Facile synthesis of yolk-shell magnetic mesoporous carbon microspheres for efficient enrichment of low abundance peptides

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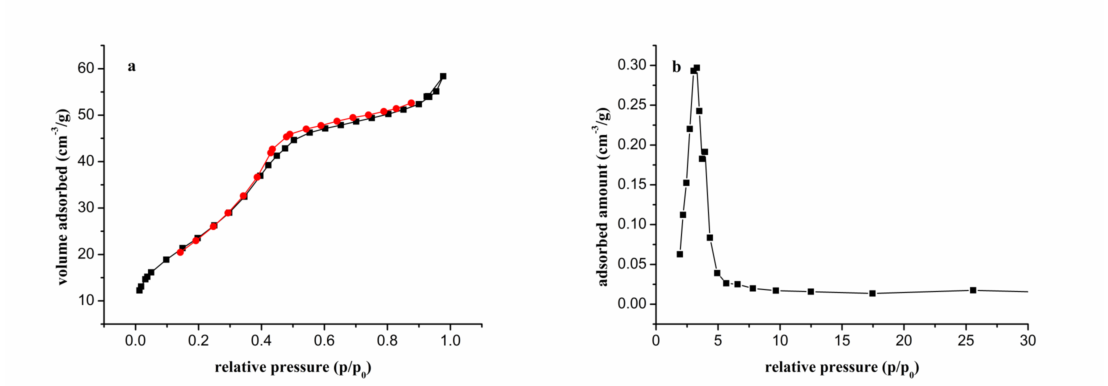
1. Mass spectrometric analysis of BSA

RPLC -MS/MS system consisted of an LTQ mass spectrometer (Thermo Fisher Scientific) with a nanospray source. A capillary column was first manually pulled to a fine point as spray tip, and then packed with C18 AQ beads (3 μm, 120 Å, Michrom Bio Resources). 0.1% (vol/vol) formic acid in water and 0.1 % (vol/vol) formic acid in acetonitrile were applied as the mobile phases.

For identification of peptides of BSA with an LTQ-MS, gradient elution from 5% to 35% (vol/vol) of the 0.1% (vol/vol) formic acid in acetonitrile in 90 min was performed to elute each sample in 1D RPLC-MS/MS. All MS and MS/MS spectra were acquired in the data dependent mode with the six most intense ions were fragmented by CID

2. Data processing and analysis of BSA

For peptide identification, the MS/MS spectra in one acquired raw file were converted to a single .mgf file using MSQuant (http://msquant.alwaysdata.net/msq). Then the .mgf files were searched against the BSA database with Mascot (Matrix Science). FDRs given are those originating from the internal Mascot decoy database search function. Peptides with FDR < 1% (rank 1 and bold red) were accepted for identification. Carbamidomethylation on cysteine was set as a fixed modification. the .mgf files were searched using fully tryptic cleavage and up to two missed cleavage sites, oxidation (+15.9949 Da) on methionine was set as variable modifications. The mass tolerances were 2 Da for parent masses and 0.8 Da for fragment masses.



Surface area (m^2/g)	Pore volume (cc/g)	Pore size (nm)
130.14	0.12	3.028

Fig.S1 N_2 adsorption-desorption isotherms (a) and pore size distribution of Fe_2O_3@nSiO_2@mSiO_2 (b).

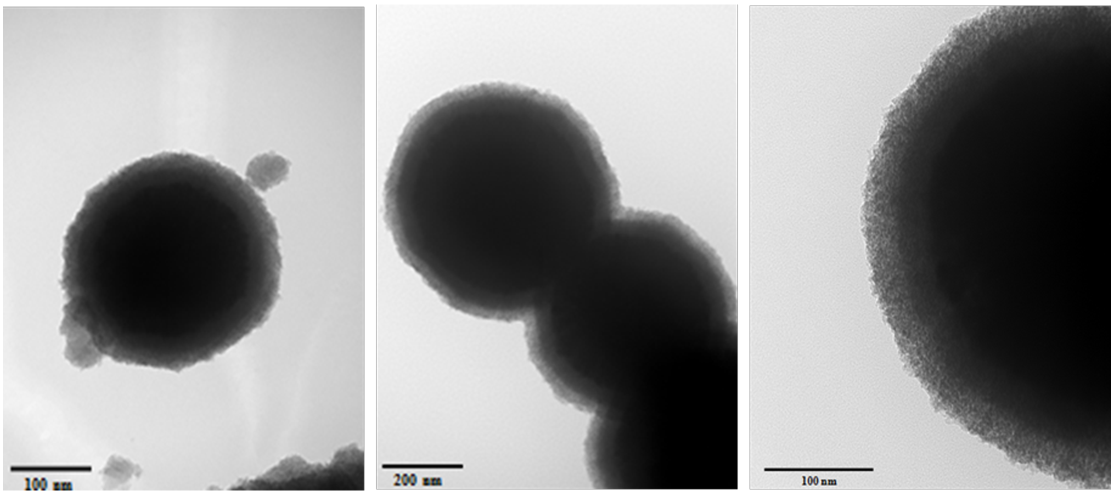


Fig.S2 TEM images of Fe_2O_3@nSiO_2@mSiO_2

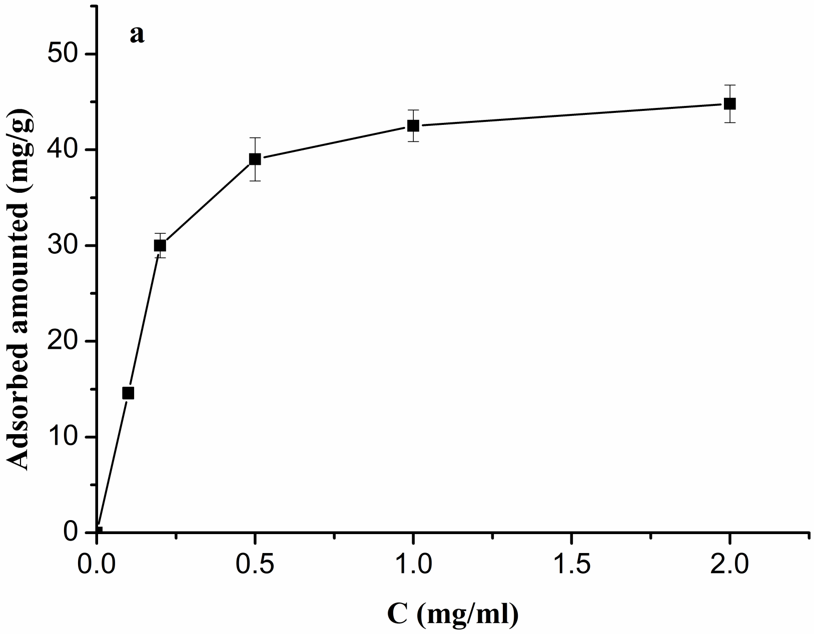


Fig.S3 The adsorption amount of Rhodamine B by Fe_2O_3@nSiO_2@mSiO_2 affected by the amount of added Rhodamine B

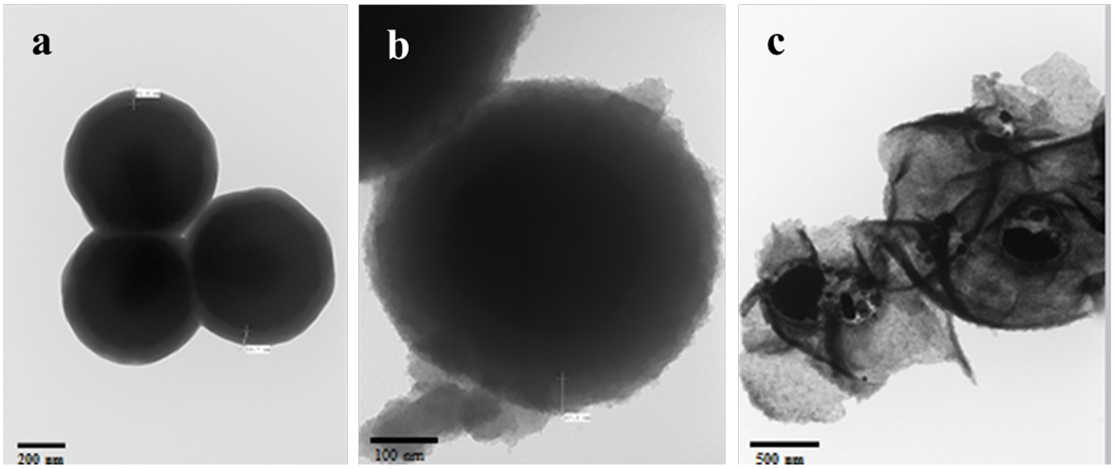


Fig.S4 TEM images of Fe_3O_4@nSiO_2 (a), Fe_3O_4@nSiO_2@C_{18} (b) and sample with 42 nm inner shell thickness collected after sulphonation process (c).

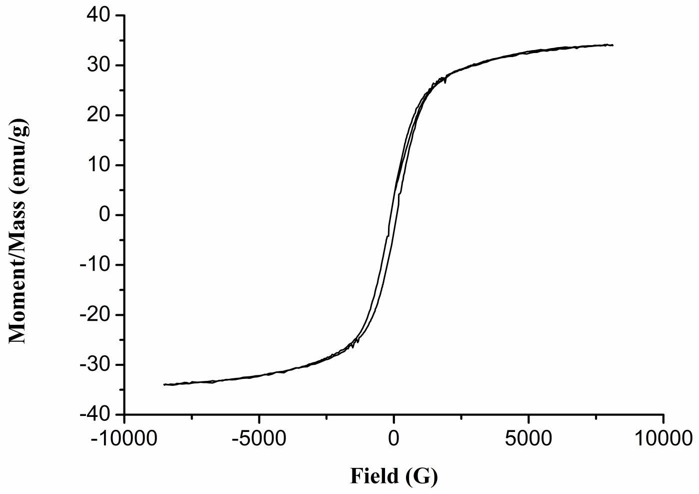


Fig.S5 Room-temperature magnetization curve of YSMMCS

Table S1. The search results of 5 nM BSA digests after enrichment with Fe_2O_3@$nSiO_2$@$mSiO_2$ nanoparticles

Sequence	MH+	pI	Ions-score	HydroScore
R.VATVSLPR.S	843.6862	9.72	52.66	0.8
K.TVMENFVAFVDK.C	1399.5797	4.37	70.44	0.5667
R.MPCTEDYLSLILNR.L	1724.6328	4.37	92.9	0.0643
R.RHPEYAVSVLLR.L	1439.8617	8.75	54.34	-0.1333
R.HPEYAVSVLLR.L	1285.5838	6.75	31.67	0.2636
K.APVLSDSSCK.S	1064.1524	5.87	31.59	0.09
K.LVVSTQTALA.-	1001.9152	5.52	68.87	1.39
R.M*PCTEDYLSLILNR.L	1742.4808	4.37	88.57	0.0643
R.RPCFSALTPDETYVPK.A	1881.8988	6.06	37.58	-0.5375
R.NECFLSHK.D	1035.8958	6.74	23.35	-0.725
R.LCVLHEK.T	899.3367	6.74	27.31	0.5286
K.QTALVELLK.H	1013.7559	6	49.06	0.6444
R.KVPQVSTPTLVEVSR.S	1640.3286	8.75	91.82	-0.0667
K.SLHTLFGDELCK.V	1419.8519	5.3	60.55	0.0583
K.LGEYGFQNALIVR.Y	1480.0953	6	85.86	0.2923
K.YICDNQDTISSK.L	1444.1661	4.21	41.03	-0.8333
K.LVNELTEFAK.T	1163.8094	4.53	52.37	0.13
K.HLVDEPQNLIK.Q	1306.4864	5.32	41.95	-0.5818
K.GACLLPK.I	758.4889	8.22	34.41	0.8571
K.TVM*ENFVAFVDK.C	1416.4088	4.37	72.76	0.5667
K.DLGEEHFK.G	975.5167	4.65	40.81	-1.425
K.KQTALVELLK.H	1141.4198	8.59	41.68	0.19
K.LVTDLTK.V	789.6011	5.84	34.44	0.4286
K.AEFVEVTK.L	924.4635	4.53	39.71	0.175

K.VPQVSTPTLVEVSR.S	1512.6602	5.97	69.23	0.2071
R.FKDLGEEHFK.G	1249.8746	5.45	44.27	-1.25
R.LSQKFPK.A	847.5794	10	33.32	-1.0143
K.CCTESLVNR.R	1139.8543	5.99	44.23	0
K.YLYEIAR.R	927.5562	6	25.05	-0.0714

Table S2. The search results of 5 nM BSA digests after enrichment with YSMMCS nanoparticles

Sequence	MH+	pI	Ions-score	HydroScore
K.LKECCDKPLLEK.S	1531.1621	6.17	23.19	-0.6167
K.TVMENFVAFVDK.C	1399.9666	4.37	60.62	0.5667
R.RHPEYAVSVLLR.L	1440.1333	8.75	62.15	-0.1333
K.LVVSTQTALA.-	1001.8782	5.52	59.03	1.39
R.M*PCTEDYLSLILNR.L	1741.7911	4.37	101.43	0.0643
K.PDPNTLCDEFK.A	1336.6899	4.03	58.29	-1.1545
R.RPCFSALTPDETYVPK.A	1879.4243	6.06	56.63	-0.5375
R.ETYGDMADCCEK.Q	1479.1754	3.92	76.57	-0.9667
K.QTALVELLK.H	1015.3943	6	52.79	0.6444
K.CCAADDKEACFAVEGPK.L	1928.898	4.32	53.31	-0.1235
R.LGEHNIDVLEGNEQFINAAK.I	2209.309	4.4	70.69	-0.435
K.ECCHGDLLECADDRADLAK.Y	2248.6852	4.23	41.03	-0.4579
K.LVNELTEFAK.T	1163.1131	4.53	61.09	0.13
K.YNGVFQECCQAEDK.G	1747.9439	4.14	83.16	-0.9143
K.TVM*ENFVAFVDK.C	1415.1444	4.37	72.43	0.5667
K.EACFAVEGPK.L	1108.0455	4.53	24.71	0.02
K.DAIPENLPPLTADFAEDKDVCK.N	2458.5567	3.96	71.48	-0.4909
K.VPQVSTPTLVEVSR.S	1512.2415	5.97	75.09	0.2071
K.CCTESLVNR.R	1139.554	5.99	54.32	0
K.TVMENFVAFVDKCCAADDKEACFAVEGPK.L	3309.585	4.3	81.43	0.1621
R.VATVSLPR.S	843.0977	9.72	42.13	0.8
K.LSSPATLNSR.V	1045.7722	9.75	42.58	-0.33
K.EYEATLEECCAK.D	1502.5272	4.09	81.61	-0.625
K.ECCHGDLLECADDR.A	1748.6737	4.1	73.84	-0.6214
-.FPTDDDDK.I	952.9826	3.77	24.36	-2.175
R.MPCTEDYLSLILNR.L	1724.2369	4.37	102.39	0.0643
R.HPEYAVSVLLR.L	1285.3062	6.75	20.52	0.2636
K.FPKAEFVEVTK.L	1296.0244	6.14	24.9	-0.1182
R.ETYGDM*ADCCEK.Q	1495.0356	3.92	41.02	-0.9667
K.DAFLGSFLYEYSR.R	1568.3315	4.37	87.23	-0.0846
R.LCVLHEK.T	897.6735	6.74	33.21	0.5286
R.KVPQVSTPTLVEVSR.S	1640.477	8.75	102.26	-0.0667
K.SLHTLFGDELCK.V	1420.4581	5.3	59.3	0.0583
K.LGEYGFQNALIVR.Y	1479.897	6	89.15	0.2923
K.YICDNQDTISSK.L	1444.0387	4.21	72.95	-0.8333
K.HLVDEPQNLIK.Q	1303.9521	5.32	56.31	-0.5818

R.CCTKPESER.M	1168.404	6.13	20.12	-1.5
K.DDSPDLPK.L	887.7196	3.93	20.17	-1.825
K.LFTFHADICTLPDTEK.Q	1908.5748	4.54	64.81	0.0437
K.DLGEEHFK.G	974.8889	4.65	36.42	-1.425
K.KQTALVELLK.H	1141.5075	8.59	60.23	0.19
K.ECCDKPLLEK.S	1292.3303	4.68	46.62	-0.73
R.PCFSALTPDETYVPK.A	1725.0262	4.37	36.64	-0.2733
K.AEFVEVTK.L	922.5591	4.53	42.42	0.175
K.TCVADESHAGCEK.S	1463.5285	4.65	79.64	-0.5154
K.LKPDPNTLCDEFK.A	1576.2524	4.56	54.75	-0.9846
K.DAIPENLPPLTADFAEDK.D	1956.38	3.77	32.78	-0.5611
R.FKDLGEEHFK.G	1250.0815	5.45	48.85	-1.25
R.LSQKFPK.A	847.6196	10	25.92	-1.0143
R.NECFLSHKDDSPDLPK.L	1902.9841	4.66	29.85	-1.275
K.YLYEIAR.R	929.3817	6	22.98	-0.0714

Table S3. The search results of 20 μL human serum after enrichment with Fe_2O_3@nSiO_2@mSiO_2 nanoparticles

Sequence	MH+	pI	Ions-scoe	HydroScore
K.GSEM*VVAGKLQ.D	1134.5827	6	33.35	0.3091
M.ADEAGSEADHEGTHSTK.R	1741.7257	4.49	26.27	-1.5412
R.SEAYNTFSER.R	1203.5286	4.53	35.33	-1.4
A.DEAGSEADHEGTHST.K	1542.5946	4.17	58.95	-1.6067
A.TKTAKDALSSVQESQVAQQA.R	2090.0729	5.73	42.12	-0.66
R.PGVLSSRQLGLPGPPDVPDHA.A	2109.1087	5.22	49.63	-0.3524
S.SSYSKQFTSSTSYNR.G	1742.799	9.7	78.39	-1.4267
S.SKITHRIHWESASLL.R	1777.9694	8.51	51.81	-0.26
K.HTLNQIDEVK.V	1196.6268	5.32	37.96	-0.93
E.SSSHHPGIAEFPSRG.K	1565.7456	6.66	55.41	-0.8333
A.EDPQGDAAQKTD.T	1274.5505	4.04	40.96	-2
S.YNRGDSTFES.K	1175.4963	4.37	41.49	-1.62
K.AGAEPASEREVS.-	1202.5662	4.25	35.69	-0.75
K.YYLQGAKIPKPEASFSPR.R	2052.0908	9.53	42.75	-0.7778
S.SRQLGLPGPPDVPDHAAYHPF.R	2271.1294	5.93	55.65	-0.6714
Y.NRGDSTFESK.S	1140.528	6.07	41.98	-1.88
A.SRGASQAGAPQGR.V	1242.6306	12	35.49	-1.1538
T.SYNRGDSTFES.K	1262.5293	4.37	28.75	-1.5455
K.RLAVYQAGAREGAER.G	1646.8727	8.74	25.35	-0.7267
R.SSKITHRIHWESASLLR.S	2021.1019	10.83	70.23	-0.5412
T.LLTEAPLNPK.A	1095.6407	6	26.34	-0.16
L.SRSGGGGGGGLGSGGSIRSSY.S	1812.8587	10.83	58.93	-0.5143
R.NVHSAGAAGSRM*NFRPGVLSSRQLGLPGPPDVPDHAAYHP.F	4149.0556	8.76	27.4	-0.475
I.SSSKGSLGGGF.S	983.4804	8.47	46.91	-0.1909
K.SYKMADEAGSEADHEGTHST.K	2122.8631	4.49	53.7	-1.32

