Supporting Information

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SI Materials and Methods

Preparation of NSP4 Inclusion Body Material. The DNA sequence encoding human neutrophil serine protease 4 (NSP4) was amplified from human bone marrow cDNA using primers DJ2064B 5'-GGCAGATCATATGGAAATCATCGGCGGCCACGAAGTG-ACC-3' and DJ1715 5'-GGGAATTCTTATTAACGACGAAC-CACGTCCCA-3' (Metabion). The PCR product was digested with *Nde* II/*Eco* RI and subcloned into the expression vector pET24c(+) (Novagen). Positive clones were verified by sequence analysis and transformed into the *Escherichia coli* strain B834 (DE3) (Novagen).

Overnight cultures of transformed *E. coli* strain B834 were grown in Luria-Bertani (LB) broth containing 50 µg/mL kanamycin, 2% (wt/vol) glucose, and inoculated in LB/kanamycin without glucose. Expression was induced at an $A_{600 \text{ nm}}$ of 0.5–0.8 by adding isopropyl-1-thio- β -D-galactopyranoside to a final concentration of 1 mM. Cultures were grown shaking at 150 rotations per minute at 37 °C for 3–4 h after induction and harvested by centrifugation.

Pelleted bacteria were lysed in 50 mM Tris-HCl, 2 mM MgCl₂ containing 10 μ g/mL DNase I and 0.25 mg/mL lysozyme, pH 7.2, by sonification. Inclusion body (IB) material was obtained by centrifugation and two washing steps in 50 mM Tris-HCl, 60 mM EDTA, 1.5 M NaCl, 6% Triton X-100, pH 7.2, and in 50 mm Tris-HCl, 60 mm EDTA, pH 7.2.

Solubilization of IB was performed in an end-over-end rotator in 6 M guanidinium hydrochloride, 100 mM Tris-HCl, 20 mM EDTA, 15 mM GSH, 150 mM GSSG, pH 8.0, overnight at room temperature. Solubilized IB were then dialized against 6 M guanidinium hydrochloride, pH 5.0, at 4 °C. Protein concentration was determined by measuring the absorbance at 280 nm (spectrophotometer ND-1000; Peqlab).

Expression of S-Tag-NSP4 in HEK 293 Cells Using the "Flp-In" System. The pcDNA5/FRT expression vector (Invitrogen) was complemented by an Igk-chain secretion signal using the oligoduplex DJ2972 5'-Pho-CTAGCCACCATGGAGACAGACACACTCC-TGCTATGGGTACTGCTGCTCTGGGTACCAGGTTCCAC-3' and DJ2973 5'-Pho-GTGGAACCTGGTACCCAGAGCAGCA-GTACCCATAGCAGGAGTGTGTCTGTCTCCATGGTGG-3' (Metabion), followed by an S-tag peptide using the oligoduplex DJ3151 5'-Pho-GTGAAAGAAACCGCTGCTGCTAAATTCG-AACGCCAGCACATGGACAGCGGAAGCGGTGGACAC-3' and DJ3152 5'-Pho-GTGTCCACCGCTTCCGCTGTCCATGT-GCTGGCGTTCGAATTTAGCAGCAGCGGTTTCTTTCAC-3'. The cDNA-sequence of mature NSP4, starting at the conserved Ile-Ile-Gly-Gly-motif, was amplified from human bone marrow cDNA with DJ3215 5'-TGGACACGTGGATGACGACGACAAGATC-ATCGGGGGGCCACGAG-3' and DJ3216 5'-CCCCACCGGTC-TTCCGAACCACGTCCCAGATCCA-3' (Metabion), thereby introducing an enterokinase cleavage site (DDDDK) at the mature amino terminus. The resulting PCR product was digested with Pml I/ Age I and cloned into the reading frames of the N-terminal S-tag and the C-terminal 6xHis-tag of the pcDNA5/FRT vector. The construct was verified by sequence analysis.

HEK 293 cells (Invitrogen) were cultured in DMEM (Life Technologies) supplemented with 10% FCS. One day before transfection, 1.4×10^6 flp-in HEK 293 cells were plated in 35-mm cell culture dishes and incubated in 3 mL DMEM containing 10% FCS. Cells were transfected by adding 1.8 mg pOG44 (encoding the flp-in recombinase; Invitrogen) and 0.2 mg pcDNA5/FRT/S-tag-NSP4/H6 in 100 mL serum-free OptiMEM medium and 7 mL FuGENE HD transfection reagent (Roche). Starting at 48 h after

transfection, the medium was replaced with DMEM containing 10% FCS and 75 µg/mL hygromycin B (Invitrogen) every 2–3 d. Two weeks posttransfection, visible circular hygromycin B-resistant colonies were pooled and cultured until a desired number of plates had reached confluence. Expression of recombinant S-tag-NSP4 was tested by Western blot analysis with S-protein conjugated to HRP (Novagen). For protein expression, cells were cultured in DMEM supplemented with 5% FCS and 75 µg/mL hygromycin B for 8–10 d before the supernatant was harvested.

Purification of S-Tag-NSP4 from HEK 293 Supernatant. Harvested cell-culture supernatant was filtered through a 0.22- μ m membrane (Millipore), concentrated fivefold, and dialyzed against binding buffer (20 mM Na₂HPO₄; 500 mM NaCl; 50 mM imidazole, pH 7.5) at 4 °C. The 6xHis-tagged S-tag-NSP4 was purified using nickel-affinity chromatography. The protein solution was applied to a HisTrap HP column (GE Healthcare) previously equilibrated in binding buffer. The column was washed with binding buffer, and bound proteins were eluted applying a linear imidazole gradient from 50 mM to 1 M imidazole in 20 mM Na₂HPO₄, 500 mM NaCl, pH 7.5. Fractions were collected and analyzed for S-tag-NSP4 by SDS/PAGE and silver-staining. The expected size is 31 kDa. S-tag-NSP4 containing fractions were pooled and concentrated. Protein concentration was determined by measuring the absorbance at 280 nm.

Processing of S-Tag-NSP4 by Enterokinase. Purified S-tag-NSP4 was dialyzed against 20 mM Tris-HCl, 500 mM NaCl, pH 7.4 at 4 °C. After dialysis, CaCl₂ was added to a final concentration of 2 mM. The amino-terminal extension, the S-tag peptide and the enterokinase (EK) recognition sequence, was cleaved off by Tag-Off High Activity Enterokinase (Merck) to generate mature 6xHis-tagged NSP4. EK cleavage was accomplished by 1 U EK per 50 µg S-tag-NSP4 for 16 h at room temperature. Conversion of S-tag-NSP4 was verified by SDS/PAGE and subsequent silverstaining. There is a molecular weight shift of ~3 kDa after removal of the synthetic propeptide. Converted NSP4 was subsequently purified by nickel-affinity chromatography according to the manufacturers' instructions (Ni-NTA; Qiagen).

Production of Granzymes A, B, K, M, H, and Proteinase 3. Granzymes (Gzms) A, B, K, M, and H were expressed as inclusion body proteins, refolded and converted into the active mature form as previously reported (1–5). Proteinase 3 (PR3) was produced as described by Korkmaz et al. (6).

Production of NSP4 Precursor in HEK 293 EBNA Cells. The DNA sequence encoding the full length reading frame of NSP4 (natural NSP4) was amplified from human bone marrow cDNA using primers DJ539 5'-TCGGCGGCCGCACCACGTCCCAGATC-CAGG-3' and DJ583 5'-CGGAATTCTGCCATGGGGCTCG-GGTTGA-3' (Metabion). The PCR product was digested with *Eco* RI and the target vector pcDNA3.1 (Invitrogen) was digested with *Bsp* 120I, complemented by the Klenow enzyme and subsequently digested with *Eco* RI. After subcloning in frame with the C-terminal cMyc-6xHis-tag, positive clones were verified by sequence analysis.

The HEK 293 cell line stably expressing Epstein–Barr virus nuclear antigen-1 (HEK293E) was grown as suspension culture in Freestyle 293 Expression Medium (Invitrogen), supplemented with 0.1% Pluronic F-68, 25 μ g/mL Geneticin G418 and 0.5% Bacto TC Lactalbumin Hydrolysate. Before transfection of HEK293E with natural NSP4, cells were brought to 1 × 10⁶ cells/mL. Poly-

ethylene imine (PEI)/DNA complexes were prepared by adding PEI to DNA, both prediluted in Optipro serum free medium (Invitrogen) and incubation for 15 min at room temperature before adding to cell culture. Per 1 mL cell culture, 2 μ g PEI and 1 μ g DNA were used.

Cell culture supernatant was harvested after 72–96 h by 10-min centrifugation at $1,000 \times g$ and purified as described above for S-tag-NSP4.

ELISA. The specificity of anti-NSP4 positive mAbs was tested in ELISA by coating 1 μ g NSP4 IB material or 100 ng per well of each of the Gzms A, B, K, M, H, neutrophil elastase (NE), cathepsin G (CG), PR3, azurocidin (AZU), and native NSP4 produced in HEK 293. NE, AZU, and CG were purchased from Elastin products, Sigma-Aldrich, and Calbiochem, respectively. Hybridoma culture supernatants were diluted 1:20 and bound mAbs were detected with HRP-labeled goat anti-rat IgG+IgM antibodies diluted 1:4,000 (112-035-068; Jackson Immunoresearch).

Isolation of Different Blood Cell Populations and Preparation of Total Cell Lysates. Peripheral blood mononuclear cells (PBMCs) and polymorphonuclear cells (PMNs) were obtained by Ficoll gradient centrifugation. Residual erythrocytes were removed by dextran sedimentation and hypertonic treatment. For total cell lysates, cells were taken in 50 mM Tris/HCl, 150 mM NaCl, 0.5 mM EDTA, 1 mM PMSF, 0.5% Nonidet P-40, pH 7.4, incubated on ice for 20 min, and underwent 4×30 s ultrasonication (Sonorex TK52; Bandelin Electronic). Cell debris and DNA were pelleted by centrifugation for 10 min at 20,000 $\times g$ and 4 °C.

SDS/PAGE and Immunoblotting. To examine the specificity of the developed rat mAbs in immunoblotting, 100 ng of each tested protein was separated by reducing SDS/PAGE and analyzed by silver-staining and immunoblotting. For the latter, proteins were transferred to a Hybond-ECL membrane (GE Healthcare) and

- Andrade F, Fellows E, Jenne DE, Rosen A, Young CS (2007) Granzyme H destroys the function of critical adenoviral proteins required for viral DNA replication and granzyme B inhibition. *EMBO J* 26:2148–2157.
- Fellows E, Gil-Parrado S, Jenne DE, Kurschus FC (2007) Natural killer cell-derived human granzyme H induces an alternative, caspase-independent cell-death program. *Blood* 110:544–552.
- Hink-Schauer C, Estébanez-Perpiñá E, Kurschus FC, Bode W, Jenne DE (2003) Crystal structure of the apoptosis-inducing human granzyme A dimer. Nat Struct Biol 10:535–540.

probed with the mAbs against NSP4 (1:30) and HRP-labeled goat anti-rat antibodies (Jackson Immunoresearch) in a dilution of 1:10,000.

Total cell lysates of isolated PBMCs or PMNs were resolved by reducing SDS/PAGE and analyzed by Western blotting, as described above, using anti-NSP4 mAbs.

Immunohistochemistry. Formalin-fixed, paraffin-embedded human tissue samples from bone marrow, lymph node, spleen, neural network, pancreas, prostate, and arteries were routinely embedded for light microscopy and sectioned into 2- μ m slides. Immunostaining was carried out after antigen retrieval by microwaving in citrate buffer (3 × 5 min, 600 W) after dewaxing of the sections. The rat hybridoma supernatants were diluted 1:30 and incubated with the sections overnight at 4 °C. Negative control slides were stained in parallel omitting the incubation with primary antibodies. Slides were developed using the Ultravision LP staining kit (Thermo Fisher Scientific). Sections were counterstained with hematoxylin.

Conversion of NSP4 Precursor by Dipeptidyl Peptidase I. Dipeptidyl peptidase I (DPPI) was first activated at 37 °C in 50 mM sodium acetate, 100 mM NaCl, 1 mM dithioerythritol (DTE), pH 5.5 for 60 min. NSP4 precursor was incubated with 0.5 U/mg activated DPPI in 50 mM sodium acetate, 100 mM NaCl, pH 5.5 for 4 h at room temperature.

Edman Sequencing. Ten micrograms of NSP4 precursor before and after incubation with DPPI was separated by reducing SDS/ PAGE and transferred to Immobilon-P transfer membrane (Millipore) in 90 mM Tris-borate, 1 mM EDTA, and 10% methanol. Membrane was stained with Coomassie blue and the bands representing NSP4 were analyzed by N-terminal Edman sequencing according to standard procedure.

- Kurschus FC, et al. (2004) Killing of target cells by redirected granzyme B in the absence of perforin. FEBS Lett 562:87–92.
- Wilharm E, et al. (1999) Generation of catalytically active granzyme K from *Escherichia* coli inclusion bodies and identification of efficient granzyme K inhibitors in human plasma. J Biol Chem 274:27331–27337.
- Korkmaz B, Kuhl A, Bayat B, Santoso S, Jenne DE (2008) A hydrophobic patch on proteinase 3, the target of autoantibodies in Wegener granulomatosis, mediates membrane binding via NB1 receptors. J Biol Chem 283:35976–35982.



Fig. S1. NSP4 protein expression screen. Staining of different human tissue samples using anti-NSP4 mAbs and the Ultravision LP staining kit. NSP4 was not detected in (A) neural network, (B) pancreas, (C) prostate, or (D) arteries. (Scale bars, 100 μm.)

