

## Supplementary Materials

Figure S1. Protein patterns from pooled crude plasma samples

Figure S2. Protein patterns from pooled WGA-bound plasma fraction

Figure S3. Protein patterns from pooled WGA-unbound plasma fraction

Figure S4. Total protein gels and immunoblots of C9 from crude plasma, WGA-bound plasma and WGA-unbound plasma fractions obtained from the study cohort.

Figure S5. Total protein gels and immunoblots of FN1 from crude plasma, WGA-bound plasma and WGA-unbound plasma fractions obtained from the study cohort.

Figure S6. Total protein gels and immunoblots of C9 and FN1 from individual samples in the study cohort.

Figure S7. Total protein gels and immunoblots of C9 and FN1 from individual samples in the validation cohort.

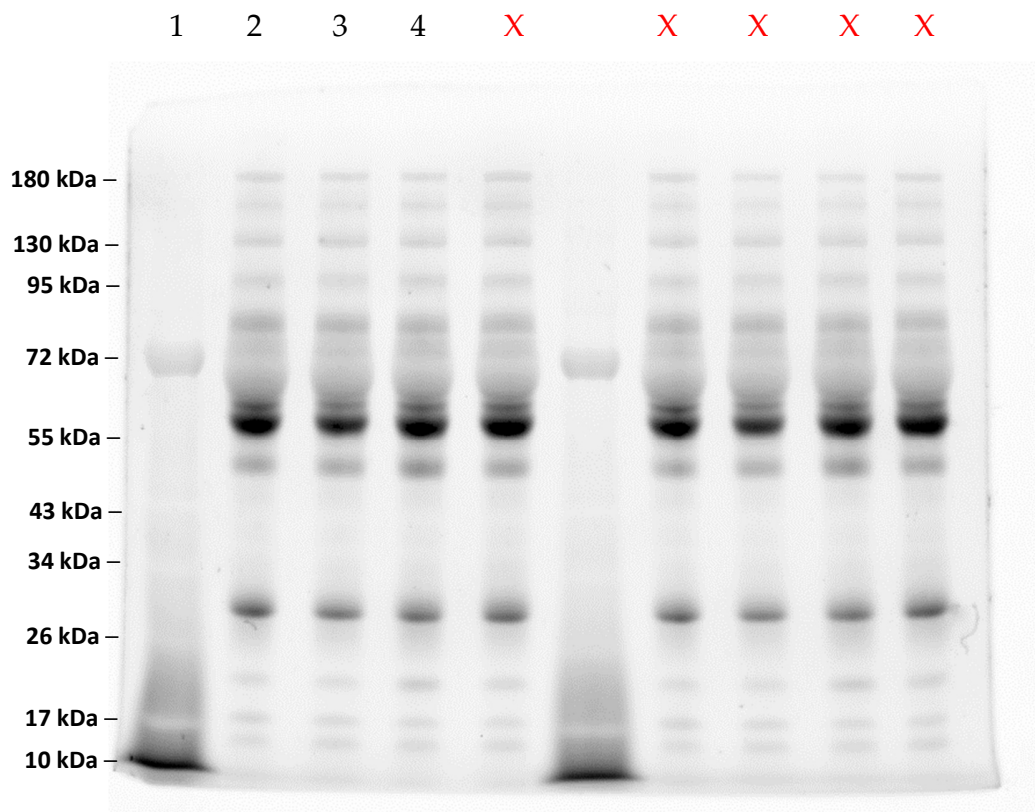
Table S1. List of the accepted peptides used in protein quantification.

Table S2. The 80 WGA-enriched plasma proteins selected for protein quantification.

Table S3. List of the 62 WGA-enriched plasma proteins containing at least 2 peptides and their fold change in non-metastatic and metastatic CRC patients compared to those of the healthy controls.

Table S4. N-linked glycosylated searched against 20 WGA-enriched glycoproteins of the pooled sample of healthy control, non-metastatic and metastatic CRC patient groups

Table S5. Glycated peptides searched against 20 WGA-enriched glycoproteins of the pooled sample of healthy control, non-metastatic and metastatic CRC patient groups



**Figure S1.** Protein patterns from pooled crude plasma samples

Lane 1: Pre-stained Protein Markers

Lane 2: Pooled crude plasma of healthy controls (10 µg)

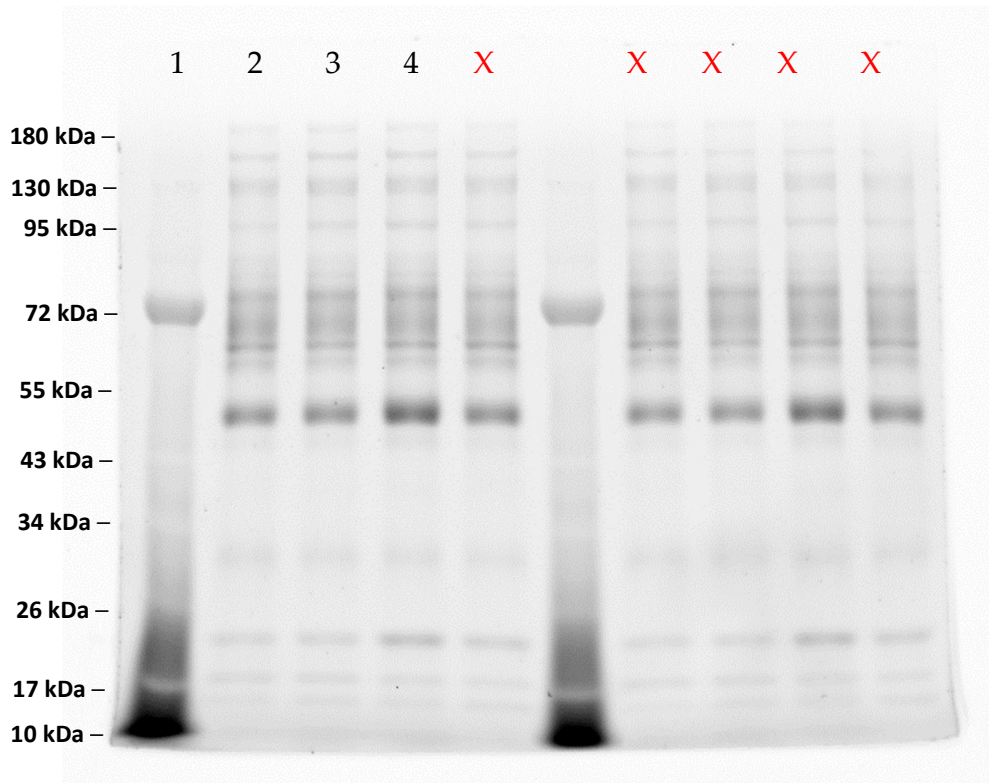
Lane 3: Pooled crude plasma of non-metastatic CRC patients (10 µg)

Lane 4: Pooled crude plasma of metastatic CRC patients (10 µg)

**X** means protein bands from other conditions and authors focus only the proteins in three conditions (healthy controls, non-metastasis and metastasis CRC patients).

#### Densitometry analysis

Pooled crude plasma samples	Lane 2: Healthy control	Lane 3: Non-metastatic CRC	Lane 4: Metastatic CRC
total protein intensity	11989295	11647984	12549313
Normalized total protein intensity (compared to healthy control)	1.00	0.97	1.05



**Figure S2.** Protein patterns from pooled WGA-bound plasma fraction

Lane 1: Pre-stained Protein Markers

Lane 2: Pooled WGA-bound plasma fraction of healthy controls (5  $\mu$ g)

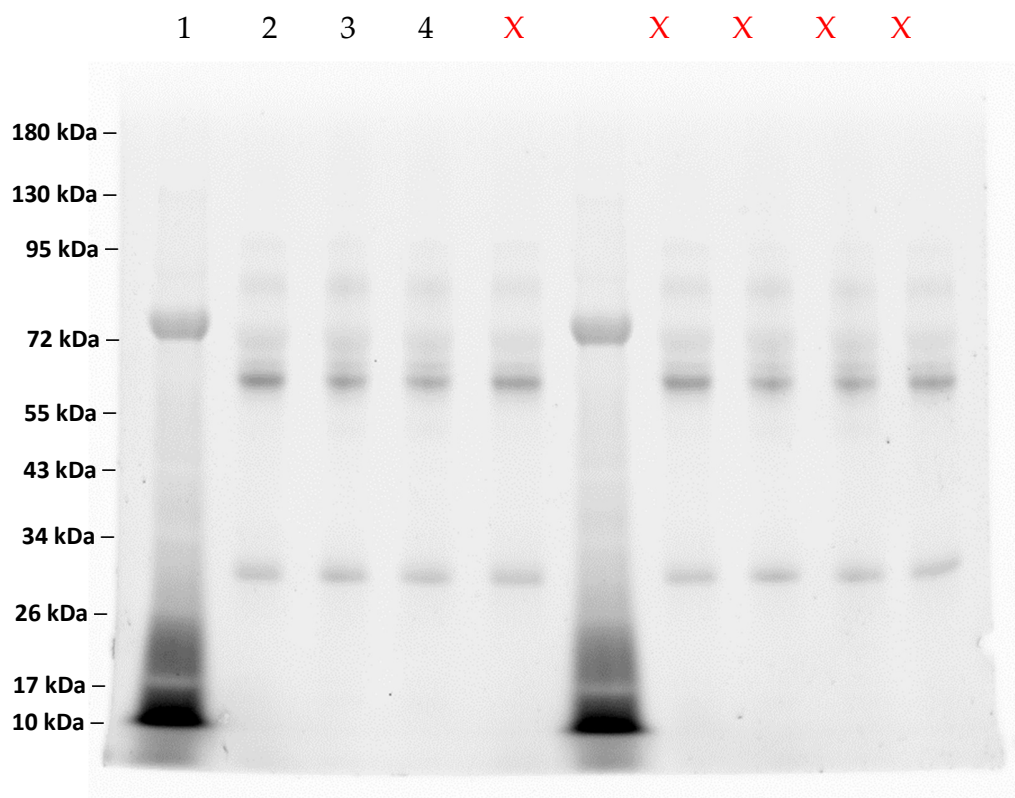
Lane 3: Pooled WGA-bound plasma fraction of CRC patients (5  $\mu$ g)

Lane 4: Pooled WGA-bound plasma fraction of metastatic CRC patients (5  $\mu$ g)

**X means protein bands from other conditions and authors focus only the proteins in three conditions (healthy controls, non-metastasis and metastasis CRC patients).**

### Densitometry analysis

WGA-bound plasma fraction	Lane 2: Healthy control	Lane 3: Non-metastatic CRC	Lane 4: Metastatic CRC
total protein intensity	9386693	8903096	9999975
Normalized total protein intensity (compared to healthy control)	1.00	0.95	1.07



**Figure S3.** Protein patterns from pooled WGA-unbound plasma fraction

Lane 1: Pre-stained Protein Markers

Lane 2: Pooled WGA-unbound plasma fraction of healthy controls (5 µg)

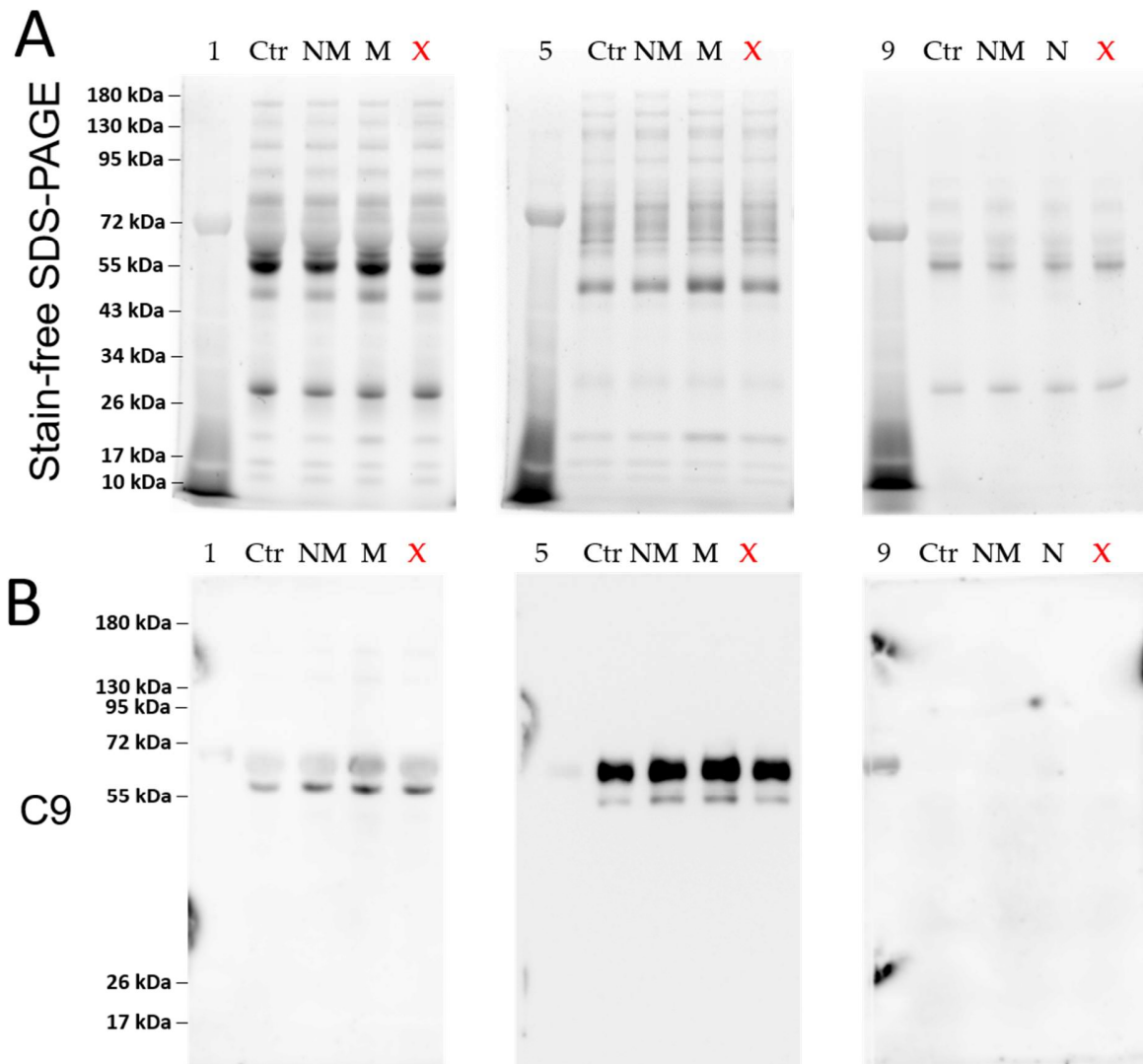
Lane 3: Pooled WGA-unbound plasma fraction of CRC patients (5 µg)

Lane 4: Pooled WGA-unbound plasma fraction of metastatic CRC patients (5 µg)

**X means protein bands from other conditions and authors focus only the proteins in three conditions (healthy controls, non-metastasis and metastasis CRC patients).**

### Densitometry analysis

WGA-unbound plasma fraction	Lane 2: Healthy control	Lane 3: Non-metastatic CRC	Lane 4: Metastatic CRC
total protein intensity	1925352	1618552	1588311
Normalized total protein intensity (compared to healthy control)	1.00	0.84	0.82

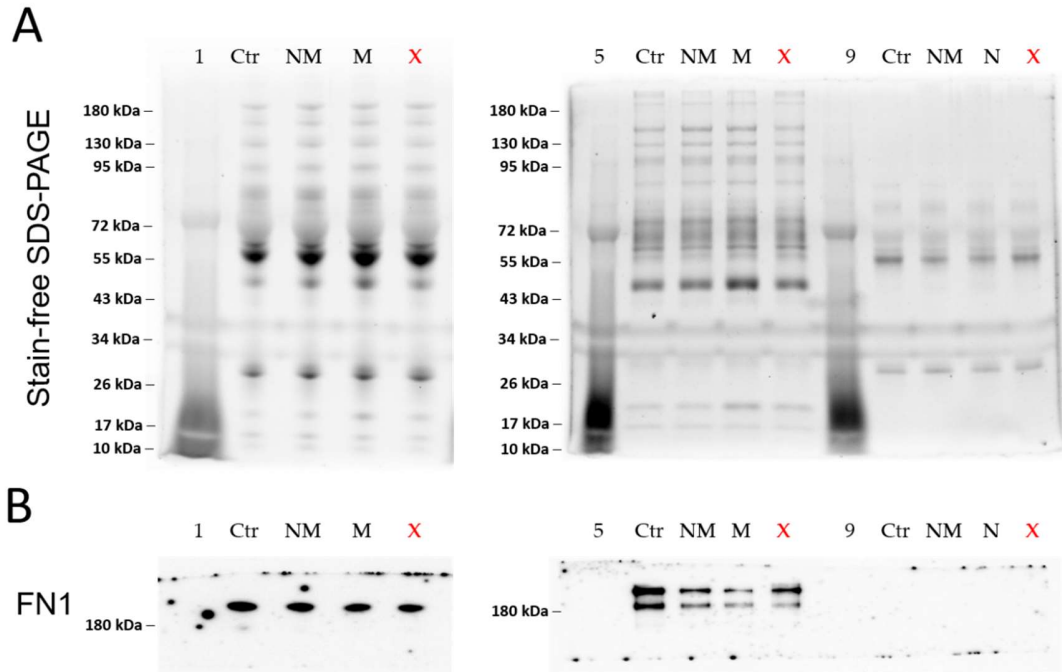


**Figure S4.** Total protein gels and immunoblots of C9 from crude plasma, WGA-bound plasma and WGA-unbound plasma fractions obtained from the study cohort. (A) Total protein gels performed by 10% stain-free SDS-PAGE. (B) Immunoblots of C9. Crude plasma (10  $\mu$ g), WGA-bound plasma fraction (5  $\mu$ g), and WGA-unbound plasma fraction (5  $\mu$ g) were from healthy control (Ctr), non-metastatic (NM) and metastatic CRC (M) patient groups, respectively. \*lane 1, 5, 9: Pre-stained Protein Markers, X means protein bands from other conditions and authors focus only the proteins in three conditions (healthy controls, non-metastasis and metastasis CRC patients).

## Densitometry analysis

	Pooled crude plasma (lane 2-4)			Pooled WGA-bound plasma fraction (lane 6-8)			Pooled WGA-unbound plasma fraction (lane 10-12)		
	Crt	NM- CRC	M- CRC	Crt	NM- CRC	M- CRC	Crt	NM- CRC	M- CRC
total protein intensity	11989 295	1164 7984	12549 313	93866 93	89030 96	9999 975	17370 37	1526 846	165249 7
C9 intensity (up)	53268 8	6011 53	13882 85	15989 954	22000 154	2851 8073	ND	ND	ND
C9 intensity (down)	55415 3	1126 339	14258 23	64345 4	18909 34	2147 486	ND	ND	ND
C9 intensity (up+down)	10868 41	1727 492	28141 08	16633 408	23891 088	3066 5559	ND	ND	ND
C9/Total protein intensity ratio	0.09	0.15	0.22	1.77	2.68	3.07	-	-	-
Normalized ratio (compared to healthy control)	1.00	1.64	2.47	1.00	1.51	1.73	-	-	-

Note: Crt = Healthy controls, NM-CRC= non metastatic CRC patients, M-CRC= metastatic CRC patients, ND = indicated undetectable.

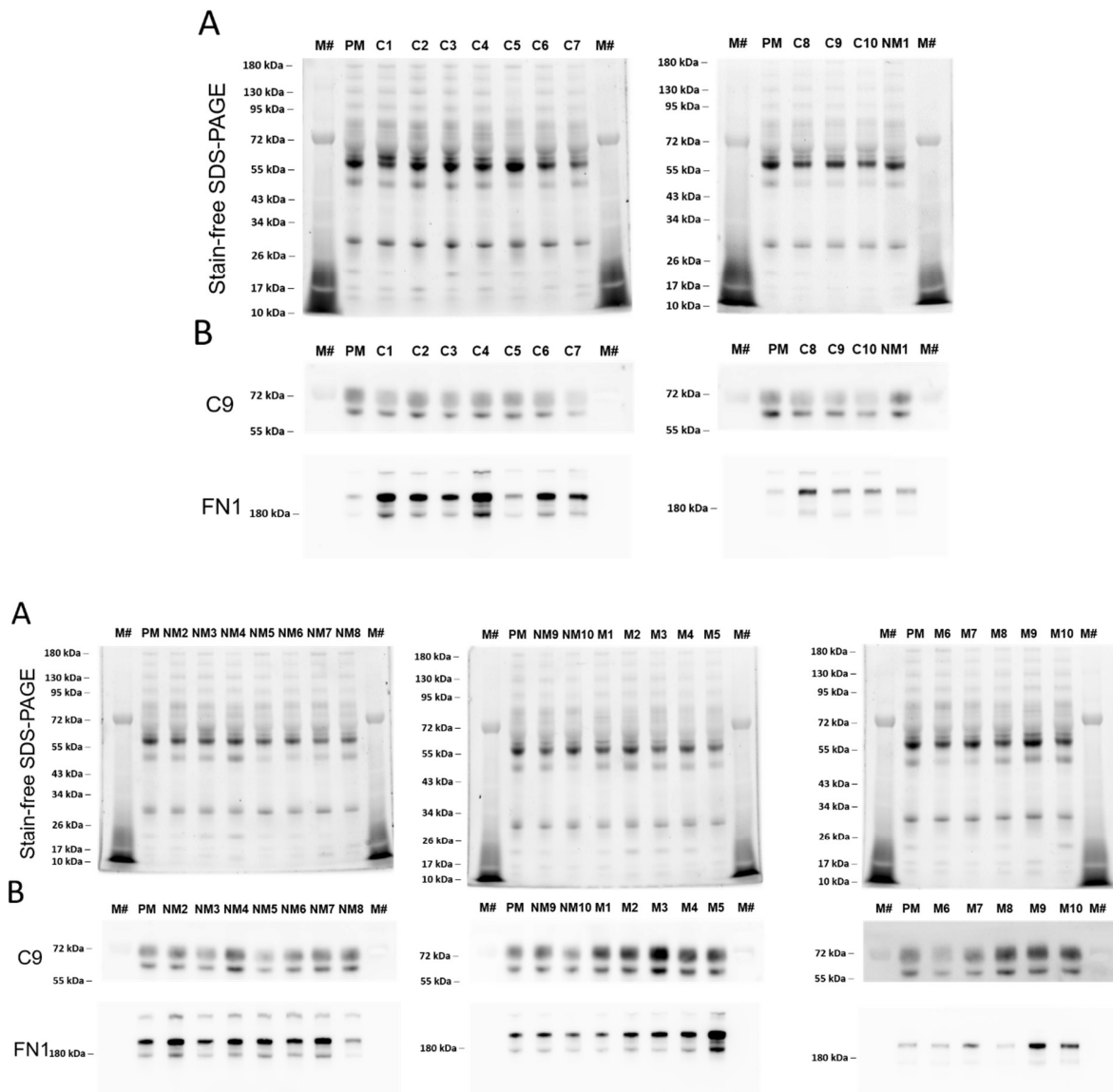


**Figure S5.** Total protein gels and immunoblots of FN1 from crude plasma, WGA-bound plasma and WGA-unbound plasma fractions obtained from the study cohort. (A) Total protein gels performed by 10% stain-free SDS-PAGE. (B) Immunoblots of C9. Crude plasma (10  $\mu$ g), WGA-bound plasma fraction (5  $\mu$ g), and WGA-unbound plasma fraction (5  $\mu$ g) were from healthy control (Ctr), non-metastatic (NM) and metastatic CRC (M) patient groups, respectively. \*lane 1, 5, 9: Pre-stained Protein Markers, **X means protein bands from other conditions and authors focus only the proteins in three conditions (healthy controls, non-metastasis and metastasis CRC patients).**

### Densitometry analysis

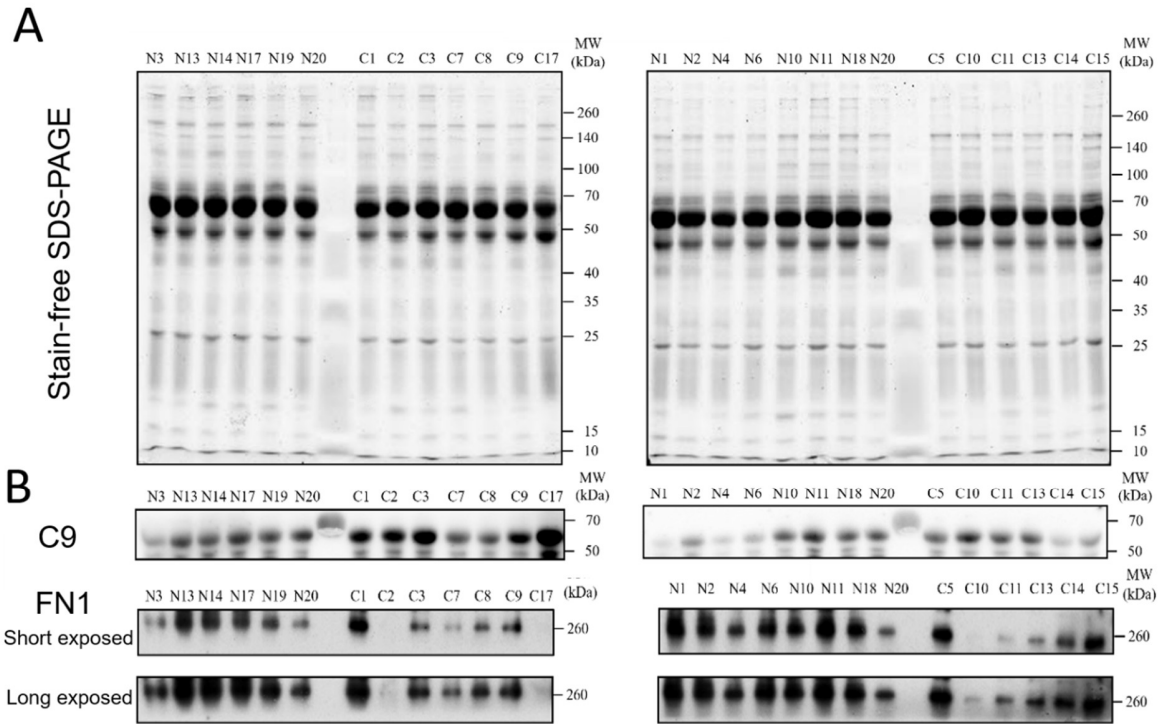
	Pooled crude plasma (lane 2-4)			Pooled WGA-bound plasma fraction (lane 6-8)			Pooled WGA-unbound plasma fraction (lane 10-12)		
	Crt	NM- CRC	M- CRC	Crt	NM- CRC	M- CRC	Crt	NM- CRC	M- CRC
total protein intensity	82462 49	1010 5944	11882 239	39960 26	38961 96	4648 245	15082 04	1337 398	134431 0
FN1 intensity (down)	15556 380	9810 423	64560 55	23743 950	92443 36	5041 287	ND	ND	ND
FN1/Total protein intensity ratio	1.89	0.97	0.54	5.94	2.37	1.08	-	-	-
Normalized ratio (compared to healthy control)	1.00	0.51	0.29	1.00	0.40	0.18	-	-	-

Note: Crt = Healthy controls, NM-CRC= non metastatic CRC patients, M-CRC= metastatic CRC patients



**Figure S6.** Total protein gels and immunoblots of C9 and FN1 from individual samples in the study cohort. (A) Total protein gels performed by 10% stain-free SDS-PAGE. (B) Immunoblots of C9 and FN1. Healthy controls (C1-C10), non-metastatic CRC patients (NM1-NM10), metastatic CRC patients (M1-M10), PM = a pooled plasma sample for protein normalization of each gel and immunoblot. M# = protein standard marker. Crude plasma samples (10 ug) were loaded in each lane.





**Figure S7.** Total protein gels and immunoblots of C9 and FN1 from individual samples in the validation cohort. (A) Total protein gels performed by 10% stain-free SDS-PAGE. (B) Immunoblots of C9 and FN1. Healthy controls (N1, N13, N14, N17, N19, N20, N1, N2, N4, N6, N10, N11, and N18), non-metastatic CRC patients (C5, C10, C11, C13, C14, and C15) metastatic CRC patients (C1, C2, C3, C7, C8, C9, and C17), N20 = a plasma sample for protein normalization of each gel and immunoblot. Crude serum samples (10 ug) were loaded in each lane.

**Supplementary Table S1. List of the accepted peptides used in protein quantification**

#	Charge	m/z	Measured mass	Score	Sequence	Accession	Anova	Normalized MS peak intensities								
								Healthy control			Non-metastatic CRC			Metastatic CRC		
								Ctrl1	Ctrl2	Ctrl3	NM1	NM2	NM3	M1	M2	M3
								7538	2	492.723	983.432	12.71	FSGSSSGAER	sp A0A075	0.000162	3865.8
1399	3	583.243	1746.707	17.06	CSGEEQSLEQCQHR	sp O43866	0.004865	18313.9	18285.8	17976.4	17704.9	14522.5	16048.8	23182.9	20031.6	20305.1
1482	2	574.281	1146.547	8.01	LVGGDNLCSGR	sp O43866	0.003399	15880.9	15737.9	15806.1	14516.5	15134.0	12674.3	11564.3	10985.7	10848.8
2728	2	496.295	990.576	3.58	LTPPLYVGK	sp O75460	1.39E-06	3976.7	3074.3	3786.1	5531.1	5140.3	6221.3	2023.1	1793.4	1786.1
3309	3	349.514	1045.521	7.14	YAVSEAAAHK	sp O75636	5.70E-06	2824.1	2411.9	2897.9	3012.4	2862.3	2992.2	1509.5	1471.0	1675.6
8547	3	512.218	1533.632	10.07	CNGHASLCNTNTGK	sp O75882	0.008709	1732.8	1516.0	1840.8	1394.5	1393.1	1417.8	1787.1	1726.6	1967.3
157	2	735.868	1469.720	16.06	EVGPTNADPVLAK	sp P00450	0.006089	147701.7	176880.2	176178.2	211575.5	271772.2	196592.2	283706.6	239971.9	296675.0
193	2	686.386	1370.758	15.06	GAYPLSIEPIGVR	sp P00450	0.015124	96273.4	79784.7	113265.2	129964.5	172923.8	127779.5	116685.8	124635.5	126566.0
294	4	648.281	2589.097	11.02	TYCSEPEKVDKDNEDFQI	sp P00450	3.00E-06	157220.4	174267.9	154744.7	180311.1	199722.4	177611.1	100278.1	100032.8	101846.5
350	2	760.376	1518.738	15.06	ALYLQYTDETFR	sp P00450	0.00015	69626.0	66417.7	73291.6	105373.1	123060.6	105837.2	94260.9	81669.4	75469.7
373	3	844.421	2530.240	11.84	SVPPSASHVAPTETFTYE	sp P00450	0.000321	220695.2	272040.2	236530.3	296223.1	311579.0	306225.9	383860.7	392368.5	334768.2
398	2	470.719	939.424	7.10	YTVNQCR	sp P00450	0.000258	30616.7	29932.2	27334.6	34449.8	32927.6	38182.1	40756.4	45736.8	43095.0
407	3	638.050	1911.128	11.80	TTIEKPVWLGFGLPIIK	sp P00450	0.000647	83160.8	91507.1	89746.7	120084.1	145365.1	112004.2	100140.3	95275.1	93275.2
410	4	340.688	1358.722	5.99	AETGDKVYVHLK	sp P00450	3.99E-05	22945.2	25812.2	23731.7	29708.0	31926.8	30549.7	36147.4	37955.8	34096.3
447	4	854.929	3415.688	9.97	QKDVDKEFYLFPTVFDEN	sp P00450	0.031199	133433.4	123528.5	140156.7	195928.8	144974.8	177206.0	153536.5	169442.5	160313.4
484	3	835.714	2504.120	16.38	SGAGTEDSACIPWAYYS	sp P00450	0.000533	139022.6	105574.3	131372.7	177268.2	145654.4	152480.8	97214.3	96334.8	96827.1
637	3	533.271	1596.792	9.55	QYTDSTFRVPVER	sp P00450	7.83E-05	25486.7	21045.1	25455.4	30265.0	37575.6	28713.4	53610.8	64169.5	70174.6
691	2	735.425	1468.836	18.06	DIASGLIGPLICK	sp P00450	6.19E-05	66263.8	63465.9	61794.4	88191.1	78887.0	88595.3	51980.3	55910.9	47432.3
750	3	724.364	2170.069	15.90	LISVDTEHSNIYLQNGPDF	sp P00450	0.000406	52215.3	46280.0	51807.4	64651.6	77047.7	64034.2	49974.8	45566.8	52766.2
753	4	295.909	1179.606	3.15	IYHSHIDAPK	sp P00450	0.006808	9985.3	9309.0	10519.9	11553.1	11239.3	12403.4	11912.4	11564.8	12368.9
819	3	522.915	1565.723	6.17	VNKDDEEFIESNK	sp P00450	3.03E-06	29072.2	35965.5	28838.0	44228.3	35795.4	46224.6	9892.4	10467.1	12359.2
822	2	509.236	1016.458	7.34	QYTDSTFR	sp P00450	5.16E-07	19179.5	18949.8	19595.5	26277.6	29361.5	25477.0	11644.5	11248.3	11287.7
856	3	825.361	2473.062	18.70	MFTTAPDQVDKEDDFQ	sp P00450	0.001325	49597.0	58283.6	55872.4	85384.5	120324.5	84651.3	59263.1	51575.7	76608.3
863	4	575.549	2298.165	10.18	MYSAVDPTKDIFTGLIGF	sp P00450	6.62E-07	25660.0	26017.8	27318.9	34876.3	33792.2	35803.6	48007.6	48121.3	44880.8
871	4	600.282	2397.097	12.95	HYYIGIETTWDYASDHGF	sp P00450	0.027927	39819.7	30630.9	30192.0	49102.2	37498.3	44143.7	45519.9	48464.0	41141.5
875	6	414.728	2482.323	6.97	KAEEEHLGILGPQLHADV	sp P00450	0.003815	19493.7	24680.9	17533.2	25684.5	26145.6	23327.7	33486.9	29616.0	41838.0
922	4	693.865	2771.431	8.29	ERGPEEEHLGILGPVIWA	sp P00450	1.94E-05	68007.4	61992.5	66923.0	97181.1	96469.9	94140.4	95941.4	93307.7	82893.5

923	3	444.546	1330.617	3.89	EYTDASFTNRK	sp P00450	0.00018	14523.5	14001.5	14112.8	19123.1	19757.1	18915.7	17421.4	14698.6	15953.0
964	2	602.269	1202.523	15.02	EYTDASFTNR	sp P00450	3.02E-06	19880.9	18695.5	21366.5	29239.5	27390.7	27678.6	14256.5	14266.1	15950.5
1083	5	431.821	2154.068	2.44	NLASRPYTFHSHGITYYK	sp P00450	0.000145	20035.4	21083.5	20804.2	25223.0	26638.7	24898.7	15184.7	15174.0	18514.6
1086	3	765.015	2292.022	12.70	FNKNNEGTYSPNYPNQ	sp P00450	2.94E-08	30619.1	31062.6	27607.3	38812.6	43767.3	40736.0	120189.0	111182.1	118612.4
1098	2	788.433	1574.852	18.06	DLYSGLIGPLIVCR	sp P00450	2.46E-05	55703.4	45286.7	59484.6	88304.4	84971.5	89185.2	40123.0	44836.3	43502.5
1150	2	716.323	1430.632	17.11	QSEDSTFYLGGER	sp P00450	0.016738	29326.7	38321.2	31388.8	38161.4	33346.5	35234.9	35124.5	28373.1	30113.8
1159	3	635.279	1902.816	12.16	NNEGTYSPNYPNQRS	sp P00450	0.003528	31857.9	31043.2	29109.2	38160.7	33345.2	36725.8	40012.5	35330.9	37387.9
1168	3	829.768	2486.283	16.17	GPEEEHLGILGPVIWAEV	sp P00450	0.004874	85554.2	97111.6	80692.4	109733.1	91958.7	116340.0	78181.1	82718.1	76589.9
1251	4	631.793	2523.143	10.56	TYSDHPEKVNKDDEEFIE	sp P00450	2.73E-05	36293.9	53661.6	36566.3	47570.1	51896.0	49244.7	13351.2	16132.2	16598.8
1326	4	607.272	2425.061	7.64	MFTTAPDQVDKEDDFQ	sp P00450	0.000921	26875.2	22967.6	26741.3	30872.0	45802.8	34276.1	20025.2	21129.8	23555.1
1352	3	525.958	1574.852	15.27	DLYSGLIGPLIVCR	sp P00450	4.92E-05	25272.5	20610.9	27344.9	37281.6	34922.6	36791.8	18420.0	20155.2	19493.0
1408	3	529.919	1586.736	4.08	RQSEDSTFYLGGER	sp P00450	0.000779	14729.7	15928.3	15376.5	19670.4	24154.6	19977.9	17593.3	17822.6	18414.2
1416	5	505.636	2523.144	3.75	TYSDHPEKVNKDDEEFIE	sp P00450	1.03E-05	22412.3	29704.9	25636.0	32981.1	27859.4	32166.7	9811.8	10414.9	11992.0
1422	3	507.254	1518.739	9.23	ALYLQYTDETFR	sp P00450	4.18E-05	9792.0	8826.8	10752.5	15711.1	14962.3	14730.2	12970.0	12196.1	11563.4
1437	4	563.547	2250.161	8.52	MYSAVDPTKDIFTGLIGF	sp P00450	0.004708	23708.7	25990.0	23327.0	24747.5	27160.7	27302.5	37080.8	39835.9	27136.3
1446	4	575.548	2298.164	7.92	KLISVDTEHSNIYLQNGPI	sp P00450	0.035185	16377.0	22800.1	20016.9	20562.9	21250.4	19323.3	24591.3	20706.6	24300.8
1447	3	490.619	1468.836	15.27	DIASGLIGPLIICK	sp P00450	2.31E-05	17477.3	16596.0	17081.4	23750.2	20834.2	23295.3	13537.5	15354.5	13482.6
1497	4	539.524	2154.067	3.39	NLASRPYTFHSHGITYYK	sp P00450	0.010603	18490.9	24459.7	18661.9	20372.4	30845.7	22696.7	11992.7	12095.4	16640.8
1665	4	632.305	2525.192	11.16	HYYIGIETTWDYASDHGF	sp P00450	0.002816	22121.9	23505.9	23825.8	32858.3	47649.3	31828.6	24525.3	26697.8	21431.3
1726	3	800.039	2397.095	19.96	HYYIGIETTWDYASDHGF	sp P00450	0.021721	35153.9	27231.3	26748.1	41470.4	32415.6	38866.1	40218.2	40688.2	33157.6
1732	3	457.927	1370.759	9.20	GAYPLSIEPIGVR	sp P00450	0.004751	6055.0	5633.4	6809.1	7708.6	10293.5	8366.3	7756.0	9303.2	7879.6
1759	5	561.678	2803.353	1.46	WYLFMGNEVDVHAAFF	sp P00450	0.000141	17365.2	14478.3	18577.0	24661.6	23788.3	22213.1	14612.1	13787.7	14147.1
1776	5	506.046	2525.192	10.33	HYYIGIETTWDYASDHGF	sp P00450	0.001982	15122.1	17045.9	17031.9	23529.5	28081.6	23964.8	17996.1	20169.2	16766.3
1802	4	564.797	2255.160	16.96	KAEEEHLGILGPQLHADV	sp P00450	0.023705	15478.3	23123.4	16057.7	20171.3	39811.7	21623.2	11053.8	10836.0	15114.1
1896	3	326.151	975.432	6.50	TYSDHPEK	sp P00450	0.003735	7400.9	6157.0	7482.4	11964.7	8640.1	11481.9	2524.6	4554.9	3351.8
2001	3	533.317	1596.930	11.69	DIASGLIGPLIICK	sp P00450	2.07E-06	10192.7	7485.4	9238.5	9634.0	8869.3	10655.2	35670.1	33911.0	29537.6
2235	3	1133.893	3398.657	17.76	QKDVDKEFYLFPTVFDEN	sp P00450	0.001503	32268.1	32642.6	27144.6	54968.3	45798.9	45636.7	62277.9	46435.7	49322.1
2311	3	864.039	2589.095	16.88	TYCSEPEKVDKDNEDFQI	sp P00450	1.99E-05	23821.0	24413.9	19613.6	31417.5	37033.6	35641.1	13412.5	12440.9	10499.7
2313	3	905.456	2713.346	18.17	HYYIAAEEIWNYPAPSGID	sp P00450	3.46E-08	35394.7	37073.0	38415.3	78517.4	58391.9	74426.3	9385.0	9315.0	8460.2
2341	5	775.392	3871.925	11.99	NMATRPYSIHAHGVQTE	sp P00450	0.000122	16220.5	16614.2	18867.3	30668.5	40787.7	32063.5	34986.5	35399.5	30530.4
2352	3	1054.184	3159.532	18.52	DVDKEFYLFPTVFDENES	sp P00450	3.78E-06	25069.5	24647.2	26655.6	44632.3	41730.7	41577.2	36821.5	35511.4	31279.8
2427	5	452.039	2255.159	7.16	KAEEEHLGILGPQLHADV	sp P00450	0.000756	6831.8	8871.9	8232.2	11291.7	15282.4	10625.7	5916.3	4647.2	6968.6
2553	3	890.426	2668.255	20.38	GVYSSDVFDFIPGTQYL	sp P00450	4.10E-05	12660.4	9777.6	12690.2	30141.7	23664.8	27360.4	17775.1	17499.0	17402.7
2595	4	575.794	2299.149	3.43	KLISVDTEHSNIYLQNGPI	sp P00450	0.00707	17328.8	20470.0	15642.0	23048.3	29543.2	22795.0	22902.7	21256.4	26853.3

