

Supporting information

Functionalizing with Glycopeptide Dendrimers Significantly Enhances the Hydrophilicity of the Magnetic Nanoparticles

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Experiment details

Materials and reagents

Tetraethoxysilane (TEOS), 3-aminopropyltriethoxysilane (APTES), ammonia solution (25%), 1-(3-dimethylaminopropyl)-3-ethylcarbodiimide hydrochloride (EDC), N-hydroxysuccinimide (NHS), human serum immunoglobulin G (human IgG), trypsin, dithiothreitol (DTT), iodoacetamide (IAA) and 2,5-dihydroxyl benzoic acid (DHB) were purchased from Sigma-Aldrich (St, Louis, MO, USA). PNGase F was obtained from New England Biolabs (Ipswich, MA). Acetonitrile (ACN), trifluoroacetic acid (TFA) and formic acid were purchased from Merck (Darmstadt, Germany). Tris and urea were purchased from BioRad (Hercules, CA, USA). The branched oligopeptides with N₃-modification as shown in **Scheme S1** were obtained from Chinese Peptides Company (Hangzhou, China). Copper(II) sulfate, ascorbic acid, iron(III) chloride hexahydrate (FeCl₃·6H₂O), sodium acetate (NaAc), potassium carbonate (K₂CO₃), potassium dihydrogen phosphate (KH₂PO₄), ammonium bicarbonate (NH₄HCO₃), anhydrous ethanol, anhydrous methanol, isopropanol and dichloromethane were obtained from Tianjin Kermel plant of chemical reagent (Tianjin, China). β-D-maltose octaacetate was purchased from Bonuo Chemical (Dalian, China). Pure water was prepared with a Milli-Q system (Millipore, Bedford, MA, USA).

20 Synthesis of magnetic nanoparticles

Synthesis of NH₂-modification of Fe₃O₄@SiO₂ (MNPs-NH₂):

Fe₃O₄ nanoparticles were synthesized according to the method reported previously.^[1] 150 mg of the prepared Fe₃O₄ nanoparticles which were washed with ethanol and water for six times were redispersed in 200 mL ethanol/water (80:20, v/v) and sonicated for 1 h. After the addition of 2 mL ammonia solution, 1.0 mL TEOS was added dropwise. The mixed solution was stirred for 8 h at room temperature. After being washed with ethanol, water and isopropanol, the obtained Fe₃O₄@SiO₂ MNPs were redispersed in 50 mL isopropanol. The mixture was sonicated for 1 h, followed by the addition of 1.0 mL APTES. Then the system was stirred for 24 h at

room temperature. The resulting magnetic nanoparticles were collected with a magnet.

Synthesis of $\text{Fe}_3\text{O}_4@\text{SiO}_2\text{-dN}_3$ (MNPs-d N_3):

20 mg N_3 -modification of peptides were dissolved in PBS solution (10 mM, 5 PH=5.5), followed by the addition of 50 mg EDC and 50 mg NHS. Then the solution was shook for 30 min. After the addition of 20 mg MNPs-NH₂, the system was sonicated for 5 min and shook at room temperature for 36 h. And every 4 h, another 50mg EDC and 50 mg NHS were added into the solution. After 36 h, the MNPs-d N_3 was obtained, washed with ethanol and water for six times and then dispersed in 4 mL 10 methanol/water (50:50, v/v) for further use.

Synthesis of $\text{Fe}_3\text{O}_4@\text{SiO}_2\text{-N}_3$ (MNPs-N₃):

In a dried flask under nitrogen, the obtained 20 mg MNPs-NH₂ were dispersed in 40 ml anhydrous dichloromethane. After the addition of 1.5mL distilled triethylamine, the whole solution was put in an ice bath under argon atmosphere and cooled to 0°C. 15 Then 1mL 2-bromoisobutyryl bromide was added, leaving mechanically stirred for 2 h at 0 °C and then at room temperature for 16 h. The obtained MNPs (denoted as $\text{Fe}_3\text{O}_4@\text{SiO}_2\text{-Br}$ MNPs) were isolated and washed with dichloromethane, ethanol and water for three times, respectively, and dried in the vacuum oven overnight at 50°C. 50 mg $\text{Fe}_3\text{O}_4@\text{SiO}_2\text{-Br}$ MNPs was dispersed in 30 mL N, N-dimethylformamide 20 solution containing 230 mg sodium azide and 167 mg ammonium chloride for 26 h at 50°C. The obtained materials (designed as MNPs-N₃) were isolated, washed with N, N-dimethylformamide, water, and methanol, and dried in the vacuum oven overnight at 50°C.

Synthesis of 1-propargyl-O-maltose:

25 1-propargyl-O-maltose was synthesized according to a reported method.^[2] 10.0 g β -D-maltose octaacetate was dissolved in 150 mL dichloromethane, followed by the addition of 1.0 mL propargylalcohol. Then the mixture into which 3.0 mL boron trifluoride/ether was added was stirred at 0°C for 1 h and at room temperature for additional 4 h. After the addition of 5.0 g potassium carbonate and being stirred for 30 30 min, the system was filtered and the filtrate was concentrated. The 1-propargyl-acetyl-

maltose (m/z at 697.2 $[M+Na]^+$) was obtained and was dissolved in 30 mL anhydrous methanol. Then 12 mL sodium methoxide in methanol (1 M) was added dropwise and the solution was stirred at room temperature for about 6 h. After quenched by neutralization, the reaction solution was filtered, concentrated and dried in the vacuum oven overnight at room temperature. 1-propargyl-O-maltose was obtained and used without further treatment. $[M+Na]^+=402.8$; 1H NMR (500 MHz, D_2O , HOD): 5.38 (d, $J=3.09$ Hz, 1H), 4.63 (d, $J=7.95$ Hz, 1H), 3.91-3.53 (m, 12H), 3.38 (t, $J=9.55$ Hz, 1H), 3.30 (t, $J=8.72$ Hz, 1H); ^{13}C NMR (125 MHz, D_2O): 98.18 (α Glc1), 97.32 (β Glc1), 76.18 ($-CH_2-CCH$), 74.51, 73.87, 72.39 ($-CH_2-CCH$), 70.57, 70.51, 70.44, 69.39, 67.09, 65.59, 58.40 (Glc6), 58.24 (Glc6), 54.28($-CH_2-CCH$)

Synthesis of dM-MNPs or M-MNPs

MNPs-d N_3 or MNPs-N $_3$ were dispersed in 4 mL methanol/water (50:50, v/v) and sonicated for 30 min. 30 μ L catalysts solution (ascorbic acid : copper (II) sulfate = 200:100, mM/mM) was added, followed by the addition of 5 mg 1-propargyl-O-maltose. Then this system was shook about 12 h. The resulting MNPs were collected, rinsed with methanol, ethanol and water for nine times and dried in the vacuum oven at 40°C.

Characterization

Transmission electron microscopy (TEM) image was obtained by JEOL JEM-2000 EX transmission electron microscope (JEOL, Tokyo, Japan). Fourier-transformed infrared spectroscopy (FT-IR) characterization has been performed on Thermo Nicolet 380 spectrometer using KBr pellets (Nicolet, Wisconsin, USA). The saturation magnetization curve was carried out at room temperature on the Physical Property Measurement System 9T (Quantum Design, San Diego, USA). The water contact angles were measured with an OCA20 contact angle system (Dataphysics, Germany) at ambient temperature. Proton nuclear magnetic resonance (1H NMR) spectra were recorded on a Bruker 500 MHz spectrometer. Carbon nuclear magnetic resonance (^{13}C NMR) spectra were recorded on a Bruker 125 MHz spectrometer. Elemental analyses were performed on Vario EL III (Elementar, Hanau, Germany). And the amount of maltose functionalized on the surface of magnetic nanoparticles

were calculated based the change of carbon content between before and after click reaction according to a reported method.⁴

$$\chi_{\text{maltose}}(\text{nmol. mg}^{-1}) = \frac{\%X * 10^6}{(AM)n100(1 - \%X(MW)/(AM)n100)} \quad \text{Eq. S1}$$

where %X is the percent of carbon increase in the bonded support as determined by
5 elemental analysis, *AM* is the atomic mass of carbon, *MW* is the molecular weight of the species bonded to the surface of support, *n* is the number of carbon atoms present in the bonded species.

Trypsin digest of proteins

2 mg human IgG was dissolved in 1 mL denaturing buffer containing 100 mM
10 NH₄CO₃ and 8 M urea. After addition of 20 μL DTT (1 M) and being kept at 60°C for 1 h, the protein was alkylated by 7.4 mg IAA at room temperature in the dark for 40 min. Then the solution was diluted by 7 mL NH₄HCO₃ (100mM) and digested with trypsin (protein: enzyme = 25:1, w/w) for 16 h. After digest being quenched by the addition of pure FA, the peptide mixture was desalted by SPE column, lyophilized
15 and kept at -20°C for long time use.

The proteins (2 mg) from mouse liver were dissolved in 1 mL denaturing buffer containing 50 mM Tris-HCl and 8 M urea. After addition of 20 μL DTT (1 M) at 60°C for 1 h, the proteins were alkylated by 7.4 mg IAA at room temperature in the dark for 40 min. Then the solution was diluted by 7 mL 50 mM Tris-HCl and digested
20 with trypsin (protein: enzyme = 25:1, w/w) for 16 h. Digestion was stopped by pure FA, and the peptides mixture were desalted by SPE column, lyophilized and kept at -20°C for long time use.

Enrichment of glycopeptides

20 μg dM-MNPs was washed three times and suspended in 400 μL
25 ACN/H₂O/TFA (88:7:5, v/v/v). And glycopeptide mixtures which were dissolved in ACN/H₂O/TFA (88:7:5, v/v/v) were added. The enrichment was carried out gently at room temperature for 30 min. After washed by ACN/H₂O/TFA (88:7:5, v/v/v) to remove non-glycopeptides, the MNPs was incubated with 2×10 μL ACN/H₂O/TFA

(30:69.9:0.1, v/v/v) to collect glycopeptides. The collected peptides were analyzed by MALDI-TOF MS, or deglycosylation for LC-MS/MS analyses.

800 μg dM-MNPs was washed three times and suspended in 400 μL ACN/H₂O/TFA (88:10:2, v/v/v). And glycopeptide mixtures which were dissolved in 5 ACN/H₂O/TFA (88:10:2, v/v/v) were added. The enrichment was carried out gently at room temperature for 30 min. After washed by ACN/H₂O/TFA (88:10:2, v/v/v) to remove non-glycopeptides, the MNPs was incubated with 2 \times 30 μL ACN/H₂O/TFA (30:69.9:0.1, v/v/v) to collect glycopeptides. The collected peptides were deglycosylation for LC-MS/MS analyses.

10 **Deglycosylation of glycopeptides by PNGase F**

Glycopeptides collected from enrichment procedure were lyophilized and re-dissolved in 30 μL NH₄HCO₃ (10 mM), followed by addition of 50 units of PNGase F (0.1 μL). Then the reaction was carried out at 37°C for 12 h and quenched by heating to 100°C. And the peptide was analyzed by MALDI-TOF MS.

15 **Evaluation of binding capacity of dM-MNPs**

Different amounts (5-100 μg) of dM-MNPs were used to treat 3 μg human IgG digest for four independent times. Then 4 \times 0.5 μL of the elution was analyzed with MALDI-TOF MS. When the peak intensity of six selected glycopeptides reach maximum, the total amount of glycopeptides were bonded onto the MNPs. The 20 binding capacity was calculated by the amount of human IgG to MNPs.

Recovery estimation of enrichment of glycopeptides

Two aliquot of human IgG tryptic digest (3 μg) were labeled with light and heavy isotopes by using a stable isotope dimethyl labeling approach according to a reported method.^[3] The heavy-tagged tryptic digest was enriched with dM-MNPs and the 25 elution was added into light-tagged tryptic digest. The mixture was then enriched with dM-MNPs and analyzed by MALDI-TOF MS. The recovery was calculated by the peak intensity ration of heavy isotope-labeled glycopeptides to the light isotope-labeled glycopeptides.

Measurement of adsorption isotherm

1 mg dM-MNPs or M-MNPs were added into 400 μ L HRP solution (88%ACN+0.1%TFA). The mixture was shaken overnight at room temperature. Then magnetic materials were collected and washed by 88%ACN+0.1%TFA. HRP adsorbed onto materials were released in 30%ACN+0.1%TFA. The amount of released HRP was determined by UV-vis spectrophotometry at 403 nm.

Mass spectrometry

Standard glycopeptides were analyzed on an AB Sciex 5800 MALDI-TOF/TOF mass spectrometer (AB, SCIEX, USA) with a pulsed Nd/YAG laser at 355 nm in linear positive ion mode. As a kind matrix, 25 mg DHB was dissolved in 1 mL ACN/H₂O/H₃PO₄ (70:29:1, v/v/v). 0.5 μ L of standard glycopeptides and 0.5 μ L matrix were dropped onto plate stepwisely for next analysis.

The proteins from mouse liver were analyzed on a Thermo Q Exactive mass spectrometer (Thermo, San Jose, CA) with a nanospray ion source and a U3000 RSLCnano system (Thermo, San Jose, CA, USA). After being enriched and lyophilized, the tryptic peptides were re-dissolved in FA/H₂O (0.1:99.9, v/v) and loaded on a trap column (200 μ m i.d.) with C₁₈ AQ beads (5 μ m, 120 Å, Daiso, Osaka, Japan). After the peptides were separated by a capillary analysis column (75 μ m i.d.) with C₁₈ AQ beads (3 μ m, 120 Å, Daiso, Osaka, Japan) in a linear gradient where ACN/H₂O/FA (buffer B, 80:19.9:0.1, v/v) was programmed as: from 0 to 4% for 15 min, from 4 to 45% for 145 min and from 45 to 90% for 5 min at a flow rate of 0.3 μ L/min, the separation system was equilibrated by FA/H₂O (buffer A, 0.1:99.9, v/v) for 15 min and peptides were analyzed in a data-independent MS/MS collision induced dissociation (CID) mode. And full mass scan was acquired from m/z 400 to 2000 with resolution of 70 000. The 12 most intense ions with charge ≥ 2 and above an intensity threshold of 10^4 were selected for MS/MS. The dynamic exclusion was set as 30s.

Database searching

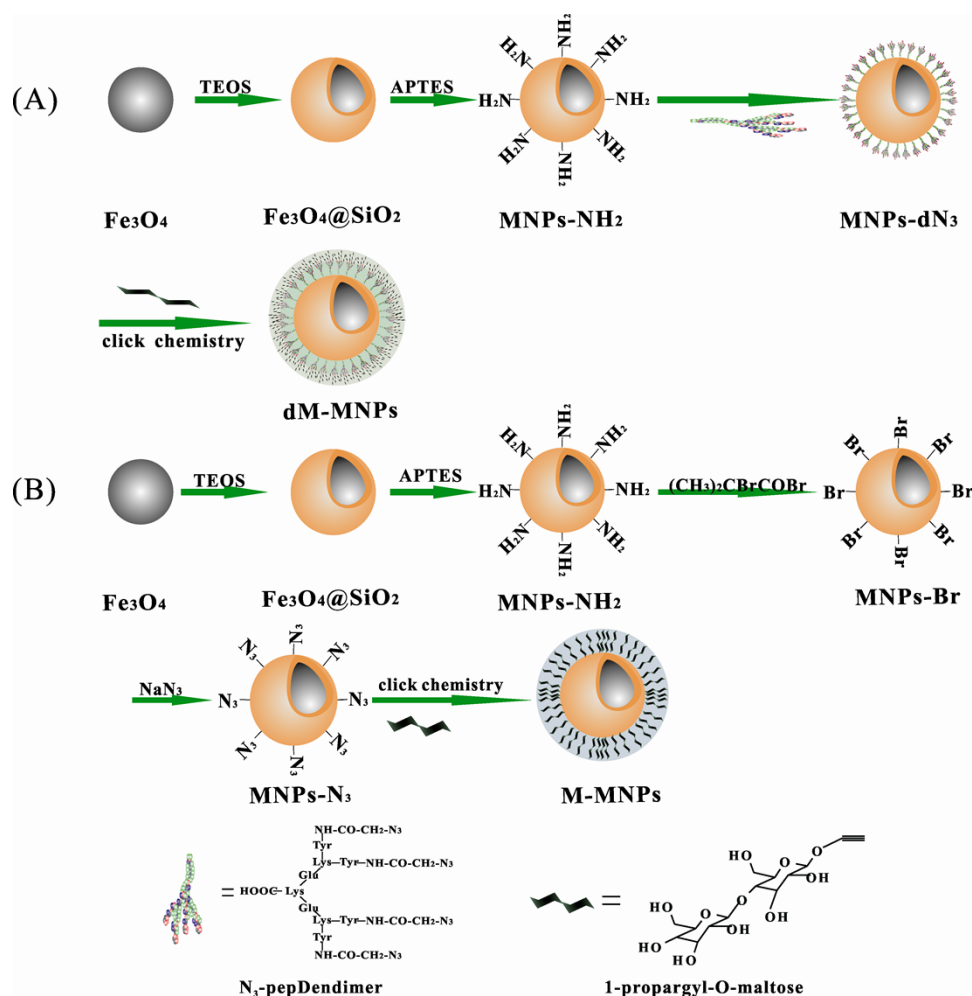
All the LC-MS/MS raw files were analyzed with Maxquant software (version 1.3.0.5) against a database (uniprot. mouse. fasta, downloaded on Dec 11, 2013). The mass tolerances were 20 ppm for initial precursor ions and 0.5 Da for fragment ions.

And for trypsin restriction, two missed cleavages were allowed. The cut off false discovery (FDR) for peptide identifications was controlled to < 1%. Only glycopeptides with N-!P-S/T or the N-X-C were considered as highly reliable results.

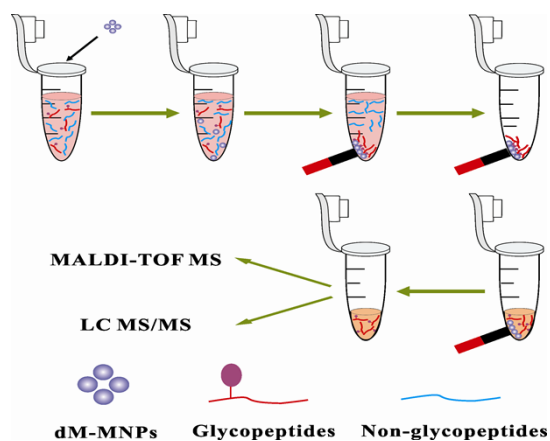
References

- 5 [1] J. Ge, Q. Zhang, T. Zhang, Y. Yin, *Angew. Chem. Int. Ed.* 2008, **47**, 8924-8928.
 [2] Z. Xiong, L. Zhao, F. Wang, J. Zhu, H. Qin, R. Wu, W. Zhang, H. Zou, *Chem. Commun.* 2012, **48**, 8138-8140.
 [3] P. J. Boersema, R. Raijmakers, S. Lemeer, S. Mohammed, A. J. Heck, *Nat. Protoc.* 2009, **4**, 484-494.
 10 [4] C. E. Kibbey, M. E. Meyerhoff, *Anal. Chem.* 1993, **65**, 2189-2196.

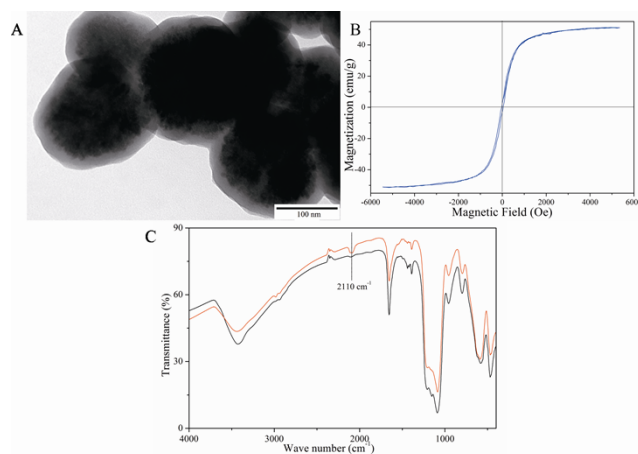
Supplementary Schemes, Tables and Figures



Scheme S1 Illustration of consecutive steps for synthesis of dM-MNPs and M-MNPs.



