

# MATRIX SCIENCE Mascot Search Results

## Peptide View

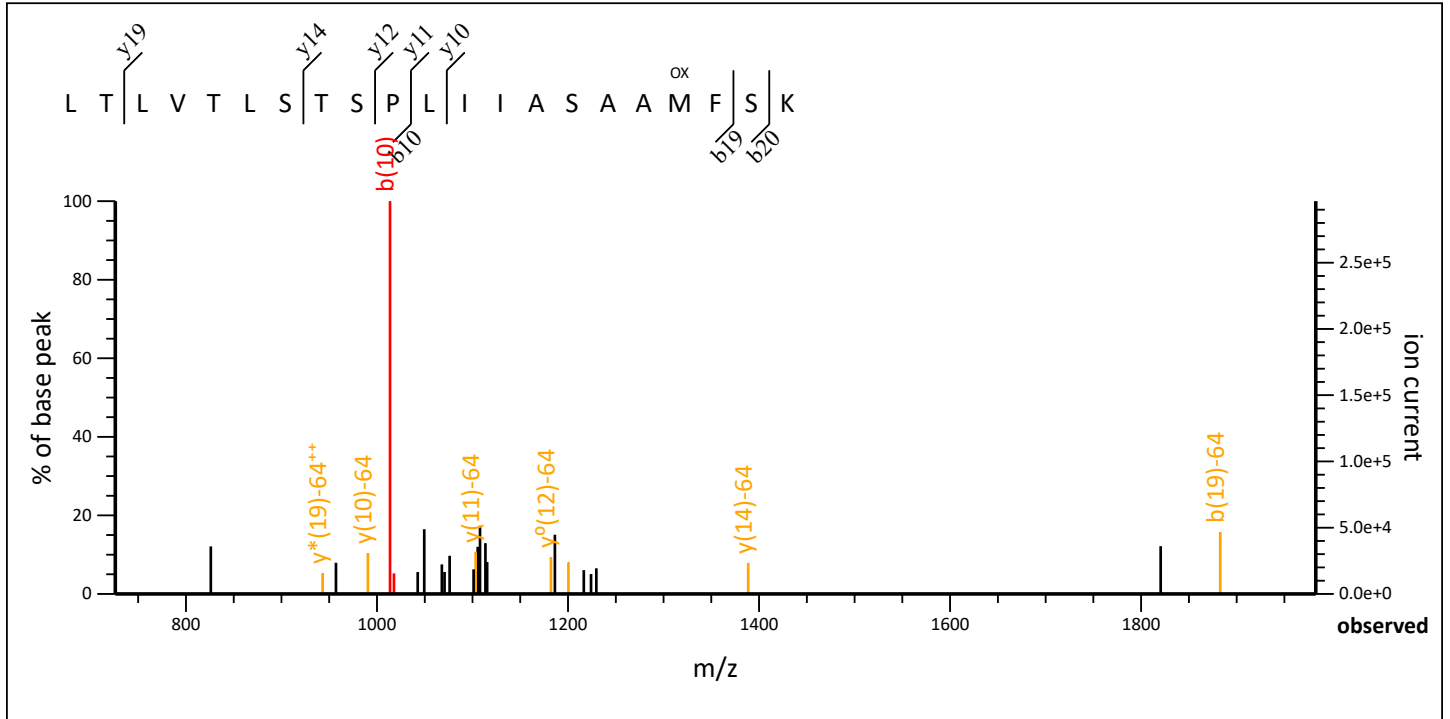
MS/MS Fragmentation of **LTLVTLSTSPLIIASAAMFSK**

Found in **XP\_004418995.1** in **NCBIprot**, PREDICTED: ATP-binding cassette sub-family B member 5 [Ceratotherium simum simum]

Match to Query 98: 2180.155448 from(1091.085000,2+) intensity(8989877.0000) index(90)

Title: Cmpd 91, +MSn(1091.08), 10.4 min

Data file LM\_26%.mgf



Label all possible matches  Label matches used for scoring

Monoisotopic mass of neutral peptide Mr(calc): 2179.2174

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

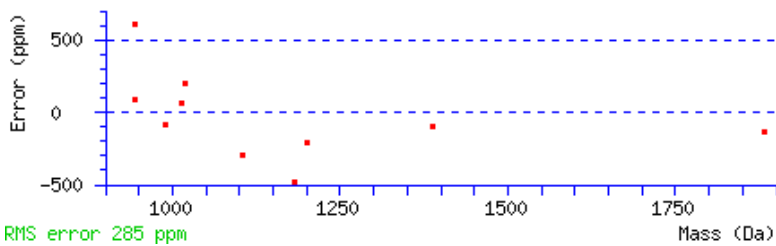
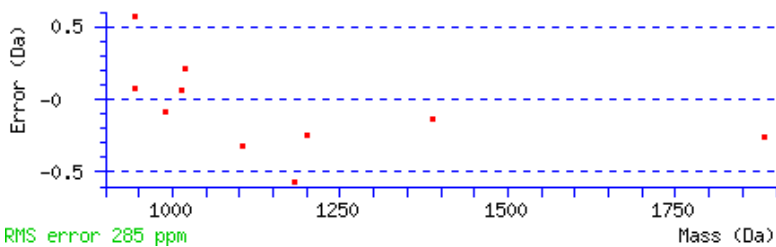
M18 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000