DNAS

Table S1. NSP4 cleavage sites from a chymotryptic peptide library

Nonprime sequence (inferred from database)	Prime-side sequence (LC-MS/MS)	PeptideProphet probability score	X!Tandem hyperscore	Mass accuracy (ppm)	Neutral mass (Da)	Examplary protein accession	Discarded from PICS profile
QFDAAFVPEV	AAQKAPASP	0.86	25.6	-0.7	955.5	17888	
YHGRVQALAD	AAREAGLQF	0.96	25.2	0.6	1049.5	17897	
AHEAGEFFMR	AGSATVRPTEGAGGTL	1.00	45.5	-0.3	1531.7	17875	
AHEAGEFFMR	AGSATVRPTEGAGGTL	1.00	45.6	-1.5	1531.7	17875	
GAVIAYEPVW	AIGTGKSATPAQAQAVH	1.00	52.6	-0.8	1722.9	17903	
GAVIAYEPVW	AIGTGKSATPAQAQAVH	1.00	49.6	-1.7	1722.9	17903	
NFNVPFVVVR	AISDVADQQSHL	1.00	50.3	-0.9	1370.6	17863	
NFNVPFVVVR	AISDVADQQSHL	1.00	53.9	-1.3	1370.6	17863	
MSFELPALPY	AKDALAPH	0.97	32.1	-0.7	937.5	17879	Х
MSFELPALPY	AKDALAPH	0.99	29.3	-2.2	937.5	17879	Х
KLDLERTVIR	APADGWVTNL	0.84	26.8	2.0	1130.5	17896	
LAVDESFQPT	AVGFAEALNNKDKPE	1.00	45.9	2.2	1745.9	17899	
LCRNCKIVKR	DGVIRVIC	0.85	31.6	-0.9	1018.5	17896	
SLXGTIIVGR	DIAHAKL	0.96	36.5	-0.5	882.5	17878	
SLXGTIIVGR	DIAHAKL	0.83	34.3	-0.2	882.5	17878	
KLTKRMRVIR	EKVDATKQY	1.00	35.7	-0.9	1224.6	17904	
KLTKRMRVIR	EKVDATKQY	0.99	32.8	-1.1	1224.6	17904	
NNPFFVSLKD	GAQKEADKLGY	0.95	38.2	-0.3	1322.7	17901	
NNPFFVSLKD	GAQKEADKLGY	0.97	38.1	-0.5	1322.7	17901	
GIANTFIAAQ	GHDVGKSLY	0.82	29.7	1.7	1090.5	17892	
KPEDAVLDVQ	GIATVTPAIVQ	0.97	41.8	-1.2	1156.6	17899	
KPEDAVLDVQ	GIATVTPAIVQ	0.97	38.1	-0.9	1156.6	17899	
KPEDAVLDVQ	GIATVTPAIVQAC	0.90	35	-3.0	1387.7	17899	
GQNVEFEIQD	GQKGPAAVNVTAI	0.90	27.1	-2.2	1340.7	17881	
HVIAGKAVAL	KEAMEPEFKTY	0.85	36.9	-2.1	1515.7	17889	Х
SGVRAIDTKC	KIEQAPGQH	0.99	28.1	-0.9	1122.5	17896	
PDEGIPAVCF	KLKDGEDPGY	0.99	27.9	-0.8	1264.6	17877	Х
PDEGIPAVCF	KLKDGEDPGY	0.94	31.1	-2.7	1264.6	17877	Х
PDEGIPAVCF	KLKDGEDPGY	0.97	30.8	-2.6	1264.6	17877	Х
KNPQKNLYTF	KNQASNDLPN	1.00	24.6	-1.1	1215.6	87082	X
KNPQKNLYTF	KNQASNDLPN	0.97	19.9	-1.1	1215.6	87082	X
SGGAGIQADL	KTFSALGAY	0.81	30.9	-7.4	1072.5	17884	X
MVEVFLERGY	KVVSGGTDNHLF	0.99	41.4	-0.6	1388.7	17889	Х
AKSVKFKYPR	QRKTVVADGVGQGY	0.93	29.2	-3.0	1592.8	17863	
WRQKGTGRAR	SGSIKSPIW	0.89	30.7	0.0	1089.6	1/89/	
ARPPLVVISR	SHADAELKEY	1.00	42.2	-2.0	12/7.6	17906	
ARPPLVVISR	SHADAELKEY	1.00	42.1	-2.0	1277.6	17906	
KEASAGKLVR	TLAAVRDAKEAA	1.00	42.3	-1.9	1330.7	17904	
KEASAGKLVR	TLAAVRDAKEAA	1.00	39.5	-1.0	1330.7	17904	
LSQYDFPGDD	TPIVRGSAL	0.97	31	-1.0	1000.5	17897	
RDXKGAVASL	TSVAKLPF	0.83	24.9	0.5	977.5	17871	Х
VVNTIRGIVK	VAAVKAPGF	1.00	41.8	-1.2	974.5	17905	
KHLPEPFRIR	VIEPVKR	0.91	41.5	1.3	955.6	87082	
KHLPEPFKIR	VIEPVKK	0.98	41./	-0.7	955.0 1000 F	8/082	
DIVWDFRLPR	VKSISASGH	0.98	33.5	-1.4	1000.5	1/8//	v
MSTAKL	VKSKATNLLY	0.99	27.3	-0.6	12/9./	1/8/0	X
CKPTSPGRRH	VVKVVNPELH	0.90	29.1	-1.9	1248.7	1/89/	
CKPTSPGRRH	VVKVVNPELH	0.94	29.4	-1.0	1248.7	1/89/	

Nonprime-side sequences are reported up to the position P10. X denotes ambiguous nonprime side residues. A small number of cleavage sites have P1 residues, which correspond to a potential cleavage-site of the digestion protease used for library generation. These cases might be related to incomplete amine protection during library preparation. Hence, prime-side cleavage products with such amino-termini are omitted from the proteomic identification of protease cleavage sites (PICS) analysis, as well as prime-side cleavage products with amino termini that correspond to a protein amino terminus. One exemplary protein is stated for each identified peptide sequence. X!Tandem was applied to assign peptides to tandem mass spectra and the X!Tandem hyperscore is reported together with the PeptideProphet probability score. C signifies carboxyamidomethylated cysteine and K signifies diversely by LC-MS/MS; however, the set of sequences was rendered nonredundant before analysis in the form of sequence logos.

Table S2. NSP4 cleavage sites from a GluC peptide library

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Nonprime sequence (inferred from database)	Prime-side sequence	PeptideProphet probability	X!Tandem	Mass accuracy	Neutral	Examplary protein	Discarded from PICS
				(PPIII)			Profile
GYTLNGRTIR	AAMVTVAKAKA	1.00	43.6	-2.3	1203.7	17889	
GYTLNGRTIR	AAMVTVAKAKA	1.00	50.5	-1.6	1203.7	17889	
KYYDDRVWLR	AGQTSMIARLE	0.93	37.1	-0.6	1203.0	17892	
KIIDPRVWLR	AGQTSMIARLE	1.00	40.2	-0.2	1203.0	17092	
CONCREAMENT	AGQTSMIARLE	0.97	40.6 25.4	-0.6	1203.0	17092	
SUASUSIIIR	AKQAVIK	0.78	23.4	-1.4	1079 E	17004	
PFLEHDDANR	ALMGANMQR	0.99	30 41 0	-0.7	1078.5	17904	
FORTAVCEAE	ALMGANMQR	0.80	27.2	-2.1	1076.5	17904	Y
r QF IAVGFAL VI FUNUDMAR	ALNINGDAFE	1.00	22	-0.0	1170.6	17891	~
KIEHAVPPAK	ALVAGGVRVLE	1.00	70 J	-2.8	1170.6	17881	
	ANCCUTTANEDI KM	0.93	30.3	-0.4 -0.8	1536.7	17886	
APDOTTTIVR	ANSSTITALFLIM	0.95	37	-0.0 -1.0	1536.7	17886	
LAVDESEOPT	AVGEDEDINNKDKPF	1.00	53 5	0.0	1745 9	17899	
HVSPGALDAE	AYGUKSTIED	1.00	35.5	73	1197.6	17905	x
GCVELVOPGG	FDELVOIYE	0.91	27.5	0.5	1242 5	14569	X
VALKEAMEPE	FKTYOOOVAK	1.00	33.1	0.5	1383 7	17889	x
LVVSTLNNPF	FUSTKDGAOKE	1.00	46.1	-4.4	1364 7	17901	~
LVVSTLNNPF	FVSLKDGAOKE	1.00	42.3	-3.6	1364 7	17901	
LTASTUTOYR	CATIPREAMPA	0.96	29.6	-0.5	1212.6	87082	
ESGVLNOOPY	GENTREE	0.56	23.0	-2.2	957.4	17877	
ESGVLNOOPY	GENTREE	1.00	27.3	0.3	957.4	17877	
GNGDCHIILB	GGKEPNYSAK	0.90	30.1	-15	1193.6	17869	
GNGDCHIILR	GGKEPNYSAK	0.97	33.3	0.3	1193.6	17869	
TTHKTLAGPR	GGLILAKGGSEE	1.00	37.2	-0.4	1245.6	17889	
TTHKTLAGPR	GGLILAKGGSEE	1.00	37.4	-0.5	1245.6	17889	
TEEYGNMIDM	GILDPTKVTR	0.97	43.4	-1.5	1214.7	17905	
TEEYGNMIDM	GILDPTKVTR	0.82	36.2	-2.5	1214.7	17905	
GAILVVAATD	GPMPOTRE	0.99	34.8	0.3	1002.4	17897	
YTSPRVMOAO	GSOLTNKYAE	0.93	29.5	-0.9	1225.6	17889	
IEDVFSISGR	GTVVTGRVE	0.97	38	-1.3	1004.5	17897	
IEDVFSISGR	GTVVTGRVE	0.96	41.7	-2.4	1004.5	17897	
ARGAIFGLTR	GVNANHIIR	0.82	38.9	-2.3	1080.5	17903	
ARGAIFGLTR	GVNANHIIR	1.00	50.6	-1.4	1080.5	17903	
GDGVGMAIRA	GVPVQDM	0.80	22.6	-1.6	832.3	17869	
QLQQVLMMSR	HNLRAPLANNGSVLE	0.75	37.4	1.9	1691.8	17872	
QLQQVLMMSR	HNLRAPLANNGSVLE	1.00	52.6	1.0	1691.8	17872	
SNYFFDTTQG	HSQINGCTVR	0.77	25.4	-0.8	1258.6	87082	
IVGGGIANTF	IAAQGHDVGKSLYE	0.99	38.6	0.4	1602.8	17892	
IVGGGIANTF	IAAQGHDVGKSLYE	1.00	38.8	-0.1	1602.8	17892	
WWMLHEETVY	KGGDTVTLNE	0.75	28.5	-0.9	1148.5	87082	
GKSASAKSLF	KLQTLGLTQ	1.00	35.2	-1.1	1116.6	17887	
GKSASAKSLF	KLQTLGLTQ	1.00	31.7	-0.8	1116.6	17887	
KNPQKNLYTF	KNQASNDLPN	1.00	33.4	-1.6	1215.6	87082	
KNPQKNLYTF	KNQASNDLPN	0.99	21.7	-2.3	1215.6	87082	
KNPQKNLYTF	KNQASNDLPN	1.00	30	-1.4	1215.6	87082	
VYIEGQLRTR	KWTDQSGQDRYTTE	1.00	38.5	-0.3	1829.8	17904	
VYIEGQLRTR	KWTDQSGQDRYTTE	1.00	42	0.4	1829.8	17904	
ETGYSNKVLD	LIAHISK	0.91	34.5	-0.8	896.5	17880	
QKEADKLGYN	LVVLDSQNNPAKE	1.00	37.5	-0.7	1541.8	17901	
SNYQPSPMVR	MMKADAAPVSAQE	0.99	35.2	1.5	1463.6	17892	
SNYQPSPMVR	MMKADAAPVSAQE	1.00	35	0.0	1463.6	17892	
AQKEADKLGY	NLVVLDSQNNPAKE	0.95	37.6	0.9	1655.8	17901	
AQKEADKLGY	NLVVLDSQNNPAKE	1.00	37.9	-0.2	1655.8	17901	
AQKEADKLGY	NLVVLDSQNNPAKE	1.00	44.7	-0.2	1655.8	17901	
KDPLDNTYTR	NMYIVKH	0.99	32	-0.6	1019.5	17874	
KDPLDNTYTR	NMYIVKH	1.00	28.4	-0.1	1019.5	17874	
AESVKNIFGY	QYTIPTHQGRGAE	0.95	35.1	-0.3	1544.7	87082	
AESVKNIFGY	QYTIPTHQGRGAE	1.00	39.2	-0.9	1544.7	87082	
GINCNLTLLF	SFAOARACAE	1.00	31.2	-2.7	1197.5	17861	

Table S2. Cont.

Nonnrime

AC PNAS

sequence (inferred from database)	Prime-side sequence (LC-MS/MS)	PeptideProphet probability score	X!Tandem hyperscore	Mass accuracy (ppm)	Neutral mass (Da)	Examplary protein accession	Discarded from PICS profile
YAKDGISYTF	SIVPNALGKDDE	0.91	36.7	-2.3	1372.7	17871	
YAKDGISYTF	SIVPNALGKDDE	0.99	40.1	0.6	1372.7	17871	
EMFGYATQLR	SLTKGRASYTME	0.78	32.3	-0.1	1458.7	17897	
KGLNVMQNLL	TAHPDVQAVFAQNDE	1.00	34.4	4.9	1728.8	17901	
KGLNVMQNLL	TAHPDVQAVFAQNDE	1.00	48.3	-2.1	1728.7	17901	
KGLNVMQNLL	TAHPDVQAVFAQNDE	1.00	41	-2.0	1728.7	17901	
CKKNPQKNLY	TFKNQASNDLPN	0.91	24.4	-0.7	1463.7	87082	
CKKNPQKNLY	TFKNQASNDLPN	1.00	30.8	1.3	1463.7	87082	
CKKNPQKNLY	TFKNQASNDLPN	0.98	24	-0.3	1463.7	87082	
SVKNIFGYQY	TIPTHQGR	0.93	33.5	-1.2	996.5	87082	
SVKNIFGYQY	TIPTHQGR	1.00	37.3	-0.3	996.5	87082	
SVKNIFGYQY	TIPTHQGRGAE	0.76	34.3	-1.4	1253.6	87082	
KEASAGKLVR	TLAAVRDAKEAA	0.95	34.8	-1.4	1330.7	17904	
VQVNEADALY	TNPAQARE	1.00	41.3	-2.3	973.4	87082	
VQVNEADALY	TNPAQARE	1.00	38.6	-2.2	973.4	87082	
EHAVPMAKAL	VAGGVRVLE	1.00	47.4	-1.0	986.5	17881	
MVMPGDNIKM	VVTLIHPI	1.00	28.6	3.2	978.6	17897	
GVKLINAVQD	VYLDSKITIA	0.91	25.8	-1.6	1237.7	87082	
KTTTTERILF	YTGVNHKIGE	0.96	34.8	-0.1	1232.6	17897	
KTTTTERILF	YTGVNHKIGE	0.95	32.9	0.2	1232.6	17897	

Nonprime-side sequences are reported up to the position P10. X denotes ambiguous nonprime side residues. A small number of cleavage sites have P1 residues, which correspond to a potential cleavage-site of the digestion protease used for library generation. These cases might be related to incomplete amine protection during library preparation. Hence, prime-side cleavage products with such amino-termini are omitted from the PICS analysis, as well as prime-side cleavage products with amino terminini that correspond to a potein amino terminus. One exemplary protein is stated for each identified peptide sequence. X! Tandem was applied to assign peptides to tandem mass spectra and the X!Tandem hyperscore is reported together with the PeptideProphet probability score. C signifies carboxyamidomethylated cysteine and K signifies di-methylated lysine. Some peptides were identified repeatedly by LC-MS/MS; however, the set of sequences was rendered nonredundant before analysis in the form of sequence logos.

