

Supplementary Materials: Multiplex detection of 24 staphylococcal enterotoxins in culture supernatant using Liquid Chromatography coupled to High Resolution Mass Spectrometry.

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Table S1. Origin of *Staphylococcus aureus* strains.

Strain	Accession no.	sample origin	Bacteria count (cfu/g)	Related publication	SE detected in food (official method)	Date of isolation	Geographical location	Strain origin
05CEB51		Rice	NA ⁽¹⁾	/	NA	2005	France	SFPO ⁽²⁾
05CEB52	ERS4338 875	Human	NA	Merda et al, 2020	NA	2005	France	SFPO
05CEB53		Human	NA	/	NA	2005	France	SFPO
06CEB196		Coconut beads	NA	/	Vidas: positive	2006	France	SFPO
06CEB83		Cheese	NA	/	Vidas: positive	2006	France	Own Check
08CEB393		Wrap salmon	NA	/	Vidas: positive	2008	France	SFPO
08CEB402		Blood sausage	NA	/	Vidas: positive	2008	France	SFPO
09CEB231		Fruit tart on pastry cream	NA	/	Vidas: positive	2009	France	SFPO
09CEB303	ERS4338 887	unknown	NA	Merda et al, 2020	NA	1997	Japan	SFPO
09CEB314	ERS4338 888	Cheese	NA	Merda et al, 2020	Vidas: positive	2009	France	SFPO
10CEB282		Steak	NA	/	Vidas: positive	2010	France	SFPO
10CEB401		Chicken	NA	/	Vidas: positive	2010	France	SFPO
11CEB110		Merguez	NA	/	Vidas: positive	2011	France	SFPO
12CEB137		Sheep's cheese	NA	/	Vidas: positive	2012	France	SFPO
12CEB368		Semi-cooked foie gras	NA	/	Vidas: positive	2012	France	SFPO
12CEB496		Chicken Sandwich	NA	/	Vidas: positive	2012	France	SFPO
12CEB512		Cottage cheese	NA	/	Ridascreen: negative	2012	France	SFPO
13CEB193	ERS4338 917	Matured cheese	NA	Merda et al, 2020	Vidas: positive	2013	France	SFPO
13CEB437		Sausage Sandwich	NA	/	Ridascreen: negative	2013	France	SFPO
14A / FRI361	ERS4338 950	Meat	NA	Merda et al, 2020	NA	1962	United Kingdom	Reference Strain
14SBCL1004		Ham	NA	/	Vidas: positive	2014	France	SFPO
14SBCL770		Pork stir-fry	NA	/	Ridascreen: negative	2014	France	SFPO

Strain	Accession no.	sample origin	Bacteria count (cfu/g)	Related publication	SE detected in food (official method)	Date of isolation	Geographical location	Strain origin
15SBCL115 1		Cream puff	1.80E+08	/	Vidas: positive	2015	France	SFPO
15SBCL142 8	ERS4338 968	Cheese	6.40E+05	Merda et al, 2020	NA	2015	France	SFPO
15SBCL143 8	ERS4338 971	Cheese	1.00E+06	Merda et al, 2020	NA	2015	France	SFPO
15SBCL452		Paëlla	1.60E+06	/	Vidas: positive	2015	France	SFPO
16SBCL102 8		Coriander Turkey	1.60E+03	/	No food sample	2016	France	SFPO
16SBCL120 4		Chicken - rice	1.00E+04	/	Ridascreen: negative	2016	France	SFPO
16SBCL136 8		Beef Bourguignon	10-100	/	No food sample	2016	France	SFPO
16SBCL246		Marinated salmon	1.10E+03	/	NA	2016	France	SFPO
16SBCL259		Kitchen tool	NA	/	No food sample	2016	France	SFPO
16SBCL899		Semolina couscous	NP	/	Vidas: positive	2016	France	SFPO
17SBCL25		Chicken	3.30E+05	/	Vidas: negative Ridascreen: negative	2017	France	SFPO
17SBCL330		vegetable	No food sample	/	NA	2017	France	SFPO
17SBCL693		Cream cake	1.50E+08	/	Vidas: positive	2017	France	SFPO
18SBCL601		Paella with meat	1.10E+09	/	Vidas: positive	2018	France	SFPO
18SBCL855		sandwich	< 400	/	Vidas: negative	2018	France	SFPO
19SBCL105 9		Raw milk	1.00E+07	/	Vidas: positive	2019	France	Own Check
19SBCL591		Ham	1.40E+08	/	Vidas : positive	2019	France	SFPO
20SBCL08		Raw milk cheese	1.00E+06	/	Vidas : positive	2020	France	Own Check
337E		Pasteurized milk cheese	NA	Letertre et al 2003b	NA	unknown	unknown	SFPO
349E		ribs	NA	Letertre et al 2003a	NA	unknown	unknown	SFPO
352E		fresh cheese	NA	Letertre et al 2003a	NA	unknown	unknown	SFPO
356E		cheese	NA	Letertre et al 2003a	NA	unknown	unknown	SFPO
42A / FRIS6	ERS4339 010	unknown	NA	Merda et al, 2020	NA	2001	unknown	Reference Strain
43A / FRI137	ERS4339 011	Human	NA	Merda et al, 2020	NA	2001	unknown	Reference Strain
44A / FRI1230	ERS4339 012	Breast milk	NA	Merda et al, 2020	NA	2001	unknown	Reference Strain
45A / FRI1151M	ERS4339 013	unknown	NA	Merda et al, 2020	NA	2001	unknown	Reference Strain

Strain	Accession no.	sample origin	Bacteria count (cfu/g)	Related publication	SE detected in food (official method)	Date of isolation	Geographical location	Strain origin
46A / FRI326	ERS4339014	Chicken tetrazzini	NA	Merda et al, 2020	NA	2001	unknown	Reference Strain

NA: Not available. SFPO: Staphylococcal food poisoning outbreaks

Table S2. Peptides database of 24 SEs.

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEA	GLIVFHTSTEPSVNYDLFGA QGQYSNTLLR	1109.893	3+	14.9	18	y ⁹⁺ , y ¹⁰⁺ , y ¹²⁺	2, 3	1, 4		0.67	18.28	x	
SEA	NVTVQELDLQAR	693.3728	2+	9.5	21	y ⁹⁺ , y ⁸⁺ , y ¹⁰⁺	1, 3, 4	2		1.27	9.65	x	x
SEA	QNTVPLETVK	564.8166	2+	7.3	18	y ⁶⁺ , y ⁶⁺⁺ , y ⁸⁺	1, 2, 3, 4			1.00	0.00	x	x
SEA	SELQGTALGNLK	615.8381	2+	8.5	21	y ⁸⁺ , y ⁹⁺ , y ¹⁰⁺	3, 4	1, 2		0.18	3.46		
SEA	YNLYNSDVFDGK	717.8304	2+	10	18	y ⁸⁺ , y ⁹⁺ , y ¹⁰⁺	1, 3, 4	2		0.77	8.34	x	x
SEA	GFFTDHSWYNDLLVDFDSK	769.3515	3+	15.9	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	3	1, 2, 4		0.18	0.00		
SEA	QIYYNEK	560.7691	2+	6	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 3, 4	2	SEE1, 2, 3	0.48	17.08		
SEA	SELQGAALGNLK	600.8328	2+	8.5	18	y ⁶⁺ , y ⁸⁺ , y ⁹⁺	1	2, 3, 4		0.25	0.00		
SEA	GLIVFHTSTEPSVNYDLFGA QGQNSNTLLR	1093.5529	3+	14.4	18	y ⁹⁺ , y ¹⁰⁺ , y ¹²⁺	1, 4	2, 3		0.76	16.19		
SEA	GFFTNHSWYNDLLVDFDSK	769.0235	3+	15.4	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	1, 4	2, 3		0.04	120.85		
SEA	EVTVQELDLQAR	700.8726	2+	9.8	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	2	1, 3, 4	SEE1, 2, 3	0.61	0.00	x	
SEA	SELQGVALDNLR	657.8542	2+	10.1	18	y ⁵⁺ , y ⁶⁺ , y ⁸⁺	2	1, 3, 4		0.86	0.00		
SEB	ESQDPKPKDELHK	507.2511	3+	3.2	15	y ⁶⁺ , y ⁸⁺⁺ , y ¹⁰⁺⁺	1, 2, 3, 4			0.50	19.06		
SEB	FIENENSWYDMMPAPGDK	764.331	3+	14.3	18	y ⁴⁺ , y ⁶⁺ , y ¹²⁺	1	2, 3, 4		0.01	13.03		
SEB	FTGLMENMK	535.7541	2+	8.9	18	y ⁵⁺ , y ⁷⁺ , y ⁸⁺	1, 3, 4	2	SEC 1, 2, 7, 8, 13	3.79	1.01		
SEB	IEVYLTTK	483.779	2+	8.4	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	1, 2, 3, 4			1.00	0.00	x	x
SEB	LGNYDNVR	475.7381	2+	4.1	21	y ⁴⁺ , y ⁶⁺ , y ⁷⁺	1, 2, 3, 4			0.29	7.17		
SEB	NLLSFDVQTNK	639.8381	2+	10.7	15	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3, 4			0.52	2.71		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEB	SIDQFLYFDLIYSIK	932.9902	2+	18.1	18	y ⁸⁺ , y ⁹⁺ , y ¹⁰⁺	1, 2, 3, 4			0.43	17.40		
SEB	VLYDDNHVSAINVK	529.6106	3+	8.3	15	y ¹¹⁺⁺ , y ¹²⁺⁺ , y ¹³⁺⁺	1, 2, 3, 4			4.04	10.63	x	x
SEB	VTAQELDYLTR	654.8433	2+	9.7	21	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4			1.53	1.04	x	x
SEB	YLMMYNDNK	596.2623	2+	8	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	1, 2, 3, 4		SEC 1, 2, 3, 4, 5, 7, 8, 10, 11, 13	0.92	0.72		
SEB	LYEFNNSPYETGYIK	919.4358	2+	10.8	21	y ⁸⁺ , y ⁹⁺ , y ¹¹⁺	1, 2, 3, 4			0.38	0.01		
SEB	FTVLMENMK	556.7776	2+	10.4	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	2	1, 3, 4		1.27	2.70		
SEC	ESQPDPTPDELHK	498.2353	3+	5.4	15	y ⁶⁺ , y ⁸⁺⁺ , y ¹⁰⁺⁺	1, 2, 3, 4, 7, 8, 10, 11, 13	5		1.00	0.00	x	
SEC	FLAHDLIYNISDK	516.9401	3+	11.1	15	y ³⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 3, 4, 5, 7, 8, 10, 11, 13			0.09	13.67		
SEC	IEVHLTTK	314.1869	3+	6.2	18	y ⁵⁺⁺ , y ⁶⁺⁺ , y ⁷⁺⁺	1, 2, 3, 4, 5, 7, 8, 11, 13	10		0.40	10.80	x	
SEC	NLYEFNNSPYETGYIK	962.9518	2+	11.3	21	y ⁸⁺ , y ¹¹⁺ , y ¹²⁺	1, 2, 3, 4, 5, 7, 8, 10, 11, 13		SEIU 1, 4, 5, 6, 9	0.35	7.03	x	x
SEC	NTISFEVQTDK	641.3197	2+	8.4	18	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3, 4, 5, 7, 8, 10, 11, 13			0.04	1.20		
SEC	SSEFTGTMGNMK	430.5215	3+	7.2	18	y ²⁺ , y ⁴⁺ , y ⁵⁺	3, 4, 5, 11	1, 2, 7, 8, 10, 13		0.01	15.25		
SEC	SVTAQELDIK	552.3008	2+	7.8	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4, 5, 7, 8, 10, 11, 13			0.96	3.01	x	
SEC	TELLNEDLAK	573.3061	2+	8.6	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	2, 3, 4, 5, 7, 8, 10, 11,	1		0.55	18.15		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptid e ratio	CV% ratio	Specific peptide	Heavy peptid e
SEC	YLMMYNDNK	596.2623	2+	8	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	13 1, 2, 3, 4, 5, 7, 8, 10, 11, 13		SEB 1, 2, 3, 4	0.30	0.31		
SEC	YLYDDHYVSATK	492.2331	3+	7.3	15	y ⁹⁺⁺ , y ¹⁰⁺⁺ , y ¹¹⁺⁺	3, 4, 5, 11	1, 2, 7, 8, 10, 13		1.31	0.04		
SEC	FTGLMENMK	535.7541	2+	8.9	18	y ⁵⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 7, 8, 13	3, 4, 5, 10, 11		0.61	4.72		
SEC	LQNVLIR	428.2742	2+	8	21	y ³⁺ , y ⁴⁺ , y ⁵⁺	1, 2, 3, 4, 7, 8, 10, 11, 13	5	SEB 1, 3, 4	0.01	5.30		
SEC	VLYDDHYVSATK	470.9015	3+	6.9	18	y ⁹⁺⁺ , y ¹⁰⁺⁺ , y ¹¹⁺⁺	1	2, 3, 4, 5, 7, 8, 10, 11, 13		1.14	1.68		
SEC	TELLNEGLAK	544.3033	2+	8.3	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1	2, 3, 4, 5, 7, 8, 10, 11, 13		0.47	4.37		
SED	IPINLWINGVQK	697.9114	2+	13.2	21	y ⁷⁺ , y ⁹⁺ , y ¹¹⁺⁺	1, 2, 3, 5			0.07	13.16		
SED	LYNNDTLGGK	547.7775	2+	5.2	18	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3, 5			1.00	0.00	x	x
SED	NVDVYAIR	475.2587	2+	8	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 3, 5			0.69	1.51		
SED	NVTVQELDAQAR	672.3493	2+	7.7	21	y ⁷⁺ , y ⁸⁺ , y ¹⁰⁺	1, 2, 3, 5			1.65	1.12	x	
SED	STGDQFLENTLLYK	814.912	2+	12.3	21	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3, 5			0.67	3.12		
SED	VSYDLFDVK	543.2793	2+	11.3	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 5			1.08	12.29	x	x
SED	NPIIGENK	442.7454	2+	4.2	18	y ⁴⁺ , y ⁵⁺ , y ⁷⁺⁺	1, 2, 3, 5			0.02	10.26		
SED	IEFDSSDESK	578.7539	2+	5.3	21	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	3	1, 2, 5		0.01	13.72		
SED	IEFDSSDGSK	542.7433	2+	5	18	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 5	3		0.06	11.79		
SEE	ESDDQFLENTLLFK	849.9147	2+	14.2	18	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3			0.28	11.57		
SEE	EVTVQELDLQAR	700.8726	2+	9.8	21	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3		SEA 2	1.30	13.38	x	x
SEE	FGLYNSDSFGGK	646.3013	2+	9.7	21	y ⁷⁺ , y ⁸⁺	1, 2, 3			1.00	0.00	x	x