2861	4	713.847	2851.359	11.79	WYLFMGNEVDVHAAFF	sp P00450	7.69E-05	14922.6	13715.7	15340.3	31444.3	23949.4	30665.4	12474.1	11290.6	9275.9	
2932	4	850.672	3398.660	12.70	QKDVDKEFYLFPTVFDE	sp P00450	3.60E-05	14135.9	15108.1	13798.5	21382.2	18417.4	20970.8	26622.3	25367.3	23492.8	
2947	2	1253.067	2504.119	15.17	SGAGTEDSACIPWAYYS	sp P00450	1.74E-05	37844.7	29004.1	31992.7	54448.7	47723.1	45566.0	23104.6	19161.0	20572.5	
3036	2	666.316	1330.617	8.36	EYTDASFTNRK	sp P00450	0.01025	6011.6	8240.2	5687.1	8877.4	13202.3	9198.6	6591.7	5193.3	5640.0	
3112	2	790.890	1579.765	6.02	QYTDSTFRVPVER	sp P00450	1.43E-06	5507.6	6149.0	5283.8	7278.6	7063.6	6125.5	17493.3	17748.2	15615.9	
3225	4	404.200	1612.770	9.40	PYTFHSHGITYYK	sp P00450	2.17E-07	4917.3	4911.4	4875.2	8329.3	10597.8	7537.1	1485.7	1128.2	1191.2	
3407	3	381.886	1142.636	3.98	DIFTGLIGPMK	sp P00450	0.007279	2574.5	2974.3	2295.8	2867.9	4015.5	2572.1	2438.6	2127.1	1967.2	
3428	2	488.723	975.431	6.91	TYSDHPEK	sp P00450	2.87E-05	7054.1	6113.0	6807.8	11832.5	9056.6	11275.7	2216.3	2111.9	2579.2	
3981	5	527.094	2630.432	5.61	IYHSHIDAPKDIASGLIG	sp P00450	4.99E-08	2579.6	2950.3	2961.4	3397.6	4243.6	2937.1	19711.8	19563.2	19858.0	
4018	4	1016.243	4060.943	7.07	SGAGTEDSACIPWAYYS	sp P00450	2.05E-08	18279.8	16056.5	17947.3	21072.6	17440.9	17278.7	93676.4	83432.1	87769.4	
4119	3	783.064	2346.169	15.64	MYSAVDPTKDIFTGLIG	sp P00450	3.09E-05	5148.8	5192.0	4397.0	11160.4	9649.7	11229.4	14182.5	10785.5	15034.1	
5748	2	956.570	1911.126	13.95	TTIEKPVWLGLGPIIK	sp P00450	0.008893	6351.2	8482.4	6905.2	10812.1	17072.1	10431.6	7723.2	7583.5	6742.9	
5935	4	790.890	3159.532	12.84	DVDKEFYLFPTVFDE	sp P00450	8.20E-05	6000.7	5464.4	6473.1	9903.6	8407.9	8710.5	7556.3	8464.5	6689.3	
6142	4	856.658	3422.605	18.90	GDSVVWYLF	SAGNEADV	sp P00450	0.002134	16401.1	15196.0	16102.2	20497.1	16593.6	22702.3	20942.1	22566.5	21099.7
6285	3	924.817	2771.429	18.97	ERGPEEEHLGILGPVI	WAEV	sp P00450	0.003822	11388.1	9183.0	9295.5	14678.2	17181.2	15680.3	12395.5	11875.0	10280.8
6695	3	1139.570	3415.687	18.71	QKDVDKEFYLFPTVFDE	sp P00450	0.002975	7857.6	7197.7	7304.0	14569.7	9782.8	11876.8	8309.3	8839.9	8685.5	
7295	4	1016.999	4063.965	20.35	IDTINLFPATLFDAYM	VASQ	sp P00450	1.72E-06	5196.4	5436.6	5440.8	17546.3	14013.7	16061.6	7605.5	8847.8	7988.7
7608	3	1141.875	3422.603	22.69	GDSVVWYLF	SAGNEADV	sp P00450	0.001288	16825.8	16640.2	17356.6	23202.8	19303.4	25826.4	22726.4	23606.5	23587.5
7619	4	622.578	2486.284	6.64	GPEEEHLGILGPVI	WAEV	sp P00450	0.000754	5287.6	5695.8	5689.8	7096.9	6956.0	7876.2	4230.5	5189.1	5160.1
8217	2	596.327	1190.640	8.56	DIFTGLIGPMK	sp P00450	0.0016	973.8	943.9	1183.1	2040.8	2110.0	1849.3	1523.5	1251.1	1125.0	
8311	6	761.910	4565.413	6.84	GPEEEHLGILGPVI	WAEV	sp P00450	1.21E-06	6445.0	7518.9	6370.5	5689.3	6050.0	6809.3	17177.3	15486.6	16145.5
9254	5	552.713	2758.526	11.00	IYHSHIDAPKDIASGLIG	sp P00450	6.50E-08	538.2	753.7	555.3	589.2	739.6	462.6	16161.6	15886.3	11332.6	
10046	4	679.344	2713.347	12.43	HYYIAAEEIWNYP	SGID	sp P00450	6.40E-08	3507.8	3484.3	3316.9	6283.7	5222.9	6458.7	609.8	563.2	404.2
11846	3	1354.660	4060.959	23.25	SGAGTEDSACIPWAYYS	sp P00450	3.08E-08	4616.2	4329.5	5590.0	5729.2	4645.8	4679.4	31160.4	27814.8	30420.7	
13220	4	996.494	3981.948	16.30	SVPPSASHVAPTETFT	YEE	sp P00450	1.38E-06	498.8	1067.3	1002.8	229.0	499.9	563.4	26747.5	31083.4	27557.3
19790	3	901.779	2702.315	18.38	EFYLFPTVFDE	NESLLEI	sp P00450	0.000247	911.6	814.3	822.5	1689.2	1409.8	1621.5	469.2	659.6	406.7
27152	2	507.217	1012.418	6.94	TYCSEPEK	sp P00450	8.65E-06	1858.3	1611.5	1932.6	3116.3	2277.9	3063.8	972.3	893.4	814.7	
597	2	574.780	1147.546	9.21	SGIECQLWR	sp P00734	0.028851	28010.6	36827.5	29160.0	34188.6	40474.3	33500.3	37857.8	39735.5	52662.7	
673	3	628.638	1882.891	10.75	TFGSGEADCGLRPL	FEK	sp P00734	2.44E-05	54237.9	61570.8	58557.1	63919.7	71617.6	66314.5	58486.2	53579.3	55712.4
715	3	744.757	2231.250	12.95	GQPSVLQVVNLPI	VERPV	sp P00734	0.017617	65718.2	49739.4	52455.7	71647.0	52049.1	65125.1	78660.6	92722.3	72696.0
733	3	665.689	1994.044	14.90	LAVTTHGLPCLAWA	SAQ	sp P00734	0.005189	48927.7	56280.8	45161.0	52753.5	67114.4	47823.1	73541.9	67943.4	59435.1
1108	5	698.375	3486.838	11.52	LKKPVAFSDYIHP	CLPDI	sp P00734	0.005392	37979.3	35189.8	43928.9	47569.9	66948.3	46327.5	71721.5	62804.4	52450.8
1114	2	597.805	1193.595	15.02	ELLESYIDGR	sp P00734	1.82E-06	20185.9	20603.1	18650.6	22506.3	25939.1	22191.9	13310.5	13047.6	12305.4	
1207	2	781.369	1560.723	15.06	TATSEYQTFNPR	sp P00734	0.000127	30925.0	34539.9	29489.8	38679.9	42408.3	36888.5	47832.2	45874.5	39463.8	

1243	3	738.010	2211.008	17.64	DKLAACLEGNCAEGLGT	sp P00734	0.00283	41330.4	29144.3	35122.8	43335.4	49910.9	39533.4	55913.0	50539.3	60317.8
1288	3	397.199	1188.574	6.76	YGFYTHVFR	sp P00734	0.001059	9403.6	12005.0	9910.5	10403.8	12570.5	10412.9	12820.4	12140.3	14190.6
1310	2	503.255	1004.495	6.03	ETWTANVGK	sp P00734	0.002858	9657.1	9060.0	10057.9	12324.0	15581.6	11773.0	13994.1	12136.6	13021.0
1406	2	437.744	873.473	5.28	VTGWGNLK	sp P00734	0.011407	8091.7	7600.4	8121.4	7809.8	10639.4	9373.1	8654.2	8311.5	9252.0
1946	3	655.309	1962.904	11.67	HQDFNSAVQLVENFCR	sp P00734	1.86E-08	17628.4	16640.4	18218.0	21921.8	20171.7	23512.5	7841.2	7051.0	7242.4
1951	4	503.754	2010.987	12.44	TFGSGEADCGLRPLFEK	sp P00734	6.61E-05	7904.7	10042.8	8175.1	7344.7	10301.4	7562.1	22910.4	21567.9	31607.2
2097	2	486.217	970.419	7.01	YTACETAR	sp P00734	0.001293	13655.6	11288.9	12688.7	16594.4	13768.0	16259.1	21212.7	20517.5	23653.2
2399	3	521.249	1560.724	6.38	TATSEYQTTFFNPR	sp P00734	0.000139	8075.5	8871.7	8914.8	9879.9	9480.9	9829.2	14234.6	13440.8	11505.2
4868	2	367.683	733.352	1.45	SPFNNR	sp P00734	0.000686	4983.5	4273.4	5185.5	5817.4	4851.5	5640.6	6536.6	6593.1	6631.4
5568	3	718.986	2153.936	12.12	NPDSSTTGPWCYTTDPT	sp P00734	2.99E-08	5901.5	6533.1	6029.7	13576.6	11081.2	12598.8	1685.9	1666.7	1292.5
6616	3	493.546	1477.616	10.67	GDACEGDSGGPFVMK	sp P00734	2.67E-05	3456.4	3620.4	3520.6	4184.2	4233.6	4165.0	2873.6	2923.8	2803.2
8119	3	752.057	2253.148	13.10	TLDEFTIIQNLQPQYQFR	sp P00736	0.025234	3310.4	2532.0	3086.9	5392.0	3547.2	4150.5	3900.5	4532.2	3831.0
1	2	602.322	1202.630	13.20	VTSIQDWVQK	sp P00738	7.09E-05	1825986.9	1965019.3	1718245.7	1555540.2	1937719.7	1684234.1	3138003.3	3045356.8	2868703.6
2	2	490.751	979.488	8.00	VGYSVSGWGR	sp P00738	0.000507	826944.5	862480.2	764133.2	687875.2	1028514.4	736483.0	1546695.0	1450848.6	1893256.9
8	2	720.337	1438.659	16.11	TEGDGVYTLNNEK	sp P00738	0.027277	1051184.7	1109335.4	1101632.6	1121799.2	1308181.8	1065101.5	1279575.2	1314373.9	1639145.5
22	3	570.289	1707.846	10.19	LRTEGDGVYTLNNEK	sp P00738	0.000159	482534.4	492469.1	547805.8	438020.4	591857.1	526338.2	857333.6	853019.6	933199.8
30	5	687.325	3431.590	6.99	AVGDKLPECEADDGCPK	sp P00738	9.23E-05	1199447.7	1310342.2	1120443.4	1243566.7	1471497.4	1179491.9	2662172.9	2588919.9	3629565.9
31	4	447.485	1785.911	4.06	VMPICLPSKDYAEVGR	sp P00738	0.000545	283024.5	357940.8	319038.4	288835.9	424777.8	294246.9	610627.8	632728.5	721567.6
32	6	572.939	3431.593	5.11	AVGDKLPECEADDGCPK	sp P00738	4.23E-06	969327.2	959696.5	908728.6	991145.3	1047575.2	918697.6	2070501.5	2125199.8	2652680.0
33	3	1292.230	3873.667	22.09	YQEDTCYGDAGSAFAVH	sp P00738	9.32E-06	3482244.6	3239077.9	3143999.6	4028940.7	3710935.0	3856817.4	5550005.0	5116913.3	5039350.0
43	3	425.551	1273.632	6.77	HYEGSTVPEKK	sp P00738	0.004037	384038.7	311622.9	370275.8	406284.1	335955.1	397377.7	831590.4	1770137.2	969667.3
47	2	352.191	702.367	1.44	VSVNER	sp P00738	0.008702	249765.3	219262.7	256573.9	275498.2	212774.1	267568.1	427293.1	449832.9	475048.1
49	3	401.884	1202.631	7.00	VTSIQDWVQK	sp P00738	3.09E-06	133232.9	132821.7	133419.8	120237.3	127126.9	118400.5	241055.3	261855.3	256299.2
61	4	969.425	3873.670	15.30	YQEDTCYGDAGSAFAVH	sp P00738	3.78E-06	1831943.2	1780758.1	1890538.1	2146798.8	1941403.8	2086090.2	2862076.7	2911148.0	2890065.4
63	3	553.944	1658.811	6.01	YVMLPVADQDQCIR	sp P00738	3.93E-05	481706.4	541313.4	467339.8	432720.0	518934.9	495200.6	944455.2	841484.7	1088361.0
65	2	854.414	1706.813	15.11	YVMLPVADQDQCIR	sp P00738	0.000193	311218.0	426311.1	313176.6	449019.4	564768.9	449920.2	876234.9	928439.0	742977.3
74	4	531.770	2123.050	13.01	SPVGVQPILNEHTFCAGM	sp P00738	0.000276	282212.1	367348.6	253927.8	246849.0	251856.0	276148.9	570643.6	485264.1	632564.3
81	2	405.194	808.373	3.79	DYAEVGR	sp P00738	0.002224	105099.4	88249.9	102513.9	127479.2	113173.4	123327.6	91976.6	92877.1	91302.9
95	3	569.946	1706.815	14.27	YVMLPVADQDQCIR	sp P00738	3.59E-05	150924.3	186056.8	153304.1	205493.4	240604.3	194384.7	390911.9	419634.6	344029.6
98	1	980.495	979.488	3.17	VGYSVSGWGR	sp P00738	0.016542	225576.7	300515.3	180121.1	176137.5	395934.9	218557.1	458731.5	432396.1	749356.0
126	3	596.311	1785.910	12.97	VMPICLPSKDYAEVGR	sp P00738	0.012628	137762.7	208809.5	170082.6	138522.8	287562.6	166157.9	347468.1	334954.2	447476.7
138	2	854.929	1707.844	12.75	LRTEGDGVYTLNNEK	sp P00738	0.000959	205712.6	226497.3	213777.7	209061.6	320253.4	251793.7	392674.3	403357.2	427393.0
149	3	599.010	1794.008	14.90	VVLHPNYSQVDIGLIK	sp P00738	0.005809	140205.9	195832.0	134075.2	120708.9	142188.7	114657.0	251867.1	203994.0	204515.1
160	3	703.680	2108.019	17.70	TEGDGVYTLNNEKQWINI	sp P00738	3.05E-09	69768.0	94975.2	76622.7	47925.1	50406.0	57345.9	643101.3	597171.3	655516.5

173	2	471.755	941.495	5.94	QKVSVNER	sp P00738	2.72E-08	33990.5	33606.8	34128.2	42398.2	33383.3	37844.3	143542.6	127050.0	137613.3
174	3	708.690	2123.047	17.95	SPVGVQPILNEHTFCAGM	sp P00738	0.001495	209460.5	284403.4	183230.2	182497.7	169764.9	190810.5	414877.9	342038.7	561541.8
177	3	320.514	958.521	5.24	QKVSVNER	sp P00738	0.001992	55857.3	46464.3	55541.3	60922.1	45325.5	57975.8	149710.7	322844.0	194100.4
212	3	480.561	1438.661	7.99	TEGDGVYTLNNEK	sp P00738	0.000522	71494.0	65483.1	73173.0	76156.1	76691.7	72751.2	89028.5	88143.5	101113.0
221	2	637.823	1273.632	14.71	HYEGSTVPEKK	sp P00738	0.002683	149157.5	124756.4	160488.7	146981.9	125763.7	181604.7	561305.6	1126028.1	696141.5
246	1	1203.637	1202.630	6.54	VTSIQDWVQK	sp P00738	1.44E-05	188046.7	210586.3	165396.7	169577.1	214335.9	181154.1	422814.5	420678.5	420118.9
306	3	570.289	1707.845	3.30	LRTEGDGVYTLNNEK	sp P00738	5.08E-08	28880.1	38089.3	35851.4	21374.4	27599.9	22152.3	218194.9	209318.3	256865.5
335	3	570.617	1708.830	7.79	LRTEGDGVYTLNNEK	sp P00738	6.64E-05	77506.3	88459.8	79167.9	85311.0	111723.7	90069.3	166988.6	156185.1	154809.4
356	4	858.904	3431.587	19.34	AVGDKLPECEADDGCPK	sp P00738	0.002593	176699.2	233728.2	162261.9	182761.9	277085.5	182496.7	451398.5	392461.5	685101.1
408	4	319.415	1273.632	5.67	HYEGSTVPEKK	sp P00738	0.000714	46139.4	39667.2	48024.6	51578.7	42295.9	50858.4	117688.2	187639.5	122814.9
425	2	573.776	1145.537	9.01	HYEGSTVPEK	sp P00738	0.000606	80338.0	67308.8	61311.4	105651.2	87432.1	91725.4	133821.2	115457.9	168368.7
432	4	595.309	2377.209	7.97	LRTEGDGVYTLNNEKQW	sp P00738	5.99E-10	15915.5	19870.2	17087.2	13117.6	9949.9	10500.4	261527.7	249111.9	255865.0
438	5	593.276	2961.343	12.83	LPECEADDGCPKPEIAH	sp P00738	0.00606	139768.9	145568.9	129539.4	165662.9	191238.3	164798.3	180796.0	170800.5	207071.8
602	2	480.268	958.521	3.65	QKVSVNER	sp P00738	0.000387	25800.5	20955.1	23733.1	29725.1	21811.7	28573.9	83256.3	221296.9	118004.5
680	2	352.683	703.351	1.43	VSVNER	sp P00738	0.001237	7887.6	7048.3	8707.4	8851.5	7899.1	9730.4	15936.5	15869.3	13881.7
749	3	382.853	1145.537	3.97	HYEGSTVPEK	sp P00738	0.002326	27829.7	22874.6	27228.8	32832.6	25446.7	30533.5	54938.5	52764.3	52589.0
844	2	471.754	941.494	7.18	QKVSVNER	sp P00738	0.000574	20697.0	17109.1	20623.0	23265.6	16851.3	22812.2	65849.6	134189.3	82256.1
929	3	704.009	2109.006	18.64	TEGDGVYTLNNEKQWINI	sp P00738	1.28E-05	31219.6	26156.5	35863.1	28676.3	29693.3	30559.3	70628.2	77520.9	82219.9
1009	3	389.843	1166.508	3.42	YQCKNYYK	sp P00738	5.68E-05	8418.2	8136.4	9198.6	9811.1	6825.4	9054.9	21452.6	19293.3	18503.4
1527	4	334.674	1334.665	1.41	NANFKFTDHLK	sp P00738	6.56E-08	3764.0	4091.7	3608.4	3333.0	4114.0	3360.8	14134.3	13390.1	14726.6
1551	3	793.409	2377.205	16.88	LRTEGDGVYTLNNEKQW	sp P00738	2.63E-09	4418.4	6854.9	5618.7	4182.0	3784.9	3466.9	104809.5	103809.5	103351.0
1598	4	543.771	2171.054	12.67	SPVGVQPILNEHTFCAGM	sp P00738	6.32E-05	10282.0	8680.8	10713.1	15144.4	10332.5	13408.7	24514.7	28379.1	28703.0
1607	2	1055.017	2108.019	14.75	TEGDGVYTLNNEKQWINI	sp P00738	9.16E-07	11371.7	18991.0	9655.1	7692.6	11188.8	9408.8	127341.7	111790.7	132362.1
2065	2	917.964	1833.913	9.02	VMPICLPSKDYAEVGR	sp P00738	0.001089	13575.7	14910.9	11292.2	18195.1	25545.2	18784.1	36013.5	37870.3	73051.2
2189	4	459.486	1833.915	3.55	VMPICLPSKDYAEVGR	sp P00738	5.95E-05	5282.1	5898.7	5388.9	6347.7	8726.8	7175.5	15139.0	15755.8	22818.5
2604	2	584.261	1166.508	1.47	YQCKNYYK	sp P00738	2.68E-05	5096.9	4654.7	5156.1	5730.2	5455.2	6091.8	10891.1	9272.2	9780.5
2638	2	602.324	1202.634	11.67	VTSIQDWVQK	sp P00738	8.08E-05	6382.2	7579.5	7004.3	6781.9	6785.6	6401.9	11494.8	10139.6	12172.3
2679	3	389.843	1166.508	3.34	YQCKNYYK	sp P00738	3.38E-08	3393.4	3269.2	3838.8	3383.9	3646.2	3751.8	9759.4	9616.3	9256.2
2686	3	389.515	1165.524	3.67	YQCKNYYK	sp P00738	1.09E-05	5183.5	4439.6	5306.9	5342.1	4390.7	5005.6	12273.6	12301.1	11798.3
2968	4	532.016	2124.035	10.61	SPVGVQPILNEHTFCAGM	sp P00738	0.000828	11533.8	11973.3	10558.3	10877.6	14105.3	9688.9	20740.9	18277.8	23496.3
3250	2	352.683	703.351	1.43	VSVNER	sp P00738	8.01E-05	7901.9	6995.0	8416.9	9133.3	7286.9	8656.4	16666.8	16248.8	16775.2
3716	4	659.378	2633.484	10.83	QLVEIEKVVLPNYSQVD	sp P00738	2.60E-09	585.3	561.3	482.9	206.7	208.2	346.0	34393.5	29620.9	30842.3
3808	4	449.509	1794.007	6.72	VVLHPNYSQVDIGLIK	sp P00738	0.00196	2733.5	4358.8	3226.1	2474.5	3188.6	2623.3	6355.7	5392.1	5555.9
5108	3	320.842	959.506	4.31	QKVSVNER	sp P00738	0.000122	2442.3	1915.0	2484.4	2778.7	2156.9	2625.7	8059.6	7632.3	8438.4

6128	4	1301.080	5200.292	19.86	YQEDTCYGDAGSAFAVH	sp P00738	6.85E-11	7489.9	6718.9	5877.6	8295.1	6405.3	8418.6	587627.2	611586.0	555979.3
6136	5	775.741	3873.669	10.09	YQEDTCYGDAGSAFAVH	sp P00738	0.005964	7203.5	7659.9	10541.6	9752.4	9667.8	9159.7	14912.6	16353.8	13462.7
9004	2	583.770	1165.524	1.44	YQCKNYK	sp P00738	0.00448	1563.1	1367.5	1530.1	1737.4	1439.7	1630.7	3861.0	3591.0	4304.6
16091	3	873.160	2616.457	16.97	QLVEIEKVVLHPNYSQVD	sp P00738	0.001689	65.8	47.0	0.1	49.9	112.7	56.2	8138.5	9346.8	7886.8
27030	3	500.625	1498.854	7.65	SDLGAVISLLWGR	sp P00739	0.000879	186.6	156.7	165.9	204.8	243.7	181.9	190.4	239.3	180.6
28762	2	750.434	1498.854	15.06	SDLGAVISLLWGR	sp P00739	0.004421	335.0	266.4	266.6	241.7	356.1	318.8	358.0	349.2	241.7
7583	3	677.024	2028.051	7.63	NKPGVYTDVAYYLAWIR	sp P00748	9.04E-05	2912.1	3270.4	3431.3	3866.9	3749.5	3577.6	2063.9	2029.0	1552.2
3899	2	754.848	1507.681	17.06	VSEADSSNADWVTK	sp P00751	0.045155	6227.4	8906.0	5907.1	5736.4	6518.2	4941.6	8406.8	7704.5	9933.7
4975	3	939.132	2814.373	17.38	LLQEGQALEYVCPSPGFYF	sp P00751	0.000479	10347.3	9266.7	8831.4	9212.0	8609.8	8542.6	16221.6	15656.6	11922.9
6231	3	326.191	975.552	5.82	VASYGVKPR	sp P00751	0.008795	838.5	741.9	963.5	634.7	606.4	716.3	880.9	1054.8	1191.0
6902	3	590.664	1768.970	6.77	DFHINLFQVLPWLK	sp P00751	0.026015	2992.4	2333.0	2735.0	3191.3	2432.8	2920.5	3945.5	4063.1	3282.6
485	3	411.581	1231.721	6.30	ANRPFLVFIR	sp P01008	0.021803	27002.9	34159.1	30416.7	22271.5	30341.4	22870.2	30515.9	32234.5	35096.5
525	3	447.560	1339.659	9.11	TSDQIHFFFAK	sp P01008	0.012541	31183.8	37750.5	40149.6	28973.1	30268.1	31153.0	26343.2	30378.7	26584.5
670	2	394.211	786.407	3.89	VANPCVK	sp P01008	0.04335	14461.4	13081.3	15692.8	12358.7	10250.9	13064.1	16338.8	15949.7	14393.4
986	3	404.553	1210.637	7.46	FRIEDGFSLK	sp P01008	4.98E-05	15019.0	14701.2	15481.8	11527.2	13715.6	11524.9	7002.7	7031.3	9065.2
1174	2	381.214	760.413	1.40	VWELSK	sp P01008	0.048319	7674.0	8708.4	7487.7	5564.9	7962.8	6491.6	8808.0	8793.4	9743.4
1361	3	558.954	1673.841	6.51	LQPLDFKENAEQSR	sp P01008	0.017902	19257.2	27451.6	16189.9	11985.4	16000.9	11346.2	21431.0	22383.3	28808.2
1462	3	764.390	2290.147	15.38	AFLEVNEEGSEAAASTAV	sp P01008	0.012858	52011.0	46226.2	48148.5	42450.8	38580.6	45660.4	47311.0	47882.2	44630.3
1601	4	605.067	2416.239	10.92	SKLPGIVAEGRDDLYVSD	sp P01008	0.004379	26501.0	33368.5	29221.9	17127.3	21969.0	18637.6	30535.8	25503.7	32252.6
1960	4	508.500	2029.969	11.29	ATEDEGSEQKIPEATNRR	sp P01008	3.66E-05	15416.1	13299.7	13722.9	11966.3	11779.1	10965.1	21594.0	21595.6	18544.2
2016	2	459.265	916.515	1.39	RVWELSK	sp P01008	0.041104	7349.0	9063.9	8889.9	6041.1	6918.4	6137.4	7229.5	6730.0	6713.9
2666	3	600.973	1799.898	7.74	EQLQDMGLVDLFSPEK	sp P01008	8.12E-08	13856.9	13805.1	15059.0	11581.8	11990.3	11093.7	5104.6	4462.0	4749.5
2936	2	420.212	838.409	5.72	FDTISEK	sp P01008	1.69E-08	4154.0	3921.4	4531.2	4099.6	4171.1	4240.7	1254.4	1322.4	1340.0
3038	2	350.691	699.367	2.11	SLNPNR	sp P01008	0.027669	8944.7	7239.4	8267.7	8246.4	5919.8	7120.8	8624.7	8512.6	11095.7
4218	3	326.839	977.495	5.27	FSPENTRK	sp P01008	0.017651	5213.8	4198.5	5026.4	4753.3	3676.8	4195.2	4654.9	4654.8	4755.1
10435	4	761.139	3040.526	11.51	FRIEDGFSLKEQLQDMGL	sp P01008	2.06E-06	2196.2	2471.6	2146.0	2551.1	2434.0	2066.8	9191.0	8905.2	7075.3
17601	3	767.049	2298.124	11.28	NDNDNIFLSPLSISTAFAM	sp P01008	0.001145	1243.4	1087.7	1002.3	1587.1	950.4	1284.6	439.0	361.1	520.7
21601	4	856.433	3421.702	16.52	VEKELTPEVLQEWLDELE	sp P01008	1.06E-05	692.8	815.9	885.7	488.4	490.4	826.8	3960.6	3491.7	3433.5
24442	4	876.750	3502.972	12.67	ITDVIPSEAINELTVLVN	sp P01008	0.000287	1269.4	1241.1	1026.6	680.3	558.0	635.9	1532.3	1873.0	1268.3
33173	3	935.857	2804.550	7.58	ITDVIPSEAINELTVLVN	sp P01008	0.016346	416.4	434.5	417.1	539.5	447.1	612.1	511.0	498.4	547.0
311	3	360.181	1077.522	5.32	FLENEDRR	sp P01009	0.030685	28536.5	27043.3	31545.1	29322.9	27444.3	27289.7	30564.7	28218.2	31889.6
415	2	444.756	887.498	6.99	AVLTIDEK	sp P01009	0.029195	29241.4	42833.0	29392.2	26849.9	40672.3	29048.9	20700.9	20117.7	22293.3
440	2	504.754	1007.494	6.33	QINDYVEK	sp P01009	4.52E-07	40781.1	48394.8	39636.3	32158.7	37154.5	38892.0	12556.3	13240.0	11527.8
561	3	697.372	2089.093	10.19	ELDRDVFALVNYIFFK	sp P01009	0.000394	65984.9	63123.7	55124.6	75108.0	71767.1	68162.7	44650.0	38615.4	39182.7

609	4	334.199	1332.767	4.15	LVDKFLEDVKK	sp P01009	0.000142	18464.9	22568.2	19105.5	17620.7	26649.2	16935.6	6668.5	7774.6	8349.0
627	3	721.712	2162.114	19.64	VFSNGADLSGVTEEAPLk	sp P01009	5.90E-09	44757.1	40836.2	43593.7	36490.3	35889.5	33342.8	111899.3	103552.1	100702.2
643	3	284.837	851.488	8.58	SASLHLPK	sp P01009	0.028255	14024.8	16550.6	14653.8	13469.3	14271.4	13471.2	14853.6	14661.4	13535.5
674	4	547.267	2185.038	12.70	LYHSEFTVNFQDTEEAK	sp P01009	5.27E-06	64080.2	76493.0	62610.4	61645.4	75768.2	62701.5	24214.2	21543.0	27642.4
769	3	721.384	2161.129	20.70	VFSNGADLSGVTEEAPLk	sp P01009	1.43E-05	35588.2	45490.8	35726.8	25634.4	27253.7	22880.1	82321.7	83838.6	69057.8
972	2	821.437	1640.860	15.06	ITPNLAIEFAFSLYR	sp P01009	2.89E-05	72388.0	59057.2	73623.6	75153.6	68189.4	70956.1	42201.5	41190.6	35930.1
981	5	356.760	1778.763	1.44	TDTSHHDQDHTFNK	sp P01009	0.001575	16318.3	8158.6	12555.9	18604.7	13957.9	17601.2	5019.3	3352.2	4901.1
997	2	917.958	1833.901	19.95	VFSNGADLSGVTEEAPLk	sp P01009	1.93E-06	52308.2	62080.0	63586.8	71718.4	91997.9	68755.0	23484.5	23221.8	24053.7
1184	5	630.511	3147.520	11.60	GKWERPFVFKDTEEEEDF	sp P01009	8.14E-05	55316.8	70733.0	54020.1	49517.9	63074.4	49428.8	26245.3	24617.5	26901.6
1196	3	400.538	1198.594	7.00	LGMFNIQHCK	sp P01009	0.001892	13270.0	11918.4	14596.8	11575.2	11447.0	11166.9	14101.7	14388.0	15547.8
1282	3	858.786	2573.337	19.38	TLNQPDSQLQLTTGNLFP	sp P01009	2.20E-06	46777.4	42481.0	48117.6	57251.0	48473.8	59664.0	20743.5	19403.2	17925.9
1332	4	445.698	1778.763	4.52	TDTSHHDQDHTFNK	sp P01009	0.005134	15251.3	6537.4	11386.8	20073.5	14954.3	17566.9	3880.8	2076.3	3397.6
1336	3	859.115	2574.322	21.38	TLNQPDSQLQLTTGNLFP	sp P01009	2.62E-06	60302.5	44181.2	56661.7	81816.8	72369.8	76237.4	18870.6	18996.8	14642.4
1355	3	547.961	1640.860	13.27	ITPNLAIEFAFSLYR	sp P01009	6.44E-05	32374.8	25298.0	30169.7	31331.4	25374.1	30059.9	17168.3	16872.8	15220.1
1421	2	917.465	1832.916	17.95	VFSNGADLSGVTEEAPLk	sp P01009	4.06E-05	36019.4	49042.4	34369.8	38470.2	42616.2	34956.1	14088.9	15170.6	12372.4
1704	4	452.750	1806.970	7.34	FNKPFVFLMIEQNTK	sp P01009	0.034116	20950.0	33855.4	23714.8	23714.3	34506.4	21115.7	31119.6	34537.4	43132.3
2126	3	612.308	1833.903	15.07	VFSNGADLSGVTEEAPLk	sp P01009	4.62E-06	13493.3	14264.9	15242.2	16755.8	20533.1	15180.6	6377.8	5881.9	6204.2
2169	3	402.565	1204.673	4.83	LVDKFLEDVKK	sp P01009	0.001324	6051.4	8909.6	6844.4	6080.9	8200.0	5552.2	2764.6	2588.2	3831.5
2411	3	293.505	877.493	1.42	FLEDVKK	sp P01009	9.71E-11	3766.2	3876.2	3662.4	3946.7	3540.0	3860.4	594.8	546.1	601.1
2503	3	593.928	1778.763	10.47	TDTSHHDQDHTFNK	sp P01009	0.003432	10580.7	5124.4	9774.0	13270.5	10868.1	14469.7	3212.0	2019.3	2795.0
2522	3	721.712	2162.114	19.64	VFSNGADLSGVTEEAPLk	sp P01009	8.54E-06	9259.6	9222.9	9310.6	7531.3	9841.9	7599.6	19214.7	22011.3	19266.7
2587	2	366.209	730.403	3.74	SPLFMGK	sp P01009	0.002927	12555.4	11105.5	13602.2	11454.9	9777.4	11434.5	16258.7	15829.3	17559.2
2614	4	339.681	1354.695	5.80	RLGMFNIQHCK	sp P01009	0.008525	4821.8	4242.4	4978.3	4334.4	3816.0	4585.6	4781.3	5093.7	5986.2
2788	3	729.353	2185.036	18.70	LYHSEFTVNFQDTEEAK	sp P01009	0.00035	20718.0	25253.5	19568.7	19331.0	25189.3	18171.1	9846.3	8501.4	11481.2
2871	2	538.813	1075.612	9.00	LSSWVLLMK	sp P01009	0.001236	3766.8	2934.2	3831.6	4817.6	5549.7	5200.7	4989.7	4884.3	4274.9
4197	2	461.718	921.420	2.21	FLENEDR	sp P01009	0.000152	2017.2	2037.4	2170.8	2095.7	2384.4	2048.4	1705.7	1420.8	1524.0
4247	3	686.654	2056.941	11.49	LYHSEFTVNFQDTEEAK	sp P01009	5.55E-05	9004.5	10461.4	9596.2	10670.4	12107.0	9594.3	4126.8	3776.0	5268.9
6612	5	635.911	3174.519	4.19	LYHSEFTVNFQDTEEAK	sp P01009	5.43E-07	2140.4	2083.9	1652.0	362.8	288.8	685.6	9962.5	11429.2	9333.7
8152	5	593.488	2962.405	6.29	WERPFVFKDTEEEEDFHV	sp P01009	1.27E-08	4051.3	4412.3	4052.4	4025.3	4432.5	3705.1	722.6	698.4	834.1
8231	4	690.137	2756.520	7.75	IVDLVKELDRDVFALVN\	sp P01009	1.81E-10	923.1	753.1	851.9	343.0	378.8	307.3	9913.4	10949.9	9542.6
8830	4	523.280	2089.092	11.41	ELDRDVFALVNYIFFK	sp P01009	2.11E-05	1835.4	1526.0	1551.0	1950.2	1826.5	1653.3	884.8	769.6	774.7
26588	2	788.926	1575.837	15.06	DTVFALVNYIFFK	sp P01009	4.41E-06	629.4	718.3	467.6	781.5	708.9	833.1	110.7	117.0	72.3
35758	4	941.253	3760.982	9.83	TLNQPDSQLQLTTGNLFP	sp P01009	6.83E-07	61.5	72.8	125.2	33.9	58.3	25.3	1760.2	1876.6	1715.8
206	2	531.298	1060.582	12.98	EIGELYLPK	sp P01011	0.04515	73347.5	91565.6	98385.2	91169.8	93143.3	99286.6	104754.8	117378.4	108341.8