Table S3. NSP4 cleavage sites from a tryptic peptide library

PNAS PNAS

UNLEGGEVOR AAAPSCARTSCR 1.00 58.1 1.0 1119.5 17891 VERNCGEVOR ALDUINGLOA 1.00 41.7 0.5 1259.6 17873 EEARLITTYO ALDUINGLOA 1.00 41.7 0.5 1259.6 17873 EEARLITTYO ALDUINGLOA 0.08 33 -0.5 1048.5 17891 ELEGUVVCQC ACGRARYDACK 1.00 53.8 -0.5 1215.6 87082 ERANNINVN ALACUINTROLA 1.00 49.6 -3.1 1835.9 17892 VUBKATELTA ALACUINTROLA 0.65 33 -1.4 931.5 17897 VUBKATELTA ALACUINT 0.74 391 -1.9 1062.5 87082 ETRANGEPRA ALACUINT 0.94 3.0 1136.6 17905 COUNTATUL ALACUINT 0.91 1.6 1308 -3.3 1015.5 17802 EIANGEPRA ALACUNT 0.81 30.8 -3.3 1158.6 17905	sequence (inferred from database)	Prime-side sequence (LC-MS/MS)	PeptideProphet probability score	X!Tandem hyperscore	Mass accuracy (ppm)	Neutral mass (Da)	Examplary protein accession	Discarded from PICS profile
VILGOCRYCH AMAPEGASTOSR 1.00 55 -0.5 1119.5 17831 EEARKITTYQ ALIDYINGQA 1.00 45.3 -1.5 1259.6 17873 EEARKITTYQ ALIDYINGQA 1.00 57.2 -2.8 1215.6 87082 LEEGVVQCD AGGIARYDARCK 1.00 57.2 -2.8 1215.6 87082 ERAKININN ALACGARTORACK 1.00 77.6 0.4 1835.9 17892 VIDEGATTITA ALACCIMANTWOLK 0.04 9.6 -3.1 1835.9 17897 VIDEGATTITA ALACCIMANTWOLK 0.05 32.8 -7.5 9.31.5 17887 VIDEGATTITA ALACCIMANT 0.99 9.7.9 -0.4 1062.5 87082 HIPADOFFRA ALACLIMA 0.9 9.7.9 -0.4 1082.5 87082 HIPADOFFRA ALACLIMAN 0.9 45.5 -0.1 115.6 17895 HIPADOFFRA ALACLIMAN 0.9 9.45.5 -0.1 158.6	VHLEGGFVGM	AAAPSGASTGSR	1.00	58.1	1.0	1119.5	17891	
EARLETTYQ ALIPLINGUA 1.00 41.7 0.5 1253.6 17873 HERGENYURA AATBCINGUA 0.00 33 -0.5 10045.5 17891 HERGENYURA AATBCINGUAR 1.00 53.8 -0.5 10145.5 87082 HERGENYURA AAGUARAYDARK 1.00 53.8 -0.5 1215.6 87082 HERGENYURA AAGUARAYDARK 1.00 49.6 -3.1 1835.9 17892 VIDHKYTITA ALACEDYK 0.74 39.1 -1.9 1062.5 87082 VIDHKYTITA ALACEDYK 0.74 39.1 -1.9 1062.5 87082 VIDHKYTITA ALACEDYK 0.81 30.8 -3.3 1015.5 17893 GOUTTATAYL AQAITESCLK 0.83 49.5 4.0 1158.6 17905 GOUTTATAYL AQAITESCLK 0.83 49.5 4.0 1158.6 17893 LAVDESUPP AVGERARIANK 0.09 45.4 0.6 1248.6 17	VHLEGGFVGM	AAAPSGASTGSR	1.00	55	-0.5	1119.5	17891	
ELALETTYO ALTEYINGGA 1.00 45.3 -1.5 129.6 (7873 LEEGGYVGG AGGUARYUNGK 1.00 57.2 -2.8 1215.6 87082 LEEGGYVGG AGGUARYUNGK 1.00 57.2 -2.8 1215.6 87082 EWARNINN ALTROMATINTQUER 1.00 77.6 0.4 1835.9 17892 EWARNINN ALTROMATINTQUER 1.00 49.6 -3.1 1835.9 17892 VURKTULTA ALTYULAK 0.65 33 -1.4 931.5 17897 VURKTULTA ALTYULAK 0.65 33 -1.4 931.5 17897 VURKTULTA ALTYULAK 0.65 32.8 -7.5 931.5 17897 VURKTULTA ALTYULAK 0.85 32.8 -7.5 931.5 17897 UNRKTULTA ALTYULAK 0.81 30.8 -3.3 1015.5 17888 GUCTTARVL AQLITICLK 0.81 30.8 -3.3 1015.5 17888 GUCTTARVL AQLITICLK 0.99 45.5 -0.1 118.6 17905 GUCTTARVL AQLITICLK 0.90 45.4 0.1 118.6 17905 GUCTTARVL AQLITICLK 0.90 57.1 0.4 77.5 17888 UNREGRYT ANDALANNER 1.00 57.4 0.4 77.5 17888 UNREGRYT ANDALANNER 1.00 57.4 0.4 77.5 17897 LAVIDERYPT ANDALANNER 1.00 41.7 -1.1 118.5 17877 CONTROLOGNER 1.00 47.9 -30 111.5 17877 CONTROLOGNER 1.00 47.9 -1.8 125.8 7 17891 LAVIDERYPT ANDALANNER 1.00 47.7 -1.1 1108.5 17877 CONTROLOGNER 1.00 47.9 -30 111.5 17877 CONTROLOGNER 1.00 47.9 -30 111.5 17877 CONTROLOGNER 1.00 47.2 -1.7 156.6 17877 CONTROLOGNER 1.00 47.2 -1.7 157.8 17899 VURSENTISL CALOCOMMER 1.00 47.2 -1.7 157.8 17899 VURSENTISL CALOCOMANER 0.09 33 -1.6 1387.7 17904 CON	EEAEKITTVQ	AAIDYINGHQA	1.00	41.7	0.5	1259.6	17873	
HEBCOYVOM ADSOLVERS 0.98 33 -0.5 1048.5 17891 LEETGVVCQ ADGHAAVDACK 1.00 57.2 -28 1215.6 87082 LEETGVVCQ ADGHAAVDACK 1.00 57.2 -28 1215.6 87082 EVAANHINVN ATARCYARTNYCQLR 1.00 77.6 0.4 1835.9 17892 VUNKYTLIA ATTYLAK 0.65 33 -14 931.5 17897 VUNKYTLIA ATTYLAK 0.85 32.8 -7.5 931.5 17897 VUNKYTLIA ATTYLAK 0.85 32.8 -7.5 931.5 17897 VUNKYTLIA ATTYLAK 0.85 32.8 -7.5 931.5 17897 UNKYTLIA ATTYLAK 0.83 0.99 37.9 -0.4 1082.5 87082 HIPADEFAQ ALACELYK 0.99 37.9 -0.4 1082.5 87082 HIPADEFAQ ALACELYK 0.99 47.9 -0.4 1082.5 87082 HIPADEFAQ ALACELYK 0.99 45.5 -0.1 1158.6 17905 GOGTTATYL AQAITEGLK 0.99 45.4 0.6 1284.6 17899 LAVEEFOFT AVGFARLANNK 0.99 45.4 0.6 1284.6 17899 LAVEEFOFT AVGFARLANNKDFF 1.00 57.1 0.4 1745.9 17899 LAVEEFOFT AVGFARLANNKDFF 1.00 38 0.0 1188.5 87082 KVONACYVV AVLAELAN 1.00 41.7 -1.1 1108.5 17877 GUNTIGEEA CHLGGMAK 1.00 37.9 -30 1118.5 17877 GUNTIGEEA CHLGGMAK 1.00 42.2 -1.7 1161.5 17897 GUNTIGEEA CHLGGMAK 1.00 42.4 -4.3 1161.5 17897 GUNTIGEEA CHLGGMAK 1.00 42.4 -4.3 1161.5 17897 GUNTIGEEA CHLGGMAK 1.00 42.4 -4.3 1161.5 17897 GUNTIGEEA CHLGGMAK 1.00 43.8 -0.9 1164.6 17877 TOTMITAND CHEMADYK 1.00 42.2 -1.7 1161.5 17897 GUNTIGEEA CHLGGMAK 1.00 57.3 2.7 1607.7 17964 HERACHTR CHEMADYK 1.00 42.4 -4.3 1161.5 17897 GUNTIGEEA GUNTGGALGGAK 1.00 57.3 2.7 1607.7 17964 HERACHTR CHEMADYK 1.00 42.4 -4.3 1161.5 17897 GUNTIGEEA GUNTGGALGGAK 1.00 57.3 2.7 1607.7 17964 HERACHTR CHEMADYK 1.00 41.9 -0.4 124.6 17877 HERACHTR CHEMADYK 1.00 41.9 -0.4 124.6 17877 HERACHTR CHEMADYK 1.00 42.7 3.7 120.6 17889 HIPADEFENCT 1.00 57.3 2.7 1607.7 17964 HERACHTR CHEMADYK 1.00 57.1	EEAEKITTVQ	AAIDYINGHQA	1.00	45.3	-1.5	1259.6	17873	
LEELGUVQQC AGGBARYDACK 1.00 57.2 -2.8 1215.6 87082 ENAMENINW ALLACYARINHTQUER 1.00 77.6 0.4 1835.9 17892 ENAMENINW ALLACYARINHTQUER 1.00 49.6 -3.1 1835.9 17892 VINEKYTLTA ALTYUAK 0.65 33 -1.4 931.5 17897 VINEKYTLTA ALTYUAK 0.65 32 -1.5 931.5 17897 VINEKYTLTA ALTYUAK 0.68 32.8 -7.5 931.5 17897 VINEKYTLTA ALTYUAK 0.99 37.9 -0.4 1082.5 87082 VINEKYTLTA ALTYUAK 0.99 37.9 -0.4 1082.5 87082 VINEKYTLTA ALTYUAK 0.99 37.9 -0.4 1082.5 87082 VINEKYTLTA ALTYUAK 0.99 45.5 -0.1 1158.6 17905 GCOTTATYU AQALITECLK 0.90 45.5 -0.1 1158.6 17905 COCTTATYU AQALITECLK 0.90 45.4 0.6 1248.6 17899 LAVDESFQF AVGRARINK 1.00 49.6 2.3 1248.6 17899 LAVDESFQF AVGRARINK 1.00 57.1 0.4 1745.9 17899 VINEKYTLTA VAGARALINK 1.00 57.1 0.4 1745.9 17899 VINEKYTLTA VAGARALINK 1.00 57.1 0.4 1745.9 17899 VINEKYTLTA VAGARALINKNEPE 1.00 57.1 0.4 1745.9 17899 VINEKYTLTA VAGARALINKNEPE 1.00 57.1 0.4 1745.9 17899 VINEKYTATY AVGRARALINKNEPE 1.00 41.7 -1.1 1108.5 17877 VINEKYTLTA VAGARALINKNEPE 1.00 44.8 0.4 1113.5 17877 VINEKYTY AVGRARALINKNEPE 1.00 44.8 0.4 1113.5 17877 CINTIGSEA CHLOGAMK 1.00 47.9 -3.0 113.5 17871 CINTIGSEA CHLOGAMK 1.00 57.1 -0.7 1	HLEGGFVGMA	AAPSGASTGSR	0.98	33	-0.5	1048.5	17891	
LEBIGVOQQ ACCHARVORCK 1.00 33.8 -0.5 1215.6 87082 ENARHITUN ALLAPEYDATNUTQUER 1.00 77.6 0.4 1835.9 (72892 VDEKTTLE ALTSTVLAK 0.65 331.4 931.5 (72897 VDEKTTLE ALTSTVLAK 0.85 32.8 -7.5 931.5 (72897 VDEKTTLE ALTSTVLAK 0.85 32.8 -7.5 931.5 (72897 VDEKTTLE ALTSTVLAK 0.85 32.8 -7.5 931.5 (72897 VDEKTTLE ALTSTVLAK 0.99 37.9 -0.4 1082.5 87082 HIPADOPPAQ ALACELYK 0.99 37.9 -0.4 1082.5 87082 COCTTATVL AQALTECLK 0.99 45.5 -0.1 1158.6 (7395 COCTTATVL AQALTECLK 0.83 49.5 4.0 1158.6 (7395 COCTTATVL AQALTECLK 0.83 49.5 4.0 1158.6 (7395 LAVDESPEPT AVGRARAINK 0.99 45.4 0.6 1248.6 (7289 LAVDESPEPT AVGRARAINK 0.99 45.4 0.6 1248.6 (7289 LAVDESPEPT AVGRARAINKERE 1.00 57.1 0.4 1745.9 (7289 LAVDESPEPT AVGRARAINKERE 1.00 57.1 0.4 1745.9 (7289 LAVDESPEPT AVGRARAINKERE 1.00 57.1 0.4 1745.9 (7289 LAVDESPEPT AVGRARAINKERE 1.00 41.7 -1.1 1108.5 (7877 CONTATVL AQALTECLK 0.84 35.2 0.1 1108.5 (7877 CONTATVL ANDELEK 1.00 44.8 0.4 1113.5 (7877 CONTATVL ANDELEK 1.00 44.8 0.4 1113.5 (7877 CONTATVL ANDELEK 1.00 42.4 -4.3 1161.5 (7877 CONTATVL ANDELEK 1.00 42.4 -4.3 1161.5 (7877 CONTATVK ANDELEK 1.00 45.2 -3.1 156.6 (7777 CONTATVK 1.00 42.4 -4.3 1161.5 (7877 CONTATVK 1.00 45.2 -3.1 156.6 (7777 CONTATVK 1.00 45.2 -3.1 156.6 (7777 CONTATVK 1.00 45.2 -3.1 156.6 (7777 CONTATVK 1.00 45.2 -3.1 157.7 (7904 CARAQULAT CONTATVK 1.00 45.4 -1.3 157.7 (7904 CARAQULAT CONTATVK 1.00 45.4 -1.3 157.7 (7904 CARAQULAT CONTATVK 1.00 45.4 -1.4 156.6 (7877 CONTATV CONTATVK 1.00 45.7 -2.5 188.0 (7899 CONTATV 1.5 CONTATVK 1.00 45.7 -2.5 188.0 (7899 CONTATV 1.5 CONTATVK 1.00 45.7 -2.5 188.0 (7899 CONTATV 1.5 CONTATVENTENTENT 1.00 53.3 -1.6 (7879 CONTATVENTENTENTENTENTENTENTENTENTENTENTE	LEEIGVVCQQ	AGGHAAFVDAGK	1.00	57.2	-2.8	1215.6	87082	
EMARHENDM ALTAPEYIASINETQUER 1.00 //.6 0.4 185.9 /7892 WARKHENDM ALTAPEYIASINETQUER 1.00 496 -3.1 185.9 /7897 VUBEKTILTA ALTTVLAK 0.65 33 -14 991.5 /7897 VUBEKTILTA ALTTVLAK 0.65 32 -7.5 991.5 /7897 VUBEKTILTA ALTTVLAK 0.74 39.1 -1.9 1082.5 87082 HIPADOPEAQ ALACELYK 0.09 37.9 -04 1082.5 87082 HIPADOPEAQ ALACELYK 0.09 41.8 0.2 1082.5 87082 HIPADOPEAQ ALACELYK 0.09 45.5 -0.1 1158.6 17905 GOGTTATVL AQAITESLE 0.90 45.5 -0.1 1158.6 17905 GOGTTATVL AQAITESLE 0.90 45.4 0.6 1248.6 17899 LAVDESFQPT AVGRADALINK 1.00 49.6 2.3 1248.6 17899 LAVDESFQPT AVGRADALINK 0.09 45.4 0.6 1248.6 17899 LAVDESFQPT AVGRADALINK 0.09 45.4 0.6 1248.6 17899 LAVDESFQPT AVGRADALINKOPE 1.00 57.1 0.4 1745.9 17899 NEDEAVA.16.4 XAGGULTGOVK 1.00 61.9 -1.8 1258.7 17861 LAVDESFQPT AVGRADALINKOPE 1.00 37.1 0.4 1745.9 17899 NEDEAVA.16.4 XAGGULTGOVK 1.00 61.9 -1.8 1258.7 17861 LAVDESFQPT AVGRADALINKOPE 1.00 44.8 0.4 1113.5 17877 GORTATVL AMAILEE 1.00 48.4 0.4 1113.5 17877 CONTAGULT AVGRADALINKOPE 1.00 47.9 -1.1 1108.5 17877 CONTAGULT AVGRADALINKOPE 1.00 42.5 -1.7 1108.5 17877 CONTAGULT AVGRADALINKOPE 1.00 47.9 -3.0 1113.5 17877 CONTAGULT AVGRADALINKOPE 1.00 47.9 -3.0 1113.5 17877 CONTAGULT AVLADETAK 0.84 35.2 0.1 1108.5 17877 CONTAGULT AVLADETAK 0.84 35.2 0.1 1108.5 17877 CONTAGULT CONTAGUNK 1.00 42.5 -3.1 156.6 17877 CONTAGULT CONTAGUNK 1.00 42.5 -3.1 156.6 17877 CONTAGULT CONTAGUNK 1.00 45.2 -3.1 156.6 17877 CONTAGULT CONTAGUNK 1.00 45.2 -3.1 156.6 17877 CONTAGULT CONTAGUNK 1.00 45.8 -1.6 13577 17904 VDESFORTVL CEGLADVVK 1.00 45.8 -1.6 13577 17904 VDESFORTVL CEGLADVVK 1.00 45.9 -1.7 1161.5 17881 DESKRITISL GALTGGOALGOAK 1.00 65.8 -1.6 13577 17904 VDESFORTVL GEAVINANCE 0.97 41.7 2.7 157.8 17899 VDESFORTVL GEAVINANCE 0.98 36.5 1.3 102.4 17877 VDESFORTVL GEAVINANCE 0.98 36.5 1.3 102.4 17877 VDESFORTVL GEAVINANCE 0.98 36.5 1.3 102.4 17877 VEEDAVING GEAVINANCE 0.98 36.5 1.3 102.4 17877 VEEDAVING GEAVINANCE 0.98 36.5	LEEIGVVCQQ	AGGHAAFVDAGK	1.00	53.8	-0.5	1215.6	87082	
