Supplementary Online Content

Mongan D, Föcking M, Healy C, et al; European Network of National Schizophrenia Networks Studying Gene-Environment Interactions (EU-GEI) High Risk Study Group. Development of proteomic prediction models for transition to psychotic disorder in the clinical high-risk state and psychotic experiences in adolescence. *JAMA Psychiatry*. Published online August 26, 2020. doi:10.1001/jamapsychiatry.2020.2459

eAppendix.

This supplementary material has been provided by the authors to give readers additional information about their work.

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Sequence	N-term cleavage window	C-term cleavage window	Amino acid before	First amino acid	Second amino acid	Second last amino acid	Last amino acid	Amino acid after	A Count	R Count	N Count	D Count	C Count	Q Count	E Count	G Count	H Count	I Count	L Count	K Count	M Count	F Count	P Count	S Count	T Count	W Count	Y Count	V Count	U Count	O Count	Length	Missed cleavages	Mass	Proteins	Leading razor protein	Start position	End position	Unique (Groups)	Unique (Proteins)	Charges	PEP	Score	id	Protein group IDs	Mod. peptide IDs	Evidence IDs	MS/MS IDs	Best MS/MS	Oxidation (M) site IDs	MS/MS Count
AAAITSDILEALGR	EDDLSSFRAAAITSDI	DILEALGRDGHFTLFA	R	A	A	G	R	D	4	1	0	1	0	0	1	1	0	2	2	0	0	0	0	1	1	0	0	0	0	0	14	0	1399.767	sp|Q15063	sp|Q15063|PC	252	265	yes	yes	2	6.60E-32	134.75	1	464	1	14;15;16;17;	12;3;4;5;6;7	19		21
AACLLPK	ECCQAADKAACLLPKL	KAACLLPKLDELRDEG	K	A	A	P	K	L	2	0	0	0	1	0	0	0	0	0	2	1	0	0	1	0	0	0	0	0	0	0	7	0	771.4313	sp|P02768	sp|P02768|ALI	199	205	yes	no	2	0.036669	91.093	5	11	5	784;785;786;	469;470	469		2
AADIEQQAVFAVFDENK	LDRRGIQRAADIEQQA	FAVFDENKSWYLEDNI	R	A	A	N	K	S	4	0	1	2	0	2	2	0	0	1	0	1	0	2	0	0	0	0	0	2	0	0	17	0	1893.911	sp|P12259	sp|P12259|FA	539	555	no	no	2	0.0009138	81.565	9	264;23	9	1136;1137;11	656;657	656		2
AAFTECCQAADK	LFFAKRYKAAFTECCQ	ECCQAADKAACLLPKL	K	A	A	D	K	A	4	0	0	1	2	1	1	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0	12	0	1370.56	sp|P02768	sp|P02768|ALI	187	198	yes	no	2	2.26E-27	154.85	12	11	12	1301;1302;13	701;702;70	714		98
ACEPGVDYVYK	TLEERLDKACEPGVDY	PGVDYVYKTRLVKVQL	K	A	C	Y	K	T	1	0	0	1	1	0	1	1	0	0	0	1	0	0	1	0	0	0	2	2	0	0	11	0	1299.581	sp|P01024	sp|P01024|CO	1536	1546	no	no	2	0.0008667	83.998	31	97;24	31	4262;4263;42	1742;1743	1764		30
ADDKETCFAEEGK	AFVEKCCKADDKETCF	TCFAEEGKKLVAASQA	K	A	D	G	K	K	2	0	0	2	1	0	3	1	0	0	0	2	0	1	0	0	1	0	0	0	0	0	13	1	1498.625	sp|P02768	sp|P02768|ALI	585	597	yes	no	2;3	1.50E-86	238.01	36	11	36	4923;4924;49	1966;1967	1981		36
ADDKETCFAEEGKK	AFVEKCCKADDKETCF	CFAEEGKKLVAASQAA	K	A	D	K	K	L	2	0	0	2	1	0	3	1	0	0	0	3	0	1	0	0	1	0	0	0	0	0	14	2	1626.72	sp|P02768	sp|P02768|ALI	585	598	yes	no	2	0.053376	78.864	37	11	37	5190;5191	2002	2002		1
AEAESLYQSK	EDIAQKSKAEAESLYQ	AESLYQSKYEELQITA	K	A	E	S	K	Y	2	0	0	0	0	1	2	0	0	0	1	1	0	0	0	2	0	0	1	0	0	0	10	0	1124.535	sp|P04264	sp|P04264|K2	367	376	yes	no	2	0.03571	58.433	51	178	51	8761;8762;87	4046	4046		1
AEFAEVSK	RLSQRFPKAEFAEVSK	AEFAEVSKLVTDLTKV	K	A	E	S	K	L	2	0	0	0	0	0	2	0	0	0	0	1	0	1	0	1	0	0	0	1	0	0	8	0	879.4338	sp|P02768	sp|P02768|ALI	250	257	yes	no	2	0.020189	97.798	65	11	65	10521;10522	4692;4693	4705		63
AEFAEVSKLVTDLTK	RLSQRFPKAEFAEVSK	KLVTDLTKVHTECCHG	K	A	E	T	K	V	2	0	0	1	0	0	2	0	0	0	2	2	0	1	0	1	2	0	0	2	0	0	15	1	1649.888	sp|P02768	sp|P02768|ALI	250	264	yes	no	3	0.05102	35.757	66	11	66	10826	4755	4755		1
AEFVEVTK	RLSQKFPKAEFVEVTK	AEFVEVTKLVTDLTKV	K	A	E	T	K	L	1	0	0	0	0	0	2	0	0	0	0	1	0	1	0	0	1	0	0	2	0	0	8	0	921.4808	CON__P02	CON__P02769	249	256	yes	yes	2	0.064911	52.786	69	12	69	11334;11335	4889;4890	4889		2
AETECQNTEYQQLLDIK	EEQLQQIRAETECQNT	YQQLLDIKIRLENEIQ	R	A	E	I	K	I	1	0	1	1	1	3	3	0	0	1	2	1	0	0	0	0	2	0	1	0	0	0	17	0	2081.958	sp|P13645	sp|P13645|K1	423	439	yes	no	2	7.61E-73	153.34	81	15	83	13168;13169	5805;5806	5805		2
AEVDDVIQVR	GILGPIIRAEVDDVIQ	VDDVIQVRFKNLASRP	R	A	E	V	R	F	1	1	0	2	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	10	0	1142.593	sp|P12259	sp|P12259|FA	1650	1659	no	no	2	0.001033	111.95	82	264;23	84	13172;13173	5807	5807		1
AFLDCCEYITQLR	LQGDACVKAFLDCCEY	CEYITQLRQQHSRDGA	K	A	F	L	R	Q	1	1	0	1	2	1	1	0	0	1	2	0	0	1	0	0	1	0	1	0	0	0	13	0	1687.77	CON__Q2L	CON__Q2UVX4	721	733	yes	yes	2	3.43E-22	133.81	86	24	88	13662;13663	5990;5991	5990		5
AGALNSNDAFVLK	RAVEVLPKAGALNSND	SNDAFVLKTPSAAYLW	K	A	G	L	K	T	3	0	2	1	0	0	0	1	0	0	2	1	0	1	0	1	0	0	0	1	0	0	13	0	1318.688	sp|P06396	sp|P06396|GE	585	597	yes	no	2	3.07E-21	127.4	99	204	101	18423;18424	8314;8315	8322		163
AGKEPGLQIWR	VEHPEFLKAGKEPGLQ	EPGLQIWRVEKFDLVP	K	A	G	W	R	V	1	1	0	0	0	1	1	2	0	1	1	1	0	0	1	0	0	1	0	0	0	0	11	1	1253.688	sp|P06396	sp|P06396|GE	62	72	yes	no	3	2.67E-05	80.916	111	204	113	20608;20609	9421;9422	9423		4
AGLENTVAETECR	LQSQLSMKAGLENTVA	TVAETECRYALQLQQI	K	A	G	C	R	Y	2	1	1	0	1	0	3	1	0	0	1	0	0	0	0	0	2	0	0	1	0	0	13	0	1448.657	sp|P13646	sp|P13646|K1	343	355	yes	no	2	0.0003256	77.379	113	276	115	20678;20679	9426	9426		1
AIGGGLSSVGGGSSTIK	GFSSSSGRAIGGGLSS	GGGSSTIKYTTTSSSS	R	A	I	I	K	Y	1	0	0	0	0	0	0	6	0	2	1	1	0	0	0	4	1	0	0	1	0	0	17	0	1446.768	sp|P02538	sp|P02538|K2	534	550	yes	no	2	2.81E-21	112.43	142	5	144	23653;23654	10488	10488		1
ALEEANADLEVK	ASYLDKVRALEEANAD	ANADLEVKIRDWYQRQ	R	A	L	V	K	I	3	0	1	1	0	0	3	0	0	0	2	1	0	0	0	0	0	0	0	1	0	0	12	0	1300.651	sp|P02533	sp|P02533|K1	135	146	no	no	2	0.063193	45.137	169	4;276;13	172	26461;26462	11442	11442		1
ALEESNYELEGK	ASYLDKVRALEESNYE	SNYELEGKIKEWYEKH	R	A	L	G	K	I	1	0	1	0	0	0	4	1	0	0	2	1	0	0	0	1	0	0	1	0	0	0	12	0	1380.641	sp|P13645	sp|P13645|K1	166	177	yes	no	2	3.13E-10	136.63	170	15	173	26465;26466	11443;114	11443		16
ALLEMQQTK	QEAPLEWKALLEMQQT	LLEMQQTKMVLETFGG	K	A	L	T	K	M	1	0	0	0	0	2	1	0	0	0	2	1	1	0	0	0	1	0	0	0	0	0	9	0	1060.559	CON__P02	CON__P02672	253	261	yes	yes	2	0.0032584	95.909	187	8	190	30170;30171	13331	13331		1
APSTYGGGLSVSSSR	VLAGGSCRAPSTYGGG	GLSVSSSRFSSGGACG	R	A	P	S	R	F	1	1	0	0	0	0	0	3	0	0	1	0	0	0	1	5	1	0	1	1	0	0	15	0	1424.69	sp|P02533	sp|P02533|K1	42	56	yes	no	2	0.0031687	58.676	245	4	251	39281;39282	17257	17257		1
APVLSDSSCK	PSLLQCLKAPVLSDSS	VLSDSSCKSSYPGQIT	K	A	P	C	K	S	1	0	0	1	1	0	0	0	0	0	1	1	0	0	1	3	0	0	0	1	0	0	10	0	1062.502	CON__P00	CON__P00761	148	157	yes	yes	2	0.0020818	88.948	248	1	254	39503;39504	17296;172	17296		3
AQGYSGLSVK	YWDTNPTRAQGYSGLS	GYSGLSVKVVNSTTGP	R	A	Q	V	K	V	1	0	0	0	0	1	0	2	0	0	1	1	0	0	0	2	0	0	1	1	0	0	10	0	1008.524	sp|P07996	sp|P07996|TS	1055	1064	yes	no	2	0.009768	73.233	252	223	258	39836;39837	17336;173	17336		4
AQPVQVAEGSEPDGFWEALGGK	QELLRVLRAQPVQVAE	FWEALGGKAAYRTSPR	R	A	Q	G	K	A	3	0	0	1	0	2	3	4	0	0	1	1	0	1	2	1	0	1	0	2	0	0	22	0	2271.081	sp|P06396	sp|P06396|GE	627	648	yes	yes	2;3	0	246.96	260	204	266	43422;43423	21035;210	21526		582
AQYEDIAQK	DSIIAEVKAQYEDIAQ	QYEDIAQKSKAEAESL	K	A	Q	Q	K	S	2	0	0	1	0	2	1	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0	9	0	1064.514	sp|P04264	sp|P04264|K2	356	364	yes	yes	2	0.052609	57.047	265	178	271	44528;44529	21826	21826		1
AQYEEIANR	DSIIAEVKAQYEEIAN	QYEEIANRSRTEAESW	K	A	Q	N	R	S	2	1	1	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	9	0	1092.52	sp|P13647	sp|P13647|K2	344	352	yes	no	2	0.029369	66.073	266	16	272	44558;44559	21827	21827		1
ASLENSLEETK	LQSQLSMKASLENSLE	ENSLEETKGRYCMQLA	K	A	S	T	K	G	1	0	1	0	0	0	3	0	0	0	2	1	0	0	0	2	1	0	0	0	0	0	11	0	1219.593	sp|P02533	sp|P02533|K1	353	363	no	no	2	6.63E-05	99.815	281	4;13	287	46153;46154	22458	22458		1
ATDAEADVASLNR	KLEQAEKKATDAEADV	ADVASLNRRIQLVEEE	K	A	T	N	R	R	4	1	1	2	0	0	1	0	0	0	1	0	0	0	0	1	1	0	0	1	0	0	13	0	1331.632	sp|P07951	sp|P07951|TP	78	90	no	no	2	1.82E-07	92.611	293	222;241	299	47508;47509	22942;229	22943		2
AVEVLPK	ANSAGATRAVEVLPKA	RAVEVLPKAGALNSND	R	A	V	P	K	A	1	0	0	0	0	0	1	0	0	0	1	1	0	0	1	0	0	0	0	2	0	0	7	0	754.4589	sp|P06396	sp|P06396|GE	578	584	yes	no	2	0.043895	87.582	328	204	334	53469;53470	25190;251	25190		2
AVMDDFAAFVEK	KATKEQLKAVMDDFAA	DFAAFVEKCCKADDKE	K	A	V	E	K	C	3	0	0	2	0	0	1	0	0	0	0	1	1	2	0	0	0	0	0	2	0	0	12	0	1341.628	sp|P02768	sp|P02768|ALI	570	581	yes	no	2;3	9.55E-14	121.6	345	11	351;352	59453;59454	28762;287	28772	3	674