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEE	GFFTGHPWYNDLLVDLGSK	722.6933	3+	15.6	15	y ⁹⁺ y ⁶⁺ , y ⁷⁺ , y ¹⁷⁺⁺	1	2, 3		1.73	18.59		
SEE	GLIVFHSSEGSTVSYDLFDAQ GQYPDTLLR	1105.877 1	3+	15.2	21	y ⁶⁺ , y ⁹⁺ , y ¹²⁺	1, 3	2		0.72	0.36		
SEE	QIYYNEK	560.7691	2+	6.1	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 3		SEA 1, 3, 4	1.16	13.32	x	
SEE	QTTVPIDK	451.2531	2+	5	21	y ²⁺ , y ⁴⁺ , y ⁶⁺	1, 2, 3			1.17	15.40	x	x
SEE	SELQGIALSNLR	650.8646	2+	9.8	21	y ⁵⁺ , y ⁶⁺ , y ⁸⁺	2	1, 3		0.05	11.77		
SEG	ELVPFVPYK	546.3104	2+	12.2	18	y ³⁺ , y ⁶⁺ , y ⁶⁺⁺	1, 2, 3, 4, 5, 7			2.30	16.41	x	
SEG	FLNIYGDNK	542.2771	2+	9.1	21	y ⁴⁺ , y ⁵⁺ , y ⁷⁺	1, 2, 3, 4, 5, 7			0.65	13.29	x	x
SEG	NMVTIQELDYK	677.3396	2+	10.2	21	y ⁶⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3, 4, 5, 7			1.21	3.78	x	
SEG	QFLSHDLIFPIEYK	583.9785	3+	13.7	18	y ⁵⁺ , y ⁵⁺⁺ , y ⁶⁺	1, 2, 3, 4, 5, 7			3.09	17.47	x	
SEG	QSLGFTITTNK	605.3273	2+	9.3	21	y ⁴⁺ , y ⁶⁺ , y ⁸⁺	1, 2, 3, 4, 5, 7			1.00	0.00	x	x
SEG	GTMGNVMNLYTSPPEGR	961.9586	2+	11.5	21	y ⁶⁺ , y ⁹⁺ , y ¹²⁺	3, 7	1, 2, 4, 5		1.12	6.47		
SEG	LYEFDGSAFESGYIK	863.404	2+	12.3	18	y ¹¹⁺ , y ¹²⁺ , y ¹³⁺	1, 2, 3, 4, 5, 7			0.28	14.82		
SEH	VIGANVWVDGIQK	699.8906	2+	11.2	21	y ⁷⁺ , y ⁹⁺ , y ¹¹⁺	1, 2, 4	3		0.74	7.95		
SEH	DYSFDIYDLK	639.7981	2+	12.7	15	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4			0.18	2.25		
SEH	ETELIR	380.7136	2+	4.7	15	y ¹⁺ , y ²⁺ , y ³⁺	1, 2, 3, 4			0.45	9.22		
SEH	FATADLAQK	482.7585	2+	6.5	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4			0.66	3.43	x	x
SEH	GLIEFDMK	476.7441	2+	11	15	y ²⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 3, 4			0.77	15.76	x	
SEH	NVDIYGASFYYK	720.3457	2+	11	15	y ⁷⁺ , y ⁸⁺ , y ¹⁰⁺	2, 3, 4	1		0.32	81.21		
SEH	SVDIYGASFYYK	706.8403	2+	11.1	18	y ⁷⁺ , y ⁸⁺ , y ¹⁰⁺	1	2, 3, 4		0.25	46.56		
SEH	NVTLQELDIK	586.8297	2+	10.3	15	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4			0.71	27.18	x	x
SEH	SDDISHIDVNLYTK	540.6019	3+	9.8	15	y ¹⁰⁺⁺ , y ¹²⁺⁺ , y ¹³⁺⁺	1, 2, 3, 4			1.00	0.00	x	x
SEH	SELTDLALANAYGQYNHPFI K	789.0656	3+	13	18	y ¹⁵⁺⁺ , y ¹⁸⁺⁺ , y ¹⁹⁺⁺	1, 2, 3, 4			0.01	14.94		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEI	LVTAQEIDVK	558.319	2+	8	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4, 5, 6, 8, 10, 11, 12, 13, 15		SEK 5, 8	1.00	0.00	x	x
SEI	SFSYDLFYTGDLVPSFLK	719.3577	3+	17.2	18	y ⁶⁺ , y ⁶⁺⁺ , y ¹⁰⁺	1, 3, 4, 5, 10	2, 6, 8, 11, 12, 13, 15		0.02	15.85		
SEI	VLFHLNNEK	371.8732	3+	7.6	15	y ⁶⁺⁺ , y ⁷⁺⁺ , y ⁸⁺⁺	3, 4, 15	6, 8, 10, 11, 12, 13		2.98	19.46	x	
SEI	VLFHLNDEK	372.2012	3+	7.9	15	y ²⁺ , y ⁷⁺⁺ , y ⁸⁺⁺	6, 8, 10, 11, 12, 13	3, 4, 15		1.33	10.72	x	
SEI	YLQEEYNIYGHNNTGK	648.3025	3+	7.6	18	y ⁸⁺ , y ¹⁴⁺⁺ , y ¹⁵⁺⁺	1, 3, 4, 6, 8, 11, 13, 15	2, 5, 10, 12		0.64	16.21	x	x
SEI	YLQEEYNIYGHNNNGK	653.9700	3+	7.4	15	y ¹²⁺⁺ , y ¹³⁺⁺ , y ¹⁴⁺⁺	5, 10	1, 2, 3, 4, 6, 8, 11, 12, 13, 15		0.38	8.06		
SEI	HDYIDLK	452.2322	2+	6.7	21	y ²⁺ , y ⁵⁺ , y ⁶⁺	2, 3, 4, 6, 12, 15	1, 5, 8, 10, 11, 13		2.17	11.31		
SEI	QGDIGVGNLR	514.7778	2+	7.1	21	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 3, 4, 5, 6, 8, 10, 11, 12, 13, 15			0.73	13.24	x	x
SEI	IPINLWVNGK	579.3436	2+	11.6	21	y ⁷⁺ , y ⁸⁺ , y ⁹⁺⁺	4, 6, 8, 11, 13, 15	5, 10, 12		0.25	11.75		
SEI	IPINLWINGK	586.3515	2+	12.4	21	y ⁷⁺ , y ⁸⁺ , y ⁹⁺⁺	5, 10	1, 2, 3, 4, 6, 8, 11, 12, 13, 15		0.28	12.69		
SEIJ	SFFISHSQYNDLLVQFDSK	759.0392	3+	14	18	y ⁶⁺ , y ⁷⁺ , y ⁷⁺⁺	1, 2, 3, 4			0.04	25.71		
SEIJ	IMTEDQFLDYTLLEK	626.3182	3+	16.5	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4			0.11	2.08	x	
SEIJ	TVVPLDIVK	492.3104	2+	11.3	21	y ⁶⁺ , y ⁶⁺⁺ , y ⁷⁺	1, 2, 3, 4			0.01	35.15		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptid e ratio	CV% ratio	Specific peptide	Heavy peptid e
SEIJ	QYNLYNPSTFGGK	744.8595	2+	9.6	18	y ⁸⁺ , y ⁹⁺ , y ¹¹⁺	2, 3	1, 4		0.34	1.52	x	
SEIJ	SELSSITLNNLR	673.8673	2+	10.8	18	y ⁴⁺ , y ⁶⁺ , y ⁹⁺	1, 2, 3, 4			1.00	0.00	x	
SEIJ	VTIQELDLQAR	643.3592	2+	10.1	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4			0.75	11.44	x	
SEK	DFVDLK	368.6974	2+	8.4	18	y ²⁺ , y ³⁺ , y ⁴⁺	1, 3, 5, 7, 8	2, 4, 9		0.08	1.81		
SEK	DNDTPIANQLQFSNESYDLIS ESK	910.091	3+	13.4	18	y ⁸⁺ , y ¹⁵⁺⁺ , y ²⁰⁺⁺	1, 2, 3, 4, 5, 7, 8, 9			0.01	15.76		
SEK	FYSGFNIGK	516.7611	2+	9.5	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4, 5, 7, 8, 9			1.00	0.00	x	
SEK	NIPINIWINGNHK	766.9202	2+	11.6	21	y ⁷⁺ , y ¹¹⁺ , y ¹¹⁺⁺	1, 2, 3, 4, 5, 7, 8, 9			0.18	3.37	x	
SEK	QGDIGIDNLR	550.7884	2+	8.2	21	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 3, 4, 5, 7, 8, 9			0.81	7.52	x	
SEK	VTFHLNNNDTFSYDLFYTG DGLPK	965.1154	3+	14.4	18	y ⁸⁺ , y ⁹⁺ , y ¹⁰⁺	1, 2, 3, 4, 5, 7	8, 9		0.23	14.11		
SEK	YLQEEYNIYGHNGTK	610.2882	3+	7.6	18	y ⁷⁺ , y ¹²⁺⁺ , y ¹³⁺⁺	1, 2, 3, 4, 5, 7, 8, 9			0.06	15.72		
SEK	FVTAQEIDVK	575.3111	2+	8.5	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 4, 7	2, 3, 5, 8, 9		1.52	3.31		
SEK	LVTAQEIDVK	558.319	2+	8	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	5, 8	1, 2, 3, 4, 7, 9	SEI 1, 2, 3, 4, 5, 6, 8, 10, 11, 12, 13, 15, 17	1.22	5.14	x	
SEK	FVTAQEIDIK	582.319	2+	9.4	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	2, 9	1, 3, 4, 5, 7, 8		0.04	24.52		
SEL	FYSGFDK	432.2003	2+	6.7	21	y ²⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 4, 5, 6, 7, 8, 9, 10, 12, 13			0.51	1.51	x	
SEL	IIPINLIINGK	604.3923	2+	14	15	y ⁷⁺ , y ⁹⁺ , y ⁹⁺⁺	1, 2, 4, 5, 6, 7, 8, 9, 10, 12, 13			2.87	9.07	x	
SEL	MVTAQEIDVK	567.2972	2+	7.7	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 4, 5, 6, 7,			1.12	12.32		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEL	NVDVFGISYK	571.298	2+	11.1	15	y ₆ ⁺ , y ₇ ⁺ , y ₈ ⁺	8, 9, 10, 12, 13, 1, 2, 4, 5, 6, 7, 8, 9, 10, 12, 13			1.36	15.18	x	
SEL	YEYVNLK	464.7424	2+	7.4	18	y ₄ ⁺ , y ₅ ⁺ , y ₆ ⁺	5, 6, 7, 8, 9, 12, 13	10		1.00	0.00	x	
SEL	YLQDEFNIYGHNDTGK	638.627	3+	9.4	15	y ₈ ⁺ , y ₁₃ ⁺⁺ , y ₁₄ ⁺⁺	5, 6, 7, 8, 9, 10, 12, 13			0.50	18.91		
SEL	TIYGGVTK	419.7371	2+	4.7	15	y ₅ ⁺ , y ₆ ⁺ , y ₇ ⁺	5, 6, 7, 8, 9, 10, 12, 13			0.89	1.74		
SEL	NVDIFGISYK	578.3059	2+	12.1	18	y ₅ ⁺ , y ₆ ⁺ , y ₈ ⁺	8, 12	1, 2, 4, 5, 6, 7, 9, 10, 13		1.11	5.34		
SEM	DVGVLNLR	443.2613	2+	9.8	18	y ₃ ⁺ , y ₄ ⁺ , y ₆ ⁺	1, 2, 3, 4, 5, 6, 8, 9, 15			1.00	0.00	x	x
SEM	ILFHLNDGSSFSYDLFDGTGTG QAESFLK	1037.164 5	3+	16.2	18	y ₈ ⁺ , y ₁₂ ⁺ , y ₁₃ ⁺	3, 4, 8, 15	1, 2, 5, 6, 9		0.13	18.46		
SEM	LVTAQEIDTK	559.3086	2+	6.5	18	y ₆ ⁺ , y ₇ ⁺ , y ₈ ⁺	3, 4, 6, 8, 15	1, 2, 5, 9		0.68	2.98	x	
SEM	IVTAQEIDTK	559.3086	2+	6.3	21	y ₆ ⁺ , y ₇ ⁺ , y ₈ ⁺	1, 2, 5, 9	3, 4, 6, 8, 15		0.61	0.22	x	
SEM	YLQEEYNIYGFNDTNK	1005.957 6	2+	10.8	21	y ₇ ⁺ , y ₈ ⁺ , y ₁₂ ⁺	1, 2, 3, 4, 5, 6, 8, 9, 15			0.10	4.11	x	
SEM	YIYGGVTLAGDYLEK	831.4247	2+	12.2	18	y ₉ ⁺ , y ₁₂ ⁺ , y ₁₃ ⁺	3, 4, 6, 8, 15	1, 2, 5, 9		0.19	13.32		
SEM	YMYGGVTLAGDYLEK	840.4029	2+	11.9	18	y ₉ ⁺ , y ₁₂ ⁺ , y ₁₃ ⁺	1, 2, 5, 9	3, 4, 6, 8, 15		0.02	23.85		
SEN	DGVQQEGFVIK	610.3195	2+	9	18	y ₆ ⁺ , y ₇ ⁺ , y ₈ ⁺	1, 2, 3, 5, 6, 7, 8	4, 9		0.42	8.70		
SEN	GSVGAEFFQFYSDNR	862.3892	2+	12.8	21	y ₈ ⁺ , y ₉ ⁺ , y ₁₀ ⁺	1, 2, 3, 4, 5, 6, 7, 8	9		0.97	3.94		
SEN	ISTDQLLNNTIILK	793.4616	2+	13.3	18	y ₇ ⁺ , y ₈ ⁺	1, 2, 3	9		0.15	25.87		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEN	NIDISVLK	451.2713	2+	10.2	15	y ⁹⁺ y ⁴⁺ , y ⁵⁺ , y ⁶⁺	4, 5, 6, 7, 8 1, 2, 3, 5, 6, 7, 8	4, 9		1.92	3.79	x	
SEN	NIDIYGLYFGNK	708.8615	2+	13.2	18	y ⁷⁺ , y ⁸⁺ , y ¹⁰⁺	3, 5, 7	1, 2, 4, 6, 8, 9		1.44	20.30	x	
SEN	VTVQELDTK	516.7822	2+	6.4	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4, 5, 6, 7, 8, 9			1.00	0.00	x	x
SEO	FLDFDLLFK	579.3157	2+	16.7	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 5, 6, 7, 8, 9, 14, 19, 21	4		0.44	128.25	x	
SEO	GNLPDQYLQIYNDNK	598.9601	3+	11.05	18	y ⁵⁺ , y ⁸⁺ , y ¹²⁺⁺	1, 2, 3, 4, 6, 7, 9, 14, 19, 21	5, 8		0.08	3.52		
SEO	SSVDPIALHNINDDYINNR	724.0223	3+	10.4	21	y ⁵⁺ , y ⁸⁺ , y ¹⁵⁺⁺	3, 6, 8, 21	1, 2, 4, 5, 7, 9, 14, 19		0.59	2.71		
SEO	TVDIYGVYYK	610.8135	2+	10	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4, 5, 6, 7, 8, 9, 14, 19, 21			1.00	0.00	x	
SEO	VTAQELDIK	508.7848	2+	7.3	18	y ⁶⁺ , y ⁸⁺ , y ⁸⁺⁺	1, 2, 3, 4, 5, 6, 7, 8, 9, 14, 19, 21			0.42	42.96	x	x
SEO	SINWLDGISAK	602.322	2+	11.8	18	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	6, 21	1, 2, 3, 4, 5, 7, 8, 9, 14, 19		0.18	99.54		
SEO	SINWLDGISAEFK	740.3775	2+	14.7	21	y ⁸⁺ , y ⁹⁺ , y ¹¹⁺	3, 8, 14	1, 2, 4, 5, 6, 7, 9, 19, 21		0.22	90.40		
SEO	ESFYDDLFIK	744.3583	2+	14.8	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 3, 4, 5, 6, 7, 9, 14, 19, 21	8		0.03	141.42		
SEP	ESNDQFLK	490.7378	2+	5.4	18	y ²⁺ , y ³⁺ , y ⁶⁺	2, 3, 4			0.17	0.13		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEP	EVTVQELDLQSR	708.8701	2+	9.4	21	y ₆ ⁺ , y ₇ ⁺ , y ₈ ⁺	2, 3	4		0.89	4.40	x	
SEP	GLIEFHPSSGDSVGYDLFGA QGQYPDTQLR	1085.5178	3+	14	18	y ₆ ⁺ , y ₉ ⁺ , y ₁₂ ⁺	2, 3, 4			1.12	0.55	x	
SEP	QNTVPLGTVK	528.806	2+	7	21	y ₆ ⁺ , y ₇ ⁺ , y ₈ ⁺	2, 3, 4			1.00	0.00	x	
SEP	SELQGTALSCLR	644.8464	2+	8.7	18	y ₄ ⁺ , y ₈ ⁺ , y ₉ ⁺	2, 3, 4		SEE 3	0.45	7.47	x	x
SEQ	DVGVINLR	443.2613	2+	9.3	15	y ₃ ⁺ , y ₄ ⁺ , y ₆ ⁺	1, 2, 3, 4, 5			2.08	2.74	x	
SEQ	EVTAQEIDIK	573.3061	2+	7.7	18	y ₅ ⁺ , y ₆ ⁺ , y ₈ ⁺	1, 2, 3, 4, 5			1.00	0.00	x	x
SEQ	FNSGFNK	407.1981	2+	3.6	18	y ₂ ⁺ , y ₅ ⁺ , y ₆ ⁺	1, 2, 3, 4, 5			0.30	6.16		
SEQ	ITFHLNNETSFTYDLFYTG QAESFLK	1082.1873	3+	16.2	18	y ₁₀ ⁺ , y ₁₁ ⁺ , y ₂₀ ⁺⁺	5	1, 2, 3, 4		0.03	16.10		
SEQ	ITFHLNNEPSFTYDLFYTG QAESFLK	1080.8557	3+	16.2	18	y ₁₀ ⁺ , y ₁₁ ⁺ , y ₁₂ ⁺	1, 2, 3, 4	5		0.13	18.50		
SEQ	NFYTNYQPETLQGVSSGNFS TSHQLEYIDGK	881.9115	4+	12.2	18	y ₁₇ ⁺⁺ , y ₁₉ ⁺⁺ , y ₂₀ ⁺⁺	5	1, 2, 3, 4		0.10	0.87		
SEQ	NIPINLWVNGK	634.3615	2+	12.5	15	y ₇ ⁺ , y ₉ ⁺ , y ₉ ⁺⁺	1, 2, 3, 4, 5			0.94	7.98	x	
SEQ	QNTISTDEVSTQK	725.8546	2+	5.2	21	y ₈ ⁺ , y ₉ ⁺ , y ₁₁ ⁺	5	1, 2, 3, 4		0.05	0.04		
SEQ	YLQNEYNIYGFNK	833.399	2+	10.4	21	y ₅ ⁺ , y ₈ ⁺ , y ₁₀ ⁺	1, 2, 3, 4, 5			0.33	3.47		
SEQ	YMYGGITLANQNLDKPR	651.9999	3+	9.9	15	y ₁₁ ⁺⁺ , y ₁₄ ⁺⁺ , y ₁₅ ⁺⁺	1, 2, 3, 4, 5			1.50	5.12		
SEQ	YTLYSQFHNEYEAK	896.9125	2+	8.6	21	y ₈ ⁺ , y ₉ ⁺ , y ₁₀ ⁺	1, 2, 3, 4, 5			0.02	2.22		
SEQ	LQGVSSGNFSTSHQLEYIDG K	756.3695	3+	9.6	18	y ₁₆ ⁺⁺ , y ₁₇ ⁺⁺ , y ₁₉ ⁺⁺	1, 2, 3, 4	5		0.99	1.24		
SEQ	NFYANYQPEK	637.296	2+	7.2	18	y ₃ ⁺ , y ₇ ⁺ , y ₈ ⁺	2	1, 3, 4, 5		0.65	1.94		
SER	DLVPFIPYK	546.3104	2+	13.6	18	y ₃ ⁺ , y ₆ ⁺ , y ₆ ⁺⁺	1, 2, 4, 5			2.64	4.10		
SER	FVNIYGDNK	535.2693	2+	7.7	18	y ₄ ⁺ , y ₅ ⁺ , y ₇ ⁺	1, 2, 4, 5			5.16	1.96	x	x
SER	GTMGNVESLYK	599.7923	2+	8.3	18	y ₅ ⁺ , y ₈ ⁺ , y ₉ ⁺	1, 2, 4, 5			0.02	141.42		
SER	NIIVPVTVDNK	606.3533	2+	10.1	15	y ₇ ⁺ , y ₈ ⁺ , y ₉ ⁺	1, 2, 4, 5			3.84	8.19		
SER	QFLGHDLIFPIPYSEYK	689.691	3+	14.47	18	y ₆ ⁺ , y ₆ ⁺⁺ , y ₈ ⁺	1, 2, 5	4		2.43	48.26		
SER	TVTVQELDYK	598.3139	2+	8.1	18	y ₆ ⁺ , y ₇ ⁺	1, 2, 4,			2.33	9.17	x	x