298	3	370.190	1107.548	3.45	WRDSLEFR	sp P01011	0.009167	22483.0	31333.0	24821.7	22781.1	34051.2	26850.3	40518.6	42787.1	47951.0
308	3	365.549	1093.626	8.57	NLAVSQVVHK	sp P01011	0.001561	32597.5	31690.7	30820.1	35719.9	37835.8	32242.6	38776.5	40097.4	45254.1
480	2	432.746	863.477	1.45	LINDYVK	sp P01011	0.020863	18660.7	18753.5	20361.3	21117.4	24465.1	21098.1	24758.5	24074.1	30271.4
619	3	636.659	1906.956	18.11	AVLDVFEEGTEASAATAV	sp P01011	0.009607	52870.3	44727.5	51838.9	68426.1	62227.7	59489.2	46098.8	49379.8	38491.5
716	4	455.994	1819.945	4.95	EQLSLLDRFTEDAKR	sp P01011	1.35E-06	19526.0	21724.7	23829.3	18930.7	19725.6	19237.9	38598.4	38472.3	40496.8
944	2	383.691	765.368	1.86	DSLEFR	sp P01011	0.00043	8609.4	9512.6	8884.8	9309.2	12571.1	10595.6	6594.9	6125.0	5653.3
996	2	351.724	701.433	2.14	ITDLIK	sp P01011	3.82E-06	8820.2	11998.7	9319.8	10705.9	14919.7	11598.5	3071.0	2947.1	3413.7
1107	2	954.484	1906.954	19.90	AVLDVFEEGTEASAATAV	sp P01011	0.003627	52170.8	51535.6	50160.2	76385.3	65840.4	60038.2	48957.8	46363.6	38625.5
1686	3	887.132	2658.374	12.16	FNRPFMIIVPTDTQNIFFI	sp P01011	0.000199	23667.0	22692.4	23710.6	57806.8	42341.8	54591.8	34550.5	33478.0	27810.9
1821	3	405.916	1214.726	7.80	ITLLSALVETR	sp P01011	0.024085	4975.1	3728.3	4656.9	7014.4	5095.8	6436.9	5587.8	6001.0	4973.9
1874	3	742.381	2224.121	15.90	GTHVDLGLASANVDFAFS	sp P01011	1.95E-07	40512.7	41288.4	38267.3	61855.4	54285.7	51736.8	15461.9	16011.7	12753.8
2006	3	607.656	1819.945	10.72	EQLSLLDRFTEDAKR	sp P01011	8.41E-05	9111.7	10985.3	11085.3	8477.7	10096.3	9275.6	18976.4	16189.1	19990.1
2315	2	711.346	1420.677	14.06	DEELSCTVVELK	sp P01011	1.22E-05	9635.1	11220.0	9611.8	12866.2	15408.3	13512.7	4952.9	4522.9	3336.8
2840	4	544.773	2175.064	10.15	RLYGSEAFATDFQDSAAV	sp P01011	6.44E-05	5412.6	7618.0	7370.4	6247.2	5513.3	6093.9	13530.9	12646.5	15191.3
4316	2	1148.590	2295.166	17.90	DYNLNDILLQLGIEEAFTS	sp P01011	0.010748	11224.8	9545.4	11028.8	22820.1	13666.9	15742.9	12011.0	9148.0	8910.6
5454	2	355.672	709.330	3.36	FTEDAK	sp P01011	0.002804	2797.2	2369.3	2963.9	3662.6	3034.3	3479.7	1982.4	1979.2	1769.4
5700	3	916.486	2746.437	14.91	ITDLIKDLDSQTMMVLVN	sp P01011	0.001404	7401.4	6298.3	7870.8	11231.5	10125.7	10841.1	10917.4	10414.3	9315.6
8214	4	665.601	2658.375	12.28	FNRPFMIIVPTDTQNIFFI	sp P01011	6.09E-05	2140.9	1957.5	2162.1	4731.4	3775.6	4547.5	3123.3	3022.9	2602.7
11037	4	687.617	2746.437	9.79	ITDLIKDLDSQTMMVLVN	sp P01011	0.001392	1986.2	1754.3	2159.5	3063.6	2660.0	2694.6	2908.8	2716.2	2543.6
18606	3	766.391	2296.152	17.11	DYNLNDILLQLGIEEAFTS	sp P01011	2.06E-05	1231.4	1100.3	1397.4	2351.6	2046.1	2604.2	952.3	809.4	906.5
19027	4	733.896	2931.554	6.83	GKITDLIKDLDSQTMMVLN	sp P01011	1.87E-05	761.0	832.2	1033.6	674.9	568.7	813.8	3015.5	3124.2	2435.6
23935	3	1079.894	3236.661	21.44	DYNLNDILLQLGIEEAFTS	sp P01011	1.47E-06	473.9	282.6	496.3	335.2	391.5	625.8	6492.1	6317.8	6870.0
26335	4	810.173	3236.662	12.27	DYNLNDILLQLGIEEAFTS	sp P01011	4.99E-08	201.0	146.4	241.3	172.1	161.8	170.3	3452.7	2793.3	2895.5
2042	3	607.980	1820.919	1.47	SLDFTELDVAAEKIDR	sp P01019	0.000884	12772.3	13198.2	13959.8	9280.8	7944.4	8661.5	11186.0	10944.8	8205.4
3582	3	575.014	1722.019	15.11	VLSALQAVQGLLVAQGR	sp P01019	1.30E-07	10140.9	7893.8	9886.6	9099.9	6493.8	8299.7	660.4	933.6	826.2
3789	3	822.464	2464.371	20.22	ADSQAQLLLSTVVGVFATA	sp P01019	1.78E-06	19535.2	14816.8	17398.1	14998.4	10668.6	11893.3	3250.0	3126.2	3618.5
4173	3	633.369	1897.087	7.23	QPFVQGLALYTPVVLPR	sp P01019	1.44E-06	8596.6	7269.5	9287.9	7096.3	8402.1	6996.3	2892.7	2898.2	3084.4
8584	4	1067.832	4267.297	21.51	TIHLTMPQLVLQGSYDLQ	sp P01019	0.011823	12172.1	11249.4	11359.6	11861.9	11080.6	11658.6	15730.4	13436.8	16970.5
8770	4	617.101	2464.373	19.38	ADSQAQLLLSTVVGVFATA	sp P01019	6.00E-06	4157.6	3016.6	3801.5	3051.6	2318.3	2395.9	801.3	611.0	707.3
13044	6	1085.393	6506.314	4.06	VGEVLNSIFFELEADEREI	sp P01019	0.000251	6570.5	7020.1	7637.3	4560.8	3727.8	4215.2	8429.0	8997.0	6657.8
24	2	628.326	1254.637	12.89	AIGYLNTGYQR	sp P01023	0.020008	472502.9	558501.5	480847.5	454616.8	468112.4	465249.9	612050.7	547767.0	683834.5
77	3	558.292	1671.855	13.06	TEHPFTVEEFVLPK	sp P01023	0.000173	282200.1	243858.1	298641.1	291417.0	289229.7	288907.9	195031.8	169468.1	162044.1
89	2	697.844	1393.673	17.11	NEDSLVQVQTDK	sp P01023	3.27E-07	412859.8	424119.8	399517.1	334063.7	402005.0	354129.4	156857.2	157389.6	145813.7
92	2	669.830	1337.645	14.06	NALFCLESAWK	sp P01023	1.96E-05	214528.3	300793.9	246436.1	226679.3	208845.4	221727.6	107561.8	113071.3	103667.4

97	3	796.405	2386.192	22.17	QQNAQGGFSSTQDTVVA	sp P01023	0.017023	496861.3	521419.1	526125.6	462746.0	520903.0	438950.2	365735.7	360518.9	446848.9
117	2	324.216	646.418	1.40	VIFIR	sp P01023	2.08E-05	58698.4	68888.2	55807.5	60669.2	74612.7	59054.7	25917.6	24130.6	30265.2
129	2	523.799	1045.583	12.80	FEVQTVPK	sp P01023	2.00E-06	158710.5	181227.6	177421.4	150275.5	149012.5	145838.8	85581.5	88432.4	96191.1
130	2	924.944	1847.874	20.95	QFSFPLSSEPFQGSYK	sp P01023	0.000838	449561.7	544526.3	430636.5	409137.4	330747.4	409373.4	288905.2	271401.2	273696.0
133	3	633.966	1898.876	14.90	FSGQLNSHGCFYQQVK	sp P01023	4.43E-05	275374.6	307433.4	265326.5	297025.0	327314.7	286150.6	171653.2	180206.0	192780.8
134	2	574.815	1147.616	11.79	QGIPFFGQVR	sp P01023	5.12E-05	222644.7	227197.0	226141.5	232393.8	206036.4	215243.9	134427.5	149341.3	120806.0
143	2	503.739	1005.464	3.73	FQVDNNNR	sp P01023	9.08E-05	102201.5	91251.4	110804.9	105048.9	88535.5	106384.5	58261.0	53964.6	53649.2
145	2	414.733	827.451	6.76	SDIAPVAR	sp P01023	1.15E-09	78995.3	77970.3	77776.7	74954.2	77807.4	77249.8	27476.2	28746.9	25744.1
155	3	473.538	1417.593	4.49	HYDGSYSTFGER	sp P01023	0.010671	119347.3	110276.4	108682.1	105590.4	106192.1	105183.6	108330.8	107231.1	113024.0
156	5	651.924	3254.583	12.49	YDVENCLANKVDLSFSPS	sp P01023	0.000329	388374.7	444256.3	396036.4	367389.4	527199.0	367425.2	208543.8	218255.6	180744.3
161	3	616.966	1847.876	14.11	QFSFPLSSEPFQGSYK	sp P01023	0.005881	192938.9	227450.6	201626.6	180969.0	140890.8	164986.7	144752.9	149454.2	138751.7
179	3	374.217	1119.630	7.80	SIYKPGQTVK	sp P01023	0.000332	70468.0	67584.4	77196.2	83130.3	64716.4	78309.5	46723.5	40364.3	41008.9
180	3	704.030	2109.070	13.88	LHTEAQIQEEGTVELTG	sp P01023	2.48E-05	278854.8	402243.7	302608.4	300311.1	329161.1	333809.2	141494.0	136071.7	152335.5
190	3	295.192	882.556	6.28	DLKPAIVK	sp P01023	2.50E-06	44710.0	40551.5	43606.6	42591.8	43157.8	39535.9	23202.3	24999.0	26326.6
215	4	387.207	1544.797	10.96	LHVVEEPTETVR	sp P01023	0.004499	79077.9	100526.5	89276.9	80806.7	85625.1	86264.0	64508.3	72587.5	66274.5
224	5	668.504	3337.484	5.54	SPCYGYQWVSEEHEEAH	sp P01023	4.16E-06	271734.2	338801.3	265140.1	275312.4	266925.3	253461.0	128711.2	115846.7	109752.0
228	3	594.009	1779.006	15.90	DTVIKPLLVEPEGLEK	sp P01023	1.08E-05	155478.2	142172.7	154043.4	160210.3	207434.5	147855.3	54849.0	56517.2	45092.9
235	2	709.803	1417.592	14.12	HYDGSYSTFGER	sp P01023	0.049291	152122.7	161316.0	130470.5	142284.2	157389.4	142758.9	127211.7	119369.3	133189.1
237	4	559.226	2232.874	5.61	KYSDASDCHGEDSQAFCS	sp P01023	0.000213	157808.1	163778.2	147299.7	141761.8	150509.1	150606.1	114002.3	119992.8	104741.4
238	2	317.700	633.386	1.34	VFQLK	sp P01023	8.40E-06	38205.8	38675.1	39678.8	35986.3	42457.7	33734.7	20461.9	20537.4	20707.5
243	2	445.235	888.456	5.84	SLNEEAVK	sp P01023	0.020608	53764.4	42966.0	49572.8	44724.9	39447.3	44802.9	51014.9	42928.0	45714.9
244	2	383.211	764.408	3.92	GEAFTLK	sp P01023	1.07E-06	50895.0	52576.0	50570.3	48750.5	67907.2	52609.1	13075.6	13231.0	16307.9
247	3	539.955	1616.844	11.11	TEVSSNHVLIYLDK	sp P01023	1.94E-06	134068.2	156524.0	131726.6	128332.5	156185.4	117696.1	34440.2	36801.9	42784.0
251	3	362.210	1083.609	6.82	GHFSISIPVK	sp P01023	5.75E-06	59677.4	75216.5	64767.2	64175.1	73394.5	55437.4	20285.0	20638.8	25220.2
253	2	403.706	805.398	4.84	GPTQEFK	sp P01023	9.72E-05	68621.1	61640.9	75806.4	70455.5	60375.3	68107.8	38170.0	43244.8	41935.4
261	3	309.188	924.541	8.96	TGTHGLLVK	sp P01023	2.91E-06	40893.9	39784.7	44584.0	47930.5	40624.1	46608.1	16060.8	15338.6	16129.2
262	2	923.023	1844.031	15.90	LLIYAVLPTGDVIGDSAK	sp P01023	6.23E-06	293530.3	242787.6	291668.1	323471.2	225997.9	269729.9	73150.0	88257.8	72898.4
284	3	615.685	1844.033	18.11	LLIYAVLPTGDVIGDSAK	sp P01023	4.71E-05	150249.5	116923.7	141855.1	170745.3	110531.9	137579.8	48032.4	53088.4	47014.9
287	3	550.618	1648.833	7.48	SSSNEEVMFLTVQVK	sp P01023	0.018151	100613.4	140024.6	104025.5	80392.8	109521.1	73969.2	55759.4	55782.9	78531.8
290	3	522.617	1564.829	12.16	ALLAYAFALAGNQDK	sp P01023	4.39E-06	85941.2	69157.8	89014.6	90725.8	77303.9	86927.4	34656.9	34081.5	29641.5
300	4	513.019	2048.046	13.00	VDLSFSPSQSLPASHAHL	sp P01023	4.76E-06	122766.5	153864.2	122573.3	129315.6	128636.9	119091.9	40035.2	40109.6	53020.3
318	3	745.298	2232.872	16.96	KYSDASDCHGEDSQAFCS	sp P01023	1.50E-05	160125.0	163321.0	148169.8	143345.9	155061.4	155227.0	103120.0	107611.1	94040.3
319	3	362.865	1085.573	3.59	SASNMAIVDK	sp P01023	9.98E-08	47912.0	44884.9	45141.2	47655.3	43462.7	48251.3	17821.4	19528.0	20132.1
322	5	1070.761	5348.769	14.18	DTVIKPLLVEPEGLEKETT	sp P01023	1.19E-06	679370.6	676385.1	653905.4	568909.9	497730.8	589035.2	#####	1151941.2	#####

323	3	796.763	2387.268	17.90	AYIFIDEAHITQALIWLSQLF sp P01023	0.00015	207374.2	179530.9	211225.1	242172.2	162338.4	194612.9	85216.3	94182.0	82921.2
325	2	613.280	1224.546	8.00	YDVENCLANK sp P01023	1.40E-08	80711.2	76807.0	73131.3	96866.7	89030.9	81806.2	15133.5	12607.3	16274.5
345	2	783.421	1564.828	15.90	ALLAYAFALAGNQDK sp P01023	2.95E-05	119931.0	87980.6	121567.9	131539.7	111313.8	134100.7	48487.6	45384.9	37761.1
363	4	1227.616	4906.435	20.84	APVGHFYEPQAPSAEVEI sp P01023	0.015555	418969.9	351414.4	409639.6	480815.7	430644.5	454060.0	476717.2	410961.5	461237.1
367	4	820.414	3277.627	15.44	VSVQLEASPAFLAVPVEK sp P01023	0.000825	200739.5	175858.7	233493.1	225222.7	239486.2	225989.2	157071.9	126341.0	125397.6
370	3	702.599	2104.774	18.95	YSDASDCHGEDSQAFCE sp P01023	0.007323	149035.8	121276.9	117356.9	111424.8	105876.9	106266.3	100860.1	90773.8	79547.6
391	3	471.872	1412.595	8.67	EQAPHICANGR sp P01023	6.65E-08	82201.8	69484.2	77640.4	91168.5	85513.7	86092.9	27587.2	27208.5	24131.4
422	2	630.291	1258.567	14.06	VGFYESDVMGR sp P01023	0.036243	43964.5	50226.5	48628.0	52421.5	66632.7	58166.7	62310.6	59618.3	78885.6
423	3	666.371	1996.091	17.11	LLLQQVSLPELPGEYSMK sp P01023	4.24E-07	133727.1	136373.6	116570.7	132083.5	108047.9	123482.4	27665.5	29581.7	20866.2
429	4	835.378	3337.481	15.83	SPCYGYQWVSEEHEEA sp P01023	2.06E-05	181954.8	254124.5	165117.7	172731.0	199649.2	168594.3	66740.5	61281.1	54099.5
461	4	1040.292	4157.140	15.25	DTVIKPLLVEPEGLEKETT sp P01023	7.56E-06	325377.9	223653.9	319073.8	365479.4	253640.6	308064.3	66405.4	80227.3	68050.3
462	2	410.712	819.410	6.31	QSSEITR sp P01023	0.039906	91558.3	74806.5	85770.1	104479.7	72417.3	88125.2	66370.3	62066.8	82856.4
483	4	383.180	1528.693	6.55	TAQEGDHGSHVYTK sp P01023	0.014693	97799.4	84107.5	97694.1	109002.9	93452.9	108784.9	53586.0	74466.5	52756.0
492	3	628.688	1883.043	18.11	VSVQLEASPAFLAVPVEK sp P01023	7.21E-09	88513.3	71887.2	72298.2	101627.0	82327.9	98149.5	9091.8	8740.5	7763.7
505	3	1055.195	3162.562	18.52	YNILPEKEEFPFALGVQTL sp P01023	7.27E-10	312793.6	257491.2	289170.0	385925.6	370176.9	356648.7	36891.8	33663.3	31137.6
543	2	605.826	1209.638	10.83	LPPNVVEESAR sp P01023	3.68E-07	207155.7	255478.3	208627.7	225142.3	291557.7	226527.7	58485.9	55926.7	61145.8
548	4	791.648	3162.563	15.73	YNILPEKEEFPFALGVQTL sp P01023	4.72E-10	188389.3	159007.3	180648.5	223799.3	206965.0	201961.3	22210.4	22310.0	19873.1
624	3	471.544	1411.611	9.92	EQAPHICANGR sp P01023	1.79E-06	35579.0	33527.6	38378.7	32483.0	32566.6	33896.4	14898.7	13587.9	11462.6
676	3	451.620	1351.837	10.26	GVPIPNKVFIR sp P01023	5.42E-08	8788.7	10644.9	9168.0	7848.4	8782.8	7058.8	60664.0	59529.0	77284.8
693	3	937.488	2809.442	16.17	VVSMDFHPLNELIPLV sp P01023	0.000417	114023.1	123242.8	126594.2	173376.2	120800.8	169338.8	71513.3	75405.7	76055.6
700	3	419.220	1254.637	6.08	AIGYLNTGYQR sp P01023	0.005949	18336.7	17930.6	19000.4	18260.5	16847.9	18521.1	23594.0	20745.5	25631.7
723	6	847.775	5080.606	10.99	LLIYAVLPTGDVIGDSAKY sp P01023	5.75E-08	91620.4	89044.0	96164.6	65211.1	63660.6	72510.7	221191.3	251672.6	248983.6
734	2	836.934	1671.853	13.12	TEHPFTVEEFVLPK sp P01023	2.47E-05	73620.1	59814.9	70423.2	73630.4	86695.9	74106.1	35385.8	27864.1	26772.5
736	4	820.168	3276.642	16.44	VSVQLEASPAFLAVPVEK sp P01023	0.005301	100428.5	130615.9	95452.0	77085.9	94112.1	88652.2	65059.4	70524.2	66244.6
759	2	777.896	1553.777	18.11	VTGEGCVYLQTSLK sp P01023	1.64E-09	135836.7	167032.0	140819.4	166533.9	172999.1	179984.2	28345.6	26275.5	28968.2
767	4	474.270	1893.051	8.37	GHFSISIPVKSDIAPVAR sp P01023	0.000806	21933.8	35227.5	23398.6	19121.2	23513.7	17550.0	42783.0	49399.1	63625.3
777	2	942.528	1883.042	17.95	VSVQLEASPAFLAVPVEK sp P01023	2.34E-09	89716.5	76849.6	72320.0	109517.9	95681.9	115231.2	8815.5	8302.4	7080.7
780	5	982.294	4906.435	16.55	APVGHFYEPQAPSAEVEI sp P01023	0.019983	151482.1	125542.0	144976.0	167083.7	142438.4	153681.1	171649.6	150048.2	166632.2
843	2	567.796	1133.578	11.72	SASNMAIVDK sp P01023	0.000106	21449.8	21398.0	18212.7	25414.4	36872.3	23794.7	7186.9	6587.6	10021.1
888	3	574.651	1720.930	11.25	ALLAYAFALAGNQDKR sp P01023	2.26E-05	46032.8	33587.6	32338.7	40795.3	29521.7	36408.8	11954.9	11267.3	10104.6
899	3	790.728	2369.164	12.16	QQNAQGGFSSTQDTVVA sp P01023	2.39E-07	65925.7	60474.5	60178.4	67827.5	63450.2	66957.0	25734.3	28995.5	28201.8
966	4	814.653	3254.582	16.49	YDVENCLANKVDSLFSFSPS sp P01023	0.001846	86740.0	118267.7	89953.7	71070.6	147756.9	80549.8	38763.5	39444.5	27856.4
977	2	560.822	1119.630	11.28	SIYKPGQTVK sp P01023	2.49E-05	22572.2	22302.6	24230.6	26988.0	26235.5	27175.2	12230.8	10123.3	11224.4
980	3	799.722	2396.145	19.38	ETTFNSLLCPSGGEVSEE sp P01023	7.13E-08	77287.5	68578.7	73527.2	104091.8	84323.9	104931.6	21565.2	18450.9	17758.2

1006	4	619.562	2474.220	17.38	SLFTDLEAENDVLHC VAF	sp P01023	0.049453	45813.7	35253.3	39613.3	38731.8	26555.8	33015.3	29205.3	30282.0	27336.5
1041	3	691.982	2072.925	14.95	MCPQLQQYEMHGPEGLF	sp P01023	0.003909	35969.0	43534.8	43598.9	49014.5	54387.4	52297.7	52451.1	53395.2	54635.3
1069	3	634.294	1899.861	14.90	FSGQLNSHGCFYQQVK	sp P01023	0.004493	43301.0	37808.6	36898.7	39434.9	51164.4	37253.3	24235.4	20734.7	29070.6
1104	2	624.840	1247.665	12.79	LSFYLLIMAK	sp P01023	4.46E-08	22724.5	22102.3	26096.2	31527.6	27794.1	32572.4	7234.1	7991.1	8151.2
1117	3	446.889	1337.645	5.75	NALFCLESAWK	sp P01023	9.96E-06	11882.3	13066.5	14728.0	12314.6	10579.8	11397.7	5618.7	6152.5	5276.8
1125	4	820.414	3277.627	15.44	VSVQLEASPAFLAVPVEK	sp P01023	0.000467	52570.3	54814.3	54357.4	48845.2	45912.7	54583.9	38337.3	41096.5	33683.8
1197	3	515.939	1544.797	13.17	LHVVEEPTHTVTR	sp P01023	0.004916	20549.5	30073.4	22975.0	20798.0	26279.0	22790.4	14757.3	16666.4	15241.4
1205	3	465.565	1393.674	8.02	NEDSLVVFQTDK	sp P01023	5.79E-05	19369.6	20733.5	20005.4	16882.4	18551.1	17369.2	9006.9	8460.0	6188.9
1214	2	566.302	1130.589	7.28	QGIPFFGQVR	sp P01023	4.67E-07	21870.2	24304.6	21640.4	23543.2	21126.2	25749.3	10006.2	10318.4	9437.2
1252	4	508.265	2029.031	4.36	SGGRTEHPFTVEEFVLPK	sp P01023	1.29E-06	7866.0	10068.0	8414.4	5028.0	6868.7	5473.3	44357.8	45260.7	72199.9
1257	3	510.571	1528.692	8.37	TAQEGDHGSHVYTK	sp P01023	0.012117	54392.7	44428.7	52795.5	60031.9	52137.6	58850.0	17590.6	38414.1	19052.0
1305	4	597.824	2387.269	12.89	AYIFIDEAHITQALIWLSQF	sp P01023	8.12E-05	32458.4	26265.4	34711.1	39151.1	26006.8	31303.5	12469.0	12793.0	12386.8
1307	2	849.425	1696.836	15.90	SSSNEEVMFLTVQVK	sp P01023	2.64E-06	40272.0	40711.8	47150.8	57818.6	54381.0	60960.8	28257.9	28242.9	25044.4
1343	3	682.373	2044.096	17.11	LLLQQVSLPELPGEYSMK	sp P01023	7.15E-08	31799.5	27789.0	30507.6	51837.1	44895.0	55081.7	10577.5	10450.8	8735.8
1350	2	504.715	1007.415	3.65	QKDNGCFR	sp P01023	0.001025	13126.8	14038.6	14177.6	16493.7	15105.6	15230.5	11477.6	11368.1	9483.5
1428	3	349.535	1045.583	5.04	FEVQVTPK	sp P01023	3.62E-06	8376.9	8478.9	9151.1	7544.2	8033.3	7920.7	4365.9	4275.7	5004.5
1454	4	597.556	2386.193	12.28	QQNAQGGFSSTQD TVVA	sp P01023	0.005939	24328.2	24587.5	26646.3	24757.4	24602.1	21501.2	16236.2	17255.6	19545.0
1478	2	916.432	1830.849	19.90	QFSFPLSSEPFQGSYK	sp P01023	0.000395	50684.7	42979.6	47112.3	54410.7	48442.0	51632.1	25035.5	29922.3	18820.5
1505	2	809.428	1616.842	14.17	TEVSSNHVLIYLDK	sp P01023	5.03E-05	38964.6	53112.1	34934.2	32079.7	54892.4	31948.2	8099.4	8897.8	11964.1
1521	4	703.368	2809.442	11.29	VVSMDFHPLNELIPLV	sp P01023	2.67E-05	31306.7	31822.4	34455.5	45669.4	37031.2	48232.3	19974.1	20861.2	20057.5
1524	4	814.411	3253.615	19.44	QQNAQGGFSSTQD TVVA	sp P01023	4.18E-05	40948.0	47159.4	37080.8	25114.2	20126.0	21698.6	48228.9	48239.1	42102.0
1526	2	950.445	1898.876	12.95	FSGQLNSHGCFYQQVK	sp P01023	0.000337	33394.6	50273.6	30002.3	47543.1	55439.6	45201.3	16789.8	15539.0	20625.0
1555	4	691.366	2761.436	8.12	VVSMDFHPLNELIPLV	sp P01023	0.000315	36728.4	35914.3	44950.0	39347.0	31140.3	36423.0	17465.9	20886.0	14115.8
1564	3	721.733	2162.178	13.10	VSNQTLSLFFTVLQDVPV	sp P01023	1.06E-06	31602.4	38563.1	32474.4	35898.5	34231.3	37814.6	9492.6	10058.5	7233.2
1572	4	779.160	3112.613	11.44	FRVVSMDENFHPLNELIP	sp P01023	4.31E-05	29857.5	21956.0	27535.0	30588.3	24586.1	31346.3	63606.3	59446.4	53655.4
1589	3	342.488	1024.441	4.15	QKDNGCFR	sp P01023	0.014574	18558.5	14435.7	16122.7	19964.8	15250.1	17529.6	16067.4	17377.6	18567.1
1649	3	451.551	1351.632	6.38	DMYSFLEDMGLK	sp P01023	7.06E-07	12373.8	14362.5	12083.4	13409.8	15731.1	14199.2	4091.1	3287.7	4398.8
1668	3	400.894	1199.661	5.27	LSFYLLIMAK	sp P01023	2.60E-06	13016.8	16005.6	12766.7	10832.9	14328.6	11992.2	3537.5	4052.5	3469.1
1721	3	566.620	1696.839	9.71	SSSNEEVMFLTVQVK	sp P01023	2.86E-05	15581.9	14942.2	18186.2	22901.5	19725.0	22676.3	12140.2	12150.4	12195.9
1783	3	443.593	1327.756	6.00	KLSFYLLIMAK	sp P01023	2.76E-05	12966.3	21263.3	13607.7	12145.7	16368.6	12634.7	3494.4	3157.4	4115.6
1793	2	463.277	924.540	9.50	TGTHGLLVK	sp P01023	3.30E-06	8872.4	9185.5	10059.9	11095.7	10998.1	11325.2	2615.1	2485.9	2751.2
1795	4	675.864	2699.426	14.91	TEHPFTVEEFVLPKFEVQ	sp P01023	4.34E-08	7993.2	7237.7	8200.2	4467.8	3719.3	3587.5	49564.2	64167.9	40021.2
1828	2	402.199	802.384	4.61	QSSEITR	sp P01023	6.04E-06	5484.9	5549.1	5405.9	6787.3	6247.7	6946.6	3519.6	3184.8	2748.0
1833	4	419.230	1672.891	3.47	LHVVEEPTHTVTRK	sp P01023	0.023599	13018.3	11144.5	12861.3	10931.1	13592.1	10701.6	10262.0	9585.0	9804.4

1867	3	459.594	1375.760	3.31	KLSFYLLIMAK	sp P01023	5.27E-06	11344.4	7356.2	10090.7	14099.2	10699.5	13007.7	2312.7	2741.1	2845.1
1904	3	764.335	2289.984	18.11	DLTGFPGLNDQDNEDC	sp P01023	1.79E-06	31043.5	36830.1	31014.1	36684.0	29100.8	34530.4	12007.5	12699.7	10703.4
1949	2	543.794	1085.573	7.77	SASNMAIVDK	sp P01023	5.41E-09	12981.7	12603.8	11975.9	12882.2	12560.2	13107.1	4114.3	3977.1	4039.9
1988	2	765.354	1528.693	14.91	TAQEGDHGSHVYTK	sp P01023	0.014772	49354.1	43519.6	48066.9	59985.6	52601.7	66098.1	34222.1	28470.6	28169.9
1996	6	818.747	4906.436	15.42	APVGHFYEPQAPSAEVEI	sp P01023	0.030029	43475.6	35799.9	41393.8	47073.8	39926.4	44659.6	48082.7	41763.9	44813.7
2021	2	504.223	1006.431	3.36	KKDNGCFR	sp P01023	0.010389	8032.8	7254.6	8435.1	8608.9	7719.6	8339.0	6402.7	6775.0	5151.0
2083	4	897.950	3587.771	19.05	ETTFNSLLCPSGGEVSEE	sp P01023	3.94E-06	106152.9	85165.2	94846.0	107936.0	86672.9	99577.4	34796.1	33732.8	28487.1
2099	3	713.025	2136.052	12.95	HNVIYINGITYTPVSSSTNEK	sp P01023	5.34E-05	25099.9	27608.4	22027.6	25376.1	29926.3	23069.8	8483.6	6620.1	10818.3
2114	5	832.435	4157.141	17.46	DTVIKPLLVEPEGLEKETT	sp P01023	6.57E-06	48048.2	30150.4	43946.1	49560.8	36040.9	46248.6	8532.0	9756.8	8936.4
2196	2	890.509	1779.004	16.01	DTVIKPLLVEPEGLEK	sp P01023	4.65E-05	29719.7	25739.7	25323.0	26403.3	49630.8	29514.0	7284.8	7823.3	5572.3
2233	4	763.650	3050.571	18.29	LLIYAVLPTGDVIGDSAKY	sp P01023	7.50E-05	31415.8	26204.3	27939.4	29060.9	23035.9	29994.9	14347.9	12655.6	10871.4
2236	4	528.276	2109.073	8.11	LHTEAQIQEEGTVVELTG	sp P01023	0.000134	12137.4	16098.1	14187.0	12768.4	12834.9	14374.3	8709.8	8810.0	8698.3
2258	1	803.390	802.383	1.46	QSSEITR	sp P01023	0.000147	12119.9	16268.4	11071.7	12622.8	17159.8	14157.4	5948.4	6132.0	5455.7
2309	5	1038.706	5188.493	16.02	AVDQSVLLMKPDAELSA	sp P01023	1.47E-06	57823.8	45665.1	52746.8	83372.8	103092.6	85170.9	19386.9	16695.0	13201.0
2334	5	858.054	4285.232	6.31	KDTVIKPLLVEPEGLEKET	sp P01023	2.93E-07	42345.6	39302.2	31730.6	43830.4	36904.5	39397.1	8468.7	9510.2	7546.6
2346	3	1196.931	3587.770	17.83	ETTFNSLLCPSGGEVSEE	sp P01023	1.08E-06	146680.6	121053.7	139007.3	148975.4	128909.2	141184.2	43928.0	44113.3	34185.9
2381	6	892.469	5348.768	13.39	DTVIKPLLVEPEGLEKETT	sp P01023	7.57E-07	64660.6	63169.7	60534.6	54472.6	46480.5	52913.2	105472.7	109034.5	100507.6
2534	5	613.929	3064.609	4.54	FRVVSMDENFHPLNELIP	sp P01023	0.000188	18703.8	14872.8	15998.2	12968.0	11299.4	14207.2	24869.7	23953.5	24251.5
2622	1	1099.579	1098.572	5.57	QTVSWAVTPK	sp P01023	0.014245	12277.3	18354.3	15923.6	15991.2	27121.0	18072.1	15046.9	13776.9	13478.8
2745	4	624.831	2495.296	4.25	NEDSLVVFQTDKSIYKPG	sp P01023	7.68E-08	7769.1	9958.8	8957.9	4538.3	5811.3	4982.8	29907.7	30742.9	32121.3
2755	3	383.546	1147.616	6.71	QGIPFFGQVR	sp P01023	0.001314	5913.4	5004.6	5702.8	5662.7	4332.6	5115.7	3514.7	3212.6	2937.3
2907	3	632.024	1893.050	14.70	GHFSISIPVKSDIAPVAR	sp P01023	0.004079	7273.7	13468.4	6588.4	5342.4	8092.4	5580.8	14197.6	16637.4	21897.9
2949	2	1238.116	2474.217	15.22	SLFTDLEAENDVLHCVAF	sp P01023	0.005765	44764.5	32375.8	31741.5	40642.4	24569.3	32682.7	17560.9	20336.2	18455.3
3088	6	543.438	3254.585	8.57	YDVENCLANKVDLSFSPS	sp P01023	3.56E-05	12803.0	14961.6	12824.4	11699.0	16678.6	11860.4	5554.3	6068.4	5372.0
3154	2	707.305	1412.595	14.12	EQAPHICANGR	sp P01023	7.37E-09	15003.8	14213.8	13760.0	18051.2	22069.8	17270.4	3344.7	3262.0	3231.9
3387	3	441.240	1320.699	7.75	PVPGHVTVSICR	sp P01023	7.06E-08	6563.6	8212.2	6923.8	7908.8	9857.2	8174.1	1195.1	1127.4	1321.9
3405	2	339.697	677.379	3.22	TTVMVK	sp P01023	0.010167	5945.8	5046.6	5968.6	7988.3	6487.3	8419.1	3822.0	4016.5	4348.4
3448	4	377.958	1507.802	2.30	TGTHGLLVKQEDMK	sp P01023	0.000176	11461.7	9092.4	11381.6	8801.1	7153.4	9226.2	20374.3	19721.3	22904.7
3629	4	1298.131	5188.494	19.81	AVDQSVLLMKPDAELSA	sp P01023	1.29E-05	37632.0	27797.3	32337.5	57748.8	78032.2	54583.2	12577.9	8934.6	7248.1
3661	4	963.002	3847.977	16.30	KYFPETWIWDLVVVNSA	sp P01023	0.000314	59046.0	54805.5	66971.1	56845.3	54584.4	58682.8	37044.8	40168.2	35724.8
3691	5	1017.128	5080.603	5.72	LLIYAVLPTGDVIGDSAKY	sp P01023	7.94E-05	16412.4	20938.5	14706.3	8927.5	15196.3	14089.0	45411.7	52035.7	43414.5
3880	2	513.228	1024.441	1.38	KKDNGCFR	sp P01023	0.046617	11198.7	8007.4	7543.2	12477.2	9181.7	10020.2	9245.4	8335.0	12021.2
3959	4	1338.199	5348.766	16.23	DTVIKPLLVEPEGLEKETT	sp P01023	2.42E-05	45984.3	50225.5	47327.8	44471.7	38134.3	46629.2	81985.3	79319.5	74923.0
4244	4	859.433	3433.704	12.70	IAQWQSFQLEGGLKQFSI	sp P01023	5.95E-07	9100.9	8178.4	6482.1	5810.8	5021.3	5427.6	22810.1	26739.6	25117.8

4365	4	892.673	3566.664	18.44	HNVIYINGITYTPVSSSTNEK sp P01023	2.04E-06	13780.5	10068.4	13146.3	25857.3	21486.7	31682.1	4702.2	4147.5	3909.7
5294	5	612.328	3056.603	7.02	SGGRTEHPFTVEEFVLPK sp P01023	7.72E-11	781.9	624.2	646.5	229.0	241.7	188.3	20146.9	20400.5	19478.6
5516	6	579.451	3470.659	1.32	HNVIYINGITYTPVSSSTNEK sp P01023	1.89E-06	6946.9	9466.8	7156.4	7212.1	8713.1	8023.9	1962.6	1697.3	2027.5
6297	3	1636.484	4906.431	11.76	APVGHFYEPQAPSAEVEI sp P01023	0.015981	24699.9	21709.3	26873.9	31530.8	25106.7	30270.6	28538.7	27323.8	26718.3
6507	6	896.801	5374.761	5.73	LHVVEEPTHTVTRKYFPE sp P01023	1.90E-08	9786.1	9832.3	9414.3	5192.2	4144.7	5515.8	32046.6	34747.1	33891.2
6798	6	771.933	4625.553	14.09	TEVSSNHVLIYLDKVSNQ sp P01023	5.90E-09	8870.3	8166.0	8394.8	5105.9	4983.2	5143.7	17879.6	20232.6	20233.8
7293	3	611.291	1830.850	15.11	QFSFPLSSEPFQGSYK sp P01023	0.004802	3525.3	3025.4	4242.5	4174.2	3439.1	3588.6	1887.9	2657.0	1697.8
7574	4	1073.347	4289.358	20.97	SSGSLLNNAIKGGVEDEV sp P01023	5.39E-09	7440.2	7748.3	8445.4	4507.3	3592.2	3891.7	37783.5	38319.0	33811.6
7606	2	724.827	1447.639	16.06	DMYSFLEDMGLK sp P01023	2.65E-05	2308.5	1617.8	2195.2	4577.3	3796.2	5067.4	1361.4	1287.3	1123.8
7954	3	885.498	2653.473	12.57	SDIAPVARLLIYAVLPTGD sp P01023	5.66E-08	8791.3	8326.5	9585.0	7102.9	7333.5	7540.6	1915.0	1395.2	1640.5
8299	3	931.157	2790.451	11.90	AFQPPFFVELTMPYSVIRG sp P01023	1.75E-06	3208.0	4283.6	3503.1	4006.0	2955.1	3377.3	10390.2	11221.5	10693.5
8405	3	1145.574	3433.701	21.44	IAQWQSFQLEGGLKQFSI sp P01023	1.24E-05	5865.3	5807.2	3860.5	4202.7	3390.3	3268.1	15789.8	17626.9	15733.5
9134	3	1283.666	3847.975	14.09	KYFPETWIWDLVVVNSA sp P01023	8.00E-05	24307.5	22156.9	26931.0	24699.5	23336.2	25042.4	13977.2	16248.4	13637.4
9781	4	541.552	2162.178	12.44	VSNQTLSLFFTVLQDVPV sp P01023	2.71E-07	2017.0	2431.8	2148.7	2363.2	2328.0	2426.2	612.8	553.5	468.4
9979	4	757.688	3026.722	14.52	VSNQTLSLFFTVLQDVPV sp P01023	2.34E-08	1680.2	1675.0	1890.7	986.2	845.1	969.0	5121.8	5284.7	5452.9
10891	2	1082.095	2162.176	17.90	VSNQTLSLFFTVLQDVPV sp P01023	2.23E-05	4603.5	6091.1	5108.4	5459.7	5300.6	6157.5	1080.0	1480.1	739.7
11196	6	1301.493	7802.913	9.58	APVGHFYEPQAPSAEVEI sp P01023	1.44E-06	8449.5	12359.8	9694.1	4519.1	4858.5	5566.8	37346.8	50196.1	39277.4
11931	4	941.260	3761.009	7.07	TEVSSNHVLIYLDKVSNQ sp P01023	0.006296	5762.6	7424.9	4659.7	3837.2	3085.2	2841.9	3805.8	4168.5	4035.7
12835	5	770.603	3847.978	14.58	KYFPETWIWDLVVVNSA sp P01023	0.001699	6752.2	6351.0	8054.5	6360.4	5839.7	6571.8	4191.0	4551.1	3856.7
13692	5	1087.955	5434.737	15.26	APVGHFYEPQAPSAEVEI sp P01023	1.20E-08	2545.6	2461.5	3065.2	1352.5	1153.6	1312.6	18728.6	17650.3	17854.0
14561	5	858.879	4289.360	16.18	SSGSLLNNAIKGGVEDEV sp P01023	1.77E-08	1862.6	1772.0	2036.4	929.5	724.6	917.2	9748.5	9968.3	9283.9
14593	5	926.118	4625.552	16.15	TEVSSNHVLIYLDKVSNQ sp P01023	3.78E-07	3648.7	3767.1	3465.7	1967.4	2260.4	2082.7	8529.5	8471.4	7515.5
17370	4	948.514	3790.025	6.80	AFQPPFFVELTMPYSVIRG sp P01023	0.00304	3652.0	3622.1	4040.8	2945.0	2292.6	2449.0	3536.3	2896.5	3492.3
19873	4	1359.692	5434.739	6.78	APVGHFYEPQAPSAEVEI sp P01023	1.86E-09	1559.6	1852.6	1516.9	983.7	857.4	816.5	13710.4	14256.0	14052.5
24252	6	715.901	4289.361	15.45	SSGSLLNNAIKGGVEDEV sp P01023	3.46E-09	617.9	546.8	517.0	237.0	223.5	266.4	3502.6	3322.4	3013.8
24315	5	753.209	3761.011	7.73	TEVSSNHVLIYLDKVSNQ sp P01023	0.004577	1312.5	1555.8	1047.6	875.4	672.3	606.5	720.9	856.2	795.4
30917	6	627.842	3761.011	6.90	TEVSSNHVLIYLDKVSNQ sp P01023	0.007649	543.5	689.7	430.1	311.1	346.5	272.9	367.2	475.1	395.6
35516	3	722.061	2163.162	8.32	VSNQTLSLFFTVLQDVPV sp P01023	8.76E-05	254.5	240.5	203.2	403.3	273.8	285.4	75.1	66.7	34.8
273	3	733.383	2197.126	12.43	VPVAVQGEDTVQSLTQG sp P01024	0.001397	149569.1	118739.5	145572.6	181907.8	249680.3	208037.7	105018.5	123630.5	91657.4
283	2	645.308	1288.602	16.11	SGSDEVQVGQQR sp P01024	1.03E-06	72620.6	65407.2	67809.3	106258.6	112654.0	101894.6	69766.7	67120.4	70495.4
313	2	444.746	887.477	4.00	IWDVVEK sp P01024	1.03E-06	33964.1	34706.1	35136.7	41840.4	47709.8	38426.5	38615.7	36017.4	42319.1
347	3	596.662	1786.965	11.52	SGIPIVTSPYQIHFTK sp P01024	0.020642	75869.2	69177.4	88801.4	94294.0	107358.0	94085.3	107469.9	107984.8	101182.2
372	3	397.867	1190.579	7.46	SDDKVTLLEER sp P01024	0.000303	28720.4	24097.3	25457.5	37664.7	40015.1	34680.5	26940.6	24438.2	28349.5
412	2	403.245	804.476	7.59	TFISPIK sp P01024	0.037616	20685.0	23661.0	21161.2	23012.2	25708.7	25604.0	24629.0	24997.8	26081.3