Scheme S2 The workflow of *N*-glycopeptides enrichment from biological samples by using dM-MNPs and M-MNPs.



5 **Figure S1** (A) TEM image and (B) hysteresis loop of M-MNPs, (C) FT-IR spectra of (a) MNPs-N₃ and M-MNPs.

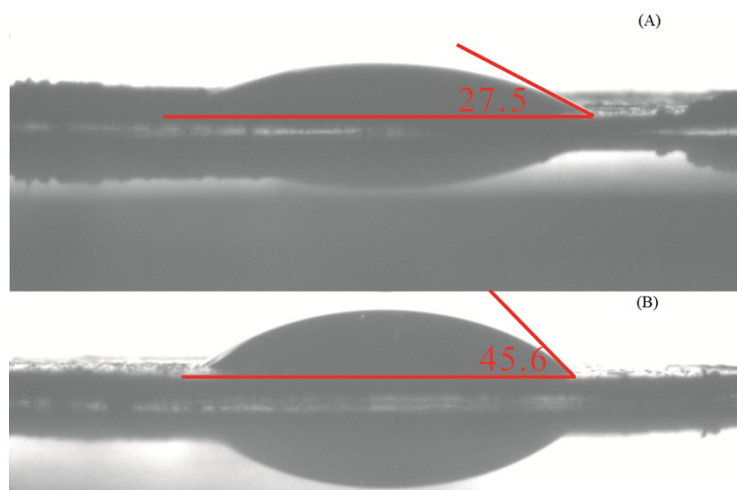


Figure S2 The water contact angles of A) dM-MNPs and (B) M-MNPs.

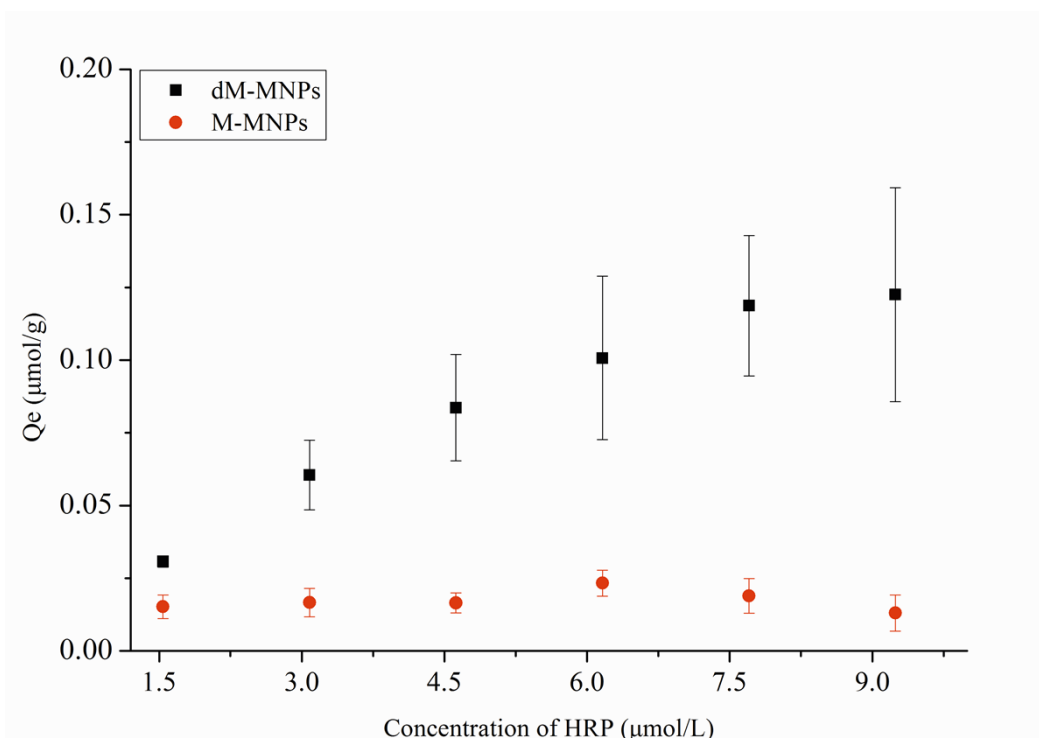


Figure S3 Binding isotherms for the binding of dM-MNPs and M-MNPs with HRP.

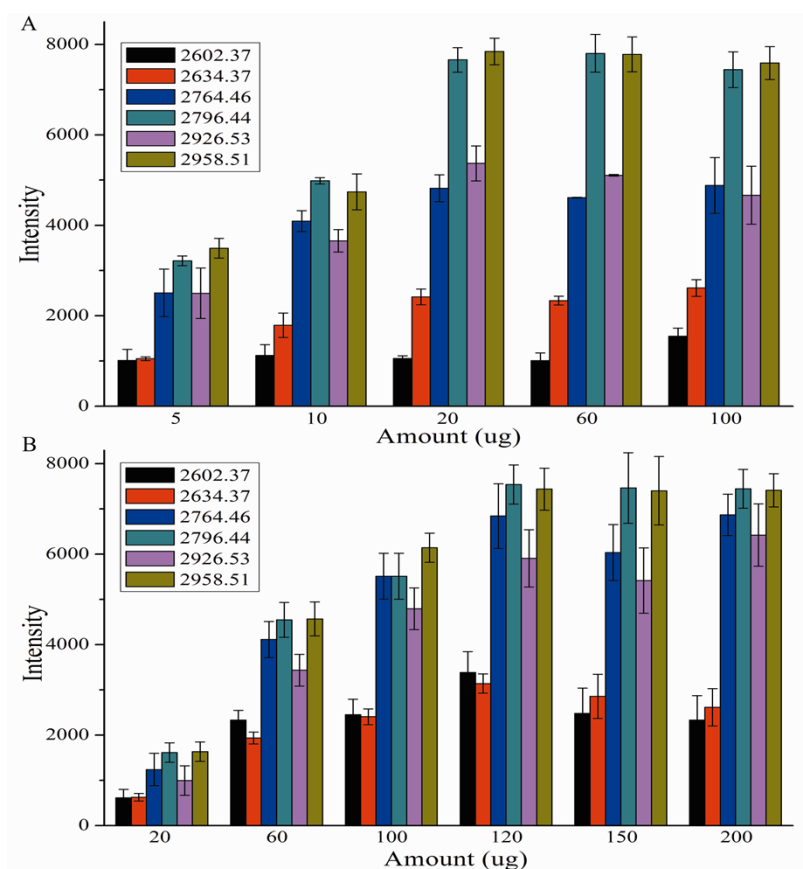
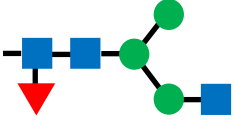
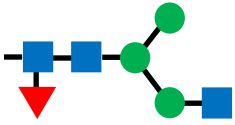
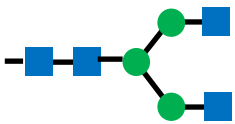
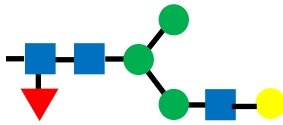
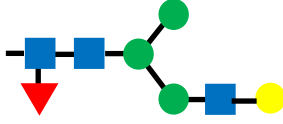
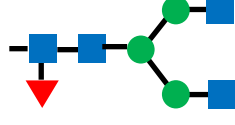
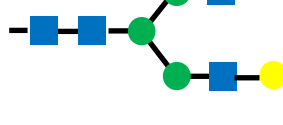
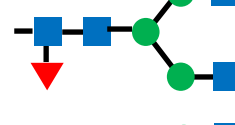
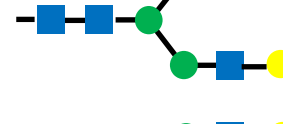
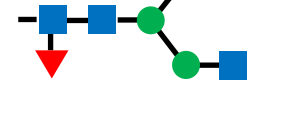


Figure S4 The intensity of six selected N-glycopeptides from 3 μ g human IgG tryptic digest after enrichment by different amount of (A) dM-MNPs and (B) M-MNPs.

Table S1. Molecular masses and glycan structure of the *N*-glycopeptides from human IgG after enrichment by dM-MNPs. N* denotes the N-linked glycosylation sites

Peak number	m/z	Glycan structure	Amino acid sequence
I1	2399.28		EEQFN*STFR
I2	2431.26		EEQYN*STYR
I3	2488.27		EEQYN*STYR
I4	2561.35		EEQFN*STFR
I5	2593.32		EEQYN*STYR
I6	2602.37		EEQFN*STFR
I7	2619.37		EEQFN*STFR
I8	2634.37		EEQYN*STYR
I9	2650.35		EEQYN*STYR
I10	2764.46		EEQFN*STFR

I11	2778.43		EEQFN*STFR
I12	2796.44		EEQYN*STYR
I13	2805.45		EEQFN*STFR
I14	2812.43		EEQYN*STYR
I15	2819.43		EEQFN*STFR
I16	2837.45		EEQYN*STYR
I17	2853.51		EEQYN*STYR
I18	2926.53		EEQFN*STFR
I19	2958.51		EEQYN*STYR
I20	2967.53		EEQFN*STFR
I21	2981.46		EEQFN*STFR
I22	2999.51		EEQYN*STYR

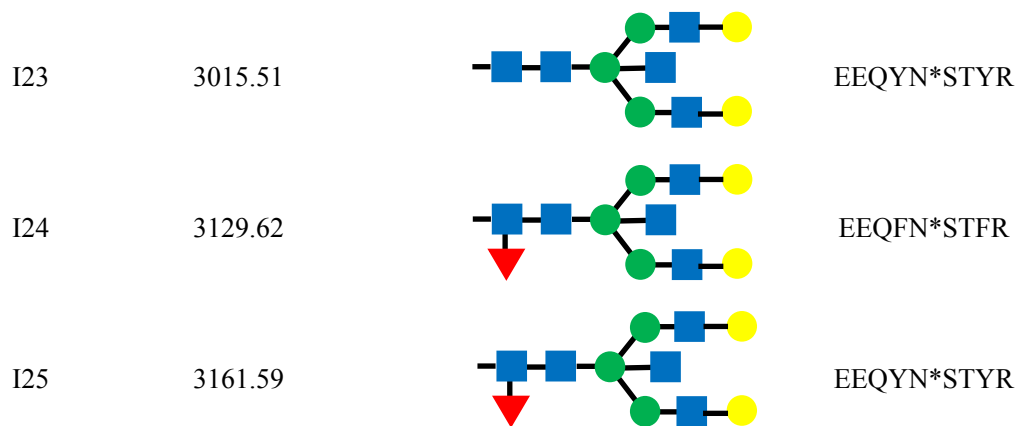


Table S2 Recovery of six selected glycopeptides from human IgG digest

Peak number	m/z	Recovery±S.D. (%; n=5)
I7	2602.40	78±1.9
I9	2634.38	91±5.8
I12	2764.49	89±6.0
I14	2796.47	92±4.7
I20	2926.56	90±9.0
I21	2958.54	91±4.6

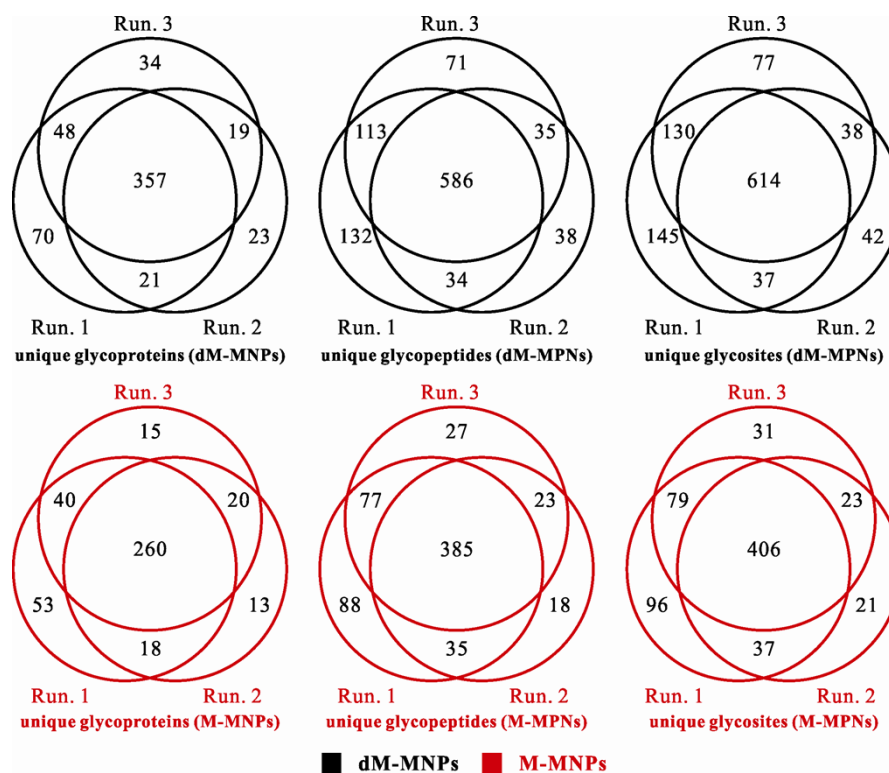


Figure S5 Overlap of *N*-glycoproteins, *N*-glycopeptides and *N*-glycosylation sites identified by dM-MNPs and M-MNPs.

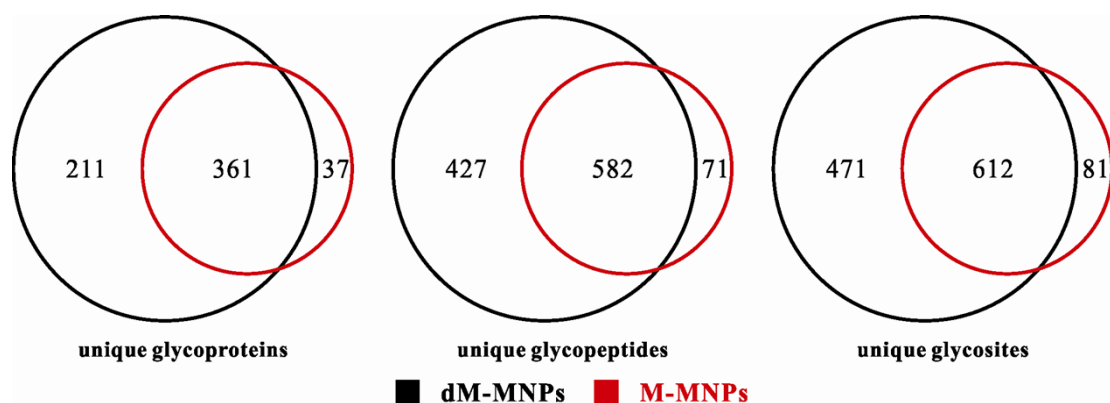


Figure S6 Overlaps of the identified *N*-glycoproteins, unique *N*-glycopeptides and *N*-glycosylation sites by using dM-MNPs and M-MNPs for protein sample extracted from mouse liver.

5 **Table S3** List of identified *N*-glycopeptides from protein sample extracted from mouse liver by dM-MNPs. N* denotes the *N*-linked glycosylation sites.

No	Protein	Protein names	Modified sequence
1	A2A7A7	GDH/6PGL endoplasmic bifunctional protein	_NIN*SSCRPHPGAWLR_
2	A2AJQ3	Protein dpy-19 homolog 4	_GVYELTHNN*K_
3	A2AQ53	Fibrillin-1	_AWGTPCELCPNVN*TSEYK_ _DACGN*GTCR_ _N*CTDIDECR_ _VLPFN*VTDYCQLVR_ _CTDLDECSN*GTHMCSQHAD CK_
4	A2AQJ6	Transmembrane protein 87A	_LFQN*CSELYK_ _QEAKEN*ATN*VTFTGDK_
5	A2ARA8	Integrin alpha-8	_VN*GTKEPIEFK_
6	A2AS37	Protein AI182371	_LEIVPIIYDN*DSLQVQTDK_
7	A2AW86	Lymphocyte antigen 75	_LAN*ISGEEQK_
8	A6H584	Collagen alpha-5(VI) chain	_SSAN*QSEFQQQIQK_ _SN*DSVLEPANR_ _AEQITIHAIGIGEAN*KTQLR_ _YQEIIIELESSLN*KTQWK_ _DLGMFAPN*MTR_ _DLQNFLN*VTSSVDVK_
9	A6X935	Inter alpha-trypsin inhibitor, heavy	_ISASGAELEALEAQVLN*LSL

		chain 4	K_ _VSGQMhMQN*ITFQTEASVA QqEK_ _GLMllLN*DTQHFSNNVK_ _VYVGN*ASVAQDITQLQK_
10	B1AQF4	Dual specificity protein phosphatase 3	
11	B1AR74	Breast carcinoma-amplified sequence 3 homolog	_LTSQDSYNN*FTNNNPGNPR_
12	B1ATV0	H(+)/Cl(-) exchange transporter 5	_LCDYENHFN*TSK_
13	B2RT14	MCG14318, isoform CRA_h	_TCTNILHN*ESLLHHLN*SSSF DVVFTDPVFPcGALLAK_ _N*MSTVLLK_
14	B2RT89	Predicted gene, EG434674	_CWAPILDN*DTASDN*GSR_ _FAQPQWHLHLN*GTFSN*E TEPDTEPCVDGWVYDR_
15	B2RXS4	Plexin-B2	_EKIEANRN*ACYTGAR_ _SCVAITDAFPQN*MSR_ _AMSN*ISVR_ _TEAGVFEYVADPTFEN*FTG GVKK_ _QGPQAGGTTLTIN*GTHLDT GSKEDVR_ _LSHDGN*ETLPLHLYVK_ _CVYEALCSN*VTSECPPPvIT R_ _VVFLSPAVPEEPEAYN*LTVL IR_
16	B5THE2	Maltase-glucoamylase	_IDCYPDEHGASEAN*CSAR_ _IwVN*SSDGISPvIGK_ _LVIIIDPAISN*NSFSSNPYGP YDR_ _YGYEN*DTEIANLYDEMvAK _ _VILILDPAISGN*ETEPYPAFT R_ _RQDPVSWN*K_ _GCIWEASN*TTR_ _FSVN*QTLLTHEK_ _VWPDYPN*ITVDPSLGWDHQ

17	B8JK39	Protein Itga9	VEQYR_ _VLN*LTDNTYFK_ _N*QTVFER_
18	D3YW52	Alpha-2-macroglobulin	_VN*LSFPSAQSLPASDTHLK_ _IN*VSYTGERPSSNMVIVDVK _ _SLGEVN*FTATAEALQSPELC GNK_ _LTN*QTLGFSFAVEQDIPVK_ _GAMITHQNIIN*DCSGFIK_
19	D3Z041	Long-chain-fatty-acid--CoA ligase 1	_LLNDYVSN*QTQGMIK_ _N*ATSYPPMCSQDAVAVQLL SDMLSTKK_ _CN*VSSPIFK_ _KCEAN*LTLSSPAR_ _TSSEFCQPVSLHGSN*HTSK_ _KFN*STQIAAMAPEHEEPR_
20	D3Z451	MCG54087	
21	D3Z5G7	Protein Ces1b	
22	D3Z627	Integrin alpha-L	
23	D3Z6W7	Glucoside xylosyltransferase 1	
24	E0CYM8	Tyrosine-protein phosphatase non- receptor type substrate 1	_GIAN*LSNFIR_
25	E9PV38	Protein Ces2g	_LN*LTEEEK_ _DGTSQPAICPQN*VTMNMEG LK_ _ALN*GSALYTGSSLDIVR_ _QLINALQIN*NTAVGHALVLP ARR_ _GPPGVN*GTQGFQGCPCGQR_ _SLN*CTVK_
26	E9PWQ3	Protein Col6a3	
27	E9PXN7	UDP-glucuronosyltransferase 1-9	
28	E9PXU2	Disintegrin and metalloproteinase domain-containing protein 17	_MFSN*CSK_ _KCQEAIN*ATCK_
29	E9PXX8	Protein Macc1	_NQN*ITAR_
30	E9PYN1	Cell adhesion molecule 1	_DVTVIEGEVATISCQVN*KSD DSVIQLLNPNR_ _VSLTN*VSISDEGR_ _FQLLN*FSSSELK_ _NLMIDIQKDTAVEGEEIEVN*

