spot id.	protein short name	protein full name	prot acc N° (uniprot)	Mw	unique peptides	sequence coverage	peptides identified (truncated)
protein quality control & degradation (q)							
q1a	psb3 ac.	Proteasome beta 3 subunit	Q9R1P1	22966	8	51%	DAVSGMGVIVHVIEK - FGIQAQMVTTDFQK - FGPY
q1b	psb3 bas	Proteasome beta 3 subunit	Q9R1P1	22966	8	50%	DAVSGMGVIVHVIEKDK - FGIQAQMVTTDFQK - FG
q2a	sae1 ac	SUMO-activating enzyme subunit 1	Q9R1T2	38620	2	7%	AQNLNPMVDVK - VSQGVEDGPEAK
q2b	sae1 bas	SUMO-activating enzyme subunit 1	Q9R1T2	38620	16	60%	AQNLNPMVDVK - DPPHNNFFFFDGMK - EALEVDW
q3	psd13	Proteasome regulatory subunit 13	Q9WVJ2	42810	18	57%	CAWGQQPDLAANEAQLLR - DLPVSEQQER - DVPA
q4	brcc3	Lys63-deubiquitinase brcc36	P46737	36151	3	13%	FTYTGTEMR - VCLESAVELPK - VEISPEQLSAASTE
q5	ube2n	Ubiquitin conjugating enzyme 2N	P61088	17139	9	72%	ICLDILK - ICLDILKDK - LELFLPEEYPMAAPK - LLA
q6	psd10	Proteasome regulatory subunit 10	Q9Z2X2	25084	10	52%	ASTNIQDTEGNTPLHLACDEER - DHYDATAMHR - F
q7	psmd8	Proteasome regulatory subunit 8	Q9CX56	39932	5	20%	GWVLGPNNYYSFASQQQKPEDSTIPSTELAK - HPVS
q8	psme2	Proteasome activator complex subunit 2	P97372	27058	16	72%	AFYAELYHIISSNLEK - ALVHERDEAAYGALR - AMV
q9	prs7	Proteasome regulatory subunit 7	P46471	48636	21	51%	ACLIFFDEIDAIGGAR - ALDEGDIALLK - EVVETPLL
q10	psb4	Proteasome beta 4 subunit	P99026	29117	8	49%	AIHSWLTR - FDGGVVIAADMLGSYGSLAR - FQIAT
protein production & folding (f)							
f1	if2b	Translation initiation factor 2 subunit 2	Q99L45	38093	27	75%	CSVASIK - DASDDLDDLNFFNQK - DDGISFSSQTAW
f2	dnjc9	DnaJ homolog subfamily C member 9	Q91WN1	30042	3	9%	GSEEELNDIK - ELGLEEGVDNLK
				30060	4	15%	ELGLEEGVDNLK - GSEEELNDIK - ISLEDIQAFEK -
f3	tcpz	T-complex protein 1 subunit zeta	P80317	57958	10	23%	ALQFLEQVK - AQAALAVNISAAR - AQLGVQAFAD
f4	ppie	Peptidyl-prolyl cis-trans isomerase E	Q9QZH3	33450	6	24%	EEEGPEPPK - EEEGPEPPKAEAQEGEPTAK - HVVFG
f5a*	hyou1 ac	Hypoxia up-regulated protein 1	Q9JKR6	111183	28	36%	AANSLEAFIFETQDK - AEPPLNASAGDQEEK - AHF
f5b	hyou1 med	Hypoxia up-regulated protein 1	Q9JKR6	111 183,1	36	47%	AANSLEAFIFETQDK - AEPPLNASAGDQEEK - AHF
f5c	hyou1 bas	Hypoxia up-regulated protein 1	Q9JKR6	111 183,1	30	42%	AANSLEAFIFETQDK - AEPPLNASAGDQEEK - AHF
homeostasis (h)							
h1	frih	Ferritin heavy chain	P09528	21067	6	36%	ELGDHVTNLR - IFLQDIK - MGAPEAGMAEYLFDK -
h2*	fril	Ferritin light chain	P29391	20803	4	27%	ALFQDVQKPSQDEWGK - LLEFQNDR - MGNHLTNL
h3a	blvra ac	Biliverdin reductase A	Q9CY64	33525	13	51%	DLKDPHSSAFLNLIGYVSR - ELGSLDNVR - FGFPAF
h3b*	blvra bas	Biliverdin reductase A	Q9CY64	33525	14	59%	DLKDPHSSAFLNLIGYVSR - ELGSLDNVR - FGFPAF
h4	blvrb	Biliverdin reductase B	Q923D2	22197	5	31%	IAIFGATGR - LPSEGPQPAHVVVGDVR - LQDVTDD
h5	nmrl1	NmrA-like family domain-containing protein 1	Q8K2T1	34377	16	57%	ALLEDGTFR - AQTLDQWLEQHK - DIGVPMTSVR -
h6	pddc1	Parkinson disease 7 domain-containing protein 1	Q8BFQ8	23278	3	19%	LESIDGAR - LPLIVEDFVK - YHALLIPSCPGALTDLA
h7	txd12	Thioredoxin domain-containing protein 12	Q9CQU0	19049	6	43%	DEDFSPDGGYIPR - EAAASGLPLMVIIHK - ILFLDPS
h8	prdx1ox	Peroxiredoxin 1, oxidized form	P35700	22263	2	11%	QITINDLPVGR - TIAQDYGVLK
				22160	3	18%	ADEGISFR - QITINDLPVGR - QGGLGPMNIPLISDPK
h9	lgul	Lactoylglutathione lyase	Q9CPU0	20811	9	54%	DFLLQQTMLR - FEELGVK - FSLYFLAYEDKNDIPK -
energy & lipid metabolism (e)							
e1a	idhc ac	Isocitrate dehydrogenase, cytoplasmic	O88844	46676	16	46%	ALEDVCIETIEAGFMTK - ATDFVVPGPGK - CATITP
e1b*	idhc bas	Isocitrate dehydrogenase, cytoplasmic	O88844	46676	13	37%	AKLDNNTELSFFAK - ALEDVCIETIEAGFMTK - CAT
e2	pfkal	6-phosphofructokinase, liver type	P12382	85361	24	40%	AIGVLTSGGDAQGMNAAVR - AMDEERFDEAIQLR -