497	3	374.512	1120.514	3.65	LCRDELCR	sp P01024	0.000484	14144.7	12217.4	15782.5	17897.5	14688.6	18040.9	26527.4	25335.4	24353.0
552	2	701.422	1400.830	14.06	SSLSVPYVIVPLK	sp P01024	7.72E-05	57675.3	61182.6	53120.5	80068.8	57117.5	69824.9	31378.8	31446.9	33033.6
601	3	606.304	1815.889	15.11	SNLDEDIIAEENIVSR	sp P01024	0.012798	38990.9	35633.1	41787.5	40819.6	41483.9	43522.8	47257.5	45035.7	43789.6
615	3	620.304	1857.889	4.20	VFLDCCNYITELRR	sp P01024	0.026115	43249.3	43235.4	43721.2	46037.6	59645.0	51427.6	76809.6	67346.8	50539.8
652	2	650.798	1299.581	11.10	ACEPGVDYVYK	sp P01024	0.000147	42247.7	43371.4	35215.1	46713.8	60447.7	51578.0	24822.1	23325.7	27983.5
667	3	624.684	1871.030	11.95	TELRPGETLNVNFLLR	sp P01024	0.000137	45168.7	40664.6	50530.9	61230.4	51202.3	59079.3	26535.8	26204.6	27763.1
714	2	421.772	841.529	6.40	VVLVAVDK	sp P01024	0.003411	14745.4	18433.4	14984.6	17403.8	26601.1	18972.8	11759.5	10844.4	10793.4
779	3	504.613	1510.818	14.27	LVAYYTLIGASGQR	sp P01024	0.000108	20492.9	19318.2	20094.4	28536.4	27175.0	26337.8	20815.9	18147.3	17907.5
798	2	402.727	803.440	5.85	SVQLTEK	sp P01024	0.000306	14475.0	13002.0	14004.0	15800.2	14954.1	17367.1	20376.1	22322.6	22822.6
800	3	384.875	1151.603	6.56	FISLGEACKK	sp P01024	0.042322	14292.1	17619.2	13682.7	16778.5	18275.3	16422.0	19047.7	18059.5	19030.8
810	2	570.275	1138.535	6.36	FYYIYNEK	sp P01024	9.18E-08	24006.4	29880.7	25381.4	36368.2	38699.9	38834.6	8322.5	8671.3	9951.2
834	2	365.691	729.367	3.42	TLDPER	sp P01024	0.040345	15654.4	13425.1	16298.0	18811.6	15129.4	18655.2	21868.1	22794.1	22670.8
836	2	366.201	730.387	5.57	AEDLVGK	sp P01024	0.000682	12766.3	11463.5	12126.5	15612.3	14237.9	16208.0	11558.8	11969.2	12122.0
848	2	542.283	1082.552	7.63	GYTQQLAFR	sp P01024	0.000565	17613.8	15017.6	19077.5	25251.7	30643.6	25268.5	13969.7	15559.5	16281.3
948	3	463.905	1388.692	10.07	KQELSEAEQATR	sp P01024	0.002164	12972.1	12751.4	15406.8	19346.5	18257.5	17851.8	14555.0	14638.3	15696.0
971	2	340.703	679.391	3.36	FLTTAK	sp P01024	0.03696	8796.1	7236.8	9982.0	9937.8	10066.6	10766.0	10484.3	11049.8	9651.2
1001	2	417.249	832.483	3.89	LPYSVVR	sp P01024	6.42E-08	11399.1	13394.5	12038.1	16858.9	22493.6	16471.5	2565.4	2410.2	2661.6
1032	2	756.415	1510.816	17.06	LVAYYTLIGASGQR	sp P01024	0.000162	28636.6	26148.3	27458.9	39897.3	41101.1	37578.0	26737.6	24990.4	21174.6
1074	2	449.743	897.472	2.80	AVLYNYR	sp P01024	9.85E-07	10331.5	12332.2	10507.0	14845.0	20069.3	16034.1	3529.5	4139.7	4179.4
1096	2	555.818	1109.622	12.12	VLLDGVQNPR	sp P01024	0.003915	15122.1	12282.8	13494.4	18677.6	21854.9	18372.7	13456.9	13757.4	14505.9
1112	2	385.233	768.451	1.47	VVPEGIR	sp P01024	1.35E-05	11942.2	11905.8	12589.2	15637.4	16317.6	15788.6	17529.3	16584.6	16486.3
1120	2	596.297	1190.579	5.94	SDDKVTLEER	sp P01024	2.07E-06	16212.9	14550.8	14361.4	24811.4	25694.4	22608.3	13243.6	12534.2	14086.2
1143	2	444.233	886.452	1.43	NEQVEIR	sp P01024	1.51E-09	12165.9	11781.5	11964.0	18828.9	16201.2	16467.3	4172.2	4152.8	3957.4
1147	3	542.967	1625.878	14.46	RIPIEDGSGEVLSR	sp P01024	0.001912	16178.0	20467.2	17442.0	21941.2	21576.0	22485.9	27747.5	24128.5	28930.6
1153	3	320.855	959.542	2.00	SVQLTEKR	sp P01024	0.001223	3003.4	2318.7	2869.6	3339.8	3314.4	4106.9	6976.8	7315.7	5751.4
1154	3	413.579	1237.716	6.75	KVLLDGVQNPR	sp P01024	0.001479	11865.4	12983.1	12975.8	16463.2	15104.3	15853.5	14260.6	13975.6	16465.1
1166	3	552.937	1655.789	6.82	LDKACEPGVDYVYK	sp P01024	0.001814	16411.0	18472.3	15110.5	18675.3	20795.9	22190.2	20062.3	20318.0	21922.4
1180	3	722.673	2164.998	13.21	AYYENSPQQVFSTEFVh	sp P01024	1.20E-07	50657.7	43201.1	49015.6	65673.2	55587.6	63762.8	17084.7	14900.2	14782.6
1193	3	320.519	958.536	3.48	EALKLEEK	sp P01024	8.87E-05	5411.2	4946.3	4912.0	7211.8	6614.9	6687.4	7382.7	7006.7	6731.7
1208	3	815.442	2443.304	12.43	EPGQDLVVLPLSITDFIP	sp P01024	2.09E-06	40971.0	37359.1	44938.3	75055.9	60645.5	68288.6	22491.6	20168.8	17781.0
1224	2	512.761	1023.508	9.44	FISLGEACK	sp P01024	0.006047	9753.7	9074.5	8915.4	12922.0	15253.0	11898.7	9906.6	12461.4	10244.3
1231	2	595.815	1189.616	7.29	DFDFVPPVVR	sp P01024	6.94E-08	18136.3	17027.8	17852.6	30476.1	19843.6	26861.7	3127.6	2905.7	3084.2
1232	3	614.669	1840.986	8.78	VHQYFNVELIQPQAVK	sp P01024	4.78E-07	24952.9	34149.4	27921.9	44607.6	49174.8	37614.7	5647.3	4474.4	4316.1
1262	3	619.291	1854.851	15.64	SEETKENEGFTVTAEGK	sp P01024	1.91E-05	33279.0	38409.0	35731.0	40857.6	31491.2	45961.1	13708.2	15454.2	15380.1

1271	3	404.900	1211.678	11.11	VTIKPAPETEK	sp P01024	9.44E-09	12087.0	10770.2	12477.2	17200.2	15789.6	17107.0	3739.6	3183.5	3416.1
1278	3	540.285	1617.834	13.99	TKKQELSEAEQATR	sp P01024	4.27E-07	13374.4	13165.9	13344.9	16438.6	16003.2	14495.3	27726.1	27641.1	30735.7
1279	3	294.864	881.571	3.21	LKGPLLNK	sp P01024	0.00016	5401.4	6026.6	5529.6	7827.0	8130.7	6879.9	4677.7	4355.4	4902.6
1296	3	314.516	940.525	3.47	EALKLEEK	sp P01024	6.49E-05	4867.0	4474.7	4521.4	6055.4	5661.7	5924.0	6312.3	6159.3	6201.2
1354	2	314.179	626.344	1.33	FLYGK	sp P01024	7.76E-07	5258.7	6032.4	5470.1	7789.5	7362.1	7297.8	2632.1	2873.0	2820.0
1375	4	395.959	1579.806	6.13	AKDQLTCNKFDLK	sp P01024	1.02E-05	13050.5	12647.9	12423.8	16270.3	18270.3	16180.5	8503.2	8567.3	8271.5
1449	2	641.267	1280.519	10.69	CAEENCFIQK	sp P01024	0.000194	13398.9	13210.8	14623.7	16052.3	16363.9	18020.0	22932.7	25446.4	22306.1
1470	2	939.992	1877.970	16.90	EYVLPSFEVIVEPTEK	sp P01024	6.89E-08	48897.4	40680.1	46270.7	77838.8	64402.3	77013.2	8025.9	9418.0	6886.3
1514	5	321.768	1603.803	4.33	FYHPEKEDGKLNK	sp P01024	0.000179	8979.4	8146.0	9367.1	12777.0	10989.6	11113.3	7956.0	7517.4	7540.7
1533	4	368.692	1470.739	1.41	AAVYHHFISDGVV	sp P01024	0.000311	8811.9	11009.1	8697.8	12763.5	11580.4	12076.7	6934.9	7101.1	7686.0
1628	2	685.870	1369.726	15.06	TIYTPGSTVLYR	sp P01024	5.27E-06	20064.0	20219.4	20846.7	32091.8	23618.7	36984.8	4658.6	4455.7	6673.6
1636	4	405.466	1617.835	1.30	TKKQELSEAEQATR	sp P01024	1.87E-06	7374.4	6530.3	7575.2	8886.3	7739.4	8036.9	14077.3	14370.8	15192.1
1664	2	631.305	1260.596	18.06	QELSEAEQATR	sp P01024	1.84E-05	11523.3	11865.9	11428.0	14457.8	15139.4	14049.9	9795.2	8365.9	9045.6
1681	3	795.794	2384.360	11.97	SSLSVPYVIVPLKTGLQEV	sp P01024	3.50E-05	19021.1	15806.3	19166.7	17258.8	13212.7	16044.2	52148.0	65662.6	38325.6
1701	2	531.748	1061.482	15.11	ADIGCTPGSGK	sp P01024	1.02E-05	10986.5	9475.3	11881.0	15772.2	15514.8	16426.4	6358.8	6707.0	6389.8
1766	2	349.158	696.302	3.67	FSCQR	sp P01024	0.004564	13313.5	11869.2	12986.9	18895.0	14026.9	16767.8	19607.4	18155.3	19431.0
1805	3	665.350	1993.030	10.82	KVEGTAFVIFIGIQDGEQR	sp P01024	1.56E-08	32459.9	32404.3	30586.3	44484.5	48325.5	48562.7	16641.8	16227.5	15263.5
1807	3	600.983	1799.927	11.69	VELLHNPAFCSLATTK	sp P01024	6.80E-06	15837.1	20247.1	19295.3	22483.7	29108.4	24199.8	7898.1	8841.5	8469.4
1848	3	386.873	1157.599	3.24	YISKYELDK	sp P01024	6.42E-09	7402.8	6450.2	7756.8	11812.2	10909.2	10992.5	1574.9	1913.1	1728.7
1854	2	673.355	1344.695	16.06	EVVADSVVVDVK	sp P01024	1.69E-08	18757.1	20873.8	19139.2	28731.6	25978.9	26488.4	8055.4	7050.6	7243.1
1858	3	275.497	823.468	4.60	ASHLGLAR	sp P01024	0.009146	7210.6	5740.8	6855.9	9398.7	7325.9	8761.4	10655.7	10891.4	11280.7
1866	3	469.879	1406.616	9.51	VSHSEDDCLAFK	sp P01024	2.63E-08	8753.3	12387.3	9309.4	16971.3	15501.7	16491.5	406.3	602.0	660.5
1880	3	716.364	2146.070	12.69	DAPDHQELNLDVSLQLPES	sp P01024	1.15E-07	30567.9	26105.7	22369.8	39886.8	36278.6	37557.0	6348.4	7585.5	7098.2
1916	2	366.172	730.330	1.33	WEDPGK	sp P01024	4.82E-09	6090.3	5387.4	5793.7	8694.6	8372.4	8194.1	1670.3	1670.3	1462.2
1919	2	851.901	1701.787	14.11	VFLDCCNYITELR	sp P01024	0.004415	21260.5	19665.7	19098.6	30166.7	23413.5	21768.3	14830.1	16728.8	12186.3
1952	4	633.333	2529.302	8.08	TMQALPYSTVGNSSNYLI	sp P01024	0.001196	14584.8	18062.7	14476.0	20610.7	29866.6	17413.5	9682.6	9489.0	6992.8
1968	2	834.373	1666.732	15.06	VYAYYNLEESCTR	sp P01024	7.30E-05	39497.8	49869.6	37335.1	51226.6	54871.4	48608.8	19419.9	21590.0	25828.4
1987	3	719.701	2156.082	19.11	ILLQGTPVAQMTEDAVDA	sp P01024	0.00256	21048.8	13871.0	19797.7	34526.5	28168.2	32737.9	18489.3	17269.9	17495.2
1997	3	868.348	2602.023	19.90	DTWVEHWPEEDECQDEI	sp P01024	2.26E-06	28003.8	30802.3	31605.0	46076.9	51175.5	51169.1	12460.5	14597.8	10885.9
2027	3	717.741	2150.203	18.11	QLYNVEATSYPALLALLQLI	sp P01024	1.86E-07	24963.1	16147.9	25474.5	41827.0	32682.3	40083.8	2606.0	2890.5	2318.0
2122	3	401.546	1201.615	3.68	NTMILEICTR	sp P01024	5.62E-05	5851.9	7375.7	6288.6	6843.5	8932.4	6993.3	2382.5	2488.7	3062.8
2148	3	943.184	2826.531	14.91	QVREPGQDLVVLPLSITTI	sp P01024	0.0025	27299.5	17624.0	18069.2	27301.4	20102.4	28976.5	44477.1	41923.6	37872.4
2202	4	733.618	2930.444	11.50	SEFPESWLWNVEDLKEP	sp P01024	0.000323	129455.7	106206.6	116928.6	160486.1	137314.8	160348.4	96505.4	99571.5	89771.3
2214	3	302.193	903.556	3.36	GVFVLNKK	sp P01024	0.000328	3074.5	2980.9	3073.0	4393.5	4543.0	4234.3	2532.8	2460.8	2415.2



2216	3	286.833	857.478	1.34	IFTVNHK	sp P01024	2.06E-06	3695.5	3477.3	4442.9	5626.4	4859.8	5290.3	1560.5	1817.2	1842.6
2300	4	432.776	1727.075	7.30	VVLVAVDKGVFVLNKK	sp P01024	0.00201	4120.1	6701.0	3801.1	4137.2	6210.2	5266.1	10552.9	10387.3	12566.6
2303	2	480.275	958.535	1.42	EALKLEEK	sp P01024	0.001367	4828.9	4850.1	4223.8	5989.1	6652.9	5766.2	6586.3	6102.9	6129.8
2360	4	485.248	1936.962	8.57	SGQSEDRQPVPQGQMTI	sp P01024	0.00381	9491.3	8416.0	9582.3	12213.1	9995.4	10584.5	9450.6	10257.4	9992.4
2403	3	753.042	2256.103	12.78	VQLSNDFDEYIMAIEQTIK	sp P01024	0.000761	11369.1	9266.2	10784.2	25786.9	18137.2	20499.1	13291.4	12216.8	10924.0
2413	5	676.537	3377.650	12.00	LESEETMVAEHDAQGD	sp P01024	0.000751	18862.2	20089.4	17543.3	29088.7	27449.6	26385.8	25979.7	24420.6	22467.4
2559	3	662.663	1984.966	12.75	SGQSEDRQPVPQGQMTI	sp P01024	0.000602	10583.2	13472.8	11131.6	18194.4	21623.8	19070.8	15974.1	15190.2	16282.5
2605	3	832.055	2493.144	22.38	DYAGVFS DAGLFTTSSSC	sp P01024	1.73E-05	26416.4	20859.4	22665.8	35973.0	26741.4	33844.0	12227.8	12170.6	11944.5
2655	4	401.957	1603.801	3.86	FYHPEKEDGKLNK	sp P01024	3.74E-06	7096.0	6371.0	7406.9	9384.9	9744.2	9263.1	5255.8	5598.4	5273.7
2698	3	860.109	2577.305	15.17	TMQALPYSTVGNSSNYLI	sp P01024	0.004173	11800.8	8036.3	7646.3	19165.6	15681.0	22777.2	8698.3	11358.5	7979.2
2872	4	497.504	1985.986	6.88	KVFLDCCNYITELRR	sp P01024	0.0006	5599.4	6847.1	6169.0	6644.0	8027.3	6673.8	11730.6	9418.1	11538.9
2911	3	797.415	2389.223	18.91	EVVADSVWVDVKDSCVG	sp P01024	0.001446	13869.3	11652.3	15399.9	18410.5	14344.3	16186.1	23596.6	26542.5	20500.9
2926	3	556.585	1666.733	9.58	VYAYYNLEESCTR	sp P01024	6.28E-07	12680.1	13653.6	11833.5	17137.5	16669.7	15050.6	6974.7	6171.5	6310.6
3040	2	601.814	1201.614	6.24	NTMILEICTR	sp P01024	0.000271	6749.0	8885.9	7283.0	8102.4	11351.1	8685.4	3373.8	3176.0	4019.5
3072	3	626.997	1877.970	11.73	EYVLPSEFIVIEPTEK	sp P01024	3.29E-07	11717.8	9986.9	11222.6	16911.1	15144.5	17045.4	1955.1	1500.0	1201.1
3105	4	641.830	2563.290	11.96	QKPDGVFQEDAPVIHQEI	sp P01024	5.79E-05	8180.5	11045.7	8242.4	15077.3	16498.7	13834.0	5658.2	5005.5	3884.7
3109	2	439.763	877.511	2.25	LMNIFLK	sp P01024	3.74E-06	2109.3	2166.1	2147.2	4169.5	5477.4	4409.8	1222.2	1168.8	900.8
3252	2	668.370	1334.726	16.06	APSTWLTAYVVK	sp P01024	8.82E-08	8282.0	6214.9	6469.9	12965.7	9552.8	11503.5	1235.3	1057.9	959.4
3382	3	568.270	1701.788	5.41	VFLDCCNYITELR	sp P01024	0.001679	6287.9	5711.9	5857.8	8406.1	6784.0	6646.4	4504.1	4683.3	3788.8
3403	2	568.294	1134.574	14.06	QPSSAFAAFVK	sp P01024	0.02777	4650.9	3366.3	4256.0	6209.5	4757.8	7050.4	3332.6	4235.4	3889.5
3530	4	1030.771	4119.053	14.43	NNNEKDMALTAFLVLSLQI	sp P01024	0.000318	23824.9	17512.6	23104.3	24751.1	28167.4	23676.4	35673.9	32972.4	33191.7
3556	4	387.704	1546.785	5.74	SDDKVTLEERLDK	sp P01024	2.09E-08	2196.1	2035.2	1975.7	1764.1	2006.4	1657.9	6764.1	6586.2	6559.1
3702	2	437.225	872.436	4.64	QLANGVDR	sp P01024	1.01E-07	3018.1	3015.0	3227.5	5064.0	4360.0	5196.1	593.9	656.5	451.9
3711	3	497.927	1490.758	8.39	GQGTLSSVVTMYHAK	sp P01024	1.04E-06	3375.4	4165.1	3367.9	5375.6	5978.2	5980.9	2000.8	1986.6	2027.1
3845	2	436.734	871.453	4.41	QLANGVDR	sp P01024	2.97E-07	3308.2	3111.2	3470.3	4542.4	4482.7	4168.2	1606.2	1592.4	1458.8
4097	3	893.758	2678.251	11.33	YGGGGYGSTQATFMVFC	sp P01024	5.99E-07	10283.6	11056.2	11447.1	24392.0	18269.1	22666.9	5313.2	4308.0	4402.8
4468	2	695.353	1388.691	13.12	KQELSEAEQATR	sp P01024	9.16E-05	3619.8	4011.1	3934.5	6059.0	7185.2	5891.8	3786.3	3472.1	3703.4
4992	4	831.459	3321.807	12.64	QLYNVEATSYALLALLQLI	sp P01024	0.001919	7193.0	7424.7	7539.2	7928.7	8586.7	10056.7	6761.4	5457.0	5516.8
5064	3	1108.275	3321.805	24.44	QLYNVEATSYALLALLQLI	sp P01024	0.002818	11484.5	10584.5	11812.5	12380.3	12211.0	15326.1	10197.7	8463.8	8257.1
5468	4	744.636	2974.513	15.52	AEDLVGKSLYVSATVILHf	sp P01024	2.03E-06	5034.5	4003.2	5062.1	5066.5	4193.0	5357.3	14077.3	14062.0	12521.9
5475	4	1009.538	4034.124	14.96	WEDPGKQLYNVEATSYA	sp P01024	1.35E-06	10654.9	8726.6	10297.6	7486.4	7047.9	7466.3	16126.8	16312.7	15035.1
5784	4	707.641	2826.533	12.18	QVREPGQDLVVLPLSITTI	sp P01024	0.001032	4619.8	3161.7	3344.1	5311.8	3821.0	5063.9	7438.3	7656.5	6883.3
5969	3	334.499	1000.475	3.34	NRWEDPGK	sp P01024	1.16E-07	1308.7	1238.0	1439.4	1727.4	1596.6	1727.5	644.8	611.0	636.7
6115	2	1222.658	2443.302	16.17	EPGQDLVVLPLSITTFDFIP	sp P01024	7.13E-06	9338.8	8663.9	10574.5	19856.3	15181.2	17939.1	4733.6	4634.4	3384.3

6307	3	641.997	1922.970	10.50	DSITTWEILAVSMSDKK	sp P01024	1.78E-06	4881.6	3586.4	4258.4	9265.9	8256.9	8472.5	1771.6	1156.0	1384.8
6910	3	783.744	2348.209	8.40	NNNEKDMALTAFLVLSLQI	sp P01024	1.66E-08	5554.2	4610.6	5125.8	11431.2	10987.2	12167.1	907.7	1255.1	1044.9
7620	2	1129.057	2256.100	16.95	VQLSNDFDEYIMAIEQTIK	sp P01024	0.001364	4600.5	3443.8	4430.6	11172.3	7809.8	8750.2	4719.7	4505.4	3846.3
7700	4	313.152	1248.580	3.41	FYHPEKEDGK	sp P01024	3.07E-05	2568.6	2203.1	2486.2	3834.9	2880.6	3931.5	839.3	815.8	886.7
8820	2	1076.108	2150.201	21.90	QLYNVEATSYALLALLQLI	sp P01024	1.93E-06	6861.1	4205.7	7747.8	12800.7	8789.1	12180.9	896.5	923.9	725.6
9215	4	1007.246	4024.954	8.73	AYYENSPQQVFSTEFEVt	sp P01024	0.000932	6406.0	6562.3	8269.5	6977.7	6617.0	7793.9	7504.8	7831.1	8745.9
9342	3	739.750	2216.227	21.11	VFSLAVNLIADSQVLCGA	sp P01024	3.30E-07	5418.8	4840.8	5676.0	12230.7	10865.0	10944.0	1151.9	896.4	633.7
9909	3	917.112	2748.313	15.17	YFKPGMPFDLMVFTNPI	sp P01024	3.32E-06	5529.4	4364.1	4454.5	11678.1	14188.2	12400.7	5169.6	4544.8	4412.7
11070	5	824.818	4119.055	6.51	NNNEKDMALTAFLVLSLQI	sp P01024	9.67E-07	2024.6	1731.6	1951.1	2581.1	2366.9	2425.2	4001.8	3598.8	3430.9
11484	3	955.181	2862.522	11.59	WEDPGKQLYNVEATSYA	sp P01024	1.14E-09	3738.3	3684.7	3747.4	6022.6	6563.8	6039.6	1082.8	1238.0	1197.2
12272	3	824.738	2471.191	20.11	GICVADPFVETVMQDFFI	sp P01024	7.38E-08	2030.9	1928.7	2501.9	5099.5	4796.0	5906.3	551.8	469.0	425.7
13552	3	1000.505	2998.492	11.59	EYVLPSEVIVEPTEKIFY	sp P01024	1.29E-05	2631.2	1645.3	2596.2	1916.4	1560.8	1906.5	5236.5	5299.0	5021.0
14888	3	1094.887	3281.638	22.96	QDSLSSQNQLGVLPLSW	sp P01024	0.000106	3149.5	2950.7	3012.8	8674.4	7489.8	6887.7	1106.0	2281.2	1683.3
16170	3	937.509	2809.505	15.91	QVREPGQDLVVLPLSITTI	sp P01024	4.63E-07	1108.8	1106.2	1142.3	1890.3	1832.1	1685.0	4218.4	3557.7	4012.8
16370	4	716.638	2862.522	7.79	WEDPGKQLYNVEATSYA	sp P01024	8.80E-10	1392.5	1401.6	1367.3	2321.1	2342.5	2257.7	312.5	345.8	361.7
16781	3	720.646	2158.916	10.94	QCQDLGAFTESMVFVFC	sp P01024	0.002006	1100.3	757.8	1361.5	1990.2	1722.1	1980.0	774.5	846.6	733.3
17486	5	807.832	4034.126	6.78	WEDPGKQLYNVEATSYA	sp P01024	6.67E-06	1493.8	1210.0	1405.3	1058.4	946.2	1024.2	2224.1	2197.4	2006.5
24450	4	985.034	3936.108	16.05	EPGQDLVVLPLSITDFIP	sp P01024	0.01031	1550.4	1603.7	1660.3	1643.1	1342.1	1537.9	1448.6	1347.2	1135.5
25219	3	753.369	2257.086	12.78	VQLSNDFDEYIMAIEQTIK	sp P01024	0.008401	348.6	287.0	334.2	721.6	662.4	630.1	498.5	396.1	277.7
29328	4	880.954	3519.789	15.65	DMALTAFLVLSLQEAKDIC	sp P01024	0.007729	450.2	531.0	709.4	1245.3	863.5	1015.1	349.4	581.3	275.0
10288	3	682.349	2044.025	10.75	SYFPESWLWEVHLVPR	sp P01031	0.025497	4637.2	3672.1	4919.2	5847.0	4718.1	6041.2	5873.1	6091.5	6083.9
15331	3	947.141	2838.400	13.04	YGGGFYSTQDTINAIEGL	sp P01031	7.28E-05	1919.0	1362.8	1581.6	2968.0	2779.6	3324.7	1264.1	981.0	1128.2
20678	3	705.692	2114.055	12.16	YIYPLDSLWIEYWPR	sp P01031	9.96E-05	665.4	621.7	780.9	1188.7	1185.0	1255.4	407.4	534.5	329.4
22106	3	872.179	2613.514	16.17	GLLVGEILSAVLSQEGINII	sp P01031	0.009449	799.0	777.2	1085.3	1372.6	1375.7	1447.9	828.6	1021.0	919.3
24458	5	856.024	4275.083	1.99	GSAEAEIAMSVPVYFVt	sp P01031	0.000559	933.7	879.2	809.3	1179.1	1274.6	1270.4	1739.0	1468.3	1225.1
29129	3	840.453	2518.336	15.38	VDDGVASFVNLNPSGVT	sp P01031	2.61E-07	695.3	714.7	609.5	1405.6	1362.3	1438.2	338.7	349.2	266.2
489	2	626.299	1250.584	15.06	TVGSDTFYSFK	sp P01042	0.007536	40396.9	48634.0	41782.4	47470.1	48703.2	45517.8	55694.4	57502.7	72902.8
623	3	838.078	2511.213	19.91	IASFSQNCDIYPGKDFVQI	sp P01042	0.002753	92777.8	117151.1	85909.1	107999.2	103375.7	100865.7	157298.7	163969.3	131009.0
668	3	505.558	1513.653	9.40	TWQDCEYKDAAK	sp P01042	0.017559	20036.6	29697.6	27950.2	24576.7	23230.6	25574.8	33971.9	39140.3	34705.0
713	2	538.739	1075.462	14.02	EGDCPVQSGK	sp P01042	0.016331	25551.5	21018.0	24890.5	26851.8	23569.1	29941.8	36991.3	40467.9	35348.0
741	2	515.773	1029.531	6.94	YFIDFVAR	sp P01042	4.01E-05	15617.5	15832.6	18580.4	18847.5	17326.0	19386.8	26998.4	27160.4	25823.0
761	2	502.289	1002.563	8.49	QVVAGLNFR	sp P01042	0.034526	15426.2	17744.7	15279.7	12803.0	19505.9	14623.6	19705.6	22700.0	25809.4
1485	2	583.280	1164.546	16.06	AATGECTATVGK	sp P01042	0.003873	13251.3	11546.1	14150.3	16659.0	13588.7	17074.0	10492.1	10526.0	11498.9
1749	2	692.336	1382.657	16.06	ENFLFLTPDCK	sp P01042	1.46E-05	16114.8	10907.9	14553.6	23665.5	23366.3	22751.3	8203.5	8516.5	7678.9

2226	3	537.256	1608.747	8.73	YEIKEGDCPVQSGK	sp P01042	3.09E-05	8383.0	9040.8	7451.3	8409.5	8515.4	6917.9	15852.2	16257.9	15874.2
2823	2	350.722	699.429	1.46	VQVVAGK	sp P01042	0.02762	6455.8	5606.2	7425.3	6891.0	5740.1	7155.5	10432.4	9778.1	10508.6
2874	3	386.882	1157.625	2.10	KYFIDFVAR	sp P01042	0.014978	2317.6	2777.0	2557.7	2603.8	3483.2	2489.2	3558.9	3833.3	5174.7
2989	3	814.374	2440.100	16.11	SLWNGDTGECTDNAYIDI	sp P01042	0.001263	18694.5	14597.1	16241.2	20463.2	17061.0	17389.1	22491.6	19576.0	23246.9
3386	4	628.811	2511.215	11.90	IASFSQNCDIYPGKDFVQI	sp P01042	0.007532	8594.9	11163.4	8133.3	10702.0	9766.1	9725.3	14971.8	15651.0	11697.7
3738	3	272.505	814.492	4.15	AVDAALKK	sp P01042	0.029063	2962.6	2401.2	3081.4	3659.5	2738.5	3158.6	4419.1	4231.2	5235.0
4748	4	591.558	2362.203	12.54	KLQSLDCNAEVVVPW	sp P01042	0.000112	2179.0	3144.3	2902.8	2736.8	2873.5	2209.0	7048.0	6639.5	9641.0
7402	3	300.822	899.445	1.30	CPGRPWK	sp P01042	0.005902	1535.0	1251.7	1505.6	1414.0	1093.1	1383.8	2442.4	2595.5	2540.9
266	2	695.311	1388.607	14.11	SSEDPNEDIVER	sp P01591	0.016262	101308.2	140875.8	99598.9	95682.3	96601.1	94321.1	135552.3	125785.0	148637.8
467	3	427.882	1280.624	7.79	FVYHLSDLCK	sp P01591	0.014793	30259.8	33132.6	27385.3	26731.5	30634.0	24045.1	34019.0	30321.7	34455.4
746	2	828.920	1655.825	16.90	CYTAVVPLVYGGETK	sp P01591	0.009354	59050.2	55281.7	68731.3	49252.0	62271.3	52740.8	71622.6	73884.5	68033.2
946	2	400.748	799.482	1.45	IVLVDNK	sp P01591	0.005765	11232.6	17155.3	11525.9	11584.8	11704.6	10736.7	7313.7	7610.8	9475.7
1549	4	353.187	1408.719	6.06	FVYHLSDLCKK	sp P01591	0.001274	6878.8	8605.7	7200.0	5481.1	7118.1	6419.2	9358.6	10641.3	11274.6
2066	2	791.843	1581.672	11.32	MVETALTPDACYPD	sp P01591	0.017912	17771.1	21897.6	21351.6	20759.0	18370.9	20856.4	26409.8	32133.4	26331.6
2336	2	820.407	1638.799	14.90	CYTAVVPLVYGGETK	sp P01591	0.002061	18475.0	16508.4	19277.1	19033.3	15929.3	16450.1	21967.6	24379.0	22737.3
2186	2	525.257	1048.499	4.06	ITCQGDSLR	sp P01714	0.00396	6792.2	6909.6	6474.9	6672.1	4817.5	5637.0	6977.8	6211.2	6731.2
9005	3	636.329	1905.966	11.54	ALEWLALIYWDDDKR	sp P01817	0.000211	4251.2	2995.8	3437.8	3319.9	2603.3	3057.5	1575.7	1568.5	1322.9
30432	3	705.405	2113.194	11.14	LDIQGTGQLLFSVVINQLF	sp P01833	3.03E-05	56.7	23.3	97.5	122.4	110.6	87.3	1233.7	1100.2	1430.4
54	2	435.183	868.351	5.54	SFNRGEC	sp P01834	0.006454	114163.8	104808.3	129491.5	102796.9	84974.0	112780.9	159031.3	163395.2	150243.1
233	3	712.662	2134.965	20.11	VDNALQSGNSQESVTEQ	sp P01834	4.76E-05	193575.1	226953.9	180758.6	196682.6	221982.0	190365.6	82596.2	96570.5	74943.2
234	4	536.026	2140.077	14.70	HKVYACEVTHQGLSSPV	sp P01834	3.62E-06	120022.2	118367.0	108194.4	110524.6	115131.3	104817.0	175303.2	172711.1	167425.6
608	2	751.884	1501.753	16.06	DSTYLSSTLTLSK	sp P01834	5.76E-08	119728.5	112637.4	121686.4	137241.9	145661.0	138270.2	54702.3	47400.6	44840.8
1055	2	1068.489	2134.964	19.90	VDNALQSGNSQESVTEQ	sp P01834	0.000393	78444.8	101876.0	62205.5	77857.2	110025.4	74778.2	28774.5	34881.3	28976.8
2569	2	435.675	869.335	1.46	SFNRGEC	sp P01834	0.001035	4528.3	4163.0	4893.6	4681.2	3745.4	4171.8	5497.5	5666.6	5700.6
6497	4	1041.009	4160.007	14.38	VQWKVDNALQSGNSQE	sp P01834	8.35E-10	1981.3	2157.9	2104.9	1050.0	1303.2	1644.7	102982.0	98524.5	78862.4
8308	2	435.675	869.335	1.46	SFNRGEC	sp P01834	0.001588	952.1	904.0	1045.7	809.6	767.1	883.5	1065.4	1309.4	1277.1
13199	4	931.983	3723.901	11.82	TVAAPSVFIFPPSDEQLK	sp P01834	5.54E-08	8725.8	6942.1	8196.2	7355.7	4924.0	6346.5	61155.4	58626.9	56887.2
326	3	559.940	1676.798	14.06	FNWYVDGVEVHNAK	sp P01857	0.002222	86955.8	89440.0	83022.7	60851.7	78089.5	62669.6	44020.5	44527.0	60304.7
428	3	713.682	2138.024	20.90	TPEVTCVVVDVSHEDPE	sp P01857	1.34E-05	159247.4	155321.7	177716.1	113453.6	123262.7	114166.3	66886.9	72416.3	81203.1
513	2	593.828	1185.641	16.06	GPSVFPLAPSSK	sp P01857	0.023927	59646.6	64488.2	62000.6	42925.5	33942.6	53282.1	46536.6	44954.9	54554.9
935	2	937.466	1872.917	14.90	TTPPVLDSDGSFFLYSK	sp P01857	0.008322	130907.6	84358.1	111195.8	86147.8	69914.0	91341.6	64507.4	59930.6	57398.6
1063	4	711.871	2843.455	14.78	THTCPPCPAPELLGGPS	sp P01857	7.26E-05	156076.7	132716.8	151937.2	99348.4	87822.1	100913.9	83221.5	84529.0	78336.6
1339	5	1343.470	6712.315	14.08	DYFPEPVTVSWNSGALT	sp P01857	0.002428	223058.4	169016.8	209021.9	211277.5	236451.2	214047.7	127876.8	162331.7	126009.8
1914	5	667.735	3333.641	7.35	SCDKTHTCPPCPAPELLC	sp P01857	0.002161	66570.3	68835.1	68952.5	52416.3	66578.4	50045.1	86096.1	77705.6	78567.1

