

Proteasome Interacting Proteins identified with a unique peptide (p-value < 0,001)

Hit	Accession - ID	Description	Score	MW	PI	Coverage	Peptides	Peptides R&G	Valid protein		
<a href="#">34</a>	<a href="#">P62263 - RS14_HUMAN</a>	40S ribosomal protein S14 - Homo sapiens (Human)	71.95	16262.53	10.07	7	1				
Query	m/z	Charge	Exp. mass	Theo. mass	Delta	Miss. clv.	Score	pValue	Rank	Sequence	Position
<a href="#">888</a>	527.79	2	1053.56	1053.56	0.00015	0	49	0.000545	1	TPGPGAQSALR	107-117

Hit	Accession - ID	Description	Score	MW	PI	Coverage	Peptides	Peptides R&G	Valid protein		
<a href="#">37</a>	<a href="#">P62877 - RBX1_HUMAN</a>	RING-box protein 1 - Homo sapiens (Human)	101.33	12265.74			3				
Query	m/z	Charge	Exp. mass	Theo. mass	Delta	Miss. clv.	Score	pValue	Rank	Sequence	Position
<a href="#">2215</a>	854.3806	2	1706.746648	1706.741745	0.004903	0	72	3.53244007153291e-006	1	AAAMDVDTPSGTNSGAGK + Acetyl (Protein N-term); Oxidation (M)	2-19

Hit	Accession - ID	Description	Score	MW	PI	Coverage	Peptides	Peptides R&G	Valid protein		
<a href="#">43</a>	<a href="#">Q59G24 - Q59G24_HUMAN</a>	Activated RNA polymerase II transcription cofactor 4 variant - Homo sapiens (Human)	63.00	15125.79			3				
Query	m/z	Charge	Exp. mass	Theo. mass	Delta	Miss. clv.	Score	pValue	Rank	Sequence	Position
<a href="#">1714</a>	630.8082	2	1259.601848	1259.59935	0.002498	0	63	2.65879827439268e-005	1	EQISDIDDAVR	122-132

Hit	Accession - ID	Description	Score	MW	PI	Coverage	Peptides	Bold&Red Peptides	Valid protein
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<a href="#">48</a>	<a href="#">Q13765 - NACA_HUMAN</a>	Nascent polypeptide-associated complex subunit alpha - Homo sapiens (Human)	81.70	23369.71		6	1	1			
Query	m/z	Charge	Exp. mass	Theo. mass	Delta	Miss. clv.	Score	pValue	Rank	Sequence	Position
<a href="#">2249</a>	807.9207	2	1613.826848	1613.826019	0.000829	0	81	<a href="#">7.72424799385339e-007</a>	1	<a href="#">IEDLSQQAQLAAAEK</a>	<a href="#">128-142</a>

# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **TPGPGAQSALR**

Found in **RS14\_HUMAN**, P62263|RS14\_HUMAN 40S ribosomal protein S14 - Homo sapiens (Human)

Match to Query 888: 1053.556848 from(527.785700,2+)

Title: OTMPB070622\_20.712.712.2.dta

Data file D:\data\_LTQOrbitrap\Marie-Pierre Bousquet\OTMPB070622\_20.RAW

Click mouse within plot area to zoom in by factor of two about that point

Or,  to  Da

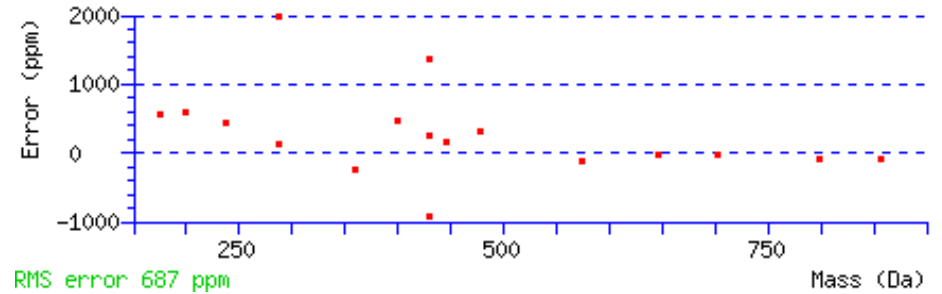
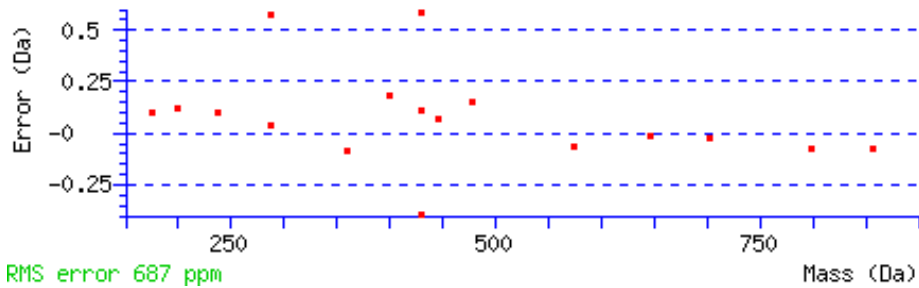
**Monoisotopic mass of neutral peptide Mr(calc):** 1053.5567

