

S-1

Title: Multiplex detection of protein toxins using MALDI-TOF-TOF tandem mass spectrometry: Application in unambiguous toxin detection from bio-aerosol

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Supplementary Data

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Supplementary figure S1: Annotated MS and MS/MS spectra for three toxins; epsilon toxin (ETX), staphylococcus enterotoxin B (SEB), and alpha toxin (PLC).

Supplementary figure S2: ClustalW alignment showing prevalence of precursor peptides, selected for inclusion list, among known sequences of category A and category B protein toxins [epsilon toxin (ETX); staphylococcus enterotoxin B (SEB); and alpha toxin (PLC)]

METHODS

In-gel Digestion. Gel pieces were destained at room temperature with 200 μ L of destaining solution (ACN/50 mM NH_4HCO_3 in H_2O 50:50 v/v) for 1 h. Gel pieces were dried and 100 ng trypsin (Promega, USA) in 50mM NH_4HCO_3 was added to the gel piece. Tryptic digestion was carried out overnight at 37°C. Peptides were extracted with 60% acetonitrile and 0.1% trifluoroacetic acid (TFA), vacuum dried, and resuspended in 0.5% TFA before MS analysis.

In-sol Digestion. In-sol tryptic digestion was carried out in a total reaction volume of 30 μ L. Protein samples were reduced with 1.5 μ L of 100 mM dithiothreitol by heating at 60°C for 15 min. After cooling to room temperature, 3 μ L of 100 mM iodoacetamide was added and then incubated in the dark at room temperature for 15 min. Enzymatic digestions were performed at 37°C for 3 h after the addition of either 100 ng trypsin and the reaction was stopped with 3 μ L of TFA at a final concentration of 0.5%. Digests were stored at –20°C until further use.

MALDI-TOF-TOF Analysis of Tryptic Protein Digests.

Digested proteins were analysed by Applied Biosystem 4800 plus MALDI TOF/TOF Analyzer (AB Sciex, USA). The digested peptides were mixed with equal volume of the CHCA matrix solution (10 mg/ml) and spotted onto the target plate. A default calibration was applied using a six component peptide standards in a mass range of 905-3660 Da, spotted onto 13 calibration points on 384-well MALDI plate. MS mass spectra were recorded in the reflector positive mode using a laser operated at a 200 Hz repetition rate with a wavelength of 355 nm. The accelerated voltage was operated at 2 kV. The MS/MS mass spectra were acquired by the data dependent acquisition method and for a routine identification and generation of reference spectra, 20 strongest precursors were selected between 850 and 4000 Da and filtered with a signal-to-noise ratio greater than 20 from one MS scan. Fragmentation of precursor ion selected by timed ion

selector (TIS) was carried out by collision induced dissociation (CID) using air as collision gas at 1 kV energy and a recharge pressure threshold of 1.5×10^{-6} .

All MS and MS/MS spectra were obtained by accumulation of at least 1200 and 1600 laser shots, respectively. MS and MS/MS data were analyzed and peak list were generated using the 4000 Series Explorer Software v. 3.5 (Applied Biosystem, USA). A peak intensity filter was used with no more than 50 peaks per 200 Da in the setting parameter of MASCOT search after acquisition. MS/MS peaks were selected based on a signal-to-noise ratio greater than 10 over a mass range of 60–20 Da below the precursor mass. MS and MS/MS data were analyzed using Protein Pilot version 4.0 (Applied Biosystem) employing the MASCOT 2.0 search engine (Matrix Science, London, UK). The peak list was searched against all entries with 16338050 sequences at non-redundant protein sequence database of ncbi. Search parameters were as follows: trypsin digestion with one missed cleavage, variable modifications (oxidation of methionine and carbamidomethylation of cysteine), and the peptide mass tolerance of 50 ppm for precursor ion and mass tolerance of ± 0.6 Da for fragment ion with +1 charge state. For all proteins successfully identified by MS/MS, MASCOT score greater than 62 was accepted as significant (p -value < 0.05).

Supplementary Table S1: Unique peptides from tryptic digest of seven different protein toxins used for generation of inclusion list for directed search from unknown samples.

Toxin	Peptide sequence ^a	Position	m/z _{obsrvd}	MS or MS/MS	Unique peptide	Conserved ^b
ETX	ASYDNVDTLIEKGR**	47-56	1580.789	MS/MS	Y	17/17
	ASYDNVDTLIEK**	47-58	1367.716	-do-	Y	17/17
	YNTKYNYLK**	61-69	1206.599	-do-	Y	17/17
	YYPNAMAYFDK**	74-84	1382.656	-do-	Y	17/17
	YYPNAMAYFDK (M)**	74-84	1398.653	-do-	Y	17/17
	YYPNAMAYFDKVTINPQGNDFYINNPK**	74-100	3197.690	-do-	Y	17/17
	VTINPQGNDFYINNPK*	85-100	1833.998	-do-	Y	16/17
	VELDGEPSMNYLEDVYVGK**	101-119	2157.110	-do-	Y	17/17
	NTDTVTATTTHTVGTISIATAK**	141-162	2219.220	-do-	Y	17/17
	FTVPFNETGVSLTTSYSFANTNTNTNSK**	163-190	3042.596	-do-	Y	17/17
	EITHNVPSQDILVPANTTVEVIAYLK*	191-216	2864.606	-do-	Y	16/17
	LVGQVSGSEWGEIPSYLAFPR**	226-246	2292.276	-do-	Y	17/17
	FSLSDTVNKSDLNEDGTININGK*	251-273	2481.229	-do-	Y	16/17
	GNYSAVMGDELIVK**	274-287	1495.804	-do-	Y	17/17
	NLNTNNVQEYVIPVDK**	290-305	1860.033	-do-	Y	17/17
	NLNTNNVQEYVIPVDKK**	290-304	1988.139	-do-	Y	17/17
	SNDSNIVKYR**	309-318	1195.597	-do-	Y	17/17
	SLSIKAPGIK*	319-328	1013.619	-do-	Y	13/17
SEB	FTGLMENMK**	16 - 24	1070.548	MS/MS	Y	28/28
	VLYDDNHVSAINVK**	25 - 38	1586.910	-do-	Y	28/28
	SIDQFLYFDLIYSIK**	39 - 53	1865.077	-do-	Y	28/28
	SIDQFLYFDLIYSIKDTK**	39 - 56	2209.282	-do-	Y	28/28
	LGNYDNVR**	57 - 64	950.508	-do-	Y	28/28
	DKYVDVFGANYYYQCYFSK*	78 - 96	2430.240	-do-	Y	22/28
	YVDVFGANYYYQCYFSK*	80 - 96	2187.095	-do-	Y	22/28
	TCMYGGVTEHNGNQLDKYR*	111 - 129	2243.137	-do-	Y	20/28
	VFEDGKNLLSFDVQTNK**	135 - 151	1954.118	-do-	Y	28/28
	NLLSFDVQTNK**	141 - 151	1278.739	-do-	Y	28/28
	KVTAQELDYLTR**	153 - 164	1436.859	-do-	Y	28/28
	VTAQELDYLTR**	154 - 164	1308.755	-do-	Y	28/28
	KLYEFNNSPYETGYIK**	172 - 187	1966.082	-do-	Y	28/28
	LYEFNNSPYETGYIK**	173 - 187	1837.974	-do-	Y	28/28
	FIENENSFWDMMMPAPGDK	188 - 206	2291.133	-do-	Y	17/28

	FIENENSFWDMMMPAPGDKFDQSK	188 - 211	2896.464	-do-	Y	17/28
	FIENENSFWDMMMPAPGDKFDQSK (M)	188 - 211	2912.480	-do-	Y	17/28
	YLMMYNDNK**	212 - 220	1191.575	-do-	Y	28/28
PLC	DNSWYLAYSIPDTGESQIR**	109-127	2215.153	MS/MS	Y	78/78
	QATFYLGEAMHYFGDIDTPYHPANVTAVDSAGHVK*	144-178	3823.148	-do-	Y	74/78
	FETFAEER*	179-186	1028.513	-do-	Y	76/78
	SIYYSHASMSHSWDDWDYAAK*	230-250	2520.157	-do-	Y	73/78
	GTAGYIYR**	259-266	900.495	-do-	Y	78/78
	IDDIQNMWIR*	346-355	1303.712	-do-	Y	76/78

^a Peptides with one star are sequences conserved among >75% of the total number of sequences of a given type used for alignment.

Peptides with two stars are sequences conserved among all the sequences of a given type used for alignment.

^b Number of toxin sequences in which the given peptide is conserved (numerator) out of the total sequences of a given type used for aligned (denominator).

Supplementary Table S2: Unique peptides from different toxins after tryptic digestion based on global BLAST search at ncbi.nlm.nih.gov.

Toxin	Peptide sequence	Closest match	% identity	Seq. Cov. ^a	E-value	Unique
ETX	K.ASYDNVDTLIEK.G	Hypothetical protein, Thermovibrio ammonificans, gb ADU97379.1	80%	83%	1.1	Y
	K.YYPNAMAYFDK.V	Hypothetical protein, Bacillus cereus, gb EEK53323.1	82%	81%	0.64	Y
	K.YYPNAMAYFDK.V (M)	Hypothetical protein, Bacillus cereus, gb EEK53323.1	82%	81%	0.64	Y
	K.GNYSAVMGDELIVK.V	Amidotransferase HisH, Brevibacterium linens, ref ZP_05915542.1	58%	85%	4.6	Y
	K.VTINPQGNDFYINNP.K	Hypothetical protein, Tetrahymena thermophila, gb EAR95052.1	83%	75%	0.28	Y
	R.NLNTNNVQEYVIPVDK.K	tRNA pseudouridine synthase B, Clostridium botulinum C, gb EGO87817.1	53%	93%	1.1	Y
	R.NLNTNNVQEYVIPVDKK.E	Hypothetical protein, Caenorhabditis brenneri, gb EGT38343.1	75%	70%	0.94	Y
	K.VELDGEPSMNYLEDVYVGK.A	Hypothetical protein, Magnetococcus sp., gb ABK45445.1	63%	78%	0.33	Y
	K.NTDTVTATTTHTVGTSIQATAK.F	Hypothetical protein, Chaetomium thermophilum var., gb EGS23090.1	71%	90%	0.72	Y
	K.LVGQVSGSEWGEIPSYLAFPR.D	Binding-protein-dependent transport systems, I. pallida, gb ADV61231.1	83%	57%	1.2	Y
	K.FTVPFNETGVSLTTSYSFANTNTNTNSK.E	Hypothetical protein, Paenibacillus larvae subsp., gb EFX46729.1	52%	75%	0.76	Y
	K.SNDSNIVKYR.S	Conserved hypothetical protein, Bacteroides sp., gb EEZ27961.1	89%	90%	2.1	Y
	R.YNTKYNYLK.R	Conserved hypothetical protein, Enterococcus faecalis, gb EFU05370.1	88%	88%	9.8	Y
	R.SLSIKAPGIK.-	Hypothetical protein, Methylosinus trichosporium, gb EFH04309.1	89%	90%	35	Y
	K.ASYDNVDTLIEKGR.Y	Hypothetical protein, Thermovibrio ammonificans, gb ADU97379.1	80%	71%	1.6	Y
	K.YNYLKR.M	Hypothetical protein, Dictyostelium discoideum, gb EAL64711.1	100%	100%	79	N
	K.FSLSDTVNKSDDLNEGTININGK.G	Leucine-rich repeat-containing protein, Fluviicola taffensis, gb AEA44745.1	56%	82%	0.15	Y