e3a	galK ac	Galactose kinase	Q9R0N0	42295	13	33%	AFMEEFGAEPELAVSAPGR - GYALLIDCR - HSLGSS
e3b*	galK bas	Galactose kinase	Q9R0N0	42295	15	51%	AEHSFAGVPCGIMDQLIALLGQK - AFMEEFGAEPEL
e4	pipnb	Phosphatidylinositol transfer protein beta isoform	P53811	31487	7	31%	ELANTPDCPR - IFTNLHR - MEDETQKELETMR - ML
e5	fpps bas	Farnesyl pyrophosphate synthase	Q920E5	40583	11	30%	ALYEALDLQSAFFK - CSWLVVQCLLR - ELGHPEIGD
DNA metabolism and repair (d)							
d1a	pcna ac	Proliferating cell nuclear antigen	P17918	28786	13	66%	AEDNADTLALVFEAPNQEK - ATPLSPTVTLSMSADV
d1b	pcna bas	Proliferating cell nuclear antigen	P17918	28786	11	54%	AEDNADTLALVFEAPNQEK - ATPLSPTVTLSMSADV
d2	rfc2	Replication factor C subunit 2	Q9WUK4	38726	22	68%	ALLGPALKDAVLELNASNDR - DAVLELNASNDR - E
d3	dnph1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	Q80VJ3	18977	4	29%	EDQALYSR - FQVWDYAEEEVETMLHR - GGREDQA
d4	tatd3	Putative deoxyribonuclease TATDN3	Q3U1C6	32437	6	28%	DLDVALPIIEK - IMQLSER - LLAIGEVGLDFTPR - NE
d5	rfa2	Replication protein A 32 kDa subunit	Q62193	29718	2	9%	APTNIVYK - IGDVEISQVTIVGIIR
RNA and nucleotide metabolism (r)							
r1	tsnax	Translin-associated protein X	Q9QZE7	32927	5	20%	AVTTGLQEYVEAVSFQHFIK - DASLSSPVMLAFK - S
r2	sarnp	SAP domain-containing ribonucleoprotein	Q9D1J3	23533	5	28%	FGISSVPTK - FGIVTSSAGTGTTEDTEAK - FGLNVSS
r3	osgep	Probable tRNA N6-adenosine threonylcarbamoyltransferase	Q8BWU5	36301	8	31%	DGTVLANPR - EALIVGGVGCNLR - GAQLFATDER -
r4	bt3L4	Transcription factor BTF3 homolog 4	Q9CQH7	17315	4	23%	DDGTVIHFNNPK - KLAEQFPR - LAEQFPR - LAVNN
r5a	strap ac	Serine-threonine kinase receptor-associated protein	Q9Z1Z2	38443	16	65%	AATAAADFTAK - CVLPEEDSGELAKPK - EFLVAGG
r5b*	strap bas	Serine-threonine kinase receptor-associated protein	Q9Z1Z2	38443	20	70%	AATAAADFTAK - ALWCSDDK - ALWCSDDKQILSA
r6a	prps1 a	Ribose-phosphate pyrophosphokinase 1	Q9D7G0	34835	12	53%	ENISEWR - FSNQETCVEIGESVR - IFSGSSHQDLSQK
r6b	prps1 b	Ribose-phosphate pyrophosphokinase 1	Q9D7G0	34835	9	31%	FSNQETCVEIGESVR - IFSGSSHQDLSQK - INNACFE
r7	pihd1	PIH1 domain-containing protein 1	Q9WTM5	51114	13	34%	AAGVVLEMIR - ALESDMAPVLIMATNR - AVLIAGQ
r8	bpnt1	3'(2'),5'-bisphosphate nucleotidase 1	Q9Z0S1	33197	12	45%	ASAYVFASPGCK - CVIAEGDLGIVQK - HMNSAGVL
r9	adk	adenosine kinase	P55264	40150	2	7%	ELFDELVK - VFTLNLSAPFISQFFK
cytoskeleton (c)							
c1	caza2	F-actin-capping protein subunit alpha-2	P47754	32967	6	29%	DIQDSLTVSNEVQTAK - FTVTPSTTQVVGILK - IVEA
c2	rhoA	Transforming protein RhoA	Q9QUI0	21768	13	79%	DGVREVFEMATR - DLRNDEHTR - DQFPEVYVPTV
c3	rab14	Ras-related protein Rab-14	Q91V41	23898	16	82%	ADLEAQR - FMADCPHTIGVEFGTR - GAAGALMVY
c4	twf1	Twinfilin-1	Q91YR1	40081	18	53%	DAFQALEK - EDVSLHGYK - EDVSLHGYKK - EFGG
c5	cof1 1PO4	cofilin-1, monophosphorylated form	P18760	18560	8	57%	AVLFCLSEDKK - EILVGDVGQTVDDPYTTFVK - HE
c6a	lsp1 ac	Lymphocyte-specific protein 1	P19973	36714	8	38%	EEDEEEAAR - EPDPEDAVGGSGEAEEHLIR - LQQY
c6b	lsp1 bas	Lymphocyte-specific protein 1	P19973	36714	11	49%	CEEQEELHAEDSEGLTTQWR - EEDEEEAAR - EPDP
c7	twf2 ac	Twinfilin-2	Q9Z0P5	39472	20	63%	AVLPLLDAQEPCYLLFR - DDLSLAGYQK - DELFGT
c8	rras	Ras-related protein R-Ras	P10833	23764	9	52%	AGNGFLLVFAINDR - ICTVDGIPAR - KYQEQELPPSP
mitochondria (m)							
m1a	sucb2 ac	Succinate-CoA ligase [GDP-forming] subunit beta, mitochondrial	Q9Z2I8	46841	2	5%	AQILAGGR - LEGTNVQEAQNILK
m1b	sucb2 bas	Succinate-CoA ligase [GDP-forming] subunit beta, mitochondrial	Q9Z2I8	46841	8	24%	ETYLAILMDR - FFVANTAK - INFDDNAEFR - LEGT
m2	coq9	Ubiquinone biosynthesis protein COQ9, mitochondrial	Q8K1Z0	35083	2	6%	LNQVLEEEQK - LVQLGQAEK
m3	mtx2	Metaxin-2	O88441	29758	14	60%	AIGWGNK - AKGHSLSDGLDEVQK - ANAEYMSPSG
m4a	phb ac.	Prohibitin	P67778	29821	14	74%	AAELIANSLATAGDGLIELR - AATFGLILDDVSLTHL
m4b	phb	Prohibitin	P67778	29821	12	53%	AAIISAEGDSK - DLQNVNITLR - EFTEAVEAK - FDA
m5	eftu	Elongation factor Tu, mitochondrial	Q8BFR5	49509	10	25%	AEAGDNLGALVR - DLDKPFLLPVESVYSIPGR - EHL
m6	thtm	3-mercaptopyruvate sulfurtransferase	Q99J99	33023	5	24%	ALVSAQWVAEALK - AQPEHIISEGR - DGIEPGHIPGS