**Ions Score:** 49 **Expect:** 0.00054

**Matches (Bold Red):** 17/102 fragment ions using 34 most intense peaks

#	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	102.0550	51.5311			84.0444	42.5258	T								11
2	<b>199.1077</b>	100.0575			181.0972	91.0522	P	953.5163	<b>477.2618</b>	936.4898	468.7485	935.5057	468.2565		10
3	256.1292	128.5682			<b>238.1186</b>	119.5629	G	<b>856.4635</b>	<b>428.7354</b>	839.4370	420.2221	838.4530	419.7301		9
4	353.1819	177.0946			335.1714	168.0893	P	<b>799.4421</b>	<b>400.2247</b>	782.4155	391.7114	781.4315	391.2194		8
5	410.2034	205.6053			392.1928	196.6001	G	<b>702.3893</b>	351.6983	685.3628	343.1850	684.3787	342.6930		7
6	481.2405	241.1239			463.2300	232.1186	A	<b>645.3679</b>	323.1876	628.3413	314.6743	627.3573	314.1823		6
7	609.2991	305.1532	592.2726	296.6399	591.2885	296.1479	Q	<b>574.3307</b>	<b>287.6690</b>	557.3042	279.1557	556.3202	278.6637		5
8	696.3311	348.6692	679.3046	340.1559	678.3206	339.6639	S	<b>446.2722</b>	223.6397	<b>429.2456</b>	215.1264	<b>428.2616</b>	214.6344		4
9	767.3682	384.1878	750.3417	375.6745	749.3577	375.1825	A	<b>359.2401</b>	180.1237	342.2136	171.6104				3
10	880.4523	440.7298	863.4258	432.2165	862.4417	431.7245	L	<b>288.2030</b>	144.6051	271.1765	136.0919				2
11							R	<b>175.1190</b>	88.0631	158.0924	79.5498				1



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

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

Other BLAST [web gateways](#)

**All matches to this query**

Score	Mr(calc):	Delta	Sequence
48.8	1053.5567	0.0001	<a href="#">TPGPGAQSALR</a>
7.5	1053.5567	0.0001	<a href="#">VVGKKGESH</a>
7.5	1053.5567	0.0001	<a href="#">VVGKKGESH</a>
0.6	1053.5567	0.0001	<a href="#">VVGSNISHK</a>

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



# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AAAMDVDTPSGTNSGAGK**

Found in **RBX1\_HUMAN**, P62877|RBX1\_HUMAN RING-box protein 1 - Homo sapiens (Human)

Match to Query 2215: 1706.746648 from(854.380600,2+)

Title: OTMPB070706\_23.984.984.2.dta

Data file D:\data\_LTQOrbitrap\Marie-Pierre Bousquet\OTMPB070706\_23.RAW

Click mouse within plot area to zoom in by factor of two about that point

Or,  to  Da

**Monoisotopic mass of neutral peptide Mr(calc):** 1706.7417

**Variable modifications:**

**N-term** : Acetyl (Protein N-term)

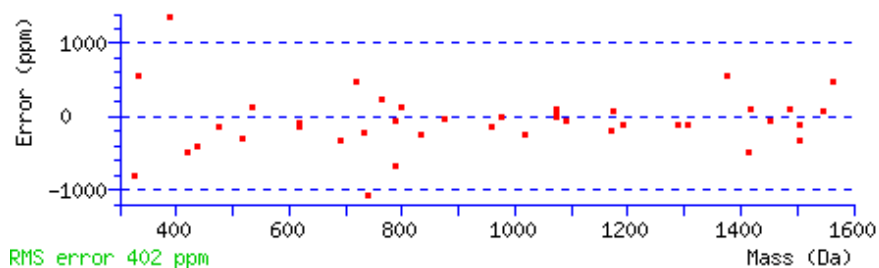
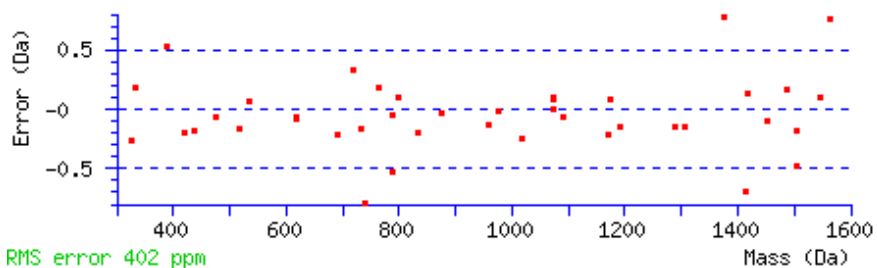
**M4** : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

