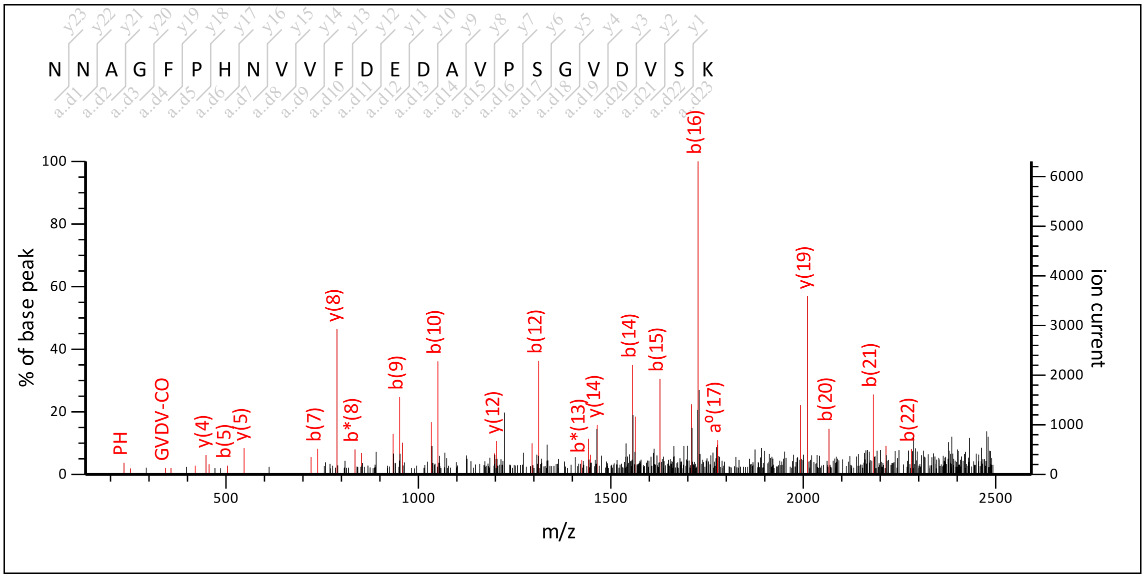
Table S2

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 0

MS/MS Fragmentation of **NNAGFPHNVVFDEDAVPSGVDVSK**
Found in **gi|115465862** in **NCBInr**, Os06g0101600 [Oryza sativa Japonica Group]

Match to Query 31: 2513.339624 from(2514.346900,1+) intensity(0.0000) index(12)
Title: Label: H6, Spot_Id: 228929, Peak_List_Id: 257551, MSMS Job_Run_Id: 24925, Comment:
Data file ppw_H6_138985133400.txt



135.09 to 2592.79

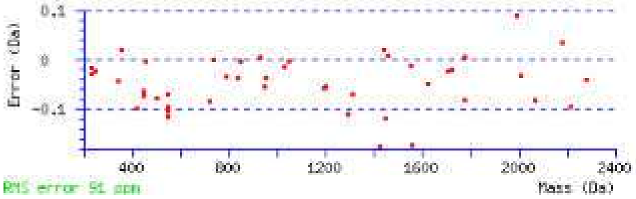
Label all possible matches ○ Label matches used for scoring ●

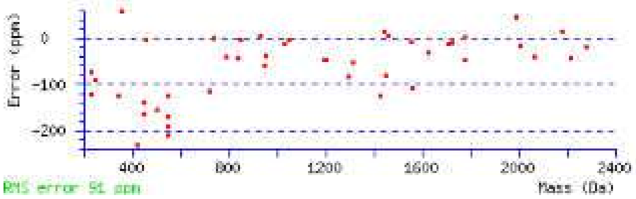
Monoisotopic mass of neutral peptide Mr(calc): 2513.1823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 7.9e-05
Matches : 45/461 fragment ions using 86 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495	N						24
2	87.0553	201.0982	184.0717		229.0931	212.0666		158.0924	N	2341.1095	2340.1143	2400.1466	2383.1201	2382.1361	23
3	44.0495	272.1353	255.1088		300.1302	283.1037			A	2270.0724		2286.1037	2269.0772	2268.0931	22
4	30.0338	329.1568	312.1302		***357.1517***	340.1252			G			**2215.0666**	2198.0400	2197.0560	21
5	120.0808	476.2252	459.1987		***504.2201***	487.1936			F	2065.9825		2158.0451	2141.0186	2140.0346	20
6	70.0651	573.2780	556.2514		601.2729	584.2463		547.2623	P	1968.9298	1967.9345	**2010.9767**	1993.9502	1992.9661	19
7	110.0713	710.3369	693.3103		***738.3318***	721.3052			H	1831.8708		1913.9239	1896.8974	1895.9134	18
8	87.0553	824.3798	807.3533		***852.3747***	835.3482		781.3740	N	1717.8279	1716.8327	**1776.8650**	1759.8385	1758.8545	17
9	72.0808	923.4482	906.4217		***951.4431***	934.4166		909.4326	V	1618.7595	1631.7799	1662.8221	1645.7956	1644.8115	16
10	72.0808	1022.5166	1005.4901		***1050.5116***	1033.4850		1008.5010	V	1519.6911	1532.7115	**1563.7537**	1546.7271	1545.7431	15
11	120.0808	1169.5851	1152.5585		***1197.5800***	1180.5534			F	1372.6227		**1464.6853**	1447.6587	1446.6747	14
12	88.0393	1284.6120	1267.5854	1266.6014	***1312.6069***	1295.5804	1294.5963	1240.6222	D	1257.5957	1256.6005	1317.6169	1300.5903	1299.6063	13
13	102.0550	1413.6546	1396.6280	1395.6440	***1441.6495***	1424.6230	1423.6389	1355.6491	E	1128.5531	1127.5579	**1202.5899**	1185.5634	1184.5794	12
14	88.0393	1528.6815	1511.6550	1510.6710	***1556.6764***	1539.6499	1538.6659	1484.6917	D	1013.5262	1012.5310	1073.5473	1056.5208	1055.5368	11
15	44.0495	1599.7186	1582.6921	1581.7081	***1627.7136***	1610.6870	1609.7030		A	942.4891		**958.5204**	941.4938	940.5098	10
16	72.0808	1698.7871	1681.7605	1680.7765	***1726.7820***	1709.7554	1708.7714	1684.7714	V	843.4207	856.4411	887.4833	870.4567	869.4727	9
17	70.0651	1795.8398	1778.8133	1777.8293	1823.8347	1806.8082	1805.8242	1769.8242	P	746.3679	745.3727	**788.4149**	771.3883	770.4043	8
18	60.0444	1882.8719	1865.8453	1864.8613	1910.8668	1893.8402	1892.8562	1866.8769	S	659.3359	658.3406	691.3621	674.3355	673.3515	7
19	30.0338	1939.8933	1922.8668	1921.8828	1967.8882	1950.8617	1949.8777		G			604.3301	587.3035	586.3195	6

20	72.0808	2038.9617	2021.9352	2020.9512	***2066.9566***	2049.9301	2048.9461	2024.9461	**V**	503.2460	516.2664	**547.3086**	530.2821	529.2980	**5**
21	88.0393	2153.9887	2136.9621	2135.9781	***2181.9836***	2164.9570	2163.9730	2109.9988	**D**	388.2191	387.2238	**448.2402**	431.2136	430.2296	**4**
22	72.0808	2253.0571	2236.0305	2235.0465	***2281.0520***	2264.0255	2263.0414	2239.0414	**V**	289.1506	302.1710	333.2132	316.1867	315.2027	**3**
23	60.0444	2340.0891	2323.0626	2322.0785	2368.0840	2351.0575	2350.0735	2324.0942	**S**	202.1186	201.1234	234.1448	217.1183	216.1343	**2**
24	101.1073								**K**	74.0237	73.0284	147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NA	158.0924	186.0873	**NAG**	215.1139	243.1088	**NAGF**	362.1823	390.1772
NAGFP	459.2350	487.2300	**NAGFPH**	596.2940	624.2889	**AG**	101.0709	129.0659
AGF	248.1394	276.1343	**AGFP**	345.1921	373.1870	**AGFPH**	482.2510	510.2459
AGFPHN	596.2940	624.2889	**AGFPHNV**	695.3624	723.3573	**GF**	177.1022	205.0972
GFP	274.1550	302.1499	**GFPH**	411.2139	439.2088	**GFPHN**	525.2568	553.2518
GFPHNV	624.3253	652.3202	**FP**	217.1335	245.1285	**FPH**	354.1925	382.1874
FPHN	468.2354	496.2303	**FPHNV**	567.3038	595.2987	**FPHNVV**	666.3722	694.3671
PH	207.1240	235.1190	**PHN**	321.1670	349.1619	**PHNV**	420.2354	448.2303
PHNVV	519.3038	547.2987	**PHNVVF**	666.3722	694.3671	**HN**	224.1142	252.1091
HNV	323.1826	351.1775	**HNVV**	422.2510	450.2459	**HNVVF**	569.3194	597.3144
HNVVFD	684.3464	712.3413	**NV**	186.1237	214.1186	**NVV**	285.1921	313.1870
NVVF	432.2605	460.2554	**NVVFD**	547.2875	575.2824	**NVVFDE**	676.3301	704.3250
VV	171.1492	199.1441	**VVF**	318.2176	346.2125	**VVFD**	433.2445	461.2395
VVFDE	562.2871	590.2821	**VVFDED**	677.3141	705.3090	**VF**	219.1492	247.1441
VFD	334.1761	362.1710	**VFDE**	463.2187	491.2136	**VFDED**	578.2457	606.2406
VFDEDA	649.2828	677.2777	**FD**	235.1077	263.1026	**FDE**	364.1503	392.1452
FDED	479.1773	507.1722	**FDEDA**	550.2144	578.2093	**FDEDAV**	649.2828	677.2777
DE	217.0819	245.0768	**DED**	332.1088	360.1038	**DEDA**	403.1460	431.1409
DEDAV	502.2144	530.2093	**DEDAVP**	599.2671	627.2620	**DEDAVPS**	686.2992	714.2941
ED	217.0819	245.0768	**EDA**	288.1190	316.1139	**EDAV**	387.1874	415.1823
EDAVP	484.2402	512.2351	**EDAVPS**	571.2722	599.2671	**EDAVPSG**	628.2937	656.2886
DA	159.0764	187.0713	**DAV**	258.1448	286.1397	**DAVP**	355.1976	383.1925
DAVPS	442.2296	470.2245	**DAVPSG**	499.2511	527.2460	**DAVPSGV**	598.3195	626.3144
AV	143.1179	171.1128	**AVP**	240.1707	268.1656	**AVPS**	327.2027	355.1976
AVPSG	384.2241	412.2191	**AVPSGV**	483.2926	511.2875	**AVPSGVD**	598.3195	626.3144
AVPSGVDV	697.3879	725.3828	**VP**	169.1335	197.1285	**VPS**	256.1656	284.1605
VPSG	313.1870	341.1819	**VPSGV**	412.2554	440.2504	**VPSGVD**	527.2824	555.2773
VPSGVDV	626.3508	654.3457	**PS**	157.0972	185.0921	**PSG**	214.1186	242.1135
PSGV	313.1870	341.1819	**PSGVD**	428.2140	456.2089	**PSGVDV**	527.2824	555.2773
PSGVDVS	614.3144	642.3093	**SG**	117.0659	145.0608	**SGV**	216.1343	244.1292
SGVD	331.1612	359.1561	**SGVDV**	430.2296	458.2245	**SGVDVS**	517.2617	545.2566
GV	129.1022	157.0972	**GVD**	244.1292	272.1241	**GVDV**	343.1976	371.1925
GVDVS	430.2296	458.2245	**VD**	187.1077	215.1026	**VDV**	286.1761	314.1710
VDVS	373.2082	401.2031	**DV**	187.1077	215.1026	**DVS**	274.1397	302.1347
VS	159.1128	187.1077						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.4	2513.1823	0.1573	NNAGFPHNVVFDEDAVPSGVDVSK
34.0	2513.1459	0.1937	NNAGFPHNVVFDEDEVPGGVDASK
6.8	2513.3278	0.0118	DARIFPQEIIEFPAVLVDGATGR
3.3	2513.2142	0.1255	KTMDVQLYTEVMESVQTIDAGR
2.6	2513.2299	0.1097	GLEQSYDTPNPQLIAVSNQHFR
1.9	2513.2591	0.0805	GNQFEVLVDSINGDFFLTKGWK
0.9	2513.1203	0.2194	AGDPYEMFTHDELIVMGRDASK
0.8	2513.2121	0.1275	YVQLANVYAAEGNWAEMGRISR
0.2	2513.0958	0.2438	KDFGYSFLCHGLGQGNTYDFST

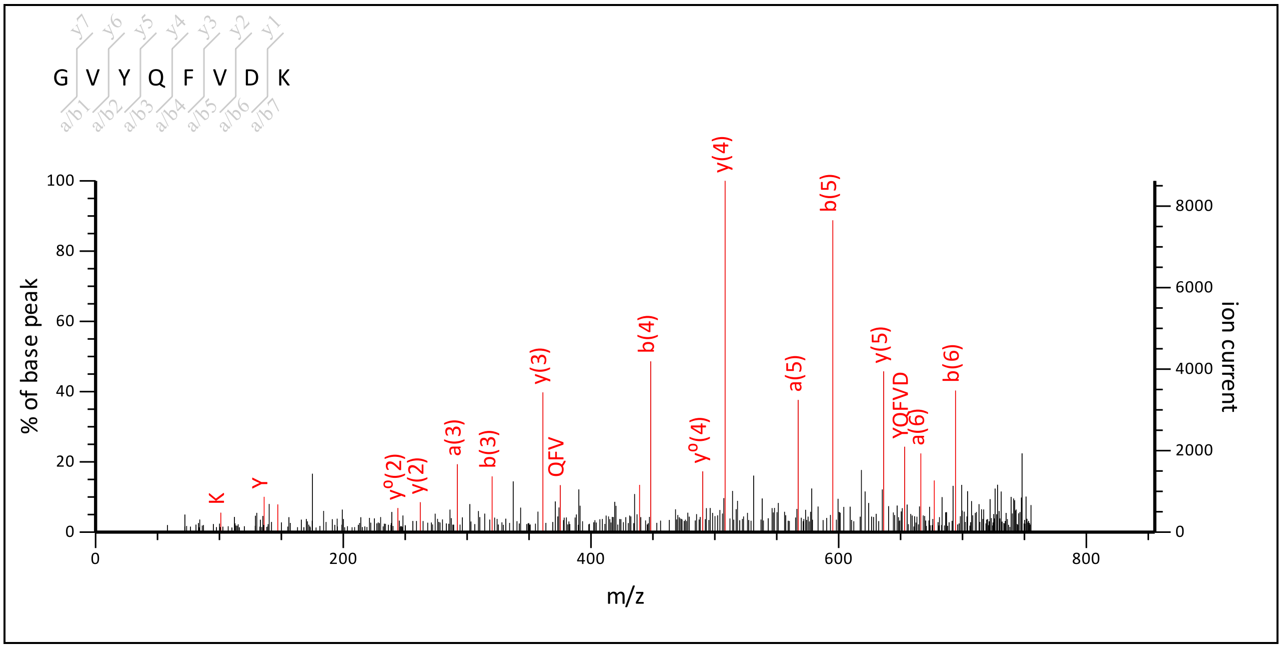
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 2

MS/MS Fragmentation of **GVYQFVDK**
Found in **gi|1835731** in **NCBInr**, photosystem II 10 kDa polypeptide [Oryza sativa Indica Group]

Match to Query 51: 954.464404 from(955.471680,1+) intensity(0.0000) index(6)
Title: Label: K5, Spot_Id: 219748, Peak_List_Id: 225860, MSMS Job_Run_Id: 21792, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K5_136842223800.txt



0 to 855.27

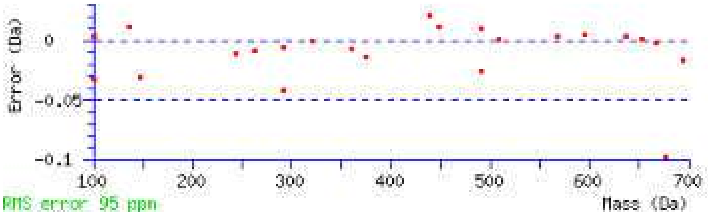
Label all possible matches ○ Label matches used for scoring ●