EVARUMENTEDA ALACEDEVEK 1.00 49.6 -3.1 183.9 1492 VUNEKTELTA ALTTVIJAK 0.85 32.8 -7.5 931.5 17897 VUNEKTELTA ALTTVIJAK 0.85 32.8 -7.5 931.5 17897 HIFADQFFAQ ALACEDEVEK 0.74 39.1 -1.9 1082.5 87082 UNEKTELTA QALACEDEVEK 0.99 37.9 -0.4 1082.5 87082 EVMSGLGGFG ALCALPOK 0.81 30.8 -3.3 1015.5 17888 GOGTTTATVL AQALITECLK 0.83 49.5 -0.1 1158.6 17905 COGTTTATVL AQALITECLK 0.83 49.5 4.0 1158.6 17905 LAVDESFQFT AVCEALANKE 0.99 45.4 0.6 1248.6 17899 LAVDESFQFT AVCEALANKENEE 1.00 57.1 0.4 1745.9 17899 LAVDESFQFT AVCEALANKENEE 1.00 57.1 0.4 1745.9 17899 LAVDESFQFT AVCEALANKENEE 1.00 38 0.0 1188.5 87082 LAVDESFQFT AVCEALANKENEE 1.00 37.9 -1.8 1258.7 17861 LAVDESFQFT AVCEALANKENEE 1.00 37.9 -1.8 1258.7 17861 LAVDESFQFT AVCEALANKENEE 1.00 37.9 -1.8 1258.7 17861 LAVDESFQFT AVCEALANKENEE 1.00 37.9 -3.0 1113.5 17877 CTHTIGSEE CHLOGENEK 1.00 42.5 -1.7 1161.5 17877 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17877 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17877 CTHTIGSEE CHLOGENEK 1.00 42.5 -1.7 1161.5 17887 CTHTIGSEE CHLOGENEK 1.00 37.9 -3.0 1113.5 17877 CTHTIGSEE CHLOGENEK 1.00 42.5 -1.7 1161.5 17887 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17877 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17887 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17887 CTHTIGSEE CHLOGENEK 1.00 42.5 -1.7 1161.5 17887 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17877 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17877 CTHTIGSEE CHLOGENEK 1.00 47.9 -3.0 1113.5 17881 DIDRITKLAR EAVRGARL 0.99 31 -0.5 931.5 17881 DIDRITKLAR EAVRGARL 0.99 31 -0.5 931.5 17881 DIDRITKLAR EAVRGARL 0.99 31 -0.5 931.5 17881 DIDRITKLAR EAVRGARL 0.99 38 0.6 123.46 17877 T9704 VESEFQTAVO GEALINKENEE 0.97 417 2.7 1575.8 17899 VESEFQTAVO GEALINKENEE 0.97 417 2.7 1575	EWAKHNINVN	AIAPGYMATNNTQQLR	1.00	//.6	0.4	1835.9	17892	
VDERKTITIAR Altrivia 0.05 33 -1.4 931.5 17897 HIPADQFPAQ ALLCELYK 0.74 391 -1.9 1082.5 87062 HIPADQFPAQ ALLCELYK 0.74 391 -1.9 1082.5 87062 HIPADQFPAQ ALLCELYK 0.00 41.8 0.2 1082.5 87062 COCTTRATVL AQALITECLK 0.90 45.5 -0.1 1158.6 17905 COCTTRATVL AQALITECLK 0.80 45.5 -0.1 1158.6 17905 LAVDESPQFT AVCFAZALNEK 1.00 49.6 2.3 1245.6 17899 LAVDESPQFT AVCFAZALNEKKER 1.00 57.1 0.4 174.5 17861 LAVDESPQFT AVGFAZALNEKKER 1.00 51.9 -1.8 128.5 17861 LAVDESPQFT AVGFAZALNEKKER 1.00 51.6 -1.4 138.5 17877 VOLASYQVA ATLABELAR 1.00 37.6 -1.7 1161.5 1787	EWAKHNINVN	AIAPGYMATNNTQQLR	1.00	49.6	-3.1	1835.9	17892	
VDREATLINA ALTERLEX 0.74 39.1 -1.9 102.5 87062 HIPADQFPAQ ALACELYK 0.99 37.9 -0.4 108.25 87062 HIPADQFPAQ ALACELYK 0.98 37.9 -0.4 108.25 87062 GEOTTATVL AQALITECLK 0.81 30.8 -3.3 1015.5 17888 GEOTTATVL AQALITECLK 0.83 49.5 4.0 1158.6 17905 LAVDESPQPT AVCFALADNR 0.99 45.4 0.6 1248.6 17899 LAVDESPQPT AVCFALADNR 0.99 45.4 0.6 1248.6 17899 LAVDESPQPT AVCFALADNR 0.99 45.4 0.6 1248.6 17899 LAVDESPQPT AVCFALADNRCKPE 1.00 57.1 0.4 1745.9 17899 LAVDESPQPT AVCFALADNRCKPE 1.00 57.1 0.4 1745.9 17899 LAVDESPQPT AVCFALADNRCKPE 1.00 38 0.0 1188.5 87062 CONTACT AVCFALADNRCKPE 1.00 37.9 -1.0 1180.5 17877 FVQUASYOVA ALADELAK 0.84 352 0.1 1108.5 17877 FVQUASYOVA ALADELAK 0.84 352 0.1 1108.5 17877 CONTACTVA AVLADELAK 0.84 352 0.1 1108.5 17877 FVQUASYOVA ALADELAK 0.84 352 0.1 1108.5 17877 FVQUASYOVA ALADELAK 0.99 31 -0.5 31.1 51.5 17887 CONTACTVA CONDENVER 1.00 42.5 -1.7 1161.5 17897 FPRIVANOV CPERADONK 1.00 42.5 -1.7 1161.5 17897 FPRIVANOV CPERADONK 1.00 57.6 -1.4 1546.6 17877 FPRIVANOV CPERADONK 1.00 57.6 -1.4 1546.6 17877 FPRIVANOV CPERADONK 1.00 57.8 -2.1 357.7 17904 CENTROSEA 041.6 AUX02.7 17881 FPRIVANOV CPERADONK 1.00 57.8 -2.1 357.7 17904 FVDESPQETA GALADENKER 0.97 41.7 2.7 157.8 17891 FDIDITIKLAR EAVERARL 0.99 31 -0.5 931.5 17881 FDIDITIKLAR EAVERARL 0.00 57.3 -2.1 357.7 17904 FVDESPQETAV GEALADENKER 0.97 41.7 2.7 157.8 17899 FVDESPQETAV GEALADENKER 0.07 45.9 0.9 157.8 17899 FVDESPQETAV GEALADENKER 0.97 41.7 2.7 157.8 17899 FVEDENLOVOK GEALAMENTER 0.97 41.7 2.7 157.8 17899 FVEDENLOVOK GEALAMENTER 0.97 41.7 2.7 157.8 17899 FVEDENLOVOK GEALAMENTER 0.97 3.3 1.6 188.9 17899 FVEDENLOVOK	VDHGKTTLTA	AITTVLAK	0.65	33	-1.4	931.5	17897	
H PADQPFAQ ALACELYK 0.99 37.9 -0.4 1082.5 87082 HTPADQPFAQ ALACELYK 0.09 37.9 -0.4 1082.5 87082 HTPADQPFAQ ALACELYK 0.09 47.5 -0.1 105.5 17888 GDGTTTATYL AQAITEGLK 0.90 45.5 -0.1 105.6 17905 GDGTTTATYL AQAITEGLK 0.83 49.5 -0.1 105.6 17905 LAVDESPQPT AVGRAALMNK 0.09 45.4 0.6 1246.6 17899 LAVDESPQPT AVGRAALMNK 0.09 45.4 0.6 1246.6 17899 LAVDESPQPT AVGRAALMNKKEFE 1.00 53.4 0.4 1745.9 17899 HAVDESPQT AVGRAALMNKKEFE 1.00 53.4 0.4 1745.9 17899 HEADDESPQT AVGRAALMNKKEFE 1.00 53.4 0.4 1745.9 17899 HEADDESPQT AVGRAALMNKKEFE 1.00 57.1 0.4 1745.9 17899 HEADDESPQT AVGRAALMNKKEFE 1.00 57.1 0.4 1745.9 17897 HYQUASYQVA AYLABELAK 1.00 41.7 -1.1 1108.5 17877 HYQUASYQVA AYLABELAK 1.00 41.7 -1.1 1108.5 17877 HYQUASYQVA AYLABELAK 1.00 42.5 -1.7 1161.5 17877 HYQUASYQVA AYLABELAK 1.00 42.5 -1.7 1161.5 17877 TFTHRIFARVD CHGHADYVK 1.00 42.5 -1.7 1161.5 17877 TFTHRIFARVD CHGHADYVK 1.00 42.5 -1.7 1161.5 17897 TFTHRIFARVD CHGHADYVK 1.00 51.6 -1.4 1546.6 17877 TFTHRIFARVD CHGHADYVK 1.00 45.2 -1.7 1161.5 17897 TFTHRIFARVD CHGHADYVK 1.00 45.2 -1.1 357.7 17904 DESKCTINSL GALTCOQALCOAK 1.00 65.8 -1.6 1357.7 17904 DESKCTINSL GALTCOQALCOAK 1.00 65.8 -1.6 1357.7 17904 DESKCTINSL GALTCOQALCOAK 1.00 65.8 -1.6 1357.7 17904 DESKCTINSL GALTCOQALCOAK 1.00 43.9 0.9 1575.8 17881 DESKCTINSL GALTCOQALCOAK 1.00 57.3 -2.1 931.5 17881 DESKCTINSL GALTCOQALCOAK 1.00 57.3 -2.1 931.5 17881 DESKCTINSL GALTCOQALCOAK 1.00 45.7 -2.5 1888.0 17899 YDESFOPTAV GFAALMNKKEFE 0.87 45.9 0.9 1575.8 17899 HERKLYTEFE GFTUSTVAK 1.00 41.1 -1.6 164.6 4894 AFTDEVATELAK 2.4 12.0 14.7 -1.7 107.5 17877 HYDRIFKLAR EAVEGAAL 1.00 57.3 -2.5 1880.0 17899 HERKLYTEFE GFTUSTVAK 1.00 45.7 -2.5 1887.0 17897 HERKLYTEFE GFTUSTVAK 1.00 57.1 -0.7 1887.9 17899 HERKLYTEFE GFTUSTVAK 1.00 57.1 -0.7 1887.9 17899 HERKLYTEFE GFTUSTVAK 1.00 57.1 -0.7 1887.9 17899 HERKLYTEFE GFTUSTVAK 1.00 57.1 -0.7 1887.9 17899 HERKLYTE	VDHGKTTLTA	AITTVLAK	0.85	32.8	-7.5	931.5	17897	
HIPADQPPRQ ALACEDYK 0.99 37.9 -0.4 1082.5 87082 EVMGCLGGFG ALCALPOK 0.81 30.8 -3.3 1015.5 17888 COUCTTATVL AQAITECLK 0.81 30.8 -3.3 1015.5 17888 COUCTTATVL AQAITECLK 0.83 49.5 -0.1 1158.6 17905 COUCTTATVL AQAITECLK 0.83 49.5 -0.1 1158.6 17905 LAVDESPOPT AVGFARALNNK 0.99 45.4 0.6 1288.6 17899 LAVDESPOPT AVGFARALNNK 0.99 45.4 0.6 1288.6 17899 LAVDESPOPT AVGFARALNNKNKPE 1.00 57.1 0.4 1745.9 17899 NPDEAVAIGA AVGFARALNNKNKPE 1.00 57.1 0.4 1745.9 17899 NPDEAVAIGA AVGFARALNNKNKPE 1.00 57.1 0.4 1745.9 17899 NPDEAVAIGA AVGGARALNNKNKPE 1.00 38 0.0 1188.5 87082 KVUNASYOVA AYLADEIAK 1.00 41.7 -1.1 1108.5 17877 CTNTIGSSEA CMLGGMARK 1.00 44.8 0.4 1113.5 17877 CTNTIGSSEA CMLGGMARK 1.00 44.8 0.4 1113.5 17877 TFTRNYAHVD CPEHADYVK 1.00 42.4 -4.3 1115.5 17887 TFTRNYAHVD CPEHADYVK 1.00 42.4 -4.3 1151.5 17887 TFTRNYAHVD CPEHADYVK 1.00 45.2 -1.7 155.8 17897 CONNEGMARK 1.00 55.8 -2.1 156.6 17877 DYNETYKLAR EAVEGAKL 1.00 55.8 -2.1 357.7 17904 ESKGYINSL GALTGGALQAK 1.00 65.8 -1.6 1357.7 17904 ESKGYINSL GALTGGALQAK 1.00 65.8 -1.6 1357.7 17904 ESKGYINSL GALTGGALQAK 1.00 65.8 -1.6 1357.7 17904 ESKKGYINSL GALTGGALQAK 1.00 65.8 -1.6 1357.7 17905 KTDGVVYTLS GFVESQAQAEEXVK 1.00 47.7 2.7 1575.8 17899 VDESPQETAV GFARALNNKNEPE 0.87 45.9 0.9 1164.6 48994 APAELLEFEF GFTVONVAK 1.00 47.9 -2.5 1887.9 1789 VDESPQETAV GFARALNNKNEPE 0.87 45.9 0.9 1164.6 48994 APAELLEFEF GFTVONVAK 1.00 45.7 -2.5 1887.9 17899 VDESPQETAV GFARALNNKNEPE 0.88 52 4.7 1107.5 17867 KTDGVVYTLS GFVESQAQAEEXVK 1.00 45.7 -2.5 1067.7 17908 KTDGVVYTLS GFVESQAQAEEXVK 1.00 45.7 -2.5 1067.7 17908 KTDGVVYTLS GFVESQAQAEEXVK 1.00 45.7 -2.5 1067.7 17905 CTANGTSTRYPEVPHY 1.00 50.1 0.0 477.7 1	HIPADQFPAQ	ALACELYK	0.74	39.1	-1.9	1082.5	87082	
H1PADQPPAQ ALGAEDYK 1.00 41.8 0.2 0.82.5 87082 EVMGGLGGTS ALCALPCK 0.90 45.5 -0.1 1158.6 17905 GOOTTTATVL AQAITESCLK 0.80 45.5 -0.1 1158.6 17905 LAVDESPOPT AVGFAELINNK 1.00 49.6 2.3 128.6 17899 LAVDESPOPT AVGFAELINNK 0.99 45.4 0.6 128.6 17899 LAVDESPOPT AVGFAELINNKDKPE 1.00 53.4 0.4 1745.9 17899 LAVDESPOPT AVGEVALLEDVK 1.00 61.9 -1.8 128.7 17861 DLINFKMTPV AWGHAELANNKDKPE 1.00 38 0.0 1188.5 17877 CYUNASYQVA AYLADEIAK 0.84 35.2 0.1 1108.5 17877 CYNNASYQVA AYLADEIAK 0.84 35.2 0.1 1108.5 17877 CYNNASYQVA AYLADEIAK 0.94 45.5 -1.7 1161.5 17897 CYNNICSSEA CMLGGMAMK 1.00 42.5 -1.1 151.5	HIPADQFPAQ	ALACELYK	0.99	37.9	-0.4	1082.5	87082	
EVMENDERYE ALLALPUK 0.81 0.8 -3.3 1015. 1788 COUTTATVL AQAITTEGLK 0.80 45.5 -0.1 1158.6 17905 COUTTATVL AQAITTEGLK 0.83 49.5 -0.0 1158.6 17905 LAVDESPERT AVGERALINKER 0.99 45.4 0.6 128.6 17899 LAVDESPERT AVGERALINKERE 1.00 57.1 0.4 1745.9 17899 LAVDESPERT AVGERALINKERE 1.00 38 0.0 1188.5 87082 KVQNASYQVA AYLADEIAK 0.84 35.2 0.1 1108.5 17877 CONTIGESEA CMLGOMARK 1.00 44.7 -1.1 1108.5 17877 CINTIGESEA CMLGOMARK 1.00 44.8 0.4 1113.5 17877 TPTERNARVD CPGHADVK 1.00 42.4 -4.3 1161.5 17897 TPTERNARVD CPGHADVK 1.00 42.4 -4.3 1161.5 17897 TPTERNARVD CPGHADVK 1.00 42.5 -1.7 1161.5 17897 CONACOUNT CONVER 1.00 45.2 -3.1 156.6 17877 TPTERNARVD CPGHADVK 1.00 45.2 -3.1 156.6 17877 TPTERNARVD CPGHADVK 1.00 45.2 -3.1 156.6 17877 CONNORNARY COTWODENNER 1.00 55.8 -1.6 1357.7 17904 ESKRYINSL GALTGGALQAK 1.00 65.8 -2.1 135.7 17904 VDESPERTV GEREALINKERE 0.87 45.9 0.9 157.8 17881 PESKRYINSL GALTGGALQAK 1.00 45.2 -3.1 156.6 17877 TVDESTELLA EAVEGAL 0.99 31 -0.5 931.5 17881 ESKRYINSL GALTGGALQAK 1.00 65.8 -1.6 1357.7 17904 ESKRYINSL GALTGGALQAK 1.00 45.7 2.7 1575.8 17899 VDESPERTV GEREALINKERE 0.87 45.9 0.9 157.8 17899 VDESPERTV GEREALINKERE 0.87 45.9 0.9 157.8 17899 VDESPERTV GEREALINKERE 0.87 45.9 0.9 157.8 17899 VDESPERTV GEREALINKERE 0.87 45.9 0.9 156.8 1607.7 17904 APAELLEEEF GETVONVAR 1.00 47.1 -1.6 1164.6 48994 APAELLEEFE GETVONVAR 1.00 47.1 -1.7 1575.8 17899 VDESPERTV GEREALINKERE 0.87 45.9 0.9 156.8 17877 VESSERTV GEREALINKERE 0.87 45.9 0.9 157.8 17899 VESSERTV GEREALINKERE 0.97 41.7 2.7 1575.8 17899 VESSERTV GEREALINKERE 0.97 41.7 2.7 1575.8 17899 VESSERTV GEREALINKERE 0.97 41.7 17883 CENTROVAR 0.00 47.0 1.00 57.1 -0.7 1887.9 17899 VESSERTV GEREALINKERE 0.98 36.5 1.3 1020.4 17897 VESSERTV	HIPADQFPAQ	ALACELYK	1.00	41.8	0.2	1082.5	87082	