m7	htra2	Serine protease HTRA2, mitochondrial	Q9JIY5	49349	4	11%	AGLRPGDVILAIGEK - LAQNAEDVYEAVR - NSWFG
m8	hmgCL	Hydroxymethylglutaryl-CoA lyase, mitochondrial	P38060	34238	8	30%	EVSVFGAVSELFTR - FAGVMQAAQAASISVR - FPGI
m9	acadl	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	P51174	47909	16	37%	AFVDSCLQLHETK - AQDTAELFFEDVR - AQDTAEL
m10	vdac2	Voltage-dependent anion-selective channel protein 2	Q60930	31621	5	22%	LTFDTTFSPNTGK - LTLSALVDGK - SCSGVEFSTSGS
m11	odp2 ac	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	Q8BMF4	67943	17	33%	AAPAAAAAMAPPGPR - DIDSFVPSK - DVPLGAPLC
m12a	fkbp4 ac	Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	51573	6	14%	ALELDSNNEK - LQAFSAAIESCNK - LYANMFER - T
m12b	fkbp4 med	Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	51573	23	61%	AEVAAGDHPTDAEMK - AEVAAGDHPTDAEMKGER
m12c*	fkbp4 bas	Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	51573	25	62%	AEVAAGDHPTDAEMK - AEVAAGDHPTDAEMKGER
lysosome & vesicles (L)							
L1	catZ	Cathepsin Z	Q9WUU7	33978	4	15%	GSLSGR - NVNGVNYASVTR - HGIPDETcNNYQAK
L2	snap23	Synaptosomal-associated protein 23	O09044	23262	2	11%	IEEGMDQINK - ILGLAIESQDAGIK
L3	snx6 ac.	Sorting nexin 6	Q6P8X1	46650	18	41%	DVDDFFEHER - EKLEDFFK - IGSSLYALGTQDSTDI
L4	ssrd	Translocon-associated protein subunit delta	Q62186	18937	5	37%	FFDEESYSLLR - NNEDVSIIPPLFTVSVDHR - SAHAG
L5	vps25	Vacuolar protein-sorting-associated protein 25	Q9CQ80	20748	7	42%	AEIITVSDGR - ALQALQQEHK - AMSFEWPWQYR -
L6a	anxa4 ac	Annexin A4	P97429	35918	12	46%	AASGFNATEDAQTLR - AEIDMLDIR - DEGNYLDDA
L6b	anxa4 bas	Annexin A4	P97429	35918	17	52%	AASGFNATEDAQTLR - AASGFNATEDAQTLRK - AE
L7	snf8	Vacuolar-sorting protein SNF8	Q9CZ28	28865	5	24%	FAQDVSQDDLIR - GTVLAEDQLAQMSK - NGGLITL
L8	nsf1c	NSFL1 cofactor p47	Q9CZ44	40710	11	39%	DLIHDQDEEEEEEEGQR - EANLLNAVIVQR - EFVAV
Signalling (s)							
s1	cab39 ac	Calcium-binding protein 39	Q06138	39871	3	8%	LLGELLLDR - TEDEQFNDEK - VFVANPNK
s2	gbb1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	P62874	37378	7	24%	ACADATLSQITNNIDPVGR - AGVLAGHDNR - KACA
s3	ppp1ca	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	P62137	37514	10	39%	AHQVVEDGYEFFAK - EIFLSQPILLELEAPLK - GNH
s4	14-3-3 eps	14-3-3 protein epsilon	P62259	29175	16	55%	AASDIAMTELPPTHPIR - DNLTLWTSDMQGDGEEQ
s5	mk14	Mitogen-activated protein kinase 14	P47811	41289	3	9%	LVGTPGAELLK - NYIQSLAQMPK - YIHSADIIHR
s6	arl3	ADP-ribosylation factor-like protein 3	Q9WUL7	20487	11	69%	FEETGQELTELLEEEK - ILLLGLDNAGK - LNVWDIG
s7	gbb2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	P62880	37332	11	51%	ACGDSTLTQITAGLDPVGR - ADQELLMYSHDNIICG
s8	pde6d	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta	O55057	17348	3	29%	ELNFSSAEQMEK - FFDDDLLVSTSK - ILWQGTEDLS
s9	cpped	Serine/threonine-protein phosphatase CPPED1	Q8BFS6	35248	3	9%	AVFSGHYHR - LTEQAVEAINK - TLDAFSSEK
s10a	ptpn6 ac	Tyrosine-protein phosphatase non-receptor type 6	P29351	67560	7	13%	DLSGPDAETLLK - GQESEYGNITYPPAVR - KLEIIQS
s10b*	ptpn6 bas	Tyrosine-protein phosphatase non-receptor type 6	P29351	67560	7	13%	DLSGPDAETLLK - GQESEYGNITYPPAVR - KLEIIQS
s11	ctbp1	C-terminal-binding protein 1	O88712	47535	2	4%	VGQAVALR - VQSVEQIR
cell death control (a)							
a1a	bid ac.	BH3-interacting domain death agonist	P70444	21952	4	31%	HLAQIGDEMDHNIQPTLVR - IEPDSESQEEIIHNIAR -
a1b	bid bas.	BH3-interacting domain death agonist	P70444	21952	8	52%	AMLIMTMLLAK - DVFHTTVNFINQNLFSYVR - HLA
a2b	Casp 3 bas	Caspase-3	P70677	31476	3	11%	EDILELMDSVSK - LFIIQACR - SGTDVDAANLR
a2a	casp3 mod	Caspase-3	P70677	31476	10	48%	EDILELMDSVSK - ETFMGLK - IPVEADFLYAYSTAP
inflammation (i)							
i1	in35	Interferon-induced 35 kDa protein homolog	Q9D8C4	31875	7	30%	FVVSNLK - IPFSVPEVPLVFQGQTK - LQELQQLK - V
i2	anxa1	Annexin A1	P10107	38736	19	54%	AAYLQENGKPLDEVLR - AAYLQENGKPLDEVLRK -
i3	myd88	Myeloid differentiation primary response protein MyD88	P22366	33754	8	27%	DFPSILR - ELETRPDPTR - LLELLALLDR - LSLFLNP