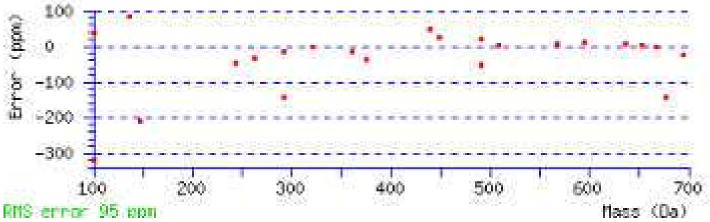
Monoisotopic mass of neutral peptide Mr(calc): 954.4811
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.67
Matches : 23/97 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	30.0338	30.0338			58.0287			44.0495	G						8
2	72.0808	129.1022			157.0972			115.0866	V	854.4043	867.4247	898.4669	881.4403	880.4563	7
3	136.0757	**292.1656**			**320.1605**				Y	691.3410		799.3985	782.3719	781.3879	6
4	101.0709	420.2241	403.1976		**448.2191**	431.1925		363.2027	Q	563.2824	562.2871	***636.3352***	619.3086	618.3246	5
5	120.0808	**567.2926**	550.2660		**595.2875**	578.2609			F	416.2140		***508.2766***	491.2500	490.2660	4
6	72.0808	**666.3610**	649.3344		**694.3559**	677.3293		652.3453	V	317.1456	330.1660	***361.2082***	344.1816	343.1976	3
7	88.0393	781.3879	764.3614	763.3774	809.3828	792.3563	791.3723	737.3981	D	202.1186	201.1234	***262.1397***	245.1132	244.1292	2
8	101.1073								K	74.0237	73.0284	***147.1128***	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VY	235.1441	263.1390	VYQ	363.2027	391.1976	VYQF	510.2711	538.2660
VYQFV	609.3395	637.3344	YQ	264.1343	292.1292	YQF	411.2027	439.1976
YQFV	510.2711	538.2660	YQFVD	625.2980	653.2930	QF	248.1394	276.1343
QFV	347.2078	375.2027	QFVD	462.2347	490.2296	FV	219.1492	247.1441

FVD	334.1761	362.1710	**VD**	187.1077	215.1026			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.3	954.4811	-0.0167	GVYQFVDK
28.3	954.3964	0.0680	SSDMASVDK
26.9	954.3964	0.0680	TDGSSMVDK
25.6	954.4117	0.0527	FNDAMVDK
24.4	954.4077	0.0568	MTSSTSDAR
24.4	954.3865	0.0779	NFADMGER
24.3	954.5076	-0.0432	VYGKFWR
24.2	954.4447	0.0197	NFGEFVDK
24.2	954.4845	-0.0200	TMKSFVDK
23.8	954.4593	0.0051	VYGRMADK

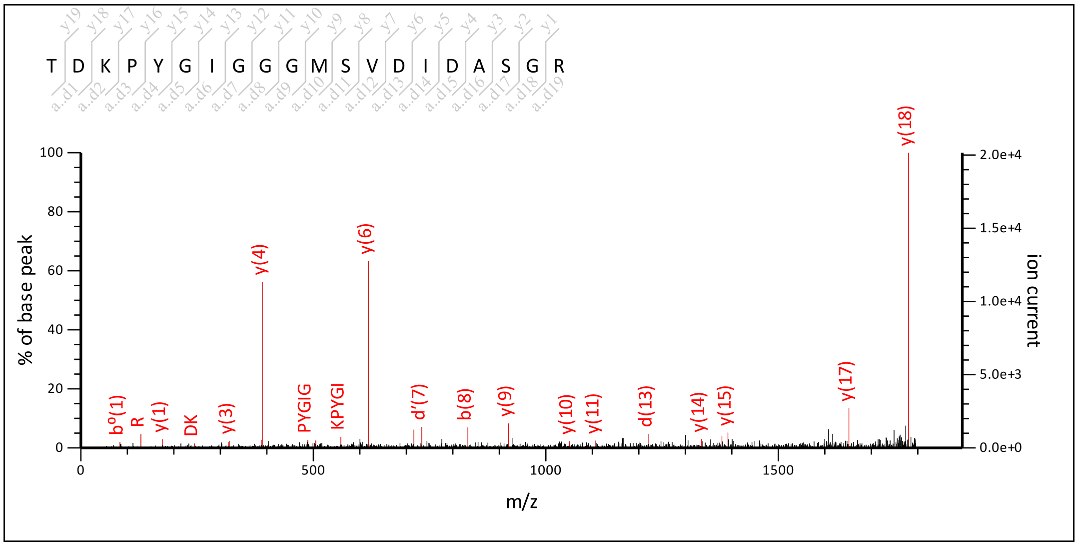
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 2

MS/MS Fragmentation of **TDKPYGIGGGMSVDIDASGR**
Found in **gi|1835731** in **NCBInr**, photosystem II 10 kDa polypeptide [Oryza sativa Indica Group]

Match to Query 175: 1994.933424 from(1995.940700,1+) intensity(0.0000) index(27)
Title: Label: K5, Spot_Id: 219748, Peak_List_Id: 225865, MSMS Job_Run_Id: 21792, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K5_136842223800.txt



0 to 1895.7

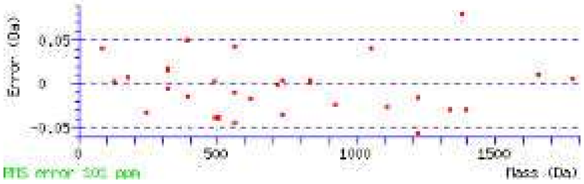
Label all possible matches ○ Label matches used for scoring ●

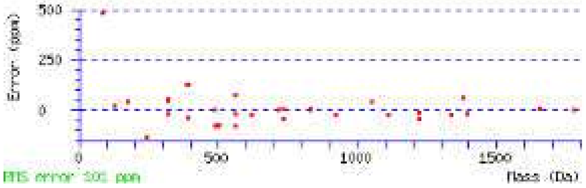
Monoisotopic mass of neutral peptide Mr(calc): 1994.9368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 124 **Expect:** 6.1e-10
Matches : 33/401 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	88.0393	189.0870		171.0764	217.0819		199.0713	145.0972		D	1834.8752	1833.8800		1894.8964	1877.8698
3	101.1073	317.1819	300.1554	299.1714	345.1769	328.1503	327.1663	260.1241		K	1706.7803	1705.7850		***1779.8694***	1762.8429
4	70.0651	414.2347	397.2082	396.2241	442.2296	425.2031	424.2191	388.2191		P	1609.7275	1608.7322		***1651.7744***	1634.7479
5	136.0757	577.2980	560.2715	559.2875	605.2930	588.2664	587.2824			Y	1446.6642			1554.7217	1537.6951
6	30.0338	634.3195	617.2930	616.3089	662.3144	645.2879	644.3039			G				***1391.6584***	1374.6318
7	86.0964	747.4036	730.3770	729.3930	775.3985	758.3719	757.3879	719.3723	733.3879	I	1276.5586	1289.5790	1303.5947	***1334.6369***	1317.6103
8	30.0338	804.4250	787.3985	786.4145	**832.4199**	815.3934	814.4094			G				***1221.5528***	1204.5263
9	30.0338	861.4465	844.4199	843.4359	889.4414	872.4149	871.4308			G				1164.5314	1147.5048
10	30.0338	918.4680	901.4414	900.4574	946.4629	929.4363	928.4523			G				***1107.5099***	1090.4834
11	104.0528	1049.5084	1032.4819	1031.4979	1077.5034	1060.4768	1059.4928	989.5051		M	974.4538	973.4585		***1050.4884***	1033.4619
12	60.0444	1136.5405	1119.5139	1118.5299	1164.5354	1147.5088	1146.5248	1120.5456		S	887.4217	886.4265		***919.4480***	902.4214
13	72.0808	1235.6089	1218.5823	1217.5983	1263.6038	1246.5773	1245.5932	1221.5932		V	788.3533	801.3737		***832.4159***	815.3894
14	88.0393	1350.6358	1333.6093	1332.6253	**1378.6307**	1361.6042	1360.6202	1306.6460		D	673.3264	672.3311		***733.3475***	716.3210
15	86.0964	1463.7199	1446.6933	1445.7093	1491.7148	1474.6883	1473.7042	1435.6886	1449.7042	I	560.2423	573.2627	587.2784	***618.3206***	601.2940
16	88.0393	1578.7468	1561.7203	1560.7363	1606.7418	1589.7152	1588.7312	1534.7570		D	445.2154	444.2201		***505.2365***	488.2100
17	44.0495	1649.7840	1632.7574	1631.7734	1677.7789	1660.7523	1659.7683			A	374.1783			***390.2096***	373.1830
18	60.0444	1736.8160	1719.7894	1718.8054	1764.8109	1747.7843	1746.8003	1720.8211		S	287.1462	286.1510		***319.1724***	302.1459
19	30.0338	1793.8374	1776.8109	1775.8269	1821.8324	1804.8058	1803.8218			G				232.1404	215.1139
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DK	216.1343	244.1292	DKP	313.1870	341.1819	DKPY	476.2504	504.2453

DKPYG	533.2718	561.2667	**DKPYGI**	646.3559	674.3508	**KP**	198.1601	226.1550
KPY	361.2234	389.2183	**KPYG**	418.2449	446.2398	**KPYGI**	531.3289	559.3239
KPYGIG	588.3504	616.3453	**KPYGIGG**	645.3719	673.3668	**PY**	233.1285	261.1234
PYG	290.1499	318.1448	**PYGI**	403.2340	431.2289	**PYGIG**	460.2554	488.2504
PYGIGG	517.2769	545.2718	**PYGIGGG**	574.2984	602.2933	**YG**	193.0972	221.0921
YGI	306.1812	334.1761	**YGIG**	363.2027	391.1976	**YGIGG**	420.2241	448.2191
YGIGGG	477.2456	505.2405	**YGIGGGM**	608.2861	636.2810	**YGIGGGMS**	695.3181	723.3130
GI	143.1179	171.1128	**GIG**	200.1394	228.1343	**GIGG**	257.1608	285.1557
GIGGG	314.1823	342.1772	**GIGGGM**	445.2228	473.2177	**GIGGGMS**	532.2548	560.2497
GIGGGMSV	631.3232	659.3181	**IG**	143.1179	171.1128	**IGG**	200.1394	228.1343
IGGG	257.1608	285.1557	**IGGGM**	388.2013	416.1962	**IGGGMS**	475.2333	503.2282
IGGGMSV	574.3017	602.2967	**IGGGMSVD**	689.3287	717.3236	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGM**	275.1172	303.1122	**GGGMS**	362.1493	390.1442
GGGMSV	461.2177	489.2126	**GGGMSVD**	576.2446	604.2395	**GGGMSVDI**	689.3287	717.3236
GG	87.0553	115.0502	**GGM**	218.0958	246.0907	**GGMS**	305.1278	333.1227
GGMSV	404.1962	432.1911	**GGMSVD**	519.2232	547.2181	**GGMSVDI**	632.3072	660.3021
GM	161.0743	189.0692	**GMS**	248.1063	276.1013	**GMSV**	347.1748	375.1697
GMSVD	462.2017	490.1966	**GMSVDI**	575.2858	603.2807	**GMSVDID**	690.3127	718.3076
MS	191.0849	219.0798	**MSV**	290.1533	318.1482	**MSVD**	405.1802	433.1751
MSVDI	518.2643	546.2592	**MSVDID**	633.2912	661.2862	**SV**	159.1128	187.1077
SVD	274.1397	302.1347	**SVDI**	387.2238	415.2187	**SVDID**	502.2508	530.2457
SVDIDA	573.2879	601.2828	**SVDIDAS**	660.3199	688.3148	**VD**	187.1077	215.1026
VDI	300.1918	328.1867	**VDID**	415.2187	443.2136	**VDIDA**	486.2558	514.2508
VDIDAS	573.2879	601.2828	**VDIDASG**	630.3093	658.3042	**DI**	201.1234	229.1183
DID	316.1503	344.1452	**DIDA**	387.1874	415.1823	**DIDAS**	474.2195	502.2144
DIDASG	531.2409	559.2358	**ID**	201.1234	229.1183	**IDA**	272.1605	300.1554
IDAS	359.1925	387.1874	**IDASG**	416.2140	444.2089	**DA**	159.0764	187.0713
DAS	246.1084	274.1034	**DASG**	303.1299	331.1248	**AS**	131.0815	159.0764
ASG	188.1030	216.0979	**SG**	117.0659	145.0608			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
123.8	1994.9368	-0.0033	TDKPYGIGGGMSVDIDASGR
14.8	1994.8826	0.0508	MGCASASWIEAVVDEASGR
14.6	1994.8795	0.0539	GHGMCGMNTMVSAVVTSTR
13.2	1995.0115	-0.0781	RNTWVFVFGNIGWSQGK
12.9	1994.9983	-0.0649	DTMLANVAATSELFLLDR
12.1	1994.9553	-0.0219	TNMAAEDVEFLEAMLRR
11.4	1994.9078	0.0257	VASCDIPIPYMDEGSSVR
11.1	1994.9302	0.0032	CPPHLNPSSSSCISSPIR
10.9	1995.0637	-0.1302	EILSGIAVPGLNVVDENTR
10.7	1995.0762	-0.1428	ISITAPLHASPHRPAGAGSR

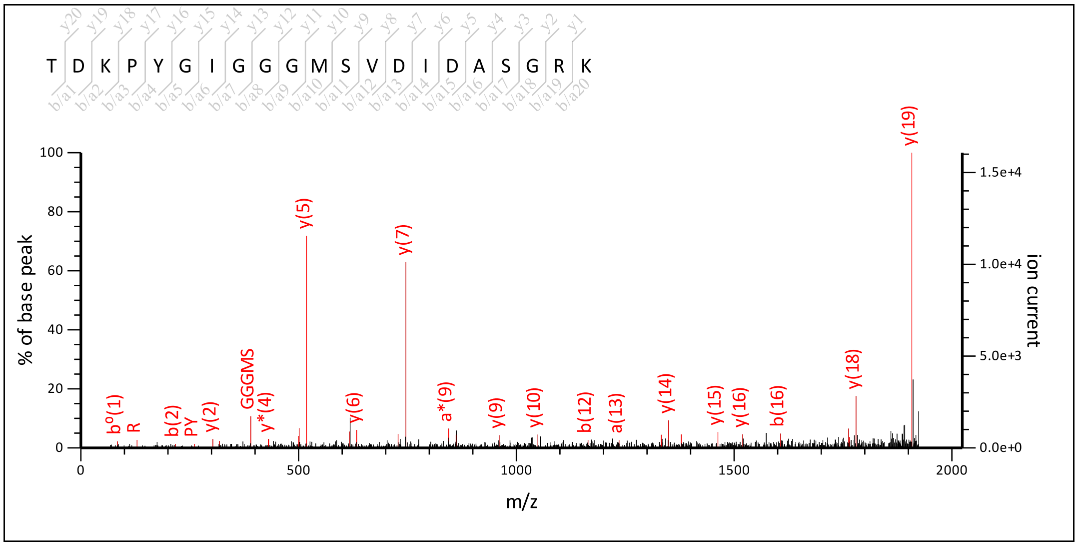
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 2

MS/MS Fragmentation of **TDKPYGIGGGMSVDIDASGRK**
Found in **gi|1835731** in **NCBInr**, photosystem II 10 kDa polypeptide [Oryza sativa Indica Group]

Match to Query 179: 2123.028324 from(2124.035600,1+) intensity(0.0000) index(29)
Title: Label: K5, Spot_Id: 219748, Peak_List_Id: 225867, MSMS Job_Run_Id: 21792, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K5_136842223800.txt



0 to 2023.87

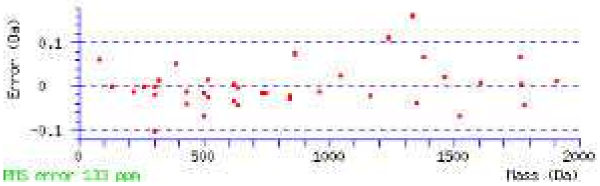
Label all possible matches ○ Label matches used for scoring ●