R.ILGGHLDAKG.S	980.5528	6.74	30.17	0.21
S.YKM*ADEAGSEADHEGTHST.K	2051.824	4.49	43.21	-1.3474
R.RHPDYSVVL.L	1085.5743	6.74	37.88	-0.3
K.ATEHLSTLSEKAKPALEDLR.Q	2209.1861	5.53	30.08	-0.675
R.QLGLPGPPDVPDHAAYHPFR.R	2184.0976	5.98	41.8	-0.665
R.QLGLPGPPDVPDH.A	1341.68	4.2	59.09	-0.7
G.HEQQHGLGHGHKF.K	1511.7259	7.1	31.73	-1.6769
K.RPPGFSPF.R	904.4678	9.75	36.65	-0.6125
F.KYYLQGAKIPKPEASFSPR.R	2180.1872	9.82	41.28	-0.9421
L.SRSGGGGGGGLGSGGSIR.S	1475.7315	12	69.72	-0.4389
S.SKITHRIHWE.S	1306.7036	8.51	29.56	-1.17
K.VTM*QNLNDR.L	1106.5253	5.81	46.48	-1.0333
S.KQFTSSTSYN.R	1162.5371	8.59	41.33	-1.32
K.SLEDKTERELLESYIDGR.I	2153.0701	4.36	82.82	-1.2222
Y.NRGDSTFESKSY.K	1390.6236	6.07	50.03	-1.7417
K.MADEAGSEADHEGTHSTKR.G	2028.8673	4.86	63.53	-1.5158
G.GGGGGGLGSGGSIR.S	1088.5437	9.75	40.96	-0.1
A.DEAGSEADHEGTHSTKRGHA.K	2091.9058	5.29	46.87	-1.715
Y.GSGGGSYGSGGGGGGGRGSY.G	1590.6529	8.59	56.9	-0.775
K.SSSYSKQFTSSTSYNR.G	1829.8303	9.7	82.23	-1.3875
R.GKSSSYSKQFTSSTSYNRGDSTFESKSY.K	3116.4105	9.31	35.92	-1.4071
L.APLAEDVRGNLR.G	1310.718	6.12	27.77	-0.5083
S.SYSKQFTSSTSY.N	1385.6225	8.22	70.04	-1.05
K.KTETQEKNPLPSKETIEQEKQAGES.-	2829.4081	4.77	50.36	-1.912
L.SALTSDNHGATY.A	1236.5494	5.06	25.28	-0.625
T.SSTSYNRGDSTFESKSY.K	1915.8307	5.79	48.09	-1.4882
S.SRQLGLPGPPDVPDHA.A	1655.8504	5.19	54.3	-0.7875
K.SSSYSKQFTSSTSYNRGDSTFESKS.Y	2768.2261	8.15	32.15	-1.352
S.GGGGGGGLGSGGSIR.S	1145.5666	9.75	58.11	-0.12
R.SSKITHRIHWE.S	1393.7327	8.51	48.51	-1.1364
K.KVPQVSTPTLVEVSR.N	1639.9378	8.75	60.12	-0.0667
Q.FTSSTSYNRGD.S	1234.5338	6.09	44.79	-1.2909
G.DFLAEGGGVR.G	1020.511	4.37	55.96	-0.01
K.YYLQGAKIPKPEA.S	1477.8059	8.43	30.22	-0.7
K.ENAGEDPGLAR.Q	1128.5289	4.14	45.41	-1.2273
K.GRPPKAGAEPASEREVS.-	1737.888	6.23	56.66	-1.2353
K.SYKM*ADEAGSEADHEGTHST.K	2138.8573	4.49	47.78	-1.32
T.IEGVDAEDGHGPGEQQK.R	1765.7948	4.17	63.07	-1.4294
K.SHALQLNNRQ.I	1180.6187	9.49	26.68	-1.31
K.YYLQGAKIPKPGLDHTEASFSPR.R	2575.3295	8.44	73.07	-0.7826
K.TETQEKNPLPSKETI.E	1714.8842	4.78	27.32	-1.54
R.NVHSGSTFFKYY.L	1449.6779	8.51	33.25	-0.5083
R.SSKITHRIHWESAS.L	1638.8354	8.51	39.94	-0.8786
K.DLGEENFK.A	951.4422	4.14	29.79	-1.4625

R.DAHKSEVAHRFKDLGEENFKALVLIA.F	2937.5559	6.04	46.45	-0.2962
K.LDDDLEHQGGHVLDHGH.K	1893.8483	4.68	35.58	-1.1412
L.GPLVEQGRV.R	954.5374	6	30.04	-0.1889
H.NLGHGHKHERDQGHGHQ.R	1943.91	7.16	48.64	-2.3353
K.HNLGHGHKHERDQGHG.H	1815.8494	7.16	30.7	-2.2625
F.LSSLTETIEGVDAEDGHGPGEQQK.R	2497.166	4.08	66.14	-0.9667
I.THRIHWESASLLR.S	1605.8609	9.32	54.63	-0.6308
R.IHWESASL.L	942.4677	5.24	35.04	0.1125
S.HHPGIAEFPSRG.K	1304.6496	6.92	33.15	-0.8417
K.VPQVSTPTLVEVSR.N	1511.843	5.97	65.48	0.2071
G.VVSLGSPSGEVSHPR.K	1507.7852	6.72	47.42	-0.1333
S.ALEEYTKKLNTQ.-	1437.7594	6.19	37.81	-1.2583
R.HYEGSTVPEKK.T	1274.6383	6.76	41.34	-1.6909
L.ESFKVSFLSALEEYTKKLNTQ.-	2462.2805	6.32	55.19	-0.5381
R.SGGGGGGGLGSGGSIR.S	1232.5976	9.46	87.91	-0.1625
G.SPM*YSIITPNILRL.E	1633.8986	8.46	107.26	0.5857
K.VSFLSALEEYTKKLNTQ.-	1971.0441	6.11	45.86	-0.3471
S.KITHRIHWESASLLR.S	1847.0399	10.84	32.66	-0.5067
R.AATVGSLAGQPLQERAQAWGERLR.A	2565.3652	9.56	41.27	-0.4833
P.GPPDVPDHAAYHPF.R	1519.6992	5.05	28	-0.7786
L.DDDLEHQGGHVLDHGHKH.K	2045.9187	5.49	46.42	-1.6833
W.NSGALTSGVH.T	942.4649	6.74	47.13	0
A.KVEQAVETEPEPEL.R	1597.7954	3.98	56.2	-1.0571
L.PPTSAHGNVAEGETKPD.P	1706.7991	4.83	49.89	-1.2412
R.M*NFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3288.6359	6.69	52.72	-0.4067
R.HTFM*GVVSLGSPSGEVSHPRKT.R	2326.1608	8.76	46.88	-0.2818
R.GLSAIRERLGPLVEQGRVR.A	2106.2243	11.52	33.85	-0.3158
R.EGVQKEDIPPADLSDQVPDTESETR.I	2755.2949	3.85	34.96	-1.324
Q.KPRLLLFSPSVVHLGVPLSVGVQLQDVPRGQVVKGSVF.L	4052.3451	11	55.82	0.5526
A.RYQWVRCNPDSNSANCLEEKGPM*FELLPGESNKIPRL.R	4307.0698	6.3	25.32	-0.8838
R.SEETKENEGFTV.T	1369.6123	4.09	38.31	-1.4167
S.YNRGDSTFESKSY.K	1553.6872	6.07	46.84	-1.7077
T.SYNRGDSTFESKSY.K	1640.7175	5.79	42.18	-1.6429
K.SKEQLTPLIK.K	1156.6938	8.31	34.39	-0.58
K.KSLEDKTERELLESYIDGR.I	2281.1672	4.66	49.81	-1.3632
K.DGAGDVAFVK.H	978.4885	4.21	37.66	0.31
Y.KMADEAGSEADHEGTH.S	1684.6862	4.49	59.33	-1.425
D.PEVRPTSAVAA.-	1097.5952	6.43	39.81	0.1
R.GLSAIRER.L	901.5216	9.6	25.66	-0.45
A.KIPKPGLDHTEASFSPR.R	1880.0026	8.6	26.72	-1.0059
A.EDPQGDAAQKT.D	1159.523	4.03	27.82	-1.8636
Y.NRGDSTFES.K	1012.4334	4.37	26.25	-1.6556
R.LTPYADEFKVKIDQTVEELR.R	2394.2567	4.51	42.21	-0.625
M.ADEAGSEADHEGTH.S	1425.5517	4.17	53.63	-1.4857

R.AHYDLRHTFM*GVVSLGSPSGEVSHPR.K	2852.3906	7.07	68.24	-0.3269
K.RLAVYQAGAREGAE.R	1490.7716	6.28	44.28	-0.4571
T.SYNRGDSTFESKS.Y	1477.6572	5.79	33.89	-1.6692
Y.LQGAKIPKPGLDHTEASFSPR.R	2249.2019	8.6	52.35	-0.7333
G.SEM*VVAGKLQ.D	1077.562	5.72	34.99	0.38
A.TVGSLAGQPLQERAQAWGERL.R	2267.1903	5.81	31.87	-0.5095
H.RIHWESASL.L	1098.5694	6.75	40.88	-0.4
M.IEQNTKSPLFM*GKVVNPTQK.-	2275.2108	9.7	30.85	-0.68
A.TVGSLAGQPLQERA.Q	1426.7647	5.66	56.41	-0.25
K.ITHRIHWESAS.L	1336.6763	6.92	32.24	-0.6182
R.GNTEGLQKSLAELGGHLDQQVEEFRR.R	2911.4723	4.96	52.53	-1.0269
K.SSSYSKQFTSSTSYNRGDSTF.E	2337.0271	8.22	41.36	-1.181
R.NGFKSHALQLNNR.Q	1498.7859	11	32.99	-1.1231
S.STSYNRGDSTFES.K	1450.6079	4.37	33.41	-1.4231
R.M*NFRPGVLSSRQLGLPGPPDVPDHAAYHPFR.R	3444.7385	8.53	25.53	-0.5387
K.SLEDKTERELLESYIDG.R	1996.9698	4.08	43.46	-1.0294
E.FVSETESRGSESGIFTNTKESSSHHPGIAEFPSRG.K	3751.7541	5.45	30.87	-0.8629
R.GASQAGAPQGR.V	999.4974	9.75	44.2	-0.8818
K.VDNALQSGNSQESVTEQDSK.D	2135.9678	3.92	86.51	-1.285
K.SSSYSKQFTSSTSYNRGDST.F	2189.9586	8.22	47.02	-1.38
K.AGVETTTPSK.Q	990.5084	6.05	47.64	-0.63
F.LSSLTETIEGVDAEDGHGPGEQQKR.K	2653.2702	4.35	36.7	-1.108
K.LQHLENELTHDIITK.F	1803.9596	5.27	27.33	-0.5867
K.TETQEKNPLPSKETIEQEKQAGES.-	2701.3205	4.48	47.98	-1.8292
R.REYHTEKLVTSKGDKEL.R	2033.0665	6.77	59.32	-1.5
R.ENADSLQASLRPHADELKA.K	2065.0303	4.75	47.11	-0.9053
D.WVQKTIAEN.-	1088.5738	6	33.69	-0.6111
K.SLAELGGHLDQQVEEF.R	1771.8501	4	62.72	-0.35
S.GEGDFLAEGGGVR.G	1263.5965	4.14	94.62	-0.3385
L.TETIEGVDAEDGHGPGEQQKR.K	2253.0404	4.35	38.37	-1.6048
A.DEAGSEADHEGTH.S	1354.5145	4.17	79.03	-1.7385
W.GQGTTVTVSSASTK.G	1323.6741	8.75	58.29	-0.2286
Y.RSGGGFSSGSAG.I	1026.4611	9.75	37.92	-0.425
E.EKGPM*FELLPGESNKIPRL.R	2171.1555	6.33	25.24	-0.6368
F.NWYVDGVEVHNAK.T	1530.7338	5.32	51.42	-0.7154
G.DSTFESKSY.K	1063.4571	4.37	49.13	-1.3889
R.HRHPDEAAF.F	1079.5031	5.99	31.17	-1.4556
K.ATEHLSTLSEK.A	1215.6213	5.4	44.82	-0.7
Y.STTAVVTNPKE.-	1146.6003	5.94	36.69	-0.4727
S.EM*VVAGKLQ.D	990.5288	6.1	42.22	0.5111
R.AATVGSLAGQPLQERAQAWGERL.R	2409.2622	6.19	48.27	-0.3087
R.AAPGQEPPEHM*AELQ.R	1620.7323	4.24	54.65	-0.9867
D.SGPRRYTIAALLSPYSYSTTAVVTNPKE.-	3042.587	9.52	41.89	-0.325
K.AGFAGDDAPR.A	976.45	4.21	39.95	-0.57

R.NVHSGSTFFKYYLQGAKIPKPEA.S	2582.3398	9.4	31.95	-0.5478
M.NFRPGVLSSRQLGLPGPPDVPDHA.A	2526.3185	6.75	35.21	-0.525
R.AELQEGARQKLHELQEKLSPLGEEM*RDRA.R	3377.7213	5.14	35.65	-1.2552
A.EEAGARVQQNVPSGTDTGDPQSKPLG.D	2638.267	4.32	76.61	-1.1538
H.GLGHGHEQQHGLGH.G	1463.6896	6.42	28.4	-1.2643
R.NEQEQPLGQWHLS.K	1565.7349	4.51	59.82	-1.5615
R.SLDRNLPSDSQDLGQHGLEED.F	2325.0558	4.1	61.83	-1.3714
Y.VKVTSIQDWVQKTIAEN.-	1959.0489	6.04	75.34	-0.2941
R.GHVLAKELEAFR.E	1369.7596	6.76	39.91	-0.0667
R.TQVNTQAEQLR.R	1287.6656	5.66	56.55	-1.2364
G.VLSSRQLGLPGPPDVPDHAAYHPF.R	2570.3494	5.98	59.59	-0.2875
R.GSESGIFTNTKESSSHHPGIAEFPSR.G	2759.2988	6.02	41.24	-0.8846
M.NFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3141.6025	6.92	46.68	-0.4862
K.TDTSHHDQDHPTFNK.I	1779.7696	5.68	25.06	-2.18
L.GLPGPPDVPDH.A	1100.5384	4.2	28.01	-0.8545
R.ISASAEELRQ.R	1103.57	4.53	48.38	-0.47
M.ADEAGSEADHEGTHST.K	1613.6296	4.17	64.11	-1.3937
Q.KENAGEDPGLA.R	1100.5216	4.14	34.59	-1.1727
R.ISASAEELR.Q	975.5103	4.53	49.36	-0.1333
G.LGHGHEQQHGLGHGHKF.K	1875.9107	7.16	45.07	-1.2941
R.NVHSGSTFFKYYLQGA.K	1818.8769	8.51	90.56	-0.275
D.FLAEGGGVR.G	905.4843	6	48.45	0.3778
K.ESSSHHPGIAEFPS.R	1481.6651	5.23	25.63	-0.7929
T.HRIHWESASLL.R	1348.7092	6.92	37.88	-0.2727
K.ESSSHHPGIAEFPSRG.K	1694.7883	6.01	38.92	-1
L.M*IEQNTKSPLFM*GKVVNPTQK.-	2422.2445	9.7	84.41	-0.5571
K.SSSYSKQF.T	933.431	8.31	27.36	-1.1375
R.SLAPYAQDTQEKLNHQLEGLTFQM*.K	2778.3383	4.65	26.89	-0.7125
I.THRIHWESASLL.R	1449.7592	6.62	33.01	-0.3083
K.SSSYSKQFTSSTSYN.R	1673.7299	8.22	77.25	-1.18
V.SETESRGSESGIFTNTKESSSHHPGIAEFPSRG.K	3505.6181	5.44	52.39	-1.1273
Y.KM*ADEAGSEADHEGTHST.K	1888.7595	4.49	48.02	-1.35
R.THLAPYSDELR.Q	1301.6489	5.29	34.5	-0.8818
Y.YLQGAKIPKPEASFSPR.R	1889.0278	9.7	32.9	-0.7471
K.VVEEQESR.V	975.4746	4.25	32.97	-1.3625
A.DEAGSEADHEGTHSTKR.G	1826.7896	4.87	52.75	-1.9118
S.SSHHPGIAEFPSRG.K	1478.7144	6.66	30.01	-0.8357
D.SGEGDFLAEGGGVR.G	1350.6285	4.14	86.91	-0.3714
R.HLSQDTGSPSGM*RPWEDLPSQDTGSPS.R	2885.2624	4.22	63.09	-1.2556
S.FLSALEEYTKKLNTQ.-	1784.9393	6.14	77.33	-0.62
L.SALEEYTKKLNTQ.-	1524.7895	5.86	49.15	-1.2231
C.GKPKNPANPVQ.R	1149.6374	10	39.61	-1.5909
I.HWESASLLR.S	1098.5693	6.75	49.1	-0.4778
G.HGLGHGHEQQHGLGHGHKF.K	2069.9914	7.21	64.4	-1.3474

R.GDSTFESKSYKM*ADEAGSEADHEGTHST.K	2990.2221	4.43	30.84	-1.3286
K.DDNPNLPR.L	940.4486	4.21	41.11	-2.2375
K.LVNEVTEFAK.T	1149.6152	4.53	44.28	0.17
K.AEFAEVSK.L	880.4415	4.53	39.59	-0.1375
V.LSSRQLGLPGPPDVPDHAAYHPF.R	2471.2512	5.98	53.86	-0.4826
T.FM*GVVSLGSPSGEVSHPR.K	1858.9121	6.75	36.09	0.1278
A.TASRGASQAGAPQGR.V	1414.7148	12	42.58	-0.9267
A.LLSPYSYSTTAVVTNPKE.-	1970.0106	6.22	82.4	-0.1889
R.NLPSDSQDLGQHGLEED.F	1853.8148	3.94	54.91	-1.4
I.NVKVGGNSKGTLKVL.R	1513.8895	10.3	30.31	-0.08
E.GDFLAEGGGVR.G	1077.533	4.37	70.14	-0.0455
R.GHGLGHGHEQQHGLGHGH.K	1851.8488	6.62	46.32	-1.3833
A.DEAGSEADHEGTHS.T	1441.5461	4.17	57.05	-1.6714
R.FKDLGEENFK.A	1226.6054	4.68	31.3	-1.28
H.GLGHGHEQQHGLGHGH.K	1657.7697	6.54	45	-1.3312
K.M*ADEAGSEADHEGTHSTKR.G	2044.8627	4.86	40.66	-1.5158
Y.KFQNALLVR.Y	1088.6569	11	55.52	0.1111
M.NFRPGVLSSRQL.G	1373.7652	12	36.18	-0.4167
S.SYSKQFTSSTSYNRGDSTFES.K	2379.0344	5.79	45.9	-1.3095
K.SSSYSKQFT.S	1034.4791	8.31	42.49	-1.0889
P.GQEPPEHM*AELQ.R	1381.606	4.24	31.66	-1.4
K.MADEAGSEADHEGTHSTK.R	1872.7655	4.49	26.29	-1.35
K.SLAELGGHLDQQVEEFR.R	1927.9506	4.4	72.01	-0.5941
T.IEGVDAEDGHGPGEQQ.K	1637.7036	3.83	39.97	-1.275
K.SSSYSKQFTSSTSYNRGDSTFESKSYK.M	3059.3862	9.3	58.09	-1.4444
R.SSKITHRIHWESASL.L	1751.9183	8.51	37.28	-0.5667
F.WDLDPEVRPTSAVAA.-	1626.814	4.03	75.74	-0.2
F.RPGVLSSRQLGLPGPPDVPDHAAYHPF.R	2880.4889	6.92	37.22	-0.4963
R.NVHSGSTFFKYYLQGAKIPKPEASFSPR.R	3156.6259	9.82	60.66	-0.625
R.GSESGIFTNTKESSSHHPGIAEFPS.R	2603.2029	5.33	27.49	-0.74
R.NVHSGSTFF.K	995.4583	6.74	31.28	0.0444
K.ITHRIHWESASLLR.S	1718.9446	9.61	32.62	-0.2643
Q.HLDNFSNQIGKHY.K	1572.756	6.92	39.25	-1.2077
K.KQTALVELVK.H	1128.6994	8.59	53.37	0.23
K.ITHRIHWESASLL.R	1562.8425	6.92	47.77	0.0615
R.GKSSSYSKQFTSSTSYNRGDSTFES.K	2738.2153	8.43	56.9	-1.336
T.FM*GVVSLGSPSGEVSHPRKT.R	2088.0547	8.75	34.72	-0.115
R.QLGLPGPPDVPDHAA.Y	1483.7537	4.2	68	-0.3667
R.TFHPLRSEAYNTFSER.R	1954.9405	6.42	27.74	-1.0875
V.SETESRGSESGIFTNTKESSSHHPGIAEFPSRGK.S	3633.7186	6.01	25.85	-1.2088
R.RPHFFFPK.S	1075.5833	11	34.48	-0.8
R.QLGLPGPPDVPDHAAYHP.F	1880.9301	5.05	30.81	-0.6444
G.VVSLGSPSGEVSHPRKT.R	1736.9273	8.73	38.45	-0.3882
K.SPELQAEAK.S	972.5001	4.53	40.85	-1.0444