4022	6	1119.727	6712.315	9.84	DYFPEPVTVSWNSGALT:sp P01857	0.001655	42589.3	33126.1	41122.4	38062.1	46843.7	41074.3	25419.3	28443.9	25272.9
8191	6	1336.836	8014.972	10.63	STSGGTAALGCLVKDYFF sp P01857	3.97E-08	5364.8	4729.6	7006.6	3447.2	3243.4	4392.2	60417.9	55862.8	56459.0
1190	4	554.551	2214.174	12.54	VVSVLTVVHQDWLNGKE sp P01859	0.017326	24507.0	25013.9	26424.2	18620.7	27527.9	17882.5	25644.8	26986.2	26014.0
1309	2	412.748	823.482	5.52	GLPAPIEK sp P01859	0.047624	10300.8	11222.0	11026.1	8840.1	11150.1	8426.9	9828.6	8842.2	10132.8
1314	3	598.669	1792.986	11.89	VVSVLTVVHQDWLNGK sp P01859	0.000203	29268.3	33799.8	24253.7	19344.7	16792.7	18698.9	13706.5	15864.6	13783.6
2409	3	598.997	1793.970	11.85	VVSVLTVVHQDWLNGK sp P01859	0.000193	25118.2	18367.0	23610.5	21297.2	17753.0	21526.4	9406.4	10065.2	7197.9
3819	3	970.140	2907.398	20.78	CCVECPCPAPPVAGPS' sp P01859	0.017773	48575.9	42757.1	40224.6	38720.8	31852.5	39775.1	38478.2	40644.5	31946.9
4219	4	554.304	2213.187	4.12	VVSVLTVVHQDWLNGKE sp P01859	2.43E-07	3661.4	3168.2	3925.2	2062.6	1803.2	1526.1	7378.7	7350.6	7067.0
3076	3	452.551	1354.632	10.85	TPLGDTTHTCPR sp P01860	1.58E-05	5040.0	4891.2	4673.8	2909.9	2421.5	3067.9	4621.1	4650.8	4106.6
3273	2	593.753	1185.492	13.02	SCDTPPPCPR sp P01860	6.75E-07	15565.2	14435.6	13980.9	9311.4	9213.0	9074.3	16370.6	15499.6	14054.5
11230	5	1341.064	6700.284	7.14	DYFPEPVTVSWNSGALT:sp P01860	0.000814	16235.9	10765.8	14327.3	9392.2	8382.1	8434.8	8019.2	8187.5	7149.6
1453	3	981.825	2942.453	20.78	YGPPCPCPAPEFLGGP:sp P01861	0.00028	149968.8	124585.6	135172.9	89079.1	68258.6	85954.2	142236.7	142224.4	124135.9
2287	2	951.469	1900.923	14.90	TTPVLDSGDSFFLYSR sp P01861	0.001344	45676.1	33100.4	41127.5	27694.6	24367.6	25684.6	29196.5	26240.7	24984.9
2356	2	415.735	829.456	2.24	GLPSSIEK sp P01861	4.82E-05	7658.4	9566.9	7501.9	4321.9	5290.3	4610.6	8051.5	7778.4	7895.2
3135	4	1264.894	5055.545	14.51	DYFPEPVTVSWNSGALT:sp P01861	0.00187	67597.5	60340.5	71480.1	58661.9	40792.5	50353.3	43111.3	47238.5	39784.5
4696	4	736.621	2942.455	12.98	YGPPCPCPAPEFLGGP:sp P01861	8.39E-05	23554.0	20088.6	21726.0	14061.8	11076.2	13072.5	27897.9	25612.0	23469.2
171	3	572.960	1715.858	14.90	FTCTVHTDLPSPLK sp P01871	0.007228	253836.8	281329.4	245407.2	207048.0	253816.2	198301.0	200459.7	181416.8	232463.7
216	2	625.322	1248.630	16.06	LICQATGFSPR sp P01871	0.033649	109828.4	131196.6	129926.3	95305.8	130828.3	97236.0	117416.2	119223.5	122112.1
223	2	515.297	1028.579	10.87	QIQVSWLR sp P01871	0.005851	77751.4	101564.6	97213.6	68981.3	83046.0	70956.8	72033.1	82932.9	69625.0
252	2	809.408	1616.802	19.90	QVGSGVTTDQVQAEAK sp P01871	0.000627	163535.1	224313.0	161291.2	136281.4	168191.5	134776.0	86298.5	82612.6	98125.1
272	2	455.215	908.415	6.94	DGFFGNPR sp P01871	0.00245	50337.1	59566.7	56041.1	38659.1	46816.1	38199.9	52028.0	50450.8	65666.8
307	2	386.720	771.425	1.43	EQLNLR sp P01871	0.000545	28033.0	30382.5	29477.6	25274.9	27956.7	23764.8	25027.4	21993.8	23532.4
375	4	931.692	3722.737	20.69	YFAHSILTVEEEWNTGE sp P01871	1.76E-06	406571.2	327774.2	417019.5	371312.7	331075.0	348221.3	140584.6	131374.6	111615.3
451	4	444.259	1773.009	2.15	GVALHRPDVYLLPPAR sp P01871	0.011526	104472.1	139641.0	93614.0	76673.8	93443.2	75180.8	85685.2	91050.2	110305.5
533	2	450.769	899.524	7.31	VSVFVPPR sp P01871	2.46E-05	54633.7	56747.5	53950.7	41545.3	42916.6	41704.5	43529.7	42045.1	48359.7
565	2	431.766	861.518	7.32	VTSTLTIK sp P01871	8.09E-05	33335.1	35592.0	31013.4	24135.4	30270.9	24933.5	17189.0	17063.4	16914.8
584	5	842.606	4207.995	11.94	YFAHSILTVEEEWNTGE sp P01871	4.68E-10	140827.2	141872.0	124651.7	62704.4	61686.1	67888.3	348254.1	336367.9	341527.3
657	5	546.479	2727.360	8.43	YAATSQVLLPSKDVMMQG' sp P01871	0.023522	50135.2	67794.8	58534.7	40243.4	51996.2	36762.1	58784.1	58398.9	73977.6
663	2	428.233	854.451	7.48	GQPLSPEK sp P01871	0.022391	35556.3	30769.5	36961.9	28259.0	23616.7	29636.8	27437.6	27944.5	29588.5
679	3	539.941	1616.803	11.83	QVGSGVTTDQVQAEAK sp P01871	0.000265	34981.8	45685.2	35259.3	28342.2	29453.8	28469.4	18573.0	18349.2	20988.9
879	2	639.359	1276.703	16.11	YAATSQVLLPSK sp P01871	1.73E-09	38173.5	40504.2	40073.5	30339.7	31041.3	28380.7	16670.5	16534.3	16705.6
934	4	694.847	2775.359	16.97	YAATSQVLLPSKDVMMQG' sp P01871	0.009148	39575.2	51768.2	48740.4	38474.3	40745.3	47203.3	57306.2	58057.6	72560.8
1005	2	819.470	1636.926	11.95	VFAIPPSFASIFLTK sp P01871	0.001274	147759.6	121943.9	123640.0	129536.6	103046.1	127086.8	88474.7	86411.0	74071.7
1228	3	490.562	1468.663	9.85	DVMQGTDEHVVCK sp P01871	0.005038	23214.6	20083.7	23325.4	15866.5	12590.4	16584.9	10698.6	11086.6	11143.6

1432	2	406.735	811.456	2.03	QTISRPK	sp P01871	0.001285	8672.0	8094.7	9557.2	7776.2	7378.0	7719.7	7713.5	7434.6	7958.1
1460	3	518.264	1551.770	9.29	YVTSAPMPEPQAPGR	sp P01871	7.72E-05	26174.7	30009.8	24472.7	16872.3	20397.5	17998.8	14101.5	15757.6	15540.5
1475	2	693.922	1385.830	13.06	NVPLPVIAELPPK	sp P01871	0.000288	193482.3	174820.1	184747.6	136330.0	123903.1	144094.5	156556.7	157604.9	136359.0
1480	3	417.217	1248.631	7.09	LICQATGFSPR	sp P01871	0.01017	9045.9	10275.4	10243.8	7637.8	9297.2	7750.0	8927.3	9612.2	9810.4
1886	2	506.784	1011.553	6.87	QIQVSWLR	sp P01871	0.000315	7885.9	6936.8	7593.3	6292.2	5964.7	7273.4	8572.3	8420.5	7850.2
2063	3	546.649	1636.926	16.11	VFAIPPSFASIFLTK	sp P01871	0.000994	35186.3	28251.0	31260.4	30852.3	23106.2	29274.2	19948.4	20594.1	17435.3
2160	2	441.715	881.415	6.07	ESGPTTYK	sp P01871	6.67E-05	38686.2	35279.2	42243.4	34953.2	30010.4	31608.5	23885.5	23855.1	23122.4
2192	3	644.661	1930.962	12.63	EGKQVGSVTTDQVQAE	sp P01871	2.47E-07	5773.9	3727.6	4179.2	2758.0	3538.0	2188.9	35863.1	39890.7	34920.4
2307	3	915.114	2742.319	22.38	ESATITCLVTGFSPADVF	sp P01871	0.000941	28523.7	27329.7	32655.6	33152.9	28140.8	32236.4	36738.1	35872.7	33669.1
2474	2	800.895	1599.776	17.90	QVGSVTTDQVQAEAK	sp P01871	7.52E-05	19348.1	22802.7	24744.3	17522.9	21778.9	17025.4	8850.0	9296.1	11314.5
2785	4	1053.006	4207.995	16.89	YFAHSILTVEEEWNTGE	sp P01871	2.83E-08	35754.4	33127.0	28645.2	11363.6	12659.5	14296.0	86930.3	84544.8	82745.9
3864	3	462.951	1385.831	11.32	NVPLPVIAELPPK	sp P01871	0.001136	30914.8	26482.8	30038.9	21836.2	18947.2	22813.4	23224.8	25233.1	21963.0
7487	2	808.846	1615.678	15.06	ESDWLGQSMFTCR	sp P01871	5.67E-05	1932.9	1378.0	1785.9	4949.6	4981.9	5737.3	763.2	1181.1	1100.5
21239	4	686.587	2742.319	14.66	ESATITCLVTGFSPADVF	sp P01871	0.027259	792.4	657.6	991.3	896.2	688.2	836.1	1065.8	1107.5	914.9
26043	4	1070.820	4279.253	3.19	VFAIPPSFASIFLTKSTKLT	sp P01871	3.39E-05	3547.4	3148.6	4701.8	1447.7	1269.3	1274.8	3781.5	5155.6	5035.9
40762	3	298.820	893.437	2.14	VQHPNGNK	sp P01871	0.0296	816.8	159.5	147.4	789.6	801.4	623.5	192.6	298.7	168.7
64	2	918.479	1834.944	19.95	QEPSQGTTFVAVTSILR	sp P01876	0.048493	992146.2	797441.5	840272.8	785830.3	662289.0	730525.1	652990.7	731096.2	741465.5
100	3	865.048	2592.123	23.17	DLCGCYSVSSVLPGCAEI	sp P01876	0.003918	691078.6	434988.0	542777.5	436966.4	409886.4	476480.1	310175.4	309768.7	251444.4
211	4	573.040	2288.129	6.81	KGDTFSCMVGHEALPLAI	sp P01876	0.020965	187507.3	213123.6	168709.1	156868.4	145718.5	161836.3	183506.7	167698.7	207123.2
213	4	879.405	3513.592	18.44	SAVQGPPERDLCGCYSV	sp P01876	3.81E-08	291903.0	259863.9	305992.5	145334.9	168646.7	141576.3	819593.0	839972.2	775769.4
227	4	585.041	2336.134	11.81	KGDTFSCMVGHEALPLAI	sp P01876	0.028579	118864.4	133963.5	112113.2	127506.4	135515.3	122511.9	148614.1	141605.1	133274.5
282	3	514.248	1539.724	13.88	DASGVFTWTPSSGK	sp P01876	0.03871	74567.5	77743.7	72656.0	60800.8	66261.6	55856.3	95999.4	81860.5	68207.1
376	3	1056.844	3167.512	18.90	NFPPSQDASGDLYTTSSC	sp P01876	0.008971	#####	#####	#####	1168159.0	1032524.9	#####	#####	1358872.0	#####
510	5	458.633	2288.131	4.10	KGDTFSCMVGHEALPLAI	sp P01876	0.000736	53776.4	51303.0	52903.9	46498.2	44838.7	46644.8	55052.0	55143.0	60468.1
526	4	1195.348	4777.361	18.11	VFPLSLCSTQPDGNVIAI	sp P01876	0.037543	649930.7	630640.9	808220.2	736672.2	591418.6	720532.6	804813.1	892859.7	715925.3
541	2	909.966	1817.918	17.90	QEPSQGTTFVAVTSILR	sp P01876	0.032087	133800.4	134169.0	143416.2	151792.7	146264.2	145849.7	124100.5	143073.8	135827.9
712	4	792.885	3167.512	17.18	NFPPSQDASGDLYTTSSC	sp P01876	0.009971	471924.4	423435.3	444605.0	396243.6	336051.2	345681.1	447324.4	489670.0	418341.5
1725	4	649.038	2592.124	12.43	DLCGCYSVSSVLPGCAEI	sp P01876	0.001052	28435.7	20175.1	27847.8	19640.0	20951.5	19213.1	11878.5	14664.9	13658.2
1789	5	956.480	4777.362	19.42	VFPLSLCSTQPDGNVIAI	sp P01876	0.03415	148072.5	140433.9	179674.9	166196.2	129219.2	156595.5	158623.1	176815.8	146433.0
3053	4	691.615	2762.429	12.09	QEPSQGTTFVAVTSILRV	sp P01876	4.84E-06	26519.3	23994.8	27594.2	21315.5	18145.8	21088.3	11188.1	11257.9	10558.2
3411	4	1195.347	4777.357	18.55	VFPLSLCSTQPDGNVIAI	sp P01876	0.001067	94628.0	77025.3	97803.3	92545.2	78850.0	86590.6	66699.1	65659.5	64077.9
7126	3	879.118	2634.333	11.90	QEPSQGTTFVAVTSILRV	sp P01876	0.005485	10895.6	7373.4	10220.6	7687.9	6192.1	6908.5	4888.6	5541.1	3397.9
24274	6	797.234	4777.361	16.23	VFPLSLCSTQPDGNVIAI	sp P01876	0.002406	2720.7	2063.7	2928.0	2586.3	2207.3	2711.9	2155.7	2039.9	2195.2
30171	3	1593.459	4777.355	16.28	VFPLSLCSTQPDGNVIAI	sp P01876	0.003823	5227.6	4350.9	5442.1	5183.5	5064.6	5682.3	3694.9	3337.0	2931.5

309	2	756.853	1511.691	18.95	DASGATFTWTPSSGK	sp P01877	7.79E-06	114961.6	120323.1	126510.8	120778.2	112101.7	128751.8	188132.1	167775.6	170906.6
829	4	988.192	3948.737	12.37	DLCGCYSVSSVLPGCAQI	sp P01877	2.32E-05	126257.5	97489.6	114014.8	99475.1	87150.5	92713.2	48474.1	46590.7	46804.7
1958	5	975.048	4870.205	11.09	SAVQGPPELDLCGCYSV	sp P01877	3.48E-07	38453.1	37737.0	33995.7	21580.1	28309.9	21099.3	113082.8	121610.2	117840.7
1515	2	480.270	958.526	7.89	TAVNALWGK	sp P02042	0.040196	6530.4	7253.4	7203.3	7386.7	11159.2	7754.9	9659.4	8696.7	9955.1
457	4	605.566	2418.233	11.32	EVDLKDYEDQQKQLEQV	sp P02671	6.13E-06	45494.5	65502.7	50292.4	31062.4	32849.7	35699.9	107527.4	125884.4	107176.1
464	2	514.757	1027.499	7.05	NSLFEYQK	sp P02671	0.004584	27175.6	28831.5	34721.1	22245.2	26991.8	27581.3	38549.8	35936.2	39847.1
504	2	786.843	1571.672	18.90	GGSTSYGTGSETESPR	sp P02671	0.000648	96864.0	86817.5	90138.8	86260.3	69464.4	82365.4	62941.2	59677.0	58392.0
529	2	760.871	1519.728	15.11	GLIDEVNQDFTNR	sp P02671	0.000289	69642.9	59278.3	59831.3	50877.1	41789.1	44039.9	51240.9	53665.3	55249.5
538	2	505.760	1009.506	11.87	VTSGSTTTTR	sp P02671	0.004198	23892.8	22302.1	26433.1	20133.6	16005.6	19215.3	29208.9	46180.6	32779.0
697	2	464.778	927.541	7.07	QLEQVIAK	sp P02671	3.21E-05	21591.1	24013.2	21601.3	18747.0	20287.1	16839.0	10303.7	10936.2	10705.3
709	3	507.584	1519.729	10.13	GLIDEVNQDFTNR	sp P02671	0.001687	27914.8	22310.0	23572.6	20602.7	16766.4	17909.7	21885.2	25919.8	23893.5
726	3	501.253	1500.738	3.41	MELERPGNEITR	sp P02671	1.43E-05	19361.2	20147.1	19865.5	18842.7	23140.0	18866.3	34531.6	32858.5	36333.6
842	3	577.588	1729.742	10.18	GDFSSANNRDNTYNR	sp P02671	2.88E-09	20120.3	18291.6	20136.9	14213.8	14853.9	13625.2	52667.8	49867.9	53454.8
914	3	369.561	1105.663	7.23	VQHIQLLQK	sp P02671	0.001853	20281.6	24156.3	17683.7	14309.3	20805.3	15363.7	10180.5	9862.8	9929.4
1072	3	503.908	1508.703	7.40	EVDLKDYEDQQK	sp P02671	0.009663	23952.3	30193.0	26339.0	24831.1	30748.4	22016.1	17643.2	16730.2	19833.2
1129	4	669.521	2674.053	6.79	HQSACKDSDWPFCSDEI	sp P02671	8.25E-06	43675.4	33178.8	43098.7	25711.8	21019.1	26542.5	67625.6	70372.5	65745.8
1450	2	570.781	1139.547	15.06	GSESGIFTNTK	sp P02671	0.001963	13287.7	16433.1	12242.4	9706.5	11729.6	9869.8	17185.0	19717.2	17269.7
1908	3	807.084	2418.230	16.88	EVDLKDYEDQQKQLEQV	sp P02671	0.000162	14478.6	24470.6	16536.7	9738.4	12555.5	12732.1	35070.0	41883.7	31407.1
2019	3	485.252	1452.734	6.01	MELERPGNEITR	sp P02671	5.82E-06	11660.2	10410.1	11069.1	7906.9	8048.6	8130.7	13665.3	13375.3	13443.3
2033	3	481.268	1440.782	8.10	MKPVPDLVPGNFK	sp P02671	0.000652	14200.7	17811.0	13859.2	11327.2	13361.2	10644.0	21247.4	22346.1	29391.4
2293	3	655.289	1962.844	19.11	NPSSAGSWNSGSSGPGI	sp P02671	2.90E-05	16037.8	20664.4	19384.5	14890.0	15018.3	13548.0	8849.9	9641.8	9498.8
2616	4	472.476	1885.874	3.89	HRHPDEAAFFDTASTGK	sp P02671	2.37E-05	9030.4	10700.1	10429.9	7148.9	6017.8	6962.3	13742.1	15552.4	15985.1
2676	4	880.134	3516.505	11.51	GGSTSYGTGSETESPRN	sp P02671	1.95E-05	25014.6	19372.6	26280.6	15043.7	17677.4	15542.8	35772.2	41754.8	40481.7
2894	4	345.943	1379.743	6.44	TVIGPDGHKEVTK	sp P02671	0.001661	4479.4	3976.1	4747.9	3049.0	3049.1	3344.9	2941.1	2918.2	3163.2
2966	2	484.216	966.417	7.63	GDFSSANNR	sp P02671	0.000287	21422.7	19232.9	22824.2	18085.9	15380.6	16723.5	16053.1	15951.4	14700.9
3061	2	368.648	735.281	5.58	CPSGCR	sp P02671	0.012928	14360.9	12203.1	15375.1	11090.0	9935.5	12007.8	13991.9	14755.3	11189.2
3137	2	982.377	1962.740	15.90	DSDWPFCSDEDWNYK	sp P02671	4.04E-06	44159.7	39722.0	47303.7	37548.2	31868.9	34896.2	19154.4	18149.6	16821.5
3495	2	595.776	1189.538	14.02	QFTSSTSYNR	sp P02671	0.013569	6085.2	6987.2	6570.9	5010.9	4260.7	4752.6	5699.4	5120.3	4608.5
3516	4	497.258	1985.004	3.19	NNKDSHSLTTNIMEILR	sp P02671	0.04713	4454.7	7952.3	4770.4	4380.3	9056.2	4033.7	11235.0	11927.6	9736.5
3518	3	625.991	1874.952	7.29	GLIDEVNQDFTNRINK	sp P02671	6.95E-10	1193.4	1061.6	1219.9	772.6	903.5	730.6	26053.3	21333.4	20822.8
3636	2	391.676	781.336	3.14	DNTYNR	sp P02671	0.00629	10086.0	8254.2	9908.9	7920.7	6657.5	7895.1	4965.4	7993.4	5094.1
3669	3	367.549	1099.626	2.05	RLEVDIDIK	sp P02671	0.012686	2716.0	4958.4	3100.9	3122.7	5353.6	2666.4	1532.1	1562.8	2310.7
3833	3	655.254	1962.741	11.78	DSDWPFCSDEDWNYK	sp P02671	1.27E-05	16225.6	15521.8	18681.4	13100.2	10855.6	13810.5	7480.2	7335.6	6844.9
5093	3	577.916	1730.726	10.27	GDFSSANNRDNTYNR	sp P02671	0.000305	4784.1	4089.7	4464.5	4024.0	3551.7	4176.6	4741.1	4947.6	5261.0

6797	3	894.344	2680.009	17.64	DSDWPFCSDEDWNYKCI	sp P02671	1.11E-07	5288.5	4045.1	4358.1	1851.3	1098.4	1457.5	22011.3	23156.0	19198.1
12487	3	1043.474	3127.400	15.90	EVVTSSEDCPEAMDL	sp P02671	0.036221	4608.0	4111.3	3985.3	4071.1	3717.5	4408.4	2738.0	2334.6	2286.5
226	2	422.749	843.483	2.43	SILENLR	sp P02675	8.53E-05	38908.1	47692.9	40391.2	30688.4	30602.0	26288.0	51976.0	53164.5	62626.3
292	2	654.813	1307.612	17.06	QGFGNVATNTDGGK	sp P02675	0.000325	97233.5	89078.2	97368.6	72352.5	60255.3	73280.5	96306.8	85156.7	94099.8
304	5	817.610	4083.015	7.25	KAPDAGGCLHADPDLGV	sp P02675	0.003639	232715.1	233735.1	282582.9	194554.1	192135.9	219343.5	265691.5	218599.0	213615.1
386	2	620.264	1238.513	11.98	EDGGGWYNR	sp P02675	0.000693	57997.1	69438.7	57875.4	42350.2	41919.9	40400.2	73278.2	70267.2	57982.2
424	2	490.726	979.437	13.02	QDGSVDFGR	sp P02675	0.000383	30801.3	38702.7	34226.2	24346.4	22128.4	23367.1	35855.7	36010.4	45284.5
595	3	850.079	2547.216	20.91	TPCTVSCNIPVVSQKECE	sp P02675	1.20E-05	75043.9	104950.0	75762.1	48419.9	45106.3	57911.4	179848.0	167057.4	179916.2
598	2	359.217	716.419	2.46	ISQLTR	sp P02675	8.32E-05	16795.1	14959.2	16295.3	11813.4	11507.6	12978.6	17166.1	19301.7	19378.5
665	2	893.400	1784.785	13.90	NYCGLPGEYWLGNDK	sp P02675	0.00262	103946.1	89503.1	85529.5	71287.3	67748.5	80635.0	61169.8	68902.1	64906.1
711	4	592.798	2367.163	12.60	AHYGGFTVQNEANKYQI	sp P02675	4.53E-05	39717.2	44260.0	39538.1	30100.7	37933.9	30227.4	77540.7	69518.2	81541.8
782	4	969.970	3875.850	6.62	DNENVVNEYSSELEKHQI	sp P02675	4.22E-06	99172.4	88686.0	105347.7	76510.5	63100.2	70627.6	156510.0	147242.8	151202.7
991	3	512.580	1534.719	6.03	AHYGGFTVQNEANK	sp P02675	0.000175	27122.6	29840.4	25582.9	16656.7	18905.9	17887.0	25471.4	24191.2	24253.7
1088	2	426.235	850.456	4.21	YQISVNK	sp P02675	0.002823	11403.2	11259.9	9325.0	7739.7	8003.7	6998.0	9991.5	8191.7	8199.2
1201	2	516.786	1031.558	4.13	IRPFFPQQ	sp P02675	0.000804	27739.0	28113.0	27181.3	17448.7	21848.7	18282.9	28222.2	25029.4	30582.1
1256	3	651.007	1949.999	18.90	EEAPSLRPAPPPISGGGY	sp P02675	7.53E-05	41422.5	54789.0	50552.4	30431.8	28455.2	28689.6	30983.5	28947.0	32825.8
1395	5	847.221	4231.068	1.46	QVKDNENVVNEYSSELEI	sp P02675	2.33E-07	59984.7	57696.5	58933.7	33379.8	30912.3	35146.9	104615.5	93704.2	87616.3
1418	4	669.835	2675.310	11.87	TPCTVSCNIPVVSQKECE	sp P02675	2.37E-06	25805.4	30788.6	23606.5	15212.1	19208.2	15758.9	61974.5	57117.4	75242.5
1429	3	828.739	2483.195	14.64	NYCGLPGEYWLGNDKIS	sp P02675	5.97E-06	20982.7	20740.0	25034.3	12757.9	12334.7	17136.8	54753.0	53859.2	51137.8
1559	4	559.556	2234.195	6.55	KREEAPSLRPAPPPISGG	sp P02675	0.007233	24170.8	34109.8	23446.4	14775.3	20831.7	15903.0	25001.3	24390.8	30370.0
1675	3	709.701	2126.080	11.24	HQLYIDETVNSNIPTNLR	sp P02675	6.30E-06	30331.5	27654.2	32911.9	22837.2	23977.1	23746.1	15168.6	16813.8	17284.3
1772	2	354.672	707.329	1.45	WDPYK	sp P02675	2.99E-06	4415.4	4865.5	4520.6	3254.5	3551.6	2963.9	6334.6	6375.5	6357.6
1822	4	585.049	2336.168	12.57	KGGETSEMYLIQPDSSVK	sp P02675	0.031306	18928.0	22091.4	17364.0	15368.8	21782.2	13377.6	24787.3	23756.2	26425.5
1932	3	370.185	1107.532	7.54	QDGSVDFGRK	sp P02675	2.21E-07	3990.5	3793.8	4476.6	3065.7	2771.5	2905.0	6850.7	7017.7	7115.7
2123	4	597.050	2384.173	12.80	KGGETSEMYLIQPDSSVK	sp P02675	0.000145	11541.6	15440.5	11642.9	12604.8	13379.7	12332.0	23782.2	21343.6	26863.1
2275	5	447.846	2234.194	1.43	KREEAPSLRPAPPPISGG	sp P02675	1.46E-06	11569.6	12339.4	10740.0	7591.2	7398.6	6780.7	13640.8	13754.7	14951.5
2408	3	359.519	1075.535	1.37	ECEEIIRK	sp P02675	0.008533	3712.8	3516.4	3954.2	2849.3	2839.1	3069.7	3463.1	3219.4	2983.6
2602	3	513.897	1538.670	8.93	LESDVSAQMEYCR	sp P02675	0.004055	9707.4	9954.3	9358.1	6175.1	6840.0	6517.8	9178.4	8308.5	7182.4
2644	4	1021.760	4083.012	10.61	KAPDAGGCLHADPDLGV	sp P02675	0.008707	32722.4	37120.7	40803.0	27536.7	30062.3	33533.1	35685.4	32762.2	29344.7
2689	2	490.705	979.395	10.13	CHAANPNGR	sp P02675	1.49E-05	6862.9	5083.4	6361.2	6108.0	5368.2	6083.1	10483.3	10098.2	10583.5
2815	2	834.862	1667.710	14.06	YYWGGQYTWDMAK	sp P02675	0.000363	9276.6	9100.3	10602.1	10886.0	10189.0	9479.9	14916.6	17415.0	12450.9
4253	3	515.571	1543.691	3.20	HGTDDGVVWMNWK	sp P02675	0.000375	2971.9	3113.9	3160.2	3514.6	2993.0	2819.4	5092.3	4408.6	4497.6
4805	4	944.206	3772.795	15.96	QGFGNVATNTDGGKNYCC	sp P02675	3.39E-07	2539.3	2841.6	2326.1	916.5	380.6	898.8	37580.0	35973.0	30298.7
4807	4	555.534	2218.106	10.09	MGPTELLIEMEDWKGDK	sp P02675	1.63E-07	3357.9	2908.9	2982.6	3340.5	2783.9	3118.7	9686.7	11645.5	10810.6

4953	2	490.213	978.411	9.87	CHAANPNGR	sp P02675	0.000225	6532.1	5686.2	6830.2	4648.2	3756.9	4211.1	7257.2	7367.1	8004.4
6022	3	1025.802	3074.385	20.52	QGFGNVATNTDGKNYCC	sp P02675	9.56E-08	5522.7	4821.6	5386.4	2282.5	1731.7	2573.7	23630.6	25311.2	21201.3
8565	2	419.696	837.378	1.36	GSWYSMR	sp P02675	0.00094	1838.9	1475.1	1829.2	1353.5	989.6	1257.8	2188.5	2302.2	2338.9
12723	4	792.628	3166.484	15.27	NSVDELNNNVEAVSQTS	sp P02675	0.002558	2613.7	2563.3	2467.9	2352.9	1847.7	2664.4	2755.1	2596.7	2455.3
14365	2	490.704	979.394	8.66	CHAANPNGR	sp P02675	0.000526	3046.6	2576.5	3213.1	2628.8	1883.3	2535.6	5117.0	5123.9	4454.6
260	5	743.355	3711.740	5.60	VAQLEAQCQEPCKDTVQ	sp P02679	0.000233	219510.3	241050.9	193657.0	150670.5	131176.1	162597.5	256383.1	238172.1	280237.1
296	3	736.353	2206.036	14.90	EGFGHLSPTGTTEFWLGI	sp P02679	0.000276	161323.8	137146.1	136351.7	113979.5	98140.1	104294.9	129487.6	141259.3	146772.1
382	3	806.366	2416.077	18.11	FGSYCPTTCGIADFLSTY	sp P02679	0.00861	149517.5	128276.0	124981.2	118109.4	95194.3	126963.8	177014.3	165618.1	140229.8
393	3	431.924	1292.751	13.06	QSGLYFIKPLK	sp P02679	0.003982	39462.7	52250.1	36082.4	27370.9	28077.4	27657.7	38839.8	41136.0	47088.3
430	4	692.839	2767.328	11.59	VAQLEAQCQEPCKDTVQ	sp P02679	0.001335	108204.0	89999.1	98008.2	103747.7	98222.8	95890.1	73705.8	68855.3	78656.8
443	3	497.920	1490.740	13.06	YEASILTHDSSIR	sp P02679	0.006965	46179.7	54982.8	42787.9	38624.8	50029.2	40291.9	32123.8	27575.2	34765.1
445	3	345.514	1033.521	8.79	VGPEADKYR	sp P02679	7.65E-06	28947.1	25436.5	26724.9	22416.0	19980.3	22405.6	34712.2	34439.7	34417.3
473	3	561.659	1681.955	10.63	IHLISTQSAIPYALR	sp P02679	0.018645	51041.5	62748.2	57552.1	44846.1	62678.8	46034.9	41123.3	37795.5	32666.0
496	4	387.209	1544.809	7.58	LTIGEGQQQHHLGGAK	sp P02679	1.30E-05	58622.9	52641.2	55738.2	48756.4	43032.7	41081.1	54639.3	52874.9	51932.6
508	2	757.368	1512.722	15.11	YLQEIYNSNNQK	sp P02679	0.002135	59801.9	79517.2	66908.6	43263.1	59643.7	48968.2	80819.6	85325.8	94648.0
555	2	559.268	1116.522	7.24	VELEDWNGR	sp P02679	0.007753	36278.6	36963.1	34470.1	25825.0	32016.2	25396.3	28305.4	26044.6	30767.4
605	2	597.747	1193.480	6.57	DNCCILDER	sp P02679	0.000211	33017.4	34460.0	31648.5	22465.5	23472.4	19996.9	39116.6	39236.9	52906.4
633	2	426.225	850.435	1.33	NWIIQYK	sp P02679	0.000746	19900.1	21618.8	18983.6	15832.4	17624.5	15855.3	21734.1	21229.4	24251.7
881	4	618.822	2471.257	4.34	AIQLTYNPDESSKPNMID	sp P02679	0.003267	45170.9	59170.7	42329.9	35921.6	39332.6	29066.2	67567.9	58097.7	56739.2
911	3	362.842	1085.505	4.12	TSTADYAMFK	sp P02679	0.000173	12163.3	13533.5	12973.4	8862.0	8793.2	8583.7	12924.4	11726.7	11006.3
959	2	638.870	1275.725	7.89	QSGLYFIKPLK	sp P02679	0.006588	19107.6	19769.2	23681.7	18235.8	16993.7	19276.9	27584.3	25874.2	22216.4
1213	4	503.979	2011.888	4.38	CHAGHLNGVYYQGGTYS	sp P02679	0.00443	19631.9	24952.8	20670.3	15942.8	15303.0	15603.7	20396.3	23793.0	30723.1
1290	3	505.248	1512.722	5.63	YLQEIYNSNNQK	sp P02679	2.06E-06	13973.8	15012.3	16188.8	10716.3	10004.3	10947.0	18853.8	18881.3	19411.0
1396	3	336.851	1007.531	7.39	LDGSVDFKK	sp P02679	0.000439	6302.6	5878.4	5530.7	4677.8	4790.3	4644.1	6325.4	6594.7	6911.9
1528	2	559.761	1117.507	6.36	VELEDWNGR	sp P02679	0.000313	24274.3	23823.4	22574.1	19597.5	23075.2	19286.3	15213.9	12188.2	13845.1
1588	2	567.762	1133.509	8.55	TSTADYAMFK	sp P02679	0.000484	9208.2	8902.0	9436.0	8861.6	11488.9	9193.9	13572.3	12741.1	14534.8
1798	3	840.761	2519.262	18.17	AIQLTYNPDESSKPNMID	sp P02679	0.000359	28601.1	24490.9	29149.9	27564.7	35280.8	28171.1	58360.1	54370.3	47145.1
1829	3	515.943	1544.808	7.45	LTIGEGQQQHHLGGAK	sp P02679	0.035905	6537.1	5511.7	7192.2	4584.6	4840.1	6472.8	7555.8	6239.4	8180.5
1884	2	482.214	962.414	6.37	DCQDIANK	sp P02679	0.002376	20311.6	17188.4	20490.0	16775.6	13542.6	16633.2	10870.8	10846.8	11482.4
1931	2	1209.045	2416.074	19.90	FGSYCPTTCGIADFLSTY	sp P02679	0.030078	54242.0	44872.3	46926.9	41578.3	35731.8	45433.7	69420.1	60449.3	48968.6
1941	3	888.082	2661.223	16.94	ANQQFLVYCEIDGSGNG	sp P02679	0.00546	36242.1	33755.4	35078.7	35395.3	29170.9	36771.5	34384.4	33165.0	30233.2
2250	2	440.724	879.434	5.93	LDGSVDFK	sp P02679	0.000136	6244.2	6956.0	6365.6	2966.5	3797.8	3190.8	4935.0	5171.3	4523.6
2945	2	517.768	1033.521	6.46	VGPEADKYR	sp P02679	1.61E-05	6362.1	6093.7	5989.8	5503.5	5465.5	5569.5	7138.9	7026.4	7491.6
3573	4	696.124	2780.465	11.70	IHLISTQSAIPYALRVELE	sp P02679	2.70E-08	5891.4	5113.4	4667.6	2644.7	2400.2	1804.8	27723.9	26840.2	27115.0



3894	2	757.861	1513.707	14.06	YLQEIYNSNNQK	sp P02679	0.000425	6262.1	6782.6	6920.6	5521.5	7487.0	6710.0	10187.3	8442.2	9084.9
4512	4	696.370	2781.450	7.68	IHLISTQSAIPYALRVELEI	sp P02679	2.90E-08	3871.4	3549.8	4216.8	2654.7	2070.5	2071.1	15722.5	17486.0	16295.7
7541	4	592.300	2365.172	7.47	MLEEIMKYEASILTHDSSI	sp P02679	1.01E-07	1750.2	1584.9	1903.8	1758.5	1437.9	1372.1	7171.3	7325.7	6179.3
520	3	604.636	1810.887	14.64	IVLGQEQDSYGGKFDR	sp P02743	0.000305	47082.4	45984.8	42817.3	45503.9	47409.4	47299.2	58829.3	52939.1	54589.1
682	2	382.727	763.439	3.27	VVFVPR	sp P02743	0.002626	12507.5	12887.1	12939.2	13219.1	11447.1	12015.4	14979.4	16005.5	17290.9
1066	2	578.805	1155.595	14.02	VEYSLYIGR	sp P02743	0.034335	16117.6	19416.5	17430.0	20049.4	21360.6	19290.4	12240.2	12033.3	18003.9
1275	2	643.899	1285.783	10.96	GYVIKPLVWV	sp P02743	0.003842	19368.8	17223.5	19243.1	24793.4	21072.3	24857.0	17333.7	17213.3	14401.0
1348	2	703.840	1405.665	16.06	AYSLSYNTQGR	sp P02743	5.08E-05	22143.4	28538.4	29583.2	29812.0	32136.3	31982.1	13135.2	15302.3	13245.0
1444	2	406.201	810.388	3.64	AYSDLR	sp P02743	0.000438	8383.6	7352.9	7639.0	8778.7	8784.1	8048.3	6558.1	6251.2	6233.4
2688	2	621.878	1241.741	9.24	LSPIYNLVPVK	sp P02748	0.000106	5906.3	5237.0	5561.7	9615.4	8223.0	8205.5	10235.8	11186.7	9273.4
5564	2	728.361	1454.707	10.54	AIEDYINEFSVR	sp P02748	0.001819	3416.5	2368.4	3198.8	5094.0	3740.4	4764.2	6450.8	6637.6	5243.6
6255	3	930.485	2788.432	21.99	GTVIDVDFVNWASSIND	sp P02748	0.001767	4582.2	3787.1	5707.1	10632.3	8340.3	8562.5	7077.1	8117.3	7076.5
19937	4	698.116	2788.434	16.27	GTVIDVDFVNWASSIND	sp P02748	0.014429	642.6	462.0	698.2	1269.2	815.1	1113.5	930.2	983.4	873.0
1370	2	495.281	988.547	6.50	VAAGAFQGLR	sp P02750	0.001009	7054.2	7451.6	6016.6	8062.2	10712.9	7796.1	12373.9	12198.4	15812.4
1407	2	358.719	715.424	1.47	VLDLTR	sp P02750	0.000283	3739.2	4571.4	3863.9	3916.3	5726.6	4189.7	8589.3	8565.3	10722.0
1494	2	406.736	811.457	1.43	GPLQLER	sp P02750	1.60E-06	4320.5	5109.3	4645.8	4817.1	5905.2	5388.3	10878.5	10870.3	11129.3
1617	3	384.876	1151.606	7.54	ALGHLDLSGNR	sp P02750	0.002238	4236.2	5579.5	4643.4	4953.0	6984.7	5188.1	9176.6	8603.0	11903.2
1635	4	740.903	2959.581	15.78	LQELHLSSNGLESLSPEF	sp P02750	0.00136	24859.1	17620.0	23546.4	29062.0	21510.0	30832.3	48052.9	47069.7	42469.5
2095	2	450.780	899.546	7.56	GQTLAVAK	sp P02750	0.01911	4755.9	5560.2	4623.4	5106.9	6930.6	4979.7	6985.9	7446.0	7911.4
2296	2	485.257	968.499	3.27	YLFLNGNK	sp P02750	2.27E-05	3313.9	3576.1	3540.4	4161.3	4816.2	4829.5	8541.2	9068.9	6814.6
2642	3	632.009	1893.004	11.51	ENQLEVLEVSWLHGLK	sp P02750	3.23E-05	8621.2	8322.7	9951.2	14006.5	13648.3	13956.6	6906.5	6572.7	5462.8
3855	3	829.042	2484.106	20.11	DGFDISGNPWICDQNLSC	sp P02750	0.019813	11570.7	9033.4	10213.5	13352.5	13207.5	14192.9	10344.4	10729.8	10491.1
4822	3	679.702	2036.083	13.16	TLDLGENQLETLPDCLR	sp P02750	0.000155	16884.1	15126.0	17580.8	20111.7	15001.5	19072.3	30342.0	30746.3	29151.1
8338	3	780.779	2339.314	17.38	NALTGLPPGLFQASATLD	sp P02750	1.12E-06	3728.1	3535.1	3795.8	7453.4	7027.1	8181.6	2335.3	1861.1	1850.6
9616	3	270.821	809.442	2.22	LHLEGNK	sp P02750	0.001762	793.3	683.4	823.7	924.7	784.6	889.6	1545.9	1538.5	1561.3
10841	4	1054.583	4214.303	9.77	NALTGLPPGLFQASATLD	sp P02750	1.23E-05	4502.5	3058.4	4198.5	6029.7	4528.4	5584.8	11554.5	13876.4	12744.7
15088	2	1243.059	2484.103	17.90	DGFDISGNPWICDQNLSC	sp P02750	0.001832	3646.1	2868.1	2805.7	4344.5	3857.0	5019.1	2860.8	2745.0	2750.2
3070	3	551.267	1650.779	7.22	LLCQCLGFGSGHFR	sp P02751	0.000169	9909.0	13032.8	9590.3	6516.3	6582.9	5887.3	5702.1	5292.1	6963.1
7288	3	643.021	1926.041	13.67	FLATTPNSLLVSWQPPR	sp P02751	0.000583	6063.6	5254.3	6483.0	4137.5	2918.5	4384.7	3256.0	3429.4	2561.1
8798	3	355.518	1063.532	7.28	VGDTYERPK	sp P02751	0.00217	2048.7	1805.7	2102.1	1451.7	1258.5	1404.4	960.1	1001.8	1073.9
12687	3	642.689	1925.045	15.11	VTWAPPSIDLTNFLVR	sp P02751	8.09E-06	3023.9	2986.7	3210.0	2360.0	1765.1	2068.6	1470.9	1378.6	1265.4
17112	3	842.128	2523.361	22.38	DLEVVAATPTSLISWDAL	sp P02751	1.28E-06	2768.2	2153.9	2656.0	2489.1	1882.8	2397.0	501.8	474.6	327.9
3951	2	599.818	1197.621	6.65	YWGVASFQK	sp P02753	0.000439	4366.6	3774.7	3901.7	5418.6	4568.4	5220.0	3190.6	3022.1	3445.5
5078	3	434.892	1301.653	6.69	QRQEELCLAR	sp P02753	2.81E-05	2046.0	2064.7	2155.0	2266.8	2569.3	2356.9	1338.7	1452.9	1311.3