AWAYYSAVNPEK	ESPGSACRAWAYYSAV	YSAVNPEKDIHSGLIG	R	A	W	E	K	D	3	0	1	0	0	0	1	0	0	0	0	1	0	0	1	1	0	1	2	1	0	0	12	0	1397.662	sp|P12259	sp|P12259|FA	1727	1738	no	no	2	2.36E-07	98.943	359	264;23	367	63327;63328	30751;307	30758		16
CCAAADPHECYAK	TYETTLEKCCAAADPH	DPHECYAKVFDEFKPL	K	C	C	A	K	V	4	0	0	1	3	0	1	0	1	0	0	1	0	0	1	0	0	0	1	0	0	0	13	0	1551.591	sp|P02768	sp|P02768|ALI	384	396	yes	no	2;3	3.23E-05	107.45	377	11	385	65448;65449	31594;315	31605		14
CCTESLVNR	PVSDRVTKCCTESLVN	CTESLVNRRPCFSALE	K	C	C	N	R	R	0	1	1	0	2	0	1	0	0	0	1	0	0	0	0	1	1	0	0	1	0	0	9	0	1137.491	sp|P02768	sp|P02768|ALI	500	508	no	no	2	6.15E-11	151.27	381	11;12	389	66012;66013	31641;316	31694		57
CFLAFTQTK	KGTKVHMKCFLAFTQT	FLAFTQTKTFHEASED	K	C	F	T	K	T	1	0	0	0	1	1	0	0	0	0	1	1	0	2	0	0	2	0	0	0	0	0	9	0	1114.548	sp|P05452	sp|P05452|TE	81	89	yes	yes	2	1.96E-08	145.63	400	196	408	69320;69321	32990;329	33036		65
CFSGQCISK	EGCGERFRCFSGQCIS	FSGQCISKSLVCNGDS	R	C	F	S	K	S	0	0	0	0	2	1	0	1	0	1	0	1	0	1	0	2	0	0	0	0	0	0	9	0	1085.463	sp|P10643	sp|P10643|CO	91	99	no	no	2	0.021364	70.816	401	252	409	69506;69507	33055;330	33055		3
CGDLEEELK	RAEVSELKCGDLEEEL	GDLEEELKNVTNNLKS	K	C	G	L	K	N	0	0	0	1	1	0	3	1	0	0	2	1	0	0	0	0	0	0	0	0	0	0	9	0	1091.481	sp|P67936	sp|P67936|TP	154	162	no	no	2	0.0048007	90.657	402	413;222	410	69561;69562	33058;330	33058		6
CYDGYTLR	LSDEISFRCYDGYTLR	CYDGYTLRGSANRTCQ	R	C	Y	L	R	G	0	1	0	1	1	0	0	1	0	0	1	0	0	0	0	0	1	0	2	0	0	0	8	0	1046.449	CON__Q3K	CON__Q3KUS7	131	138	yes	yes	2	1.84E-05	143.85	452	26	460	75009;75010	35211;352	35225		55
DAEAWFNEK	QLAEQNRKDAEAWFNE	AEAWFNEKSKELTTEI	K	D	A	E	K	S	2	0	1	1	0	0	2	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	9	0	1108.483	sp|P13645	sp|P13645|K1	335	343	yes	no	2	0.0002766	131.06	456	15	464	75381;75382	35376;353	35382		16
DAEEWFFTK	KMAEKNRKDAEEWFFT	AEEWFFTKTEELNREV	K	D	A	T	K	T	1	0	0	1	0	0	2	0	0	0	0	1	0	2	0	0	1	1	0	0	0	0	9	0	1171.519	sp|P02533	sp|P02533|K1	301	309	yes	no	2	0.0048619	82.279	457	4	465	75474;75475	35392;353	35392		2
DAFLGSFLYEYSR	CKNYQEAKDAFLGSFL	SFLYEYSRRHPEYAVS	K	D	A	S	R	R	1	1	0	1	0	0	1	1	0	0	2	0	0	2	0	2	0	0	2	0	0	0	13	0	1566.736	CON__P02	CON__P02769	347	359	yes	yes	2	0.0003825	70.942	459	12	467	75546;75547	35395;353	35395		4
DCVGDVTENQICNK	PTPQFGGKDCVGDVTE	TENQICNKQDCPIDGC	K	D	C	N	K	Q	0	0	2	2	2	1	1	1	0	1	0	1	0	0	0	0	1	0	0	2	0	0	14	0	1650.698	sp|P07996	sp|P07996|TS	530	543	yes	yes	2	8.59E-43	188.28	477	223	485	77655;77656	36129;361	36131		10
DDNPNLPR	NECFLQHKDDNPNLPR	DDNPNLPRLVRPEVDV	K	D	D	P	R	L	0	1	2	2	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	8	0	939.441	sp|P02768	sp|P02768|ALI	131	138	yes	no	2	8.12E-20	139.92	485	11	493	79540;79541	37017;370	37030		44
DIEALFVSESK	MQELLPAKDIEALFVS	ALFVSESKKLTRKAV	K	D	I	S	K	K	1	0	0	1	0	0	2	0	0	1	1	1	0	1	0	2	0	0	0	1	0	0	11	0	1236.624	CON__Q3K	CON__Q3KUS7	626	636	yes	yes	2	0.037449	62.2	549	26	557	91370;91371	42807;428	42808		2
DIQYLPLIK	AINLLPSRDIQYLPLI	IQYLPLIKMSTITGPV	R	D	I	I	K	M	0	0	0	1	0	1	0	0	0	2	2	1	0	0	1	0	0	0	1	0	0	0	9	0	1101.643	CON__P02	CON__P02672	220	228	yes	yes	2	0.0078555	80.229	562	8	571	93316;93317	43815;438	43821		11
DLASIAR	PIQSVFTRDLASIARL	RDLASIARLRIAKGGV	R	D	L	A	R	L	2	1	0	1	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0	0	0	7	0	744.413	sp|P07996	sp|P07996|TS	190	196	yes	no	2	0.064545	77.496	575	223	584	94642;94643	44319	44319		1
DLGEENFK	SEVAHRFKDLGEENFK	DLGEENFKALVLIAFA	K	D	L	F	K	A	0	0	1	1	0	0	2	1	0	0	1	1	0	1	0	0	0	0	0	0	0	0	8	0	950.4345	sp|P02768	sp|P02768|ALI	37	44	yes	no	2	0.011583	110.63	589	11	598	95986;95987	44850;448	44864		59
DNCQYVYNVDQR	GDGILNERDNCQYVYN	YVYNVDQRDTDMDGVG	R	D	N	Q	R	D	0	1	2	2	1	2	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	12	0	1572.663	sp|P07996	sp|P07996|TS	811	822	yes	yes	2	4.94E-27	153.12	611	223	622	100728;1007	47623;476	47625		7
DPDQTDGLGLSYLSSHIANVER	KQFFKNWRDPDQTDGL	SHIANVERVPFDAATL	R	D	P	E	R	V	1	1	1	3	0	1	1	2	1	1	3	0	0	0	1	3	1	0	1	1	0	0	22	0	2386.14	sp|P06396	sp|P06396|GE	398	419	yes	yes	2;3	0	305.54	625	204	636	102780;1027	48464;484	48467		272
DQIVDLTVGNNK	YNTIDDLKDQIVDLTV	DLTVGNNKTLLDIDNT	K	D	Q	N	K	T	0	0	2	2	0	1	0	1	0	1	1	1	0	0	0	0	1	0	0	2	0	0	12	0	1314.678	sp|P35527	sp|P35527|K1	213	224	yes	no	2	0.0004898	92.538	641	19	652	104452;1044	49236;492	49237		2
DSQEEEKTEALTSAK	QVFVWVGKDSQEEEKT	TEALTSAKRYIETDPA	K	D	S	A	K	R	2	0	0	1	0	1	4	0	0	0	1	2	0	0	0	2	2	0	0	0	0	0	15	1	1664.774	sp|P06396	sp|P06396|GE	714	728	yes	no	2	0.0026906	81.565	666	204	677	107964;1079	50861	50861		1
DSSTWLTAFVLK	SYAAWLSRDSSTWLTA	WLTAFVLKVLSLAQEQ	R	D	S	L	K	V	1	0	0	1	0	0	0	0	0	0	2	1	0	1	0	2	2	1	0	1	0	0	12	0	1366.713	sp|P0C0L4	sp|P0C0L4|CO	1073	1084	no	no	2	0.0008185	88.495	668	245;2	679	108081;1080	50890;508	50890		6
DVWGIEGPIDAAFTR	PGYPKLIRDVWGIEGP	PIDAAFTRINCQGKTY	R	D	V	T	R	I	2	1	0	2	0	0	1	2	0	2	0	0	0	1	1	0	1	1	0	1	0	0	15	0	1645.81	sp|P04004	sp|P04004|VT	198	212	no	no	2;3	6.68E-168	223.08	710	168	722	113227;1132	52849;528	53795		947
DYIFGDYIER	MEKALQERDYIFGDYI	IFGDYIERLWAYLTIE	R	D	Y	E	R	L	0	1	0	2	0	0	1	1	0	2	0	0	0	1	0	0	0	0	2	0	0	0	10	0	1289.593	CON__Q0V	CON__Q0V8M	547	556	yes	yes	2	2.12E-15	141.52	722	21	735	115663;1156	54654;546	54665		101
ECCEKPLLEK	DSISSKLKECCEKPLL	CEKPLLEKSHCIAEVE	K	E	C	E	K	S	0	0	0	0	2	0	3	0	0	0	2	2	0	0	1	0	0	0	0	0	0	0	10	1	1304.611	sp|P02768	sp|P02768|ALI	301	310	yes	no	2;3	5.96E-31	177.7	759	11	772	120685;1206	56557;565	56561		22
ECEEIIR	NIPVVSGKECEEIIRK	KECEEIIRKGGETSEM	K	E	C	I	R	K	0	1	0	0	1	0	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	7	0	947.4382	sp|P02675	sp|P02675|FIB	240	246	no	no	2	0.0013323	143.37	762	143;9	775	121525;1215	56905;569	56917		30
EDGGGWWYNR	DPRKQCSKEDGGGWWY	GGGWWYNRCHAANPNG	K	E	D	N	R	C	0	1	1	1	0	0	1	3	0	0	0	0	0	0	0	0	0	2	1	0	0	0	10	0	1238.511	sp|P02675	sp|P02675|FIB	427	436	no	no	2	1.07E-24	166.96	775	143;9	788	123082;1230	57563;575	57712		165
EEAPSLR	HRPLDKKREEAPSLRP	REEAPSLRPAPPPISG	R	E	E	L	R	P	1	1	0	0	0	0	2	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	7	0	800.4028	sp|P02675	sp|P02675|FIB	54	60	no	no	2	0.0083222	113.08	788	143;9	802	125050;1250	58740;587	58741		9
EFNAETFTFHADICTLSEK	VDETYVPKEFNAETFT	DICTLSEKERQIKKQT	K	E	F	E	K	E	2	0	1	1	1	0	3	0	1	1	1	1	0	3	0	1	3	0	0	0	0	0	19	0	2259.015	sp|P02768	sp|P02768|ALI	525	543	yes	no	2;3	2.40E-41	135.81	820	11	834	129252;1292	60923;609	60923		11
EGGQTAPASTR	IYKGGTSREGGQTAPA	QTAPASTRLFQVRANS	R	E	G	T	R	L	2	1	0	0	0	1	1	2	0	0	0	0	0	0	1	1	2	0	0	0	0	0	11	0	1073.51	sp|P06396	sp|P06396|GE	554	564	yes	no	2	0.0056445	70.908	838	204	852	131651;1316	61781;617	61781		2
EIETYHNLLEGGQEDFESSGAGK	SIKMRLEKEIETYHNL	FESSGAGKIGLGGRGG	K	E	I	G	K	I	1	0	1	1	0	1	5	4	1	1	2	1	0	1	0	2	1	0	1	0	0	0	23	0	2509.125	sp|P35527	sp|P35527|K1	450	472	yes	no	3	3.29E-12	79.143	856	19	872	134876	63624	63624		1
ELANELR	RKVTEENKELANELRR	KELANELRRPPLCYHN	K	E	L	L	R	R	1	1	1	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	7	0	843.445	sp|P07996	sp|P07996|TS	307	313	yes	no	2	0.041523	88.734	876	223	894	139169;1391	65587;655	65588		2
ELTTEIDNNIEQISSYK	AWFNEKSKELTTEIDN	IEQISSYKSEITELRR	K	E	L	Y	K	S	0	0	2	1	0	1	3	0	0	3	1	1	0	0	0	2	2	0	1	0	0	0	17	0	1995.964	sp|P13645	sp|P13645|K1	346	362	yes	no	2	2.57E-14	136.93	914	15	932	145321;1453	68669;686	68670		2
EPAHLMSLFGGK	QSRVVQGKEPAHLMSL	LMSLFGGKPMIIYKGG	K	E	P	G	K	P	1	0	0	0	0	0	1	2	1	0	2	1	1	1	1	1	0	0	0	0	0	0	12	0	1285.649	sp|P06396	sp|P06396|GE	531	542	yes	no	2;3	5.26E-09	112.36	936	204	954	148789;1487	70174;701	70179		32
EPGLQIWR	PEFLKAGKEPGLQIWR	EPGLQIWRVEKFDLVP	K	E	P	W	R	V	0	1	0	0	0	1	1	1	0	1	1	0	0	0	1	0	0	1	0	0	0	0	8	0	997.5345	sp|P06396	sp|P06396|GE	65	72	yes	no	2	5.11E-13	126.24	941	204	959	150037;1500	70989;709	71020		236
EQLGPVTQEFWDNLEK	TSTFSKLREQLGPVTQ	EFWDNLEKETEGLRQE	R	E	Q	E	K	E	0	0	1	1	0	2	3	1	0	0	2	1	0	1	1	0	1	1	0	1	0	0	16	0	1931.927	sp|P02647	sp|P02647|AP	86	101	no	no	2;3	1.05E-122	198.14	953	136;17	971	151692;1516	71667;716	71893		244
EQQALQTVCLK	AQEVALLKEQQALQTV	ALQTVCLKGTKVHMKC	K	E	Q	L	K	G	1	0	0	0	1	3	1	0	0	0	2	1	0	0	0	0	1	0	0	1	0	0	11	0	1316.676	sp|P05452	sp|P05452|TE	63	73	yes	no	2	2.08E-38	195.7	958	196	977	154080;1540	72978;729	73013		50