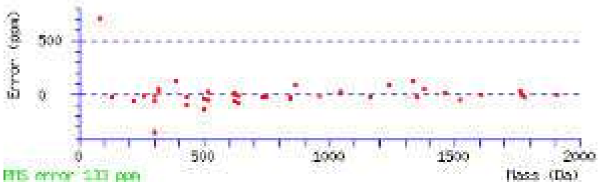
Monoisotopic mass of neutral peptide Mr(calc): 2123.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 79 **Expect:** 1.9e-05
Matches : 43/424 fragment ions using 57 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	88.0393	189.0870		171.0764	**217.0819**		199.0713	145.0972		D	1962.9702	1961.9749		2022.9913	2005.9648
3	101.1073	317.1819	300.1554	299.1714	345.1769	328.1503	327.1663	260.1241		K	1834.8752	1833.8800		***1907.9644***	1890.9378
4	70.0651	414.2347	397.2082	396.2241	442.2296	425.2031	424.2191	388.2191		P	1737.8225	1736.8272		***1779.8694***	1762.8429
5	136.0757	577.2980	560.2715	559.2875	605.2930	588.2664	587.2824			Y	1574.7591			1682.8166	1665.7901
6	30.0338	634.3195	617.2930	616.3089	662.3144	645.2879	644.3039			G				***1519.7533***	1502.7268
7	86.0964	747.4036	730.3770	729.3930	775.3985	758.3719	757.3879	719.3723	733.3879	I	1404.6536	1417.6740	1431.6897	***1462.7319***	1445.7053
8	30.0338	804.4250	787.3985	786.4145	832.4199	815.3934	814.4094			G				***1349.6478***	1332.6212
9	30.0338	**861.4465**	844.4199	843.4359	889.4414	872.4149	871.4308			G				1292.6263	1275.5998
10	30.0338	918.4680	901.4414	900.4574	946.4629	929.4363	928.4523			G				***1235.6049***	1218.5783
11	104.0528	1049.5084	1032.4819	1031.4979	1077.5034	1060.4768	1059.4928	989.5051		M	1102.5487	1101.5535		1178.5834	1161.5568
12	60.0444	1136.5405	1119.5139	1118.5299	**1164.5354**	1147.5088	1146.5248	1120.5456		S	1015.5167	1014.5215		***1047.5429***	1030.5164
13	72.0808	**1235.6089**	1218.5823	1217.5983	1263.6038	1246.5773	1245.5932	1221.5932		V	916.4483	929.4687		***960.5109***	943.4843
14	88.0393	1350.6358	1333.6093	1332.6253	**1378.6307**	1361.6042	1360.6202	1306.6460		D	801.4213	800.4261		***861.4425***	844.4159
15	86.0964	1463.7199	1446.6933	1445.7093	1491.7148	1474.6883	1473.7042	1435.6886	1449.7042	I	688.3373	701.3577	715.3733	***746.4155***	729.3890
16	88.0393	1578.7468	1561.7203	1560.7363	**1606.7418**	1589.7152	1588.7312	1534.7570		D	573.3103	572.3151		***633.3315***	616.3049
17	44.0495	1649.7840	1632.7574	1631.7734	1677.7789	1660.7523	1659.7683			A	502.2732			***518.3045***	501.2780
18	60.0444	1736.8160	1719.7894	1718.8054	**1764.8109**	1747.7843	1746.8003	1720.8211		S	415.2412	414.2459		447.2674	430.2409
19	30.0338	1793.8374	1776.8109	1775.8269	1821.8324	1804.8058	1803.8218			G				360.2354	343.2088
20	129.1135	1949.9386	1932.9120	1931.9280	1977.9335	1960.9069	1959.9229	1864.8746		R	202.1186	201.1234		***303.2139***	286.1874
21	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

DK	216.1343	244.1292	**DKP**	313.1870	341.1819	**DKPY**	476.2504	504.2453
DKPYG	533.2718	561.2667	**DKPYGI**	646.3559	674.3508	**KP**	198.1601	226.1550
KPY	361.2234	389.2183	**KPYG**	418.2449	446.2398	**KPYGI**	531.3289	559.3239
KPYGIG	588.3504	616.3453	**KPYGIGG**	645.3719	673.3668	**PY**	233.1285	261.1234
PYG	290.1499	318.1448	**PYGI**	403.2340	431.2289	**PYGIG**	460.2554	488.2504
PYGIGG	517.2769	545.2718	**PYGIGGG**	574.2984	602.2933	**YG**	193.0972	221.0921
YGI	306.1812	334.1761	**YGIG**	363.2027	391.1976	**YGIGG**	420.2241	448.2191
YGIGGG	477.2456	505.2405	**YGIGGGM**	608.2861	636.2810	**YGIGGGMS**	695.3181	723.3130
GI	143.1179	171.1128	**GIG**	200.1394	228.1343	**GIGG**	257.1608	285.1557
GIGGG	314.1823	342.1772	**GIGGGM**	445.2228	473.2177	**GIGGGMS**	532.2548	560.2497
GIGGGMSV	631.3232	659.3181	**IG**	143.1179	171.1128	**IGG**	200.1394	228.1343
IGGG	257.1608	285.1557	**IGGGM**	388.2013	416.1962	**IGGGMS**	475.2333	503.2282
IGGGMSV	574.3017	602.2967	**IGGGMSVD**	689.3287	717.3236	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGM**	275.1172	303.1122	**GGGMS**	362.1493	390.1442
GGGMSV	461.2177	489.2126	**GGGMSVD**	576.2446	604.2395	**GGGMSVDI**	689.3287	717.3236
GG	87.0553	115.0502	**GGM**	218.0958	246.0907	**GGMS**	305.1278	333.1227
GGMSV	404.1962	432.1911	**GGMSVD**	519.2232	547.2181	**GGMSVDI**	632.3072	660.3021
GM	161.0743	189.0692	**GMS**	248.1063	276.1013	**GMSV**	347.1748	375.1697
GMSVD	462.2017	490.1966	**GMSVDI**	575.2858	603.2807	**GMSVDID**	690.3127	718.3076
MS	191.0849	219.0798	**MSV**	290.1533	318.1482	**MSVD**	405.1802	433.1751
MSVDI	518.2643	546.2592	**MSVDID**	633.2912	661.2862	**SV**	159.1128	187.1077
SVD	274.1397	302.1347	**SVDI**	387.2238	415.2187	**SVDID**	502.2508	530.2457
SVDIDA	573.2879	601.2828	**SVDIDAS**	660.3199	688.3148	**VD**	187.1077	215.1026
VDI	300.1918	328.1867	**VDID**	415.2187	443.2136	**VDIDA**	486.2558	514.2508
VDIDAS	573.2879	601.2828	**VDIDASG**	630.3093	658.3042	**DI**	201.1234	229.1183
DID	316.1503	344.1452	**DIDA**	387.1874	415.1823	**DIDAS**	474.2195	502.2144
DIDASG	531.2409	559.2358	**DIDASGR**	687.3420	715.3369	**ID**	201.1234	229.1183
IDA	272.1605	300.1554	**IDAS**	359.1925	387.1874	**IDASG**	416.2140	444.2089
IDASGR	572.3151	600.3100	**DA**	159.0764	187.0713	**DAS**	246.1084	274.1034
DASG	303.1299	331.1248	**DASGR**	459.2310	487.2259	**AS**	131.0815	159.0764
ASG	188.1030	216.0979	**ASGR**	344.2041	372.1990	**SG**	117.0659	145.0608
SGR	273.1670	301.1619	**GR**	186.1349	214.1299			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.7	2123.0317	-0.0034	TDKPYGIGGGMSVDIDASGRK
17.4	2123.0504	-0.0220	TFNMGVGMVLVVNQEVSQR
14.7	2122.9953	0.0330	MVEVNADGKIYAAEGAADAGR
13.3	2122.9841	0.0442	TMEISINDYPLTNPDTSGR
12.7	2122.9511	0.0773	LNEMAEVQSAMELGDDTVR
12.7	2122.9511	0.0773	LNEMAEVQSAMELGDDTVR
12.6	2123.0205	0.0078	GLSSPSMDEGALFATPSTSIR
12.0	2123.0019	0.0265	SVEDDSIPSFSGGIDDSLRK
11.7	2123.0429	-0.0146	ISYNLAMANVDEIRQSQR
11.2	2123.1627	-0.1343	SLTGFVGLIASLVFLDQSTR

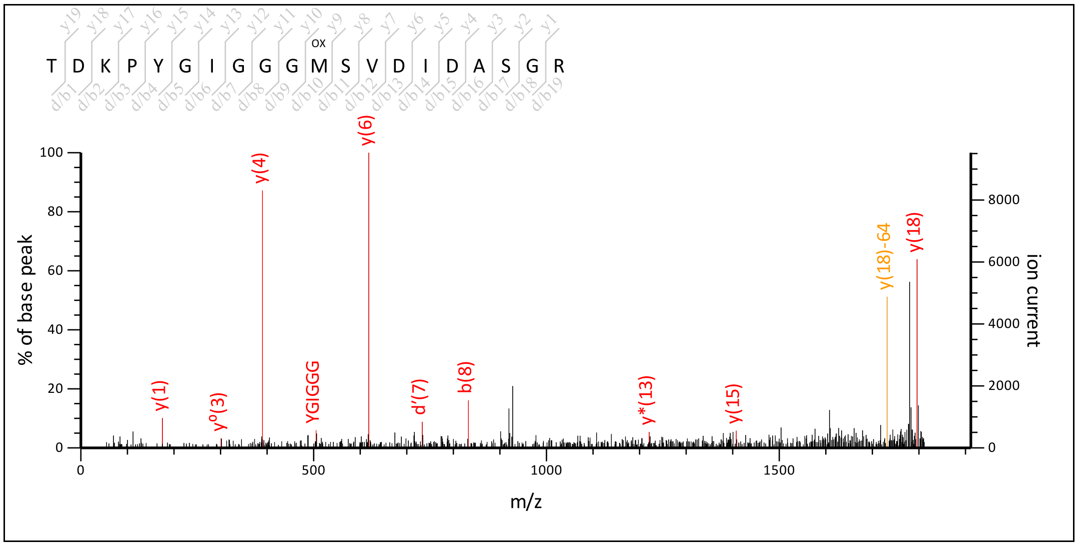
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 2

MS/MS Fragmentation of TDKPYGIGGGMSVDIDASGR
Found in gi|1835731 in NCBInr, photosystem II 10 kDa polypeptide [Oryza sativa Indica Group]

Match to Query 177: 2010.909624 from(2011.916900,1+) intensity(0.0000) index(28)
Title: Label: K5, Spot_Id: 219748, Peak_List_Id: 225866, MSMS Job_Run_Id: 21792, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K5_136842223800.txt



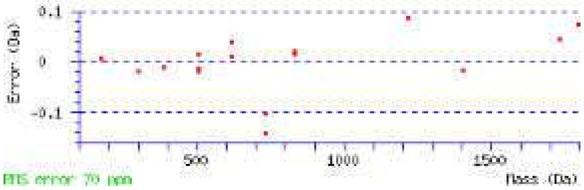
0 to 1911.46

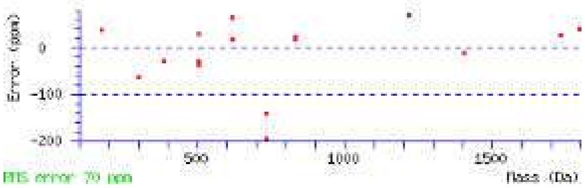
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2010.9317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 **Expect:** 0.017
Matches : 16/551 fragment ions using 18 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	88.0393	189.0870		171.0764	217.0819		199.0713	145.0972		D	1850.8701	1849.8749		1910.8913	1893.8647
3	101.1073	317.1819	300.1554	299.1714	345.1769	328.1503	327.1663	260.1241		K	1722.7752	1721.7799		***1795.8643***	1778.8378
4	70.0651	414.2347	397.2082	396.2241	442.2296	425.2031	424.2191	388.2191		P	1625.7224	1624.7272		1667.7694	1650.7428
5	136.0757	577.2980	560.2715	559.2875	605.2930	588.2664	587.2824			Y	1462.6591			1570.7166	1553.6901
6	30.0338	634.3195	617.2930	616.3089	662.3144	645.2879	644.3039			G				***1407.6533***	1390.6267
7	86.0964	747.4036	730.3770	729.3930	775.3985	758.3719	757.3879	719.3723	733.3879	I	1292.5536	1305.5740	1319.5896	1350.6318	1333.6053
8	30.0338	804.4250	787.3985	786.4145	832.4199	815.3934	814.4094			G				1237.5477	1220.5212
9	30.0338	861.4465	844.4199	843.4359	889.4414	872.4149	871.4308			G				1180.5263	1163.4997
10	30.0338	918.4680	901.4414	900.4574	946.4629	929.4363	928.4523			G				1123.5048	1106.4783
11	120.0478	1065.5034	1048.4768	1047.4928	1093.4983	1076.4717	1075.4877	989.5051		M	974.4538	973.4585		1066.4834	1049.4568
12	60.0444	1152.5354	1135.5088	1134.5248	1180.5303	1163.5038	1162.5197	1136.5405		S	887.4217	886.4265		919.4480	902.4214
13	72.0808	1251.6038	1234.5773	1233.5932	1279.5987	1262.5722	1261.5882	1237.5882		V	788.3533	801.3737		***832.4159***	815.3894
14	88.0393	1366.6307	1349.6042	1348.6202	1394.6257	1377.5991	1376.6151	1322.6409		D	673.3264	672.3311		***733.3475***	716.3210
15	86.0964	1479.7148	1462.6883	1461.7042	1507.7097	1490.6832	1489.6992	1451.6835	1465.6992	I	560.2423	573.2627	587.2784	***618.3206***	601.2940
16	88.0393	1594.7418	1577.7152	1576.7312	1622.7367	1605.7101	1604.7261	1550.7519		D	445.2154	444.2201		***505.2365***	488.2100
17	44.0495	1665.7789	1648.7523	1647.7683	1693.7738	1676.7472	1675.7632			A	374.1783			***390.2096***	373.1830
18	60.0444	1752.8109	1735.7843	1734.8003	1780.8058	1763.7793	1762.7952	1736.8160		S	287.1462	286.1510		319.1724	302.1459
19	30.0338	1809.8324	1792.8058	1791.8218	1837.8273	1820.8007	1819.8167			G				232.1404	215.1139
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DK	216.1343	244.1292	**DKP**	313.1870	341.1819	**DKPY**	476.2504	504.2453
DKPYG	533.2718	561.2667	**DKPYGI**	646.3559	674.3508	**KP**	198.1601	226.1550
KPY	361.2234	389.2183	**KPYG**	418.2449	446.2398	**KPYGI**	531.3289	559.3239
KPYGIG	588.3504	616.3453	**KPYGIGG**	645.3719	673.3668	**PY**	233.1285	261.1234
PYG	290.1499	318.1448	**PYGI**	403.2340	431.2289	**PYGIG**	460.2554	488.2504
PYGIGG	517.2769	545.2718	**PYGIGGG**	574.2984	602.2933	**YG**	193.0972	221.0921
YGI	306.1812	334.1761	**YGIG**	363.2027	391.1976	**YGIGG**	420.2241	448.2191
YGIGGG	477.2456	505.2405	**YGIGGGM**	624.2810	652.2759	**GI**	143.1179	171.1128
GIG	200.1394	228.1343	**GIGG**	257.1608	285.1557	**GIGGG**	314.1823	342.1772
GIGGGM	461.2177	489.2126	**GIGGGMS**	548.2497	576.2446	**GIGGGMSV**	647.3181	675.3130
IG	143.1179	171.1128	**IGG**	200.1394	228.1343	**IGGG**	257.1608	285.1557
IGGGM	404.1962	432.1911	**IGGGMS**	491.2282	519.2232	**IGGGMSV**	590.2967	618.2916
GG	87.0553	115.0502	**GGG**	144.0768	172.0717	**GGGM**	291.1122	319.1071
GGGMS	378.1442	406.1391	**GGGMSV**	477.2126	505.2075	**GGGMSVD**	592.2395	620.2345
GG	87.0553	115.0502	**GGM**	234.0907	262.0856	**GGMS**	321.1227	349.1176
GGMSV	420.1911	448.1860	**GGMSVD**	535.2181	563.2130	**GGMSVDI**	648.3021	676.2971
GM	177.0692	205.0641	**GMS**	264.1013	292.0962	**GMSV**	363.1697	391.1646
GMSVD	478.1966	506.1915	**GMSVDI**	591.2807	619.2756	**MS**	207.0798	235.0747
MSV	306.1482	334.1431	**MSVD**	421.1751	449.1701	**MSVDI**	534.2592	562.2541
MSVDID	649.2862	677.2811	**SV**	159.1128	187.1077	**SVD**	274.1397	302.1347
SVDI	387.2238	415.2187	**SVDID**	502.2508	530.2457	**SVDIDA**	573.2879	601.2828
SVDIDAS	660.3199	688.3148	**VD**	187.1077	215.1026	**VDI**	300.1918	328.1867
VDID	415.2187	443.2136	**VDIDA**	486.2558	514.2508	**VDIDAS**	573.2879	601.2828
VDIDASG	630.3093	658.3042	**DI**	201.1234	229.1183	**DID**	316.1503	344.1452
DIDA	387.1874	415.1823	**DIDAS**	474.2195	502.2144	**DIDASG**	531.2409	559.2358
ID	201.1234	229.1183	**IDA**	272.1605	300.1554	**IDAS**	359.1925	387.1874
IDASG	416.2140	444.2089	**DA**	159.0764	187.0713	**DAS**	246.1084	274.1034
DASG	303.1299	331.1248	**AS**	131.0815	159.0764	**ASG**	188.1030	216.0979
SG	117.0659	145.0608						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.2	2010.9317	-0.0221	TDKPYGIGGGMSVDIDASGR
11.0	2010.8614	0.0482	SEATSSIGAESDDGSSAPTSR
10.1	2010.9342	-0.0245	ESSSTIDVSDSDNVVSSKR
9.9	2010.9027	0.0069	VASCDIPIPYMDEGSSVR
8.1	2010.8371	0.0725	SDSSNNECVLQCVEGASR
8.1	2010.9763	-0.0667	MILMPCYLQLDLGLCR
8.1	2010.9763	-0.0667	MILMPCYLQLDLGLCR
8.0	2010.8991	0.0105	TDNNSVRSGYNADNVTER
7.6	2010.8614	0.0482	ESSATTVSPDSENDTTNTR
6.9	2011.0011	-0.0915	SQPYGISTNGVVGSLFETR