456	2	607.341	1212.667	14.06	TVAACNLPIVR	sp P02760	0.004089	46023.3	45725.6	40103.3	57503.5	73256.6	54922.3	70980.7	59031.9	83899.4
574	2	704.886	1407.758	13.62	AFIQLWAFDAVK	sp P02760	0.001086	45516.5	41663.5	45915.7	65116.8	50949.0	70966.4	67925.0	73803.2	70745.9
650	2	854.879	1707.743	15.95	EYCGVPGDGDEELLR	sp P02760	2.64E-05	73294.9	80763.2	81124.7	101047.5	109226.8	106284.5	129023.0	117419.8	123605.0
2665	2	483.711	965.407	7.27	ECLQTCR	sp P02760	0.012549	6259.2	5323.1	6491.5	11156.8	7976.9	10187.9	5159.6	5805.4	5139.5
3082	2	836.367	1670.719	12.00	CVLFPYGGCQGNNGNK	sp P02760	4.29E-05	12044.5	14176.0	12087.0	18957.8	20481.0	20238.1	12581.9	13183.1	9906.6
3543	3	470.260	1407.758	8.05	AFIQLWAFDAVK	sp P02760	0.009431	3783.4	2974.6	3438.8	4699.8	3653.6	5381.0	4730.2	5438.1	5043.0
3590	3	776.015	2325.022	9.60	CVLFPYGGCQGNNGNKFY	sp P02760	0.001888	6780.4	7023.9	8741.9	10111.5	10712.8	7966.4	13912.6	13996.0	13301.2
3843	3	373.503	1117.488	5.72	FYSEKECR	sp P02760	0.001468	2022.4	1804.4	2217.2	3315.4	2447.0	2935.5	4741.1	5139.7	4426.3
4162	3	649.615	1945.823	11.29	GVCEETSGAYEKTDTDGI	sp P02760	0.000673	8261.6	6090.5	7358.7	9700.1	8293.5	9436.5	5018.9	5333.2	5325.6
4739	4	693.557	2770.197	9.65	CVLFPYGGCQGNNGNKFY	sp P02760	1.75E-05	3309.2	3284.6	2547.6	2770.5	1362.3	3227.3	18893.0	20574.5	24670.6
25	4	438.995	1751.949	7.98	YVGGQEHFALLILR	sp P02763	0.002236	338949.2	440603.6	345982.5	387615.9	547383.6	385780.4	712844.2	679690.8	708016.7
38	3	414.212	1239.616	12.77	SDVVYTDWKK	sp P02763	5.14E-05	149478.9	184611.1	137319.0	165241.1	205412.9	165564.0	381298.6	336680.7	393014.1
106	3	584.990	1751.949	13.95	YVGGQEHFALLILR	sp P02763	0.006213	168168.9	235726.5	176118.4	182062.8	299665.3	194506.9	401029.3	332045.1	399048.6
108	2	620.815	1239.615	13.87	SDVVYTDWKK	sp P02763	0.001226	109152.7	156296.7	93506.5	128357.5	193596.5	132416.8	290732.7	282869.5	349370.5
114	2	556.768	1111.521	12.29	SDVVYTDWK	sp P02763	0.015501	111025.8	133951.5	131712.5	140933.3	181403.9	136462.5	156170.7	148909.4	206345.4
240	2	871.907	1741.800	16.06	EQLGEFYEALDCLR	sp P02763	1.29E-06	203462.3	201113.4	214324.6	297998.5	254666.1	290407.5	110604.0	123144.7	110876.9
437	3	581.608	1741.802	10.28	EQLGEFYEALDCLR	sp P02763	3.33E-06	62736.9	59046.5	70098.0	88368.5	77442.9	89490.1	38933.3	39326.5	39265.6
857	5	972.664	4858.286	11.15	TYMLAFDVNDEKNWGLS	sp P02763	1.06E-05	158672.2	127516.7	165604.2	237093.7	214491.5	236279.0	373364.9	431808.4	434206.0
1024	5	618.306	3086.493	11.28	TYMLAFDVNDEKNWGLS	sp P02763	9.59E-07	42521.7	44258.9	41534.8	60479.7	57972.6	62061.2	30540.2	26681.0	27175.8
1608	4	858.917	3431.641	12.23	NWGLSVYADKPETTKEQ	sp P02763	3.10E-05	49622.4	39128.8	43356.8	57575.2	53485.6	56832.0	31522.2	28770.7	34528.1
1871	4	772.630	3086.492	20.52	TYMLAFDVNDEKNWGLS	sp P02763	5.37E-08	30505.0	32931.2	30049.0	42105.7	42956.6	42903.3	21248.4	21033.3	21618.1
2074	3	570.290	1707.849	8.41	NWGLSVYADKPETTK	sp P02763	0.012276	12058.3	15334.0	13379.9	16203.9	24096.9	15941.6	13578.0	12389.8	14651.1
5835	3	694.352	2080.035	11.69	EQLGEFYEALDCLRIPK	sp P02763	2.37E-08	2069.1	1629.8	1776.7	2204.4	1630.0	2181.7	23503.1	25918.4	23227.9
7656	5	963.059	4810.261	13.38	TYMLAFDVNDEKNWGLS	sp P02763	0.003362	17126.1	11165.9	15347.3	16857.3	11822.4	16121.9	26784.5	29023.2	24472.9
299	2	424.221	846.428	6.09	CNLLAEK	sp P02765	0.000688	38058.9	35905.4	39975.9	44270.9	41914.3	39808.8	44891.9	45193.3	48702.7
394	2	401.682	801.350	3.48	QYGFCK	sp P02765	0.023566	25523.2	25967.8	22904.4	25859.8	30496.2	24467.0	30168.3	32669.4	27220.0
455	5	971.892	4854.422	17.97	HTLNQIDEVKVWPQQPSI	sp P02765	0.006463	265200.5	192096.2	253769.6	234592.0	242533.2	304268.1	393923.0	375731.5	345223.6
610	3	1121.855	3362.544	12.95	QPNCCDPETEEAALVAID	sp P02765	0.000677	232978.8	208218.9	270062.9	296804.8	224400.7	251135.6	144598.2	143425.9	130004.6
718	4	508.257	2028.998	3.08	QLKEHAVEGDCDFQLLK	sp P02765	0.007089	33861.3	35552.5	31562.0	38947.3	43870.4	36993.1	36221.4	42208.8	36598.2
989	3	554.260	1659.758	13.06	EHAVEGDCDFQLLK	sp P02765	0.00034	28793.3	36214.9	25689.2	28601.1	30804.8	28432.5	17523.1	15617.2	14900.7
1000	3	671.664	2011.970	13.70	QLKEHAVEGDCDFQLLK	sp P02765	0.006313	23858.4	31873.4	28059.0	27813.7	30922.3	26595.4	37780.5	39973.1	42018.7
1060	3	860.441	2578.302	16.38	AQLVPLPPSTYVEFTVSG	sp P02765	0.003878	223873.3	192915.8	208604.8	248452.4	209896.3	240728.3	183455.6	179464.3	166878.9
1697	3	399.547	1195.620	4.97	HTLNQIDEVK	sp P02765	6.27E-06	6574.1	8170.7	8197.8	8848.9	8214.8	9858.4	3190.1	3716.4	3328.0
1705	1	830.409	829.402	1.44	CNLLAEK	sp P02765	0.001037	13994.1	17190.0	15168.0	17980.4	23098.8	17947.1	13415.7	14754.6	12115.9

1899	3	1226.611	3676.811	17.69	VWPQQPSGELFEIEIDTLI sp P02765	3.69E-06	114797.8	92277.3	108240.9	159773.9	125324.3	139667.5	47405.4	46638.5	42588.6
2076	4	920.211	3676.814	18.90	VWPQQPSGELFEIEIDTLI sp P02765	8.94E-06	73200.2	62326.6	75977.6	96014.0	77858.4	83375.5	36127.1	33305.4	29348.4
2218	4	841.644	3362.546	19.18	QPNCCDDPETEEAALVAID sp P02765	0.000236	41590.6	36282.8	43377.5	50134.1	40415.0	45361.7	25705.8	26126.0	22397.0
2433	2	598.817	1195.620	12.09	HTLNQIDEVK sp P02765	7.84E-06	7002.6	9971.9	8332.6	9465.2	11373.0	11312.6	2925.1	3424.9	2754.7
3156	4	611.564	2442.225	11.88	QLKEHAVEGDCDFQLLKI sp P02765	1.21E-05	3558.3	5675.6	2941.2	2289.7	3672.2	2057.9	23833.9	25691.1	36344.0
3310	6	810.079	4854.427	14.18	HTLNQIDEVKVWPQQPS sp P02765	0.002317	21915.0	16766.3	21766.7	21425.6	21153.2	25751.9	35392.9	33514.6	29881.5
3505	3	1093.888	3278.642	7.70	AQLVPLPPSTYVEFTVSG sp P02765	2.53E-11	3824.4	3619.1	3715.7	1575.9	1620.2	2127.4	120235.0	115493.6	109604.5
4293	2	360.183	718.351	1.39	EATEAAK sp P02765	0.011823	12572.0	10977.6	13212.7	18097.3	14932.4	18256.3	15135.2	15570.2	12065.6
4341	3	489.213	1464.617	15.80	CDSSPDAEDVRK sp P02765	0.00013	3420.0	2989.6	3752.1	3714.0	3209.9	3375.9	2489.0	2292.2	2301.2
4879	4	607.307	2425.199	14.83	QLKEHAVEGDCDFQLLKI sp P02765	3.84E-09	2589.1	2959.7	2570.2	1505.1	1563.8	1721.5	19107.4	17854.8	14897.5
7637	4	820.669	3278.645	15.65	AQLVPLPPSTYVEFTVSG sp P02765	3.68E-09	782.1	606.9	659.6	146.1	242.8	124.3	28447.4	26580.6	23662.8
22298	3	1122.184	3363.530	10.86	QPNCCDDPETEEAALVAID sp P02765	2.89E-06	2607.3	2251.7	2732.9	3122.6	3160.2	3477.1	1362.4	1271.5	1117.7
22678	3	1122.183	3363.528	14.90	QPNCCDDPETEEAALVAID sp P02765	1.15E-05	3426.9	3107.4	3535.3	5424.7	4158.5	5094.0	1704.5	1226.3	1445.6
378	2	697.816	1393.617	17.11	AADDTWEPFASGK sp P02766	0.010034	73066.9	83548.1	72362.9	76429.8	75457.1	66380.4	63612.8	60968.5	54160.0
389	4	785.886	3139.515	17.52	TSESGELHGLTTEEEFVE sp P02766	0.009326	217977.4	177252.6	210961.4	209134.6	181836.8	201669.6	161626.7	149634.5	143550.9
554	3	456.259	1365.755	12.21	GSPAINVAHVFR sp P02766	0.000334	40606.1	44245.0	39630.9	40805.6	54665.2	40850.1	29222.3	25493.6	31553.1
1056	4	613.558	2450.203	3.76	ALGISPFHEHAEVFTANI sp P02766	0.00101	43909.1	51516.3	46011.8	44799.6	60780.6	51215.8	31327.6	29029.1	41134.9
2253	3	819.056	2454.148	16.17	TSESGELHGLTTEEEFVE sp P02766	5.30E-07	25029.9	24338.6	21868.6	26703.2	23159.9	28700.1	6684.2	8009.9	7228.6
3299	2	1245.145	2488.276	16.91	YTIAALLSPYSYSTTAVVT sp P02766	0.028959	21839.8	20316.1	25409.7	28042.7	34529.8	24353.2	21737.7	20338.2	18324.2
232	2	575.312	1148.609	9.90	LVNEVTEFAK sp P02768	0.00042	113791.5	100054.7	84639.2	74039.9	88642.2	75717.5	48874.9	44163.0	52784.1
268	3	682.371	2044.091	15.90	VFDEFKPLVEEPQNLIK sp P02768	0.01082	180655.2	111191.6	152403.3	117155.7	100094.9	143624.3	94734.7	87129.2	68249.3
276	2	722.326	1442.637	16.06	YICENQDSISSK sp P02768	6.08E-06	128473.8	145990.7	126238.2	90227.5	94730.5	88363.8	87542.8	85831.3	79871.1
280	2	395.240	788.466	4.41	LVTDLTK sp P02768	8.60E-06	32805.2	35214.3	31675.4	24750.5	30906.5	23578.5	18301.8	18892.5	18264.5
329	2	464.251	926.488	5.95	YLYEIAR sp P02768	0.007481	39355.6	50681.8	50640.4	31163.0	43745.9	33873.3	31282.1	26732.6	32861.1
337	3	358.853	1073.537	3.63	LDELRDEGK sp P02768	3.57E-05	34835.7	27739.1	32623.8	24723.2	21911.3	23801.2	18967.4	15576.7	16958.2
343	2	686.288	1370.561	15.06	AAFTECCQAADK sp P02768	1.90E-08	117041.7	118720.2	107680.0	76968.1	86400.9	82507.0	36124.1	38656.7	39603.2
361	2	569.753	1137.492	7.42	CCTESLVNR sp P02768	1.41E-07	56318.5	58087.3	52677.7	42873.2	41102.0	38625.6	23355.4	22928.7	23481.0
392	2	749.794	1497.573	17.06	TCVADESAENCDK sp P02768	0.000127	101497.8	88008.3	113806.0	77620.7	65295.0	82570.0	46858.0	46672.1	38971.0
401	3	547.318	1638.934	13.90	KVPQVSTPTLVEVSR sp P02768	0.000249	75894.1	96789.4	88392.5	64215.8	69198.5	54772.8	47584.4	47287.7	53482.5
441	2	480.786	959.557	5.60	FQNALLVR sp P02768	3.33E-07	44863.3	55122.4	45708.9	34628.5	35339.5	29575.8	11500.9	12170.1	13111.5
454	2	500.807	999.599	11.90	QTALVELVK sp P02768	0.01454	37082.1	52543.8	35376.0	23078.8	33819.7	22671.0	22148.4	22205.7	25722.3
458	2	492.748	983.482	7.51	TYETTLEK sp P02768	8.56E-05	44000.1	37081.2	40084.9	31430.8	36140.3	27209.2	17991.0	21217.5	19303.4
459	4	407.688	1626.722	6.89	ADDKETCFAEEGKK sp P02768	1.45E-06	43960.3	41376.7	41896.6	30234.6	26395.4	29223.2	27489.0	27375.6	28865.0
491	3	409.541	1225.601	6.16	FKDLGEENFK sp P02768	0.001615	30558.4	42619.0	31865.1	21920.8	28078.0	22537.2	18848.1	19138.7	20255.1

532	2	507.304	1012.594	15.27	LVAASQAALGL	sp P02768	0.002073	33352.6	38135.8	37128.5	24390.8	21674.7	25875.7	23195.5	27394.9	21646.9
535	3	518.205	1551.593	13.06	CCAAADPHECYAK	sp P02768	0.001172	57185.7	46738.8	60236.9	38971.8	37838.1	40970.4	32332.1	34577.3	32377.0
569	5	517.830	2584.116	5.82	VHTECCHGDLLLECADDR	sp P02768	0.011962	52641.8	71334.1	57077.9	46713.0	54308.1	38927.2	38725.5	36009.0	45573.7
579	4	647.036	2584.115	10.76	VHTECCHGDLLLECADDR	sp P02768	0.002704	73361.4	115463.3	78766.6	57305.9	92452.4	52207.0	33179.5	28923.3	38692.2
603	2	440.724	879.434	6.32	AEFAEVSK	sp P02768	0.000208	21280.0	20759.5	19302.3	15613.0	17606.6	13378.2	9804.7	10881.3	11496.4
732	3	637.650	1909.928	10.49	RPCFSALEVDETYVPK	sp P02768	8.61E-09	86327.7	96948.2	100669.9	63897.4	75207.9	69826.0	18690.6	19075.6	19006.7
764	4	475.505	1897.990	7.84	RHPYFYAPELFFAK	sp P02768	0.001749	37131.1	32989.6	40944.0	26811.7	21040.8	27217.6	24704.7	24174.0	21541.7
820	3	432.216	1293.625	5.06	AVMDDFAAFVEK	sp P02768	6.35E-07	21152.9	22243.6	20834.4	12304.9	12752.3	12296.0	12047.2	11369.0	12339.0
887	3	339.851	1016.532	5.76	SLHTLFGDK	sp P02768	8.87E-06	14316.0	20339.6	14944.6	11061.4	14678.8	10371.3	3330.0	3154.5	3901.2
900	3	489.953	1466.837	9.96	RHPDYSVLLLLR	sp P02768	0.03971	25250.5	51535.8	29060.1	16405.1	34427.9	21105.8	14434.2	13205.0	16554.2
909	2	386.724	771.432	3.51	AACLLPK	sp P02768	1.16E-07	24011.5	25574.3	24277.5	16804.4	17287.1	16320.4	10522.5	10392.4	11653.1
928	3	543.248	1626.722	13.99	ADDKETCFAEEGKK	sp P02768	4.64E-08	33128.8	31693.5	31487.3	22040.3	20617.8	22530.4	18882.8	17818.6	18477.9
984	5	528.052	2635.223	4.43	QEPERNECFLQHKDDNP	sp P02768	0.000136	70570.8	89736.7	68350.0	46169.7	56545.3	47412.1	37795.6	39546.1	38792.4
1003	4	483.766	1931.034	7.08	SLHTLFGDKLCTVATLR	sp P02768	0.001017	27120.2	35625.9	27077.7	16062.4	25768.3	17113.3	13163.6	12185.0	9934.2
1021	2	829.381	1656.748	17.06	QNCLEFQLGEYK	sp P02768	1.05E-07	67427.6	69838.8	52849.6	42109.8	42826.0	44526.3	13414.8	11223.1	11944.0
1073	4	623.328	2489.283	17.11	ALVLIIFAQYLQQC PFEDI	sp P02768	0.000169	42171.8	49991.3	42452.4	38061.0	28986.8	35178.2	24087.4	22897.0	19313.5
1145	4	637.048	2544.163	7.69	EFNAETFTFHADICTLSEK	sp P02768	9.99E-07	44919.3	49985.3	47783.6	32400.2	38132.3	36173.3	15653.9	16493.6	12890.3
1160	3	516.271	1545.792	5.84	LKECCEKPLLEK	sp P02768	0.000477	27731.7	28053.9	26361.4	20882.6	21110.5	17713.7	22801.3	20849.1	15694.9
1220	4	367.717	1466.837	3.10	RHPDYSVLLLLR	sp P02768	0.014447	14183.7	20763.6	15273.7	10756.4	13544.2	9704.2	8008.4	8538.2	10103.0
1298	3	633.670	1897.990	11.06	RHPYFYAPELFFAK	sp P02768	0.002547	31831.5	28469.6	35535.6	22269.5	25770.8	23368.2	21141.0	24936.3	19663.1
1330	3	830.768	2489.281	21.90	ALVLIIFAQYLQQC PFEDI	sp P02768	0.00058	50436.9	66711.9	50509.7	49303.1	36545.2	46018.5	28883.1	27776.5	23242.9
1371	2	768.290	1534.566	13.12	CCAAADPHECYAK	sp P02768	0.000798	31704.3	37928.3	33420.8	26760.4	35530.5	24042.7	17421.6	14328.7	17704.4
1372	3	867.105	2598.294	21.64	QNCLEFQLGEYK FQNAI	sp P02768	1.62E-06	36543.3	28706.1	34521.9	19358.8	15180.9	15943.8	43805.8	42024.7	36427.4
1400	5	683.126	3410.596	10.07	TCVADESAENCDKSLHTL	sp P02768	2.87E-08	22683.9	31269.7	24686.8	9304.6	9446.4	8716.8	56284.4	60680.9	50877.0
1557	4	655.557	2618.197	11.73	QEPERNECFLQHKDDNP	sp P02768	5.04E-05	37279.8	39472.7	34804.0	28832.6	35625.2	31253.2	18826.0	16210.3	19715.8
1618	2	537.776	1073.537	6.07	LDEL RDEGK	sp P02768	4.02E-06	13290.0	10915.7	11885.4	8624.3	9147.4	8624.5	5748.7	4726.8	5281.2
1644	2	671.822	1341.630	14.06	AVMDDFAAFVEK	sp P02768	0.010765	14954.9	12971.5	13600.2	14781.3	9153.6	12870.8	11441.6	10464.4	10885.0
1784	3	553.257	1656.750	9.78	QNCLEFQLGEYK	sp P02768	9.59E-08	20555.7	20136.7	17519.0	12976.0	11144.4	12837.5	4599.8	3989.6	4230.2
2107	4	659.813	2635.223	11.39	QEPERNECFLQHKDDNP	sp P02768	0.008344	37019.9	56187.0	33231.1	23598.7	37023.6	25269.2	18361.1	21036.1	22118.7
2337	3	481.886	1442.637	6.92	YICENQDSISSK	sp P02768	5.24E-05	6878.2	8445.5	7995.8	5566.2	5224.5	5370.3	5884.6	5068.1	5626.8
2384	3	840.077	2517.210	21.90	MPCAEDYLSVVLNQLCVI	sp P02768	2.58E-05	31929.6	25137.7	26425.0	24732.5	21589.2	27781.5	13565.8	13046.3	13047.4
2509	3	709.001	2123.982	18.70	AAFTECCQAADKAACLLF	sp P02768	1.59E-07	18518.7	19881.1	18635.6	8289.2	9792.5	8487.6	41545.8	42519.8	58847.8
2592	6	740.354	4436.081	7.12	RPCFSALEVDETYV PKEF	sp P02768	7.04E-06	25556.4	17738.3	25127.3	11938.2	11779.4	13278.5	31349.4	35416.5	30361.9
2726	3	581.637	1741.890	1.88	HPYFYAPELFFAK	sp P02768	1.87E-06	15153.8	14905.9	16029.5	9339.1	8007.9	9599.7	8082.2	8587.5	7946.5

2910	3	754.013	2259.017	15.95	EFNAETFTFHADICTLSEK	sp P02768	3.54E-08	26327.9	28177.8	21950.5	22951.2	19707.8	21752.7	3525.8	3359.6	2649.7
2917	3	644.685	1931.033	12.70	SLHTLFGDKLCTVATLR	sp P02768	0.004849	11315.3	17345.1	10756.5	7202.8	12529.8	6844.0	5361.5	4942.6	3340.3
3083	3	435.878	1304.612	5.75	ECCEKPLLEK	sp P02768	7.61E-07	5166.9	5013.2	5044.4	3592.0	3393.0	3396.0	2680.7	2221.9	2691.3
3414	2	492.293	982.572	6.52	QTALVELVK	sp P02768	0.002608	3025.2	2930.0	3422.3	2578.8	2000.3	2783.9	2135.7	2028.3	1981.2
3681	5	888.223	4436.077	17.49	RPCFSALEVDETYVPKEF	sp P02768	1.83E-06	22861.4	15873.4	19214.1	8639.8	9811.8	9774.8	28847.8	31516.0	24840.7
4405	3	992.121	2973.340	19.78	SHCIAEVENDEMPADLPS	sp P02768	4.55E-05	29721.3	27799.1	28704.5	30707.0	28420.2	29833.1	14663.3	13667.9	9641.2
4938	4	380.450	1517.771	2.20	LDELRDEGKASSAK	sp P02768	2.83E-12	174.4	194.0	161.9	102.8	101.6	100.4	5942.7	6408.3	7260.2
4939	2	776.804	1551.593	14.12	CCAAADPHECYAK	sp P02768	5.70E-05	8326.8	7461.7	7875.8	5647.1	7088.9	6036.3	3404.8	3294.5	3396.8
5025	5	740.382	3696.872	17.56	FKDLGEENFKALVLIAFAC	sp P02768	3.94E-05	13332.0	11110.2	12360.6	5714.0	4954.8	6954.4	9526.0	7414.7	7233.9
5985	2	812.398	1622.782	14.06	DVFLGMFLYEYAR	sp P02768	0.000118	10455.8	8633.3	10340.0	11949.2	8354.3	10048.2	4638.9	4531.2	4368.2
6552	3	541.935	1622.784	11.32	DVFLGMFLYEYAR	sp P02768	9.26E-05	4640.8	3689.5	4806.6	5529.3	3568.8	4467.8	1754.7	1641.6	1549.2
11496	3	861.430	2581.267	15.64	QNCLEFEQLGEYKFNQAI	sp P02768	5.80E-05	3486.4	2675.8	3345.6	2290.1	1866.3	1799.3	2929.6	3003.9	2814.3
13368	4	905.977	3619.880	8.12	ALVLIAFAYLQCCPFEDI	sp P02768	4.61E-08	3210.7	2913.8	2746.3	2053.8	1921.1	2392.9	14611.7	13960.8	11657.9
14003	5	925.882	4624.373	14.38	VFDEFKPLVEEPQNLIKQI	sp P02768	3.21E-07	777.6	437.7	865.4	476.5	535.7	436.3	11944.4	9787.0	9614.4
9653	3	936.187	2805.541	11.20	LAQKVPTADLEDVPLAE	sp P02774	7.65E-05	6198.5	5100.7	6943.7	4144.7	2735.4	3435.2	12172.3	12553.8	10986.3
15241	3	789.430	2365.267	12.43	VPTADLEDVPLAEDITNII	sp P02774	0.000177	3177.8	3299.2	2615.0	2259.9	1845.4	1885.0	1602.5	1365.6	1554.1
4483	3	606.607	1816.800	10.23	EGTCPEAPTDECKPVK	sp P02787	1.14E-06	7209.4	8576.4	7968.1	5980.9	6128.8	6145.0	3686.5	3831.5	3314.0
5982	3	724.372	2170.093	17.67	SAGWNIPIGLLYCDLPEPI	sp P02787	7.15E-06	8269.2	7493.6	7724.4	6527.0	5662.8	6521.1	4702.0	4918.5	4781.9
73	2	610.808	1219.601	8.17	NFPPSPVDAEFR	sp P02790	0.002302	227562.0	191195.0	223144.8	286695.8	356698.4	316420.6	332729.9	371257.0	299196.7
87	2	748.344	1494.673	11.16	YYCFQGNQFLR	sp P02790	0.001584	227645.5	190003.0	228215.0	299975.5	361992.6	330297.0	345466.5	391318.8	309994.8
172	3	381.549	1141.627	9.07	QGHNSVFLIK	sp P02790	0.02705	63738.5	82864.2	68252.9	90101.8	113973.9	86323.9	95323.1	92318.3	112484.5
196	3	377.223	1128.647	1.45	RLWWLDLK	sp P02790	0.03283	46798.5	35314.2	42841.5	58797.8	50089.9	61051.9	48176.8	52011.7	50111.9
209	4	783.617	3130.440	22.83	CSPHLVLSALTSDNHGAT	sp P02790	0.004987	301753.7	242150.9	260584.1	426127.8	340732.0	436527.9	338420.2	339243.9	336970.3
230	3	788.728	2363.161	19.90	LLQDEFPGIPSPLDAAVEI	sp P02790	7.46E-07	299075.1	271679.5	259850.3	475513.6	383165.1	407135.9	129932.5	134575.2	116220.8
248	3	499.232	1494.675	6.00	YYCFQGNQFLR	sp P02790	0.001271	56113.8	44819.3	57397.1	72465.3	74014.9	74920.1	79103.2	99742.6	81951.3
302	3	613.301	1836.883	18.90	SGAQATWTELPWPHEK	sp P02790	4.16E-06	195540.7	171190.1	190271.7	279098.3	336589.7	299078.0	110924.7	113282.5	94827.3
351	2	571.299	1140.584	14.06	GGYTLVSGYPK	sp P02790	2.53E-06	105080.8	107504.0	111330.3	164754.5	190927.5	162760.2	81697.7	74952.0	87049.6
358	4	945.710	3778.813	18.83	SLGPNSCSANGPGLYLIH	sp P02790	3.22E-08	132023.6	134703.0	164654.1	146595.9	135565.4	145757.2	508952.1	511255.5	502922.6
388	2	563.307	1124.599	6.30	QGHNSVFLIK	sp P02790	0.000931	32290.8	42749.0	38312.3	43643.5	49606.0	48963.2	59484.4	60810.6	69590.7
404	2	565.331	1128.647	1.43	RLWWLDLK	sp P02790	0.002938	40099.3	35645.5	34737.6	57245.1	47956.9	60763.3	40037.6	43699.7	40492.8
544	4	821.386	3281.516	17.90	SLGPNSCSANGPGLYLIH	sp P02790	0.044193	107938.3	100694.2	115452.7	146959.7	114227.9	139845.2	105434.6	103838.4	75897.3
653	3	365.496	1093.467	2.17	DYFMPCPGR	sp P02790	0.003039	23700.5	28489.0	23383.5	30499.6	31500.5	29062.8	31530.0	32853.4	34709.9
897	2	511.737	1021.459	7.20	VDGALCMEK	sp P02790	5.37E-07	11544.8	12243.6	12200.6	21414.9	24496.6	21303.0	9802.0	9536.4	9015.9
990	4	362.201	1444.774	6.55	GDKVVVYPPEKK	sp P02790	4.49E-05	37909.0	42738.2	34273.7	49384.8	54748.6	47637.6	65871.7	68592.7	67899.5

1039	4	805.625	3218.470	10.47	DGWHWSPIAHQWPQGP	sp P02790	3.18E-07	102784.3	80169.2	100718.9	183855.0	151254.4	180000.8	39523.5	39163.1	35069.3
1101	2	571.743	1141.471	9.50	DYFMPCPGR	sp P02790	9.79E-06	11850.3	12941.4	12192.7	21398.3	21521.4	20683.4	23405.2	24145.1	29721.1
1164	3	591.339	1770.996	15.11	LYLVQGTQVYVFLTK	sp P02790	1.37E-08	40867.8	33827.0	39598.3	69892.8	60202.3	67676.3	13488.7	12606.1	12582.4
1331	4	421.979	1683.888	1.35	FDPVRGEVPPRYPR	sp P02790	2.26E-06	66768.7	74667.3	67810.4	78943.7	96142.6	78987.4	167025.1	164373.6	190996.9
1401	3	381.877	1142.609	7.77	QGHNSVFLIK	sp P02790	0.004725	4966.6	5088.0	4930.4	7229.6	9339.9	7050.5	7607.1	6476.4	8510.4
1451	3	325.493	973.456	4.14	VDGALCMEK	sp P02790	0.019636	15542.0	13496.4	15918.4	20341.4	18078.9	20196.4	10967.5	11406.0	11846.4
1495	3	423.564	1267.670	8.13	FDPVRGEVPPR	sp P02790	3.10E-05	26106.8	28308.1	25714.2	38538.7	48454.7	38281.7	20474.1	20264.4	21712.2
1504	4	711.090	2840.330	15.91	SGAQATWTELPWPHEK\	sp P02790	1.46E-07	24012.1	24320.9	25588.4	39705.0	45840.2	36605.7	70115.7	67617.5	69147.2
1506	4	625.315	2497.232	14.38	EVGTPHGIILDSVDAAFIC	sp P02790	0.024329	20880.2	14218.8	18102.9	27536.5	22837.9	23448.4	15697.0	18515.5	16965.3
1666	3	423.564	1267.670	1.45	FDPVRGEVPPR	sp P02790	0.001028	31999.9	34962.5	33043.6	40913.4	50620.4	42057.2	30633.1	29754.2	34277.6
1670	3	382.551	1144.630	5.67	VWVYPPEKK	sp P02790	0.006238	18289.7	20563.0	17188.5	24820.4	28555.2	23225.4	24988.2	24440.6	26421.0
1840	2	563.307	1124.600	6.06	QGHNSVFLIK	sp P02790	0.029967	8197.2	11582.6	8980.8	12446.6	17713.4	12619.3	13529.6	13512.7	17213.1
2156	3	512.266	1533.776	9.66	WKNFSPVDAAFR	sp P02790	5.05E-08	6077.4	6725.1	5652.5	7382.6	7999.3	6844.9	33061.1	31848.1	27922.6
2159	3	266.487	796.439	2.82	LHIMAGR	sp P02790	4.21E-06	1627.5	1461.3	1723.5	3525.6	3440.0	3242.0	2749.2	2642.3	2503.8
2245	2	886.505	1770.995	16.90	LYLVQGTQVYVFLTK	sp P02790	1.13E-08	35268.9	28550.0	31996.7	59802.1	53965.4	60383.7	10145.0	8780.7	8884.2
2388	5	1105.524	5522.586	10.80	LLQDEFPGIPSPLDAAVE\	sp P02790	5.87E-05	35648.9	36032.5	46369.0	60056.6	68137.3	62624.0	72281.6	79591.5	93191.5
2830	2	487.735	973.456	6.05	VDGALCMEK	sp P02790	0.003948	12655.2	11087.1	13137.8	17109.9	15284.3	17399.8	8480.7	8708.5	8528.5
3499	4	783.365	3129.431	12.46	GECQAEGVLFFQGDREV	sp P02790	2.81E-07	20649.7	16530.2	18214.6	27273.8	26942.5	27627.7	5644.5	5487.2	4249.0
3525	4	361.450	1441.771	6.91	QGHNSVFLIKGDK	sp P02790	1.20E-07	1524.8	1745.1	1552.1	2203.4	2255.4	2075.1	5981.1	6485.3	6263.7
4172	6	1016.677	6094.020	12.54	DGWHWSPIAHQWPQGP	sp P02790	3.09E-06	31409.2	29934.7	38986.2	23133.5	23459.7	23708.6	68695.8	71871.6	75681.6
4188	3	1060.152	3177.435	21.52	GECQAEGVLFFQGDREV	sp P02790	1.26E-07	15783.1	15269.0	15406.9	40068.6	38059.8	44460.5	7910.1	8909.6	6848.9
4946	4	389.706	1554.793	1.38	SHKWDRELISER	sp P02790	4.07E-09	688.9	671.8	770.4	854.0	949.9	877.5	8815.4	7616.2	7132.3
5279	3	504.897	1511.669	2.28	DVRDYFMPCPGR	sp P02790	2.78E-06	821.6	984.5	937.7	2027.0	1837.2	1515.5	6643.0	6797.6	4541.6
5387	5	559.473	2792.328	1.40	SGAQATWTELPWPHEK\	sp P02790	1.67E-06	4467.2	5352.0	4915.8	5734.5	6207.3	5300.7	13741.1	12624.9	14622.4
5574	5	995.297	4971.447	11.07	DGWHWSPIAHQWPQGP	sp P02790	1.13E-05	20498.8	19153.7	23952.8	17453.2	14652.3	17718.7	37321.7	41189.9	39090.0
6144	4	866.652	3462.579	5.56	GECQAEGVLFFQGDREV	sp P02790	3.53E-05	6717.9	4017.2	5956.2	6391.6	5497.5	6307.6	12188.3	14140.9	12362.6
9792	4	795.367	3177.438	12.78	GECQAEGVLFFQGDREV	sp P02790	3.26E-08	3857.5	3508.2	3743.9	9382.7	8878.7	10345.7	1803.6	1838.5	1505.5
9805	3	481.597	1441.769	7.17	QGHNSVFLIKGDK	sp P02790	1.69E-05	543.2	709.3	563.7	728.6	1147.7	807.4	2418.9	2788.4	2422.4
16838	5	1219.812	6094.023	13.54	DGWHWSPIAHQWPQGP	sp P02790	4.31E-06	6963.0	6259.7	8084.1	6742.5	6770.7	6134.0	17897.6	15030.5	15987.0
6116	3	665.953	1994.836	10.36	WTPYQGCEALCCPEPK	sp P04003	0.000102	2897.5	2765.5	3048.0	3960.0	2910.6	3611.3	7057.8	7192.3	9127.7
755	2	336.193	670.371	2.17	TYLTK	sp P04004	0.000128	11665.3	12824.8	11599.6	9986.6	11205.1	10394.8	11317.9	11115.7	11805.3
858	3	399.858	1196.552	8.52	CTEGFNVDKK	sp P04004	0.0303	15682.6	13337.6	16117.5	13951.6	13256.4	15283.4	16957.9	17799.5	16204.4
1093	4	871.344	3481.346	16.04	CQCDELCSYQSCCTDY	sp P04004	0.00555	102588.0	89437.7	90698.6	74960.2	77677.7	76901.8	82716.5	81310.1	76153.3
1121	2	590.769	1179.524	12.87	CTEGFNVDKK	sp P04004	0.011056	10869.7	13472.3	12605.8	14699.8	19130.3	15502.0	17382.6	18688.5	17570.4

1907	2	438.241	874.467	3.87	QPQFISR	sp P04004	0.018255	13522.7	14152.9	12774.1	11937.6	12652.7	12335.8	11419.1	11533.1	12197.0
2401	2	711.831	1421.648	15.06	FEDGVLPDYPR	sp P04004	3.61E-08	33420.1	36614.7	34601.4	40092.1	39845.1	38366.9	11977.6	12291.6	10567.3
2996	3	556.265	1665.772	8.17	DWHGVPGQVDAAMAGR	sp P04004	0.004255	5474.2	6456.4	6072.7	6922.8	9121.4	7908.6	8652.8	8324.5	11407.9
3068	2	506.825	1011.635	14.02	TGISPLALIK	sp P04114	0.010474	4407.5	4557.4	4819.5	3597.5	5363.7	3782.9	4925.2	4797.9	5044.0
3307	3	822.798	2465.372	19.38	IADFELPTIIVPEQTIEIPSII	sp P04114	0.000827	12044.6	11948.4	10802.6	13782.2	15970.2	12943.4	9826.1	10279.7	10349.1
3623	3	514.296	1539.865	5.98	LLSGGNTLHLVSTTK	sp P04114	0.030521	4256.7	6815.3	4243.8	4314.9	6659.5	4609.0	3497.2	3529.3	4176.0
4639	2	371.733	741.451	1.36	AAIQALR	sp P04114	0.005115	1203.4	1422.7	1261.9	1273.5	1437.8	1263.0	1600.9	1682.4	1581.0
4751	2	431.246	860.477	5.69	ITLPDFR	sp P04114	1.59E-06	1590.4	2098.6	1894.9	2407.4	2326.4	2691.2	607.6	693.8	501.3
5119	2	569.781	1137.547	3.81	QGFFPDSVNK	sp P04114	0.000737	5441.2	8403.6	7136.0	8224.6	10537.3	8664.7	2829.8	2743.8	3129.9
8667	3	719.719	2156.135	14.46	HSITNPLAVLCEFISQSIIK	sp P04114	0.004527	4508.0	3873.7	5332.1	4411.0	3377.6	3888.6	5890.8	6194.0	5658.8
9593	3	1147.589	3439.746	17.90	YSQPEDSLIPFFEITVPES	sp P04114	0.000302	8111.6	7836.5	6685.7	12828.4	11587.6	11350.7	8740.6	7366.5	8238.4
14117	4	860.944	3439.748	15.18	YSQPEDSLIPFFEITVPES	sp P04114	0.002157	3127.8	2957.7	2941.9	4449.9	4286.9	4405.2	3479.4	3128.2	3612.7
16190	4	915.950	3659.772	14.44	NKADYVETVLDSTCSSTV	sp P04114	1.01E-06	3086.0	2997.2	3185.7	4651.7	3971.1	4041.6	862.1	892.7	572.0
21313	5	1026.753	5128.731	8.99	LPEIAIPEFIPTLNLDNFQ	sp P04114	0.000377	2658.5	3248.0	2838.3	3235.9	2565.6	2468.7	436.9	299.3	555.9
33042	4	743.177	2968.681	15.99	VHANPLLIDVVTYLVALIPI	sp P04114	1.18E-08	520.1	614.9	554.7	693.6	603.4	669.3	120.5	132.5	114.2
951	2	562.810	1123.605	7.64	DGYLFQLLR	sp P04196	0.042669	17926.8	22435.1	18742.1	18159.3	15298.1	18671.0	25070.6	17760.7	14986.8
1337	3	507.561	1519.661	5.89	YKEENDDFASFR	sp P04196	6.87E-08	15646.5	16265.6	15370.7	19824.9	19793.8	20178.9	11881.5	11449.3	12826.3
1488	3	608.970	1823.887	15.67	ADLFYDVEALDLESPIK	sp P04196	0.000572	20927.9	19056.9	20657.9	24073.1	21052.8	24501.6	22209.6	24345.7	22356.4
1508	3	314.863	941.568	3.27	ALDLINKR	sp P04196	0.002465	5491.7	7706.3	5416.1	5180.8	7709.8	5312.2	4788.9	4380.9	4532.5
1548	2	411.728	821.441	6.61	QIGSVYR	sp P04196	0.001268	5704.1	6256.3	5959.5	6649.5	6154.8	6200.7	7489.6	6707.5	6077.6
1573	3	429.568	1285.683	5.60	RPSEIVIGQCK	sp P04196	0.001974	9325.9	7792.3	9509.8	10956.0	10206.4	10897.0	12117.5	10663.0	10071.2
1661	2	745.850	1489.686	16.06	GGEGTGYFVDFSVR	sp P04196	0.000284	22585.1	18506.9	21269.7	22855.5	20390.4	21432.1	24497.6	23659.5	22454.0
1770	3	378.516	1132.526	1.40	HPNVFGFCR	sp P04196	0.00021	5897.0	6084.8	5606.5	6415.7	7074.7	5888.5	8851.5	7588.0	9908.8
2423	2	912.950	1823.886	17.90	ADLFYDVEALDLESPIK	sp P04196	0.003746	19249.9	18383.7	22659.8	26195.7	22540.1	28490.9	22320.5	25099.8	21717.0
2613	2	841.900	1681.786	17.06	DSPVLIDFFEDTER	sp P04196	0.00065	14612.9	15650.1	21625.2	22762.7	18876.9	25326.0	12014.5	11120.2	11241.7
3979	3	561.603	1681.787	9.95	DSPVLIDFFEDTER	sp P04196	0.000864	5098.3	5354.6	6903.3	8227.4	5930.4	8822.9	4332.4	3698.9	3762.8
4115	4	473.472	1889.858	6.78	YKEENDDFASFRVDR	sp P04196	2.09E-06	2060.0	2630.0	2924.5	1704.2	2247.3	1824.8	10417.7	9334.1	10415.1
6544	3	667.991	2000.953	10.50	DSPVLIDFFEDTERYR	sp P04196	0.00079	3057.5	2825.5	3287.0	3049.9	2280.9	3103.0	5068.8	4703.8	4659.4
1079	2	632.831	1263.648	16.06	SGLSTGWTQLSK	sp P04217	0.007366	27363.4	21082.0	23785.2	17796.2	21396.9	16724.6	22073.0	21594.5	25377.6
1223	4	537.768	2147.042	12.80	IFFHLNAVALGDGGHYTC	sp P04217	0.04644	23843.4	28807.2	21503.8	14750.9	21238.6	14461.5	17100.2	17035.3	14915.0
1674	2	403.251	804.488	3.95	GVTFLLR	sp P04217	0.011604	4686.8	5861.9	4825.3	4145.2	4081.7	3867.5	5436.7	5151.4	7073.1
1839	3	626.006	1874.996	17.11	VTLCVAPLSGVDFQLR	sp P04217	5.40E-05	18641.4	17355.2	16952.2	13041.6	11407.0	11777.1	12430.7	11344.8	11287.9
1903	2	363.730	725.445	2.22	ELLVPR	sp P04217	0.020106	4402.4	4962.3	4412.8	2753.2	4468.6	3095.5	4422.3	4228.1	4072.8
2105	3	824.405	2470.194	12.43	SWVPHTFESESDPVELL	sp P04217	0.00559	26632.6	18922.6	27868.7	20915.5	23803.4	20572.2	17430.2	16149.8	18622.2