ETCFAEEGK	KCCKADDKETCFAEEG	TCFAEEGKKLVAASQA	K	E	T	G	K	K	1	0	0	0	1	0	3	1	0	0	0	1	0	1	0	0	1	0	0	0	0	0	9	0	1069.439	sp|P02768	sp|P02768|ALI	589	597	yes	no	2	0.0007412	114.5	983	11	1003	159284;1592	75632;756	75635		8
ETYGEMADCCAK	LCTVATLRETYGEMAD	EMADCCAKQEPERNEC	R	E	T	A	K	Q	2	0	0	1	2	0	2	1	0	0	0	1	1	0	0	0	1	0	1	0	0	0	12	0	1433.526	sp|P02768	sp|P02768|ALI	106	117	yes	no	2	2.46E-10	117.31	999	11	1020;1021	161742;1617	76505;765	76513		108
EVLLTGIQTQGAK	WIQVDMQKEVLLTGIQ	GIQTQGAKHYLKPYYT	K	E	V	A	K	H	1	0	0	0	0	2	1	2	0	1	2	1	0	0	0	0	2	0	0	1	0	0	13	0	1356.761	CON__Q28	CON__Q28107	1957	1969	yes	yes	2	1.21E-65	180.67	1012	23	1034	165336;1653	78306;783	78404		107
EVQGFESATFLGYFK	NGRAVQHREVQGFESA	ATFLGYFKSGLKYKKG	R	E	V	F	K	S	1	0	0	0	0	1	2	2	0	0	1	1	0	3	0	1	1	0	1	1	0	0	15	0	1721.83	sp|P06396	sp|P06396|GE	148	162	yes	no	2;3	4.78E-85	181.32	1015	204	1038	166435;1664	78933;789	79150		298
EVSFDVELPK	VNRADTAKEVSFDVEL	SFDVELPKTAFITNFT	K	E	V	P	K	T	0	0	0	1	0	0	2	0	0	0	1	1	0	1	1	1	0	0	0	2	0	0	10	0	1161.592	sp|Q06033	sp|Q06033|ITI	76	85	no	no	2	9.66E-05	107.57	1018	436;21	1041	167350;1673	79408;794	79535		130
EVVADSVWVDVK	LIGASGQREVVADSVW	DSVWVDVKDSCVGSLV	R	E	V	V	K	D	1	0	0	2	0	0	1	0	0	0	0	1	0	0	0	1	0	1	0	5	0	0	12	0	1344.693	sp|P01024	sp|P01024|CO	545	556	no	no	2	1.40E-07	120.09	1022	97;24	1045	167816;1678	79581;795	79643		67
FASFIDK	QIKTLNNKFASFIDKV	KFASFIDKVRFLEQQN	K	F	A	D	K	V	1	0	0	1	0	0	0	0	0	1	0	1	0	2	0	1	0	0	0	0	0	0	7	0	826.4225	sp|P35908	sp|P35908|K2	189	195	no	no	2	0.044508	87.284	1055	20;16;5;18;0;1	1079	175741;1757	83671;836	83671		3
FDLVPVPTNLYGDFFTGDAYVILK	LQIWRVEKFDLVPVPT	GDAYVILKTVQLRNGN	K	F	D	L	K	T	1	0	1	3	0	0	0	2	0	1	3	1	0	3	2	0	2	0	2	3	0	0	24	0	2703.384	sp|P06396	sp|P06396|GE	76	99	yes	yes	2	0.01132	55.66	1069	204	1093	177643;1776	84600	84600		0
FEMEQNLR	TLDDFRIKFEMEQNLR	FEMEQNLRQGVDADIN	K	F	E	L	R	Q	0	1	1	0	0	1	2	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	8	0	1065.491	sp|P35527	sp|P35527|K1	243	250	yes	no	2	0.057343	65.038	1083	19	1107	179509;1795	85342	85342		1
FEQLELR	RLPMSVRRFEQLELRP	RFEQLELRPVLYNYLD	R	F	E	L	R	P	0	1	0	0	0	1	2	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	7	0	933.492	sp|P0C0L4	sp|P0C0L4|CO	846	852	no	no	2	2.26E-05	154.11	1084	245;246;2	1108	179535;1795	85343;853	85377		147
FFVAPFPEVFGK	VLNENLLRFFVAPFPE	PFPEVFGKEKVNELSK	R	F	F	G	K	E	1	0	0	0	0	0	1	1	0	0	0	1	0	4	2	0	0	0	0	2	0	0	12	0	1383.723	CON__P02	CON__P02662	23	34	yes	yes	2	0.0016832	87.149	1099	6	1125	181310;1813	85942;859	85942		19
FKDLGEENFK	HKSEVAHRFKDLGEEN	DLGEENFKALVLIAFA	R	F	K	F	K	A	0	0	1	1	0	0	2	1	0	0	1	2	0	2	0	0	0	0	0	0	0	0	10	1	1225.598	sp|P02768	sp|P02768|ALI	35	44	yes	no	2;3	5.86E-07	136.57	1118	11	1144	184476;1844	87325;873	87328		15
FKPTLSQQQK	NKTKAHIRFKPTLSQQ	PTLSQQQKSPEQQETV	R	F	K	Q	K	S	0	0	0	0	0	3	0	0	0	0	1	2	0	1	1	1	1	0	0	0	0	0	10	1	1203.661	sp|Q14624	sp|Q14624|ITI	215	224	no	no	2;3	0.0001333	136.27	1119	463	1145	184656;1846	87340;873	87342		7
FLEQQNQVLETK	ASFIDKVRFLEQQNQV	QNQVLETKWELLQQLD	R	F	L	T	K	W	0	0	1	0	0	3	2	0	0	0	2	1	0	1	0	0	1	0	0	1	0	0	12	0	1475.762	sp|Q86Y46	sp|Q86Y46|K2	152	163	yes	no	2	4.86E-08	107.15	1131	25	1157	186478;1864	88213;882	88214		2
FLEQQNQVLQTK	ASFIDKVRFLEQQNQV	QNQVLQTKWELLQQVD	R	F	L	T	K	W	0	0	1	0	0	4	1	0	0	0	2	1	0	1	0	0	1	0	0	1	0	0	12	0	1474.778	sp|P04264	sp|P04264|K2	200	211	no	no	2	3.33E-66	189.72	1132	178;20	1158	186482;1864	88215;882	88251		50
FLVNLVK	ELQRKTDRFLVNLVKL	RFLVNLVKLKHELTDE	R	F	L	V	K	L	0	0	1	0	0	0	0	0	0	0	2	1	0	1	0	0	0	0	0	2	0	0	7	0	831.5218	sp|P43652	sp|P43652|AF	550	556	no	no	1;2	1.77E-17	159.75	1144	362;30	1170	187713;1877	88687;886	88738		109
FPVFMGR	VLWDQQHKFPVFMGRV	KFPVFMGRVYDPRA__	K	F	P	G	R	V	0	1	0	0	0	0	0	1	0	0	0	0	1	2	1	0	0	0	0	1	0	0	7	0	852.4316	sp|P05155	sp|P05155|IC1	488	494	no	no	2	1.48E-13	166.66	1160	191	1187	190857;1908	90385;903	90418		230
FQDLVDAVR	IPPVPDDKFQDLVDAV	QDLVDAVRAEKGFLLL	K	F	Q	V	R	A	1	1	0	2	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	2	0	0	9	0	1061.551	sp|P07996	sp|P07996|TS	75	83	yes	no	2	6.08E-19	163.9	1163	223	1190	191387;1913	90648;906	90649		46
FQMIPLDPK	ISETDFRRFQMIPLDP	QMIPLDPKGTSQNDPN	R	F	Q	P	K	G	0	0	0	1	0	1	0	0	0	1	1	1	1	1	2	0	0	0	0	0	0	0	9	0	1087.574	sp|P07996	sp|P07996|TS	960	968	yes	no	2	0.033409	63.565	1169	223	1196	191900;1919	90808;908	90808		3
FQNALLVR	FEQLGEYKFQNALLVR	FQNALLVRYTKKVPQV	K	F	Q	V	R	Y	1	1	1	0	0	1	0	0	0	0	2	0	0	1	0	0	0	0	0	1	0	0	8	0	959.5553	sp|P02768	sp|P02768|ALI	427	434	yes	no	2	4.55E-19	153.88	1170	11	1197	191988;1919	90811;908	91097		388
FSSSSGYGGGSSR	GGGGGGGRFSSSSGYG	GYGGGSSRVCGRGGGG	R	F	S	S	R	V	0	1	0	0	0	0	0	4	0	0	0	0	0	1	0	6	0	0	1	0	0	0	13	0	1234.521	sp|P35527	sp|P35527|K1	47	59	yes	no	2	0.0037294	62.466	1199	19	1226	197094;1970	93089	93089		1
FTGSQPFGQGVEHATANK	NCLPCPPRFTGSQPFG	VEHATANKQVCKPRNP	R	F	T	N	K	Q	2	0	1	0	0	2	1	3	1	0	0	1	0	2	1	1	2	0	0	1	0	0	18	0	1874.891	sp|P07996	sp|P07996|TS	624	641	yes	yes	3	0.0044293	28.472	1210	223	1237	198696;1986	93778;937	93778		5
FTVSNVNAAGSK	ASGRKLEKFTVSNVNA	VNVAAGSKVTFELTYE	K	F	T	S	K	V	2	0	2	0	0	0	0	1	0	0	0	1	0	1	0	2	1	0	0	2	0	0	12	0	1178.63	sp|Q06033	sp|Q06033|ITI	138	149	no	no	2	1.85E-07	100.88	1219	436;21	1247	200056;2000	94428;944	94431		5
FVFGTTPEDILR	QGVLQNVRFVFGTTPE	TTPEDILRNKGCSSST	R	F	V	L	R	N	0	1	0	1	0	0	1	1	0	1	1	0	0	2	1	0	2	0	0	1	0	0	12	0	1393.724	sp|P07996	sp|P07996|TS	217	228	yes	no	2	6.57E-21	140.75	1223	223	1251	200327;2003	94449;944	94452		81
GAFLYEPCGVSMPVLSTGVLR	NISVSSSKGAFLYEPC	VLSTGVLRSNGGCSIV	K	G	A	L	R	S	1	1	0	0	1	0	1	3	0	0	3	0	1	1	2	2	1	0	1	3	0	0	21	0	2252.133	CON__Q9N	CON__Q9NSB4	447	467	yes	yes	2	0.0059265	50.675	1241	29	1270	203205;2032	95523	95523	7	1
GASQAGAPQGR	VRAATASRGASQAGAP	QAGAPQGRVPEARPNS	R	G	A	G	R	V	3	1	0	0	0	2	0	3	0	0	0	0	0	0	1	1	0	0	0	0	0	0	11	0	998.4894	sp|P06396	sp|P06396|GE	33	43	yes	yes	2	0.0001397	93.992	1246	204	1275	203504;2035	95609;956	95612		4
GFEPGVTNILK	TPGVFIGKGFEPGVTN	PGVTNILKTTQGSKIF	K	G	F	L	K	T	0	0	1	0	0	0	1	2	0	1	1	1	0	1	1	0	1	0	0	1	0	0	11	0	1173.639	sp|Q15063	sp|Q15063|PC	576	586	yes	no	2	0.032876	68.846	1303	464	1333	215078;2150	101901;10	101902		2
GFLLLASLR	VDAVRAEKGFLLLASL	FLLLASLRQMKKTRGT	K	G	F	L	R	Q	1	1	0	0	0	0	0	1	0	0	4	0	0	1	0	1	0	0	0	0	0	0	9	0	988.607	sp|P07996	sp|P07996|TS	87	95	yes	no	2	0.001161	104.75	1310	223	1340	215887;2158	102346;10	102361		16
GFSCGSAIVGGGK	QCVRGGPRGFSCGSAI	SAIVGGGKRGAFSSVS	R	G	F	G	K	R	1	0	0	0	1	0	0	5	0	1	0	1	0	1	0	2	0	0	0	1	0	0	13	0	1195.566	sp|P19013	sp|P19013|K2	14	26	yes	no	2	0.020161	53.327	1318	18	1348	217425	103258	103258		1
GFSSGSAVVSGGSR	GGGGGGFRGFSSGSAV	AVVSGGSRRSTSSFSC	R	G	F	S	R	R	1	1	0	0	0	0	0	4	0	0	0	0	0	1	0	5	0	0	0	2	0	0	14	0	1253.6	sp|P35908	sp|P35908|K2	21	34	yes	no	2	2.13E-12	103.34	1320	20	1350	217590;2175	103349;10	103349		2
GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR	GSSRVCGRGGGGSFGY	GGFGGGSRGFGGASGG	R	G	G	S	R	G	1	1	0	0	0	0	0	17	0	0	1	0	0	3	0	7	0	0	2	0	0	0	32	0	2704.154	sp|P35527	sp|P35527|K1	64	95	yes	no	3	3.38E-13	45.685	1331	19	1361	219410	104439	104439		1
GGSGGSYGGGGSGGGYGGGSGSR	GSYGRGSRGGSGGSYG	YGGGSGSRGGSGGSYG	R	G	G	S	R	G	0	1	0	0	0	0	0	15	0	0	0	0	0	0	0	5	0	0	2	0	0	0	23	0	1790.72	sp|P35527	sp|P35527|K1	491	513	yes	no	2	2.79E-42	114.63	1336	19	1366	219742;2197	104489;10	104490		2
GGSGGSYGR	GKIGLGGRGGSGGSYG	GSGGSYGRGSRGGSGG	R	G	G	G	R	G	0	1	0	0	0	0	0	5	0	0	0	0	0	0	0	2	0	0	1	0	0	0	9	0	796.3464	sp|P35527	sp|P35527|K1	479	487	yes	no	2	0.035051	62.546	1337	19	1367	219748	104491	104491		1
GGTLGTPQTGSENDALYEYLR	ASEDCISRGGTLGTPQ	DALYEYLRQSVGNEAE	R	G	G	L	R	Q	1	1	1	1	0	1	2	4	0	0	3	0	0	0	1	1	3	0	2	0	0	0	21	0	2241.055	sp|P05452	sp|P05452|TE	102	122	yes	no	2;3	4.20E-269	242.07	1340	196	1370	219999;2200	104590;10	104594		273
GGVASGFK	KSGLKYKKGGVASGFK	GGVASGFKHVVPNEVV	K	G	G	F	K	H	1	0	0	0	0	0	0	3	0	0	0	1	0	1	0	1	0	0	0	1	0	0	8	0	721.3759	sp|P06396	sp|P06396|GE	170	177	yes	no	2	0.023459	76.035	1341	204	1371	220310;2203	104863;10	104863		15
GGVNDNFQGVLQNVR	IARLRIAKGGVNDNFQ	QGVLQNVRFVFGTTPE	K	G	G	V	R	F	0	1	3	1	0	2	0	3	0	0	1	0	0	1	0	0	0	0	0	3	0	0	15	0	1615.807	sp|P07996	sp|P07996|TS	202	216	yes	no	2	1.79E-85	183.78	1343	223	1373	220424;2204	104880;10	104925		46