**Ions Score:** 73 **Expect:** 3.5e-006

**Matches (Bold Red):** 41/246 fragment ions using 60 most intense peaks

#	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	114.0549	57.5311					A								18
2	185.0921	93.0497					A	1594.7013	797.8543	1577.6748	789.3410	1576.6908	788.8490		17
3	256.1292	128.5682					A	1523.6642	762.3358	1506.6377	753.8225	1505.6537	753.3305		16
4	403.1646	202.0859					M	1452.6271	726.8172	1435.6006	718.3039	1434.6166	717.8119		15
5	518.1915	259.5994			500.1810	250.5941	D	1305.5917	653.2995	1288.5652	644.7862	1287.5811	644.2942		14
6	617.2599	309.1336			599.2494	300.1283	V	1190.5648	595.7860	1173.5382	587.2727	1172.5542	586.7807		13
7	732.2869	366.6471			714.2763	357.6418	D	1091.4964	546.2518	1074.4698	537.7385	1073.4858	537.2465		12
8	833.3346	417.1709			815.3240	408.1656	T	976.4694	488.7383	959.4429	480.2251	958.4588	479.7331		11
9	930.3873	465.6973			912.3768	456.6920	P	875.4217	438.2145	858.3952	429.7012	857.4112	429.2092		10
10	1017.4194	509.2133			999.4088	500.2080	S	778.3690	389.6881	761.3424	381.1748	760.3584	380.6828		9
11	1074.4408	537.7240			1056.4303	528.7188	G	691.3369	346.1721	674.3104	337.6588	673.3264	337.1668		8
12	1175.4885	588.2479			1157.4779	579.2426	T	634.3155	317.6614	617.2889	309.1481	616.3049	308.6561		7
13	1289.5314	645.2693	1272.5049	636.7561	1271.5209	636.2641	N	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323		6
14	1376.5635	688.7854	1359.5369	680.2721	1358.5529	679.7801	S	419.2249	210.1161	402.1983	201.6028	401.2143	201.1108		5
15	1433.5849	717.2961	1416.5584	708.7828	1415.5743	708.2908	G	332.1928	166.6001	315.1663	158.0868				4
16	1504.6220	752.8147	1487.5955	744.3014	1486.6115	743.8094	A	275.1714	138.0893	258.1448	129.5761				3
17	1561.6435	781.3254	1544.6169	772.8121	1543.6329	772.3201	G	204.1343	102.5708	187.1077	94.0575				2
18							K	147.1128	74.0600	130.0863	65.5468				1



NCBI BLAST search of [AAAMDVDTPSGTNSGAGK](#)

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

Other BLAST [web gateways](#)

### All matches to this query

Score	Mr(calc):	Delta	Sequence
72.8	1706.7417	0.0049	<a href="#">AAAMDVDTPSGTNSGAGK</a>

7.4	1706.7457	0.0009	<a href="#">TMHSSWEESDELLK</a>
5.1	1706.7530	-0.0063	<a href="#">NDECVLEDNSQRTK</a>
1.5	1706.7505	-0.0038	<a href="#">CTQEGCGKHFASPSK</a>
0.1	1706.7530	-0.0063	<a href="#">DSRGAGQEQGMPAGK</a>

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



# **MASCOT** Mascot Search Results

## Peptide View

MS/MS Fragmentation of **EQISDIDDAVR**

Found in **Q59G24\_HUMAN**, Q59G24|Q59G24\_HUMAN Activated RNA polymerase II transcription cofactor

4 variant - Homo sapiens (Human)

Match to Query 1714: 1259.601848 from(630.808200,2+)