	K.EITHNVPSQDILVPANTTVEVIAYLK.K	Hypothetical protein, Clostridium botulinum, ref YP_002650769.1	61%	69%	0.22	Y
	K.YYPNAMAYFDKVTINPQGNDIFYINNP.K.V	Hypothetical protein, Trichomonas vaginalis, gb EAX92806.1	50%	81%	0.23	Y
SEB	LGNYDNVR	Putative RNA-processing protein, C. maquilensis, ref YP_001540802.1	100%	87%	23	Y
	NLLSFDVQTNK	Nonribosomal peptide synthase, Aspergillus fumigatus, gb EDP56272.1	89%	81%	5.2	Y
	LYEFNNSPYETGYIK	Chain A, Streptococcal Superantigen (Ssa) From Streptococcus Pyogenes >pdb 1BXT	100	100 %	1e-07	Y
	NVTVQELDLQAR (A)	Enterotoxin A [Staphylococcus caprae] >gb ABG66464.1	100	100	0.002	Y
	YNLYNSDVFDGK (A)	Enterotoxin A [Staphylococcus caprae] >gb ABG66458.1	100	100	3e-04	Y
	K.FTGLMENMK.V	Enterotoxin sec variant [Staphylococcus aureus] gb AAP37184.1	100	100	0.18	Y
	K.VLYDDNHVSAINVK.S	Enterotoxin SEU, Staphylococcus aureus subsp. Aureus, >gb EFB55455.1	77	92	0.11	Y
	K.SIDQFLYFDLIYSIK.D	Hypothetical protein, Plasmodium chabaudi chabaudi, >emb CAH84993.1	69	86	1.4	Y
	K.SIDQFLYFDLIYSIKDTK.L	ABC transporter, putative [Plasmodium falciparum 3D7] >emb CAD51237.1	63	83	0.45	Y
	K.LGNYDNVR.V	KH type 1 domain protein, C. maquilensis, ref YP_001540802.1	100	87	69	Y
	K.DKYVDVFGANYYYQCYFSK.K	Enterotoxin SEU, S aureus subsp. aureus WBG10049] >gb EFB55455.1	68	94	8e-07	Y
	K.YVDVFGANYYYQCYFSK.K	Enterotoxin SEU, S aureus subsp. aureus WBG10049] >gb EFB55455.1	80	88	3e-05	Y
	K.TCMYGGVTEHNGNQLDKYR.S	Enterotoxin SEU, S aureus subsp. aureus WBG10049] >gb EFB55455.1	88	89	2e-07	Y
	R.VFEDGKNLLSFDVQTNK.K	Enterotoxin SEU, S aureus subsp. aureus WBG10049] >gb EFB55455.1	65	100	0.29	Y
	K.NLLSFDVQTNK.K	Nonribosomal peptide synthase, Aspergillus fumigatus A1163] gb EDP56272.1	89	781	15	Y
	K.KVTAQELDYLTR.H	ZYRO0B08998p [Zygosaccharomyces rouxii] >emb CAR26409.1	90	83	1.8	Y
	K.VTAQELDYLTR.H	ZYRO0B08998p [Zygosaccharomyces rouxii] >emb CAR26409.1	90	90	1.7	Y
	K.KLYEFNNSPYETGYIK.F	Chain A, Streptococcal Superantigen (Ssa)	100	93	1e-07	Y

	K.LYEFNNSPYETGYIK.F	From Streptococcus Pyogenes pdb 1BXT A Chain A, Streptococcal Superantigen (Ssa)	100	100	1e-07	N
	K.FIENENSFWYDMMPAPGDK.F	From Streptococcus Pyogenes >pdb 1BXT Type C enterotoxin, partial [Staphylococcus intermedius] gb AAB50248.1	85	100	4e-10	Y
	K.FIENENSFWYDMMPAPGDKFDQSK.Y	Type C enterotoxin, partial [Staphylococcus intermedius] gb AAB50248.1	88	100	3e-15	Y
	K.FIENENSFWYDMMPAPGDKFDQSK.Y	Type C enterotoxin, partial [Staphylococcus intermedius] gb AAB50248.1	88	100	3e-15	Y
	K.YLMMYNDNK.M	Enterotoxin sec variant [Staphylococcus aureus]	100	100	0.023	Y
PLC	K.DNSWYLAYSIPDTGESQIR.K	Glycogen operon protein, Lyngbya sp., gb EAW39224.1	65%	78%	0.93	Y
	K.QATFYLGAMHYFGDIDTPYHPANVTAVDSAGHVK.F	Phosphatidylcholine-specific phospholipase C, Bacillus mycoides, gb ACX71492.1	54%	80%	0.006	Y
	K.FETFAEER.K	DNA polymerase, Glomerella graminicola, gb EFQ33299.1	88%	100%	4723	Y
	K.GTAGYIYR.F	Methyltransferase, Selenomonas sp. oral taxon, gb EFM24268.1	88%	100%	22	Y
	K.IDDIQNMWIR.K	Cell surface protein A, Rhodococcus erythropolis, gb EEN89176.1	88%	80%	0.74	Y
	K.SIYYSHASMSHSWDDWDYAAK.V	Phospholipase C precursor, Clostridium sardiniense, dbj BAD15292.1	83%	85%	1e-09	Y

^aSeq. Cov. = sequence coverage

Supplementary table S3: Optimization of in-sol digestion for MS-based detection of toxins using ETX protein.

Sample	MOWSE score	Sequence Coverage	Peptides (MS/MS ion score)												RMS error
			E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	
Pellet resuspended in TFE															
5000 ng	1222	63	71	82	125	144	42	179	103	179	46	83	155	116	46
1250 ng	1214	63	76	79	127	126	28	164	95	167	65	73	81	135	39
300 ng	899	55	33	66	129	111	23	113	-	162	31	40	69	125	32
150 ng	275	25	-	22	93	33	-	-	-	61	-	-	-	67	29
75 ng	176	22	-	-	79	15	-	-	-	38	-	-	-	44	26
38 ng	ND	ND	-	-	-	-	-	-	-	-	-	-	-	-	-
Pellet resuspended in NH ₄ HCO ₃															
5000 ng	1150	63	42	72	132	106	15	199	69	177	85	41	49	127	27
1250 ng	1097	55	60	79	125	120	34	117	-	187	100	76	75	125	17
300 ng	868	63	21	76	111	115	32	82	9	140	51	35	77	119	16
150 ng	445	32	-	38	129	50	-	-	-	74	24	-	49	82	14
75 ng	118	11	-	-	95	-	-	-	-	23	-	-	-	-	9
38 ng	65	11	-	-	39	-	-	-	-	26	-	-	-	-	10

Supplementary table S4: Directed search of ETX from samples of increasing complexity.

Sample	MOWSE score	Sequence Coverage	Peptides (MS/MS ion score)												RMS error
			E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	
ETX															
1000 ng	1213	48	83	95	126	125	58	149	-	161	-	105	142	129	44
500 ng	997	42	62	81	142	132	-	84	-	159	-	87	124	127	47
125 ng	448	27	19	66	129	62	-	-	-	-	-	39	45	88	50
31 ng	106	13	-	36	55	-	-	-	-	-	-	-	-	15	44
ETX + Mix 1 (1:1)															
1000 ng	1202	56	104	72	139	170	48	131	16	181	-	110	108	123	32
500 ng	783	48	60	71	139	123	23	12	-	46	-	76	110	125	32
125 ng	243	19	-	26	101	10	-	-	-	-	-	-	51	56	38
31 ng	ND	ND	-	-	-	-	-	-	-	-	-	-	-	-	-
ETX + Mix 2 (1:1)															
1000 ng	911	42	61	72	151	147	-	77	-	133	-	48	90	134	32
500 ng	639	33	56	75	136	60	-	-	-	14	-	45	111	142	24
125 ng	226	19	-	36	66	27	-	-	-	-	-	-	37	60	32
31 ng	ND	ND	-	-	-	-	-	-	-	-	-	-	-	-	-
ETX + Mix 3 (1:1)															
1000 ng	844	48	63	73	151	120	21	39	-	71	-	68	111	129	18
500 ng	609	27	42	82	131	97	-	-	-	-	-	69	98	92	26
125 ng	199	13	-	44	83	-	-	-	-	-	-	-	17	54	21
31 ng	ND	ND	-	-	-	-	-	-	-	-	-	-	-	-	-

Mix 1 = cOTC; Mix 2 = cOTC+CBL ; Mix 3 = cOTC+CBL+ HP2918+ ABC

Supplementary table S5: Directed search of ETX from blind samples. Ten ml Tris buffer alone or spiked with ETX and or other proteins of varying complexity were subjected to enrichment and cleanup, and for detection of ETX using MS and MSMS analysis.

Sample	MOWSE score	Sequence Coverage	Peptides (MS/MS ion score)												RMS error
			E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	
S1	No hit	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S2	767	49	-	68	127	83	-	135	42	185	21	-	-	106	23
S3	615	34	-	61	128	63	-	45	-	186	-	-	-	133	18
S4	499	34	-	36	104	35	-	45	-	180	-	-	-	59	45
S5	No hit	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S6	648	34	-	59	135	67	-	67	-	178	-	-	74	68	52
S7	No hit	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S8	No hit	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S9	1114	63	49	59	125	77	67	203	78	170	59	35	56	114	55
S10	831	55	-	49	116	99	35	135	36	176	41	-	38	105	52

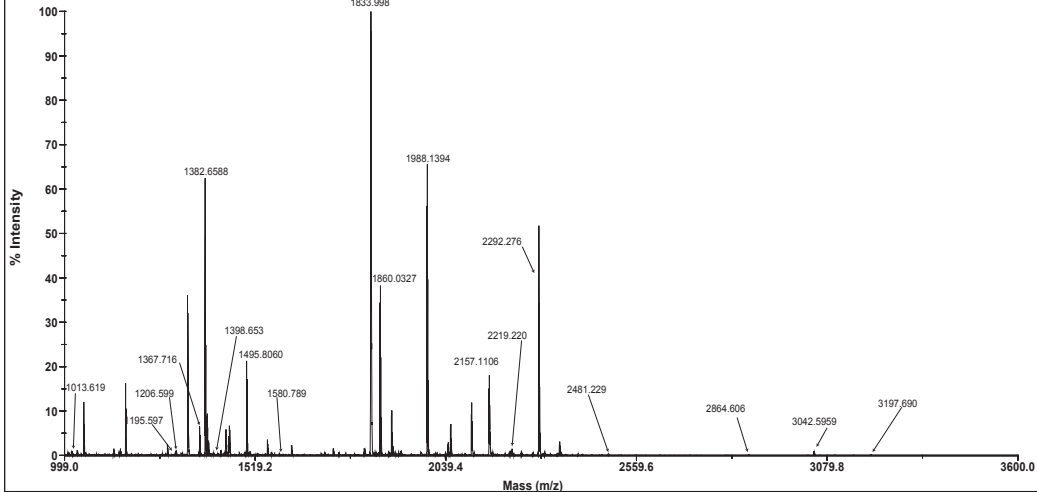
S1 = Tris buffer; **S2** = 2 µg ETX; **S3** = 1 µg ETX; **S4** = 1 µg ETX and 4 µg *E. coli* lysate; **S5** = 2 µg cOTC; **S6** = 1 µg ETX and 2 µg cOTC; **S7** = 4 µg *E. coli* lysate; **S8** = 4 µg LEC; **S9** = 2 µg ETX and 8 µg LEC; **S10** = 4 µg ETX, 10 µg *E. coli* lysate, 3 µg cOTC, and 8 µg LEC.

LEC = lysate of environmental microbial consortium.

Fig: S1 Below

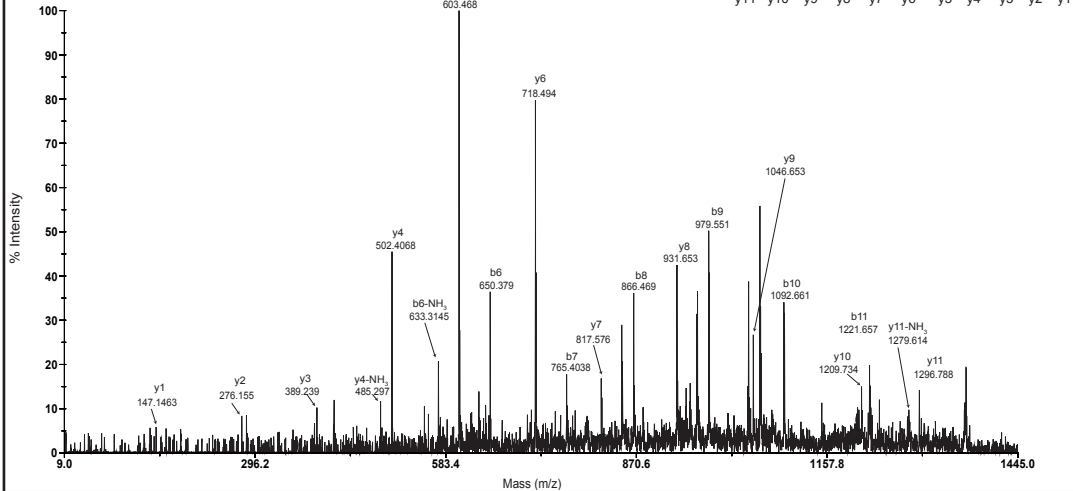
ETX MS

EPSILON TOXIN (ETX)