GGWTVIQNR	YCDMKTEKGGWTVIQN	GWTVIQNRQDGSVDFG	K	G	G	N	R	Q	0	1	1	0	0	1	0	2	0	1	0	0	0	0	0	0	1	1	0	1	0	0	9	0	1029.536	CON__P02	CON__P02676	281	289	yes	yes	2	2.10E-05	135.87	1344	9	1374	220481;2204	104926;10	104928		13
GHLFLQTDQPVYNPGQR	NLLFSSRRGHLFLQTD	PVYNPGQRVRYRVFAL	R	G	H	Q	R	V	0	1	1	1	0	3	0	2	1	0	2	0	0	1	2	0	1	0	1	1	0	0	17	0	1968.981	CON__P01	CON__P01030	138	154	yes	yes	2;3	0.0021004	43.628	1348	2	1378	221805;2218	105718;10	105730		35
GLESQTK	DGKKTFFRGLESQTKL	RGLESQTKLVNGQSHI	R	G	L	T	K	L	0	0	0	0	0	1	1	1	0	0	1	1	0	0	0	1	1	0	0	0	0	0	7	0	761.3919	sp|P0C0L4	sp|P0C0L4|CO	298	304	no	no	2	0.0098551	107.74	1372	245;246;2	1402	226680;2266	108937;10	108937		2
GPDPSSPAFR	GSGRRLVKGPDPSSPA	DPSSPAFRIEDANLIP	K	G	P	F	R	I	1	1	0	1	0	0	0	1	0	0	0	0	0	1	3	2	0	0	0	0	0	0	10	0	1029.488	sp|P07996	sp|P07996|TS	51	60	yes	no	2	1.52E-06	114.28	1420	223	1451	231987;2319	111013;11	111029		18
GSLGGGFSSGGFSGGSFSR	SLRISSSKGSLGGGFS	FSGGSFSRGSSGGGCF	K	G	S	S	R	G	0	1	0	0	0	0	0	8	0	0	1	0	0	3	0	6	0	0	0	0	0	0	19	0	1706.765	sp|P13645	sp|P13645|K1	41	59	yes	no	2	4.98E-17	101.2	1460	15	1491	240602;2406	115085;11	115085		4
GSSGGGCFGGSSGGYGGLGGFGGGSFR	FSGGSFSRGSSGGGCF	GFGGGSFRGSYGSSSF	R	G	S	F	R	G	0	1	0	0	1	0	0	15	0	0	1	0	0	3	0	5	0	0	1	0	0	0	27	0	2341.977	sp|P13645	sp|P13645|K1	60	86	yes	no	2	3.78E-15	78.021	1465	15	1496	242933;2429	116111	116111		1
GTLLALER	LRQMKKTRGTLLALER	GTLLALERKDHSGQVF	R	G	T	E	R	K	1	1	0	0	0	0	1	1	0	0	3	0	0	0	0	0	1	0	0	0	0	0	8	0	871.5127	sp|P07996	sp|P07996|TS	102	109	yes	yes	2	0.017874	101.28	1480	223	1511	244041;2440	116505;11	116506		7
GTSQNDPNWVVR	QMIPLDPKGTSQNDPN	NDPNWVVRHQGKELVQ	K	G	T	V	R	H	0	1	2	1	0	1	0	1	0	0	0	0	0	0	1	1	1	1	0	2	0	0	12	0	1371.653	sp|P07996	sp|P07996|TS	969	980	yes	no	2	7.41E-23	145.17	1484	223	1515	244253;2442	116555;11	116588		37
GVFVLNK	VVLVAVDKGVFVLNKK	KGVFVLNKKNKLTQSK	K	G	V	N	K	K	0	0	1	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	0	2	0	0	7	0	775.4592	sp|P01024	sp|P01024|CO	601	607	no	no	2	0.013131	103.41	1498	97;24	1529	245788;2457	117241;11	117241		44
GYTQQLAFR	GALELIKKGYTQQLAF	YTQQLAFRQPSSAFAA	K	G	Y	F	R	Q	1	1	0	0	0	2	0	1	0	0	1	0	0	1	0	0	1	0	1	0	0	0	9	0	1082.551	sp|P01024	sp|P01024|CO	1052	1060	no	no	2	7.06E-15	162.51	1528	97;24	1559	250562;2505	119258;11	119264		120
HGGGGGGFGGGGFGSR	SSFSCLSRHGGGGGGF	GGGGFGSRSLVGLGGT	R	H	G	S	R	S	0	1	0	0	0	0	0	11	1	0	0	0	0	2	0	1	0	0	0	0	0	0	16	0	1319.576	sp|P35908	sp|P35908|K2	46	61	yes	no	3	0.014711	27.149	1542	20	1573	251852;2518	119705	119705		1
HLVDEPQNLIK	STVFDKLKHLVDEPQN	DEPQNLIKQNCDQFEK	K	H	L	I	K	Q	0	0	1	1	0	1	1	0	1	1	2	1	0	0	1	0	0	0	0	1	0	0	11	0	1304.709	CON__P02	CON__P02769	402	412	yes	yes	2	3.26E-145	230.06	1560	12	1591	253942;2539	120384;12	120387		22
HPDYSVVLLLR	FLYEYARRHPDYSVVL	YSVVLLLRLAKTYETT	R	H	P	L	R	L	0	1	0	1	0	0	0	0	1	0	3	0	0	0	1	1	0	0	1	2	0	0	11	0	1310.735	sp|P02768	sp|P02768|ALI	362	372	yes	no	2;3	1.82E-06	124.92	1566	11	1597	254815;2548	120764;12	120779		47
HPYFYAPELLFFAK	YLYEIARRHPYFYAPE	PELLFFAKRYKAAFTE	R	H	P	A	K	R	2	0	0	0	0	0	1	0	1	0	2	1	0	3	2	0	0	0	2	0	0	0	14	0	1741.887	sp|P02768	sp|P02768|ALI	170	183	yes	no	2;3	1.40E-38	146.11	1569	11	1600	255148;2551	120835;12	120877		68
HVVPNEVVVQR	GGVASGFKHVVPNEVV	PNEVVVQRLFQVKGRR	K	H	V	Q	R	L	0	1	1	0	0	1	1	0	1	0	0	0	0	0	1	0	0	0	0	5	0	0	11	0	1274.71	sp|P06396	sp|P06396|GE	178	188	yes	no	2;3	1.37E-20	140.83	1590	204	1621	258848;2588	122611;12	122629		227
IALGGLLFPASDLR	NNSQLIMRIALGGLLF	LFPASDLRLPLVPALD	R	I	A	L	R	L	2	1	0	1	0	0	0	2	0	1	4	0	0	1	1	1	0	0	0	0	0	0	14	0	1441.829	CON__Q6T	CON__Q6T181	169	182	yes	yes	2	8.95E-20	121.83	1605	28	1636	263336;2633	124642;12	124642		24
IEDANLIPPVPDDK	DPSSPAFRIEDANLIP	IPPVPDDKFQDLVDAV	R	I	E	D	K	F	1	0	1	3	0	0	1	0	0	2	1	1	0	0	3	0	0	0	0	1	0	0	14	0	1534.788	sp|P07996	sp|P07996|TS	61	74	yes	no	2	2.25E-12	103.21	1637	223	1668	270450;2704	128543;12	128573		43
IEGEPEFR	GPTLTKVKIEGEPEFR	IEGEPEFRLKIEGETI	K	I	E	F	R	L	0	1	0	0	0	0	3	1	0	1	0	0	0	1	1	0	0	0	0	0	0	0	8	0	975.4662	sp|Q15063	sp|Q15063|PC	705	712	yes	no	2	0.063928	53.166	1647	464	1678	272588	129353	129353		1
IEISELNR	GDSVRNSKIEISELNR	IEISELNRVIQRLRSE	K	I	E	N	R	V	0	1	1	0	0	0	2	0	0	2	1	0	0	0	0	1	0	0	0	0	0	0	8	0	972.524	sp|P04264	sp|P04264|K2	396	403	no	no	2	0.0003384	134.66	1651	178;20	1682	273507;2735	130015;13	130015		6
IIAATIENAQPILQIDNAR	TIEDLRNKIIAATIEN	ILQIDNARLAADDFRT	K	I	I	A	R	L	4	1	2	1	0	2	1	0	0	5	1	0	0	0	1	0	1	0	0	0	0	0	19	0	2063.138	sp|P08779	sp|P08779|K1	178	196	yes	no	2;3	1.44E-08	81.565	1686	13	1717	276822;2768	131550;13	131550		2
IIDGVPVEITEK	PIIKKYTKIIDGVPVE	VPVEITEKETREERII	K	I	I	E	K	E	0	0	0	1	0	0	2	1	0	3	0	1	0	0	1	0	1	0	0	2	0	0	12	0	1311.729	sp|Q15063	sp|Q15063|PC	736	747	yes	no	2	0.013888	55.401	1688	464	1719	276977;2769	131587;13	131588		4
IITHPNFNGNTLDNDIMLIK	EQFINAAKIITHPNFN	DNDIMLIKLSSPATLN	K	I	I	I	K	L	0	0	4	2	0	0	0	1	1	4	2	1	1	1	1	0	2	0	0	0	0	0	20	0	2282.173	CON__P00	CON__P00761	78	97	yes	yes	2;3	2.13E-140	168.1	1707	1	1738;1739	279144;2791	132246;13	132390	0	191
ILPLTVCK	AQDERSKRILPLTVCK	ILPLTVCKMHVLHCQG	R	I	L	C	K	M	0	0	0	0	1	0	0	0	0	1	2	1	0	0	1	0	1	0	0	1	0	0	8	0	942.5572	sp|P10643	sp|P10643|CO	737	744	no	no	2	0.026264	84.244	1731	252	1763	281838;2818	133588;13	133588		12
IMADSGPIYDK	VVMYEGKKIMADSGPI	DSGPIYDKTYAGGRLG	K	I	M	D	K	T	1	0	0	2	0	0	0	1	0	2	0	1	1	0	1	1	0	0	1	0	0	0	11	0	1208.575	sp|P07996	sp|P07996|TS	1131	1141	yes	no	2	0.018398	59.067	1738	223	1770	282417;2824	133749;13	133749		1
IPESGGDNSVFDIFELTGAAR	MHVCGTNRIPESGGDN	FELTGAARKGSGRRLV	R	I	P	A	R	K	2	1	1	2	0	0	2	3	0	2	1	0	0	2	1	2	1	0	0	1	0	0	21	0	2194.054	sp|P07996	sp|P07996|TS	21	41	yes	no	2	3.41E-22	136.81	1751	223	1783	284337;2843	134157;13	134165		8
IQLVEEELDR	DVAALNRRIQLVEEEL	LVEEELDRAQERLATA	R	I	Q	D	R	A	0	1	0	1	0	1	3	0	0	1	2	0	0	0	0	0	0	0	0	1	0	0	10	0	1242.646	sp|P67936	sp|P67936|TP	56	65	no	no	2	1.29E-24	166.16	1772	413;210;222;2	1804	287378;2873	135376;13	135416		49
ISIGGGSCAISGGYGSR	YGLGGSKRISIGGGSC	ISGGYGSRAGGSYGFG	R	I	S	S	R	A	1	1	0	0	1	0	0	6	0	3	0	0	0	0	0	4	0	0	1	0	0	0	17	0	1597.752	sp|P02538	sp|P02538|K2	70	86	no	no	2	9.89E-06	78.486	1789	5	1821	289840	136410	136410		1
ISISTSGGSFR	YNLGGSKRISISTSGG	STSGGSFRNRFGAGAG	R	I	S	F	R	N	0	1	0	0	0	0	0	2	0	2	0	0	0	1	0	4	1	0	0	0	0	0	11	0	1110.567	sp|P13647	sp|P13647|K2	74	84	yes	no	2	3.60E-05	103.55	1791	16	1823	289906;2899	136414;13	136416		3
ISYIIGK	DLWGEKPKISYIIGKD	KISYIIGKDTWVELWP	K	I	S	G	K	D	0	0	0	0	0	0	0	1	0	3	0	1	0	0	0	1	0	0	1	0	0	0	7	0	792.4745	CON__Q2L	CON__Q2UVX4	1617	1623	yes	yes	2	0.054812	82.263	1797	24	1829	290491;2904	136511;13	136512		3
ITQVLHFTK	AFRLFETKITQVLHFT	TQVLHFTKDVKAAANQ	K	I	T	T	K	D	0	0	0	0	0	1	0	0	1	1	1	1	0	1	0	0	2	0	0	1	0	0	9	0	1085.623	sp|P0C0L4	sp|P0C0L4|CO	1647	1655	no	no	2;3	0.0014327	117.89	1820	245;246;2	1852	295309;2953	139212;13	139323		119
KGGVASGFK	FKSGLKYKKGGVASGF	GGVASGFKHVVPNEVV	K	K	G	F	K	H	1	0	0	0	0	0	0	3	0	0	0	2	0	1	0	1	0	0	0	1	0	0	9	1	849.4709	sp|P06396	sp|P06396|GE	169	177	yes	no	2	0.0081668	113.71	1882	204	1915	304194;3041	143178	143178		1
KGYTQQLAFR	QGALELIKKGYTQQLA	YTQQLAFRQPSSAFAA	K	K	G	F	R	Q	1	1	0	0	0	2	0	1	0	0	1	1	0	1	0	0	1	0	1	0	0	0	10	1	1210.646	sp|P01024	sp|P01024|CO	1051	1060	no	no	3	0.0038452	53.124	1886	97;24	1919	304478;3044	143266	143266		1
KLVAASQAALGL	TCFAEEGKKLVAASQA	ASQAALGL________	K	K	L	G	L	-	4	0	0	0	0	1	0	1	0	0	3	1	0	0	0	1	0	0	0	1	0	0	12	1	1140.687	sp|P02768	sp|P02768|ALI	598	609	yes	no	2	4.36E-09	115.7	1893	11	1926	305251;3052	143513;14	143521		13
KQTALVELLK	PDTEKQIKKQTALVEL	TALVELLKHKPKATEE	K	K	Q	L	K	H	1	0	0	0	0	1	1	0	0	0	3	2	0	0	0	0	1	0	0	1	0	0	10	1	1141.707	CON__P02	CON__P02769	548	557	yes	yes	2	1.53E-05	115.78	1903	12	1936	306241;3062	143736	143736		1
KQTALVELVK	SEKERQIKKQTALVEL	TALVELVKHKPKATKE	K	K	Q	V	K	H	1	0	0	0	0	1	1	0	0	0	2	2	0	0	0	0	1	0	0	2	0	0	10	1	1127.691	sp|P02768	sp|P02768|ALI	549	558	yes	no	2;3	2.25E-23	163.65	1904	11	1937	306287;3062	143737;14	143753		141
KVPQVSTPTLVEVSR	ALLVRYTKKVPQVSTP	PTLVEVSRNLGKVGSK	K	K	V	S	R	N	0	1	0	0	0	1	1	0	0	0	1	1	0	0	2	2	2	0	0	4	0	0	15	1	1638.931	sp|P02768	sp|P02768|ALI	438	452	no	no	2;3	9.89E-138	161.49	1912	11;12	1945	307522;3075	144442;14	144496		306
