GN=KANK1 , Q14678 KN motif and ankyrin repeat domain-containing protein 1

					OS=Homo sapiens GN=KANK1 PE=1 SV=3 ,
IAILTC(464.28596)PFEPK PK	NA,NA,C253,NA	;;X;X;	1.45998;;X;X;	1.45998	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 , B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 , P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 ,
VVMALGDYMGASCHAC(470.29977)IGGTNVR	NA,NA	;;X;X;	1.53735;;X;X;	1.53735	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 ,
IAILTC(464.28596)PFEPK PK	NA,NA,C253,NA	;;X;;	1.4657;;X;1.2822;;	1.37395	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 , B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 , P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 ,
LNQVC(464.28596)FDDDG TSSPQDR	NA,NA	;;X;X;	0.82111;;X;X;	0.82111	Q8N1F7 Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 ,
AHGC(470.29977)FPEGR	NA,NA,NA	;;X;X;	1.37899;;X;X;	1.37899	Q7Z5L9-2 Isoform 2 of Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 , Q7Z5L9 Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2 ,
NFYGGNGIVGAQVPLGAGI ALAC(464.28596)K	NA,NA,NA,C219,NA,NA,C188,NA,NA,NA	;;;X;	1.39009;;1.7665;;X;	1.578295	P08559 Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 , P08559-4 Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 , P08559-2 Isoform 2 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 ,
AVILGPPGSGKGTVC(464.28596)QR	C22,NA,NA	U;;X;X;	1.76181;;X;X;	1.76181	P27144 Adenylate kinase 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 ,
AAQGPPAPAVPPNTDVM(15.994915)AC(470.29977)TQTALLQK	M144,C146,M150,C152,M113,C115,NA	;;X;X;	1.63246;;X;X;	1.63246	H0YEB6 Sjogren syndrome/scleroderma autoantigen 1 (Fragment) OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 , O60232 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 , G3V1B8 Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 ,

SC(464.28596)GSSTPDEFP TDIPGTK	NA,NA	,,,X;	0.74678,,1.38952,, X;	1.06815	P41091 Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3 ,
VIGIEC(470.29977)SSISDY AVK	NA,C119,C101,C95,C95,N A,NA	,,,X;X;	1.80169,1.71978,1. 12524,,X;X;	1.71978	E9PKG1 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 , H7C211 Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 , Q99873-4 Isoform 4 of Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 , Q99873 Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2 , Q99873-2 Isoform 2 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 , Q99873-3 Isoform 3 of Protein arginine N- methyltransferase 1 OS=Homo sapiens GN=PRMT1 ,
LLSNM(15.994915)MC(46 4.28596)QYR	NA,NA,NA,NA	,,X;X;	1.42524,,X;X;	1.42524	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 , X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 , P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 ,
LQDAFSSIGQSC(470.2997 7)HLDLPQIAVVGGQSAGK	C27,NA,NA,C27,NA,NA	,,X;X;	1.20404,,X;X;	1.20404	P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 , P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 ,
LQDAFSSIGQSC(470.2997 7)HLDLPQIAVVGGQSAGK	C27,NA,NA,C27,NA,NA	,,X;X;	1.41242,,X;X;	1.41242	P50570-5 Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-4 Isoform 4 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570 Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2 , P50570-3 Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2 , P50570-2 Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2 ,
SC(464.28596)PSFSASSE GTR	C9,C9,C9,NA,NA	,,X,,,;	1.38594,,X;1.10306 ,,	1.2445	D6RCP9 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 , P27707 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 , D6RFG8 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 , D6RG38 Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1 ,
SSVNC(464.28596)PFSSQ	NA,NA	U,,X;X;	0.61877,,X;X;	0.61877	Q08211 ATP-dependent RNA helicase A OS=Homo sapiens

DM(15.994915)K					GN=DHX9 PE=1 SV=4 ,
NMITGTSQADC(464.28596)AVLIVAAGVGEFEAGISK	NA,NA,NA	;;X;X;	2.04357;;X;X;	2.04357	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 ,
GLTDL SAC(464.28596)K	NA,NA	;;X;X;	1.38969;;X;X;	1.38969	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
MLQPC(464.28596)GPPA DKPEEN	NA,NA	U;;X;X;	1.66822;;X;X;	1.66822	Q9BWJ5 Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1 ,
C(464.28596)TVVSETISSK	NA,NA,NA	;;X;X;	1.52976;;X;X;	1.52976	Q68D10 Protein SPT2 homolog OS=Homo sapiens GN=SPTY2D1 PE=1 SV=3 , Q68D10-2 Isoform 2 of Protein SPT2 homolog OS=Homo sapiens GN=SPTY2D1 ,
TTSSANNPNLMYQDEC(464.28596)DRR	C507,C586,NA,NA,C505,NA	;;X;;	1.21458;;X;1.40276;;	1.30867	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 , Q92841-2 Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 , Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 ,
QVC(470.29977)QLPGLFS YAQHIASIDGR	NA,NA	;;X;X;	1.67506;;X;X;	1.67506	Q9Y6C9 Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 ,
LNISFPATGC(470.29977)QK	NA,NA	;;;;	1.4112,1.43815,1.76842;;1.33528;;1.2815;;	1.4112	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
KLLDLVQQSC(470.29977)NYK	NA,C30,NA	;;X;;	1.58665;;X;1.52064;;	1.553645	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 , P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 ,
EHAASLC(470.29977)R	NA,NA	;;X;X;	1.30574;;X;X;	1.30574	Q9H0A8 COMM domain-containing protein 4 OS=Homo sapiens GN=COMMD4 PE=1 SV=1 ,
C(470.29977)PFTGNVSIR	C60,NA	;;X;;	1.53646,1.48404;;X;1.26181;;	1.48404	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
AKC(464.28596)ELSSSVQT DINLPYLT(15.994915)DS SGPK	NA,NA,NA	;;X;X;	1.65683;;X;X;	1.65683	P38646 Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 ,

TSC(464.28596)GSPNYAA PEVISGR	C200,NA,C200,C174,NA	;;X;X;	2.45698;;X;X;	2.45698	Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 , A0A087WXX9 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=1 , Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 , P54646 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=2 ,
HELQANC(470.29977)YEE VKDR	C177,NA,NA,C139,NA	;;;;;	1.46006;;1.22943;;1.14319;;	1.22943	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 , G3V1A4 Cofilin 1 (Non-muscle), isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 , P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 ,
WSAAC(470.29977)AYLHP ALSR	C242,NA,NA	U;;X;X;	1.6501;;X;X;	1.6501	Q8NE62 Choline dehydrogenase, mitochondrial OS=Homo sapiens GN=CHDH PE=1 SV=2 ,
IIFVVGPGSGKGTQC(464.28596)EK	C41,NA,NA	;;X;X;	1.31455;;X;X;	1.31455	Q5T9B7 Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=1 , P00568 Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 ,
KLNCQVIGASVDSHFC(470.29977)HLAWVNTPK	C83,C83,NA	;;X;X;	3.39842;;X;X;	3.39842	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 , A0A0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 ,
LTAC(470.29977)QVATAF NLSR	NA,C425,C425,NA	;;X;X;	1.62509;;X;X;	1.62509	O95671-3 Isoform 3 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671-2 Isoform 2 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671 N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3 ,
LTAC(470.29977)QVATAF NLSR	NA,C425,C425,NA	;;X;X;	2.01209;;X;X;	2.01209	O95671-3 Isoform 3 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671-2 Isoform 2 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671 N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3 ,
AAVPLGGFLC(464.28596) NVADK	NA,NA,NA	U;;X;X;	1.49481;;X;X;	1.49481	Q7L8L6 FAST kinase domain-containing protein 5, mitochondrial OS=Homo sapiens GN=FASTKD5 PE=1 SV=1 ,

GLIAAIC(470.29977)AGPT ALLAHEIGFGSK	NA,C86,NA,NA	,,;,;	1.28013,1.23897,,1. 25574,,1.24761,;	1.251675	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
AAVPLGGFLC(464.28596) NVADK	NA,NA,NA	U,,X;X;	1.21321,,X;X;	1.21321	Q7L8L6 FAST kinase domain-containing protein 5, mitochondrial OS=Homo sapiens GN=FASTKD5 PE=1 SV=1 ,
GLIAAIC(470.29977)AGPT ALLAHEIGFGSK	NA,C86,NA,NA	,,;,;	1.2557,,1.11444,,1. 24395,;	1.24395	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
LDVGNFSWGSEC(464.285 96)CTRK	NA,NA	U,,X;X;	1.54882,,X;X;	1.54882	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
MAGIFDVNTC(470.29977) YGSPQSPQLIR	NA,NA,NA,C428,NA,NA	,,X;X;	1.37926,,X;X;	1.37926	Q9BTX1-2 Isoform 2 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1 Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 PE=1 SV=2 , Q9BTX1-4 Isoform 4 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1-5 Isoform 5 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1-6 Isoform 6 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 ,
ADASSTPSFQQAFASSC(46 4.28596)TISSNGPGQRR	NA,NA	,,X;X;	6.37796,,X;X;	6.37796	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
VLPSTPYFALGLGM(15.99 4915)FPGKGGMVAPGMT C(470.29977)QY	M422,C436,NA,NA,NA	,,X;X;	4.16138,,X;X;	4.16138	Q9Y238-3 Isoform 3 of Deleted in lung and esophageal cancer protein 1 OS=Homo sapiens GN=DLEC1 , Q9Y238-2 Isoform 2 of Deleted in lung and esophageal cancer protein 1 OS=Homo sapiens GN=DLEC1 , Q9Y238 Deleted in lung and esophageal cancer protein 1 OS=Homo sapiens GN=DLEC1 PE=2 SV=2 ,
YGIIC(464.28596)M(15.99 4915)EDLIHEYTVGK	C186,M187,NA	,,X;X;	1.51788,,X;X;	1.51788	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
YGIIC(464.28596)M(15.99 4915)EDLIHEYTVGK	C186,M187,NA	,,X;X;	1.63021,1.5471,,X; X;	1.588655	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
SPHSPSIATPPSQSSSC(46 4.28596)SDAPM(15.99491 5)LSTVHSAK	C240,M245,NA,NA,C242, M247,NA,C242,M247,NA, C240,M245,NA,NA	,,X;X;	1.30652,,X;X;	1.30652	E9PQN2 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=1 , E9PK91 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1

					SV=1 , Q9NYF8 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 , Q9NYF8-4 Isoform 4 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 , E9PKI6 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=1 , E9PK09 Bcl-2-associated transcription factor 1 (Fragment) OS=Homo sapiens GN=BCLAF1 PE=1 SV=7 , Q9NYF8-3 Isoform 3 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 , Q9NYF8-2 Isoform 2 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 , E9PJA7 Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=1 ,
TVVNGKEC(464.28596)INF ASFNFLGLLDNPR	NA,NA	,,X;X;	3.44747,,X;X;	3.44747	O15269 Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1 ,
TIQFVDWC(470.29977)PT GFK	C347,NA,C417,NA,NA,C34 7,NA	,,,,X;	1.61967,1.83993,,1. 62078,,X;	1.62078	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 ,
IVGYFVSGC(464.28596)DP SIM(15.994915)GIGPVPAI SGALKK	NA,NA,C287,M292,NA,NA	,,X;X;	2.01486,,X;X;	2.01486	A0A0B4J2A4 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 , P42765 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 ,
AGSDGESIGNC(470.29977))PFSQR	C35,NA	U,,U,,X;	1.55027,,1.652,,X;	1.601135	Q9Y696 Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 ,
LLAPDC(464.28596)EIIQEV GKLYPLEIVFGM(15.99491 5)NGR	C215,M233,NA	U,,X;X;	1.5425,,X;X;	1.5425	Q9NQ75 Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 ,
GYWASLDASTQTTHLTPN NLIGC(470.29977)IIGR	C293,NA	U,,X;X;	1.66653,,X;X;	1.66653	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
VGLSGAPADAC(464.28596))STAQK	C394,NA	U,,X;X;	1.39474,,X;X;	1.39474	Q8NFW8 N-acylneuraminate cytidyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 ,

KGVSASAVPFTPSSPLLSC(464.28596)SQEGSR	NA,NA,NA,NA	;;X;X;	1.68266;;X;X;	1.68266	Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 , J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 , Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 ,
GC(470.29977)LELIKETGVPIAGR	NA,NA,NA,NA,NA	;;X;X;	1.48666;;X;X;	1.48666	P11586 C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 , F5H2F4 C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=1 ,
LC(464.28596)SSSSSDTSSR	NA,C385,NA,NA	;;X;;;	1.43558;;X;1.35822;;	1.3969	Q86WB0 Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 , Q86WB0-2 Isoform 2 of Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 , C9J0I9 Nuclear-interacting partner of ALK OS=Homo sapiens GN=ZC3HC1 PE=1 SV=1 ,
AIVFSGC(464.28596)GR	C70,NA	U;;X;X;	1.5624;;X;X;	1.5624	Q9BUL9 Ribonuclease P protein subunit p25 OS=Homo sapiens GN=RPP25 PE=1 SV=1 ,
CC(464.28596)ILALVCWITVLLQCSK	C6,NA	U;;X;X;	1.38927;;X;X;	1.38927	Q6UXB1 Insulin growth factor-like family member 3 OS=Homo sapiens GN=IGFL3 PE=1 SV=1 ,
C(470.29977)ASQAGMTAYGTR	C132,C127,NA,NA	;;X;X;	3.76298;;X;X;	3.76298	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 ,
C(470.29977)ASQAGMTAYGTR	C132,C127,NA,NA	;;;X;X;	5.62001,1.39661;;X;X;	3.50831	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 ,
PC(464.28596)SEETPAISPSKR	C3,NA,C3,NA,NA	;;X;;;	1.50935;;X;1.11308;;	1.311215	P33316-2 Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT , H0YNJ9 Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=1 ,
LQFHDVAGDIFHQQC(470.29977)K	C415,C385,NA,NA	;;X;X;	1.23947;;X;X;	1.23947	P11413-3 Isoform 3 of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD , P11413 Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 , P11413-2 Isoform Long of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD ,

VIDPVTGKPC(470.29977)A GTTYLESPLSSETTQLSK	C195,NA,C100,NA,C100,N A,NA	;;X;X;	1.43664;;X;X;	1.43664	I3L0E3 HCG1984214, isoform CRA_a OS=Homo sapiens GN=hCG_1984214 PE=3 SV=1 , E9PE17 28S ribosomal protein S17, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS17 PE=3 SV=1 , Q9Y2R5 28S ribosomal protein S17, mitochondrial OS=Homo sapiens GN=MRPS17 PE=1 SV=1 ,
VIDPVTGKPC(470.29977)A GTTYLESPLSSETTQLSK	C195,NA,C100,NA,C100,N A,NA	;;X;X;	1.5619;;X;X;	1.5619	I3L0E3 HCG1984214, isoform CRA_a OS=Homo sapiens GN=hCG_1984214 PE=3 SV=1 , E9PE17 28S ribosomal protein S17, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS17 PE=3 SV=1 , Q9Y2R5 28S ribosomal protein S17, mitochondrial OS=Homo sapiens GN=MRPS17 PE=1 SV=1 ,
AAAENLPVPAELPIEDLC(46 4.28596)SLTSQSLPIELTSV VPESTEDILLK	C65,C65,NA	;;X;X;	1.33541;;X;X;	1.33541	Q96JB2-2 Isoform 2 of Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 , Q96JB2 Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3 ,
QGEYGLASIC(470.29977)N GGGGASAM(15.994915)LI QKL	NA,NA,NA	U;;U;X;	1.4716;;1.56192;;X;	1.51676	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
C(470.29977)EFEEVQGFL DQVAHKLPFAAK	NA,NA,NA,NA,NA	;;X;X;	1.63871;;X;X;	1.63871	E9PI14 39S ribosomal protein L16, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL16 PE=1 SV=1 , Q9NX20 39S ribosomal protein L16, mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1 ,
C(470.29977)EFEEVQGFL DQVAHKLPFAAK	NA,NA,NA,NA,NA	;;;X;X;	1.63634,1.61539;;X ;X;	1.625865	E9PI14 39S ribosomal protein L16, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL16 PE=1 SV=1 , Q9NX20 39S ribosomal protein L16, mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1 ,
VQVSDPESTVAVAFPTIPH C(470.29977)SM(15.9949 15)ATLIGLSIK	C93,M95,NA	;;X;X;	1.45693;;X;X;	1.45693	Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 ,
LTIVSDPSHC(464.28596) NVLR	C87,NA,NA	;;;X;X;	1.32453,1.44781;;X ;X;	1.38617	P78346-2 Isoform 2 of Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 , P78346 Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1 ,
LILDVFC(470.29977)GSQ M(15.994915)HFVR	C476,M480,C446,M450,N A,NA	;;X;X;	1.33677;;X;X;	1.33677	P11413-3 Isoform 3 of Glucose-6-phosphate 1- dehydrogenase OS=Homo sapiens GN=G6PD , P11413

					Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 , P11413-2 Isoform Long of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD ,
SSSSVTTSETQPC(470.29977)TPSSSDYDLQR	NA,NA	;;X;X;	1.29245;;X;X;	1.29245	P50552 Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 ,
IGVHVVDQVLTMEPYCC(464.28596)RDM(15.994915)LSLSDK	C584,M587,C584,M587,NA	;;X;X;	5.1984;;X;X;	5.1984	Q70CQ1-2 Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 49 OS=Homo sapiens GN=USP49 , Q70CQ1 Ubiquitin carboxyl-terminal hydrolase 49 OS=Homo sapiens GN=USP49 PE=1 SV=1 ,
VQEAPIDEHWIEC(470.29977)NDGVFQR	NA,C91,NA	;;X;X;	1.4151;;X;X;	1.4151	Q14353-2 Isoform 2 of Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT , Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 ,
SC(470.29977)GPASQSTLGLK	C232,NA,NA,C254,NA,NA,NA,C255,NA	;;X;X;	1.23653;;X;X;	1.23653	Q9BXS6-7 Isoform 7 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , H0YMD2 Nucleolar and spindle-associated protein 1 (Fragment) OS=Homo sapiens GN=NUSAP1 PE=1 SV=1 , Q9BXS6-2 Isoform 2 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6-3 Isoform 3 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6-4 Isoform 4 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6 Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 PE=1 SV=1 , Q9BXS6-6 Isoform 6 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6-5 Isoform 5 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 ,
VQVSDPESTVAVAFPTIPH C(470.29977)SMATLIGLSIK	C93,NA	;;X;X;	4.30562;;X;X;	4.30562	Q9Y3D0 Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1 ,
AYEYVEC(470.29977)PIR	NA,NA	U;;X;X;	1.75525;;X;X;	1.75525	P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 ,
DC(470.29977)DLQEDVLA CFFSLLKPAITAVEVATLPR	NA,NA	U;;X;X;	4.08209;;X;X;	4.08209	D6RAT4 Cellular nucleic acid-binding protein (Fragment) OS=Homo sapiens GN=CNBP PE=1 SV=7 ,
HLYTLDGDDIINALC(464.28	NA,NA	;;X;X;	1.0515;;X;X;	1.0515	P63244 Receptor of activated protein C kinase 1 OS=Homo

596)FSPNR					sapiens GN=RACK1 PE=1 SV=3 ,
HLTLDGGDIINALC(464.28596)FSPNR	NA,NA	;;X;X;	1.3649;;X;X;	1.3649	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
LVAFC(470.29977)PFASSQ VALENANAVSEGVVHEDLR	NA,NA	;;X;;	1.42608;;X;1.30676;;	1.36642	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
LVAFC(470.29977)PFASSQ VALENANAVSEGVVHEDLR	NA,NA	;;X;;	1.71249,1.77478;;X;1.74799;;	1.74799	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
NLPFPTYFPDGDDEELPEDL YDENVC(464.28596)QPGA PSITFA	C365,NA,NA,NA,C338,NA,NA	;;X;;	1.72105;;X;1.35425;;	1.53765	E7ETU7 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , H0Y9G6 39S ribosomal protein L3, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , P09001 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 ,
NAFAC(464.28596)FDEEA TGTIQEDYLR	NA,NA,NA,NA	;;X;X;	1.27056;;X;X;	1.27056	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 , J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 , O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 ,
TLLLC(464.28596)GYPNVG K	NA,NA	;;X;X;	1.39459;;X;X;	1.39459	Q9BZE4 Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 ,
M(15.994915)ININILSVC(464.28596)K	NA,NA	;;X;X;	1.9194;;X;X;	1.9194	Q53GQ0 Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 ,
TTSLC(464.28596)AGPSAS KNEYEK	C730,C676,NA	;;X;X;	1.88854;;X;X;	1.88854	Q9BWU0 Kanadaplin OS=Homo sapiens GN=SLC4A1AP PE=1 SV=1 , A0A087X0M4 Kanadaplin OS=Homo sapiens GN=SLC4A1AP PE=1 SV=1 ,
FM(15.994915)LVLASNLP EQFDC(464.28596)AINSR	M402,C415,M448,C461,NA	;;X;X;	0.62215;;X;X;	0.62215	Q5T9A4-3 Isoform 3 of ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B , Q5T9A4 ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1 ,
ISELSGC(464.28596)TPDPR	NA,NA,NA	;;X;X;	0.80161;;X;X;	0.80161	Q9H9P8 L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=L2HGDH PE=1 SV=3 ,
LVILANNC(470.29977)PALR	C52,C52,NA	;;X;X;	0.89752;;X;X;	0.89752	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 , E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 ,
C(470.29977)ASQVGM(15.994915)TAPGTR	C215,M221,C204,M210,NA,NA	;;X;	1.46505;;1.24887;;X;	1.35696	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,

LAEQC(470.29977)GGLQG FLIFRSFGGTGSGFTSLLM(15.994915)ER	C96,M121,NA,NA	;;X;X;	4.54578;;X;X;	4.54578	A6NHL2-2 Isoform 2 of Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 , A6NHL2 Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2 ,
SSGEIVYC(470.29977)GQV FEK	NA,NA	;;X;X;	1.72031;;X;X;	1.72031	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 ,
GLPHCSC(470.29977)AEF QDSLNFYHPSGLSLHLR	C58,C48,NA	;;X;X;	0.59577;;X;X;	0.59577	Q9NYF3 Protein FAM53C OS=Homo sapiens GN=FAM53C PE=1 SV=1 , D6RHW3 Protein FAM53C (Fragment) OS=Homo sapiens GN=FAM53C PE=1 SV=7 ,
GVPGAIVNVSSQC(470.299 77)SQR	NA,NA	;;X;X;	1.19182;;X;X;	1.19182	Q7Z4W1 L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 ,
LVMSYVAAVC(464.28596) GK	C129,NA,C129,NA	;;X;X;	2.04469;;X;X;	2.04469	O43795 Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3 , E9PDF6 Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=1 , O43795-2 Isoform 2 of Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B ,
GVPGAIVNVSSQC(470.299 77)SQR	NA,C137,NA,NA	;;X;;	1.21338;;X;1.59441 ;;	1.403895	Q7Z4W1 L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 , J3QS36 L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=1 SV=1 , J3KS22 L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=1 SV=7 ,
PC(470.29977)GEDWLSHP LGIVQGFFAQNGVNPDWE K	NA,C3,NA	;;X;X;	1.53178;;X;X;	1.53178	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 , Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP ,
IIPGFM(15.994915)C(464. 28596)QGGDFTR	M61,C62,M61,C62,M61,C 62,NA	;;X;X;	1.44701;;X;X;	1.44701	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
PC(470.29977)GEDWLSHP LGIVQGFFAQNGVNPDWE K	NA,C3,NA	;;X;X;	1.27913;;X;X;	1.27913	Q9BTE3 Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2 , Q9BTE3-2 Isoform 2 of Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP ,
ADDTFEALC(470.29977)IE PFSSPELPDVM(15.99491 5)KPQDSGSSANEQAVQ	NA,NA,C84,M98,NA,NA,N A,NA	;;X;X;	1.24119;;X;X;	1.24119	I3L0M9 Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1 , Q15370 Transcription elongation factor B polypeptide 2

					OS=Homo sapiens GN=TCEB2 PE=1 SV=1 , B8ZZU8 Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=1 SV=1 ,
ALANVNIGSLIC(470.29977))NVGAGGPAPAAGAAPAG GPAPSTAAAPAEK	NA,NA,NA	,,;X;X;	1.28692,1.28692,,;X; ;X;	1.28692	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 , P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 ,
ALANVNIGSLIC(470.29977))NVGAGGPAPAAGAAPAG GPAPSTAAAPAEK	NA,NA	,,;;;X;	1.35679,1.35679,,;1.46115,,;X;	1.35679	P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 ,
ALANVNIGSLIC(470.29977))NVGAGGPAPAAGAAPAG GPAPSTAAAPAEK	NA,NA,NA	,,;,;,;,;,;	1.33949,1.30666,1.33949,1.30666,,;1.41083,,;1.36746,1.36746,,;	1.33949	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 , P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 ,
AATGEEVSAEDLGGADLHC(464.28596)R	NA,NA,NA	,,;,;,;	1.54064,,;1.11391,,;1.17146,,;	1.17146	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
LFNC(470.29977)SASLDWPR	NA,NA,NA	,;X;X;	4.34945,,;X;X;	4.34945	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
C(464.28596)EFDSQASAPR	NA,NA	,;X;X;	1.34396,,;X;X;	1.34396	O43542 DNA repair protein XRCC3 OS=Homo sapiens GN=XRCC3 PE=1 SV=1 ,
M(15.994915)SSYAFFVQTC(470.29977)R	NA,M13,C23,M13,C23,NA,M13,C23,NA	,;X;X;	1.54545,,;X;X;	1.54545	P26583 High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 , Q5T7C4 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=1 , B2RPK0 Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1 , D6R9A6 High mobility group protein B2 (Fragment) OS=Homo sapiens GN=HMGB2 PE=1 SV=1 , P09429 High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3 ,
LHLDEYPC(470.29977)SLVGNWNTWYGEQDQAVHLWR	C106,C123,NA	,;X;X;	1.57654,,;X;X;	1.57654	Q9BPW8 Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 , H7C2U6 Protein NipSnap homolog 1 (Fragment) OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 ,
LHLDEYPC(470.29977)SLVGNWNTWYGEQDQAVHL	C106,C123,NA	,;X;X;	1.4575,,;X;X;	1.4575	Q9BPW8 Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 , H7C2U6 Protein NipSnap

WR					homolog 1 (Fragment) OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 ,
ADASSTPSFQQAFASSC(464.28596)TISSNGPGQR	C688,NA,NA	,,;;X;	0.66619,,1.34367,,X;	1.00493	Q68CZ2-2 Isoform 2 of Tensin-3 OS=Homo sapiens GN=TNS3 , Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
AVC(470.29977)M(15.994915)LSNTTAIAEAWAR	NA,C376,M377,NA,NA,NA ,C376,M377,NA,NA	,,;;,X;	1.89668,,1.41834,1.37764,,X;	1.41834	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
TMVNLALENAC(470.29977)DEATYQLGLDMEELEEIEE DAGLGNGGLGR	C109,NA,NA	U,,X;X;	0.5197,,X;X;	0.5197	P11217 Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 ,
C(470.29977)LHNFLTDGV PAEGAFTEDFQGLR	C316,NA,C268,NA	,;X;X;	1.44679,,X;X;	1.44679	G3V1A6 Gasdermin domain containing 1, isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 , P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 ,
AVC(470.29977)M(15.994915)LSNTTAIAEAWAR	NA,C376,M377,NA,NA,NA ,C376,M377,NA,NA	,,;;,X;	2.16376,1.71874,,1.73851,,X;	1.73851	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
TMVNLALENAC(470.29977)DEATYQLGLDMEELEEIEE DAGLGNGGLGR	C109,NA,NA	U,,X;X;	0.51948,,X;X;	0.51948	P11217 Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 ,
C(470.29977)LHNFLTDGV PAEGAFTEDFQGLR	C316,NA,C268,NA	,;X;;	1.44036,,X;1.60559 ,;	1.522975	G3V1A6 Gasdermin domain containing 1, isoform CRA_d OS=Homo sapiens GN=GSDMD PE=1 SV=1 , P57764 Gasdermin-D OS=Homo sapiens GN=GSDMD PE=1 SV=1 ,

AQLVEIVGC(464.28596)HFR	NA,NA	U,,X;X;	1.50562,,X;X;	1.50562	O75446 Histone deacetylase complex subunit SAP30 OS=Homo sapiens GN=SAP30 PE=1 SV=1 ,
ALVDGPC(464.28596)TQVR	NA,C42,NA	,,X;X;	1.48992,,X;X;	1.48992	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 , P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 ,
LQC(464.28596)FGDVIIPNPLDTFGNVQM(15.994915)ASSTDQTEALPLVVR	C411,M429,NA	U,,X;X;	1.44632,,X;X;	1.44632	Q92786 Prospero homeobox protein 1 OS=Homo sapiens GN=PROX1 PE=1 SV=2 ,
IC(470.29977)ALENELAALR	NA,NA,NA,NA	,,X;X;	1.29846,,X;X;	1.29846	Q15390 Mitochondrial fission regulator 1 OS=Homo sapiens GN=MTFR1 PE=1 SV=2 , Q15390-2 Isoform 2 of Mitochondrial fission regulator 1 OS=Homo sapiens GN=MTFR1 , H0YBZ4 Mitochondrial fission regulator 1 (Fragment) OS=Homo sapiens GN=MTFR1 PE=1 SV=1 ,
LQC(464.28596)FGDVIIPNPLDTFGNVQM(15.994915)ASSTDQTEALPLVVR	C411,M429,NA	U,,X;X;	2.27844,,X;X;	2.27844	Q92786 Prospero homeobox protein 1 OS=Homo sapiens GN=PROX1 PE=1 SV=2 ,
C(464.28596)PARPPPSGSQGLLEEMLAASSSK	NA,NA	U,,X;X;	1.03855,,X;X;	1.03855	Q9C0C2 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4 ,
VLVTTNVC(464.28596)AR	NA,C367,NA,C392,NA,C393,NA,C310,NA	,,X;;;,	1.42871,,X;1.23247,1.1804,,	1.23247	Q9UMR2-3 Isoform 3 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B , Q9UMR2 ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 , Q9NUU7-2 Isoform 2 of ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A , Q9NUU7 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 , H3BQK0 ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 , F6QDS0 HCG2043426, isoform CRA_b OS=Homo sapiens GN=hCG_2043426 PE=1 SV=1 , I3L352 ATP-dependent RNA helicase DDX19A (Fragment) OS=Homo sapiens GN=DDX19A PE=1 SV=1 ,
C(470.29977)EFQDAYVLLSEKK	NA,NA,NA	U,U,,X;X;	1.37258,1.41374,,X;X;	1.39316	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
NC(470.29977)LTNFHGM DLTR	C96,NA	,,X;X;	1.53296,,X;X;	1.53296	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 ,
NC(470.29977)LTNFHGM DLTR	NA,NA,C96,NA,NA	,,X;;;,	1.44571,,X;1.30725,,	1.37648	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal

					protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
NC(470.29977)LTNFHGM DLTR	C96,NA	,,X;X;	1.50884,,X;X;	1.50884	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 ,
SSLPEFQAPEAEPEPGEPLL QVTLVDC(464.28596)PGH ASLIR	C93,NA,C93,NA	,,X;X;	1.8412,,X;X;	1.8412	P57772 Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC PE=1 SV=4 , P57772-2 Isoform 2 of Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC , C9J8T0 Selenocysteine-specific elongation factor OS=Homo sapiens GN=EEFSEC PE=1 SV=1 ,
LC(470.29977)YVALDFEQE MATAASSSSLEK	NA,NA,NA,NA,NA,NA	,,,;	1.35565,,1.28113,,1 .32945,;	1.32945	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 , Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 ,
GLYGIKDDVFLSVPC(464.2 8596)ILGQNGISDLVK	C322,NA,NA	,,X;X;	1.23445,,X;X;	1.23445	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA , P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 ,
SGGSGGC(470.29977)SGA GGASNCGTGSGR	NA,NA,NA,NA	,,,X;	1.60024,,1.47136,, X;	1.5358	E9PI68 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=1 , A0A087WUC6 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=1 , Q15005 Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3 ,
ISSVLAGGSC(464.28596)R	C40,NA,NA	,,X;X;	2.43153,,X;X;	2.43153	P08779 Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 ,
ICDEC(470.29977)NYGSYQ GR	C49,NA	U,,X;X;	1.57454,,X;X;	1.57454	Q7RTV0 PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1 ,
LTPGC(464.28596)EAEAET EAICFFVQQFTDM(15.9949 15)EHNR	C2359,M2378,NA	,,,X;X;	1.27407,1.39465,,X ;X;	1.33436	P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 ,
SLC(464.28596)NLEESITSA GR	NA,NA,NA	,,X;X;	3.26882,,X;X;	3.26882	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
LIC(464.28596)LVTGSPSIR	C590,NA,NA	U,,X;X;	2.03917,,X;X;	2.03917	Q6PI48 Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1 ,

GSDELSTC(470.29977)VT NGPFIMSSNSASAANGNDS K	NA,NA	;;X;X;	2.35591;;X;X;	2.35591	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
AYHEQLSVAEITNAC(470.2 9977)FEPANQMVK	NA,NA,NA,NA,NA	;;X;X;	1.54536;;X;X;	1.54536	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
AYHEQLSVAEITNAC(470.2 9977)FEPANQMVK	NA,NA,NA,NA,NA	;;X;X;	1.64233,1.84162;;X; X;	1.741975	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
QGEYGLASIC(464.28596)N GGGGASAM(15.994915)LI QK	NA,NA,NA	U;;U;;X;	1.88967;;1.6637;;X;	1.776685	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
VNAAGTDPSSPVGFVLGVD LLHIFPLEGATFLC(470.299 77)PADVTDPR	NA,NA,NA	U;;X;X;	1.45354;;X;X;	1.45354	Q9UI43 rRNA methyltransferase 2, mitochondrial OS=Homo sapiens GN=FTSJ2 PE=1 SV=1 ,
ITSEQAM(15.994915)QDP YFLEDPLPTSDVFAGC(464. 28596)QIPYPK	NA,NA,NA,NA	;;X;X;	1.46597;;X;X;	1.46597	P49336-2 Isoform 2 of Cyclin-dependent kinase 8 OS=Homo sapiens GN=CDK8 , P49336 Cyclin-dependent kinase 8 OS=Homo sapiens GN=CDK8 PE=1 SV=1 , A0A0D9SF22 Cyclin-dependent kinase 8 (Fragment) OS=Homo sapiens GN=CDK8 PE=1 SV=3 ,
LPSGLGC(464.28596)STVL SPEGSAQFAAQIFGLSNHLV WSK	C374,NA	;;;X;	1.36705;;1.49286;; X;	1.429955	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
LPSGLGC(464.28596)STVL SPEGSAQFAAQIFGLSNHLV WSK	C374,NA	;;X;X;	1.86216;;X;X;	1.86216	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
QQYLC(470.29977)QPLLD AVLANIR	C507,NA,C618,C552,NA	;;X;X;	1.81051;;X;X;	1.81051	Q96RN5-3 Isoform 3 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 , Q96RN5-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 ,

					Q96RN5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=2 , G3V1P5 Mediator of RNA polymerase II transcription subunit 15 OS=Homo sapiens GN=MED15 PE=1 SV=1 ,
C(470.29977)SEGSFLLTTF PRPVTVEPMDQLDDEEGLP EK	NA,NA	,,X;X;	1.34684,,X;X;	1.34684	Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 ,
LGEWVGLC(464.28596)K	NA,NA	U,,X;X;	1.39248,,X;X;	1.39248	P25398 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 ,
YIELFLNSC(464.28596)PK	NA,NA,NA,NA,NA,NA	,,,X;X;	1.65418,1.18665,,X; X;	1.420415	F5H5I6 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=2 , H0YAK1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 , H0Y8R1 G-rich sequence factor 1 (Fragment) OS=Homo sapiens GN=GRSF1 PE=1 SV=1 , Q12849-5 Isoform 2 of G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 , Q12849 G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=3 ,
EINHFFC(464.28596)EAPA VLKLAC(470.29977)ADTAL YETVMYVCCV	C229,C239,NA	U,,X;X;	0.41092,,X;X;	0.41092	O43869 Olfactory receptor 2T1 OS=Homo sapiens GN=OR2T1 PE=3 SV=3 ,
VC(470.29977)ALLSCTSHK DYPFHEEF	C299,NA	U,,X;X;	1.69107,,X;X;	1.69107	P15121 Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3 ,
HLNEIDLFHC(470.29977)I DPNDSK	C62,NA,C58,NA	,,X;X;	0.8781,,X;X;	0.8781	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 ,
QVC(464.28596)QLPGLFS YAQHIASIDGR	NA,NA	,,X;X;	1.70384,,X;X;	1.70384	Q9Y6C9 Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 ,
ELDSLNNC(464.28596)LG DAGILQLVESVR	NA,NA	,,X;X;	1.38722,,X;X;	1.38722	P13489 Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 ,
DADADAGGGADGGDGRG GHSC(470.29977)R	NA,NA	U,,X;X;	1.33051,,X;X;	1.33051	Q14657 EKC/KEOPS complex subunit LAGE3 OS=Homo sapiens GN=LAGE3 PE=1 SV=2 ,
VAC(464.28596)AEWQES R	C87,C87,NA	,,X;X;	1.43653,,X;X;	1.43653	O75663 TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 , O75663-2 Isoform 2 of TIP41-like protein OS=Homo sapiens GN=TIPRL ,

TCLPAPC(470.29977)PSSS NISLWNILR	NA,C484,C520,NA,NA	;;X;X;	1.22049;;X;X;	1.22049	Q9H4L5-2 Isoform 1b of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 , Q9H4L5-3 Isoform 1c of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 , Q9H4L5 Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1 , Q9H4L5-4 Isoform 1d of Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 ,
SVM(15.994915)ESSDRC(4 70.29977)ALSSPSLAFTPPI K	M114,C120,NA,NA,NA	;;X;X;	1.88634;;X;X;	1.88634	Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 ,
EFEFSQLPLKVEFLEC(464.2 8596)SAK	C246,NA	;;X;X;	1.0909;;X;X;	1.0909	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
LC(464.28596)PLKDEPWPI HPWEPGSFR	C105,NA,NA,NA,C78,NA,N A	;;X;X;	1.56145;;X;X;	1.56145	E7ETU7 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , H0Y9G6 39S ribosomal protein L3, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , P09001 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 ,
LC(464.28596)PLKDEPWPI HPWEPGSFR	C105,NA,NA,NA,C78,NA,C 78,NA,NA	;;;X;	1.72741;;2.58357;; X;	2.15549	E7ETU7 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , H0Y9G6 39S ribosomal protein L3, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , E9PF06 39S ribosomal protein L3, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL3 PE=1 SV=1 , P09001 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1 ,
EEC(464.28596)PVFTPPG GETLDQVK	C114,NA,C55,NA,NA	;;X;X;	1.41221;;X;X;	1.41221	Q9NQ88 Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 , A0A0U1RQD1 Chromosome 12 open reading frame 5, isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 ,
LSAPGC(464.28596)WAAC TNFSR	NA,NA,NA	;;X;X;	1.53078;;X;X;	1.53078	Q04941 Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1 , Q04941-2 Isoform 2 of Proteolipid protein 2 OS=Homo sapiens GN=PLP2 ,
SIPLEC(464.28596)PLSSPK	NA,NA,NA	;;X;X;	2.18902;;X;X;	2.18902	Q92667 A-kinase anchor protein 1, mitochondrial OS=Homo sapiens GN=AKAP1 PE=1 SV=1 ,
EQNYC(464.28596)ESR	C160,NA,NA	;;X;X;	1.48852;;X;X;	1.48852	Q7L5D6 Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1 , Q7L5D6-2 Isoform 2 of Golgi

					to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 ,
LADQC(464.28596)TGLQG FLVFHSGGGTSGSFTSLM ER	C129,NA,NA,NA	,,X;X;	1.46441,,X;X;	1.46441	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha- 1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
GLDYEGGGC(470.29977)R	C691,NA,NA	,,,X;	1.43086,,1.53004,, X;	1.48045	O60568 Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 ,
VM(15.994915)TIAPGLFG TPLLTSLPEKVC(464.28596)NFLASQVPFPSR	NA,NA	U,,X;X;	1.42235,,X;X;	1.42235	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
VM(15.994915)TIAPGLFG TPLLTSLPEKVC(464.28596)NFLASQVPFPSR	NA,NA	U,,X;X;	1.47636,,X;X;	1.47636	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
INDALSC(464.28596)EYEC R	NA,NA,NA	,,X;X;	0.87187,,X;X;	0.87187	Q52LJ0 Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 , Q52LJ0-2 Isoform 2 of Protein FAM98B OS=Homo sapiens GN=FAM98B ,
C(470.29977)PEALFQPSFL GM(15.994915)ESCGIHET TFNSIMK	NA,NA,NA	,,,X;X;	1.52566,1.54384,,X ;X;	1.53475	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
M(15.994915)DVLGTVGSC (464.28596)GAPNFR	NA,NA	U,,X;X;	1.14611,,X;X;	1.14611	Q9ULE6 Paladin OS=Homo sapiens GN=PALD1 PE=1 SV=3 ,
LDC(464.28596)NIEIQNAI ELTKPQYLSM(15.994915)I DLLESVDYMVR	NA,C279,M298,NA,C322, M341,NA	,,,X;X;	1.7967,2.03456,,X; X;	1.91563	Q709C8-3 Isoform 3 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C , Q709C8-4 Isoform 4 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C , Q709C8 Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1 , Q709C8-2 Isoform 2 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C ,
GC(470.29977)IVDANLSVL NLVIVK	NA,NA	,,X;X;	1.52549,,X;X;	1.52549	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
YWLC(464.28596)AATGPS IK	NA,NA	,,,X;	1.6675,,1.60735,,X;	1.637425	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
LQGINC(470.29977)GPDF TPSFANLGR	NA,NA,NA,C662,C575,C46 6,NA,NA,NA,NA,NA,NA	,,X;X;	1.38457,,X;X;	1.38457	Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 , Q04637-3

					Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 , Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , E7EUV4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 , Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 , Q04637-7 Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 ,
ALSAVHSPTFCQLAC(470.29977)GQDGQLK	NA,C255,NA,C272,NA	;;X;X;	1.27575;;X;X;	1.27575	Q8IY67 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 , Q8IY67-2 Isoform 2 of Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 , A0A087WZ13 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 , E9PAU2 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 ,
YC(470.29977)FPNYVGRP K	C34,C34,NA	;;X;X;	1.08758;;X;X;	1.08758	P61163 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 , R4GMT0 Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 ,
NLVQC(470.29977)GDFPH LLVYGPSGAGKK	NA,C32,NA	;;X;X;	2.08313;;X;X;	2.08313	P40938 Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2 , P40938-2 Isoform 2 of Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 ,
SQAPC(470.29977)ANKDE ADLSSK	C300,NA,NA	;;X;;;	1.27658;;X;1.30644;;	1.29151	Q96SK2-2 Isoform 2 of Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 , Q96SK2 Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 ,
QC(464.28596)EGITSPEGS	NA,NA,NA,NA	;;X;X;	1.68531;;X;X;	1.68531	Q9Y570-4 Isoform 4 of Protein phosphatase methylesterase

K					1 OS=Homo sapiens GN=PPME1 , Q9Y570-2 Isoform 2 of Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 , Q9Y570 Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 ,
IIPLEGLQLPSPTATSQLPL ESDAVEC(464.28596) LNY QHYKGSDFDCELR	NA,NA,NA	,,X;X;	1.3917,,X;X;	1.3917	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
LVVPATQC(464.28596)GS LIGK	C109,NA	U,U,,U,,X;	1.41248,2.07875,,1. 37871,,X;	1.41248	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
C(464.28596)M(15.99491 5)QLTDFILK	NA,C54,M55,NA	,,,,X;	1.47895,,1.35283,, X;	1.41589	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 , P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 ,
EKLNLS(464.28596)IHSP VVNELM(15.994915)R	NA,NA	U,,X;X;	1.43222,,X;X;	1.43222	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
ATILDLS(464.28596)NK	NA,NA	U,,X;X;	1.16505,,X;X;	1.16505	Q96AG4 Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRR59 PE=1 SV=1 ,
ECPSDEC(464.28596)GAG VFMASHFDR	C126,NA	U,,X;X;	1.70773,,X;X;	1.70773	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
C(464.28596)M(15.99491 5)QLTDFILK	NA,C54,M55,NA	,,X;X;	1.73225,,X;X;	1.73225	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 , P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 ,
C(470.29977)PQPLFKVGA MAAAPLTIAIQR	NA,NA,NA,NA	,,X;X;	1.74525,,X;X;	1.74525	C9JY47 HERV-H LTR-associating protein 1 OS=Homo sapiens GN=HHLA1 PE=4 SV=2 , C9JL84 HERV-H LTR-associating protein 1 OS=Homo sapiens GN=HHLA1 PE=2 SV=1 , C9JL84-2 Isoform 2 of HERV-H LTR-associating protein 1 OS=Homo sapiens GN=HHLA1 ,
C(470.29977)SFDVVKR	C169,NA	U,,X;X;	1.70692,,X;X;	1.70692	Q9Y678 Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 ,
QPAIMPGQSYGLEDGSC(4 64.28596)SYK	NA,NA,NA	,,X,,,;	1.5024,,X;1.35105,,	1.426725	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
TTTPNM(15.994915)NPAI NYQPQSSSVPC(464.2859 6)QR	M292,C308,NA	U,,X;X;	1.66243,,X;X;	1.66243	Q8WXI9 Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1 ,

TISPEHVIQALESLGFGSYISE VKEVLQEC(470.29977)K	NA,NA	U,,X;X;	0.98578,,X;X;	0.98578	Q01658 Protein Dr1 OS=Homo sapiens GN=DR1 PE=1 SV=1 ,
QPAIMPGQSYGLEDGSC(4 64.28596)SYKDFSES	C89,NA,NA,NA	,,,,,,X;	1.54626,1.57203,1. 96324,2.24121,,1.5 9371,,X;	1.59371	M0QYT0 Uncharacterized protein (Fragment) OS=Homo sapiens PE=1 SV=1 , M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
SC(470.29977)AHDWVYE	NA,NA,NA	,,X;X;	0.84513,,X;X;	0.84513	P22392-2 Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 , Q32Q12 Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=1 SV=1 ,
DC(470.29977)GGAAQLA GPAAEADPLGR	C8,NA,NA,C8,C8,C8,C8,NA	,,X;X;	1.41556,,X;X;	1.41556	Q9Y508 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LNV3 E3 ubiquitin-protein ligase RNF114 (Fragment) OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LNT1 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 , A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 ,
DC(464.28596)DPGEVVK	NA,NA,C133,NA,NA	,,X;X;	1.00109,,X;X;	1.00109	Q9NYK5 39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3 , Q9NYK5-2 Isoform 2 of 39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 ,
SLAQSLYPC(470.29977)SA QQLNEDLR	C80,NA	,,X;X;	1.60322,,X;X;	1.60322	Q6P988 Palmitoleoyl-protein carboxylesterase NOTUM OS=Homo sapiens GN=NOTUM PE=1 SV=2 ,
C(470.29977)EFQDAYVLLS EK	NA,NA,NA	U,U,,U,,U,,	1.45763,1.37683,,1. 54467,,1.73976,,	1.50115	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
FLVHNVKELEVLLM(15.994 915)C(470.29977)NK	M90,C91,M108,C109,M90 ,C91,NA	,,X;X;	1.48767,,X;X;	1.48767	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens

					GN=RPL32 PE=1 SV=1 ,
QATC(470.29977)CIPPMT M(15.994915)SISLSVPESR APGESGPQLAR	C994,M1001,NA	U,,X;X;	0.9528,,X;X;	0.9528	Q5JTC6 APC membrane recruitment protein 1 OS=Homo sapiens GN=AMER1 PE=1 SV=2 ,
C(464.28596)PLIFLPPVSGT ADVFFR	NA,C44,NA,C44,NA,NA,C4 4,NA	,,X;X;	1.88618,,X;X;	1.88618	Q9NZD8 Maspardin OS=Homo sapiens GN=SPG21 PE=1 SV=1 , H0YKM6 Maspardin OS=Homo sapiens GN=SPG21 PE=1 SV=1 , H0YLT5 Maspardin (Fragment) OS=Homo sapiens GN=SPG21 PE=1 SV=7 , H0YLBW1 Maspardin (Fragment) OS=Homo sapiens GN=SPG21 PE=1 SV=7 , H0YKBO Maspardin (Fragment) OS=Homo sapiens GN=SPG21 PE=1 SV=1 , Q9NZD8-2 Isoform 2 of Maspardin OS=Homo sapiens GN=SPG21 , H0YMB7 Maspardin (Fragment) OS=Homo sapiens GN=SPG21 PE=1 SV=1 ,
RGSDELFSTC(470.29977)V TNGPFIM(15.994915)SSN SASAANGNDSK	NA,NA	,,X;X;	6.582,,X;X;	6.582	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
IAVHC(464.28596)TVR	C72,NA,NA,NA	,,,;	1.27799,,1.34411,,1 .21146,,	1.27799	P62913 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 , Q5VVC8 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 , P62913-2 Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 ,
LTISYC(464.28596)R	C82,NA,C82,NA,NA	,,X;X;	0.19528,,X;X;	0.19528	J3KS15 Peptidyl-tRNA hydrolase ICT1, mitochondrial (Fragment) OS=Homo sapiens GN=ICT1 PE=1 SV=1 , Q14197 Peptidyl-tRNA hydrolase ICT1, mitochondrial OS=Homo sapiens GN=ICT1 PE=1 SV=1 ,
VAASC(464.28596)GAIQYI PTELDQVRK	C134,NA	,,X;X;	1.35454,,X;X;	1.35454	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 ,
VDEFPLC(464.28596)GHM (15.994915)VSDEYEQLSSE ALEAAR	C49,M52,C49,M52,NA	,,,;	1.42954,1.28684,,1. 29995,,1.27252,,	1.293395	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
VDEFPLC(464.28596)GHM (15.994915)VSDEYEQLSSE ALEAAR	C49,M52,C49,M52,NA	,,,;	1.43897,,1.28595,,1 .24827,,	1.28595	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
VPAFEGDDGFC(464.28596)VFESNAIAYYSNEELR	C68,NA,NA	,,,X;X;	1.19803,1.76908,1. 22725,,X;X;	1.22725	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,

NNTQVLINC(464.28596)R	C36,C36,C46,NA	;;X;X;	1.31902;;X;X;	1.31902	P62316 Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 , P62316-2 Isoform 2 of Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 , K7ERG4 Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 ,
VSVHC(470.29977)PVFDY VPPELITLFISNIGGNAPSYIY R	C310,NA	U;;X;X;	1.47133;;X;X;	1.47133	P49770 Translation initiation factor eIF-2B subunit beta OS=Homo sapiens GN=EIF2B2 PE=1 SV=3 ,
SC(470.29977)ANPNVGFQ R	NA,NA,C124,NA,NA	;;X;X;	1.96523;;X;X;	1.96523	S4R3M1 Dual-specificity protein phosphatase 22 OS=Homo sapiens GN=DUSP22 PE=1 SV=1 , Q9NRW4 Dual specificity protein phosphatase 22 OS=Homo sapiens GN=DUSP22 PE=1 SV=1 , Q9NRW4-2 Isoform 2 of Dual specificity protein phosphatase 22 OS=Homo sapiens GN=DUSP22 , S4R378 Dual-specificity protein phosphatase 22 OS=Homo sapiens GN=DUSP22 PE=1 SV=1 ,
HTSC(470.29977)SSAGND SKPVQEAPSVAR	C793,C706,NA,NA	;;X;X;	1.63394;;X;X;	1.63394	Q9P246-2 Isoform 2 of Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 , H0Y860 Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=1 , Q9P246 Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=2 ,
DLC(470.29977)FSPGLM(1 5.994915)EASHVVNDVNE AVQLVFRK	NA,NA	,,,,,;	1.36505,1.3296,1.3 1114;;1.23255;;1.20 991;;	1.31114	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 ,
LASSIRNPVHC(464.28596) FDLASLDPR	NA,NA	U;;X;X;	2.14361;;X;X;	2.14361	O43159 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 ,
LSLDGQNIYNAC(470.2997 7)CTLR	NA,NA	;;X;X;	2.89495;;X;X;	2.89495	P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
GVLLYGPPGC(470.29977) GK	C137,NA	;;X;X;	1.31523;;X;X;	1.31523	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 ,
TLC(464.28596)GTPNYIAP EVLSK	C212,NA	U;;X;X;	1.52517;;X;X;	1.52517	P53350 Serine/threonine-protein kinase PLK1 OS=Homo sapiens GN=PLK1 PE=1 SV=1 ,
GLC(464.28596)ESVVEADL VEALEK	C84,NA,NA,NA,NA,NA,NA	;;X;X;	1.15789;;X;X;	1.15789	Q8WVV9-5 Isoform 5 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL , Q8WVV9-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL , C9IYN3 Heterogeneous nuclear ribonucleoprotein L-like

					OS=Homo sapiens GN=HNRNPLL PE=1 SV=2 , D6W592 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRPLL PE=1 SV=1 , Q8WVV9 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 , B7WPG3 Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1 ,
IIPGFM(470.29977)QGG DFTR	C62,C62,C62,NA	;;X;X;	1.45311;;X;X;	1.45311	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
ETC(470.29977)SLWPGQA LSLQVEQLLHHR	NA,NA	;;X;X;	1.253;;X;X;	1.253	P19623 Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 ,
ETC(470.29977)SLWPGQA LSLQVEQLLHHR	NA,NA	;;X;X;	1.84384;;X;X;	1.84384	P19623 Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 ,
LHLDDEYPC(464.28596)SL VGNWNTWYGEQDQAVHL WR	C106,C123,NA	;;X;X;	1.4447;;X;X;	1.4447	Q9BPW8 Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 , H7C2U6 Protein NipSnap homolog 1 (Fragment) OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 ,
ELEVLLMC(464.28596)NK	C91,C109,C91,NA	;;;X;	1.24938,1.68535;;1.61949;;X;	1.61949	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
LPLC(470.29977)SLPGEPG NGPDQQLQR	C75,NA	U;;X;X;	1.30388;;X;X;	1.30388	Q96GX2 Putative ataxin-7-like protein 3B OS=Homo sapiens GN=ATXN7L3B PE=3 SV=2 ,
IAVYSC(470.29977)PFDG M(15.994915)ITETK	C225,M230,NA	;;X;X;	1.37549;;X;X;	1.37549	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 ,
IVGYFVSGC(470.29977)DP SIM(15.994915)GIGPVPAI SGALKK	NA,NA,C287,M292,NA,NA	;;X;X;	2.01486;;X;X;	2.01486	A0A0B4J2A4 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 , P42765 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 ,
NSQWVPTLPNSSHHLDAVP C(470.29977)STTINR	C138,C138,C138,NA,NA,NA,NA,NA,NA	;;X;X;	1.25143;;X;X;	1.25143	Q12824 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 PE=1 SV=2 , Q12824-2

					Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 , G5E975 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, isoform CRA_c OS=Homo sapiens GN=SMARCB1 PE=1 SV=1 ,
LHTAANAATATETTC(464.28596)QDVAATPVAR	C33,NA,NA	U,,X;X;	1.27997,,X;X;	1.27997	Q9NP92 28S ribosomal protein S30, mitochondrial OS=Homo sapiens GN=MRPS30 PE=1 SV=2 ,
NSQWVPTLPNSSHHLDVPC(470.29977)STTINR	C138,C138,C138,NA,NA,NA,NA,NA,NA	,,X,,,;	1.40338,,X;1.4275,,;	1.41544	Q12824 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 PE=1 SV=2 , Q12824-2 Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 , G5E975 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, isoform CRA_c OS=Homo sapiens GN=SMARCB1 PE=1 SV=1 ,
LQDLSSC(464.28596)ITQGK	NA,NA,NA	,,X;X;	1.78655,,X;X;	1.78655	P29590-11 Isoform PML-11 of Protein PML OS=Homo sapiens GN=PML , P29590 Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 ,
C(470.29977)SDNSSYEEPLSPISASSSTR	C205,NA,C205,NA,C711,C346,NA,NA	,,,,X;	1.42638,,1.53838,,X;	1.48238	Q8IXK0-2 Isoform 2 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 , A0A0A0MSI2 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 , Q8IXK0 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 , Q8IXK0-3 Isoform 3 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 , Q8IXK0-4 Isoform 4 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 , B3KPJ4 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 , Q8IXK0-5 Isoform 5 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 ,
ALANSLAC(464.28596)QGK	NA,C393,NA,NA	,,X;X;	1.24823,,X;X;	1.24823	P04075 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 , P04075-2 Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA , J3KPS3 Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=1 SV=1 ,
NAGNC(470.29977)LSPAV	NA,NA,NA	,,X;X;	1.56814,,X;X;	1.56814	O43175 D-3-phosphoglycerate dehydrogenase OS=Homo

IVGLLK					sapiens GN=PHGDH PE=1 SV=4 , Q5SZU1 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 ,
TSSVSNPQDSVGSPC(464.28596)SR	NA,NA,C108,NA,NA	;;X;X;	1.74934;;X;X;	1.74934	P49023 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3 , F5GZ78 Paxillin OS=Homo sapiens GN=PXN PE=1 SV=1 , P49023-2 Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN , P49023-3 Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN ,
NAGNC(470.29977)LSPAV IVGLLK	NA,NA,NA	;;X;X;	1.50497;;X;X;	1.50497	O43175 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 , Q5SZU1 D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1 ,
SSIINSLKQEQM(15.994915)C(470.29977)NVGVSMG LTR	M267,C268,M267,C268,NA	;;X;X;	1.80187;;X;X;	1.80187	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
AEGKVESDFFC(470.29977)QLGHFNLLLEDYPK	C97,C73,NA,C73,NA,NA	;;X;X;	2.21688;;X;X;	2.21688	O15550 Lysine-specific demethylase 6A OS=Homo sapiens GN=KDM6A PE=1 SV=2 , A0A087X0R0 Lysine-specific demethylase 6A OS=Homo sapiens GN=KDM6A PE=1 SV=1 , F8W8R6 Lysine-specific demethylase 6A OS=Homo sapiens GN=KDM6A PE=1 SV=2 , F5H6S1 Lysine-specific demethylase 6A OS=Homo sapiens GN=KDM6A PE=1 SV=2 , F5H5V6 Lysine-specific demethylase 6A OS=Homo sapiens GN=KDM6A PE=1 SV=2 ,
GGNAVVDGC(470.29977)GK	NA,NA,NA	;;X;X;	1.53675;;X;X;	1.53675	P48506 Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 , E1CEI4 Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=1 ,
YDNSLKIISNASC(470.29977)TTNCLAPLAK	C152,NA	;;X;X;	1.40689;;X;X;	1.40689	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
VC(464.28596)TLAIIDPGD SDIIR	C92,C92,NA	;;;X;X;	1.56282,1.56994,1.45172;;X;X;	1.56282	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 , E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 ,
VC(464.28596)TLAIIDPGD SDIIR	C92,C92,NA	;;X;X;	2.14759;;X;X;	2.14759	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 , E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 ,

LECEPNC(464.28596)R	NA,NA	,,;X;	1.27702,,1.24914,,X;	1.26308	Q969Q0 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3 ,
LLPAITILGC(464.28596)R	NA,NA,NA	,;X;X;	1.54293,,;X;X;	1.54293	Q96IJ6 Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1 , Q96IJ6-2 Isoform 2 of Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA ,
ILGNTFGM(15.994915)C(470.29977)VLQDFEALTPNLAR	M120,C121,NA,NA	,;X;X;	1.62592,,;X;X;	1.62592	E9PMU0 RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=1 , Q9H0A0 RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=2 ,
VELPTC(470.29977)MYR	NA,NA	,;X;X;	1.77375,,;X;X;	1.77375	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 ,
QVLMGPYNPDTC(464.28596)PEVGFFDVLGNDR	NA,NA	U,,U,,U,,	1.44833,,1.53629,,1.49641,,	1.49641	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 ,
VIGSGC(470.29977)NLDSAR	C192,NA,NA,NA	,,;X;	1.65759,2.12715,,1.61878,,X;	1.65759	P00338-3 Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA , P07195 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 , P00338 L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 ,
LGPGRPLPTFPTSEC(464.28596)TSDVEPDTR	C73,NA,NA	,;X;X;	1.83231,,;X;X;	1.83231	Q8TDD1 ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 , Q8TDD1-2 Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 ,
AFAFVTFADDQIAQSLC(464.28596)GEDLIK	NA,C244,C244,C244,NA,NA,NA	,,;X;X;	1.54039,1.37565,,X;X;	1.45802	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
LHM(15.994915)TIFSQSVSPC(464.28596)GK	NA,NA	,;X;X;	1.39811,,;X;X;	1.39811	Q86W42 THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1 ,
AFAFVTFADDQIAQSLC(464.28596)GEDLIK	NA,C244,C244,C244,NA,NA,NA	,,;X;,,	1.11983,1.04302,1.34503,,X;1.563,,	1.23243	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,

					B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
QLFALSC(464.28596)TAEE QGVLPDDLSGVIR	C75,NA,NA	;;X;X;	1.45816;;X;X;	1.45816	P04899 Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 , P04899-4 Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 ,
SLPSAVYC(464.28596)IED K	C674,NA	U;;U;;X;	1.73632;;2.79277;;X;	2.264545	O43290 U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 ,
SGEFPVSDYFSLSGSC(470.29977)PSSPLPSPAPSVAGS VASSSGSLR	C498,NA	;;X;X;	1.56741;;X;X;	1.56741	Q5SNT2 Transmembrane protein 201 OS=Homo sapiens GN=TMEM201 PE=1 SV=1 ,
NAFAC(470.29977)FDEEA TGTIQEDYLR	NA,NA,NA,NA	;;X;X;	1.27056;;X;X;	1.27056	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 , J3QRS3 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 , O14950 Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 ,
C(470.29977)HIDLSGIVEE VK	NA,NA,C244,NA,NA	;;X;X;	4.44514;;X;X;	4.44514	Q6KB66-2 Isoform 2 of Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 , Q6KB66 Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2 ,
VSLDPELEEALTSASDTELC(470.29977)DLAAILGM(15.994915)HNLITNTK	C132,M140,NA	U;;U;;U;;	1.2115;;1.13134;;1.17062;;	1.17062	Q9NYL9 Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 ,
SPQPVC(464.28596)SPAG SEGTPK	C279,NA	;;X;X;	2.03474;;X;X;	2.03474	Q6KC79 Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2 ,
LSGGLGAGSC(470.29977) R	NA,C40,NA,NA,NA,NA	;;X;X;	2.16598;;X;X;	2.16598	contaminant_KERATIN12 no description, Q04695 Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 , K7EPJ9 Keratin, type I cytoskeletal 17 (Fragment) OS=Homo sapiens GN=KRT17 PE=1 SV=1 ,
YGINTTDIFQTVDLWEGKN M(15.994915)AC(464.28596)VQR	M122,C124,NA,NA,NA	;;X;X;	1.56243;;X;X;	1.56243	P37802 Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 , P37802-2 Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2 , X6RJP6 Transgelin-2 (Fragment) OS=Homo sapiens GN=TAGLN2 PE=1 SV=1 ,
GVSASAVPFTPSSPLLSC(47	NA,NA,NA,NA	;;X;X;	0.98527;;X;X;	0.98527	Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo

0.29977)SQEGSR					sapiens GN=GIT1 PE=1 SV=2 , J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 , Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 ,
LNISFPATGC(464.28596)QK	NA,NA	,,,,;	1.47302,,1.3491,,1.3052,,	1.3491	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
LNISFPATGC(464.28596)QK	NA,NA	,,,,;	1.43815,1.76842,,1.33438,,1.28064,,	1.386265	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
LDSLGLCSVSC(464.28596)ALEFIPNSK	C256,NA	U,,U,,X;	1.20895,,1.54116,,X;	1.375055	Q9BSH4 Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1 ,
LTFSLGGSDNFKHLNEIDLFHC(470.29977)IDPNDSK	C62,NA,C58,NA	,,X;X;	1.48509,,X;X;	1.48509	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 ,
AAAPAPEEEMDEC(470.29977)EQALAAEPK	C266,NA,NA	,,,,;	1.24425,1.73174,,1.31141,,1.17868,,	1.27783	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
GC(470.29977)WDSIHVVEVQEK	NA,NA,C176,NA,NA,C135,NA,NA,NA,NA	,,X;;	1.37466,,X;1.22495,,	1.299805	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 , P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB , B1AK88 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK87 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 ,
VNPLGGAVALGHPLGC(470.29977)TGAR	NA,NA,NA	,,X;X;	2.38793,,X;X;	2.38793	P09110 3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 ,
VVVWGECDSTDDC(470.29977)IEHNIGPCSSVLVDVGGA VTAVSVCPVLHPSQR	C635,NA,C679,NA	,,X;X;	3.89336,,X;X;	3.89336	Q6IA86 Elongator complex protein 2 OS=Homo sapiens GN=ELP2 PE=1 SV=2 , Q6IA86-6 Isoform 6 of Elongator complex protein 2 OS=Homo sapiens GN=ELP2 , Q6IA86-3 Isoform 3 of Elongator complex protein 2 OS=Homo sapiens GN=ELP2 ,
NM(15.994915)GLSPPASS	NA,NA	,,X;X;	1.0418,,X;X;	1.0418	Q9HC52 Chromobox protein homolog 8 OS=Homo sapiens

TSTSSTC(470.29977)R					GN=CBX8 PE=1 SV=3 ,
AATMSAVEAATC(464.28596)R	NA,C266,NA,C129,NA	;;X;X;	0.90415;;X;X;	0.90415	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 , Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 , Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL , B5MD87 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2 ,
KAAAPAPEEEM(15.994915)DEC(464.28596)EQALAAEPK	M263,C266,NA,NA	;;X;;	1.20563;;X;1.14844;;	1.177035	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
SWC(470.29977)PDCVQAEPVVR	NA,NA	;;;X;X;	1.45861,1.35549;;X;X;	1.40705	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 ,
SWC(470.29977)PDCVQAEPVVR	NA,NA	;;;X;X;	1.4289,1.70616;;X;X;	1.56753	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 ,
C(464.28596)AVSDVEM(15.994915)QEHYDEFFEEVFTEMEK	NA,NA,C67,M74,NA	;;;X;X;	1.40209,1.40209;;X;X;	1.40209	Q01081 Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3 , P0DN76 Splicing factor U2AF 35 kDa subunit-like protein OS=Homo sapiens GN=U2AF1L5 PE=3 SV=1 , Q01081-2 Isoform 2 of Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 ,
TFVDFFSQC(470.29977)LH EEYR	NA,NA	U;;U;X;	1.3452;;1.53102;;X;	1.43811	Q53GQ0 Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 ,
SLTGC(464.28596)WSAGTISK	NA,NA,C49,NA,NA	;;X;X;	1.50575;;X;X;	1.50575	Q6KB66-2 Isoform 2 of Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 , Q6KB66 Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2 ,
LLQPPKGVLLYGPPGC(464.28596)GK	C137,NA	;;X;X;	1.70833;;X;X;	1.70833	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 ,
TLETANC(470.29977)M(15.994915)SSQTK	C96,M97,NA,NA,NA,NA	;;X;X;	1.52051;;X;X;	1.52051	P50416-2 Isoform 2 of Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A , P50416 Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 ,
VPPFPLPLEPC(464.28596)TQEFLWR	C42,NA,NA	;;X;X;	1.44611;;X;X;	1.44611	Q12789 General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 , Q12789-3 Isoform 2 of General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 ,

AYHEQLTVAEITNAC(464.28596)FEPANQM(15.994915)VK	C295,M302,NA	,,;,;	1.34666,1.39169,;0.96404,;1.14611,;	1.246385	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
SGDAAIVDM(15.994915)VPGKPMC(464.28596)VESFSDYPPLGR	NA,NA	,;X;X;	1.36196,;X;X;	1.36196	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
AYHEQLTVAEITNAC(464.28596)FEPANQM(15.994915)VK	C295,M302,C365,M372,NA	,,;,;X;	1.22817,1.5866,1.43262,;1.47889,;X;	1.455755	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 ,
ALIVGHC(464.28596)MPGPR	NA,NA,NA	U,;X;X;	1.46406,;X;X;	1.46406	Q6P1L8 39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 ,
SGDAAIVDM(15.994915)VPGKPMC(464.28596)VESFSDYPPLGR	NA,NA,NA	,,;,;X;	1.40769,1.4103,;1.29358,;X;	1.40769	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
TC(470.29977)YPLESRPSLS LGTITDEEM(15.994915)K	C1921,M1940,NA	,;X;X;	1.62314,;X;X;	1.62314	A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 ,
C(464.28596)M(15.994915)TNTPVVVR	C120,M121,NA,C120,M121,NA,NA,NA,NA	,,;,;X;	1.59785,;1.75934,;X;	1.678595	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 ,
SGDAAIVDMVPGKPM(15.994915)C(470.29977)VESFSDYPPLGR	NA,NA	,;X;X;	1.42613,;X;X;	1.42613	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
SGDAAIVDMVPGKPM(15.994915)C(470.29977)VESFSDYPPLGR	NA,NA	,;X;X;	1.66096,;X;X;	1.66096	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
C(470.29977)FLAQPVTLID IYTHWQQTSELGR	NA,NA,NA,NA,NA,NA,C38,C38,C38,NA	,;X;X;	1.18646,;X;X;	1.18646	E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 , Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-6 Isoform 6 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 , Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-3 Isoform 3 of Treacle protein

					OS=Homo sapiens GN=TCOF1 , Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 , J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 ,
SLTLLPHGTPNSASPC(464.28596)SQR	NA,NA	U,,X;X;	0.75885,,X;X;	0.75885	Q9BXB5 Oxysterol-binding protein-related protein 10 OS=Homo sapiens GN=OSBPL10 PE=1 SV=2 ,
ELEVLLM(15.994915)C(470.29977)NK	M90,C91,M108,C109,M90,C91,NA	,,,,X;	1.60172,1.76874,,1.12235,,X;	1.60172	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
ALADAQIPYSAVDQACVGYVFGDSTC(470.29977)GQR	NA,NA	,,X;X;	2.04658,,X;X;	2.04658	P22307 Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 ,
VSDTVVEPYNATLSVHQLVE NTDETYC(464.28596)IDNE ALYDIC(464.28596)FR	C201,C211,C201,C211,NA,C183,C193,C201,C211,NA	,,X;X;	1.52594,,X;X;	1.52594	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
VSDTVVEPYNATLSVHQLVE NTDETYC(464.28596)IDNE ALYDIC(464.28596)FR	C201,C211,C201,C211,NA,C183,C193,C201,C211,NA	,,,,X;X;	1.66942,1.5818,1.82714,,X;X;	1.66942	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
VGVGTC(464.28596)GIAD KPMTQYQDTSK	C214,NA	U,,X;X;	1.12495,,X;X;	1.12495	O75940 Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1 ,
YLAEVAC(470.29977)GDDR	C134,NA	,,X;X;	0.89818,,X;X;	0.89818	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 ,
IFVGNVSAAC(470.29977)TSQELR	C90,NA	,,X;X;	1.02501,,X;X;	1.02501	Q96PK6-5 Isoform 5 of RNA-binding protein 14 OS=Homo sapiens GN=RBM14 ,
SGAELALDYLC(464.28596)R	C75,NA,C107,C92,NA	,,X;X;	1.40379,,X;X;	1.40379	H7C0T1 Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=1 SV=1 , Q9BRJ6 Uncharacterized protein C7orf50 OS=Homo sapiens

					GN=C7orf50 PE=1 SV=1 , C9JQV0 Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=1 SV=1 , H7C2R9 Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=1 SV=1 ,
C(470.29977)MQLTDFILK	NA,C54,NA	,,X;X;	1.52197,,X;X;	1.52197	E7EPB3 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=1 , P50914 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4 ,
ALAPLLAFVTKPNSALESC(464.28596)SFAR	NA,NA	U,,X;X;	1.33086,,X;X;	1.33086	P46060 Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 ,
NIC(470.29977)FTVWDVG GQDK	NA,NA	,,X;X;	1.51323,,X;X;	1.51323	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 ,
FC(464.28596)PAGVYEFVP VEQGDGFR	NA,NA,C514,NA,NA	,,X;X;	0.74371,,X;X;	0.74371	Q16134 Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 , Q16134-3 Isoform 2 of Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH ,
VCETDGC(464.28596)SSE AK	C14,C10,C14,NA	,,,,,;	1.64221,,1.45853,,1.27577,,	1.45853	D6RF24 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=1 , H0Y9L0 Methionine aminopeptidase 1 (Fragment) OS=Homo sapiens GN=METAP1 PE=1 SV=1 , P53582 Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=2 ,
RGPC(464.28596)IYNEDN GIHK	C208,NA	,,X;X;	1.40158,,X;X;	1.40158	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
SDLYEVIQSTLDGLLC(470.29977)TSLPVWLENHTALTVM(15.994915)ASK	NA,NA	,,X;X;	1.548,,X;X;	1.548	P22102 Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 ,
IHMGSC(470.29977)AENT AK	NA,NA,NA	U,,U;X;	1.43424,,1.36572,,X;	1.39998	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
FDPTQFQDC(464.28596)II QGLTETGTDLEAVAK	NA,C39,C35,NA,NA,C35,NA,C39,C35,NA	,,,,,,;	1.29035,1.2243,0.82995,1.40883,,1.0779,,0.88291,,	1.1511	C9JWF5 Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=7 , C9JV57 Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=1 , Q7L1Q6 Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 , C9IZ80 Basic leucine zipper and W2 domain-

					containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=1 , C9J188 Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=7 , C9JFN4 Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=1 , Q7L1Q6-3 Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 , Q7L1Q6-4 Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 , Q7L1Q6-2 Isoform 2 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 ,
IC(464.28596)PVEFNPNFV AR	NA,NA,NA	,,,X;	1.1733,,1.06,,X;	1.11665	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 , F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 ,
GLFGAGGAAGGC(464.28596)GVAGAGADGYGYLAPP K	NA,NA	U,,X;X;	2.24492,,X;X;	2.24492	P58012 Forkhead box protein L2 OS=Homo sapiens GN=FOX2 PE=1 SV=1 ,
IC(464.28596)PVEFNPNFV AR	NA,NA,NA	,,,X;	1.28091,,1.08676,,X;	1.183835	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 , F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 ,
EM(15.994915)FPYEASTP TGISASC(470.29977)R	M308,C323,NA,NA,NA,NA ,NA,NA	,,,X;	1.5275,,1.49092,,X;	1.50921	G5E972 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 , P42167 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 , P42167-2 Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO ,
LVSSPCC(470.29977)IVTST YGTANM(15.994915)ER	C590,M602,NA	U,,X;X;	1.41354,,X;X;	1.41354	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 ,
AALEALGSC(464.28596)LN NK	NA,NA,C70,NA,NA	,,X;X;	1.30076,,X;X;	1.30076	P34897 Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 , P34897-3 Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 ,
LGNNC(464.28596)VFAPA	C58,NA	,,X;X;	1.09079,,X;X;	1.09079	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2

DVTSEKDVQTALALAK					OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
FHSNTWKNTTFC(464.28596)K	NA,NA	U,,X;X;	1.15776,,X;X;	1.15776	H7C5E0 Uncharacterized protein C3orf30 (Fragment) OS=Homo sapiens GN=C3orf30 PE=1 SV=1 ,
YATSCYSCC(470.29977)PR	C173,NA,NA	,,,,X;	2.08197,1.61316,,1.66481,,X;	1.66481	Q13057-2 Isoform 2 of Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY , Q13057 Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4 ,
ESFIIIEQSFLLC(470.29977)EDLLYGRM(15.994915)SFR	C49,M57,NA,NA,NA	,,X;X;	5.62254,,X;X;	5.62254	H3BNT4 M-phase phosphoprotein 6 OS=Homo sapiens GN=MPHOSPH6 PE=1 SV=1 , Q99547 M-phase phosphoprotein 6 OS=Homo sapiens GN=MPHOSPH6 PE=1 SV=2 , H3BU96 M-phase phosphoprotein 6 OS=Homo sapiens GN=MPHOSPH6 PE=1 SV=1 ,
APPWVPAM(15.994915)GFTLAPSLGC(470.29977)FVGSR	M9,C19,NA,NA	,,,,;	2.43381,,2.52879,,2.55327,,	2.52879	B1AH87 Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=1 SV=1 , P30536 Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 ,
DVQIGDIVTVGEC(470.29977)RPLSK	C131,NA	,,,,X;	1.45503,1.44872,1.49887,,1.37672,,X;	1.451875	P62280 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3 ,
AAC(464.28596)LPLPGYR	NA,NA	,,X;X;	0.62917,,X;X;	0.62917	P13796 Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 ,
IIPGFMC(464.28596)QGGDFTR	C62,C62,C62,NA	,,X;X;	1.2383,,X;X;	1.2383	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
AHSNPDFLPVDNC(464.28596)LQSVLGQR	C703,NA,NA	,,X;X;	1.4679,,X;X;	1.4679	Q5VSL9-2 Isoform 2 of Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 , Q5VSL9 Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 PE=1 SV=1 ,
IIPGFMC(464.28596)QGGDFTR	C62,C62,C62,NA	,,X;X;	1.45311,,X;X;	1.45311	F8WE65 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , C9J5S7 Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=1 SV=1 , P62937 Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 ,
EITSLDTENIDEILNNADVALVNFYADWC(470.29977)R	C58,NA	U,U,,X;X;	1.17138,1.43746,,X;X;	1.30442	Q9BS26 Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 ,
EITSLDTENIDEILNNADVAL	C58,NA	U,U,,U,,X;	1.3721,1.40169,,1.4	1.40169	Q9BS26 Endoplasmic reticulum resident protein 44

VNFYADWC(470.29977)R			5585,;X;		OS=Homo sapiens GN=ERP44 PE=1 SV=1 ,
FSPNSSNP IIVSC(464.28596)GWDK	NA,NA	,;X;X;	1.60031,;X;X;	1.60031	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
GWSGNSWGGISLGPPDPG PC(464.28596)GETYEDFDT R	NA,NA,NA	,;X;X;	2.20027,;X;X;	2.20027	P82675 28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5 PE=1 SV=2 ,
ILQDDIESLM(15.994915)P IVYTPTVGLAC(470.29977) SQYGHIFR	M108,C120,NA,NA	,;X;X;	1.84654,;X;X;	1.84654	P23368 NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1 ,
C(470.29977)TKEEHLCTQR	NA,C226,C205,C201,C210, NA	,;X;X;	1.11254,;X;X;	1.11254	J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , P06753-2 Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 , A0A087WWU8 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , Q5VU61 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 , Q5HYB6 Epididymis luminal protein 189 OS=Homo sapiens GN=DKFZp686J1372 PE=1 SV=1 ,
LQGINC(464.28596)GPDF TPSFANLGR	NA,NA,NA,C662,C575,C46 6,NA,NA,NA,NA,NA,NA	,;X;X;	1.3827,;X;X;	1.3827	Q04637 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 , Q04637-3 Isoform B of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , E9PGM1 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 , Q04637-8 Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , Q04637-4 Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , Q04637-6 Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , E7EUV4 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 , Q04637-5 Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , Q04637-9 Isoform 9 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 , E7EX73 Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 , Q04637-7 Isoform 7 of Eukaryotic

					translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 ,
KC(464.28596)GETAFIAPQ CEM(15.994915)PIEWVVC R	C81,M93,NA	,;X;X;	1.25979,,X;X;	1.25979	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
QGEYGLASIC(464.28596)N GGGGASAMLIQKL	NA,NA,NA	U,U,,X;X;	1.44471,1.81041,,X ;X;	1.62756	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
M(15.994915)PC(464.285 96)QLHQVIVAR	M638,C640,NA	,;X;X;	1.61108,,X;X;	1.61108	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 ,
VC(464.28596)EEIAIIPSK	C35,NA	,;X;X;	1.38737,,X;X;	1.38737	P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 ,
SC(464.28596)GHQTSASSL K	NA,NA	U,,X;X;	1.4563,,X;X;	1.4563	Q9HB90 Ras-related GTP-binding protein C OS=Homo sapiens GN=RRAGC PE=1 SV=1 ,
VVNSETPVVVFHAQWC(4 64.28596)GPCK	C90,NA,C90,NA,NA	,,;,;,;	1.44923,1.25175,,1. 26488,,1.56937,,;	1.357055	Q99757 Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=2 , F8WDN2 Thioredoxin, mitochondrial OS=Homo sapiens GN=TXN2 PE=1 SV=1 ,
NHLLPDIVTC(464.28596)V QSSR	C184,NA	U,U,,X;U,,;	1.45399,1.37047,,X ;1.35286,,;	1.37047	Q9BSD7 Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 ,
NMMAAC(470.29977)DPR	C303,C650,C303,NA	,,;,;,X;	1.53692,1.53692,,0. 92854,0.92854,,X;	1.23273	A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
TLC(464.28596)LTC(470.2 9977)IVSGDPTPEISWLKND QPVTFLDR	NA,NA,NA	,;X;X;	1.40468,,X;X;	1.40468	Q5VTT5-3 Isoform 3 of Myomesin-3 OS=Homo sapiens GN=MYOM3 , Q5VTT5 Myomesin-3 OS=Homo sapiens GN=MYOM3 PE=2 SV=1 ,
WTQTLSELDLAVPFC(470.2 9977)VNFR	C188,NA	U,U,,X;X;	1.66962,1.14014,,X ;X;	1.40488	Q9Y266 Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 ,
VDEFPLC(470.29977)GHM VSDEYEQLSSEALEAAR	C49,NA	,;X;X;	1.3691,,X;X;	1.3691	P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
TIC(470.29977)SHVQNMI K	NA,C74,NA	,;X;X;	0.93134,,X;X;	0.93134	D6RAN4 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=7 , P32969 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 ,
VFAEC(464.28596)NDESF WFR	C38,C38,NA,C38,C38,C38, C38,NA,C38,NA	,;X;X;	0.53203,,X;X;	0.53203	Q9NX40-2 Isoform 2 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 , D6RIT9 OCIA domain- containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 , D6RG39 OCIA domain-containing

					protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 , D6RA54 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 , Q9NX40-4 Isoform 4 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 , Q9NX40 OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 , D6RC55 OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 , Q9NX40-3 Isoform 3 of OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 , D6RDI5 OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=1 SV=1 ,
VDEFPLC(470.29977)GHM VSDEYEQLSSEALEAAR	C49,NA	,,;X;X;	1.54854,1.59212,,X; X;	1.57033	P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
TATAVAHC(470.29977)K	C25,C25,NA	,,,,,;	1.39699,1.47278,,1. 34633,,1.23957,,	1.37166	M0R210 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1 , P62249 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 ,
ADIIVSELLGSFADNELSPEC(464.28596)LDGAQHFLKD DGVSIPEYTSFLAPISSSK	NA,C388,NA,NA,NA	,;X;X;	1.49166,,X;X;	1.49166	O14744 Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4 , O14744-3 Isoform 3 of Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 , O14744-5 Isoform 5 of Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 , O14744-2 Isoform 2 of Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 ,
M(15.994915)LQPC(470.29977)GPPADKPEEN	NA,NA	U,,X;X;	1.44556,,X;X;	1.44556	Q9BWJ5 Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1 ,
LM(15.994915)HLFTSGDC(464.28596)K	M83,C91,NA	U,,X;X;	1.19938,,X;X;	1.19938	Q8WXD5 Gem-associated protein 6 OS=Homo sapiens GN=GEMIN6 PE=1 SV=1 ,
DLAGC(464.28596)IHGLSN VK	C418,NA,NA,NA,NA	,;X;X;	2.22914,,X;X;	2.22914	P48735 Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 , P48735-2 Isoform 2 of Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 ,
STPYEC(470.29977)GFDP M(15.994915)SPAR	C39,M44,NA	U,,U;X;	2.15327,,1.87668,, X;	2.014975	P03897 NADH-ubiquinone oxidoreductase chain 3 OS=Homo sapiens GN=MT-ND3 PE=1 SV=1 ,
NPLC(464.28596)PLGQTV QSEIFR	C115,NA	U,,X;X;	2.07567,,X;X;	2.07567	Q9Y5R8 Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 ,
FHADSV(464.28596)K	NA,NA	U,,X;U,,	1.64755,,X;1.21941	1.43348	Q9BW61 DET1- and DDB1-associated protein 1 OS=Homo