CONTINATVL AQALITECLAR 0.90 49.5 -0.1 1188.6 17905 CONTINATVL AQALITECLAR 0.83 49.5 4.0 1158.6 17905 CONTINATVL AQALITECLAR 0.83 49.5 4.0 1158.6 17899 LAVDESPOPT AVGFRAALNNK 0.99 45.4 0.6 1248.6 17899 LAVDESPOPT AVGFRAALNNKKYEFE 1.00 53.4 0.4 1745.9 17899 HYDEAVAIGA AVQGVLTGDVK 1.00 51.9 -1.8 1258.7 17861 DLAVERSPOYT AVGFRAALNNKKYEFE 1.00 38 0.0 1188.5 8708.2 KVQNASYQVA AYLADELAK 0.84 35.2 0.1 1108.5 17877 GTNTIGSSEA CMLOGMARK 1.00 44.7 -1.1 1108.5 17877 GTNTIGSSEA CMLOGMARK 1.00 47.9 -3.0 1113.5 17877 GTNTIGSSEA CMLOGMARK 1.00 42.5 -1.7 1161.5 17897 CTNTIGSSEA CMLOGMARK 1.00 451.6 -1.4 1546.6 17877 TPTRIYAND CPGHADYVK 1.00 42.5 -1.7 1161.5 17897 CTNTIGSSEA CMLOGMARK 1.00 51.6 -1.4 1546.6 17877 CMARGULAFF COTWDEWIK 1.00 55.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 57.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 65.8 -1.6 1357.7 17904 ESKKYINSL GALIGGALQAK 1.00 65.8 -1.6 1357.7 17904 VDESTOPTAVA GFRAALQAR 1.00 45.2 0.3 1154.6 48994 APAELLEFEF GFTVDWVAK 1.00 43.1 -0.5 1357.7 17904 VDESTOPTAVA GFRAALQAR 1.00 65.8 -1.6 1357.7 17904 VDESTOPTAVA GFRAALNKKKFE 0.97 41.7 2.7 1575.8 17889 VDESTOPTAV GFRAALNKKKFE 0.97 41.7 2.7 1575.8 17899 VDESTOPTAV GFRAALNKKKFE 0.87 45.9 0.9 1575.8 17899 VDESTOPTAV GFRAALNKKKFE 0.97 41.7 2.7 1575.8 17899 VDESTOPTAV GFRAALNKKKFE 0.87 45.9 0.9 1575.8 17899 VDESTOPTAV GFRAALNKKKFE 0.88 35.2 4.7 1107.5 17877 KEGNVPAFTL GERATOLVWAR 1.00 41.9 -0.4 1234.6 17877 REGNVPAFTL GERATOLVWAR 1.00 41.9 -0.4 1234.6 17877 VESTOPTAVK GFRAALNKKK 1.00 57.1 -0.7 1887.9 17898 VGVDVVARAT GLADASYSK 0.88 35.2 4.7 1107.5 17877 KTEMAVYAR GLADASYSK 0.98 36.5 1.3 1020.4 17905 CTAAGTASIW GFRAGAAKK 1.00 75.9 -0.9 1307.6 17889 VGVDVVARAT GLADASYSK 0.95 36.5 -2.6 1020.4 1790	EVMGGLGGFG	ALCALPQK	0.81	30.8	-3.3	1015.5	1/888	
COCTTATVL AAAITTEGLK 0.83 49.5 4.0 1158.6 17905 LAVDESPOPT AVGFRAAINNK 0.99 45.4 0.6 1248.6 17899 LAVDESPOPT AVGFRAAINNKKKPE 1.00 57.1 0.4 1745.9 17899 LAVDESPOPT AVGFRAAINNKKKPE 1.00 57.1 0.4 1745.9 17899 LAVDESPOPT AVGFRAAINNKKKPE 1.00 61.9 -1.8 1258.7 17861 LAVDESPOPT AVGFRAAINNKKKPE 1.00 41.7 -1.1 1108.5 17877 CHLARDANGA AVGAGVLARK 1.00 44.8 0.4 1113.5 17877 CTMTIGSSEA CMLGGMANK 1.00 42.4 -4.3 1161.5 17897 GNARQNLAFF COTMODENVEK 1.00 45.2 -3.1 1546.6 17877 GNARQNLAFF COTMODENVEK 1.00 51.6 -1.4 1546.6 17877 GNARQNLAFF COTMODENVEK 1.00 56.8 -2.1 1357	GDGTTTATVL	AQAIITEGLK	0.90	45.5	-0.1	1158.6	17905	
LAVDESPOPT AVGPRAALINNK 1.00 49.6 2.3 1248.6 17899 LAVDESPOPT AVGPRAALINNK NEPE 1.00 53.4 0.4 1745.9 17899 LAVDESPOPT AVGPRAALINNKINKPE 1.00 53.4 0.4 1745.9 17899 NPDEXVAIGA AVQGVIJCOVK 1.00 51.9 -1.8 125.7 17861 DLNPKAMTFV AVRMLHEE 1.00 38 0.0 1188.5 87082 KVQINASYQVA AYLADEIAK 1.00 41.7 -1.1 1108.5 17877 GVMTSYQVA AYLADEIAK 1.00 44.7 -1.1 1108.5 17877 GVMTSYQVA AYLADEIAK 1.00 44.7 -1.1 1108.5 17877 GVMTSYQVA AYLADEIAK 1.00 44.7 -1.1 1108.5 17877 GVMTSSEA CMLGGMARK 1.00 42.5 -1.7 1161.5 17897 TPTRHYAHVD CPGHADYVK 1.00 42.5 -1.7 1161.5 17897 TPTRHYAHVD CPGHADYVK 1.00 45.2 -3.1 1154.6 17877 GVMTGSSEA CMLGGMARK 1.00 45.2 -3.1 1161.5 17897 TPTRHYAHVD CPGHADYVK 1.00 45.2 -3.1 1161.5 17897 TPTRHYAHVD CPGHADYVK 1.00 51.6 -1.4 1546.6 17877 GNARGNLAFF C2VMDDENVIK 1.00 55.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 65.8 -2.1 1357.7 17904 VDESPQPTAV GPABALINKICKEE 0.97 41.7 2.7 1575.8 17899 VDESPQPTAV GPABALINKICKEE 0.97 41.7 2.7 1575.8 17899 VDESPQTAV GPABALINKICKEE 0.97 41.7 1.7 17908 KTDQKVVTLS GPVESQAQABEAVK 1.00 57.3 2.7 1607.7 17908 KTDQKVVTLS GPVESQAQABEAVK 1.00 57.3 2.7 1607.7 17908 KTDQKVVTLS GPVESQAQABEAVK 1.00 57.1 -0.7 1887.9 17891 KFDQKUDVQ GIAVVPFAVPH 1.00 55.1 -0.7 1887.9 17899 KFDQKUDVQ GIAVVPFAVPH 1.00 55.1 -0.7 1887.9 17899 KFDQKUDVQ GIAVVPFAVPH 1.00 55.1 -0.7 1887.9 17899 KFDQKUDVQ	GDGTTTATVL	AQAIITEGLK	0.83	49.5	4.0	1158.6	17905	
LAVDESUPT AVGRAEALANNER 0.99 45.4 0.6 1246.6 17899 LAVDESUPT AVGRAEALANNERVE 1.00 57.1 0.4 1745.9 17889 LAVDESUPT AVGRAEALANNERVE 1.00 57.1 0.4 1745.9 17889 DLAVEANTEV AVMARTHEE 1.00 57.1 0.4 1745.9 17869 EVVINASYQVA AVLADELAN 0.4 1.00 41.7 -1.1 108.5 17877 GUNTICOSEA CHLCGNAMK 1.00 41.7 -1.1 108.5 17877 GUNTICOSEA CHLCGNAMK 1.00 44.8 0.4 1113.5 17877 GUNTICOSEA CHLCGNAMK 1.00 42.4 -4.3 1161.5 17897 TPTRILYAMVD CPCHADVK 1.00 42.5 -1.7 1161.5 17897 TPTRILYAMVD CPCHADVK 1.00 45.2 -3.1 1546.6 17877 GUNTICOSEA CHLCGNAMK 1.00 51.6 -1.4 1546.6 17877 GUNTICOSEA CHLCGNAMK 1.00 55.8 -2.1 1357.7 17881 DYDRITKLAR EAVEGAL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGAL 1.00 65.8 -2.1 1357.7 17904 VDESUPTAVE GRAEAQAQAK 1.00 65.8 -1.6 1357.7 17904 VDESUPTAVE GRAEAQAQAK 1.00 43.2 -1 1357.7 17904 VDESUPTAVE GRAEAQAQAK 1.00 43.2 -1 1357.7 17904 VDESUPTAVE GRAEALANNERVEE 0.87 45.9 0.9 1575.8 17889 APAELLEFE GTVDNVAK 1.00 41.1 -1.6 1164.6 48994 APAELLEFE GTVDNVAK 1.00 43.2 -2.1 1357.7 17904 VDESUPTAVE GRAEALANNERVEE 0.87 45.9 0.9 1575.8 17889 APAELLEFE GTVDNVAK 1.00 43.2 -2.1 1357.7 17904 VDESUPTAVE GRAEALANNERVE 0.97 41.7 2.7 1575.8 17899 APAELLEFE GTVDNVAK 1.00 43.6 -0.8 1607.7 17908 KTDQKVTLS GVVESQAQAEEAVK 1.00 45.3 -2.1 1357.7 17904 VDESUPTAVE GRAEALANNERVE 0.97 41.7 2.7 1575.8 17899 APAELLEFE GTVDNVAK 1.00 43.6 -0.8 1607.7 17908 KTDQKVTLS GVVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17908 KTDQKVTLS GVVESQAAEEAVK 1.00 57.3 2.7 1607.7 17908 KTDQKVTLS GVESQAAEEAVK 1.00 57.3 2.7 1607.7 17908 KTDQKVTLS GVESQAAEEAVK 1.00 57.1 -0.7 1887.9 17897 KFEDAVLDV GIATVTATVACTOPK 1.00 57.1 -0.7 1887.9 17899 HYLDMAHVA GUNAGVENPUPH 1.00 53.1 -0.7 1879 KFEDAVLDV GIATVTATVACTOPK 1.00 57.1 -0.7 1879 KFEDAVLDV GIATVTATVACTOPK 1.00 55.1 -2.5 1880. 17899 HYLDMAHVA GUNAGVENPUPH 1.00 50.1 0.0 1477.7 17889 ILFUMAHVA GUNAGVENEVEK 0.83 36.6 -2.5 1560.7 17877 KLGPTEFICT GREDEGIFAV	LAVDESFQPT	AVGFAEALNNK	1.00	49.6	2.3	1248.6	17899	
LAVDESPQPT AVGFAREALANKDRPE 1.00 53.4 0.4 1745.9 17899 LAVDESPQT AVGFAREALANKDRPE 1.00 57.1 0.4 1745.9 17889 NPDEZVATGA AVGGOVLTCDVK 1.00 51.9 -1.8 1258.7 17861 DAPRAMPY AWWHLHEE 1.00 38 0.0 1188.5 87082 KVQNASYQVA AYLADELAK 1.00 41.7 -1.1 1108.5 17877 GTNTIGSSEA CHLGGNAMK 1.00 44.8 0.4 1113.5 17877 GTNTIGSSEA CHLGGNAMK 1.00 42.2 -0.1 1108.5 17877 TPTRNYANV CFGALDVK 1.00 42.2 -4.3 1161.5 17897 GNARQNLATF CQTWDENVHK 1.00 45.2 -3.1 1546.6 17877 GNARQNLATF CQTWDENVHK 1.00 51.6 -1.4 1546.6 17877 TPTRNYANV CFGALDVK 1.00 55.6 -1.4 1546.6 17877 DYDRITKLAR EAVEGAL 1.00 37.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAL 1.00 55.8 -1.6 1357.7 17904 ESKKGYINSI GALTGGALQQAK 1.00 65.8 -2.1 335.7 17904 VDESPQPTAV GFARALNNKDRPE 0.97 41.7 2.7 1575.8 17899 VDESPQPTAV GFARALNNKDRPE 0.87 45.9 0.9 1164.6 48994 APAELLEFEF GFTVDNVAK 1.00 41.1 -1.6 1164.6 48994 APAELLEFEF GFTVDNVAK 1.00 41.9 -0.4 1234.6 17877 KTOQKVTLS GFVESQAERAVK 1.00 45.2 -3.1 6 1357.7 17904 ESKKGYINSI GALTGGALQQAK 1.00 65.8 -2.1 931.5 17881 DYDRITKLAR EAVEGALL 1.00 37.8 -2.1 931.5 17881 ESKKGYINSI GALTGGALQQAK 1.00 65.8 -2.1 1357.7 17904 VDESPQPTAV GFARALNNKDRPE 0.97 41.7 2.7 1575.8 17899 VDESPQPTAV GFARALNNKDRPE 0.97 41.7 2.7 1575.8 17899 KTDQKVVTLS GFVESQAAERAVK 1.00 45.7 -2.5 1888.0 17897 RGWQPAPTL GGEATDIVVNR 1.00 57.3 2.7 1607.7 17908 RGWQPAPTL GGEATDIVVNR 1.00 57.3 2.7 1607.7 17908 RGWQPAPTL GGEATDIVVNR 1.00 57.1 -0.7 1887.9 17899 KFDDAVLDVQ GIATVTFAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 KFDDAVLDVQ GIATVTFAIVQACTQDK 1.00 55.1 -0.7 1887.9 17899 KFDDAVLDVQ GIATVTFAIVQACTQDK 1.00 55.9 -0.3 1503.7 8782 KLGPYEFICT GRPGEJFAVCFK 0.83 36.6 -2.5 1560.7 17877 KLG	LAVDESFQPT	AVGFAEALNNK	0.99	45.4	0.6	1248.6	17899	
LAVDESPOPT AUGRAELIANKERPE 1.00 57.1 0.4 1745.9 77899 PIDEAVAIGA AVGGOVLTEDVK 1.00 61.9 -1.8 1258.7 17861 DLAPKANTEV AWMLHEE 1.00 38 0.0 1188.5 87082 KVQNASYQVA AYLADELAK 1.00 41.7 -1.1 1108.5 17877 GTMTIGSSEA CHLGGNAMK 1.00 47.7 -1.1 1108.5 17877 GTMTIGSSEA CHLGGNAMK 1.00 47.9 -3.0 1113.5 17877 TPTRHYAHVD CPGHADYVK 1.00 42.4 -4.3 1161.5 17897 TPTRHYAHVD CPGHADYVK 1.00 42.5 -1.7 1161.5 17897 TPTRHYAHVD CPGHADYVK 1.00 45.2 -3.1 1546.6 17877 GNARQNLAFF CQTNDDENVHK 1.00 45.2 -3.1 1546.6 17877 UNDRITKLAR EAVEGAL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGAL 0.99 31 -0.5 931.5 17881 ESKKGYINSL GALTGGALQQAK 1.00 65.8 -2.1 1357.7 17904 VDESPOPTAV GFAEAUQAK 1.00 65.8 -2.1 1357.7 17904 VDESPOPTAV GFAEAUNKDRFE 0.97 41.7 2.7 1575.8 17899 VDESPOPTAV GFAEAUNKDRFE 0.87 45.9 0.9 1575.8 17899 VDESPOPTAV GFAEAUNKDRFE 0.87 45.9 0.9 1575.8 17899 APAELLFEFF GFTVDNVAK 1.00 49.6 -0.8 1607.7 17904 APAELLFEFF GFTVDNVAK 1.00 49.6 -0.8 1607.7 17908 AFAELLFEFF GFTVDNVAK 1.00 41.1 -1.6 1164.6 48994 AFAELLFEFF GFTVDNVAK 1.00 49.6 -0.8 1607.7 17908 KTDQKVTLS GFVESQAQAEEAVK 1.00 47.7 2.7 1877 KTQKVTLS GFVESQAQAEEAVK 1.00 47.7 2.7 1889 VGVDVAAA 0.00 14.7 7.7 17809 VGVDVAAA 0.00 14.7 7.7 17808 KTDQKVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17808 KTDQKVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17807 VGVSTAAAVQ GFVESVPH 1.00 56.9 -0.3 1503.7 16879 VGVDVAAA 0.00 177.7 17889 V	LAVDESFQPT	AVGFAEALNNKDKPE	1.00	53.4	0.4	1745.9	17899	