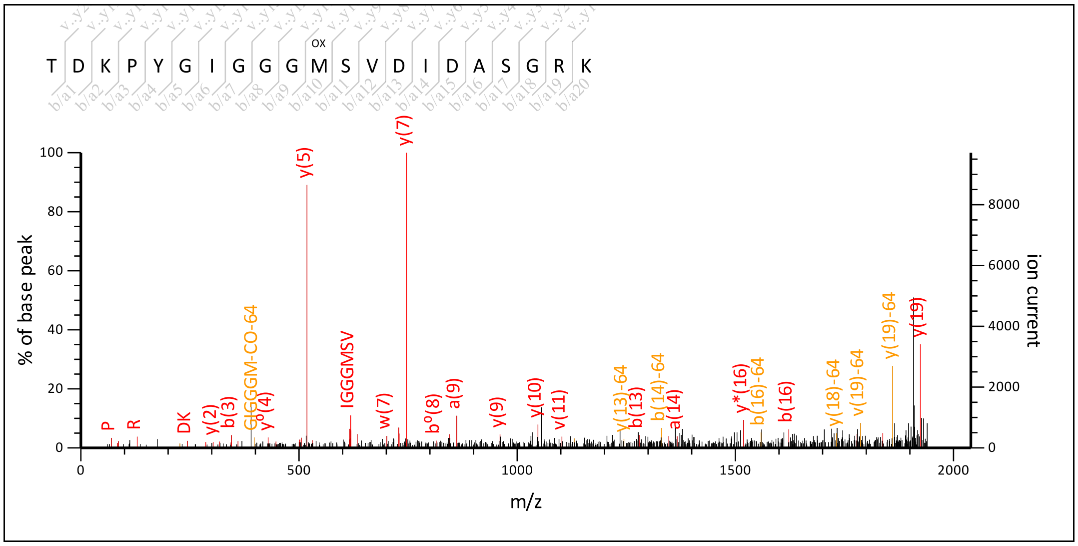
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 2

MS/MS Fragmentation of **TDKPYGIGGGMSVDIDASGRK**
Found in **gi|1835731** in **NCBInr**, photosystem II 10 kDa polypeptide [Oryza sativa Indica Group]

Match to Query 181: 2139.007324 from(2140.014600,1+) intensity(0.0000) index(30)
Title: Label: K5, Spot_Id: 219748, Peak_List_Id: 225869, MSMS Job_Run_Id: 21792, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K5_136842223800.txt



0 to 2039.73

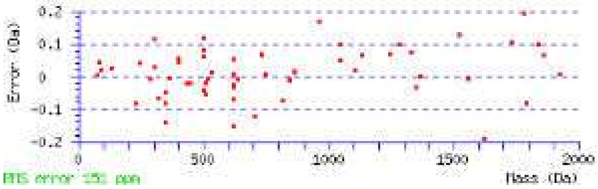
Label all possible matches ○ Label matches used for scoring ●

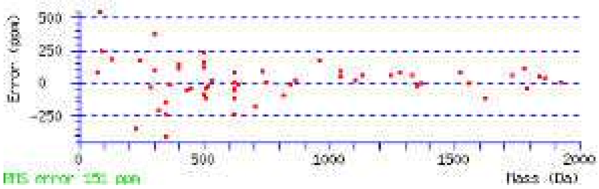
Monoisotopic mass of neutral peptide Mr(calc): 2139.0266
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.05
Matches : 64/609 fragment ions using 112 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	88.0393	189.0870		171.0764	217.0819		199.0713	145.0972		D	1914.9668	1913.9716		1974.9879	1957.9614
3	101.1073	317.1819	300.1554	299.1714	**345.1769**	328.1503	327.1663	260.1241		K	1786.8719	1785.8766		***1859.9610***	1842.9345
4	70.0651	414.2347	397.2082	396.2241	442.2296	425.2031	424.2191	388.2191		P	1689.8191	1688.8238		***1731.8660***	1714.8395
5	136.0757	577.2980	560.2715	559.2875	605.2930	588.2664	587.2824			Y	1526.7558			1634.8133	1617.7867
6	30.0338	634.3195	617.2930	616.3089	662.3144	645.2879	644.3039			G				1471.7499	1454.7234
7	86.0964	747.4036	730.3770	729.3930	775.3985	758.3719	757.3879	719.3723	733.3879	I	1356.6502	1369.6706	1383.6863	1414.7285	1397.7019
8	30.0338	804.4250	787.3985	786.4145	832.4199	815.3934	814.4094			G				1301.6444	1284.6179
9	30.0338	861.4465	844.4199	843.4359	889.4414	872.4149	871.4308			G				***1244.6230***	1227.5964
10	30.0338	918.4680	901.4414	900.4574	946.4629	929.4363	928.4523			G				1187.6015	1170.5749
11	56.0495	1001.5051	984.4785	983.4945	1029.5000	1012.4734	1011.4894	989.5051		M	1102.5487	1101.5535		***1130.5800***	1113.5535
12	60.0444	1088.5371	1071.5106	1070.5265	1116.5320	1099.5055	1098.5215	1072.5422		S	1015.5167	1014.5215		***1047.5429***	1030.5164
13	72.0808	1187.6055	1170.5790	1169.5950	1215.6004	1198.5739	1197.5899	1173.5899		V	916.4483	929.4687		***960.5109***	943.4843
14	88.0393	1302.6325	1285.6059	1284.6219	**1330.6274**	1313.6008	1312.6168	1258.6426		D	801.4213	800.4261		***861.4425***	844.4159
15	86.0964	1415.7165	1398.6900	1397.7060	1443.7114	1426.6849	1425.7009	1387.6852	1401.7009	I	688.3373	701.3577	715.3733	***746.4155***	729.3890
16	88.0393	1530.7435	1513.7169	1512.7329	**1558.7384**	1541.7118	1540.7278	1486.7536		D	573.3103	572.3151		***633.3315***	616.3049
17	44.0495	1601.7806	1584.7540	1583.7700	1629.7755	1612.7489	1611.7649			A	502.2732			***518.3045***	501.2780
18	60.0444	1688.8126	1671.7861	1670.8020	1716.8075	1699.7810	1698.7970	1672.8177		S	415.2412	414.2459		***447.2674***	430.2409
19	30.0338	1745.8341	1728.8075	1727.8235	1773.8290	1756.8024	1755.8184			G				***360.2354***	343.2088
20	129.1135	1901.9352	1884.9086	1883.9246	1929.9301	1912.9035	1911.9195	1816.8712		R	202.1186	201.1234		***303.2139***	286.1874

21	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DK	216.1343	244.1292	DKP	313.1870	341.1819	DKPY	476.2504	504.2453
DKPYG	533.2718	561.2667	DKPYGI	646.3559	674.3508	KP	198.1601	226.1550
KPY	361.2234	389.2183	KPYG	418.2449	446.2398	KPYGI	531.3289	559.3239
KPYGIG	588.3504	616.3453	KPYGIGG	645.3719	673.3668	PY	233.1285	261.1234
PYG	290.1499	318.1448	PYGI	403.2340	431.2289	PYGIG	460.2554	488.2504
PYGIGG	517.2769	545.2718	PYGIGGG	574.2984	602.2933	PYGIGGGM	657.3355	685.3304
YG	193.0972	221.0921	YGI	306.1812	334.1761	YGIG	363.2027	391.1976
YGIGG	420.2241	448.2191	YGIGGG	477.2456	505.2405	YGIGGGM	560.2827	588.2776
YGIGGGMS	647.3148	675.3097	GI	143.1179	171.1128	GIG	200.1394	228.1343
GIGG	257.1608	285.1557	GIGGG	314.1823	342.1772	GIGGGM	397.2194	425.2143
GIGGGMS	484.2514	512.2463	GIGGGMSV	583.3198	611.3148	GIGGGMSVD	698.3468	726.3417
IG	143.1179	171.1128	IGG	200.1394	228.1343	IGGG	257.1608	285.1557
IGGGM	340.1979	368.1928	IGGGMS	427.2300	455.2249	IGGGMSV	526.2984	554.2933
IGGGMSVD	641.3253	669.3202	GG	87.0553	115.0502	GGG	144.0768	172.0717
GGGM	227.1139	255.1088	GGGMS	314.1459	342.1408	GGGMSV	413.2143	441.2092
GGGMSVD	528.2413	556.2362	GGGMSVDI	641.3253	669.3202	GG	87.0553	115.0502
GGM	170.0924	198.0873	GGMS	257.1244	285.1193	GGMSV	356.1928	384.1878
GGMSVD	471.2198	499.2147	GGMSVDI	584.3039	612.2988	GGMSVDID	699.3308	727.3257
GM	113.0709	141.0659	GMS	200.1030	228.0979	GMSV	299.1714	327.1663
GMSVD	414.1983	442.1932	GMSVDI	527.2824	555.2773	GMSVDID	642.3093	670.3042
MS	143.0815	171.0764	MSV	242.1499	270.1448	MSVD	357.1769	385.1718
MSVDI	470.2609	498.2558	MSVDID	585.2879	613.2828	MSVDIDA	656.3250	684.3199
SV	159.1128	187.1077	SVD	274.1397	302.1347	SVDI	387.2238	415.2187
SVDID	502.2508	530.2457	SVDIDA	573.2879	601.2828	SVDIDAS	660.3199	688.3148
VD	187.1077	215.1026	VDI	300.1918	328.1867	VDID	415.2187	443.2136
VDIDA	486.2558	514.2508	VDIDAS	573.2879	601.2828	VDIDASG	630.3093	658.3042
DI	201.1234	229.1183	DID	316.1503	344.1452	DIDA	387.1874	415.1823
DIDAS	474.2195	502.2144	DIDASG	531.2409	559.2358	DIDASGR	687.3420	715.3369
ID	201.1234	229.1183	IDA	272.1605	300.1554	IDAS	359.1925	387.1874
IDASG	416.2140	444.2089	IDASGR	572.3151	600.3100	DA	159.0764	187.0713
DAS	246.1084	274.1034	DASG	303.1299	331.1248	DASGR	459.2310	487.2259
AS	131.0815	159.0764	ASG	188.1030	216.0979	ASGR	344.2041	372.1990
SG	117.0659	145.0608	SGR	273.1670	301.1619	GR	186.1349	214.1299





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.3	2139.0266	-0.0193	TDKPYGIGGGMSVDIDASGRK
11.5	2138.9976	0.0097	AFGDALDSIPMMLAENSGLR
9.4	2139.0354	-0.0280	DVNAWSTMITGFARNGMLR
7.7	2138.9725	0.0348	TTDPDDIMLNFARGECIR
7.5	2139.0444	-0.0370	GVLEVNPDALAEADKADQER
7.2	2138.9392	0.0681	SSEVDVEYPSWLSENDQR
6.9	2139.0300	-0.0227	NAMSTTVNDVMVGITSAGLSR

6.8	2139.0241	-0.0168	SRPESMAALMEGFWIGIGR
6.7	2138.9539	0.0534	TDTPYGTGGGMALPDGKDASGR
6.6	2139.0630	-0.0557	MASKAATPSSPSFILTSGASGR

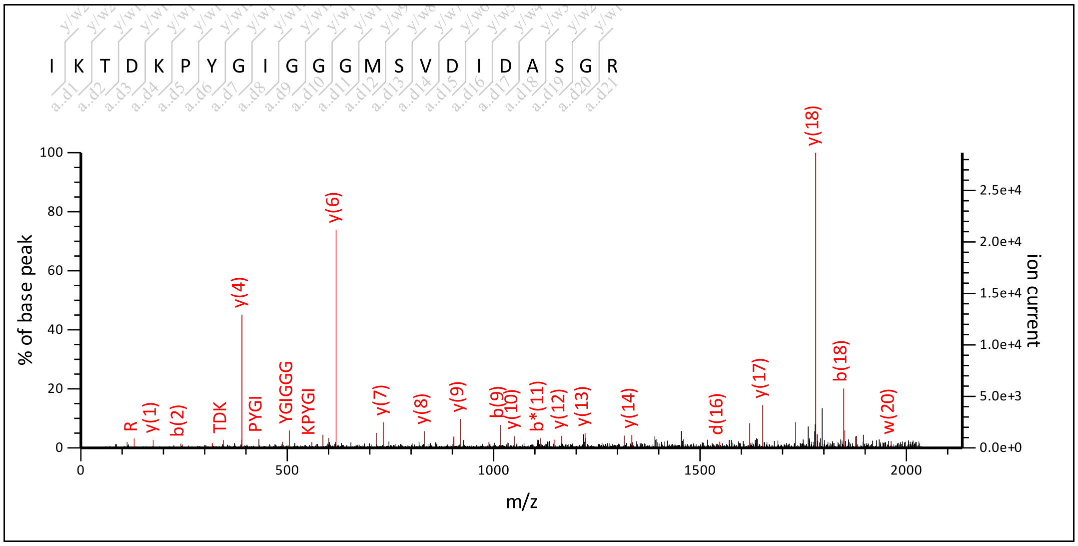
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 2

MS/MS Fragmentation of **IKTDKPYGIGGGMSVDIDASGR**
Found in **gi|1835731** in **NCBInr**, photosystem II 10 kDa polypeptide [Oryza sativa Indica Group]

Match to Query 185: 2236.110624 from(2237.117900,1+) intensity(0.0000) index(31)
Title: Label: K5, Spot_Id: 219748, Peak_List_Id: 225862, MSMS Job_Run_Id: 21792, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K5_136842223800.txt