KYLYEIAR	DNEETFLKKYLYEIAR	KYLYEIARRHPYFYAP	K	K	Y	A	R	R	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	0	2	0	0	0	8	1	1054.581	sp|P02768	sp|P02768|ALI	161	168	yes	no	3	0.0040738	92.439	1916	11	1949	308237;3082	144784;14	144784		1
KYVLPNFEVK	SSTQFEVKKYVLPNFE	VLPNFEVKITPGKPYI	K	K	Y	V	K	I	0	0	1	0	0	0	1	0	0	0	1	2	0	1	1	0	0	0	1	2	0	0	10	1	1235.691	sp|P0C0L4	sp|P0C0L4|CO	235	244	no	no	2;3	8.21E-20	163.16	1920	245;246;2	1953	308366;3083	144819;14	144844		81
LAADDFR	LLQIDNARLAADDFRL	RLAADDFRLKYENEVA	R	L	A	F	R	L	2	1	0	2	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	7	0	806.3923	sp|P13645	sp|P13645|K1	229	235	no	no	2	0.01709	100.07	1926	15;4;276;13;2	1959	310098;3100	145589;14	145589		2
LAELEEALQK	ALKDARNKLAELEEAL	ELEEALQKAKQDMARL	K	L	A	Q	K	A	2	0	0	0	0	1	3	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	10	0	1142.618	sp|P13647	sp|P13647|K2	432	441	yes	no	2	0.0008874	97.431	1933	16	1966	310818	145826	145826		1
LATALQK	ELDRAQERLATALQKL	RLATALQKLEEAEKAA	R	L	A	Q	K	L	2	0	0	0	0	1	0	0	0	0	2	1	0	0	0	0	1	0	0	0	0	0	7	0	743.4541	sp|P67936	sp|P67936|TP	70	76	no	no	2	0.036891	90.986	1956	413;210;222;2	1990	313801;3138	147125	147125		1
LCNNPTPQFGGK	GGVQKRSRLCNNPTPQ	PTPQFGGKDCVGDVTE	R	L	C	G	K	D	0	0	2	0	1	1	0	2	0	0	1	1	0	1	2	0	1	0	0	0	0	0	12	0	1331.629	sp|P07996	sp|P07996|TS	518	529	yes	no	2	5.43E-06	93.098	1967	223	2001	315592;3155	147806;14	147807		6
LCTVATLR	LHTLFGDKLCTVATLR	LCTVATLRETYGEMAD	K	L	C	L	R	E	1	1	0	0	1	0	0	0	0	0	2	0	0	0	0	0	2	0	0	1	0	0	8	0	932.5113	sp|P02768	sp|P02768|ALI	98	105	yes	no	1;2	2.73E-10	157.9	1973	11	2007	316341;3163	148063;14	148174		133
LDELRDEGK	KAACLLPKLDELRDEG	DELRDEGKASSAKQRL	K	L	D	G	K	A	0	1	0	2	0	0	2	1	0	0	2	1	0	0	0	0	0	0	0	0	0	0	9	1	1073.535	sp|P02768	sp|P02768|ALI	206	214	yes	no	2	0.011982	128.27	1977	11	2011	317477;3174	148298	148298		1
LDTLAQEVALLK	MFEELKSRLDTLAQEV	AQEVALLKEQQALQTV	R	L	D	L	K	E	2	0	0	1	0	1	1	0	0	0	4	1	0	0	0	0	1	0	0	1	0	0	12	0	1312.76	sp|P05452	sp|P05452|TE	51	62	yes	yes	2;3	1.79E-56	182.64	1989	196	2023	319029;3190	148793;14	148999		252
LEALKEGGGSLAEYHAK	LRQRLTARLEALKEGG	SLAEYHAKASEQLKAL	R	L	E	A	K	A	3	0	0	0	0	0	3	3	1	0	3	2	0	0	0	1	0	0	1	0	0	0	17	1	1771.911	CON__P15	CON__P15497	201	217	yes	yes	3	3.52E-06	64.507	1998	17	2032	320295;3202	149401;14	149404		4
LECEINTYR	VLLDVRARLECEINTY	ECEINTYRSLLESEDC	R	L	E	Y	R	S	0	1	1	0	1	0	2	0	0	1	1	0	0	0	0	0	1	0	1	0	0	0	9	0	1196.55	sp|Q15323	sp|Q15323|K1	349	357	yes	no	2	0.0080688	79.906	2001	22	2035	320681;3206	149633	149633		1
LEGLEDALQK	ALKDAKNKLEGLEDAL	GLEDALQKAKQDLARL	K	L	E	Q	K	A	1	0	0	1	0	1	2	1	0	0	3	1	0	0	0	0	0	0	0	0	0	0	10	0	1114.587	sp|P02538	sp|P02538|K2	427	436	no	no	2	0.037264	57.96	2010	5	2045	322355;3223	150290	150290		1
LENEIQTYR	QLLDIKIRLENEIQTY	ENEIQTYRSLLEGEGS	R	L	E	Y	R	S	0	1	1	0	0	1	2	0	0	1	1	0	0	0	0	0	1	0	1	0	0	0	9	0	1164.578	sp|P13645	sp|P13645|K1	442	450	yes	no	2	4.75E-06	140.5	2026	15	2061	324524;3245	150938;15	150938		2
LEQEIATYR	ILLDVKTRLEQEIATY	EQEIATYRRLLEGEDA	R	L	E	Y	R	R	1	1	0	0	0	1	2	0	0	1	1	0	0	0	0	0	1	0	1	0	0	0	9	0	1121.572	sp|P02533	sp|P02533|K1	408	416	no	no	2	0.0008217	109.71	2029	4;276;13	2064	325069;3250	151126;15	151126		3
LEVDIDIK	AQLVDMKRLEVDIDIK	LEVDIDIKIRSCRGSC	R	L	E	I	K	I	0	0	0	2	0	0	1	0	0	2	1	1	0	0	0	0	0	0	0	1	0	0	8	0	943.5226	sp|P02671	sp|P02671|FIB	169	176	no	no	2	0.033438	71.501	2036	142;8	2072	326127;3261	151771;15	151771		2
LFACSNK	KMDAHPPRLFACSNKI	RLFACSNKIGRFVIEE	R	L	F	N	K	I	1	0	1	0	1	0	0	0	0	0	1	1	0	1	0	1	0	0	0	0	0	0	7	0	838.4007	sp|P06396	sp|P06396|GE	669	675	yes	no	2	0.0034928	132.96	2040	204	2076	326513;3265	151890;15	151891		4
LGEHNIDVLEGNEQFINAAK	YKSRIQVRLGEHNIDV	EQFINAAKIITHPNFN	R	L	G	A	K	I	2	0	3	1	0	1	3	2	1	2	2	1	0	1	0	0	0	0	0	1	0	0	20	0	2210.097	CON__P00	CON__P00761	58	77	yes	yes	2;3;4	0	401.16	2060	1	2097	329596;3295	153643;15	153644		438
LGEYGFQNALIVR	QNCDQFEKLGEYGFQN	FQNALIVRYTRKVPQV	K	L	G	V	R	Y	1	1	1	0	0	1	1	2	0	1	2	0	0	1	0	0	0	0	1	1	0	0	13	0	1478.788	CON__P02	CON__P02769	421	433	yes	yes	2	2.93E-27	136.57	2064	12	2101	330805;3308	154314;15	154338		26
LHVDPENFR	LSELHCDKLHVDPENF	HVDPENFRLLGNVLVC	K	L	H	F	R	L	0	1	1	1	0	0	1	0	1	0	1	0	0	1	1	0	0	0	0	1	0	0	9	0	1125.557	sp|P68871	sp|P68871|HB	97	105	no	no	2;3	4.58E-10	119.41	2096	416;132;27	2133	337108;3371	156666;15	156711		52
LKECCEKPLLEK	NQDSISSKLKECCEKP	CEKPLLEKSHCIAEVE	K	L	K	E	K	S	0	0	0	0	2	0	3	0	0	0	3	3	0	0	1	0	0	0	0	0	0	0	12	2	1545.79	sp|P02768	sp|P02768|ALI	299	310	yes	no	2;3	1.17E-07	116.55	2116	11	2154	339861;3398	157902;15	157903		3
LLALGTPENPSWLSIHLQDQK	QLAAGSGRLLALGTPE	SIHLQDQKVVLSSGSG	R	L	L	Q	K	V	1	0	1	1	0	2	1	1	1	1	5	1	0	0	2	2	1	1	0	0	0	0	21	0	2359.254	CON__Q6T	CON__Q6T181	264	284	yes	yes	3	3.23E-05	64.723	2120	28	2158	340346;3403	157984	157984		1
LLDNWDTLASTLSK	LGKQLNLKLLDNWDTL	TLASTLSKVREQLGPV	K	L	L	S	K	V	1	0	1	2	0	0	0	0	0	0	4	1	0	0	0	2	2	1	0	0	0	0	14	0	1575.814	CON__P15	CON__P15497	69	82	yes	yes	2	1.61E-06	109.24	2128	17	2166	341760;3417	158781;15	158790		10
LLVVYPWTQR	VGGEALGRLLVVYPWT	VVYPWTQRFFESFGDL	R	L	L	Q	R	F	0	1	0	0	0	1	0	0	0	0	2	0	0	0	1	0	1	1	1	2	0	0	10	0	1273.718	sp|P68871	sp|P68871|HB	32	41	no	no	2;3	7.43E-09	157.68	2178	416;132;417;4	2217	350909;3509	163721;16	163898		188
LNDLEDALQQAK	ALKDAKNKLNDLEDAL	EDALQQAKEDLARLLR	K	L	N	A	K	E	2	0	1	2	0	2	1	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	12	0	1356.689	sp|P04264	sp|P04264|K2	444	455	yes	no	2	7.20E-06	91.265	2184	178	2223	351465;3516	164025;16	164026		2
LNDLEEALQQAK	ALKDARNKLNDLEEAL	EEALQQAKEDLARLLR	K	L	N	A	K	E	2	0	1	1	0	2	2	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	12	0	1370.704	sp|P35908	sp|P35908|K2	442	453	yes	no	2	5.67E-10	137.95	2185	20	2224	351672;3516	164027;16	164031		5
LPYSVVR	QDFFIDLRLPYSVVRN	RLPYSVVRNEQVEIRA	R	L	P	V	R	N	0	1	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	1	2	0	0	7	0	832.4807	sp|P01024	sp|P01024|CO	835	841	no	no	2	0.002772	143.18	2228	97;24	2268	358154;3581	167344;16	167345		3
LQSSSASYGGGFGGGSCQLGGGR	________________	SCQLGGGRGVSTCSTR	R	L	Q	G	R	G	1	1	0	0	1	2	0	9	0	0	2	0	0	1	0	5	0	0	1	0	0	0	23	0	2145.95	sp|P13646	sp|P13646|K1	5	27	no	no	3	0.044586	15.128	2252	276	2292	362402	169569	169569		1
LRVDPVNFK	LSDLHAHKLRVDPVNF	RVDPVNFKLLSHCLLV	K	L	R	F	K	L	0	1	1	1	0	0	0	0	0	0	1	1	0	1	1	0	0	0	0	2	0	0	9	1	1086.619	CON__P01	sp|P69905|HB	92	100	no	no	2	0.007141	74.92	2256	419;3	2296	362649;3626	169613;16	169614		2
LSFNPTQLEEQCHI	KALPMHIRLSFNPTQL	QLEEQCHI________	R	L	S	H	I	-	0	0	1	0	1	2	2	0	1	1	2	0	0	1	1	1	1	0	0	0	0	0	14	0	1714.799	CON__P02	CON__P02754	149	162	yes	yes	2	9.10E-05	80.916	2264	10	2304	363473;3634	169856;16	169857		3
LSPLAQELR	KVQELQDKLSPLAQEL	SPLAQELRDRARAHVE	K	L	S	L	R	D	1	1	0	0	0	1	1	0	0	0	3	0	0	0	1	1	0	0	0	0	0	0	9	0	1025.587	CON__P15	CON__P15497	164	172	yes	yes	2	0.0006329	125.31	2289	17	2329	366756;3667	171242;17	171242		3
LSSPATLNSR	DNDIMLIKLSSPATLN	SPATLNSRVATVSLPR	K	L	S	S	R	V	1	1	1	0	0	0	0	0	0	0	2	0	0	0	1	3	1	0	0	0	0	0	10	0	1044.556	CON__P00	CON__P00761	98	107	yes	yes	2	1.58E-08	138.26	2295	1	2335	367328;3673	171531;17	171545		80
LTPLYELVK	LPQVIKQKLTPLYELV	TPLYELVKEVPCASVK	K	L	T	V	K	E	0	0	0	0	0	0	1	0	0	0	3	1	0	0	1	0	1	0	1	1	0	0	9	0	1074.633	sp|P10643	sp|P10643|CO	421	429	no	no	2	0.0064957	93.374	2318	252	2358	370722;3707	173136;17	173147		61
LTSLSDR	ALRADLEKLTSLSDRY	KLTSLSDRYVSHFETE	K	L	T	D	R	Y	0	1	0	1	0	0	0	0	0	0	2	0	0	0	0	2	1	0	0	0	0	0	7	0	790.4185	sp|P0C0L4	sp|P0C0L4|CO	1504	1510	no	no	2	1.52E-06	154.09	2324	245;246;2	2364	371606;3716	173501;17	173507		27
LVAASQAALGL	CFAEEGKKLVAASQAA	ASQAALGL________	K	L	V	G	L	-	4	0	0	0	0	1	0	1	0	0	3	0	0	0	0	1	0	0	0	1	0	0	11	0	1012.592	sp|P02768	sp|P02768|ALI	599	609	yes	no	1;2	1.13E-07	114.78	2339	11	2379	374341;3743	174753;17	175184		524
LVILEGELER	KYEEVARKLVILEGEL	ILEGELERAEERAEVS	K	L	V	E	R	A	0	1	0	0	0	0	3	1	0	1	3	0	0	0	0	0	0	0	0	1	0	0	10	0	1169.666	sp|P67936	sp|P67936|TP	133	142	no	no	2	1.05E-19	157.91	2361	413;222	2401	377899;3779	176250;17	176292		104
LVNELTEFAK	CPFDEHVKLVNELTEF	NELTEFAKTCVADESH	K	L	V	A	K	T	1	0	1	0	0	0	2	0	0	0	2	1	0	1	0	0	1	0	0	1	0	0	10	0	1162.623	CON__P02	CON__P02769	66	75	yes	yes	2	4.51E-11	144.12	2367	12	2407	378574;3785	176557;17	176559		31