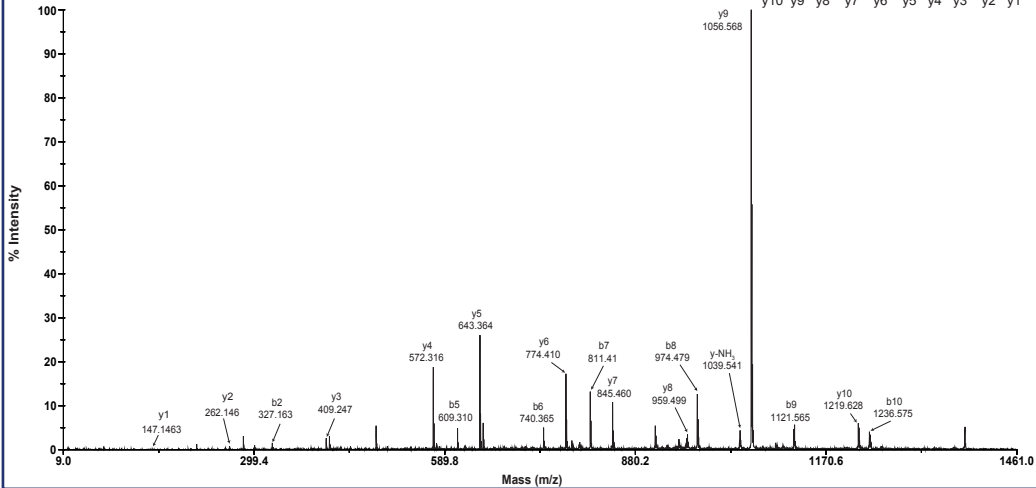
Precursor 1367.7

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y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1



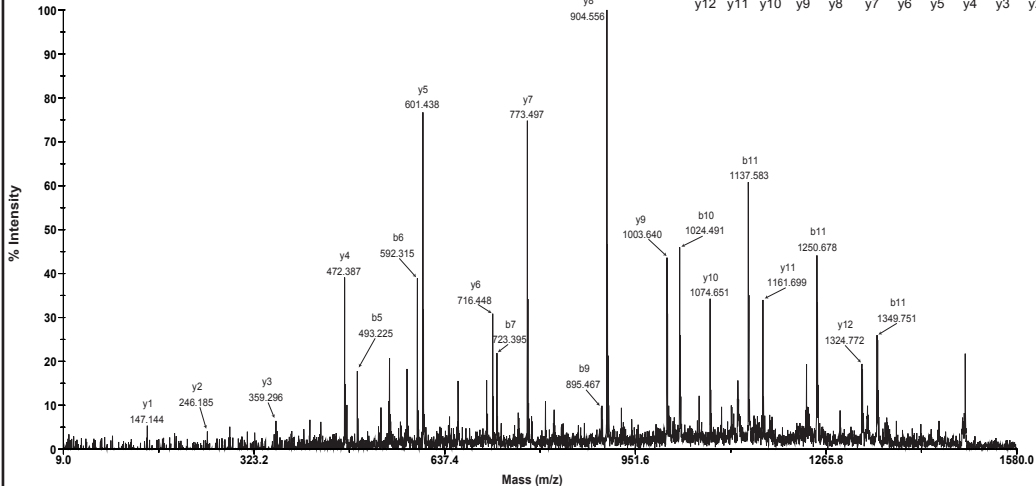
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y10 y9 y8 y7 y6 y5 y4 y3 y2 y1



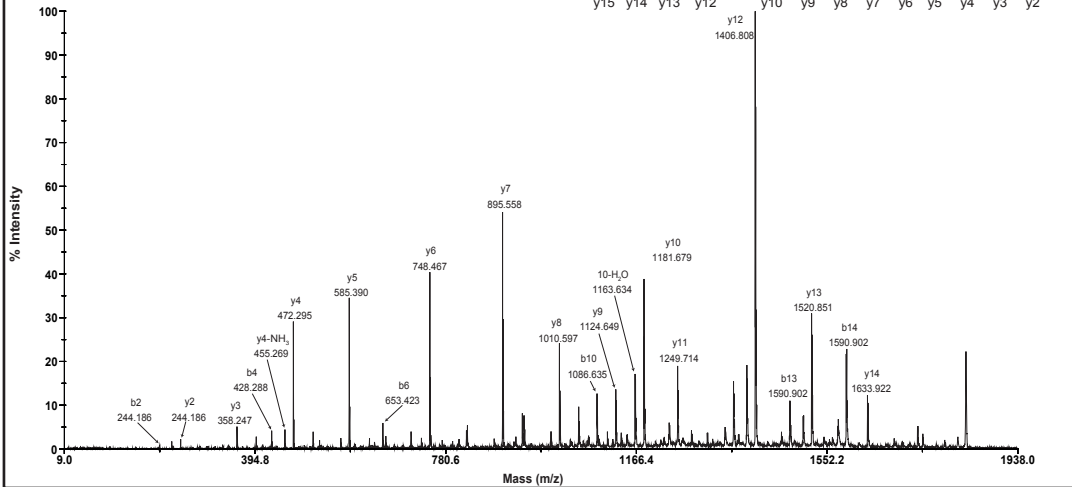
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y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1

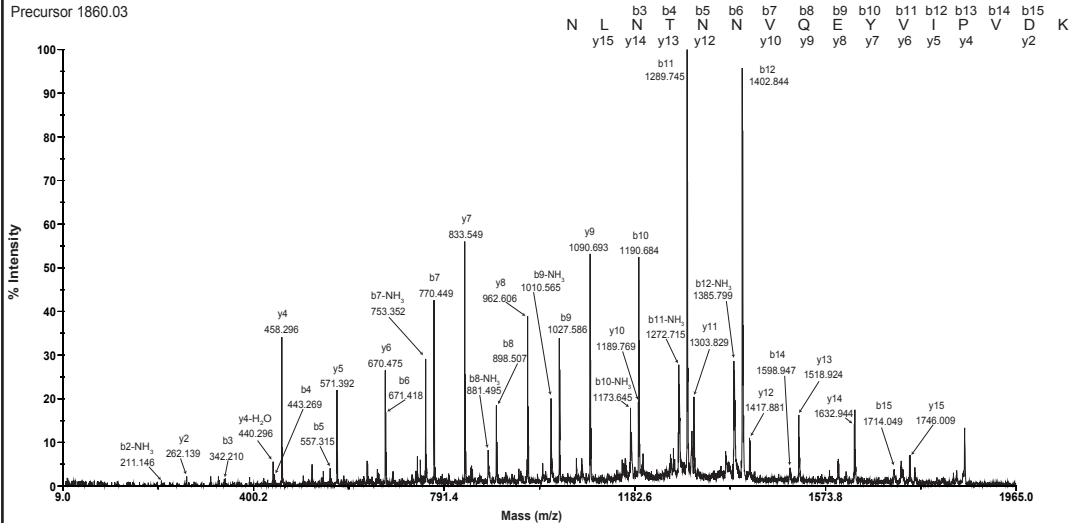


Precursor 1834

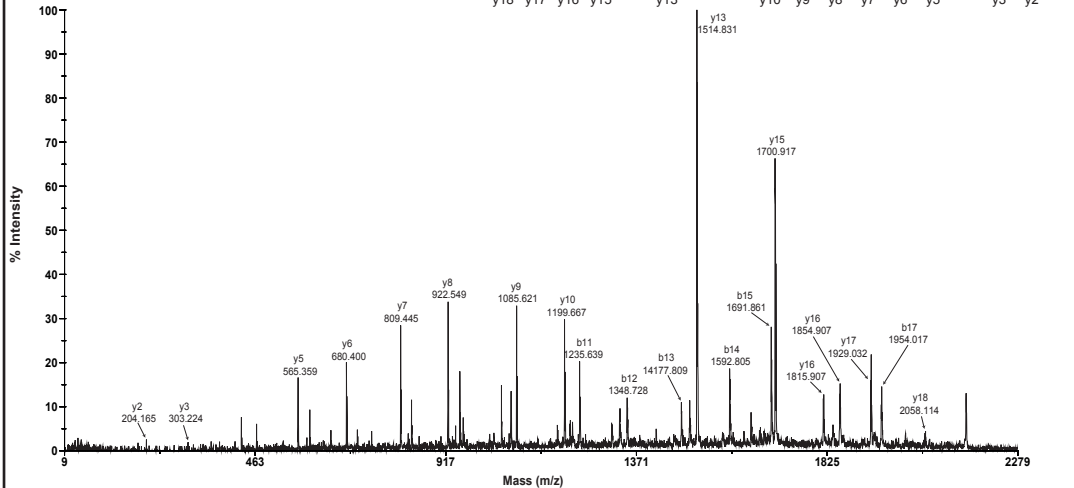
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y15 y14 y13 y12 y12 y10 y9 y8 y7 y6 y5 y4 y3 y2 K



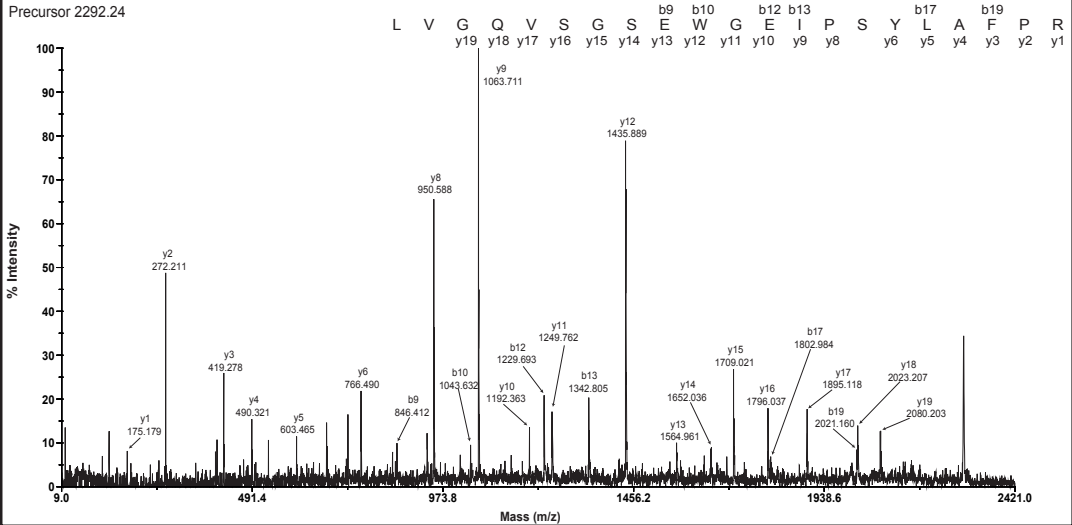
Precursor 1860.03



Precursor 2157.11

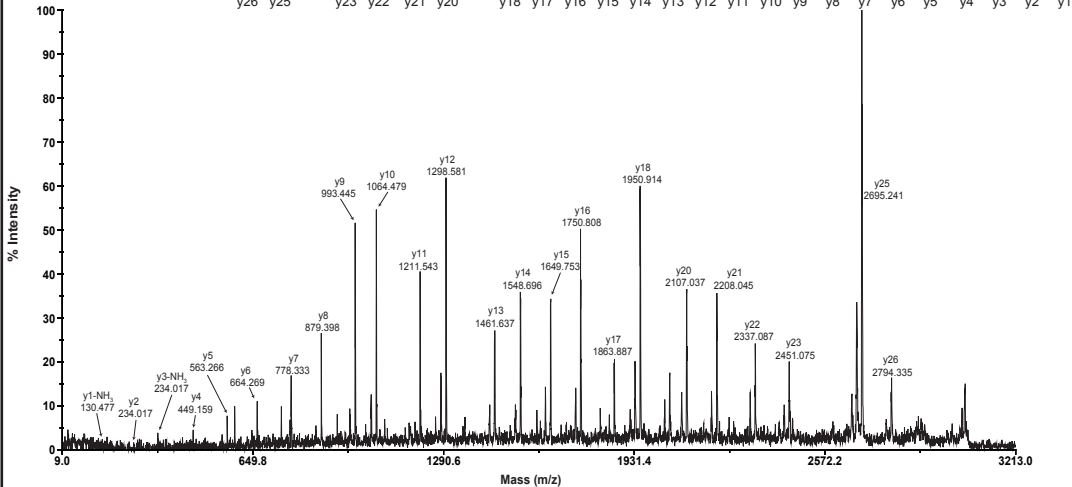


Precursor 2292.24



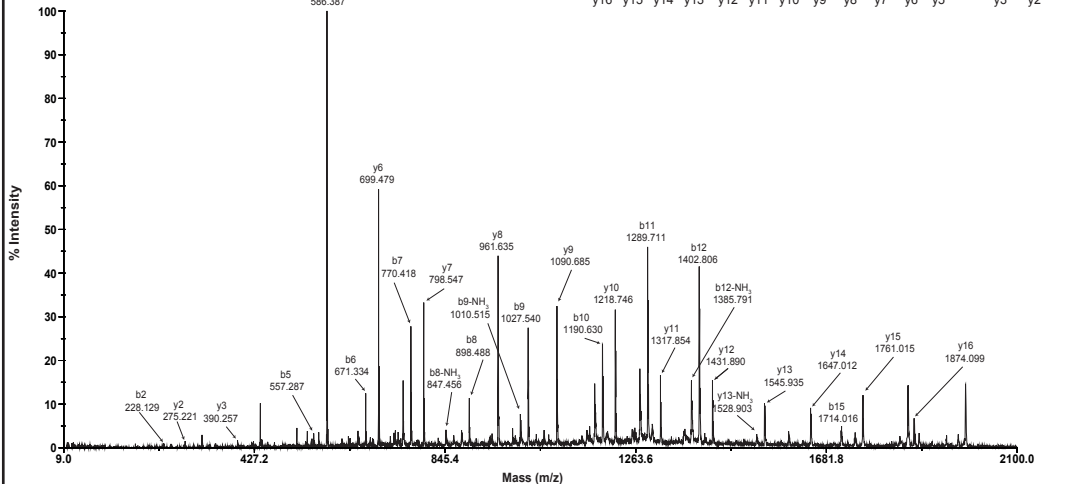
Precursor 3042.51

F T V P F N E T G V S L T T S Y S F A N T N T N T N S K
y26 y25 y23 y22 y21 y20 y18 y17 y16 y15 y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1