5175	2	1236.104	2470.193	8.90	SWVPHTFESELSDPVELL	sp P04217	0.020631	14868.7	11648.2	16520.2	12225.9	15741.7	11767.9	9554.3	8761.8	12161.7
8821	2	814.905	1627.795	8.61	CEGPIPDVTFELLR	sp P04217	0.002514	3254.4	2686.6	3585.2	3058.9	3047.9	3301.6	1708.6	2172.8	1542.3
13674	2	1076.088	2150.161	16.95	SLPAPWLSMAPVSWITP	sp P04217	0.003245	2511.6	2166.5	2975.8	3283.1	2601.1	3101.1	2249.6	2836.7	2639.0
297	2	455.736	909.457	6.33	TLYSSSPR	sp P05155	5.73E-05	43870.1	38363.1	40837.1	47682.1	51528.6	43038.4	68065.0	64891.0	70019.0
377	2	558.799	1115.584	13.15	LLDSLPSDTR	sp P05155	0.02121	37880.0	46982.4	47016.8	51334.3	72082.2	49107.2	40024.7	33493.4	43120.5
474	2	593.354	1184.694	10.79	FQPTLLTLPR	sp P05155	0.000506	57333.8	56354.2	57634.9	75442.1	66785.0	67732.4	47981.3	52927.2	44140.9
571	3	609.665	1825.972	16.90	GVTSVSQIFHSPDLAIR	sp P05155	7.47E-05	51097.9	59454.7	52635.3	69494.1	96969.5	67915.1	32696.3	26338.1	24007.5
640	3	406.870	1217.589	7.54	DFTCVHQALK	sp P05155	8.96E-08	23218.6	23119.2	21970.3	25324.7	26849.7	26344.1	14283.8	13918.2	14832.8
823	2	659.412	1316.810	15.06	LVLNIAIYLSAK	sp P05155	0.001438	33943.1	29421.0	33505.8	44408.3	32914.6	45196.5	28726.2	26521.2	24208.5
902	2	325.169	648.324	2.00	VYDPR	sp P05155	0.03362	9141.5	7834.1	9412.7	10077.3	8200.2	10312.4	10848.5	11253.3	12356.1
904	4	616.820	2463.251	12.54	TNLESILSYPKDFTCVHQ	sp P05155	8.14E-06	23911.3	30054.9	28308.9	21366.2	17611.8	21758.6	64912.8	82133.0	65492.2
3009	3	395.905	1184.694	1.82	FQPTLLTLPR	sp P05155	0.002516	4054.2	3568.2	4069.4	5103.8	4232.5	4574.3	3391.6	3612.6	3596.1
4515	3	872.473	2614.398	18.90	TLLVFEVQQPFLFVLWDC	sp P05155	2.76E-09	12328.1	10286.0	11484.4	18186.0	17334.2	16000.5	2484.2	2407.7	2239.0
6933	3	1022.879	3065.615	12.74	KVETNMAFSPFSIASLLT	sp P05155	1.55E-05	6851.0	6441.8	7141.9	13827.4	12705.0	12541.8	11158.9	12519.6	9224.9
12137	4	755.410	3017.613	8.14	KVETNMAFSPFSIASLLT	sp P05155	0.004815	3639.5	2819.7	3433.2	4369.3	4151.7	3984.7	3229.2	3027.5	2354.2
13249	4	654.607	2614.399	8.20	TLLVFEVQQPFLFVLWDC	sp P05155	6.54E-07	1369.6	1447.4	1325.0	2443.7	2140.3	2072.1	204.5	213.4	351.6
15562	4	767.411	3065.616	16.90	KVETNMAFSPFSIASLLT	sp P05155	2.10E-06	1451.7	1506.4	1503.1	2919.4	2555.0	2682.4	2445.7	2751.2	2256.4
16584	3	805.801	2414.382	15.91	LLDSLPSDTRLVLLNIAIYL	sp P05155	5.96E-05	703.4	644.0	993.3	1152.8	956.7	896.2	3176.2	3325.8	2863.0
4657	2	560.825	1119.635	7.49	QFPILLDFK	sp P05546	6.12E-06	3501.7	3199.0	3712.9	3742.1	3315.8	3404.3	2028.7	2136.3	1969.3
5851	3	761.060	2280.158	12.90	AILQSGSFNAPWAVTSLY	sp P06276	0.000979	6869.6	6902.8	7833.2	7231.6	7460.1	7217.6	4975.5	4701.5	5681.3
4020	3	677.321	2028.942	14.64	DSGVPDRFSGSGSGTDF	sp P06310	0.000624	6099.5	6759.4	6317.2	4554.6	5377.8	5690.6	8928.4	9101.1	11986.4
10267	2	373.178	744.341	4.47	DSGVPDR	sp P06310	1.53E-05	2646.6	2339.0	2931.8	2842.0	2196.9	2608.5	1224.6	1257.9	1128.1
1942	2	561.820	1121.625	11.17	LLIYWASTR	sp P06312	0.009812	10539.9	12540.5	11302.1	8918.4	11849.2	9631.1	9893.8	10385.5	9751.5
2711	2	380.186	758.357	1.45	ESGVPDR	sp P06312	0.000174	4565.0	3851.5	4428.7	4747.4	4001.2	4938.7	1480.3	1749.0	1422.6
20795	2	364.701	727.388	2.07	VNVGDPK	sp P06681	0.000683	696.7	584.1	705.9	657.0	516.6	700.9	1064.6	1040.6	1061.7
27809	2	674.868	1347.722	5.54	QHLGDVNLNPL	sp P06681	0.012116	252.5	192.7	317.6	291.8	222.3	282.5	409.5	440.3	391.7
2916	2	882.963	1763.912	16.90	WSAGLTSSQVDLYIPK	sp P08185	0.038504	18048.5	12055.7	17571.4	16550.5	11402.2	16503.8	10223.2	10453.5	8470.3
10265	4	701.872	2803.460	18.78	KNIFISPVISMALAMLSL	sp P08185	0.001137	3735.5	3668.6	4197.3	3882.8	3103.3	3612.2	2815.0	2688.4	2694.1
11761	3	892.795	2675.363	15.17	NIFISPVISMALAMLSLG	sp P08185	2.08E-05	3280.9	2881.7	3007.7	4568.5	4381.0	4349.8	2555.9	2210.6	2158.7
21376	3	910.803	2729.387	16.17	FNQPFIIIFDHTWSSLF	sp P08185	1.89E-05	1065.1	1290.1	1395.2	877.0	686.9	858.8	2054.9	2198.2	2052.8
3742	3	509.927	1526.758	9.81	SIDVACHPGYALPK	sp P08603	6.08E-05	3112.1	3503.1	3093.2	3311.7	3817.4	3276.6	4847.3	4869.4	5229.3
2305	2	656.847	1311.680	10.99	LGNQEPGGQTALK	sp P08697	1.94E-06	16033.2	15229.5	15084.0	12081.8	12710.2	11146.0	7893.4	8117.8	7466.1
3451	3	710.380	2128.119	13.90	WFLLEQPEIQVAHFPPK	sp P08697	9.73E-06	19759.3	15235.9	18359.1	16242.3	11132.7	14741.0	5068.4	4134.9	4458.5
5901	5	884.657	4418.250	6.35	GFPIKEDFLEQSEQLFGA	sp P08697	0.000371	12180.4	11861.5	11657.9	9655.9	13137.3	8713.9	5844.3	4769.6	4973.4



17187	3	908.479	2722.415	12.22	HQMDLVATLSQLGLQELF	sp P08697	0.001135	1286.7	1496.4	1679.5	1994.5	2099.2	2025.4	734.3	1178.0	826.5
1358	2	684.365	1366.716	15.06	DSSTWLTAFVLK	sp P0C0L4	0.000142	12192.7	16140.6	12276.1	35920.3	26061.5	33538.5	21376.7	20951.5	18393.5
2633	3	1044.830	3131.467	19.99	LQETSNWLLSQQADGS	sp P0C0L4	4.69E-05	21880.3	20300.8	24249.1	41963.7	33154.9	45211.1	17353.3	18027.3	17526.8
4375	3	543.320	1626.938	12.10	PVAFSVVPTAAAASLK	sp P0C0L4	1.31E-06	3575.8	2961.6	3088.5	7405.8	5044.1	8621.7	698.4	890.0	796.6
5569	3	456.579	1366.716	7.43	DSSTWLTAFVLK	sp P0C0L4	6.14E-05	1289.0	1496.9	1429.6	3614.2	2564.0	2941.3	1976.4	2070.7	1987.4
6055	2	814.475	1626.936	11.89	PVAFSVVPTAAAASLK	sp P0C0L4	1.17E-05	4396.3	3551.0	3561.9	8945.6	5823.5	10232.7	832.2	1120.5	590.0
1959	4	775.140	3096.531	16.99	LQETSNWLLSQQADGS	sp P0C0L5	0.002937	19850.8	14884.8	18956.3	32705.5	26180.6	28368.5	16730.9	19059.4	19061.3
2535	3	1033.184	3096.530	21.78	LQETSNWLLSQQADGS	sp P0C0L5	0.002842	22348.2	15961.2	20856.9	36583.5	30389.5	33156.9	16178.7	20707.1	19962.6
3021	2	655.363	1308.711	14.06	GSSTWLTAFVLK	sp P0C0L5	0.000393	6582.6	5779.8	6652.8	4719.9	4835.7	5809.5	8734.8	7476.8	7410.8
4416	5	924.874	4619.332	11.17	VLSLAQEQVGGSPKQLQI	sp P0C0L5	1.26E-06	10306.4	9173.8	8700.6	11795.2	10624.4	12190.5	32476.3	31440.6	27397.5
889	3	772.065	2313.174	15.17	VTTVASHTSDSDVPSGV1	sp P10909	0.014798	48691.8	45741.0	51593.3	46279.5	65279.2	49828.3	68923.2	62627.2	70661.8
1499	2	644.824	1287.633	13.83	ELDESLQVAER	sp P10909	0.001393	13714.2	18813.6	16838.4	15735.9	13557.1	14527.5	21103.0	20398.2	23048.5
1937	2	697.353	1392.691	15.06	ASSIIDELFQDR	sp P10909	0.000601	17012.7	15695.9	18469.4	16144.5	13828.0	16425.1	10630.6	11544.1	10580.2
2168	2	356.177	710.340	3.63	SYQWK	sp P10909	7.46E-05	4257.1	4208.9	4051.7	3990.9	4113.3	4010.2	4671.4	5065.8	4862.9
3272	2	536.786	1071.557	7.28	EIQNAVNGVK	sp P10909	0.00236	4465.6	3912.9	4289.0	4316.9	4303.9	4538.3	3319.8	3635.0	3503.9
4999	4	500.748	1998.964	4.44	EPQDTHYHLPFSLPHR	sp P10909	0.039649	5059.7	5849.8	5009.2	4330.2	4735.5	4374.8	4824.7	4468.4	3343.0
5651	3	408.176	1221.506	3.40	EGDDDRTVCR	sp P10909	0.023444	3764.3	3195.0	3913.6	3993.8	3098.3	3348.9	4690.3	4623.6	5144.0
8809	3	649.000	1943.979	9.37	ASSIIDELFQDRFFTR	sp P10909	1.20E-06	1795.5	1603.6	1596.2	1194.2	958.2	1039.3	3059.2	4125.7	3480.5
186	4	309.432	1233.700	4.66	EHVAHLLFLR	sp P19652	0.03369	45393.2	57683.5	50966.9	49024.7	66687.4	46709.1	32044.6	36115.3	45747.2
368	3	408.869	1223.584	7.88	SDVMYTDWKK	sp P19652	5.35E-06	46927.0	47841.3	44937.9	46949.0	42637.3	45140.7	74643.2	71748.5	67236.5
416	2	548.752	1095.489	6.07	SDVMYTDWK	sp P19652	0.002664	62464.1	61066.6	64538.5	58687.6	67299.0	56275.5	54549.0	55572.4	55517.4
534	3	704.997	2111.970	16.11	EQLGEFYALDCLCIPR	sp P19652	4.69E-05	119838.2	84541.4	106607.6	126271.6	88544.7	107859.6	36772.1	40900.7	37663.7
550	5	360.197	1795.951	4.10	YEGGREHVAHLLFLR	sp P19652	6.06E-05	16464.8	21929.7	18226.8	15541.6	24585.5	18037.8	53486.0	49198.0	62575.1
592	4	449.995	1795.951	6.33	YEGGREHVAHLLFLR	sp P19652	0.005722	20899.8	35258.5	22467.6	17325.5	37763.3	21787.6	62878.5	56153.1	88465.1
973	3	366.170	1095.489	2.12	SDVMYTDWK	sp P19652	0.004652	14775.5	13952.1	15837.3	14063.3	15828.2	13303.6	13392.8	13427.9	12968.1
1081	3	424.870	1271.588	9.32	SDVMYTDWKK	sp P19652	1.07E-05	9056.2	9124.1	9157.1	11855.2	13904.2	11438.1	19411.9	18454.5	20793.7
1648	5	622.503	3107.478	7.16	TLMFGSYLDDEKNWGLS	sp P19652	2.47E-09	32285.9	34052.1	32080.5	37534.1	34738.7	35236.9	9583.8	10344.3	10617.7
1865	2	1056.991	2111.967	16.95	EQLGEFYALDCLCIPR	sp P19652	7.44E-05	59970.5	38662.2	48714.5	67165.8	43115.7	55758.1	15742.6	18240.8	16211.5
2348	5	1050.895	5249.439	5.99	TLMFGSYLDDEKNWGLS	sp P19652	1.41E-05	46527.7	42303.6	46369.8	65708.8	61604.5	60517.9	92650.0	125090.8	103071.5
2368	4	789.879	3155.486	6.78	TLMFGSYLDDEKNWGLS	sp P19652	6.37E-06	24838.6	20995.6	25258.2	40026.1	33569.1	38953.6	12288.7	12748.2	9598.8
651	3	494.592	1480.755	10.86	IYGNQDTSSQLKK	sp P19823	0.000507	22614.7	22097.3	19412.8	24780.3	22369.2	26236.3	38372.8	37579.7	30885.6
655	2	791.932	1581.849	17.90	IQPSGGTNINEALLR	sp P19823	0.014859	55030.4	66928.4	58370.1	59862.7	74717.9	61624.1	72390.2	62013.8	71906.1
662	2	669.365	1336.716	11.05	FYNQVSTPLLR	sp P19823	0.000737	30448.7	28962.7	34464.9	35743.3	28205.4	37379.6	52027.7	53201.6	49086.1
938	4	921.695	3682.749	16.09	NVQFNYPHTSVTDVTQNI	sp P19823	0.000188	90952.6	80375.6	93459.8	103755.2	91373.1	103612.1	56780.6	60940.9	57770.4

1198	2	396.722	791.430	2.24	ALYAQAR	sp P19823	0.025929	7100.0	4964.5	6589.2	6934.6	7302.3	7422.6	8714.1	8831.8	7860.7
1200	3	473.915	1418.722	7.74	VQFELHYQEVK	sp P19823	0.00118	11927.7	16760.4	15557.0	18036.2	20473.7	16901.9	11872.4	10903.9	13513.1
1255	2	423.746	845.478	5.87	IYLQPGR	sp P19823	0.001836	9474.4	10787.0	9478.5	11167.9	13515.7	10344.2	8787.9	8877.0	9095.3
1260	4	367.957	1467.797	3.50	AHVSFKPTVAQQR	sp P19823	0.000128	10254.7	9898.7	9832.1	13299.1	11579.5	11545.6	15282.7	14598.6	14110.6
1373	3	611.354	1831.039	11.95	KLWAYLTINQLLAER	sp P19823	0.026986	23668.3	20858.4	21184.7	30832.3	27496.4	25559.5	25807.5	23948.6	23312.6
1440	2	415.243	828.471	8.97	SLAPATAAK	sp P19823	0.0036	7808.8	7166.6	8447.7	9912.3	9361.0	9256.4	8869.7	8457.5	8279.8
1534	3	597.325	1788.954	7.38	HLEV DVWVIEPQGLR	sp P19823	9.70E-05	18583.0	16622.4	19024.1	24663.1	21922.7	23633.5	19738.4	22395.7	19850.4
1715	2	514.294	1026.573	7.19	TEVNVLPGAK	sp P19823	0.000328	11736.6	12936.5	11872.4	12977.0	18183.4	15390.6	8399.3	8406.8	8957.3
2417	3	946.139	2835.396	20.17	AGELEVFNGYFVHFFAPC	sp P19823	0.00357	34006.2	36767.3	31767.7	49223.7	37122.7	44858.4	27180.8	29052.2	23854.9
2482	3	490.273	1467.797	9.91	AHVSFKPTVAQQR	sp P19823	0.000205	6906.2	7181.4	6988.8	8666.5	8792.3	8184.2	10906.1	9776.1	9158.7
2750	3	528.291	1581.851	10.66	IQPSGGTNINEALLR	sp P19823	0.002706	6372.1	6960.3	7175.6	6906.9	7599.0	7073.7	8914.2	8124.7	8479.6
4605	2	308.693	615.372	1.46	TAGLVR	sp P19823	0.034328	4369.0	3790.3	4534.6	5143.3	4041.2	4964.3	6166.5	6357.0	6352.7
7509	3	568.655	1702.944	9.72	LWAYLTINQLLAER	sp P19823	0.005256	2949.5	1835.8	2418.5	3328.8	2674.8	3397.5	2251.3	2261.5	2050.1
8629	4	709.856	2835.396	12.43	AGELEVFNGYFVHFFAPC	sp P19823	0.004303	4305.9	4478.0	4022.1	6454.3	4219.2	5499.6	2931.2	3416.8	3223.5
21826	4	1138.832	4551.301	11.15	FDPAKLDQIESVITATSAN	sp P19823	0.000303	2042.2	1880.6	1904.2	3627.2	2609.4	3227.7	1506.7	1426.9	1407.6
23461	4	941.766	3763.036	16.58	AIFILNEANNLGLDPNSV	sp P19823	0.000128	4524.5	4429.6	4749.8	5916.8	5062.0	5681.2	3341.1	2709.8	2180.4
25831	5	911.267	4551.300	14.31	FDPAKLDQIESVITATSAN	sp P19823	0.000168	993.5	960.5	856.3	1562.1	1136.7	1366.5	536.2	611.0	684.6
28928	3	1255.352	3763.033	15.30	AIFILNEANNLGLDPNSV	sp P19823	0.000105	4930.9	4940.3	4531.5	6375.0	5634.8	6481.4	3285.3	3000.0	2211.5
824	3	669.341	2005.001	6.88	FAHYVVT SQVVNTANEAF	sp P19827	0.01996	49578.9	51129.9	43566.4	51137.6	72290.7	52335.2	45834.9	39653.8	55958.8
1004	2	580.815	1159.615	12.71	EVAFDLEIPK	sp P19827	0.030678	21815.0	19602.6	21965.5	21353.2	20044.6	23252.0	19160.9	15528.7	12442.3
1087	2	579.318	1156.622	16.06	AAISGENAGLVR	sp P19827	0.038338	18093.1	20709.5	18777.4	19881.3	21568.4	18230.7	18671.1	18077.8	20115.4
1132	2	735.865	1469.716	18.11	QYYEGSEIVVAGR	sp P19827	0.001122	29284.3	35609.9	31239.3	36768.6	38060.8	32086.3	46944.4	40488.4	53827.4
1250	2	545.302	1088.589	13.98	LDAQASFLPK	sp P19827	0.001588	26043.7	29848.1	25767.2	29336.3	32317.2	28183.5	20628.9	18146.3	22996.7
1397	2	420.217	838.419	5.47	VTYDVSR	sp P19827	3.30E-05	8513.9	10005.6	8647.1	10498.5	11232.7	11101.2	4893.7	5579.7	6193.9
1442	6	842.430	5048.539	13.06	IYEDHDATQQLQGFYSQ	sp P19827	0.003899	74132.8	61094.7	73361.2	87660.3	71244.8	77170.2	99795.4	100866.6	94052.6
2178	2	781.454	1560.894	17.06	LWAYLTIQELLAK	sp P19827	0.018584	19394.1	14946.2	17438.6	22141.7	18382.6	20147.3	16345.8	16388.0	11436.8
2188	2	839.427	1676.839	16.90	GFSLDEATNLNGGLLR	sp P19827	0.017484	20955.2	21392.1	18385.1	28031.6	22770.6	24899.0	20362.7	18351.4	19725.1
2286	3	429.246	1284.717	5.77	KA AISGENAGLVR	sp P19827	0.00091	6320.0	6348.7	5783.5	7420.9	7605.7	7182.9	7256.0	7481.2	7362.5
2573	3	542.636	1624.886	10.86	VTFQLTYEEVLKR	sp P19827	3.48E-07	10287.3	10741.2	9384.6	13450.8	14043.9	11207.7	4053.2	3914.7	3495.3
2627	3	521.306	1560.895	11.32	LWAYLTIQELLAK	sp P19827	0.011047	7909.6	5940.3	7256.6	9377.4	7648.7	8171.1	7554.0	7952.0	5930.1
3286	3	334.539	1000.594	4.15	ELAAQTIKK	sp P19827	0.021365	1830.1	1569.4	2038.3	2070.8	1862.4	2287.2	2884.6	3189.1	3885.0
3500	4	751.140	3000.530	16.65	TAFISDFAVTADGNAFIGC	sp P19827	7.31E-06	11944.4	9792.1	10380.8	10946.9	9713.1	10002.4	23095.0	20992.5	19141.1
4839	5	663.934	3314.633	10.71	KGHVLF RPTVSQQQSCPC	sp P19827	0.005237	8688.6	12977.2	9024.1	11401.7	15337.2	14127.7	8164.6	7237.2	7374.0
5320	3	328.535	982.583	5.41	ELAAQTIKK	sp P19827	0.035645	977.9	865.4	1063.4	1072.3	990.2	1222.8	1398.2	1584.1	1917.5

8744	4	1002.009	4004.008	13.77	GIEILNQVESLPELSNH/ sp P19827	7.50E-05	11087.2	10130.5	11545.2	25819.6	21092.1	20625.5	11380.9	11165.3	8618.0
10014	3	719.696	2156.066	11.45	ILGDMQPGDYFDLVLFGT sp P19827	0.00044	1383.4	1216.4	1408.0	2420.1	2672.9	3349.7	1793.7	1931.4	1516.7
10027	3	725.033	2172.079	19.11	TAFISDFAVTADGNAFIGE sp P19827	4.78E-06	5470.1	4897.8	5249.3	7711.1	5767.7	6482.7	2393.7	2378.7	2364.8
18692	2	1079.039	2156.063	16.90	ILGDMQPGDYFDLVLFGT sp P19827	0.000284	903.5	955.7	1055.4	1780.3	1978.0	2430.6	1025.8	1194.2	1229.8
2183	3	848.703	2543.087	17.38	SQCTYSNPEGTVVLACD( sp P22792	0.000537	32188.3	34201.8	34240.6	26508.0	24408.7	25390.3	38310.0	30448.6	38237.6
2649	2	801.437	1600.860	16.90	LSNNALSGLPQGVFGK sp P22792	0.014114	15828.8	14248.0	17055.8	15457.4	14250.1	14760.1	11987.0	13983.7	11108.7
2719	3	812.428	2434.262	15.90	VVFLNTQLCQFRPDAFGC sp P22792	0.013707	25545.7	18675.1	20989.1	23626.0	15157.4	18704.6	12980.4	13796.2	13144.0
4557	4	762.182	3044.697	16.99	TLNLAQNLLAQLPEELFHI sp P22792	0.004253	9363.4	9014.6	9099.7	11343.1	9519.9	8564.7	10744.2	9886.5	10633.8
4675	2	617.285	1232.556	11.01	CLAYDFYPGK sp P25311	0.00593	3598.9	3951.2	3280.3	2168.1	2474.8	2299.3	3653.5	2682.1	3254.4
4746	3	801.743	2402.206	15.90	HVEDVPAFQALGSLNDLC sp P25311	0.007464	10720.3	11551.3	11798.4	8926.0	6794.4	9219.0	10823.5	11049.5	12517.4
10383	3	800.759	2399.255	15.38	ILLMDLNEEDPTVLELGIT sp P27169	1.01E-07	3055.2	3047.8	2839.8	3880.1	3632.8	3787.0	1680.8	1578.7	1571.6
6521	2	657.845	1313.676	4.12	DFALQNPSAVPR sp P35858	0.004081	3404.3	3341.4	3360.8	2314.0	2514.9	2485.5	2870.9	2583.2	3425.8
7338	2	727.942	1453.869	9.17	NLIAAVAPGAFLGLK sp P35858	4.44E-07	3054.8	3858.0	3269.6	3095.4	3031.6	2641.9	776.1	792.3	635.5
7382	4	334.447	1333.761	1.39	LSHNAIASLRPR sp P35858	0.003474	1138.2	1126.4	1004.7	857.7	997.8	868.4	745.6	794.5	758.3
9511	2	835.979	1669.943	16.90	VAGLLEDTFPGLLGLR sp P35858	6.98E-05	3139.4	3002.2	3260.3	2919.5	2210.3	3089.6	895.2	1074.8	844.4
13634	3	557.655	1669.943	12.16	VAGLLEDTFPGLLGLR sp P35858	1.45E-05	1316.7	1111.7	1233.5	1036.4	812.8	955.2	319.9	397.6	271.6
29174	4	953.498	3809.965	19.09	DNGLVGIEEQSLWGLAEI sp P35858	0.002982	995.3	917.9	1150.5	767.0	824.8	749.9	682.1	689.9	809.7
1550	2	527.799	1053.584	4.29	LPNNVLQEK sp P43652	0.000363	21416.4	23601.2	21869.9	16390.4	23661.4	17087.8	10159.8	10601.2	12150.0
1682	3	530.948	1589.823	10.83	ESLLNHFLYEVAR sp P43652	3.63E-07	18752.1	16481.3	15209.9	12944.2	11384.4	11593.9	6080.9	5986.0	5937.9
1719	3	642.614	1924.821	15.64	SCCEEQNKVNCLQTR sp P43652	0.00143	23184.6	23818.1	24711.6	16787.2	15471.8	17385.4	18274.1	20172.2	17202.7
1737	4	673.348	2689.364	7.56	LKHELTDEELQSLFTNFAI sp P43652	0.002155	25778.2	27719.3	31812.4	22668.1	30450.5	22518.1	16925.3	17010.0	17507.3
1950	2	811.855	1621.695	17.06	AESPEVCFNeesPK sp P43652	3.05E-08	27947.9	26728.5	28058.3	22231.2	25558.5	26302.4	8733.9	8699.2	8834.7
1957	3	438.870	1313.587	9.73	TINPAVDHCKK sp P43652	0.005097	9561.5	8940.8	10268.6	8003.6	6868.9	7166.4	7098.1	7476.0	5878.1
2100	2	692.794	1383.574	12.15	FTDSENVQER sp P43652	1.35E-07	17766.8	18675.6	18916.8	16331.0	12601.4	13985.0	4152.5	3593.4	3478.4
2373	4	411.959	1643.807	2.10	GQCIINSNKDDRPK sp P43652	0.00529	7763.0	8002.8	7896.9	5782.0	4790.8	6520.1	5350.4	6152.2	5744.3
2639	4	622.097	2484.358	12.07	RNPFVFAPTLLTVAVHFEI sp P43652	0.005107	19971.3	15635.2	17906.1	16181.6	13412.8	15292.0	12353.7	12185.1	11734.1
3097	2	516.809	1031.603	1.33	AIPVTQYLK sp P43652	2.83E-05	9561.2	12002.3	9502.2	8392.1	10184.1	8499.5	3095.4	3998.6	4092.7
4074	3	366.859	1097.556	4.06	ICAMEGLPQK sp P43652	7.41E-07	3213.4	2570.9	3179.8	2502.6	2637.2	2455.1	957.4	761.6	850.5
4192	3	831.362	2491.063	18.64	FTDSENVQERDADPDTI sp P43652	2.90E-06	6940.1	8333.5	8017.1	3661.7	4249.7	3404.2	13103.7	11820.5	15776.5
4221	2	944.474	1886.933	15.90	SDVGFLPPFPPTLDPEEK sp P43652	0.000143	18805.8	17862.4	15709.0	13887.7	11763.5	13616.5	8969.3	9778.1	8584.1
4689	2	514.218	1026.421	7.92	CQAYESNR sp P43652	3.28E-06	9013.8	7830.8	9732.8	6661.7	5851.8	6548.0	3521.5	3509.1	2950.9
4920	2	415.706	829.398	4.72	AFSSYQK sp P43652	4.78E-08	2266.0	1961.2	2464.9	2187.6	1778.0	2111.9	415.3	342.3	374.8
6666	3	629.985	1886.935	14.67	SDVGFLPPFPPTLDPEEK sp P43652	7.53E-05	5359.5	4984.9	4897.2	4438.0	3408.2	3962.7	2560.5	2912.5	2695.7
6953	3	1006.117	3015.328	22.04	ELISLVEDVSSNYDGCCE sp P43652	1.67E-09	15357.4	16891.0	18425.9	16077.6	17136.6	14970.7	1757.4	1617.8	1990.5

8075	3	566.919	1697.734	7.39	EGKFTDSENVQCER	sp P43652	0.007777	2268.6	1957.3	1775.0	1617.6	1570.9	1232.5	1361.4	1493.8	1624.2
12335	4	754.840	3015.331	12.32	ELISLVEDVSSNYDGCCE	sp P43652	1.56E-05	5205.6	3857.9	5444.8	3942.8	5098.5	4829.7	500.0	445.8	183.9
34	2	657.837	1313.659	15.06	VNVDEVGGEALGR	sp P68871	0.000178	364307.8	317298.8	324504.9	458338.8	471184.3	437947.9	598138.3	515895.8	676254.5
46	2	466.765	931.515	11.08	SAVTALWGK	sp P68871	0.039258	151270.3	199594.4	144741.1	173235.9	221299.2	166629.8	196360.9	204967.8	272198.6
59	4	445.005	1775.989	11.95	LLGNVLCVLAHHFGK	sp P68871	5.54E-05	208965.6	184525.8	185442.9	181185.6	191111.3	204833.7	307944.7	316603.7	282796.9
101	2	689.855	1377.695	15.06	EFTPPVQAAYQK	sp P68871	0.000531	270712.9	275449.3	286098.6	326429.4	431918.6	328345.2	431225.9	395870.0	450940.1
267	3	438.894	1313.660	9.42	VNVDEVGGEALGR	sp P68871	1.23E-05	39091.7	33869.3	35677.0	51742.2	49132.9	48329.2	67017.7	60893.9	73009.5
328	3	460.239	1377.696	10.02	EFTPPVQAAYQK	sp P68871	3.98E-06	50788.3	47458.9	55488.4	60603.2	67233.6	60578.1	82202.9	80260.9	86359.6
418	3	670.987	2009.939	18.11	FFESFGDLSTPDAVMGNF	sp P68871	0.007239	71009.5	107248.9	89242.1	85932.7	82286.9	94664.8	121591.6	127462.7	110908.6
439	5	518.055	2585.238	1.47	GTFATLSELHCCLKHVDP	sp P68871	0.021653	59809.6	63086.8	60567.8	66486.1	84685.6	67166.8	74963.5	70461.6	78369.6
499	3	686.989	2057.945	17.11	FFESFGDLSTPDAVMGNF	sp P68871	3.01E-05	45577.9	39147.8	43221.2	73262.1	61689.1	77622.0	91517.1	81945.7	73305.0
519	3	593.004	1775.989	11.06	LLGNVLCVLAHHFGK	sp P68871	0.001011	47290.3	44466.3	40398.3	43169.0	41988.9	52972.4	68188.9	71406.7	56330.3
797	2	1029.979	2057.943	17.90	FFESFGDLSTPDAVMGNF	sp P68871	0.001587	48190.9	31604.6	49783.0	81345.1	71247.7	91048.1	96561.6	80906.2	63620.8
2028	1	932.521	931.514	3.91	SAVTALWGK	sp P68871	0.008324	10501.6	16779.6	8942.3	15011.4	24156.1	14042.1	11351.8	12300.6	17764.5
2177	5	628.142	3135.676	4.16	LLGNVLCVLAHHFGKEF	sp P68871	0.001987	19119.4	13757.4	19407.8	19021.5	16991.0	19759.2	31867.2	25352.2	24600.0
3183	6	707.026	4236.113	4.91	VLGAFSDGLAHLNLTGK	sp P68871	1.96E-08	4027.8	3990.4	5107.2	2442.7	2093.2	3049.4	56365.5	41265.3	49542.9
9954	4	829.420	3313.653	12.55	LLVVYPWTQRFFESFGDI	sp P68871	2.22E-07	2750.5	2976.8	3055.0	6156.5	5693.5	6117.5	5801.5	6547.0	5853.1
44	3	510.584	1528.730	10.46	VGAHAGEYGAEALER	sp P69905	0.032486	210000.6	287454.2	199090.6	248129.3	310755.7	241298.3	287942.9	309870.6	281091.9
52	4	459.229	1832.888	7.34	TYFPHFDLSHGSAQVK	sp P69905	0.00945	224138.9	295977.9	239890.9	257702.8	288063.9	276892.6	321913.5	323653.8	391930.0
69	2	536.282	1070.550	11.80	MFLSFPTTK	sp P69905	0.000935	105103.2	113344.4	116254.2	159777.9	198457.8	150424.2	216928.5	176247.6	164100.5
96	3	391.228	1170.662	8.79	VLSPADKTNVK	sp P69905	8.88E-06	64999.0	61570.4	70777.1	84733.3	72979.8	78099.4	125812.0	127972.6	110992.7
239	3	611.970	1832.887	15.01	TYFPHFDLSHGSAQVK	sp P69905	0.024113	102807.4	147151.5	105500.5	128281.9	149968.3	138280.8	144978.1	148358.3	183213.6
478	2	365.211	728.408	2.43	VLSPADK	sp P69905	0.027337	44260.5	37337.5	44946.6	56528.9	45171.8	54034.6	49600.5	48663.9	56503.6
493	5	600.105	2995.489	14.69	VADALTNAVAHVDDMPN	sp P69905	0.000694	54541.0	62408.6	54089.1	91571.4	73854.3	84878.0	73583.9	70358.7	69418.9
644	2	266.648	531.281	1.45	AAWGK	sp P69905	0.00292	18064.5	14330.7	17430.6	22189.1	16758.0	20877.8	28630.2	28988.6	32694.0
727	2	626.862	1251.710	16.06	FLASVSTVLTSK	sp P69905	0.002957	33040.3	37004.5	31689.3	48745.7	64792.5	47291.9	33641.5	30724.7	26172.6
742	3	341.856	1022.545	2.18	MFLSFPTTK	sp P69905	0.003053	17823.8	22901.5	19513.0	19435.2	24346.8	22060.9	27890.3	27601.0	31889.7
1138	2	586.338	1170.662	13.91	VLSPADKTNVK	sp P69905	3.84E-06	9428.9	8360.6	9212.5	12574.9	12478.6	11968.1	19398.0	20193.5	18404.5
1247	6	710.563	4257.334	10.43	LLSHCLLVTLAAHLPAEFT	sp P69905	0.000314	91576.5	85716.0	90679.0	92382.0	79756.7	80525.7	137765.0	133061.5	123359.6
1619	5	605.734	3023.634	12.24	LLSHCLLVTLAAHLPAEFT	sp P69905	0.000938	31044.4	28249.7	29334.9	47228.4	40933.6	43951.8	31802.3	32129.3	36421.9
1654	5	625.724	3123.582	11.42	KVADALTNAVAHVDDMPI	sp P69905	0.002284	17606.2	17435.8	16770.9	27906.0	24945.9	27226.5	26848.5	27156.0	18150.9
1917	5	852.473	4257.329	17.02	LLSHCLLVTLAAHLPAEFT	sp P69905	0.002979	73078.6	68074.8	71403.4	74492.8	64628.6	61435.8	112116.3	92192.7	92134.4
2407	4	756.915	3023.632	19.83	LLSHCLLVTLAAHLPAEFT	sp P69905	0.007884	23429.2	23250.7	26486.6	41099.2	34046.7	35720.4	25918.3	29810.9	29886.8
10885	6	763.756	4576.493	9.92	LLSHCLLVTLAAHLPAEFT	sp P69905	4.22E-08	4381.9	5330.0	4711.0	2851.9	3042.4	3143.6	16601.6	15337.6	15300.8