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptid e ratio	CV% ratio	Specific peptide	Heavy peptid e
SER	QQFSFTISTNK	650.8302	2+	9.7	18	y ⁸⁺ , y ⁶⁺ , y ⁹⁺	5 1, 2, 4, 5			0.08	20.94		
SER	SEFINK	369.1951	2+	3.3	18	y ²⁺ , y ³⁺ , y ⁴⁺	5 1, 2, 4, 5			1.00	0.00		
SER	TIDASSVK	410.7242	2+	2.8	15	y ⁵⁺ , y ⁶⁺ , y ⁷⁺⁺	5 1, 2, 4, 5			0.80	27.23		
SER	AVIAENVK	422.2504	2+	4.8	15	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	5 1, 2, 4, 5			9.45	3.47	x	
SER	NWLTNNK	445.23	2+	5.9	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	5 1, 2, 4, 5			0.44	2.73		
SES	EPTIQELDLK	593.3217	2+	9.8	18	y ³⁺ , y ⁵⁺ , y ⁶⁺	1, 3			0.79	16.79		
SES	GFMITTDK	456.7284	2+	7.9	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 3			0.31	11.35		
SES	NSIGVNVFK	489.2744	2+	9.1	18	y ²⁺ , y ⁶⁺ , y ⁷⁺	1, 3			6.92	0.19	x	
SES	SELDSTALYNIK	677.3485	2+	9.9	18	y ⁸⁺ , y ⁹⁺ , y ¹⁰⁺	1, 3			1.00	0.00	x	x
SES	TNSTQLLSNDLIFDDITLK	717.7108	3+	15.5	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 3			1.00	0.05		
SES	TSYSQDNIILDIK	755.3934	2+	11.3	21	y ⁵⁺ , y ⁸⁺ , y ¹⁰⁺	1, 3			4.70	4.69	x	
SES	YSVDFLK	436.2316	2+	9.9	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 3			5.08	2.35	x	
SET	EGLKDFYSK	362.8537	3+	7	15	y ¹⁺ , y ²⁺ , y ³⁺	1			0.82	NR		
SET	FYDGDISK	472.7216	2+	6	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	1			1.00	NR	x	
SET	INTLDDKILNQFK	521.291	3+	10.9	15	y ⁹⁺⁺ , y ¹¹⁺⁺ , y ¹²⁺⁺	1			0.63	NR		
SET	ISHFDIYMEK	428.2094	3+	9	15	y ³⁺ , y ⁴⁺ , y ⁹⁺⁺	1			0.44	NR		
SET	IDVYTNK	426.7267	2+	4.4	15	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1			0.05	NR		
SET	ELEIGNR	415.722	2+	5.1	18	y ³⁺ , y ⁴⁺ , y ⁶⁺⁺	1			0.06	NR		
SET	INTLDDK	409.7163	2+	2.5	18	y ²⁺ , y ⁵⁺ , y ⁶⁺	1			0.25	NR		
SET	HSPLDKPTNISYR	509.9353	3+	6.7	18	y ⁵⁺ , y ¹¹⁺⁺ , y ¹²⁺⁺	1			0.55	NR	x	
SET	VGDYVDAWGHIINNKPIGK	699.369	3+	11.4	18	y ¹⁴⁺⁺ , y ¹⁵⁺⁺ , y ¹⁸⁺⁺	1			0.63	NR	x	
SEIU	ASEFTGLMDNMR	686.3052	2+	10.6	18	y ⁵⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 4, 5, 6, 9, 7, 17			0.93	0.84	x	