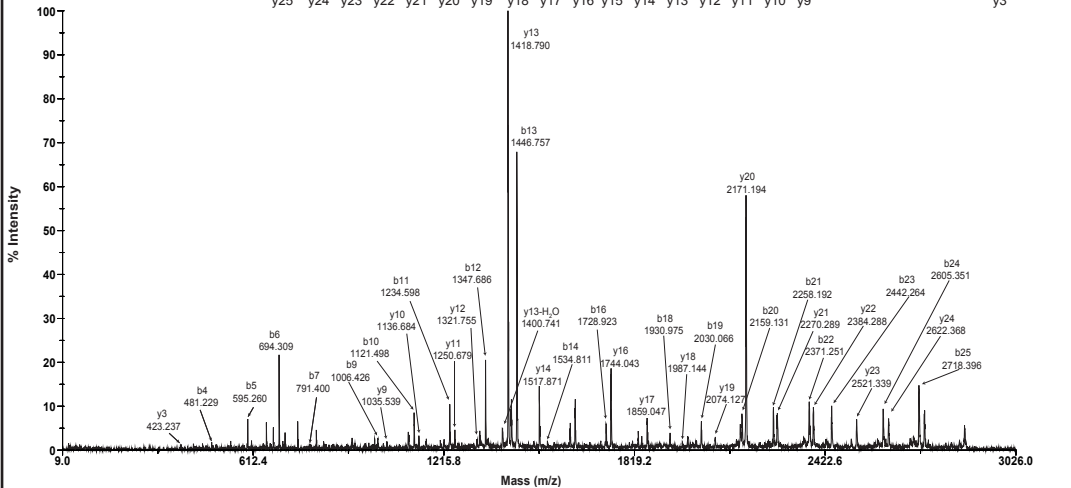
Precursor 1988.14

N L N T N N V Q E Y V I P V D K K
y16 y15 y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y3 y2



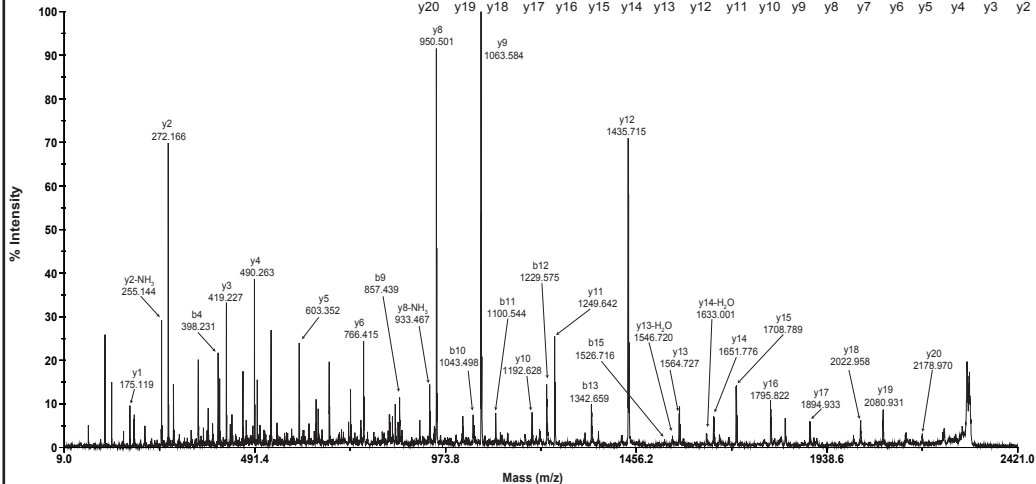
Precursor 2864.6

E I T H N V P S Q D I L V P A N T T V E V I A Y L K
y25 y24 y23 y22 y21 y20 y19 y18 y17 y16 y15 y14 y13 y12 y11 y10 y9 y3



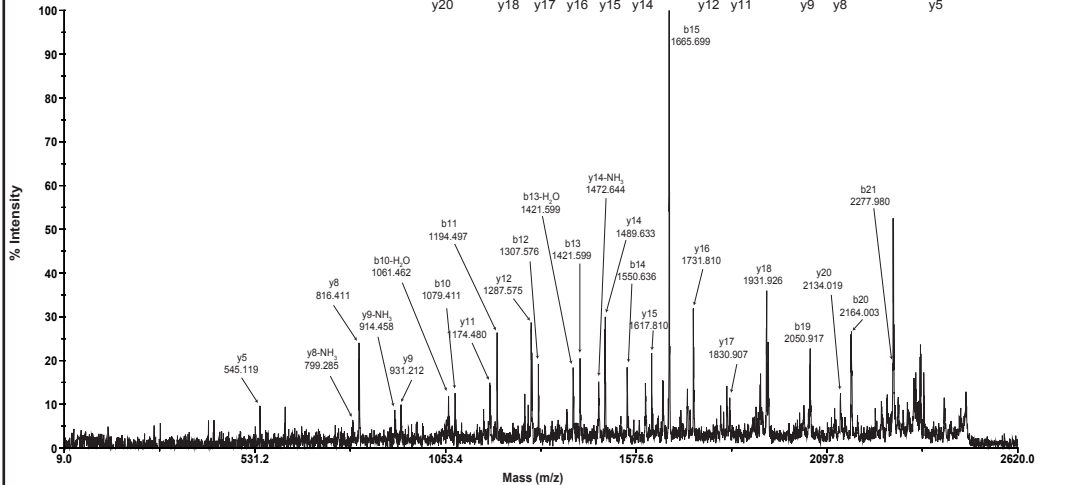
Precursor 2292.16

L V G Q V S G S b9 b10 b11 b12 b13 b15 Y L A b19 P R
y20 y19 y18 y17 y16 y15 y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1



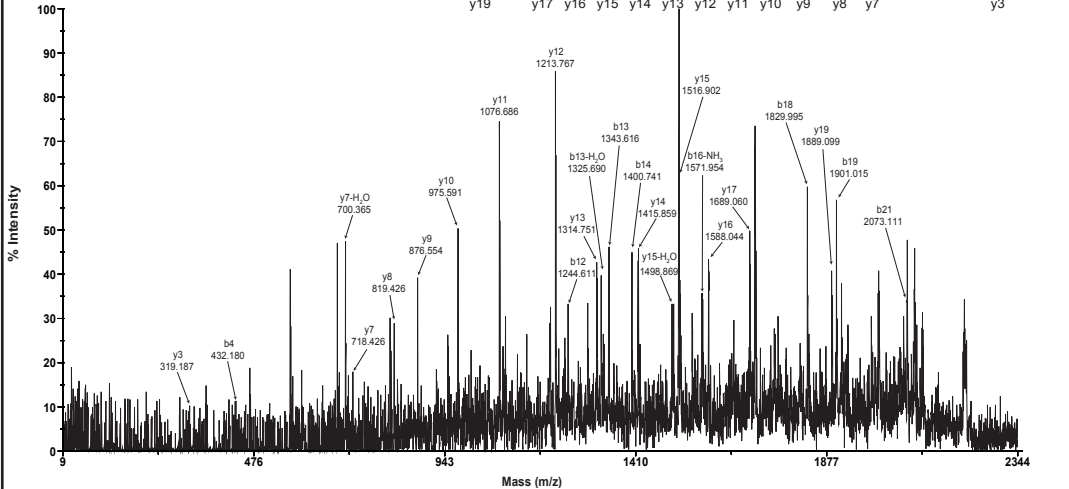
Precursor 2481.09

F S L S D T V N K b10 b11 b12 b13 b14 b15 b17 b18 b19 b20 b21
y20 y18 y17 y16 y15 y14 y12 y11 y9 y8 y5



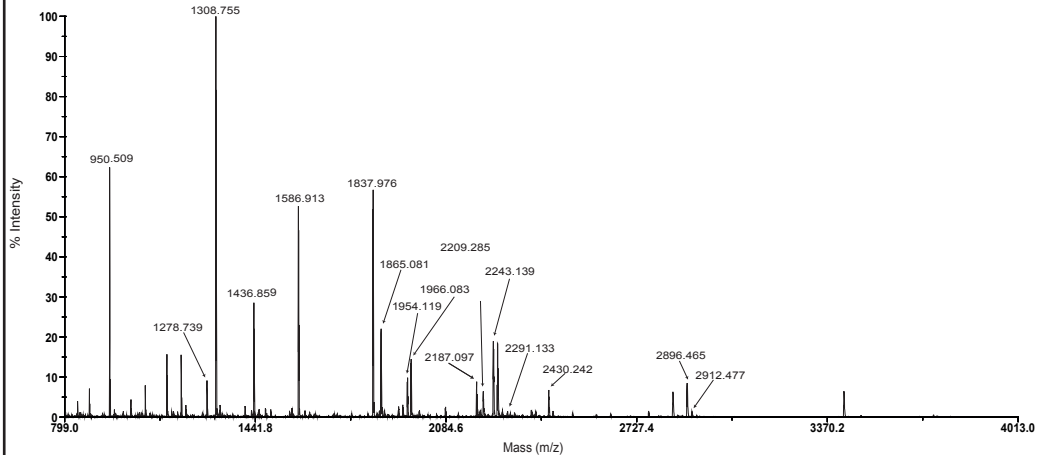
Precursor 2219.22

N T D b4 T V T b7 A T T T H T b12 T b13 V b14 G T b16 S I b18 Q b19 A T b21 A K
y19 y17 y16 y15 y14 y13 y12 y11 y10 y9 y8 y7 y3

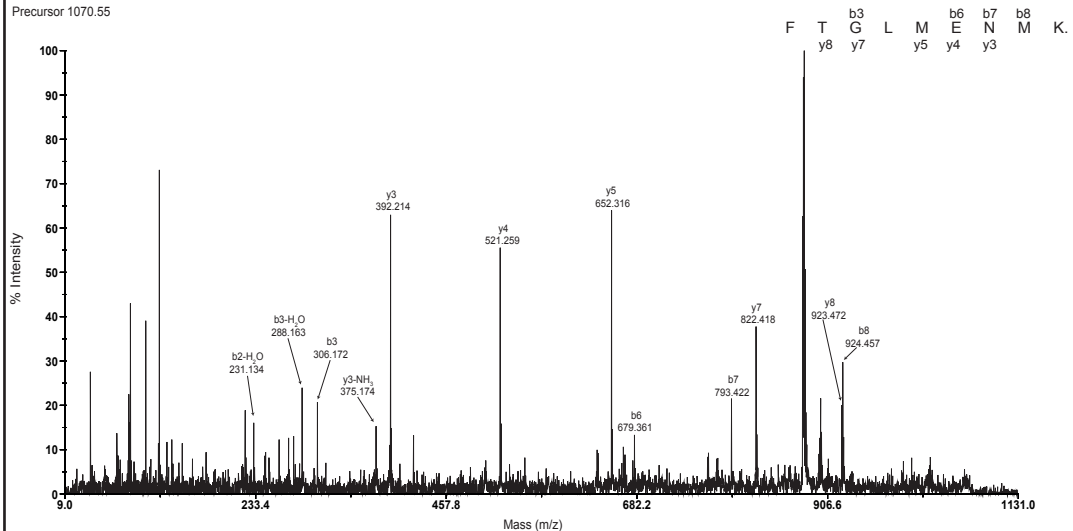


SEB MS

STAPH ENTEROTOXIN B (SEB)