			CTAMASKPATTIR_
			_VDDEMPQHAVLSGPNLFINN
			LN*KTDN*GTYSR_
31	E9PZ16	Basement membrane-specific heparan sulfate proteoglycan core protein	_LCN*ECSDGSFHLSK_ _LTVPSSQN*SSFR_ _TDEAN*CSVK_ _GVN*VTMPSQPGVPPLSSTQL QIDPALQEFQLVDLSR_ _ALVN*FTR_ _SLTQGSLLVGNLAPVN*GTSQ GK_
32	E9PZD8	Ceruloplasmin	_EYEGAVYPDN*TTDFQR_
33	E9Q035	Serotransferrin	_N*STLCLDLGIPLK_
34	E9Q414	Apolipoprotein B-100	_LPQQIHHYLN*ASDWER_ _ESMN*FSSK_
35	E9Q433	Killer cell lectin-like receptor 2	_ALN*DSLHYLNR_
36	E9Q4S7	Receptor-type tyrosine-protein phosphatase eta	_GPDGTEGLSSTVN*GSTDPSA VTDIR_ _LTWSNAN*GTASYR_ _TN*STQVSDVR_
37	E9Q5P0	Serine protease hepsin	_TAGAN*GTSGFFCVDEGGLP LAQR_
38	E9Q649	Beta-1,3-galactosyl-O-glycosyl- glycoprotein beta-1,6-N- acetylglucosaminyltransferase 4	_DNVN*CSGVYEHEPLEIGK_
39	E9Q6A6	Collagen alpha-6(VI) chain	_LGN*FSELATHN*QTFLK_ _DLSVFAPN*MTEIHK_ _VGLVTYSN*ETR_
40	E9Q6C2	Complement C1s-A subcomponent	_KITAN*STWQPKAK_
41	E9Q6C7	Latrophilin-2	_SLGQFLSTEN*ATIK_
42	E9Q6D8	Protein C6	_VLN*FTMK_
43	E9Q8B5	Protein Gm4788	_NN*STWFK_
44	E9Q8I0	Complement factor H	_CIN*GTINYPTCV_ _DNSCVDPPHVPN*ATIVTR_

45	E9Q9F1	Potassium voltage-gated channel subfamily KQT member 5	_LTEFTHN*STMDYK_ _WDPEPN*CTSK_ _IQCVDGN*WTTLPVCIEEER_ _SASAN*ISR_
46	E9QJY0	Low affinity cationic amino acid transporter 2	_ISEEFLKN*ISASAR_
47	E9QN70	Laminin subunit beta-1	_VN*ASTTDPNSTVEQSALTR_
48	E9QPX1	Collagen alpha-1(XVIII) chain	_DGQQN*ISLLYTEPGASQTQT GASFR_
49	F7BJK1	Protein Pcdh1 (Fragment)	_AN*DSDQGANAIEIDYTFHQA PEVVR_
50	F7BWT7	Tetraspanin-15	_N*TTDVVNTMCGYK_
51	F8VQG4	Protein H2-T24	_QYYN*SSGTQSQR_
52	F8VQJ3	Laminin subunit gamma-1	_VN*SSLHSQISR_ _KYEQAKN*ISQDLEK_ _CDQCEENYFYN*R_ _VNDN*KTAAEEALR_ _TLAGEN*QTALEIEELNR_ _RIPAIN*R_ _LLNN*LTSIK_ _IASAVQKN*ATSTK_
53	F8WIJ0	Solute carrier family 12 member 4	_TVVVDN*ETVATR_
54	F8WJ05	Inter-alpha-trypsin inhibitor heavy chain H1	_AN*LSSQVLK_ _N*LTNMSK_
55	G3UW85	Enhancer of rudimentary homolog	_TYADYESVN*ECMEGVCK_
56	G3UWA6	4F2 cell-surface antigen heavy chain	_LMNAPLYLAEWQN*ITK_

57	G3UXA6	Polypyrimidine tract-binding protein 3	_AQAALQAVSAVQSGN*LSLP GATANEGTLLPGQSPVLR_
58	G3X8T3	Lysosomal protective protein	_LWTSLQTHCCAQN*K_ _LDPPCTN*TTAPSNYLNNPYV R_ _MYVTN*DTEVAENNYEALK DFFR_
59	G3X8V6	Oncostatin-M-specific receptor subunit beta	_NLGPN*TTSTTITSDDFKPGV R_
60	G3X8X3	Large neutral amino acids transporter small subunit 3	_TN*TTQDEQHQTSCDQQEK _
61	G3X924	Plasmalemma vesicle-associated protein	_ADSLYSQVVGLSASQAN*LS K_
62	G3X925	Pyruvate kinase	_EVN*KTCEALLFK_ _LN*FSHGSHEYHAESIANIR_ _TVWVDYHN*ITQVVAVGGR_
63	G3X943	MCG18706, isoform CRA_b	_FVEQN*STGSKGN*SSR_
64	G3X973	Stabilin-1	_WQIHN*ISGK_ _N*SSITLPADSR_ _AYTIFVPTN*HSLETQGN*NS VLGIDTVR_ _FCN*ESMGNCGSTGLAQPCH SDAHCVIQEGVAR_ _KGCADYCN*QTITKR_
65	G3X9D6	Apolipoprotein N, isoform CRA_a	_TQN*GSLPAVTR_ _ASVVN*VTQHCTMESWESM NEVAR_
66	G5E8C4	Transmembrane and TPR repeat-containing protein 3	_AN*ESRLEEADQLYR_
67	G5E8F8	Integrin beta	_SN*LTVLR_
68	G5E8G3	Neurotrimin	_AMDN*VTVR_
69	G5E8Q8	MCG115189	_LLQQSN*QSSQFLHSVER_ _MDYNSFQGTPSN*ETK_ _ANEQVIQNLN*HTYK_
70	G5E8U1	Sulfate anion transporter 1	_N*NDSTLN*NSATTLIIGLQD CR_

71	H3BL08	Ceramide synthase 6	_FWLPHN*VTWADLK_
72	J3QPG5	Sulfated glycoprotein 1	_TN*SSFIQGFVDHVKEDCDRL GPGVSDICK_ _FSELIVNN*ATEELLVK_ _LVLYLEHNLEKN*STK_ _DN*ATQEEILHYLEK_ _LSQALGN*ITVVQK_
73	K3W4M4	ATP-dependent (S)-NAD(P)H- hydrate dehydratase	_LSQALGN*ITVVQK_
74	K3W4R4	Collagen alpha-1(XIV) chain	_AIN*ASAN*ITSDGVEVLGR_ _VVDKGN*GSKPTSPEEVK_ _SFMVN*WTQSPGKVEK_
75	O08530	Sphingosine 1-phosphate receptor 1	_HYN*YTGK_
76	O08532	Voltage-dependent calcium channel subunit alpha-2/delta-1	_SFSGLLD CGN*CSR_ _DAVNN*ITAK_
77	O08603	Retinoic acid early-inducible protein 1-beta	_TMTSGDPGETAN*ATEVKK_
78	O08677	Kininogen-1	_EGN*CSAQSGLA WQDCDFK DAEEAATGECTATVGKR_ _IAN*FSQSCTLYSGDDLVEAL PKPCPGCPR_
79	O08692	Myeloid bactenecin (F1)	_DCDFLEDGEERN*CTGK_
80	O08705	Sodium/bile acid cotransporter	_MEAHN*VSAPFN*FSLPPGFG HR_
81	O08966	Solute carrier family 22 member 1	_YEVDWN*QSTLDCVDPLSSL AAN*R_
82	O09009	Beta-1,3-N- acetylglucosaminyltransferase radical fringe	_MINTN*CSAVR_
83	O09043	Napsin-A	_ASSSFRPN*GTK_
84	O09159	Lysosomal alpha-mannosidase	_QN*FSFCR_ _ELN*ISICPVSQTSER_ _RDDYRPTWTLN*QTEPVAGN YYPVNTR_

85	O09164	Extracellular superoxide dismutase [Cu-Zn]	_AN*LTWTVK_ _LEAYFSLEGFPAEQN*ASNR_
86	O35114	Lysosome membrane protein 2	_N*QSVGDPNVDLIR_ _TMVFPVMYLN*ESVLIDKET ANQLK_ _TSLDWWTDDTCNMIN*GTDG DSFHPLISK_ _NMVLQN*GTK_ _NKANIQFGEN*GTTISAVTNK
87	O35343	Importin subunit alpha-4	- _VQN*TSLEAIVQNASSDNQGI QLSAVQAAR_
88	O35598	Disintegrin and metalloproteinase domain-containing protein 10	_EGICNGFTALCPASDPKPN*F TDCNR_
89	O35604	Niemann-Pick C1 protein	_IN*TTSDEKDPTNPFR_ _TEQLIQAPN*TSVHIYEPYPA GADVPPGPPLNK_ _LYN*VTHQFCN*ASVMDPTC VR_ _LIASN*ITETMR_ _ACN*ATNWIEYMFNK_
90	O35607	Bone morphogenetic protein receptor type-2	_ISHEN*GTILCSK_
91	O35632	Hyaluronidase-2	_FDAAGTSVHGGVPQN*GSLC AHLPLK_ _RNPSANTFLHLN*ASSFR_
90	O35887	Calumenin	_N*ATYGYVLDDPDDGFNY K_
93	O54890	Integrin beta-3	_CNNGN*GTFECGVCR_ _NAVN*CTYKNEDDCVVR_
94	O55060	Thiopurine S-methyltransferase	_EFFAEQN*LSYTEEPLAEIAG AK_
95	O55111	Desmoglein-2	_YVQN*GTYTAK_
96	O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	_TASEMVLADDN*FSTIVAAV EEGR_

97	O70423	Membrane primary amine oxidase	_YLYLASN*HSNK_
98	O70570	Polymeric immunoglobulin receptor	_TN*QSCSELVIDSTEK_ _ANLINFPEN*NTFVINIEQLTQ DDTGSIK_
99	O88325	Alpha-N-acetylglucosaminidase	_SVYN*CSGEACSGHNR_ _LLLTAAPN*LTTSPAFR_
100	O88342	WD repeat-containing protein 1	_MTVN*ESEQLVSCSMDDTVR -
101	O88507	Ciliary neurotrophic factor receptor subunit alpha	_VN*GTDLAPDLLN*GSQILIR -
102	O88531	Palmitoyl-protein thioesterase 1	_FFN*DSIVDPVDSEWFGFYR_ _CVN*ESYKK_
103	O88668	Protein CREG1	_VN*KTEEDYAR_ _VVTPEEYFN*VTLQ_
104	O88783	Coagulation factor V	_SN*ETALSPDLN*QTSPSMST DR_
105	O88792	Junctional adhesion molecule A	_AFMN*SSFTIDPK_
106	O88829	Lactosylceramide alpha-2,3-sialyltransferase	_LNSAPVEGYSEHVGN*KTTIR -
107	O89017	Legumain	_SHTN*TSHVMQYGN*K_
108	O89020	Afamin	_HVEDKFN*ETTQR_
109	O89023	Tripeptidyl-peptidase 1	_SSSHLPPSSYFN*ASGR_ _DVGSGTTN*NSQACAQFLEQ YFHNSDLTEFMR_ _QRYN*LTAK_
110	P00186	Cytochrome P450 1A2	_KSEEMLNIVNN*SKDFVENV TSGNAVDFFPVLRL_
111	P01029	Complement C4-B	_FSDGLESN*R_ _N*TTCQDLQIEVK_ _ALN*VTLSSMGRNGLK_
112	P01592	Immunoglobulin J chain	_EN*ISDPTSPLRR_
113	P01869	Ig gamma-1 chain C region, membrane-bound form	_EEQFN*STFR_

114	P01872	Ig mu chain C region secreted form	_IMESHPN*GTFSAK_
115	P01897	H-2 class I histocompatibility antigen, L-D alpha chain	_TLLGYYN*QSAGGTHTLQW MYGCDVGS DGR_ _EQN*YTCR_ _YLKNGN*ATLLR_
116	P01900	H-2 class I histocompatibility antigen, D-D alpha chain	_YYN*QSAGGSHTLQWMAGC DVESDGR_ _YLKNGN*ATLLR_
117	P01902	H-2 class I histocompatibility antigen, K-D alpha chain	_EQN*YTCHVHHK_ _YLELGN*ETLLR_
118	P01921	H-2 class II histocompatibility antigen, A-D beta chain	_GECYYTN*GTQR_
119	P02301	Histone H3.3C	_FQSA AIGALQEASEAYLVGLF EDTN*LCAIHAK_
120	P03953	Complement factor D	_LSQN*ASLGPHVRPLPLQYED KEVEPGTLC DVAGWGVVTHA GR_
121	P03987	Ig gamma-3 chain C region	_EAQYN*STFR_
122	P04228	H-2 class II histocompatibility antigen, A-D alpha chain	_SN*FTPATNEAPQATVFPK_
123	P04939	Major urinary protein 3	_AFVEN*ITVLENSLVFK_
124	P05202	Aspartate aminotransferase, mitochondrial	_HFIEQGIN*VCLCQSYAK_
125	P06339	H-2 class I histocompatibility antigen, D-37 alpha chain	_LGN*ETLQR_
126	P06683	Complement component C9	_GAGEVSPA EHSSKPTN*ISAK _ _MSPWSN*WSECDPCLK_ _TDNGKTVN*ITR_
127	P06684	Complement C5	_AFN*ECCTIANK_
128	P06797	Cathepsin L1	_YRAEFAVAN*DTGFVDIPQQ EK_

129	P06802	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1	_MN*ASFSLK_ _VYN*GSVPFEER_
130	P07309	Transthyretin	_TLGISPFHEFADVFTAN*DS GHR_
131	P07758	Alpha-1-antitrypsin 1-1	_GDHTQILEGLQFN*LTQTSE ADIHK_
132	P07759	Serine protease inhibitor A3K	_YTGN*ASALLILPDQGR_ _FN*LTETPEADIHQGFNLLQ SLSQPEDQDQINIGNAMFIEK_ _NLINDYVSN*QTQGMIK_
133	P08101	Low affinity immunoglobulin gamma Fc region receptor II	_ATVN*DSGEYR_ _YHHYSSN*FSIPK_ _EDTVTLTCEGTHNPGN*SSTQ WFHNGR_
134	P08113	Endoplasmin	_TDDEVVQREEEAIQLDGLN* ASQIR_ _GVVDSDDLPLN*VSR_ _HNN*DTQHIWESDSNEFSVIA DPR_ _LGVIEDHSN*R_
135	P08607	C4b-binding protein	_CEQEASEDLKPALTGN*K_ _LACLN*GTVLR_ _LVGSPFIGCTVVN*K_
136	P09055	Integrin beta-1	_KEN*SSEICSNNGECVCGQCV CR_ _CHEGN*GTFECGACR_ _SCGECIQAGPNCGWCTN*TT FLQEGMPTSAR_ _SYCKNGVN*GTGENGRK_ _KDTCAQECSHFN*LTK_ _NPCTSEQN*CTSPFSYK_
137	P09242	Alkaline phosphatase, tissue-nonspecific isozyme	_N*RTDVEYELDEK_ _CN*TTQGNEVTSILR_
138	P09470	Angiotensin-converting enzyme	_STEVSN*HTLK_
139	P10126	Elongation factor 1-alpha 1	_VETGVLKPGMVVTFAPVN*V TTEVK_
140	P10404	MLV-related proviral Env polyprotein	_THQALCN*TTQK_
141	P10493	Nidogen-1	_CVAN*YTGNGR_
142	P10605	Cathepsin B	_ILRGEN*HCGIESEIVAGIPR_

143	P11247	Myeloperoxidase	_QN*TTWQAGR_ _SYN*DSVDPR_
144	P11276	Fibronectin	_RHEEGHMLN*CTCFGQGR_ _N*YTDCTSEGRR_ _LDAPTNLQFVN*ETDR_ _DQCIVDDITYNVN*DTFHKR_
145	P11438	Lysosome-associated membrane glycoprotein 1	_EN*VSDPSLTITFGR_ _YSVQHMYFTYN*LSDTEHFP NAISK_ _DATIQAYLSSGN*FSK_ _LN*MTLPDALVPTFSISN*HSL K_ _GYLLTLN*FTKN*TTR_ _AFNISP*DTSSGSCGINLVTL K_ _VYMKN*VTVVLRL_
146	P11609	Antigen-presenting glycoprotein CD1d1	_CLQMSSFAN*R_ _VLNADQGTSATVQMLLN*DT CPLFVR_
147	P11688	Integrin alpha-5	_IYLRN*ESEFR_ _HPGN*FSSLSCDYFAVN*QSR _ _TEKDPQNDPVGTCYLSTEN*F TR_
148	P11835	Integrin beta-2	_LN*FTGPGEPDSLR_
149	P11881	Inositol 1,4,5-trisphosphate receptor type 1	_VETGEN*CTSPAPK_
150	P12246	Serum amyloid P-component	_LIPHLEKPLQN*FTLCFR_
151	P12265	Beta-glucuronidase	_YGIVVIDECPGVGIVLPQSFG N*ESLR_ _IAN*ETGGHGSQPR_ _ITIAIN*NLTLPHTLPPGTIVYK _
152	P13597	Intercellular adhesion molecule 1	_GDHGAN*FSCR_ _TELDLRPQGLALFSN*VSEAR _ _EAFLPQGGSVQVN*CSSSCK_ _QEMN*GTIVCHAFSSHGN*V TR_ _LDETDCCLGN*WTWQEGSQQ _

153	P14094	Sodium/potassium-transporting ATPase subunit beta-1	TLK_ _LDWLGN*CSGLNDDSYGYR_ _YLQPLLAVQFTN*LTVDTEIR
154	P14152	Malate dehydrogenase, cytoplasmic	- _NVIIWGN*HSSTQYPDVNHA K_
155	P14211	Calreticulin	_SGTIFDNFLITNDEAYAEFEFG N*ETWGVTK_
156	P14429	H-2 class I histocompatibility antigen, Q7 alpha chain	_TAQSYYN*QSK_
157	P15116	Cadherin-2	_SN*ISILR_ _ILSQAPSTPSPNMFTINN*ETG DIITVAAGLDR_ _RN*WTINR_
158	P15208	Insulin receptor	_SHGCTAEGLCCHKECLGN*C SEPDDPTK_ _TWSPPFESDDSQKHN*QSEY DDSAECCSCPK_ _GLSPGN*YSVR_ _HN*LITQGK_
159	P15209	BDNF/NT-3 growth factors receptor	_ITN*ISSDDSGK_
160	P16294	Coagulation factor IX	_TIPHHQYN*ATINK_
	P16301	Phosphatidylcholine-sterol acyltransferase	_IVYN*HSSGR_ _AELSN*HTRPVILVPGCLGNR
161	P16406	Glutamyl aminopeptidase	- _GWLN*GSLVGFYK_ _MGDREALGN*ASQLFDSWL K_ _YGMQNSGNEAAWN*YTLEQ YQK_ _VNYEGGTWDWIAEALSSN*H TR_
162	P16858	Glyceraldehyde-3-phosphate dehydrogenase	_IVSN*ASCTTNCLAPLAK_
163	P17047	Lysosome-associated membrane glycoprotein 2	_EASHYSIHDIIVLSYN*TSDST VFPGAVAK_ _LN*NSQIK_ _VPFIFNINPATTN*FTGSCQPQ