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEIU	FLQHDLLFK	387.5536	3+	10.3	18	y ¹⁺ , y ²⁺ , y ⁸⁺	10, 11 1, 2, 4, 5, 7, 9, 10, 11, 17	6		0.04	9.01	x	
SEIU	NITAEIDYK	597.8037	2+	7.3	18	y ⁶⁺ , y ⁷⁺ , y ⁸⁺	1, 2, 4, 5, 6, 7, 9, 10, 11, 17			1.03	2.59	x	
SEIU	YLLIYNDNK	578.3059	2+	9.4	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	1, 2, 4, 5, 6, 7, 9, 10, 11, 17			1.00	0.00	x	
SEX	GNIVINTK	429.7558	2+	5.4	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 3, 4, 5, 7, 9, 10, 12, 14, 15, 16, 17, 22, 24, 25, 28, 34, 36, 41, 45			4.69	3.11	x	
SEX	NVTFELVK	475.2713	2+	9.8	18	y ²⁺ , y ⁵⁺ , y ⁶⁺	1, 4, 7, 12, 14, 17, 22, 24, 10, 15, 25, 28, 16, 45 34, 36, 41	3, 5, 9,		2.33	3.93	x	
SEX	INLEGTYR	483.2562	2+	7	18	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	1, 4, 5, 7, 9, 12, 14, 15, 17, 22, 24, 25, 28, 34, 36, 41, 45			7.38	7.15		
SEX	IHLEGTYTVAGR	439.5701	3+	7.6	18	y ³⁺ , y ⁴⁺ , y ⁵⁺	1, 4, 5, 15, 24, 25, 28, 34, 45	3, 7, 9, 10, 12, 14, 16, 17, 22, 36, 41		2.51	15.36		
SEX	EVVTLK	344.7156	2+	5.2	18	y ²⁺ , y ³⁺ , y ⁴⁺	1, 3, 4, 5, 7, 9, 10, 12,	17, 41		2.68	1.86		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEX	NWVYSERPLNENQVR	635.3185	3+	8.5	18	y ₁₁ ⁺⁺ , y ₁₂ ⁺⁺ , y ₁₃ ⁺⁺	14, 15, 16, 22, 24, 25, 28, 34, 36, 45	10, 34		5.49	2.57	x	
SEX	ELDHIIR	299.1714	3+	6.4	18	y ₃ ⁺ , y ₄ ⁺⁺ , y ₅ ⁺⁺	14, 15, 16, 17, 22, 24, 25, 34, 36, 41, 45	28		3.27	2.73	x	
SEX	INTADIK	387.7214	2+	3.6	18	y ₂ ⁺ , y ₅ ⁺ , y ₆ ⁺	3, 5, 9, 10, 28, 45	15, 16, 17, 22, 24, 25, 34, 36, 41		4.40	9.03		
SEX	NITLTK	351.7109	2+	3.3	18	y ₂ ⁺ , y ₃ ⁺ , y ₄ ⁺	1, 3, 4, 5, 7, 9, 10, 12, 14, 15, 16, 17, 22, 24, 25, 28, 34, 36, 41, 45			1.00	0.00		
SEY	TVLYNTDYLK	615.3243	2+	9.4	18	y ₆ ⁺ , y ₇ ⁺ , y ₈ ⁺	1, 2, 3, 4, 6, 7			3.17	4.99	x	
SEY	VNPDSLLEVK	557.3111	2+	10.1	18	y ₈ ⁺ , y ₈ ⁺⁺ , y ₉ ⁺⁺	1, 2, 3, 4, 6, 7			5.00	2.03	x	
SEY	EVTGVGENYIDVK	711.8592	2+	9.1	18	y ₇ ⁺ , y ₈ ⁺ , y ₁₀ ⁺	6	1, 2, 3, 4, 7		0.99	1.44		
SEY	YDPISK	361.6896	2+	3.4	21	y ₃ ⁺ , y ₄ ⁺	1, 2, 3,			1.08	0.29		

Toxin	Peptide	m/z	z	RT (min)	EC %	Fragment s	Variant present	Variant absent	Commun SE	Peptide ratio	CV% ratio	Specific peptide	Heavy peptide
SEY	VDTYNVR	433.722	2+	3.3	21	y ⁴⁺ , y ⁵⁺ , y ⁶⁺	4, 6, 7			1.00	0.00	x	
SEY	MNLFVNGHQTK	430.2204	3+	7.2	18	y ⁷⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3, 4, 6, 7			0.15	3.79		
SEY	TFDFDNISHIDIYMK	620.2942	3+	13.8	18	y ¹²⁺ , y ¹³⁺ , y ¹⁴⁺	1, 2, 3, 4, 6, 7			1.43	19.21		
SEY	VTNLSYR	426.7323	2+	4.3	18	y ³⁺ , y ⁵⁺ , y ⁶⁺	1, 2, 3, 4, 6, 7			1.28	2.16	x	
SEZ	SSQYTGSWHNIWYLYNSDP VNAK	910.7576	3+	12.9	18	y ⁵⁺ , y ⁸⁺ , y ⁹⁺	1, 2, 3, 5			0.41	1.35	x	
SEZ	YLMYR	429.7307	2+	9.1	15	y ³⁺ , y ⁴⁺ , y ⁵⁺	1, 2, 3, 5			0.77	3.55	x	
SEZ	IQPIVVK	398.7682	2+	7.5	15	y ²⁺ , y ³⁺ , y ⁴⁺	1, 2, 3, 5			1.00	0.00	x	
SEZ	INLYHLGGTSYETGYIK	643.6633	3+	10.9	18	y ⁶⁺ , y ¹⁵⁺ , y ¹⁶⁺	1, 2, 3, 5			0.36	0.80	x	
SEZ	YYWYDMMPPDPGFTQSK	1014.929	2+	14.1	18	y ⁷⁺ , y ⁹⁺ , y ¹⁰⁺	1, 2, 3, 5			0.25	11.57	x	
TSST 1	HQLTQIHGLYR	455.9177	3+	8	18	y ⁴⁺ , y ⁵⁺ , y ⁹⁺	1, 3, 5, 6	2, 4		0.16	6.05		
TSST 1	LPTPIELPLK	560.8524	2+	13	21	y ⁷⁺ , y ⁹⁺	1, 2, 3, 4, 5, 6			0.79	18.63	x	
TSST 1	ITMNDGSTYQSDLSK	830.3802	2+	7.6	21	y ¹⁰⁺ , y ¹¹⁺ , y ¹²⁺	1, 2, 3, 4, 5, 6			1.00	0.00	x	
TSST 1	NTDGSISLIIFSPYYSPAFTK	1209.615	2+	16.5	18	y ⁵⁺ , y ¹¹⁺ , y ¹²⁺	1, 3, 6	2, 4, 5		1.08	6.79		
TSST 1	QLAISTLDFEIR	703.3879	2+	13.7	18	y ⁸⁺ , y ⁹⁺ , y ¹⁰⁺	1, 3, 5, 6	2, 4		4.75	10.82	x	
TSST 1	QLAISTLDFK	568.3215	2+	11.6	18	y ⁵⁺ , y ⁶⁺ , y ⁷⁺	2, 4	1, 3, 5, 6		1.71	4.72	x	
TSST 1	DLLDWYSSGSDAFTNSEVLD NSLGSMR	993.7819	3+	16.6	18	y ⁸⁺ , y ⁹⁺ , y ¹⁰⁺	2, 4, 5	1, 3, 6		0.02	8.31		
TSST 1	FEYNTEKPPINIDEIK	650.6667	3+	10.96	18	y ⁹⁺ , y ¹³⁺ , y ¹⁴⁺	1, 2, 3, 4, 5, 6			0.15	6.51		
TSST 1	HQLTQTHGLYR	451.9056	3+	4.2	18	y ⁴⁺ , y ⁹⁺ , y ¹⁰⁺	2, 4	1, 3, 5, 6		0.22	8.13		

Figure S1. Sequence alignment of 24 SE and 164 variants.**SEA**

a_2	MKKRKTAFILTLCLIVIMLVTSPLVNG	SEKSEEIKEKDLHKKSELQGVALDNLQIYYHNG	60
a_3	--MKKTAFTLLLFIALTLTTSPLVNG	SEKSEEINEKDLRKKSELQGTALGNLQIYYNE	58
a_1	--MKKTAFTLLLFIALTWTTSPVNG	SEKSEEINEKDLRKKSELQGAALGNLQIYYNE	58
a_4	--MKKTAFTLLLFIALTWTTSPVNG	SEKSEEINEKDLRKKSELQGTALGNLQIYYNE	58
	:*** * * * .: .*****:***:*****.*.***:***:*		
a_2	KAITENKESDNQFLQHTILFNGFFTDHPWYNDLLVDFDSKVLADKYKGKKVDLYGAYYGY		120
a_3	KAKTENKESHQFLQHTILFKGFFTDHWSYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGY		118
a_1	KAKTENKESHQFLQHTILFKGFFTNHSYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGY		118
a_4	KAKTENKESHQFLQHTILFKGFFTNHSYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGY		118
	** *****.:*****:***.* *****.:*****:*****		
a_2	QCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWLDGKQNTVPLETVKTNKKEVTVQE		180
a_3	QCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWLDGKQNTVPLETVKTNKKNVTVQE		178
a_1	QCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWLDGKQNTVPLETVKTNKKNVTVQE		178
a_4	QCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWLDGKQNTVPLETVKTNKKNVTVQE		178
	*****:*****:*****:*****		
a_2	LDLQARHYLHGKYNLYNSDTFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYR		240
a_3	LDLQARRYLQEKYNLYNSDVFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYR		238
a_1	LDLQARRYLQEKYNLYNSDVFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYR		238
a_4	LDLQARRYLQEKYNLYNSDVFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYR		238
	*****:*.: *****.***** ***** *****		
a_2	DNKTINSENMHIDIYLYTT	259	
a_3	DNKTINSENMHIDIYLYTS	257	
a_1	DNKTINSENMHIDIYLYTS	257	
a_4	DNKTINSENMHIDIYLYTS	257	
	*****:*****:		

SEB

b_3	MYNRLFVSRVILIFALILVIYTPNVLA	ESQDPKPDELHKASKFTGLMENMKVLYDDNHV	60
b_1	MYKRLFISHVILIFALILVISTPNVLA	ESQDPKPDELHKSSKFTGLMENMKVLYDDNHV	60
b_2	MYKRLFISHVILIFVILVISTPNVLA	ESQDPKPDELHKASKFTVLMENMKVLYDDNHV	60
b_4	MYKRLFISHVILIFVILVISTPNVLA	ESQDPKPDELHKASKFTGLMENMKVLYDDNHV	60
	..*.*.*:*****.***** ***** *****:***** *****		
b_3	SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQC		120
b_1	SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQC		120
b_2	SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQC		120
b_4	SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQC		120

b_3	YFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK		180
b_1	YFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK		180
b_2	YFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK		180
b_4	YFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK		180
	*****:*****:*****		
b_3	KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPGDKFDQSKY		240
b_1	KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPGDKFDQSKY		240
b_2	KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPGDKFDQSKY		240
b_4	KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPGDKFDQSKY		240
	*****:*****:*****		
b_3	LMMYNDNKLVDSDKVKIEVYLTTKKK	266	
b_1	LMMYNDNKMVDSKDVKIEVYLTTKKK	266	
b_2	LMMYNDNKLVDSDKVKIEVYLTTKKK	266	
b_4	LMMYNDNKLVDSDKVKIEVYLTTKKK	266	

*****:*****

SEC

c_10	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_5	MYKRLFISRVILIFALILVISTPNVLA	ESQPDMPDDLHKSSEFTGTMGNMKYLYDDHYV	60
c_11	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_3	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_4	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_2	MNKSRLFISCVILIFSLILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_1	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_13	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_7	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
c_8	MNKSRLFISCVILIFALILVLFTPNVLA	ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYV	60
	* * * * * : * * * * * : * * * * * : * * * * * : * * * * *		
c_10	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_5	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_11	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_3	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_4	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_2	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_1	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_13	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_7	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
c_8	SATKVMVDKFLAHDLIYNISDKKLKNYDIVKTELLNEDLAKKYKDEVVDVYGSNYYVNC		120
	***** : ***** : ***** : ***** : *****		
c_10	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_5	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_11	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_3	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_4	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_2	CFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_1	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_13	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_7	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
c_8	YFSSKDNVGKVTGGKTCMYGGITKHEGNHFDNGNLQNVLRVYENKRNTISFEVQTDKKS		180
	***** : ***** : ***** : ***** : *****		
c_10	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_5	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_11	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_3	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_4	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_2	VTAQELDIKARSFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_1	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_13	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFEQSKY		240
c_7	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
c_8	VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKY		240
	***** : ***** : ***** : ***** : *****		
c_10	LMMYNDNKTVDSTQFHLDEISKR--	264	
c_5	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_11	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_3	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_4	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_2	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_1	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_13	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_7	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
c_8	LMMYNDNKTVDSSKSVKIEVHLTTKNG	266	
	***** : ***** : ***** : ***** : *****		

SED

d_5	MKKFNILIALFFFTSLVISPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSYADKNP	60
d_3	MKKFNILIALFFFTSLVISPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSYADKNP	60
d_1	MKKFNILIALFFFTSLVISPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSYADKNP	60
d_2	MKKFNILIALFFFTSLVISPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSYADKNP	60

d_5	IIGENKSTGDQFLENTLLYKNFFTDLINFEDLLINFNSKEMAHFKSKNVDVYAIRYSIN	120
d_3	IIGENKSTGDQFLENTLLYKKFFTDLINFEDLLINFNSKEMAHFKSKNVDVYAIRYSIN	120
d_1	IIGENKSTGDQFLENTLLYKKFFTDLINFEDLLINFNSKEMAHFKSKNVDVYAIRYSIN	120
d_2	IIGENKSTGDQFLENTLLYKKFFTDLINFEDLLINFNSKEMAHFKSKNVDVYAIRYSIN	120
*****:*****		
d_5	CYGGEIDKTACTYGGVTPHEGNKLKERKKIPINLWINGVQKEVSLDKVQTDKKNVTVQEL	180
d_3	CYGGEIDKTACTYGGVTPHEGNKLKERKKIPINLWINGVQKEVSLDKVQTDKKNVTVQEL	180
d_1	CYGGEIDKTACTYGGVTPHEGNKLKERKKIPINLWINGVQKEVSLDKVQTDKKNVTVQEL	180
d_2	CYGGEIDRTACTYGGVTPHEGNKLKERKKIPINLWINGVQKEVSLDKVQTDKKNVTVQEL	180
*****:*****		
d_5	DAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRIYSD	240
d_3	DAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDESXVSYDLFDVKGDFPEKQLRIYSD	240
d_1	DAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRIYSD	240
d_2	DAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRIYSD	240
***** *****		
d_5	NKTLSTEHLHIDIYLYEK	258
d_3	NKTLSTEHLHIDIYLYEK	258
d_1	NKTLSTEHLHIDIYLYEK	258
d_2	NKTLSTEHLHIDIYLYEK	258