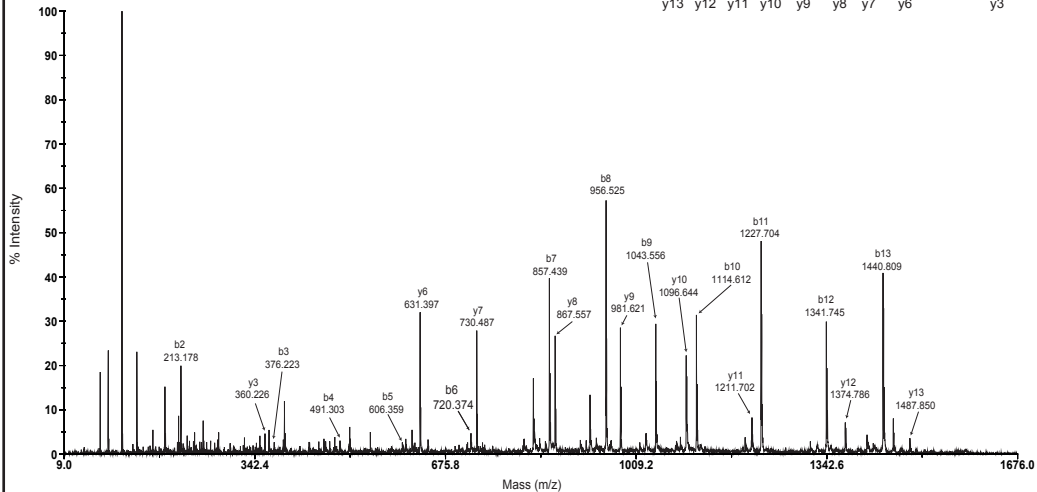


Precursor 1070.55



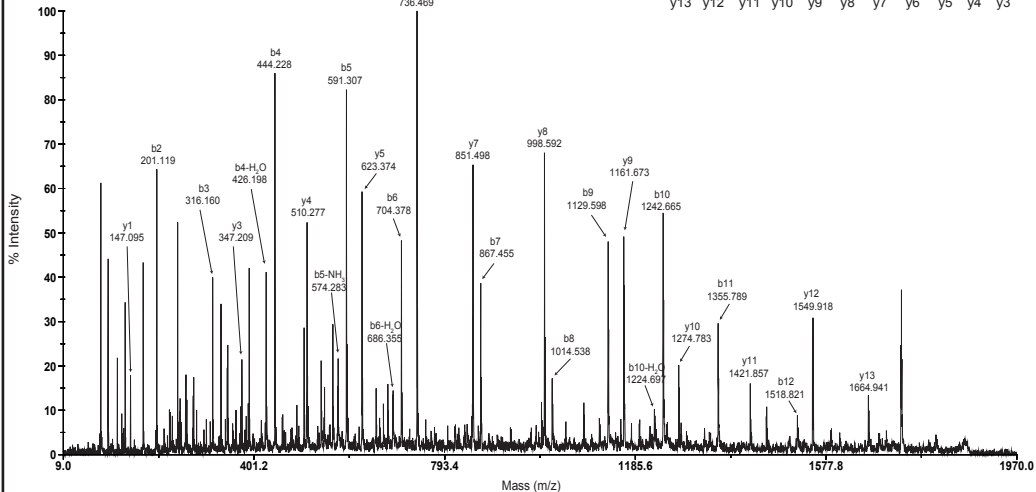
Precursor 1586.91

V	b2	b3	b4	b5	b6	b7	b8	b9	b10	b11	b12	b13	
	L	Y	D	D	N	H	V	S	A	I	N	V	K
	y13	y12	y11	y10	y9	y8	y7	y6			y3		



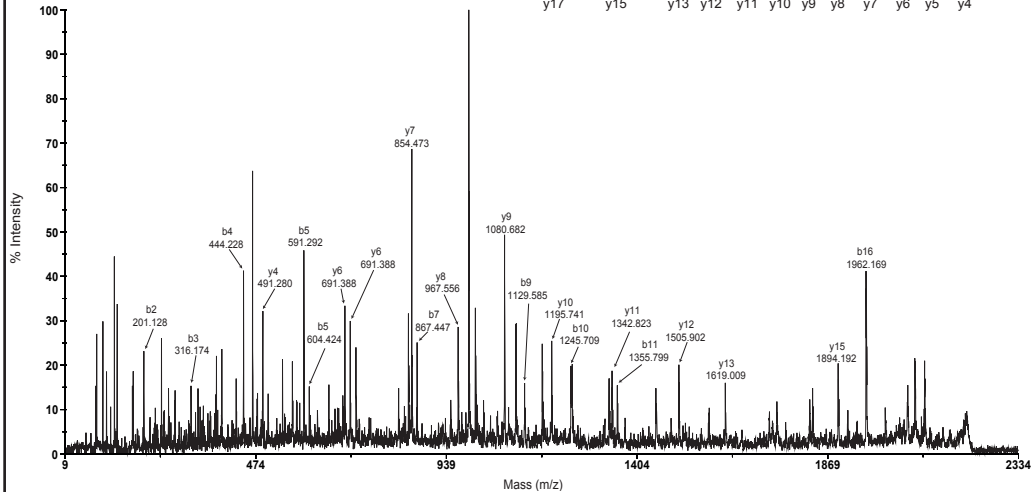
Precursor 1865.08

S I D Q F L Y F D L I Y S I K
y13 y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y1



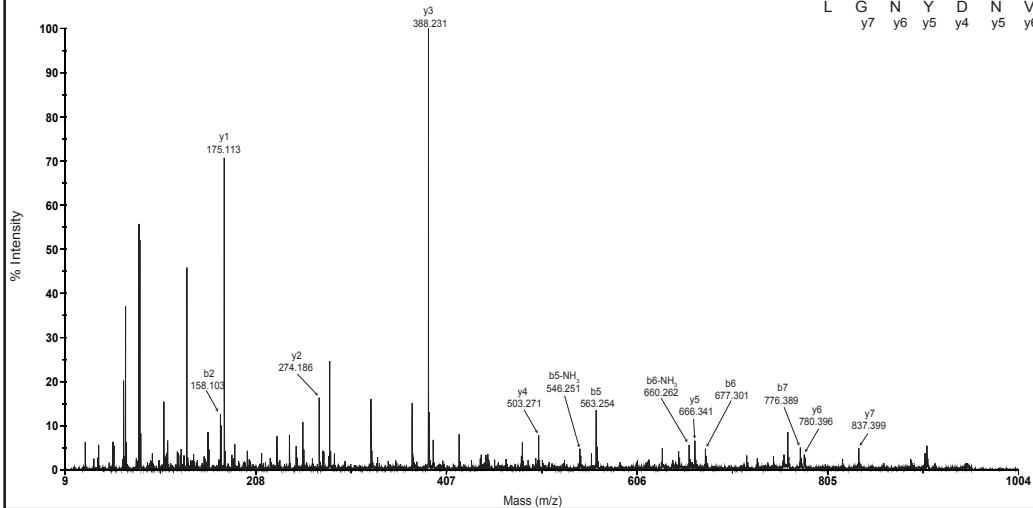
Precursor 2209.28

S I D Q F L Y F D L I Y S I K D T K
y17 y15 y13 y12 y11 y10 y9 y8 y6 y5 y4

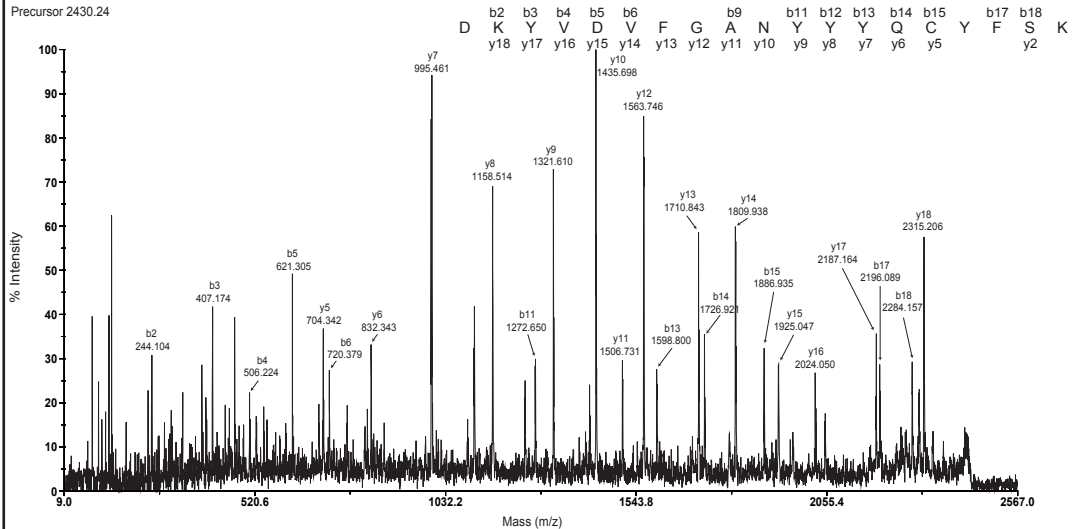


Precursor 950.509

L	b2	b3		b5	b6	b7	
	G	N	Y	D	N	V	R
	y7	y6	y5	y4	y5	y6	y7

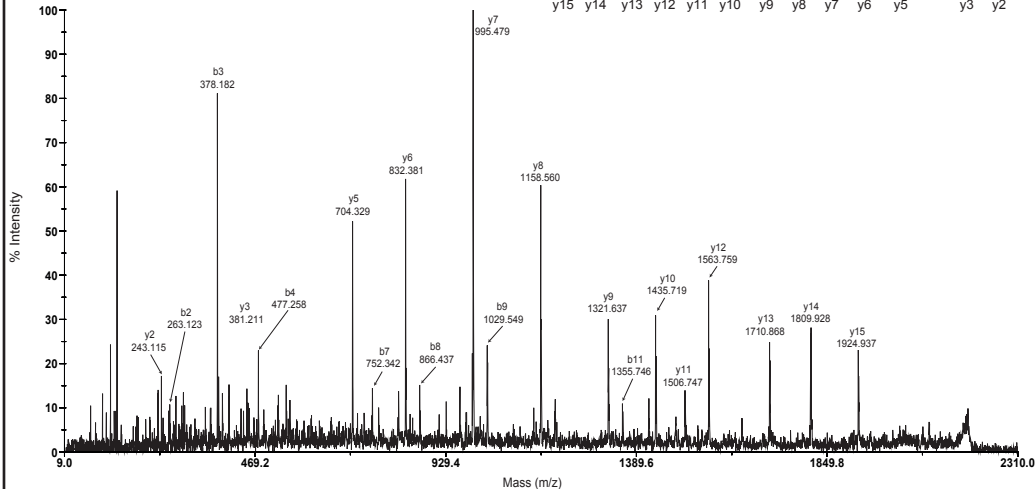


Precursor 2430.24



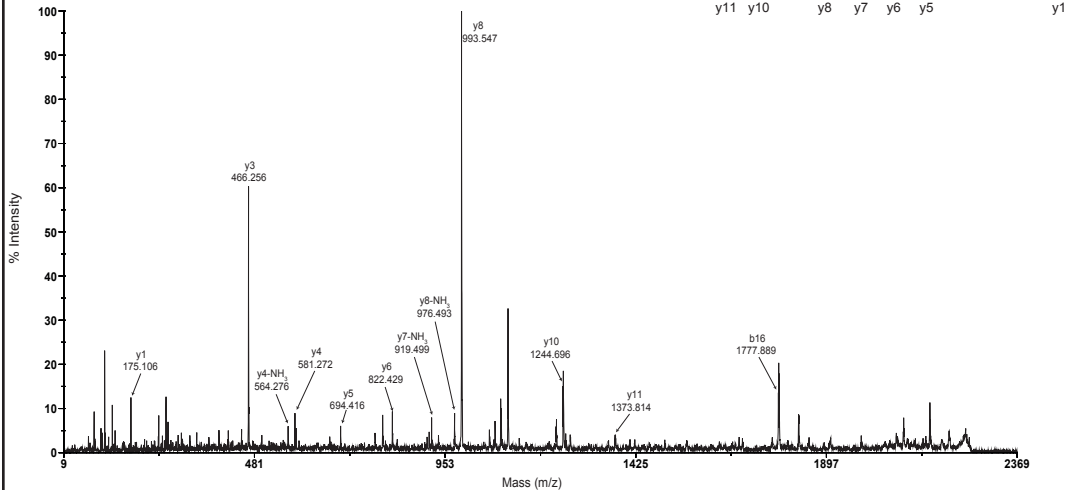
Precursor 2187.1

Y V D V F G A N Y Y Y Q C Y F S K
y15 y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y3 y2

