

# MATRIX SCIENCE Mascot Search Results

## Peptide View

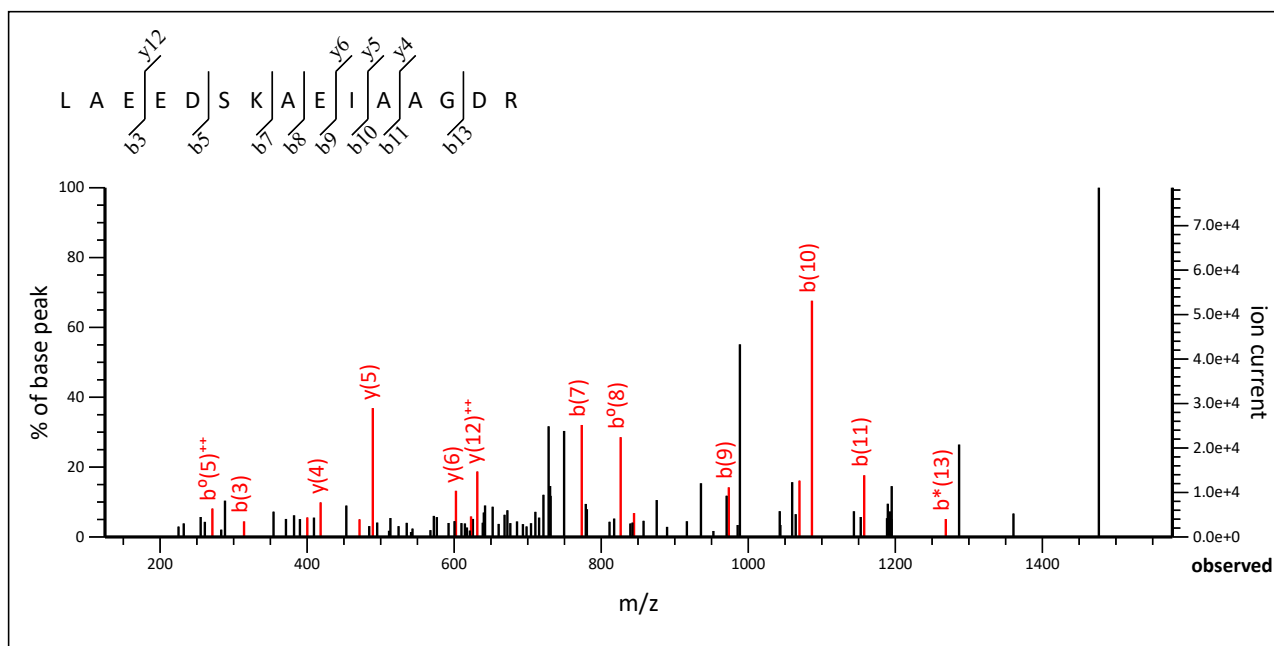
MS/MS Fragmentation of **LAEEDSKAEIAAGDR**

Found in **XP\_006862759.1** in **NCBIprot**, PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP4 isoform X2 [Chrysochloris asiatica]

Match to Query 17: 1573.743448 from(787.879000,2+) intensity(1005291.0000) rtinseconds(324.609) scans(MS: 217/223 MSMS: 218/225) index(1)

Title: Cmpd 2, +MS2(787.88), 5.4 min #218-225

Data file LM\_18%.mgf



?  125.05 to 1576.8

Label all possible matches  Label matches used for scoring

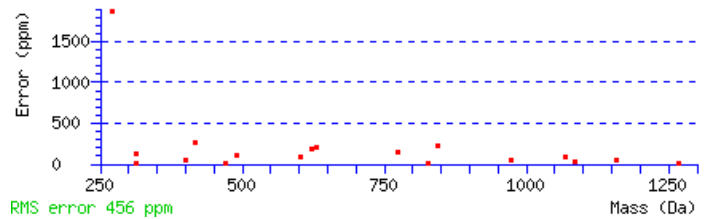
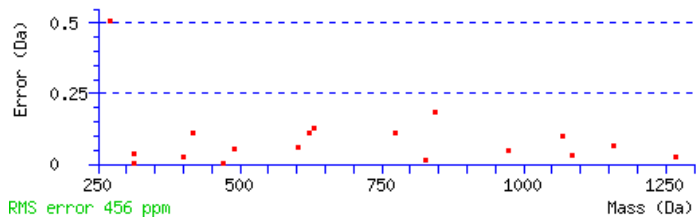
Monoisotopic mass of neutral peptide Mr(calc): 1573.7583