K.LVAASQAALGL.-	1013.5994	5.52	36.41	1.6455
R.DAHKSEVAHRFKDLGEENFKA.L	2428.1986	6.04	29.33	-1.2286
G.HGLGHGHEQQHGLGHGH.K	1794.8283	6.62	64.58	-1.4412
K.ALGISPFHEHAEVVFTANDSGPR.R	2451.2057	5.28	30.41	-0.1522
V.LKPEEEAPAPEVGASKPEGI.D	2048.0549	4.33	57.65	-0.77
F.TSSTSYNRGDSTFESKSY.K	2016.8785	5.73	36.88	-1.4444
L.SSRQLGLPGPPDVPDHAAYHPF.R	2358.1578	5.93	53.29	-0.6773
S.KITHRIHWESASLL.R	1690.9393	8.76	47.08	-0.2214
R.GRELTTQRQLM*QERAEEGKGPSKAQRGSLE.H	3386.6556	8.59	29.91	-1.5533
H.WESASLLR.S	961.5097	6	39.15	-0.1375
H.RIHWESASLLR.S	1367.7545	9.61	60.69	-0.3909
R.M*NFRPGVLS.S	1036.5241	9.5	38.58	0.2111
A.DSGEGDFLAEGGGVR.G	1465.6555	3.92	105.82	-0.58
R.IGEIKEETTSHL.R	1356.7003	4.75	40.16	-0.6167
R.RAVPPNNSNAAEDDLPTVELQGVVPR.G	2758.4084	4.32	42.02	-0.5962
Y.LQGAKIPKPEASFSPR.R	1725.9658	9.99	30.08	-0.7125
G.GGGGGLGSGGSIR.S	1031.523	9.75	37.64	-0.0769
K.SSSYSKQFTSSTSYNRGDSTFESKSY.K	2931.2894	8.11	66.98	-1.35
Y.SKQFTSSTSYN.R	1249.5712	8.31	55.54	-1.2727
S.SSYSKQFTSST.S	1222.5594	8.31	43.64	-1.0273
F.LSALEEYTKKLNTQ.-	1637.8742	6.14	50.95	-0.8643
K.SYKM*ADEAGSEADHEGTHSTK.R	2266.9516	4.86	37.62	-1.4429
A.EDPQGDAAQKTDTSHHDQ.D	1979.8308	4.34	34.43	-2.1611
R.AQAWGERL.R	930.4797	6.05	25.34	-0.675
R.LAPLAEDVRGNL.R	1267.7005	4.37	49.57	0.1833
K.MADEAGSEADHEGTHST.K	1744.67	4.17	67.23	-1.2
R.ILGGHLDAKGSFPWQAKM*.V	1972.0087	8.6	51.01	-0.1167
C.FSALEVDETYVPK.E	1497.7448	4.14	61.21	-0.1538
S.YSKQFTSSTSYNRGDSTFESKSY.K	2670.1928	8.38	44.41	-1.4217
K.YLYEIAR.R	927.4937	6	31.94	-0.0714
P.GLDHTEASFSPR.R	1316.6229	5.32	38.47	-0.8833
K.SHALQLNN.R	896.4589	6.46	35.97	-0.6375
R.NVHSAGAAGSRM*NFRPGVLSS.R	2131.0468	12	28.5	-0.1381
R.SSRIGEIKEETTSHL.R	1686.865	5.47	26.17	-0.9
S.SLGGGFGGGSR.G	951.4655	9.46	51.55	-0.1727
R.TSSDHTDHTYLSSTFTKGERA.L	2341.0693	5.93	29.5	-1.2048
R.NGFKSHALQLN.N	1228.6436	8.76	37.5	-0.6
R.TGKEKVTSGSTTTT.R	1397.7114	8.26	37.01	-0.9786
E.SFKVSFLSALEEYTKKLNTQ.-	2333.2141	8.16	49.59	-0.39
R.SEETKENEGFTVTAEGK.G	1855.8553	4.32	57.28	-1.3941
N.FRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3027.5581	6.92	28.84	-0.3786
R.RPHFFFPKSRIV.R	1530.8692	12.01	31.4	-0.25
K.HQTVPQNTGGK.N	1166.5919	8.76	28.71	-1.5636
L.PGPPDVPDHAAYHPF.R	1616.7493	5.05	37.23	-0.8333

I.GEIKEETTSHL.R	1243.6171	4.75	43.7	-1.0818
R.GNTEGLQKSLAELGGHLDQQVEEFR.R	2755.3672	4.57	63.92	-0.888
K.M*ADEAGSEADHEGTH.S	1572.5855	4.17	41.38	-1.26
A.ATASRGASQAGAPQGR.V	1485.7513	12	51.48	-0.7562
S.SHHPGIAEFPSRG.K	1391.682	6.66	26.49	-0.8385
S.SRQLGLPGPPDVPDHAA.Y	1726.8874	5.19	43.11	-0.6353
K.M*ADEAGSEADHEGTHST.K	1760.6652	4.17	90.39	-1.2
S.SSGSVGESSSKGP.R	1165.5341	5.72	29.37	-0.8308
R.SLEHSEGPVGRDPAGPPDGGPDTEPR.A	2626.215	4.29	37.24	-1.4346
Y.GSGGGSYGSGGGGGGHGSY.G	1514.5897	6.74	32.81	-0.7263
R.M*NFRPGVLSSRQLGLPGPPDVPDHA.A	2673.3569	6.5	57.09	-0.428
Y.FVELGTQPATQ.-	1190.6057	4	36.36	-0.1182
F.KVSFLSALEEYTKKLNTQ.-	2099.1348	8.43	88.47	-0.5444
R.PGVLSSRQLGLPGPPDVPDHAAYHP.F	2577.3208	6	70.41	-0.468
S.RQLGLPGPPDVPDHAAYHPF.R	2184.0995	5.98	38.28	-0.665
R.IHWESASLLR.S	1211.6534	6.75	44.56	0.02
R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2602.3088	3.92	36.01	-0.44
R.GHGLGHGHEQQHGLGHGHKF.K	2127.0135	7.21	40.41	-1.3
R.DAHKSEVAHRFKDLGEENFKALVL.I	2753.4351	6.04	40.29	-0.5833
L.PWLKEKLQDEDLGFL.-	1830.9619	4.32	62.8	-0.68
Y.VKVTSIQHWVQKTIAEN.-	1981.0865	8.57	52.45	-0.2765
R.M*NFRPGVLSSRQLGLPGPPDVPDHAAYHP.F	3141.5666	6.69	45.62	-0.5172
S.SKITHRIHWESA.S	1464.7708	8.51	42.27	-0.8917
K.TYETTLEK.C	984.4891	4.53	27.82	-1.3125
K.VKSPELQAEAK.S	1199.6638	6.11	27.61	-0.8273
I.GEIKEETTSHLR.S	1399.7177	5.5	35.95	-1.3667
G.HGHEQQHGLGHGHKF.K	1705.8048	7.16	45.27	-1.6933
L.FQVLPWLKEKLQDEDLGFL.-	2318.2472	4.32	35.53	-0.1526
R.VGEAAHALGNTGHEIGR.Q	1688.8462	6	47.48	-0.3412
K.LSPLGEEM*R.D	1047.5136	4.53	41.98	-0.5333
F.VELGTQPATQ.-	1043.5365	4	36.71	-0.41
G.LGHGHEQQHGLGH.G	1406.6671	6.42	40.41	-1.3308
F.TVNFGDTEEAKK.Q	1338.6535	4.68	27.09	-1.2333
R.RHPDYSVVLLLR.L	1467.8423	8.75	68.64	0.0333
Y.KMADEAGSEADHEGTHST.K	1872.7675	4.49	88.21	-1.35
T.ADSGEGDFLAEGGGVR.G	1536.6934	3.92	118.96	-0.4313
K.KTETQEKNPLPSKETI.E	1842.9812	6.23	29.47	-1.6875
H.SAGAAGSRM*NFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3945.9504	8.51	28.18	-0.3605
K.SGSDEVQVGQQR.T	1289.6086	4.37	73.3	-1.3333
Y.YLQGAKIPKPGLDHTEASFSPR.R	2412.266	8.5	27.97	-0.7591
S.SRQLGLPGPPDVPDHAAYHP.F	2124.0602	5.93	55.18	-0.845
R.GKSSSYSKQFTSSTSYNR.G	2014.9473	10	50.9	-1.4722
R.SSKITHRIHWESASLL.R	1865.0009	8.51	59.97	-0.2938
R.RHDWGHEKQ.R	1192.5614	6.92	30.51	-2.9556

S.SSYSKQFTSSTSYN.R	1586.6971	8.22	66.03	-1.2071
G.RPPKAGAEPASEREVS.-	1680.8662	6.23	35.44	-1.2875
K.SSSYSKQFTSSTSYNRGDSTFESKSYKM*.A	3206.4194	9.3	33.39	-1.325
K.GPSVFPLAPSSK.S	1186.6463	8.75	27.89	0.0917
R.SLLEGEGSSGGGGR.G	1262.5964	4.53	44.38	-0.6214
S.SHHPGIAEFPS.R	1178.5594	5.93	25.56	-0.5455
A.LEEYTKKLNTQ.-	1366.7205	6.14	44.56	-1.5364
K.MADEAGSEADHEGTH.S	1556.5914	4.17	51.59	-1.26
K.SLHTLFGDK.L	1017.5361	6.46	39.69	-0.2333
S.YSKQFTSST.S	1048.4949	8.59	33.81	-1.0778
R.GSESGIFTNTKESSSHHPG.I	1958.8857	6	31.3	-1.1421
K.HNLGHGHKHERDQGHGHQ.R	2080.9676	7.21	41.35	-2.3833
R.QLGLPGPPDVPDHAAYHPF.R	2027.9979	5.05	67.62	-0.4632
A.DEAGSEADHEGTHSTK.R	1670.6893	4.49	42.14	-1.75
F.LSALEEYTKKLNT.Q	1509.8156	6.14	39.49	-0.6615
R.NVHSGSTFFKYYLQGAKIPKPGLDHTEASFSPR.R	3679.8666	9.4	52.39	-0.6515
P.SKETIEQEKQAGES.-	1563.75	4.49	45.65	-1.8
R.HTFM*GVVSLGSPSGEVSHPR.K	2097.0186	6.92	76.45	-0.08
L.SRSGGGGGGGLGSGGSIRSS.Y	1649.7952	12	58.09	-0.475
K.SSSYSKQFTS.S	1121.5122	8.31	34.18	-1.06
S.FKVSFLSALEEYTKKLNTQ.-	2246.2069	8.43	61.64	-0.3684
K.SSSYSKQFTSSTSYNRGDSTFES.K	2553.0994	5.79	54.21	-1.2652
R.GKSSSYSKQFTSSTSYN.R	1858.8476	9.53	66.59	-1.2941
R.M*NFRPGVLSSRQLGLPGPPDVPDHAA.Y	2744.3952	6.5	35.77	-0.3423
L.NQAQEHFGK.D	1058.5022	6.75	27.49	-1.8778
S.SYSKQFTSST.S	1135.5279	8.31	31.74	-1.05
R.QLGLPGPPDVPDHA.A	1412.7158	4.2	50.88	-0.5214
R.IGEIKEETTSHLR.S	1512.802	5.5	57.57	-0.9154
R.GSESGIFTNTKESSSHHPGIAEFPSRG.K	2816.3252	6.02	55.07	-0.8667
R.GDSTFESKS.Y	957.4166	4.37	33.71	-1.2889
R.APNHAVVTR.K	964.5332	9.8	64.54	-0.1667
F.VSETESRGSESGIFTNTKESSSHHPGIAEFPSRG.K	3604.6894	5.45	34.22	-0.9706
D.AHKSEVAHRFKDLGEENFKALVL.I	2638.4108	6.97	30.58	-0.4565
R.AELQEGAR.Q	873.4425	4.53	43.52	-1
R.DAHKSEVAHRF.K	1296.6448	6.92	32.06	-1.0909
F.LM*IEQNTKSPLFM*GKVVNPTQK.-	2535.3323	9.7	66.33	-0.3591
K.TGLQEVEVK.A	1002.5467	4.53	38.25	-0.3667
K.MADEAGSEADHEGTHSTKRGHA.K	2293.985	5.28	37.92	-1.3909
K.SSSYSKQFTSSTSY.N	1559.6864	8.22	44.99	-1.0143
T.SSTSYNRGDSTFES.K	1537.6396	4.37	52.54	-1.3786
A.HKSEVAHRFKDLGEENFKALVL.I	2567.3693	6.93	49.46	-0.5591
R.NVHSAGAAGSRM*NFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	4296.1262	8.76	25.85	-0.3951
D.VPDHAAYHPF.R	1153.5323	5.97	26.21	-0.38
V.SLGSPSGEVSHPR.K	1309.651	6.47	52.64	-0.8

S.SKITHRIHWESASLLR.S	1934.0688	10.83	47.92	-0.525
K.GSEM*VVAGKLQDR.G	1405.7098	6.07	56.37	-0.3538
D.SGEGDFLAEGGGV.R	1194.528	3.57	49.36	-0.0538
P.GVLSSRQLGLPGPPDVPDHA.A	2012.0562	5.21	42.27	-0.29
R.SSKITHRIHWESA.S	1551.8021	8.51	44.16	-0.8846
L.SRSGGGGGGGLGSGGSIRSSYSRF.S	2203.059	11.71	40.05	-0.5542
K.SSSYSKQFTSSTSYNRGDSTFESKSYKM*ADEAGSEADHEGTHS.K	4801.0318	5.01	38.13	-1.35
L.GHGHEQQHGLGHGHKF.K	1762.8262	7.16	25.01	-1.6125
R.DAHKSEVAHRFKDLGEENFKAL.V	2541.283	6.04	37.85	-1
R.AHYDLRHTFM*GVVSLGSPSGEVSHPRKT.R	3081.5344	8.65	57.61	-0.4679
R.DAHKSEVAHRFKDLGEENFKALVLIAF.A	3084.5751	6.04	35.95	-0.1815
S.YSKQFTSSTSYNRGDSTFES.K	2292.0042	6.07	27.13	-1.335
S.STSYNRGDSTFESKSY.K	1828.798	5.79	25	-1.5312
H.GLGHGHEQQHGLGHGHKF.K	1932.9321	7.16	30.05	-1.2444
P.M*LGEFVSETESRGSESGIFTNTKESSSHHPGIAEFPSRG.K	4197.9387	5.05	28.82	-0.7282
R.SQHLDNFSNQIGKHY.K	1787.8454	6.66	31.52	-1.3333
R.DAHKSEVAHRFK.D	1424.7386	8.6	27.76	-1.325
L.EEYTKKLNTQ.-	1253.6374	6.24	39.56	-2.07
K.NAEELKARISASAEELRQ.R	2015.0515	4.95	40.31	-0.9
K.FQNALLVR.Y	960.5631	9.75	35.13	0.6125
R.ARYQWVRCNPDSNSANCLEEKGPM*FELLPGESNKIPRLRT.D	4635.2521	8.07	31.86	-0.9025
G.VLSSRQLGLPGPPDVPDHA.A	1955.0335	5.21	25.8	-0.2842
R.VTEPISAESGEQVER.V	1630.7915	4.09	84.12	-0.7733
A.DSGEGDFLAEGGGV.R	1309.5372	3.43	51.7	-0.3
R.TATSEYQTFFNPR.T	1561.7282	5.66	62.35	-1.0308
R.NVHSGSTFFKYYLQGAKIPKPEAS.F	2669.3715	9.4	49.76	-0.5583
T.NTKESSSHHPGIAEFPSRG.K	2037.9733	6.93	35.2	-1.2684
L.GLPGPPDVPDHAAYHPF.R	1786.8543	5.05	57.98	-0.5353
L.PVLESFKVSFLSALEEYTKKLNTQ.-	2771.4865	6.64	41.38	-0.2042
Q.FTSSTSYNRGDSTFES.K	1785.7579	4.37	38.89	-1.075
R.IGEIKEETT.V	1019.5263	4.25	26.58	-0.8
F.KVSFLSALEEYTKKLNT.Q	1971.0818	8.43	52.48	-0.3706
I.SASAEELRQ.R	990.4856	4.53	60.31	-1.0222
K.QFTSSTSYNRGDSTFES.K	1913.8126	4.37	58.81	-1.2176
R.NVHSAGAAGSRM*NF.R	1434.6535	9.76	42.17	-0.2
R.GHVLAKELEAFREA.K	1569.845	5.5	71.27	-0.1786
K.AQYEDIAQK.S	1065.5211	4.37	34.94	-1.2333
S.SSYSKQFTSSTSY.N	1472.6543	8.22	52.15	-1.0308
R.GKSSSYSKQFTSST.S	1494.7074	9.7	33.31	-1.1714
D.EAGSEADHEGTHST.K	1427.5677	4.39	43.72	-1.4714
K.SSSYSKQFTSSTS.Y	1396.6228	8.31	74.57	-0.9923
K.LDELRDEGK.A	1074.543	4.32	43.74	-1.6889
G.EGDFLAEGGGVR.G	1206.5751	4.14	79.2	-0.3333
K.VFDEFKPLVEEPQNLIK.Q	2045.096	4.41	64.52	-0.3471

R.GDSTFESKSYK.M	1248.5743	6.07	41.2	-1.5273
R.THLAPYSDELRQR.L	1585.8081	6.42	28.61	-1.3615
K.REEAPSLRPAPPPISGGGY.R	1951.003	6.14	25.79	-0.8526
R.PGVLSSRQLGLPGPPDVPDHAAYHPF.R	2724.3768	6	67.14	-0.3423
M.NFRPGVLS.S	889.4896	9.75	37.69	0
S.SYSKQFTSSTSYN.R	1499.6645	8.22	85	-1.2385
K.FNWYVDGVEVHNAK.T	1677.802	5.32	35.31	-0.4643
A.VPPNNSNAAEDDLPTVELQGVVPR.G	2531.2324	3.92	29.63	-0.5333
Q.FTSSTSYNRGDSTFESKSY.K	2163.9468	6.07	33.19	-1.2211
R.PGVLSSRQLGLPGPPDVPDHAA.Y	2180.146	5.22	51.45	-0.2545
R.GDSTFESKSY.K	1120.4794	4.37	63.34	-1.29
A.EDPQGDAAQKTDTSHHDQD.H	2094.8596	4.3	39.16	-2.2316
E.TQEKNPLPSKETIEQEKQAGES.-	2471.2263	4.65	44.97	-1.8045
G.HGLGHGHEQQHGLGH.G	1600.7473	6.54	56.64	-1.3933
D.LRQGLLPVLESFKVSFLSALEEYTKKLNTQ.-	3451.9865	8.43	29.74	-0.0633
K.KNAEELKARISASAEELRQ.R	2143.1493	6.29	28.94	-1.0579
R.DAHKSEVAHRFKD.L	1539.767	6.93	34.41	-1.4923
Q.DEPPQSPWDRVKDLATVY.V	2116.0408	4.23	32.09	-1.1333
D.LRHTFM*GVVSLGSPSGEVSHPRKT.R	2595.3461	10.84	53.11	-0.2875
R.GVKLTDVAPVSFF.L	1379.7575	5.84	67.54	0.9923
E.NAGEDPGLAR.Q	999.4856	4.37	41.28	-1
R.TLEIPGNSDPNM*IPDGDFNSYVR.V	2567.1827	3.84	75.86	-0.7174
L.GEYKFQNAL.L	1069.5307	6	28.77	-0.8556
S.YSKQFTSSTSYN.R	1412.6331	8.5	70.94	-1.275
K.SLAELGGHLDQQVEEFRR.R	2084.0535	4.83	49.94	-0.8111
P.GVLSSRQLGLPGPPDVPDHAAYHPF.R	2627.3369	5.98	66.96	-0.292
L.APLAEDVRGNL.R	1154.6176	4.37	46.01	-0.1455
G.GSKGPLDQLE.K	1043.5377	4.75	54.31	-1
K.LDDDLEHQGGHVLDHGHKH.K	2158.9996	5.49	37.1	-1.3947
K.WQEEM*ELYR.Q	1299.5675	4.25	35.58	-1.6667
L.AEDVRGNL.R	873.4433	4.37	32.54	-0.7
L.TETIEGVDAEDGHGPGEQQ.K	1968.8403	3.77	61.84	-1.3316
K.SYKMADEAGSEADHEGTHSTKR.G	2407.0593	5.37	76.32	-1.5818
L.DNFSNQIGKHY.K	1322.6119	6.74	32.4	-1.4818
F.SALEVDETYVPK.E	1350.6794	4.14	37.13	-0.4
S.TSYNRGDSTFESKSY.K	1741.7669	5.73	38.92	-1.58
S.SRQLGLPGPPDVPDH.A	1584.8112	5.19	29.13	-0.96
T.HRIHWESASLLR.S	1504.8129	9.61	44.69	-0.625
G.TQQPQQDEM*PSPTFLTQVKESLSSY.W	2885.3547	4.14	69.93	-1.072
G.SPSGEVSHPRKT.R	1281.6553	8.49	33.06	-1.4667
L.DVSLQLPSR.S	1014.558	5.84	45.13	-0.3222
R.NVHSAGAAGSRMN.F	1271.5908	9.76	47.28	-0.4308
R.HDWGHEKQ.R	1036.4595	5.99	34.51	-2.7625
K.VSFLSALEEYTK.K	1386.7165	4.53	69.39	0.1583