i4	casp1	Caspase-1	P29452	45642	9	25%	DSEEDFLTDAIFEDDGIKK - FSFEQPEFR - GSLFIESL
miscellaneous (u)							
u1	mtna	Methylthioribose-1-phosphate isomerase	Q9CQT1	39411	5	14%	AGAGGPGLAALVAFVR - DLGQVAAQEAER - FAED
u2	cryl1	Lambda-crystallin homolog	Q99KP3	35209	4	12%	EIDGFVLNR - IFAQLDR - LQYAVISEAWR - VPDDPE
u3	ppac	Low molecular weight phosphotyrosine protein phosphatase	Q9D358	18192	3	24%	IDSAATSTYEVGNPPDYR - IELLGSYDPQK - SPIAEA
u4a	clic4 ac	Chloride intracellular channel protein 4	Q9QYB1	28731	15	71%	AGSDGESIGNCPFSQR - DEFTNTCPSDKEVEIAYSDV
u4b	clic4 bas	Chloride intracellular channel protein 4	Q9QYB1	28731	26	91%	AGSDGESIGNCPFSQR - DEFTNTCPSDK - DEFTNTC
u5	lhpp	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Q9D7I5	29144	10	71%	AFQVLMELENPVLISLGK - ALEYACGIK - ELVGVLQ
u6	amrp	Alpha-2-macroglobulin receptor-associated protein	P55302	42217	16	43%	AEEGYENLLSPSDMAHIK - DAQMVHSNALNEDTQ
u7	mat2b	Methionine adenosyltransferase 2 subunit beta	Q99LB6	37392	3	14%	LETLGIGQR - RPDVVESQPDAASQLNVGASGNLAK
u9	fa49b	Protein FAM49B	Q921M7	36749	11	41%	AWGAVVPLVGK - DAEGILEDLQSYR - DQPPNSVEG
u10	cdc42	Cell division control protein 42 homolog	P60766	21259	4	27%	CVVVGDGAVGK - NVFDEAILAALEPPEPK - TCLLIS
u11	spre	Sepiapterin reductase	Q64105	27884	7	29%	ALAPQLAR - EELGAQQPDLK - ELPRPEGLQR - LLL

YTEPVIAGLDPK - IFPMGDR - LNLYELK - LYIGLAGLATDVQTVAQR - NCVAIAADR - QIKPYTLMSMVANLLYEK
PYYTEPVIAGLDPK - GKNCVAIAADR - LNLYELK - LYIGLAGLATDVQTVAQR - NCVAIAADR - QIKPYTLMSMVANLLYEKR