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

Ions Score: 16 Expect: 7.2e+02

Matches : 18/150 fragment ions using 44 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	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							15
2	185.1285	93.0679					A	1461.6816	731.3444	1444.6550	722.8312	1443.6710	722.3392	14
3	<b>314.1710</b>	157.5892			296.1605	148.5839	E	1390.6445	695.8259	1373.6179	687.3126	1372.6339	686.8206	13
4	443.2136	222.1105			425.2031	213.1052	E	1261.6019	<b>631.3046</b>	1244.5753	<b>622.7913</b>	1243.5913	622.2993	12
5	558.2406	279.6239			540.2300	<b>270.6186</b>	D	1132.5593	566.7833	1115.5327	558.2700	1114.5487	557.7780	11
6	645.2726	323.1399			627.2620	<b>314.1347</b>	S	1017.5323	509.2698	1000.5058	500.7565	999.5218	500.2645	10
7	<b>773.3676</b>	387.1874	756.3410	378.6742	755.3570	378.1821	K	930.5003	465.7538	913.4738	457.2405	912.4898	456.7485	9
8	<b>844.4047</b>	422.7060	827.3781	414.1927	<b>826.3941</b>	413.7007	A	802.4054	401.7063	785.3788	393.1930	784.3948	392.7010	8
9	<b>973.4473</b>	487.2273	956.4207	478.7140	955.4367	478.2220	E	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	7
10	<b>1086.5313</b>	543.7693	<b>1069.5048</b>	535.2560	1068.5208	534.7640	I	<b>602.3257</b>	301.6665	585.2991	293.1532	584.3151	292.6612	6
11	<b>1157.5685</b>	579.2879	1140.5419	570.7746	1139.5579	570.2826	A	<b>489.2416</b>	245.1244	472.2150	236.6112	<b>471.2310</b>	236.1191	5
12	1228.6056	614.8064	1211.5790	606.2931	1210.5950	605.8011	A	<b>418.2045</b>	209.6059	401.1779	201.0926	<b>400.1939</b>	200.6006	4
13	1285.6270	643.3172	<b>1268.6005</b>	634.8039	1267.6165	634.3119	G	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
14	1400.6540	700.8306	1383.6274	692.3174	1382.6434	691.8253	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
15							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of [LAEEDSKAEIAAGDR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

#### All matches to this query

Score	Mr(calc)	Delta	Sequence
16.3	1573.7583	-0.0149	<a href="#">LAEEDSKAEIAAGDR</a>
14.1	1573.7995	-0.0560	<a href="#">MAAAGARLSPGSGSGLR</a>
13.3	1572.7678	0.9756	<a href="#">RMEAGEATPLTGAGGR</a>
12.8	1573.7419	0.0015	<a href="#">AREVMAWNQAENR</a>
11.8	1574.7842	-1.0407	<a href="#">VVGYAQDQVDGHLR</a>
11.3	1574.7181	-0.9746	<a href="#">RMNSLMDEDIAHK</a>
11.0	1572.7090	1.0345	<a href="#">MEQDDPGEALAE LR</a>
10.8	1573.7155	0.0280	<a href="#">CPQSGTTLSPAENR</a>
10.6	1574.7787	-1.0353	<a href="#">LSSLQSLDLEAEDR</a>
10.4	1574.7776	-1.0342	<a href="#">VRYAPYAVSPCHR</a>

Mascot: <http://www.matrixscience.com/>