Title: OTMPB070706\_25.2144.2144.2.dta

Data file D:\data\_LTQOrbitrap\Marie-Pierre Bousquet\OTMPB070706\_25.RAW

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

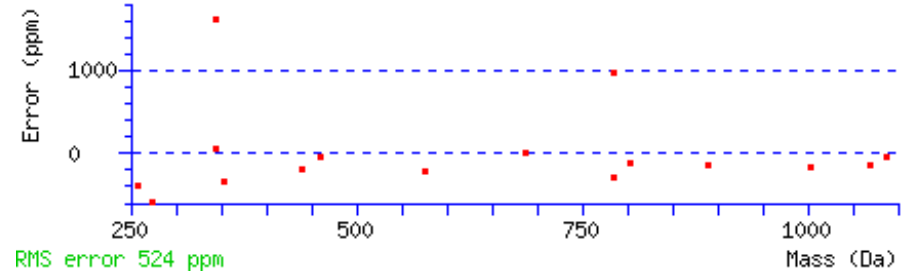
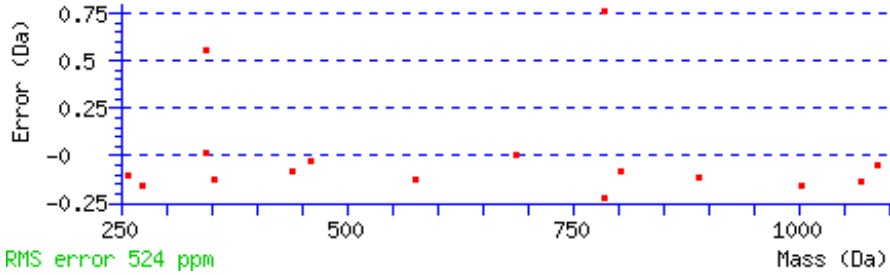
**Monoisotopic mass of neutral peptide Mr(calc):** 1259.5994

**Ions Score:** 63 **Expect:** 2.7e-005

**Matches (Bold Red):** 16/112 fragment ions using 24 most intense peaks

#	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	130.0499	65.5286			112.0393	56.5233	E							11
2	<b>258.1084</b>	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1131.5640	566.2857	1114.5375	557.7724	1113.5535	557.2804	10
3	371.1925	186.0999	354.1660	177.5866	<b>353.1819</b>	177.0946	I	<b>1003.5055</b>	502.2564	986.4789	493.7431	985.4949	493.2511	9
4	458.2245	229.6159	441.1980	221.1026	<b>440.2140</b>	220.6106	S	<b>890.4214</b>	445.7143	873.3949	437.2011	872.4108	436.7091	8
5	573.2515	287.1294	556.2249	278.6161	555.2409	278.1241	D	<b>803.3894</b>	402.1983	786.3628	393.6850	785.3788	393.1930	7
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	I	<b>688.3624</b>	<b>344.6849</b>	671.3359	336.1716	670.3519	335.6796	6
7	801.3625	401.1849	<b>784.3359</b>	392.6716	<b>783.3519</b>	392.1796	D	<b>575.2784</b>	288.1428	558.2518	279.6295	557.2678	279.1375	5
8	916.3894	458.6984	899.3629	450.1851	898.3789	449.6931	D	<b>460.2514</b>	230.6293	443.2249	222.1161	442.2409	221.6241	4
9	987.4265	494.2169	970.4000	485.7036	969.4160	485.2116	A	<b>345.2245</b>	173.1159	328.1979	164.6026			3
10	<b>1086.4950</b>	543.7511	1069.4684	535.2378	<b>1068.4844</b>	534.7458	V	<b>274.1874</b>	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



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

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

Other BLAST [web gateways](#)

**All matches to this query**

Score	Mr(calc):	Delta	Sequence
63.0	1259.5994	0.0025	<a href="#">EQISDIDDAVR</a>
4.0	1259.6041	-0.0022	<a href="#">PTAGSVGGGMGRR</a>
2.2	1259.6081	-0.0062	<a href="#">LHFCDSNVVR</a>
1.7	1259.6081	-0.0062	<a href="#">GMGWKPGEGIGR</a>
0.5	1259.5968	0.0050	<a href="#">ASPSPFCPELR</a>
0.1	1259.5968	0.0050	<a href="#">AVLSACSSYFR</a>

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

# **MASCOT** Mascot Search Results

## Peptide View

MS/MS Fragmentation of **IEDLSQQAQLAAAEK**

Found in **NACA\_HUMAN**, Q13765|NACA\_HUMAN Nascent polypeptide-associated complex subunit alpha - Homo sapiens (Human)

Match to Query 2249: 1613.826848 from(807.920700,2+)