			SAQLR_ _VQPFN*VTK_ _CNSVLTYN*LTPVVQK_ _DLGPALAN*SSHVDK_ _VYTYADTPNDFQLSN*FSLPE EDTK_ _RMELSVGAIQAN*R_ _ITLEVFDVPKPSIEIN*KTEAS TDSCHLR_ _YYHGELSYLN*VTRK_ _TQLTCSLN*SSGVDIVGHR_ _TSDTGEEEAITN*STEANGKY VVVSTPEK_ _SQTISNLDVNVDPGTYVCN* ATNAQGTR_ _VCDGN*STNPR_
164	P17439	Glucosylceramidase	
165	P18181	CD48 antigen	
166	P18242	Cathepsin D	
167	P18572	Basigin	
168	P19137	Laminin subunit alpha-1	
169	P19221	Prothrombin	_WVLTAAHCILYPPWDKN*FT ENDLLVR_ _YPHKPEIN*STTHPGADLK_ _SLSN*STAR_ _LLYISAEDFSIDHSPN*STAGP SCSLLQEAFR_
170	P19324	Serpin H1	
171	P20060	Beta-hexosaminidase subunit beta	
172	P21614	Vitamin D-binding protein	_ICQN*LSKK_
173	P22272	Interleukin-6 receptor subunit alpha	_ALEVAN*GTVTSLPGATVTLI CPGK_
174	P23953	Carboxylesterase 1C	_EGASEEETN*LSK_ _NIQAVNEIATLSQCN*DTSSA AMVQCLR_ _N*ATSYPPMCSQDAGWAK_ _QTPEYQN*R_ _TLMSAEANLAGLFPNEVQH FNPN*ISWQIPVHTVPITEDR_ _YHGFLN*TSYHR_ _YEQLQN*ETR_
175	P24638	Lysosomal acid phosphatase	
176	P24668	Cation-dependent mannose-6-phosphate receptor	_LRPLFN*K_ _EASN*HSSGAGLVQINK_ _GSNFN*ISK_ _LQTPLN*YTEFQKPICLPSK_
177	P26262	Plasma kallikrein	

178	P26618	Platelet-derived growth factor receptor alpha	_NN*LSVVAR_
179	P26928	Hepatocyte growth factor-like protein	_GTTN*TTSAGVPCQR_
180	P27046	Alpha-mannosidase 2	_DSVIN*LSESVEDGPR_ _GSPGN*ASQGSIIHLHSPQLAL QADPR_
181	P27773	Protein disulfide-isomerase A3	_VDCTANTN*TCNK_
182	P28653	Biglycan	_MIEN*GSLSFPLTLR_ _LLQVVYLHSNN*ITK_
183	P28654	Decorin	_YIQVVYLHNNN*ISAVGQND FCR_ _LGLSFNSITVMEN*GSLANVP HLR_ _ISDTN*ITAIPQGLPTSLTEVH LDGNKITK_
184	P28665	Murinoglobulin-1	_EVNSQLDNN*GCSTQEVN*IT ELQSK_ _TIEQERN*ASFVYTK_ _SLDEEAIKEN*NSIHWK_ _SLGNVN*FSVSAEAQQSSEPC GSEVATVPETGRK_ _YLN*ETQQLTQK_ _ICLHLYQLN*ETVTVTASLVS QSGR_
185	P28666	Murinoglobulin-2	_EVNSKLDNN*GCSTQEVN*IT ELQSK_
186	P28843	Dipeptidyl peptidase 4	_QLITEEKIPN*NTQWITWSPE GHK_ _LDFIVLN*ETR_ _N*STVMSR_
187	P29416	Beta-hexosaminidase subunit alpha	_SAEGTFFIN*K_
188	P29533	Vascular cell adhesion protein 1	_N*TTISVHPSTR_
189	P29699	Alpha-2-HS-glycoprotein	_RPFVVYEMEVDLTLETCHA LDPTPLAN*CSVR_

			CPLLTPFN*DTNVVHTVNTA LAAFNTQNN*GTYFK _ALN*SSTEDGIKR_
190	P29754	Type-1A angiotensin II receptor	
191	P29788	Vitronectin	_N*NTNTGVQPENTSPPGDLNP R_
192	P30204	Macrophage scavenger receptor types I and II	_FQN*FSMATDQR_ _VLNN*ITNDLR_
193	P31428	Dipeptidase 1	_RN*WTETEVR_
194	P31809	Carcinoembryonic antigen-related cell adhesion molecule 1	_MTLSQN*NSILR_ _GN*TTAIDKEIAR_ _TLTLLN*VTRN*DTGPYVCET R_ _TTVKN*ITVLEPVTQPFLQVT N*TTVK_
195	P31809-3	Isoform 3 of Carcinoembryonic antigen-related cell adhesion molecule 1	_FHVHQPVTQPFLQVTN*TTV K_
196	P31996	Macrosialin	_KAWGISVLNPN*KTK_
197	P32020	Non-specific lipid-transfer protein	_HSVN*NTYSQFQDEYSLEEV MK_
198	P32261	Antithrombin-III	_SLTFN*ESYQDVSEVVYGAK _ _VTINNWVAN*KTEGR_ _LGACN*DTLK_
199	P32507	Poliovirus receptor-related protein 2	_MVN*TTFICTATNAVGTGR_
200	P33587	Vitamin K-dependent protein C	_IVN*GTLTK_ _EILVHPN*YTR_
201	P34927	Asialoglycoprotein receptor 1	_SLSCQMAAFRGN*GSER_ _QN*FSN*LTVSTEDQVK_
202	P35492	Histidine ammonia-lyase	_EGLALIN*GTQMITSLGCEAL ER_
203	P35762	CD81 antigen	_TFHETLN*CCGSNALTTLTTT ILR_
204	P35917	Vascular endothelial growth factor receptor 3	_ADN*YTYEHLR_

205	P35918	Vascular endothelial growth factor receptor 2	_VVGND*DTGAYK_
206	P36552	Coproporphyrinogen-III oxidase, mitochondrial	_AGVSISVVHGN*LSEEAANQ MR_
207	P38647	Stress-70 protein, mitochondrial	_GAVVGIDLGTTN*SCVAVME GK_
208	P40237	CD82 antigen	_EMGNTVMDIIRN*YTAN*AT SSR_ _CCGWVSHYN*WTENEELMG FTK_ _NYTAN*ATSSR_ _KGFCEADN*STVSENNPEDW PVNTEGCMK_
209	P41233	ATP-binding cassette sub-family A member 1	_YPTPGEAPGVVGNFN*K_ _EAFN*ETNQAIQTISR_
210	P41593	Parathyroid hormone/parathyroid hormone-related peptide receptor	_FMTN*ETR_
211	P42703	Leukemia inhibitory factor receptor	_LKN*ITDISQK_ _KVPSN*STETVIESDQFQPGV R_ _LGVQMHPGQEIHN*FTLTGR_ _GSALPHPSN*ATWEIK_ _IEGLTN*ETYR_
212	P43006	Excitatory amino acid transporter 2	_VLVAPPSEEAN*TTK_ _AVISMLN*ETMNEAPEETK_
212	P43277	Histone H1.3	_ALAAAGYDVEKN*NSR_
213	P43406	Integrin alpha-V	_TAADATGLQPILNQFTPAN*V SR_ _AN*TTQPGIVEGGQVLK_ _LSCAFKTEN*QTR_
214	P45700	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	_TCHESYN*R_
215	P46978	Dolichyl-diphosphooligosaccharide--protein	_VMSWWDYGYQITAMAN*R_ _TILVDN*NTWN*NTHISR_

		glycosyltransferase subunit STT3A	
216	P49182	Heparin cofactor 2	_NGN*MSGISDQR_ _DFVN*ASSK_
218	P50172	Corticosteroid 11-beta-dehydrogenase isozyme 1	_QSN*GSIAVISSLAGK_
219	P50427	Steryl-sulfatase	_WHN*GSAVWK_
220	P50429	Arylsulfatase B	_IYAGMVSLMDEAVGN*VTK_
221	P50608	Fibromodulin	_LYLDHNN*LTR_
222	P51660	Peroxisomal multifunctional enzyme type 2	_ICDFSN*ASKPQTIQESTGGIV EVLHK_
223	P51830	Adenylate cyclase type 9	_NPCN*SSVLQDGR_
224	P51885	Lumican	_LGSFDGLVN*LTFIYLQHNQL K_
225	P52430	Serum paraoxonase/arylesterase 1	_HAN*WLTPLK_ _ITVVYAEN*GTVLQGTTVAS VYK_
226	P52592	Sphingosine 1-phosphate receptor 2	_VLEHYN*YTK_
227	P52793	Ephrin-A1	_HIVFWN*SSNPK_
228	P54751	CMP-N-acetylneuraminic-beta-galactosamide-alpha-2,3-sialyltransferase 1	_KPNN*LSDTVK_ _TGVHDGDFEYN*ITTTLAAIN K_
229	P55065	Phospholipid transfer protein	_IKVSN*VSCEASVSK_
230	P55292	Desmocollin-2	_AN*YTILK_
231	P55302	Alpha-2-macroglobulin receptor-associated protein	_VIDLWDLAQSAN*FTEK_
232	P56528	ADP-ribosyl cyclase 1	_N*PCNITREDYAPLVK_ _LVTQTIPCN*K_
233	P57716	Nicastrin	_TSLDLWMHTDPMSQKN*ESV K_ _AN*NSWFQSILK_ _KIYIPLN*K_ _LLN*ATHQIGCQSSISGDTGVI HVVEKEEDLK_

234	P57757	Cystinosin	_SKN*LTIVELPDEVIVPR_
235	P62702	40S ribosomal protein S4, X isoform	_FDTGN*LCMVTGGANLGR_
236	P63028	Translationally-controlled tumor protein	_TEGAIDDSLIGGN*ASAEGPE GEGTESTVVTGVDIVMNHHL QETSFTK_
237	P63038	60 kDa heat shock protein, mitochondrial	_LVQDVAN*NTNEEAGDGTTT ATVLAR_
238	P68373	Tubulin alpha-1C chain	_AYHEQLTVAEITN*ACFEPAN QMVK_
239	P70194	C-type lectin domain family 4 member F	_SSTEN*TSAELHVLGR_ _GSLQSANDLSSQTQGFLQHS MDN*ISAIQTVR_ _GSN*NSGHDN*HSQFVR_ _LRDYEEN*SSSCHK_ _CGNCN*LTSLEDEDFCK_
240	P70274	Selenoprotein P	_CGNCN*LTSLEDEDFCK_
241	P70302	Stromal interaction molecule 1	_LAVTN*TTMTGTVLK_
242	P70387	Hereditary hemochromatosis protein homolog	_CQALDFFPQN*ITMR_
243	P70389	Insulin-like growth factor-binding protein complex acid labile subunit	_N*NSLQTFVPQPGLER_ _N*LTQLPDGIPVSTR_
244	P70665	Sialate O-acetyltransferase	_AVAYGEKN*LTFQGPLPK_
245	P70699	Lysosomal alpha-glucosidase	_LEN*LSSTESGYTATLTR_ _GVFITN*ETGQPLIGK_
246	P80313	T-complex protein 1 subunit eta	_EGTDSSQGIPQLVSN*ISACQ VIAEAVR_
247	P97300	Neuroplastin	_KKENGVFEEISN*SSGR_ _KN*ASNMEYR_ _AN*ATIEVK_
248	P97328	Ketohexokinase	_GVDVSQVTWQSQGDTPCSC CIVN*NSN*GSR_
249	P97333	Neuropilin-1	_IAYSNN*GSDWK_ _RGPECSQN*YTAPTGVK_
250	P97370	Sodium/potassium-transporting ATPase subunit beta-3	_IIDLIPDGYPQISCLPKEEN*AT IATYPEFGVLDLK_

251	P97449	Aminopeptidase N	_LVEDLESFLKPYSVEEQKN*L TSCPDGAPFIQHGPDYR_ _SGQEDHYWLDVEKN*QSAK_ _NPNN*NTIHPNLR_ _KLN*YTLK_ _N*ATLVNEADKLR_ _SN*VTRPSEFNWIWIPIFLK _ _FTCN*QTTDVIIIHSK_ _QQCLEEAQLEN*ETTGCSK_
252	P97751	Vasoactive intestinal polypeptide receptor 1	
253	P97821	Dipeptidyl peptidase 1	_SDIN*CSVMEATEEK_
254	P97927	Laminin subunit alpha-4	_RPASN*ISASIQR_
255	P97927		_HVTDMN*STIHLR_
256	P98063	Bone morphogenetic protein 1	_AAGN*SSALGGQGTSQGQQR _
257	P98064	Isoform 2 of Mannan-binding lectin serine protease 1	_DKSGAVN*SSAAR_
258	P98064	Mannan-binding lectin serine protease 1	_FGYILHTDN*R_ _NN*LTTYK_
259	P98086	Complement C1q subcomponent subunit A	_VLTNQESPYQN*HTGR_
260	P99026	Proteasome subunit beta type-4	_VN*DSTMLGASGDYADFQYL K_
261	Q00560	Interleukin-6 receptor subunit beta	_GSN*FTAICVLK_ _EQVTVIN*R_
262	Q01279	Epidermal growth factor receptor	_YADANN*VCHLCHAN*CTY GCAGPGLQGCEVWPSGPK_ _CDPSCP*N*GSCWGGGEENCQ K_ _DIVQNVFMSN*MSMDLQSH SSCPK_ _DCVSCQN*VSR_ _EFVENSECIQCHPECLPQAMN *ITCTGR_ _TCPAGIMGEN*NTLVWK_ _DTLSIN*ATNIK_

263	Q01339	Beta-2-glycoprotein 1	_YTSFEYPKN*ISFACNPGFFLN *GTSSSK_ _DYRPSAGN*NSLYQDTVVFK _ _CLPHFAMIGN*DTVMCTEQG N*WTRLPECLEVK_
264	Q02788	Collagen alpha-2(VI) chain	_N*MTLFSDLVAEK_ _RGTFTDCALAN*MTQQIR_ _MALLQYGSQNQQQVAFPLT YN*VTTIHEALER_ _TASVSIN*QTEPPK_
265	Q03145	Ephrin type-A receptor 2	_DN*DSLITRK_
266	Q03311	Cholinesterase	_ETFLLN*TTCVK_
267	Q04592	Proprotein convertase subtilisin/kexin type 5	
268	Q04857	Collagen alpha-1(VI) chain	_RN*FTAADWGHSR_ _ENYAELLDDGFLKN*ITAQIC IDKK_
269	Q05685	Folate receptor beta	_NACCSVN*TSQELHK_
270	Q06770	Corticosteroid-binding globulin	_DLFTN*QSDFADTTK_ _GSTQYLENLGFN*MSK_ _VPMMVQSGN*ISYFR_ _QELN*DSLQVAER_ _RN*STGCLK_ _AFPEVCN*ETMMALWEECKP CLK_
271	Q06890	Clusterin	
272	Q07113	Cation-independent mannose-6- phosphate receptor	_LSYKDQVLQLVYEN*GSPCP SLSDLR_ _AGIN*ASYSEK_ _MN*YTGGDTCHK_ _HQN*QTLR_ _AACAVRPQEVTMVN*GTLTN PVTGK_ _ISTN*ITLVCKPGDLESAPVLR _ _SLLEFN*TTMGCQPSDSQHR_ _IGCFALSEPGN*GSDAGAAST TAREEGDSWVLN*GTK_
273	Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	

274	Q07456	Protein AMBP	_KEDSCQLN*YSEGPCLGMQE R_
275	Q07797	Galectin-3-binding protein	_APIPTALDTN*SSK_ _GLN*LTEDTYKPR_ _ALGYEN*ATQALGR_
276	Q07968	Coagulation factor XIII B chain	_TYEN*GSSVEYR_ _KEQETCLAPELEHGN*YSTTQ R_
277	Q08857	Platelet glycoprotein 4	_VISNN*CTSYGVLDIGK_ _QFWIFDVQNPDDVAKN*SSK _ _VFNGKDN*ISK_ _RPYIVPILWLN*ETGTIGDEK_ _SVQTNVQVQ*QGSSSQNTTTP TTK_
278	Q0GNC1	Inverted formin-2	_LLPAFN*TTSGLPYPR_
279	Q2HXL6	ER degradation-enhancing alpha-mannosidase-like 3	
280	Q2VLH6	Scavenger receptor cysteine-rich type 1 protein M130	_LAGGENN*CSGR_ _LTNEAHKEN*CTGR_
281	Q3T9X0	Protein Slc2a9	_AFYN*GTWYR_
282	Q3TAS6	UPF0510 protein INM02	_GSEVEDEDLELFN*TSVQLRP PSTAPGPETAAFIER_
283	Q3TCN2	Putative phospholipase B-like 2	_SDLNPAN*GSYPFQALHQR_ _LEDGFHPDAVAWAN*LTNAI R_
284			_AMSSN*ETAAYK_ _VMSWWDYGYQIAGMAN*R_ _TTLVDN*NTWN*NSHIALVG K_
285	Q3TQC7	Ectonucleoside triphosphate diphosphohydrolase 5	_GYLTSFEMFN*STFK_
286	Q3TQN1	Protein-tyrosine sulfotransferase 2	_LGYDPYANPPNYGNPDPIVIN *NTHR_
287	Q3U9N4	Granulins	_VGNVECGEGHFCHDN*QTCC K_ _CPTN*NTCCK_

288	Q3UDW8	Heparan-alpha-glucosaminide N-acetyltransferase	_FGEFGN*YSLLVQHASSGAN K_
289	Q3UMW8	Ceroid-lipofuscinosis neuronal protein 5 homolog	_KIETN*YTK_ _IFLYSGEPIYLG*ETSIFGPK_
290	Q3UP75	UDP-glucuronosyltransferase 3A1	_KEN*SSYQVINWR_
291	Q3UQ28	Peroxidasin homolog	_ILCDNSDN*ITR_
292	Q3UUQ7	GPI inositol-deacylase	_LHVAQPEN*DSHVALLK_
293	Q3V1K7	Solute carrier organic anion transporter family member 2B1	_SQVFYTN*CSCVAGN*GTVP AGSCESACSR_
294	Q3V3R4	Integrin alpha-1	_GELQSEN*SSLTLSSNR_ _DSCESNQN*ITCR_ _VTLDFN*LTPENGPVLDDA LPNSVHGHIPFAK_ _LDLPVN*TSIPN*VTEIK_ _EN*MTFGSTLVTNPK_ _ANQIVIPHN*TTFQTEPTK_ _YN*HTGQVVIYK_ _QTQVGIVQYGAN*VTHEFNL NK_ _AHFSSLN*LTIR_ _VYVYAVN*QTR_
295	Q4KL18	Transmembrane protein 171	_KN*NLSSSR_
296	Q4PZA2	Endothelin-converting enzyme 1	_N*SSVEAFK_ _QQTECMVQQYSN*YSVNGEP VNGR_ _FFN*FSWR_ _HLLN*ATASVSEAERK_ _QVSTLIN*NTDK_ _DYYLN*KTENEK_ _LGGWN*ITGPWAK_ _LLGGGDEDAIRPQMQQILDF ETALAN*ITIPQEK_ _ACMN*ETRIEELR_