R.MNFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3272.643	6.69	42.86	-0.4067
V.TPLQLFEGR.R	1060.5799	5.66	38.12	-0.4222
L.GLPGPPDVPDHAA.Y	1242.6112	4.2	36.74	-0.4462
L.SVTWSESGQGVTAR.N	1464.7108	5.72	57.76	-0.4857
R.RPHFFFPKSR.I	1318.7179	12.01	34.65	-1.17
A.ELGGHLDQQVEEF.R	1500.6973	4	34.89	-0.8
L.VEEPQNLIK.Q	1069.5889	4.53	35.77	-0.7778
P.GAPGPLTLKEVEELE.Q	1581.8376	4.33	31.88	-0.3467
R.WLQGSQELPR.E	1213.6324	6	38.71	-1.11
M.VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRF.F	4564.3998	5.59	36.16	0.0317
A.ALLSPYSYSTTAVVTNPKE.-	2041.0455	6.26	101.04	-0.0842
R.QLGLPGPPDVPDHAAY.H	1646.82	4.2	49.6	-0.425
R.TGKEKVTSGSTTTTR.R	1553.8127	9.99	40.22	-1.2133
A.KVEQAVETEPEPELR.Q	1753.897	4.33	83.13	-1.2867
S.GEGDFLAEGGGV.R	1107.4941	3.57	67.81	0.0083
R.RGHVLAKELEAFREA.K	1725.9399	6.76	31.83	-0.4667
G.KKLVAASQAALGL.-	1269.7907	10	29.23	0.7923
S.SRIGEIKEETTSHL.R	1599.8344	5.47	48.75	-0.9071
A.TVGSLAGQPLQER.A	1355.7276	5.66	45.54	-0.4077
S.RSGGGGGGGLGSGGSIRSS.Y	1562.7628	12	50.77	-0.4579
S.SSHHPGIAEFPS.R	1265.5918	5.93	37.46	-0.5667
K.AGVETTKPSK.Q	1017.5572	8.64	39.97	-0.95
Y.FVELGTQPAT.Q	1062.5463	4	38.5	0.22
K.DDPDAPLQPVTPLQL.F	1618.8324	3.42	36.91	-0.48
R.NLPSDSQDLGQHGLEEDFM*.L	2147.9237	3.77	114.74	-1.0053
K.SAVQGPPER.D	940.4856	5.72	29.49	-1.1
K.YYLQGAKIPKPGLDHTEA.S	2001.0443	6.75	37.79	-0.7278
A.EEAGARVQQNVPSGTDTGD.P	1930.8718	4.12	50.76	-1.1579
R.ARYQWVRCNPDSNSANCLEEKGPM*FELLPGESNKIPR.L	4265.0275	6.34	34.24	-0.9378
Y.YLQGAKIPKPEA.S	1314.7418	8.5	29.56	-0.65
K.SEVAHRFKDLGEENFKALVL.I	2302.2176	5.51	61.59	-0.26
R.DAHKSEVAHRFKDLGEENFK.A	2357.1623	6.04	29.46	-1.38
L.FEKKSLEDKTERELLESYIDGR.I	2685.3727	4.77	32.62	-1.3864
K.SLEDKTERELLESYI.D	1824.9232	4.25	49.63	-0.9067
K.AVM*DDFAAFVEK.C	1358.6302	4.03	65.04	0.575
L.LVVYPWTQRF.F	1308.7108	8.75	46.37	0.25
T.ADSGEGDFLAEGGGV.R	1380.5922	3.43	64.83	-0.16
K.KLVAASQAALGL.-	1141.6937	8.75	52.39	1.1833
E.YTKKLNTQ.-	995.5523	9.7	32.42	-1.7125
T.ATSEYQTFFNPR.T	1460.6798	6.05	41.77	-1.0583
A.QKENAGEDPGLA.R	1228.5798	4.14	52.32	-1.3667
G.SPM*YSIITPNILR.L	1520.7974	8.46	32.22	0.3385
R.QAGAAGSRMNFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3970.9357	8.76	30.81	-0.4316
K.M*ADEAGSEADHEGTHSTK.R	1888.7612	4.49	39.39	-1.35

G.GSKGPLDQLEKGGETAQSAD.P	1987.9579	4.5	36.21	-1.155
A.TSEYQTFFNPR.T	1389.6446	5.66	63.43	-1.3182
R.RVEPYGENFN.K	1224.5649	4.53	29.82	-1.48
S.LTETIEGVDAEDGHGPGEQQK.R	2210.0218	4.08	39.62	-1.2095
T.SEYQTFFNPR.T	1288.595	5.72	42.91	-1.38
L.GSPSGEVSHPRKT.R	1338.6754	8.75	28.99	-1.3846
K.QTALVELVK.H	1000.6038	6	34.28	0.6889
K.DDPDAPLQPVTPLQLFEGR.R	2108.056	3.84	81.1	-0.6737
A.VDSGNDVTDIADD.G	1335.556	3.41	33.79	-0.6308
E.FVSETESRGSESGIFTNTKESSSHHPGIAEFPS.R	3538.6323	4.98	30.71	-0.7667
R.DAHKSEVAHRFKDLG.E	1709.8728	6.92	34.89	-1.0667
G.SPM*YSIITPNILRLE.S	1762.9428	5.94	53.4	0.3133
R.DAHKSEVAHRFKDL.G	1652.8513	6.92	29.69	-1.1143
R.VTEPISAESGEQVERVNEPSILEM*S.R	2746.3099	3.9	30.35	-0.436
G.EGDFLAEGGGV.R	1050.4746	3.57	60.38	0.0455
K.SYKM*ADEAGSEADHEGTHSTKR.G	2423.0527	5.37	32.63	-1.5818
Y.LSLTPEQWK.S	1101.5941	6	35.74	-0.8111
R.GPPASSPAPAPK.F	1076.5732	8.75	54.38	-0.7083
K.SSSYSKQFTSST.S	1309.5904	8.31	52.86	-1.0083
K.VTSIQDWVQK.T	1203.6414	5.81	39.18	-0.39
R.VGFYESDVM*GR.G	1275.5679	4.37	50.75	-0.1182
K.KEKHTHHAPLSPR.T	1537.835	9.99	35.82	-1.8846
R.LVRPEVDVM*.C	1073.5662	4.37	43.74	0.5778
R.SSRIGEIKEETTSHLR.S	1842.9667	6.49	33.53	-1.125
K.YYLQGAKIPKPEAS.F	1564.8376	8.43	35.37	-0.7071
A.EDPQGDAAQKTDTSHHD.Q	1851.7743	4.49	51.47	-2.0824
K.SSSYSKQFTSSTSYNRGDSTFESK.S	2681.1917	8.15	35.23	-1.375
K.SVLGQLGITK.V	1015.6152	8.47	32.21	0.66
S.YKMADEAGSEADHEGTHST.K	2035.8307	4.49	45.66	-1.3474
G.YRSGGGFSSGSAG.I	1189.5229	8.75	29.45	-0.4923

Table S4. The search results of 20 µL human serum after enrichment with YSMMCS nanoparticles

Sequence	MH+	pI	Ions-score	HydroScore
M.ADEAGSEADHEGTHSTK.R	1741.7257	4.49	31.74	-1.5412
F.KYYLQGAKIPKPEA.S	1605.9001	9.4	24.87	-0.9286
G.DFLAEGGGV.R	864.4108	3.67	66.53	0.4889
R.ARYQWVRCNPDSNSANCLEEKGPMFELLPGESNKIPRL.R	4362.1198	6.34	29.84	-0.8132
S.SSYSKQFTSSTSYNR.G	1742.797	9.7	82.31	-1.4267
A.EEAGARVQQNVPSGTDTG.D	1815.848	4.14	74.56	-1.0278
D.DQEQSQVAEKPMEGES.R	1791.7696	3.91	73.62	-1.725
S.YNRGDSTFES.K	1175.4968	4.37	40.18	-1.62
K.YYLQGAKIPKPEASFSPR.R	2052.0911	9.53	37.11	-0.7778
D.GAGDVAFVKHSTIFENLANKADRD.Q	2575.2895	5.53	52.21	-0.3875
L.DDDLEHQGGHVLDHGHKHKHGHGHGKHKN.K	3263.5438	6.81	26.93	-2.0517

S.SRQLGLPGPPDVPDHAAYHPF.R	2271.1321	5.93	59.38	-0.6714
D.LPTVELQGVVPR.G	1307.7695	6	81.62	0.3667
D.LDPEVRPTSAVAA.-	1325.7063	4.37	54.14	0.1077
D.QEQSQVAEKPMEGES.R	1676.7425	4.09	70.63	-1.6067
T.SYNRGDSTFES.K	1262.5295	4.37	50.77	-1.5455
D.PQGDAAQKTDTSHHDQDH.P	1987.8488	5.1	44.78	-2.1444
K.KNAEELKARISASAEELRQ.R	2143.1506	6.29	33.38	-1.0579
R.RDAHKSEVAHRFKD.L	1695.8671	8.6	45.44	-1.7071
R.SSKITHRIHWESASLLR.S	2021.0977	10.83	71.58	-0.5412
L.SRSGGGGGGGLGSGGSIRSSY.S	1812.8596	10.83	64.37	-0.5143
C.DIQM*TQSPSSLSASVGD.T	1738.7797	3.89	106.5	-0.2647
G.HGHEQQHGLGH.G	1236.5615	6.42	55.75	-1.8818
K.SYKMADEAGSEADHEGTHST.K	2122.859	4.49	92.67	-1.32
R.KNPKFM*ETVAEKALQEYRKKHREE.-	3005.5627	9.31	35.61	-1.8125
R.ILGGHLDAKG.S	980.5525	6.74	44.46	0.21
S.YKM*ADEAGSEADHEGTHST.K	2051.824	4.49	47.6	-1.3474
R.ILGGHLDAKGSFPWQAKM*VSHH.N	2432.2241	8.61	30.11	-0.2318
D.KTERELLESYIDGR.I	1708.8868	4.87	54.12	-1.2857
K.QFTSSTSYNRGDST.F	1550.6727	5.84	38.15	-1.3714
D.SQEEEKTEALTSAKRYIETD.P	2328.1203	4.54	42.17	-1.495
G.HEQQHGLGHGHKF.K	1511.7258	7.1	55.08	-1.6769
R.NVHSAGAAGSRMNFRPGVLSS.R	2115.0516	12	36.66	-0.1381
D.PQEHENINGVPPHLGHPFHWGGHE.R	2722.2675	5.87	35.42	-1.275
D.PLDRAMAELAA.-	1157.5988	4.37	55.08	0.3273
D.SARQSTLDKEL.-	1247.6595	5.79	34.51	-1.0727
Q.DEPPQSPWDRVKDLATVYVDVLKD.S	2785.4075	4.31	38.08	-0.7958
R.SVQLTEKRM*D.K	1222.6097	5.91	29.52	-1.05
K.SLEDKTERELLESYIDGR.I	2153.0725	4.36	39.57	-1.2222
M.ADEAGSEADHEGT.H	1288.4924	3.83	63.2	-1.3538
A.DEAGSEADHEGTHSTKRGHA.K	2091.9091	5.29	35.91	-1.715
K.SSSYSKQFTSSTSYNR.G	1829.8266	9.7	103.29	-1.3875
R.DAHKSEVAHRFKDLGEE.N	1967.9569	5.48	66.39	-1.3529
R.GKSSSYSKQFTSSTSYNRGDSTFESKSY.K	3116.4047	9.31	65.48	-1.4071
K.MADEAGSEADHEGTHS.T	1643.6226	4.17	83.88	-1.2313
S.SYSKQFT.S	860.4155	8.31	26.03	-1.1714
L.APLAEDVRGNLR.G	1310.7185	6.12	50.52	-0.5083
S.SYSKQFTSSTSY.N	1385.6218	8.22	55.65	-1.05
S.SRQLGLPGPPDVPDHA.A	1655.8491	5.19	39.03	-0.7875
G.VNDNEEGF.F	923.3742	3.57	34.13	-1.3625
K.FKLDDDLEHQGGHVLDHGHKH.K	2434.1672	5.84	29.07	-1.3143
A.TVGSLAGQPLQ.E	1070.5848	5.18	27.4	0.2455
R.SSKITHRIHWE.S	1393.7349	8.51	47.33	-1.1364
H.LDNFSNQIGKHY.K	1435.6972	6.74	26.03	-1.0417
F.DTASTGKTFPG.F	1081.5168	5.84	30.36	-0.7364

K.GRPPKAGAEPASEREVS.-	1737.8884	6.23	47.83	-1.2353
G.KPKNPANPVQ.R	1092.6159	10	45.16	-1.71
K.TETQEKNPLPSKETI.E	1714.8861	4.78	48.67	-1.54
R.NVHSGSTFFKYY.L	1449.6796	8.51	31.66	-0.5083
R.SSKITHRIHWESAS.L	1638.8349	8.51	51.62	-0.8786
K.LDDDLEHQGGHVLDHGH.K	1893.8485	4.68	44.07	-1.1412
E.QNTKSPLFM*GKVVNPTQK.-	2033.083	10.3	61.06	-0.8111
D.PLDRAM*AEL.A	1031.5202	4.37	34.52	0
L.SPYSYSTTAVVTNPKE.-	1743.8437	5.94	104.07	-0.6875
C.HPNSPLDEENLTQENQD.R	1979.8542	4.01	72.09	-2.0765
A.QAWGERL.R	859.442	6	33.41	-1.0286
D.PAHGGAPPEM*ASN.R	1251.5419	5.25	41.19	-0.7154
G.DAAQKTDTSHHDQD.H	1568.6566	4.72	62.08	-2.1357
D.PQGDAAQKTDTSHHDQDHP.T	2084.9033	5.1	35.64	-2.1158
D.PKKGHIYQGSEADSVFSGFLIFPSA.-	2682.3586	7.16	62.04	-0.056
I.THRIHWESASLLR.S	1605.8609	9.32	51.98	-0.6308
S.HHPGIAEFPSRG.K	1304.65	6.92	49.08	-0.8417
A.EDPQGDAAQKTDTSH.H	1599.6877	4.22	62.45	-1.9133
T.ATVVASSAPGV.G	958.5212	5.57	23.42	1.2455
G.VVSLGSPSGEVSHPR.K	1507.7858	6.72	57.03	-0.1333
A.QDEERDSGKEQGHT.R	1615.6945	4.5	43.19	-2.7429
D.LATVYVDVLKDSGRD.Y	1650.8681	4.68	86.01	-0.0067
E.PPQSPWDRVKD.L	1324.6643	6.56	33.8	-1.9273
L.DNFSNQIGKHY.K	1322.612	6.74	34.64	-1.4818
P.GPPDVPDHAAYHPF.R	1519.6959	5.05	59.7	-0.7786
D.QEQSQVAEKPM*EGESRNR.N	2118.9832	4.95	49.93	-2.0333
L.PPTSAHGNVAEGETKPD.P	1706.7976	4.83	69.61	-1.2412
G.SATGRSKSSEKRQAVD.T	1706.8782	9.98	33.06	-1.4875
N.TKSPLFMGKVVNPTQK.-	1774.9891	10.3	26.19	-0.475
R.M*NFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3288.6337	6.69	42.15	-0.4067
R.HTFM*GVVSLGSPSGEVSHPRKT.R	2326.1625	8.76	45.4	-0.2818
D.AYLAPNNLKPVVAEFYGSKED.P	2325.179	4.87	62.92	-0.3857
C.HPNSPLDEENLTQENQDRGTHVD.L	2645.1815	4.41	76.89	-1.887
D.DDLEHQGGHVLDHGHKH.K	1930.8874	5.83	40.62	-1.5765
S.YNRGDSTFESKSY.K	1553.6865	6.07	63.13	-1.7077
T.SYNRGDSTFESKSY.K	1640.7187	5.79	65.03	-1.6429
K.KSLEDKTERELLESYIDGR.I	2281.1658	4.66	44.8	-1.3632
Y.KMADEAGSEADHEGTH.S	1684.6864	4.49	57	-1.425
D.PEVRPTSAVAA.-	1097.5953	6.43	48.69	0.1
R.GLSAIRER.L	901.5217	9.6	28.39	-0.45
A.KIPKPGLDHTEASFSPR.R	1880.0015	8.6	33.34	-1.0059
A.EDPQGDAAQKT.D	1159.5225	4.03	33.89	-1.8636
P.NSPLDEENLTQENQDRGTHVD.L	2411.071	4.16	59.64	-1.8381
G.SPSGEVSHPRKT.R	1281.6551	8.49	41.42	-1.4667

K.SSSYSKQFTSSTSYNRGD.S	2001.8782	8.22	98.4	-1.45
C.SVM*HEALHNHYTQKSLSLSPG.K	2352.1389	6.78	49.6	-0.5667
K.RLAVYQAGAREGAE.R	1490.7716	6.28	58.36	-0.4571
A.EDPQGDAAQKTDTSHHDQDHPTFNK.I	2819.2285	4.77	31.28	-2.1
S.YSTTAVVTNPKE.-	1309.6649	6.22	63.95	-0.5417
K.ITHRIHWE.S	1091.5727	6.93	30.18	-0.875
D.LRHTFMGVVSLGSPSGEVSHPRKT.R	2579.3518	10.84	66.05	-0.2875
R.NVHSAGAAGSRMN.F	1271.591	9.76	46.18	-0.4308
R.HDWGHEKQ.R	1036.4593	5.99	36.99	-2.7625
A.TVGSLAGQPLQERAQAWGERL.R	2267.1888	5.81	24.02	-0.5095
N.GQPENNYKTTPPMLDSD.G	1906.8502	4.27	41.14	-1.6412
D.DNIKTYSDHPEKVNKD.D	1902.9201	5.53	33.21	-1.975
R.MNFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3272.6452	6.69	36.03	-0.4067
L.LESYIDGR.I	952.4742	4.37	34.26	-0.7125
K.SSSYSKQFTSSTSYNRGDSTF.E	2337.0249	8.22	53.4	-1.181
R.ILGGHLDAKGSF.P	1214.6528	6.74	62.42	0.3417
D.PLDRAMAELA.A	1086.5612	4.37	41.37	0.18
A.VDSGNDVTD.I	921.38	3.67	47.52	-0.8333
E.PASEREVS.-	874.427	4.53	30.17	-1.0875
R.NGFKSHALQLNNR.Q	1498.7872	11	47.17	-1.1231
D.GDFNSYVR.V	957.443	5.84	46.69	-0.875
K.LDDDLEHQGGH.V	1235.5286	4.21	38.14	-1.5545
D.PQTFYYAVAVVKKD.S	1628.8692	8.83	61.5	-0.05
D.AGSAFAVHDLEED.T	1360.6021	4.12	59.24	-0.1692
R.GASQAGAPQGR.V	999.4974	9.75	44.11	-0.8818
K.LDDDLEHQGGHVLDHGHKHKHGHGHGKH.K	3134.4904	6.5	35.73	-1.725
D.RVKDLATVYVDVLKDSGRD.Y	2149.1611	6.21	50.23	-0.4105
K.TETQEKNPLPSKETIEQEKQAGES.-	2701.3148	4.48	59.24	-1.8292
D.WVQKTIAEN.-	1088.5778	6	34.53	-0.6111
M.ADEAGSEADHEG.T	1187.4445	3.83	48.47	-1.4083
S.GEGDFLAEGGGVR.G	1263.5971	4.14	99.31	-0.3385
A.EDPQGDAAQKTDTSHHDQDHP.T	2328.9732	4.44	48.59	-2.2476
D.KSLHTLFGD.K	1017.5361	6.75	43.06	-0.2333
N.FRPGVLSSRQLGLPGPPDVPDHA.A	2412.2775	6.75	29.42	-0.3957
R.SVQLTEKRMD.K	1206.6145	5.91	43.47	-1.05
G.VNDNEEGFF.S	1070.4421	3.57	43.27	-0.9
R.HRHPDEAAF.F	1079.502	5.99	33.35	-1.4556
R.AATVGSLAGQPLQERAQAWGERL.R	2409.2631	6.19	58.03	-0.3087
A.VDSGNDVTDIAD.D	1220.5283	3.52	72	-0.3917
D.WILEKTQSSDGKAQMQSPA.-	2105.0328	6.07	36.52	-0.9211
D.SGPRRYTIAALLSPYSYSTTAVVTNPKE.-	3042.5844	9.52	66.24	-0.325
R.REYHTEKLVTSKGDKELR.T	2189.1681	8.44	43.18	-1.6667
R.GHGLGHGHEQQHGLGHGHKFKLDDD.L	2713.2734	6.28	39.7	-1.464
H.GLGHGHEQQHGLGH.G	1463.6888	6.42	58.54	-1.2643