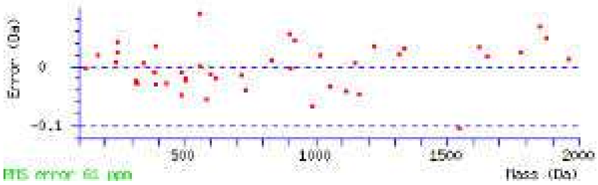
0 to 2135.37

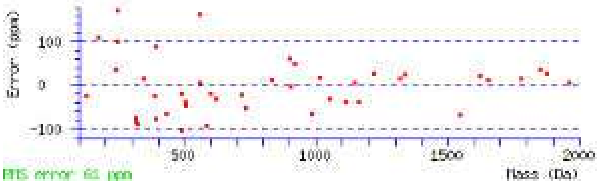
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2236.1158
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92  Expect: 7.7e-07
Matches : 45/445 fragment ions using 60 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		I					
2	101.1073	214.1914	197.1648		**242.1863**	225.1598		157.1335		K	2050.9498	2049.9546		2124.0390	2107.0124
3	74.0600	315.2391	298.2125	297.2285	343.2340	326.2074	325.2234	299.2442	301.2234	T	1949.9022	1962.9226	1964.9018	1995.9440	1978.9175
4	88.0393	430.2660	413.2395	412.2554	458.2609	441.2344	440.2504	386.2762		D	1834.8752	1833.8800		1894.8964	1877.8698
5	101.1073	558.3610	541.3344	540.3504	**586.3559**	569.3293	568.3453	501.3031		K	1706.7803	1705.7850		***1779.8694***	1762.8429
6	70.0651	655.4137	638.3872	637.4032	683.4087	666.3821	665.3981	629.3981		P	1609.7275	1608.7322		***1651.7744***	1634.7479
7	136.0757	818.4771	801.4505	800.4665	846.4720	829.4454	828.4614			Y	1446.6642			1554.7217	1537.6951
8	30.0338	875.4985	858.4720	857.4880	**903.4934**	886.4669	885.4829			G				1391.6584	1374.6318
9	86.0964	988.5826	971.5560	970.5720	**1016.5775**	999.5510	998.5669	960.5513	974.5669	I	1276.5586	1289.5790	1303.5947	***1334.6369***	1317.6103
10	30.0338	1045.6041	1028.5775	1027.5935	1073.5990	1056.5724	1055.5884			G				***1221.5528***	1204.5263
11	30.0338	1102.6255	1085.5990	1084.6150	1130.6204	1113.5939	1112.6099			G				***1164.5314***	1147.5048
12	30.0338	1159.6470	1142.6204	1141.6364	1187.6419	1170.6154	1169.6313			G				1107.5099	1090.4834
13	104.0528	1290.6875	1273.6609	1272.6769	1318.6824	1301.6558	1300.6718	1230.6841		M	974.4538	973.4585		***1050.4884***	1033.4619
14	60.0444	1377.7195	1360.6930	1359.7089	1405.7144	1388.6879	1387.7038	1361.7246		S	887.4217	886.4265		***919.4480***	902.4214
15	72.0808	1476.7879	1459.7614	1458.7773	1504.7828	1487.7563	1486.7723	1462.7723		V	788.3533	801.3737		***832.4159***	815.3894
16	88.0393	1591.8149	1574.7883	1573.8043	**1619.8098**	1602.7832	1601.7992	1547.8250		D	673.3264	672.3311		***733.3475***	716.3210
17	86.0964	1704.8989	1687.8724	1686.8884	1732.8938	1715.8673	1714.8833	1676.8676	1690.8833	I	560.2423	573.2627	587.2784	***618.3206***	601.2940
18	88.0393	1819.9259	1802.8993	1801.9153	**1847.9208**	1830.8942	1829.9102	1775.9360		D	445.2154	444.2201		***505.2365***	488.2100
19	44.0495	1890.9630	1873.9364	1872.9524	1918.9579	1901.9313	1900.9473			A	374.1783			***390.2096***	373.1830
20	60.0444	1977.9950	1960.9685	1959.9844	2005.9899	1988.9634	1987.9794	1962.0001		S	287.1462	286.1510		***319.1724***	302.1459
21	30.0338	2035.0165	2017.9899	2017.0059	2063.0114	2045.9848	2045.0008			G				232.1404	215.1139
22	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KT	202.1550	230.1499	**KTD**	317.1819	345.1769	**KTDK**	445.2769	473.2718
KTDKP	542.3297	570.3246	**TD**	189.0870	217.0819	**TDK**	317.1819	345.1769
TDKP	414.2347	442.2296	**TDKPY**	577.2980	605.2930	**TDKPYG**	634.3195	662.3144
DK	216.1343	244.1292	**DKP**	313.1870	341.1819	**DKPY**	476.2504	504.2453
DKPYG	533.2718	561.2667	**DKPYGI**	646.3559	674.3508	**KP**	198.1601	226.1550
KPY	361.2234	389.2183	**KPYG**	418.2449	446.2398	**KPYGI**	531.3289	559.3239
KPYGIG	588.3504	616.3453	**KPYGIGG**	645.3719	673.3668	**PY**	233.1285	261.1234
PYG	290.1499	318.1448	**PYGI**	403.2340	431.2289	**PYGIG**	460.2554	488.2504
PYGIGG	517.2769	545.2718	**PYGIGGG**	574.2984	602.2933	**YG**	193.0972	221.0921
YGI	306.1812	334.1761	**YGIG**	363.2027	391.1976	**YGIGG**	420.2241	448.2191
YGIGGG	477.2456	505.2405	**YGIGGGM**	608.2861	636.2810	**YGIGGGMS**	695.3181	723.3130
GI	143.1179	171.1128	**GIG**	200.1394	228.1343	**GIGG**	257.1608	285.1557
GIGGG	314.1823	342.1772	**GIGGGM**	445.2228	473.2177	**GIGGGMS**	532.2548	560.2497
GIGGGMSV	631.3232	659.3181	**IG**	143.1179	171.1128	**IGG**	200.1394	228.1343
IGGG	257.1608	285.1557	**IGGGM**	388.2013	416.1962	**IGGGMS**	475.2333	503.2282
IGGGMSV	574.3017	602.2967	**IGGGMSVD**	689.3287	717.3236	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGM**	275.1172	303.1122	**GGGMS**	362.1493	390.1442
GGGMSV	461.2177	489.2126	**GGGMSVD**	576.2446	604.2395	**GGGMSVDI**	689.3287	717.3236
GG	87.0553	115.0502	**GGM**	218.0958	246.0907	**GGMS**	305.1278	333.1227
GGMSV	404.1962	432.1911	**GGMSVD**	519.2232	547.2181	**GGMSVDI**	632.3072	660.3021
GM	161.0743	189.0692	**GMS**	248.1063	276.1013	**GMSV**	347.1748	375.1697
GMSVD	462.2017	490.1966	**GMSVDI**	575.2858	603.2807	**GMSVDID**	690.3127	718.3076
MS	191.0849	219.0798	**MSV**	290.1533	318.1482	**MSVD**	405.1802	433.1751
MSVDI	518.2643	546.2592	**MSVDID**	633.2912	661.2862	**SV**	159.1128	187.1077
SVD	274.1397	302.1347	**SVDI**	387.2238	415.2187	**SVDID**	502.2508	530.2457
SVDIDA	573.2879	601.2828	**SVDIDAS**	660.3199	688.3148	**VD**	187.1077	215.1026
VDI	300.1918	328.1867	**VDID**	415.2187	443.2136	**VDIDA**	486.2558	514.2508
VDIDAS	573.2879	601.2828	**VDIDASG**	630.3093	658.3042	**DI**	201.1234	229.1183
DID	316.1503	344.1452	**DIDA**	387.1874	415.1823	**DIDAS**	474.2195	502.2144
DIDASG	531.2409	559.2358	**ID**	201.1234	229.1183	**IDA**	272.1605	300.1554
IDAS	359.1925	387.1874	**IDASG**	416.2140	444.2089	**DA**	159.0764	187.0713
DAS	246.1084	274.1034	**DASG**	303.1299	331.1248	**AS**	131.0815	159.0764
ASG	188.1030	216.0979	**SG**	117.0659	145.0608			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
92.2	2236.1158	-0.0052	IKTDKPYGIGGGMSVDIDASGR
13.5	2236.0212	0.0894	DDLLESGMADAMSVSANQRAR
13.3	2236.0179	0.0927	SASPRFSGGGGSGSGSGSSMPPTPK
11.9	2235.9855	0.1251	FFGKGSSTQSGSMSPTSDWAR
11.8	2236.0819	0.0287	VTEEGSSSQSEDVKAISTNLR
11.4	2236.0946	0.0160	KEDPWNSIMAGAATGGFLSLR
11.2	2236.0286	0.0820	EMHMKGSASVEDGQMVSLLR
10.9	2236.0980	0.0126	VNFATITPRETNMDGCVALK
10.7	2236.0356	0.0750	IGGFRSAVDAAATTGEEQADDR

9.8	2236.0286	0.0820	EMHMKGSASVEDGQMVSLLR

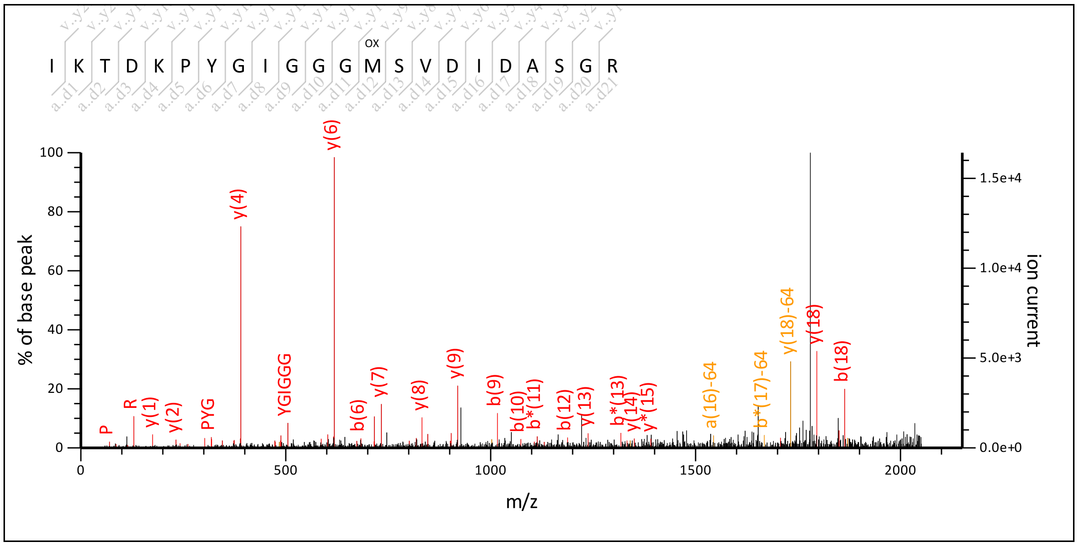
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 2

MS/MS Fragmentation of **IKTDKPYGIGGGMSVDIDASGR**
Found in **gi|1835731** in **NCBInr**, photosystem II 10 kDa polypeptide [Oryza sativa Indica Group]

Match to Query 187: 2252.092624 from(2253.099900,1+) intensity(0.0000) index(32)
Title: Label: K5, Spot_Id: 219748, Peak_List_Id: 225863, MSMS Job_Run_Id: 21792, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K5_136842223800.txt



0 to 2150.76

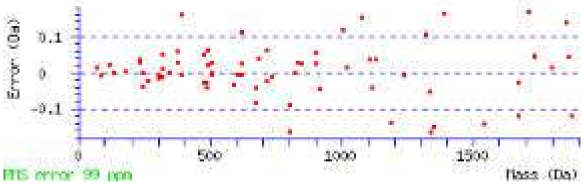
Label all possible matches ○ Label matches used for scoring ●

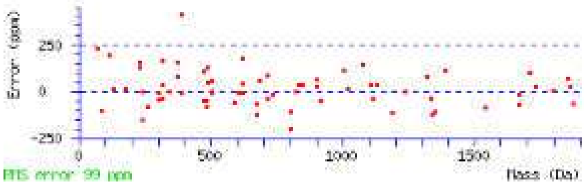
Monoisotopic mass of neutral peptide Mr(calc): 2252.1107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 68 **Expect:** 0.0002
Matches : 75/606 fragment ions using 140 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			***114.0913***			44.0495		**I**					
2	101.1073	214.1914	197.1648		***242.1863***	225.1598		157.1335		**K**	2066.9448	2065.9495		2140.0339	2123.0074
3	74.0600	315.2391	298.2125	297.2285	343.2340	326.2074	325.2234	299.2442	301.2234	**T**	1965.8971	1978.9175	1980.8967	2011.9389	1994.9124
4	88.0393	430.2660	413.2395	412.2554	458.2609	441.2344	440.2504	386.2762		**D**	1850.8701	1849.8749		1910.8913	1893.8647
5	101.1073	558.3610	541.3344	540.3504	***586.3559***	569.3293	568.3453	501.3031		**K**	1722.7752	1721.7799		***1795.8643***	1778.8378
6	70.0651	655.4137	638.3872	637.4032	***683.4087***	666.3821	665.3981	629.3981		**P**	1625.7224	1624.7272		***1667.7694***	1650.7428
7	136.0757	818.4771	801.4505	800.4665	***846.4720***	829.4454	828.4614			**Y**	1462.6591			1570.7166	1553.6901
8	30.0338	875.4985	858.4720	857.4880	***903.4934***	886.4669	885.4829			**G**				1407.6533	1390.6267
9	86.0964	988.5826	971.5560	970.5720	***1016.5775***	999.5510	998.5669	960.5513	974.5669	**I**	1292.5536	1305.5740	1319.5896	***1350.6318***	1333.6053
10	30.0338	1045.6041	1028.5775	1027.5935	***1073.5990***	1056.5724	1055.5884			**G**				***1237.5477***	1220.5212
11	30.0338	1102.6255	1085.5990	1084.6150	***1130.6204***	1113.5939	1112.6099			**G**				1180.5263	1163.4997
12	30.0338	1159.6470	1142.6204	1141.6364	***1187.6419***	1170.6154	1169.6313			**G**				1123.5048	1106.4783
13	120.0478	1306.6824	1289.6558	1288.6718	1334.6773	1317.6508	1316.6667	1230.6841		**M**	974.4538	973.4585		1066.4834	1049.4568
14	60.0444	1393.7144	1376.6879	1375.7038	1421.7093	1404.6828	1403.6988	1377.7195		**S**	887.4217	886.4265		***919.4480***	902.4214
15	72.0808	1492.7828	1475.7563	1474.7723	1520.7777	1503.7512	1502.7672	1478.7672		**V**	788.3533	801.3737		***832.4159***	815.3894
16	88.0393	1607.8098	1590.7832	1589.7992	1635.8047	1618.7781	1617.7941	1563.8199		**D**	673.3264	672.3311		***733.3475***	716.3210
17	86.0964	1720.8938	1703.8673	1702.8833	1748.8888	1731.8622	1730.8782	1692.8625	1706.8782	**I**	560.2423	573.2627	587.2784	***618.3206***	601.2940
18	88.0393	1835.9208	1818.8942	1817.9102	***1863.9157***	1846.8891	1845.9051	1791.9309		**D**	445.2154	444.2201		***505.2365***	488.2100
19	44.0495	1906.9579	1889.9313	1888.9473	1934.9528	1917.9263	1916.9422			**A**	374.1783			***390.2096***	373.1830
20	60.0444	1993.9899	1976.9634	1975.9794	2021.9848	2004.9583	2003.9743	1977.9950		**S**	287.1462	286.1510		***319.1724***	302.1459