297	Q571E4	N-acetylgalactosamine-6-sulfatase	_TGEAN*LTQLYTQEALDFIQT QHAR_
298	Q59IW6	Protein Abi3bp	_QVIQN*VTHR_
299	Q5F2E7	Nuclear fragile X mental retardation-interacting protein 2	_TVQN*SSVSPSSSSSSSTGET QTQSSSR_
300	Q5FWI3	Transmembrane protein 2	_TTN*ASASDPR_ _VLENEKFDTHEYHN*ESR_ _GDPSIISVN*GTDFTFR_ _HPNCVN*VTK_
301	Q5PT54	Sodium/bile acid cotransporter 5	_VLQVVN*VTK_
302	Q5SUF2	Luc7-like protein 3	_ESDTKNEVN*GTSEDIKSEGD TQSN_
303	Q5U431	G-protein coupled receptor 39	_GLNCN*LSR_
304	Q60590	Alpha-1-acid glycoprotein 1	_ESQTIGDQCVYN*STHLGFQR -
305	Q60675	Laminin subunit alpha-2	_ICNQN*SSNPYQR_
306	Q60709	Amyloid-like protein 2	_RN*QSLSLLYK_
307	Q60738	Zinc transporter 1	_SSVEIIN*STQAPMR_
308	Q60805	Tyrosine-protein kinase Mer	_SDN*GSYFCK_ _QPESVN*VTR_
309	Q60932	Voltage-dependent anion-selective channel protein 1	_TKSENGLEFTSSGSANTETTK VN*GSLETK_
310	Q61001	Laminin subunit alpha-5	_QLLAN*SSALEETILGHQGR_ _LN*ASIADLQSK_ _VFDLHQNMGSVN*VSVGCTP AQLIETSR_ _QELSQDN*ATLK_ _EALNQAVN*TTR_

311	Q61009	Scavenger receptor class B member 1	_LN*VTSPDLFR_ _LTYN*ESR_ _ESGIQN*VSTCR_ _EHSFLFDIHPVTGIPMN*CSV K_ _FTAPDTLAFAN*GSVYPPNEGF CPCR_
312	Q61029	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	_ASSN*ESLVANR_
313	Q61129	Complement factor I	_FN*VSLIYGR_ _WGEVDLIGN*CSQFYPPDRYY EK_ _FSHN*GTCAAEGK_ _AQAALDKAN*ASR_
314	Q61292	Laminin subunit beta-2	
315	Q61391	Neprilysin	_SCIN*ESAIDSR_ _EIAN*ATTKPEDR_
316	Q61469	Lipid phosphate phosphohydrolase 1	_IN*CSDGYIEDYICQGNEEK_
317	Q61490	CD166 antigen	_TVNSLN*VSAISIPEHDEADDI SDENR_ _N*ATGDYK_ _LSLSEN*YTLSIANAK_ _IIISPEEN*VTLTCTAENQLER_ _DSYPDGN*ITWYRNGK_ _VEFDDKGNVITSYGNPILLN* SSIPEDATIK_ _LDN*YSTQELGR_ _NVALVAGDTGN*ATGLGEQ GPTR_
318	Q61503	5'-nucleotidase	
319	Q61508	Extracellular matrix protein 1	
320	Q61526	Receptor tyrosine-protein kinase erbB-3	_HFN*DSGACVPR_ _YQTVDSSNIDGFVN*CTK_
321	Q61543	Golgi apparatus protein 1	_GN*ITEYQCHQYITK_ _LN*LTTDPK_

322	Q61549	EGF-like module-containing mucin-like hormone receptor-like 1	_VINEECKEN*ESINLAAR_
323	Q61606	Glucagon receptor	_LYSDQCHHN*LSELLPPPELV CN*R_
324	Q61614	Endothelin-1 receptor	_TCMLN*ATSK_
325	Q61646	Haptoglobin	_NLFLN*HSETASAK_ _VVLHPN*HSVVDIGLIK_ _N*LTSPVGVQPILNEHTFCAG LTK_ _CVVHYEN*STVPEKK_ _GDEKEN*ITAEALDLSLK_
326	Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	
327	Q61735	Leukocyte surface antigen CD47	_DAMVGN*YTCEVTELSR_ _SYIFIYDGNKN*STTTDQN*FT SAK_
328	Q61739	Integrin alpha-6	_YQTLN*CSVNVR_
329	Q61830	Macrophage mannose receptor 1	_TSYCN*ESFYFLCK_ _WECKN*DTLFGIK_
330	Q62000	Mimecan	_VIHLQFNSSSLTDDTFCKAN* DTR_
331	Q62009	Periostin	_GVN*ETLLVNELK_
332	Q62086	Serum paraoxonase/arylesterase 2	_IQNILSEKPSVTTVYINN*GSV LQGSSVATIYDRK_ _QPNMN*LTQLK_
333	Q62087	Serum paraoxonase/lactonase 3	_VSTLYANN*GSVLQGSTVAS VYHK_ _VIQLGTLVDN*LTVDPATGDI LAGCHPNPMK_
334	Q62192	CD180 antigen	_LIN*LTFLDLTR_
335	Q62313	Trans-Golgi network integral membrane protein 1	_TDAELN*ETARPLSPVNPK_
336	Q62351	Transferrin receptor protein 1	_QKN*ITAFN*ETLFR_

337	Q62470	Integrin alpha-3	_VWN*STFIEDYKDFDR_ _DLAVGDDYTN*R_ _TSIPTINMEN*K_
338	Q63836	Selenium-binding protein 2	_CN*VSNTHSHCLASGEVMV NTLGDLQGNGK_
339	Q63880	Carboxylesterase 3A	_PLLAHMQLPPEIMPTVIDEYL DN*GSDESATR_ _NVN*ISYTVN*DSFFPQRPQK _ _KNVN*ISYTVNDSFFPQRPQK _
340	Q63886	UDP-glucuronosyltransferase 1-1	_KFPVPFQKEN*VTATLVELGR _
341	Q63961	Endoglin	_KLN*ASIVTSFVELPLVSN*VS LR_ _VN*ITVLPSTSR_ _N*TTSAAMVHCLR_ _N*ATSYPPMCQDPVTGQIV NDLLTNRK_
342	Q64176	Carboxylesterase 1E	_N*TTSAAMVHCLR_ _N*ATSYPPMCQDPVTGQIV NDLLTNRK_
343	Q64449	C-type mannose receptor 2	_ASN*ASKPGTLER_ _VTPVCN*ASLPAQR_ _KVEVEAVN*ATAVK_
344	Q64487	Receptor-type tyrosine-protein phosphatase delta	_KVEVEAVN*ATAVK_
345	Q64695	Endothelial protein C receptor	_QLNAYN*R_
346	Q64726	Zinc-alpha-2-glycoprotein	_DTTGSHTFQGMFGCEITNN*R _
347	Q64735	Complement component receptor 1-like protein	_CTPPPYVENAVMLSEN*R_ _IN*YTCNQGYR_ _YN*VTSFK_
348	Q69ZQ1	Uncharacterized family 31 glucosidase KIAA1161	_YN*VTSFK_
349	Q6DYE8	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3	_LN*LSEGEVAATVK_

350	Q6GQT6	Sterol regulatory element-binding protein cleavage-activating protein	_LPEN*QTLPGELPEHAGPAEG VHDSR_
351	Q6GQT9	Nodal modulator 1	_VTNSNANAAGPLIVAGYN*V SGSVR_
352	Q6P5F7	Protein tweety homolog 3	_VWDTAAALN*R_
353	Q6P6J9	Thioredoxin domain-containing protein 15	_ENLFGQLQGAGGFQDREEEYY AEPGVTEAEPVATEDAN*STD SLK_ _IFIFN*QTGIEAK_
354	Q6P9J9	Anoctamin-6	_LN*ITCESSK_ _NTDKENPYIGLGN*YTLCR_
355	Q6PD26	GPI transamidase component PIG-S	_IYN*ASELPVRVEVDMVR_
356	Q6PEM8	Proton-coupled folate transporter	_FSTELGYN*GTR_
357	Q6PGD0	Apoptosis-related protein 3	_GFTQLQTLILPQDVPCPGGSN AWDN*VTSFK_
358	Q6XLQ8	Calumenin	_N*VTYGTYLDDPDPDDGFNY K_
359	Q71KU9	Fibrinogen-like protein 1	_IDLDFEKN*SSFAQYQSFK_
360	Q75N73	Zinc transporter ZIP14	_YGKN*DSLTLTQLK_ _SLLDHLHVGVRDN*VSQPK_
361	Q7TN73	CAS1 domain-containing protein 1	_MN*ITSIAPLLEK_
362	Q7TQD7	Unconventional myosin-Ib	_AAHIFN*ESLVCHQIR_
363	Q80V26	Inositol monophosphatase 3	_QVALQTFGN*QTSIIPAGGAG YK_
364	Q80WQ6	Inactive rhomboid protein 2	_WQN*DTGPSDKSDLSQK_

365	Q80XL7	Metallophosphoesterase 1	_ASDAN*CSGEDAAPPEER_ _KLN*CSQEVPGSSQCDREPEP R_
366	Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	_TIQLN*VCNSEEVEK_
367	Q80YX1	Tenascin	_LLQTAEHN*ISGAER_
368	Q8BFR4	N-acetylglucosamine-6-sulfatase	_TPMTN*SSIR_ _YPHNHHVVN*NTLEGN*CSS K_ _YYN*YTLSINGK_ _GPGIKPN*QTSK_ _GDRN*LTWR_
369	Q8BG07	Phospholipase D4	_ELGAIYN*CSNLAQDLEK_ _N*ISVVVATHSPTLAK_
370	Q8BG19	Transmembrane and TPR repeat- containing protein 4	_NLADQGN*QTAAIK_
371	Q8BGQ4	Protein O-mannosyl-transferase 2	_FSGAN*DTDFR_
372	Q8BGT0	Osteopetrosis-associated transmembrane protein 1	_NIGN*TSEGPR_
373	Q8BH24	Transmembrane 9 superfamily member 4	_KCEVLCN*QSNKPITLTVEQS R_
374	Q8BH35	Complement component C8 beta chain	_AVN*GSLVK_
375	Q8BHC0	Lymphatic vessel endothelial hyaluronic acid receptor 1	_NKNPQMN*FTEANEACK_
376	Q8BHG3	Cell cycle control protein 50B	_QGN*YSAGLPR_
377	Q8BI84	Melanoma inhibitory activity protein 3	_TGN*SSPASVER_

378	Q8BJ83	TM2 domain-containing protein 3	_NFVIN*MTCR_ _DHIHCLGN*R_ _YFAN*CTVR_
379	Q8BJS4	SUN domain-containing protein 2	_ALSPN*STISSAPK_
380	Q8BK48	Pyrethroid hydrolase Ces2e	_IVAN*LSGCAAVNSETLMCC LR_
381	Q8BKU8	Transmembrane protein 87B	_KTMFN*STEIK_
382	Q8BLF1	Neutral cholesterol ester hydrolase 1	_GNYDFVEAMIVNN*HTSLDV ER_
383	Q8BLK3	Limbic system-associated membrane protein	_GTDN*ITVR_
384	Q8BLY1	SPARC-related modular calcium- binding protein 1	_LN*NTNVR_
385	Q8BM72	Heat shock 70 kDa protein 13	_N*STIQAANLAGLK_
386	Q8BM88	Cathepsin O	_YPAEGQRPIPN*VSLPLR_ _WLN*ETQLK_
387	Q8BNX1	C-type lectin domain family 4 member G	_DDIGACRN*CCSVTK_
388	Q8BS35	Alkylglycerol monooxygenase	_SPGAQDN*VSVSQGMR_
389	Q8BSY0	Aspartyl/asparaginyl beta- hydroxylase	_GGGGN*SSSSGSGSGSGSGSP STGSSGSSSPGAR_ _VYEEVLN*VTPNDGFAK_
390	Q8BTJ4	Ectonucleotide pyrophosphatase/phosphodiesterase family member 4	_SN*YSVIDLTPVAAILPK_ _IN*VTEVYDKLK_
391	Q8BVL6	Protein Rarres1 (Fragment)	_NEKPRPAVN*VTCAR_
392	Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	_DGTVTAGN*ASGVSDGAGA VIIASEDAVKK_
393	Q8BXA5	Cleft lip and palate transmembrane protein 1-like protein	_VKDLMVIN*R_ _TVN*VSVPPK_

394	Q8BXZ1	Protein disulfide-isomerase TMX3	_LVAIAVIDEKN*TSLEHTR_
395	Q8BY89	Choline transporter-like protein 2	_TCNPETFPLRN*ESLQCPTAR_
			KN*ITDLVEGAK
			GVL MVGN*ETTYEDGHGAR
396	Q8BYB9	Protein O-glucosyltransferase 1	_FLSYN*VTR_
397	Q8C0Z1	Protein ITFG3	_NTN*SSNN*LTR_
			_KPILGHYKPD TLAVVIEN*GT
			SIDR_
398	Q8C129	Leucyl-cystinyl aminopeptidase	_TN*QSAELIQPVATNGK_
			DIILHSTGHN*ISR
399	Q8C165	Probable carboxypeptidase PM20D1	_GAIQIPTVSFSHEESN*TTALA
			EFGEYIRK_
			HYAN*ITNGMYR
			_GALDLMLQVN*MTPGHSSAP
			PK_
400	Q8C196	Carbamoyl-phosphate synthase [ammonia], mitochondrial	_ILDYHQEACN*GCIISVGGQI
			PNNLAVPLYKNGVK_
			ALENN*MSLDEIVR
			_VAGLLVLN*YSNDYNHWLA
			TK_
			DGSIDLVINLPNN*NTK
401	Q8C341	Protein osteopotenia	_SISEN*ATATTEPK_
402	Q8C7X2	Uncharacterized protein KIAA0090	_FINYN*QTVSR_
403	Q8C8K1	Ephrin type-B receptor 4	_SVVHHLN*GSTLR_
404	Q8CDV7	Ectonucleoside triphosphate diphosphohydrolase 1	_VVN*VSELYGTPCTK_
405	Q8CG14	Complement C1s-A subcomponent	_ITAN*STWEPDKAK_
406	Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	_EAGLPPNIIQFVPADGPTFGD
			TVTSSEHL CGIN*FTGSVPTFK_

407	Q8CID3	Protein FAM20A	_DLGTASHN*FSGALPR_
408	Q8CIF4	Biotinidase	_WNPCLEPFRFN*DTEVLQR_ _YQFNTNVVFSND*GTLVDR_ _GVQIIVFPEDGIHGFN*FTR_ _GHLIAQVATNPQGLTGTGN* TTSEMDPSHR_
409	Q8CIM7	Cytochrome P450 2D26	_GTTLIPN*LSSVLKDETVWEK PLR_
410	Q8CJ91	CD209 antigen-like protein B	_IPIFQGQN*ESIQEK_
411	Q8CJH3	Plexin-B1	_YTSDPN*VTSVGPSK_
412	Q8JZZ0	UDP-glucuronosyltransferase 3A2	_VSQVLHEGGHN*VTK_
413	Q8K094	Poliovirus receptor	_ISWPSNVN*GSHR_
414	Q8K0B2	Probable lysosomal cobalamin transporter	_GN*STLAVPK_
415	Q8K0E8	Fibrinogen beta chain	_YKGTAGNALMDGASQLVGE N*R_
416	Q8K0L2	Ectonucleoside triphosphate diphosphohydrolase 8	_QSLNTVN*DTVWK_
417	Q8K0R6	Glycolipid transfer protein domain-containing protein 2	_AAGVLEDVYN*RTQGLLAG HGLLQLA_
418	Q8K297	Procollagen galactosyltransferase 1	_TALWVATDHNTDN*TSAILR _ _AMN*TSQVEAMGIQMLPGY R_
419	Q8K299	Scavenger receptor class A member 5	_LVN*GSGPHQGR_
420	Q8K2C7	Protein OS-9	_YHSQTYGN*GSK_
421	Q8K385	Ferric-chelate reductase 1	_HSQQPLITYEKYN*VTDTPK_

422	Q8K389	CDK5 regulatory subunit-associated protein 2	_LHSEN*VTK_
423	Q8K441	ATP-binding cassette sub-family A member 6	_TSLLVIN*NTESNIEDFLQSLK_
424	Q8K442	ATP-binding cassette sub-family A member 8-A	_KILASPNEEN*MTELISMR_ _NYN*FTLACNTK_
425	Q8K4G1	Isoform 2 of Latent-transforming growth factor beta-binding protein 4	_N*ATSVDSGAPGGAAPGGPG FR_
426	Q8K4Q8	Collectin-12	_VQSLQTLAAN*NSALAK_ _ETLQN*NSFLITTVN*K_ _DLQDLHKDTEN*R_
427	Q8QZR3	Pyrethroid hydrolase Ces2a	_TVAN*LSGCEATDSEALIHCL R_
428	Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	_EN*GTITAAN*ASTLNDGAA ALVLMTAEAAQR_
429	Q8R084	Protein Ugt2b1	_WVGN*WTYELKK_
430	Q8R0F3	Sulfatase-modifying factor 1	_FVN*STGYLTEAEK_
431	Q8R0I0	Angiotensin-converting enzyme 2	_CDISN*STEAGQK_
432	Q8R121	Protein Z-dependent protease inhibitor	_ETYFN*LSKK_ _EGN*FTSTFDKK_
433	Q8R143	Pituitary tumor-transforming gene 1 protein-interacting protein	_VGCSEYTN*R_
434	Q8R180	ERO1-like protein alpha	_WGHN*VTEFQQR_
435	Q8R1J9	Torsin-2A	_SWVQGN*LTACGR_

436	Q8R1V4	Transmembrane emp24 domain-containing protein 4	_FTFTSHTPGDHDQICLHSN*STR_ R_
437	Q8R242	Di-N-acetylchitobiase	_QVN*GSVSGSQWNK_ _
438	Q8R2E9	ERO1-like protein beta	_LGAIN*STLSN*ESK_ _YSQAAN*STKELDDCEQANK _
439	Q8R2Q8	Bone marrow stromal antigen 2	_TQDSLLQAETQAN*SCN*LTV VTLQESLEKK_ _N*TTHLLQR_ _
440	Q8R2R1	Protein O-mannosyl-transferase 1	_FVHVN*TSAILK_ _
441	Q8R366	Immunoglobulin superfamily member 8	_IGPGEPELLELCN*VSGALPPPG R_ _
442	Q8R3G9	Tetraspanin-8	_ILN*ETLYENAK_ _
443	Q8R3H7	Heparan sulfate 2-O-sulfotransferase 1	_YHVLHIN*TTK_ _
444	Q8R420	ATP-binding cassette sub-family A member 3	_YHAN*TSAQQLFQK_ _
445	Q8R4G6	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A	_RQN*QSLVYGK_ _
446	Q8R4U0	Stabilin-2	_NAN*CSTVSPGQTQCTCQK_ _YGPQCN*R_ _CDNN*DTIIVR_ _VLLN*LTTVAANHGYTK_ _ITN*GTVGVR_ _
447	Q8VBZ3	Cleft lip and palate transmembrane protein 1 homolog	_DYYPIN*ESLASLPLR_ _
448	Q8VCC2	Liver carboxylesterase 1	_TAASILWQAYPILN*ISEK_ _