SEE

e_1	MKKTAFILLLFIALTLTTSPLVNGSEKSEEINEKDLRKKSELQRNALSNLRQIYYYNEKA	60
e_2	MKKTAFILLLFIALTLTTSPLVNGSEKSEEINEKDLRKKSELQGIALSNLRQIYYYNEKA	60
e_3	MKKTAFILLLFIALTLTTSPLVNGSEKSEEINEKDLRKKSELQGTALSNLRQIYYYNEKA	60
***** *****		
e_1	ITENKESDDQFLENTLLFKGFFTGHWPYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC	120
e_2	ITENKESDDQFLENTLLFKDFFTGHWPYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC	120
e_3	ITENKESDDQFLENTLLFKDFFTGHWPYNDLLVDLGSKDATNKYKGKKVDLYGAYYGYQC	120
*****.*****		
e_1	AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELD	180
e_2	AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELD	180
e_3	AGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELD	180

e_1	LQARHYLHGKFLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQQQYPTLLRIYRDN	240
e_2	LQARHYLHEKFLYNSDSFGGKVQRGLIVFHPSEGSTVSYDLFDAQQQYPTLLRIYRDN	240
e_3	LQARHYLHEKFLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQQQYPTLLRIYRDN	240
***** *****		
e_1	KTINSENHIDLYLYTT	257
e_2	KTINSENHIDLYLYTT	257
e_3	KTINSENHIDLYLYTT	257

SEH

h_1	MINKIKILFSFLALLLSFTSYAKA	EDLHDKSELTDLALANAYGQYNHPFIKENIKSDEIS	60
h_4	MINKIKILFSFLALLLSFTSYAKA	EDLHDKSELTDLALANAYGQYNHPFIKENIKSDEIS	60
h_2	MINKIKILFSFLALLLSFTSYAKA	EDLHDKSELTDLALANAYGQYNHPFIKENIKSDEIS	60
h_3	MINKIKILFSFLALLLSFTSYAKA	EDLHDKSELTDLALANAYGQYNHPFIKENIKSDEIS	60

h_1	GEKDLIFRNQGDGNDLRVKFATADLAQKFKNKSVDIYGASFYYKCEKISENISECLYGG		120
h_4	GEKDLIFRNQGDGNDLRVKFATADLAQKFKNKSVDIYGASFYYKCEKISENISECLYGG		120
h_2	GEKDLIFRNQGDGNDLRVKFATADLAQKFKNKSVDIYGASFYYKCEKISENISECLYGG		120
h_3	GEKDLIFRNQGDGNDLRVKFATADLAQKFKNKSVDIYGASFYYKCEKISENISECLYGG		120

h_1	TTLNSEKLAQERVIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKD		180
h_4	TTLNSEKLAQERVIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKD		180
h_2	TTLNSEKLAQERVIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKD		180
h_3	TTLNSEKLAQERAIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKD		180
* *****			
h_1	SEISKGLIEFDMKTPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYTKKS		240
h_4	SEISKGLIEFDMKTPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYTKKS		240
h_2	SEISKGLIEFDMKTPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYTKKS		240
h_3	SEISKGLIEFDMKTPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYTKKS		240

h_1	IINENF	246	
h_4	V-----	241	
h_2	V-----	241	
h_3	V-----	241	
:			

SEI

i_2	MKKFKYSFIVVFILFFNVNDFSIA	QGDIGVGNLNRFYTKHDYIDLKGLIDKNLPSANQLE	60
i_12	MKKFKYSFIVVFILFFNVNDFSIA	QGDIGVGNLNRFYTKHDYIDLKGLIDKNLPSANQLE	60
i_6	MKKFKYSFILVFILFFNIKDLTYA	QGDIGVGNLNRFYTKHDYIDLKGVTDKNLPIANQLE	60
i_15	MKKFKYSFILVFILFFNIKDLTYA	QGDIGVGNLNRFYTKHDYIDLKGVTDKNLPIANQLE	60
i_3	MKKFKYSFILVFILFFNIKDLTYA	QGDIGVGNLNRFYTKHDYIDLKGVTDKNLPIANQLE	60
i_4	MKKFKYSFILVFILFFNIKDLTYA	QGDIGVGNLNRFYTKHDYIDLKGVTDKNLPIANQLE	60
i_8	MKKFKYSFIVVFILFFNVYDLSIA	QGDIGVGNLNRFYTKYDYIDLKGVTDKNLPTANQLE	60
i_11	MKKFKYSFIVVFILFFNVYDLSIA	QGDIGVGNLNRFYTKYDYIDLKGVTDKNLPTANQLE	60
i_13	MKKFKYSFIVVFILFFNVNDFSIA	QGDIGVGNLNRFYTKYDYIDLKGVTDKNLPIANQLE	60
i_17	MKKFKYSFIVVFILFFNVDDLTYA	QGDIGVGNLNRFYTKYDYIDLKGVTDKNLPIANQLE	60
i_1	MKKIKYSFILVFILFFNIKDLTYA	QGDIGVGNLNRFYTKYDYIDLKGVTDKNLPIANQLE	60
i_5	MKKIKYSFILVFILFFNIKDLTYA	QGDIGVGNLNRFYTKYDYIDLKGVTDKNLPIANQLE	60
i_10	MKKIKYSFILFFILFFNIKDLTYA	QGDIGVGNLNRFYTKYDYIDLKGVTDKNLPIANQLE	60
:**:***:***: *:*****:*****: *****			
i_2	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_12	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_6	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_15	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_3	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_4	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_8	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_11	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_13	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_17	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_1	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_5	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120
i_10	FSTGTNDLISESNNWDEISKFKGKKLDIFGIDYNGPCKSKYMYGGATLSGQYLSARKIP		120

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i_2	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_12	INLLVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_6	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIY-----	165
i_15	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_3	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_4	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_8	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_11	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_13	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_17	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_1	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNSTGKGKEYGYKSK	180
i_5	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNNNGKGKEYGYKSK	180
i_10	INLWVNGKHKTISTDKIATNKKLVTAQEIDVKLRRLQEEYNIYGHNNNGKGKEYGYKSK	180
.**:*****:*****		
i_2	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_12	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_6	-----GDGLPVSFLKIYEDNKIIIESEKFHLDVEISYVD	198
i_15	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_3	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_4	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_8	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_11	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_13	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_17	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_1	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_5	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
i_10	FYSGFNKGKVLFHLNDEKSFSDLFYTGDPVPSFLKIYEDNKIIIESEKFHLDVEISYVD	240
::*****		
i_2	SNK	243
i_12	SNK	243
i_6	SN-	200
i_15	SN-	242
i_3	SN-	242
i_4	SN-	242
i_8	SN-	242
i_11	SN-	242
i_13	SN-	242
i_17	SN-	242
i_1	SN-	242
i_5	SN-	242
i_10	SN-	242
**		

SEJ

sej_4	MKKTIFILIFSLTLLITPLVYSDSKNETIKEKNLHKKSELSSITLNNLRHIYFFNEKG	60
sej_2	MKKRIFILIFSLTLLITPLVYSDSKNETIKEKNLHKKSELSSITLNNLRHIYFFNEKG	60
sej_1	MKKTIFILIFSLTLLITPLVYSDSKNETIKEKNLHKKSELSSITLNNLRHIYFFNEKG	60
sej_3	MKKTIFILIFSLTLLITPLVYSDSKNETIKEKNLHKKSELSSITLNNLRHIYFFNEKG	60

sej_4	ISEKIMTEDQFLDYTLFLKSFESHQSQYNDLLVQFDSKETVNKFKGKQVDLYGSYYGFQC	120
sej_2	ISEKIMTEDQFLDYTLFLKSFESHQSQYNDLLVQFDSKETVNKFKGKQVDLYGSYYGFQC	120
sej_1	ISEKIMTEDQFLDYTLFLKSFESHQSQYNDLLVQFDSKETVNKFKGKQVDLYGSYYGFQC	120
sej_3	ISEKIMTEDQFLDYTLFLKSFESHQSQYNDLLVQFDSKETVNKFKGKQVDLYGSYYGFQC	120

sej_4	SGGKSNKTACMYGGVTLHENNQLYDTKKIPINLWIDSIRTVVPLDIVKTNKKKVTIQELD	180
sej_2	SGGKPNKTACMYGGVTLHENNQLYDTKKIPINLWIDSIRTVVPLDIVKTNKKKVTIQELD	180
sej_1	SGGKPNKTACMYGGVTLHENNQLYDTKKIPINLWIDSIRTVVPLDIVKTNKKKVTIQELD	180
sej_3	SGGKPNKTACMYGGVTLHENNQLYDTKKIPINLWIDSIRTVVPLDIVKTNKKKVTIQELD	180

sej_4	LQARYYLHKQYNLYNPSTFDGKIQKGLIVFHTSKEPLVSYDLFNVIGQYPDKLLKIYQDN	240
sej_2	LQARYYLHKQYNLYNPSTFDGKIQKGLIVFHTSKEPLVSYDLFNVIGQYPDKLLKIYQDN	240
sej_1	LQARYYLHKQYNLYNPSTFDGKIQKGLIVFHTSKEPLVSYDLFNVIGQYPDKLLKIYQDN	240
sej_3	LQARYYLHKQYNLYNPSTFDGKIQKGLIVFHTSKEPLVSYDLFNVIGQYPDKLLKIYQDN	240

sej_4	KIIESENMHIDIYLYTSLIVLISLPLVL	268
sej_2	KIIESENMHIDIYLYTSLIVLISLPLVL	268
sej_1	KIIESENMHIDIYLYTSLIVLISLPLVL	268
sej_3	KIIESENMHIDIYLYTSLIVLISLPLVL	268

SEK

k_2	MKKLISILLINIIILGVSNNASAQGDIGIDNLRNFYTKKDFINLKDVKDNDTPIANQLQF	60
k_9	MKKLISILLINIIILGVSNNASAQGDIGIDNLRNFYTKKDFINLKDVKDNDTPIANQLQF	60
k_7	MKKLIVIIILINIITLSVNSASAQGDIGIDNLRNFYTKKDFVLDKDVKDNDTPIANQLQF	60
k_4	MKKLISILLINIIILGVSNSASAQGDIGIDNLRNFYTKKDFIDLDKDVKDNDTPIANQLQF	60
k_1	MKKLISILLINIIILGVSNSASAQGDIGIDNLRNFYTKKDFVLDKDVKDNDTPIANQLQF	60
k_3	MKKLISILLINIIILGVSNSASAQGDIGIDNLRNFYTKKDFVLDKDVKDNDTPIANQLQF	60
k_5	MKKLISILLINIIILGVSNNASAQGDIGIDNLRNFYTKKDFVLDKDVKDNDTPIANQLQF	60
k_8	MKKLISILLINIIILGVSNNASAQGDIGIDNLRNFYTKKDFVLDKDVKDNDTPIANQLQF	60

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k_2	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKPRNIPI	120
k_9	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKPRNIPI	120
k_7	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKPRNIPI	120
k_4	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKSRNIPI	120
k_1	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKSRNIPI	120
k_3	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKSRNIPI	120
k_5	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKSRNIPI	120
k_8	SNESYDLISESKDFNKFNSFKGKKLDVFGISYNGQCNTKYIYGGITATNEYLDKSRNIPI	120
*****:*****.*****:*****		
k_2	NIWINGNHKTISTNKVSTNKKFVTAQEIDIKLRRYLQEEYNIYGHNGTKKGEEYGHKSKE	180
k_9	NIWINGNHKTISTNKVSTNKKFVTAQEIDIKLRRYLQEEYNIYGHNGTKKGEEYGHKSKE	180
k_7	NIWINGNHKTISTNKVSTNKKFVTAQEIDVKLRLKYLQEEYNIYGHNGTKKGEEYGHKSKE	180
k_4	NIWINGNHKTISTNKVSTNKKFVTAQEIDVKLRLKYLQEEYNIYGHNGTKKGEEYGHKSKE	180
k_1	NIWINGNHKTISTNKVSTNKKFVTAQEIDVKLRLKYLQEEYNIYGHNGTKKGEEYGHKSKE	180
k_3	NIWINGNHKTISTNKVSTNKKFVAAQEIDVKLRLKYLQEEYNIYGHNGTKKGEEYGHKSKE	180
k_5	NIWINGNHKTISTNKVSTNKKLVTAQEIDVKLRLKYLQEEYNIYGHNGTKKGEEYGHKSKE	180
k_8	NIWINGNHKTISTNKVSTNKKLVTAQEIDVKLRLKYLQEEYNIYGHNGTKKGEEYGHKSKE	180
*****:*:*****:***:*****		
k_2	YSGFNIGKVTFHLNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
k_9	YSGFNIGKVTFHSNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
k_7	YSGFNIGKVTFHLNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
k_4	YSGFNIGKVTFHLNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
k_1	YSGFNIGKVTFHLNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
k_3	YSGFNIGKVTFHLNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
k_5	YSGFNIGKVTFHLNNNDTFSYDLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
k_8	YSGFNIGKVTFHLNNNDTFSYGLFYTGDDGLPKSFLKIYEDNKTVESEKFHLDVDISYKE	240
***** *****.*****		
k_2	TK	242
k_9	TK	242
k_7	TI	242
k_4	TI	242
k_1	TI	242
k_3	TI	242
k_5	TI	242
k_8	TI	242
*		