R.NEQEQPLGQWHLS.K	1565.7331	4.51	59.02	-1.5615
Y.VKVTSIQDWVQKTIAEN.-	1959.0558	6.04	55	-0.2941
D.PNHFRPAGLPEKY.-	1525.7917	9.01	38.97	-1.2846
Y.YLQGAKIPKPGLDHTEAS.F	1925.0104	6.75	23.55	-0.7
Y.LQGAKIPKPGLDHTEA.S	1674.9191	6.75	27.92	-0.6562
G.VLSSRQLGLPGPPDVPDHAAYHPF.R	2570.3141	5.98	40.96	-0.2875
D.LEEVKAKVQPYLDD.F	1646.8657	4.5	56.66	-0.7429
M.NFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3141.5988	6.92	48.2	-0.4862
S.RIGEIKEETTSHL.R	1512.802	5.5	39.19	-0.9154
D.SEIDAELKNIL.-	1244.674	4.14	59.74	-0.0273
G.EIKEETTSHL.R	1186.5955	4.75	23.94	-1.15
R.ISASAEELRQ.R	1103.5684	4.53	60.98	-0.47
R.GHGLGHGHEQQHG.L	1350.6037	6.42	43.45	-1.6538
G.LGHGHEQQHGLGHGHKF.K	1875.9117	7.16	42.14	-1.2941
G.SEM*VVAGKLQDR.G	1348.6896	5.79	23.75	-0.35
R.NVHSGSTFFKYYLQGA.K	1818.8812	8.51	65.92	-0.275
E.ALHNHYTQKSLSLSPG.K	1752.9018	8.65	70.53	-0.6563
D.FLAEGGGVR.G	905.4841	6	55.02	0.3778
K.M*ADEAGSEADHEGTHS.T	1659.6178	4.17	23.41	-1.2313
Q.FTSSTSYNRGDST.F	1422.6134	5.84	37.45	-1.2077
D.TQNIFFM*SKVTNPKQA.-	1869.9539	10	77.91	-0.475
L.M*IEQNTKSPLFM*GKVVNPTQK.-	2422.2491	9.7	76.88	-0.5571
D.DQEQSQVAEKPMEGESR.N	1947.8698	4.25	66.15	-1.8882
N.NYKTTPPVLD.S	1147.5999	6.09	52.16	-0.88
R.SLAPYAQDTQEKLNHQLEGLTFQM*.K	2778.3376	4.65	39.75	-0.7125
I.THRIHWESASLL.R	1449.7607	6.62	68.2	-0.3083
K.SSSYSKQFTSSTSYN.R	1673.728	8.22	79.75	-1.18
V.M*HEGLHNHYTQKSLSLSPG.K	2152.051	6.81	29.01	-0.9211
Y.KM*ADEAGSEADHEGTHST.K	1888.7592	4.49	93.51	-1.35
D.PEVKFNWYVD.G	1296.6257	4.67	52.49	-0.7
K.KKEKHTHHAPLSPR.T	1665.9289	10.29	38.2	-2.0286
A.DEAGSEADHEGTHSTKR.G	1826.7889	4.87	66.57	-1.9118
S.SSHHPGIAEFPSRG.K	1478.7147	6.66	41.66	-0.8357
K.SEVAHRFKD.L	1088.5495	6.48	28.22	-1.1778
M.ADEAGSEADHEGTHSTKR.G	1897.8253	4.87	37	-1.7056
D.DQEQSQVAEKPMEGESRN.R	2061.9122	4.25	61.5	-1.9778
A.DEAGSEADHEG.T	1116.4082	3.83	54.57	-1.7
K.IIIIKKGHAKDSQRY.K	1770.0388	10	34.55	-0.6067
A.KVEQAVETEPEPELR.Q	1753.8969	4.33	29.65	-1.2867
R.NVHSAGAAGSRM*NFRPGVLSSRQLGLPGPPD.V	3161.6049	11.7	23.86	-0.4
R.NVHSAGAAGSRM*.N	1173.5432	9.76	25.41	-0.175
C.GKPKNPANPVQ.R	1149.6378	10	34.84	-1.5909
P.LVEQGRVR.A	956.5647	9.6	30.99	-0.525
A.RHFWQQDEPPQSPWDRVKD.L	2451.1584	5.53	48.27	-2.1579

R.GDSTFESKSYKM*ADEAGSEADHEGTHST.K	2990.2137	4.43	49.33	-1.3286
R.SEETKENEGF.T	1169.4953	4.09	49.78	-2.05
V.LSSRQLGLPGPPDVPDHAAYHPF.R	2471.2487	5.98	29.91	-0.4826
D.GSPAYRVPVAVQGED.T	1544.7692	4.67	68.71	-0.3267
S.YNRGDSTFESKS.Y	1390.6249	6.07	31.48	-1.7417
D.LRHTFMGVVSLGSPSGEVSHPR.K	2350.1857	9.61	26.89	-0.1045
D.DQEQSQVAEKPM*EGGGCGV.E	1964.8687	4	27.68	-0.9368
K.LHELQEKLSPLGEEM*RDRA.R	2267.144	4.96	25.94	-1.1053
A.TASRGASQAGAPQGR.V	1414.7147	12	41.71	-0.9267
N.SQESVTEQDSKD.S	1352.5815	4.12	71.53	-1.9833
H.NLGHGHKHERDQGHGH.Q	1815.8497	7.16	35.38	-2.2625
R.GHGLGHGHEQQHGLGHGH.K	1851.8496	6.62	70.52	-1.3833
I.IAIM*SGLGFCISFGIRCNLGVAIVEMVNNS.T	3144.5942	5.99	24.71	1.2733
D.NALQSGNSQESVTEQDSKD.S	2036.9005	4.12	108.98	-1.5737
A.DEAGSEADHEGTHS.T	1441.5461	4.17	56.69	-1.6714
D.LEEVKAKVQPYLD.D	1531.8355	4.87	51.19	-0.5308
D.LRHTFM*GVVSLGSPSGEVSHPR.K	2366.2009	9.61	68.79	-0.1045
D.VAFVKHQTVPQNTGGKNPD.P	2037.0518	8.57	37.97	-0.8789
Y.YLQGAKIPKPEAS.F	1401.7751	8.5	31.26	-0.6615
H.GLGHGHEQQHGLGHGH.K	1657.7688	6.54	59.29	-1.3312
D.DQEQSQVAEKPMEGGGC.G	1792.7696	4	48.5	-1.2706
K.M*ADEAGSEADHEGTHSTKR.G	2044.8638	4.86	38.04	-1.5158
N.GQPENNYKTTPPVLDSD.G	1874.8776	4.27	52.04	-1.5059
E.KNPLPSKETIEQEKQAGES.-	2113.0755	4.95	55.75	-1.6842
S.SYSKQFTSSTSYNRGDSTFES.K	2379.0371	5.79	58.12	-1.3095
Y.FVELGTQPAT.Q	1062.5474	4	38.67	0.22
P.GQEPPEHM*AELQ.R	1381.6054	4.24	51.25	-1.4
K.MADEAGSEADHEGTHSTK.R	1872.767	4.49	55.22	-1.35
D.GLDEDSDRAIEGR.T	1432.6673	4.11	50.8	-1.3846
A.TVGSLAGQPLQE.R	1199.6275	4.6	38.59	-0.0667
D.AVRGSPAINVAVHVFRKAAD.D	2078.1637	10.84	51.62	0.36
F.RPGVLSSRQLGLPGPPDVPDHAAYHPF.R	2880.4843	6.92	35.65	-0.4963
M.GKVVNPTQK.-	970.5683	10	35.64	-1.0111
D.QEQSQVAEKPMEGESR.N	1832.8427	4.49	64.86	-1.7875
R.GSESGIFTNTKESSSHHPGIAEFPS.R	2603.1976	5.33	47.11	-0.74
A.PEEHPVLL.T	933.5052	4.51	24.64	-0.2
D.GKAQMQSPA.-	917.4512	8.75	42.85	-0.9111
D.YVSQFEGSALGKQLNLKLLD.N	2223.2023	6.19	29.78	-0.06
K.YYLQGAKIPKPGLDHTEA.S	2001.0457	6.75	23.47	-0.7278
D.KTERELLESYIDG.R	1552.785	4.41	25.4	-1.0385
R.GGSTSYGTGSETESPR.N	1572.6778	4.53	55.11	-1.3312
A.EEAGARVQQNVPSGTDTGD.P	1930.8732	4.12	79.31	-1.1579
Q.HLDNFSNQIGKHY.K	1572.7562	6.92	45.98	-1.2077
D.PQGDAAQKTDTSHHDQ.D	1735.763	5.14	60.67	-1.9938

R.RHDWGHEKQR.K	1348.6625	8.76	37.3	-3.11
L.DHTEASFSPR.R	1146.5183	5.32	27.51	-1.4
D.PAHGGAPPEMASN.R	1235.5479	5.25	32.55	-0.7154
L.GPLVEQGRVR.A	1110.6376	9.6	28.99	-0.62
R.QLGLPGPPDVPDHAA.Y	1483.7537	4.2	47.95	-0.3667
Y.YLQGAKIPKPEA.S	1314.7425	8.5	27.8	-0.65
R.TFHPLRSEAYNTFSER.R	1954.9409	6.42	29.49	-1.0875
R.SEETKENEGFTVT.A	1470.6582	4.09	43.23	-1.3615
T.SYNRGDSTFESKSYKMADEAGSEADHEGTHST.K	3494.4678	4.69	49.4	-1.4781
L.SSRQLGLPGPPDVPDHAAYHPF.R	2358.1606	5.93	24.71	-0.6773
R.DAHKSEVAHRFKDLGEENFK.A	2357.1615	6.04	38.92	-1.38
Q.SGNSQESVTEQDSKD.S	1610.6789	4.12	53.85	-1.9
H.WESASLLR.S	961.5103	6	38.19	-0.1375
H.RIHWESASLLR.S	1367.7552	9.61	49.63	-0.3909
R.M*NFRPGVLS.S	1036.5244	9.5	40.22	0.2111
D.APVIHQEMIGGLRNNNEKD.M	2135.0652	5.54	47.72	-0.9368
A.DSGEGDFLAEGGGVR.G	1465.6547	3.92	115.99	-0.58
R.NGFKSHALQLNNRQIR.G	1896.03	12.01	26.99	-1.1312
T.SAHGNVAEGETKPD.P	1411.6438	4.83	80.71	-1.2286
R.MNFRPGVLSSRQLGLPGPPDVPDHA.A	2657.3752	6.5	75.35	-0.428
D.MPNALSALSDLHAHKLRVD.P	2088.1047	6.7	47.77	-0.0947
K.SSSYSKQFTSSTSYNRGDSTFESKSY.K	2931.2806	8.11	57.58	-1.35
Y.SKQFTSSTSYN.R	1249.5697	8.31	57.57	-1.2727
A.EDPQGDAAQKTDTSHHDQ.D	1979.8317	4.34	46.52	-2.1611
T.IEQEKQAGES.-	1118.5321	4.25	28.63	-1.63
R.GHGLGHGHEQQHGLGH.G	1657.7698	6.54	52.54	-1.3312
R.LAPLAEDVRGNL.R	1267.6997	4.37	51.51	0.1833
R.QGLLPVLESFKVSFLSALEEYTKKLNTQ.-	3182.7375	6.23	32.64	-0.0429
S.RQLGLPGPPDVPDHA.A	1568.8185	5.21	32.62	-0.7867
V.TCFYGEGFF.G	1070.4433	4	27.67	0.5111
S.VMHEALHNHYTQKSLSLSPG.K	2249.1156	7	24.83	-0.555
K.RPPGFSPFR.S	1060.5684	12	30.34	-1.0444
D.DQEQSQVAEKPM*EGESR.N	1963.8667	4.25	55.86	-1.8882
D.PDRFRPDGLPKKY.-	1588.8584	9.72	26.7	-1.8231
R.NVHSAGAAGSRM*NFRPGVLSS.R	2131.0473	12	26.94	-0.1381
H.NHYTQKSLSLSPG.K	1431.7232	8.6	53.29	-0.9923
R.NVHSAGAAGSRMNFR.P	1574.7595	12	53.84	-0.4867
N.FRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	3027.5544	6.92	34.93	-0.3786
T.ADSGEGDFLAEGGGV.R	1380.5913	3.43	80.74	-0.16
L.PGPPDVPDHAAYHPF.R	1616.7518	5.05	47.01	-0.8333
R.GNTEGLQKSLAELGGHLDQQVEEFR.R	2755.3421	4.57	73.69	-0.888
K.M*ADEAGSEADHEGTH.S	1572.587	4.17	45.1	-1.26
A.ATASRGASQAGAPQGR.V	1485.7506	12	39.45	-0.7562
S.SRQLGLPGPPDVPDHAA.Y	1726.8873	5.19	58.2	-0.6353

D.EAGSEADHEGTHSTKRGHA.K	1976.8804	5.77	36.21	-1.6211
M.ADEAGSEADHEGTHS.T	1512.5843	4.17	55.31	-1.44
S.ASAEELRQ.R	903.4548	4.53	55.86	-1.05
A.RHFWQQD.E	1016.4696	6.75	34.59	-2.3286
Y.FVELGTQPATQ.-	1190.6053	4	43.3	-0.1182
R.ILGGHLDAKGSFPWQAKM*VSH.H	2295.1699	8.61	37.4	-0.0905
A.VGTSAAPVPSDNH.-	1251.5976	5.08	34	-0.3154
A.QKENAGEDPGLA.R	1228.5803	4.14	24.14	-1.3667
L.SSRQLGLPGPPDVPDHA.A	1742.8831	5.19	28.28	-0.7882
R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2602.3099	3.92	52.91	-0.44
R.NLAKGKEESLDSDLY.A	1681.8276	4.32	57.89	-1.0267
D.EDSDRAIEG.R	991.4326	3.92	30.07	-1.4889
D.GLKPTIDKPSED.S	1299.6748	4.78	47.67	-1.2583
R.DAHKSEVAHRFKDLGEENFKALVL.I	2753.4301	6.04	47.48	-0.5833
D.GHGPGEQQKRKIVLD.P	1661.9089	8.6	27.59	-1.32
K.GSEM*VVAGKLQDRGPD.V	1674.8124	4.78	47.49	-0.6313
A.HKSEVAHRFKDLG.E	1523.8074	8.6	32.37	-1.1
D.SGKEQGHTRRHDWGHEKQ.R	2173.0385	8.38	29.5	-2.6389
R.NEQEQPLGQWH.L	1365.6181	4.51	63.43	-2.1182
R.THLAPYSDELRQ.R	1429.7067	5.29	33.22	-1.1
A.EDPQGDAAQ.K	930.38	3.49	29.29	-1.7667
G.LGHGHEQQHGLGH.G	1406.6671	6.42	49.57	-1.3308
R.GHGLGHGHEQQHGLGHGHKFKL.D	2368.1909	8.63	39.4	-1.1864
D.PLDRAM*AELAA.-	1173.5937	4.37	52.63	0.3273
K.LDDDLEHQ.G	984.4277	3.84	31.11	-1.6375
G.HGHEQQHGLGHGH.K	1430.6435	6.54	35.39	-1.8692
T.ADSGEGDFLAEGGGVR.G	1536.6932	3.92	107.3	-0.4313
K.TEHLASSSED.S	1075.4541	4.37	31.83	-1.12
S.SRQLGLPGPPDVPDHAAYHP.F	2124.0628	5.93	43.1	-0.845
D.DLEHQGGHVLDHGHKH.K	1815.864	6.15	36.17	-1.4562
D.AHKSEVAHRFKD.L	1424.7398	8.65	25.69	-1.325
R.SSKITHRIHWESASLL.R	1864.9978	8.51	69.78	-0.2938
D.AGLVYDAYLAPNNLKPVVAEFYGSKED.P	2943.478	4.5	32.41	-0.1296
N.RGDSTFESKSY.K	1276.5815	6.07	32.98	-1.5818
H.TFM*GVVSLGSPSGEVSHPRKT.R	2189.1055	8.44	37.22	-0.1429
K.QFTSSTSYNRGD.S	1362.5938	6.09	49.22	-1.475
R.LGPLVEQGRV.R	1067.621	6	46.52	0.21
K.SSSYSKQFTSSTSYNRGDSTFESKSYKM*.A	3206.4199	9.3	40.29	-1.325
G.GSKGPLDQLEKGGETAQSAD.P	1987.955	4.5	76.33	-1.155
A.EDPQGDAAQKTDT.S	1375.5969	3.84	48.68	-1.9
D.PLDRAM*AELA.A	1102.5567	4.37	47.53	0.18
D.GSGEVVLSRKVLLD.G	1471.8498	6.19	38.18	0.4429
R.PAPPPISGGGY.R	1012.5098	5.95	41.8	-0.3091
G.NSQESVTEQDSKD.S	1466.6232	4.12	61.28	-2.1