LVNEVTEFAK	CPFDEHVKLVNEVTEF	NEVTEFAKTCVADESA	K	L	V	A	K	T	1	0	1	0	0	0	2	0	0	0	1	1	0	1	0	0	1	0	0	2	0	0	10	0	1148.608	sp|P02768	sp|P02768|ALI	66	75	yes	no	2	1.32E-19	156.51	2368	11	2408	378756;3787	176588;17	176811		227
LVPFATELHER	YAGDLQKKLVPFATEL	FATELHERLAKDSEKL	K	L	V	E	R	L	1	1	0	0	0	0	2	0	1	0	2	0	0	1	1	0	1	0	0	1	0	0	11	0	1310.698	sp|P06727	sp|P06727|AP	80	90	no	no	2;3	9.57E-47	180.44	2371	206	2411	379323;3793	176837;17	176864		295
LVRPEVDVMCTAFHDNEETFLK	DDNPNLPRLVRPEVDV	DNEETFLKKYLYEIAR	R	L	V	L	K	K	1	1	1	2	1	0	3	0	1	0	2	1	1	2	1	0	2	0	0	3	0	0	22	1	2649.257	sp|P02768	sp|P02768|ALI	139	160	yes	no	3;4	5.44E-135	168.75	2378	11	2418;2419	380187;3801	177238;17	177377	4	154
LVTDLTK	AEFAEVSKLVTDLTKV	KLVTDLTKVHTECCHG	K	L	V	T	K	V	0	0	0	1	0	0	0	0	0	0	2	1	0	0	0	0	2	0	0	1	0	0	7	0	788.4644	sp|P02768	sp|P02768|ALI	258	264	no	no	2	0.0035307	135.87	2379	11;12	2420	380519;3805	177394;17	177414		57
LVVQIDNAK	CTKSENARLVVQIDNA	VVQIDNAKLAADDFRT	R	L	V	A	K	L	1	0	1	1	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	2	0	0	9	0	998.5761	sp|Q15323	sp|Q15323|K1	127	135	yes	no	2	0.0052707	85.212	2382	22	2423	381069;3810	177545	177545		1
MFLSFPTTK	YGAEALERMFLSFPTT	FLSFPTTKTYFPHFDL	R	M	F	T	K	T	0	0	0	0	0	0	0	0	0	0	1	1	1	2	1	1	2	0	0	0	0	0	9	0	1070.547	CON__P01	sp|P69905|HB	33	41	no	no	2	0.0005768	126.52	2420	419;3	2465;2466	389687;3896	183205;18	183208	1	94
MIGFPSSAGSVSPR	LLEGQDAKMIGFPSSA	SAGSVSPRSTSVTTTS	K	M	I	P	R	S	1	1	0	0	0	0	0	2	0	1	0	0	1	1	2	4	0	0	0	1	0	0	14	0	1391.687	sp|P13646	sp|P13646|K1	416	429	yes	no	2	0.029009	47.559	2424	276	2471	390563	183503	183503		1
MPCTEDYLSLILNR	CTKPESERMPCTEDYL	YLSLILNRLCVLHEKT	R	M	P	N	R	L	0	1	1	1	1	0	1	0	0	1	3	0	1	0	1	1	1	0	1	0	0	0	14	0	1723.827	CON__P02	CON__P02769	469	482	yes	yes	2	0.0002463	81.017	2438	12	2487	392218	184161	184161	6	1
MSTITGPVPR	IQYLPLIKMSTITGPV	TITGPVPREFKSQLQE	K	M	S	P	R	E	0	1	0	0	0	0	0	1	0	1	0	0	1	0	2	1	2	0	0	1	0	0	10	0	1057.559	CON__P02	CON__P02672	229	238	yes	yes	2	0.0064443	87.476	2443	8	2494	392763;3927	184303	184303	2	1
MTLDDFR	LLDIDNTRMTLDDFRI	RMTLDDFRIKFEMEQN	R	M	T	F	R	I	0	1	0	2	0	0	0	0	0	0	1	0	1	1	0	0	1	0	0	0	0	0	7	0	896.4062	sp|P35527	sp|P35527|K1	234	240	yes	no	2	0.0091192	110.34	2445	19	2496	392814;3928	184311;18	184315		5
MYEQEWVR	IYSLPGLKMYEQEWVR	MYEQEWVRLHLLNIGG	K	M	Y	V	R	L	0	1	0	0	0	1	2	0	0	0	0	0	1	0	0	0	0	1	1	1	0	0	8	0	1139.507	sp|P12259	sp|P12259|FA	1820	1827	no	no	2	0.013263	107.32	2459	264;23	2511	394085;3940	184774;18	184777		20
NALWHTGNTPGQVR	TGPGEHLRNALWHTGN	GNTPGQVRTLWHDPRH	R	N	A	V	R	T	1	1	2	0	0	1	0	2	1	0	1	0	0	0	1	0	2	1	0	1	0	0	14	0	1549.775	sp|P07996	sp|P07996|TS	1078	1091	yes	no	3	6.16E-13	78.401	2472	223	2527	396457;3964	185842;18	185842		8
NECFLQHK	CAKQEPERNECFLQHK	NECFLQHKDDNPNLPR	R	N	E	H	K	D	0	0	1	0	1	1	1	0	1	0	1	1	0	1	0	0	0	0	0	0	0	0	8	0	1074.492	sp|P02768	sp|P02768|ALI	123	130	yes	no	2;3	0.0045731	96.285	2481	11	2536	397610;3976	186305;18	186310		46
NEQVEIR	RLPYSVVRNEQVEIRA	RNEQVEIRAVLYNYRQ	R	N	E	I	R	A	0	1	1	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	7	0	886.4508	sp|P01024	sp|P01024|CO	842	848	no	no	2	0.012299	104.11	2484	97;24	2539	398497;3984	186647;18	186647		2
NFFNPPIISR	TNTKGHVKNFFNPPII	FNPPIISRFIRVIPKT	K	N	F	S	R	F	0	1	2	0	0	0	0	0	0	2	0	0	0	2	2	1	0	0	0	0	0	0	10	0	1203.64	sp|P12259	sp|P12259|FA	2190	2199	no	no	2	5.91E-07	127.68	2489	264;23	2544	399019;3990	186776;18	186779		135
NIVELMR	KDSNTLTKNIVELMRG	KNIVELMRGDFAKANN	K	N	I	M	R	G	0	1	1	0	0	0	1	0	0	1	1	0	1	0	0	0	0	0	0	1	0	0	7	0	873.4742	CON__P02	CON__P02672	111	117	yes	yes	2	0.050527	84.359	2522	8	2577	405241;4052	189780	189780		1
NLDLDSIIAEVK	ILSMDNSRNLDLDSII	DSIIAEVKAQYEEIAQ	R	N	L	V	K	A	1	0	1	2	0	0	1	0	0	2	2	1	0	0	0	1	0	0	0	1	0	0	12	0	1328.719	sp|P35908	sp|P35908|K2	342	353	no	no	2	3.80E-08	108.43	2528	20;16;5;0	2583	406473;4064	190027;19	190064		39
NLDLDSIIAEVR	VLSMDNNRNLDLDSII	DSIIAEVRAQYEEIAQ	R	N	L	V	R	A	1	1	1	2	0	0	1	0	0	2	2	0	0	0	0	1	0	0	0	1	0	0	12	0	1356.725	sp|P19013	sp|P19013|K2	315	326	no	no	2	1.55E-08	129.16	2529	18;25	2584	406610;4066	190066	190066		1
NMQDMVEDYR	SRLDSELKNMQDMVED	QDMVEDYRNKYEDEIN	K	N	M	Y	R	N	0	1	1	2	0	1	1	0	0	0	0	0	2	0	0	0	0	0	1	1	0	0	10	0	1299.522	sp|P04264	sp|P04264|K2	258	267	yes	no	2	0.017083	66.692	2549	178	2606	410078;4100	191945;19	191945		2
NQILNLTTDNANILLQIDNAR	YKTIDDLKNQILNLTT	LLQIDNARLAADDFRL	K	N	Q	A	R	L	2	1	5	2	0	2	0	0	0	3	4	0	0	0	0	0	2	0	0	0	0	0	21	0	2366.255	sp|P13645	sp|P13645|K1	208	228	yes	no	3	0.0010822	27.904	2578	15	2635	414474;4144	194069	194069		1
NTLIIYLDK	LDKAFSDRNTLIIYLD	TLIIYLDKVSHSEDDC	R	N	T	D	K	V	0	0	1	1	0	0	0	0	0	2	2	1	0	0	0	0	1	0	1	0	0	0	9	0	1091.623	sp|P01024	sp|P01024|CO	1442	1450	no	no	2	0.005094	87.258	2600	97;24	2658	417411;4174	195844;19	195844		24
NVQDAIADAEQR	AHVKKQCKNVQDAIAD	AIADAEQRGEHALKDA	K	N	V	Q	R	G	3	1	1	2	0	2	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	12	0	1328.632	sp|P35908	sp|P35908|K2	419	430	yes	no	2	3.96E-06	94.616	2608	20	2666	418310;4183	196188	196188		1
NWETEITAQPDGGK	TGARIAYKNWETEITA	TAQPDGGKTENCAVLS	K	N	W	G	K	T	1	0	1	1	0	1	2	2	0	1	0	1	0	0	1	0	2	1	0	0	0	0	14	0	1544.711	sp|P05452	sp|P05452|TE	156	169	yes	no	2;3	0	301.6	2614	196	2672	419032;4190	196593;19	196600		219
NYSPYYNTIDDLK	KGPAAIQKNYSPYYNT	YNTIDDLKDQIVDLTV	K	N	Y	L	K	D	0	0	2	2	0	0	0	0	0	1	1	1	0	0	1	1	1	0	3	0	0	0	13	0	1604.736	sp|P35527	sp|P35527|K1	200	212	yes	no	2	2.03E-12	114.86	2624	19	2682	420387;4203	197197;19	197198		2
PALPAGTEDTAK	MLQVLGPKPALPAGTE	AGTEDTAKEDAANRKL	K	P	A	A	K	E	3	0	0	1	0	0	1	1	0	0	1	1	0	0	2	0	2	0	0	0	0	0	12	0	1169.593	sp|P06396	sp|P06396|GE	278	289	yes	no	2	9.72E-14	121.5	2631	204	2689	420902;4209	197280;19	197289		52
PCFSALEVDETYVPK	TESLVNRRPCFSALEV	VDETYVPKEFNAETFT	R	P	C	P	K	E	1	0	0	1	1	0	2	0	0	0	1	1	0	1	2	1	1	0	1	2	0	0	15	0	1753.823	sp|P02768	sp|P02768|ALI	510	524	yes	no	2	2.82E-74	172.92	2638	11	2696	422426;4224	198404;19	198430		35
PEVDVMCTAFHDNEETFLK	PNLPRLVRPEVDVMCT	DNEETFLKKYLYEIAR	R	P	E	L	K	K	1	0	1	2	1	0	3	0	1	0	1	1	1	2	1	0	2	0	0	2	0	0	19	0	2281.003	sp|P02768	sp|P02768|ALI	142	160	yes	no	3	7.02E-05	59.252	2650	11	2708	423215;4232	198609	198609		1
PFDAFTDLK	EEELCSGKPFDAFTDL	FDAFTDLKNGSLFAFR	K	P	F	L	K	N	1	0	0	2	0	0	0	0	0	0	1	1	0	2	1	0	1	0	0	0	0	0	9	0	1052.518	sp|P04004	sp|P04004|VT	160	168	no	no	2	3.32E-69	201.39	2651	168	2709	423233;4232	198610;19	198629		213
PLVEEPQNLIK	AKVFDEFKPLVEEPQN	EEPQNLIKQNCELFEQ	K	P	L	I	K	Q	0	0	1	0	0	1	2	0	0	1	2	1	0	0	2	0	0	0	0	1	0	0	11	0	1278.718	sp|P02768	sp|P02768|ALI	403	413	yes	no	2	2.91E-81	200.6	2694	11	2752	428312;4283	200213;20	200217		142
PNSMVVEHPEFLK	QGRVPEARPNSMVVEH	VEHPEFLKAGKEPGLQ	R	P	N	L	K	A	0	0	1	0	0	0	2	0	1	0	1	1	1	1	2	1	0	0	0	2	0	0	13	0	1525.76	sp|P06396	sp|P06396|GE	49	61	yes	yes	2;3	1.15E-12	117.14	2700	204	2758	428972;4289	200676;20	200699		33
PVQGVAYVR	QARYIYGKPVQGVAYV	VQGVAYVRFGLLDEDG	K	P	V	V	R	F	1	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0	1	3	0	0	9	0	987.5502	sp|P0C0L4	sp|P0C0L4|CO	275	283	no	no	2	2.46E-16	148.33	2734	245;246;2	2792	435125;4351	203144;20	203158		128
QCANLQAAIADAEQR	SEIDHVKKQCANLQAA	AIADAEQRGEMALKDA	K	Q	C	Q	R	G	5	1	1	1	1	3	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	15	0	1657.784	sp|P02538	sp|P02538|K2	401	415	no	no	3	0.030042	33.147	2757	5	2815	437681	204374	204374		1
QCANLQNAIADAEQR	AEIDNVKKQCANLQNA	AIADAEQRGELALKDA	K	Q	C	Q	R	G	4	1	2	1	1	3	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	15	0	1700.79	sp|P13647	sp|P13647|K2	406	420	no	no	2	8.47E-05	82.171	2758	16	2816	437682;4376	204375	204375		1
QDGSVDFGR	GWTVIQNRQDGSVDFG	DGSVDFGRKWDPYKQG	R	Q	D	G	R	K	0	1	0	2	0	1	0	2	0	0	0	0	0	1	0	1	0	0	0	1	0	0	9	0	979.4359	sp|P02675	sp|P02675|FIB	286	294	no	no	2	0.0007412	114.5	2766	143;9	2824	438352;4383	204703;20	204705		25
QEIECQNQEYSLLLSIK	EAQITDVRQEIECQNQ	YSLLLSIKMRLEKEIE	R	Q	E	I	K	M	0	0	1	0	1	3	3	0	0	2	3	1	0	0	0	2	0	0	1	0	0	0	17	0	2094.03	sp|P35527	sp|P35527|K1	428	444	yes	no	2	1.49E-47	164.11	2777	19	2835	439883	205231	205231		1