21	30.0338	2051.0114	2033.9848	2033.0008	2079.0063	2061.9797	2060.9957			G				232.1404	215.1139	
22	129.1135									R	74.0237	73.0284		175.1190	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KT	202.1550	230.1499	KTD	317.1819	345.1769	KTDK	445.2769	473.2718
KTDKP	542.3297	570.3246	TD	189.0870	217.0819	TDK	317.1819	345.1769
TDKP	414.2347	442.2296	TDKPY	577.2980	605.2930	TDKPYG	634.3195	662.3144
DK	216.1343	244.1292	DKP	313.1870	341.1819	DKPY	476.2504	504.2453
DKPYG	533.2718	561.2667	DKPYGI	646.3559	674.3508	KP	198.1601	226.1550
KPY	361.2234	389.2183	KPYG	418.2449	446.2398	KPYGI	531.3289	559.3239
KPYGIG	588.3504	616.3453	KPYGIGG	645.3719	673.3668	PY	233.1285	261.1234
PYG	290.1499	318.1448	PYGI	403.2340	431.2289	PYGIG	460.2554	488.2504
PYGIGG	517.2769	545.2718	PYGIGGG	574.2984	602.2933	YG	193.0972	221.0921
YGI	306.1812	334.1761	YGIG	363.2027	391.1976	YGIGG	420.2241	448.2191
YGIGGG	477.2456	505.2405	YGIGGGM	624.2810	652.2759	GI	143.1179	171.1128
GIG	200.1394	228.1343	GIGG	257.1608	285.1557	GIGGG	314.1823	342.1772
GIGGGM	461.2177	489.2126	GIGGGMS	548.2497	576.2446	GIGGGMSV	647.3181	675.3130
IG	143.1179	171.1128	IGG	200.1394	228.1343	IGGG	257.1608	285.1557
IGGGM	404.1962	432.1911	IGGGMS	491.2282	519.2232	IGGGMSV	590.2967	618.2916
GG	87.0553	115.0502	GGG	144.0768	172.0717	GGGM	291.1122	319.1071
GGGMS	378.1442	406.1391	GGGMSV	477.2126	505.2075	GGGMSVD	592.2395	620.2345
GG	87.0553	115.0502	GGM	234.0907	262.0856	GGMS	321.1227	349.1176
GGMSV	420.1911	448.1860	GGMSVD	535.2181	563.2130	GGMSVDI	648.3021	676.2971
GM	177.0692	205.0641	GMS	264.1013	292.0962	GMSV	363.1697	391.1646
GMSVD	478.1966	506.1915	GMSVDI	591.2807	619.2756	MS	207.0798	235.0747
MSV	306.1482	334.1431	MSVD	421.1751	449.1701	MSVDI	534.2592	562.2541
MSVDID	649.2862	677.2811	SV	159.1128	187.1077	SVD	274.1397	302.1347
SVDI	387.2238	415.2187	SVDID	502.2508	530.2457	SVDIDA	573.2879	601.2828
SVDIDAS	660.3199	688.3148	VD	187.1077	215.1026	VDI	300.1918	328.1867
VDID	415.2187	443.2136	VDIDA	486.2558	514.2508	VDIDAS	573.2879	601.2828
VDIDASG	630.3093	658.3042	DI	201.1234	229.1183	DID	316.1503	344.1452
DIDA	387.1874	415.1823	DIDAS	474.2195	502.2144	DIDASG	531.2409	559.2358
ID	201.1234	229.1183	IDA	272.1605	300.1554	IDAS	359.1925	387.1874
IDASG	416.2140	444.2089	DA	159.0764	187.0713	DAS	246.1084	274.1034
DASG	303.1299	331.1248	AS	131.0815	159.0764	ASG	188.1030	216.0979
SG	117.0659	145.0608						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.0	2252.1107	-0.0181	IKTDKPYGIGGGMSVDIDASGR
14.4	2252.1140	-0.0214	QSSSLVETAIMSTMNNISIAR
11.4	2251.8958	0.1969	MGEADDARDAVEEMDVDGGDR
10.8	2252.1073	-0.0147	TVVAGQNEFEVFKADLENSR
10.6	2252.1037	-0.0110	KCSIIMELMDGDLLALMQR
9.8	2252.1284	-0.0358	LEAHANDVLETLDTLLSENR
9.2	2252.1702	-0.0776	NSFRPNFTAEGLYGGALLGR

8.9	2252.0610	0.0316	TVSDRPFNDHRYFIDDQK
8.7	2251.9751	0.1176	MATQTLDSHQTSTTDEETEK
8.5	2251.9677	0.1249	DTQSTQDVADGTTTDVDNVDR

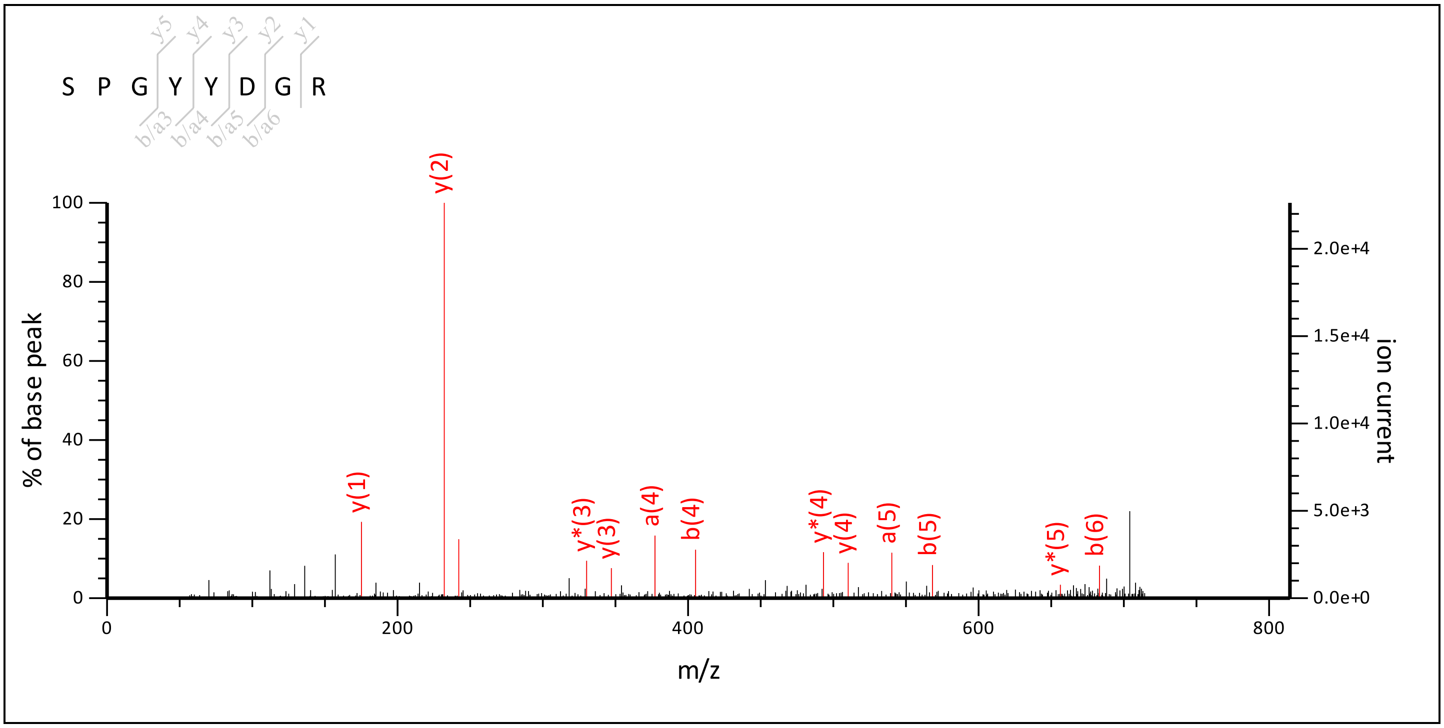
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 4

MS/MS Fragmentation of **SPGYYDGR**
Found in **gi|671740** in **NCBInr**, ribulose-bisphosphate carboxylase [synthetic construct]

Match to Query 7: 913.384024 from(914.391300,1+) intensity(0.0000) index(1)
Title: Label: J5, Spot_Id: 219747, Peak_List_Id: 225845, MSMS Job_Run_Id: 21791, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J5_136842222100.txt

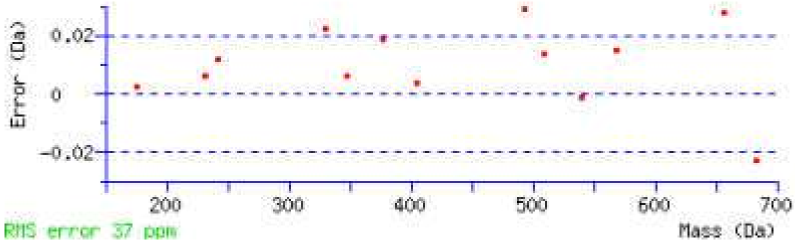


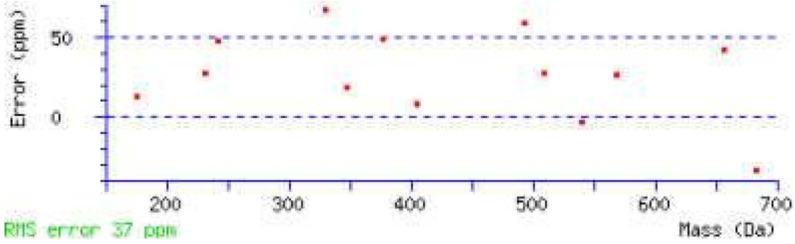
0 to 814.34

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 913.3930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 3.9
Matches : 13/28 fragment ions using 21 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	60.0444	88.0393	S			8
2	157.0972	185.0921	P	827.3682	810.3417	7
3	214.1186	***242.1135***	G	730.3155	713.2889	6
4	**377.1819**	***405.1769***	Y	673.2940	656.2675	5
5	**540.2453**	***568.2402***	Y	***510.2307***	493.2041	4
6	655.2722	***683.2671***	D	***347.1674***	330.1408	3
7	712.2937	740.2886	G	***232.1404***	215.1139	2
8			R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.0	913.3930	-0.0090	SPGYYDGR
27.0	913.3930	-0.0090	SPGYYDGR
24.2	913.4076	-0.0236	RMTYDGR
22.1	913.3964	-0.0123	ASVMYDGR
22.1	913.4294	-0.0453	FEKYDGR
22.1	913.3786	0.0054	MCLYDGR
16.3	913.4042	-0.0202	GGSGYFNGR
15.7	913.4657	-0.0817	QLYYATR
15.2	913.3964	-0.0123	YMSLGDGR
14.1	913.4254	-0.0413	QVPENDGR

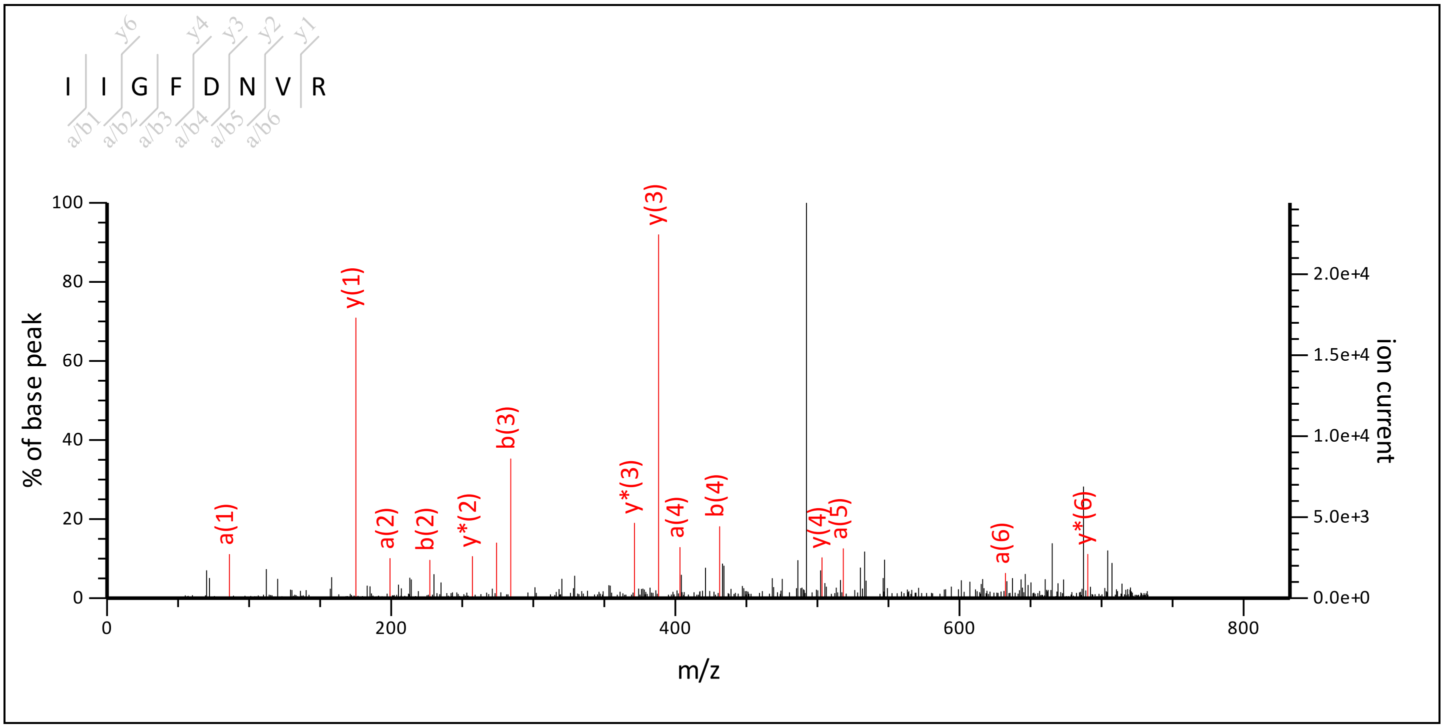
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 4

MS/MS Fragmentation of **IIGFDNVR**
Found in **gi|671740** in **NCBInr**, ribulose-bisphosphate carboxylase [synthetic construct]

Match to Query 11: 932.502614 from(933.509890,1+) intensity(0.0000) index(2)
Title: Label: J5, Spot_Id: 219747, Peak_List_Id: 225844, MSMS Job_Run_Id: 21791, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J5_136842222100.txt

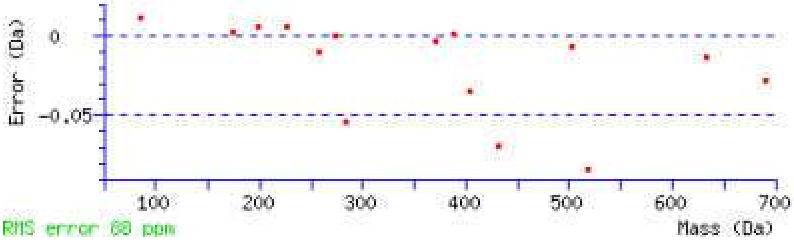


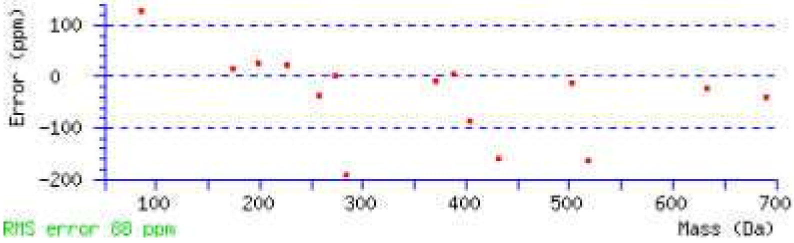
0 to 832.59

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 932.5080
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 4.8
Matches : 15/32 fragment ions using 28 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	***86.0964***		114.0913		I			8
2	***199.1805***		**227.1754**		I	820.4312	803.4046	7
3	256.2020		**284.1969**		G	707.3471	690.3206	6
4	***403.2704***		**431.2653**		F	650.3256	633.2991	5
5	***518.2973***		546.2922		D	***503.2572***	486.2307	4
6	***632.3402***	615.3137	660.3352	643.3086	N	***388.2303***	371.2037	3
7	731.4087	714.3821	759.4036	742.3770	V	***274.1874***	257.1608	2
8					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.8	932.5080	-0.0054	IIGFDNVR
24.8	932.5728	-0.0702	LITAMKLK
24.5	932.4352	0.0674	DNADPFVR
23.5	932.5113	-0.0087	KTAMVEVR
22.3	932.5080	-0.0054	VFLADNVR
21.9	932.4749	0.0277	VMSIDNVR
21.8	932.5331	-0.0305	LLGFDQIK
21.1	932.4862	0.0165	LERMNVR
21.1	932.5080	-0.0054	LVAFDNVR
20.9	932.4134	0.0892	GDGAMNNVR