			;;		sapiens GN=DDA1 PE=1 SV=1 ,
IKSGEEDFESLASQFSDC(470.29977)SSAK	NA,C113,NA,NA	,,,,;	1.38924,1.46656,1.37611,;1.27441,;1.10802,;	1.37611	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 , K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 , Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 ,
TSC(470.29977)GSPNYAA PEVISGR	C200,NA,C200,C174,NA	;;X;X;	2.45698,;X;X;	2.45698	Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 , A0A087WXX9 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=1 , Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 , P54646 5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Homo sapiens GN=PRKAA2 PE=1 SV=2 ,
C(470.29977)WDPSPQAYF TLPR	NA,C354,C348,NA	;;X;X;	1.28765,;X;X;	1.28765	I3L0Z8 Segment polarity protein dishevelled homolog DVL-2 (Fragment) OS=Homo sapiens GN=DVL2 PE=1 SV=1 , O14641 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 , I3L2N2 Segment polarity protein dishevelled homolog DVL-2 OS=Homo sapiens GN=DVL2 PE=1 SV=1 ,
QLKEDLSSIILLSEEDLQMLV DAPC(470.29977)SDLAQE LR	C154,C154,NA	;;X;X;	1.15749,;X;X;	1.15749	O00273-2 Isoform DFF35 of DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA , O00273 DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1 ,
IISNASC(470.29977)TTNCL APLAK	C152,NA	,,,,;	1.35851,1.40638,;1.24796,1.37926,;1.13228,;	1.35851	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
IISNASC(470.29977)TTNCL APLAK	C152,NA	,,,,;	1.41671,1.43758,1.49107,;1.37264,1.38967,;1.22513,1.17545,;	1.38967	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
IKADPDGPEAQAEAC(470.29977)SGER	C18,NA	;;X;X;	1.49918,;2.00849,;X;	1.753835	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
VAASC(470.29977)GAIQYI PTELDQVRK	C134,NA	;;X;X;	1.35454,;X;X;	1.35454	Q7L2H7 Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 ,

TPC(470.29977)NAGTFSQ PEK	C129,C129,NA,NA	,,,X;	1.3387,,1.78752,,X;	1.56311	O43684 Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 , J3QT28 Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=1 SV=1 , O43684-2 Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 ,
YSTGSDSASFHTTPSM(15. 994915)C(470.29977)LNP DLEGPPLEAYTIQGQYAIPQ PDLTK	M216,C217,NA,NA	,,,,X;	1.3958,,1.39789,1.3 2254,,X;	1.3958	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,
SILSPGGSC(470.29977)GPI K	NA,NA,C215,NA,NA	,,X;X;	1.2502,,X;X;	1.2502	P78347 General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 , P78347-4 Isoform 4 of General transcription factor II-I OS=Homo sapiens GN=GTF2I , P78347-3 Isoform 3 of General transcription factor II-I OS=Homo sapiens GN=GTF2I , P78347-2 Isoform 2 of General transcription factor II-I OS=Homo sapiens GN=GTF2I ,
M(15.994915)GVEAVIAL EATPDTPAC(470.29977)V VSLNGNHAVR	NA,NA,NA,NA,NA	,,X;X;	0.71566,,X;X;	0.71566	Q01813-2 Isoform 2 of ATP-dependent 6- phosphofructokinase, platelet type OS=Homo sapiens GN=PFBK , Q01813 ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFBK PE=1 SV=2 ,
SIHLAC(464.28596)TAGIF DAYVPPEGDAR	C80,NA,NA,NA,NA	,,X;X;	1.76395,,X;X;	1.76395	A0A087X2D5 39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=1 , Q9BRJ2 39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=2 ,
AFLDNPGILSELC(464.2859 6)GTLSR	NA,C272,C272,NA	,,X;X;	1.09463,,X;X;	1.09463	B4E1N1 Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=1 , Q6NXX6 Armadillo repeat- containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=2 , Q6NXX6-2 Isoform 2 of Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 ,
NDPPM(15.994915)EAAG FTAQVILNHPGQISAGYAP VLDC(464.28596)HTAHIA K	NA,NA	,,X;X;	1.6698,,X;X;	1.6698	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
PM(15.994915)C(464.285 96)IPPSYADLGK	NA,NA	,,X;X;	1.28384,,X;X;	1.28384	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
VM(15.994915)TIAPGLFG	NA,NA	U,U,,U,,U,,	1.32032,1.47879,,1.	1.455965	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2

TPLLTSLPEKVC(470.29977) NFLASQVPFPSR			67102,,1.43314,;		OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
FQGIKHEC(464.28596)QA NGPEDLNR	C118,NA,NA	,;X;X;	1.06794,,X;X;	1.06794	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN , P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 ,
AHQLVLPPC(464.28596)D VVIK	NA,C279,NA,NA,NA	,;X;X;	0.43873,,X;X;	0.43873	F8W881 Constitutive coactivator of PPAR-gamma-like protein 2 OS=Homo sapiens GN=FAM120C PE=1 SV=2 , Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR- gamma-like protein 1 OS=Homo sapiens GN=FAM120A , Q9NX05 Constitutive coactivator of PPAR-gamma-like protein 2 OS=Homo sapiens GN=FAM120C PE=2 SV=3 , Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 ,
KC(470.29977)PFYAAEQD K	C319,NA,NA,NA	,;X;X;	1.74731,,X;X;	1.74731	A0A087WT44 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=1 , P30519 Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2 , P30519-2 Isoform 2 of Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 ,
LNLSC(464.28596)IHSPVV NELM(15.994915)R	NA,NA	U,,X;X;	1.24184,,X;X;	1.24184	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
LNLSC(464.28596)IHSPVV NELM(15.994915)R	NA,NA	U,,X;U,;	1.86633,,X;1.68031 ,,	1.77332	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
SYC(464.28596)NDQSTGD IK	C106,NA	U,,U,,X;	1.18437,,1.34652,, X;	1.265445	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 ,
VTHLVANC(464.28596)TQ GEK	NA,C221,NA,C221,NA	,;X;X;	1.78571,,X;X;	1.78571	Q9H8V3-4 Isoform 4 of Protein ECT2 OS=Homo sapiens GN=ECT2 , Q9H8V3-3 Isoform 3 of Protein ECT2 OS=Homo sapiens GN=ECT2 , Q9H8V3-2 Isoform 2 of Protein ECT2 OS=Homo sapiens GN=ECT2 , Q9H8V3 Protein ECT2 OS=Homo sapiens GN=ECT2 PE=1 SV=4 ,
KAAAPAPEEEMDEC(470.2 9977)EQALAAEPK	C266,NA,NA	,;X;;	1.19369,,X;1.15839 ,,	1.17604	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
GLPWSC(470.29977)SADE VM(15.994915)R	C22,M28,NA	U,,X;X;	1.97927,,X;X;	1.97927	P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 ,
GFGFVC(470.29977)FSSPE EATK	NA,NA,C339,NA,NA,NA,N A,C339,NA	,;X;X;	0.94684,,X;X;	0.94684	B1ANR0 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC4 PE=1 SV=1 , Q13310 Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1 ,

					Q13310-2 Isoform 2 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 , P11940 Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 , A0A087WTT1 Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1 , Q13310-3 Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 , P11940-2 Isoform 2 of Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 , Q9H361 Polyadenylate-binding protein 3 OS=Homo sapiens GN=PABPC3 PE=1 SV=2 ,
GGGGGPC(470.29977)GF QPASR	C17,NA	U,,X;X;	1.18235,,X;X;	1.18235	Q96QR8 Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3 ,
ISLGLPVGAVINC(470.29977)ADNTGAK	NA,NA	,,X;X;	1.50044,,X;X;	1.50044	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 ,
LGGSLIVAFEGC(470.29977)PV	C146,NA,NA	,,,X;X;	1.39286,1.40791,,X;X;	1.400385	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN , P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 ,
FNNWGGSLSLGHPFGATG C(470.29977)R	C413,NA,C413,NA,NA	,,X;;	1.53599,,X;1.44296 ,;	1.489475	P55084 Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 , P55084-2 Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB ,
FNNWGGSLSLGHPFGATG C(470.29977)R	C413,NA,C413,NA,NA	,,X;X;	2.78507,,X;X;	2.78507	P55084 Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 , P55084-2 Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB ,
LQSGIC(464.28596)HLFR	NA,NA,NA	,,,X;	1.59877,,1.68132,,X;	1.640045	P14868 Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 ,
C(470.29977)MTNTPVVVR	C120,NA,C120,NA,NA,NA,NA	,,X;X;	1.52259,,X;X;	1.52259	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 ,
TFTVLLFC(464.28596)ILM DPQPELWIESNYPQAPWE NITLWC(470.29977)R	C22,C49,NA	U,,X;X;	4.79163,,X;X;	4.79163	Q8N6C5-2 Isoform 2 of Immunoglobulin superfamily member 1 OS=Homo sapiens GN=IGSF1 ,
KGTVLLADNVIC(470.29977)	C173,NA	,,X;X;	1.28174,,X;X;	1.28174	P21964 Catechol O-methyltransferase OS=Homo sapiens

7)PGAPDFLAHVR					GN=COMT PE=1 SV=2 ,
SVAAGC(464.28596)PVLL GKDNPSGPGSR	NA,NA	U,,X;X;	1.17928,,X;X;	1.17928	Q9NQS1 Cell death regulator Aven OS=Homo sapiens GN=AVEN PE=1 SV=1 ,
KGTVLLADNVIC(470.2997 7)PGAPDFLAHVR	C173,NA	,,X;X;	1.14552,,X;X;	1.14552	P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 ,
LC(470.29977)EPEVLNSLE ETYSPPFR	C177,C261,C261,NA,C224, NA,NA,NA,NA,NA,NA,NA	,,X;;;	1.01486,,X;0.78962 ,,	0.90224	H0YJA2 Zinc finger CCCH domain-containing protein 14 (Fragment) OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-5 Isoform 5 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7-3 Isoform 3 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , G3V5I6 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-10 Isoform 10 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , G3V256 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-2 Isoform 2 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7-4 Isoform 4 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7 Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1 , Q6PJT7-9 Isoform 9 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 , Q6PJT7-11 Isoform 11 of Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 ,
VNQAIWLLC(464.28596)T GAR	C155,NA,C155,NA	,,,,X;	1.31227,,1.15141,, X;	1.23184	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
GC(464.28596)SNEPYFGSL TALVCQHSITPLALPCK	NA,NA	,,X;X;	1.04485,,X;X;	1.04485	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
VNQAIWLLC(464.28596)T GAR	C155,NA,C155,NA	,,,,;	1.39978,1.36458,,1. 42364,,1.27043,,	1.38218	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S

					ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
GLPWSC(464.28596)SADE VQR	C22,C22,NA	;;X;X;	1.02571;;X;X;	1.02571	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 ,
GC(464.28596)SNEPYFGSL TALVCQHSITPLALPCK	NA,NA	;;X;X;	1.57806;;X;X;	1.57806	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
GLPWSC(464.28596)SADE VQR	C22,C22,NA	;;X;X;	1.43795;;X;X;	1.43795	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 ,
SQSVSVSGPGPGPGGLC(4 70.29977)PGPNVLLNQNN PPAPQPQHLAR	C222,NA	U;;X;X;	1.25898;;X;X;	1.25898	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 ,
FSAIQC(464.28596)AAAVP R	NA,C98,C98,NA,C98,NA,N A	;;X;X;	1.50075;;X;X;	1.50075	Q15054-3 Isoform 3 of DNA polymerase delta subunit 3 OS=Homo sapiens GN=POLD3 , E9PM91 DNA polymerase delta subunit 3 (Fragment) OS=Homo sapiens GN=POLD3 PE=1 SV=1 , E9PNC0 DNA polymerase delta subunit 3 (Fragment) OS=Homo sapiens GN=POLD3 PE=1 SV=1 , Q15054 DNA polymerase delta subunit 3 OS=Homo sapiens GN=POLD3 PE=1 SV=2 , Q15054-2 Isoform 2 of DNA polymerase delta subunit 3 OS=Homo sapiens GN=POLD3 , E9PRK3 DNA polymerase delta subunit 3 (Fragment) OS=Homo sapiens GN=POLD3 PE=1 SV=1 ,
GLEC(470.29977)SPSTPT M(15.994915)NSYFYK	NA,NA	;;X;X;	2.39938;;X;X;	2.39938	Q08AM6 Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=1 SV=1 ,
SQDC(470.29977)PWYDQ GFC(464.28596)K	C60,C68,C124,C132,NA	;;X;X;	0.02899;;X;X;	0.02899	H9KVA5 Putative cleavage and polyadenylation-specificity factor subunit 4-like protein OS=Homo sapiens GN=CPSF4L PE=4 SV=1 , A6NMK7 Putative cleavage and polyadenylation specificity factor subunit 4-like protein OS=Homo sapiens GN=CPSF4L PE=2 SV=3 ,
GSC(464.28596)STEVEKET QEK	C69,NA	U;;U;;U;;	1.2671;;1.33249;;1. 07064;;	1.2671	O75348 V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 ,
GSC(464.28596)STEVEKET QEK	C69,NA	U;;X;U;;	1.31165;;X;1.2538;;	1.282725	O75348 V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 ,

TVDSQGPTPVC(470.29977)TPTFLER	NA,NA	;;X;X;	1.29567;;X;X;	1.29567	Q9BYG3 MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1 ,
VYQPVSC(464.28596)PLSDLSENVESVVNEEK	C251,NA,C251,NA,NA	;;X;X;	1.57747;;X;X;	1.57747	Q99590 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 , A0A0A0MTP7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 , Q99590-2 Isoform 2 of Protein SCAF11 OS=Homo sapiens GN=SCAF11 , F8VXG7 Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=1 ,
VPTANVSVDLTC(470.29977)R	C247,NA	;;X;X;	1.20602;;X;X;	1.20602	P04406 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 ,
C(470.29977)EFEEVQGFLDQVAHK	NA,NA,NA,NA,NA	;;;X;	1.40928;;1.65673;;X;	1.533005	E9PI14 39S ribosomal protein L16, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL16 PE=1 SV=1 , Q9NX20 39S ribosomal protein L16, mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1 ,
SPWLAGNELTVADVVLWSVLQQIGGC(470.29977)SVTVPANVQR	NA,NA	;;X;X;	1.41438;;X;X;	1.41438	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 ,
SPWLAGNELTVADVVLWSVLQQIGGC(470.29977)SVTVPANVQR	NA,NA	;;;X;	1.35051;;1.29063;;X;	1.32057	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 ,
SPWLAGNELTVADVVLWSVLQQIGGC(470.29977)SVTVPANVQR	NA,NA	;;X;X;	1.56906;;X;X;	1.56906	Q13155 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 ,
YSNSALGHVNC(464.28596)TIK	NA,C1101,NA	;;;;	2.9645;;3.25536;;2.55683;;	2.9645	Q9NQC3-1 Isoform 1 of Reticulon-4 OS=Homo sapiens GN=RTN4 # F8W914 Reticulon OS=Homo sapiens GN=RTN4 PE=1 SV=1 #
FLVHNVKELEVLLM(15.994915)C(464.28596)NK	M90,C91,M108,C109,M90,C91,NA	;;X;X;	1.44668;;X;X;	1.44668	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
YAIC(470.29977)SALAASALPALVM(15.994915)SK	C125,M138,NA	;;;;	1.47684,1.42017;;1.34734;;1.28727;;	1.383755	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
TWYVQATC(470.29977)ATQGTGLYEGLDWLSNELSKR	NA,NA	;;X;X;	1.41838,1.53648;;X;X;	1.47743	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
YAIC(470.29977)SALAASALPALVM(15.994915)SK	C125,M138,NA	;;X;X;	1.65944;;X;X;	1.65944	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,

TWYVQATC(470.29977)AT QGTGLYEGLDWLSNELSKR	NA,NA	,,X;X;	1.05166,,X;X;	1.05166	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 ,
INPSETYPAFC(464.28596) TTCFPSEPLVGPSVR	C425,NA,NA	U,,X;X;	2.24904,,X;X;	2.24904	Q96GW9 Methionine--tRNA ligase, mitochondrial OS=Homo sapiens GN=MARS2 PE=1 SV=2 ,
NGYDYGQC(464.28596)R	C80,NA,NA	,,X;X;	1.22786,,X;X;	1.22786	S4R3G0 Serine/arginine-rich-splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 , Q13242 Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 ,
AALVTSFC(464.28596)M(1 5.994915)FKYMALYSMIQR	C542,M543,NA	U,,X;U,;	0.99831,,X;1.44317 ,,	1.22074	H0Y4Z2 Cation-transporting ATPase (Fragment) OS=Homo sapiens GN=ATP13A4 PE=1 SV=1 ,
LC(464.28596)SGPGIVGN VLVDPSAR	NA,NA,NA	,,X;X;	1.50332,,X;X;	1.50332	Q9Y5P6-2 Isoform 2 of Mannose-1-phosphate guanylttransferase beta OS=Homo sapiens GN=GMPPB , Q9Y5P6 Mannose-1-phosphate guanylttransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2 ,
EGIC(470.29977)ALGGTSE LSSEGTQHSYSEEEKYAFVN WINK	NA,NA	,,X;X;	1.28912,,X;X;	1.28912	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 ,
C(464.28596)PQVEEAIVQS GQKK	C146,C146,NA	,,X;;	1.28443,,X;1.29981 ,,	1.29212	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
C(464.28596)CLTYCFNKPE DK	C144,NA	U,,X;X;	1.57712,,X;X;	1.57712	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
LLDLVQQSC(470.29977)N YK	NA,C30,NA	,,,;,,;	1.46022,1.50427,0. 98881,,1.6128,,1.19 104,;	1.46022	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 , P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 ,
NC(464.28596)LQVLNPET R	NA,NA	,,X;X;	1.265,,X;X;	1.265	Q7Z6M1 Rab9 effector protein with kelch motifs OS=Homo sapiens GN=RABEPK PE=1 SV=1 ,
AYSPLHGGSGSYSVC(464.2 8596)SNSDTK	NA,NA,C190,NA,NA	,,X;X;	1.66792,,X;X;	1.66792	H0YAZ1 Store-operated calcium entry-associated regulatory factor (Fragment) OS=Homo sapiens GN=SARAF PE=1 SV=1 , Q96BY9 Store-operated calcium entry-associated regulatory factor OS=Homo sapiens GN=SARAF PE=1 SV=1 , H0YAN9 Store-operated calcium entry-associated regulatory factor (Fragment) OS=Homo sapiens GN=SARAF PE=1 SV=1 , Q96BY9-2 Isoform 2 of Store-operated calcium entry- associated regulatory factor OS=Homo sapiens GN=SARAF ,
VGLNAQAAC(470.29977)A	C157,NA	U,,X;X;	1.31002,,X;X;	1.31002	P48681 Nestin OS=Homo sapiens GN=NES PE=1 SV=2 ,

PR					
VGLNAQAAC(470.29977)A PR	C157,NA	U,,X;X;	1.32042,,X;X;	1.32042	P48681 Nestin OS=Homo sapiens GN=NES PE=1 SV=2 ,
YFAGNLASGGAAGATSLC(4 64.28596)FVYPLDFAR	NA,C129,C129,C129,NA	,,,,X;X;	1.50816,1.54206,1. 50816,1.54206,,X;X ;	1.52511	P12236 ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 , P12235 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 , P05141 ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 , V9GYG0 ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=1 ,
IAILTC(470.29977)PFEPK PK	NA,NA,C253,NA	,,X;;	1.46752,,X;1.28383 ,,	1.375675	E9PCA1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 , B7ZAR1 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 , P48643 T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 ,
VIDPVTGKPC(464.28596)A GTTYLESPLSSETQLSK	C195,NA,C100,NA,C100,N A,NA	,,X;X;	1.50028,,X;X;	1.50028	I3L0E3 HCG1984214, isoform CRA_a OS=Homo sapiens GN=hCG_1984214 PE=3 SV=1 , E9PE17 28S ribosomal protein S17, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS17 PE=3 SV=1 , Q9Y2R5 28S ribosomal protein S17, mitochondrial OS=Homo sapiens GN=MRPS17 PE=1 SV=1 ,
QNSDFLC(464.28596)QM DLLQEFYETTLEALKDAK	C130,NA	U,,X;X;	0.78635,,X;X;	0.78635	P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 ,
AYGGSM(15.994915)C(47 0.29977)AK	NA,NA	U,,X;X;	1.34261,,X;X;	1.34261	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 ,
C(470.29977)GYAGSNFPE HIFPALVGRPIIR	NA,C20,NA	,,X;X;	1.79921,,X;X;	1.79921	P61160-2 Isoform 2 of Actin-related protein 2 OS=Homo sapiens GN=ACTR2 , P61160 Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 ,
QNSDFLC(464.28596)QM DLLQEFYETTLEALKDAK	C130,NA	U,,X;X;	1.47163,,X;X;	1.47163	P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 ,
DAGGKSWC(470.29977)P DCVQAEPVVR	NA,NA	,,X;X;	1.37357,,X;X;	1.37357	Q9BRA2 Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1 ,
C(470.29977)AGPTPEAEL QALAR	C52,NA	U,,X;X;	1.42144,,X;X;	1.42144	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 ,
GVLLYGPPGC(464.28596) GK	C137,NA	,,X;X;	1.31523,,X;X;	1.31523	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 ,

EQHIAEC(464.28596)MAK	C124,NA	U,,X;X;	1.30769,,X;X;	1.30769	Q8TAE8 Growth arrest and DNA damage-inducible proteins-interacting protein 1 OS=Homo sapiens GN=GADD45GIP1 PE=1 SV=1 ,
DLGGIVLANAC(470.29977)GPCIGQWDRK	C448,NA,C473,NA,NA	,,X;X;	1.37554,,X;X;	1.37554	Q99798 Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 , A2A274 Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=1 ,
VLVTTNVC(470.29977)AR	NA,C367,NA,C392,NA,C393,NA,C310,NA	,,;,;,;	1.39665,,1.57516,,1.26797,1.1804,,	1.33231	Q9UMR2-3 Isoform 3 of ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B , Q9UMR2 ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 , Q9NUU7-2 Isoform 2 of ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A , Q9NUU7 ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 , H3BQK0 ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1 , F6QDS0 HCG2043426, isoform CRA_b OS=Homo sapiens GN=hCG_2043426 PE=1 SV=1 , I3L352 ATP-dependent RNA helicase DDX19A (Fragment) OS=Homo sapiens GN=DDX19A PE=1 SV=1 ,
MDILDVLTAAQELSRPGC(464.28596)LGR	C628,NA	,,X;X;	1.23086,,X;X;	1.23086	Q9Y4R8 Telomere length regulation protein TEL2 homolog OS=Homo sapiens GN=TELO2 PE=1 SV=2 ,
VSNSPSQAIEVVELASAFSLPIC(464.28596)EGLTQR	C233,NA,NA	,,X;X;	2.41477,,X;X;	2.41477	Q96EY7 Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3 ,
GYWAGLDASAQTTSHELTIPNDLIGC(464.28596)IIGR	C302,NA	,,X;X;	1.29095,,X;X;	1.29095	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 ,
TVLCGTC(464.28596)GQPADK	C479,NA,C187,NA,NA,NA	,,X;X;	0.6333,,X;X;	0.6333	P02545-4 Isoform 4 of Prelamin-A/C OS=Homo sapiens GN=LMNA , P02545-5 Isoform 5 of Prelamin-A/C OS=Homo sapiens GN=LMNA , A0A0C4DGC5 Prelamin-A/C (Fragment) OS=Homo sapiens GN=LMNA PE=1 SV=1 , P02545 Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 , P02545-3 Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA ,
GYWAGLDASAQTTSHELTIPNDLIGC(464.28596)IIGR	C302,NA	,,X;X;	1.65946,,X;X;	1.65946	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 ,
NILGGTVFREPIIC(470.29977)K	C154,NA,NA,NA,NA	,,;,;,;	1.62818,,1.55892,,1.35247,,	1.55892	P48735 Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 , P48735-2 Isoform 2

					of Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 ,
QNSDFLC(464.28596)QM DLLQEFYETTLEALK	C130,NA	U,,X;X;	1.65236,,X;X;	1.65236	P61201-2 Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 ,
EVIIVSCGPAQC(470.2997 7)QETIR	C162,C162,NA	,,,,X;	1.38425,1.063,,1.26 134,,X;	1.26134	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
EVIIVSCGPAQC(470.2997 7)QETIR	C162,C162,NA	,,X;X;	1.59723,,X;X;	1.59723	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
SGTIC(464.28596)SSELP G AFEAAGFHLNEHLYNM(15. 994915)IIR	NA,NA,NA,NA	,,,,X;	1.2172,,1.31794,,X;	1.26757	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , K7EKD8 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 ,
SGTIC(464.28596)SSELP G AFEAAGFHLNEHLYNM(15. 994915)IIR	NA,NA,C200,M222,NA	,,X;;	1.27434,,X;1.2634,,	1.26887	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , K7ELJ7 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 ,
SGTIC(464.28596)SSELP G AFEAAGFHLNEHLYNM(15. 994915)IIR	NA,NA,NA	,,X;X;	1.47703,,X;X;	1.47703	A0A0C4DGQ5 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 , P04632 Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 ,
ASGRELC(464.28596)YILLF GVGLSYCMTFFIAK	NA,NA	U,,X;X;	5.74036,,X;X;	5.74036	Q14832 Metabotropic glutamate receptor 3 OS=Homo sapiens GN=GRM3 PE=1 SV=2 ,
ASPLPPPPPPGAEPAC(46 4.28596)PGSSAAAPAYK	C128,NA	U,,X;X;	1.91955,,X;X;	1.91955	Q8NDT2 Putative RNA-binding protein 15B OS=Homo sapiens GN=RBM15B PE=1 SV=3 ,
GGNAVVDGC(464.28596) GK	NA,NA,NA	,,X;X;	1.53675,,X;X;	1.53675	P48506 Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 , E1CEI4 Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=1 ,
SSGTFLSGLSDC(464.28596)TNVTFK	C102,NA	,,X;X;	0.81573,,X;X;	0.81573	Q5JTH9 RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 ,
LGGTC(470.29977)VNVGC VPK	NA,NA,NA,NA,C102,NA,N A	,,X;X;	1.24596,,X;X;	1.24596	P00390-2 Isoform Cytoplasmic of Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR , P00390 Glutathione reductase, mitochondrial OS=Homo sapiens

					GN=GSR PE=1 SV=2 , P00390-3 Isoform 2 of Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR ,
GLHVVEIREEC(470.29977)GPLPIVVASPR	NA,NA,NA	U,,X;X;	2.09459,,X;X;	2.09459	P82675 28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5 PE=1 SV=2 ,
TYGGC(464.28596)EGPDAM(15.994915)YVK	NA,NA,NA	,,X;X;	1.97203,,X;X;	1.97203	E5RHG8 Transcription elongation factor B polypeptide 1 (Fragment) OS=Homo sapiens GN=TCEB1 PE=1 SV=1 , Q15369 Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1 ,
LVIVGDGAC(470.29977)GK	NA,NA,C180,NA,C16,NA	,,X;X;	1.9533,,X;X;	1.9533	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 , U3KQA9 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=7 , U3KQV3 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=7 , P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 , E9PQH6 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 ,
SC(470.29977)SGVEFSTGSSNTDTGK	NA,C36,NA	,,;,;	1.25184,,1.52091,,1.42107,,	1.42107	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 , P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
EALPVSLPQIPC(470.29977)LSSEFK	NA,NA	,,X;X;	1.75851,,X;X;	1.75851	Q9UHI6 Probable ATP-dependent RNA helicase DDX20 OS=Homo sapiens GN=DDX20 PE=1 SV=2 ,
SC(470.29977)SGVEFSTGSSNTDTGK	NA,C36,NA	,,;,X;	1.3231,,1.88959,,X;	1.606345	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 , P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
FLSQIESDC(464.28596)LALLQVR	NA,NA	,,X;X;	1.60952,,X;X;	1.60952	P52789 Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 ,
VTVLTHC(470.29977)NTGALATAGYGTA LGVIR	C168,NA	U,,X;X;	1.37314,,X;X;	1.37314	Q9BV20 Methylthioribose-1-phosphate isomerase OS=Homo sapiens GN=MRI1 PE=1 SV=1 ,
KVIGIEC(470.29977)SSISDYAVK	C101,NA	,,;,;	1.62241,,4.85235,,2.61227,,	2.61227	Q99873-4 Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 ,
GLELIASENFC(470.29977)SR	NA,NA,C59,NA,NA	,,X;X;	1.40318,,X;X;	1.40318	P34897 Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 , P34897-3 Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 ,

VAC(464.28596)ITEQVLT VNKR	NA,NA	,,,;	1.28454,1.34496,,1. 31754,,1.39196,;	1.33125	P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 ,
VAC(464.28596)ITEQVLT VNKR	NA,NA	,,,;	1.65688,1.32001,,1. 44109,,1.45836,;	1.449725	P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 ,
LHTPMYFFLSNLSCVDIC(47 0.29977)FTTSVAPQLLVTM (15.994915)NK	NA,NA	U,,X;X;	0.858,,X;X;	0.858	Q5TZ20 Olfactory receptor 2G6 OS=Homo sapiens GN=OR2G6 PE=2 SV=1 ,
DLSYC(470.29977)LSGMY DHR	NA,NA	U,,X;X;	1.39923,,X;X;	1.39923	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 ,
IIPTEEGLQLPSPTATSQLPL ESDAVEC(470.29977)LNY QHYKGSDFDCELR	NA,NA,NA	,,X;X;	1.39163,,X;X;	1.39163	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
IIPTEEGLQLPSPTATSQLPL ESDAVEC(470.29977)LNY QHYKGSDFDCELR	NA,NA,NA	,,X;X;	1.46216,,X;X;	1.46216	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
C(464.28596)LTQQAVALQ R	NA,C1138,NA,NA	,,X;X;	1.7736,,X;X;	1.7736	O75153 Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2 , K7EIG1 Clustered mitochondria protein homolog (Fragment) OS=Homo sapiens GN=CLUH PE=1 SV=2 , I3L2B0 Clustered mitochondria protein homolog (Fragment) OS=Homo sapiens GN=CLUH PE=1 SV=2 ,
KGLIAAIC(464.28596)AGP TALLAHEIGFGSK	NA,C86,NA,NA	,,X;X;	1.25254,,X;X;	1.25254	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
TC(464.28596) LHAILNILEK GTEGR	C1032,NA	,,X;X;	8.43439,,X;X;	8.43439	Q92621 Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 ,
KGLIAAIC(464.28596)AGP TALLAHEIGFGSK	NA,C86,NA,NA	,,,X;	1.27502,,1.12931,, X;	1.202165	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7

					PE=1 SV=1 ,
KGLIAAIC(464.28596)AGP TALLAHEIGFGSK	NA,C86,NA,NA	;;X;X;	1.2506;;X;X;	1.2506	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
VQTLLEEELGKEEC(470.29 977)FQNK	C354,C354,NA,NA	;;X;X;	1.59196;;X;X;	1.59196	Q9BVJ6-2 Isoform 2 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A , Q9BVJ6 U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1 , Q9BVJ6-3 Isoform 3 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A ,
AGIDGESIGNC(464.28596) PFSQR	NA,NA,C32,NA	;;X;X;	2.07907;;X;X;	2.07907	Q9NZA1 Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 PE=1 SV=3 , Q9NZA1-3 Isoform 3 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 , Q9NZA1-2 Isoform 1 of Chloride intracellular channel protein 5 OS=Homo sapiens GN=CLIC5 ,
IPDIVLWPTC(464.28596)H DDVVK	NA,NA,NA	U;;X;X;	1.01328;;X;X;	1.01328	O00116 Alkylidihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1 ,
WLSDEC(470.29977)TNAV VNFLSR	C345,NA,NA,NA,C345,NA, NA	;;X;X;	1.37694;;X;X;	1.37694	O75521-2 Isoform 2 of Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 , A0A0C4DGA2 Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=1 , O75521 Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 ,
C(464.28596)SHQQSPYQL LFGEPYIFEELLSLK	C289,NA,NA,NA	;;X;X;	1.82926;;X;X;	1.82926	Q96GJ1-2 Isoform 2 of tRNA (uracil(54)-C(5))- methyltransferase homolog OS=Homo sapiens GN=TRMT2B , Q96GJ1-3 Isoform 3 of tRNA (uracil(54)-C(5))- methyltransferase homolog OS=Homo sapiens GN=TRMT2B , Q96GJ1 tRNA (uracil(54)-C(5))-methyltransferase homolog OS=Homo sapiens GN=TRMT2B PE=1 SV=1 ,
C(464.28596)TVLSLEQSYA HAGLGGMASIFGLLEIAQTH YYSK	C997,NA,C1017,C954,NA, NA,NA,C1017,NA,NA	;;X;X;	1.45265;;X;X;	1.45265	Q8WVG6-3 Isoform 3 of MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD , Q8WVG6-2 Isoform 2 of MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD , Q8WVG6-7 Isoform 7 of MAP kinase-activating death domain protein OS=Homo

					sapiens GN=MADD , Q8WVG6-5 Isoform 5 of MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD , Q8WVG6-4 Isoform 4 of MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD , Q8WVG6-6 Isoform 6 of MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD , A0A0A0MRB5 MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD PE=1 SV=1 , Q8WVG6 MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD PE=1 SV=2 , Q8WVG6-8 Isoform 8 of MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD ,
YVFNLAELVPM(15.994 915)EYVGIPEC(464.28596) IK	NA,M287,C295,M165,C173,M408,C416,NA	;;X;X;	0.22475;;X;X;	0.22475	Q12982-2 Isoform 2 of BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 , Q12982 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 , H7C096 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 (Fragment) OS=Homo sapiens GN=BNIP2 PE=1 SV=1 , J3KN59 BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Homo sapiens GN=BNIP2 PE=1 SV=1 ,
FTSC(470.29977)VAFFNIL NELNDYAGQR	NA,NA,C69,NA,C69,NA,NA	;;X;X;	1.48267,1.45059;;X;X;	1.46663	Q5TON5-3 Isoform 3 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L , S4R347 Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L PE=1 SV=1 , Q5TON5-4 Isoform 4 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L , Q5TON5 Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L PE=1 SV=3 , Q5TON5-2 Isoform 2 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L , Q5TON5-5 Isoform 5 of Formin-binding protein 1-like OS=Homo sapiens GN=FNBP1L ,
TTSILC(464.28596)LAR	NA,NA,NA	;;X;X;	1.44563;;X;X;	1.44563	P35250-2 Isoform 2 of Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 , P35250 Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3 ,
LHDAIVEVVC(470.29977) LLR	NA,C470,C470,NA,C470,NA,NA,NA,NA	;;X;X;	1.35324;;X;X;	1.35324	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-3 Isoform 2

					of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 , O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 , O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L ,
GC(470.29977)TATLGNFAK	NA,NA	,,,X;	1.38709,,1.33602,,X;	1.361555	P15880 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 ,
TIIPISQC(470.29977)TPK	C212,NA,NA	,,,,,;	1.56383,,1.49844,,1.23338,,	1.49844	P40926 Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 ,
KLDTNSDGQLDFSEFLNLIGGLAM(15.994915)AC(464.28596)HDSFLK	NA,NA	U,,U,,X;	1.69393,,1.69024,,X;	1.692085	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
KLDTNSDGQLDFSEFLNLIGGLAM(15.994915)AC(464.28596)HDSFLK	M89,C91,NA	U,U,,U,,U,,	1.2262,1.33302,,1.51567,,1.43736,,	1.38519	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
KLDTNSDGQLDFSEFLNLIGGLAM(15.994915)AC(464.28596)HDSFLK	M89,C91,NA	U,,X,X;	1.99796,,X,X;	1.99796	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
DLAGAPPGEVVG(470.29977)FTPQSR	C584,NA,NA	,,X,X;	1.56857,,X,X;	1.56857	Q9Y446-2 Isoform PKP3b of Plakophilin-3 OS=Homo sapiens GN=PKP3 , Q9Y446 Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1 ,
SGDAAIVDM(15.994915)VPGKPMC(470.29977)VESFSDYPPLGR	NA,NA	,,X,X;	1.32257,,X,X;	1.32257	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
VSDTVVEPYNATLSVHQLVNTDETYC(470.29977)IDNEALYDICFR	C201,C201,NA,C183,C201,NA	,,,X;	1.62886,,1.67268,,X;	1.65077	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
SGDAAIVDM(15.994915)VPGKPMC(470.29977)VESF	NA,NA	,,,X,X;	1.33106,1.40769,1.74723,,X,X;	1.40769	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,

SDYPPLGR					
VSDTVVEPYNATLSVHQLVE NTDETYC(470.29977)IDNE ALYDICFR	C201,C201,NA,C164,C183, C201,NA	,,X,;;	1.17859,,X;1.32878 ,,	1.253685	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
AGAVVAVPTDTLYGLACAA SC(464.28596)SAALR	C99,NA,NA	U,,X;X;	1.42567,,X;X;	1.42567	Q86U90 YrdC domain-containing protein, mitochondrial OS=Homo sapiens GN=YRDC PE=1 SV=1 ,
LLDVLSGHEGPISGLC(464.2 8596)FNPM(15.994915)K	NA,C508,M512,NA	,,X;X;	1.71153,,X;X;	1.71153	A0A0B4J2E5 Protein LOC102724159 OS=Homo sapiens GN=LOC102724159 PE=1 SV=1 , Q15269 Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=2 SV=2 ,
YSDVEVPASVTGYSFASDG DSGTC(470.29977)SPLR	NA,NA,C430,NA,C430,C43 0,C430,C430,NA	,,,X;X;	1.53876,2.67574,,X ;X;	2.10725	P35611-3 Isoform 3 of Alpha-adducin OS=Homo sapiens GN=ADD1 , P35611-5 Isoform 5 of Alpha-adducin OS=Homo sapiens GN=ADD1 , P35611 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 , E7ENY0 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 , P35611-4 Isoform 4 of Alpha-adducin OS=Homo sapiens GN=ADD1 , E7EV99 Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=1 , P35611-6 Isoform 6 of Alpha-adducin OS=Homo sapiens GN=ADD1 , P35611-2 Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1 ,
KIWC(464.28596)FGPDGT GPNILTDITK	C651,NA	U,,X;X;	0.96806,,X;X;	0.96806	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
GLGQEC(470.29977)VLSSS PAVLALQTSLVFSR	NA,NA	,,X;X;	1.4512,,X;X;	1.4512	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 ,
EENVGLHQTLDTLNLNC(464.28596)I	C283,NA,NA	,,X;X;	1.03259,,X;X;	1.03259	P67936-2 Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 , P67936 Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 ,
NM(15.994915)MAAC(46 4.28596)DPR	M299,C303,M299,C303,M 646,C650,M299,C303,NA, M281,C285,M299,C303,N A	,,,,,X;	1.6589,1.6589,,1.48 069,1.48069,,X;	1.569795	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens

					PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
VWNLANC(470.29977)K	NA,NA	,,,X;X;	1.45476,1.82835,,X; ;X;	1.641555	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
TATGC(464.28596)YIGWCK	NA,NA,C74,NA	,,X;X;	1.33644,,X;X;	1.33644	A0A087WUX8 MICOS complex subunit OS=Homo sapiens GN=APOOL PE=1 SV=1 , Q6UXV4 MICOS complex subunit MIC27 OS=Homo sapiens GN=APOOL PE=1 SV=1 , A0A087WYF7 MICOS complex subunit OS=Homo sapiens GN=APOOL PE=1 SV=1 ,
WEALHAAECPC(470.29977)GPSLIR	NA,NA	U,,X;X;	1.16017,,X;X;	1.16017	P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 ,
LNLSC(470.29977)IHSPVVNELM(15.994915)R	NA,NA	U,,X;U,,	1.3291,,X;1.11035,,	1.219725	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
LNLSC(470.29977)IHSPVVNELM(15.994915)R	NA,NA	U,,X;X;	1.21044,,X;X;	1.21044	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
LNLSC(470.29977)IHSPVVNELM(15.994915)R	NA,NA	U,,X;U,,	1.86633,,X;1.68031,,	1.77332	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
AKVDEFPLC(464.28596)GHM(15.994915)VSDEYEQLSSEALEAAR	C49,M52,NA	,,,,X;	1.43857,1.51248,,1.32644,,X;	1.43857	P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
AKVDEFPLC(464.28596)GHM(15.994915)VSDEYEQLSSEALEAAR	C49,M52,C49,M52,NA	,,,,,;	1.42221,1.47207,,1.18107,,1.20576,,	1.313985	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
AKVDEFPLC(464.28596)GHM(15.994915)VSDEYEQLSSEALEAAR	C49,M52,C49,M52,NA	,,,,,;	1.22971,1.44908,,1.25264,,1.2468,,	1.24972	X1WI28 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE=1 SV=6 , P27635 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4 ,
QMAGC(464.28596)LEDCTR	C174,NA,NA	,,X;X;	1.54572,,X;X;	1.54572	O00411 DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 ,
SIQFVDWC(464.28596)PTGFK	NA,C347,NA,NA	,,,X;	1.49452,,1.41343,,X;	1.453975	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,

DTQTSITDSC(470.29977)A VYR	C100,NA	U,U,U;;X;X;	2.11136,1.65951,2. 11303;;X;X;	2.11136	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
EC(470.29977)LPLIIFLR	NA,NA,NA	U,U,U;;U;;U;;	1.16065,1.40176,1. 38923;;1.34619;;1.2 6754;;	1.34619	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
EC(470.29977)LPLIIFLR	NA,NA,NA	U;;X;X;	1.38787;;X;X;	1.38787	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
ELEVLLM(15.994915)C(46 4.28596)NK	M90,C91,M108,C109,M90 ,C91,NA	;;;X;	1.60172;;0.7546;;X;	1.17816	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
AC(464.28596)DLPWVHF PDTER	NA,NA	;;X;;	1.395;;X;1.24656;;	1.32078	H7BX11 Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 ,
GNHEC(464.28596)ASINR	NA,C126,C83,NA	;;;;;	1.33499;;1.10196;;0 .78489;;	1.10196	P62136-2 Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA , P62140 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 , P62136 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 ,
VEPC(470.29977)SLTPGYT K	C219,NA,NA,NA,NA,NA	;;X;X;	1.9037;;X;X;	1.9037	Q96EB1-3 Isoform 3 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1-2 Isoform 2 of Elongator complex protein 4 OS=Homo sapiens GN=ELP4 , Q96EB1 Elongator complex protein 4 OS=Homo sapiens GN=ELP4 PE=1 SV=2 , G5E9D4 Elongation protein 4 homolog (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=ELP4 PE=1 SV=1 ,
GALMANFLTQGQVC(470. 29977)CNGTR	C288,NA	;;X;X;	1.77733;;X;X;	1.77733	P49189 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 ,
AGQC(470.29977)VIGLQM (15.994915)GTNK	C164,M170,C153,M159,N A,C155,M161,NA	;;;;;	1.47991,1.49033;;1. 43001;;1.38396;;	1.45496	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
TIYAGNALC(470.29977)TV	C155,NA,NA	;;;;;	1.43769;;1.69875;;1	1.69875	P13804 Electron transfer flavoprotein subunit alpha,

K			.72812,;		mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 ,
DSGAALGLGIALHSPC(464.28596)YAQVR	NA,C269,NA	,;X;X;	2.10815,;X;X;	2.10815	K7ESE6 Glucose-6-phosphatase 3 (Fragment) OS=Homo sapiens GN=G6PC3 PE=1 SV=1 , Q9BUM1 Glucose-6-phosphatase 3 OS=Homo sapiens GN=G6PC3 PE=1 SV=2 ,
ATDSKEPPGELC(464.28596)PDVLYR	NA,C46,NA,NA,NA	,;X;X;	0.71166,;X;X;	0.71166	Q9BUK6 Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 PE=1 SV=1 , Q9BUK6-2 Isoform 2 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 , Q9BUK6-3 Isoform 3 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 , Q9BUK6-7 Isoform 7 of Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 ,
C(470.29977)HVQTIQLCR	NA,C153,C153,NA	,;X;X;	1.86121,;X;X;	1.86121	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 , O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 , B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 ,
IFGSIPM(15.994915)QAC(464.28596)QQK	M152,C155,M152,C155,M152,C155,M152,C155,NA	,;X;X;	1.64141,;X;X;	1.64141	F5H6J5 Zinc finger CCHC domain-containing protein 8 (Fragment) OS=Homo sapiens GN=ZCCHC8 PE=1 SV=1 , Q6NZY4-2 Isoform 2 of Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 , Q6NZY4 Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2 , F5GX80 Zinc finger CCHC domain-containing protein 8 (Fragment) OS=Homo sapiens GN=ZCCHC8 PE=1 SV=1 ,
LPITVLNGAPGFINLC(464.28596)DALNAWQLVK	NA,C240,NA	,;X;X;	1.95899,;X;X;	1.95899	P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 , P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC ,
LPITVLNGAPGFINLC(464.28596)DALNAWQLVK	NA,C240,NA	,;;X;	1.37765,;1.28086,;X;	1.329255	P31939 Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 , P31939-2 Isoform 2 of Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC ,
C(470.29977)LLIHPNPESA LNEEAGR	NA,C147,NA	,;X;X;	1.38824,;X;X;	1.38824	Q16763 Ubiquitin-conjugating enzyme E2 S OS=Homo sapiens GN=UBE2S PE=1 SV=2 , K7EPJ1 Ubiquitin-conjugating enzyme E2 S (Fragment) OS=Homo sapiens GN=UBE2S PE=1 SV=1 ,
SGQGAFGNM(15.994915)C(470.29977)R	M95,C96,NA	,,,;	1.9808,1.50597,;1.3633,;1.26725,;	1.42115	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,

AWVWNTHADFADEC(470.29977)PKPELLAIR	NA,C132,C132,C209,NA,C132,NA	;;X;X;	1.25231;;X;X;	1.25231	C9JXG8 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=2 , P43487 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 , C9JJ34 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=1 , F6WQW2 Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 , C9JGV6 Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=1 SV=7 , P43487-2 Isoform 2 of Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 ,
HSM(15.994915)NPFC(464.28596)EIAVEEAVR	M129,C133,M129,C133,NA	;;X;;	1.36068,1.57123;;X;1.20562;;	1.36068	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
AAAPAPEEEM(15.994915)DEC(464.28596)EQALAAE PK	M263,C266,NA,NA	;;X;;	1.20379;;X;1.14988;;	1.176835	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
HSM(15.994915)NPFC(464.28596)EIAVEEAVR	M129,C133,M129,C133,NA	;;X;X;	1.5504,2.07132;;X;X;	1.81086	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
AAAPAPEEEM(15.994915)DEC(464.28596)EQALAAE PK	M263,C266,NA,NA	;;X;X;	1.28734;;X;X;	1.28734	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
SLLINAVEASC(470.29977)IR	NA,NA,C262,NA,C262,NA,NA,NA,NA,C188,C262,NA	;;X;;	1.58602;;X;1.35942;;	1.47272	E2QRB3 Pyrroline-5-carboxylate reductase 1, isoform CRA_c OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , A0A087WTV6 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , J3KR12 Uncharacterized protein OS=Homo sapiens PE=4 SV=1 , Q96C36 Pyrroline-5-carboxylate reductase 2 OS=Homo

					sapiens GN=PYCR2 PE=1 SV=1 ,
SLLINAVEASC(470.29977)IR	C262,NA,C262,NA,NA,NA,C262,NA	,,,;X;X;	1.81931,1.57984,1.85032,,;X;X;	1.81931	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , Q96C36 Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 ,
INISEGNC(470.29977)PER	NA,C54,C54,C54,C54,NA	,,,,,;	1.37663,1.45394,,1.33466,,1.24054,;	1.355645	Q15366-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366-6 Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 , Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
LREC(464.28596)LPLIIFLR	NA,NA,NA	U,,;X;X;	1.40259,,;X;X;	1.40259	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
IVGIGYNGM(15.994915)PNGC(464.28596)SDDVLPWR	NA,M67,C71,NA	,;X;X;	1.6277,,;X;X;	1.6277	P32321 Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1 SV=2 , P32321-2 Isoform 2 of Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD ,
LREC(464.28596)LPLIIFLR	NA,NA,NA	U,,;X;X;	1.52395,,;X;X;	1.52395	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
ISWTC(464.28596)INTTLTC(470.29977)EVMNGTDP ELNLYQDGKHLK	C139,C146,NA	U,,;X;X;	0.7009,,;X;X;	0.7009	P06729 T-cell surface antigen CD2 OS=Homo sapiens GN=CD2 PE=1 SV=2 ,
NNLLC(464.28596)NGLSLK	NA,NA,C77,NA	,;X;X;	1.50593,,;X;X;	1.50593	Q9NVH0-2 Isoform 2 of Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 , Q9NVH0 Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2 , C9JLF4 Exonuclease 3'-5' domain-containing protein 2 (Fragment) OS=Homo sapiens GN=EXD2 PE=1 SV=1 ,
VHPAM(15.994915)ATAAGGC(470.29977)R	NA,NA,NA	,,,,,;	1.68748,,1.67358,,1.23192,;	1.67358	H7C0N4 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 , H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 ,

YATSCYSCC(464.28596)PR	C173,NA,NA	,,;,;	2.08197,1.61316,;1.66481,;1.31488,;	1.638985	Q13057-2 Isoform 2 of Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY , Q13057 Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4 ,
LALQQQLIC(470.29977)K	C69,NA	,;X;X;	1.27591,;X;X;	1.27591	Q8IWX8 Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=3 ,
GC(464.28596)IVDANLSVL NLVIVK	NA,NA	,,;,;	1.49578,;1.35828,;1.31725,;	1.35828	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
C(470.29977)PGESLINPGF K	NA,NA	U,;X;X;	2.62704,;X;X;	2.62704	Q9BUH6 Protein PAXX OS=Homo sapiens GN=C9orf142 PE=1 SV=2 ,
GC(464.28596)IVDANLSVL NLVIVK	NA,NA	,;X;X;	1.52549,;X;X;	1.52549	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
IQFNDLQSLLC(464.28596) ATLQNVLR	C440,C440,NA	,;X;X;	1.3531,;X;X;	1.3531	Q14974 Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 , Q14974-2 Isoform 2 of Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 ,
IGFPETEEEEIEIASNSDC(464.28596)IFPSAPDVK	C353,NA,NA	,,;X;	1.24575,;1.54331,;X;	1.39453	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP , Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 ,
LFTEYPC(470.29977)GSGN VYAGVLAVAR	C280,NA	U,;X;X;	1.57505,;X;X;	1.57505	Q8IU81 Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens GN=IRF2BP1 PE=1 SV=1 ,
SAVDLSC(464.28596)SR	C144,NA,NA	,;X;X;	1.53221,;X;X;	1.53221	Q9Y446-2 Isoform PKP3b of Plakophilin-3 OS=Homo sapiens GN=PKP3 , Q9Y446 Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1 ,
ALANVNIGSLIC(464.28596))NVGAGGPAPAAGAAPAG GPAPSTAAAPAEKK	NA,NA,NA	,,;X;X;	0.85189,0.85189,;X; ;X;	0.85189	P05386-2 Isoform 2 of 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 , P05386 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 ,
TTSSANNPNLM(15.994915)YQDEC(470.29977)DRR	M502,C507,M581,C586,NA,NA,M500,C505,NA	,;X,;;	1.65772,;X;1.22355 ,;	1.440635	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 , Q92841-2 Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 , Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 ,

C(470.29977)PQVEEAIVQS GQK	C146,C146,NA	;;X;X;	1.71091;;X;X;	1.71091	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
TLGSGAC(464.28596)GEV K	NA,C140,NA,C140,NA	;;X;X;	2.45621;;X;X;	2.45621	O96017-13 Isoform 13 of Serine/threonine-protein kinase Chk2 OS=Homo sapiens GN=CHK2 , O96017 Serine/threonine-protein kinase Chk2 OS=Homo sapiens GN=CHK2 PE=1 SV=1 , O96017-9 Isoform 9 of Serine/threonine-protein kinase Chk2 OS=Homo sapiens GN=CHK2 , O96017-4 Isoform 4 of Serine/threonine-protein kinase Chk2 OS=Homo sapiens GN=CHK2 ,
VM(15.994915)AEANHFID LSQIPC(470.29977)NGK	NA,NA	;;X;X;	2.014;;X;X;	2.014	O15294 UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3 ,
AFQYVETHGEVC(464.2859 6)PANWTPDSPTIKPSAAS K	NA,NA,NA	;;;;	1.47484;;1.31649;;1 .12761,;	1.31649	P30048 Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 ,
INEIVYFLPFC(464.28596)H SELIQLV NK	C572,NA,NA,C371,C513,N A,NA	;;;X;	1.35848;;1.08011,; X;	1.219295	Q9H078 Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1 , Q9H078-4 Isoform 4 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB , Q9H078-2 Isoform 2 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB , Q9H078-5 Isoform 5 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB , Q9H078-3 Isoform 3 of Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB , H0YGM0 Caseinolytic peptidase B protein homolog (Fragment) OS=Homo sapiens GN=CLPB PE=1 SV=1 ,
VC(470.29977)EEIAIIPSKK	C35,NA	;;X;X;	1.72644;;X;X;	1.72644	P08708 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 ,
AFQYVETHGEVC(464.2859 6)PANWTPDSPTIKPSAAS K	NA,NA,NA	;;X;X;	1.29018;;X;X;	1.29018	P30048 Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 ,
VC(470.29977)EEIAIIPSKK	NA,C35,C35,NA	;;;X;;	1.99418,1.61388;;X ;1.48354,;	1.61388	H0YN88 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 , A0A075B716 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=1 , P08708 40S

					ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 ,
VC(470.29977)TLAIIDPGD SDIIR	C92,C92,NA	,,,;X;	2.4781,1.82395,,1.94212,,X;	1.94212	P62888 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 , E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 ,
LDEC(470.29977)EEAFQG TK	C103,NA,NA,NA,NA,NA,NA	,;X;X;	1.03589,,;X;X;	1.03589	P61289-3 Isoform 3 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 , B3KQ25 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , K7ESG5 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289-2 Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 ,
NTGQTC(464.28596)VCSN QFLVQR	NA,NA,NA,NA,NA,NA,NA,NA	,;X;,,;	1.3171,1.31673,,;X;0.834,,;	1.31673	C9J8Q5 Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=1 , P01763 Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1 , P51649 Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 , P51649-2 Isoform 2 of Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 ,
SVAAGC(470.29977)PVLL GKDNPSGPSR	NA,NA	U,,;X;X;	1.17928,,;X;X;	1.17928	Q9NQS1 Cell death regulator Aven OS=Homo sapiens GN=AVEN PE=1 SV=1 ,
C(470.29977)TAGQILSHP WVSDDASQENNM(15.994915)QAEVTGK	NA,C657,M678,NA,NA,NA,C640,M661,NA	,;X;X;	2.02837,,;X;X;	2.02837	Q8N568-2 Isoform 2 of Serine/threonine-protein kinase DCLK2 OS=Homo sapiens GN=DCLK2 , Q8N568-3 Isoform 3 of Serine/threonine-protein kinase DCLK2 OS=Homo sapiens GN=DCLK2 , G5E9L9 Doublecortin and CaM kinase-like 2, isoform CRA_c OS=Homo sapiens GN=DCLK2 PE=1 SV=1 , A0A0U1RR70 Serine/threonine-protein kinase DCLK2 OS=Homo sapiens GN=DCLK2 PE=1 SV=1 , Q8N568 Serine/threonine-protein kinase DCLK2 OS=Homo sapiens GN=DCLK2 PE=2 SV=4 ,
LLACIASRPGQC(470.29977)GR	NA,NA	,;X;,,;	1.57034,,;X;1.28488,,;	1.42761	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
VTVLTHC(464.28596)NTG	C168,NA	U,,;X;X;	1.37314,,;X;X;	1.37314	Q9BV20 Methylthioribose-1-phosphate isomerase

ALATAGYGTALGVIR					OS=Homo sapiens GN=MRI1 PE=1 SV=1 ,
IPGGIIEDSC(464.28596)VL R	NA,C168,NA,NA	;;X;X;	1.7146;;X;X;	1.7146	P49368-2 Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 , B4DUR8 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 , P49368 T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 ,
KGVSASAVPFTPSSPLLSC(4 70.29977)SQEGSR	NA,NA,NA,NA	;;X;X;	1.69046;;X;X;	1.69046	Q9Y2X7 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2 , J3QRU8 ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=1 , Q9Y2X7-3 Isoform 3 of ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 ,
YWLC(470.29977)AATGPS IK	NA,NA	;;X;X;	1.6151;;X;X;	1.6151	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
C(470.29977)EGINISGNFY R	NA,NA	;;X;X;	1.50692;;X;X;	1.50692	MOQYS1 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=1 SV=2 ,
ISEVFDC(470.29977)WFES GSM(15.994915)PYAQVH YPFENKR	NA,NA,NA	;;X;X;	2.1086;;X;X;	2.1086	P41252 Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 ,
YWLC(470.29977)AATGPS IK	NA,NA	;;;X;	1.6675;;1.61745;;X;	1.642475	P63244 Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3 ,
C(470.29977)EGINISGNFY R	NA,NA	;;X;X;	1.51772;;X;X;	1.51772	MOQYS1 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=1 SV=2 ,
C(464.28596)ASQVGMTA PGTR	C215,C204,NA,NA	;;X;X;	1.399;;X;X;	1.399	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
TDETYCIDNEALYDIC(464.2 8596)FR	C211,C558,NA	;;X;;;	1.65998;;X;5.04801 ;;	3.353995	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
C(464.28596)ASQVGMTA PGTR	C215,C204,NA,NA	;;X;X;	1.42755;;X;X;	1.42755	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
VVEPYNATLSIHLVENTDE TYC(470.29977)IDNEALYD IC(464.28596)FR	C548,C558,NA	;;X;X;	0.45775;;X;X;	0.45775	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
VVEPYNATLSIHLVENTDE TYC(470.29977)IDNEALYD	C548,C558,NA	;;X;X;	0.09346;;X;X;	0.09346	A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,

IC(464.28596)FR					
ETC(464.28596)SLWPGQA LSLQVEQLLHHR	NA,NA	;;X;X;	1.84632;;X;X;	1.84632	P19623 Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 ,
ETC(464.28596)SLWPGQA LSLQVEQLLHHR	NA,NA	;;X;X;	1.2383;;X;X;	1.2383	P19623 Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 ,
YIYDQC(470.29977)PAVA GYGPIELPDYNR	C453,NA,NA	U;;U;X;	1.16029;;1.4298;;X;	1.295045	P31930 Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 ,
VC(470.29977)ENIPIVLCG NKVDIK	NA,NA,NA,NA,NA	;;X;X;	24.38969;;X;X;	24.38969	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 , J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 , B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 , F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 ,
LSGFGQSGSFC(464.28596) R	NA,NA,NA,C117,NA,NA,C1 17,C117,NA	;;X;X;	0.30847;;X;X;	0.30847	Q9UHK6-4 Isoform 3 of Alpha-methylacyl-CoA racemase OS=Homo sapiens GN=AMACR , V9GYP4 Alpha-methylacyl- CoA racemase OS=Homo sapiens GN=AMACR PE=1 SV=1 , D6RB81 Alpha-methylacyl-CoA racemase OS=Homo sapiens GN=AMACR PE=1 SV=1 , Q9UHK6-5 Isoform 4 of Alpha- methylacyl-CoA racemase OS=Homo sapiens GN=AMACR , V9GZ45 Alpha-methylacyl-CoA racemase OS=Homo sapiens GN=AMACR PE=1 SV=1 , V9GYU9 Alpha-methylacyl-CoA racemase OS=Homo sapiens GN=AMACR PE=1 SV=1 , Q9UHK6-2 Isoform 2 of Alpha-methylacyl-CoA racemase OS=Homo sapiens GN=AMACR , Q9UHK6 Alpha-methylacyl- CoA racemase OS=Homo sapiens GN=AMACR PE=1 SV=2 ,
SEHPPLC(470.29977)GR	C1156,NA	;;X;X;	0.78631;;X;X;	0.78631	Q15393 Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 ,
SLPGPAPC(464.28596)LK	NA,NA	;;X;X;	1.45245;;X;X;	1.45245	H0Y360 AMP deaminase 2 (Fragment) OS=Homo sapiens GN=AMPD2 PE=1 SV=1 ,
EVPQHPS(464.28596)LFF QYNTQLGPPYHILVDTNFN FSIK	NA,C54,C42,NA,NA	;;X;X;	1.01639;;X;X;	1.01639	G3V5S9 rRNA-processing protein FCF1 homolog OS=Homo sapiens GN=FCF1 PE=1 SV=1 , Q9Y324 rRNA-processing protein FCF1 homolog OS=Homo sapiens GN=FCF1 PE=2 SV=1 , G3V1S4 Chromosome 14 open reading frame 111, isoform CRA_a OS=Homo sapiens GN=FCF1 PE=1 SV=1 ,
CPPKCLPQCPAPCSPAVSSC CGPISGGCCGPSSGGCCNS	C72,NA	U;;X;X;	1.08451;;X;X;	1.08451	O14633 Late cornified envelope protein 2B OS=Homo sapiens GN=LCE2B PE=2 SV=1 ,

GAGGCC(470.29977)LSHHR					
VGLGIC(464.28596)YDM(15.994915)R	NA,NA	,;X;X;	1.32119,,;X;X;	1.32119	Q9NQR4 Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 ,
FTTSC(470.29977)M(15.994915)TGYSPLQLGLSSGGSGSYSPGVITYSPVSGYNK	C157,M158,C158,M159,NA	,;X;;	1.38633,,;X;1.56397,,;	1.47515	Q96SK2-2 Isoform 2 of Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 , Q96SK2 Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 ,
ESLNASIVDAINQAADC(464.28596)WGIR	C167,NA,NA	,;;X;	1.30366,,;1.10467,,;X;	1.204165	Q9UJZ1 Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 ,
FTTSC(470.29977)M(15.994915)TGYSPLQLGLSSGGSGSYSPGVITYSPVSGYNK	C157,M158,C158,M159,NA	,;;X;	2.49696,,;3.96536,,;X;	3.23116	Q96SK2-2 Isoform 2 of Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 , Q96SK2 Transmembrane protein 209 OS=Homo sapiens GN=TMEM209 PE=1 SV=2 ,
ANNNAAVAPTTC(464.28596)PLQPVTDPFAFSR	C46,NA,NA	,;X;X;	1.33756,,;X;X;	1.33756	F1T0I1 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 , J3KNL6 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 ,
LQDSFC(464.28596)SGQTLWELLSHFPQIR	C106,NA,NA	,;X;X;	1.43141,,;X;X;	1.43141	J3QL04 Tether-containing UBX domain for GLUT4 (Fragment) OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 , Q9BZE9 Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 ,
LDINLLDNVVNC(470.29977)LYHGEQAQQR	NA,NA	,;X;X;	1.42966,,;X;X;	1.42966	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 ,
GC(464.28596)WDSIHVVEVQEK	NA,NA,C176,NA,NA,C135,NA,NA,NA,NA	,;;X;;	0.88681,1.37466,,;X;1.23346,,;	1.23346	P47756 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 , P47756-2 Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB , B1AK88 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_d OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK87 Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 , B1AK85 F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=1 ,
LQDSFC(464.28596)SGQTLWELLSHFPQIR	C106,NA,NA	,;X;X;	2.3118,,;X;X;	2.3118	J3QL04 Tether-containing UBX domain for GLUT4 (Fragment) OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 , Q9BZE9 Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 ,
LDINLLDNVVNC(470.29977)	NA,NA	,;X;;	1.41916,,;X;1.05775	1.238455	O14980 Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 ,

7)LYHGEGAQQR			,,		
QGEYGLASIC(470.29977)N GGGGASAM(15.994915)LI QK	NA,NA,NA	U,,X;U,,	1.69499,,X;1.37527 ,,	1.53513	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
GSSC(470.29977)FECTHY QSFLEYR	C188,NA	,,X;X;	1.52374,,X;X;	1.52374	P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 ,
SVHYC(464.28596)PATK	NA,C193,NA	,,X;;	1.49922,,X;1.64887 ,,	1.574045	P25205 DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 , P25205-2 Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 ,
VC(470.29977)ENIPIVLG NK	NA,NA,NA,NA,NA	,,X;X;	1.39959,,X;X;	1.39959	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 , J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 , B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 , F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 ,
VC(470.29977)ENIPIVLG NK	NA,NA,NA,NA,NA	,,X;X;	12.04805,,X;X;	12.04805	P62826 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 , J3KQE5 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 , B5MDF5 GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=1 , F5H018 GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=7 ,
LGGSLIVAFEGC(464.28596)PV	C146,NA,NA	,,,X;;;	1.41846,1.3984,0.7 0963,,X;1.23444,1. 19646,,	1.23444	P60981-2 Isoform 2 of Destrin OS=Homo sapiens GN=DSTN , P60981 Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 ,
VVMALGDYM(15.994915) GASC(464.28596)HACIGG TNVR	NA,NA	,,X;X;	1.60726,,X;X;	1.60726	P60842 Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 ,
NCAVSC(464.28596)AGEK	C141,NA,NA	,,X;;	1.81503,,X;1.52861 ,,	1.67182	Q15813 Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1 , Q15813-2 Isoform 2 of Tubulin- specific chaperone E OS=Homo sapiens GN=TBCE ,
YRNPVSQC(464.28596)M R	NA,C50,C50,C50,NA,NA,N A	,,X;X;	1.57997,,X;X;	1.57997	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein

					43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
IVGYFVSGC(464.28596)DP SIM(15.994915)GIGPVPAI SGALK	NA,NA,C287,M292,NA,NA	;;;X;	1.5548;;0.93666;;X;	1.24573	A0A0B4J2A4 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 , P42765 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 ,
IGIASQALGIAQTALDC(470. 29977)AVNYAENR	NA,NA,C285,NA,NA	;;X;X;	1.71702;;X;X;	1.71702	P16219 Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 , E9PE82 Short-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 ,
LGTLPFC(470.29977)CP WEQLTQDWESR	C705,NA	U;;X;X;	1.43308;;X;X;	1.43308	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 ,
ILGNTFGM(15.994915)C(4 64.28596)VLQDFEALTPNL LAR	M120,C121,NA,NA	;;X;X;	1.62592;;X;X;	1.62592	E9PMU0 RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=1 , Q9H0A0 RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=2 ,
GHSAC(470.29977)EPENL EFSSFM(15.994915)FWR	C147,M158,NA	U;;X;X;	1.61382;;X;X;	1.61382	Q9ULX3 RNA-binding protein NOB1 OS=Homo sapiens GN=NOB1 PE=1 SV=1 ,
SGDAAIVDMVPGKPM(15. 994915)C(464.28596)VES FSDYPPLGR	NA,NA	;;X;X;	1.44307;;X;X;	1.44307	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
VIIVQAC(464.28596)R	C173,C258,NA,C328,NA,C 258,NA,C202,C211,NA	;;X;X;	1.18397;;X;X;	1.18397	P51878-3 Isoform 3 of Caspase-5 OS=Homo sapiens GN=CASP5 , P49662-4 Isoform 4 of Caspase-4 OS=Homo sapiens GN=CASP4 , P51878-6 Isoform 6 of Caspase-5 OS=Homo sapiens GN=CASP5 , P51878-5 Isoform 5 of Caspase-5 OS=Homo sapiens GN=CASP5 , P51878-2 Isoform 2 of Caspase-5 OS=Homo sapiens GN=CASP5 , P49662 Caspase-4 OS=Homo sapiens GN=CASP4 PE=1 SV=1 , P51878 Caspase-5 OS=Homo sapiens GN=CASP5 PE=1 SV=3 , P49662-2 Isoform 2 of Caspase-4 OS=Homo sapiens GN=CASP4 , A0A087WZP8 Caspase OS=Homo sapiens GN=CASP4 PE=1 SV=1 ,
SGDAAIVDMVPGKPM(15. 994915)C(464.28596)VES FSDYPPLGR	NA,NA,NA	;;;X;	1.66096;;1.3083;;X;	1.48463	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
IC(464.28596)SHSAPEQQ	C19,NA	U;;X;X;	1.95764;;X;X;	1.95764	O75683 Surfeit locus protein 6 OS=Homo sapiens GN=SURF6

AR					PE=1 SV=3 ,
C(464.28596)LGPPTTPGPY R	C56,C56,NA,NA,NA,NA	,,X;X;	0.76069,,X;X;	0.76069	P29372-4 Isoform 3 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372 DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 , A2IDA3 DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 , P29372-5 Isoform 4 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372-2 Isoform 2 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG ,
NM(15.994915)ITGTSQAD C(470.29977)AVLIVAAGV GEFEAGISK	NA,NA,NA	,,X;X;	1.38929,,X;X;	1.38929	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 ,
NM(15.994915)ITGTSQAD C(470.29977)AVLIVAAGV GEFEAGISK	NA,NA,NA,NA	,,,X;	0.97248,1.03871,,1. 22003,,X;	1.03871	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 , A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
NFPAIGGTGPTSDTGWGC(464.28596)M(15.994915) LR	NA,C74,M75,C74,M75,NA	,,X;X;	1.10739,,X;X;	1.10739	Q9Y4P1-2 Isoform 2 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B , Q9Y4P1 Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B PE=1 SV=2 , Q9Y4P1-6 Isoform 6 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B ,
C(464.28596)GAQDKEHPR	NA,NA	U,,X;X;	1.51098,,X;X;	1.51098	Q96GX9 Methylthioribulose-1-phosphate dehydratase OS=Homo sapiens GN=APIP PE=1 SV=1 ,
IIC(464.28596)SAGLSLLAE ER	NA,NA,NA	,,,X;X;	1.42833,1.24308,,X ;X;	1.335705	Q9BV86 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 , S4R338 N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=1 ,
QVLMGPYPNDTC(470.299 77)PEVGFFDVLGNDR	NA,NA	U,,U,,U,,	1.43189,,1.53546,,1 .49641,,	1.49641	Q9H3P7 Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 ,
C(470.29977)HTPPLYR	NA,NA,NA	,,X,,,	1.45368,,X;1.26774 ,,	1.36071	M0R117 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=1 , Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 ,
LNIISNLDC(464.28596)VN EVIGIR	C402,C357,NA,C390,NA	,,,X;	1.40423,1.5481,,1.5 7984,,X;	1.5481	P30154-2 Isoform 2 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B , P30154-4 Isoform 4 of

					Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B , P30154 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3 , P30153 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 ,
C(464.28596)NLEEISNYG VSGFQTTEHFLTAVHR	C342,NA	U,U,;X;X;	1.99323,1.3939,;X; X;	1.693565	Q9NVN8 Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens GN=GNL3L PE=1 SV=1 ,
QPAIM(15.994915)PGQSY GLEDGSC(470.29977)SYK DFSESR	NA,NA,NA	,;X;X;	1.18125,;X;X;	1.18125	MOQXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
NTGIIC(470.29977)TIGPAS R	NA,NA	,;X;X;	1.42685,;X;X;	1.42685	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 ,
C(470.29977)M(15.99491 5)QEIPQEIQK	NA,NA	,;X;X;	3.13805,;X;X;	3.13805	Q8NB16 Mixed lineage kinase domain-like protein OS=Homo sapiens GN=MLKL PE=1 SV=1 ,
IVGYFVSGC(470.29977)DP SIM(15.994915)GIGPVPAI SGALK	NA,NA,C287,M292,NA,NA	,;X;X;	1.57815,;X;X;	1.57815	A0A0B4J2A4 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 , P42765 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 ,
SGGLQTPEC(470.29977)LS R	NA,NA	,;X;X;	1.44395,;X;X;	1.44395	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 ,
C(464.28596)LKVSTSTTK	C283,NA,NA,C283,NA,NA	,;X;X;	0.18298,;X;X;	0.18298	P15529-3 Isoform D of Membrane cofactor protein OS=Homo sapiens GN=CD46 , P15529-11 Isoform C of Membrane cofactor protein OS=Homo sapiens GN=CD46 , P15529-14 Isoform I of Membrane cofactor protein OS=Homo sapiens GN=CD46 , P15529-6 Isoform J of Membrane cofactor protein OS=Homo sapiens GN=CD46 , P15529-8 Isoform M of Membrane cofactor protein OS=Homo sapiens GN=CD46 ,
GLC(470.29977)AIAQAESL R	NA,NA	,,;,;,;	1.59847,;1.33185,1. 37922,;1.14783,;	1.355535	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 ,
GHSSDSNPAIC(464.28596) R	C31,NA	,,;,X;	1.58715,;1.23816,; X;	1.412655	Q5JTH9 RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 ,
LADQC(470.29977)TGLQG	C129,NA,NA,NA	,;X;X;	1.43987,;X;X;	1.43987	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens

FLVFHSFGGGTSGFTSLLMER					GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
SEFYANEAC(464.28596)K	NA,NA,C381,NA,C219,NA,NA	;;X;X;	0.92079;;X;X;	0.92079	A0A087X0W7 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 , A0A087WT95 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 , P49753 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 ,
LQILNSIFPGIGC(464.28596)PVPR	NA,NA	U;;X;X;	1.4035;;X;X;	1.4035	Q9NX47 E3 ubiquitin-protein ligase MARCH5 OS=Homo sapiens GN=MARCH5 PE=1 SV=1 ,
SKDVYGYSSC(464.28596)R	NA,NA	U;;X;X;	4.59821;;X;X;	4.59821	Q8N9Z2 Coiled-coil domain-containing protein 71L OS=Homo sapiens GN=CCDC71L PE=2 SV=2 ,
DLM(15.994915)ANATC(470.29977)FR	M1442,C1447,NA,M2128,C2133,NA	;;X;X;	1.76589;;X;X;	1.76589	H7C1M2 Protein SON (Fragment) OS=Homo sapiens GN=SON PE=1 SV=1 , P18583-5 Isoform D of Protein SON OS=Homo sapiens GN=SON , P18583-2 Isoform A of Protein SON OS=Homo sapiens GN=SON ,
AATM(15.994915)SAVEAATC(464.28596)R	NA,M258,C266,NA,M121,C129,NA	;;X;X;	1.42483;;X;X;	1.42483	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 , Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 , Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL , B5MD87 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2 ,
LGTTAGQM(15.994915)C(470.29977)SGLPGLSSVDINFGDSINESEGIPLKR	M474,C475,NA,NA	;;X;X;	1.42405;;X;X;	1.42405	A0A087WV66 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1 , P46013 Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 ,
LGYILTC(470.29977)PSNLGTGLR	C347,NA,C347,NA,NA	;;X;X;	1.31162;;X;X;	1.31162	P12532-2 Isoform 2 of Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A , P12532 Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 ,
LNPQC(464.28596)IPYTLQNHYYR	NA,C497,NA,NA	;;X;X;	1.66227;;X;X;	1.66227	O95453-2 Isoform 2 of Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN , O95453-3 Isoform 3 of Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN , O95453 Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN PE=1 SV=1 ,

GNVAGDSKNDPPM(15.994915)EAAGFTAQVILNHPGQISAGYAPVLDCHTAHIAC(470.29977)K	NA,NA	,,;X;X;	1.7648,1.48699,,;X;X;	1.625895	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
TIAEC(470.29977)LADELINAAK	C172,NA,C172,NA	,,;,;,;	1.37174,1.39591,,;1.58215,,;1.2708,,;	1.383825	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , MOR0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , MOR0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
VLQSEFC(470.29977)NAVR	NA,C47,NA,NA	,;X;X;	1.34335,,;X;X;	1.34335	Q9NUP9 Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1 , G3V1D4 Lin-7 homolog C (C. elegans), isoform CRA_b OS=Homo sapiens GN=LIN7C PE=1 SV=1 ,
GNVAGDSKNDPPM(15.994915)EAAGFTAQVILNHPGQISAGYAPVLDCHTAHIAC(470.29977)K	NA,NA	,;X;X;	1.93635,,;X;X;	1.93635	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
TIAEC(470.29977)LADELINAAK	C172,NA,C172,NA	,,;,;,;	1.39967,,;1.58461,,;1.34789,,;	1.39967	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , MOR0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , MOR0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
C(464.28596)AGPTPEAELQALAR	C52,NA	U,,;X;X;	1.4962,,;X;X;	1.4962	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 ,
DILKEM(15.994915)FPYEA STPTGISASC(470.29977)R	M308,C323,NA,NA,NA,NA,NA,NA	,;X;X;	1.13741,,;X;X;	1.13741	G5E972 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=1 , P42167 Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 , P42167-2 Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO ,
DYVLNC(470.29977)SILNP LLTLLTK	NA,NA	,;X;X;	1.2263,,;X;X;	1.2263	O60684 Importin subunit alpha-7 OS=Homo sapiens GN=KPNA6 PE=1 SV=1 ,
VTEDENDIEIPSEDDGTVL LSTVTAQFPGAC(470.29977)GLR	NA,C39,C39,C39,NA,NA,NA	,,;X;X;	1.67148,2.1752,,;X;X;	1.92334	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens

					GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
VLC(470.29977)PINYPLSP TR	C454,NA,NA	,,X;X;	1.99938,,X;X;	1.99938	Q96LD4 Tripartite motif-containing protein 47 OS=Homo sapiens GN=TRIM47 PE=1 SV=2 , Q96LD4-2 Isoform 2 of Tripartite motif-containing protein 47 OS=Homo sapiens GN=TRIM47 ,
VETNQDWSLM(15.994915) C(464.28596)PNECPGLDE VWGEEFEKLYASYEK	NA,NA	,,X;X;	1.85157,,X;X;	1.85157	P23921 Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1 ,
VLVVGAGGIGC(470.29977) JELLK	C30,NA	,,X;X;	1.44551,,X;X;	1.44551	Q9UBT2 SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2 ,
VDDEILGFISEATPLGGIQAA STESC(464.28596)NQQLD LALCR	NA,NA,NA	U,U,,X;U,;	1.83742,1.90829,,X ;1.59667,;	1.83742	P42166 Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 ,
VDDEILGFISEATPLGGIQAA STESC(464.28596)NQQLD LALCR	NA,NA,NA	U,,X;X;	3.7697,,X;X;	3.7697	P42166 Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 ,
SFEC(470.29977)LLGLNSN IGIR	C88,NA,NA,NA	,,X;X;	1.91777,,X;X;	1.91777	H3BTQ7 Origin recognition complex subunit 6 OS=Homo sapiens GN=ORC6 PE=1 SV=1 , H3BT22 Origin recognition complex subunit 6 OS=Homo sapiens GN=ORC6 PE=1 SV=1 , Q9Y5N6 Origin recognition complex subunit 6 OS=Homo sapiens GN=ORC6 PE=1 SV=1 ,
YGAVDPLLALLAVPDM(15. 994915)SSLAC(464.28596) GYLR	M218,C223,NA	U,,X;X;	1.44844,,X;X;	1.44844	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 ,
AAIGC(464.28596)GIVESIL NWVK	NA,C431,NA,C486,NA	,,,X;	1.66846,,2.7375,,X;	2.20298	P11388-3 Isoform 3 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A , P11388-2 Isoform 2 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A , P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 , P11388-4 Isoform 4 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A ,
LPSLPLVQGELVGG LTC(470 .29977)LTAQTHSLLQHQL QLTLLDQYIR	C213,NA,NA,NA,NA	,,X;X;	1.3083,,X;X;	1.3083	Q7Z7H8 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 , Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10, mitochondrial