NPDEEXVIGA AVQCGVUTCDVK 1.00 61.9 -1.8 1258.7 17861 LIMPRATTY AWMILHEE 1.00 41.7 -1.1 1108.5 17877 GTNTIGSSEA CMLGGMAMK 1.00 41.7 -1.1 1108.5 17877 GTNTIGSSEA CMLGGMAMK 1.00 42.4 -4.3 1161.5 17897 GTNTIGSSEA CMLGGMAMK 1.00 42.4 -4.3 1161.5 17897 GTNTIGSSEA CMLGGMAMK 1.00 42.5 -1.7 1161.5 17897 GTNRONLATF COTWDDENVIK 1.00 45.2 -3.1 1546.6 17877 GNARONLATF COTWDDENVIK 1.00 37.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 65.8 -1.6 1357.7 17904 VDESFQPTAV GFAEALNNKDKFE 0.97 41.7 2.7 1575.8 17899 AFAELLEFE GFTVDNVVAK 1.00 48.9 -0.9 1164.6 48	LAVDESFQPT	AVGFAEALNNKDKPE	1.00	57.1	0.4	1745.9	17899	
DLAPKANTLY AWMULHEE 1.00 38 0.0 1188.5 87.082 KVQNASYQVA AYLADELAK 0.04 41.7 -1.1 1108.5 17877 GTNTIGSSEA CHLGGMAMK 1.00 44.8 0.4 1113.5 17877 GTNTIGSSEA CHLGGMAMK 1.00 42.4 -4.3 1161.5 17897 GNARGNLATF CORMORAVK 1.00 42.5 -1.7 1161.5 17897 GNARGNLATF COTWDENVEK 1.00 45.2 -3.1 1546.6 17877 GNARGNLATF COTWDENVEK 1.00 51.6 -1.4 1546.6 17877 DYDRITKLAR EAVEGAKL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGAKL 0.09 37.8 -2.1 935.7 17904 DESKRGYINSL GALTGGOALQOAK 1.00 65.8 -1.6 1357.7 17904 DESKRGYINSL GALTGGOALQOAK 1.00 41.1 -1.6 164.6 48994 </td <td>NPDEAVAIGA</td> <td>AVQGGVLTGDVK</td> <td>1.00</td> <td>61.9</td> <td>-1.8</td> <td>1258.7</td> <td>1/861</td> <td></td>	NPDEAVAIGA	AVQGGVLTGDVK	1.00	61.9	-1.8	1258.7	1/861	
EVQLANSTOVA ATLADETAK 1.00 41.7 -1.1 1108.5 17877 GTNTIGSSEA CHLGGMAMK 1.00 44.8 0.4 1113.5 17877 GTNTIGSSEA CHLGGMAMK 1.00 37.9 -3.0 1113.5 17877 GTNTIGSSEA CHLGGMAMK 1.00 42.4 -4.3 1161.5 17897 GNRENLATF COMDENVIK 1.00 45.2 -1.7 1161.5 17877 GNARONLATF COWDENVIK 1.00 51.6 -1.4 1546.6 17877 GNARONLATF COWDENVIK 1.00 37.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 37.8 -2.1 931.5 17881 ESKKGYINSL GALTGGOALQOAK 1.00 65.8 -1.6 1357.7 17904 VDESEQPTAV GFARALINNEREE 0.97 41.7 2.7 1575.8 17899 VDESEQPTAV GFARALINNEREE 0.87 45.9 0.9 1575.8 17	DLNPKAMTPV	AWWMLHEE	1.00	38	0.0	1188.5	87082	
EVQNASTQVA AYLADBIAK 0.84 35.2 0.1 1005.5 17877 CTNTTIGSERA CMLGGMAMK 1.00 37.9 -3.0 1113.5 17877 CTPTRHYANUD CPGHADYVK 1.00 42.4 -4.3 1161.5 17897 TPTRHYANUD CPGHADYVK 1.00 42.5 -1.7 1161.5 17897 GNARQNLATF CQTMDDENVHK 1.00 45.2 -3.1 1546.6 17877 GNARQNLATF CQTMDDENVHK 1.00 51.6 -1.4 1546.6 17877 GNARQNLATF CQTMDDENVHK 1.00 57.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 65.8 -1.6 1357.7 17904 ESKKGYINSL GALTGGQALQQAK 1.00 65.8 -1.6 1357.7 17904 VDESPQPTAV GFABALMNEKPE 0.87 45.9 0.9 1575.8 17899 APAELLFEF GFUVDNVAK 1.00 41.1 -1.6 1164.6 <t< td=""><td>KVQNASYQVA</td><td>AYLADEIAK</td><td>1.00</td><td>41.7</td><td>-1.1</td><td>1108.5</td><td>1/8//</td><td></td></t<>	KVQNASYQVA	AYLADEIAK	1.00	41.7	-1.1	1108.5	1/8//	
CITHICSSEA CHLGBAAMK 1.00 44.8 0.4 111.5. 17877 CTNTICSSEA CMLGGAMK 1.00 42.4 -4.3 1161.5 17877 TPTRHYAHVD CPGHADYVK 1.00 42.5 -1.7 1161.5 17897 GNARQNLATF CQTMDDENVHK 1.00 45.2 -3.1 1546.6 17877 GNARQNLATF CQTMDDENVHK 1.00 51.6 -1.4 1546.6 17877 GNARQNLATF CQTMDDENVHK 1.00 37.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGALQAX 1.00 65.8 -2.1 1357.7 17904 VDESFOPTAV GFABALINKDKPE 0.97 41.7 2.7 1575.8 17899 APAELLFEF GFTVDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDGKVVILS GPVESQAQAEEAVK 1.00 45.3 -2.7 1607.7	KVQNASYQVA	AYLADEIAK	0.84	35.2	0.1	1108.5	1/8//	
CTHTICSSEA CALGGMAMK 1.00 37.9 -3.0 1113.5 17877 TPTRHYAHVD CPGHADYVK 1.00 42.4 -4.3 1161.5 17897 GNARQNLAFF CQTWDDENVHK 1.00 42.5 -1.7 1161.5 17897 GNARQNLAFF CQTWDDENVHK 1.00 45.2 -3.1 1546.6 17877 GNARQNLAFF CQTWDDENVHK 1.00 37.8 -2.1 931.5 17881 DYDRITKLAR EAVEGALL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGALL 0.00 37.8 -2.1 935.7 17904 VDESFQPTAV GALTGGQALQAR 1.00 65.8 -1.6 1357.7 17904 VDESFQPTAV GFAEALNNKDRFE 0.87 45.9 0.9 1575.8 17899 APAELLFEF GFTVDNVAK 1.00 41.1 -1.6 1164.6 48994 AFTDGKVVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1575.8 <td< td=""><td>GINTIGSSEA</td><td>CMLGGMAMK</td><td>1.00</td><td>44.8</td><td>0.4</td><td>1113.5</td><td>1/8//</td><td></td></td<>	GINTIGSSEA	CMLGGMAMK	1.00	44.8	0.4	1113.5	1/8//	
TPTRHYAHVD CPGHADYVK 1.00 42.4 -4.3 1161.5 17897 GNARQNLATF CQTWDDENVHK 1.00 42.5 -1.7 1161.5 17897 GNARQNLATF CQTWDDENVHK 1.00 51.6 -1.4 1546.6 17877 GNARQNLATF CQTWDDENVHK 1.00 51.6 -1.4 1546.6 17877 GNARQNLATF CQTWDDENVHK 1.00 57.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 65.8 -2.1 1357.7 17904 ESKKGYINSL GALTGQALQAK 1.00 65.8 -1.6 1357.7 17904 VDESFQPTAV GFAEALNNKDKPE 0.97 41.7 2.7 1575.8 17899 VDESFQPTAV GFAEALNNKDKPE 0.87 45.9 0.9 1576.8 17899 APAELLFEEF GFTVDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 47.3 2.7 1607.7 17908 RGWQVPAFTL GGEATDIVVMR 1.00 47.7	GTNTIGSSEA	CMLGGMAMK	1.00	37.9	-3.0	1113.5	1/8//	
TPTRTARHOD CPCHADYVK 1.00 42.5 -1.7 1101.5 17897 CNARQULATF CQTWDDENVHK 1.00 45.2 -3.1 1546.6 17877 GNARQULATF CQTWDDENVHK 1.00 51.6 -1.4 1546.6 17877 DYDRITKLAR EAVEGAKL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 65.8 -2.1 931.5 17881 ESKKGYINSL GALTGQOALQQAK 1.00 65.8 -2.1 1357.7 17904 VDESEPPTAV GFAEALNNKDKPE 0.97 41.7 2.7 1575.8 17899 VDESEPPTAV GFAEALNNKDKPE 0.87 45.9 0.9 156.4 48994 APAELLFEEF GFTVDNVVAK 1.00 38.3 -0.9 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 KTDQKVVTLS GFVESQAQAEEAVK 1.00 41.9 -0.4 1234.6 17877 EAVAIGAAVQ GGAZTDIVVMR 1.00 45.7 -	TPTRHYAHVD	CPGHADYVK	1.00	42.4	-4.3	1101.5	17897	
GNARQNLATP CQTWDDENVHK 1.00 45.2 -3.1 1546.6 17877 DYDRITKLAR EAVEGAKL 0.99 31 -0.5 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 37.8 -2.1 937.7 17904 ESKKGYINSL GALTGQOALQQAK 1.00 65.8 -1.6 1357.7 17904 ESKKGYINSL GALTGQOALQQAK 1.00 65.8 -1.6 1357.7 17904 VDESFQPTAV GFAEALNNKDKPE 0.97 41.7 2.7 1575.8 17899 APAELLFEEF GFTVDNVVAK 1.00 38 -0.9 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17908 KTDQKVVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17908 KTDQKVVTLS GEVESQAQAEEAVK 1.00 55.3 -1.1 960.5 <td>TPTRHYAHVD</td> <td>CPGHADYVK</td> <td>1.00</td> <td>42.5</td> <td>-1.7</td> <td>1101.5</td> <td>1/89/</td> <td></td>	TPTRHYAHVD	CPGHADYVK	1.00	42.5	-1.7	1101.5	1/89/	
CAMARQULATY CUTMDDENVER 1.00 51.5 -1.4 1946.0 17877 DYDRITYLAR EAVEGAKL 1.00 37.8 -2.1 931.5 17881 DYDRITKLAR EAVEGAKL 1.00 65.8 -2.1 1357.7 17904 ESKKGYINSL GALTGGQALQQAK 1.00 65.8 -1.6 1357.7 17904 VDESFQPTAV GFAEALMNKDKPE 0.97 41.7 2.7 1575.8 17899 VDESFQPTAV GFAEALMNKDKPE 0.87 45.9 0.9 1164.6 48994 APAELLFEEF GFTVDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 KTQQKVVTLS GFVESQAQAEEAVK 1.00 41.9 -0.4 1234.6 17877 RGWQVPAFTL GEATDLVVMR 0.99 38.3 -1.1 960.5 17861 KYLSDHYLG GIATUTVANA 0.90 38.3 -1.1 10.5	GNARQNLATE	CQTWDDENVHK	1.00	45.2	-3.1	1546.6	1/8//	
DIDRITIALRR EAVEGARL 0.99 31 -0.3 951.3 17661 DYDRITIALRR EAVEGARL 1.00 37.8 -2.1 931.5 17881 ESKKGYINSL GALTGGQALQQAK 1.00 65.8 -2.1 1357.7 17904 VDESFQPTAV GFAEALNNKDKPE 0.97 41.7 2.7 1575.8 17899 VDESFQPTAV GFAEALNNKDKPE 0.87 45.9 0.9 1575.8 17899 APAELLFEEF GFTVDNVVAK 1.00 38 -0.9 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 RGWQVPAFTL GGEATDIVVMR 0.99 38.3 -1.1 960.5 17861 KYLDBAVUDQ GIATVTPAIVQACTQDK 0.00 45.7 -2.5 1888.0 17899 KPEDAVLOVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6	GNARQNLATF	CQTWDDENVHK	1.00	51.0 51	-1.4	1540.0	1/8//	v
DIDENTIALRAR EAVEDAAL 1.00 57.8 -2.1 531.3 17861 ESKRGYINSL GALTGGQALQQAK 1.00 65.8 -2.1 1357.7 17904 VDESFQPTAV GFAEALNKDKDFE 0.97 41.7 2.7 1575.8 17899 VDESFQPTAV GFAEALNKDKDFE 0.87 45.9 0.9 1575.8 17899 APAELLFEEF GFTVDNVVAK 1.00 38 -0.9 1164.6 48994 APAELLFEEF GFTVDNVVAK 1.00 49.6 -0.8 1607.7 17908 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 RGQUPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 EAVAIGAAVQ GOUTGDVK 0.90 38.3 -1.1 960.5 17861 KYLSDHKVLQ GIAUTYPAIVQACTQDK 1.00 45.7 -2.5 188.0 17899 KPEDAVLDVQ GIATYTPAIVQACTQDK 1.00 57.3 -1.6 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1	DIDRIIKLAR	EAVEGALL	1.00	ו כ ס ד כ	-0.5	931.3	17001	×
ESKRGYLNGLA 1.00 0.30 -2.1 137.7 17904 ESKRGYLNSL GALTGQQALQQAK 1.00 65.8 -1.6 1357.7 17904 VDESFQPTAV GFAEALNNKDKPE 0.97 41.7 2.7 1575.8 17899 APAELLFEF GFTVDNVVAK 1.00 38 -0.9 1164.6 48994 APAELLFEF GFTVDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.4 1234.6 17877 RGWQVPAFTL GEATDIVVMR 0.99 38 0.6 1234.6 17877 EAVAIGAAVQ GGVLTGDVK 0.90 38.3 -1.1 960.5 17861 KYLSDHPKLQ GIAQQNSFK 0.88 35.2 4.7 1107.5 17877 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 <	DIDRIIKLAR	CALECCALOON	1.00	57.0	-2.1	1257.7	17001	^
ESKROTINGL GALTGOURDURA 1.00 0.3.6 -1.0 137.7 17504 VDESFQPTAV GFAEALINNKDKPE 0.97 41.7 2.7 1575.8 17899 VDESFQPTAV GFAEALINNKDKPE 0.87 45.9 0.9 1575.8 17899 APAELLFEEF GFTVDNVVAK 1.00 38 -0.9 1164.6 48994 APAELLFEEF GFTVDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 RGWQVPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 RGWQVPAFTL GGEATDIVVMR 0.90 38.3 -1.1 960.5 17861 KYLSDHYLQ GIAQNSFK 0.88 35.2 4.7 1107.5 17877 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 VKPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 18	ESKKGIINSL	GALIGGQALQQAK	1.00	65.8	-2.1	1357.7	17904	
VDESPQFIAV GFARALINKENPE 0.37 41.7 2.7 157.3 17693 VDESPQFIAV GFARALINKENPE 0.37 45.9 0.9 157.8 17899 APAELLFEEF GFTVDNVVAK 1.00 38 -0.9 1164.6 48994 APAELLFEEF GFTVDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 RGWQVPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 RGWQVPAFTL GGEATDIVVMR 0.90 38.3 -1.1 960.5 17861 KYLSDHYLQ GIATVTPAIVQACTQDK 1.00 45.7 -2.5 1886.0 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 <td< td=""><td>UDECEODENU</td><td>CEAEAINNYDYDE</td><td>0.97</td><td>05.8 /1 7</td><td>-1.0</td><td>1557.7</td><td>17904</td><td></td></td<>	UDECEODENU	CEAEAINNYDYDE	0.97	05.8 /1 7	-1.0	1557.7	17904	