SGEK - EEAGGGGGGGISEEEAAQYDR - FDAVCLTCCSR - FFTGDVFGYHGYTFANLGEHEFVEEK - GLTMLDHEQVSPEDPGAQFLIQTGSVGR - GSGIVECLGPQ - KPESFFTK - LDSSETTMVK - NDVFDS
FLQQSQSSGPGQAAVWHR - ETIEDVEEMLNNLPGVTSVHSR - FLGCVDIK - GSIDEVDKR - LEELYTK - LEELYTKK - LELWCTDVK - LNIGDLQATK - LYENFISEFEHR - QLTFEEIAK - QMTDPNVALTFLE
AER
EPVPGIK - LLAEPVPGIKAEPDESNAR - TNEAQAIETAR - TVLLSIQALLSAPNPDDPLANDVAEQWK - WSPALQIR - YFHVVIAGPQDSPFEGGTFK
LVTQGASIYIENK - FLVTQGASIYIENKEEK - GAHVNAVNQNGCTPLHYAASK - GGLGLILKR - LDELKER - MVHILLFYK - NRHEIAVMLLEGGANPDAK - TPLQVAK
LEQYLMEGSYNK - ILFAEATR - LKLVLLELNFLPTTGTK - LVLLELNFLPTTGTK
LDLR - APLDIPIPDPPPK - APLDIPIPDPPPKDDEMETDK - ASKDTHVMDYR - CILVITWIQHLIPK - DEAAYGALR - DTHVMDYR - IEDGNDFGVAIQEK - IISLSQLLQEDSLNVADLSSLR - KIISLSQLLQEDS
HPER - FDDGAGGDNEVQR - FVNLGIEPPK - FVNLGIEPPKGVLLFGPPGTGK - FVVDLSDQVAPTDIEEGMR - GVLLFGPPGTGK - IINADSEDPK - IINADSEDPKYIINVK - INELTGIK - KIEFSLPDLEGR - L
TEK - GVEIEGPLSAQTNWDIAHMISGFE - QPVLSQTEAR - QVLGQMVIDEELLGDGHSYSPR - TQNPMVTGTSVLGVK - VNDSTMLGASGDYADFQYLK

AGSER - DEALEDEDSK - DVDADEEDSR - DYTYEELLNR - EKNPDMVAGEK - EVEPEPTEEK - EVEPEPTEEKDVDADEEDSR - EYVTCHTCR - FPEEDEILEK - FPEEDEILEKDEALEDEDSK - FVMKPPQV

QAYLDFK
LLIIPK - GIDPFSLDALAK - GLVLDHGAR - IITEGFEAAK - SETDTSLIR - TEVNSGFFYK - VCGDSDKGFVVINQK - VLAQNSGFDLQETLVK
EVTEGLDVLR - SDVVPMTAENFR - SNPQVYMDIK - VLYVGGLAEEVDDK
LDESGVLSLDR - DAVIYPILVEFTR - DEPAEQGELK - EAGMQPQLQIR - EEAEPPAEETSQPPPSEPK - EVEEEPGLR - EVQYLLNK - FLGDSAAGMAIK - FPEHELIVDPQR - LCQGLFFR - LEELTLR - LFNE
LDESGVLSLDR - AVGKEELGK - DAVITVPAFFNQAER - DEPAEQGELKEEAEPPAEETSQPPPSEPK - EAGMQPQLQIR - FLGDSAAGMAIK - FPEHELIVDPQR - KLCQGLFFR - KTPVTVTLK - KYPDYESK
LDESGVLSLDR - DAVITVPAFFNQAER - DAVIYPILVEFTR - DKLAELR - EAGMQPQLQIR - EVEEEPGLR - FLGDSAAGMAIK - KYPDYESK - LEELTLR - LGNTISSLFGGGTSSDAK - LIPEMDQVFTEVEM

QNYHQDAEAAINR - SVNQSLLELHK - YFLHQSHEER
R - NLNQALLDLHALGSAR
SGISR - FGVVVVGVGR - FTASPLEEEKFGFPAFSGISR - KFGVVVVGVGR - LLGQVSAEDLAAEK - MTVQLETQNK - NIFLKDQDIFIQK - QISLEDALR - SGSLEEVPNVGVNK - SPLSWIEEK - SQEVDVAYI
SGISR - FGVVVVGVGR - FTASPLEEEKFGFPAFSGISR - HVLVEYPMALSFAAAQELWELAAQK - KFGVVVVGVGR - LLGQVSAEDLAAEKK - MTVQLETQNK - NIFLKDQDIFIQK - RELGSLDNVR - SPLS
HIR - NIVTAMK - TGLTTLAQAVQAGYEVTVLVR
FYTLKPDR - GEVEEYFR - HTAEEYAALLSK - KLVVVFGATGAQGGSVAR - LAAGHFDGKGEVEEYFR - LGFQGAQDLANMFR - LGLHYVVYSGLENIR - LGLHYVVYSGLENIRK - LLADLAK - LPCYFEN
SSGSLAR
GK - SWCGACK - VRPEIINESGNPSYK - YFYVSAEQVVQGMK