					OS=Homo sapiens GN=MRPL10 ,
LTALDYHNPAGFNC(464.28596)KDETEFR	C19,NA	,,;,;	1.50774,,1.5068,,1.19123,,	1.5068	Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 ,
FALAC(470.29977)NASDKI IEPIQSR	NA,NA,NA	,,X,,;	1.49121,,X;1.38971 ,,	1.44046	P35250-2 Isoform 2 of Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 , P35250 Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3 ,
VAC(470.29977)ITEQVLT VNKR	NA,NA	,,;,;	1.28454,1.34496,,1.31754,,1.39196,,	1.33125	P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 ,
VAC(470.29977)ITEQVLT VNKR	NA,NA	,,;,;	1.65688,1.32086,,1.44439,,1.45836,,	1.451375	P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1 ,
VALEGLRPTIPPGISPHVC(470.29977)K	C361,NA,C453,NA	,,;,;	1.61321,,2.8936,,1.52013,,	1.61321	Q13418-2 Isoform 2 of Integrin-linked protein kinase OS=Homo sapiens GN=ILK , Q13418 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 , A0A0A0MTH3 Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=1 ,
EFHQAGKPIGLCC(464.28596)IAPVLA	C188,NA	,,X;X;	1.96127,,X;X;	1.96127	A0A096LP16 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
EFHQAGKPIGLCC(464.28596)IAPVLA	C188,NA	,,X;X;	2.14522,,X;X;	2.14522	A0A096LP16 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
EFHQAGKPIGLCC(464.28596)IAPVLA	C188,NA	,,X;X;	1.64927,,X;X;	1.64927	A0A096LP16 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
C(470.29977)SEGSFLLTTF PRPVTVEPM(15.994915)D QLDDEEGLPEK	C119,M138,NA,NA	,,X,,;	1.58199,,X;1.31178 ,,	1.446885	Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO , Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 ,
LALFNPDC(470.29977)W DR	C44,NA	U,,X;X;	1.64722,,X;X;	1.64722	O00483 Cytochrome c oxidase subunit NDUF44 OS=Homo sapiens GN=NDUF44 PE=1 SV=1 ,
LVIVGDGAC(464.28596)G K	NA,NA,C180,NA,C16,NA	,,X;X;	1.9533,,X;X;	1.9533	Q5JR08 Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=7 , U3KQA9 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=7 , U3KQV3 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=7 , P08134 Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1 , E9PQH6 Rho-related GTP-binding protein RhoC

					(Fragment) OS=Homo sapiens GN=RHOC PE=1 SV=1 ,
LALFNPVC(470.29977)WDR	C44,NA	U,,X;X;	1.68703,,X;X;	1.68703	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 ,
HFLSDTGMAC(464.28596)R	NA,NA	,,X;X;	1.9503,,X;X;	1.9503	Q5TFE4 5'-nucleotidase domain-containing protein 1 OS=Homo sapiens GN=NT5DC1 PE=1 SV=1 ,
C(470.29977)IAMM(15.994915)CNEFFEGFPDKQPR	C81,M85,NA	U,U,,X;X;	0.08392,0.0,,X;X;	0.04196	P26447 Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 ,
GLELIASENFC(464.28596)SR	NA,NA,C59,NA,NA	,,X;X;	1.28199,,X;X;	1.28199	P34897 Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 , P34897-3 Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 ,
TPC(464.28596)SSLLPLLNAHAATSGK	C307,NA,NA,NA,C367,NA,C397,NA	,,,,X;	1.09612,,1.25972,,X;	1.17792	B8ZZZ7 DNA polymerase-transactivated protein 6, isoform CRA_b OS=Homo sapiens GN=SPATS2L PE=1 SV=1 , Q9NUQ6-4 Isoform 4 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L , A0A0A0MSG5 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=1 , Q9NUQ6 SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2 , Q9NUQ6-2 Isoform 2 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L , Q9NUQ6-3 Isoform 3 of SPATS2-like protein OS=Homo sapiens GN=SPATS2L ,
THTYEC(464.28596)R	NA,NA,C1137,NA	,,X;X;	2.24216,,X;X;	2.24216	C9J4M6 DNA-directed RNA polymerase subunit beta OS=Homo sapiens GN=POLR2B PE=1 SV=2 , C9J2Y9 DNA-directed RNA polymerase subunit beta OS=Homo sapiens GN=POLR2B PE=1 SV=2 , P30876 DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1 ,
GC(464.28596)LLYGPPGTGK	NA,NA,NA	,,X,,,;	1.384,,X;1.123,,;	1.2535	A0A087X2I1 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 , P62333 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 ,
MPC(470.29977)QLHQVIVAR	C640,NA	,,X;X;	1.63487,,X;X;	1.63487	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 ,
TQYSCYC(464.28596)CK	NA,C229,NA	,,X,,,;	1.4818,,X;0.89976,,;	1.19078	Q9UGI8 Testin OS=Homo sapiens GN=TES PE=1 SV=1 , Q9UGI8-2 Isoform 2 of Testin OS=Homo sapiens GN=TES ,
VMALQEAC(464.28596)EAYLVGLFEDTNLC(464.2859	C97,C111,NA	U,,X;X;	13.0115,,X;X;	13.0115	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,

6)AIHAK					
NSC(470.29977)PLTPVVSK	NA,NA,NA	U,,X;X;	2.0492,,X;X;	2.0492	Q6IN84 rRNA methyltransferase 1, mitochondrial OS=Homo sapiens GN=MRM1 PE=1 SV=1 ,
LC(470.29977)YVALDFEQE M(15.994915)ATAASSSL EK	NA,NA,NA,NA,NA,NA	,,;,;	1.31566,,1.19573,,1 .14266,;	1.19573	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 , Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 ,
FQSSAVM(15.994915)ALQ EASEAYLVGLFEDTNLC(470 .29977)AIHAK	NA,NA	U,U,,U;X;	1.38652,1.41774,,1. 40509,,X;	1.40509	Q71DI3 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 ,
LKGC(464.28596)SNEPYFG SLTALVCQHSITPLALPCK	NA,NA	,,X;X;	1.42438,,X;X;	1.42438	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
FGVIC(464.28596)LEDLIHE IAFPGK	NA,NA	U,U,,X;X;	1.8804,1.89888,,X; X;	1.88964	Q6DKI1 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1 ,
LKGC(464.28596)SNEPYFG SLTALVCQHSITPLALPCK	NA,NA	,,X;X;	1.3836,,X;X;	1.3836	Q68CZ2 Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 ,
HELQANC(464.28596)YEE VKDR	C177,NA,NA,C139,NA	,,;,;	1.46006,,1.22111,,1 .14319,;	1.22111	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 , G3V1A4 Cofilin 1 (Non-muscle), isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 , P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 ,
THC(470.29977)PYAVALPE VAPAQPLTEALR	C143,NA	,,X;X;	1.88612,,X;X;	1.88612	Q6PIG6 BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 ,
LVVPATQC(470.29977)GS LIGK	C109,NA	U,U,,U;X;	1.41248,1.99499,,1. 37578,,X;	1.41248	Q15365 Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 ,
STC(464.28596)SLTPALAA HFSENLK	NA,NA,NA,NA,NA	,,X;X;	0.9379,,X;X;	0.9379	Q9BTA9 WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=3 , Q9BTA9- 5 Isoform 4 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC , Q9BTA9-2 Isoform 2 of WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC , A0A0A0MRT2 WW domain- containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=1 ,
AYGGSMC(464.28596)AK	NA,NA	U,,U;X;	1.36868,,1.32301,, X;	1.345845	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 ,
GC(470.29977)AFVTFTR	C176,C177,NA,NA,NA	,,X;X;	1.60728,,X;X;	1.60728	Q92879-4 Isoform 4 of CUGBP Elav-like family member 1 OS=Homo sapiens GN=CELF1 , G5EA30 CUG triplet repeat,

					RNA binding protein 1, isoform CRA_c OS=Homo sapiens GN=CELF1 PE=1 SV=1 ,
YKVC(464.28596)NYGLTFT QK	NA,NA	;;X;X;	1.65324;;X;X;	1.65324	Q9Y277 Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 ,
FCSFSPC(464.28596)IEQV QR	C209,NA	;;;X;	1.7066;;1.10704;;X;	1.40682	Q96FX7 tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens GN=TRMT61A PE=1 SV=1 ,
KLLDLVQQSC(464.28596) NYK	NA,C30,NA	;;X;;;	1.58665;;X;1.52064 ;;	1.553645	B1AHD1 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=1 , P55769 NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 ,
C(464.28596)SILAAANPAY GR	C482,NA	;;X;X;	0.73695;;X;X;	0.73695	P33993 DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 ,
C(464.28596)PQVEEAIVQS GQK	C146,C146,NA	;;X;X;	1.71091;;X;X;	1.71091	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
QC(464.28596)PIMDPAW EAPGVPIIDAIIFGGR	NA,NA,NA	;;X;X;	0.00386;;X;X;	0.00386	Q16822 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 ,
QC(464.28596)PIMDPAW EAPGVPIIDAIIFGGR	C297,NA,NA,NA,NA	;;;X;	0.00985;;1.63894;; X;	0.824395	B4DW73 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=1 , Q16822 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 ,
QC(464.28596)PIMDPAW EAPGVPIIDAIIFGGR	NA,NA,NA	;;X;X;	0.00787;;X;X;	0.00787	Q16822 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 ,
C(464.28596)EFEEVQGFL DQVAHKLPFAAK	NA,NA,NA,NA,NA	;;X;X;	1.6674;;X;X;	1.6674	E9PI14 39S ribosomal protein L16, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL16 PE=1 SV=1 , Q9NX20 39S ribosomal protein L16, mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1 ,
C(464.28596)EFEEVQGFL DQVAHKLPFAAK	NA,NA,NA,NA,NA	;;;X;X;	1.63634,1.66725;;X ;X;	1.651795	E9PI14 39S ribosomal protein L16, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL16 PE=1 SV=1 , Q9NX20 39S ribosomal protein L16, mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1 ,
NCGC(470.29977)LGASPN LEQLQEENLK	C34,NA,NA	;;X;X;	0.53395;;X;X;	0.53395	P54136 Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 ,
RPYGVGLLIAGYDDM(15.9 94915)GPHIFQTC(464.285	M146,C154,NA,NA	;;X;X;	1.29699;;X;X;	1.29699	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 , P25786 Proteasome subunit

96)PSANYFDCR					alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 ,
RPYGVGLLIAGYDDM(15.994915)GPHIFQTC(464.28596)PSANYFDCR	M146,C154,NA,NA	;;X;X;	1.34645;;X;X;	1.34645	P25786-2 Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 , P25786 Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 ,
KVAEPELM(15.994915)GTPDGTC(464.28596)YPPPPVPR	NA,M1882,C1889,NA	;;X;X;	0.91065;;X;X;	0.91065	F8VPD4 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 , P27708 CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 ,
M(15.994915)ALDALLQEI ALSEPQLC(464.28596)EVLQVAGPDR	NA,NA,NA	;;X;X;	1.30002;;X;X;	1.30002	C9J6P4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=1 , Q7Z2W4 Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3 ,
C(464.28596)LSEQSVAISR	NA,NA,NA	;;X;X;	1.1593;;X;X;	1.1593	P41134-2 Isoform ID-B of DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 , P41134 DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 PE=1 SV=3 ,
C(464.28596)TSAEEFVQR	C37,NA	;;X;X;	0.59376;;X;X;	0.59376	O60231 Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 OS=Homo sapiens GN=DHX16 PE=1 SV=2 ,
NVGIAFLIDDVLDFTSC(470.29977)SDQM(15.994915)GKPTSADLK	C276,M280,C276,M280,NA	;;X;X;	1.3704;;X;X;	1.3704	Q5T2R2-3 Isoform 3 of Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 , Q5T2R2 Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 PE=1 SV=1 ,
VQEAPIDEHWIIEC(464.28596)NDGVFQR	NA,C91,NA	;;X;X;	1.5028;;X;X;	1.5028	Q14353-2 Isoform 2 of Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT , Q14353 Guanidinoacetate N-methyltransferase OS=Homo sapiens GN=GAMT PE=1 SV=1 ,
NM(15.994915)ITGTSQADC(464.28596)AVLIVAAGVGEFEAGISK	NA,NA,NA,NA	;;;X;	1.38929,1.01723,0.84152;;1.16761;;X;	1.09242	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 , A0A087WVQ9 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
NM(15.994915)ITGTSQADC(464.28596)AVLIVAAGVGEFEAGISK	NA,NA,NA	;;;X;X;	0.97248,1.04011;;X;X;	1.006295	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , Q05639 Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 ,
DSGYGDIWC(464.28596)PERGEFLAPPR	C213,C176,NA,C228,C228,NA,NA	;;X;;	1.49629;;X;1.2798;;	1.388045	J3KP06 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , F8WD26 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , Q8WWI1-4

					Isoform 4 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 , Q8WWI1 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 , Q8WWI1-3 Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 , Q8WWI1-2 Isoform 2 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 ,
ANC(470.29977)IDSTASAE AVFASEVKK	C268,NA	;;X;X;	1.35499;;X;X;	1.35499	P22087 rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2 ,
AHSNPDFLPVDNC(470.29 977)LQSVLGQR	C703,NA,NA	;;X;X;	1.46269;;X;X;	1.46269	Q5VSL9-2 Isoform 2 of Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 , Q5VSL9 Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 PE=1 SV=1 ,
NPSTVC(464.28596)LCPE QPTCSNADSR	C42,C42,NA	;;X;X;	0.30017;;X;X;	0.30017	Q9H7E9-2 Isoform 2 of UPF0488 protein C8orf33 OS=Homo sapiens GN=C8orf33 , Q9H7E9 UPF0488 protein C8orf33 OS=Homo sapiens GN=C8orf33 PE=1 SV=1 ,
IGFPETEEEEIEIASNSDC(470.29977)IFPSAPDVKA	C353,NA,NA	;;X;;;	1.14008;;X;1.07518 ;;	1.10763	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP , Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 ,
TAGQTGM(15.994915)C(4 64.28596)GGVR	NA,NA	;;X;X;	1.7004;;X;X;	1.7004	Q5VTL8 Pre-mRNA-splicing factor 38B OS=Homo sapiens GN=PRPF38B PE=1 SV=1 ,
IGFPETEEEEIEIASNSDC(470.29977)IFPSAPDVKA	C353,NA,NA	;;X;X;	1.25673;;1.01935;; X;	1.13804	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP , Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 ,
SAQPSPHYM(15.994915)A APSSGQIYGSGPQGYNTQP VPVSGQC(464.28596)PPP STR	NA,NA,M235,C262,NA,NA ,NA	;;X;X;	1.39316;;X;X;	1.39316	A0A087WZF1 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 , C9JXK9 Lipoma-preferred partner (Fragment) OS=Homo sapiens GN=LPP PE=1 SV=1 , C9JUT4 LIM domain containing preferred translocation partner in lipoma, isoform CRA_e OS=Homo sapiens GN=LPP PE=1 SV=1 , Q93052 Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1 ,
SSYLNIIVGLVGSIDNDFC(47 0.29977)GTDM(15.99491 5)TIGTDSALHR	C241,M245,NA,C170,M17 4,NA,NA	;;X;X;	1.55532;;X;X;	1.55532	P08237-3 Isoform 3 of ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM , P08237 ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 ,
ASFENNCEIGC(464.28596)	C15,NA	;;X;X;	0.81061;;X;X;	0.81061	P56537 Eukaryotic translation initiation factor 6 OS=Homo

FAK					sapiens GN=EIF6 PE=1 SV=1 ,
LALFNPDCV(464.28596)W DRNNPEPWNK	C44,NA	U,,X;X;	1.63254,,X;X;	1.63254	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 ,
LALFNPDCV(464.28596)W DRNNPEPWNK	C44,NA	U,,X;X;	1.64023,,X;X;	1.64023	O00483 Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1 ,
TFVGT(464.28596)WM(15.994915)A PEVMEQVR	C218,M220,NA,NA,C218, M220,NA	,,X;X;	1.17047,,X;X;	1.17047	Q9UEW8 STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens GN=STK39 PE=1 SV=3 , O95747 Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 , C9JIG9 Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 , Q9UEW8-2 Isoform 2 of STE20/SPS1-related proline-alanine-rich protein kinase OS=Homo sapiens GN=STK39 ,
VLPMNTGVEAGETAC(470.29977)K	NA,NA,NA	U,,X;X;	1.80484,,X;X;	1.80484	P04181 Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 ,
DSEDPQTLLFSATC(464.28596)PHWVFNVAK	C310,C310,NA	,,X;X;	1.13159,,X;X;	1.13159	Q9NR30 Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 , Q9NR30-2 Isoform 2 of Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 ,
NC(464.28596)LTNFGHM(15.994915)DLTR	NA,NA,C96,M103,NA,NA	,,;,;	1.42979,,1.35003,,1.28238,,	1.35003	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
NC(464.28596)LTNFGHM(15.994915)DLTR	NA,NA,C96,M103,NA,NA	,,X;,;	1.42018,,X;1.34782,,	1.384	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
TDC(464.28596)SPIQFESA WALTNIASGTSEQTK	C133,NA	U,U,,X;X;	1.14875,0.82461,,X;X;	0.98668	P52292 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 ,
AYEYVEC(464.28596)PIR	NA,NA	U,,U,,X;	1.88291,,3.41817,,X;	2.65054	P53701 Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 ,
IAQLIC(470.29977)ER	C134,NA,NA	,,X;X;	1.44734,,X;X;	1.44734	P33316-2 Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT ,

FHFGDSL(464.28596)TH KGEIPALPPCK	C265,NA	,,X;X;	1.4501,,X;X;	1.4501	O75439 Mitochondrial-processing peptidase subunit beta OS=Homo sapiens GN=PMPCB PE=1 SV=2 ,
KITAFVPNDGC(464.28596) LNFIEENDEVLVAGFGR	NA,NA	,,X;X;	1.4563,,X;X;	1.4563	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
HVVC(464.28596)AAETGS GK	NA,NA	U,,X;U,,	1.83762,,X;1.80842 ,,	1.82302	Q9NUL7 Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=1 SV=2 ,
KITAFVPNDGC(464.28596) LNFIEENDEVLVAGFGR	NA,NA	,,,X;X;	1.6229,1.62603,,X; X;	1.624465	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
HTLDGAAC(464.28596)LL NSNKYFPSR	C102,C170,NA,NA,NA,NA	,,X;X;	1.30602,,X;X;	1.30602	Q9Y3A3-2 Isoform 2 of MOB-like protein phocein OS=Homo sapiens GN=MOB4 , S4R3N1 Protein HSPE1-MOB4 OS=Homo sapiens GN=HSPE1-MOB4 PE=3 SV=1 , Q9Y3A3-3 Isoform 3 of MOB-like protein phocein OS=Homo sapiens GN=MOB4 , Q9Y3A3 MOB-like protein phocein OS=Homo sapiens GN=MOB4 PE=1 SV=1 , B4DM50 MOB-like protein phocein OS=Homo sapiens GN=MOB4 PE=1 SV=1 ,
YSYVC(470.29977)PDLVK	C235,NA	,,X;X;	1.49891,,X;X;	1.49891	P61158 Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3 ,
SLLINAVEASC(464.28596)I R	C262,NA,C262,NA,NA,NA, C262,NA	,,,X;X;	1.44453,1.58602,1. 51301,,X;X;	1.51301	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , Q96C36 Pyrroline-5- carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 ,
SLLINAVEASC(464.28596)I R	C262,NA,C262,NA,NA,NA, C262,NA	,,,X;X;	1.57984,1.8555,,X; X;	1.71767	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , Q96C36 Pyrroline-5- carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1 ,
RSIQFVDWC(464.28596)P TGFK	NA,NA,NA,NA	,,X;X;	1.66933,,X;X;	1.66933	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A

					chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
LIC(470.29977)LVTGSPSIR	C590,NA,NA	U,,X;X;	2.02209,,X;X;	2.02209	Q6PI48 Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1 ,
GAVEC(470.29977)CPNCR	NA,NA	,,X;X;	1.34441,,X;X;	1.34441	P31689 DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 ,
KGLIAAIC(470.29977)AGP TALLAHEIGFGSK	NA,C86,NA,NA	,,X;X;	1.25555,,X;X;	1.25555	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
KGLIAAIC(470.29977)AGP TALLAHEIGFGSK	NA,C86,NA,NA	,,X;X;	1.2752,,X;X;	1.2752	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
KGLIAAIC(470.29977)AGP TALLAHEIGFGSK	NA,C86,NA,NA	,,X;X;	1.25467,,X;X;	1.25467	Q99497 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 , K7ELW0 Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1 , K7EN27 Protein deglycase DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=1 SV=1 ,
TQNLPC(464.28596)QLIS R	NA,NA	,,,X;	1.33646,,1.48834,, X;	1.4124	P37268 Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 ,
YGIIC(464.28596)MEDLIH EIYTVGKR	C186,NA,NA	,,,;	1.45638,,1.33108,,1 .24077,,	1.33108	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
YGIIC(464.28596)MEDLIH EIYTVGKR	C186,NA,NA	,,X,;	1.44229,,X;1.07878 ,,	1.260535	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
YGIIC(464.28596)MEDLIH EIYTVGKR	C186,NA,NA	,,X,;	1.42277,,X;1.29361 ,,	1.35819	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
NC(464.28596)SETQYESK	C112,NA	U,,X;X;	1.36461,,X;X;	1.36461	P61981 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 ,
GSSC(464.28596)FECTHY QSFLEYR	C188,NA	,,X;X;	1.68902,,X;X;	1.68902	P21964 Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2 ,

NC(470.29977)NDFQYESK	C112,NA	,,X;X;	1.2834,,X;X;	1.2834	Q04917 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 ,
LADQC(470.29977)TGLQG FLVFHSFGGGTGSFGFTSLLM (15.994915)ER	C129,M154,NA,NA,NA	,,,X;X;	1.43974,1.38268,,X; X;	1.41121	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 ,
LADQC(470.29977)TGLQG FLVFHSFGGGTGSFGFTSLLM (15.994915)ER	C129,M154,C129,M154,C199,M224,NA,NA	,,,X;	1.58311,,1.94909,,X;	1.7661	Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , F5H5D3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 ,
FTLDC(470.29977)THPVED GIM(15.994915)DAANFEQ FLQER	NA,NA	U,,U,,X;	1.68137,,1.39276,,X;	1.537065	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 ,
GVPGAIVNVSSQC(464.28596)SQR	NA,C137,NA	,,,X;	1.19182,,1.41476,,X;	1.30329	Q7Z4W1 L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 , J3QS36 L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=1 SV=1 ,
FTLDC(470.29977)THPVED GIM(15.994915)DAANFEQ FLQER	NA,NA	U,,X;X;	1.44006,,X;X;	1.44006	P35268 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 ,
GVPGAIVNVSSQC(464.28596)SQR	NA,NA	,,X;X;	1.21338,,X;X;	1.21338	Q7Z4W1 L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 ,
VC(464.28596)ISILHAPGD DPM(15.994915)GYESSAE R	NA,NA,NA	,,X,,,;	1.4698,,X;1.38927,,;	1.429535	P60604-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 , P60604 Ubiquitin-conjugating enzyme E2 G2 OS=Homo sapiens GN=UBE2G2 PE=1 SV=1 ,
EQC(464.28596)CYNCGKP GHLAR	C80,NA,C92,NA,C87,NA,NA,NA,NA	,,X;X;	1.491,,X;X;	1.491	P62633-7 Isoform 7 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633 Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 , P62633-5 Isoform 5 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-4 Isoform 4 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-3 Isoform 3 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-8 Isoform 8 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP

					sapiens GN=CNBP , P62633-6 Isoform 6 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-2 Isoform 2 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP ,
AYHEQLSVAEITNAC(470.29977)FEPANQM(15.994915)VK	NA,NA,NA,NA,NA	;;X;X;	1.45946;;X;X;	1.45946	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
AYHEQLSVAEITNAC(470.29977)FEPANQM(15.994915)VK	NA,NA,NA,NA,NA	;;X;X;	1.50452;;X;X;	1.50452	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
LFTEYPC(464.28596)GSGN VYAGVLAVAR	C280,NA	U;;X;X;	1.57505;;X;X;	1.57505	Q8IU81 Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens GN=IRF2BP1 PE=1 SV=1 ,
LC(464.28596)YVALDFEQE MATAASSSSLEK	NA,NA,NA,NA,NA,NA	,,,,;	1.35315,1.34667;;1.58679;;1.32927;;	1.34991	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 , Q6S8J3 POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 ,
SDVC(470.29977)TPGGTTI YGLHALEQGGLR	NA,C235,NA,C98,NA	;;X;X;	1.58721;;X;X;	1.58721	A0A0A0MQS1 Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=1 SV=1 , Q53H96 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3 , Q53H96-2 Isoform 2 of Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL , B5MD87 Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2 ,
LGTAPFC(464.28596)CP WEQLTQDWESR	C705,NA	U;;U;X;	1.43308;;1.30657;;X;	1.369825	Q99575 Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2 ,
LC(464.28596)GSGFQSIVN GCQEICVK	NA,NA,C92,NA,NA	;;X;X;	0.98598;;X;X;	0.98598	A0A0B4J2A4 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 , P42765 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 ,
QSELEPVVSLVDVLEEDDEELE	NA,NA,NA,NA,C35,NA	;;X;X;	1.17156;;X;X;	1.17156	HOYJA0 Putative E3 ubiquitin-protein ligase UBR7

NEAC(470.29977)AVLGGS DSEK					(Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 , G3V2G3 Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 , G3V253 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=1 , G3V336 Putative E3 ubiquitin-protein ligase UBR7 (Fragment) OS=Homo sapiens GN=UBR7 PE=1 SV=1 , Q8N806 Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 ,
LLDVLSGHEGPISGLC(470.29977)FNPM(15.994915)K	NA,C508,M512,NA	,,X;X;	1.71153,,X;X;	1.71153	A0A0B4J2E5 Protein LOC102724159 OS=Homo sapiens GN=LOC102724159 PE=1 SV=1 , Q15269 Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=2 SV=2 ,
GC(464.28596)TIVKPFNLS QGK	C301,C301,NA	,,X;X;	0.36674,,X;X;	0.36674	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 , Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 ,
TGNGPM(15.994915)SVC(470.29977)GR	NA,M490,C493,NA,NA,NA,NA	,,,X;	1.11663,,1.44457,,X;	1.2806	O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 , O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , A0A087X1A5 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 , Q5JW30 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 ,
DVPLADPGLDNDVGVEVG GSGGC(470.29977)LEER	NA,NA	U,,X;X;	1.43051,,X;X;	1.43051	Q9NPA3 Mid1-interacting protein 1 OS=Homo sapiens GN=MID1IP1 PE=1 SV=1 ,
LVSSPC(470.29977)CIVTST YGWTANM(15.994915)ER	C589,M602,NA	U,,X;X;	1.38037,,X;X;	1.38037	P08238 Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 ,
AVC(464.28596)MLSNTTA IAEAWAR	NA,NA,NA,NA,NA,C376,NA,NA	,,X;X;	1.92037,,X;X;	1.92037	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65 Tubulin

					alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
AVC(464.28596)MLSNTTA IAEAWAR	NA,NA,NA,NA,NA,NA,C37 6,NA,NA	,,;,;,;	1.56869,1.57584,1. 57681,,1.4693,,1.33 99,;	1.56869	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
FM(15.994915)TPVIQDNP SGWGPC(470.29977)AVPE QFR	M5,C19,NA,NA,NA	,,;,;,;	1.38412,,1.91522,,1 .30811,;	1.38412	O15371-2 Isoform 2 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D , O15371 Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 , O15371-3 Isoform 3 of Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D ,
AVC(464.28596)MLSNTTA IAEAWAR	NA,C376,NA,NA,NA,C376, NA,NA	,,;,;,X;	1.91209,1.8566,,2.0 5043,,X;	1.91209	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , P68363 Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
C(470.29977)ASQVGMTA PGTR	C215,C204,NA,NA	,,X;X;	1.42755,,X;X;	1.42755	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
HGELWC(464.28596)AVSK	C913,NA	,,X;X;	1.5709,,X;X;	1.5709	O94906 Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 ,
LLACIASRPGQC(464.2859	NA,NA	,,;,X;	1.57034,,1.4658,,X;	1.51807	P62241 40S ribosomal protein S8 OS=Homo sapiens

6)GR					GN=RPS8 PE=1 SV=2 ,
LLACIASRPGQC(464.28596)GR	NA,NA	,,;,;	1.54453,,1.73571,,1.28207,,	1.54453	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
FVIHC(470.29977)NSPVW GADKCEELLEK	C275,NA,NA	,,X;X;	1.96509,,X;X;	1.96509	O75367-3 Isoform 3 of Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY , O75367 Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4 ,
LSAPGC(470.29977)WAAC TNFSR	NA,NA,NA	,,X;X;	1.53078,,X;X;	1.53078	Q04941 Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1 , Q04941-2 Isoform 2 of Proteolipid protein 2 OS=Homo sapiens GN=PLP2 ,
M(15.994915)TNHC(464.28596)VFSANEDHETIR	M93,C97,M93,C97,NA	,,X;X;	1.44386,,X;X;	1.44386	E7ETZ4 Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens GN=BZW2 PE=1 SV=1 , Q9Y6E2 Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens GN=BZW2 PE=1 SV=1 ,
IQVGICLLLVLC(470.29977)ERFTFFEVVCNM(15.994915)IPFCTIK	C52,M64,NA	U,,X;X;	2.16006,,X;X;	2.16006	A6NIM6 Solute carrier family 15 member 5 OS=Homo sapiens GN=SLC15A5 PE=3 SV=2 ,
AVLLVGLC(464.28596)DS GK	C73,NA	,,X;X;	1.36563,,X;X;	1.36563	Q9Y5M8 Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 ,
KLFAPQQILQC(464.28596)SPAN	C230,NA,NA,NA	,,X;X;	1.50865,,X;X;	1.50865	P04183 Thymidine kinase, cytosolic OS=Homo sapiens GN=TK1 PE=1 SV=2 , K7ERV3 Thymidine kinase OS=Homo sapiens GN=TK1 PE=1 SV=1 ,
STSSSC(464.28596)HAPAV TQHAPYFK	NA,NA,NA	U,,X;X;	1.20424,,X;X;	1.20424	P30048 Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 ,
NIDPKPC(470.29977)TPR	C85,NA,C85,C85,NA	,,X;X;	1.33114,,X;X;	1.33114	K7EQ55 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=2 , Q96EP5-2 Isoform 2 of DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 , Q96EP5 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=1 , K7EK33 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=2 ,
AVAILC(470.29977)NHQR	NA,NA	U,,U,,U,,	1.42276,,1.39115,,1.5022,,	1.42276	P11387 DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 ,
DLNYC(470.29977)FSGM(15.994915)SDHR	C267,M271,C267,M271,C267,M271,NA	,,X;X;	1.52786,,X;X;	1.52786	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 , P55795 Heterogeneous

					nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 ,
IISDNLTYC(470.29977)K	NA,NA	,;X;X;	1.55473,,X;X;	1.55473	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
DLNYC(470.29977)FSGM(15.994915)SDHR	C267,M271,C267,M271,C 267,M271,NA	,,,X;X;	1.5823,1.77565,,X; X;	1.678975	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 , P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 ,
YGIIC(464.28596)MEDLIH EIYTVGK	C186,NA	,;X;X;	1.45447,,X;X;	1.45447	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
HC(470.29977)SQVDSVR	NA,NA,C112,NA	,;X;X;	1.72908,,X;X;	1.72908	Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN , Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 , Q14247-2 Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN ,
NVGIAFLIDDVLDFTSC(46 4.28596)SDQM(15.99491 5)GKPTSADLK	C276,M280,C276,M280,N A	,;X;X;	1.3704,,X;X;	1.3704	Q5T2R2-3 Isoform 3 of Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 , Q5T2R2 Decaprenyl-diphosphate synthase subunit 1 OS=Homo sapiens GN=PDSS1 PE=1 SV=1 ,
YGIIC(464.28596)MEDLIH EIYTVGK	C186,NA,NA	,,,;,,;	1.50487,1.47894,,1. 34849,,1.29818,,;	1.413715	P18124 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 , A8MUD9 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 ,
VC(464.28596)EDLDTSVN LAWTSGTNCTR	C199,NA	,;X;X;	1.88096,,X;X;	1.88096	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
GNVAGDSKNDPPM(15.99 4915)EAAGFTAQVIILNHPG QISAGYAPVLDLC(464.2859 6)HTAHIACK	NA,NA,NA	,,,;X;	1.66911,,1.61202,, X;	1.640565	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , A0A087WVQ9 Elongation factor 1- alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
HLNEIDLFHC(464.28596)I DPNSK	C62,NA,C58,NA	,;X;;	0.88628,,X;0.39394 ,,	0.64011	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 ,
C(470.29977)PICVPCGLR	NA,NA	,;X;X;	1.31414,,X;X;	1.31414	Q9HAV4 Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 ,

ADQQYEC(470.29977)VAE IGEGAYGK	C15,NA	U,U,;X;X;	1.59012,2.04124,;X ;X;	1.81568	Q00534 Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1 ,
VAM(15.994915)KHPSAVT AC(464.28596)NLDLENLV TDSNR	M316,C325,NA	U,;X;X;	3.44581,;X;X;	3.44581	Q9Y678 Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 ,
IQCTLQDVGSALATPC(470. 29977)SSAR	NA,NA,NA,C80,NA,NA,NA	,;X;X;	1.33835,;X;X;	1.33835	Q96EY8 Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 , S4R3P5 Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=1 SV=1 ,
RPLNPLASGQGTSEENTFYS WLEGLC(470.29977)VEK	C241,NA	U,;X;X;	1.35972,;X;X;	1.35972	Q96HE7 ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2 ,
KLVNSVAGC(464.28596)A DDALAGLVACNPNLQLLQG HR	C14,NA,NA,NA,NA	,;X;X;	2.48224,;X;X;	2.48224	A0A087WUL0 Triokinase/FMN cyclase OS=Homo sapiens GN=TKFC PE=1 SV=1 , Q3LXA3 Triokinase/FMN cyclase OS=Homo sapiens GN=TKFC PE=1 SV=2 , H0YCY6 Triokinase/FMN cyclase (Fragment) OS=Homo sapiens GN=TKFC PE=1 SV=1 , Q3LXA3-2 Isoform 2 of Triokinase/FMN cyclase OS=Homo sapiens GN=TKFC ,
SEGGFIWAC(470.29977)K	NA,NA	U,;X;X;	1.40372,;X;X;	1.40372	O75874 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 ,
NMM(15.994915)AAC(47 0.29977)DPR	M300,C303,NA,M300,C30 3,M300,C303,M647,C650, M300,C303,M300,C303,N A,M263,C266,M282,C285, M300,C303,NA	,,,,;X,;;	1.52685,1.30379,1. 52685,1.30379,;X;1 .29252,1.29252,;	1.30379	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 , P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
NQSFC(470.29977)PTVNL DK	NA,C70,NA,NA	,,,,;X;	1.41138,;1.35699,; X;	1.384185	P46776 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2 , E9PLL6 60S ribosomal protein L27a

					OS=Homo sapiens GN=RPL27A PE=1 SV=1 , E9PID9 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1 ,
LC(464.28596)DFGVSGQLI DSM(15.994915)ANSFVGT R	C114,M126,C207,M219,C 211,M223,NA,NA	;;X;;	0.86318;;X;1.24156 ;;	1.05237	G5E9C7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 , Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 , P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 , Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 ,
SYC(470.29977)AEIAHNVS SK	C96,C114,C96,NA	;;X;X;	1.41462;;X;X;	1.41462	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
SYC(470.29977)AEIAHNVS SK	C96,C114,C96,NA	;;X;;	1.35709;;X;1.26511 ;;	1.3111	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
VLPM(15.994915)NTGVEA GETAC(470.29977)K	NA,NA,NA	U;;U;;X;	1.41973;;2.04645;; X;	1.73309	P04181 Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1 ,
LHTGPLPEQC(470.29977) R	C163,NA,NA,NA	;;X;X;	1.59586;;X;X;	1.59586	A0JLT2-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 , J3KR33 Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 PE=1 SV=1 , A0JLT2 Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 PE=1 SV=2 ,
NVQLLSQFVSPFTGC(470.2 9977)IYGR	NA,NA,NA	U;;U;;X;	1.42143;;1.37381;; X;	1.39762	Q9Y3D5 28S ribosomal protein S18c, mitochondrial OS=Homo sapiens GN=MRPS18C PE=1 SV=1 ,
VQPQWSPPAGTQPC(464. 28596)R	C110,NA,NA	;;X;X;	1.35872;;X;X;	1.35872	P49589-3 Isoform 3 of Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS ,
EAVTSM(15.994915)GGKS SC(470.29977)PVCGISYSF EHLQANQHLANIVER	NA,M404,C410,NA,NA	;;X;X;	0.30404;;X;X;	0.30404	Q9BYJ4 Tripartite motif-containing protein 34 OS=Homo sapiens GN=TRIM34 PE=1 SV=2 , B2RNG4 Protein TRIM6-TRIM34 OS=Homo sapiens GN=TRIM6-TRIM34 PE=2 SV=1 ,

					Q9BYJ4-2 Isoform 2 of Tripartite motif-containing protein 34 OS=Homo sapiens GN=TRIM34 ,
HIGDGC(464.28596)CLTR	NA,C202,NA	,,;,;	1.43892,,1.33878,,1.21816,;	1.33878	A0A087WZT2 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=1 , Q6UX53 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=2 ,
VWAVLPSSPEAC(464.28596)GAASLQER	C170,NA,NA	U,,X;X;	1.63584,,X;X;	1.63584	Q5T440 Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1 ,
VICAEEPIC(464.28596)KDFPETNNILK	C456,NA	,,X;X;	1.65825,,X;X;	1.65825	P49915 GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 ,
QPAIMPGQSYGLEDGSC(470.29977)SYKDFSES	NA,NA,NA	,,;,;	1.54626,1.97516,2.24121,,1.57268,,1.45231,;	1.57268	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
VC(464.28596)AKPWAPDM(15.994915)TLPGISPPPEK	NA,C195,M203,NA	,,X;X;	1.39366,,X;X;	1.39366	Q96FF9 Sororin OS=Homo sapiens GN=CDCA5 PE=1 SV=1 , B5MBX0 Sororin OS=Homo sapiens GN=CDCA5 PE=1 SV=1 ,
C(464.28596)ELENCQPFVVELHKG	C100,NA	,,X;X;	0.70989,,X;X;	0.70989	Q06203 Amidophosphoribosyltransferase OS=Homo sapiens GN=PPAT PE=1 SV=1 ,
LRLPDSGDSC(464.28596)ASASQVAGIAGAHHAQSLA VLPVESP	NA,NA	U,,X;X;	5.43537,,X;X;	5.43537	A0A0A0MSF3 Cyclin-L2 OS=Homo sapiens GN=CCNL2 PE=1 SV=1 ,
VS DTVVEPYNATLSVHQLVE NTDETYC(464.28596)IDNE ALYDICFR	C201,C201,NA,C183,C201,NA	,,X;X;	1.56467,1.57367,,X;X;	1.56917	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
VS DTVVEPYNATLSVHQLVE NTDETYC(464.28596)IDNE ALYDICFR	C201,C201,NA,C164,C183,C201,NA	,,;,;	1.33756,,1.44156,,1.31351,;	1.33756	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , K7ESM5 Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=1 SV=1 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin

					beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
SNNYVQEPEC(464.28596) R	C69,NA,NA	;;X;X;	0.80386;;X;X;	0.80386	Q7Z6M4 Transcription termination factor 4, mitochondrial OS=Homo sapiens GN=MTERF4 PE=1 SV=3 ,
VSDTVVEPYNATLSVHQLVE NTDETYC(464.28596)IDNE ALYDICFR	C201,C201,NA,C183,C201, NA	;;X;X;	2.45662;;X;X;	2.45662	P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 , Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
LVFLAC(470.29977)CVAPT NPR	C301,NA	U;;X;X;	2.01896;;X;X;	2.01896	Q14566 DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 ,
SQSVSVSGPGPGPGGLC(4 64.28596)PGPNVLLNQNN PPAPQPQLAR	C222,NA	U;;X;X;	1.30247;;X;X;	1.30247	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 ,
GFVTM(15.994915)TLESLE EIQDVSC(464.28596)AWK	M590,C603,NA	U;;X;X;	1.58873;;X;X;	1.58873	Q9BQ39 ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1 ,
AC(464.28596)SVGAVPGIT K	C278,NA	U,U;;X;X;	2.17548,1.49906;;X ;X;	1.83727	Q9NVN8 Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens GN=GNL3L PE=1 SV=1 ,
FALAC(464.28596)NASDKI IEPIQSR	NA,NA,NA	;;X;;;	1.49121;;X;1.38971 ;;	1.44046	P35250-2 Isoform 2 of Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 , P35250 Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3 ,
SVLLCGIEAQAC(464.2859 6)ILNTTLDLLDR	C114,NA,NA,NA	;;X;X;	1.04587;;X;X;	1.04587	K7ENV7 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=7 , K7EKW4 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=1 , Q96AB3 Isochorismatase domain-containing protein 2 OS=Homo sapiens GN=ISOC2 PE=1 SV=1 ,
SVLLCGIEAQAC(464.2859 6)ILNTTLDLLDR	C114,NA,NA,NA	;;X;X;	1.43807,1.27022;;X ;X;	1.354145	K7ENV7 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=7 , K7EKW4 Isochorismatase domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ISOC2 PE=1 SV=1 , Q96AB3 Isochorismatase domain-containing protein 2 OS=Homo sapiens GN=ISOC2 PE=1 SV=1 ,
LHYGTDPC(470.29977)TG QPFRFPLVSVR	C137,NA,C139,NA	;;X;X;	1.47656;;X;X;	1.47656	Q8NFF5 FAD synthase OS=Homo sapiens GN=FLAD1 PE=1 SV=1 , Q8NFF5-3 Isoform 3 of FAD synthase OS=Homo

					sapiens GN=FLAD1 , Q8NFF5-2 Isoform 2 of FAD synthase OS=Homo sapiens GN=FLAD1 ,
ALSAVHSPTFCQLAC(464.28596)GQDGLK	NA,C255,NA,C272,NA	,,X;X;	1.27575,,X;X;	1.27575	Q8IY67 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 , Q8IY67-2 Isoform 2 of Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 , A0A087WZ13 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 , E9PAU2 Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 ,
LKGLGC(470.29977)QTLG PHNPTPPPSLDM(15.994915)FAEELAEETPTPTQR	C234,M250,NA	U,,X;X;	1.11623,,X;X;	1.11623	O95400 CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens GN=CD2BP2 PE=1 SV=1 ,
PM(15.994915)C(470.29977)IPPSYADLGK	NA,NA	,,X;X;	1.28384,,X;X;	1.28384	P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
IVQTLC(464.28596)TVR	C147,NA	,,X;X;	2.1562,,X;X;	2.1562	Q96D53 AarF domain-containing protein kinase 4 OS=Homo sapiens GN=ADCK4 PE=1 SV=2 ,
LLDIAC(470.29977)WIHHK	C117,C102,NA,C82,NA	,,X;X;	2.9885,,X;X;	2.9885	F8WD96 Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 , C9JH19 Cathepsin D (Fragment) OS=Homo sapiens GN=CTSD PE=1 SV=1 , P07339 Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1 , F8W787 Cathepsin D (Fragment) OS=Homo sapiens GN=CTSD PE=1 SV=1 ,
VSDTVVEPYNATLSVHQLVE NTDETYC(470.29977)IDNE ALYDIC(464.28596)FR	C201,C211,NA	,,X;X;	3.16517,,X;X;	3.16517	Q9BUF5 Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 ,
IINDNATYC(470.29977)R	NA,NA	,,,X;	1.6454,,1.31063,,X;	1.478015	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
VTDGALVVVDCVSGVC(470.29977)VQTETVLR	C136,NA	U,,X;X;	0.95577,,X;X;	0.95577	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
VTDGALVVVDCVSGVC(470.29977)VQTETVLR	C136,NA	U,U,,X;U,;	1.20592,1.45957,,X;1.35362,,	1.35362	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
LASSIRNPVHC(470.29977)FDLASLDPR	NA,NA	U,,X;X;	2.16463,,X;X;	2.16463	O43159 Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 ,
LDTNSDGQLDFSEFLNLIGG LAM(15.994915)AC(464.28596)HDSFLK	M89,C91,NA	U,U,,X;X;	1.3736,1.21879,,X;X;	1.296195	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
LDTNSDGQLDFSEFLNLIGG	M89,C91,NA	U,,X;X;	1.43359,,X;X;	1.43359	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11