QEYEQLIAK	TKTLNDMRQEYEQLIA	EYEQLIAKNRKDIENQ	R	Q	E	A	K	N	1	0	0	0	0	2	2	0	0	1	1	1	0	0	0	0	0	0	1	0	0	0	9	0	1120.576	sp|P35527	sp|P35527|K1	328	336	yes	no	2	0.0008402	118.74	2783	19	2841	440349;4403	205387	205387		1
QGSFQGGFR	QASAWLTRQGSFQGGF	GSFQGGFRSTQDTVIA	R	Q	G	F	R	S	0	1	0	0	0	2	0	3	0	0	0	0	0	2	0	1	0	0	0	0	0	0	9	0	982.4621	sp|P0C0L4	sp|P0C0L4|CO	1292	1300	no	no	2	7.51E-56	193.16	2797	245;246;2	2855	443642;4436	206771;20	206785		83
QGVDADINGLR	FEMEQNLRQGVDADIN	DADINGLRQVLDNLTM	R	Q	G	L	R	Q	1	1	1	2	0	1	0	2	0	1	1	0	0	0	0	0	0	0	0	1	0	0	11	0	1156.584	sp|P35527	sp|P35527|K1	251	261	yes	no	2	0.012767	63.184	2798	19	2856	443857;4438	206855;20	206855		2
QISNLQQSISDAEQR	SEIDNVKKQISNLQQS	SISDAEQRGENALKDA	K	Q	I	Q	R	G	1	1	1	1	0	4	1	0	0	2	1	0	0	0	0	3	0	0	0	0	0	0	15	0	1715.844	sp|P04264	sp|P04264|K2	418	432	yes	no	2	2.98E-97	228.83	2809	178	2867	445325;4453	207511;20	207511		4
QNCELFEQLGEYK	EEPQNLIKQNCELFEQ	FEQLGEYKFQNALLVR	K	Q	N	Y	K	F	0	0	1	0	1	2	3	1	0	0	2	1	0	1	0	0	0	0	1	0	0	0	13	0	1656.745	sp|P02768	sp|P02768|ALI	414	426	yes	no	2;3	2.55E-205	247.31	2834	11	2892	447991;4479	208546;20	209046		505
QSLEASLAETEGR	LQSQLALKQSLEASLA	SLAETEGRYCVQLSQI	K	Q	S	G	R	Y	2	1	0	0	0	1	3	1	0	0	2	0	0	0	0	2	1	0	0	0	0	0	13	0	1389.674	sp|P13645	sp|P13645|K1	387	399	yes	no	2	7.39E-30	145.55	2850	15	2908	450818;4508	210060;21	210060		4
QTALVELLK	DTEKQIKKQTALVELL	TALVELLKHKPKATEE	K	Q	T	L	K	H	1	0	0	0	0	1	1	0	0	0	3	1	0	0	0	0	1	0	0	1	0	0	9	0	1013.612	CON__P02	CON__P02769	549	557	yes	yes	2	0.023237	69.825	2857	12	2915	451415;4514	210216;21	210217		6
QTALVELVK	EKERQIKKQTALVELV	TALVELVKHKPKATKE	K	Q	T	V	K	H	1	0	0	0	0	1	1	0	0	0	2	1	0	0	0	0	1	0	0	2	0	0	9	0	999.5965	sp|P02768	sp|P02768|ALI	550	558	yes	no	2	0.0010544	96.331	2858	11	2916	451494;4514	210222;21	210347		147
QTQVSVLPEGGETPLFK	ITKMDYPKQTQVSVLP	GGETPLFKQFFKNWRD	K	Q	T	F	K	Q	0	0	0	0	0	2	2	2	0	0	2	1	0	1	2	1	2	0	0	2	0	0	17	0	1828.957	sp|P06396	sp|P06396|GE	374	390	yes	no	2;3	1.30E-135	195.71	2863	204	2921	452436;4524	210532;21	210843		408
QVLDNLTMEK	DADINGLRQVLDNLTM	LDNLTMEKSDLEMQYE	R	Q	V	E	K	S	0	0	1	1	0	1	1	0	0	0	2	1	1	0	0	0	1	0	0	1	0	0	10	0	1189.601	sp|P35527	sp|P35527|K1	262	271	yes	no	2	0.061949	51.528	2875	19	2933	454259	211390	211390		1
RFEQLELR	LRLPMSVRRFEQLELR	RFEQLELRPVLYNYLD	R	R	F	L	R	P	0	2	0	0	0	1	2	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	8	1	1089.593	sp|P0C0L4	sp|P0C0L4|CO	845	852	no	no	2	4.55E-21	172.94	2888	245;246;2	2946	456610;4566	212307;21	212323		25
RHPDYSVVLLLR	MFLYEYARRHPDYSVV	YSVVLLLRLAKTYETT	R	R	H	L	R	L	0	2	0	1	0	0	0	0	1	0	3	0	0	0	1	1	0	0	1	2	0	0	12	1	1466.836	sp|P02768	sp|P02768|ALI	361	372	yes	no	3	4.35E-08	100.38	2894	11	2952	457158;4571	212417;21	212448		39
RHPEYAVSVLLR	SFLYEYSRRHPEYAVS	YAVSVLLRLAKEYEAT	R	R	H	L	R	L	1	2	0	0	0	0	1	0	1	0	2	0	0	0	1	1	0	0	1	2	0	0	12	1	1438.805	CON__P02	CON__P02769	360	371	yes	yes	3	0.000159	73.082	2895	12	2953	457280;4572	212456;21	212457		3
RLEVDIDIK	RAQLVDMKRLEVDIDI	LEVDIDIKIRSCRGSC	K	R	L	I	K	I	0	1	0	2	0	0	1	0	0	2	1	1	0	0	0	0	0	0	0	1	0	0	9	1	1099.624	sp|P02671	sp|P02671|FIB	168	176	no	no	2	0.0086913	115.7	2899	142;8	2957	457693;4576	212565;21	212565		3
RPCFSALEVDETYVPK	CTESLVNRRPCFSALE	VDETYVPKEFNAETFT	R	R	P	P	K	E	1	1	0	1	1	0	2	0	0	0	1	1	0	1	2	1	1	0	1	2	0	0	16	1	1909.924	sp|P02768	sp|P02768|ALI	509	524	yes	no	2;3;4	7.37E-63	182.23	2905	11	2963	458216;4582	212693;21	212713		346
SEDCFILDHGK	PFAQGALKSEDCFILD	CFILDHGKGKIFVWK	K	S	E	G	K	D	0	0	0	2	1	0	1	1	1	1	1	1	0	1	0	1	0	0	0	0	0	0	11	0	1319.582	sp|P06396	sp|P06396|GE	328	338	yes	no	2;3	7.56E-20	168.8	2976	204	3034	469135;4691	217454;21	217647		194
SGGGFSSGSAGIINYQR	FSSRSGYRSGGGFSSG	AGIINYQRRTTSSSTR	R	S	G	Q	R	R	1	1	1	0	0	1	0	5	0	2	0	0	0	1	0	4	0	0	1	0	0	0	17	0	1656.786	sp|P04264	sp|P04264|K2	13	29	yes	no	2	1.17E-05	95.094	3011	178	3069	475054;4750	221105	221105		1
SGGGGGGGLGSGGSIR	FSSSYLSRSGGGGGGG	LGSGGSIRSSYSRFSS	R	S	G	I	R	S	0	1	0	0	0	0	0	10	0	1	1	0	0	0	0	3	0	0	0	0	0	0	16	0	1231.591	sp|P35527	sp|P35527|K1	14	29	yes	no	2	7.72E-07	90.731	3012	19	3070	475056;4750	221106;22	221106		3
SHCIAEVENDEMPADLPSLAADFVESK	CEKPLLEKSHCIAEVE	AADFVESKDVCKNYAE	K	S	H	S	K	D	4	0	1	3	1	0	4	0	1	1	2	1	1	1	2	3	0	0	0	2	0	0	27	0	2973.337	sp|P02768	sp|P02768|ALI	311	337	yes	no	2;3;4;5	4.49E-172	144.68	3027	11	3085;3086	478270;4782	222982;22	222993	5	215
SILENLR	PTNLRVLRSILENLRS	RSILENLRSKIQKLES	R	S	I	L	R	S	0	1	1	0	0	0	1	0	0	1	2	0	0	0	0	1	0	0	0	0	0	0	7	0	843.4814	sp|P02675	sp|P02675|FIB	200	206	no	no	2	0.0033176	141.98	3035	143;9	3094	479782;4797	223917;22	223925		14
SISISVAR	LVNLGGSKSISISVAR	SISISVARGGGRGSGF	K	S	I	A	R	G	1	1	0	0	0	0	0	0	0	2	0	0	0	0	0	3	0	0	0	1	0	0	8	0	831.4814	sp|P04264	sp|P04264|K2	75	82	yes	no	2	0.0006531	102.77	3046	178	3105	480750;4807	224281;22	224284		6
SITLFVQEDR	LLATGQWKSITLFVQE	TLFVQEDRALYIDCE	K	S	I	D	R	A	0	1	0	1	0	1	1	0	0	1	1	0	0	1	0	1	1	0	0	1	0	0	10	0	1206.625	sp|P07996	sp|P07996|TS	155	164	yes	no	2	0.000144	105.52	3048	223	3107	481303;4813	224545;22	224549		27
SLDLDSIIAEVK	ILSMDNNRSLDLDSII	DSIIAEVKAQYEDIAQ	R	S	L	V	K	A	1	0	0	2	0	0	1	0	0	2	2	1	0	0	0	2	0	0	0	1	0	0	12	0	1301.708	sp|P04264	sp|P04264|K2	344	355	no	no	2	6.34E-33	161.17	3059	178	3118	483816;4838	225826;22	225938		113
SLHTLFGDELCK	ESHAGCEKSLHTLFGD	LFGDELCKVASLRETY	K	S	L	C	K	V	0	0	0	1	1	0	1	1	1	0	3	1	0	1	0	1	1	0	0	0	0	0	12	0	1418.686	CON__P02	CON__P02769	89	100	yes	yes	3	0.0099359	35.523	3072	12	3132	486616;4866	227208	227208		1
SLHTLFGDK	ESAENCDKSLHTLFGD	LHTLFGDKLCTVATLR	K	S	L	D	K	L	0	0	0	1	0	0	0	1	1	0	2	1	0	1	0	1	1	0	0	0	0	0	9	0	1016.529	sp|P02768	sp|P02768|ALI	89	97	yes	no	2;3	0.0004974	111.17	3073	11	3133	486644;4866	227209;22	227212		245
SLLEGEGSSGGGGR	ENEIQTYRSLLEGEGS	GSSGGGGRGGGSFGGG	R	S	L	G	R	G	0	1	0	0	0	0	2	6	0	0	2	0	0	0	0	3	0	0	0	0	0	0	14	0	1261.59	sp|P13645	sp|P13645|K1	451	464	yes	no	2	1.09E-20	126.71	3076	15	3136	487304;4873	227494;22	227494		2
SLNNQFASFIDK	SREREQIKSLNNQFAS	QFASFIDKVRFLEQQN	K	S	L	D	K	V	1	0	2	1	0	1	0	0	0	1	1	1	0	2	0	2	0	0	0	0	0	0	12	0	1382.683	sp|P04264	sp|P04264|K2	186	197	yes	no	2	2.13E-48	175.86	3079	178	3139	487376;4873	227500;22	227513		26
SLSSEMYVK	AIITQGCKSLSSEMYV	LSSEMYVKSYTIHYSE	K	S	L	V	K	S	0	0	0	0	0	0	1	0	0	0	1	1	1	0	0	3	0	0	1	1	0	0	9	0	1042.501	sp|P12259	sp|P12259|FA	2143	2151	no	no	2	0.01821	72.485	3088	264;23	3149	488511;4885	228043	228043		1
SLVGLGGTK	GGGGFGSRSLVGLGGT	LVGLGGTKSISISVAG	R	S	L	T	K	S	0	0	0	0	0	0	0	3	0	0	2	1	0	0	0	1	1	0	0	1	0	0	9	0	830.4862	sp|P35908	sp|P35908|K2	62	70	yes	no	2	0.0010813	105.14	3094	20	3155	489246;4892	228272;22	228272		3
SLVNLGGSK	AGGGFGSRSLVNLGGS	LVNLGGSKSISISVAR	R	S	L	S	K	S	0	0	1	0	0	0	0	2	0	0	2	1	0	0	0	2	0	0	0	1	0	0	9	0	873.492	sp|P04264	sp|P04264|K2	66	74	yes	no	2	0.0006043	105.14	3096	178	3157	489338;4893	228282;22	228289		10
SLYNLGGSK	GVGGYGSRSLYNLGGS	LYNLGGSKRISISTSG	R	S	L	S	K	R	0	0	1	0	0	0	0	2	0	0	2	1	0	0	0	2	0	0	1	0	0	0	9	0	937.4869	sp|P13647	sp|P13647|K2	64	72	yes	no	2	0.0008556	119.41	3098	16	3159	489408;4894	228293;22	228293		2
SPAQILQWQVLSNTVPAK	YAKPAAVRSPAQILQW	LSNTVPAKSCQAQPTT	R	S	P	A	K	S	2	0	1	0	0	3	0	0	0	1	2	1	0	0	2	2	1	1	0	2	0	0	18	0	1979.084	CON__P02	CON__P02668	69	86	yes	yes	2;3	9.66E-30	115.57	3109	7	3170	491050;4910	229273;22	229275		3
SQYEALVETNR	NRVLNETRSQYEALVE	EALVETNRREVEQWFT	R	S	Q	N	R	R	1	1	1	0	0	1	2	0	0	0	1	0	0	0	0	1	1	0	1	1	0	0	11	0	1308.631	sp|Q15323	sp|Q15323|K1	230	240	yes	no	2	0.03187	61.353	3139	22	3201	495291;4952	231363	231363		1
SQYEQLAEQNR	TQLLNNMRSQYEQLAE	EQLAEQNRKDAEAWFN	R	S	Q	N	R	K	1	1	1	0	0	3	2	0	0	0	1	0	0	0	0	1	0	0	1	0	0	0	11	0	1364.632	sp|P13645	sp|P13645|K1	323	333	yes	no	2	1.20E-07	114.5	3140	15	3202	495293;4952	231364;23	231365		5
SSGSSYPSLLQCLK	ISGWGNTKSSGSSYPS	PSLLQCLKAPVLSDSS	K	S	S	L	K	A	0	0	0	0	1	1	0	1	0	0	3	1	0	0	1	5	0	0	1	0	0	0	14	0	1525.745	CON__P00	CON__P00761	134	147	yes	yes	2	3.36E-38	141.95	3149	1	3212	496446;4966	231807;23	232004		224
TAAENDFVTLK	YEDEINKRTAAENDFV	ENDFVTLKKDVDNAYM	R	T	A	L	K	K	2	0	1	1	0	0	1	0	0	0	1	1	0	1	0	0	2	0	0	1	0	0	11	0	1207.609	sp|P35908	sp|P35908|K2	276	286	yes	no	2	1.51E-11	125.48	3211	20	3276	507144;5071	237474;23	237474		3