449	Q8VCF1	Soluble calcium-activated nucleotidase 1	_ISHYN*DTYPLSPPQR_
450	Q8VCG4	Complement component C8 gamma chain	_SLPVN*DSVLDVFER_ _VREAN*LTEDQILFFPK_
451	Q8VCI0	Phospholipase B-like 1	_TIYN*WSGYPLLVHK_ _TVLDKNGDAYGYYN*DSIK_ _RDQGN*VTDMASMK_ _FN*ETLHR_
452	Q8VCM8	Nicalin	_VIYN*LTEK_
453	Q8VCS0	N-acetylmuramoyl-L-alanine amidase	_LEPEHLQLQN*ISQEQLAQVA TLATK_
454	Q8VCS9	Transporter	_GVSSSEN*FTSPVMEFWER_
455	Q8VCT4	Carboxylesterase 1D	_DGASEEETN*LSK_ _N*TTSYPPMCSQDAVGGQVL SELFTNRK_
456	Q8VCU1	Carboxylesterase 3B	_NVN*ISYIVN*DSFFPQRPEK_ _YAFQELLGDISFIPTLN*FSK_
457	Q8VCU2	Phosphatidylinositol-glycan-specific phospholipase D	_NLN*YTER_ _LSSSPN*VTISCK_ _VN*GTLTQVLLVGAPTHDDV SK_
458	Q8VCV9	Sodium-dependent glucose transporter 1A	_LAWGTAPAQN*HTESDLDTL MLN*R_
459	Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial	_GATLSHHNIVN*NSMLIGQR_
460	Q8VDB2	Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase	_YDKSEVDGAAAMLN*YTHIL MEAVPGHPALYR_
461	Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	_IISAN*GCKVDNSSLTGESEPP TR_ _GVGIISEGN*ETVEDIAAR_
462	Q8VEK0	Cell cycle control protein 50A	_NEDRPIAPCGAIANSMFN*DT LELYLVAN*ESDPKPIPIPLK_ _CLSPN*VTSCACTIN*FTLK_

			DDLHPTLPAGQYFLN*ITYNY PVHSDGR
463	Q8VEK3	Heterogeneous nuclear ribonucleoprotein U	_GN*FTLPEVAECFDEITYVEL QKEEAQK_
464	Q8VHI3	GDP-fucose protein O-fucosyltransferase 2	_SQHLN*STDAADK_
465	Q8VI47	Canalicular multispecific organic anion transporter 1	_QN*GTDNSPSQR_
466	Q91V08	C-type lectin domain family 2 member D	_WTDNTEYN*NTIPIRGEER_ _TEQIPVN*K_
467	Q91VI7	Ribonuclease inhibitor	_LQLEYCN*LTATSCEPLASVL R_
468	Q91WN2	Transmembrane protein 150A	_HVCNVENWSYN*ESCSPDPA EQGGPK_
469	Q91WU0	Expressed sequence AU018778	_N*ATTYPPMCSQDAAR_
470	Q91X72	Hemopexin	_SWSTVGN*CTAALR_ _N*GTAHGN*STHPMHSR_
471	Q91XL1	Leucine-rich HEV glycoprotein	_MFSQN*DTR_
472	Q91Y47	Coagulation factor XI	_VYGGIVN*QSEINEGTAFFR_ _GMNYN*SSVVK_ _LESAMN*YTDFQRPICLPSKG DR_
473	Q91Y74	CMP-N-acetylneuraminase-beta-galactosamide-alpha-2,3-sialyltransferase 4	_SMAGSGHN*VSQEAIAIKR_
474	Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	_TILPAAAQDVYYRDEIGN*VS TSHLLILDDSVEMEIRPR_
475	Q91ZJ9	Hyaluronidase-1	_EELGTYPYYTPTGEPVFGGLP QN*ASLVTHLAHTFQDIK_
476	Q91ZX7	Prolow-density lipoprotein	_VDIPQQPMGIIAVAN*DTN*S

receptor-related protein 1

CELSPCR_
_WQCDYDN*DCGDNSEDEESC
TPRPCSESEFSCANGR_
_WLCDGDN*DCGNSEDESN*A
TCSAR_
_VWVCDRDN*DCVDGSDEPA
N*CTQMTCGVDEFR_
_INNGGCQDLCLLTHQGHVN*
CSCR_
_MGCQHHCVPTPSGPTCYCN*
SSFQLQADGK_
GVTHLN*ISGLK
LTSCATN*ASMCGDEAR
MHLN*GSNVQVLHR
DGSCIGN*SSR
CN*ASSQFLCSSGR
TCVSN*CTASQFVCK
LHKDN*TTCYEFK
QTGDVTCN*CTDGR
LN*GTDPIVAADSKR
IETILLN*GTDRK
RGCKDN*ATDSVPLR
VNRFN*STEYQVVTR
_AFIN*GTGVETVVSADLPNA
HGLAVDWVSR_
LYWISSGN*HTINR
FGTCSQLCN*NTK
CDMDGQN*R
_TCPLDEFQCN*NTLCKPLAW
K_
_LYWTDGDN*ISMANMDGSN
*HTLLFSGQK_
KLNLDGSN*YTLLK
GPCSHLCLINYN*R
WTGHN*VTVVQR
_DGGSTTAGN*SSQVSDGAAA
VLLAR_
_N*GSYDIGMACGVESMSLSG
MGNPGNISSR_
SFGN*ISER

477 Q921H8 3-ketoacyl-CoA thiolase A,
peroxisomal

478 Q921L8 Polypeptide N-
acetylgalactosaminyltransferase 11

479	Q923B6	Metalloreductase STEAP4	_LRN*ATITQALTNK_
480	Q924Z4	Ceramide synthase 2	_LWLVPVN*LTWADLEDKDGR_
481	Q925Q3	Sodium/potassium/calcium exchanger 6	_AVCGLN*TSDRCDFVR_
482	Q925U4	ER degradation-enhancing alpha- mannosidase-like 1	_VIN*SSSNCNRVPDER_
483	Q99J21	Mucolipin-1	_GHVDPAN*DTFDIDPR_
484	Q99JR5	Tubulointerstitial nephritis antigen- like	_GRADECALPYLGATCYCDLF CN*R_
485	Q99JY8	Lipid phosphate phosphohydrolase 3	_LRPHFLSVCDPDFSQIN*CSE GYIQNYR_
486	Q99K41	EMILIN-1	_LGALN*NSLLLLLEDR_ _LEKLEGLLAN*VSR_ _LN*LTAQQLSQLEGLLQAR_ _LEDRFN*STLGPSEEQEKNWP GGPGR_ _ESN*STSLTQAALLEK_
487	Q99KF1	Transmembrane emp24 domain- containing protein 9	_FTFSTHTPGEHQICLHSN*STK _
488	Q99KI0	Aconitate hydratase, mitochondrial	_HPN*GTQETILLN*HTFNETQI EWR_
489	Q99MB1	Toll-like receptor 3	_LTHIPDDLPSN*ITVLN*LTHN QLR_
490	Q99MQ4	Asporin	_ITDIEN*GTFANIPR_
491	Q99PG0	Arylacetamide deacetylase	_AMLLNQHVPMESSHLLQFVN *WSSLLPER_
492	Q9CPW5	Translocon-associated protein subunit beta	_IAPASN*VSHTVVLRLK_ _AGYFN*FTSATITYLAQEDGP VVIGSTSAPGQGGILAQR_
493	Q9CQ88	Tetraspanin-31	_NTQADVIN*ASWSVLSN*STR _ _SFDCCGLFN*LTTLR_
494	Q9CQF9	Prenylcysteine oxidase	_MSN*ITFR_ _LLN*QTLR_

495	Q9CQW3	Vitamin K-dependent protein Z	_CSLLHSN*ISVK_
496	Q9CQX5	Claudin domain-containing protein 1	_SPIQEN*SSDSNK_ _YN*GSLGLWR_
497	Q9CRA0	Ecto-ADP-ribosyltransferase 4	_SAGN*MSTYNCQLLK_
498	Q9CY50	Translocon-associated protein subunit alpha	_YPQDYQFYIQN*FTALPLNTV VPPQR_ _DLNGNVFQDAVFN*QTVTVI ER_
499	Q9CYA0	Cysteine-rich with EGF-like domain protein 2	_N*ETHSICSACDESK_
500	Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	_VVELLADIVQN*SSLEDSQIE KER_
501	Q9D1H9	Microfibril-associated glycoprotein 4	_RFN*GSVSFFR_ _VDLEDFEN*NTAYAK_
502	Q9D304	E3 ubiquitin-protein ligase RNF128	_VPHTGVN*R_
503	Q9D404	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	_GPN*HSVSTACTTGAHAVGD SFR_
504	Q9D6Z1	Nucleolar protein 56	_LAALALASSEN*SSTPEECE VNEK_
505	Q9D7N9	Adipocyte plasma membrane-associated protein	_AGPN*GTLFVVDAYK_
506	Q9D8C2	Tetraspanin-13	_SYNPN*DTCPASCAK_
507	Q9D8N1	Uncharacterized protein C11orf24 homolog	_AVN*QSMLR_
508	Q9DAU1	Protein canopy homolog 3	_VVMDIPYELWN*ETSAEVAD LKK_

509	Q9DB05	Alpha-soluble NSF attachment protein	_AIAHYEQSADYYKGEESN*SS ANK_
510	Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	_AVAQGN*LSSADVQAAK_
511	Q9DBB9	Carboxypeptidase N subunit 2	_LQDLEITGSPVSN*LSAHIFSN *LSSLEK_ _LSLDSN*NLTALHPALFHN*L SR_ _LQLLN*LSR_ _AFSGSPN*LTK_
512	Q9DBD0	Inhibitor of carbonic anhydrase	_SCHTAVGTSEGWNVPMGLIY N*QTGSCK_ _DLLFSDDTECLSNLQN*K_
513	Q9DBH5	Vesicular integral-membrane protein VIP36	_VFPYISVMVNN*GSLSYDHS KDGR_
514	Q9DBI0	Transmembrane protease serine 6	_ELLVDELLSN*SSTLASYK_
515	Q9DBN1	Protein 1300002K09Rik	_QIN*ITCDNPVDR_
516	Q9DBU0	Transmembrane 9 superfamily member 1	_IIFAN*VSVR_
517	Q9DBX3	Sushi domain-containing protein 2	_SQLVN*ETHWQYYGTSDTR_ _MPN*GTQAR_ _FCILDVMSTGSSSVGN*ATR_ _CCGVSN*YTDWFEVYN*ATR
518	Q9DCK3	Tetraspanin-4	- _FQVPCPLAHNLAN*ATGN*FS HMOVVAEEK_
519	Q9DCP2	Sodium-coupled neutral amino acid transporter 3	- _FQVPCPLAHNLAN*ATGN*FS HMOVVAEEK_
520	Q9EPK6	Nucleotide exchange factor SIL1	_FN*SSSSSLEEK_
521	Q9EPR4	Solute carrier family 23 member 2	_CN*TTEITVAN*GTAEELLEHI WHPR_

522	Q9EPT5	Solute carrier organic anion transporter family member 2A1	_QPIYLN*CSCVTGGSASAK_
523	Q9EQG7	Ectonucleotide pyrophosphatase/phosphodiesterase family member 5	_VQPIVAVADEGWYILQN*K_
524	Q9EQH2	Endoplasmic reticulum aminopeptidase 1	_CFN*AMEVDALN*SSHPVSTP VENPAQIR_
525	Q9EQJ0	Two pore calcium channel protein 1	_LTPNCCN*TSTVADAYR_
526	Q9ER39	Torsin-1A	_GN*VSACAR_
527	Q9ER41	Torsin-1B	_FTECCHEERPLN*TSALK_
528	Q9ERU9	E3 SUMO-protein ligase RanBP2	_LNSN*NSASPHR_
529	Q9ESB3	Histidine-rich glycoprotein	_LPPLNIGEVLTLPEANFPSFSL PNCN*R_ _YSN*ESQDLSVNGYN*CTTSS VSSALR_ _N*CSTQHFPR_ _LQEGALPQLPPGYPPHSGAN* R_
530	Q9ET22	Dipeptidyl peptidase 2	_ALAGLVYN*SSGTEPCYDIYR _
531	Q9ET30	Transmembrane 9 superfamily member 3	_IVDVN*LTSEGK_
532	Q9JHJ3	Lysosomal protein NCU-G1	_LLEFDSTN*ASEGAQPPGKPY PPYSLAK_
533	Q9JI71	Delta-like protein 4	_TDEQN*DTLTR_
534	Q9JIL4	Na(+)/H(+) exchange regulatory cofactor NHE-RF3	_AGVLADDHLIEVNGENVEN* ASHEEVVEK_

535	Q9JIM1	Equilibrative nucleoside transporter 1	_YFTNRLDVSQN*VSSDTDQS CESTK_
536	Q9JJF9	Signal peptide peptidase-like 2A	_IAQEGGAAALLIAN*NSVLIPS SR_
537	Q9JJK5	Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein	_GAESTEQPDNSN*QTQHPGD SSSDGLR_
538	Q9JL3	Solute carrier organic anion transporter family member 1B2	_YATENDISSLHN*STLTCLVN *QTTSLTGTSPEIMEK_
539	Q9JJR8	Transmembrane protein 9B	_ENPGHIYNKN*ISQK_
540	Q9JJX6	P2X purinoceptor 4	_GVAVTN*TSQLGFR_ _CVPFN*ASVK_ _AAEN*FTLLVK_ _NILPN*ITTSYLK_
541	Q9JKF6	Poliovirus receptor-related protein 1	_ADANPPATEYHWTTLN*GSL PK_ _NPN*GTVTVISR_
542	Q9JKR6	Hypoxia up-regulated protein 1	_DKN*GTRAEPPLN*ASAGDQ EEK_ _FQISPQLQFSPEEVLGMVLN* YSR_ _LSALDNLLN*HSSIFLK_ _EN*GTDAVQEEEEESPAEGSK DEPAEQGELK_ _VIN*DTWAWKN*ATLAEQA K_ _VFGSQN*LTTVK_ _QYCTEQN*ATLVK_ _RN*LTWEESK_
543	Q9JL99	C-type lectin domain family 1 member B	_RN*LTWEESK_
544	Q9QUN9	Dickkopf-related protein 3	_GGN*GTICDNQR_

545	Q9QWR8	Alpha-N-acetylgalactosaminidase	_VN*YTEVSR_
546	Q9QXC1	Fetuin-B	_VLYLPAYN*CTLRPVSK_
547	Q9QXZ6	Solute carrier organic anion transporter family member 1A1	_SVGTGTNMVFQN*CSCIGSSG N*SSAVLGLCK_ _YKYETTISPTSN*LSSNSFLCI EN*R_
548	Q9QY81	Nuclear pore membrane glycoprotein 210	_GLMVGN*GSVLGVVQAVDA ETGK_ _IEAVLPAEFFEVLSSSQN*GSY HHR_ _GATN*NTCIIR_
549	Q9QYC7	Vitamin K-dependent gamma-carboxylase	_VEN*GSETGPLPELQPLLEG EVK_ _N*QTLQEGEK_
550	Q9QZ25	Vascular non-inflammatory molecule 3	_LTGSAGN*YTVQCQK_
551	Q9QZC2	Plexin-C1	_GACEVRPLGNLN*R_ _DQAGN*CTEPVSLAPPARPR_
552	Q9R013	Cathepsin F	_VYIN*DSVELSRNENK_
553	Q9R069	Basal cell adhesion molecule	_GN*LTLER_
554	Q9R098	Hepatocyte growth factor activator	_FCNIVPTEHCFLGN*GTEYR_
555	Q9R0A1	Chloride channel protein 2	_ETLVTLFDN*R_
556	Q9R0E1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	_EQYIHEN*YSR_
557	Q9R0E2	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	_EQIN*ISLDHR_
558	Q9R0L9	Sialomucin core protein 24	_TYCANEPLSN*CSQVN*R_
559	Q9R182	Angiopoietin-related protein 3	_KDGSQDFN*ETWENYEK_

560	Q9R1W5	Calcitonin gene-related peptide type 1 receptor	_IMQDPIQQAEGLYCN*R_
561	Q9WTP6	Adenylate kinase 2, mitochondrial	_LAEN*FCVCHLATGDMLR_
562	Q9WU60	Attractin	_GICN*ASDTR_ _EWLPLN*HSVNSVVVR_ _IDSTGN*VTNELR_
563	Q9WUH7	Semaphorin-4G	_GYN*SSQDLPSLVLDLVK_ _GQTQN*YSTLLLEEASER_ _N*NQTECFNHVR_
564	Q9WV54	Acid ceramidase	_SVLEN*TTSYEEAKNTLTK_
565	Q9WVJ3	Carboxypeptidase Q	_EVMNLLQPLN*VTK_
566	Q9WVL3	Solute carrier family 12 member 7	_TAFAPPDIPVCLLGN*R_ _MQVVSN*GTVTTALWR_ _CLVPHTVN*LSSAWR_
567	Q9Z0M5	Lysosomal acid lipase/cholesteryl ester hydrolase	_NYFHYN*QSFPPSYNIK_
568	Q9Z1M0	P2X purinoceptor 7	_SAEN*FTVLIK_
569	Q9Z222	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	_ETNVGN*QTVVR_
570	Q9Z2A9	Gamma-glutamyltransferase 5	_LWDPSSHPGIQN*ISR_ _QLFFN*GTETLR_ _GDHHQLSHYN*LTGVR_
571	Q9Z2G6	Protein sel-1 homolog 1	_MYSEGSDIVPQSN*ETALHYF K_ _EATIVGEN*ETYPR_
572	S4R1S4	Receptor-type tyrosine-protein phosphatase C	_SLPN*NVTSEFEVESLKPYK_

Table S4 The score and MS intensity of the N-glycopeptides identified by both dM-MNPs and M-MNPs.