SEL

l_13	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_12	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_9	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_8	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_7	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_6	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_4	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_1	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60
l_2	MKKRLLFVIVITLFISSNHTVLSNGDVGPGLNRFYTKYEYVNLKNIKDKNSPESHRL	60

1_5	MKKRLLFVIVITLFISSNHTVLSNGDVG TGNLRNFYTKY EYVNLKNVKDKNSPESHRL E	60
1_10	-----MNLKNVKDKNSPESHRL E : ****.*****	18
1_13	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_12	YSYKNDTLA EFDNEYITS DLKGKNVDIFGISYKYGNSRTIYGGVTKAENNKLGSPRII	120
1_9	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_8	YSYKNDTLA EFDNEYITS DLKGKNVDIFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_7	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_6	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_4	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_1	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_2	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_5	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII	120
1_10	YSYKNDTLA EFDNEYITS DLKGKNVDVFGISYKYGNSRTIYGGVTKAENNKLDSPRII *****.*****.***** *****.*****	78
1_13	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_12	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_9	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_8	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_7	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_6	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_4	PINLIINGKHQT VTTKCVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_1	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_2	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_5	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS	180
1_10	PINLIINGKHQT VTTKSVSTDKKMVT AQEIDVKLRKYLQDEFNIYGHNDTGKGKEYGTSS *****.*****.***** *****.*****	138
1_13	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_12	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_9	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_8	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_7	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_6	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_4	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_1	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_2	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV DSTQFHL DVEISK R	240
1_5	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV GSTQFHL DVEISK R	240
1_10	KFYSGFDKGSVVFHMDGNSF SYDLFYTG YGLPESFLKIYKDNKTV GSTQFHL DVEISK R *****. *.*****.***** *****.*****	198

SEM

m_3	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQ SINPENNHLSHQLVFSMD	60
m_8	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQ SINPENNHLSHQLVFSMD	60
m_15	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQ SINPENNHLSHQLVFSMD	60
m_4	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQ SINPENNHLSHQLVFSMD	60
m_6	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQ SINPENNHLSHQLVFSMD	60
m_1	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIESHQININPDNNLSHQLVFSKD	60
m_5	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQININPDNNRLSHQLVFSKD	60
m_2	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQININPDNNRLSHQLVFSMD	60
m_9	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQININPDNNRLSHQLVFSMD	60
m_19	MKRILII VVLLFCYSQNHIATADVGV LNLNRNYYGSYPIEDHQININPDNNRLSHQLVFSMD	60

*****.**.***:* ***** *		
m_3	NSSITAEFKNVDDVKKFKNHAVDVYGLSYSGYCLKNKYIYGGVTLAGDYLEKSRCIPINL	120
m_8	NSTITAEFKNVDDVKKFKNHAVDVYGLSYSGYCLKNKYIYGGVTLAGDYLEKSRCIPINL	120
m_15	NSTVTAEFKNVDDVKKFKNHAVDVYGLSYSGYCLKNKYIYGGVTLAGDYLEKSRRIPINL	120
m_4	NSTVTAEFKNVDDVKKFKNHAVDVYGLSYSGYCLKNKYIYGGVTLAGDYLEKSRRIPINL	120
m_6	NSTVTAEFKNVDDVKKFKNHAVDVYGLSYSGYCLKNKYIYGGVTLAGDYLEKSRRIPINL	120
m_1	NSTVTAEFKNVEDVKKFKNRAVDVYGLSYSGYCLKNKMYGGVTLAGDYLEKSRCIPINL	120
m_5	NSTVTAEFKNVEDVKKFKNRAVDVYGLSYSGYCLKNKMYGGVTLAGDYLEKSRCIPINL	120
m_2	NSTVTAEFKNVEDVKKFKNRAVDVYGLSYSGYCLKNKMYGGVTLAGDYLEKSRCIPINL	120
m_9	NSTVTAEFKNVDDVKKFKNRAVDVYGLSYSGYCLKNKMYGGVTLAGDYLEKSKYIPINL	120
m_19	NSTVTAEFKNVDDVKKFKNRAVDVYGLSYSGYCLKNKMYGGVTLAGDYLEKSKYIPINL	120
.:***:*****:*****:*****:*****:*****:*****		
m_3	WVNGEHQTISTDKVSTNKKLVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGNKSKFSS	180
m_8	WVNGEHQTISTDKVSTNKKLVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGNKSKFSS	180
m_15	WVNGEHQTISTDKVSTNKKLVTAQEIDTKLRRYLQEEYNIYGFNDTNKVRNYGNKSKFSS	180
m_4	WVNGEHQTISTDKVSTNKKLVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGNKSKFSS	180
m_6	WVNGEHQTISTDKVSTNKKLVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGNKSKFSS	180
m_1	WVNGNHKTISTDKVSTNKKIVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGTSKFFS	180
m_5	WVNGNLKTISTDKVSTNKKIVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGTSKFFS	180
m_2	WVNGEHQTISTEKVSTNKKIVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGTSKFFS	180
m_9	WVNSEHQTISTEKVSTNKKIVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGTSKFFS	180
m_19	WVNSEHQTISTEKVSTNKKIVTAQEIDTKLRRYLQEEYNIYGFNDTNKGRNYGTSKFFS	180
.: :*:*****:*****:*****:*****:*****:*****		
m_3	GFNAGKILFHLNDGSSFSYDLFDTGTGQAESFLKIYNDNKTVETEFHLDVEISYKDES	239
m_8	GFNAGKILFHLNDGSSFSYDLFDTGTGQAESFLKIYNDNKTVETEFHLDVEISYKDES	239
m_15	GFNAGKILFHLNDGSSFSYDLFDTGTGQAESFLKIYNDNKTVETEFHLDVEISYKDES	239
m_4	GFNAGKILFHLNDGSSFSYDLFDTGTGQAESFLKIYNDNKTVETEFHLDVEISYKDES	239
m_6	GFNAGKILFHLNDSSFSYDLFDTGTGQAESFLKIYNDNKTVETEFHLDVEISYKDES	239
m_1	GFNTGKISFHLNDGTSFSYDLFDTGTGQAESFLKIYNDNKTVETDKFHLDEISYKDES	239
m_5	GFNTGKISFHLNDGTSFSYDLFDTGTGQAESFLKIYNDNKTVETDKFHLDEISYKDES	239
m_2	GFNTGKISFHLNDGSSFSYDLFDTGTGQAESFLKIYNDNKTVETDKFHLDEISYKDES	239
m_9	GFNTGKVSFHLNDGSSFSYDLFDTGTGQAESFLKIYNDNKTVETDKFHLDEISYKDES	239
m_19	GFNTGKISFHLNDGSSFSYDLFDTGTGQAESFLKIYNDNKTVETDKFHLDEISYKDES	239
.:*: **.:*****:*****:*****:*****:*****:*****		

SEN

n_4	MRLFCAIAIIITLLCLINNNYVNADVDKNDLKKKSDIDSSKLFNLTSYYTDITWQLDES	60
n_5	-----MKCLINNNYVNAEVDKDKLKKKSDLDSSKLFNLTSYYTDITWQLDES	48
n_3	MRLFYIAAIIITLLCLINNNYVNAEVDKDKLKKKSDLDSSKLFNLTSYYTDITWQLDES	60
n_7	MRLFYIAAIIITLLCLINNNYVNAEVDKDKLKKKSDLDSSKLFNLTSYYTDITWQLDES	60
n_8	MRLFYIAVIIITLLCLINNNYVNAEVDKDKLKKKSDIDSSK----CYTDTITWQLDES	55
n_6	MRLFYIAVIIITLLCLINNNYVNAEVDKDKLKKKSDIDSSNLFNLTSYYTDITWQLDES	60
n_1	MRLFYIAVIIITLLCLINNNYVNAEVDKDKLKKKSDIDSSNLFNLTSYYTDITWQLDES	60
n_2	MRLFYIAVIIITLLCLINNNYVNAEVDKDKLKKKSDIDSSKLFNLTSYYTDITWQLDES	60
n_9	-----MLCFLNNNYVNADVNKNLKKKSELDSSKLFNLANYTDTVTWQLEKSN	48
n_13	MRLFYIALIIITLLCLINNNYVNADVDKNDLKKKSDLDSSKLFNLTSYYTDITWQLEKSN	60
: *:***:****:***: *****.:***: *****:****:***		
n_4	KISTDQLLNNTIILKDIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYYGNKCVGLT	120

n_5	KISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYFGNKC	108
n_3	KISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYFGNKC	120
n_7	KISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYFGNKC	120
n_8	KISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYFGNKC	115
n_6	KISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYFGNKC	120
n_1	KISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYFGNKC	120
n_2	KISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSDLANQFKGNIDIYGLYFGNKC	120
n_9	VISSDQLLNNTIIFKNIVISVLNTSSLKVEFNSSDLANQYKGRNVDIFGLYGNKC	108
n_13	VISSDQLLNNTIIFKNIVIAELNTSSLKVEFNSSDLANQYKGSNVDIFGLYGNKC	120
	*:*****:*: * *: :***** *****: * *: **: **: *****: **	
n_4	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGIQQEGFVIKTKKAKVTVQELDTKVR	180
n_5	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGVQQEGFVIKTKKAKVTVQELDTKVR	168
n_3	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGVQQEGFVIKTKKAKVTVQELDTKVR	180
n_7	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGVQQEGFVIKTKKAKVTVQELDTKVR	180
n_8	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGVQQEGFVIKTKKAKVTVQELDTKVR	175
n_6	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGVQQEGFVIKTKKAKVTVQELDTKVR	180
n_1	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGVQQEGFVIKTKKAKVTVQELDTKVR	180
n_2	EEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDGVQQEGFVIKTKKAKVTVQELDTKVR	180
n_9	GEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDDAQQEGFVIKTKKAKVTVQELDTKVR	168
n_13	GEKTSCLYGGVTIYDGNQLDEERVIGVNVFKDDAQQEGFVIKTKKAKVTVQELDTKVR	180
	***** *****:*****:*****. *****	
n_4	LENLYKIYNKDTGNIQKGCIFFHSHNHQNSFYFDLYNIKGSVGAEFFQFYSDNRTVSSS	240
n_5	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNVKGSVGAEFFQFYSDNRTVSSS	228
n_3	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNVKGSVGAEFFQFYSDNRTVSSS	240
n_7	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNVKGSVGAEFFQFYSDNRTVSSS	240
n_8	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNIKGSVGAEFFQFYSDNRTVSSS	235
n_6	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNIKGSVGAEFFQFYSDNRTVSSS	240
n_1	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNIKGSVGAEFFQFYSDNRTVSSS	240
n_2	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNIKGSVGAEFFQFYSDNRTVSSS	240
n_9	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNIKGSVGAEFFQFYSDNRTVSSS	228
n_13	LENLYKIYNKDTGNIQKGCIFFHSHNHQDSFYFDLYNIKGSVGAEFFQFYSDNRTVSSS	240
	*****: *: *: :*****:*****. *****	
n_4	NYHIDVFLYKD	251
n_5	NYHIDVFLYKD	239
n_3	NYHIDVFLYKD	251
n_7	NYHIDVFLYKD	251
n_8	NYHIDVFLYKD	246
n_6	NYHIDVFLYKD	251
n_1	NYHIDVFLYKD	251
n_2	NYHIDVFLYKD	251
n_9	NYHIDVFLYKD	239
n_13	NYHIDVFLYKD	251