11189	6	843.800	5056.754	13.99	VDPVNFKLLSHCLLVTLA	sp P69905	5.27E-05	7118.5	9052.2	8561.5	5419.2	5649.6	5401.2	8559.8	8577.1	7253.1
11638	3	540.642	1618.905	8.40	LWAYLTIEQLLEK	sp Q06033	1.78E-05	1223.1	1116.9	1177.6	1680.7	1638.8	1964.0	2434.8	2108.8	2355.1
599	3	402.228	1203.664	7.85	FKPTLSQQQK	sp Q14624	2.92E-06	17990.5	16929.0	17300.2	21090.9	17403.8	19065.2	34583.7	31766.6	32729.3
685	2	467.275	932.535	5.85	NVVFVIDK	sp Q14624	0.004237	17411.5	21356.8	17084.4	17842.9	15652.3	18192.9	22524.7	24819.7	24009.9
728	3	339.855	1016.542	7.57	FAHTVVTSR	sp Q14624	0.007277	10293.4	9004.4	10610.1	12072.1	10207.6	11551.0	14432.6	14678.5	12351.1
801	4	781.878	3123.484	15.44	FSSHVGGTLGQFYQEVL	sp Q14624	0.001063	80215.4	51061.1	66720.9	77135.7	73626.2	87426.5	37922.9	39752.8	31279.9
807	4	485.769	1939.046	7.64	NPLVWVHASPEHVVVTR	sp Q14624	0.040316	33342.4	45344.0	28581.0	36217.2	46867.9	36724.2	27926.4	33159.7	33899.1
885	3	805.732	2414.175	17.38	QGPVNLLSDPEQGVET	sp Q14624	0.04556	62291.7	37615.2	67344.2	66083.7	45809.6	69129.3	35041.6	36754.5	34745.2
968	2	642.836	1283.658	15.06	AGFSWIEVTFK	sp Q14624	0.000747	22160.2	22183.2	23401.2	29062.6	25517.5	29555.7	22702.1	24416.4	21974.5
975	2	654.334	1306.653	17.06	AEAQAQYSAAVAK	sp Q14624	0.005878	26043.9	27205.1	22490.7	26033.0	30991.0	27597.8	35252.9	35767.7	30747.9
1075	3	604.656	1810.946	5.92	SPEQQETVLDGNLIIR	sp Q14624	0.001997	21053.0	18233.2	25194.0	26232.7	25384.3	27772.0	40529.3	33042.4	34002.7
1152	2	500.283	998.552	6.73	LALDNGGLAR	sp Q14624	0.002437	9837.2	8728.0	8304.7	9896.0	12161.1	10027.1	13426.3	13235.7	14290.9
1172	2	464.759	927.504	6.33	ILDDLSPR	sp Q14624	0.007558	14241.9	17410.9	13405.8	16750.2	15804.6	15263.5	20446.1	18863.4	22298.1
1210	3	323.207	966.600	6.10	VRPQQLVK	sp Q14624	0.015064	8025.9	7464.7	7897.7	9319.3	8109.6	9016.6	9503.9	9558.7	9988.5
1461	2	500.776	999.537	6.78	LALDNGGLAR	sp Q14624	0.015831	5957.4	7826.4	7880.9	8487.5	10722.8	8767.2	10406.5	9031.9	11106.5
1472	3	552.970	1655.888	7.10	LQDRGPDVLTATVSGK	sp Q14624	0.000766	14502.2	16497.6	14490.7	16079.1	17362.9	18269.8	12986.0	11966.8	12363.8
1576	2	906.480	1810.945	13.90	SPEQQETVLDGNLIIR	sp Q14624	0.016069	27507.7	22362.4	29549.3	32304.7	35594.1	33595.4	46083.1	34620.2	34177.0
1610	5	723.145	3610.689	7.40	DTDRFSSHVGGTLGQFY	sp Q14624	0.000635	31866.2	29491.2	31150.4	28673.4	23763.1	28199.5	40703.2	47256.6	47605.4
1611	3	891.443	2671.308	22.97	QGPVNLLSDPEQGVET	sp Q14624	5.08E-07	24059.9	30608.4	22204.6	17614.9	20380.5	15797.4	99139.9	100804.1	84860.6
1694	3	987.849	2960.527	21.04	LWAYLTIQQLLEQTVSAS	sp Q14624	0.018615	44432.0	40810.7	50475.9	65306.2	54494.8	58153.5	50778.9	48692.9	39175.4
1900	4	546.781	2183.096	12.80	QLGLPGPPDVPDHAAYHI	sp Q14624	0.003852	21439.9	24850.7	21905.0	22381.1	22183.1	21428.3	16891.5	16146.3	20287.7
2005	2	415.728	829.442	3.95	SIQNNVR	sp Q14624	0.004077	12822.6	10631.5	12727.9	14227.6	11744.0	13630.3	22283.7	23393.0	25236.5
2176	3	405.892	1214.654	3.92	MNFRPGVLSSR	sp Q14624	1.23E-05	5586.9	4868.3	5284.5	5339.1	5655.7	5066.7	9352.6	9437.8	8374.2
2263	4	741.139	2960.527	19.32	LWAYLTIQQLLEQTVSAS	sp Q14624	0.007685	21296.1	19844.1	24099.7	29829.9	24783.4	28740.5	29927.6	28221.8	24416.5
2375	2	748.917	1495.820	16.06	ITFELVYEELLK	sp Q14624	0.00028	16931.5	13192.1	17264.3	21902.5	20807.4	22958.6	14852.7	16010.2	15432.7
2620	5	641.946	3204.694	12.42	AGFSWIEVTFKNPLVWV	sp Q14624	2.48E-07	12354.5	10575.6	11275.2	10945.1	8800.2	9030.5	37670.9	41887.5	39697.0
2963	4	736.160	2940.613	15.65	TGLLLLSDPKVTIGLLFV	sp Q14624	0.000494	12815.3	12092.2	14920.4	13826.7	13592.9	11352.2	19630.9	21550.7	23683.2
3205	3	375.190	1122.548	3.47	NVHSGSTFFK	sp Q14624	1.91E-05	2923.7	3188.1	2774.1	3393.2	3650.7	3466.0	4310.0	4594.5	4456.5
3271	4	1300.381	5197.495	16.06	RIHEDSDSALQLQDFYQE	sp Q14624	0.002654	35479.0	25247.2	38644.3	54909.1	49244.0	53886.7	56447.5	54908.4	54505.3
3311	3	810.454	2428.340	14.91	TGLLLLSDPKVTIGLLFV	sp Q14624	7.41E-09	17367.2	15938.6	16694.2	23384.1	22226.8	23772.2	6332.3	5667.1	5653.5
4531	5	1040.507	5197.496	17.28	RIHEDSDSALQLQDFYQE	sp Q14624	0.00168	17400.8	13021.7	19178.6	28133.5	22994.1	24667.5	27251.0	29711.7	26555.6
4688	4	1261.356	5041.395	18.28	IHEDSDSALQLQDFYQEV	sp Q14624	1.46E-05	21011.2	24822.4	24542.5	27684.3	27373.7	30549.8	32442.9	29334.0	29025.3
5970	3	499.614	1495.820	7.92	ITFELVYEELLK	sp Q14624	0.000929	2762.0	2125.0	2757.3	3762.2	3390.9	3530.4	2555.5	2723.5	2822.8
6042	4	1043.543	4170.142	17.30	ILDDLSPRDQFNLIWFSTE	sp Q14624	4.05E-07	4980.4	3996.5	4078.7	4585.7	4647.4	3448.2	37064.1	28580.8	25018.2

6425	3	800.057	2397.150	16.38	QGPVLLSDPEQGVET sp Q14624	0.000216	7688.6	6962.1	8900.8	9597.2	7361.4	9046.6	5035.9	3964.4	4119.8
6633	3	865.130	2592.368	17.38	LPEGSVSLIILLTDGDPTV sp Q14624	1.06E-06	9945.4	7328.9	7585.7	13733.1	11277.4	13809.1	3274.1	2836.2	2865.8
13072	5	1009.286	5041.396	13.55	IHEDSDSALQLQDFYQEV sp Q14624	2.26E-05	3775.3	4072.8	4016.4	4988.9	4187.5	4950.8	6046.9	5599.4	5034.6
15097	5	835.036	4170.144	1.43	ILDDLSPRDQFNLIWFSTE sp Q14624	1.28E-07	982.1	853.7	940.8	844.2	819.3	598.0	6921.2	5694.6	5575.2
26410	3	1681.474	5041.401	12.32	IHEDSDSALQLQDFYQEV sp Q14624	0.001742	2483.5	2324.4	2483.3	2702.4	2549.4	3392.0	3300.8	2237.9	3230.6
29203	4	866.926	3463.675	17.58	SFAAGIQALGGTNINDAM sp Q14624	0.000148	399.8	436.9	492.3	1038.6	833.5	1018.7	630.8	429.3	415.5
32032	3	1155.565	3463.673	17.35	SFAAGIQALGGTNINDAM sp Q14624	7.57E-05	565.6	489.9	415.5	1227.4	1019.5	1270.3	258.1	411.0	412.2
35576	5	1208.813	6039.030	12.99	SFAAGIQALGGTNINDAM sp Q14624	0.000794	561.5	518.2	607.0	512.7	336.7	569.7	1487.0	1093.8	1272.9
23997	3	961.183	2880.528	19.90	EYGVVLAPDGSTVAVEPL sp Q96PD5	0.002565	1124.6	871.0	1002.6	1701.6	1510.0	1535.0	727.1	367.4	255.7
3840	2	730.382	1458.750	16.06	FGQSGPIVLDVDR sp Q9UGM	9.13E-08	16.0	40.1	44.4	148.4	102.2	139.8	32908.2	31938.8	29266.2

Supplementary Table S2. The 80 WGA-enriched plasma proteins selected for protein quantification

					Non-metastatic CRC vs Healthy control						Metastatic CRC vs Healthy control					
UniProt	Gene	ID	Description	Peptides used	NM1/ Avg Ctr	NM2/ Avg Ctr	NM2/ Avg Ctr	LOG 10 p value	Fold change (NM/Ctr)	p-value	M1/ Avg Ctr	M2/ Avg Ctr	M3/ Avg Ctr	LOG 10 p value	Fold change (M/Ctr)	
sp Q9UGM3	DMBT1	DMBT1_HUMAN	Deleted in malignant brain tumors 1 protein	1	4.43	3.05	4.17	1.6806	0.0209	3.88	1.15	1.22	1.15	2.9189	0.0012	1.17
sp P01833	PIGR	PIGR_HUMAN	Polymeric immunoglobulin receptor	1	2.07	1.87	1.48	1.3583	0.0438	1.80	-1.35	-1.36	-1.28	2.1955	0.0064	-1.33
sp P04003	C4BPA	C4BPA_HUMAN	C4b-binding protein alpha chain	1	1.36	1.00	1.24	0.7081	>0.05	1.20	1.24	1.22	1.21	1.7400	0.0182	1.23
sp Q06033	ITIH3	ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3	1	1.43	1.40	1.68	1.5403	0.0288	1.50	1.43	1.49	1.42	2.1251	0.0075	1.44
sp P08603	CFH	CFAH_HUMAN	Complement factor H	1	1.02	1.18	1.01	0.5018	>0.05	1.07	1.61	1.62	1.59	2.3020	0.0050	1.60
sp P00736	C1R	C1R_HUMAN	Complement C1r subcomponent	1	1.81	1.19	1.39	0.9024	>0.05	1.47	1.02	-1.10	-1.09	1.4201	0.0380	-0.39
sp P02042	HBD	HBD_HUMAN	Hemoglobin subunit delta	1	1.06	1.60	1.11	0.5557	>0.05	1.25	-1.71	-1.62	-1.76	1.6317	0.0233	-1.70
sp O75882	ATRNL1	ATRNL1_HUMAN	Attractin	1	-1.22	-1.22	-1.20	5.0120	<0.0001	-1.21	-1.08	-1.18	-1.10	0.6718	>0.05	-1.12
sp P01714	IGLV3-19	LV319_HUMAN	Immunoglobulin lambda variable 3-19	1	-1.01	-1.40	-1.19	2.5872	0.0026	-1.20	20.85	18.60	24.18	0.3632	>0.05	21.21
sp P06276	BCHE	CHLE_HUMAN	Cholinesterase	1	1.00	1.04	1.00	0.4855	>0.05	1.01	-1.15	-1.15	-1.21	2.9835	0.0010	-1.17
sp P05546	SERPIND1	HEP2_HUMAN	Heparin cofactor 2	1	1.08	-1.05	-1.02	0.7001	>0.05	-0.33	1.02	1.07	-1.04	3.6544	0.0002	0.35
sp P00748	F12	FA12_HUMAN	Coagulation factor XII	1	1.21	1.17	1.12	1.6106	0.0245	1.16	1.10	1.06	1.10	2.4333	0.0037	1.09
sp O75636	FCN3	FCN3_HUMAN	Ficolin-3	1	1.11	1.06	1.10	1.4551	0.0351	1.09	-2.05	-2.10	-2.00	3.2078	0.0006	-2.05
sp A0A075B6H9	IGLV4-69	LV469_HUMAN	Immunoglobulin lambda variable 4-69	1	1.24	-1.02	1.17	0.2645	>0.05	0.46	1.60	1.53	1.66	2.9170	0.0012	1.60
sp P27169	PON1	PON1_HUMAN	Serum paraoxonase/arylesterase 1	1	1.30	1.22	1.27	2.0805	0.0083	1.26	-1.79	-2.01	-2.02	3.7121	0.0002	-1.94
sp O75460	ERN1	ERN1_HUMAN	Serine/threonine-protein kinase/endoribonuclease IRE1	1	1.53	1.42	1.72	1.6264	0.0236	1.56	1.30	1.21	1.25	3.1571	0.0007	1.25
sp P01817	HV205	HV205_HUMAN	Immunoglobulin heavy variable 2-5	1	-1.07	-1.37	-1.16	2.8053	0.0016	-1.20	-1.15	-1.18	-1.32	2.7597	0.0017	-1.21
sp Q96PD5	PGLYRP2	PGRP2_HUMAN	N-acetylmuramoyl-L-alanine amidase	1	1.70	1.51	1.54	1.9797	0.0105	1.58	1.34	1.30	1.28	1.4248	0.0376	1.30
sp P06681	C2	CO2_HUMAN	Complement C2	2	1.04	-1.24	1.07	0.3459	>0.05	0.29	1.39	1.47	1.38	3.6505	0.0002	1.42
sp P02774	GC	VTDB_HUMAN	Vitamin D-binding protein	2	-1.42	-1.99	-1.71	2.4406	0.0036	-1.71	1.51	1.53	1.38	1.9913	0.0102	1.47
sp P06310	IGKV2-30	KV230_HUMAN	Immunoglobulin kappa variable 2-30	2	-1.22	-1.19	-1.09	3.4605	0.0003	-1.17	-1.37	-2.72	-3.91	0.8236	>0.05	-2.67
sp P00739	HPR	HPTR_HUMAN	Haptoglobin-related protein	2	-1.03	1.31	1.09	0.2664	>0.05	0.46	-1.46	-1.40	-1.43	0.2515	>0.05	-1.43
sp P25311	AZGP1	ZA2G_HUMAN	Zinc-alpha-2-glycoprotein	2	-1.35	-1.61	-1.30	2.7877	0.0016	-1.42	-1.03	-1.09	1.05	0.7114	>0.05	-0.36
sp O43866	CD5L	CD5L_HUMAN	CD5 antigen-like	2	-1.06	-1.15	-1.18	3.4928	0.0003	-1.13	1.20	1.15	1.23	0.7263	>0.05	1.19
sp P02753	RBP4	RET4_HUMAN	Retinol-binding protein 4	2	1.26	1.17	1.24	1.8320	0.0147	1.22	-1.88	-1.80	-1.95	3.9514	0.0001	-1.87
sp P06312	IGKV4-1	KV401_HUMAN	Immunoglobulin kappa variable 4-1	2	-1.15	1.01	-1.08	0.7329	>0.05	-0.41	1.05	1.07	1.01	3.6891	0.0002	1.05
sp P02787	TF	TRFE_HUMAN	Serotransferrin	2	-1.26	-1.34	-1.24	3.8060	0.0002	-1.28	-1.77	-1.89	-1.90	3.6705	0.0002	-1.85
sp P01877	IGHA2	IGHA2_HUMAN	Immunoglobulin heavy constant alpha 2	3	-1.12	-1.19	-1.11	3.9034	0.0001	-1.14	-2.26	-2.27	-2.69	2.3654	0.0043	-2.41
sp P01860	IGHG3	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3	3	-1.54	-1.66	-1.62	3.7221	0.0002	-1.61	1.12	1.15	1.45	3.2581	0.0006	1.24
sp P02748	C9	CO9_HUMAN	Complement component C9	4	1.92	1.52	1.63	1.5555	0.0278	1.69	-1.36	-1.37	-1.57	1.8598	0.0138	-1.43
sp P0C0L5	C4B	CO4B_HUMAN	Complement C4-B	4	1.61	1.35	1.49	1.6373	0.0231	1.48	1.47	1.42	1.31	2.3035	0.0050	1.40
sp P00751	CFB	CFAB_HUMAN	Complement factor B	4	-1.07	-1.10	-1.17	3.6899	0.0002	-1.11	1.31	1.52	1.29	1.8904	0.0129	1.37
sp P22792	CPN2	CPN2_HUMAN	Carboxypeptidase N subunit 2	4	-1.04	-1.27	-1.19	3.0374	0.0009	-1.17	-1.08	-1.18	-1.10	3.7174	0.0002	-1.12
sp P08185	SERPINA6	CBG_HUMAN	Corticosteroid-binding globulin	4	1.08	-1.23	1.05	0.3409	>0.05	0.30	-1.45	-1.53	-1.27	3.1342	0.0007	-1.42
sp P08697	SERPINF2	A2AP_HUMAN	Alpha-2-antiplasmin	4	-1.17	-1.19	-1.27	3.6782	0.0002	-1.21	1.70	1.64	1.81	3.3709	0.0004	1.71
sp P0C0L4	C4A	CO4A_HUMAN	Complement C4-A	5	2.22	1.65	2.28	1.4556	0.0350	2.05	1.78	1.94	1.62	3.6756	0.0002	1.78
sp P01861	IGHG4	IGHG4_HUMAN	Immunoglobulin heavy constant gamma 4	5	-1.41	-1.82	-1.52	2.6408	0.0023	-1.58	-1.38	-1.30	-1.41	3.2839	0.0005	-1.36
sp P02751	FN1	FINC_HUMAN	Fibronectin	5	-1.44	-1.69	-1.51	3.0557	0.0009	-1.55	1.63	1.52	1.69	3.9954	0.0001	1.61
sp P01031	C5	CO5_HUMAN	Complement C5	6	1.53	1.39	1.61	1.7824	0.0165	1.51	1.50	1.50	1.62	1.6814	0.0208	1.54
sp P02743	APCS	SAMP_HUMAN	Serum amyloid P-component	6	1.10	1.10	1.11	3.0010	0.0010	1.11	-2.62	-2.68	-2.68	4.5590	<0.0001	-2.66
sp P01859	IGHG2	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2	6	-1.24	-1.26	-1.25	5.0495	<0.0001	-1.25	1.04	1.05	-1.06	3.3132	0.0005	0.34

sp P02766	TTR	TTHY_HUMAN	Transthyretin	6	1.03	1.04	1.00	0.7072	>0.05	1.02	-1.32	-1.41	-1.40	3.8191	0.0002	-1.37
sp P35858	IGFALS	ALS_HUMAN	Insulin-like growth factor-binding protein complex acid labile subunit	6	-1.20	-1.27	-1.23	4.0780	0.0001	-1.23	-1.64	-1.72	-1.76	3.6588	0.0002	-1.71
sp P01591	JCHAIN	IGJ_HUMAN	Immunoglobulin J chain	7	-1.16	-1.09	-1.17	3.8530	0.0001	-1.14	-2.10	-2.09	-1.96	1.9099	0.0123	-2.05
sp P04004	VTN	VTNC_HUMAN	Vitronectin	7	-1.09	-1.03	-1.06	4.1237	0.0001	-1.06	-1.17	-1.17	-1.21	4.5078	<0.0001	-1.18
sp P01019	AGT	ANGT_HUMAN	Angiotensinogen	7	-1.18	-1.39	-1.30	3.1245	0.0008	-1.29	-1.24	-1.27	-1.22	3.7820	0.0002	-1.25
sp P10909	CLU	CLUS_HUMAN	Clusterin	8	-1.05	1.09	-1.03	0.6967	>0.05	-0.33	-1.04	-1.02	-1.12	1.8484	0.0142	-1.06
sp P01834	IGKC	IGKC_HUMAN	Immunoglobulin kappa constant	9	-1.01	1.06	-1.02	0.7058	>0.05	-0.32	1.06	1.04	1.00	0.3490	>0.05	1.03
sp P04217	A1BG	A1BG_HUMAN	Alpha-1B-glycoprotein	9	-1.31	-1.12	-1.36	2.9758	0.0011	-1.26	-2.00	-1.95	-1.97	3.6628	0.0002	-1.98
sp P01857	IGHG1	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1	9	-1.25	-1.18	-1.20	4.1486	0.0001	-1.21	1.16	1.15	1.21	4.3015	<0.0001	1.17
sp P02760	AMBP	AMBP_HUMAN	Protein AMBP	10	1.36	1.38	1.40	3.1674	0.0007	1.38	-1.04	-1.04	-1.01	2.4293	0.0037	-1.03
sp P19652	ORM2	A1AG2_HUMAN	Alpha-1-acid glycoprotein 2	12	1.14	1.10	1.06	0.3826	0.0334	1.10	-1.66	-1.70	-1.97	0.3324	>0.05	-1.78
sp P04114	APOB	APOB_HUMAN	Apolipoprotein B-100	12	1.20	1.29	1.14	1.4087	0.0390	1.21	2.43	2.48	3.14	4.3344	<0.0001	2.68
sp P04196	HRG	HRG_HUMAN	Histidine-rich glycoprotein	13	1.16	1.05	1.19	1.0474	>0.05	1.13	-1.29	-1.23	-1.40	0.7782	>0.05	-1.31
sp P02750	LRG1	A2GL_HUMAN	Leucine-rich alpha-2-glycoprotein	14	1.29	1.23	1.33	2.0089	0.0098	1.28	1.14	1.16	1.12	4.4624	<0.0001	1.14
sp P02763	ORM1	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1	14	1.18	1.41	1.19	1.1401	>0.05	1.26	-1.01	1.05	1.10	2.2969	0.0050	0.38
sp P68871	HBB	HBB_HUMAN	Hemoglobin subunit beta	15	1.20	1.33	1.22	1.5893	0.0257	1.25	1.30	1.35	1.29	2.2000	0.0063	1.31
sp P05155	SERPING1	IC1_HUMAN	Plasma protease C1 inhibitor	15	1.24	1.32	1.18	1.6132	0.0244	1.25	-1.09	-1.10	-1.24	0.9416	>0.05	-1.14
sp P01042	KNG1	KNG1_HUMAN	Kininogen-1	16	1.11	1.07	1.08	1.7536	0.0176	1.09	1.11	1.09	1.02	2.6543	0.0022	1.07
sp P69905	HBA1	HBA_HUMAN	Hemoglobin subunit alpha	18	1.18	1.25	1.15	1.6009	0.0251	1.19	1.38	1.24	1.42	3.1304	0.0007	1.35
sp P00734	F2	THRB_HUMAN	Prothrombin	18	1.18	1.29	1.14	1.3545	0.0442	1.20	-1.05	-1.08	-1.04	2.4916	0.0032	-1.05
sp P01876	IGHA1	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1	18	-1.13	-1.28	-1.18	3.4045	0.0004	-1.20	-1.19	-1.21	-1.16	0.3482	>0.05	-1.19
sp P01008	SERPINC1	ANT3_HUMAN	Antithrombin-III	19	-1.29	-1.21	-1.26	3.9674	0.0001	-1.25	1.05	1.02	1.16	4.5439	<0.0001	1.08
sp P43652	AFM	AFAM_HUMAN	Afamin	19	-1.25	-1.21	-1.26	4.3004	0.0001	-1.24	-2.39	-2.56	-2.63	4.6107	<0.0001	-2.53
sp P19827	ITIH1	ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1	20	1.22	1.20	1.14	1.7732	0.0169	1.19	2.08	1.80	2.01	1.2260	>0.05	1.96
sp P19823	ITIH2	ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2	22	1.20	1.14	1.18	1.9533	0.0111	1.17	1.35	1.32	1.26	0.7576	>0.05	1.31
sp P02765	AHSG	FETUA_HUMAN	N Alpha-2-HS-glycoprotein	23	1.18	1.05	1.16	1.0702	>0.05	1.13	-1.80	-1.84	-1.62	0.8860	>0.05	-1.75
sp P01011	SERPINA3	AACT_HUMAN	Alpha-1-antichymotrypsin	24	1.30	1.24	1.22	2.0698	0.0085	1.25	-1.31	-1.35	-1.24	2.2267	0.0059	-1.30
sp P02671	FGA	FIBA_HUMAN	Fibrinogen alpha chain	32	-1.28	-1.31	-1.30	4.7869	<0.0001	-1.30	1.94	2.00	2.12	1.7400	0.0182	2.02
sp P02679	FGG	FIBG_HUMAN	Fibrinogen gamma chain	32	-1.25	-1.27	-1.25	5.0410	<0.0001	-1.26	1.40	1.37	1.40	1.5949	0.0254	1.39
sp P01871	IGHM	IGHM_HUMAN	Immunoglobulin heavy constant mu	34	-1.26	-1.21	-1.28	4.0846	0.0001	-1.25	1.04	-1.08	1.00	4.4724	<0.0001	0.32
sp P02675	FGB	FIBB_HUMAN	Fibrinogen beta chain	37	-1.40	-1.42	-1.33	3.9636	0.0001	-1.38	1.19	1.28	-1.09	2.0217	0.0095	0.46
sp P01009	SERPINA1	A1AT_HUMAN	Alpha-1-antitrypsin	37	1.03	1.10	1.00	0.5353	>0.05	1.04	1.10	1.04	1.09	4.4053	<0.0001	1.08
sp Q14624	ITIH4	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4	40	1.20	1.11	1.19	1.5999	0.0251	1.17	1.74	1.75	1.74	2.1681	0.0068	1.74
sp P02790	HPX	HEMO_HUMAN	Hemopexin	45	1.46	1.46	1.46	4.6672	<0.0001	1.46	1.12	1.05	1.02	2.3839	0.0041	1.07
sp P00738	HP	HPT_HUMAN	Haptoglobin	60	1.04	1.14	1.04	0.8076	>0.05	1.07	1.30	1.24	1.24	2.5493	0.0028	1.26
sp P02768	ALB	ALBU_HUMAN	Serum albumin	63	-1.42	-1.32	-1.81	2.4520	0.0035	-1.52	-1.50	-1.50	-1.51	4.4652	<0.0001	-1.51
sp P00450	CP	CERU_HUMAN	Ceruloplasmin	82	1.37	1.41	1.33	2.4194	0.0038	1.37	-1.55	-1.58	-2.06	2.7328	0.0019	-1.73
sp P01024	C3	CO3_HUMAN	Complement C3	128	1.40	1.38	1.38	3.7168	0.0002	1.39	1.14	1.14	1.09	4.0388	0.0001	1.12
sp P01023	A2M	A2MG_HUMAN	Alpha-2-macroglobulin	168	1.02	1.00	-1.01	0.3699	>0.05	0.33	-1.32	-1.36	-1.37	7.6089	<0.0001	-1.35



Supplementary Table S3. List of the 62 WGA-enriched plasma proteins containing at least 2 peptides and their fold change in non-metastatic and metastatic CRC patients compared to those of the healthy controls

UniProt	Gene	ID	Description	Peptides used	Non-metastatic CRC vs Healthy control		Metastatic CRC vs Healthy control	
					p-value	Fold change (NM/Ctr)	p-value	Fold change (M/Ctr)
sp P00738	HP	HPT_HUMAN	Haptoglobin	60	>0.05	1.07	0.0028	2.02
sp P02748	C9	CO9_HUMAN	Complement component C9	4	0.0278	1.69	0.0138	1.78
sp P02750	LRG1	A2GL_HUMAN	Leucine-rich alpha-2-glycoprotein	14	0.0098	1.28	0.0000	1.74
sp P02763	ORM1	A1AG1_HUMAN	Alpha-1-acid glycoprotein 1	14	>0.05	1.26	0.0050	1.71
sp P68871	HBB	HBB_HUMAN	Hemoglobin subunit beta	15	0.0257	1.25	0.0063	1.61
sp P06681	C2	CO2_HUMAN	Complement C2	2	>0.05	0.29	0.0002	1.60
sp P02760	AMBP	AMBP_HUMAN	Protein AMBP	10	0.0007	1.38	0.0037	1.60
sp P02774	GC	VTDB_HUMAN	Vitamin D-binding protein	2	0.0036	-1.71	0.0102	1.47
sp P01042	KNG1	KNG1_HUMAN	Kininogen-1	16	0.0176	1.09	0.0022	1.44
sp P0C0L5	C4B	CO4B_HUMAN	Complement C4-B	4	0.0231	1.48	0.0050	1.42
sp P00751	CFB	CFAB_HUMAN	Complement factor B	4	0.0002	-1.11	0.0129	1.40
sp P69905	HBA1	HBA_HUMAN	Hemoglobin subunit alpha	18	0.0251	1.19	0.0007	1.39
sp P02790	HPX	HEMO_HUMAN	Hemopexin	45	<0.0001	1.46	0.0041	1.31
sp Q14624	ITIH4	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4	40	0.0251	1.17	0.0068	1.31
sp P00734	F2	THRB_HUMAN	Prothrombin	18	0.0442	1.20	0.0032	1.30
sp P01877	IGHA2	IGHA2_HUMAN	Immunoglobulin heavy constant alpha 2	3	0.0001	-1.14	0.0043	1.26
sp P02675	FGB	FIBB_HUMAN	Fibrinogen beta chain	37	0.0001	-1.38	0.0095	1.25
sp P06310	IGKV2-30	KV230_HUMAN	Immunoglobulin kappa variable 2-30	2	0.0003	-1.17	>0.05	1.24
sp P00450	CP	CERU_HUMAN	Ceruloplasmin	82	0.0038	1.37	0.0019	1.23
sp P10909	CLU	CLUS_HUMAN	Clusterin	8	>0.05	-0.33	0.0142	1.19
sp P01591	JCHAIN	IGJ_HUMAN	Immunoglobulin J chain	7	0.0001	-1.14	0.0123	1.17
sp P02671	FGA	FIBA_HUMAN	Fibrinogen alpha chain	32	<0.0001	-1.30	0.0182	1.17
sp P01011	SERPINA3	AACT_HUMAN	Alpha-1-antichymotrypsin	24	0.0085	1.25	0.0059	1.14
sp P01031	C5	CO5_HUMAN	Complement C5	6	0.0165	1.51	0.0208	1.12
sp P02679	FGG	FIBG_HUMAN	Fibrinogen gamma chain	32	<0.0001	-1.26	0.0254	1.09
sp P19827	ITIH1	ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1	20	0.0169	1.19	>0.05	1.08
sp P02765	AHSG	FETUA_HUMAN	N Alpha-2-HS-glycoprotein	23	>0.05	1.13	>0.05	1.07
sp P04196	HRG	HRG_HUMAN	Histidine-rich glycoprotein	13	>0.05	1.13	>0.05	1.07
sp P05155	SERPING1	IC1_HUMAN	Plasma protease C1 inhibitor	15	0.0244	1.25	>0.05	1.05
sp P19823	ITIH2	ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2	22	0.0111	1.17	>0.05	1.03
sp P00739	HPR	HPTR_HUMAN	Haptoglobin-related protein	2	>0.05	0.46	>0.05	0.46
sp P19652	ORM2	A1AG2_HUMAN	Alpha-1-acid glycoprotein 2	12	0.0334	1.10	>0.05	0.38
sp P01876	IGHA1	IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1	18	0.0004	-1.20	>0.05	0.35
sp P01834	IGKC	IGKC_HUMAN	Immunoglobulin kappa constant	9	>0.05	-0.32	>0.05	0.34
sp P25311	AZGP1	ZA2G_HUMAN	Zinc-alpha-2-glycoprotein	2	0.0016	-1.42	>0.05	-0.36
sp O43866	CD5L	CD5L_HUMAN	CD5 antigen-like	2	0.0003	-1.13	>0.05	-0.39
sp P01008	SERPINC1	ANT3_HUMAN	Antithrombin-III	19	0.0001	-1.25	<0.0001	-1.03
sp P02743	APCS	SAMP_HUMAN	Serum amyloid P-component	6	0.0010	1.11	<0.0001	-1.05

sp P0C0L4	C4A	CO4A_HUMAN	Complement C4-A	5	0.0350	2.05	<0.0001	-1.06
sp P22792	CPN2	CPN2_HUMAN	Carboxypeptidase N subunit 2	4	0.0009	-1.17	<0.0001	-1.12
sp P01861	IGHG4	IGHG4_HUMAN	Immunoglobulin heavy constant gamma 4	5	0.0023	-1.58	<0.0001	-1.14
sp P01024	C3	CO3_HUMAN	Complement C3	128	0.0002	1.39	<0.0001	-1.17
sp P04004	VTN	VTNC_HUMAN	Vitronectin	7	0.0001	-1.06	<0.0001	-1.18
sp P01871	IGHM	IGHM_HUMAN	Immunoglobulin heavy constant mu	34	0.0001	-1.25	<0.0001	-1.19
sp P01860	IGHG3	IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3	3	0.0002	-1.61	<0.0001	-1.21
sp P04114	APOB	APOB_HUMAN	Apolipoprotein B-100	12	0.0390	1.21	<0.0001	-1.25
sp P04217	A1BG	A1BG_HUMAN	Alpha-1B-glycoprotein	9	0.0011	-1.26	<0.0001	-1.30
sp P01859	IGHG2	IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2	6	<0.0001	-1.25	<0.0001	-1.31
sp P02753	RBP4	RET4_HUMAN	Retinol-binding protein 4	2	0.0147	1.22	<0.0001	-1.33
sp P01009	SERPINA1	A1AT_HUMAN	Alpha-1-antitrypsin	37	>0.05	1.04	<0.0001	-1.35
sp P06312	IGKV4-1	KV401_HUMAN	Immunoglobulin kappa variable 4-1	2	>0.05	-0.41	<0.0001	-1.36
sp P02766	TTR	TTHY_HUMAN	Transthyretin	6	>0.05	1.02	<0.0001	-1.37
sp P01857	IGHG1	IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1	9	0.0001	-1.21	<0.0001	-1.43
sp P08185	SERPINA6	CBG_HUMAN	Corticosteroid-binding globulin	4	>0.05	0.30	0.001	-1.43
sp P01023	A2M	A2MG_HUMAN	Alpha-2-macroglobulin	168	>0.05	0.33	<0.0001	-1.51
sp P01019	AGT	ANGT_HUMAN	Angiotensinogen	7	0.0008	-1.29	<0.0001	-1.71
sp P02787	TF	TRFE_HUMAN	Serotransferrin	2	0.0002	-1.28	<0.0001	-1.87
sp P43652	AFM	AFAM_HUMAN	Afamin	19	0.0001	-1.24	<0.0001	-1.98
sp P02751	FN1	FINC_HUMAN	Fibronectin	5	0.0009	-1.55	<0.0001	-2.05
sp P35858	IGFALS	ALS_HUMAN	Insulin-like growth factor-binding protein comple	6	0.0001	-1.23	<0.0001	-2.05
sp P08697	SERPINF2	A2AP_HUMAN	Alpha-2-antiplasmin	4	0.0002	-1.21	<0.0001	-2.53
sp P02768	ALB	ALBU_HUMAN	Serum albumin	63	0.0035	-1.52	<0.0001	-2.66

Supplementary Table S4. N-linked glycosylated searched against 20 WGA-enriched glycoproteins of the pooled sample of healthy control, non-metastatic and metastatic CRC patient groups (criteria: DeltaMod > 20, Log Prob > 1.3 (p-value < 0.05) and MS/MS fragmentations containing modifications were found in at least 2 of 3 runs)

Description	N-glycosylation	Healthy control		Non-metastatic CRC		Metastatic CRC	
		Delta Mod	Log Prob	Delta Mod	Log Prob	Delta Mod	Log Prob
>sp P01023 A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3							
K.GCVLLSYLN <sup>55</sup> [+2204.772]ETVTVSASLESVR.G	HexNAc(4)Hex(5)NeuAc(2)	48.33	4.00	-	-	-	-
K.GCVLLSYLN <sup>55</sup> [+2350.830]ETVTVSASLESVR.G	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	33.45	4.73	-	-	-	-
R.GN <sup>70</sup> [+2204.772]R.S	HexNAc(4)Hex(5)NeuAc(2)	-	-	116.01	2.17	-	-
K.IITILEEEMN <sup>247</sup> [+2018.708]VSVCGLYTYGKVPVGHVTVSICR.K	HexNAc(3)Hex(6)Fuc(1)NeuAc(1)	-	-	383.31	8.27	-	-
K.IITILEEEMN <sup>247</sup> [+2262.814]VSVCGLYTYGKVPVGHVTVSICR.K	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	102.42	3.35	-	-	-	-
K.VSN <sup>1424</sup> [+1913.677]QTLSLFFTVLQDVPVR.D	HexNAc(4)Hex(5)NeuAc(1)	189.17	3.92	151.31	3.70	-	-
K.VSN <sup>1424</sup> [+2059.735]QTLSLFFTVLQDVPVR.D	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	154.10	4.04	161.60	4.13	-	-
K.VSN <sup>1424</sup> [+2226.754]QTLSLFFTVLQDVPVR.D	HexNAc(4)Hex(5)NeuAc(2)Na(1)	-	-	81.68	3.07	-	-
K.VSN <sup>1424</sup> [+2569.905]QTLSLFFTVLQDVPVR.D	HexNAc(5)Hex(6)NeuAc(2)	40.34	2.76	-	-	-	-
>sp P00738 HPT_HUMAN Haptoglobin OS=Homo sapiens OX=9606 GN=HP PE=1 SV=1							
K.MVSHHN <sup>184</sup> [+1913.677]LTTGATLINEQWLLTTAK.N	HexNAc(4)Hex(5)NeuAc(1)	145.40	3.62	156.52	2.96	200.20	2.60
K.MVSHHN <sup>184</sup> [+2018.708]LTTGATLINEQWLLTTAK.N	HexNAc(3)Hex(6)Fuc(1)NeuAc(1)	129.34	3.42	56.23	3.18	151.24	3.06
K.MVSHHN <sup>184</sup> [+2204.772]LTTGATLINEQWLLTTAK.N	HexNAc(4)Hex(5)NeuAc(2)	23.91	3.15	46.94	2.54	20.55	2.70
K.MVSHHN <sup>184</sup> [+2861.000]LTTGATLINEQWLLTTAK.N	HexNAc(5)Hex(6)NeuAc(3)	-	-	47.68	3.48	-	-
K.VVLHPN <sup>241</sup> [+1913.677]YSQVDIGLIK.L	HexNAc(4)Hex(5)NeuAc(1)	166.98	4.02	37.92	3.51	53.89	3.68
K.VVLHPN <sup>241</sup> [+2204.772]YSQVDIGLIK.L	HexNAc(4)Hex(5)NeuAc(2)	33.27	2.32	46.13	3.64	35.92	2.85
K.VVLHPN <sup>241</sup> [+2226.754]YSQVDIGLIK.L	HexNAc(4)Hex(5)NeuAc(2)Na(1)	-	-	98.82	2.95	-	-
K.VVLHPN <sup>241</sup> [+2278.809]YSQVDIGLIK.L	HexNAc(5)Hex(6)NeuAc(1)	-	-	-	-	47.30	3.18

>sp P02763 A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens OX=9606 GN=ORM1 PE=1 SV=1							
R.NEEYN <sup>56</sup> [+2204.772]K.S	HexNAc(4)Hex(5)NeuAc(2)	160.38	2.78	200.79	2.43	198.73	2.55
R.QDQCIYN <sup>93</sup> [+2861.000]TTYLVNQQR.E	HexNAc(5)Hex(6)NeuAc(3)	-	-	59.58	3.50	21.86	2.19
>sp P0C0L4 CO4A_HUMAN Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=2							
R.GLN <sup>1328</sup> [+2204.772]VTLSSSTGR.N	HexNAc(4)Hex(5)NeuAc(2)	-	-	-	-	185.59	3.48

Supplementary Table S5. Glycated peptides searched against 20 WGA-enriched glycoproteins of the pooled sample of healthy control, non-metastatic and metastatic CRC patient groups (criteria: DeltaMod > 20, Log Prob > 1.3 (p-value < 0.05) and MS/MS fragmentations containing modifications were found in at least 2 of 3 runs)

Peptide sequence	Modification	Healthy control		Non-metastatic CRC		Metastatic CRC	
		Delta	Log	Delta	Log	Delta	Log
		Mod	Prob	Mod	Prob	Mod	Prob
>sp P01023 A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3							
R.AVDQSVLLMK <sup>608</sup> [+58.005]PDAELSASSVYNLLPEKDLTGFPGLNDQDNEDCINR.H	CML	73.56	6.58	74.81	6.42	78.67	6.56
K.DTVIK <sup>901</sup> [+58.005]PLLVEPEGLEKETTFFNSLLCPSGGGEVSEELSLK.L	CML	22.30	2.69	126.19	5.80	-	-
K.DTVIKPLLVEPEGLEK <sup>912</sup> [+58.005]JETTFFNSLLCPSGGGEVSEELSLK.L	CML	83.46	2.73	-	-	-	-

Note: CML= carboxymethyllysine