P.DVAEGASPCVL.R	1060.4794	3.67	27.42	0.7727
R.FKDLGEENF.K	1098.5108	4.14	37.15	-0.9889
K.MADEAGSEADHEGTH.S	1556.5911	4.17	39.75	-1.26
S.PLFMGKVVNPTQK.-	1458.8144	10.02	23.82	-0.1692
R.GDSTFESK.S	870.3844	4.37	39.29	-1.35
L.GSPSGEVSHPRKT.R	1338.677	8.75	59.26	-1.3846
R.GSESGIFTNTKESSSHHPG.I	1958.8862	6	52.06	-1.1421
D.PERLGREGVQKED.I	1512.7772	5.01	24.27	-1.9077
R.QLGLPGPPDVPDHAAYHPF.R	2027.9957	5.05	74.03	-0.4632
K.MADEAGSEADHEGT.H	1419.5329	3.83	68.43	-1.1214
E.GKKLVAASQAALGL.-	1326.8115	10	62.57	0.7071
A.VDSGNDVTDIADD.G	1335.5544	3.41	66.74	-0.6308
R.NVHSGSTFFKYYLQGAKIPKPGLDHTEASFSPR.R	3679.8652	9.4	35.19	-0.6515
R.GHGLGHGHEQQHGLGHGHKFKLDDDLEHQGGHVLDHGHKH.K	4395.0871	6.4	28.81	-1.41
A.EEGKKLVAASQAALGL.-	1584.8957	6.24	50.23	0.1812
L.SRSGGGGGGGLGSGGSIRSS.Y	1649.7927	12	42.09	-0.475
D.DQEQSQVAEKPM*EGESRNR.N	2234.0057	4.59	39.47	-2.1105
R.DAHKSEVAHRFKDLG.E	1709.8674	6.92	55.17	-1.0667
R.DAHKSEVAHRFKDLGEEN.F	2081.9998	5.39	29.86	-1.4722
A.HGNVAEGETKPD.P	1253.576	4.83	59.78	-1.5167
R.DAHKSEVAHRFKDL.G	1652.8497	6.92	26.6	-1.1143
R.M*NFRPGVLSSRQLGLPGPPDVPDHAA.Y	2744.3918	6.5	37.83	-0.3423
S.SYSKQFTSST.S	1135.5269	8.31	42.9	-1.05
D.VAFVKHSTIFENLANKAD.R	2004.0569	6.73	57.34	0.0667
V.SAGVTGTIGSPAAVTGTIR.P	1715.8985	9.46	24.94	0.5632
E.AGSEADHEGTHST.K	1298.5241	4.63	34.05	-1.3154
R.GDSTFESKS.Y	957.4166	4.37	35.44	-1.2889
K.SYKM*ADEAGSEADHEGTHSTKR.G	2423.0529	5.37	35.61	-1.5818
A.DEAGSEADHEGTHSTKRG.H	1883.8125	4.87	43.48	-1.8278
F.VSETESRGSESGIFTNTKESSSHHPGIAEFPSRG.K	3604.6924	5.45	26.83	-0.9706
R.DAHKSEVAHRF.K	1296.645	6.92	41.33	-1.0909
R.GKSSSYSKQFT.S	1219.5955	9.7	37.69	-1.2818
P.DRVTGVDTD.P	977.4542	4.17	29.99	-0.9333
K.MADEAGSEADHEGTHSTKRGHA.K	2293.9834	5.28	62.15	-1.3909
R.QLTPYAQRME.R	1236.6046	6.22	29.53	-1.11
S.EETKENEGFTV.T	1282.5805	4.09	35.78	-1.4727
D.DDLEHQGGHVLDHGHKHKHGHGHGKHKNKG.K	3333.6326	8.44	38.56	-2.01
T.SSTSYNRGDSTFES.K	1537.6396	4.37	71.06	-1.3786
G.DAAQKTDTSHHDQDHPT.F	1903.8171	5.1	45.49	-2.0824
D.VPDHAAYHPF.R	1153.5427	5.97	48.85	-0.38
E.DPQGDAAQKTD.T	1145.5074	4.17	28.24	-1.8636
K.GSEM*VVAGKLQDR.G	1405.7109	6.07	59.05	-0.3538
D.SGEGDFLAEGGGV.R	1194.5274	3.57	57.46	-0.0538
V.ETRTIVRFNRPFLM*IIVPTDTQNIFFMSKVTNPKQA.-	4269.2643	10.9	25.16	-0.1028

Y.KM*ADEAGSEADHEGTH.S	1700.6804	4.49	50.09	-1.425
C.FAEEGKKLVAASQAALGL.-	1803.0022	6.14	49.18	0.4167
V.DESDAFHDNL.R	1162.4661	3.84	35.67	-1.31
K.SSSYSKQFTSSTSYNRGDSTFESKSYKM*ADEAGSEADHEGTHST.K	4801.0373	5.01	43.7	-1.35
K.SSSYSKQFTSSTSYNRGDSTFESKSYKMADEAGSEADHEGTHST.K	4785.0388	5.01	34.66	-1.35
V.SLGSPSGEVSHPRKT.R	1538.7891	8.49	24.97	-1
L.GHGHEQQHGLGHGHKF.K	1762.8276	7.16	36	-1.6125
R.DAHKSEVAHRFKDLGEENFKAL.V	2541.2856	6.04	34.58	-1
R.AHYDLRHTFM*GVVSLGSPSGEVSHPRKT.R	3081.5309	8.65	56.62	-0.4679
R.LAPLAEDVRGNLR.G	1423.8006	6.07	35.1	-0.1769
A.EEAGARVQQNVPSGTD.T	1657.7783	4.38	69	-1.0875
S.STSYNRGDSTFESKSY.K	1828.7982	5.79	54.73	-1.5312
D.DPDAPLQPVTPLQLFEGRRN.R	2263.1841	4.56	26.33	-0.865
R.SQHLDNFSNQIGKHY.K	1787.8433	6.66	46.05	-1.3333
A.EEAGARVQQNVPSGTDTGDPQSKPLGD.W	2753.2987	4.27	87.8	-1.2407
R.DAHKSEVAHRFK.D	1424.7387	8.6	52.08	-1.325
L.EEYTKKLNTQ.-	1253.6376	6.24	41.29	-2.07
D.PQGDAAQKTDTSHH.D	1492.677	6	37.69	-1.7786
G.HGLGHGHEQQHGLG.H	1463.6891	6.42	31.93	-1.2643
R.VTEPISAESGEQVER.V	1630.7919	4.09	102.45	-0.7733
R.AATVGSLAGQPLQER.A	1497.8021	6.05	66.07	-0.1133
R.NVHSGSTFFKYYLQGAKIPKPEAS.F	2669.3717	9.4	39.47	-0.5583
R.GHGLGHGHEQ.Q	1028.4659	6.26	34.1	-1.44
P.GQEPPEHMAELQ.R	1365.6103	4.24	37.48	-1.4
K.GSEMVVAGKLQDR.G	1389.7163	6.07	46.34	-0.3538
R.IGEIKEETT.V	1019.5263	4.25	34.33	-0.8
I.SASAEELRQ.R	990.4859	4.53	67.54	-1.0222
D.GAGDVAFVKHSTIFENLANKAD.R	2304.1585	5.49	63.89	-0.0591
P.DVSSALDKLKEFGNTLED.K	1980.9801	4.27	38.09	-0.6278
E.PEPILIPRV.R	1033.6405	6.43	38.72	0.4667
D.EAGSEADHEGTHST.K	1427.5668	4.39	49.44	-1.4714
D.STFESKSYKMADEAGSEADHEGTHST.K	2802.1787	4.63	48.6	-1.2808
P.GPPDVPDHA.A	904.4158	4.2	30.3	-1.0444
D.STFESKSY.K	948.4316	5.72	44.24	-1.125
D.PEVKFNWYVDGVEVHNAKTKPREEQ.Y	2999.5008	5.6	32.47	-1.3
A.EDPQGDAAQKTDTSHHD.Q	1851.7727	4.49	68.29	-2.0824
K.SLEDKTERE.L	1106.5329	4.62	33.47	-2.2333
S.SYSKQFTSSTSYN.R	1499.6647	8.22	96.2	-1.2385
E.EYTKKLNTQ.-	1124.5952	8.59	36.32	-1.9111
R.VAPEEHPVLLTEAPLNPK.A	1954.0669	4.75	47.49	-0.2667
S.YKMADEAGSEADHEGTHST.K	2035.8261	4.49	70.09	-1.3474
R.PGVLSSRQLGLPGPPDVPDHAA.Y	2180.145	5.22	50.08	-0.2545
R.GDSTFESKSY.K	1120.4796	4.37	56.85	-1.29
A.EDPQGDAAQKTDTSHHDQD.H	2094.8573	4.3	54.76	-2.2316

K.LDDDLEHQGGHVLDHGHKHKHGHGHGKHKN.K	3376.6276	6.81	32.47	-1.8567
K.HNLGHGHKHERDQGHGH.Q	1952.9088	7.21	47.23	-2.3176
K.GSEM*VVAGKLQ.D	1134.5827	6	48.54	0.3091
G.HGLGHGHEQQHGLGH.G	1600.7473	6.54	71.55	-1.3933
P.LAEDVRGNLR.G	1142.6276	6.07	23.92	-0.63
G.TPDVSSALDKLKEFGNTLED.K	2179.0775	4.27	47.8	-0.68
K.SQFLIKTRKKKKEKHTHHAPLSPR.T	2895.6872	11.26	49.87	-1.6042
R.SEAYNTFSER.R	1203.5277	4.53	45.12	-1.4
A.SEGGFTATGQR.Q	1110.5183	5.72	50.5	-0.9364
A.DEAGSEADHEGTHST.K	1542.5937	4.17	70.36	-1.6067
R.GDKLFGPDL.K	961.4994	4.21	41.83	-0.3222
R.PGVLSSRQLGLPGPPDVPDHA.A	2109.0763	5.22	68.03	-0.3524
S.SKITHRIHWESASLL.R	1777.9689	8.51	63.43	-0.26
D.LRQGLLPVLESFKVSFLSALEEYTKKLNTQ.-	3451.923	8.43	64.63	-0.0633
A.EDPQGDAAQKTD.T	1274.5502	4.04	53.91	-2
K.AGAEPASEREVS.-	1202.5648	4.25	40.75	-0.75
L.DDDLEHQGGHVLDHGHKHKHGHGHG.K	2756.2548	6.2	35.04	-1.8
H.VLDHGHKHKHGHGHGKHKNKG.K	2345.2348	10.18	26.07	-2.0429
A.SRGASQAGAPQGR.V	1242.6303	12	45.14	-1.1538
E.PLEKQHEKERKQEEGES.-	2081.0266	5.1	55.89	-2.7294
D.DGTGQKQIWRIEGSNKVPVD.P	2227.1476	6.22	23.85	-1.055
P.PTSAHGNVAEGETKPD.P	1609.7449	4.83	73.25	-1.2188
A.RHFWQQDE.P	1145.5119	5.51	37.54	-2.475
H.NLGHGHKHERDQGHG.H	1678.7907	7.1	63.02	-2.2
R.MNFRPGVLSSR.Q	1263.6624	12	41.76	-0.3091
R.DAHKSEVAHRFKD.L	1539.7662	6.93	44.61	-1.4923
D.LRHTFM*GVVSLGSPSGEVSHPRKT.R	2595.3447	10.84	61.76	-0.2875
L.QGAKIPKPEASFSPR.R	1612.881	9.99	25.34	-1.0133
R.QLGLPGPPDVPDH.A	1341.6795	4.2	60.54	-0.7
K.HNLGHGHKHERD.Q	1436.6906	7.1	26.7	-2.3917
V.ELGTQPATQ.-	944.4694	4	28.29	-0.9222
K.RPPGFSPF.R	904.4685	9.75	36.28	-0.6125
-.DIVM*TQSPD.S	1021.4509	3.89	55.6	-0.3333
L.SRSGGGGGGGLGSGGSIR.S	1475.7318	12	32.58	-0.4389
D.DQEQSQVAEKPM*EGESRN.R	2077.9077	4.25	34.5	-1.9778
S.SKITHRIHWE.S	1306.7015	8.51	37.98	-1.17
S.KQFTSSTSYN.R	1162.5378	8.59	32.43	-1.32
Y.NRGDSTFESKSY.K	1390.624	6.07	43.58	-1.7417
K.MADEAGSEADHEGTHSTKR.G	2028.8697	4.86	68.56	-1.5158
A.SEAEDASLLSFMQGYM*KHATKTAKD.A	2775.2953	5.54	69.44	-0.66
E.GKKLVAASQAALG.L	1213.7258	10	47.96	0.4692
D.DQEQSQVAEKPM*EGES.R	1807.7622	3.91	58.74	-1.725
K.KTETQEKNPLPSKETIEQEKQAGES.-	2829.4083	4.77	68.77	-1.912
T.SSTSYNRGDSTFESKSY.K	1915.8312	5.79	76.41	-1.4882

P.KNPANPVQ.R	867.4687	8.75	28.91	-1.45
K.SPLFMGKVVNPTQK.-	1545.8485	10	58.75	-0.2143
S.PLFM*GKVVNPTQK.-	1474.8067	10.02	32.66	-0.1692
A.KVEQAVETEPE.P	1258.6174	4.33	59.4	-1.2273
D.QEQSQVAEKPM*EGESRN.R	1962.8814	4.49	39.3	-1.8882
K.SSSYSKQFTSSTSYNRGDSTFESKS.Y	2768.226	8.15	36.46	-1.352
D.WILEKTQSSDGKAQM*QSPA.-	2121.0274	6.07	40.69	-0.9211
P.TSAHGNVAEGETKPD.P	1512.6929	4.83	81.23	-1.1933
Q.NTKSPLFMGKVVNPTQK.-	1889.0326	10.3	45.8	-0.6529
G.DFLAEGGGVR.G	1020.5111	4.37	43.96	-0.01
K.YYLQGAKIPKPEA.S	1477.8046	8.43	67.91	-0.7
D.VSLQLPSR.S	899.5315	9.72	42.87	0.075
K.SYKM*ADEAGSEADHEGTHST.K	2138.8546	4.49	118.09	-1.32
R.NLPSDSQDLGQHG.L	1367.619	4.2	55.98	-1.3154
E.QNTKSPLFMGKVVNPTQK.-	2017.0902	10.3	70.62	-0.8111
K.YYLQGAKIPKPGLDHTEASFSPR.R	2575.3319	8.44	69.98	-0.7826
R.ILGGHLDAKGSFPWQAKMVSH.H	2279.1784	8.61	34.31	-0.0905
R.GHGLGHGHEQQHGLGHGHKFKLDD.D	2598.2446	6.63	41.13	-1.3792
H.NLGHGHKHERDQGHGHQ.R	1943.9061	7.16	86.67	-2.3353
N.HYTQKSLSLSPG.K	1317.6795	8.6	43.44	-0.7833
R.TQVNTQAEQL.R	1131.5633	4	49.75	-0.91
K.SLAELGGHLDQQVEEFRR.R	2084.05	4.83	47.63	-0.8111
R.IHWESASL.L	942.4682	5.24	35.22	0.1125
S.ALEEYTKKLNTQ.-	1437.7586	6.19	58.31	-1.2583
K.LDDDLEHQGGHVLDHGHKH.K	2159.002	5.49	53.85	-1.3947
L.AEDVRGNL.R	873.4428	4.37	35.75	-0.7
S.STSYNRGDSTFESKS.Y	1665.7334	5.79	29.08	-1.5467
R.SEETKENEGFTVTAEGKGQGTLSVVTM*YHAKAKD.Q	3658.7598	5.13	24.83	-0.8324
D.QEQSQVAEKPMEGESRN.R	1946.8878	4.49	52.86	-1.8882
R.HRHPDEAAFFDTASTGK.T	1886.8764	6	59.87	-1.0882
K.SYKMADEAGSEADHEGTHSTKR.G	2407.0571	5.37	67.3	-1.5818
R.DAHKSEVAHRFKDLGEENFKALAVAR.L	2938.5589	6.93	33.47	-0.7192
G.PSTQVTAGSNHTAVLLM*DGQVF.T	2289.1022	5.08	23.67	0.2364
K.VSFLSALEEYTKKLNTQ.-	1971.0466	6.11	42.81	-0.3471
S.KITHRIHWESASLLR.S	1847.0397	10.84	25.99	-0.5067
L.DDDLEHQGGHVLDHGHKH.K	2045.9181	5.49	34.36	-1.6833
A.KVEQAVETEPEPEL.R	1597.7944	3.98	53.74	-1.0571
S.SRQLGLPGPPDVPDH.A	1584.8133	5.19	36.31	-0.96
R.EGVQKEDIPPADLSDQVPDTESETR.I	2755.2987	3.85	58.46	-1.324
A.EDPQGDAAQKTDTSHHDQDH.P	2231.9181	4.44	49.83	-2.28
T.HRIHWESASLLR.S	1504.8132	9.61	50.27	-0.625
R.SEETKENEGFTV.T	1369.611	4.09	49.9	-1.4167
P.LAEDVRGNL.R	986.5269	4.37	39.11	-0.2
D.PGLARQAPKPRKQ.R	1446.8655	12.02	27.03	-1.6615

Y.SYSTTAVVTNPKE.-	1396.6959	5.94	81.95	-0.5615
F.AEEGKKLVAASQAALGL.-	1655.9333	6.19	33.53	0.2765
N.HYTQKSLSLSLG.K	1333.711	8.6	53.61	-0.3333
Y.NRGDSTFES.K	1012.4331	4.37	24.06	-1.6556
R.LTPYADEFKVKIDQTVEELR.R	2394.2479	4.51	29.37	-0.625
M.ADEAGSEADHEGTH.S	1425.5511	4.17	63.7	-1.4857
K.GSEMVVAGKLQDRGPD.V	1658.8167	4.78	61.92	-0.6313
K.TAKDALSSVQESQVAQQA.R	1860.9296	4.37	96.99	-0.4778
V.NDNEEGFF.S	971.3746	3.57	38.29	-1.5375
D.PKFHPLHSKIIIIKKGHAKDSQRY.K	2841.6325	10.3	64.76	-0.8625
T.SYNRGDSTFESKS.Y	1477.6557	5.79	40.35	-1.6692
S.VM*HEALHNHYTQKSLSLSPG.K	2265.1102	7	26.98	-0.555
Y.LQGAKIPKPGLDHTEASFSPR.R	2249.2033	8.6	40.21	-0.7333
R.GTIRPVKGPQTSTSPASPKGLHTGGTKRM*ETTTTALKTTTTA.L	4284.2972	11.17	24.02	-0.7405
G.SATGRSKSSEKRQAVDTAVD.G	2093.0577	8.31	36.76	-1.1
A.TVGSLAGQPLQERA.Q	1426.7652	5.66	57.98	-0.25
E.EETGDGLDEDSDR.A	1437.5617	3.62	37.48	-2.1154
S.STSYNRGDSTFES.K	1450.6085	4.37	52.2	-1.4231
V.TPLQLFEGR.R	1060.5791	5.66	56.24	-0.4222
K.SLEDKTERELLESYIDG.R	1996.9666	4.08	53.69	-1.0294
E.FVSETESRGSESGIFTNTKESSSHHPGIAEFPSRG.K	3751.7579	5.45	41.74	-0.8629
K.SSSYSKQFTSSTSYNRGDST.F	2189.9587	8.22	59.79	-1.38
R.PGVLSSRQL.G	956.5532	10.18	45.59	0.0222
D.ETYVPKEFNAETFTFHAD.I	2145.9741	4.56	52.65	-0.7444
D.GVYTLNNEKQWINKAVGD.K	2049.0741	6.19	46.41	-0.7778
R.REYHTEKLVTSKGDKEL.R	2033.067	6.77	66.17	-1.5
K.SLAELGGHLDQQVEEF.R	1771.8486	4	75.54	-0.35
S.SYSKQFTSSTSYNRGDSTFESKSY.K	2757.2265	8.11	43.43	-1.3958
A.DEAGSEADHEGTH.S	1354.5145	4.17	64.48	-1.7385
R.TLDPERLGR.E	1056.5794	5.73	27.26	-1.2333
D.DDGTGQKQIWRIEGSNKVPVD.P	2342.1661	4.87	34.21	-1.1714
G.DSTFESKSY.K	1063.4584	4.37	44.51	-1.3889
Y.STTAVVTNPKE.-	1146.6004	5.94	40.89	-0.4727
-.DIVMTQSPD.S	1005.4566	3.89	51.66	-0.3333
S.EM*VVAGKLQ.D	990.5297	6.1	37.12	0.5111
R.RPHFFFPKSR.I	1318.7172	12.01	33.87	-1.17
A.GSEADHEGTHST.K	1227.4875	4.63	40.29	-1.575
R.AAPGQEPPEHM*AELQ.R	1620.7332	4.24	60.99	-0.9867
A.GFAGDDAPR.A	905.4119	4.21	40.61	-0.8333
D.PQGDAAQKTDTSHHD.Q	1607.7044	5.27	68.39	-1.8933
R.NVHSGSTFFKYYLQGAKIPKPEA.S	2582.34	9.4	32.78	-0.5478
M.NFRPGVLSSRQLGLPGPPDVPDHA.A	2526.3196	6.75	31.07	-0.525
C.SVMHEALHNHYTQKSLSLSPG.K	2336.1458	6.78	46.09	-0.5667
R.MNFRPGVLSS.R	1107.562	9.5	28.12	0.11