Title: OTMPB070622\_13.2486.2486.2.dta

Data file D:\data\_LTQOrbitrap\Marie-Pierre Bousquet\OTMPB070622\_13.RAW

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

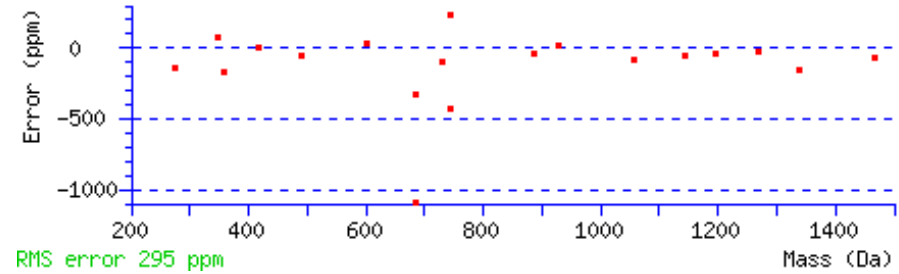
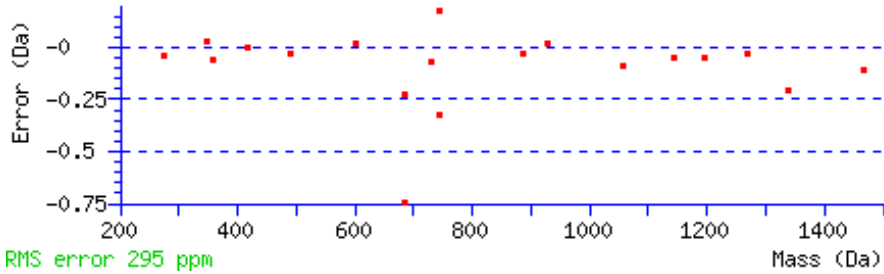
**Monoisotopic mass of neutral peptide Mr(calc):** 1613.8260

**Ions Score:** 82 **Expect:** 7.7e-007

**Matches (Bold Red):** 19/154 fragment ions using 36 most intense peaks

#	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>	#
<b>1</b>	114.0913	57.5493					<b>I</b>							<b>15</b>

2	243.1339	122.0706			225.1234	113.0653	E	1501.7493	751.3783	1484.7227	742.8650	1483.7387	742.3730	14
3	358.1609	179.5841			340.1503	170.5788	D	1372.7067	686.8570	1355.6801	678.3437	1354.6961	677.8517	13
4	471.2449	236.1261			453.2344	227.1208	L	1257.6797	629.3435	1240.6532	620.8302	1239.6692	620.3382	12
5	558.2770	279.6421			540.2664	270.6368	S	1144.5957	572.8015	1127.5691	564.2882	1126.5851	563.7962	11
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	Q	1057.5637	529.2855	1040.5371	520.7722	1039.5531	520.2802	10
7	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	Q	929.5051	465.2562	912.4785	456.7429	911.4945	456.2509	9
8	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	A	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	8
9	1013.4898	507.2485	996.4633	498.7353	995.4793	498.2433	Q	730.4094	365.7083	713.3828	357.1951	712.3988	356.7030	7
10	1126.5739	563.7906	1109.5473	555.2773	1108.5633	554.7853	L	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	6
11	1197.6110	599.3091	1180.5844	590.7959	1179.6004	590.3039	A	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	5
12	1268.6481	634.8277	1251.6216	626.3144	1250.6375	625.8224	A	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
13	1339.6852	670.3462	1322.6587	661.8330	1321.6747	661.3410	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
14	1468.7278	734.8675	1451.7013	726.3543	1450.7172	725.8623	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI BLAST search of [IEDLSQQAQLAAAEK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.7	1613.8260	0.0008	<a href="#">IEDLSQQAQLAAAEK</a>
5.7	1613.8334	-0.0066	<a href="#">KDLTYSVICKK</a>
4.5	1613.8195	0.0073	<a href="#">MKALEETVRHQEK</a>
3.9	1613.8334	-0.0066	<a href="#">LEVKMEIGLPDEK</a>

2.4	1613.8242	0.0026	<a href="#">HCMASGAVLNKVRR</a>
2.1	1613.8195	0.0073	<a href="#">KNNPQCLLNGSLGEK</a>
2.0	1613.8334	-0.0066	<a href="#">KDLTYSVICKK</a>
1.4	1613.8260	0.0008	<a href="#">KPASSSSAPQNIPK</a>
1.3	1613.8301	-0.0032	<a href="#">YITNKEEFTLQK</a>
0.9	1613.8260	0.0008	<a href="#">SKVEETTEHLVTK</a>

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