LAM(15.994915)AC(464.28596)HDSFLK					PE=1 SV=2 ,
M(15.994915)FPNAPYLPS C(464.28596)LESQPAIR	M195,C205,M200,C210,NA,NA,M195,C205,NA,NA,M127,C137,NA,M127,C137,NA	;;X;X;	1.98424;;X;X;	1.98424	J3KNN9 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , P19544-7 Isoform 7 of Wilms tumor protein OS=Homo sapiens GN=WT1 , P19544-8 Isoform 8 of Wilms tumor protein OS=Homo sapiens GN=WT1 , H0Y7K5 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , A0A0A0MT54 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , P19544 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=2 , P19544-3 Isoform 3 of Wilms tumor protein OS=Homo sapiens GN=WT1 , P19544-2 Isoform 2 of Wilms tumor protein OS=Homo sapiens GN=WT1 , H0Y3F0 Wilms tumor protein OS=Homo sapiens GN=WT1 PE=1 SV=1 , P19544-4 Isoform 4 of Wilms tumor protein OS=Homo sapiens GN=WT1 ,
LNLSC(470.29977)IHSPVV NELMR	NA,NA	U;;X;X;	1.7726;;X;X;	1.7726	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
ARDC(470.29977)LIPM(15.994915)GITSENVAER	NA,NA,NA	;;X;X;	1.30816;;X;X;	1.30816	P09110 3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 ,
AENGLLM(15.994915)TPC (464.28596)YTANFVAPEVL KR	NA,NA,M561,C564,M576,C579,M480,C483,NA,NA	;;X;X;	1.45856;;X;X;	1.45856	Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 , P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 , Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 ,
VMALQEAC(464.28596)EAYLVGLFEDTNLCIAHAK	C97,NA	U,U;;U;;X;	73.82524,61.49757,67.61176;;X;	67.61176	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
HTSC(464.28596)SSAGND SKPVQEAPSVAR	C793,C706,NA,NA	;;X;X;	1.63394;;X;X;	1.63394	Q9P246-2 Isoform 2 of Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 , H0Y860 Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=1 , Q9P246 Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=2 ,

VMALQEAC(464.28596)EAYLVGLFEDTNLCAIHAK	C97,NA	U,,X;X;	41.26063,,X;X;	41.26063	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
QPPWC(470.29977)DPLGPFVVGGEDLDPGPR	C185,C185,NA	,,X;X;	1.41754,,X;X;	1.41754	Q5QPM7 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 , Q92530 Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2 ,
HGFC(464.28596)GIPITDTGR	NA,NA	,,,,,;	1.44525,,1.28475,,1.1593,,	1.28475	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 ,
HGFC(464.28596)GIPITDTGR	NA,NA	,,,,,;	1.44026,,1.39152,,1.20325,,	1.39152	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 ,
AMAEGLREVFSHC(464.28596)PFLM(15.994915)GPIELK	C883,M887,C883,M887,NA	,,X;X;	4.67368,,X;X;	4.67368	P55160 Nck-associated protein 1-like OS=Homo sapiens GN=NCKAP1L PE=1 SV=3 , P55160-2 Isoform 2 of Nck-associated protein 1-like OS=Homo sapiens GN=NCKAP1L ,
NC(470.29977)LTNFHGM(15.994915)DLTR	NA,NA,C96,M103,NA,NA	,,X;;	1.42852,,X;1.28708,,	1.3578	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
LIDFLEC(470.29977)GK	C234,NA,NA	,,;X;	1.42229,,1.48242,,X;	1.452355	P17844 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 , J3KTA4 Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 ,
NC(470.29977)LTNFHGM(15.994915)DLTR	NA,NA,C96,M103,NA,NA	,,,,,;	1.42018,,1.36109,,1.35053,,	1.36109	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
ELELM(15.994915)FGC(470.29977)QVEGDAAETPPRPR	M274,C277,NA,NA	,,X;X;	1.72083,,X;X;	1.72083	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 , Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 ,
SM(15.994915)VSPVPSPTGTISVPNSC(464.28596)PASPR	NA,NA	,,X;X;	1.54942,,X;X;	1.54942	P85037 Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1 ,

DLC(464.28596)FSPGLM(15.994915)EASHVVNDVNEAVQLVFRK	NA,NA	,,,,,;	1.35903,1.29916,,1.23255,,1.20991,;	1.265855	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 ,
FC(470.29977)AFGGNPPVTGPR	NA,C150,NA	,,X;X;	1.07452,,X;X;	1.07452	O15446-2 Isoform 2 of DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP , O15446 DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP PE=1 SV=1 ,
DLM(15.994915)ANATC(464.28596)FR	M1442,C1447,NA,M2128,C2133,NA	,,X;X;	1.76589,,X;X;	1.76589	H7C1M2 Protein SON (Fragment) OS=Homo sapiens GN=SON PE=1 SV=1 , P18583-5 Isoform D of Protein SON OS=Homo sapiens GN=SON , P18583-2 Isoform A of Protein SON OS=Homo sapiens GN=SON ,
GTPEQPQC(470.29977)GFSNAVVQILR	C67,NA,NA	U,U,U,,U,U,,U,U,;	1.35267,1.33251,1.24215,,1.33124,1.28376,,1.22033,1.24345,;	1.28376	Q86SX6 Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 ,
NTVLC(470.29977)NVVEQFLQADLAR	C70,NA	U,U,,U,,X;	1.40089,1.47604,,1.04016,,X;	1.40089	Q14258 E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 ,
GTPEQPQC(470.29977)GFSNAVVQILR	C67,NA,NA	U,,X;X;	1.62561,,X;X;	1.62561	Q86SX6 Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 ,
ITAFVPNDGC(470.29977)LNFIEENDEVLVAGFGR	NA,NA	,,X;X;	1.4549,,X;X;	1.4549	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
ITAFVPNDGC(470.29977)LNFIEENDEVLVAGFGR	NA,NA	,,,,,;	1.39031,1.44717,1.43657,,1.35403,,1.23175,;	1.39031	P62266 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 ,
TAFQEALDAAGDKLVVDF SATWC(464.28596)GPCK	NA,NA	,,X;X;	1.42224,,X;X;	1.42224	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,
TAFQEALDAAGDKLVVDF SATWC(464.28596)GPCK	NA,NA	,,X;X;	1.35843,1.31698,,X;X;	1.337705	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,
IAVYSC(464.28596)PFDGM(15.994915)ITETK	C225,M230,NA	,,X;X;	1.37549,,X;X;	1.37549	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 ,
ATGHSGGGC(470.29977)ISQGR	NA,NA,NA,NA,NA	,,,,,;	1.64923,,2.23242,,1.69181,;	1.69181	I3L407 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=1 , I3L139 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=1 , Q9HA64 Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2 , I3L3W5 Ketosamine-3-kinase (Fragment) OS=Homo sapiens GN=FN3KRP PE=1 SV=1 ,

PPMEAAGFTAQVILNHPG QISAGYAPVLDCHTAHIAC(464.28596)K	NA,NA	,,X;X;	1.89058,,X;X;	1.89058	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
AC(470.29977)FQVGTSEE M(15.994915)K	NA,C157,M166,C729,M73 8,NA,C729,M738,C717,M 726,NA	,,X;X;	1.99475,,X;X;	1.99475	P35658-4 Isoform 4 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 , A0A0A0MSW3 Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=1 , P35658 Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 , P35658-2 Isoform 2 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 , P35658-3 Isoform 3 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 , P35658-5 Isoform 5 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 ,
EC(470.29977)EGIVPVPLA EK	NA,NA,NA	U,,X;X;	1.54225,,X;X;	1.54225	P82932 28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 ,
C(464.28596)SDNSSYEEPL SPISASSSTR	C205,NA,C205,NA,C711,C 346,NA,NA	,,,X;	1.42638,,1.53838,, X;	1.48238	Q8IXK0-2 Isoform 2 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 , A0A0A0MSI2 Polyhomeotic- like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 , Q8IXK0 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 , Q8IXK0-3 Isoform 3 of Polyhomeotic- like protein 2 OS=Homo sapiens GN=PHC2 , Q8IXK0-4 Isoform 4 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 , B3KPJ4 Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 , Q8IXK0-5 Isoform 5 of Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 ,
AVLLASDAQEC(464.28596)TLEEVVER	C332,NA,NA	,,,X,;;	0.9213,0.78963,1.7 1712,,X;1.18535,,	1.053325	Q27J81-2 Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2 , Q27J81 Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 ,
SDITKLEVDIVNAANSSLLG GGGVGDC(470.29977)IHR	C186,NA	U,,X;X;	1.43777,,X;X;	1.43777	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
GNFTLPEVAEC(464.28596) FDEITYVELQKEEAQK	NA,C629,NA	,,X;X;	1.30919,1.28454,,X ;X;	1.296865	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
GNFTLPEVAEC(464.28596) FDEITYVELQKEEAQK	NA,C629,NA	,,,X,;;	1.423,1.62117,1.41 817,,X;1.59949,,	1.511245	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2

					Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
YQEAAPNVANNTGPHAAS C(470.29977)FGAK	C517,NA,C517,NA,NA,NA, NA,NA,NA,C295,C564,NA, NA,C295,NA,C618,NA,C56 4,C564,C618,NA,C295,C51 7,NA,C295,C295,NA,C564, NA,C517,NA,NA,NA,NA	,;X;X;	1.27632,;X;X;	1.27632	O60716-23 Isoform 3C of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-30 Isoform 4B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-19 Isoform 3AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-2 Isoform 1AB of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-4 Isoform 1BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , C9JZR2 Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=2 , O60716-32 Isoform 4 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-10 Isoform 2AB of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-18 Isoform 3AB of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-3 Isoform 1AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-15 Isoform 2C of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-16 Isoform 2 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-24 Isoform 3 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-29 Isoform 4A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-8 Isoform 1 of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-5 Isoform 1A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-26 Isoform 4AB of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-11 Isoform 2AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-9 Isoform 2ABC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-7 Isoform 1C of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-28 Isoform 4BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-25 Isoform 4ABC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-21 Isoform 3A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-6 Isoform 1B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-27 Isoform 4AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-31 Isoform 4C of Catenin delta-1 OS=Homo sapiens

					GN=CTNND1 , O60716 Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 , O60716-13 Isoform 2A of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-12 Isoform 2BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-17 Isoform 3ABC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-14 Isoform 2B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-22 Isoform 3B of Catenin delta-1 OS=Homo sapiens GN=CTNND1 , O60716-20 Isoform 3BC of Catenin delta-1 OS=Homo sapiens GN=CTNND1 ,
SDITKLEVDIVNAANSSLLG GGGV DGC(470.29977)IHR	C186,NA	U,,X;X;	1.62006,,X;X;	1.62006	Q9BQ69 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 ,
LQDSFC(470.29977)SGQT LWELLSHFQIR	C106,NA,NA	,,X;X;	1.42696,,X;X;	1.42696	J3QL04 Tether-containing UBX domain for GLUT4 (Fragment) OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 , Q9BZE9 Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 ,
AAVEEGIVLGGGC(470.299 77)ALLR	NA,NA,NA	U,U,,U,U,,U,,	1.39896,1.38095,,1.36157,1.38739,,1.22679,,	1.38095	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
AAVEEGIVLGGGC(470.299 77)ALLR	NA,NA,NA	U,U,U,,U,U,, U,,	1.37591,1.48863,1.41697,,1.392,1.42282,,1.27007,,	1.404485	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
NWYVQPSC(464.28596)A TSGDGLYEGLTWLTSNYK	C155,NA	U,U,,X;X;	1.78391,1.79971,,X; X;	1.79181	P62330 ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 ,
LNCQVIGASVDSHFC(464.2 8596)HLAWVNTPK	C83,C83,NA	,,X;X;	1.5277,,X;X;	1.5277	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 , A0A0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 ,
LNCQVIGASVDSHFC(464.2 8596)HLAWVNTPK	C83,C83,NA	,,X;X;	1.53175,,X;X;	1.53175	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 , A0A0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 ,
LNCQVIGASVDSHFC(464.2 8596)HLAWVNTPK	C83,C83,NA	,,X;X;	1.52085,,X;X;	1.52085	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 , A0A0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 ,
MAGIFDVNTC(464.28596) YGSPQSPQLIR	NA,NA,NA,C428,NA,NA	,,X;X;	1.37926,,X;X;	1.37926	Q9BTX1-2 Isoform 2 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1 Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 PE=1 SV=2 , Q9BTX1-4 Isoform 4 of Nucleoporin

					NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1-5 Isoform 5 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 , Q9BTX1-6 Isoform 6 of Nucleoporin NDC1 OS=Homo sapiens GN=NDC1 ,
KAAAPAPEEEM(15.994915)DEC(470.29977)EQALAAEPK	M263,C266,NA,NA	;;;X;	1.20563;;1.32388;;X;	1.264755	P26641 Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 , P26641-2 Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G ,
KAQC(464.28596)PIVER	C66,NA,C66,NA	;;;;	1.4903;;1.34302;;1.23519;;	1.34302	P46782 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 , M0R0R2 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 , M0R0F0 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 ,
EADQKEQFSQGSNSC(470.29977)LETSLAEIFPLGK	C161,NA,C102,NA,NA	;;X;X;	1.75027;;X;X;	1.75027	Q9NQ88 Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 , A0A0U1RQD1 Chromosome 12 open reading frame 5, isoform CRA_b OS=Homo sapiens GN=TIGAR PE=1 SV=1 ,
NAIQLLASFLANNPFSC(470.29977)K	NA,NA	;;X;X;	0.91225;;X;X;	0.91225	Q15021 Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3 ,
LNCQVIGASVDSHFC(464.28596)HLAWVNTPKK	C83,C83,NA	;;X;X;	1.33068;;X;X;	1.33068	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 , A0A0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 ,
WC(470.29977)EYGLTFTEK	NA,C65,NA	;;;;X;	1.2707,1.32619;;1.57652;;X;	1.32619	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 , P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
FC(470.29977)IWTESAFR	C250,NA	;;X;;;	1.52511;;X;1.28824;;	1.406675	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
GC(470.29977)GTVLLSGPR	NA,NA,NA,NA	;;X;X;	1.40673;;X;X;	1.40673	J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 , G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 , Q07020 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 ,
GC(470.29977)GTVLLSGPR	NA,NA,NA,NA	;;X;X;	1.40939;;X;X;	1.40939	J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 , G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 , Q07020 60S ribosomal protein L18 OS=Homo sapiens

					GN=RPL18 PE=1 SV=2 ,
GLDYEGGGC(464.28596)R	C691,NA,NA	,,,X;	1.43086,,1.53004,,X;	1.48045	O60568 Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1 ,
LTFSCLGSDNFKHLNEIDLF HC(464.28596)IDPNDSK	C62,NA,C58,NA	,,X;X;	1.38191,,X;X;	1.38191	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 ,
LTFSCLGSDNFKHLNEIDLF HC(464.28596)IDPNDSK	C62,NA,C58,NA	,,X;X;	1.48509,,X;X;	1.48509	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 ,
SPVTTLLEC(464.28596)M HK	NA,C622,NA,C617,C665,NA,NA	,,X;X;	0.3085,,X;X;	0.3085	P55265-3 Isoform 3 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR , P55265-2 Isoform 2 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR , P55265-5 Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR , H0YCK3 Double-stranded RNA-specific adenosine deaminase (Fragment) OS=Homo sapiens GN=ADAR PE=1 SV=1 , P55265-4 Isoform 4 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR , P55265 Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 ,
SC(464.28596)GPASQSTL GLK	C232,NA,NA,C254,NA,NA,NA,C255,NA	,,X;X;	1.23653,,X;X;	1.23653	Q9BXS6-7 Isoform 7 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , H0YMD2 Nucleolar and spindle-associated protein 1 (Fragment) OS=Homo sapiens GN=NUSAP1 PE=1 SV=1 , Q9BXS6-2 Isoform 2 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6-3 Isoform 3 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6-4 Isoform 4 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6 Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 PE=1 SV=1 , Q9BXS6-6

					Isoform 6 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 , Q9BXS6-5 Isoform 5 of Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 ,
IGAAIQEELGYNC(470.29977)QTGGVIAEILR	NA,NA	;;X;X;	1.51364;;X;X;	1.51364	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
FSAIQC(470.29977)AAAVP R	NA,C98,C98,NA,C98,NA,N A	;;X;X;	1.48124;;X;X;	1.48124	Q15054-3 Isoform 3 of DNA polymerase delta subunit 3 OS=Homo sapiens GN=POLD3 , E9PM91 DNA polymerase delta subunit 3 (Fragment) OS=Homo sapiens GN=POLD3 PE=1 SV=1 , E9PNC0 DNA polymerase delta subunit 3 (Fragment) OS=Homo sapiens GN=POLD3 PE=1 SV=1 , Q15054 DNA polymerase delta subunit 3 OS=Homo sapiens GN=POLD3 PE=1 SV=2 , Q15054-2 Isoform 2 of DNA polymerase delta subunit 3 OS=Homo sapiens GN=POLD3 , E9PRK3 DNA polymerase delta subunit 3 (Fragment) OS=Homo sapiens GN=POLD3 PE=1 SV=1 ,
C(464.28596)ASQSGMTAY GTR	C175,C164,NA,NA	;;X;X;	1.54838;;X;X;	1.54838	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
C(464.28596)ASQSGMTAY GTR	C175,C164,NA,C166,NA	;;;;;	1.35851;;1.31382;;1 .13982;;	1.31382	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
FC(464.28596)DNSSAIQ GK	NA,NA	U;;X;X;	1.28029;;X;X;	1.28029	O15067 Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 ,
IAVYSC(464.28596)PFDG MITETK	C225,NA	;;X;X;	0.91858;;X;X;	0.91858	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 ,
VGIGRPAHPEAVQAHVLGC (464.28596)FSPAEEQLPL LLDR	NA,NA	U;;X;X;	1.50226;;X;X;	1.50226	Q86Y79 Probable peptidyl-tRNA hydrolase OS=Homo sapiens GN=PTRH1 PE=1 SV=1 ,
IAVYSC(464.28596)PFDG MITETK	C225,NA	;;X;X;	0.93961;;X;X;	0.93961	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 ,
LEGDLTGPSVGVEVPDVELE C(470.29977)PDAK	NA,NA	U;;X;X;	1.49908;;X;X;	1.49908	Q09666 Neuroblast differentiation-associated protein AHNK OS=Homo sapiens GN=AHNAK PE=1 SV=2 ,
YFDLSSYSVAVNQGH(470.	NA,NA,NA	U;;X;X;	1.89181;;X;X;	1.89181	P04181 Ornithine aminotransferase, mitochondrial

29977)HPK					OS=Homo sapiens GN=OAT PE=1 SV=1 ,
GTEAGQVGEPGIPTGEAGP SC(464.28596)SSASDKLPR	C241,NA	U,,X;X;	0.64538,,X;X;	0.64538	O15355 Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 ,
AFDLIEHYFGTEDESSIA PQ VDLNQQQYIFQQC(464.28 596)EAPM(15.994915)EG FQL	C529,M533,NA	U,,X;X;	1.43975,,X;X;	1.43975	P52294 Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3 ,
ISC(464.28596)MSKPPAP NPTPPR	NA,NA,NA	,,X;X;	1.36119,,X;X;	1.36119	P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 , P46734 Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 ,
NC(464.28596)PHVVVGTP GR	C164,NA	,,X;;	1.17757,,X;1.19485 ,,	1.18621	O00148 ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2 ,
LC(464.28596)DFGVSGQLI DSMANSFVGTR	C207,NA,NA	,,X;X;	1.31406,,X;X;	1.31406	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 , Q02750-2 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 ,
DGLTDVYNKIHM(15.9949 15)GSC(464.28596)AENTA K	NA,NA,NA	U,,X;X;	1.7273,,X;X;	1.7273	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
NTLANSC(470.29977)GTGI R	NA,NA	,,X;X;	1.25491,,X;X;	1.25491	Q96RE7 Nucleus accumbens-associated protein 1 OS=Homo sapiens GN=NACC1 PE=1 SV=1 ,
AVM(15.994915)ALQEAC(470.29977)EAYLVGLFEDT NLCAIHAK	M91,C97,NA	U,,X;X;	0.43447,,X;X;	0.43447	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
LVYSTCSLC(464.28596)QE ENEDVVRDALQQNPGA FR	NA,NA	,,X;X;	1.42414,,X;X;	1.42414	Q96P11-2 Isoform 2 of Probable 28S rRNA (cytosine-C(5))- methyltransferase OS=Homo sapiens GN=NSUN5 ,
C(464.28596)LSAAEEK	NA,C170,C170,C145,C154, NA	,,X;X;	1.15051,,X;X;	1.15051	J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , P06753-2 Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 , A0A087WWU8 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , Q5VU61 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 , Q5HYB6 Epididymis luminal protein 189 OS=Homo sapiens GN=DKFZp686J1372 PE=1 SV=1 ,

ANASIC(464.28596)FAVPD PLM(15.994915)PDPSKQP K	C95,M103,C95,M103,NA, NA	;;X;X;	6.5975;;X;X;	6.5975	O75569-2 Isoform 2 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA , O75569 Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=1 SV=1 , O75569-3 Isoform 3 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA ,
ANASIC(464.28596)FAVPD PLM(15.994915)PDPSKQP K	C95,M103,C95,M103,NA, NA	;;X;X;	1.3606;;X;X;	1.3606	O75569-2 Isoform 2 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA , O75569 Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=1 SV=1 , O75569-3 Isoform 3 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA ,
NFPAIGGTGPTSDTGWGC(470.29977)M(15.994915) LR	NA,C74,M75,C74,M75,NA	;;X;X;	1.04815;;X;X;	1.04815	Q9Y4P1-2 Isoform 2 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B , Q9Y4P1 Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B PE=1 SV=2 , Q9Y4P1-6 Isoform 6 of Cysteine protease ATG4B OS=Homo sapiens GN=ATG4B ,
EKLC(464.28596)YVALDFE NEM(15.994915)ATAASSS SLEK	NA,NA,C219,M229,NA,NA	;;X;X;	2.84987;;X;X;	2.84987	P68133 Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 , P68032 Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 ,
DLPTSPVDLVINCLDC(470. 29977)PENVFLR	C413,NA	U;;X;X;	1.82987;;X;X;	1.82987	Q96F86 Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1 ,
KGAGNPQASTLALQSNITQ C(464.28596)LLGQPWPLN EAQVQASVVK	NA,NA,NA,NA,NA,NA,C12 99,C1261,C1260,NA	;;;;;	1.39695;;1.3189;;1. 41329;;	1.39695	E7ETY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 , Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-6 Isoform 6 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 , Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 , J3KQ96

					Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 ,
C(470.29977)SHQQSPYQL LFGEPYIFEELLSLK	C289,NA,NA,NA	;;X;X;	1.82926;;X;X;	1.82926	Q96GJ1-2 Isoform 2 of tRNA (uracil(54)-C(5))-methyltransferase homolog OS=Homo sapiens GN=TRMT2B , Q96GJ1-3 Isoform 3 of tRNA (uracil(54)-C(5))-methyltransferase homolog OS=Homo sapiens GN=TRMT2B , Q96GJ1 tRNA (uracil(54)-C(5))-methyltransferase homolog OS=Homo sapiens GN=TRMT2B PE=1 SV=1 ,
CPEALFQPSFLGMESC(464.28596)GIHETTFNSIMK	NA,NA,NA	;;X;X;	1.74815;;X;X;	1.74815	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
CPEALFQPSFLGMESC(464.28596)GIHETTFNSIMK	NA,NA,NA	;;;X;X;	1.77259,1.78338;;X;X;	1.777985	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
DLDKANYLSQALQAGTVW VNC(464.28596)YDVFGAQ SPFGGYK	NA,NA,NA	;;X;X;	1.08237;;X;X;	1.08237	P05091 Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2 ,
GFTDADNTWEPEENLDC(470.29977)PELIEAFLNSQK	C69,NA	;;X;X;	1.03041;;X;X;	1.03041	Q13185 Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 ,
ITLIIGGSYGAGNYGM(15.994915)C(470.29977)GR	NA,NA,NA	;;X;X;	2.11197;;X;X;	2.11197	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
IYHPNINSNGSIC(464.28596)LDILR	C87,NA,NA	;;X;X;	1.44381;;X;X;	1.44381	P61077 Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1 , P61077-2 Isoform 2 of Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 ,
APAM(15.994915)C(470.29977)SSPRVPR	M336,C337,NA	U;;X;X;	1.39585;;X;X;	1.39585	Q96GM1-2 Isoform 2 of Phospholipid phosphatase-related protein type 2 OS=Homo sapiens GN=PLPPR2 ,
CPEALFQPSFLGMESC(464.28596)GIHETTFNSIM(15.994915)K	NA,NA,NA	;;;X;X;	1.45252,1.50897;;X;X;	1.480745	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
VC(464.28596)NVAPIAGE TK	C188,C336,NA	;;X;X;	0.85928;;X;X;	0.85928	H0YG10 Nucleolar GTP-binding protein 2 (Fragment) OS=Homo sapiens GN=GNL2 PE=1 SV=2 , Q13823 Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 ,
CPEALFQPSFLGMESC(464.28596)GIHETTFNSIM(15.994915)K	NA,NA,NA,NA,NA	;;;;;X;	1.73244,2.068,2.04905;;1.79168,1.95322;;X;	1.95322	P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 , P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
NC(464.28596)LTNFHGM	C96,NA	;;X;X;	1.53296;;X;X;	1.53296	P61247 40S ribosomal protein S3a OS=Homo sapiens

DLTR					GN=RPS3A PE=1 SV=2 ,
NC(464.28596)LTNFHGM DLTR	NA,NA,C96,NA,NA	;;X;;	1.50884;;X;1.41561 ;;	1.462225	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
M(15.994915)PC(470.299 77)QLHQVIVAR	M638,C640,NA	;;X;X;	0.9476;;X;X;	0.9476	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 ,
M(15.994915)PC(470.299 77)QLHQVIVAR	M638,C640,NA	;;X;X;	1.61108;;X;X;	1.61108	P17655 Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 ,
SQEATEAAPSC(470.29977)VGDMADTPR	C84,C241,NA,NA,NA,NA	;;X;X;	0.89978;;X;X;	0.89978	Q9UHD8-3 Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9 , Q9UHD8-5 Isoform 5 of Septin-9 OS=Homo sapiens GN=SEPT9 , Q9UHD8-7 Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9 , Q9UHD8 Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 , Q9UHD8-2 Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9 ,
NIAQIAVVMGSC(470.2997 7)TAGGAYVPAM(15.9949 15)ADENIIVR	NA,NA,NA	;;X;X;	1.68742;;X;X;	1.68742	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
LM(15.994915)EQLLSSVG FC(464.28596)TEVEEDLID AVTGLSGSGPAYAFTALDAL ADGGVK	M149,C159,NA,M149,C15 9,NA,NA,NA,NA	;;X;X;	1.77547;;X;X;	1.77547	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 ,
LFVSDGVPGC(464.28596) LPVLAAAGR	C12,NA,NA	;;X;X;	3.29533;;X;X;	3.29533	P56192 Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2 ,
VIEINPYLLGTMSGC(464.2 8596)AADQCQYWER	NA,NA,NA,NA	;;X;X;	2.45569;;X;X;	2.45569	P28062-2 Isoform 2 of Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 , X5D2R7 Proteasome subunit beta type OS=Homo sapiens GN=PSM8 PE=1 SV=1 , P28062 Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3 ,
LLNLVYDVTPELVDLVITEL GM(15.994915)IPC(464.2 8596)SSVPVVLRL	M527,C530,M505,C508,N A,M503,C506,M505,C508, NA	;;X;X;	2.06562;;X;X;	2.06562	E7ERK9 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 , Q9UI10-3 Isoform 3 of Translation initiation factor eIF-2B subunit delta

					OS=Homo sapiens GN=EIF2B4 , Q9UI10-2 Isoform 2 of Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 , A0A087WTA5 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=1 , Q9UI10 Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2 ,
LDVGNFSWGSEC(464.28596)C(464.28596)TRK	NA,NA	U,,X;X;	1.57656,,X;X;	1.57656	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
C(464.28596)ALSSPSLAFT PPIK	C120,NA,NA,NA	,,,;	1.50159,,1.2934,,1.40263,,	1.40263	Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 ,
C(464.28596)ALSSPSLAFT PPIK	C120,NA,NA,NA	,,,X;	1.47756,,1.43304,,X;	1.4553	Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 ,
LILDVFC(464.28596)GSQM(15.994915)HFVR	C476,M480,C446,M450,NA,NA	,,X;X;	1.3227,,X;X;	1.3227	P11413-3 Isoform 3 of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD , P11413 Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 , P11413-2 Isoform Long of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD ,
AC(470.29977)QSIYPLHDV FVRK	C201,NA	,,X;X;	1.60343,,X;X;	1.60343	P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 ,
HFLSDTGM(15.994915)AC(470.29977)R	NA,NA	,,X;X;	1.72796,,X;X;	1.72796	Q5TFE4 5'-nucleotidase domain-containing protein 1 OS=Homo sapiens GN=NT5DC1 PE=1 SV=1 ,
AC(464.28596)PRPEGLNF QDLK	NA,C227,NA,NA	,,X;X;	1.74753,,X;X;	1.74753	P15927-3 Isoform 3 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 , P15927-2 Isoform 2 of Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 , P15927 Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1 ,
C(464.28596)VYTYIQEFYR	NA,NA,C948,C892,NA	,,X;X;	1.67809,,X;X;	1.67809	B5MCI0 Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=1 , A0A096LNK9 Smoothelin (Fragment) OS=Homo sapiens GN=SMTN PE=1 SV=1 , A0A087WVP4 Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=1 , P53814-5 Isoform B2 of Smoothelin OS=Homo sapiens GN=SMTN ,
SLAPPDASILISNVC(464.28	NA,C274,M292,NA	,,X;X;	1.36317,,X;X;	1.36317	A0A087X0R7 Protein SENP3-EIF4A1 (Fragment) OS=Homo

596)SIGDHVAQELFQGS DLGM(15.994915)AEEA ERPGEK					sapiens GN=SEN3-EIF4A1 PE=4 SV=1 , Q9H4L4 Sentrin-specific protease 3 OS=Homo sapiens GN=SEN3 PE=1 SV=2 ,
SLAPPDASILISNVC(464.28596)SIGDHVAQELFQGS DLGM(15.994915)AEEA ERPGEK	NA,C274,M292,NA	,,X;X;	1.55329,,X;X;	1.55329	A0A087X0R7 Protein SEN3-EIF4A1 (Fragment) OS=Homo sapiens GN=SEN3-EIF4A1 PE=4 SV=1 , Q9H4L4 Sentrin-specific protease 3 OS=Homo sapiens GN=SEN3 PE=1 SV=2 ,
NDPPM(15.994915)EAAG FTAQVILNHPGQISAGYAP VLDCHTAHIAC(464.28596) K	NA,NA	,,,X;X;	1.71873,1.60552,,X; X;	1.662125	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 ,
LLHVFACAC(464.28596)P GCSTGGAR	NA,NA,NA	,,X;X;	1.27522,,X;X;	1.27522	Q9BRP1 Programmed cell death protein 2-like OS=Homo sapiens GN=PDCD2L PE=1 SV=1 , K7ESF4 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 ,
TTSSANNPNLM(15.994915)YQDEC(470.29977)DR	M502,C507,M581,C586,NA,NA,M500,C505,NA	,,X;X;	1.25176,,X;X;	1.25176	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 , Q92841-2 Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 , Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 ,
LC(464.28596)YVALDFEQE MAMVASSSSLEK	C880,NA	U,U,U,,U,,U,;	1.31744,1.20714,1.16347,,1.33806,,1.26236,,	1.26236	P0CG39 POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 ,
ANNNAAVAPTTC(470.29977)PLQPVTDPFAFSR	C46,NA,NA	,,X;X;	1.33756,,X;X;	1.33756	F1T0I1 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 , J3KNL6 Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1 ,
VC(470.29977)NFLASQVP FPSR	C205,NA	X,,,,;	X;1.33919,,1.26536,,	1.302275	Q99714 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 ,
ADIIHAC(464.28596)DIVE DAAIAYGYNNIQMTLPK	C263,NA	X,,X;	X;0.88974,,X;	0.88974	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 ,
YSTGSDSASFPHTPSM(15.994915)C(464.28596)LNP DLEGPPLEAYTIQGQYAIQ	M216,C217,NA,NA	X,,X;	X;1.32069,,X;	1.32069	Q15366-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 , Q15366 Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 ,

PDLTK					
GFNKETAAAC(470.29977)VEK	NA,NA,NA	X;;;X;	X;1.77188;;X;	1.77188	E9PGT1 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 , Q15631 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 ,
IKADPDGPEAQAEAC(470.29977)SGER	NA,NA,C18,C18,NA	X,,,,;	X;1.39409;;1.39478;;	1.394435	D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 , D6RC52 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 , Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 , J3QSY4 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
AGQPHSSSDAAQAPAEQP HSSSDAAQAPC(464.28596) JPR	C51,C51,NA,NA,NA,NA	X,,,,;	X;1.52368;;1.80206;;	1.66287	P29372-4 Isoform 3 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372 DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 , A2IDA3 DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 , P29372-5 Isoform 4 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372-2 Isoform 2 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG ,
VLTC(464.28596)TDLEQG PNFFLDFENAQPTSEKEIY NQVNVVLK	NA,NA	X;;;X;	X;1.52688;;X;	1.52688	Q9NUQ9 Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1 ,
GDSEPTPGC(464.28596)S GLGPGGVR	C13,NA,NA,C13,C13,NA	X;;;X;	X;1.52368;;X;	1.52368	Q8WW01 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSN15 PE=1 SV=1 , Q8WW01-2 Isoform 2 of tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSN15 , H0YCV5 tRNA-splicing endonuclease subunit Sen15 (Fragment) OS=Homo sapiens GN=TSN15 PE=1 SV=1 , E9PPN1 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSN15 PE=1 SV=1 , F2Z3M0 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSN15 PE=1 SV=1 ,
LLEETGIC(470.29977)VVP GSGFGQR	C477,NA	X;;;X;	X;1.95991;;X;	1.95991	Q8TD30 Alanine aminotransferase 2 OS=Homo sapiens GN=GPT2 PE=1 SV=1 ,
LGYLTC(470.29977)PSNL GTGLR	C347,NA,C347,NA,NA	X;;;X;	X;1.37007;;X;	1.37007	P12532-2 Isoform 2 of Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A , P12532 Creatine kinase U-type, mitochondrial OS=Homo sapiens

					GN=CKMT1A PE=1 SV=1 ,
LNCQVIGASVDSHFC(470.29977)HLAWVNTPK	C83,C83,NA	X;;;X;	X;1.32082;;X;	1.32082	Q06830 Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 , AOA0A0MSI0 Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1 ,
GEVPC(464.28596)TVTSAS PLEEATLSELK	C141,NA,NA	X;;;X;	X;1.56505;;X;	1.56505	P48047 ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 ,
C(464.28596)EGINISGNFY R	NA,NA	X;;;X;	X;1.36291;;X;	1.36291	M0QYS1 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=1 SV=2 ,
EEQVISLGPQVAEGENVFG VC(470.29977)HIFASFNDT FVHVTDLGSK	C31,NA	X;;;X;	X;1.07184;;X;	1.07184	P62263 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 ,
VAAAASC(464.28596)LSQ K	NA,C314,NA	X;;;X;	X;1.57478;;X;	1.57478	O95067 G2/mitotic-specific cyclin-B2 OS=Homo sapiens GN=CCNB2 PE=1 SV=1 , H1UBN3 Cyclin B2 OS=Homo sapiens GN=CCNB2V PE=1 SV=1 ,
VLDALFPCVQGGTTAIPGAF GC(464.28596)GK	C221,C221,NA	X;;;X;	X;1.02636;;X;	1.02636	P38606-2 Isoform 2 of V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A , P38606 V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 ,
GIGM(15.994915)NEPLVD C(464.28596)EGYPR	NA,NA,M52,C59,M52,C59 ,M52,C59,M52,C59,NA	X;;;X;	X;1.30373;;X;	1.30373	O00233-2 Isoform p27-S of 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 , O00233 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 , J3KN29 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 , F5H7X1 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 , F5H5V4 26S proteasome non-ATPase regulatory subunit 9 (Fragment) OS=Homo sapiens GN=PSMD9 PE=1 SV=1 , F5GX23 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=1 ,
AVM(15.994915)ALQEAC(470.29977)EAYLVGLFEDT NLCAIHAK	M91,C97,NA	X;U;;X;	X;0.71087;;X;	0.71087	P68431 Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 ,
DLC(470.29977)FSPGLM(15.994915)EASHVVNDVNE AVQLVFRK	NA,C362,M368,NA	X;;;X;	X;1.53137;;X;	1.53137	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 , Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5