Ions Score: 13 Expect: 1.4e+03

Matches : 10/310 fragment ions using 20 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	114.0913	57.5493			L							21
2	215.1390	108.0731	197.1285	99.0679	T	2003.1423	1002.0748	1986.1158	993.5615	1985.1318	993.0695	20
3	328.2231	164.6152	310.2125	155.6099	L	1902.0946	951.5510	1885.0681	943.0377	1884.0841	942.5457	19
4	427.2915	214.1494	409.2809	205.1441	V	1789.0106	895.0089	1771.9840	886.4957	1771.0000	886.0036	18
5	528.3392	264.6732	510.3286	255.6679	T	1689.9422	845.4747	1672.9156	836.9614	1671.9316	836.4694	17
6	641.4232	321.2153	623.4127	312.2100	L	1588.8945	794.9509	1571.8679	786.4376	1570.8839	785.9456	16
7	728.4553	364.7313	710.4447	355.7260	S	1475.8104	738.4088	1458.7839	729.8956	1457.7999	729.4036	15
8	829.5029	415.2551	811.4924	406.2498	T	1388.7784	694.8928	1371.7518	686.3796	1370.7678	685.8876	14

9	916.5350	458.7711	898.5244	449.7658	S	1287.7307	644.3690	1270.7042	635.8557	1269.7202	635.3637	13
10	<b>1013.5877</b>	507.2975	995.5772	498.2922	P	<b>1200.6987</b>	600.8530	1183.6721	592.3397	<b>1182.6881</b>	591.8477	12
11	1126.6718	563.8395	1108.6612	554.8343	L	<b>1103.6459</b>	552.3266	1086.6194	543.8133	1085.6354	543.3213	11
12	1239.7559	620.3816	1221.7453	611.3763	I	<b>990.5619</b>	495.7846	973.5353	487.2713	972.5513	486.7793	10
13	1352.8399	676.9236	1334.8294	667.9183	I	877.4778	439.2425	860.4512	430.7293	859.4672	430.2373	9
14	1423.8770	712.4422	1405.8665	703.4369	A	764.3937	382.7005	747.3672	374.1872	746.3832	373.6952	8
15	1510.9091	755.9582	1492.8985	746.9529	S	693.3566	347.1819	676.3301	338.6687	675.3461	338.1767	7
16	1581.9462	791.4767	1563.9356	782.4714	A	606.3246	303.6659	589.2980	295.1527	588.3140	294.6607	6
17	1652.9833	826.9953	1634.9727	817.9900	A	535.2875	268.1474	518.2609	259.6341	517.2769	259.1421	5
18	1736.0204	868.5138	1718.0099	859.5086	M	464.2504	232.6288	447.2238	224.1155	446.2398	223.6235	4
19	<b>1883.0888</b>	942.0481	1865.0783	933.0428	F	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	3
20	1970.1209	985.5641	1952.1103	976.5588	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
21					K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [LTLVTLSTSPLIASAAMFSK](#)  
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)  
 Other BLAST [web gateways](#)

#### All matches to this query

Score	Mr(calc)	Delta	Sequence
13.3	2179.2174	0.9381	<a href="#">LTLVTLSTSPLIASAAMFSK</a>
7.0	2180.1259	0.0295	<a href="#">ISSQTRETSPIQIPGGLMIH</a>
7.0	2178.9926	1.1629	<a href="#">AFSTLCYSADGQSILAGGMSK</a>
6.9	2180.1325	0.0230	<a href="#">SDLPLTPPTSKLPTVPDGEGR</a>
6.8	2179.0249	1.1305	<a href="#">MGRSESQMDITDINTPKPK</a>
5.7	2181.1026	-0.9471	<a href="#">RLLRPPPGLDSESDGTESQK</a>
4.5	2180.1372	0.0183	<a href="#">HKPPSLTRSTSMLISSAHSK</a>
4.3	2181.1286	-0.9731	<a href="#">HPKMSVGLNLDAMGAALALEK</a>
3.9	2179.0878	1.0677	<a href="#">AAALTSAGELAGPLHPAMGMAAR</a>
3.9	2179.0878	1.0677	<a href="#">AAALTSAGELAGPLHPAMGMAAR</a>