R.GHVLAKELEAFR.E	1369.7607	6.76	41.69	-0.0667
R.TQVNTQAEQLR.R	1287.6645	5.66	60.25	-1.2364
R.GSESGIFTNTKESSSHHPGIAEFPSR.G	2759.3051	6.02	74.44	-0.8846
F.SHSKSDTTLPVAITSPGPEASSAVSTTTISPD.M	3141.6013	4.75	26.92	-0.2625
D.RVKDLATVYVDVLKD.S	1733.9783	6.17	44.77	0.0933
D.APRIKKIVQKKLAGDESAD.-	2067.1918	9.53	83	-0.7632
M.ADEAGSEADHEGTHST.K	1613.6306	4.17	89.04	-1.3937
S.SRQLGLPGPPD.V	1136.6059	5.81	42.65	-0.9364
G.PRRYTIAALLSPYSYSTTAVVTNPKE.-	2898.5344	9.55	35.65	-0.3038
A.EDPQGDAAQK.T	1058.4746	4.03	46.85	-1.98
A.KEKHYYIGIIETTWDYASDHGEKKLISVD.T	3438.7232	5.47	29.41	-0.8207
E.EGKKLVAASQAALGL.-	1455.854	8.69	41.01	0.4267
K.ESSSHHPGIAEFPSRG.K	1694.7868	6.01	40.07	-1
K.SSSYSKQF.T	933.4313	8.31	48.72	-1.1375
R.KHNLGHGHKHERDQGHGHQR.G	2365.1637	9.99	40.62	-2.565
R.GDSTFESKSYKMADEAGSEADHEGTHST.K	2974.248	4.43	68.83	-1.3286
D.PDAPRIKKIVQKKLAGDESAD.-	2279.2647	8.83	62.41	-0.9333
R.GHGLGHGHEQQHGLG.H	1520.7103	6.42	57.49	-1.2067
R.ARYQWVRCNPDSNSANCLEEKGPM*FELLPGESNKIPRL.R	4378.1043	6.34	30.83	-0.8132
V.SETESRGSESGIFTNTKESSSHHPGIAEFPSRG.K	3505.6154	5.44	45.61	-1.1273
Y.YLQGAKIPKPEASFSPR.R	1889.0267	9.7	44.43	-0.7471
D.SGEGDFLAEGGGVR.G	1350.629	4.14	103.76	-0.3714
Q.DEPPQSPWDRVKD.L	1568.7336	4.42	56	-2.1692
R.SLAPYAQDTQEKLN.H	1577.779	4.37	38.79	-1.0429
P.LPPTSAHGNVAEGETKPDPD.V	2031.9624	4.49	52.59	-1.12
S.GEGDFLAEGGGV.R	1107.4956	3.57	79.73	0.0083
R.DHHHPHKPHEHGPPPPPDER.D	2350.0988	6.28	24.02	-2.66
I.HWESASLLR.S	1098.5693	6.75	49.1	-0.4778
R.GHGLGHGHEQQH.G	1293.5828	6.42	39.64	-1.7583
G.HGLGHGHEQQHGLGHGHKF.K	2069.9915	7.21	82.09	-1.3474
H.RIHWESA.S	898.4536	6.75	27.34	-0.9429
R.RGHVLAKELEAFREA.K	1725.9393	6.76	56.27	-0.4667
S.SSYSKQFTSSTS.Y	1309.5916	8.31	40.61	-1.0083
G.KKLVAASQAALGL.-	1269.7893	10	75.25	0.7923
S.SRIGEIKEETTSHL.R	1599.8336	5.47	28.48	-0.9071
D.EDSDRAIEGR.T	1147.5345	4.32	23.44	-1.79
H.RIHWESASLL.R	1211.6533	6.75	53.15	0.02
D.VAFVKHSTIFENLANKADRD.Q	2275.1821	6.73	29.56	-0.34
R.NLPSDSQDLGQHGLEED.F	1853.8166	3.94	70.98	-1.4
P.LPPTSAHGNVAEGETKPD.P	1819.8807	4.83	83.31	-0.9611
E.GDFLAEGGGVR.G	1077.5324	4.37	64.73	-0.0455
L.MIEQNTKSPLFM*GKVVNPTQK.-	2406.2545	9.7	71.53	-0.5571
F.TSSTSYNRGDSTFES.K	1638.6878	4.37	66.21	-1.3333
K.SSSYSKQFTSSTSYNRGDSTFESKSYKM.A	3190.4274	9.3	32.29	-1.325

R.ILGGHLDAKGS.F	1067.5848	6.74	42.79	0.1182
D.QEQSQVAEKPMEGESRNR.N	2102.9895	4.95	52.48	-2.0333
V.NDNEEGFFS.A	1058.4064	3.57	39.98	-1.4556
M.NFRPGVLSSRQL.G	1373.7655	12	37.74	-0.4167
Q.KPRLLLFSPSVVHLGVPLSVGVQLQD.V	2798.627	8.75	61.45	0.6346
K.SLEDKTERELLESY.I	1711.8392	4.25	23.81	-1.2929
K.SSSYSKQFT.S	1034.4803	8.31	38.14	-1.0889
N.VAEGETKPD.P	945.4528	4.38	54.01	-1.2333
D.PQGDAAQKTDTSH.H	1355.6184	5.22	62.33	-1.6692
R.PGVLSSRQLGLPGPPD.V	1589.8641	6.52	111.51	-0.3188
K.KKKEKHTHHAPLSPR.T	1794.0242	10.46	34.83	-2.1533
K.SLAELGGHLDQQVEEFR.R	1927.9553	4.4	65.48	-0.5941
R.GHGLGHGHEQQHGLGHGHKFKLDDDLEHQGGHV.L	3570.6873	6.2	25.65	-1.297
D.PLDRAMAE.L	902.4404	4.75	30.63	-0.475
K.SSSYSKQFTSSTSYNRGDSTFESKSYK.M	3059.3874	9.3	42.16	-1.4444
R.SSKITHRIHWESASL.L	1751.9182	8.51	47.54	-0.5667
S.KITHRIHWESA.S	1377.7391	8.76	33.56	-0.9
R.NVHSGSTFFKYYLQGAKIPKPEASFSPR.R	3156.6296	9.82	74.16	-0.625
D.EELLRFSN.-	1007.5167	4.53	37.94	-0.675
K.ITHRIHWESASLLR.S	1718.945	9.61	44.04	-0.2643
K.ITHRIHWESASLL.R	1562.8436	6.92	55.41	0.0615
R.GKSSSYSKQFTSSTSYNRGDSTFES.K	2738.2166	8.43	72.59	-1.336
T.NTKESSSHHPGIAEFPS.R	1824.8509	6	28.56	-1.1294
R.AAPGQEPPEHMAELQ.R	1604.7362	4.24	46.28	-0.9867
A.HKSEVAHRFKDLGE.E	1652.8504	6.93	32.73	-1.2714
A.DEAGSEADHEGT.H	1217.456	3.83	74.26	-1.6167
V.SETESRGSESGIFTNTKESSSHHPGIAEFPSRGK.S	3633.7131	6.01	28.26	-1.2088
L.PPTSAHGNVAEGETKPDPD.V	1918.8781	4.49	58.2	-1.3789
R.RPHFFFPK.S	1075.5839	11	35.27	-0.8
R.LAPLAEDVR.G	983.5533	4.37	42.46	0.2556
R.QLGLPGPPDVPDHAAYHP.F	1880.9239	5.05	43.37	-0.6444
D.GLDEDSDRAIEG.R	1276.5656	3.77	66.99	-1.125
G.VVSLGSPSGEVSHPRKT.R	1736.9297	8.73	34.79	-0.3882
D.TQNIFFMSKVTNPKQA.-	1853.9538	10	72.8	-0.475
G.HGLGHGHEQQHGLGHGH.K	1794.8265	6.62	91.51	-1.4412
R.DAHKSEVAHRFKDLGEENFKA.L	2428.1984	6.04	36.56	-1.2286
D.GDEELLRFSN.-	1179.5639	4.14	46.42	-0.93
D.AGSAFAVHD.L	874.4055	5.34	36.83	0.5
S.KITHRIHWESASLL.R	1690.9398	8.76	67.66	-0.2214
R.GHGLGHGHEQQHGLGHGHKFK.L	2255.1058	8.63	47.62	-1.4238
N.SVFLIKGD.K	878.499	5.8	32.48	0.8375
S.TSYNRGDSTFES.K	1363.5753	4.37	39.9	-1.475
D.AEDGHGPGEQQK.R	1252.5556	4.65	37.55	-2.1333
D.DQEQSQVAEKPMEGESRNR.N	2218.013	4.59	48.19	-2.1105

R.IGEIKEETTSHL.R	1356.7008	4.75	65.39	-0.6167
K.GRPPKAGAEPASER.E	1422.7444	8.75	34.27	-1.4929
D.PKFHPLHSKIIIIKKGHAKDSQ.R	2522.4691	10.18	64.47	-0.6773
A.DEAGSEADHE.G	1059.3852	4.04	46.13	-1.83
S.VLCIWVQQNVPSGTDTGDPQSKPLG.D	2639.2732	4.21	59.96	-0.304
K.M*ADEAGSEADHEGTHSTKRGHA.K	2309.9725	5.28	36.13	-1.3909
S.SSYSKQFTSSTSYNRGDSTFES.K	2466.0688	5.79	50.63	-1.2864
K.LDDDLEHQGGHVLDHGHKHKHGHGHGK.H	2997.4321	6.44	41.74	-1.6704
K.SYKMADEAGSEADHEGTHSTKRGHA.K	2672.176	5.76	61.62	-1.464
F.LSALEEYTKKLNTQ.-	1637.8757	6.14	45.77	-0.8643
R.AQAWGERL.R	930.4798	6.05	32.4	-0.675
K.MADEAGSEADHEGTHST.K	1744.6704	4.17	86.84	-1.2
S.SYSKQFTSSTS.Y	1222.5579	8.31	36.92	-1.0273
A.EDPQGDAAQKTDTSHHDQDHPT.F	2430.0175	4.44	40.06	-2.1773
K.SHALQLNN.R	896.459	6.46	35.84	-0.6375
R.SSKHSQGLRDQGNQEQD.P	1913.8685	5.47	48.51	-2.2941
D.DNIKTYSDHPEKVNKDD.E	2017.9465	4.89	26.19	-2.0647
R.SSRIGEIKEETTSHL.R	1686.8653	5.47	36.93	-0.9
Y.TQKSLSLSPG.K	1017.5585	8.41	41.78	-0.49
W.DLTDASVVCRALGFENATQALGRAAFGQGSGPIM*.L	3439.7245	4.56	29.75	0.25
R.TGKEKVTSGSTTTT.R	1397.7103	8.26	40.62	-0.9786
E.SFKVSFLSALEEYTKKLNTQ.-	2333.2382	8.16	54.53	-0.39
P.TSAHGNVAEGETKPDPD.V	1724.7722	4.48	46.07	-1.3529
R.RPHFFFPKSRIV.R	1530.869	12.01	26.84	-0.25
A.SEAEDASLLSFM*QGYM*KHATKTAKD.A	2791.2947	5.54	53.03	-0.66
N.GQPENNYKTTPPVLD.S	1672.817	4.67	55.43	-1.42
I.GEIKEETTSHL.R	1243.6174	4.75	59.31	-1.0818
I.THRIHWESAS.L	1223.592	6.62	41.3	-1.13
H.EALHNHYTQKSLSLSPG.K	1881.9457	7.01	48.07	-0.8235
K.GSEM*VVAGKLQD.R	1249.6114	4.67	56.72	-0.0083
K.M*ADEAGSEADHEGTHST.K	1760.666	4.17	103.73	-1.2
K.KLVAASQAALGL.-	1141.694	8.75	63.88	1.1833
D.SHVLLAAPPGHQLH.R	1476.8083	6.78	23.97	0.1214
R.M*NFRPGVLSSRQLGLPGPPDVPDHA.A	2673.3571	6.5	33.37	-0.428
E.YTKKLNTQ.-	995.5523	9.7	35.48	-1.7125
Y.NEDKLMAKALL.L	1245.6779	6.07	30.23	-0.1273
T.SSTSYNRGDSTFESKS.Y	1752.7689	5.79	31.98	-1.5
R.GHRPLDKKREEAPSL.R	1732.9454	8.6	28.92	-1.7
F.KVSFLSALEEYTKKLNTQ.-	2099.1357	8.43	64.09	-0.5444
R.GGSTSYGTGSETESPRNPS.S	1870.8037	4.53	92.45	-1.4316
E.DPQGDAAQKTDTSHHD.Q	1722.7311	4.72	40.45	-1.9937
Q.GDAAQKTDTSHHDQD.H	1625.6795	4.72	45.65	-2.02
N.GQPENNYKTTPPM*LD.S	1720.7995	4.67	34.31	-1.5733
S.RQLGLPGPPDVPDHAAYHPF.R	2184.0976	5.98	45.83	-0.665

R.IHWESASLLR.S	1211.6547	6.75	48.54	0.02
R.GHGLGHGHEQQHGLGHGHK.F	1979.9452	7.21	43.32	-1.5158
R.GHGLGHGHEQQHGLGHGHKF.K	2127.0091	7.21	100.14	-1.3
D.TYHYLPFSLPHR.R	1530.7863	8.31	36.6	-0.65
A.HKSEVAHRFKD.L	1353.702	8.6	30	-1.6091
R.M*NFRPGVLSSRQLGLPGPPDVPDHAAYHP.F	3141.5654	6.69	30.9	-0.5172
R.KHNLGHGHKHERDQGHGHQ.R	2209.0633	8.63	91.93	-2.4632
S.SKITHRIHWESA.S	1464.7705	8.51	43.8	-0.8917
R.GHGLGHGHEQQHGLGHGHKFKLD.D	2483.2179	7.21	48.17	-1.287
E.LLESYIDGR.I	1065.5582	4.37	50.59	-0.2111
E.DPQGDAAQKTDTSHHDQD.H	1965.8146	4.42	38.03	-2.1611
G.HGHEQQHGLGHGHKF.K	1705.8074	7.16	56.44	-1.6933
K.QFTSSTSYNRGDSTFESKSYK.M	2420.0934	8.43	25.31	-1.4571
R.EGVQKEDIPPADLSD.Q	1612.7694	3.95	62.43	-1
D.VPDHAAYHPFR.R	1309.644	6.89	43.78	-0.7545
K.SLEDKTERELLES.Y	1548.7766	4.25	44.53	-1.2923
R.VSDPKFHPLHSKIIIIKKGHAKDSQRY.K	3142.7604	10	45.44	-0.7704
D.PQSKPLGDWAAGTM*D.P	1589.7246	4.54	78.62	-0.7667
E.KQHEKERKQEEGES.-	1741.8468	5.63	24.29	-3.2214
D.AQGDVPVTVTVHD.F	1337.6701	4.51	52.88	0.1154
Y.KMADEAGSEADHEGTHST.K	1872.7678	4.49	100.92	-1.35
K.KTETQEKNPLPSKETI.E	1842.9797	6.23	48.52	-1.6875
D.ALRTHLAPYSD.E	1243.644	6.8	44.18	-0.4
R.GKSSSYSKQFTSSTSYNR.G	2014.9458	10	43.53	-1.4722
K.M*ADEAGSEADHEGTHSTK.R	1888.7564	4.49	92.74	-1.35
R.RHDWGHEKQ.R	1192.5605	6.92	35.69	-2.9556
S.SSYSKQFTSSTSYN.R	1586.6949	8.22	86.14	-1.2071
R.DAHKSEVAHRFKDLGEENF.K	2229.0688	5.39	25.68	-1.2474
L.M*IEQNTKSPLFMGKVVNPTQK.-	2406.2515	9.7	67.34	-0.5571
A.TSEYQTFFNPR.T	1389.6444	5.66	47.42	-1.3182
K.HATKTAKDALSSVQESQVAQQA.R	2298.1651	6.75	54	-0.6636
R.RVEPYGENFN.K	1224.564	4.53	45.44	-1.48
S.SHHPGIAEFPS.R	1178.5593	5.93	26	-0.5455
A.LEEYTKKLNTQ.-	1366.7208	6.14	51.14	-1.5364
H.GLGHGHKFKLDDDLEHQ.G	1945.9352	5.74	26.27	-1.2882
Q.DEPPQSPWDRVKDLATVYVD.V	2330.1275	4.2	42.62	-0.985
K.HNLGHGHKHERDQGHGHQ.R	2080.9661	7.21	78.71	-2.3833
R.SLAPYAQDTQEKLNHQLEGLTFQM.K	2762.3483	4.65	34.78	-0.7125
D.NALQSGNSQESVTEQD.S	1706.7452	3.88	93.36	-1.3562
A.EDPQGDAAQKTDTSHHDQDHPTFN.K	2691.1307	4.44	43.32	-2.025
A.DEAGSEADHEGTHSTK.R	1670.689	4.49	64.93	-1.75
F.LSALEEYTKKLNT.Q	1509.816	6.14	32.27	-0.6615
P.SKETIEQEKQAGES.-	1563.7489	4.49	59.02	-1.8
D.GVYTLNDKKQWINKAVGD.K	2049.04	8.43	51.32	-0.8

R.HTFM*GVVSLGSPSGEVSHPR.K	2097.0173	6.92	91.15	-0.08
W.FSETFQKVKEKLKIDS.-	1927.0554	8.43	35.97	-0.8625
D.PQGDAAQKTDTSHHDQD.H	1850.7868	4.72	59.78	-2.0824
K.SSSYSKQFTS.S	1121.5113	8.31	30.14	-1.06
Q.DEPPQSPWD.R	1070.4427	3.77	45.57	-2.2778
K.SSSYSKQFTSSTSYNRGDSTFES.K	2553.1024	5.79	60.5	-1.2652
R.GKSSSYSKQFTSSTSYN.R	1858.8439	9.53	100.47	-1.2941
R.QLRPEHFQEVGYAAPPSPPLS.R	2320.1775	5.4	44.32	-0.7048
A.TPLPPTSAHGNVAEGETKPD.P	2017.9841	4.83	64.92	-0.98
R.MNFRPGVLSSRQLGLPGPPDVPDHAA.Y	2728.3945	6.5	33.41	-0.3423
G.EGDFLAEGGGV.R	1050.4741	3.57	70.45	0.0455
R.QLGLPGPPDVPDHA.A	1412.7171	4.2	77.21	-0.5214
R.IGEIKEETTSHLR.S	1512.8017	5.5	61.85	-0.9154
R.SKSSEKRQAVDTAVD.G	1620.8195	5.95	53.16	-1.16
A.EDPQGDAAQKTDTSHH.D	1736.7462	4.64	42.69	-1.9937
R.GSESGIFTNTKESSSHHPGIAEFPSRG.K	2816.3215	6.02	75.47	-0.8667
D.KFLASVSTVLTSKYR.-	1699.9738	10.29	105.38	0.2133
F.LM*IEQNTKSPLFM*GKVVNPTQK.-	2535.3317	9.7	52.71	-0.3591
S.EMVVAGKLQ.D	974.5347	6.1	46.78	0.5111
D.AEDGHGPGEQQKR.K	1408.6571	5.45	24.17	-2.3154
G.VNDGDM*RLAD.G	1121.4893	4.17	35.16	-0.72
K.SYKMADEAGSEADHEGTHSTK.R	2250.9589	4.86	47.95	-1.4429
K.SSSYSKQFTSSTSY.N	1559.6857	8.22	74.71	-1.0143
V.SLGSPSGEVSHPR.K	1309.65	6.47	76.53	-0.8
D.SKSNEKAEEWGRSGKD.P	1807.8558	6.04	48.79	-2.25
S.SKITHRIHWESASLLR.S	1934.0699	10.83	52.75	-0.525
L.PGPPDVPDH.A	930.4319	4.2	35.87	-1.4222
K.SSSYSKQFTSST.S	1309.5908	8.31	45.22	-1.0083
R.SSKITHRIHWESA.S	1551.8017	8.51	49.65	-0.8846
Q.LGLPGPPDVPDHAAYHPF.R	1899.938	5.05	26.67	-0.2944
F.LMIEQNTKSPLFM*GKVVNPTQK.-	2519.3345	9.7	63.36	-0.3591
D.PQTFYYAVAVVKKDSG.F	1772.9212	8.83	42.07	-0.1187
Q.DEPPQSPWDRVKDLATVYVDVLKDSGRD.Y	3200.5852	4.39	61.9	-1.0107
R.M*NFRPGVL.S	949.4929	9.5	34.72	0.3375
K.SYKM*ADEAGSEADHEGTH.S	1950.7763	4.49	40.41	-1.3833
K.MADEAGSEADHEG.T	1318.4859	3.83	57.13	-1.1538
H.GLGHGHEQQHGLGHGHKF.K	1932.9295	7.16	57.88	-1.2444
N.TKSPLFM*GKVVNPTQK.-	1790.9842	10.3	29.18	-0.475
H.YTQKSLSLSPG.K	1180.6214	8.59	31.17	-0.5636
R.GHGLGHGHEQQHGLGHGHKFKLDDDLEHQGGH.V	3471.6175	6.2	31.6	-1.4687
R.NVHSAGAAGSRM.N	1157.5484	9.76	47.93	-0.175
F.LM*IEQNTKSPLFMGKVVNPTQK.-	2519.3342	9.7	94.72	-0.3591
L.DDDLEHQGGHVLDHGHKHKHGHGHGKHKNKG.K	3448.6606	7.31	31.02	-2.0581
A.DSGEGDFLAEGGGV.R	1309.5559	3.43	89.42	-0.3