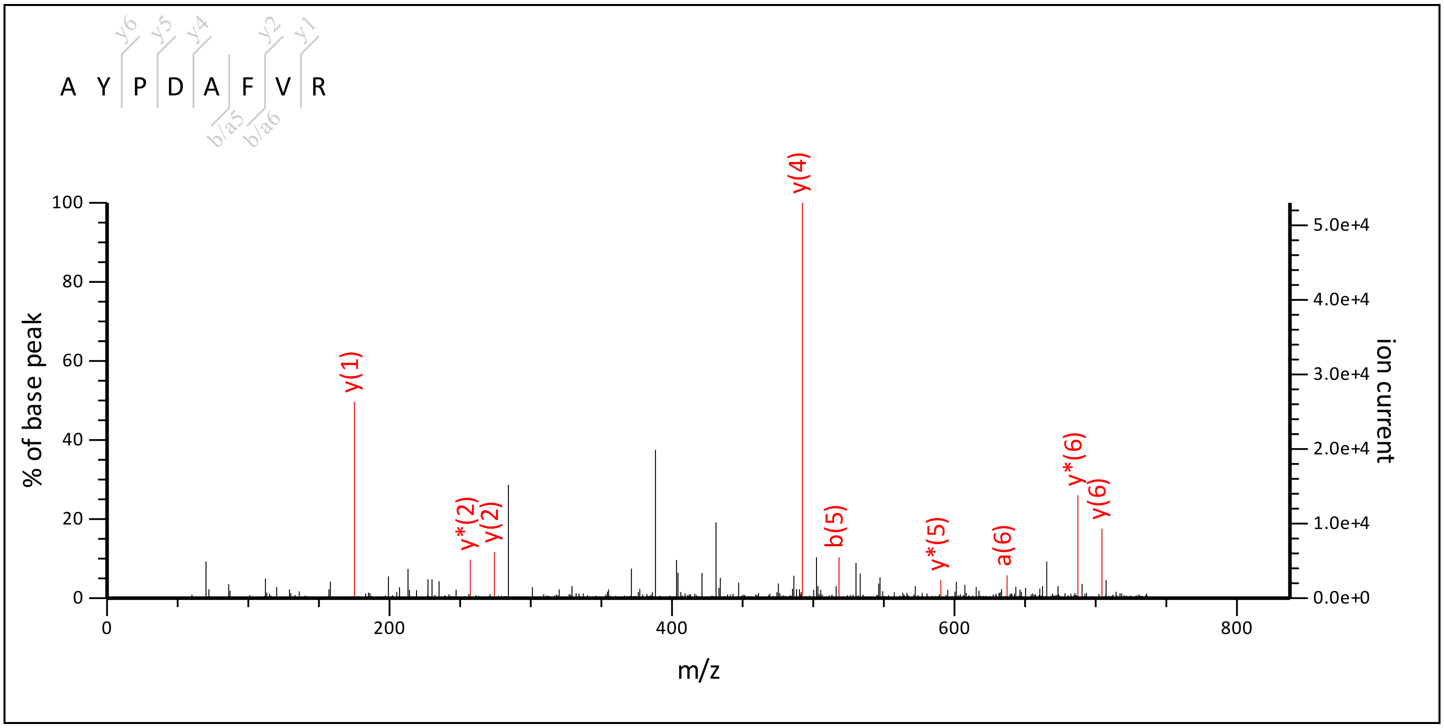
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 4

MS/MS Fragmentation of **AYPDAFVR**
Found in **gi|671740** in **NCBInr**, ribulose-bisphosphate carboxylase [synthetic construct]

Match to Query 13: 937.455374 from(938.462650,1+) intensity(0.0000) index(3)
Title: Label: J5, Spot_Id: 219747, Peak_List_Id: 225843, MSMS Job_Run_Id: 21791, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J5_136842222100.txt

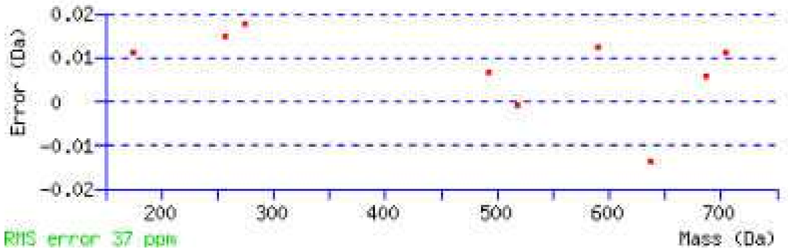


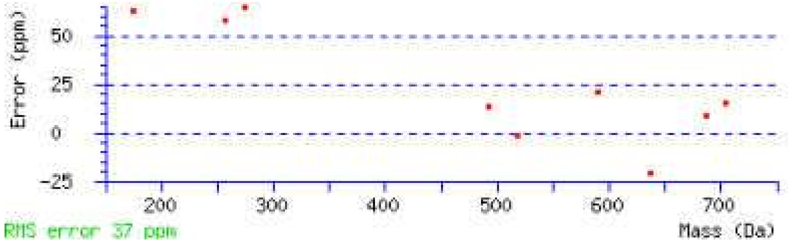
0 to 837.51

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 937.4658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 7
Matches : 9/28 fragment ions using 14 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	44.0495	72.0444	A			8
2	207.1128	235.1077	Y	867.4359	850.4094	7
3	304.1656	332.1605	P	***704.3726***	687.3461	6
4	419.1925	447.1874	D	607.3198	590.2933	5
5	490.2296	**518.2245**	A	***492.2929***	475.2663	4
6	**637.2980**	665.2930	F	421.2558	404.2292	3
7	736.3665	764.3614	V	***274.1874***	257.1608	2
8			R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.9	937.4658	-0.0104	AYPDAFVR
21.6	937.5055	-0.0502	FSSVLMVR
18.6	937.4254	0.0300	HPGEEDVR
18.4	937.4552	0.0002	FSNRCVR
18.3	937.4658	-0.0104	SWYVEVR
17.1	937.4691	-0.0138	AVPYSMVR
16.9	937.4658	-0.0104	SFPADFVR
16.7	937.5021	-0.0468	AYVPAYVR
16.2	937.4691	-0.0138	EMAVFAVR
15.4	937.5022	-0.0468	IFADAFVR

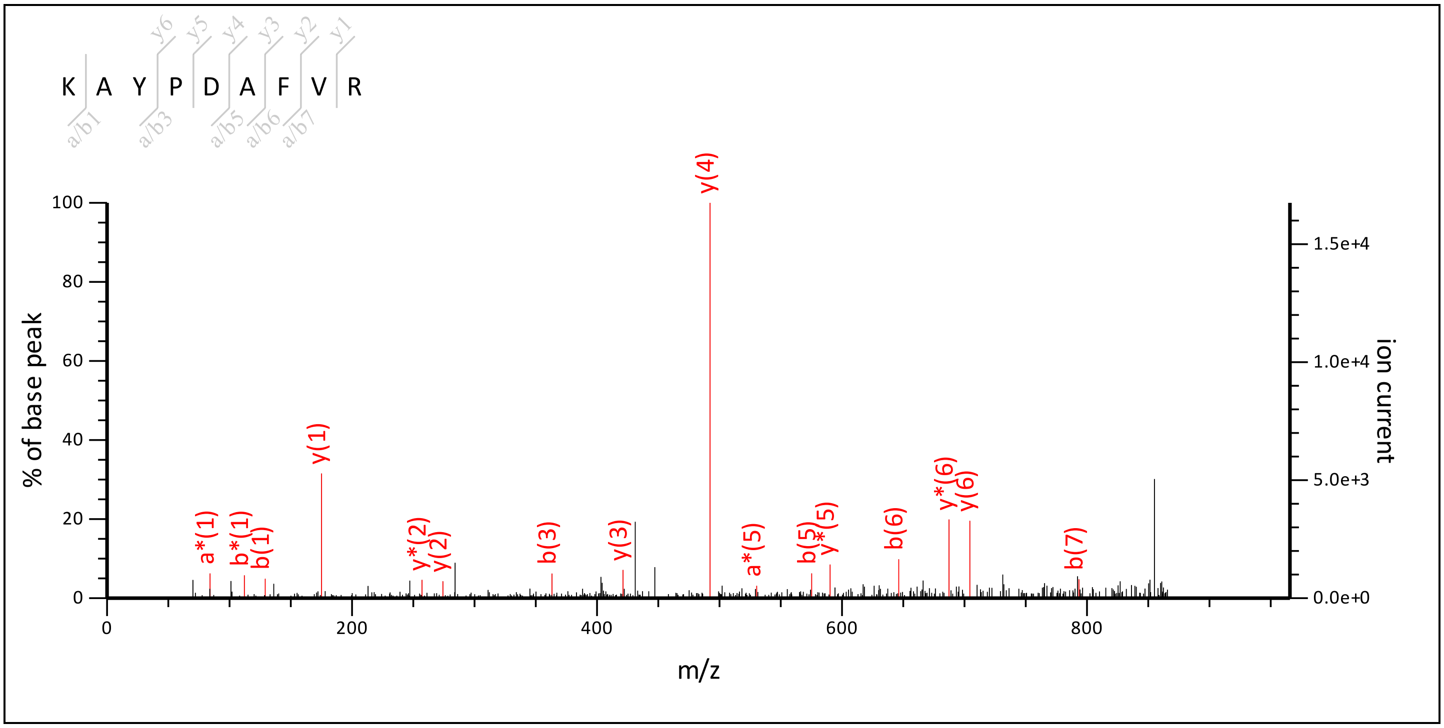
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 4

MS/MS Fragmentation of **KAYPDAFVR**
Found in **gi|671740** in **NCBInr**, ribulose-bisphosphate carboxylase [synthetic construct]

Match to Query 27: 1065.567024 from(1066.574300,1+) intensity(0.0000) index(8)
Title: Label: J5, Spot_Id: 219747, Peak_List_Id: 225847, MSMS Job_Run_Id: 21791, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J5_136842222100.txt



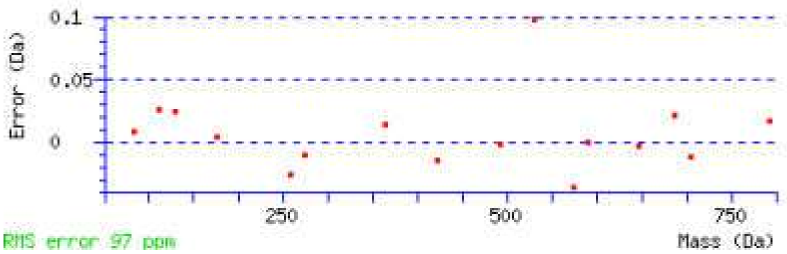
0 to 965.68

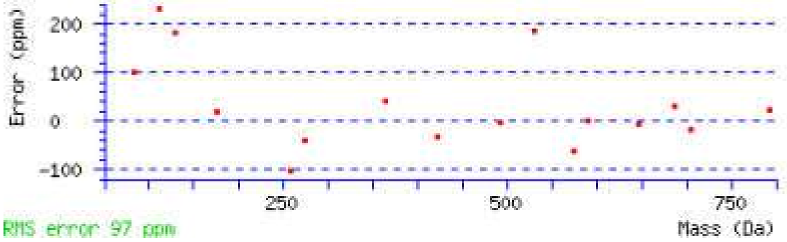
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1065.5607
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 1.2
Matches : 16/48 fragment ions using 24 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	101.1073	84.0808	***129.1022***	112.0757	**K**			**9**
2	172.1444	155.1179	200.1394	183.1128	**A**	938.4730	921.4465	**8**
3	335.2078	318.1812	***363.2027***	346.1761	**Y**	867.4359	850.4094	**7**
4	432.2605	415.2340	460.2554	443.2289	**P**	***704.3726***	687.3461	**6**
5	547.2875	530.2609	***575.2824***	558.2558	**D**	607.3198	590.2933	**5**
6	618.3246	601.2980	***646.3195***	629.2930	**A**	***492.2929***	475.2663	**4**
7	765.3930	748.3665	***793.3879***	776.3614	**F**	***421.2558***	404.2292	**3**
8	864.4614	847.4349	892.4563	875.4298	**V**	***274.1874***	257.1608	**2**

9					R	*175.1190*	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.8	1065.5607	0.0063	KAYPDAFVR
20.8	1065.5091	0.0579	KTDDDAFVR
18.1	1065.5390	0.0281	RVFDGMAVR
16.4	1065.4695	0.0975	MVRDGEMGR
14.5	1065.5311	0.0360	KMMTATEVR
14.2	1065.5125	0.0546	VSSMAKDGQK
13.1	1065.5100	0.0571	MICAFGPVR
13.0	1065.5641	0.0029	LKDAMAVFR
12.8	1065.4938	0.0732	TLSTDGESTR
12.5	1065.5567	0.0103	SQFNKTSVR

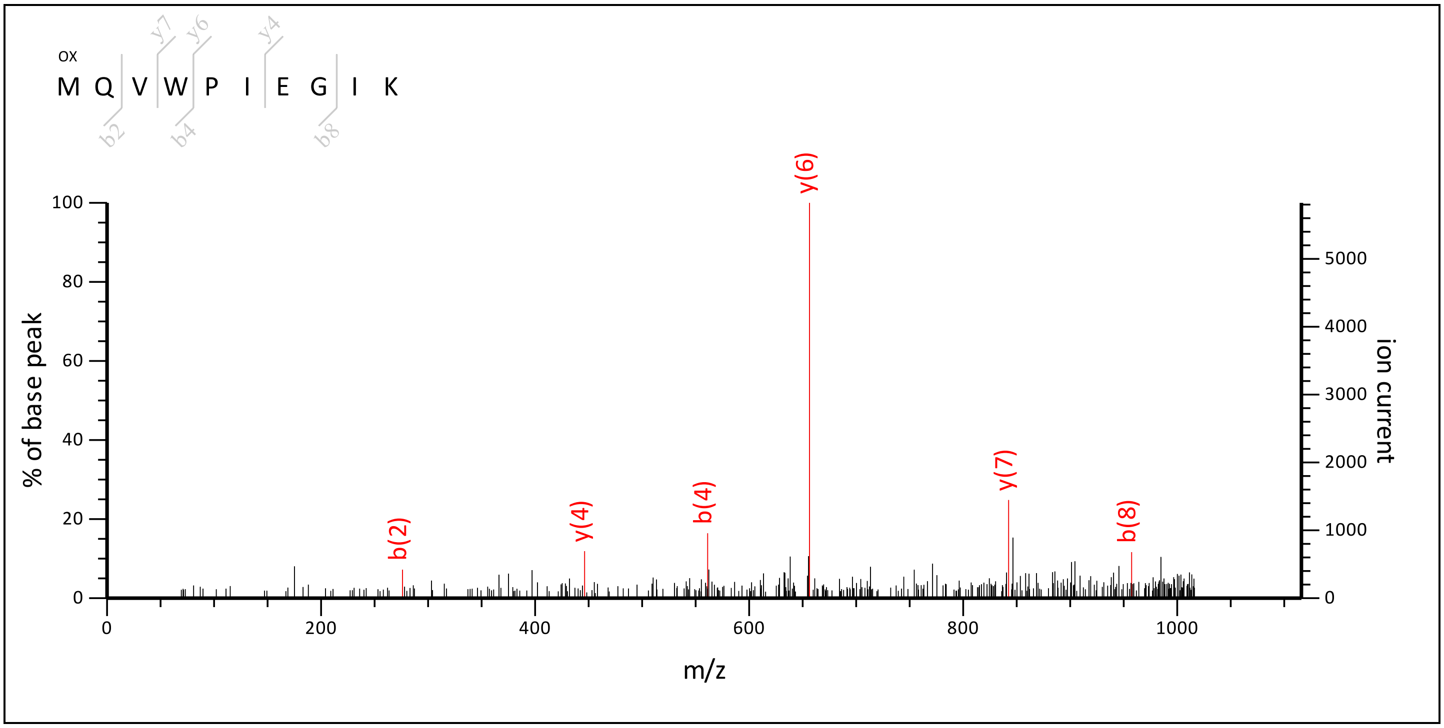
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 4

MS/MS Fragmentation of **MQVWPIEGIK**
Found in **gi|671740** in **NCBInr**, ribulose-bisphosphate carboxylase [synthetic construct]

Match to Query 42: 1215.620924 from(1216.628200,1+) intensity(0.0000) index(13)
Title: Label: J5, Spot_Id: 219747, Peak_List_Id: 225851, MSMS Job_Run_Id: 21791, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J5_136842222100.txt