SEO

o_9	MLNVILLIINLIAICNVNNAYANEENPKIEDLCKKSSVDPIALHNIEKDYVNNRFTIDKS	60
o_20	MLNVLLLIINLIAICSVNNAYANEEEKPKIEDLCKKSSVDPIALHNIEKDYVNNRFTIDKS	60
o_4	MLNVLLLIINLIAICSVNNAYANEENPKIEDLCKKSSVDDIALHNIDKDYMTNRFTINES	60
o_5	MLNVLLLIITYLIAICSVNNAYANEENPKIEDLCKKSSVDDIALHNIDKDYMTNRFTINES	60
o_1	MLNVLLLIITYLIAICSVNNAYANEENPKIEDLCKKSSVDDIALHNIDKDYMTNRFIINES	60
o_19	MLNVLLLIITYLIAICSVNNAYANEENPKIEDLCKKSSVDDIALHNIDKDYMTNRFIINES	60
o_8	MLNVLLLIILNLIAICSVNNAYANEEDPKIESLCKKSSVDPIALHNINDDYINNRFTTVKS	60
o_2	MLNVLLLIITYLIAICSVNNAYANEENPKIEDLCKKSSVDSTALHNINDDYINNRFTTVKS	60
o_7	MLNVLLLIITYLIAICSVNNAYANEENPKIEDLCKKSSVDSTALHNINDDYINNRFTTVKS	60
o_21	MLNVLLLIILNLIAICSVNNAYANEEDPKIESLCKKSSVDPIALHNINDDYINNRFTTVKS	60
o_14	MLNVLLLIILNLIAICSVNNAYANEEDPKIESLCKKSSVDPIDLHNINDDYINNRFTTVKS	60
o_3	MLNVLLLIILNLIAICSVNNAYANEEDPKIESLCKKSSVDPIALHNINDDYINNRFTTVKS	60

o_6	MLNVLLLILNLIACSVNNAYANEEDPKIESLCKKSSVDPIALHNINDDYINNRFTTVK	60
	::*****.*****.***.***** ***:..*:*:*:*	
o_9	PVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_20	PVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_4	TVLTTEKFLDIDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_5	PVLTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_1	PVLTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_19	PVLTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_8	IVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSAISKEFLGKTVDIYGVIYKAHC	120
o_2	IVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_7	IVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSEISKEYFGKTVDIYGVIYKAHC	120
o_21	IVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSAISKEFLGKTVDIYGVIYKAHC	120
o_14	IVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSAISKEFLGKTVDIYGVIYKAHC	120
o_3	IVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSAISKEFLGKTVDIYGVIYKAHC	120
o_6	IVSTTEKFLDFDILLFKNFTWLDGKSAEFKDLKVEFSSSAISKEFLGKTVDIYGVIYKAHC	120
	* *:*****:*****.:.***** *:***** *****:*****	
o_9	HGEHQVKTACTYGGITSHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_20	HGEHQVKTACTYGGITSHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_4	HGEHQVKTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_5	HGEHQVKTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_1	HGEHQVKTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_19	HGEHQVKTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_8	HGEHQVDTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_2	HGEHQMNTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_7	YGEHQMNTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_21	HGEHQVDTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_14	HGEHQVDTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_3	HGEHQVDTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
o_6	HGEHQVDTACTYGGVTPHENNKLEPKNIGVAVYKDNVNVNTFIVTTDKKKVTAQELDIK	180
	:****:..*****:* *****.***:*****	
o_9	VRTKLNNEYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_20	VRTKLNNEYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_4	VRTKLNNVYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_5	VRTKLNNVYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_1	VRTKLNNVYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_19	VRTKLNNVYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_8	VRTKLNNAYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_2	VRTKLNNAYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_7	VRTKLNNAYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_21	VRTKLNNAYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_14	VRTKLNNAYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_3	VRTKLNNAYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
o_6	VRTKLNNAYKLYDRMTSDVQKGYIKFHSSEHSEKESFYDLYIKGNLPDQYLQIYNDNKT	240
	***** *****:*****: :*:.: : :*:.*:	
o_9	IDSSDYHIDVYLF- 254	
o_20	IDSSDYHIDVYLF- 254	
o_4	IDSSDYHIDVYLF- 254	
o_5	IDSSDYHIDVYLF- 254	
o_1	IDSSDYHIDVYLF- 254	
o_19	IDSSDYHIDVYLF- 254	
o_8	VSSSNYHIDVFLYKD 255	
o_2	IDSSDYHIDVYLF- 254	
o_7	IDSSDYHIDVYLF- 254	
o_21	IDSSDYHIDVYLF- 254	
o_14	IDSSDYHIDVYLF- 254	

o_3 IDSSDYHIDVYLFT- 254
o_6 IDSSDYHIDVYLFT- 254
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SEP

p_4	MSKIKKTTFILLSFIALTLITSPFVNCSEKSEEINGKDLQKKSELQGTALSNLRQTYYYH	60
p_2	MSKIKKTTFILLSFIALTLITSPFVNCSEKSEEINGKDLQKKSELQGTALSNLRQTYYYH	60
p_3	MSKIKKITFILLSFIALTLITSPFVNCSEKSEEINGKDLQKKSELQGTALSNLRQTYYYH	60

p_4	GSAIENKESNDQFLKNTILFNDFFTGHQWYNDLLVDLGSKDTANIYKGKKVDLYGVYYG	120
p_2	GSAIENKESNDQFLKNTILFNDFFTGHQWYNDLLVDLGSKDTANIYKGKKVDLYGVYYG	120
p_3	GSAIENKESNDQFLKNTILFNDFFTGHQWYNDLLVDLGSKDTANIYKGKKVDLYGVYYG	120

p_4	YQCTGGTTFKKTACMYGGVTLHDNNQLEEEKKVPINLWIDGKQNTVPLGTVKTNKKEVTQ	180
p_2	YQCTGGTTFKKTACMYGGVTLHDNNQLEEEKKVPINLWIDGKQNTVPLGTVKTNKKEVTQ	180
p_3	YQCTGGTTFKKTACMYGGVTLHDNNQLEEEKKVPINLWIDGKQNTVPLGTVKTNKKEVTQ	180

p_4	ELELQSRHYLHETYNLYNTDAFNGKIQRGLIEFHPSSGDSVGYDLFGAQGGYPDTQLRIY	240
p_2	ELDLQSRHYLHETYNLYNTDAFNGKIQRGLIEFHPSSGDSVGYDLFGAQGGYPDTQLRIY	240
p_3	ELDLQSRHYLHETYNLYNTDAFNGKIQRGLIEFHPSSGDSVGYDLFGAQGGYPDTQLRIY	240
	** : *****	
p_4	RDNKTIKSKNMHIDIYLYTT	260
p_2	RDNKTIKSKNMHIDIYLYTT	260
p_3	RDNKTIKSKNMHIDIYLYTT	260

SEQ

q_3	MNKIFRILTVSLFFFTFLIKNNLAYADVGVINLRNFYANYEPEKLQGVSSGNFSTSHQLE	60
q_5	MNKIFRVLTVSLFFFTFLIKNNLAYADVGVINLRNFYANYEPEKLQGVSSGNFSTSHQLE	60
q_2	MNKIFRVLTVSLFFFTFLIKNNLAYADVGVINLRNFYANYEPEKLQGVSSGNFSTSHQLE	60
q_1	MNKIFRILTVSLFFFTFLIKNNLAYADVGVINLRNFYANYEPEKLQGVSSGNFSTSHQLE	60
q_4	MNKIFRILTVSLFFFTFLIKNNLAYADVGVINLRNFYANYEPEKLQGVSSGNFSTSHQLE	60
	***** : ***** : * * : * * . *****	
q_3	YIDGKYTLYSQFHNEYAKRLKDHKVDIFGISYSGLCNTKMYGGITLANQNLDKPRNIP	120
q_5	YIDGKYTLYSQFHNEYAKRLKDHKVDIFGISYSGLCNTKMYGGITLANQNLDKPRNIP	120
q_2	YIDGKYTLYSQFHNEYAKRLKDHKVDIFGISYSGLCNTKMYGGITLANQNLDKPRNIP	120
q_1	YIDGKYTLYSQFHNEYAKRLKDHKVDIFGISYSGLCNTKMYGGITLANQNLDKPRNIP	120
q_4	YIDGKYTLYSQFHNEYAKRLKDHKVDIFGISYSGLCNTKMYGGITLANQNLDKPRNIP	120

r_4	DYKVRNWLTTNNKKLYEFDGSAYETGYIKFIEENKDSFWYDLFPKKDLVPFIPYKFVNIYG *****.*****	240
r_2	DNKTIDASSVKIEVHLTTM	259
r_5	DNKTIDASSVKIEVHLTTT	259
r_1	DNKTIDASSVKIEVHLTTT	259
r_4	DNKTIDASSVKIEVHLTTT *****	259

SES

s_3	MNYSKITVSLIIILLCTFSFEFSFNRFVQADESRPKIESLKKKSELDSTALYNIKTSYSQ	60
s_1	MNYSKITVTLIIILLCTFSFEFSFNRFVQADESRPKIESLKKKSELDSTALYNIKTSYSQ *****.*****	60
s_3	DNIILDIKNKTNSTQLLSNDLIFDDITLKEWNKNSLKTENFSSEIANHFKGKKVDIFGIY	120
s_1	DNIILDIKNKTNSTQLLSNDLIFDDITLKEWNKNSLKTENFSSEIANHFKGKKVDIFGIY *****	120
s_3	YGANCIGEVSKRTGCIYGGITLHEEEKIDQKNSIGVNVFKDGSQQKGFMITTDKKEPTIQ	180
s_1	YGANCIGEVSKRTGCIYGGITLHEEEKIDQKNSIGVNVFKDGSQQKGFMITTDKKEPTIQ *****	180
s_3	ELDLKTRKVIQNYKIYNSETGNIQKGYMEFHSNSSFYYDLFNFKGKYSVDLKFYNDN	240
s_1	ELDLKTRKVIQNYKIYNSETGNIQKGYMEFHSNSSFYYDLFNFKGKYSVDLKFYNDN *****	240
s_3	KTINSSNLHIDVYLYSQ	257
s_1	KTINSSNLHIDVYLYSQ *****	257

SET

>t_1
MKKCILFIFSIILLVSISTLFIPNAKSDSREGLKDFYSKKIDVYTNKKINEKDKYSVDIEVDNYVYRINTLDDKILNQFKV
GDYVDAWGHIIINNPKIGKVIKFDGDISKHSPDKPTNISYRINLFKEQKQTEVTPEKELEIGNRYLTMKQIDYRIKSYLV
KKQQLYTEFYNGKIEISMLDGGKHFIDLSTYYYDPSNFTLDYTKISHFDIYMEK

SEU

u_11	MKLFAFLFICVKSCSLLFMLNDNPKPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKAQE	60
u_18	MKLFAFLFICVKSCSLLFMLNDNPKPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKAQE	60
u_6	MKLFAFIFICVKSCSLLFMLNGNPKPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKSQE	60
u_4	MKLFAFIFICVKSCSLLFMLNGNPKPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKSQE	60
u_5	MKLFAFIFICVKSCSLLFMLNGNPKPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKSQE	60
u_1	MKLFAFIFICVKSCSLLFMLNGNPKPEQLNKASEFTGLMDNMRYLYDDKHVSEINIKAE	60
u_7	MKLFAFIFICVKSCSLLFMLNGNPRPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKVQE	60
u_17	MKLFAFIFICVKSCSLLFMLNGNPRPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKAQE	60
u_9	MKLFAFIFICVKSCSLLFMLNGNPRPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKAQE	60
u_2	MKLFAFIFICVKSCSLLFMLNGNPRPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKAQE	60
u_10	MKLFAFIFICVKSCSLLFMLNGNPRPEQLNKASEFTGLMDNMRYLYDDKHVSETNIKAQE *****.*****.***.*****.*****	60
u_11	KFLQHDLLFKINR-----SKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSSDNMEL	115
u_18	KFLQHDLLFKING-----SKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSADNMEL	115
u_6	KFLQHDLLFEING-----SKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSSDNMEL	115
u_4	KFLQHDLLFKING-----SKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSLDNMEL	115
u_5	KFLQHDLLFKING-----SKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSSDNMEL	115
u_1	KFLQHDLLFKINGSKIDGSKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSADNMEL	120
u_7	KFLQHDLLFKINGSKIDGSKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSADNMEL	120
u_17	KFLQHDLLFKINGSKIDGSKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSADNMEL	120
u_9	KFLQHDLLFKINGSKIDGSKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCYFSADNMEL	120
u_2	KFLQHDLLFKINGSKIDGSKILKTEFNKNSLSDKYKNKNVDLFGTNYYNQCNFSADNMEL	120

u_10	KFLQHDLDFKINGSKIDGSKILKTEFNKSLSDKYKNKNVDLFGTNYYNQCYFSADNMEL *****:*** *****:*****:***** ** ** *****	120
u_11	NDGILIEKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITA	175
u_18	NDGILIGKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITA	175
u_6	NDGRLEKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITA	175
u_4	NDGRLEKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITA	175
u_5	NDGRLEKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVYENERNSLSFDIPTNKKNITA	175
u_1	NDGRLEKTCMYGGVTEHDGNQIDKNNSTDNSHNILIKVFENERNSLSFDIPTNKKNITA	180
u_7	NDGRLEKTCMYGGVTEHDGNQIDKNNLTDNSHNILIKVYENERNTLSFDISTNMKNITA	180
u_17	NDGRLEKTCMYGGVTEHDGNQIDKNNLTDNSHNILIKVYENERNTLSFDISTNMKNITA	180
u_9	NDGRLEKTCMYGGVTEHDGNQIDKNNLTDNSHNILIKVYENERNTLSFDISTNKKNITA	180
u_2	NDGRLEKTCMYGGVTEHDGNQIDKNNLTDNSHNILIKVYENERNTLSFDISTNKKNITA	180
u_10	NDGRLEKTCMYGGVTEHDGNQIDKNNLTDNSHNILIKVYENERNTLSFDISTNKKNITA *** ** *****:*****:***** ** *****	180
u_11	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGNGNTFWYDMPESGEKFPYPTKYLLI	235
u_18	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGNGNTFWYDMPESGEKFPYPTKYLLI	235
u_6	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGSGHSFWYDMPESGKKFPYPTKYLLI	235
u_4	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGSGHSFWYDMPESGKKFPYPTKYLLI	235
u_5	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGSGHSFWYDMPESGKKFPYPTKYLLI	235
u_1	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGNGHSFWYDMPESGEKFPYPTKYLLI	240
u_7	QEIDYKVRNYLLKHKDLYEFNSSPYESGYIKFIEGNGHSFWYDMPESGEKFPYPTKYLLI	240
u_17	QEIDYKVRNYLLKHKDLYEFNSSPYESGYIKFIEGNGHSFWYDMPESGEKFPYPTKYLLI	240
u_9	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGNGHSFWYDMPESGEKFPYPTKYLLI	240
u_2	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGNGHSFWYDMPESGEKFPYPTKYLLI	240
u_10	QEIDYKVRNYLLKHKDLYEFNSSPYETGYIKFIEGNGHSFWYDMPESGEKFPYPTKYLLI *****:***:*****:***** ..:****:*****:*****	240
u_11	YNDNKTVDQSQSVNVEVHLTKK	256
u_18	YNDNKTVDQSQSVNVEVHLTKK	256
u_6	YNDNKTVESKSIINVEVHLTKK	256
u_4	YNDNKTVESKSIINVEVHLTKK	256
u_5	YNDNKTVESKSIINVEVHLTKK	256
u_1	YNDNKTVESKSIINVEVHLTKK	261
u_7	YNDNKTVESKSIINVEVHLTKK	261
u_17	YNDNKTVESKSIINVEVHLTKK	261
u_9	YNDNKTVESKSIINVEVHLTKK	261
u_2	YNDNKTVESKSIINVEVHLTKK	261
u_10	YNDNKTVESKSIINVEVHLTKK *****:***:*****	261