Modified sequence	Score		Intensity		
	dM-MNPs	M-MNPs	dM-MNPs	M-MNPs	Ratio
ACMN*ETRIEELR	154.28	88.338	238580000	5157200	46.3
ADN*YTYEHLR	118.4	55.721	58332000	3000400	19.4
ADSLYSQVVGLSAS QAN*LSK	118.23	126.25	98100000	57063000	1.7
AELSN*HTRPVILVP GCLGNR	206.7	110.6	524400000	39313000	13.3
AFMN*SSFTIDPK	64.65	74.46	493860000	163600000	3.0
AFN*ECCTIANK	119.76	110.66	308220000	54767000	5.6
AFSGSPN*LTK	106.29	106.29	168950000	29880000	5.7
AFVEN*ITVLENSLV FK	204.43	192.4	3027900000	166420000 0	1.8
AFYN*GTWYR	159.37	144.09	147250000	11955000	12.3
AGIN*ASYSEK	106.29	83.397	116030000	16929000	6.9
AGPN*GTLFVVDAY K	106.13	117.92	650100000	222610000	2.9
AGYFN*FTSATITYL AQEDGPVVGSTAP GQGGILAQR	184.55	121.82	1150800000	164040000	7.0
ALAAAGYDVEKN*N SR	212.17	188.4	167310000	9723000	17.2
ALAGLVYN*SSGTEP CYDIYR	191.37	134.37	357220000	126910000	2.8
_ALGYEN*ATQALGR _	182.41	172.74	692940000	408960000	1.7
ALSPN*STISSAPK	102.73	88.552	392130000	100840000	3.9
ALVN*FTR	169.37	148.07	339320000	121170000	2.8
AMSN*ISVR	179.73	91.853	293460000	43948000	6.7
AMSSN*ETAAYK	113.63	103.22	752860000	221020000	3.4
AN*ATIEVK	101.43	103.56	205340000	38447000	5.3
AN*LSSQVLK	114.89	94.309	318970000	73013000	4.4
AN*NSWFQSILK	72.531	97.163	83332000	34740000	2.4
AN*TTQPGIVEGGQ VLK	61.641	85.619	288590000	123310000	2.3
AN*YTILK	85.265	73.616	90035000	44529000	2.0
ANQIVIPHN*TTFQT EPTK	137.44	137.44	1312700000	421240000	3.1
APIPTALDTN*SSK	142.91	151.78	424530000	141150000	3.0
AQAALDKAN*ASR	197.3	127.17	263850000	17783000	14.8
ASDAN*CSGEDAAP PEER	120.29	79.013	36724000	8000600	4.6

ASSFRPN*GTK	193.49	187.58	345340000	50990000	6.8
ATVN*DSGEYR	187.64	173.32	1251500000	623320000	2.0
AWGTPCELCPNVN* TSEYK	122.31	90.385	95664000	57843000	1.7
CDNN*DTIIVR	243.4	133.76	185860000	26364000	7.0
CDQCEENYFYN*R	130.01	122.51	13743000	18512000	0.7
CFN*AMEVDALN*S SHPVSTPVENPAQIR	198.05	164.43	526160000	105330000	5.0
CGNCN*LTSLEDEDF CK	140.74	109.35	134080000	74965000	1.8
CHEGN*GTFECGAC R	200.9	116.98	261290000	27873000	9.4
CLQMSSFAN*R	192.92	168.83	433730000	135010000	3.2
CN*ASSQFLCSSGR	169.09	156.08	136590000	69337000	2.0
CVAN*YTGN*GR	129.85	94.409	34255000	23555000	1.5
CVVHYEN*STVPEK K	183.81	151.54	937550000	172700000	5.4
CVYEALCSN*VTSEC PPPVITR	91.725	81.016	38970000	14728000	2.6
CWAPILDN*DTASD N*GSR	218.28	111.92	317270000	24023000	13.2
CWAPILDN*DTASD N*GSR	218.28	251.13	317270000	155480000 0	0.2
DAMVGN*YTCEVTE LSR	150.76	186.77	415510000	486520000	0.9
DATIQAYLSSGN*FS K	89.541	62.861	12819000	10452000	1.2
DCVSCQN*VSR	176.6	155.06	2067000000	739300000	2.8
DCDFLEDGEERN*C TGK	81.656	70.197	31431000	12385000	2.5
DFVN*ASSK	100.02	69.598	68455000	4853200	14.1
DGGSTTAGN*SSQV SDGAAAVLLAR	132.65	189.07	156810000	660760000	0.2
DGQQN*ISLLYTEPG ASQTQTGASFR	198.55	166.65	172890000	166850000	1.0
DGSCIGN*SSR	194.06	85.622	116690000	34032000	3.4
DGTSQPAICPQN*VT MNMEGLK	166.29	92.289	742350000	100210000	7.4
DGTVTAGN*ASGVS DGAGAVIIASEDAVK K	169.57	230.8	228690000	212340000 0	0.1
DIILHSTGHN*ISR	127.02	78.763	79124000	5695400	13.9
DKN*GTRAEPPLN*A SAGDQEEK	174.81	96.591	4259600000	33302000	127. 9

DKN*GTRAEPPLN*A SAGDQEEK	174.81	228.46	169940000	104320000 0	0.2
DLAVGDDYTN*R _DLGPALAN*SSH DV K_	152.54	208.6	119010000	96078000	1.2
DLLFSDDTECL SNLQ N*K	128.22	127.36	1469000000	106870000	13.7
DLQNFLN*VTSS VD VK	138.39	218.4	204300000	294160000	0.7
_DN*ATQEEILH YLEK _	121.19	113.29	138190000	48721000	2.8
DN*DSLITRK _DNVN*CSGVYE HEP LEIGK_	133.25	120.32	1056200000	185220000	5.7
DSVIN*LSESV EDGP R	166.16	148.52	278150000	51637000	5.4
DSYPDGN*ITW YRN *GK	59.579	37.477	14350000	3577100	4.0
DTLSIN*ATNIK _DTTGSHTFQGM FGC EITNN*R_	127.32	144.8	56682000	35977000	1.6
DVGSGTTN*N* SQA CAQFLEQYFHN* SDL TEFMR	150.09	118.77	337610000	402350000	0.8
DYRPSAGN*N* SLY QDTVVK	268.73	163.66	571690000	244500000	2.3
DYYLN*KTENEK _DYYPIN*ESL ASLPL R_	188.1	76.704	156300000	16267000	9.6
EAFN*ETNQAI QTIS R	255.7	200.47	962660000	165520000	5.8
EALNQAVN*TTR _EAQYN*STFR_ _EASN*HSSGAG LVQI NK_	174.02	156.15	1092300000	440560000	2.5
EATIVGEN*ET YPR _EEQFN*STFR_ _EGASEEETN* LSK_ _EGICN*GFTAL CPAS DPKPN*FTDCNR_ _EGLALIN*GTQ MITS LGCEALER_ _EGN*CSAQSG LAWQ	248.05	240.21	560470000	135800000	4.1
216.46	238.47	199350000	144200000	1.4	
194.43	145.41	292930000	42099000	7.0	
183.47	160.59	342970000	92633000	3.7	
267.34	252.73	1270800000	294090000	4.3	
188.91	179.67	934150000	452610000	2.1	
243.03	186.16	2319300000	110880000 0	2.1	
93.011	64.65	53183000	16179000	3.3	
88.79	77.641	20682000	32236000	0.6	
137.09	62.611	88820000	6740000	13.2	
188.48	136.91	909880000	123720000	7.4	

DCDFKDAEEAATGEC					
TATVGKR_					
EGN*FTSTFDKK	107.85	58.754	61916000	19391000	3.2
EILVHPN*YTR	112.36	136.63	213630000	31542000	6.8
ELGAIYN*CSNLAQ DLEK	105.9	96.544	26586000	17692000	1.5
ELLVDELLSN*SSTL ASYK	86.479	61.815	18010000	8571500	2.1
_ELN*ISICPVSQTSER _	177.84	185.12	440990000	224570000	2.0
EN*ISDPTSPLRR	157.42	97.734	378920000	78389000	4.8
EN*MTFGSTLV TNP K	83.692	59.709	104020000	5615500	18.5
EQN*YTCR	150.02	135.35	103170000	24934000	4.1
EQVTVIN*R	159.04	179.73	134480000	33517000	4.0
ESGIQN*VSTCR	252.42	237.93	4766900000	163610000 0	2.9
ESN*STSLTQAALLE K	99.566	166.6	269800000	182590000	1.5
ESQTIGDQCVYN*ST HLGFQR	116.82	82.367	311380000	98906000	3.1
ETLVTLFDN*R	144.65	148.32	15706000	31629000	0.5
EVN*SQLDN*N*GCS TQEVN*ITELQSK	220.48	105.31	1448500000	31184000	46.5
EVN*SQLDN*N*GCS TQEVN*ITELQSK	220.48	66.383	1505000000	91700000	16.4
EYEGAVYPD N*TTD FQR	202.4	209.39	924170000	601050000	1.5
FCNIVPTEHCFLGN* GTEYR	106.16	115.15	46343000	11161000	4.2
FFN*FSWR	162.51	132.09	104790000	9062800	11.6
FGTCSQLCN*N*TK	245.58	244.95	1437200000	406560000	3.5
FIN*YN*QTVSR	175.93	198.61	1512000000	768670000	2.0
FQISPQLQFSPEEVL GMVLN*YSR	290.71	237.01	482460000	346070000	1.4
FQLLN*FSSSELK	103.88	132.59	496130000	175590000	2.8
FQN*FSMATDQR	144.17	116.55	178340000	21188000	8.4
FSDGLESN*R	182.98	182.98	642390000	106440000	6.0
FSGAN*DTDFR	119.53	131.09	54521000	38483000	1.4
FSTELGYN*GTR	150.04	104.07	187820000	31188000	6.0
FTAPDTLFAN*GSVY PPNEGFCPCR	180.13	172	1327300000	526510000	2.5
_FTCN*QTDTVIIH SK _	149.59	88.311	1290100000	127180000	10.1

FTFTHTPGDHQICL HSN*STR	256.13	72.644	2956100000	84093000	35.2
FTFTHTPGEHQICL HSN*STK	264.91	70.99	3745200000	11919000	314. 2
FVN*STGYLTEAEK _GAGEVSPAEHSSKPT N*ISAK_	96.734	84.566	85767000	15052000	5.7
GATN*NTCIIR _GCIWEASN*TTR_ _GDHGAN*FSCR_ _GDPSIISVN*GTDFTF R_	141.12	56.533	551220000	13716000	40.2
GDTHTQILEGLQFN* LTQTSEADIHK	176.38	178.22	93346000	40669000	2.3
GECYYTN*GTQR _GELQSEN*SSLTLSSS NR_	124.67	117.14	94219000	44794000	2.1
GHVDPAN*DTFDIDP R	88.056	48.004	45505000	3532400	12.9
GIAN*LSNFIR _GLN*LTEDTYKPR_ _GLNCN*LSR_ _GLSPGN*YSVR_ _GN*ITEYQCHQYITK _	65.716	59.261	11295000	8424400	1.3
GN*TTAIDKEIAR	244.95	188.69	3037300000	102680000 0	3.0
GQTQN*YSTLLLEEA SER	124.67	96.113	128670000	36437000	3.5
GRADECALPYLGAT CYCDLFCN*R	196.64	205.68	180050000	104800000	1.7
GSEVEDEDLELFN*T SVQLRPPSTAPGPETA AFIER	97.417	68.044	69321000	2856100	24.3
GSN*FTAICVLK _GSPGN*ASQGSIH LH SPQLALQADPR_	198.58	183.47	8418700	6903900	1.2
GTDN*ITVR _GTTN*TTSAGVPCQ R_	183.08	184.88	555580000	142680000	3.9
GVDVSQVTWQSQG DTPCSCCIVN*N*SN* GSR	93.992	58.981	16322000	6600000	2.5
_GVDVSQVTWQSQG	159.79	159.79	63449000	10721000	5.9
	112.24	103.39	326500000	94638000	3.4
	206.1	222.25	4792600000	131960000 0	3.6
	141	106.93	27619000	40042000	0.7
	134.66	55.247	49564000	10988000	4.5
	260.66	147.5	103800000	5029000	20.6
	58.511	66.267	28787000	47847000	0.6
	79.395	66.853	1513000000	184310000	8.2
	137.9	71.379	24566000	3357100	7.3
	129.54	84.566	133140000	34828000	3.8
	108.57	66.383	39959000	91700000	0.4
	179.47	200.36	1001300000	185820000	5.4

DTPCSCCIVN*N*SN*					
GSR_					
_GVFITN*ETGQPLIG	86.944	94.728	399700000	91965000	4.3
K_					
_GVSSSEN*FTSPVME	219.97	139.04	473460000	46941000	10.1
FWER_					
GVTHLN*ISGLK	173.72	142.12	510070000	96531000	5.3
_GVVDSDDLPLN*VS	131.53	82.102	21100000	15970000	1.3
R_					
GWLN*GSLVGFYK	110.86	123.8	218960000	33464000	6.5
_GYLTSFEMFN*STFK	152.74	115.78	358740000	77351000	4.6
-					
_GYN*SSQDLPSLVLD	64.507	39.237	105410000	14876000	7.1
FK_					
HAN*WTLTPLK	166.97	196.48	788840000	223550000	3.5
HFN*DSGACVPR	96.113	45.829	20363000	5143800	4.0
_HLEN*ATASVSEAE	199.58	146.1	819420000	60209000	13.6
RK_					
HN*LTITQGK	187.99	117.67	205220000	44328000	4.6
_HNN*DTQHIWESDS	207.17	190.63	735930000	305950000	2.4
NEFSVIADPR_					
HYAN*ITN*GMYR	249.83	88.338	2889400000	185280000	15.6
IAN*ETGGHSGPR	147.33	122.45	438330000	80561000	5.4
_IAN*FSQSCTLYSGD	158.94	131.57	599300000	271330000	2.2
DLVEALPKPCPGCPR_					
_IAPASN*VSHTVVLR	239.58	239.58	13990000000	280130000	5.0
PLK_				0	
_IAQEGGAAALLIAN*	76.417	34.437	11868000	9527700	1.2
NSVLIPSSR_					
IASAVQKN*ATSTK	152.99	74.475	132290000	12954000	10.2
_IDCYPDEHGASEAN*	148.56	85.808	246490000	13604000	18.1
CSAR_					
IDSTGN*VTN*ELR	185.25	184.44	175640000	81734000	2.1
_IEAVLPAEFFEVLSSS	197.31	110.26	409340000	26957000	15.2
QN*GSYHHIR_					
IEGLTN*ETYR	161.17	188.04	249040000	148560000	1.7
IETILLN*GTDRK	164.64	179.67	156480000	63608000	2.5
IFIFN*QTGIEAK	105.25	82.362	103330000	18002000	5.7
_IGCFALSEPGN*GSD	43.803	61.583	19706000	23461000	0.8
AGAASTTAREEGDS					
WVLN*GTK_					
_IGCFALSEPGN*GSD	43.803	62.302	19706000	37672000	0.5
AGAASTTAREEGDS					
WVLN*GTK_					

IGPGEPLLELLCN*VS GALPPPGR	56.708	41.711	6366200	981190	6.5
IIDLIPDGYPQISCLP KEEN*ATIATYPEFGV LDLK	92.679	66.461	1827700000	109370000	16.7
IISPEEN*VTLTCTA ENQLER	246.68	207.82	1049000000	701030000	1.5
IISAN*GCKVDNSSL TGESEPQTR	60.939	103.27	30080000	25151000	1.2
ILCDNSDN*ITR	67.456	62.924	25445000	2553400	10.0
ILDIYHQEACN*GCII SVGGQIPN*N*LAVPL YKN*GVK	154.88	150.26	9973800000	430850000 0	2.3
ILN*ETLYENAK	147.62	119.27	135560000	67942000	2.0
IMESHPN*GTFSAK	174.37	59.185	1150000000	10119000	113. 6
IN*N*GGCQDLCLLT HQGHVN*CSCR	162.85	119.06	323960000	37965000	8.5
IN*TTSDEKDPTNPF R	160.27	82.908	60527000	17612000	3.4
IN*VSYTGERPSSN* MVIVDVK	152.09	64.723	2556800000	45345000	56.4
IN*YTCN*QGYR	161.63	180.8	1070000000	406820000	2.6
IQ*CVDGN*WTTLPV CIEER	165.71	181.4	146410000	89181000	1.6
ISASGAELEALEAQV LN*LSLK	120.56	71.535	201810000	4607700	43.8
ISWPSNVN*GSHR	145.28	62.924	68562000	2057300	33.3
ITDIEN*GTFANIPR	190.1	186.13	113310000	41894000	2.7
ITN*GTVGVR	131.06	135.79	198610000	53026000	3.7
ITVVYAEN*GTVLQ* GTTVASVYK	132.45	80.752	132970000	15896000	8.4
IVDVN*LTSEGK	162.26	162.26	1169000000	829420000	1.4
IVN*GTLTK	74.92	91.069	197600000	41161000	4.8
KEDSCQLN*YSEGPC LGMQER	231.93	169.25	322960000	29892000	10.8
KEN*SSEICSN*N*GE CVCGQCVCR	235.26	178.43	573840000	43163000	13.3
KEN*SSYQVINWR	164.9	166.97	920490000	213830000	4.3
KFPVPFQKEN*VTAT LVELGR	183.65	186.58	8822600000	558410000 0	1.6
KILASPN*EEN*MTE LISMR	228.39	225.67	1556600000	138680000	11.2
KLN*YTLK	150.88	128.61	364900000	39202000	9.3

KLNLDGSN*YTLLK	177.88	143.93	426660000	123610000	3.5
KN*ITDLVEGAK	112.02	63.602	63448000	13666000	4.6
KVPSN*STETVIESD QFQPGVR	121.63	123.83	159910000	78594000	2.0
LACLN*GTVLR	218.55	199.46	511840000	309040000	1.7
LAN*ISGEEQK	107.83	57.836	14584000	5618100	2.6
LAVTN*TTMTGTVL K	140.08	126.63	523980000	80620000	6.5
LDAPTNLQFVN*ET DR	209.39	224.34	1268600000	730480000	1.7
LDETDCLGN*WTW QEGSQQTLK	151.63	125.28	156730000	136190000	1.2
LDFIVLN*ETR	237.08	210.64	2784300000	730760000	3.8
LDLPVN*TSIPN*VTE IK	68.516	48.883	166990000	23144000	7.2
LDLPVN*TSIPN*VTE IK	67.283	290.5	91186000	934920000 0	0.0
LDN*YSTQELGR	162.72	115.29	317840000	100280000	3.2
LDPPCTN*TTAPSNY LNNPYVR	266.64	265.07	626170000	537690000	1.2
LDWLGN*CSGLNDD SYGYR	287.55	224.86	2103200000	346450000	6.1
LEN*LSSTESGYTAT LTR	134.93	149.09	151200000	84605000	1.8
LFQN*CELYK	87.298	87.298	101680000	51688000	2.0
LGACN*DTLK	82.749	108.43	774450000	257230000	3.0
LGAIN*STLSN*ESK	153.39	165.45	301950000	207690000	1.5
LGAIN*STLSNESK	153.39	119.01	376640000	99492000	3.8
_LGALN*NSLLLLLEDR _	211.06	161.63	231060000	56324000	4.1
LGGWN*ITGPWAK	97.779	126.48	240110000	60656000	4.0
LGN*ETLQR	152.63	153.04	131870000	36679000	3.6
LGVIEDHSN*R	123.63	67.726	7352400	6972000	1.1
LHVAQPEN*DSHVA LLK	103.88	63.128	494990000	27614000	17.9
LIASN*ITETMR	152.69	144.17	738700000	308740000	2.4
LLEFDSTN*ASEGAQ *PPGKPYPPYSLAK	75.226	90.633	91003000	60146000	1.5
LLLTAAPN*LTTSPA FR	143.93	125.73	342610000	101810000	3.4
LLN*QTLR	191.03	175.75	1020800000	225730000	4.5
LLPAFN*TTSGLPYP R	127.76	92.939	26987000	15181000	1.8
_LLQQSN*QSSQFLH	165.45	93.152	98807000	8295000	11.9

SVER_					
_LLQVVYLHSN*N*IT	85.287	91.207	69384000	32735000	2.1
K_					
_LMNAPLYLAEWQN*	87.647	57.52	130700000	5916700	22.1
ITK_					
LN*ASIADLQSK	160.86	149.41	33540000	53250000	0.6
LN*FTGPGEPDSLR	60.364	91.62	14463000	9294000	1.6
_LN*GTDPIVAADSKR	220.97	161.21	1758300000	189420000	9.3
-					
LN*LSEGEVAATVK	89.46	65.805	31723000	18158000	1.7
_LN*LTAFAQLSQLEGL	209.31	123.14	173080000	46910000	3.7
LQAR_					
LN*LTEEEK	157.86	157.86	709330000	168360000	4.2
LN*LTTDPK	111.95	114.89	125890000	44217000	2.8
_LN*MTLPDALVPTFS	135.26	74.338	3556100000	71183000	50.0
ISN*HSLK_					
_LN*MTLPDALVPTFS	135.26	87.963	3514600000	214400000	16.4
ISN*HSLK_					
LN*N*SQIK	134.06	145.04	1072700000	128990000	8.3
LN*VTSPDLFR	171.85	118.4	40746000	32894000	1.2
_LPPLNIGEVLTLP	105.73	76.198	59902000	7040200	8.5
EA					
NFPSFSLPNCN*R_					
LQLLN*LSR	162.25	161.02	9406300	4502200	2.1
_LQTPLN*YTEFQKPI	85.231	47.485	68079000	51486000	1.3
CLPSK_					
LRN*ATITQALTNK	186.94	113.52	312270000	46921000	6.7
_LSALDN*LLN*HSSIF	224.64	67.648	1725300000	38396000	44.9
LK_					
LSQALGN*ITVVQK	77.527	63.185	111720000	40713000	2.7
LSSPN*VTISCK	127.56	100.55	449730000	116850000	3.8
LTEFTHN*STMDYK	179.46	88.101	382060000	16911000	22.6
_LTGSAGN*YTVCQK	99.531	68.809	51113000	7056500	7.2
-					
_LTSCATN*ASMCGD	234.22	172.91	1372400000	509390000	2.7
EAR_					
LTVPSSQN*SSFR	164.9	174.84	180740000	72539000	2.5
_LTWSN*AN*GTASY	182.23	80.96	58729000	14652000	4.0
R_					
LTYN*ESR	160.03	145.04	1484900000	243870000	6.1
LVTQTIPCN*K	132.88	140.16	1311200000	381620000	3.4
_LWDPSSHPGIQN*IS	155.98	180.48	417960000	174780000	2.4
R_					
_LWLPVN*LTWADLE	241.93	79.97	1304900000	23188000	56.3
DKDGR_					