					OS=Homo sapiens GN=CECR5 ,
YTVIMNPQLC(470.29977) TQMAITIWVIGFFHALLHSV MTSR	NA,NA	X;U;;X;	X;2.64979;;X;	2.64979	P58182 Olfactory receptor 12D2 OS=Homo sapiens GN=OR12D2 PE=2 SV=2 ,
GDSEPTPGC(470.29977)S GLGPGGVR	C13,NA,NA,C13,C13,NA	X;;;X;	X;1.54045;;X;	1.54045	Q8WW01 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 , Q8WW01-2 Isoform 2 of tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 , H0YCV5 tRNA-splicing endonuclease subunit Sen15 (Fragment) OS=Homo sapiens GN=TSEN15 PE=1 SV=1 , E9PPN1 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 , F2Z3M0 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 ,
GDSEPTPGC(470.29977)S GLGPGGVR	C13,NA,NA,C13,C13,NA	X;;;X;	X;1.65234;;X;	1.65234	Q8WW01 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 , Q8WW01-2 Isoform 2 of tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 , H0YCV5 tRNA-splicing endonuclease subunit Sen15 (Fragment) OS=Homo sapiens GN=TSEN15 PE=1 SV=1 , E9PPN1 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 , F2Z3M0 tRNA-splicing endonuclease subunit Sen15 OS=Homo sapiens GN=TSEN15 PE=1 SV=1 ,
TYAIC(464.28596)GAIR	C56,C56,C56,NA	X;;;X;	X;1.31039;;X;	1.31039	Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 , Q9BYK1 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 , P63220 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 ,
EEHLC(464.28596)TQR	NA,NA,NA,C233,C212,C20 8,C217,NA	X;;;X;	X;1.12288;;X;	1.12288	P06753-5 Isoform 5 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 , P06753-7 Isoform 7 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 , J3KN67 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , P06753-2 Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 , A0A087WWU8 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 , Q5VU61 Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 , Q5HYB6 Epididymis luminal

					protein 189 OS=Homo sapiens GN=DKFZp686J1372 PE=1 SV=1 ,
GQVYTCGHGPGGRLGHGD EQTC(464.28596)LVPR	C217,C217,C217,NA	X;;;X;	X;0.95261;;X;	0.95261	E7EPI0 Inhibitor of Bruton tyrosine kinase OS=Homo sapiens GN=IBTK PE=1 SV=1 , Q9P2D0-2 Isoform 2 of Inhibitor of Bruton tyrosine kinase OS=Homo sapiens GN=IBTK , Q9P2D0 Inhibitor of Bruton tyrosine kinase OS=Homo sapiens GN=IBTK PE=1 SV=3 ,
TEEAAADTALTIMEVAEVES PLNPSC(470.29977)KIMTF R	C36,NA	X;U;;X;	X;0.90365;;X;	0.90365	Q9H3R0-4 Isoform 4 of Lysine-specific demethylase 4C OS=Homo sapiens GN=KDM4C ,
PDGPEAQAEAC(470.2997 7)SGER	C18,NA	X;;;X;	X;1.48676;;X;	1.48676	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
NIC(470.29977)FTVWDVG GQDK	NA,NA,NA	X;;;X;	X;2.16909;;X;	2.16909	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 , C9J1Z8 ADP-ribosylation factor 5 (Fragment) OS=Homo sapiens GN=ARF5 PE=1 SV=1 ,
ATYDKLC(464.28596)K	NA,NA	X;U;;U;;	X;1.21775;;1.30707 ;;	1.26241	P62851 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 ,
C(464.28596)DGDASPPSP AR	NA,NA,C15,NA	X;;;X;	X;0.30221;;X;	0.30221	E7EUV9 Histone RNA hairpin-binding protein OS=Homo sapiens GN=SLBP PE=1 SV=1 , F8W8D3 Histone RNA hairpin-binding protein OS=Homo sapiens GN=SLBP PE=1 SV=1 , Q14493 Histone RNA hairpin-binding protein OS=Homo sapiens GN=SLBP PE=1 SV=1 ,
C(470.29977)SEGSFLLTTF PRPVTVEPM(15.994915)D QLDDEEGLPEK	C119,M138,NA,NA	X;;;;;	X;1.34335;;1.2315;;	1.287425	Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO , Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 ,
DLM(15.994915)AC(470.2 9977)AQTGSGK	M221,C223,NA,M221,C22 3,M221,C223,NA	X;;;X;	X;1.68852;;X;	1.68852	O00571 ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 , A0A0D9SFB3 ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=1 , A0A0D9SF53 ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=1 , A0A0D9SG12 ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=1 ,
C(464.28596)IPALDSLTPA NEDQK	NA,NA,NA	X;U;;X;	X;1.61337;;X;	1.61337	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
YAC(470.29977)GLWGLSP	C457,NA,NA,NA	X;;;X;	X;1.26767;;X;	1.26767	Q15637-6 Isoform 6 of Splicing factor 1 OS=Homo sapiens

ASR					GN=SF1 , H7C0N4 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=1 , H7C561 Splicing factor 1 (Fragment) OS=Homo sapiens GN=SF1 PE=1 SV=7 ,
IC(470.29977)PVEFNPV AR	NA,NA,NA	X;;;X;	X;1.06;;X;	1.06	Q9UI30 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 , F5GX77 Multifunctional methyltransferase subunit TRM112-like protein OS=Homo sapiens GN=TRMT112 PE=1 SV=1 ,
EFHQAGKPIGLC(464.2859 6)CIAPVLAAK	C187,NA	X;;;X;	X;0.93017;;X;	0.93017	A0A096LP16 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
LLLDHEALSC(470.29977)L LVLLFVDEPK	C3188,NA,C3179,NA	X;;;X;	X;1.30752;;X;	1.30752	Q7Z6Z7 E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 , Q7Z6Z7-2 Isoform 2 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 , Q7Z6Z7-3 Isoform 3 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 ,
YDSYESC(464.28596)DSR	C67,C67,C117,C147,NA,N A,C66,NA	X;;;X;	X;1.66166;;X;	1.66166	Q9ULX6-2 Isoform 2 of A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L , Q9ULX6 A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3 , M0QYT7 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 , M0R010 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 , V9GZ50 A kinase (PRKA) anchor protein 8-like, isoform CRA_c OS=Homo sapiens GN=AKAP8L PE=1 SV=1 , M0R1Y5 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=2 ,
FRCPEALFQPSFLGM(15.99 4915)ESC(464.28596)GIHE TTFNSIMK	NA,NA,NA,NA,NA	X;;;X;	X;1.41393;;X;	1.41393	P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 , P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 ,
LHTGPLPEQC(464.28596) R	C163,NA,NA,NA	X;;;;;	X;0.73618;;0.63541 ;;	0.685795	A0JLT2-2 Isoform 2 of Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 , J3KR33 Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 PE=1 SV=1 , A0JLT2 Mediator of RNA polymerase II transcription subunit 19 OS=Homo sapiens GN=MED19 PE=1 SV=2 ,
EQNYC(470.29977)ESR	C160,NA,NA	X;;;X;	X;1.41696;;X;	1.41696	Q7L5D6 Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1 , Q7L5D6-2 Isoform 2 of Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4

					,
GAVFEGC(470.29977)GM(15.994915)TPNANPSQIYNIDPAR	NA,NA,NA,C274,M276,NA,NA,NA,NA,NA,NA	X;;;X;	X;0.90533;;X;	0.90533	Q9NP81 Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 PE=1 SV=1 , M0R2C6 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 , Q9NP81-2 Isoform 2 of Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 , M0R259 Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 PE=4 SV=1 , M0QWZ7 Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 PE=1 SV=1 ,
AGQPHSSSDAAQAPAEQP HSSSDAAQAPC(470.29977)PR	C51,C51,NA,NA,NA,NA	X;;;;	X;1.52368;;1.80206;;	1.66287	P29372-4 Isoform 3 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372 DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 , A2IDA3 DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 , P29372-5 Isoform 4 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372-2 Isoform 2 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG ,
AGQPHSSSDAAQAPAEQP HSSSDAAQAPC(470.29977)PR	C51,C51,NA,NA,NA,NA	X;;;X;	X;1.74139;;X;	1.74139	P29372-4 Isoform 3 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372 DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 , A2IDA3 DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 , P29372-5 Isoform 4 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372-2 Isoform 2 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG ,
LYYFQYPC(464.28596)YQEGLR	NA,NA	X;U;;U;;	X;1.33524;;1.1975;;	1.26637	Q9NRW3 DNA dC- dU-editing enzyme APOBEC-3C OS=Homo sapiens GN=APOBEC3C PE=1 SV=2 ,
TVGVQGDC(470.29977)R	C523,NA,NA	X;;;X;	X;1.42872;;X;	1.42872	P49915 GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 , P49915-2 Isoform 2 of GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS ,
C(464.28596)SDSDGLAPP QHLIR	NA,C182,NA,C143,C182,C143,NA,NA,NA	X;;;X;	X;0.86266;;X;	0.86266	P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 , P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo

					sapiens GN=TP53 , P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 ,
VAAAASC(470.29977)LSQK	NA,C314,NA	X,,,X;	X;1.57478,,X;	1.57478	O95067 G2/mitotic-specific cyclin-B2 OS=Homo sapiens GN=CCNB2 PE=1 SV=1 , H1UBN3 Cyclin B2 OS=Homo sapiens GN=CCNB2V PE=1 SV=1 ,
LLGSTIPLC(464.28596)SAQWER	C304,NA,NA,NA,NA	X,,,X;	X;0.7101,,X;	0.7101	P50416-2 Isoform 2 of Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A , P50416 Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2 ,
FAC(464.28596)HSASLTVR	NA,NA	X,,,X;	X;1.30804,,X;	1.30804	Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 ,
ADPDGPEAQAEAC(464.28596)SGER	C18,NA	X,,,X;	X;1.5789,1.68523,,X;	1.632065	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
QC(464.28596)NAAIHKK	C192,NA,NA	X,,,X;	X;2.76348,,X;	2.76348	Q05655 Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2 , Q05655-2 Isoform 2 of Protein kinase C delta type OS=Homo sapiens GN=PRKCD ,
SYC(470.29977)NDQSTGDIK	C106,NA	X;U,,X;	X;1.37779,,X;	1.37779	P00492 Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 ,
DSGYGDIWC(464.28596)PER	C213,C176,NA,C228,C228,NA,C176,NA	X,,,X;	X;1.25954,,X;	1.25954	J3KP06 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , F8WD26 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2 , Q8WWI1-4 Isoform 4 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 , Q8WWI1 LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 , Q8WWI1-3 Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 , Q8WWI1-2 Isoform 2 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7 , E9PMP7 LIM domain only protein 7 (Fragment) OS=Homo sapiens GN=LMO7 PE=1 SV=7 ,
GFNKETAAAC(464.28596)VEK	NA,NA,NA	X,,,X;	X;0.98942,,X;	0.98942	E9PGT1 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 , Q15631 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 ,
GFNKETAAAC(464.28596)	NA,NA,NA	X,,,X;	X;1.77188,,X;	1.77188	E9PGT1 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 ,

VEK					Q15631 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 ,
TVPFLPLLGGC(470.29977) IDDTILSR	C180,NA,NA,NA,NA	X,,,,;	X;1.62971,;1.30636 ,,	1.468035	Q7Z7H8 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3 , Q7Z7H8-2 Isoform 2 of 39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 ,
AEGSDVANAVLDGADC(46 4.28596)IM(15.994915)LS GETAKGDYPLEAVR	NA,NA	X,,,X;	X;0.87492,;X;	0.87492	P14618 Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 ,
DLTTAGAVTQC(470.29977)YR	NA,NA	X,,,X;	X;1.19482,;X;	1.19482	Q02543 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2 ,
TGC(470.29977)TFPEKPDF H	C318,C336,C336,NA	X,,,,;	X;1.4564,;1.18273,;	1.319565	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK , P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 , P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK ,
C(470.29977)ALSSPSLAFT PPIK	C120,NA,NA,NA	X,,,,;	X;1.29252,;1.40935 ,,	1.350935	Q8NFH5-3 Isoform 3 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5-2 Isoform 2 of Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 , Q8NFH5 Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1 ,
LSEEAEC(464.28596)PNPS TPSK	C947,NA	X;U,;X;	X;2.67956,;X;	2.67956	O94804 Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1 ,
RGPC(464.28596)IYNEDN GIIK	C208,NA	X,,,X;	X;0.94481,;X;	0.94481	P36578 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 ,
C(470.29977)M(15.99491 5)TNTPVVVR	C120,M121,NA,C120,M12 1,NA,NA,NA,NA	X,,,X;	X;2.03834,;X;	2.03834	P32322 Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2 , P32322-2 Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 , P32322-3 Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 ,
IIMTLAEDLLC(470.29977)S AAQNSR	NA,C543,C537,NA,NA,NA	X,,,X;	X;0.44533,;X;	0.44533	H0YIW3 HEAT repeat-containing protein 5A (Fragment) OS=Homo sapiens GN=HEATR5A PE=1 SV=1 , F5H619 HEAT repeat-containing protein 5A OS=Homo sapiens GN=HEATR5A PE=1 SV=1 , Q86XA9-2 Isoform 2 of HEAT repeat-containing protein 5A OS=Homo sapiens GN=HEATR5A , Q86XA9 HEAT repeat-containing protein 5A OS=Homo sapiens GN=HEATR5A PE=1 SV=2 , H7C5W6 HEAT repeat-containing protein 5A (Fragment) OS=Homo sapiens

					GN=HEATR5A PE=1 SV=1 ,
QSLFC(464.28596)PK	C27,NA	X,,,X;	X;1.72677,,X;	1.72677	Q56VL3 OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 ,
TSC(464.28596)GSPNYAA PEVISGR	C200,C200,NA	X,,,,;	X;1.70247,,1.5552,;	1.628835	Q13131 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4 , Q13131-2 Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 ,
TIC(470.29977)SHVQNM(15.994915)IK	NA,NA,C74,M80,NA	X,,,X;	X;1.39542,,X;	1.39542	D6RAN4 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=7 , E7ESE0 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=1 , P32969 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 ,
NQLKETTEAAC(464.28596) JR	NA,NA,NA	X,,,,;	X;1.84056,,4.86895 ,,	3.354755	Q9Y2Q3 Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3 , Q9Y2Q3-4 Isoform 4 of Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 ,
ALIVGHC(464.28596)M(15.994915)PGPR	NA,NA,NA	X;U,,X;	X;1.83809,,X;	1.83809	Q6P1L8 39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 ,
GLC(464.28596)AIAQAESL R	NA,NA	X,,,X;	X;1.22121,,X;	1.22121	P23396 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 ,
VDLNSNGFIC(464.28596) DYELHELFK	NA,NA	X,,,X;	X;0.96994,,X;	0.96994	P13797 Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 ,
NC(464.28596)IVLIDSTPYR QWYESHYALPLGR	NA,NA	X,,,X;	X;1.31853,,X;	1.31853	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
NFILDQC(470.29977)NVY NSGQR	NA,NA	X,,,X;	X;0.43366,,X;	0.43366	Q1KMD3 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 ,
LILADALC(464.28596)YAH TFNPK	C376,NA,NA	X,,,X;	X;1.61927,,X;	1.61927	P28838 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 , P28838-2 Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 ,
NIC(464.28596)FTVWDVG GQDK	NA,NA,NA	X,,,X;	X;2.16909,,X;	2.16909	P84085 ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2 , C9J1Z8 ADP-ribosylation factor 5 (Fragment) OS=Homo sapiens GN=ARF5 PE=1 SV=1 ,
CC(470.29977)SPLFM(15.994915)DVK	C495,M500,NA	X;U,,X;	X;0.13834,,X;	0.13834	Q7LFX5-2 Isoform 2 of Carbohydrate sulfotransferase 15 OS=Homo sapiens GN=CHST15 ,
DC(470.29977)PHISQR	C143,NA	X,,,X;	X;1.24152,,X;	1.24152	Q9Y2S7 Polymerase delta-interacting protein 2 OS=Homo sapiens GN=POLDIP2 PE=1 SV=1 ,

HSM(15.994915)NPFC(470.29977)EIAVEEAVR	M129,C133,M129,C133,NA	X,,,,;	X;1.69789,,1.58295,,	1.64042	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
GC(470.29977)IVDANLSVLNLVIVK	NA,NA	X,,,,;	X;1.40253,,1.31326,,	1.357895	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
TTC(470.29977)SSGSALGP GAGAAQPSASPLEGLDLSY PR	C12,C12,NA,NA	X,,,X;	X;1.20521,,X;	1.20521	Q96FZ5 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=2 SV=1 , F8WDZ3 CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 PE=1 SV=1 , Q96FZ5-2 Isoform 2 of CKLF-like MARVEL transmembrane domain-containing protein 7 OS=Homo sapiens GN=CMTM7 ,
C(470.29977)EFQDAYVLLSEK	NA,NA,NA	X;U,,U,;	X;1.37306,,1.27029,,	1.321675	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
IHMGSC(464.28596)AENTAK	NA,NA,NA	X;U,,X;	X;1.40744,,X;	1.40744	P24752 Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 ,
KGAGNPQASTLALQSNITQ C(470.29977)LLGQPWPLN EAQVQASVVK	NA,NA,NA,NA,NA,NA,C1299,C1261,C1260,NA	X,,,X;	X;1.3189,,X;	1.3189	E7EY2 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1 , Q13428-2 Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-6 Isoform 6 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-4 Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428 Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 , Q13428-8 Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-3 Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1 , Q13428-7 Isoform 7 of Treacle protein OS=Homo sapiens GN=TCOF1 , J3KQ96 Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=1 SV=1 ,
TAPGM(15.994915)GDQSGC(464.28596)YR	M156,C162,NA	X,,,X;	X;1.24979,,X;	1.24979	Q9BWF3 RNA-binding protein 4 OS=Homo sapiens GN=RBM4 PE=1 SV=1 ,
ADPDGPEAQAEAC(470.29977)SGER	C18,NA	X,,,X;	X;1.5789,1.68523,,X;	1.632065	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
VNGTTPC(470.29977)AFPTHYEEALKDEEK	NA,NA	X;U,,X;	X;1.95341,,X;	1.95341	O15479 Melanoma-associated antigen B2 OS=Homo sapiens GN=MAGEB2 PE=1 SV=3 ,
EGTDSSQGIPQLVSNISAC(4	NA,NA	X,,,X;	X;1.01145,,X;	1.01145	Q99832 T-complex protein 1 subunit eta OS=Homo sapiens

64.28596)QVIAEAVR					GN=CCT7 PE=1 SV=2 ,
AGEVPPAMYQFSQYVC(4 64.28596)QQTGLQIPQLPA PPK	NA,C82,C60,NA,NA	X;;;X;	X;0.29068;;X;	0.29068	K7EIR2 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 , A0A140TA84 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 , Q5XKP0 MICOS complex subunit MIC13 OS=Homo sapiens GN=MIC13 PE=1 SV=1 , A0A140TA86 MICOS complex subunit MIC13 OS=Homo sapiens GN=C19orf70 PE=1 SV=1 ,
HSM(15.994915)NPFC(46 4.28596)EIAVEEAVR	M129,C133,M129,C133,N A	X;;;;	X;1.72037;;1.30573 ;;	1.51305	P38117 Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3 , P38117-2 Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB ,
TIC(464.28596)SHVQNM(15.994915)IK	NA,NA,C74,M80,NA	X;;;X;	X;1.39542;;X;	1.39542	D6RAN4 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=7 , E7ESE0 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=1 , P32969 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1 ,
ISC(470.29977)M(15.9949 15)SKPPAPNPTPPR	NA,NA,NA	X;;;;	X;1.51465;;1.73224 ;;	1.623445	P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 , P46734 Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 ,
EYTYSKHGM(15.994915)H FTHNMFPVPNNLHMAQN AC(464.28596)ECNK	M274,C294,NA	X;U;;X;	X;9.57286;;X;	9.57286	A8MT65 Zinc finger protein 891 OS=Homo sapiens GN=ZNF891 PE=2 SV=2 ,
VDASAC(464.28596)GM(1 5.994915)ER	NA,C317,M319,C317,M31 9,NA	X;;;X;	X;1.50744;;X;	1.50744	O95671-3 Isoform 3 of N-acetylserotonin O- methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671-2 Isoform 2 of N-acetylserotonin O- methyltransferase-like protein OS=Homo sapiens GN=ASMTL , O95671 N-acetylserotonin O- methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3 ,
IATLDM(15.994915)SSDQI AANLQAVINEVC(464.2859 6)R	M262,C279,NA,NA	X;U;;X;	X;1.74703;;X;	1.74703	Q9BYD6 39S ribosomal protein L1, mitochondrial OS=Homo sapiens GN=MRPL1 PE=1 SV=2 ,
HC(464.28596)SQVDSVR	NA,NA,C112,NA	X;;;;	X;1.39048;;1.12209 ;;	1.256285	Q14247-3 Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN , Q14247 Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 , Q14247-2 Isoform

					2 of Src substrate cortactin OS=Homo sapiens GN=CTTN ,
ASDHGWVC(470.29977)D QR	C309,NA,NA	X;U;;U;;	X;1.46435;;1.22045 ;;	1.3424	Q9HC36 rRNA methyltransferase 3, mitochondrial OS=Homo sapiens GN=RNMTL1 PE=1 SV=2 ,
AMTGNAGEWC(470.2997 7)LMESDPGVFTELIK	NA,NA	X;U;;X;	X;1.05993;;X;	1.05993	Q5LJA9 Ubiquitin carboxyl-terminal hydrolase (Fragment) OS=Homo sapiens GN=UCHL5 PE=1 SV=1 ,
LEKPNEGYLEFFVDC(470.2 9977)SASATPEFEGR	C85,NA	X;U;;X;	X;1.22249;;X;	1.22249	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 ,
LLACIASRPGQC(470.2997 7)GR	NA,NA	X;;;X;	X;1.73717;;X;	1.73717	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,
AALALGSC(470.29977)LN NK	NA,NA,NA,NA,C70,NA,NA NK	X;;;X;	X;2.15527;;X;	2.15527	P34897 Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 , G3V5L0 Serine hydroxymethyltransferase, mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 , P34897-3 Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 ,
GC(464.28596)ATGSRPR	C77,C77,NA,C77,NA,NA	X;;;X;	X;1.30059;;X;	1.30059	A3KFJ8 Fibrinogen C domain-containing protein 1 OS=Homo sapiens GN=FIBCD1 PE=1 SV=1 , Q8N539 Fibrinogen C domain-containing protein 1 OS=Homo sapiens GN=FIBCD1 PE=1 SV=2 , X6RDH7 Fibrinogen C domain-containing protein 1 (Fragment) OS=Homo sapiens GN=FIBCD1 PE=1 SV=1 , Q8N539-2 Isoform 2 of Fibrinogen C domain-containing protein 1 OS=Homo sapiens GN=FIBCD1 , H0Y4Y8 Fibrinogen C domain-containing protein 1 (Fragment) OS=Homo sapiens GN=FIBCD1 PE=1 SV=1 ,
TSVPSPC(470.29977)GK	C260,NA,C260,NA,NA,NA, NA	X;;;;;	X;1.45049;;1.01491 ;;	1.2327	P49748-3 Isoform 3 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL , P49748 Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 , P49748-2 Isoform 2 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL ,
NIDPKPC(464.28596)TPR	C85,NA,C85,C85,NA	X;;;X;	X;1.59366;;X;	1.59366	K7EQ55 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=2 , Q96EP5-2 Isoform 2 of DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 , Q96EP5 DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=1 , K7EK33 DAZ-associated protein 1

					OS=Homo sapiens GN=DAZAP1 PE=1 SV=2 ,
LHDAIVEVVC(464.28596)LLR	NA,C470,C470,NA,C470,NA,NA,NA,NA	X;;;X;	X;5.89577;;X;	5.89577	O00429-6 Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-5 Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-3 Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429-2 Isoform 4 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , O00429 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 , O00429-8 Isoform 8 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L , G8JLD5 Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=1 , O00429-4 Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L ,
FQSSAVM(15.994915)ALQEASEAYLVGLFEDTNLC(470.29977)A	NA,NA	X;U;;U;;	X;0.5449;;0.57712;;	0.56101	Q71D13 Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3 ,
YKWC(470.29977)EYGLTFTEK	NA,C65,NA	X;;;X;	X;1.8176;;X;	1.8176	A0A0A0MR02 Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1 , P45880 Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 ,
TLEEFQDVYLVMEIMDANLC(470.29977)QVIHMELDER	NA,NA,C116,C116,C116,C116,C116,NA	X;;;X;	X;0.28908;;X;	0.28908	P45984-2 Isoform Alpha-1 of Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 , P45984-4 Isoform Beta-2 of Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 , P45984-5 Isoform 5 of Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 , P45984 Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 PE=1 SV=2 , J3KNK1 Mitogen-activated protein kinase OS=Homo sapiens GN=MAPK9 PE=1 SV=1 , P45984-3 Isoform Beta-1 of Mitogen-activated protein kinase 9 OS=Homo sapiens GN=MAPK9 , D7R525 Mitogen-activated protein kinase OS=Homo sapiens GN=MAPK9 PE=1 SV=1 ,
VALLELGC(470.29977)GTGANFQFYPPGCR	NA,C79,NA	X;;;X;	X;1.08075;;X;	1.08075	A0A087WZT2 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=1 , Q6UX53 Methyltransferase-like protein 7B OS=Homo sapiens GN=METTL7B PE=1 SV=2 ,
VAC(470.29977)IGAWHPA	C253,NA	X;;;X;	X;1.17137;;X;	1.17137	P39023 60S ribosomal protein L3 OS=Homo sapiens

R					GN=RPL3 PE=1 SV=2 ,
DAANC(464.28596)WTSLL ESEYAADPWVQDQM(15.9 94915)QR	NA,NA	X;U;;X;	X;1.45922;;X;	1.45922	Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 ,
NPVQC(470.29977)MR	NA,C50,C50,C50,NA,NA,NA	X;;;X;	X;3.10816;;X;	3.10816	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,
EC(464.28596)LPLIIFLR	NA,NA,NA	X;U;;X;	X;1.30929;;X;	1.30929	P62701 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 ,
DC(464.28596)GGAAQLA GPAAEADPLGR	C8,NA,NA,C8,C8,C8,C8,NA	X;;;X;	X;4.13977;;X;	4.13977	Q9Y508 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LNV3 E3 ubiquitin- protein ligase RNF114 (Fragment) OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LNT1 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LP02 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , Q9Y508-2 Isoform 2 of E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 , A0A096LNN8 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 , A0A096LPF9 E3 ubiquitin-protein ligase RNF114 OS=Homo sapiens GN=RNF114 PE=1 SV=1 ,
ETAAAC(464.28596)VEK	NA,NA,NA	X;;;X;	X;1.12024;;X;	1.12024	E9PGT1 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 , Q15631 Translin OS=Homo sapiens GN=TSN PE=1 SV=1 ,
VTELQQQLC(470.29977) TSVNTIYDNAVQGLR	NA,NA	X;U;;X;	X;0.89976;;X;	0.89976	Q96AG4 Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRR59 PE=1 SV=1 ,
C(464.28596)SEGSFLLTTF PRPVTVEPM(15.994915)D QLDDEEGLPEK	C119,M138,NA,NA	X;;;;;	X;1.32842;;1.24327 ;;	1.285845	Q15233-2 Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO , Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 ,
C(464.28596)M(15.99491 5)PTFQFFK	NA,NA	X;;;X;	X;1.30206;;X;	1.30206	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,

VNGTTPC(464.28596)AFP THYEEALKDEEK	NA,NA	X;U;;U;;	X;2.08816;;0.95688 ;;	1.52252	O15479 Melanoma-associated antigen B2 OS=Homo sapiens GN=MAGEB2 PE=1 SV=3 ,
KAC(464.28596)QIFVR	NA,NA,NA,NA	X;;;X;	X;1.55575;;X;	1.55575	P52272 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 , P52272-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM , A0A087X0X3 Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=1 ,
C(470.29977)TFCVDAGV WYYEVTVVTSQVMQIGWA TR	C352,NA	X;U;;X;	X;0.61117;;X;	0.61117	Q96DX4 RING finger and SPRY domain-containing protein 1 OS=Homo sapiens GN=RSPRY1 PE=1 SV=1 ,
VDC(470.29977)TANTNTC NK	NA,NA	X;;;X;	X;1.65225;;X;	1.65225	P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 ,
LLAIC(464.28596)QPLTYST R	C136,C136,NA	X;;;X;	X;1.78439;;X;	1.78439	P47893 Olfactory receptor 3A2 OS=Homo sapiens GN=OR3A2 PE=2 SV=3 , P47888 Olfactory receptor 3A3 OS=Homo sapiens GN=OR3A3 PE=2 SV=3 ,
TAPGM(15.994915)GDQS GC(470.29977)YR	M156,C162,NA	X;;;X;	X;1.22883;;X;	1.22883	Q9BWF3 RNA-binding protein 4 OS=Homo sapiens GN=RBM4 PE=1 SV=1 ,
GC(464.28596)QDFGWD CFQPDGYEQTYAEM(15.99 4915)PK	C129,M150,NA	X;;;X;	X;1.3201;;X;	1.3201	Q9BY32 Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2 ,
M(15.994915)C(464.2859 6)RPVILLPEDTPPFLELK	NA,M944,C945,M944,C94 5,NA	X;;;X;	X;1.64408;;X;	1.64408	P52701-4 Isoform 4 of DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 , P52701-3 Isoform 3 of DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 , P52701 DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2 ,
ADIIHAC(470.29977)DIVE DAAIAYGNNIQM(15.994 915)TLPK	C263,M280,NA	X;;;X;	X;1.45372;;X;	1.45372	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 ,
VDC(464.28596)TANTNTC NK	NA,NA	X;;;X;	X;1.65225;;X;	1.65225	P30101 Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 ,
DAANC(470.29977)WTSLL ESEYAADPWVQDQM(15.9 94915)QR	NA,NA	X;U;;X;	X;1.45922;;X;	1.45922	Q8WVJ2 NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1 ,
C(464.28596)LEELVFGDVE NDEDALLRR	C90,NA	X;U;;X;	X;1.24046;;X;	1.24046	Q9Y5J1 U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 ,

KQC(470.29977)QQLQTAI AEAEQR	C383,NA,NA	X;U;;X;	X;0.14441;;X;	0.14441	Q5XKE5 Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 ,
ADIIHAC(464.28596)DIVE DAAIAYGYNNIQM(15.994 915)TLPK	C263,M280,NA	X;;;X;	X;1.30534;;X;	1.30534	Q9NSD9 Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 ,
C(470.29977)LGHPEEFYNL VR	NA,NA	X,,,,;	X;1.33658;;1.2472;;	1.29189	P37268 Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 ,
C(464.28596)LGHPEEFYNL VR	NA,NA	X,,,,;	X;1.33658;;1.2472;;	1.29189	P37268 Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1 ,
IAVYSC(470.29977)PFDG MITETK	C225,NA	X;;;X;	X;0.78661;;X;	0.78661	P50990 T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 ,
LC(470.29977)DFGVSGQLI DSMANSFVGTR	C207,C211,NA	X;;;X;	X;2.25575;;X;	2.25575	Q02750 Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2 , P36507 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 ,
YDSYESC(470.29977)DSR	C67,C67,C117,C147,NA,N A,C66,NA	X;;;X;	X;1.64441;;X;	1.64441	Q9ULX6-2 Isoform 2 of A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L , Q9ULX6 A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3 , M0QYT7 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 , M0R010 A- kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=1 , V9GZ50 A kinase (PRKA) anchor protein 8-like, isoform CRA_c OS=Homo sapiens GN=AKAP8L PE=1 SV=1 , M0R1Y5 A-kinase anchor protein 8-like (Fragment) OS=Homo sapiens GN=AKAP8L PE=1 SV=2 ,
C(464.28596)VCDSETGLLL LPLPSDTVLEVDHTAVALR	C1421,C1396,NA	X;;;X;	X;3.72111;;X;	3.72111	A0A087X1U6 Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=1 , A0A075B730 Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 ,
ISC(464.28596)M(15.9949 15)SKPPAPNPTPPR	NA,NA,NA	X,,,,;	X;1.51465;;1.73224 ;;	1.623445	P46734-3 Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 , P46734 Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2 ,
XC(464.28596)AACLGPSLE QHLSGGVLSCEVPGSDCPG QHHSEVLHK	C2,NA	X;U;;X;	X;2.83178;;X;	2.83178	H0YJ98 Integrin alpha-7 (Fragment) OS=Homo sapiens GN=ITGA7 PE=1 SV=1 ,
TGSQGGC(464.28596)TQV	C27,NA	X;U;;X;	X;1.13359;;X;	1.13359	P62857 40S ribosomal protein S28 OS=Homo sapiens

R					GN=RPS28 PE=1 SV=1 ,
DFVNEAISHWELQSEGGQS AAPSPASWAC(464.28596) SPNLR	C76,C76,NA	X;;;X;	X;1.92206;;X;	1.92206	Q96CB9-4 Isoform 4 of 5-methylcytosine rRNA methyltransferase NSUN4 OS=Homo sapiens GN=NSUN4 , Q96CB9 5-methylcytosine rRNA methyltransferase NSUN4 OS=Homo sapiens GN=NSUN4 PE=1 SV=2 ,
ASC(470.29977)LYGQLPK	NA,NA	X;;;X;	X;1.89306;;X;	1.89306	P09211 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 ,
IKADPDGPEAQAEAC(464.28596)SGER	NA,NA,C18,C18,NA	X;;;;	X;1.39409;;1.39478 ;;	1.394435	D6RCB9 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 , D6RC52 H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1 , Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 , J3QSY4 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
GLELIASENFC(464.28596) SR	NA,NA,NA,NA,C59,NA,NA	X;;;X;	X;0.55114;;X;	0.55114	P34897 Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 , G3V5L0 Serine hydroxymethyltransferase, mitochondrial (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 , P34897-3 Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 ,
IKADPDGPEAQAEAC(464.28596)SGER	C18,NA	X;;;X;	X;2.00849;;X;	2.00849	Q9NX24 H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens GN=NHP2 PE=1 SV=1 ,
AENGLLM(15.994915)TPC (464.28596)YTANFVAPEVL K	NA,NA,M561,C564,M576, C579,M480,C483,NA,NA	X;;;X;	X;1.65413;;X;	1.65413	Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 , P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 , Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 ,
AENGLLM(15.994915)TPC (470.29977)YTANFVAPEVL K	NA,NA,M561,C564,M576, C579,M480,C483,NA,NA	X;;;X;	X;1.60788;;X;	1.60788	Q15418-2 Isoform 2 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418-4 Isoform 4 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens

					GN=RPS6KA1 , E9PGT3 Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=1 SV=1 , P51812 Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1 , Q15418-3 Isoform 3 of Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 , Q15418 Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2 ,
HPLTQELKEC(470.29977)E GIVPVPLAEK	NA,NA,NA	X;U;;U;;	X;2.02987;;1.6569;;	1.843385	P82932 28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 ,
HPLTQELKEC(470.29977)E GIVPVPLAEK	NA,NA,NA	X;U;;U;;	X;1.329;;1.20903;;	1.269015	P82932 28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 ,
PIIFLSGC(464.28596)YTM(15.994915)VSVAYIAGFVL QERVVCNER	NA,NA	X;U;;X;	X;10.96757;;X;	10.96757	Q14332 Frizzled-2 OS=Homo sapiens GN=FZD2 PE=1 SV=1 ,
TFC(464.28596)GTPEYLAP EVLEDNDYGR	C310,NA,NA,NA,NA,NA	X;;;X;	X;1.4743;;X;	1.4743	P31749 RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2 , P31751 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 , Q9Y243-2 Isoform 2 of RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 , Q9Y243 RAC-gamma serine/threonine-protein kinase OS=Homo sapiens GN=AKT3 PE=1 SV=1 , M0R0P9 RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=1 ,
AGSVATC(470.29977)QAV M(15.994915)R	C522,M526,NA	X;;;X;	X;2.02109;;X;	2.02109	O94906 Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 ,
NILGGTVFREPIIC(464.285 96)K	C154,NA,NA,NA,NA	X;;;;;	X;1.59064;;1.40425 ;;	1.497445	P48735 Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2 , P48735-2 Isoform 2 of Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 ,
APEVTILEPLQDVQLSEGQD ASFQC(470.29977)R	NA,C4271,C5228,C4271,C 4786,NA,NA	X;;;X;	X;1.48492;;X;	1.48492	Q5VST9-2 Isoform 2 of Obscurin OS=Homo sapiens GN=OBSCN , Q5VST9-3 Isoform 3 of Obscurin OS=Homo sapiens GN=OBSCN , H3BPX2 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=2 , Q5VST9 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3 , Q5VST9-6 Isoform 5 of Obscurin OS=Homo sapiens GN=OBSCN , A6NGQ3 Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=4 ,

DC(464.28596)GEYAHTR	NA,NA,NA,NA,NA	X;;;X;	X;1.93803;;X;	1.93803	Q9Y399 28S ribosomal protein S2, mitochondrial OS=Homo sapiens GN=MRPS2 PE=1 SV=1 , Q5T8A0 28S ribosomal protein S2, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS2 PE=1 SV=1 ,
SC(464.28596)NGPVLVGS PQGGVDIEEVAASNPELIFK	NA,NA,NA	X;;;X;	X;1.13744;;X;	1.13744	Q96I99 Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 ,
ATC(464.28596)APQHGAP GPGPADASK	C2535,NA,C2516,C2535,NA	X;;;;;	X;1.32598;;1.12391 ,1.34816;;	1.32598	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA , A0A087WWY3 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 , Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 , P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 ,
DLC(464.28596)FSPGLM(1 5.994915)EASHVVNDVNE AVQLVFRK	NA,C362,M368,NA	X;;;X;	X;1.53137;;X;	1.53137	Q9BXW7 Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1 , Q9BXW7-2 Isoform 1 of Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 ,
STLTDSLVC(470.29977)K	C41,NA	X;U;;U;;	X;0.94516;;0.94813 ;;	0.946645	P13639 Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 ,
VGAPTIPDSC(464.28596)L PLGM(15.994915)SQEDN QLK	NA,C274,M279,NA	X;;;X;	X;2.03152;;X;	2.03152	E9PL17 Polyribonucleotide 5'-hydroxyl-kinase Clp1 OS=Homo sapiens GN=CLP1 PE=1 SV=1 , Q92989 Polyribonucleotide 5'-hydroxyl-kinase Clp1 OS=Homo sapiens GN=CLP1 PE=1 SV=1 ,
KIIPTLEEGQLPSPTATSQLP LESDAVEC(464.28596)LNY QHYK	NA,NA,NA	X;;;X;	X;0.94689;;X;	0.94689	P61978 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 , P61978-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK ,
NFYGGNGIVGAQVPLGAGI ALAC(470.29977)K	NA,NA,NA,C219,NA,NA,C1 88,NA,NA,NA	X;;;X;	X;1.7665;;X;	1.7665	P08559 Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 , P08559-4 Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 , P08559-2 Isoform 2 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 ,
GEVPC(470.29977)TVTSAS PLEEATLSELK	C141,NA,NA	X;;;X;	X;1.56505;;X;	1.56505	P48047 ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 ,
VC(470.29977)TLAIIDPGD	C92,C92,NA	X;;;X;	X;1.39025;;X;	1.39025	P62888 60S ribosomal protein L30 OS=Homo sapiens

SDIIR					GN=RPL30 PE=1 SV=2 , E5RI99 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 ,
RNSDVMDC(470.29977)VI LDDGGFLLM(15.994915)A NHDDYTNIQIGR	NA,NA	X;;;X;	X;1.04408;;X;	1.04408	P54289-5 Isoform 5 of Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Homo sapiens GN=CACNA2D1 ,
VQYPQSQAC(470.29977)K	NA,NA	X;U;;X;	X;2.47521;;X;	2.47521	Q14204 Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 ,
HPLTQELKEC(464.28596)E GIVPVPLAEK	NA,NA,NA	X;U;;U;;	X;1.3508;;1.22889;;	1.289845	P82932 28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3 ,
NESC(470.29977)SENYTTD FIYQLYSEEGK	NA,NA,NA	X;;;X;	X;1.7773;;X;	1.7773	Q01813 ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2 ,
IDC(464.28596)FSEVPTSV FGEK	NA,NA	X;;;X;	X;2.21011;;X;	2.21011	O00567 Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 ,
C(464.28596)ASQSGM(15. 994915)TAYGTR	C175,M181,C164,M170,N A,C166,M172,NA	X;;;;;	X;1.24149;;1.18186 ;;	1.211675	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , A0A087X271 Calponin (Fragment) OS=Homo sapiens GN=CNN2 PE=1 SV=1 ,
FEYFKYIC(470.29977)PDK	NA,NA	X;X;U;;	X;X;0.77394;;	0.77394	Q8TDB6 E3 ubiquitin-protein ligase DTX3L OS=Homo sapiens GN=DTX3L PE=1 SV=1 ,
HLNEIDLFHC(464.28596)I DPNSK	C62,NA,C58,NA	X;X;;;;	X;X;0.38397;;	0.38397	A0A087WYT3 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185 Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1 , Q15185-4 Isoform 4 of Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 ,
KECENC(470.29977)DCLQ GFQLTHSLGGGTGSGMGTL LISK	C127,C474,NA	X;X;;;;	X;X;0.06624;;	0.06624	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
SEFYANEAC(464.28596)KR	NA,NA,C381,NA,C219,NA, NA	X;X;;;;	X;X;0.94484;;	0.94484	A0A087X0W7 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 , A0A087WT95 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=1 , P49753 Acyl-coenzyme A thioesterase 2, mitochondrial OS=Homo sapiens GN=ACOT2 PE=1 SV=6 ,
LC(470.29977)DSYEIRPGK	C87,C226,NA,C125,C226, NA	X;X;;;;	X;X;1.7521;;	1.7521	B4DT28 Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRPR PE=1 SV=1 , O43390-2