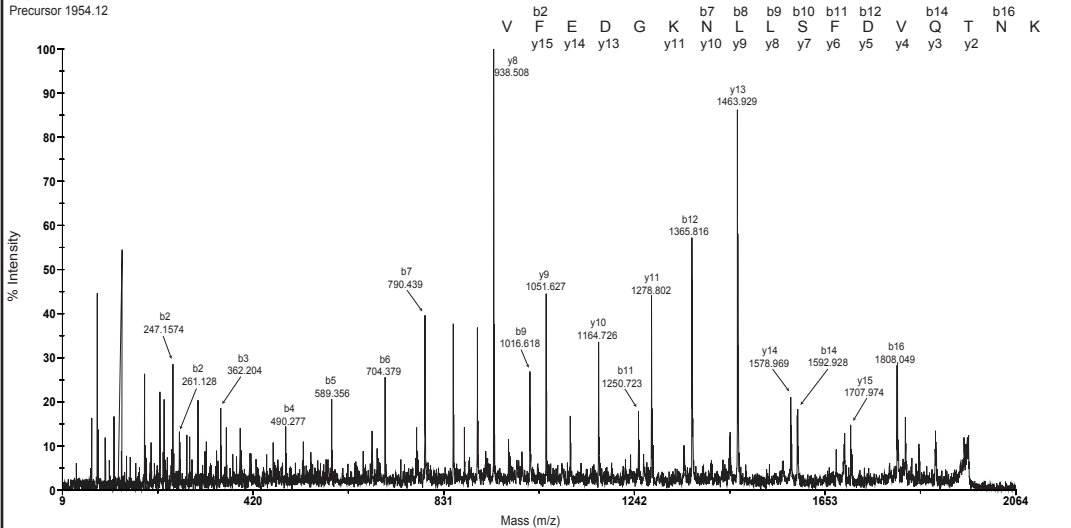


Precursor 2243.14

T C M Y G G V T E H N G N Q L b16 D K Y R
y11 y10 y8 y7 y6 y5

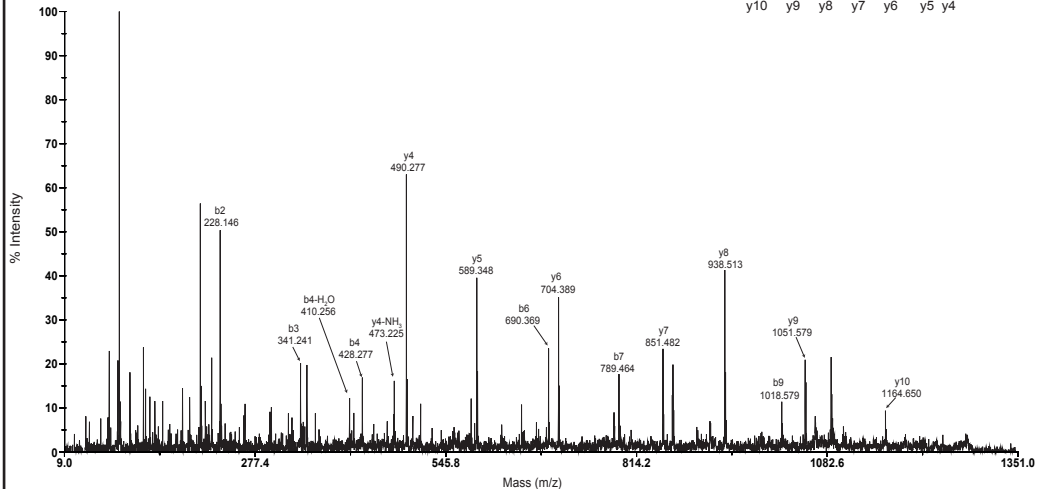


Precursor 1954.12



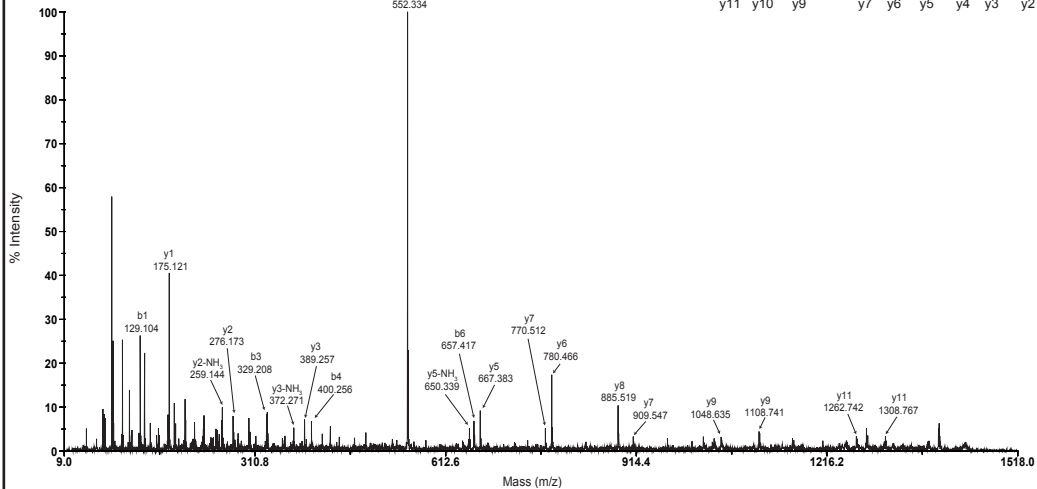
Precursor 1278.74

N	b2	b3	b4	F	D	b6	b7	T	b9	
	L	L	S	y7	y6	V	Q		N	K
	y10	y9	y8			y5	y4			



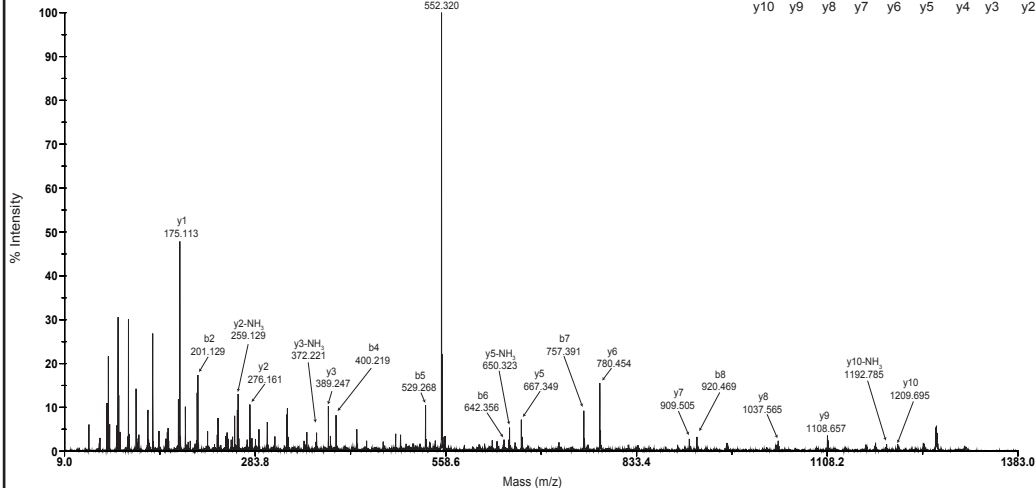
Precursor 1436.86

b1		b3	b4		b6	b7	b8	b9		b11	
K	V	T	A	Q	E	L	D	Y	L	T	R
	y11	y10	y9		y7	y6	y5	y4	y3	y2	y1

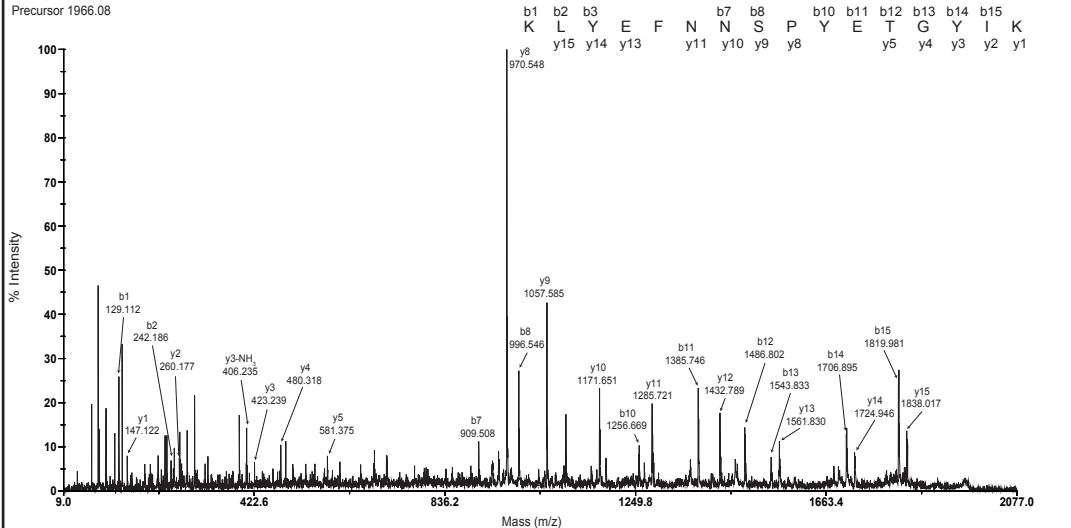


Precursor 1308.76

V	b2		b4	b5	b6	b7	b8				
	T	A	Q	E	L	D	Y	L	T	R	
	y10	y9	y8	y7	y6	y5	y4	y3	y2	y1	

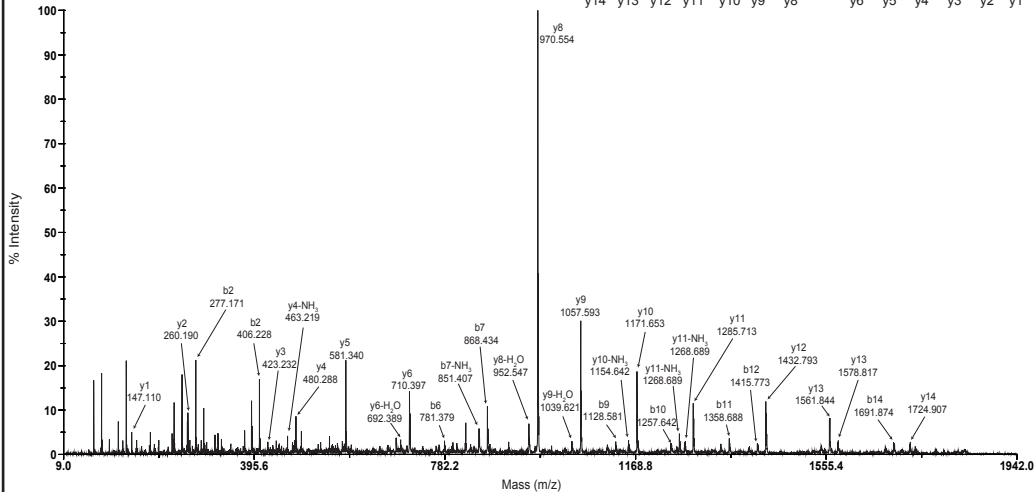


Precursor 1966.08



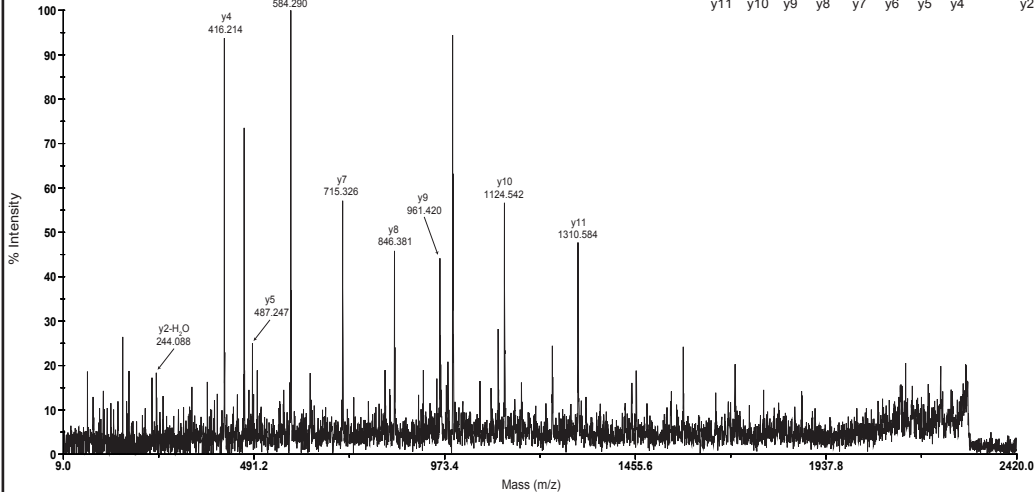
Precursor 1837.97

L	b2	b3	F	N	b6	b7		b9	b10	b11	b12	b13	b14
	Y	E			N	S	P	Y	E	T	G	Y	I
y14	y13	y12	y11	y10	y9	y8			y6	y5	y4	y3	y2