GFGHIGIAVPDVYSACK - GLAFIQDPDGYWIEILNPNK - LDFPAMK - SLDFYTR - TAWTFSR - VLGLTLLQK

EK - FKDIFQEIYDK - GQETSTNPIASIFAWSR - GWPLYLSTK - IIWELIK - LDNNTELSFFAK - LIDDMVAQAMK - LILPYVELDLHSYDLGIENR - LVTGWVKPIIIGR - NILGGTVFR - SDYLNTFEFMDK - SE
ITPDEK - DAAEAIKK - FKDIFQEIYDK - HAYGDQYR - KIQGGSVVEMQGDEMTR - LDNNTELSFFAK - LIDDMVAQAMK - SDYLNTFEFMDK - SIEDFAHSSFQMALSK - VEITYTPK - VTYMVHDFEEGGG
AMLWVSEK - ANVEHMTEK - EQWWLNLR - ETDFEHR - FDEAIQLR - GGTPSAFDR - GQVQEVGWHDVAGWLGR - HGKPISSSYVK - IMEVIDAITTTAQSHQR - ISMADYVSGELEHVTR - LNIIIIAEGAI

EYPVR - HVVSEIR - LAVLITNSNVR - LMVESHYSLR - MEELEAGR - QCEEVAQALGK - RAFMEEFGAEPELAVSAPGR - SLETSLVPLSDPK - TAQAAAAMSR - TDGLVSLLTTSK - VEELLAEAR
AVSAPGR - GYALLIDCR - HSLGSSEYPVR - HVVSEIRR - LAVLITNSNVR - LQFPLPSAQWSLEPGIPQWANYVK - MEELEAGR - QCEEVAQALGK - RAFMEEFGAEPELAVSAPGR - SLETSLVPLSDPK - TA
APEGSLVFHEK - NEPYENDGEK - SQVEPADYK - VVLPCSVQEYQVGQLYSVAEASK
AIAR - EVLEYNALGGK - GLTVVQAFQELVEPK - LDAYNQEK - LKEVLEYNALGGK - QILEENYGQK - QILEENYGQKDPEK - VGTDIQDNK - YEEDSYNR

PLVVEYK - DLSHIGDAVVISCAK - FSASGELGNGNIK - IADMGHLK - LIQGSILK - LIQGSILKK - LMDLDVEQLGIPEQEYSCVIK - LSQTSNVDKEEEAVTIEMNEPVHLTFALR - MPSGEFAR - NLAMGVNL
PLVVEYK - CAGNEDIITLR - FSASGELGNGNIK - IADMGHLK - LIQGSILKK - LMDLDVEQLGIPEQEYSCVIK - MPSGEFAR - NLAMGVNLTSMSK - SEGFDTYR - VSDYEMK
GNVPNIIIAGPPGTGK - EIGYTHMK - EKVPYTDDGLEAIIFTAQGDMR - EMIQHCVDANIDEAYK - FALACNASDK - FALACNASDKIIEPIQSR - IIEPIQSR - IIILDEADSMTDGAQQALR - LMNVIEK - LMNV
LYSR - QADVVVAEVTQPSLGVGYELGR
PCNISIAAEFIAQVK - QLPLSSICLETDSPALGPEK - YAGTDEEKEEQR

FQQELDAR - SLISMEEINK - TIFLLHR
ISR - FNVPVSLESK - ITSGIPQTER
GPGMGAPLASVAVVAR - ISNDPSPGYNIEQMAK - PAVLGFEGSANK - TPLKDSAITQR - TYVTAPGTGFLPGDTAR
IAGIEEVNMIK
DFK - FSPDGELYASGSEDGTLR - GAVWGATLNK - IGFPETAEEELEEIASENSDSIYSSTPEVK - IYDLNKPEAEPK - LWDHATMTEVK - LWQTVVGK - QGDTGDWIGTFLGHK - QILSADDK - SFEAPATINS
DK - CVLPEEDSGELAKPK - EFLVAGGEDFK - FSPDGELYASGSEDGTLR - GAVWGATLNK - GHFGPIHCVR - IGFPETAEEELEEIASENSDSIYSSTPEVK - IYDLNKPEAEPK - LWDHATMTEVK - LWQTVV
- INNACFEAVVVTNTIPQEDK - IQVIDISMILAEAIR - LNVDFALIHK - MVLVGDVK - NCTIVSPDAGGAK - THNGESVSYLFSHVPL - VAILVDDMADTCGTICHAADK - VTAVIPCFPYAR - VYAILTHGIFSG
AVVVTNTIPQEDK - MVLVGDVK - MVLVGDVKDR - NCTIVSPDAGGAK - RVTSIADR - SRAPISAK - VTAVIPCFPYAR
PGTGK - FVQCPDGELQK - GLGLDDALEPR - GTEVQVDDIKR - GTSYQSPHGIPIDLLDR - IGLETSLR - LLIVSTSPYSEK - TEALTQAFR - TQGFLALFSGDTGEIK - TTEMETIYDLGTK - VYSLFLDESR
AALR - IIQLIEGK - KWDTCAPEVILHAVGGK - LTDIHGNALQYNK - LVASAYSIAQK - LVQMSICSSLAR - QPCPSQYSAIK - SHSNQLVTDCISAMNPDTVLR - TSATDLQTK - WDTCAPEVILHAVGGK