					Isoform 2 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR , O43390-3 Isoform 3 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR , O43390-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR , O43390 Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 ,
IDSVHEELQMEVIDLQC(464.28596)NTVLK	NA,C421,NA,C874,NA	X;X;;	X;X;5.96305,;	5.96305	Q86UP8 General transcription factor II-I repeat domain-containing protein 2A OS=Homo sapiens GN=GTF2IRD2 PE=1 SV=2 , Q86UP8-6 Isoform 6 of General transcription factor II-I repeat domain-containing protein 2A OS=Homo sapiens GN=GTF2IRD2 , Q6EKJ0 General transcription factor II-I repeat domain-containing protein 2B OS=Homo sapiens GN=GTF2IRD2B PE=1 SV=1 , A0A0A0MSY2 General transcription factor II-I repeat domain-containing protein 2A OS=Homo sapiens GN=GTF2IRD2 PE=1 SV=1 ,
ALDLDSSC(470.29977)KEA ADGYQR	C508,NA,C508,C60,NA	X;X;;	X;X;1.11396,;	1.11396	P31948-2 Isoform 2 of Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 , P31948-3 Isoform 3 of Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 , P31948 Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 , H0YGI8 Stress-induced-phosphoprotein 1 (Fragment) OS=Homo sapiens GN=STIP1 PE=1 SV=1 ,
SDPSIVLLLQC(464.28596) DIQK	C187,NA	X;X;U,;	X;X;1.38591,;	1.38591	P62760 Visinin-like protein 1 OS=Homo sapiens GN=VSNL1 PE=1 SV=2 ,
M(15.994915)KLNISFPAT GC(464.28596)QK	NA,NA	X;X;;	X;X;1.22713,;	1.22713	P62753 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 ,
LDTNSDGQLDFSEFLNLIGG LAM(15.994915)AC(470.29977)HDSFLK	M89,C91,NA	X;X;U,;	X;X;1.58431,;	1.58431	P31949 Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 ,
SFFDNISC(470.29977)DDN RER	C311,C375,NA,NA,NA,C54 ,NA	X;X;;	X;X;1.0743,;	1.0743	A0A140TA76 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 , Q8ND56-2 Isoform 2 of Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A , A0A0G2JQ95 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 ,

					Q8ND56 Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A PE=1 SV=3 , Q8ND56-3 Isoform 3 of Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A , A0A096LP11 Protein LSM14 homolog A (Fragment) OS=Homo sapiens GN=LSM14A PE=1 SV=1 ,
QQPALATALC(470.29977) PHAPAASDYELSLDLKNK	NA,NA,NA	X;X;;	X;X;1.4601,;	1.4601	A0A0G2JLG2 IQ motif and SEC7 domain-containing protein 3 (Fragment) OS=Homo sapiens GN=IQSEC3 PE=1 SV=1 , Q9UPP2 IQ motif and SEC7 domain-containing protein 3 OS=Homo sapiens GN=IQSEC3 PE=2 SV=3 ,
AGQPHSSSDAAQAPAEQP HSSSDAAQAPC(464.28596))PR	C51,C51,NA,NA,NA,NA	X;X;;	X;X;1.50002,;	1.50002	P29372-4 Isoform 3 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372 DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3 , A2IDA3 DNA-3-methyladenine glycosylase (Fragment) OS=Homo sapiens GN=MPG PE=1 SV=1 , P29372-5 Isoform 4 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG , P29372-2 Isoform 2 of DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG ,
PQAFMDHTQSHGVKLTPA QYQGLSGSPAVLQEGDEGC (470.29977)K	NA,NA,NA,C285,NA	X;X;;	X;X;0.26843,;	0.26843	Q9C0A1-2 Isoform 2 of Zinc finger homeobox protein 2 OS=Homo sapiens GN=ZFHX2 , C9JSX6 Zinc finger homeobox protein 2 (Fragment) OS=Homo sapiens GN=ZFHX2 PE=4 SV=2 , Q9C0A1 Zinc finger homeobox protein 2 OS=Homo sapiens GN=ZFHX2 PE=2 SV=3 , A2RRC6 ZFHX2 protein OS=Homo sapiens GN=ZFHX2 PE=2 SV=1 ,
SQSVSVSGPGPGPGGLC(4 64.28596)PGPNVLLNQQN PPAPQPQHLAR	C222,NA	X;X;U,;	X;X;1.31239,;	1.31239	Q9H0L4 Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 ,
NCDC(464.28596)LQGFQL THSLGGGTGSGMGTLLISK	C129,C476,NA	X;X;;	X;X;6.8588,;	6.8588	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
SYC(464.28596)AEIAHNVS SK	C96,C114,C96,NA	X;X;;	X;X;1.26511,;	1.26511	P62910 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2 , F8W727 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1 , D3YTB1 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 ,
FRCPEALFQPSFLGMESC(4 70.29977)GIHETTFNSIM(1	NA,NA,NA,NA,NA	X;X;;	X;X;1.2577,;	1.2577	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens

5.994915)K					GN=ACTG1 PE=1 SV=1 ,
HELQANC(470.29977)YEE VKDR	C177,NA,NA,C139,NA	X;X;;	X;X;1.22979;;	1.22979	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 , G3V1A4 Cofilin 1 (Non-muscle), isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 , P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 ,
GDEC(464.28596)ELLGHS K	NA,NA,NA	X;X;U;;	X;X;1.15952;;	1.15952	P49411 Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 ,
NLSTFAVDGKDC(470.2997 7)K	C164,NA	X;X;;	X;X;1.0927;;	1.0927	A0A096LPI6 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
LC(464.28596)DSYEIRPGK	C87,C226,NA,C125,C226, NA	X;X;;	X;X;1.7521;;	1.7521	B4DT28 Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRPR PE=1 SV=1 , O43390-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR , O43390-3 Isoform 3 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR , O43390-4 Isoform 4 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR , O43390 Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 ,
TVFAEHISDEC(464.28596) K	C114,NA	X;X;;	X;X;1.39654;;	1.39654	P39023 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 ,
VAAASGHC(470.29977)GA FSGSDSSR	C947,NA,NA	X;X;;	X;X;1.63026;;	1.63026	Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A , Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 ,
YLAEVAC(470.29977)GDD RK	C134,NA	X;X;;	X;X;0.66117;;	0.66117	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 ,
SACGVC(464.28596)PGR	NA,NA	X;X;U;;	X;X;1.25722;;	1.25722	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 ,
ELHGQNPVVTPC(464.285 96)NK	NA,C159,C159,C159,NA	X;X;;	X;X;1.28031;;	1.28031	Q16630-2 Isoform 2 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 , Q16630-3 Isoform 3 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 , F8WJN3 Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=1 , Q16630 Cleavage and polyadenylation specificity factor subunit 6

					OS=Homo sapiens GN=CPSF6 PE=1 SV=2 ,
C(470.29977)SDSDGLAPP QHLIR	NA,C182,NA,C143,C182,C 143,NA,NA,NA	X;X;;;	X;X;0.65816;;	0.65816	P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 , P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 ,
PPM(15.994915)EAAGFTA QVIILNHPGQISAGYAPVLD C(470.29977)HTAHIACK	NA,M314,C342,NA	X;X;;;	X;X;1.19444;;	1.19444	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 ,
ISLGLPVGAVINC(470.2997 7)ADNTGAK	NA,NA	X;X;;;	X;X;1.32906;;	1.32906	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 ,
ISLGLPVGAVINC(470.2997 7)ADNTGAK	NA,NA	X;X;;;	X;X;1.23677;;	1.23677	P62829 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 ,
YTVIMNPQLC(470.29977) TQMAITIWVIGFFHALLHSV MTSR	NA,NA	X;X;U;;	X;X;1.5233;;	1.5233	P58182 Olfactory receptor 12D2 OS=Homo sapiens GN=OR12D2 PE=2 SV=2 ,
C(470.29977)ESAFLSK	NA,C36,C36,NA	X;X;;;	X;X;1.40566;;	1.40566	C9JNW5 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , C9JXB8 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 , P83731 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 ,
VTEDENDEPIEPSDDGTVL LSTVTAQFPAC(470.2997 7)GLR	NA,C39,C39,C39,NA,NA,N A	X;X;;;	X;X;1.53456,1.5437 6;;	1.53916	A0A087X260 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , A0A087WYY0 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , B1AKP7 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , Q13148 TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 , G3V162 TAR DNA binding protein, isoform CRA_d OS=Homo sapiens GN=TARDBP PE=1 SV=1 ,

FVVDVDKNIDINDVTPNC(470.29977)R	C104,C104,NA	X;X;;	X;X;1.02827;;	1.02827	P62195 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 , P62195-2 Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 ,
GAVEKGEELSC(464.28596)EER	C38,C38,NA	X;X;;	X;X;1.35542;;	1.35542	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 , P31947-2 Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN ,
AC(470.29977)DLPAWVHF PDTER	NA,NA	X;X;;	X;X;1.28326;;	1.28326	H7BXI1 Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 ,
NSFYM(15.994915)GTC(464.28596)QDEPEQLDDW NR	M1888,C1891,NA,M753,C756,NA,M768,C771,NA	X;X;;	X;X;1.51206;;	1.51206	A0A087WY61 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=1 , Q14980-2 Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 , H0YFY6 Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=1 SV=1 , Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 , Q14980-5 Isoform 5 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 ,
LTALDYHNPAGFNC(470.29977)KDETEFR	C19,NA	X;X;;	X;X;1.19123;;	1.19123	Q9Y224 UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1 ,
ATC(470.29977)APQHGAP GPGPADASK	C2535,NA,C2516,C2535,NA	X;X;;;	X;X;1.12391,1.34816;;	1.236035	P21333-2 Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA , A0A087WWY3 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1 , Q60FE5 Filamin A OS=Homo sapiens GN=FLNA PE=1 SV=1 , P21333 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 ,
QDTYVSTPSEIHSLSPEQT EDDLEEEC(464.28596)EPE EMLK	NA,C806,NA	X;X;;	X;X;1.75595;;	1.75595	O43379 WD repeat-containing protein 62 OS=Homo sapiens GN=WDR62 PE=1 SV=4 , O43379-4 Isoform 4 of WD repeat-containing protein 62 OS=Homo sapiens GN=WDR62 ,
C(470.29977)CLTYCFNKPE DK	C144,NA	X;X;U;;	X;X;1.44921;;	1.44921	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
LGPGRPLPTFPTSEC(470.29977)TSDVEPDTR	C73,NA,NA	X;X;;	X;X;2.84455;;	2.84455	Q8TDD1 ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2 , Q8TDD1-2 Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 ,
EC(470.29977)PSDECGAG VFM(15.994915)ASHFDR	C121,M132,NA	X;X;U;;	X;X;1.2079;;	1.2079	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,

IGFPETTEEEIEIASNSDC(470.29977)IFPSAPDVK	C353,NA,NA	X;X;;	X;X;1.13957;;	1.13957	Q9Y3F4-2 Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP , Q9Y3F4 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 ,
GLM(15.994915)AIDC(464.28596)PHTGIVDYR	NA,NA,NA,NA,NA,NA,NA	X;X;;	X;X;1.37246;;	1.37246	C9JVN9 L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=L2HGDH PE=1 SV=1 , Q9H9P8 L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=L2HGDH PE=1 SV=3 , Q9H9P8-2 Isoform 2 of L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=L2HGDH ,
ECENC(470.29977)DCLQG FQLTHSLGGGTGSGMGTLLI SK	C127,C474,NA	X;X;;;	X;X;0.08053,0.14066;;	0.110595	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
LPAEPPALLQTHPPC(464.28596)R	NA,NA,C102,NA,C102,NA,C102,NA,NA,NA,NA	X;X;;	X;X;0.7941;;	0.7941	Q92667 A-kinase anchor protein 1, mitochondrial OS=Homo sapiens GN=AKAP1 PE=1 SV=1 , I3L2N7 A-kinase anchor protein 1, mitochondrial (Fragment) OS=Homo sapiens GN=AKAP1 PE=1 SV=1 , I3L2A2 A-kinase anchor protein 1, mitochondrial (Fragment) OS=Homo sapiens GN=AKAP1 PE=1 SV=7 , I3L0K6 A-kinase anchor protein 1, mitochondrial (Fragment) OS=Homo sapiens GN=AKAP1 PE=1 SV=1 , Q92667-2 Isoform 2 of A-kinase anchor protein 1, mitochondrial OS=Homo sapiens GN=AKAP1 ,
RLDEC(464.28596)EEAFQ GTK	C103,NA,NA,NA,NA,NA	X;X;;	X;X;1.30305;;	1.30305	P61289-3 Isoform 3 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 , B3KQ25 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , K7ESG5 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289-2 Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 ,
YLAEVAC(464.28596)GDDRK	C134,NA	X;X;;	X;X;0.66117;;	0.66117	P27348 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 ,
SPPAC(464.28596)SQHTP PLPSTPTGPPPCSPGGNHPL C(470.29977)ALSGR	C89,C115,NA	X;X;U;;	X;X;1.91921;;	1.91921	Q3SXR2 Uncharacterized protein C3orf36 OS=Homo sapiens GN=C3orf36 PE=2 SV=1 ,

LC(464.28596)ASGAGATP DTAIEEIKEK	C31,NA,NA	X;X;;	X;X;1.53639;;	1.53639	P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 , P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 ,
NC(464.28596)LTNFHGM DLTR	NA,NA,C96,NA,NA	X;X;;	X;X;1.30725;;	1.30725	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
TVFAEHISDEC(470.29977) K	C114,NA	X;X;;	X;X;1.39654;;	1.39654	P39023 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 ,
C(464.28596)SATPSAQVK PIVSASPPSR	C498,C726,NA	X;X;;	X;X;1.0234;;	1.0234	H0Y3K4 RNA-binding protein 33 (Fragment) OS=Homo sapiens GN=RBM33 PE=1 SV=1 , Q96EV2 RNA-binding protein 33 OS=Homo sapiens GN=RBM33 PE=1 SV=3 ,
C(464.28596)SDSDGLAPP QHLIR	NA,C182,NA,C143,C182,C 143,NA,NA,NA	X;X;;	X;X;0.65816;;	0.65816	P04637-2 Isoform 2 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , J3KP33 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4 , P04637-5 Isoform 5 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , P04637-3 Isoform 3 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , A0A0U1RQC9 Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1 , P04637-4 Isoform 4 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 , P04637-6 Isoform 6 of Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 ,
SLC(470.29977)IGATYDVT DSR	NA,C356,C344,NA	X;X;;	X;X;0.90879;;	0.90879	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 , O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 , B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 ,
AATGEEVSAEDLGGADLHC(464.28596)R	NA,NA,NA	X;X;;	X;X;1.28292;;	1.28292	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
AGQC(464.28596)VIGLQM (15.994915)GTNK	C164,M170,C153,M159,N A,C155,M161,NA	X;X;;	X;X;1.1985;;	1.1985	Q99439 Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4 , B4DDF4 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , B4DUT8 Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 , A0A087X271 Calponin (Fragment) OS=Homo sapiens

					GN=CNN2 PE=1 SV=1 ,
VAGINAC(470.29977)GR	C1803,C1916,C1916,NA,NA	X;X;;	X;X;1.20076;;	1.20076	P51610-2 Isoform 2 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 , P51610 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 , P51610-4 Isoform 4 of Host cell factor 1 OS=Homo sapiens GN=HCFC1 , A6NEM2 Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 ,
IKSGEEDFESLASQFSDC(470.29977)SSAK	NA,C113,NA,NA	X;X;;	X;X;1.04706;;	1.04706	K7EN45 Peptidylprolyl isomerase (Fragment) OS=Homo sapiens GN=PIN1 PE=1 SV=1 , K7EMU7 Peptidylprolyl isomerase OS=Homo sapiens GN=PIN1 PE=1 SV=1 , Q13526 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1 ,
KENQWC(464.28596)EEK	C160,NA,NA	X;X;;	X;X;0.10677;;	0.10677	E5RJR5 S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=1 , P63208 S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2 ,
EADQKEQFSQGSPSNC(464.28596)LESLAEIFPLGK	C161,NA,NA	X;X;;	X;X;1.1534;;	1.1534	Q9NQ88 Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 ,
QNVCSGEC(470.29977)PPPK	C246,NA	X;X;U;;	X;X;1.1055;;	1.1055	A0A087WXS2 Hepatocyte nuclear factor 1-beta OS=Homo sapiens GN=HNF1B PE=1 SV=1 ,
LCMLTAELEYC(470.29977)NAPK	C866,NA,NA,NA,C584,NA,NA	X;X;;	X;X;0.61598;;	0.61598	Q9BXT4-2 Isoform 2 of Tudor domain-containing protein 1 OS=Homo sapiens GN=TDRD1 , H9KV62 Tudor domain-containing protein 1 OS=Homo sapiens GN=TDRD1 PE=1 SV=1 , H9KV63 Tudor domain-containing protein 1 OS=Homo sapiens GN=TDRD1 PE=1 SV=1 , Q9BXT4 Tudor domain-containing protein 1 OS=Homo sapiens GN=TDRD1 PE=1 SV=2 , Q9BXT4-4 Isoform 4 of Tudor domain-containing protein 1 OS=Homo sapiens GN=TDRD1 , Q9BXT4-3 Isoform 3 of Tudor domain-containing protein 1 OS=Homo sapiens GN=TDRD1 ,
TGC(470.29977)TFPEKPDFH	C318,C336,C336,NA	X;X;;	X;X;1.15606;;	1.15606	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK , P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 , P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK ,
GC(464.28596)GTVLLSGPR	NA,NA,NA,NA	X;X;;	X;X;1.03572;;	1.03572	J3QQ67 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1 , G3V203 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 ,

					Q07020 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 ,
TTSSANNPNLMYQDEC(470.29977)DRR	C507,C586,NA,NA,C505,NA	X;X;;	X;X;1.40276;;	1.40276	Q92841-3 Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , H3BLZ8 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1 , Q92841-2 Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 , Q92841 Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 , Q92841-1 Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 ,
EC(470.29977)PSDECGAG VFMASHFDR	C121,NA	X;X;U;;	X;X;1.12692;;	1.12692	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
TYAIC(470.29977)GAIR	C56,C56,C56,NA	X;X;;	X;X;1.36552;;	1.36552	Q8WVC2 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 , Q9BYK1 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 , P63220 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1 ,
QPAIMPGQSYGLEDGSC(470.29977)SYK	NA,NA,NA	X;X;;	X;X;1.35105;;	1.35105	M0QXS5 Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=1 SV=1 , P14866 Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 ,
ECPSDEC(470.29977)GAG VFMASHFDR	C126,NA	X;X;U;;	X;X;1.08745;;	1.08745	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
PVM(15.994915)SGNTAYP VISC(464.28596)PPLTPDW GVQDVWSSLR	M339,C350,NA	X;X;;	X;X;47.62757;;	47.62757	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
C(464.28596)ACASHVAK	C96,NA,C96,C95,C33,C96,NA	X;X;;	X;X;1.39139;;	1.39139	D6RFI1 Drebrin (Fragment) OS=Homo sapiens GN=DBN1 PE=1 SV=1 , Q16643-2 Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1 , Q16643-3 Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1 , D6R9W4 Drebrin (Fragment) OS=Homo sapiens GN=DBN1 PE=1 SV=1 , D6RCR4 Drebrin (Fragment) OS=Homo sapiens GN=DBN1 PE=1 SV=1 , Q16643 Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 ,
VC(470.29977)PPHM(15.994915)LPEDGANLSSAR	NA,NA,NA,NA,C29,M33,NA	X;X;;	X;X;1.41549;;	1.41549	Q9GZY8-2 Isoform 2 of Mitochondrial fission factor OS=Homo sapiens GN=MFF , A0A0A0MS29 Mitochondrial

					fission factor OS=Homo sapiens GN=MFF PE=1 SV=1 , Q9GZY8 Mitochondrial fission factor OS=Homo sapiens GN=MFF PE=1 SV=1 , H7C433 Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=1 SV=1 , E9PQX8 Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=1 SV=1 ,
C(470.29977)LAQEVNIPD WIVDLR	NA,NA,NA	X;X;;	X;X;1.44498;;	1.44498	Q9Y4W2 Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2 , Q9Y4W2-2 Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L ,
NVTQIEPFC(470.29977)LE TDRR	C630,C630,NA	X;X;;	X;X;1.46618;;	1.46618	Q9ULW0-2 Isoform 2 of Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 , Q9ULW0 Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 ,
EAELSKGESVC(470.29977) LDR	NA,NA	X;X;U;;	X;X;1.63323;;	1.63323	P62072 Mitochondrial import inner membrane translocase subunit Tim10 OS=Homo sapiens GN=TIMM10 PE=1 SV=1 ,
TGC(464.28596)TFPEKPDF H	C318,C336,C336,NA	X;X;;	X;X;1.15395;;	1.15395	P55263-4 Isoform 4 of Adenosine kinase OS=Homo sapiens GN=ADK , P55263 Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2 , P55263-2 Isoform 2 of Adenosine kinase OS=Homo sapiens GN=ADK ,
VHIPNDDAQFDASHC(464. 28596)DSDKGEFGGFSVT GK	C141,NA,NA	X;X;;	X;X;1.11017;;	1.11017	Q16576-2 Isoform 2 of Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 , Q16576 Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 ,
VHIPNDDAQFDASHC(464. 28596)DSDKGEFGGFSVT GK	C141,NA,NA	X;X;;	X;X;1.47495;;	1.47495	Q16576-2 Isoform 2 of Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 , Q16576 Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 ,
LC(470.29977)ASGAGATP DTAIEEIKEK	C31,NA,NA	X;X;;	X;X;1.47749;;	1.47749	P53384-2 Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 , P53384 Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2 ,
KC(470.29977)DLISIPK	NA,C473,C473,NA	X;X;;	X;X;1.43294;;	1.43294	Q9ULV4-2 Isoform 2 of Coronin-1C OS=Homo sapiens GN=CORO1C , Q9ULV4 Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 , Q9ULV4-3 Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C ,
AYGGSMC(470.29977)AK	NA,NA	X;X;U;;	X;X;1.33239;;	1.33239	P49207 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 ,
AALAAC(464.28596)PSSPF	C463,M472,NA,NA	X;X;;	X;X;1.3009;;	1.3009	Q8N2G8-3 Isoform 3 of GH3 domain-containing protein

PPAM(15.994915)PR					OS=Homo sapiens GN=GHDC , Q8N2G8 GH3 domain-containing protein OS=Homo sapiens GN=GHDC PE=1 SV=2 ,
AFVNPFPDYEEAAGALLAS GAAEETGC(464.28596)VR PPATTDEGPLPFHQDGK	NA,NA	X;X;U,;	X;X;1.86725,;	1.86725	Q9NS86 LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 ,
ELHGQNPVVTPC(470.299 77)NK	NA,C159,C159,C159,NA	X;X,;;	X;X;1.28031,;	1.28031	Q16630-2 Isoform 2 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 , Q16630-3 Isoform 3 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 , F8WJN3 Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=1 , Q16630 Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2 ,
GSFWTLHPDSGNM(15.99 4915)FENG(470.29977)Y LR	M242,C247,NA,NA	X;X,;;	X;X;1.8641,;	1.8641	Q9Y261 Hepatocyte nuclear factor 3-beta OS=Homo sapiens GN=FOXA2 PE=1 SV=1 , Q9Y261-2 Isoform 2 of Hepatocyte nuclear factor 3-beta OS=Homo sapiens GN=FOXA2 ,
AC(470.29977)QSIYPLHDV FVR	NA,NA,C201,NA,NA	X;X,;;	X;X;1.42822,;	1.42822	D6RB09 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=7 , D6RAT0 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=1 , P61247 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 , D6RG13 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE=1 SV=1 ,
AATGEEVSAEDLGGADLHC(470.29977)R	NA,NA,NA	X;X,;;	X;X;1.28292,;	1.28292	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
AATGEEVSAEDLGGADLHC(464.28596)RK	NA,NA,NA	X;X,;;	X;X;1.10337,;	1.10337	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
YATSCYSC(470.29977)CPR	C172,NA,NA	X;X,;;	X;X;1.32562,;	1.32562	Q13057-2 Isoform 2 of Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY , Q13057 Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4 ,
C(464.28596)VDEGLLDCK R	C208,NA,NA	X;X;U,;	X;X;0.51832,;	0.51832	Q9BSE5 Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 ,
C(464.28596)VDEGLLDCK R	C208,NA,NA	X;X;U,;	X;X;0.96265,;	0.96265	Q9BSE5 Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 ,
M(15.994915)LQPC(464.2 8596)GPPADKPEEN	NA,NA,NA	X;X;U,;	X;X;1.2998,;	1.2998	Q9BWJ5 Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1 , P01765 Ig heavy chain V-III region TIL

					OS=Homo sapiens PE=1 SV=1 ,
EADQKEQFSQGSPSNC(470.29977)LETSLAEIFPLGK	C161,NA,NA	X;X;;	X;X;1.19269;;	1.19269	Q9NQ88 Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 ,
SLC(464.28596)IGATYDVT DSR	NA,C356,C344,NA	X;X;;	X;X;0.90879;;	0.90879	O00541 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 , O00541-2 Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1 , B5MCF9 Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 ,
VTDDLVC(464.28596)LVYK TDQAQDVK	NA,NA	X;X;U;;	X;X;1.62878;;	1.62878	P49458 Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 ,
VAC(470.29977)AEWQES R	C87,NA	X;X;;	X;X;1.36806;;	1.36806	O75663 TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2 ,
MAEPEKAPALSILLYVQAFQ VGMPPPGCC(470.29977) R	NA,C853,NA	X;X;;	X;X;3.14652;;	3.14652	Q9Y2I1 Nischarin OS=Homo sapiens GN=NISCH PE=1 SV=3 , Q9Y2I1-2 Isoform 2 of Nischarin OS=Homo sapiens GN=NISCH ,
SVYLGTC(464.28596)GK	C516,NA	X;X;U;;	X;X;0.34524;;	0.34524	Q9NXV6 CDKN2A-interacting protein OS=Homo sapiens GN=CDKN2AIP PE=1 SV=3 ,
RLFDMPC(470.29977)DET LCSADSFVNDYTWGGS R	NA,NA,NA,NA	X;X;;	X;X;1.3623;;	1.3623	Q63HQ2-4 Isoform 4 of Pikachurin OS=Homo sapiens GN=EGFLAM , Q63HQ2-2 Isoform 2 of Pikachurin OS=Homo sapiens GN=EGFLAM , Q63HQ2 Pikachurin OS=Homo sapiens GN=EGFLAM PE=1 SV=2 ,
DLSYC(470.29977)LSGM(1 5.994915)YDHR	NA,NA	X;X;U;;	X;X;2.79412;;	2.79412	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 ,
NQLKETTEAAC(470.29977)R	NA,NA,NA	X;X;;	X;X;4.86895;;	4.86895	Q9Y2Q3 Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3 , Q9Y2Q3-4 Isoform 4 of Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 ,
KDC(470.29977)EVVMM(1 5.994915)IGLPGAGK	NA,C478,M483,NA	X;X;;	X;X;1.98369;;	1.98369	Q00839 Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 , Q00839-2 Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU ,
TIC(470.29977)HYIVEAGA SLMKTDQQGDTPR	C880,NA,NA,NA,C879,C879,C891,NA	X;X;;	X;X;0.2378;;	0.2378	Q13574-5 Isoform 5 of Diacylglycerol kinase zeta OS=Homo sapiens GN=DGKZ , Q13574-4 Isoform 4 of Diacylglycerol kinase zeta OS=Homo sapiens GN=DGKZ , Q13574-6 Isoform 6 of Diacylglycerol kinase zeta OS=Homo sapiens GN=DGKZ , Q13574-2 Isoform 2 of Diacylglycerol kinase zeta OS=Homo sapiens GN=DGKZ , Q13574-7 Isoform 7 of Diacylglycerol

					kinase zeta OS=Homo sapiens GN=DGKZ , Q13574 Diacylglycerol kinase zeta OS=Homo sapiens GN=DGKZ PE=1 SV=3 , Q13574-3 Isoform 3 of Diacylglycerol kinase zeta OS=Homo sapiens GN=DGKZ ,
TAVC(470.29977)DIPPRGL K	NA,C354,C354,C354,C354, NA,C336,NA	X;X;;	X;X;1.60551,;	1.60551	Q13885 Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 , P68371 Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 , A6NNZ2 Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 , Q9BVA1 Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 , Q3ZCM7 Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 , P04350 Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 , Q5JP53 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1 ,
EEC(470.29977)DKYALQS QQR	NA,NA,C179,NA,NA	X;X;;	X;X;1.69181,;	1.69181	A0A0B4J2A4 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=1 , P42765 3- ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 ,
HGFC(470.29977)GIPITDT GR	NA,NA	X;X;;	X;X;1.1593,;	1.1593	P12268 Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 ,
C(470.29977)ASQAGM(15 .994915)TAYGTR	C132,M138,C127,M133,N A,NA	X;X;;	X;X;1.21765,;	1.21765	E9PDU6 Calponin (Fragment) OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417 Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1 , Q15417-2 Isoform 2 of Calponin-3 OS=Homo sapiens GN=CNN3 ,
AYHEQLSVAEITNAC(464.2 8596)FEPANQMVK	NA,NA,NA,NA,NA,NA	X;X;;	X;X;0.95641,;	0.95641	P68366-2 Isoform 2 of Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A , Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 , P68366 Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 ,
VFC(464.28596)VEEEDSES SLQKR	C368,NA,NA	X;X;;	X;X;1.81793,;	1.81793	Q14684-2 Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B , Q14684 Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 ,
LQTEAQEDDWYDC(464.28	NA,NA	X;X;;	X;X;1.42001,;	1.42001	Q9UHI6 Probable ATP-dependent RNA helicase DDX20

596)HR					OS=Homo sapiens GN=DDX20 PE=1 SV=2 ,
LEKPNEGYLEFFVDC(464.28596)SASATPEFEGR	C85,NA	X;X;U,;	X;X;1.21746,;	1.21746	Q15024 Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 ,
NC(464.28596)DCLQGFQLTHSLGGGTGSGMGTLLISK	C127,C474,NA	X;X,;;	X;X;9.13673,;	9.13673	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
RQDSDLVQC(470.29977)GVTSPSSAEATGK	NA,NA	X;X;U,;	X;X;1.32887,;	1.32887	Q9HC52 Chromobox protein homolog 8 OS=Homo sapiens GN=CBX8 PE=1 SV=3 ,
SVLEALTSSTAM(15.994915)QCVPSDGC(470.29977)AMLLR	NA,NA	X;X;U,;	X;X;1.86504,;	1.86504	Q6ZVW7 Putative interleukin-17 receptor E-like OS=Homo sapiens GN=IL17REL PE=2 SV=2 ,
FHADSV(470.29977)K	NA,NA	X;X;U,;	X;X;1.20612,;	1.20612	Q9BW61 DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1 ,
TAFQEALDAAGDKLVVDF SATWC(464.28596)GPCK	NA,NA	X;X,;;	X;X;1.37365,;	1.37365	P10599 Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 ,
DLSYC(464.28596)LSGM(15.994915)YDHR	NA,NA	X;X;U,;	X;X;1.0231,;	1.0231	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 ,
DLSYC(464.28596)LSGM(15.994915)YDHR	NA,NA	X;X;U,;	X;X;1.57466,;	1.57466	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 ,
HEEFEEGC(470.29977)K	NA,NA,C41,C245,NA	X;X,;;	X;X;1.42207,;	1.42207	I3L3Q4 Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=1 SV=1 , Q9HC38-2 Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 , Q9HC38-3 Isoform 3 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 , F6TLX2 Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1 ,
TIQFVDWC(470.29977)PTGFK	NA,C347,NA,NA,NA,C347,NA	X;X,;;	X;X;1.42068,;	1.42068	Q13748 Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 , Q9BQE3 Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 , Q9NY65-2 Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 , C9J2C0 Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=1 SV=1 , Q71U36 Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 , Q9NY65 Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 ,

DLNYC(464.28596)FSGM(15.994915)SDHR	C267,M271,C267,M271,C267,M271,NA	X;X;;	X;X;1.35104,;	1.35104	P31943 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 , G8JLB6 Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 , P55795 Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 ,
C(470.29977)VDEGLLDCKR	C208,NA,NA	X;X;U,;	X;X;0.99703,;	0.99703	Q9BSE5 Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 ,
C(464.28596)GESGHLAR	C144,NA,C156,NA,C151,NA,NA,NA,NA	X;X;;	X;X;1.33438,;	1.33438	P62633-7 Isoform 7 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633 Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1 , P62633-5 Isoform 5 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-4 Isoform 4 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-3 Isoform 3 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-8 Isoform 8 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-6 Isoform 6 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP , P62633-2 Isoform 2 of Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP ,
LNLSC(464.28596)IHSPVVNELM(15.994915)R	NA,NA	X;X;U,;	X;X;1.15004,;	1.15004	Q9Y2X3 Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 ,
GSFWTLHPDSGNM(15.994915)FENG(464.28596)YLR	M242,C247,NA,NA	X;X;;	X;X;1.8641,;	1.8641	Q9Y261 Hepatocyte nuclear factor 3-beta OS=Homo sapiens GN=FOXA2 PE=1 SV=1 , Q9Y261-2 Isoform 2 of Hepatocyte nuclear factor 3-beta OS=Homo sapiens GN=FOXA2 ,
QDLRQEGQQLVDNSHFMSAEVTEC(464.28596)LQELEGR	C3394,NA,NA	X;X;U,;	X;X;5.69723,;	5.69723	Q9NRC6 Spectrin beta chain, non-erythrocytic 5 OS=Homo sapiens GN=SPTBN5 PE=1 SV=2 ,
SKDAAFQNVLTHVC(464.28596)LD	NA,NA	X;X;U,;	X;X;1.28875,;	1.28875	Q8NBU5 ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1 ,
NIC(470.29977)FTVWDVGGQDR	NA,C62,NA	X;X;;	X;X;1.13437,;	1.13437	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 , C9JPM4 ADP-ribosylation factor 4 (Fragment) OS=Homo sapiens GN=ARF4 PE=1 SV=1 ,
NIC(470.29977)FTVWDVGGQDR	NA,C62,NA	X;X;;	X;X;1.22931,;	1.22931	P18085 ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 , C9JPM4 ADP-ribosylation factor 4

					(Fragment) OS=Homo sapiens GN=ARF4 PE=1 SV=1 ,
HELQANC(464.28596)YEE VKDR	C177,NA,NA,C139,NA	X;X;;	X;X;1.22979;;	1.22979	E9PK25 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1 , G3V1A4 Cofilin 1 (Non-muscle), isoform CRA_a OS=Homo sapiens GN=CFL1 PE=1 SV=1 , P23528 Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 ,
FTTEIHPSC(470.29977)VT R	NA,NA	X;X;U;;	X;X;1.56325;;	1.56325	P29317 Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2 ,
RCGGELGDFTYIESPNYPG NYPANTEC(464.28596)TW TINPPK	NA,NA,C807,NA,NA,NA,NA	X;X;;	X;X;1.49432;;	1.49432	Q9NQ36 Signal peptide, CUB and EGF-like domain-containing protein 2 OS=Homo sapiens GN=SCUBE2 PE=2 SV=2 , A0A0A0MTC8 Signal peptide, CUB and EGF-like domain-containing protein 2 OS=Homo sapiens GN=SCUBE2 PE=1 SV=1 , Q9NQ36-2 Isoform 2 of Signal peptide, CUB and EGF-like domain-containing protein 2 OS=Homo sapiens GN=SCUBE2 ,
FRC(464.28596)PEALFQPS FLGM(15.994915)ESCGIH ETTFNSIMK	NA,NA,NA,NA,NA	X;X;;	X;X;1.06493;;	1.06493	P60709 Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 , P63261 Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ,
TATAVAHC(470.29977)R	NA,NA	X;X;U;;	X;X;1.08689;;	1.08689	A0A087WZ27 Zinc finger protein 90 OS=Homo sapiens GN=ZNF90 PE=4 SV=2 ,
EC(464.28596)PSDECGAG VFM(15.994915)ASHFDR	C121,M132,NA	X;X;U;;	X;X;1.2079;;	1.2079	P62979 Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 ,
ASDHGWVC(464.28596)D QR	C309,NA,NA	X;X;U;;	X;X;1.22045;;	1.22045	Q9HC36 rRNA methyltransferase 3, mitochondrial OS=Homo sapiens GN=RNMTL1 PE=1 SV=2 ,
EM(15.994915)ASC(470.29977)ITQR	NA,NA	X;X;U;;	X;X;1.2555;;	1.2555	Q969E8 Pre-rRNA-processing protein TSR2 homolog OS=Homo sapiens GN=TSR2 PE=1 SV=1 ,
VHIPNDDAQFDASHC(470.29977)DSDKGEFGGFSVT GK	C141,NA,NA	X;X;;	X;X;1.47495;;	1.47495	Q16576-2 Isoform 2 of Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 , Q16576 Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 ,
VAAASGHC(464.28596)GA FSGSDSSR	C947,NA,NA	X;X;;	X;X;1.63026;;	1.63026	Q9NZB2-6 Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A , Q9NZB2 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 ,
PPM(15.994915)EAAGFTA QVIILNHPGQISAGYAPVLD CHTAHIAAC(470.29977)K	NA,M314,C349,NA	X;X;;	X;X;1.13828;;	1.13828	P68104 Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 , P68104-2 Isoform 2 of Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 ,

AATGEEVSAEDLGGADLHC(470.29977)RK	NA,NA,NA	X;X;;	X;X;1.10337;;	1.10337	Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 ,
EC(470.29977)ENCDCLQG FQLTHSLGGGTGSGMGTLLI SK	C124,C471,NA	X;X;;;	X;X;0.03819,0.0;;	0.019095	Q13509 Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 , A0A0B4J269 Uncharacterized protein OS=Homo sapiens PE=1 SV=1 ,
WTDAFVGLSTC(470.29977)GRHMSAHR	NA,NA	X;X;U;;	X;X;0.72233;;	0.72233	A8MPS7 Carbohydrate deacetylase OS=Homo sapiens GN=YDJC PE=1 SV=1 ,
C(464.28596)AGPTPEAEL QALAR	C52,NA	X;X;U;;	X;X;1.48354;;	1.48354	Q15050 Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 ,
GAVEKGEELSC(470.29977)EER	C38,C38,NA	X;X;;	X;X;1.00293;;	1.00293	P31947 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 , P31947-2 Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN ,
ANAVC(470.29977)KLTYL QMLGYDISWAAFNIIEVMS ASK	C60,C60,NA,NA,C60,NA	X;X;;	X;X;0.49711;;	0.49711	O14617 AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=1 SV=1 , O14617-3 Isoform 3 of AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 , O14617-4 Isoform 4 of AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 , O14617-2 Isoform 2 of AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 , O14617-5 Isoform 5 of AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 ,
NLSTFAVDGKDC(464.28596)K	C164,NA	X;X;;	X;X;1.0927;;	1.0927	A0A096LP16 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 ,
PVMSGNTAYPVISC(464.28596)PPLTPDWGVQDVWSS LR	C350,NA	X;X;;	X;X;6.92262;;	6.92262	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
PVMSGNTAYPVISC(464.28596)PPLTPDWGVQDVWSS LR	C350,NA	X;X;;	X;X;47.24258;;	47.24258	P22234 Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 ,
LLLC(470.29977)GGAPLSA TTQR	C450,NA	X;X;U;;	X;X;1.46872;;	1.46872	O95573 Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 ,
C(470.29977)PQVEEAIVQS GQKK	C146,C146,NA	X;X;;	X;X;1.29981;;	1.29981	Q9BVP2 Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 , Q9BVP2-2 Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 ,
LDVGNFSWGSECC(470.29977)TR	NA,NA	X;X;U;;	X;X;1.34153;;	1.34153	P62241 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 ,

QYLEQHASGRFHCSWC(464.28596)WHTWQSAHVILFHMFLDR	NA,NA	X;X;U;;	X;X;1.60357;;	1.60357	Q5QGT7 Receptor-transporting protein 2 OS=Homo sapiens GN=RTP2 PE=1 SV=1 ,
C(470.29977)EFQDAYVLLSEKK	NA,NA,NA	X;X;U;;	X;X;1.13969;;	1.13969	P10809 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 ,
RGSDelfSTC(470.29977)V TNGPFIM(15.994915)SSN SASAANGNSK	C23,M31,NA,C23,M31,NA ,NA	X;X;;;	X;X;1.13509;;	1.13509	A0A0U1RRM4 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 , P26599-3 Isoform 3 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 , P26599-2 Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 , P26599 Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 ,
SCYDLSC(470.29977)HAR	NA,NA	X;X;U;;	X;X;1.15867;;	1.15867	P41250 Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 ,
RLDEC(470.29977)EEAFQ GTK	C103,NA,NA,NA,NA,NA	X;X;;;	X;X;1.30305;;	1.30305	P61289-3 Isoform 3 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 , B3KQ25 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , K7ESG5 Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 , P61289-2 Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 ,
LLSELDQQSTEM(15.994915)PRTGNGPMSVC(464.28596)GR	NA,M482,C493,NA,NA,NA ,NA	X;X;;;	X;X;1.70867;;	1.70867	O95793 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2 , O95793-2 Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , O95793-3 Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 , A0A087X1A5 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 , Q5JW30 Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=1 ,
FVVDVDKNIDINDVTPNC(464.28596)R	C104,C104,NA	X;X;;;	X;X;1.00089;;	1.00089	P62195 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1 , P62195-2 Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5

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PNC(464.28596)STLNFTLD LSR	NA,C494,C624,C494,NA,C 413,NA	X;X;;;	X;X;2.70375;;	2.70375	Q9NR96-3 Isoform 3 of Toll-like receptor 9 OS=Homo sapiens GN=TLR9 , Q9NR96 Toll-like receptor 9 OS=Homo sapiens GN=TLR9 PE=1 SV=2 , H0Y858 Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 , Q9NR96-4 Isoform 4 of Toll-like receptor 9 OS=Homo sapiens GN=TLR9 , Q9NR96-5 Isoform 5 of Toll-like receptor 9 OS=Homo sapiens GN=TLR9 , Q9NR96-2 Isoform 2 of Toll-like receptor 9 OS=Homo sapiens GN=TLR9 ,