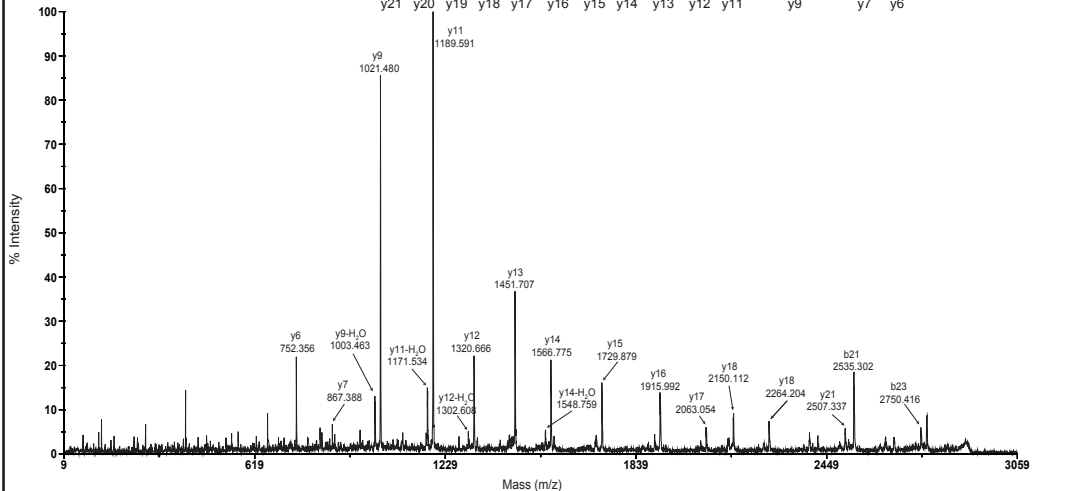
Precursor 2291.13

F I E N E N S F W Y D M M P A P G D K
y11 y10 y9 y8 y7 y6 y5 y4 y2



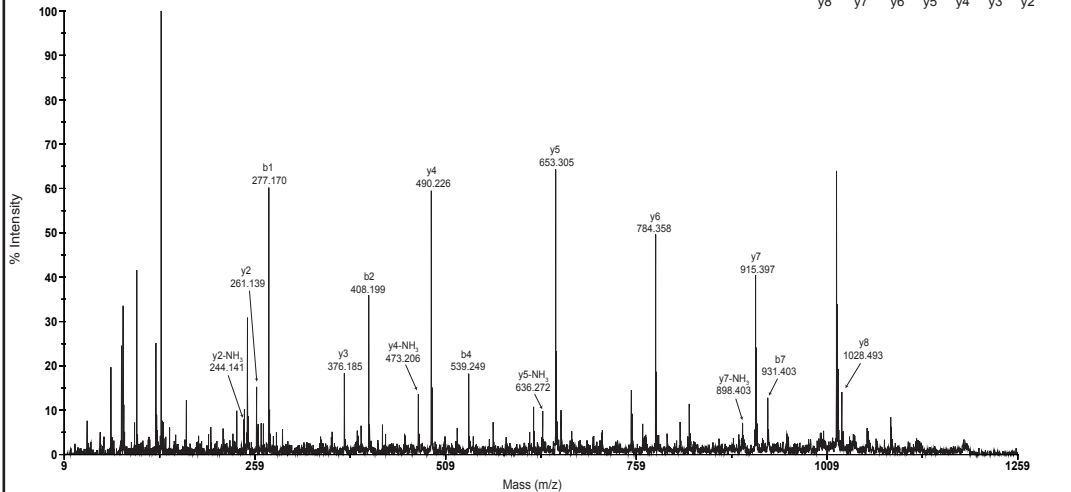
Precursor 2896.46

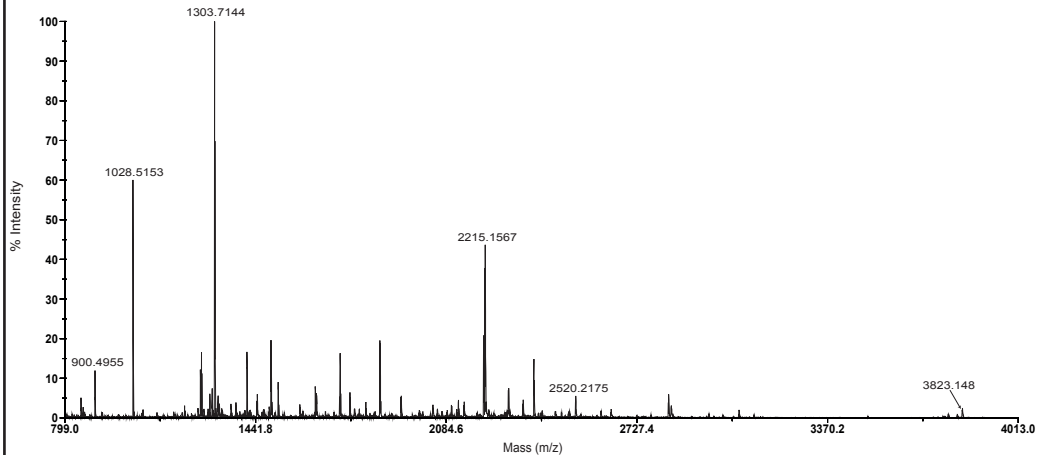
F I E N E N S F W Y D M M P A P G D K F b²¹ b²³
y²¹ y²⁰ y¹⁹ y¹⁸ y¹⁷ y¹⁶ y¹⁵ y¹⁴ y¹³ y¹² y¹¹ y⁹ y⁷ y⁶ D Q S K



Precursor 1191.58

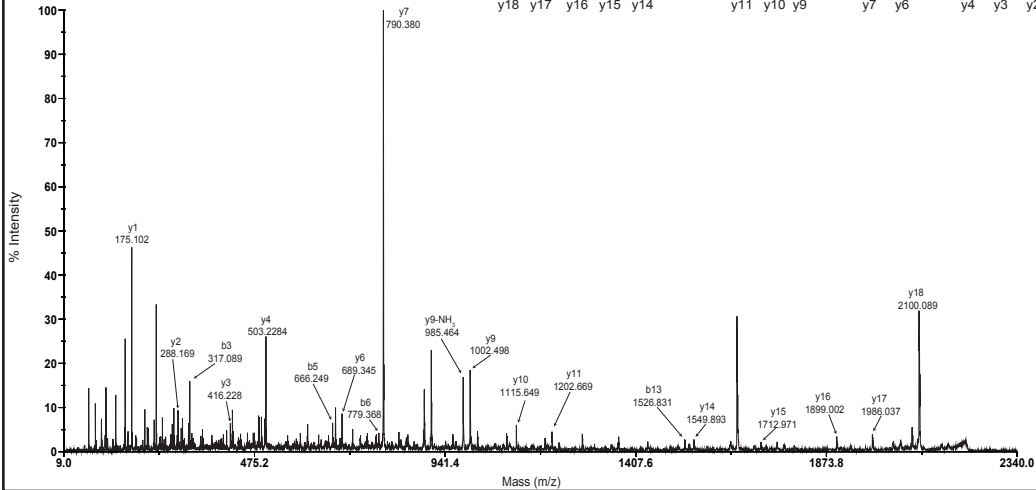
Y	b2	b3	b4	Y	N	b7	
	L	M	M	Y	N	D	N
	y8	y7	y6	y5	y4	y3	y2
							K





Precursor 2215.15

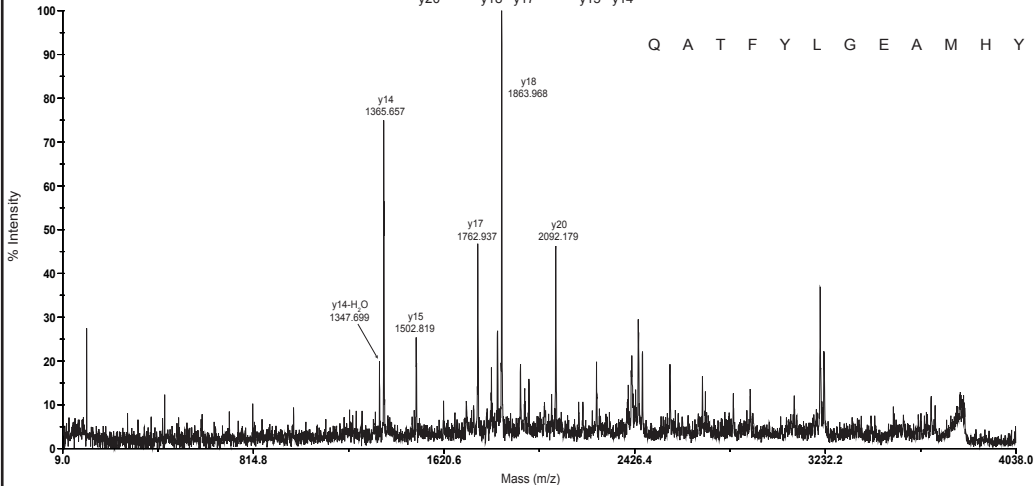
b1 D y18
b3 S y17
b4 W y16
b5 Y y15
b6 L y14
A Y S I P D b13 T G b15 E S Q I R
y11 y10 y9 y7 y6 y4 y3 y2 y1



Precursor 3823.15

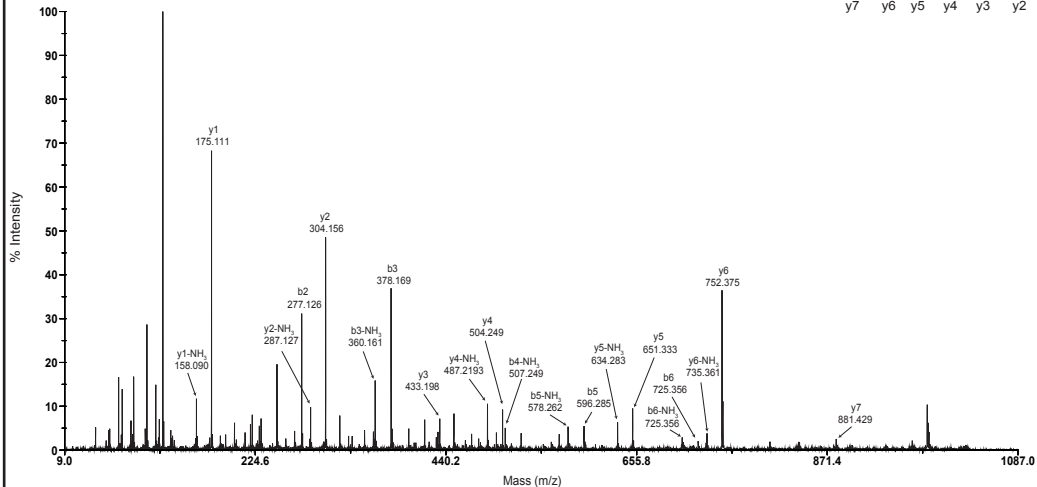
-G D I D T P Y H P A N V T A V D S A G H V K
y20 y18 y17 y15 y14