APAELLFEF GFAUNINDRE 0.07 43.3 0.03 107.53 107.53 107.53 APAELLFEF GFTVDNVVAK 1.00 38 -0.9 1164.6 48994 APAELLFEEF GFTVDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 KTDQKVVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17908 RGWQVPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 EAVAIGAAVQ GGVLTGDVK 0.90 38.3 -1.1 960.5 17861 KYLSDHFKLQ GIAQQNSFK 0.88 35.2 4.7 1107.5 17877 FPEDAVLDVQ GIATUTPAIVQACTQDK 1.00 45.7 -2.5 1888.0 17899 KPEDAVLDVQ GIATUTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 <td>VDESEQFIAV</td> <td>GFAEALNINDKPE CEAEALNINKDKPE</td> <td>0.37</td> <td>41.7</td> <td>2.7</td> <td>1575.8</td> <td>17899</td> <td></td>	VDESEQFIAV	GFAEALNINDKPE CEAEALNINKDKPE	0.37	41.7	2.7	1575.8	17899	
APAELLIPEEF GFIVDNVVAK 1.00 36 -0.5 1104.0 40594 APAELLIPEEF GFUDNVVAK 1.00 41.1 -1.6 1164.6 48994 KTDQKVVTLS GFVESQAQAEEAVK 1.00 49.6 -0.8 1607.7 17908 RGWQVPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 RGWQVPAFTL GGEATDIVVMR 0.90 38.3 -1.1 960.5 17861 KYLSDHPKLQ GIAQQNSFK 0.88 35.2 4.7 1107.5 17877 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 45.7 -2.5 1888.0 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVVAEAT GLVAGYYPPVPH 1.00 54.2 3.4 1477.7 17889 VGVDVVAEAT GLVAGYYPPVPH 1.00 56.5 -2.6 1020.4 17905 ITEGLKAVAA GMPMDLK 0.98 36.5	VDESEVEIAV	CETUDNUUNK	1.00	40.9	0.9	1164.6	17899	
AFABLIFEF GFIVUNVAR 1.00 41.1 -1.0 100.0 40.90 KTDQKVVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17908 RGQVPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 RGQVPAFTL GGEATDIVVMR 0.90 38.3 -1.1 960.5 17861 KYLSDHYLQ GIAQQNSFK 0.88 35.2 4.7 1107.5 17877 KYLSDHYLQ GIATVTPAIVQACTQDK 1.00 45.7 -2.5 1888.0 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 VGVDVVAEAT GLFITDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVVAEAT GLFITDETAR 0.00 42.7 3.7 1209.6 17889 VLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 TIEGLKAVAA GMNPMDLK 0.98 36.5	AFALLLFLEF	CETUDNUUNK	1.00	J0 /1 1	-0.9	1164.6	40994	
ALDQAVVILS GFVESQAQAEEAVK 1.00 57.3 -0.3 1007.7 17908 KTDQKVVTLS GFVESQAQAEEAVK 1.00 57.3 2.7 1607.7 17908 RGWQVPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 EAVAIGAAVQ GGVLTGDVK 0.90 38.3 -1.1 960.5 17861 KYLSDHPKLQ GIAQNSFK 0.88 35.2 4.7 1107.5 17877 KYEDAVLDVQ GIATVTPAIVQACTQDK 1.00 45.7 -2.5 1888.0 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVVAEAT GLFLTDETAR 1.00 42.7 3.7 1209.6 17880 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 54.2 3.4 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50	KENOKAMI C	GFIVDNVVAR	1.00	41.1	-1.0	1607.7	17009	
NIDQAVVIES GFVESQAQABLAYK 1.00 57.3 2.7 1007.7 17500 RGWQVPAFTL GGEATDIVVMR 0.99 38 0.6 1234.6 17877 EAVAIGAAVQ GGVLTGDVK 0.90 38.3 -1.1 960.5 17861 KYLSDHPKLQ GIAQQNSFK 0.88 35.2 4.7 1107.5 17877 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 45.7 -2.5 1888.0 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17880 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VLFVDMAHVA GLVAGVYPNPVPH 1.00 54.2 3.4 1477.7 17889 YLFVDMAHVA GLVAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 YLFVDMAHVA GLVAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 <td>KIDQKVVILS</td> <td>GF VESQAQAEEAVK</td> <td>1.00</td> <td>49.0 57.2</td> <td>-0.8</td> <td>1607.7</td> <td>17908</td> <td></td>	KIDQKVVILS	GF VESQAQAEEAVK	1.00	49.0 57.2	-0.8	1607.7	17908	
RGWQVFAFIL GGEATDIVVMR 0.39 36 0.3 1234.6 17877 RGWQVFAFIL GGEATDIVVMR 1.00 41.9 -0.4 1234.6 17877 RGWQVFAFIL GGEATDIVVMR 0.90 38.3 -1.1 960.5 17861 KYLSDHPKLQ GIAQQNSFK 0.88 35.2 4.7 1107.5 17877 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 45.7 -2.5 1888.0 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 54.2 3.4 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 <	RIDQRVVILS	CCEATDINAMD	0.99	30	2.7	1224.6	17900	
NowQVFAFILGGEATUTVNER1.0041.5-0.412.4.017.877EAVAIGAAVQGGVLTGDVK0.9038.3-1.1960.517861KYLSDHPKLQGIAQNSFK0.8835.24.71107.517877KPEDAVLDVQGIATVTPAIVQACTQDK1.0045.7-2.51888.017899KPEDAVLDVQGIATVTPAIVQACTQDK1.0057.1-0.71887.917899KPEDAVLDVQGIATVTPAIVQACTQDK1.0053.3-1.61887.917899VGVDVVAEATGLFLTDETAR0.7829.1-1.71209.617880VGVDVVAEATGLFLTDETAR1.0042.73.71209.617880VGVDVVAEATGLVAAGVYPNPVPH1.0050.10.01477.717889YLFVDMAHVAGLVAAGVYPNPVPH1.0050.10.01477.717889ITEGLKAVAAGMNPMDLK0.9836.51.31020.417905ITEGLKAVAAGPAHGGANEAALK1.0072-1.81307.617869CIAAGIASLWGPAHGGANEAALK1.0075.9-0.91307.617869NAADLAAISGQKPLITK0.7723.1-3.51027.617877KLGPYEFICTGRPDEGIPAVCFK0.8336.6-2.51560.717877NYRNHFVTILGTIQGEQFGINK1.0039.71.1150.717877	RGWQVFAFIL	CCEATDIVIME	1 00	J0 /1 0	0.0	1234.0	17877	
EAATGAATQ GUTIGDYA 0.50 36.5 -1.1 500.5 17807 KYLSDHPKLQ GIAQQNSFK 0.88 35.2 4.7 1107.5 17877 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 45.7 -2.5 1888.0 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17889 VGVDVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVAEAT GLVAAGVYPNPVPH 1.00 54.2 3.4 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GNNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 NAADLAAIS GQKPLITK 0.77 23.1 <	FAUATCANNO	CONTRODUK	0.90	28.2	-0.4	960 5	17861	
KIEDDIFIENDGLAQMOFICGLAQJ.00J.2-1.7H07.3H07.3KPEDAVLDVQGIATVTPAIVQACTQDK1.0045.7-2.51888.017899KPEDAVLDVQGIATVTPAIVQACTQDK1.0057.1-0.71887.917899VGVDVVAEATGLFLTDETAR0.7829.1-1.71209.617880VGVDVVAEATGLFLTDETAR1.0042.73.71209.617880YLFVDMAHVAGLVAAGVYPNPVPH1.0050.10.01477.717889YLFVDMAHVAGLVAAGVYPNPVPH1.0050.10.01477.717889ITEGLKAVAAGMNPMDLK0.9836.51.31020.417905ITEGLKAVAAGMNPMDLK0.9536.5-2.61020.417905CIAAGIASLWGPAHGGANEAALK1.0072-1.81307.617869NAADLAAISGQKPLITK0.7723.1-3.51027.617897KLGPYEFICTGRPDEGIPAVCFK0.8336.6-2.51560.717877KLGPYEFICTGRPDEGIPAVCFK1.0039.71.11560.717877NYRNHFVTILGTIQGEQPGFINK1.0058.9-0.31503.787082	EVALONDELO	GGVIIGDVK	0.50	35.2	-1.1 17	1107 5	17877	
KHEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1887.9 17899 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVVAEAT GLFLTDETAR 1.00 42.7 3.7 1209.6 17880 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17877 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6<	KEEDAVLDVO	GIATUTPAINOACTODK	1 00	45 7	-2.5	1888.0	17899	
KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 57.1 -0.7 1007.5 17859 KPEDAVLDVQ GIATVTPAIVQACTQDK 1.00 53.3 -1.6 1887.9 17899 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVVAEAT GLFLTDETAR 1.00 42.7 3.7 1209.6 17880 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6	KPEDAVI DVO	CIATUTRALVQACIQDA	1.00	4J.7 57 1	-2.5	1887.9	17899	
NR HARVEDY GLATYTIATYQACTODX 1.00 35.3 -1.3 1007.3 17053 VGVDVVAEAT GLFLTDETAR 0.78 29.1 -1.7 1209.6 17880 VGVDVVAEAT GLFLTDETAR 1.00 42.7 3.7 1209.6 17880 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 54.2 3.4 1477.7 17889 ITEGLKAVA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17877 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 39.7 1.1 1560.7 17877	KPEDAVI DVO	CIATUTRALVQACIQDA	1.00	53.3	-0.7	1887.9	17899	
VGVDVALATI GLF ITDETAR 1.00 22.1 1.7 1.7 1209.6 17860 VGVDVVAEAT GLF1TDETAR 1.00 42.7 3.7 1209.6 17880 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 54.2 3.4 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	VCVDVVAFAT	GLELTDETAR	0.78	29.1	-1.0 -1.7	1209.6	17880	
YLFVDMAHVA GLVAAGVYPNPVPH 1.00 54.2 3.4 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	VGVDVVAEAT	GLELTDETAR	1 00	42.7	37	1209.0	17880	
MINOMANUA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 YLFVDMAHVA GLVAAGVYPNPVPH 1.00 50.1 0.0 1477.7 17889 ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	VIEVDMAHVA	CLVAACVYPNPVPH	1.00	54.2	3.4	1205.0	17889	
ITEGLKAVAA GMNPMDLK 0.98 36.5 1.3 1020.4 17905 ITEGLKAVAA GMNPMDLK 0.98 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 0.95 36.5 -2.6 1020.4 17869 CIAAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	VIEVDMAUVA		1.00	50.1	0.0	1477.7	17889	
ITEGLIKAVAA GENTERLAK 0.30 30.5 1.5 1020.4 17305 ITEGLKAVAA GMNPMDLK 0.95 36.5 -2.6 1020.4 17905 CIAAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	TTECT KAVAA	CMNDMDI K	0.98	36.5	13	1020 /	17905	
CIAGIASLW GPAHGGANEAALK 1.00 72 -1.8 1307.6 17869 CIAAGIASLW GPAHGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	TTEGI.KAVAA	GMNPMDLK	0.95	36.5	-2.6	1020.4	17905	
CIANGINGIN GPANGGANEAALK 1.00 72 -1.6 1507.0 17609 CIAAGIASLW GPANGGANEAALK 1.00 75.9 -0.9 1307.6 17869 NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1027.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	CIAACIACIM	CPAHCCANFAATW	1 00	77	_1 &	1307 6	17869	
NAAADLAAIS GQKPLITK 0.77 23.1 -3.5 1007.6 17897 KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	CIAACIACIW	CPAHCCANEAAIN	1 00	75 9	_0 9	1307.0	17869	
KLGPYEFICT GRPDEGIPAVCFK 0.83 36.6 -2.5 1560.7 17877 KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	NAAADI.AATC	COKPLITER	0.77	73.5 73 1	_3 5	1027 6	17897	
KLGPYEFICT GRPDEGIPAVCFK 1.00 39.7 1.1 1560.7 17877 NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	NUUTOTUNETO	CREDECIDAVCER	0.77	20.1	_3.5 _2 5	1560 7	17877	
NYRNHFVTIL GTIQGEQPGFINK 1.00 58.9 -0.3 1503.7 87082	KIGDAELLOL	GREDECTEAVOER	1 00	30.0	2.5	1560.7	17877	
	NYRNHEVTT	GTIOGEOPOETNW	1 00	52.7	_0 3	1503.7	87082	
NYRNHEVITL GTLOGEOPGETNK 100 533 01 15037 97097	NYRNHEVTT	CLICCEUDCEINK	1 00	53.5	0.5	1503.7	87082	
FRNAEFLOAY GVALADGPLK 0.82 38.6 -0.2 1055.6 17875	FRNAFFLOAY	GVATADGPLK	0.82	38.6	_0.7	1055.6	17875	