AENEYQTAISENYQTMSDTTFK - LLLNNDNLLR - TKIDWNK - TSVETALR
ENYVADIEVDGK - EVFEMATR - HFCPNVPIILVGNK - HFCPNVPIILVGNKK - IGAFGYMECSAK - KLVIVGDGACGK - LRPLSYPDTDVILMCFSIDSPDSLENIPEK - LVIVGDGACGK - MKQEPVKPEEGR -
DITR - IIEVSGQK - IYQNIQDGSLDLNAAESGVQHKPSAPQGGR - KFMADCPHTIGVEFGTR - KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR - LQIWDTAGQER - LTSEPQPQR - NLTNPNTVIILIGNK - QFA
GHIKDEVFGTVK - GPAEAEATTD - HQTLQGVAFPISR - IEIDNGDELTADFLYDEVHPK - INEVQTDVSVDTK - KQLNYVQLEIDIK - MLYAATR - MLYSSCK - NETIILANTENTELR - QLNYVQLEIDIK - QL
QANCYEEVKDR - LGGSAVISLEGKPL - MLPDKDCR - NIILEEGKEILVGDVGQTVDDPYTTFVK - SSTPEEVKK - YALYDATYETK
QATESSGR - QQFWGNEGTAEGTEPSQSERPEEK - SQPTLPISTIDER - SSELDEDEGFGDWSQKPEPR - TLWETGEVQSQSASK - VHLEESNLSYREPDPEDAVGGSGEAEEHLIR
DAVGGSGEAEEHLIR - KSLWEQK - LADRTESLNR - LQQYTQATESSGR - QQFWGNEGTAEGTEPSQSERPEEK - SQPTLPISTIDER - SSELDEDEGFGDWSQKPEPR - TLWETGEVQSQSASK - VHLEESNLS
VK - EFGGGHIKDELFGTVK - ETIELVHTEPTNVAQLPSR - HLSSCAAPAPLTSAER - HQTLQGLAFPLQPEAQR - HTHEGDALESVVFIYSMPGYK - IEIGDGAELTAEFLYDEVHPK - KIEIGDGAELTAEFLYDE
PSAPR - LDILDTAGQEEFGAMR - LFTQILR - LNVDEAFEQLVR - LVVVGGGGVGK - QSFNEVGK - SEASSFSASHHMTYFEASAK

VQEAQNILK - MAENLGFLGSLK - NQAADQITK - SHNGPVIVGSPQGGVDIEEVAASSPELIFK - VMVAEALDISR

K - GEQILLSDNAASLAVQAFLQMCNLPVK - GHSLSDGLDEVQK - GHSLSDGLDEVQKAEMK - IEQHYFEDWGK - LGTQPYFFNK - MKAIGWGNK - NYSNLLAFCR - TLDQVLEDVDQCCQALSQR - VKN
FGK - DLQNVNITLR - EFTEAVEAK - FDAGELITQR - FGLALAVAGGVVNSALYNVDAGHR - GVQDIVVGEGTHFLIPWVQKPIIFDCR - ILFRPVASQLPR - IYTSIGEDYDER - KLEAAEDIAYQLSR - NITYL
GELITQR - FGLALAVAGGVVNSALYNVDAGHR - IYTSIGEDYDER - KLEAAEDIAYQLSR - NITYLPAGQSVLLQLPQ - NVPVITGSK - QVSDDLTER - VFESIGK - VLPSITTEILK
LLAK - ELAMPGEDLK - HYAHTDCPGHADYVK - KYEEIDNAPEER - LLDAVDTYIPVPTR - QIGVEHVVVYVNK - TTLTAAITK - YEEIDNAPEER
VNIPFTEFLTNEGLEK - FQGTQPEPR - THEDILENLDAR

TSGSQR - VILGSPAHR
NYPVLTPNMK - GFEEAVAAGAK - GYVSCALGCPYEGK - KNANCSIEESFQR - LLEAGDFICQALNR - NANCSIEESFQR
FFEDVRLPANALLGEENK - CIGAIAMTEPGAGSDLQGVR - GFYYLMQELPQER - LDSGSASMAK - LETPSAK - LPANALLGEENK - LPANALLGEENKGFYYLMQELPQER - QGLLGINIAEK - RLDSGSASM
SNTDTGK - WCEYGLTFTEK - YQLDPTASISAK

IVEK - DVPVGSIICITVEKPQDIEAFK - GIDLTQVK - GKISVNDFIIK - ISVNDFIIK - LQPHEFQGGTFTISNLGMFGIK - NFSAIINPPQACILAIGASEDK - NFSAIINPPQACILAIGASEDKLIPADNEK - VAPAPA

QLAVCQQR - VFVHYTGWLLDGTK - VLQLYPSNK
- AKESWEMSSAEK - ALELDSNNEK - AWDIAVATMK - EGTGTETPMIGDR - ELCFEVGEGESLDLPCGLEEAIQR - FDSSLDRK - FQIPPHAELR - GEDLTEEEDGGIIR - GEGYARPNDGAMVEVALEGYHK -
- AKESWEMSSAEK - EGTGTETPMIGDR - ELCFEVGEGESLDLPCGLEEAIQR - ESWEMSSAEK - FQIPPHAELR - FSFDLGKGEVIK - GEAHLAVNDFDLAR - GEDLTEEEDGGIIR - GEGYARPNDGAMVEV