Q A T F Y L G E A M H Y F



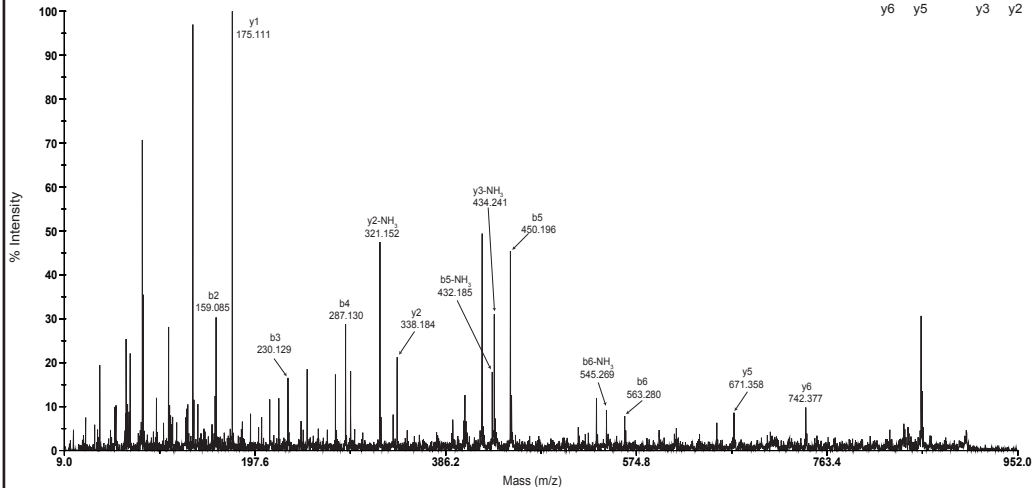
Precursor 1028.51

F	b2	b3	b4	b5	b6		
	E	T	F	A	E	E	R
	y7	y6	y5	y4	y3	y2	y1



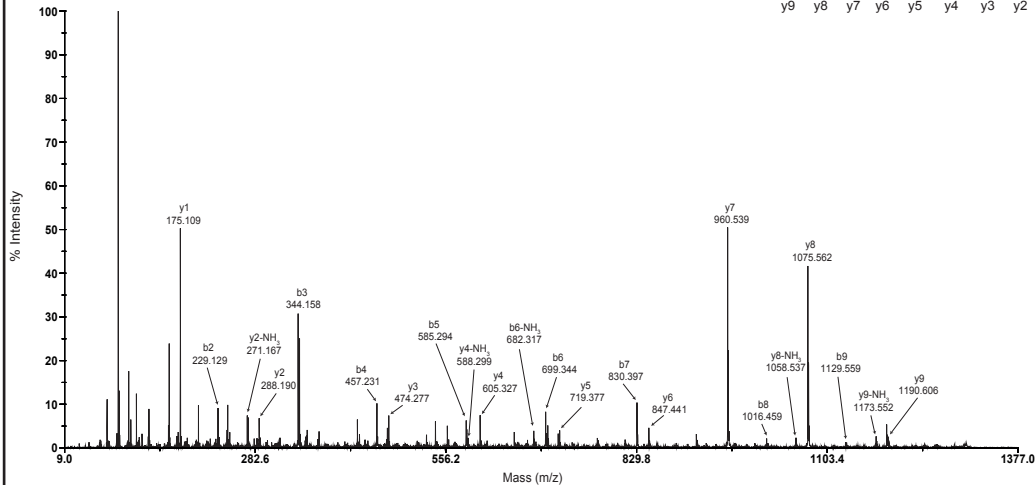
Precursor 900.495

G	b2 T	b3 A	b4 G	b5 Y	b6 I	Y	R
		y6	y5		y3	y2	y1



Precursor 1303.71

	b2	b3	b4	b5	b6	b7	b8	b9	
I	D	D	I	Q	N	M	W	I	R
	y9	y8	y7	y6	y5	y4	y3	y2	y1



Precursor 2520.22

S I^{b2} Y^{b3} Y S H A S M S^{y12} H S W D^{b14} D^{b15} W D^{b17} Y A A^{b20} K

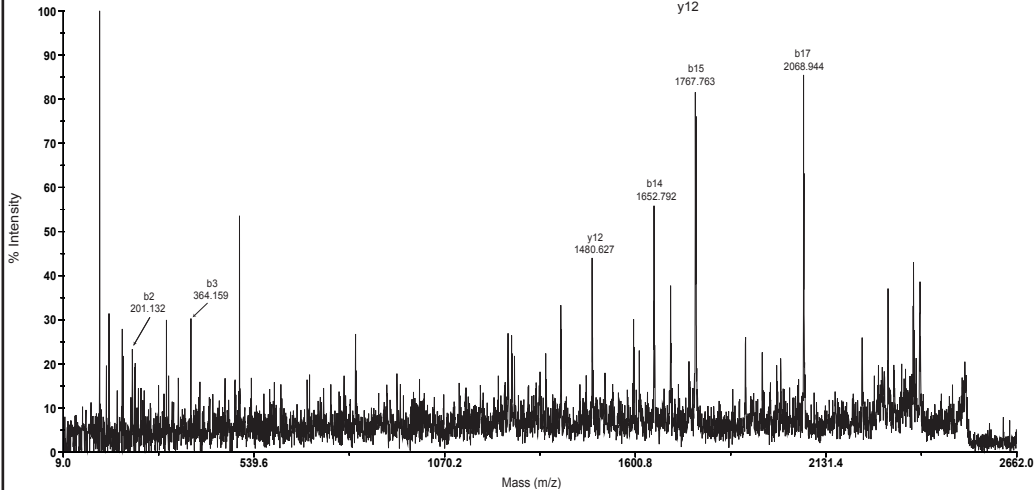


Fig: S2 Below

ETX- CLUSTAL 2.1 multiple sequence alignment

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AAA23236.1      MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
prf             MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
Q02307.1       MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
CAA43104.1     MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
ADU04573.1     MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
EDT23265.1     MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
EDT71753.1     MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
ZP_02953227.1 MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
ZP_02636519.1 MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
AAW47580.1     MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
AAA23235.1     MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
BAG75487.1     MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
YP_002291114.1 MKKNLVKSLAIASAVISIYSIVNIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 60
CAB60614.1     -----YDNVDTLIEKGR 12
CAD20125.1     -----YDNVDTLIEKGR 12
1UYJ           -----KEISNTVSNEMSKKASYDNVDTLIEKGR 28
ADF42572.1     -----SFHSYIVSPTNVAIKEISNTVSNEMSKKASYDNVDTLIEKGR 42
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```

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AAA23236.1      YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
prf             YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
Q02307.1       YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
CAA43104.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
ADU04573.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
EDT23265.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
EDT71753.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
ZP_02953227.1 YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
ZP_02636519.1 YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
AAW47580.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
AAA23235.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
BAG75487.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
YP_002291114.1 YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 120
CAB60614.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 72
CAD20125.1     YNTKYNLYLKRMEKYPNAMAYFDKGTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 72
1UYJ           YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 88
ADF42572.1     YNTKYNLYLKRMEKYPNAMAYFDKVTINPQGNDFYINNPKVELDGEPSMNYLEDVYVGHA 102
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AAA23236.1      LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
prf             LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
Q02307.1       LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
CAA43104.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
ADU04573.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
EDT23265.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
EDT71753.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
ZP_02953227.1 LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
ZP_02636519.1 LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
AAW47580.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
AAA23235.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
BAG75487.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
YP_002291114.1 LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 180
CAB60614.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 132
CAD20125.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 132
1UYJ           LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 148
ADF42572.1     LLTNDTQEQKLKLSQSFTCKNTDVTATTHTTHTVGTSTIQATAKFTVPFNETGVSLLTTSYSF 162
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AAA23236.1      ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
prf             ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
Q02307.1       ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
CAA43104.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
ADU04573.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
EDT23265.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
EDT71753.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
ZP_02953227.1 ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
ZP_02636519.1 ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
AAW47580.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
AAA23235.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
BAG75487.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
YP_002291114.1 ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 240
CAB60614.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 192
CAD20125.1     ANTNTNTNSKENTHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 192
1UYJ           ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 208
ADF42572.1     ANTNTNTNSKEITHNVPSQDILVPANTTVEVIAYLKKVNVKGNVKLVGVQSGSEWGEIPS 222
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```

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AAA23236.1      YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
prf             YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
Q02307.1       YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
CAA43104.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
ADU04573.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
EDT23265.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
EDT71753.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
ZP_02953227.1 YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
ZP_02636519.1 YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
AAW47580.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
AAA23235.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
BAG75487.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
YP_002291114.1 YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 300
CAB60614.1     YLAFPRDGYKFLSDTVIKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 252
CAD20125.1     YLAFPRDGYKFLSDTVIKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 252
1UYJ           YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 268
ADF42572.1     YLAFPRDGYKFLSDTVNKSDDLNEGDGTININGKKNYSAVMGDELIVKVRNLNTNNVQEYV 282
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AAA23236.1      IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
prf             IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
Q02307.1       IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
CAA43104.1     IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
ADU04573.1     IPVDKKEKSNDNSNIVKYRSLYIKAPGIKAAEAAAK 334
EDT23265.1     IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
EDT71753.1     IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
ZP_02953227.1 IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
ZP_02636519.1 IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
AAW47580.1     IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
AAA23235.1     IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
BAG75487.1     IPVDKKEKSNDNSNIVKYRSLYIKAPGIK----- 328
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SEB- CLUSTAL 2.1 multiple sequence alignment

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CAJ43561.1 -----IFVLILVISTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 48
ABJ97621.1 --KRLFISHVILIFVLILVISTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 58
ABJ97622.1 MYKRLFISHVILIFVLILVISTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
AAL04126.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
P01552.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
YP_005297270.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
BAH86611.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
BAH86609.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
BAH86610.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
AAW37877.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
YP_185778.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
AEV77895.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
BAH30701.1 MYKRLFISHVILIFALILVISTPNVLAESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 60
1SBB -----ESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 33
AAW19659.1 -----ESQDPDPKDELHKSSKFTGLMENMKVLYDDNHV 33
ABJ97620.1 -----IFALILVISTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 48
ABJ97619.1 -----ESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 33
ZP_06325911.1 MYKRLFISHVILIFVLILVISTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
EFB48235.1 MYKRLFISHVILIFVLILVISTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
AAP37186.1 -----DELHKASKFTGLMENMKVLYDDNHV 25
BAL14649.1 MYNRLFVSRVILIFALILVIYTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
BAH86612.1 MYNRLFVSRVILIFALILVIYTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
BAH30704.1 MYNRLFVSRVILIFALILVIYTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
BAH30703.1 MYNRLFVSRVILIFALILVIYTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
BAH30702.1 MYNRLFVSRVILIFALILVIYTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
BAH30700.1 MYNRLFVSRVILIFALILVIYTPNVLAESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 60
ABF93357.1 -----ESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 33
ABF93356.1 -----ESQDPDPKDELHKASKFTGLMENMKVLYDDNHV 33
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CAJ43561.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 108
ABJ97621.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 118
ABJ97622.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
AAL04126.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
P01552.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
YP_005297270.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH86611.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH86609.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH86610.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
AAW37877.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
YP_185778.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
AEV77895.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH30701.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
1SBB SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 93
AAW19659.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 93
ABJ97620.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 108
ABJ97619.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 93
ZP_06325911.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
EFB48235.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
AAP37186.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 85
BAL14649.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH86612.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH30704.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH30703.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH30702.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
BAH30700.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 120
ABF93357.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 93
ABF93356.1 SAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFNKDLADKYKDKYVDVFGANYYYQC 93
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CAJ43561.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 168
ABJ97621.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 178
ABJ97622.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
AAL04126.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
P01552.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
YP_005297270.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH86611.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH86609.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH86610.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
AAW37877.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
YP_185778.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
AEV77895.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH30701.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
1SBB YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 153
AAW19659.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 153
ABJ97620.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 168
ABJ97619.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 153
ZP_06325911.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
EFB48235.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
AAP37186.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 145
BAL14649.1 YFSEKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH86612.1 YFSEKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH30704.1 YFSEKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH30703.1 YFSEKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH30702.1 YFSEKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
BAH30700.1 YFSEKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
ABF93357.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 153
ABF93356.1 YFSKKTNDINSHQTDKRRKTCMYGGVTEHNGNHLDKYRSITVRVFEDGKNLLSFDVQTNKK 153
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CAJ43561.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 228
ABJ97621.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 238
ABJ97622.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
AAL04126.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
P01552.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
YP_005297270.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
BAH86611.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
BAH86609.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
BAH86610.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
AAW37877.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
YP_185778.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
AEV77895.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
BAH30701.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
1SBB KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 213
AAW19659.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 213
ABJ97620.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 228
ABJ97619.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 213
ZP_06325911.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMAPAGDKFDQSKY 240
EFB48235.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 240
AAP37186.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 205
BAL14649.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 240
BAH86612.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 240
BAH30704.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 240
BAH30703.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 240
BAH30702.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 240
BAH30700.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 240
ABF93357.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 213
ABF93356.1 KVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIESENSFWYDMMAPAGDKFDQSKY 213
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CAJ43561.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 254
ABJ97621.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 264
ABJ97622.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
AAL04126.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
P01552.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
YP_005297270.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
BAH86611.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
BAH86609.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
BAH86610.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
AAW37877.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
YP_185778.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
AEV77895.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
BAH30701.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 266
1SBB LMMYNDNKMVDSKDVKIEVYLTTKKK 239
AAW19659.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 239
ABJ97620.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 254
ABJ97619.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 239
ZP_06325911.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
EFB48235.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
AAP37186.1 LMMYNDNKLVDSDVKM----- 222
BAL14649.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
BAH86612.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
BAH30704.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
BAH30703.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
BAH30702.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
BAH30700.1 LMMYNDNKLVDSDVKIEVYLTTKKK 266
ABF93357.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 239
ABF93356.1 LMMYNDNKMVDSKDVKIEVYLTTKKK 239
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