R.TATSEYQTFFNPR.T	1561.7285	5.66	81.34	-1.0308
L.GLPGPPDVPDHAAYHPF.R	1786.8536	5.05	38.37	-0.5353
K.KEKHTHHAPLSPR.T	1537.8347	9.99	50.56	-1.8846
Q.FTSSTSYNRGDSTFES.K	1785.7558	4.37	73.62	-1.075
R.DAHKSEVAHRFKDLGE.E	1838.9139	6.05	58.74	-1.2188
K.LDDDLEHQGGHVLDHGHKHKHGHGHGKHKNKG.K	3561.7475	7.31	44.34	-1.875
A.SEAEDASLLSFMQGYMKHATKTAKD.A	2759.3008	5.54	38.14	-0.66
K.QFTSSTSYNRGDSTFES.K	1913.8142	4.37	66.3	-1.2176
R.SSRIGEIKEETTSHLR.S	1842.9671	6.49	61	-1.125
R.NVHSAGAAGSRM*NF.R	1434.654	9.76	35.99	-0.2
V.SETESRGSESGIFTNT.K	1701.757	4.25	58.06	-1.0812
L.GLPGPPDVPDHA.A	1171.5743	4.2	39.7	-0.6333
F.KYYLQGAKIPKPEAS.F	1692.9327	9.4	26.83	-0.92
S.SSYSKQFTSSTSY.N	1472.6522	8.22	58.27	-1.0308
D.YVEKGTQGKIVD.L	1336.7113	6.19	27.54	-0.6833
R.GKSSSYSKQFTSST.S	1494.707	9.7	55.31	-1.1714
K.SSSYSKQFTSSTS.Y	1396.6228	8.31	53.76	-0.9923
G.EGDFLAEGGGVR.G	1206.5758	4.14	80.27	-0.3333
R.GDSTFESKSYK.M	1248.5739	6.07	50.66	-1.5273
R.PGVLSSRQLGLPGPPDVPDHAAYHPF.R	2724.3905	6	56.16	-0.3423
K.YYLQGAKIPKPEAS.F	1564.8372	8.43	36.14	-0.7071
S.AHGNVAEGETKPD.P	1324.6131	4.83	70.82	-1.2615
D.QVTVAMTPR.S	1002.5408	9.75	54.2	0.1222
K.SSSYSKQFTSSTSYNRGDSTFESK.S	2681.197	8.15	51.61	-1.375
A.LHNHYTQKSLSLSPG.K	1681.8669	8.61	24.92	-0.82
E.RDHSHGPPLPQGPPPLLPM*SCSSCQH.A	2791.2897	7	24.94	-0.8269
R.EGVQKEDIPPAD.L	1297.6289	4.12	38.69	-1.2083
D.PNM*IPDGDFNSYVR.V	1640.7364	4.21	71.11	-0.7714
L.MIEQNTKSPLFMGKVVNPTQK.-	2390.2595	9.7	51.35	-0.5571
I.THRIHWESASL.L	1336.677	6.62	42.4	-0.6818
R.HTFMGVVSLGSPSGEVSHPRKT.R	2310.1697	8.76	93.68	-0.2818
A.AVGTSAAPVPSDNH.-	1322.6355	5.08	39.67	-0.1643
K.SYKMADEAGSEADHEGTH.S	1934.782	4.49	52.46	-1.3833
K.SLAELGGHL.D	896.4827	5.22	40.13	0.5444
K.RLAVYQAGAREGAER.G	1646.8712	8.74	32.08	-0.7267
D.LRQGLLPVLESFKVSFLSALEEYTKKLNT.Q	3323.8727	8.43	32.91	0.0552
K.PKNPANPVQ.R	964.5213	9.18	48.22	-1.4667
P.EDQESHAQGAAKAKKDLVEV.L	2153.081	4.9	32.79	-1.06
D.PTFIPAPIQAKTSPVD.E	1681.9154	6.51	40.48	0.0062
F.KYYLQGAKIPKPEASFSPR.R	2180.1867	9.82	33.43	-0.9421
D.PGDDNNDIAPR.G	1183.5325	3.93	72.31	-1.7545
D.SGRDYVSQFEGSALGKQLNLKLLD.N	2638.3873	5.95	55.03	-0.4333
S.TTAVVTNPKE.-	1059.5687	5.88	53.97	-0.44
D.PDQTDGLGLSYLSSHIANVERVPFD.A	2730.3235	4.41	75.46	-0.328

Y.GSGGGSYGSGGGGGGGGRGSY.G	1590.6521	8.59	45.94	-0.775
S.GGGGGGGGLGSGGSIR.S	1145.5659	9.75	60.99	-0.12
E.NAGEDPGLAR.Q	999.4861	4.37	31.89	-1
K.KVPQVSTPTLVEVSR.N	1639.9401	8.75	48.53	-0.0667
Q.FTSSTSYNRGD.S	1234.5335	6.09	33.3	-1.2909
D.APDHQELNLDVSLQLPSR.S	2032.0431	4.54	35.07	-0.6833
S.SRIGEIKEETT.V	1262.6589	4.78	44.68	-1.1364
K.SHALQLNNRQ.I	1180.6191	9.49	30.91	-1.31
D.QVTVAM*TPR.S	1018.5352	9.75	37.03	0.1222
K.QFTSSTSYNR.G	1190.5441	8.75	43.49	-1.38
R.DAHKSEVAHRFKDLGEENFKALVLIA.F	2937.5537	6.04	32.26	-0.2962
S.YSKQFTSSTSYN.R	1412.6345	8.5	79.39	-1.275
L.APLAEDVRGNL.R	1154.6167	4.37	52.1	-0.1455
Y.DLDPGAGSLEI.-	1086.5314	3.49	48.74	0.0182
R.SLAPYAQDTQEKL.N	1463.7363	4.37	33.86	-0.8538
D.PEVRPTSAV.A	955.5213	6.43	34.42	-0.2778
D.SGRDYVSQFEGSALGKQLNLKLLDNWD.S	3053.5207	4.86	38.43	-0.6778
Y.KMADEAGSEADHEGTHSTK.R	2000.8625	4.87	37.85	-1.4842
R.SGGGGGGGLGSGGSIR.S	1232.5986	9.46	84.56	-0.1625
D.ENPFAQGALKSED.C	1405.6606	4.38	66.79	-1.0769
I.DQNVEELKG.R	1031.5017	4.14	35.26	-1.5333
D.SSPVKAGVETTTPSKQSN.N	1817.9229	8.31	63.33	-0.9444
Q.SGNSQESVTEQD.S	1280.5249	3.88	55.6	-1.6917
K.MADEAGSEADH.E	1132.4212	3.91	54.93	-1.0091
R.IGEIKEET.T	918.4778	4.25	33.38	-0.8125
G.SEM*VVAGKLQ.D	1077.561	5.72	51.21	0.38
D.APVIHQEM*IGGLRNNNEKD.M	2151.0609	5.54	51.35	-0.9368
R.NLAKGKEESLDSD.L	1405.6811	4.5	45.65	-1.3769
G.DGLDEDSDR.A	1021.4079	3.71	38.57	-2.1556
D.LPSLAADFVESKD.V	1391.7033	4.27	88.51	0.0462
M.IEQNTKSPLFM*GKVVNPTQK.-	2275.2143	9.7	41.66	-0.68
F.SSPTAAGTPNKETA.G	1331.6444	5.72	54.18	-0.9143
R.GNTEGLQKSLAELGGHLDQQVEEFRR.R	2911.4636	4.96	46.65	-1.0269
D.SSPVKAGVETTTPSKQ.S	1616.8483	8.31	68.81	-0.7938
R.RVEPYGENFNK.A	1352.6608	6.14	31.03	-1.7
E.YKGRPPKAGAEPASEREVS.-	2029.0455	8.5	41.51	-1.3789
D.ALTNAVAHVDD.M	1125.5543	4.51	49.5	0.2909
D.AVRGSPAINVAVHVFRKAADD.T	2193.1894	8.8	43.12	0.1762
R.ISELKAEAV.K	959.5415	4.53	35.91	0.4889
F.FDTASTGKTFPG.F	1228.5855	5.84	32.69	-0.4417
P.AGAKVSELI.I	887.5324	6.05	33.63	0.8333
D.M*PNALSALSDLHAHKLRVD.P	2104.0976	6.7	53.55	-0.0947
D.QEQSQVAEKPM*EGES.R	1692.7368	4.09	30.93	-1.6067
D.PTKPDATMVVRN.R	1328.7006	9.18	40.29	-0.6583

R.IGEIKEETTSH.L	1243.6165	4.75	60.71	-1.0182
D.RARAHVDALRTHLAPYSD.E	2049.0747	8.76	31.72	-0.6833
F.EEVSGNVSPGTR.R	1231.5919	4.53	48.12	-0.9417
L.GLPGPPDVPDH.A	1100.5366	4.2	56.17	-0.8545
R.TLEIPGNSD.P	945.453	4.03	33.65	-0.6333
S.TFESKSY.K	861.399	5.66	35.35	-1.1714
S.EETKENEGF.T	1082.4637	4.09	31.32	-2.1889
K.AVHKAVLTID.E	1066.627	6.8	31.08	0.9
D.QLEKGGETAQSAD.P	1333.624	4.38	55.14	-1.2538
N.RFTQKSLSLSPG.K	1320.7283	11	36.49	-0.55
G.KKLVAASQAALG.L	1156.7056	10	55.9	0.5417
R.QLGLPGPPDVPDHAAY.H	1646.8189	4.2	42.73	-0.425
R.ASVDSGSSEEQGGSS.R	1383.5507	3.57	50.9	-0.9333
L.APLAEDVR.G	870.4685	4.37	46.91	-0.1875
R.PNFGDMLATNSTRGLN.E	1707.8025	6.27	36.47	-0.5625
L.SALEEYTKKLNTQ.-	1524.7905	5.86	69.73	-1.2231
A.GAEPASEREVS.-	1131.5283	4.25	43.37	-0.9818
L.DDDLEHQGGHV.L	1221.5125	4.21	39.82	-1.5182
R.IHWESASLL.R	1055.5517	5.24	46.89	0.5222
D.PTVRRQECSIPVCGQDQVTVAM*TPR.S	2787.3571	8.46	32.14	-0.364
R.MNFRPGVL.S	933.5007	9.5	36.33	0.3375
M.ELERPGGNEIT.R	1214.6014	4.25	31.76	-1.2091
D.TGALLFIGKILDPRGP.-	1667.9824	8.41	56.84	0.5
A.TVGSLAGQPLQER.A	1355.728	5.66	50.83	-0.4077
R.SVAQATSSSGEAPD.S	1306.5761	4.03	76.72	-0.4857
A.SSTKGQTKRNLAKGKEESLD.S	2177.1518	9.52	32.85	-1.64
S.RSGGGGGGGLGSGGSIRSS.Y	1562.7619	12	52.13	-0.4579
D.DLPTVELQGVVPR.G	1422.7932	4.37	38.93	0.0692
D.TYHYLPFSLPH.R	1374.6842	6.61	33.51	-0.3
K.TETQEKNTLPTKETIEQE.K	2119.0414	4.5	35.44	-1.8111
A.KIPKPEASFSPR.R	1356.766	9.99	34.73	-1.0917
E.GDFLAEGGGV.R	921.4313	3.67	35.92	0.4
D.KFSEFWDLD.P	1186.5416	4.27	36.9	-0.7444
R.NVHSGSTFF.K	995.4581	6.74	30.86	0.0444
D.PDAPLQPVTPLQLFEGR.R	1878.0101	4.37	67.26	-0.3412
G.VNDGDMRLAD.G	1105.4937	4.17	57.52	-0.72
R.NLAKGKEESLD.S	1203.6226	4.87	35.7	-1.2364
A.HGNVAEGETKPDPD.V	1465.6558	4.49	51.14	-1.6643
R.LFAEEKAVADTRDQADGSR.A	2079.0085	4.44	36.72	-0.9368
T.PLPPTSAHGNVAEGETKPD.P	1916.935	4.83	30.84	-0.9947
D.PDAPPSPPLGAPGLPPAGSPPDSHVLLAAPPGHQLH.R	3461.7773	5.71	32.35	-0.3083
E.DLRQGLLPVLESFKVSFLSALEEYTKKLNTQ.-	3566.948	6.25	31.26	-0.1742
S.SKITHRIHWESAS.L	1551.8026	8.51	45.17	-0.8846
P.PTSAHGNVAEGETKPDPD.V	1821.8237	4.49	38.59	-1.3667

S.SSYSKQFTSST.S	1222.5582	8.31	46.34	-1.0273
S.GNSQESVTEQDSKD.S	1523.645	4.12	78.17	-1.9786
D.APLQPVTPLQLFEGR.R	1665.931	6.05	59.7	-0.0467
D.VPVTVTVHD.F	966.5261	5.33	32.49	0.7889
R.VSDPKFHPLHSKIIIIKKGHAKDSQ.R	2823.5984	9.83	30.37	-0.6
P.GLDHTEASFSPR.R	1316.6232	5.32	47.79	-0.8833
I.EKLNM*AACTYRISVQCVTSRGSSDEL.Q	2877.3291	6.26	35.48	-0.2192
A.EDPQGDAAQKTDTS.H	1462.6296	3.84	56.88	-1.8214
R.NGFKSHALQLN.N	1228.643	8.76	48.81	-0.6
K.LVTSKGDKEL.R	1089.6154	6.07	36.24	-0.49
R.ISELKAEAVKKD.R	1330.7575	6.26	60.94	-0.575
R.SEETKENEGFTVTAEGK.G	1855.8585	4.32	57.32	-1.3941
M.NFRPGVLSSR.Q	1132.6236	12	31.62	-0.53
A.RVQQNVPSGTDTGD.P	1473.6931	4.54	39.66	-1.3
K.INVKVGGNS.K	887.4954	8.75	31.85	0.0444
K.KTETQEKNTLPTKETIEQE.K	2247.1334	4.8	36.42	-1.9211
G.VNDNEEGFFSA.R	1228.5194	3.57	35.65	-0.6455
K.MADEAGSEADHEGTHSTKRGHAKSRPV.R	2861.3364	6.23	31.01	-1.3778
Y.GSGGGSYGSGGGGGGHGSY.G	1514.5893	6.74	51.23	-0.7263
R.PGVLSSRQLGLPGPPDVPDHAAYHP.F	2577.3183	6	38.89	-0.468
D.RVKDLATVYVD.V	1278.7053	6.13	33.97	0.0727
G.SEMVVAGKLQ.D	1061.5676	5.72	48.32	0.38
P.GSSGTGGTATWKPGSS.G	1437.6601	8.75	43.84	-0.7438
F.VELGTQPATQ.-	1043.5368	4	32.37	-0.41
D.SGPRRYTIAALLSPYSYSTTAVVTNPK.E	2913.5471	9.99	32.24	-0.2074
R.ELLESYIDGR.I	1194.6002	4.14	42.24	-0.54
D.PWAKNLNEKD.Y	1214.6159	6.61	36.07	-1.87
G.RPPKAGAEPASEREVS.-	1680.8664	6.23	31.23	-1.2875
L.AEDPQGDAAQKTDTSHHDQD.H	2165.8957	4.3	36.76	-2.03
K.M*ADEAGSEADHEGT.H	1435.528	3.83	72.02	-1.1214
T.ISSNLTEMSKGVKLLAALM*.D	2022.1091	8.59	33.8	0.6842
S.YSKQFTSST.S	1048.4948	8.59	33.85	-1.0778
N.SQESVTEQD.S	1022.4276	3.88	53.74	-1.7333
K.SLQVRQDGGKSRL.K	1443.8048	10.83	37.02	-1.0769
D.TDTGALLFIGKILDPRGP.-	1884.0589	5.63	64.72	0.2111
E.EGKKLVAASQAALG.L	1342.7708	8.69	42.72	0.1857
D.EFKPLVEE.P	990.5155	4.52	34.3	-0.65
R.GPDVLTATVSGK.L	1144.6198	5.84	82.71	0.1667
L.GLPGPPDVPD.H	963.4786	3.89	32.39	-0.62
R.VNEPSILEM*S.R	1134.5343	3.8	42.55	0.07
F.VELGTQPAT.Q	915.479	4	36.12	-0.0667
D.PQSKPLGDWAAGTMD.P	1573.7329	4.54	49.97	-0.7667
K.GAVHDVKDVLDS.V	1254.6334	4.41	37.83	-0.05
T.SYNRGDSTFESK.S	1390.6228	5.79	36.6	-1.7417

R.TLDPERLG.R	900.4799	4.37	34.57	-0.825
D.LATVYVDVLKD.S	1235.6899	4.54	46.47	0.8273
R.GPPASSPAPAPK.F	1076.5734	8.75	46.87	-0.7083
G.LPGPPDVPDHAAYHPF.R	1729.8312	5.05	44.28	-0.5438
R.NVHSAGAAGSRM*NFRPGVLSSRQLGLPGPPDVPDHAAYHPF.R	4296.1189	8.76	30.02	-0.3951
S.SYSKQFTSSTSYNR.G	1655.7661	9.7	30.49	-1.4714
R.LPDRVTGVDTD.P	1187.5927	4.17	30.37	-0.5636
D.LGQHGLEED.F	997.46	4.37	35.46	-1.1556
K.ETIEQEKQAGES.-	1348.6226	4.09	39.63	-1.7083
E.FVSETESR.G	954.4531	4.53	35.98	-0.85
D.GEQRISLPESLKRIPIEDGSGEVVLSRKVLLD.G	3532.967	5.15	31.16	-0.2594
R.GRDGAIDLGYDLL.M	1377.709	3.93	31.77	0.0154
T.NTKESSSHHPGIAEFPSRG.K	2037.9748	6.93	39.47	-1.2684
L.PVLESFKVSFLSALEEYTKKLNTQ.-	2771.4911	6.64	45.51	-0.2042
T.SYNRGDSTFESKSYK.M	1768.8129	8.15	38.77	-1.7933
L.GGHLDQQVEEF.R	1258.5697	4.13	38.54	-0.9727
R.GHVLAKELEAFREA.K	1569.8369	5.5	63.43	-0.1786
V.FTANDSGPR.R	964.449	5.84	42.06	-1.1556
Y.SKQFTSSTSY.N	1135.5246	8.31	58.93	-1.05
T.QVNTQAEQLR.R	1186.6169	6	51.44	-1.29
D.PTFIPAPIQAKTSPVDEKALQD.Q	2366.2555	4.78	54.65	-0.3955
S.GNSQESVTEQD.S	1193.4918	3.88	43.64	-1.7727
M.NFRPGVLS.S	889.4894	9.75	39.98	0
K.DDPDAPLQPV.T	1066.5045	3.42	33.46	-0.9
Q.FTSSTSYNRGDSTFESKSY.K	2163.9488	6.07	51.54	-1.2211
E.TQEKNPLPSKETIEQEKQAGES.-	2471.2249	4.65	57.46	-1.8045
G.YRSGGGFSSGSAG.I	1189.5231	8.75	37.63	-0.4923