SEX

x_27	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASIQDSSSVHDKQLLKVKEVPNNSEK	60
x_28	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASIQDSSSVHDKQLLKVKEVPNNSEK	60
x_47	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASIQDSSSVHDKQFQKVEEVPNNSEK	60
x_10	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_34	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_3	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_16	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_14	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_12	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_22	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_41	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_6	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_36	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_4	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_7	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_17	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_15	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_45	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60
x_5	MFKKHHSKNSIVLKSILSLGIIYSGIFGINSKADASTQNSSSVHDKQLQKVEEVPNNSEK	60

x_9	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVVEVPNNSEK	60
x_25	MFKKYDSKNSIVLKSILSLGIIYSGSFGIYPKADASTQNSSSVQDKQLQKVVEVPNNSEK	60
x_1	MFKKYDSKNSILLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVVEVPNNSEK	60
x_24	MFKKYDSKNSIVLKSILSLGIIYGGTFGIYPKADASTQNSSSVQDKQLQKVVEVPNNSEK	60
	*****:***** **.* *** **:*** *: * **:***: **:*****	
x_27	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_28	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_47	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_10	ALVKKLYDRYSKNTINGKSNKSRNWVYSERPLNGNQVRINLEGTYRVADRVYTPKRNITL	120
x_34	ALVKKLYDRYSKNTINGKSNKSRNWVYSERPLNGNQVRINLEGTYTVAGRVYTPKRNITL	120
x_3	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRINLEGTYRVADRVYTPKRNITL	120
x_16	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRINLEGTYRVADRVYTPKRNITL	120
x_14	ALVKKLYDRYSQNTINGKSNKARNWVYSERPLNENQVRIHLEGTYRVADRVYTPKRNITL	120
x_12	ALVKKLYDRYSQNTINGKSNKARNWVYSERPLNENQVRIHLEGTYRVADRVYTPKRNITL	120
x_22	ALVKKLYDRYSQNTINGKSNKARNWVYSERPLNENQVRIHLEGTYRVADRVYTPKRNITL	120
x_41	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNGNQVRINLEGTYRVADRVYTPKRNITL	120
x_6	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYRVADRVYTPKRNITL	120
x_36	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYRVADRVYTPKRNITL	120
x_4	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_7	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVADRVYTPKRNITL	120
x_17	ALVKKLYDRYSQNTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVADRVYTPKRNITL	120
x_15	ALVKKLYDRYSKNTINGKSNKSRNWVYSERPLNGNQVRINLEGTYTVAGRVYTPKRNITL	120
x_45	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_5	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_9	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVADRVYTPKRNITL	120
x_25	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_1	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
x_24	ALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITL	120
	*****:*****:***** *****:***** **.* *****	
x_27	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_28	NKEVVTLKELDHIVRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVE	180
x_47	NKEVVTLKELDHIVRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVE	180
x_10	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVK	180
x_34	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_3	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVK	180
x_16	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVK	180
x_14	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKNRGNVE	180
x_12	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKNRENVE	180
x_22	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKNRENVE	180
x_41	NKEIVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_6	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_36	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_4	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_7	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_17	NKEVITLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKDRENVK	180
x_15	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKNRENVE	180
x_45	NKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVK	180

x_5	NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVK	180
x_9	NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVK	180
x_25	NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKNRENVE	180
x_1	NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKNRENVE	180
x_24	NKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKNGGKYTLESHKELQKNRENVE	180

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x_27	INTDDIKNVTTFELVKSVDIEQA	203
x_28	INTADIKNVTTFELVKSVDIEQA	203
x_47	INTADIKNVTTFELVKSVDIEQA	203
x_10	INTADIKNVTTFKLVSVDIEQV	203
x_34	INTDDIKNVTTFELVKSVDIEQV	203
x_3	INTADIKNVTTFKLVSVDIEQV	203
x_16	INTDDIKNVTTFKLVSVDIEQV	203
x_14	INTDDIKNVTTFELVKSVDIEQV	203
x_12	INTDDIKNVTTFELVKSVDIEQV	203
x_22	INTDDIKNVTTFELVKSVDIGQV	203
x_41	INTDDIKNVTTFELVKSVDIEQV	203
x_6	INTDDIKNVTTFELVKSVDIEQV	203
x_36	INTDDIKNVTTFELVKSVDIEQV	203
x_4	IKTDDIKNVTTFELVKRVNDIEQV	203
x_7	NNTDDIKNVTTFELVKSVDIEQV	203
x_17	INTDDIKNVTTFELVKSVDIEQV	203
x_15	INTADVENVTFDLVKSVDIEQV	203
x_45	INTADIKNVTTFKLVSVDIEQV	203
x_5	INTADIKNVTTFKLVSVDIEQV	203
x_9	INTADIKNVTTFKLVSVDIEQV	20
x_25	INTDDIKNVTTFELVKSVDIEQV	203
x_1	INTDDIKNVTTFELVKSVDIEQV	203
x_24	INTDDIKNVTTFELVKSVDIEQV	203

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SEY

y_5	MKAKLWFLLLTTLAFLIAVMGSIGIAEVGAKTGTGLITENSNDLSLKEHYAQKFEVYTNKEVT	60
y_11	MKAKLWFLLLTTLAFLIAVMGSIGIAEVEAKTTGLITENSNDLSLKEHYAQKFEVYTNKEVT	60
y_2	MKAKLCFLLLTTLAFLIAVTGSIGIAEVKAKTGTGLITENSNDLSLKEHYAQKFEVYTNKEVT	60
y_1	MKAKLWFLLLTTLAFLIAVTGSIGIAEVKAKTGTGLITENSNDLSLKEHYAQKFEVYTNKEIT	60
y_7	MKAKLWFLLLTTLAFLIAVTGSIGIAEVKAKTGTGLITENSNDLSLKEHYAQKFEVYTNKEVT	60
y_6	MKAKLWFLLLTTLAFLIAVTGSIGIAEVKAKTGTGLITENSNDLSLKEHYAQKFEVYTNKEVT	60
y_3	MKAKLWFLLLTTLAFLIAVTGSIGIAEVKAKTGTGLITENSNDLSLKEHYAQKFEVYTNKEVT	60
y_4	MKAKLWFLLLTTLAFLIAVTESIGIAEVKAKTGTGLITENSNDLSLKEHYAQKFEVYTNKEVT	60

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y_5	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
y_11	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
y_2	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
y_1	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
y_7	GVGENYIDAKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
y_6	GVGENYIDVQVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120
y_3	GVGENYIDTKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI	120

y_4	GVGENYIDTKVDTYNVRTVLYNTDYLKQFKNQDKVNIWGTLYENQQSKVYRGTVVKYDPI *****.*****:*****:*****	120
y_5	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
y_11	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
y_2	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
y_1	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
y_7	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
y_6	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
y_3	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG	180
y_4	SKVTNLSYRMNLFVNGHQTKVNPDSLLEVKNKQISLKETDFRIRKYLLEKEHLYSNYNSG *****	180
y_5	ELIEMKNGTRHKIDLGILSDSQEKTFFDNISHIDIYMK	221
y_11	ELIEMKNGTRHKIDLGILSDSQEKTFFDNISHIDIYMK	221
y_2	ELIVEMKNGARHKIDLGILSDSQEKTFFDNISHIDIYMK	221
y_1	ELIEMKNGARHKIDLGILSDSQEKTFFDNISHIDIYMK	221
y_7	ELIEMKNGARHKIDLGILSDSQEKTFFDNISHIDIYMK	221
y_6	ELIEMKNGARHKIDLGILSDSQEKTFFDNISHIDIYMK	221
y_3	ELIEMKNGARHKIDLGILSDSQEKTFFDNISHIDIYMK	221
y_4	ELIEMKNGARHKIDLGILSDSQEKTFFDNISHIDIYMK ***.*****:*****	221

SEZ

z_5	MRKVFILITLLFGYSSYSLLQAKAETQNDPNISELNKSSQYTGSWHNIWYLYNSDPVNAK	60
z_3	MRKVFILITLLFGYSSYSLLQAKAETQNDPNISELNKSSQYTGSWHNIWYLYNSDPVNAK	60
z_1	MRKVFILITLLFGYSSYSLLQAKAETQNDPNISELNKSSQYTGSWHNIWYLYNSDPVNAK	60
z_2	MRKVFILITLLFGYSSYSLLQAKAETQNDPNISELNKSSQYTGSWHNIWYLYNSDPVNAK ***:*****:*****	60
z_5	KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASSFDGKEVDIFGVNYFDQCYFSNE	120
z_3	KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASSFDGKEVDIFGVNYFDQCYFSNE	120
z_1	KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASSFDGKEVDIFGVNYFDQCYFSNE	120
z_2	KIKLSDKFLSHDFIVPINNPGHYDYVKTELKDSTMASSFDGKEVDIFGVNYFDQCYFSNE *****.*****	120
z_5	NIQCDSNQGAGSKKTCMYGGITLNNNTNNRIQPIVVKVYENDSVTLSDINIDKETVTI	180
z_3	NIQCDSNQGAGSKKTCMYGGITLNNNTNNRIQPIVVKVYENDSVTLSDINIDKETVTI	180
z_1	NIQCDSNQGAGSKKTCMYGGITLNNNTNNRIQPIVVKVYENDSVTLSDINIDKETVTI	180
z_2	NIQCDSNQGAGSKKTCMYGGITLNNNTNNRIQPIVVKVYENDSVTLSDINIDKETVTI *****.*****	180
z_5	QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYYWYDMMPDPGFTQSKYLMYIR	240
z_3	QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYYWYDMMPDPGFTQSKYLMYIR	240
z_1	QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYYWYDMMPDPGFTQSKYLMYIR	240
z_2	QELDYKVRNKLISKINLYHLGGTSYETGYIKFIENGNRYYWYDMMPDPGFTQSKYLMYIR *****	240

z_5	GNETVESAKTEIEVHLTKK	259
z_3	GNETVESAKTEIEVHLTKK	259
z_1	GNETVESAKTEIEVHLTKK	259
z_2	GNETVESAKTEIEVHLTKK	259

TSST1

TSST1_6	MNKKLLMNFFIVSPLLLATIATDFTVPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDTF	60
TSST1_1	MNKKLLMNFFIVSPLLLATIATDFTVPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDTF	60
TSST1_3	MNKKLLMNFFIVSPLLLATIATDFTVPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDTF	60
TSST1_5	MNKKLLMKFFIVSPLLLATIATGFTVPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDAF	60
TSST1_2	MNKKLLMKFFIVSPLLLATIATGFTVPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDAF	60
TSST1_4	MNKKLLMKFFIVSPLLLATIATGFTVPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDAF	60
	*****:*****.***** ***** *****:*	
TSST1_6	TNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGGKVDLNTKRTKKSQHTSEGTY	120
TSST1_1	TNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRTKKSQHTSEGTY	120
TSST1_3	TNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRTKKSQHTSEGTY	120
TSST1_5	TNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPFTFSKGEKVDLNTKRTKKSQHTSEGTW	120
TSST1_2	TNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPFTFSKGEKVDLNTKRIKKSQHTSEGTW	120
TSST1_4	TNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPFTFSKGEKVDLNTKRIKKSQHTSEGTW	120
	*****:*****:*** ***** *****:	
TSST1_6	IHFQISGVTNTEKLPTPIELPLKVKVHGKDSPLKYWPKFDDKKQLAISTLDFEIRHQLTQI	180
TSST1_1	IHFQISGVTNTEKLPTPIELPLKVKVHGKDSPLKYWPKFDDKKQLAISTLDFEIRHQLTQI	180
TSST1_3	IHFQISGVTNTEKLPTPIELPLKVKVHGKDSPLKYWPKFDDKKQLAISTLDFEIRHQLTQI	180
TSST1_5	IHFQISGVTNTEKLPTPIELPLKVKVHGKDSPLKYWPKFDDKKQLAISTLDFEIRHQLTQI	180
TSST1_2	IHFQISGVTNTEKLPTPIELPLKVKVHGKDSPLKYWPKFDDKKQLAISTLDFKIRHQLTQT	180
TSST1_4	IHFQISGVTNTEKLPTPIELPLKVKVHGKNSPLKYWPKFDDKKQLAISTLDFKIRHQLTQT	180
	*****:*****:*****	
TSST1_6	HGLYRSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN	234
TSST1_1	HGLYRSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN	234
TSST1_3	HGLYRSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN	234
TSST1_5	HGLYRSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN	234
TSST1_2	HGLYRSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN	234
TSST1_4	HGLYRSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN	234