LYWISSGN*HTINR	203.11	125.82	883700000	129570000	6.8
_MALLQYGSQN*QQQ					
VAFPLTYN*VTIHEA	156.72	68.516	419820000	10407000	40.3
LER_					
MFSQN*DTR	138.54	88.921	116190000	27009000	4.3
MIEN*GSLFLPTLR	156.24	169.04	895660000	193610000	4.6
				213980000	
MTLSQN*N*SILR	219.03	245.76	6206000000	0	2.9
N*ATLVN*EADKLR	218.75	102.97	552660000	32248000	17.1
_N*ATSYPPMCFQDP					
VTGQIVNDLLTNRK_	182.39	100.88	336750000	32119000	10.5
_N*ATTYPPMCSQDA					
AR_	181.71	113.4	3489100000	274260000	12.7
N*CSTQHFPR	162.88	54.982	115560000	3061100	37.8
_N*ETHSICSACDESC					
K_	137.19	80.632	129070000	7860700	16.4
N*GN*MSGISDQR	97.734	52.693	3322200	5888200	0.6
_N*LIN*DYVSN*QTQ				356650000	
GMIK_	206.2	226.19	7336600000	0	2.1
_N*LTSPVGVQPILNE					
HTFCAGLTK_	115.36	107.74	473620000	287170000	1.6
N*MTLFSDLVAEK	125.54	94.122	314550000	71003000	4.4
N*MVLQN*GTK	128.6	98.048	1614900000	301100000	5.4
_N*PCNITREDYAPLV					
K_	86.539	74.678	25906000	5251300	4.9
N*QTLQEGEK	161.63	73.985	125280000	3909700	32.0
N*SSITLPADSR	126.71	61.375	52917000	6327300	8.4
N*STIQAANLAGLK	311.76	62.088	232890000	58893000	4.0
N*STLCDLCIGPLK	182.53	230.91	3453400000	839710000	4.1
N*TTHLLQR	141.2	121.05	118640000	18166000	6.5
N*TTISVHPSTR	138.99	69.451	73300000	1997800	36.7
_N*VALVAGDTGN*A					
TGLGEQGPTR_	215.98	169.84	150320000	107090000	1.4
_N*VTYGTYLDDPDP					
DDGFNYK_	115.32	89.846	131710000	16755000	7.9
N*YN*FTLACNTK	201.48	186.74	1672000000	805840000	2.1
_NAN*CSTVSPGQTQ					
CTCQK_	138.91	47.082	113260000	7025200	16.1
_NAVN*CTYKNEDDC					
VVR_	179.39	78.326	178960000	19322000	9.3
NIGN*TSEGPR	185.6	135.86	130610000	31033000	4.2
NILPN*ITTSYLK	81.431	83.617	190060000	130720000	1.5
_NIN*SSCRPHPGAWL					
R_	180.95	102.5	2068800000	74657000	27.7

NIQAVNEIATLSQC N*DTSSAAMVQCLR	254.25	93.397	1472900000	57307000	25.7
NLFLN*HSETASAK	162.94	207.04	2245000000	642320000	3.5
NLN*YTER	157.9	127.84	98397000	17938000	5.5
NPCN*ITR	161.48	111.65	888420000	135750000	6.5
NPN*GTVTVISR	124.42	98.156	187790000	32756000	5.7
NPN*N*NTIHPNLR	240.41	184.03	2456600000	462220000	5.3
NTN*SSN*N*LTR	200.71	167.09	101580000	85417000	1.2
NTN*SSNN*LTR	200.71	167.09	101580000	85417000	1.2
NTQADVIN*ASWSV LSN*STR	163.45	109.28	157520000	49215000	3.2
NTQADVIN*ASWSV LSN*STR	163.45	109.28	157520000	57351000	2.7
NVN*ISYIVN*DSFFP QRPEK	158.98	226.65	243930000	923590000	0.3
NVN*ISYIVNDSFFP QRPEK	307.02	185.33	3838800000	154680000	24.8
NVN*ISYTVN*DSFF PQRPOK	207.53	231.91	1626900000	844620000	1.9
NYTAN*ATSSR	171.68	101.38	89044000	8993100	9.9
QELN*DSLQVAER	203.11	224.24	598260000	281660000	2.1
QELSQDN*ATLK	139.32	116.84	39600000	57171000	0.7
QFWIFDVQNPDDVA KN*SSK	172.66	132.62	179440000	62498000	2.9
QGN*YSAGLPR	111.06	70.977	39134000	16166000	2.4
QIN*ITCDNPVDR	149.23	71.268	76320000	11791000	6.5
QLFFN*GTETLR	104.07	81.525	154470000	83088000	1.9
QLLAN*SSALEETIL GHQGR	117.67	61.648	129940000	6192000	21.0
QN*FSN*LTVSTEDQ VK	196.67	191.57	2682000000	106010000 0	2.5
QN*FSN*LTVSTEDQ VK	196.67	191.57	2682000000	106010000 0	2.5
QN*GTDNSPSQR	86.313	66.262	11216000	980660	11.4
QN*TTWQAGR	84.615	65.347	22679000	7061000	3.2
QPNMN*LTQLK	77.379	45.307	218040000	55532000	3.9
QRYN*LTAK	133.57	149.57	559290000	48138000	11.6
QSLNTVN*DTVWK	109.96	64.224	63920000	49666000	1.3
QSN*GSIAVISSLAG K	134.25	158.89	10676000000	891690000 0	1.2
_QTGDVTCN*CTDGR	200.98	185.9	751340000	249670000	3.0
QTQVGIVQYGAN*V THEFNLNK	87.554	90.765	286610000	92383000	3.1

QVSTLIN*NTDK	171.92	171.62	490130000	194780000	2.5
RGPECSQN*YTAPTG VIK	113.33	69.935	74499000	15867000	4.7
RGTFTDCALAN*MT QQIR	285.06	178.68	1907500000	510090000	3.7
RIPAIN*R	143.02	80.462	48311000	2433400	19.9
RN*FTAADWGHRSR	190.57	65.043	708930000	12066000	58.8
RN*WTETEV	222.3	121.36	346860000	44737000	7.8
RN*WTINR	182.68	155.75	306110000	41995000	7.3
RPFVGVYEMEVDTL ETTCHALDPTPLAN* CSVR	239.24	130.41	676330000	43284000	15.6
SAEGTFFIN*K	78.655	90.108	121690000	95559000	1.3
SCIN*ESAIDSR	138.75	148.28	156010000	73996000	2.1
SCVAITDAFPQN*MS R	179.39	113.59	257140000	72463000	3.5
_SDIN*CSVMEATEEK _	166.38	111.74	78315000	38853000	2.0
SDLNPAN*GSYPFQA LHQR	174.95	103.04	273960000	10522000	26.0
_SFDCCGLFN*LTTLR _	157.22	82.069	265910000	3522000	75.5
SGQEDHYWLDVEK N*QSAK	212.21	100.67	2162200000	178220000	12.1
SLGEVN*FTATAEAL QSPCLCGNK	257.22	168.78	451110000	176960000	2.5
SLGQFLSTEN*ATIK	50.158	86.413	27801000	36352000	0.8
SLN*CTVK	122.74	127.12	337170000	34047000	9.9
_SLPVN*DSVLDVFER _	104.17	37.77	38743000	4176900	9.3
SLTQGSIVGNLAPV N*GTSQ GK	168.3	184.35	1109100000	562170000	2.0
SN*DSVLEPANR	176.42	199.09	157670000	54928000	2.9
SN*ISILR	163.62	152.47	481090000	130100000	3.7
SN*VTRPSEFNWI APIPFLK	74.048	49.089	33724000	11745000	2.9
SPGAQDN*VSVSQG MR	332.06	132.84	1018900000	171590000	5.9
SQLTISNLDVN*VDP GTIVCN*ATN*AQGT TR	189.78	200.13	476980000	195210000	2.4
_SSAN*QSEFQQIQK _	213.82	234.52	418120000	147040000	2.8
_SSHLPPSSYFN*AS	227.47	207.31	737960000	393860000	1.9

GR_					
_SSTEN* TSAELHVLG	157.75	111.74	264030000	12753000	20.7
R_					
_SVLEN* TTSYEEAKN	146.5	136.2	1164100000	485280000	2.4
TLTK_					
_SVYN* CSGEACSGH	249.66	131.35	429230000	63156000	6.8
NR_					
_SWSTVGN* CTAALR	185.25	162.49	2710400000	125710000	2.2
-				0	
_SYIFIYDGN* KN* STT	195.56	264.31	572140000	214890000	0.3
TDQN* FTSAK_				0	
_TAADATGLQPILNQF	173.77	178.32	181340000	23764000	7.6
TPAN* VSR_					
_TAASILWQAYPILN*	128.69	124.99	228200000	103310000	2.2
ISEK_					
_TAGAN* GTSGFFCV	210.98	164.98	388040000	267090000	1.5
DEGLPLAQR_					
_TALWVATDHNTDN*	214.52	58.49	120610000	41944000	2.9
TSAILR_					
TASVSIN* QTEPPK	161.1	57.804	30335000	10607000	2.9
_TCPAGIMGEN* NTL	109.48	94.007	802870000	269580000	3.0
VWK_					
_TCPLDEFQCN* NTLC	51.819	80.316	62221000	53745000	1.2
KPLAWK_					
_TCVSN* CTASQFVC	116.84	113.72	265280000	165200000	1.6
K_					
_TDAELN* ETARPLSP	141.6	48.288	102260000	10633000	9.6
VNPK_					
_TDDEVVQREEEAIQ	410.11	207.86	2138600000	578520000	3.7
LDGLN* ASQIR_					
_TEKDPQNDPVGTCY	188.44	204.21	737380000	270570000	2.7
LSTEN* FTR_					
_TELDLRPQ* GLALFS	176.73	134.29	138820000	47314000	2.9
N* VSEAR_					
TEQIPVN* K	81.296	54.776	24431000	5946500	4.1
_TIEQERN* ASFVYTK	194.01	222.45	1607700000	639060000	2.5
-					
_TILVDN* NTWN* NT	249.66	202.13	987520000	477880000	2.1
HISR_					
_TILVDNNTWN* NTHI	258.91	309.83	7398600000	850970000	8.7
SR_					
_TLAGEN* QTALEIEE	189.31	124.92	28660000	6780100	4.2
LNR_					
_TLTLLN* VTRN* DTG	447.02	165.9	3334100000	475090000	7.0

PYVCETR_					
_TLTLLN*VTRN*DTG	447.02	309.83	2439800000	143400000	1.7
PYVCETR_				0	
_TMVFPVMYLN*ESV	256.07	82.477	1171900000	27942000	41.9
LIDKETANQLK_					
_TN*QSAELIQPVATN	148.33	82.449	81172000	17413000	4.7
*GK_					
_TN*QSCSELVIDSTEK	192.24	155.09	482630000	102510000	4.7
-					
TN*STQVSDVR	156.48	97.734	53944000	38156000	1.4
_TN*TTQDEQHQWTS	119.23	56.424	23883000	10681000	2.2
CDQQEK_					
TPMTN*SSIR	155.42	110.88	133210000	13033000	10.2
_TQ*LTCSLN*SSGVD	296.72	306.77	8729900000	186150000	4.7
IVGHR_				0	
TQN*GSLPAVTR	151.79	144.7	170360000	68877000	2.5
_TSDTGEEEAITN*ST				293170000	
EAN*GKYVVVSTPEK	290.2	322.93	6036500000	0	2.1
-					
_TTLVDN*N*TWN*N	103.5	128.06	142540000	50640000	2.8
SHIALVGK_					
_TVAN*LSGCEATDSE	393.04	406.73	17195000000	818870000	2.1
ALIHCLR_				0	
_TVN*SLN*VSAISIPE	143.67	123.14	182750000	53394000	3.4
HDEADDISDENR_					
TVVVDN*ETVATR	88.021	56.122	49560000	12229000	4.1
_TYCANEPSLN*CSQV	151.8	128.06	97094000	50640000	1.9
N*R_					
_TYCANEPSLN*CSQV	151.8	91.114	97094000	127690000	0.8
N*R_					
TYEN*GSSVEYR	167.12	107.85	49262000	99360000	0.5
_VAGLLVLN*YSN*D	43.115	80.238	10585000	12400000	0.9
YNHWLATAK_					
VDCTANTN*TCNK	229.64	143.79	290110000	16554000	17.5
_VDIPQQPMGIIAVAN	127.14	50.498	77436000	66076000	1.2
*DTN*SCELSPCR_					
_VDLEDFEN*NTAYAK	161.63	176.91	389240000	592440000	0.7
K_					
VETGEN*CTSPAPK	130.1	131.13	295800000	39275000	7.5
-					
VFGSQN*LTTVK	139.86	124.1	4348000000	204730000	2.1
				0	
VFN*GKDN*ISK	112.89	104.43	279030000	64908000	4.3
VGCSEYTN*R	201.58	191.85	502360000	166400000	3.0
VGLVITYSN*ETR	137.89	113.67	200490000	75310000	2.7

VIDLWDLAQSAN*F TEK	122.93	56.407	135460000	12128000	11.2
VILILDPAISGN*ETE PYPAFTR	158.74	106.03	112000000	18318000	6.1
VIN*DTWAWKN*AT LAEQAK	169.44	124.23	385560000	184680000	2.1
VIN*DTWAWKN*AT LAEQAK	120.99	112.8	631160000	246210000	2.6
VISN*N*CTSYGVLD IGK	84.874	82.586	55884000	24398000	2.3
VISN*N*CTSYGVLD IGK	116.35	106.19	188410000	123710000	1.5
VIYN*LTEK	117.04	131.06	537030000	117470000	4.6
VLN*ADQGTSATVQ MLLN*DTCPLFVR	240.31	160.57	611480000	65487000	9.3
VLN*LTDNTYFK	94.767	89.403	153300000	26813000	5.7
VLN*N*ITNDLR	185.6	194.06	236740000	131570000	1.8
VLPFN*VTDYCQLV R	93.348	101.32	50345000	85099000	0.6
VLQVVN*VTK	81.099	90.108	268380000	101320000	2.6
VLTNQESPYQN*HT GR	169.04	164.68	178610000	50727000	3.5
_VLVAPPSEEAN*TTK _	134.61	143.94	1448200000	287570000	5.0
VLYLPAYN*CTLRP VSK	197.49	42.947	200810000	20299000	9.9
VN*GTLTQVLLVGA PTHDDVSK	102.24	34.217	119120000	54190000	2.2
VN*ITVLPSLTSR	140.45	127.56	163940000	146950000	1.1
VN*KTEEDYAR	156.48	142.71	1100900000	184840000	6.0
VN*LSFPSAQLPAS DTHLK	146.06	120.11	2173200000	714800000	3.0
VN*SSLHSQISR	229.95	142.19	388440000	55069000	7.1
VN*YTEVSR	131.06	111.95	60530000	10547000	5.7
_VNDN*KTAAEEALR _	146.5	109.22	141480000	19988000	7.1
VNRFN*STEYQVVT R	263.15	235.88	1239500000	653880000	1.9
VNYEGGTWDWIAE ALSSN*HTR	171.85	54.672	596410000	5419700	110. 0
VPFIFNINPATTN*FT GSCQPQSAQLR	179.42	109.56	66011000	57505000	1.1
VQPFN*VTK	71.692	80.684	1709300000	529690000	3.2
_VQSLQTLAAN*NSA	104.45	74.786	19181000	33907000	0.6

LAK_					
VSLTN*VSISEGR	193.28	192.15	843800000	487260000	1.7
_VSQVLHEGGHN*VT	203.05	144.73	1289900000	42884000	30.1
K_					
_VSTLYAN*N*GSVL	156.29	100.94	411360000	124860000	3.3
QGSTVASVYHK_					
_VTINNWVAN*KTEG	178.58	149.32	927880000	140610000	6.6
R_					
_VTNSNANAAGPLIV	130.65	59.539	71447000	102050000	0.7
AGYN*VSGSVR_					
VTPVCN*ASLPAQR	109.15	67.275	45342000	16869000	2.7
_VVDKGN*GSKPTSP	112.74	84.653	346620000	20341000	17.0
EEVK_					
_VVELLADIVQN*SSL	126.61	84.762	58354000	19215000	3.0
EDSQIEKER_					
_VVFLSPAVPEEPEAY	111.82	58.479	159600000	9491200	16.8
N*LTVLIR_					
_VVLHPN*HSVVDIGL	207.79	154.88	3676800000	304780000	12.1
IK_					
_VVN*VSELYGTPCT	131.66	170.52	155700000	128130000	1.2
K_					
VVTPEEYFN*VTLQ	42.629	46.985	50640000	47784000	1.1
VWDTAAALN*R	103.7	79.974	8681200	7302700	1.2
_VYGGIVN*QSEINEG	139.88	70.802	53293000	18400000	2.9
TAFFR_					
VYN*GSVPFEER	155.26	98.156	465700000	123930000	3.8
_VYTYADTPNDFQLS	98.703	92.792	235290000	138130000	1.7
N*FSLPEEDTK_					
VYVYAVN*QTR	166.34	159.4	108710000	81255000	1.3
WDPEPN*CTSK	78.653	69.721	255080000	75667000	3.4
_WLCDGDN*DCGN*S	238.56	104.63	547670000	51108000	10.7
EDESN*ATCSAR_					
_WLCDGDN*DCGN*S	114.46	163.85	34321000	273040000	0.1
EDESN*ATCSAR_					
WLN*ETQLK	82.426	82.452	87233000	25552000	3.4
_WTDNTEYN*NTIPIR	190.82	133.71	444390000	115470000	3.8
GEER_					
WTGHN*VTVVQR	199.82	191.33	963290000	121480000	7.9
_YATEN*DISSLHN*S	208.3	201.88	3646700000	435530000	8.4
TLTCLVN*QTSLTGT					
SPEIMEK_					
_YATEN*DISSLHN*S	208.3	201.88	4383900000	460220000	9.5
TLTCLVN*QTSLTGT					
SPEIMEK_					

YEQLQN*ETR	179.8	185.6	558890000	150670000	3.7
YEVDWN*QSTLDCV DPLSSLAAN*R	214.27	85.932	405190000	16743000	24.2
YEVDWN*QSTLDCV DPLSSLAAN*R	214.27	85.932	334400000	21057000	15.9
YFAN*CTVR	159.04	133.55	146900000	42892000	3.4
YGKN*DSLTLTQLK	136.17	170.74	830780000	135070000	6.2
YGPQCN*R	111.69	86.113	37456000	4730600	7.9
YLELGN*ETLLR	255.24	176.48	1463300000	491720000	3.0
YLKN*GN*ATLLR	160.75	176.95	2684400000	684420000	3.9
YLN*ETQQLTQK	192.5	199.68	8763500000	390480000 0	2.2
YLQPLLAVQFTN*LT VDTEIR	191.61	155.49	418090000	142670000	2.9
YPAEGQRPIPN*VSL PLR	145.1	74.12	97039000	5097700	19.0
YPQDYQFYIQN*FTA LPLNTVVPPQR	172.3	161.04	1483100000	254920000	5.8
YPTPGEAPGVVGNF N*K	151.22	136.17	195900000	62156000	3.2
YQTVDSSNIDGFVN* CTK	88.551	77.39	17651000	7340400	2.4
YTGN*ASALLILPDQ GR	187.75	169.15	3841300000	312540000 0	1.2
YTSFEYPKN*ISFAC NPGFFLN*GTSSSK	91.618	58.877	249860000	13440000	18.6
YTSFEYPKN*ISFAC NPGFFLN*GTSSSK	91.618	58.877	249860000	32765000	7.6
YVQN*GTYTAK	115.78	115.78	296700000	122970000	2.4