Table S3. Cont.

Nonprime

AC PNAS

sequence (inferred from database)	Prime-side sequence (LC-MS/MS)	PeptideProphet probability score	X!Tandem hyperscore	Mass accuracy (ppm)	Neutral mass (Da)	Examplary protein accession	Discarded from PICS profile
KARGITINTS	HVEYDTPTR	0.81	33.2	-2.9	1204.5	17897	
KARGITINTS	HVEYDTPTR	0.97	33.2	-1.6	1204.5	17897	
WDFRLPRVKS	ISASGHK	0.65	23.5	-1.6	814.4	17877	
WDFRLPRVKS	ISASGHK	0.70	26.8	-1.6	814.4	17877	
KNPQKNLYTF	KNQASNDLPN	1.00	26.9	-1.6	1215.6	87082	
KNPQKNLYTF	KNQASNDLPN	1.00	30.1	-2.0	1215.6	87082	
GEIEFWFAMI	KVTTIIVM	0.73	20	3.1	1019.6	48994	
NLKAMYSIAK	KYDIPVVMDSAR	1.00	38.9	1.7	1508.7	87082	Х
NLKAMYSIAK	KYDIPVVMDSAR	0.97	33.7	-1.4	1508.7	87082	Х
GETEDATIAD	LAVGTAAGQIK	0.89	37.1	-0.1	1143.6	17891	
GETEDATIAD	LAVGTAAGQIK	1.00	41.2	-0.5	1143.6	17891	
DLRCVNMVAD	LWHAPAPK	0.82	32.4	-1.5	1034.5	17877	
DLRCVNMVAD	LWHAPAPK	0.91	30	1.9	1034.5	17877	
TNTIGSSEAC	MLGGMAMK	1.00	42	-0.8	953.4	17877	
TNTIGSSEAC	MLGGMAMK	1.00	38.7	0.5	953.4	17877	
AELDDIFSVQ	NLMHPAYK	0.98	32.4	-1.6	1088.5	87082	
AELDDIFSVQ	NLMHPAYK	0.93	38.8	-1.7	1088.5	87082	
ALNMIDYGLD	NLPGGPL	0.68	26.4	-2.2	754.4	17890	
GLEEIGVVCQ	QAGGHAAFVDAGK	1.00	78.5	-1.8	1343.6	87082	
GLEEIGVVCQ	QAGGHAAFVDAGK	1.00	77.7	-1.1	1343.6	87082	
DGLEEIGVVC	QQAGGHAAFVDAGK	1.00	86.9	-0.8	1471.7	87082	
DGLEEIGVVC	QQAGGHAAFVDAGK	1.00	86.9	-0.5	1471.7	87082	
GLKQCKANPW	QQFAETHNK	1.00	44.5	-0.7	1217.5	17871	
GLKQCKANPW	QQFAETHNK	0.98	39.3	-0.8	1217.5	17871	
EHDPMEIWAT	QSSTLVEVLAK	0.93	35.3	0.2	1289.7	17903	
EHDPMEIWAT	QSSTLVEVLAK	0.97	39.3	-2.2	1289.7	17903	
AESVKNIFGY	QYTIPTHQGR	1.00	46.3	-1.7	1287.6	87082	
AESVKNIFGY	QYTIPTHQGR	1.00	46.3	-1.0	1287.6	87082	
PYIVATITSN	SAGGQPVSLANLK	0.94	35.1	0.3	1356.7	87082	
PYIVATITSN	SAGGQPVSLANLK	1.00	42	-2.4	1356.7	87082	
ARLMATMKEA	SAGKLVR	0.98	32.7	0.2	845.5	17904	
YAGQDIVSNA	SCTTNCLAPLAK	1.00	45.4	-6.1	1450.7	17880	
RKIKAAOYVA	SHPGEVCPAK	0.99	43.7	-0.6	1196.5	17868	
RKIKAAQYVA	SHPGEVCPAK	1.00	38.5	-0.8	1196.5	17868	
RKIKAAQYVA	SHPGEVCPAK	1.00	47.8	-0.8	1196.5	17868	
PFACIAAGIA	SLWGPAHGGANEAALK	0.96	39.7	1.3	1693.8	17869	
PFACIAAGIA	SLWGPAHGGANEAALK	0.97	43.9	-1.7	1693.8	17869	
HDPMEIWATO	SSTLVEVLAK	0.95	35.2	-0.8	1161.6	17903	
HDPMEIWATQ	SSTLVEVLAK	0.99	38.2	0.0	1161.6	17903	
RTMACGIAGL	SVAADSLSAIK	1.00	56.7	-0.1	1176.6	17871	
RTMACGIAGL	SVAADSLSAIK	1.00	65.1	4.3	1176.6	17871	
RTMACGIAGL	SVAADSLSAIK	1.00	50.7	-5.6	1176.6	17871	
CKKNPOKNLY	TFKNOASNDLPN	1.00	29.6	-0.6	1463.7	87082	
CKKNPOKNLY	TFKNQASNDLPN	0.98	26.7	1.4	1463.7	87082	
KEASAGKLVR	TLAAVRDAKEAA	0.99	38.5	-0.6	1330.7	17904	х
KEASAGKLVR	TLAAVRDAKEAA	0.99	43.5	-1.0	1330.7	17904	х
KEASAGKLVR	TLAAVRDAKEAA	0.99	35.7	-0.8	1330.7	17904	х
KEASAGKLVR	TLAAVRDAKEAA	0.97	34.6	0.1	1330.7	17904	х
EEKARGITIN	TSHVEYDTPTR	1.00	46.4	0.9	1392.6	17897	
EEKARGITIN	TSHVEYDTPTR	1.00	46.3	-1.4	1392.6	17897	
TTGEHEVSFO	VHSEVFAK	0.83	27.9	-0.7	1031.5	17906	
OOAVAAHKFN	VLASOPADEDR	0.81	25.5	-0.7	1305.6	17901	
PDEAVATGAA	VOGGVLTGDVK	0,99	40.8	-0.2	1187.6	17861	
PDEAVATGAA	VOGGVLTGDVK	0.99	46.6	_1 8	1187.6	17861	
MVMPGDNTKM	VVTLTHPT	0.83	26.1	0.3	978.6	17897	
MVMPGDNTKM	VVTLTHPT	0.99	29.7	_1 4	978.6	17897	
		0.00			2.0.0		

Nonprime-side sequences are reported up to the position P10. X denotes ambiguous nonprime side residues. A small number of cleavage sites have P1 residues, which correspond to a potential cleavage-site of the digestion protease used for library generation. These cases might be related to incomplete amine protection during library preparation. Hence, prime-side cleavage products with such amino-termini are omitted from the PICS analysis, as well as prime-side cleavage products with amino termini that correspond to a potential nino terminus. One exemplary protein is stated for each identified peptide sequence. X! Tandem was applied to assign peptides to tandem mass spectra and the X!Tandem hyperscore is reported together with the PeptideProphet probability score. C signifies carboxyamidomethylated cysteine and K signifies di-methylated lysine. Some peptides were identified repeatedly by LC-MS/MS; however, the set of sequences was rendered nonredundant before analysis in the form of sequence logos.