K - LGEGEGSMTK - LGEGEGSMTKEEFTK - NLVELAELELK - QELEAEYLAIFK - QELIDFK - QNEFSVVR - SAADDYNR - SADGVIVSGVK - SADGVIVSGVKDVDDFFEHER - SLVDYENANK - TFLLEY
TYEVR - VQNMALYADVSGK - YQVSWSLEHK
NLEWLDK - LIYQWVSR - QSSMTVMEAQESPLFNNVK - SSFLIMWR
LMK - FLSILCSR - GAGTDEGCLIEILASR - GLGTDDNTLIR - GLGTDEDAIIGILAYR - INQTYQQQYGR - QDAQELYEAGEK - SETSGSFEDALLAIVK - SKPSYFAER - VLVSLSAAGR
IDMLDIR - DEGNYLDDALMK - FLSILCSR - GAGTDEGCLIEILASR - GLGTDDNTLIR - GLGTDEDAIIGILAYR - INQTYQQQYGR - NHLLHVFDEYK - QDAQELYEAGEK - QDAQELYEAGEKR - RINQTY
EELHQQVLK - NGYVTVSEIK - TNLEEFASK
TGTEEDR - ELADENQTLK - FYAGGSER - HSGQDVHVVLK - LGAAPEEESAYVAGER - LGSTAPQVLNTSSPAQQAENEAK - SGQQIVGPPR - SYQDPSNAQFLESIR - TGFSLDNGDLR

DATLSQITNNIDPVGR - LFVSGACDASAK - LIIWDSYTTNK - LLLAGYDDFNCNVWDALK - LLVSASQDGK
ECASINR - ICGDIHGQYYDLLR - IYGFYDECK - LNLDSIIGR - NVQLTENEIR - TFTDCFNCLPIAAIVDEK - YGQFSGLNPGGRPITPPR - YPENFFLLR
K - EALQDVEDENQ - EDLVYQAK - KEAAENSLVAYK - KVAGMDVELTVEER - LAEQAER - LAEQAERYDEMVESMK - LICCDILDVLDK - LICCDILDVLDKHLIPAANTGESK - QMVETELK - VAGMDVE

GQR - LSCVPVLIFANK - QDLLTAAPASEIAEGLNLHTIR - QLASEDISHITPTQGFNIK - RFEETGQELTELLEEEK - SAPDQEVR - SVQSQGFK - SYFENTDILIYVIDSADR - SYFENTDILIYVIDSADRK
ITSVAFSR - ELPGHTGYLSCCR - IYAMHWGTDSR - KACGDSTLTQITAGLDPVGR - LIIWDSYTTNK - LLLAGYDDFNCNIWDAMK - LLVSASQDGK - QTFIGHESDINAVAFFPNGYAFTTGSDDATCR - TFVS

VPGVEHEAR

QK - NQGDFSLSVR - SGMVQTEAQYK - VNAADIENR - VYGLYSVTNSR
QK - NQGDFSLSVR - SGMVQTEAQYK - VNAADIENR - VYGLYSVTNSR

QELEVLGR - QLAAQFMNGSLSEEDKR
QIGDEMDHNIQPTLVR - IEPDSESQEEIIHNIAR - QELEVLGR - QLAAQFMNGSLSEEDK - QLAAQFMNGSLSEEDKR - VASHAPSLLR

YYSWR - LEFMHILTR - LFIIQACR - SGTDVDAANLR - SINNFEVK - SSFVCVILSHGDEGVIYGTNGPVELK - SVDSGIYLDSSYK - VATEFESFSLDSTFHAK

LVSGFPAGLR - VNLEDCR - VQVQPLELPVVTNIQVSSQPDNHR - VSPYVSGEIQK
ALDLELK - ALTGHLEEVVLAMLK - ALYEAGER - CLTTIVK - CQDLSVNQDLADTDAR - DITSDTSGDFR - FLENQEQEYVQAVK - GGPGSAVSPYPSFNVSSDVAALHK - GVDEATIIDILTKR - KALLALAK
R - MVVVVSDDYLQSK - QLEQTDYR - QQNQESEKPLQVAR - SLLDAWQGR

IK - LALIICNTEFQHLSPR - LANITAMDK - LLLEDLGYTVK - LQMPTADR - VGAQVDLR - VLNQEEMDK

MLEK - HLLEQTNPR - SIGDLGAR
HLAAR
VFR
AK - EVEIAYSDVAK - FLDGDEMTLADCNLLPK - FSAYIKNSRPEANEALER - GVVFSVTTVDLK - HPESNTAGMDIFAK - IEEFLEEVLCPPK - KPADLQNLAPGTHPPFITFNSEVK - LDEYLNSPLPDEIDENS
PSDKEVEIAYSDVAK - EEDKEPLIELFVK - EVEIAYSDVAK - FLDGDEMTLADCNLLPK - FSAYIK - FSAYIKNSRPEANEALER - GLLKTLQK - GMTGIWR - GVVFSVTTVDLK - GVVFSVTTVDLKR - HPES

QLGFDISEEEVTAPAPATCQILK - ETSGLMLDVGGYMK - FCTNESQK - FRPGDEHHPEVQADGYVDNLAEAVDLLLK - GLRPHLLIHEGVR - LKQSPLK - SALQAIGVEAHQAIMIGDDIVGDVGGAQQCGMR

ELGDPR - EFLHYK - EKYVLLEEK - FSSEELDK - FSSEELDKLWR - IQERDELNWK - IQEYNVLLDTLSR - KVSHQGYGSTTEFEEPR - LAELHSDLK - LIHNLNVILAR - LKHVESIGDPEHISR - LNQLWEK -
- VLITGATGLLGR
LLNALR - EAIQHPADEK - EAIQHPADEKLQEK - EIYNQVNVVLK - GLLGALTSTPYSPTQHLER - INNVPAEGENEVNNELANR - KFYEFSQR - MTNPAIQNDFSYYR - VMLETPEYR
YTTNK - TPFLLVGTQIDLR
INNAATLGDVSK - LLSPGSVMLVSAR - QLKEELGAQQPDLK - VVLAAADLGTEAGVQR