TAAENEFVALK	YEDEINKRTAAENEFV	ENEFVALKKDVDAAYM	R	T	A	L	K	K	3	0	1	0	0	0	2	0	0	0	1	1	0	1	0	0	1	0	0	1	0	0	11	0	1191.614	sp|O95678	sp|O95678|K2	247	257	yes	no	2	0.0022451	76.827	3212	0	3277	507155	237477	237477		1
TAAENEFVTLK	YEDEINKRTAAENEFV	ENEFVTLKKDVDAAYM	R	T	A	L	K	K	2	0	1	0	0	0	2	0	0	0	1	1	0	1	0	0	2	0	0	1	0	0	11	0	1221.624	sp|P02538	sp|P02538|K2	261	271	no	no	2	0.012735	63.216	3213	5;14	3278	507156;5071	237478	237478		1
TASDFITK	EERKAALKTASDFITK	TASDFITKMDYPKQTQ	K	T	A	T	K	M	1	0	0	1	0	0	0	0	0	1	0	1	0	1	0	1	2	0	0	0	0	0	8	0	881.4495	sp|P06396	sp|P06396|GE	361	368	yes	yes	2	0.022835	83.206	3224	204	3290	508458;5084	237790;23	237790		5
TCVADESAENCDK	NEVTEFAKTCVADESA	ESAENCDKSLHTLFGD	K	T	C	D	K	S	2	0	1	2	2	0	2	0	0	0	0	1	0	0	0	1	1	0	0	1	0	0	13	0	1497.571	sp|P02768	sp|P02768|ALI	76	88	yes	no	2	7.10E-47	166.86	3233	11	3299	510009;5100	238646;23	238654		59
TEAESWYQTK	EEIANRSRTEAESWYQ	AESWYQTKYEELQQTA	R	T	E	T	K	Y	1	0	0	0	0	1	2	0	0	0	0	1	0	0	0	1	2	1	1	0	0	0	10	0	1241.556	sp|P13647	sp|P13647|K2	355	364	yes	no	2	0.0086168	74.464	3243	16	3310	511506;5115	239440;23	239441		2
TEALTSAK	KDSQEEEKTEALTSAK	TEALTSAKRYIETDPA	K	T	E	A	K	R	2	0	0	0	0	0	1	0	0	0	1	1	0	0	0	1	2	0	0	0	0	0	8	0	819.4338	sp|P06396	sp|P06396|GE	721	728	yes	no	2	0.019937	96.492	3244	204	3311	511510;5115	239442;23	239442		3
TENCAVLSGAANGK	TAQPDGGKTENCAVLS	LSGAANGKWFDKRCRD	K	T	E	G	K	W	3	0	2	0	1	0	1	2	0	0	1	1	0	0	0	1	1	0	0	1	0	0	14	0	1390.651	sp|P05452	sp|P05452|TE	170	183	yes	yes	2	2.65E-16	115	3263	196	3330	514969;5149	241881;24	241881		3
TFHEASEDCISR	FLAFTQTKTFHEASED	ASEDCISRGGTLGTPQ	K	T	F	S	R	G	1	1	0	1	1	0	2	0	1	1	0	0	0	1	0	2	1	0	0	0	0	0	12	0	1450.615	sp|P05452	sp|P05452|TE	90	101	yes	no	2;3	8.50E-49	176.6	3274	196	3341	517214;5172	243806;24	243828		112
TGAQELLR	TGASEAEKTGAQELLR	TGAQELLRVLRAQPVQ	K	T	G	L	R	V	1	1	0	0	0	1	1	1	0	0	2	0	0	0	0	0	1	0	0	0	0	0	8	0	886.4872	sp|P06396	sp|P06396|GE	616	623	yes	yes	2	2.09E-30	178.08	3290	204	3357	520154;5201	245477;24	245493		60
TIVTTLQDSIR	VLELRGLRTIVTTLQD	TTLQDSIRKVTEENKE	R	T	I	I	R	K	0	1	0	1	0	1	0	0	0	2	1	0	0	0	0	1	3	0	0	1	0	0	11	0	1245.693	sp|P07996	sp|P07996|TS	289	299	yes	no	2	3.76E-68	193.1	3327	223	3395	525871;5258	247613;24	247613		164
TIYTPGSTVLYR	YLFIQTDKTIYTPGST	PGSTVLYRIFTVNHKL	K	T	I	Y	R	I	0	1	0	0	0	0	0	1	0	1	1	0	0	0	1	1	3	0	2	1	0	0	12	0	1369.724	sp|P01024	sp|P01024|CO	137	148	no	no	2	1.89E-20	138.66	3328	97;24	3396	526052;5260	247777;24	247805		143
TLLDIDNTR	DLTVGNNKTLLDIDNT	LLDIDNTRMTLDDFRI	K	T	L	T	R	M	0	1	1	2	0	0	0	0	0	1	2	0	0	0	0	0	2	0	0	0	0	0	9	0	1059.556	sp|P35527	sp|P35527|K1	225	233	yes	no	2	0.0002766	131.06	3342	19	3411	529133;5291	250149;25	250156		8
TLLEGEESR	DLEIATYRTLLEGEES	LLEGEESRMSGECAPN	R	T	L	S	R	M	0	1	0	0	0	0	3	1	0	0	2	0	0	0	0	1	1	0	0	0	0	0	9	0	1032.509	sp|P04264	sp|P04264|K2	484	492	yes	no	2	0.0033789	95.531	3343	178	3412	529160;5291	250159;25	250161		7
TNAENEFVTIK	YEDEINKRTNAENEFV	ENEFVTIKKDVDGAYM	R	T	N	I	K	K	1	0	2	0	0	0	2	0	0	1	0	1	0	1	0	0	2	0	0	1	0	0	11	0	1264.63	sp|P04264	sp|P04264|K2	278	288	yes	no	2	0.0023342	76.619	3370	178	3441	533964;5339	252436;25	252438		5
TPSAAYLWVGTGASEAEK	SNDAFVLKTPSAAYLW	TGASEAEKTGAQELLR	K	T	P	E	K	T	4	0	0	0	0	0	2	2	0	0	1	1	0	0	1	2	2	1	1	1	0	0	18	0	1836.889	sp|P06396	sp|P06396|GE	598	615	yes	yes	2;3	1.42E-235	302.28	3394	204	3466	537660;5376	254380;25	254380		225
TSSSTFQYITLLK	NTVDSVSRTSSSTFQY	FQYITLLKNMWKGRQN	R	T	S	L	K	N	0	0	0	0	0	1	0	0	0	1	2	1	0	1	0	3	3	0	1	0	0	0	13	0	1487.787	CON__P02	CON__P02676	144	156	yes	yes	2	5.39E-10	103.22	3414	9	3486	541899;5419	256280;25	256280		9
TWDPEGVIFYGDTNPK	TSSSFEVRTWDPEGVI	FYGDTNPKDWFMLGL	R	T	W	P	K	D	0	0	1	2	0	0	1	2	0	1	0	1	0	1	2	0	2	1	1	1	0	0	16	0	1837.852	sp|P04278	sp|P04278|SH	77	92	no	no	2;3	2.92E-71	162.93	3446	180;28	3518	548334;5483	260798;26	260955		175
TWNQSIALR	RFIRVIPKTWNQSIAL	WNQSIALRLELFGCDI	K	T	W	L	R	L	1	1	1	0	0	1	0	0	0	1	1	0	0	0	0	1	1	1	0	0	0	0	9	0	1087.577	sp|P12259	sp|P12259|FA	2207	2215	no	no	2	5.52E-19	164.53	3449	264;23	3521	548803;5488	260997;26	261050		71
TYEDDSPEWFK	YEKSSEGKTYEDDSPE	DDSPEWFKEDNAVQPN	K	T	Y	F	K	E	0	0	0	2	0	0	2	0	0	0	0	1	0	1	1	1	1	1	1	0	0	0	11	0	1415.588	sp|P12259	sp|P12259|FA	1685	1695	no	no	2	5.65E-06	110.76	3454	264;23	3526	549340;5493	261130;26	261130		62
TYETTLEK	VLLLRLAKTYETTLEK	TYETTLEKCCAAADPH	K	T	Y	E	K	C	0	0	0	0	0	0	2	0	0	0	1	1	0	0	0	0	3	0	1	0	0	0	8	0	983.4811	sp|P02768	sp|P02768|ALI	376	383	yes	no	2	0.015682	103.83	3455	11	3527	549465;5494	261193;26	261199		23
TYFPHFDLSHGSAQVK	FLSFPTTKTYFPHFDL	SHGSAQVKGHGKKVAD	K	T	Y	V	K	G	1	0	0	1	0	1	0	1	2	0	1	1	0	2	1	2	1	0	1	1	0	0	16	0	1832.885	CON__P01	sp|P69905|HB	42	57	no	no	2;3;4	0.00065	50.053	3456	419;3	3528	549799;5498	261216;26	261221		6
VATVSLPR	SPATLNSRVATVSLPR	VATVSLPRSCAAAGTE	R	V	A	P	R	S	1	1	0	0	0	0	0	0	0	0	1	0	0	0	1	1	1	0	0	2	0	0	8	0	841.5022	CON__P00	CON__P00761	108	115	yes	yes	2	2.55E-28	162.51	3492	1	3565	554813;5548	263453;26	263528		1501
VCNYVNWIQQTIAAN	NKPGVYTKVCNYVNWI	IQQTIAAN________	K	V	C	A	N	-	2	0	3	0	1	2	0	0	0	2	0	0	0	0	0	0	1	1	1	2	0	0	15	0	1792.857	CON__P00	CON__P00761	217	231	yes	yes	2	3.43E-65	163.77	3497	1	3570	559566;5595	265144;26	265184		77
VDALIDEIDFLR	NKVELQAKVDALIDEI	IDEIDFLRTLYDAELS	K	V	D	L	R	T	1	1	0	3	0	0	1	0	0	2	2	0	0	1	0	0	0	0	0	1	0	0	12	0	1417.745	sp|P12035	sp|P12035|K2	325	336	yes	no	2	0.0002393	78.655	3503	14	3576	560311	265439	265439		1
VDEVGGEALGR	TSLFAKVKVDEVGGEA	VGGEALGRLLVVYPWT	K	V	D	G	R	L	1	1	0	1	0	0	2	3	0	0	1	0	0	0	0	0	0	0	0	2	0	0	11	0	1100.546	CON__Q3S	CON__Q3SX09	75	85	yes	yes	2	9.68E-21	155.42	3505	27	3578	560337;5603	265441	265441		1
VDLLNQEIEFLK	IKVELQSKVDLLNQEI	NQEIEFLKVLYDAEIS	K	V	D	L	K	V	0	0	1	1	0	1	2	0	0	1	3	1	0	1	0	0	0	0	0	1	0	0	12	0	1459.792	sp|P35908	sp|P35908|K2	303	314	yes	no	2	6.34E-33	161.17	3510	20	3583	561998;5619	265920;26	265948		30
VDSLNDEINFLK	NKVELEAKVDSLNDEI	NDEINFLKVLYDAELS	K	V	D	L	K	V	0	0	2	2	0	0	1	0	0	1	2	1	0	1	0	1	0	0	0	1	0	0	12	0	1405.709	sp|P19013	sp|P19013|K2	276	287	yes	no	2	8.16E-05	84.213	3514	18	3587	562530;5625	266088	266088		1
VELEAALQQAK	LKDAHSKRVELEAALQ	EAALQQAKEELARMLR	R	V	E	A	K	E	3	0	0	0	0	2	2	0	0	0	2	1	0	0	0	0	0	0	0	1	0	0	11	0	1198.656	sp|P19013	sp|P19013|K2	416	426	yes	no	2	0.014082	61.999	3528	18	3601	564819	267280	267280		1
VFALDQK	PGQRVRYRVFALDQKM	RVFALDQKMRPSTDTI	R	V	F	Q	K	M	1	0	0	1	0	1	0	0	0	0	1	1	0	1	0	0	0	0	0	1	0	0	7	0	819.4491	sp|P0C0L4	sp|P0C0L4|CO	160	166	no	no	2	0.0022617	144.29	3547	245;246;2	3620	566662;5666	267884;26	267888		32
VFDEFKPLVEEPQNLIK	DPHECYAKVFDEFKPL	EEPQNLIKQNCELFEQ	K	V	F	I	K	Q	0	0	1	1	0	1	3	0	0	1	2	2	0	2	2	0	0	0	0	2	0	0	17	1	2044.088	sp|P02768	sp|P02768|ALI	397	413	yes	no	2;3;4	1.25E-232	239.31	3551	11	3624	567154;5671	268046;26	268401		399
VGGHAAEYGAEALER	NVKAAWGKVGGHAAEY	YGAEALERMFLSFPTT	K	V	G	E	R	M	4	1	0	0	0	0	3	3	1	0	1	0	0	0	0	0	0	0	1	1	0	0	15	0	1528.727	CON__P01	CON__P01966	18	32	yes	yes	3	0.0002212	48.823	3577	3	3651	571812;5718	270185;27	270213		29
VHTECCHGDLLECADDR	KLVTDLTKVHTECCHG	LLECADDRADLAKYIC	K	V	H	D	R	A	1	1	0	3	3	0	2	1	2	0	2	0	0	0	0	0	1	0	0	1	0	0	17	0	2085.83	sp|P02768	sp|P02768|ALI	265	281	yes	no	2;3;4	9.67E-256	294.83	3589	11	3663	572644;5726	270462;27	270473		91
VHVSEEGTEPEAMLQVLGPK	NERSGRARVHVSEEGT	MLQVLGPKPALPAGTE	R	V	H	P	K	P	1	0	0	0	0	1	4	2	1	0	2	1	1	0	2	1	1	0	0	3	0	0	20	0	2149.073	sp|P06396	sp|P06396|GE	258	277	yes	yes	2;3	2.57E-96	149.09	3590	204	3664	572963;5729	270554;27	270569		36
VILEIDNAR	TATIENNRVILEIDNA	ILEIDNARLAADDFRL	R	V	I	A	R	L	1	1	1	1	0	0	1	0	0	2	1	0	0	0	0	0	0	0	0	1	0	0	9	0	1041.582	sp|P13646	sp|P13646|K1	176	184	no	no	2	0.015106	74.127	3598	276	3673	574076	271077	271077		1
VLDELTLAR	ADINGLRRVLDELTLA	LDELTLARADLEMQIE	R	V	L	A	R	A	1	1	0	1	0	0	1	0	0	0	3	0	0	0	0	0	1	0	0	1	0	0	9	0	1028.587	sp|P02533	sp|P02533|K1	224	232	no	no	2	0.021169	70.919	3616	4;13	3691	576036;5760	271944;27	271946		3

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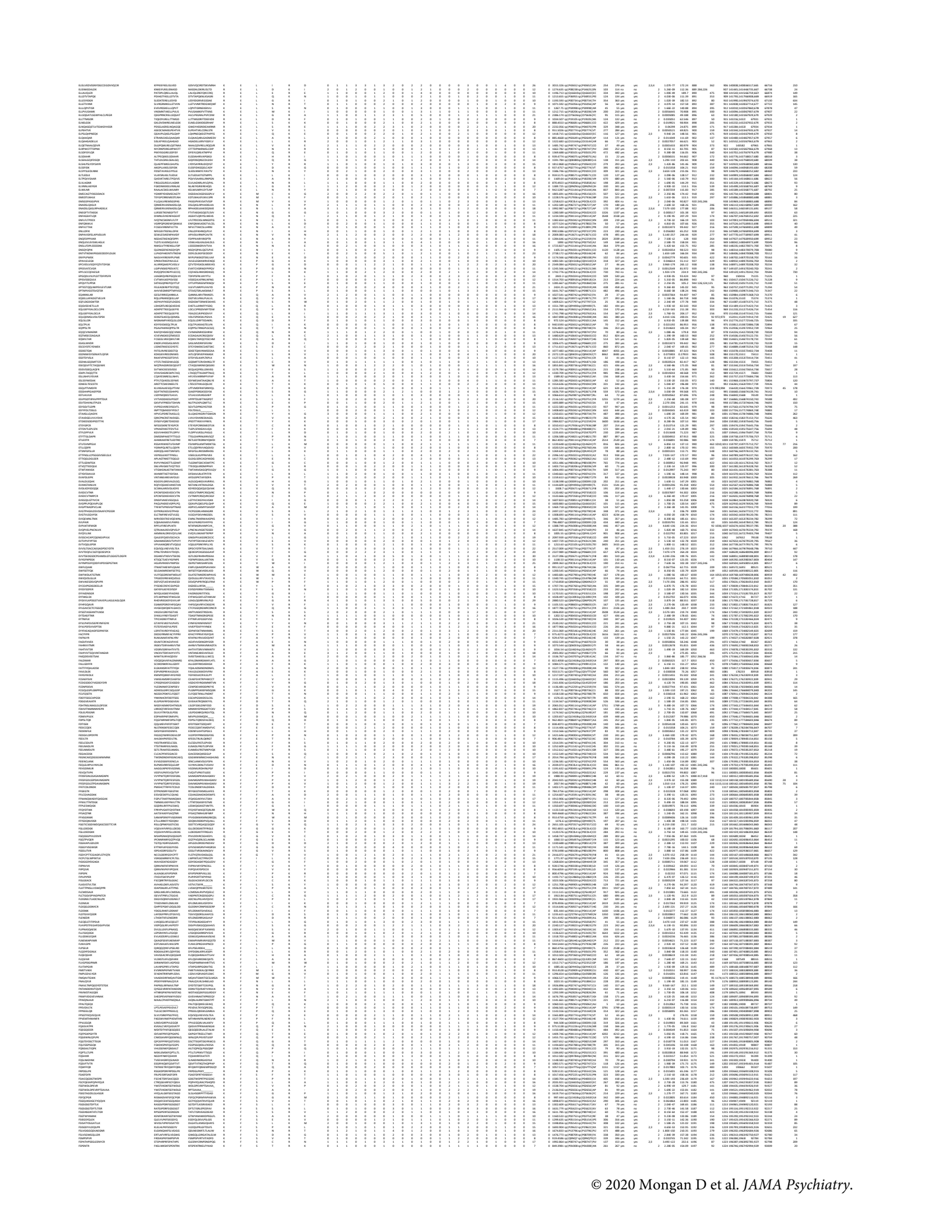

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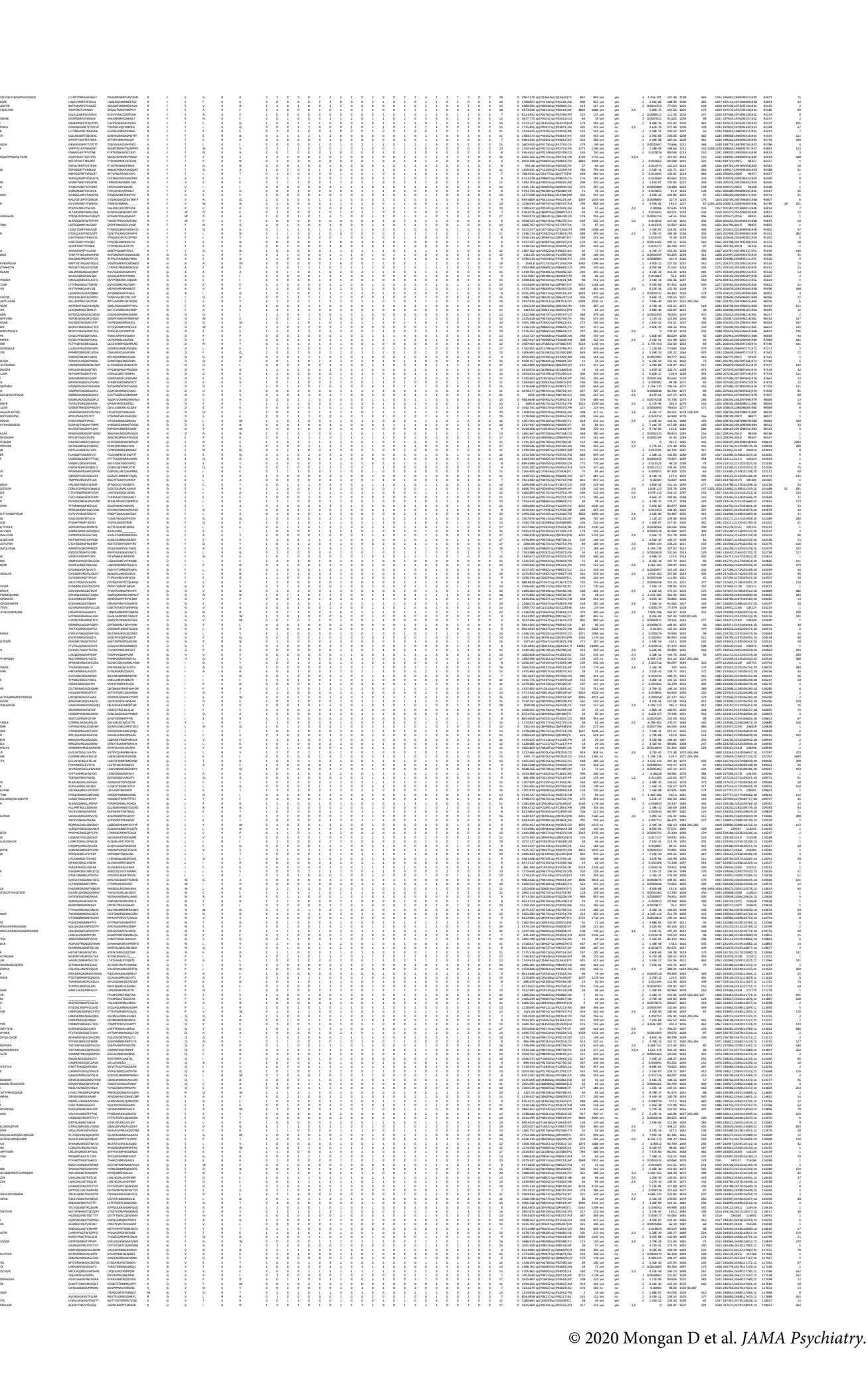

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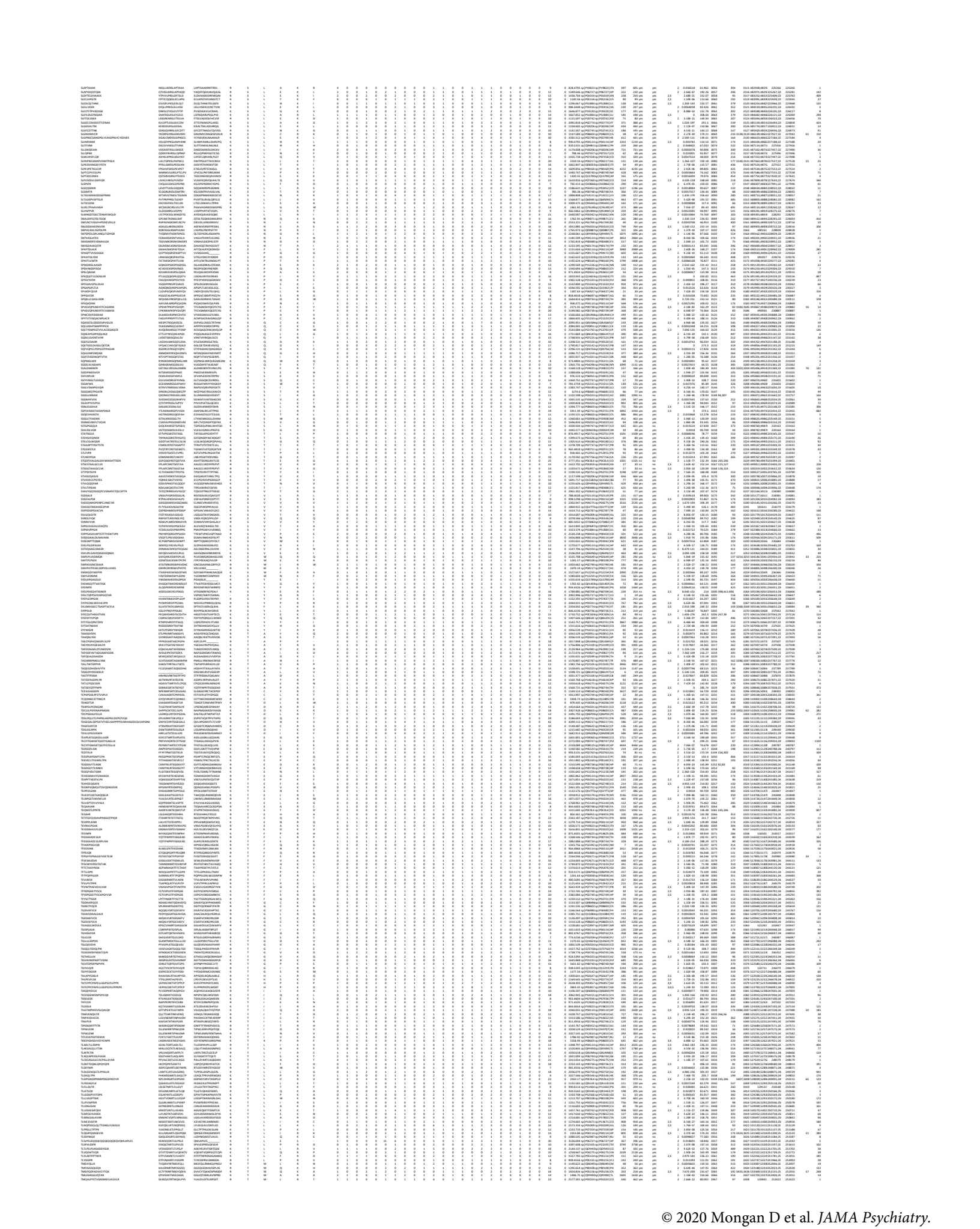

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