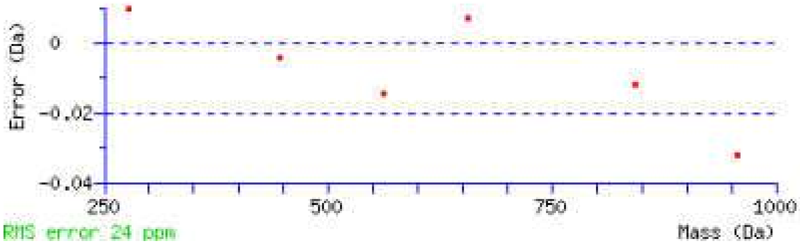
0 to 1116.05

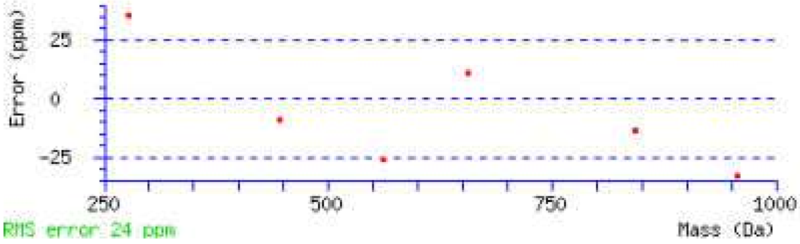
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1215.6322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 25
Matches : 6/86 fragment ions using 10 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	120.0478		148.0427		**M**			**10**
2	248.1063	231.0798	***276.1013***	259.0747	**Q**	1069.6041	1052.5775	**9**
3	347.1748	330.1482	375.1697	358.1431	**V**	941.5455	924.5189	**8**
4	533.2541	516.2275	***561.2490***	544.2224	**W**	***842.4771***	825.4505	**7**
5	630.3068	613.2803	658.3017	641.2752	**P**	***656.3978***	639.3712	**6**
6	743.3909	726.3643	771.3858	754.3593	**I**	559.3450	542.3184	**5**

7	872.4335	855.4069	900.4284	883.4019	**E**	***446.2609***	429.2344	**4**
8	929.4550	912.4284	***957.4499***	940.4233	**G**	317.2183	300.1918	**3**
9	1042.5390	1025.5125	1070.5339	1053.5074	**I**	260.1969	243.1703	**2**
10					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.5	1215.6169	0.0040	MNSILPGEDIK
26.8	1215.6360	-0.0151	GVFVRPDVDGR
20.4	1215.6652	-0.0443	FQVWPIEGIK
20.4	1215.6322	-0.0112	MQVWPIEGIK
20.4	1215.6322	-0.0112	MQVWPIEGIK
20.3	1215.5965	0.0245	MATASVRHMGR
19.0	1215.6533	-0.0324	QVALMIGEDIK
19.0	1215.6459	-0.0250	RLSDLAGEDLK
18.8	1215.5732	0.0478	DLDLVQGEDGR
17.2	1215.6976	-0.0766	KVIYGLVPDGR

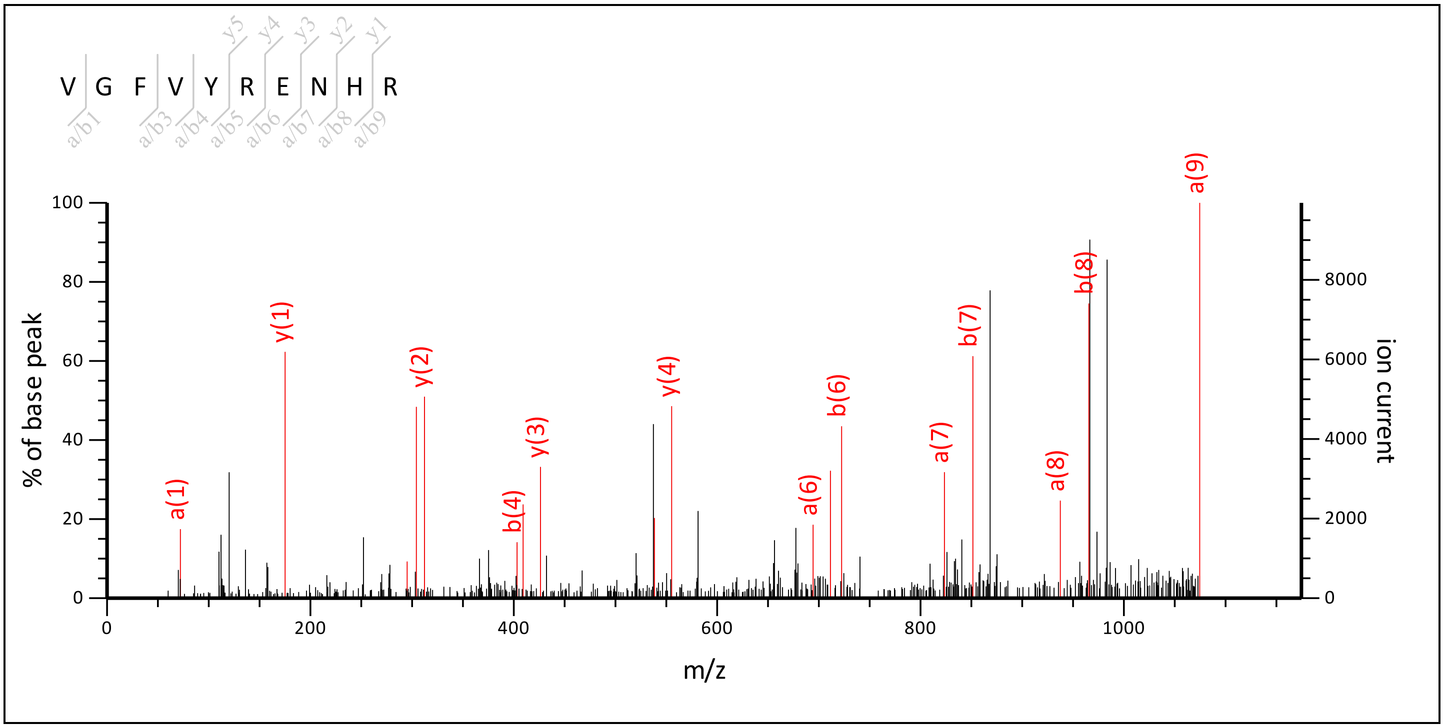
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 4

MS/MS Fragmentation of **VGFVYRENHR**
Found in **gi|671740** in **NCBInr**, ribulose-bisphosphate carboxylase [synthetic construct]

Match to Query 54: 1275.644624 from(1276.651900,1+) intensity(0.0000) index(16)
Title: Label: J5, Spot_Id: 219747, Peak_List_Id: 225842, MSMS Job_Run_Id: 21791, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J5_136842222100.txt



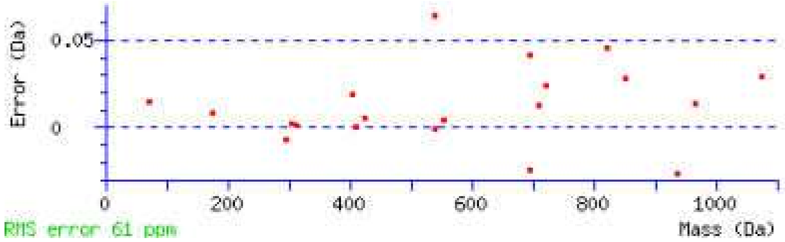
0 to 1174.58

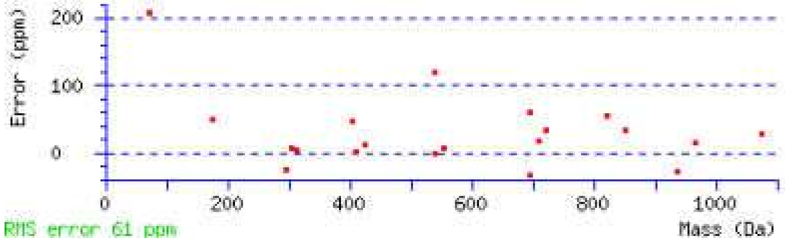
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1275.6472
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.66
Matches : 20/44 fragment ions using 33 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	***72.0808***		100.0757		**V**			**10**
2	129.1022		157.0972		**G**	1177.5861	1160.5596	**9**
3	276.1707		***304.1656***		**F**	1120.5647	1103.5381	**8**
4	375.2391		***403.2340***		**V**	973.4962	956.4697	**7**
5	***538.3024***		566.2973		**Y**	874.4278	857.4013	**6**
6	***694.4035***	677.3770	***722.3984***	705.3719	**R**	**711.3645**	694.3379	**5**
7	***823.4461***	806.4196	***851.4410***	834.4145	**E**	**555.2634**	538.2368	**4**
8	***937.4890***	920.4625	***965.4839***	948.4574	**N**	**426.2208**	409.1942	**3**

9	***1074.5479***	1057.5214	1102.5429	1085.5163	**H**	**312.1779**	295.1513	**2**
10					**R**	**175.1190**	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.6	1275.6472	-0.0026	VGFVYRENHR
23.6	1275.6221	0.0226	HWRELENHR
21.3	1275.6798	-0.0352	FYMITVPIHR
21.0	1275.6472	-0.0026	GPSPSPAKGWHR
21.0	1275.5381	0.1066	WYSGNNENHR
18.7	1275.6545	-0.0098	GRPTRGPQDHR
16.7	1275.5732	0.0715	YDDDGLAPPGTR
16.7	1275.6823	-0.0377	LPTNEIFSSLR
14.7	1275.6432	0.0014	NKPPRENHER
14.7	1275.6255	0.0192	CRPGGAPATPHR

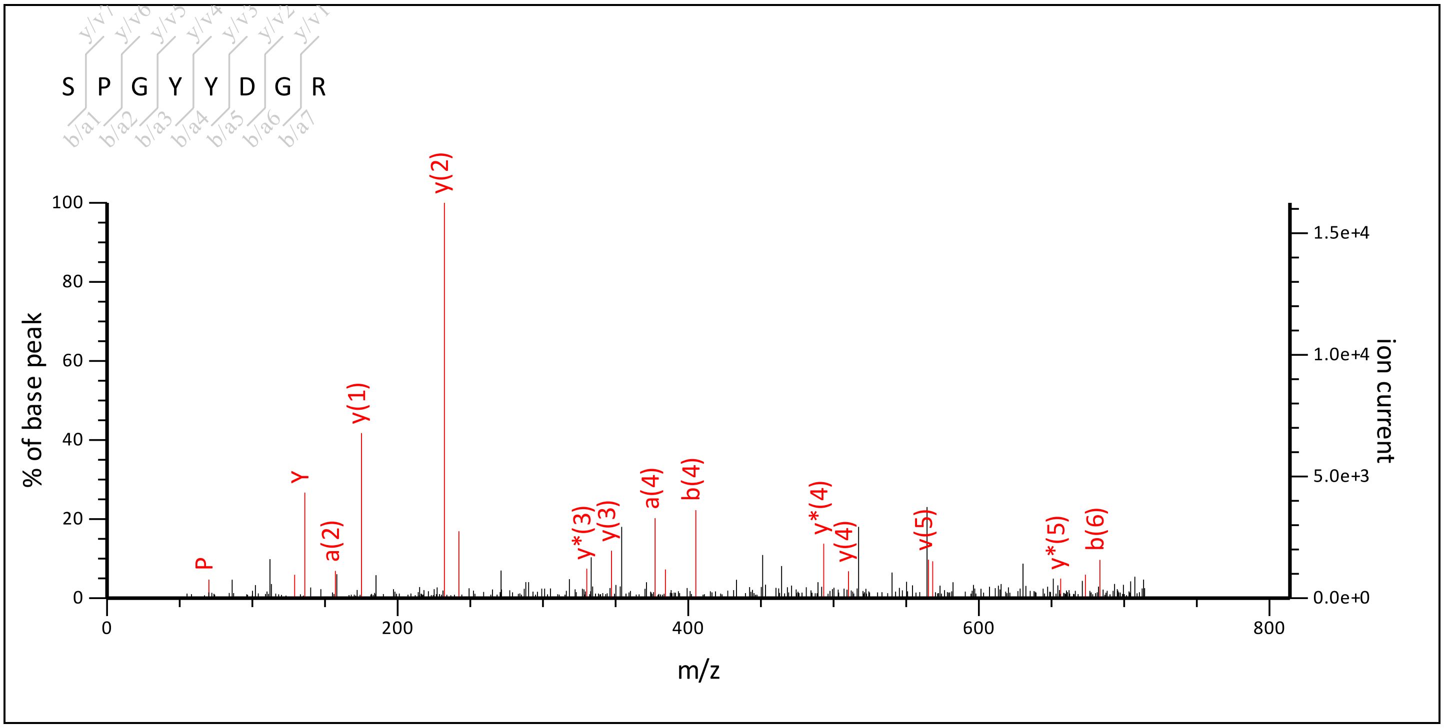
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **SPGYYDGR**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 23: 913.473924 from(914.481200,1+) intensity(0.0000) index(1)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227090, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



0 to 814.08

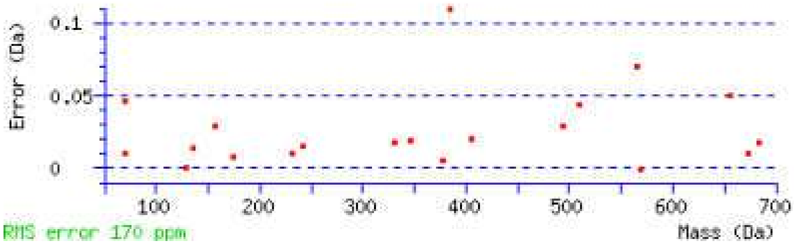
Label all possible matches ○ Label matches used for scoring ●

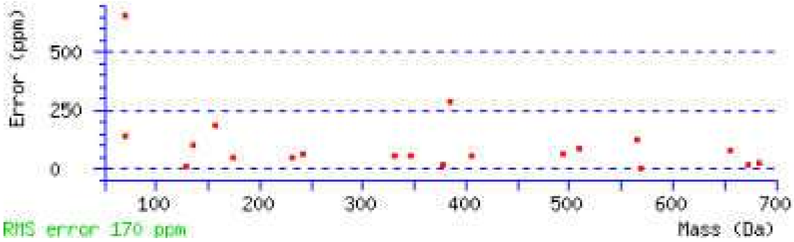
Monoisotopic mass of neutral peptide Mr(calc): 913.3930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 22
Matches : 22/96 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	60.0444	60.0444	42.0338	88.0393	70.0287	44.0495	S						8
2	70.0651	**157.0972**	139.0866	185.0921	167.0815	131.0815	P	785.3213	784.3260	827.3682	810.3417	809.3577	7
3	30.0338	214.1186	196.1081	**242.1135**	224.1030		G			730.3155	713.2889	712.3049	6
4	136.0757	**377.1819**	359.1714	**405.1769**	387.1663		Y	565.2365		***673.2940***	656.2675	655.2835	5
5	136.0757	540.2453	522.2347	**568.2402**	550.2296		Y	402.1732		***510.2307***	493.2041	492.2201	4
6	88.0393	655.2722	637.2617	**683.2671**	665.2566	611.2824	D	287.1462	286.1510	***347.1674***	330.1408	329.1568	3
7	30.0338	712.2937	694.2831	740.2886	722.2780		G			***232.1404***	215.1139		2

8	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PG	127.0866	155.0815	**PGY**	290.1499	318.1448	**PGYY**	453.2132	481.2082
PGYYD	568.2402	596.2351	**PGYYDG**	625.2617	653.2566	**GY**	193.0972	221.0921
GYY	356.1605	384.1554	**GYYD**	471.1874	499.1823	**GYYDG**	528.2089	556.2038
YY	299.1390	327.1339	**YYD**	414.1660	442.1609	**YYDG**	471.1874	499.1823
YD	251.1026	279.0975	**YDG**	308.1241	336.1190	**DG**	145.0608	173.0557





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.7	913.4294	0.0446	QLYYDGR
32.9	913.3930	0.0809	SPGYYDGR
32.9	913.3930	0.0809	SPGYYDGR
32.3	913.3964	0.0776	DYATMTGR
32.2	913.4294	0.0446	GAIYYDGR
30.1	913.5094	-0.0354	SPGRLATGR
29.3	913.5094	-0.0354	QIRAVDGR
28.3	913.4981	-0.0242	QLGVSPTGR
27.3	913.3964	0.0776	YMSLGDGR
26.7	913.5094	-0.0354	AVARAVDGR

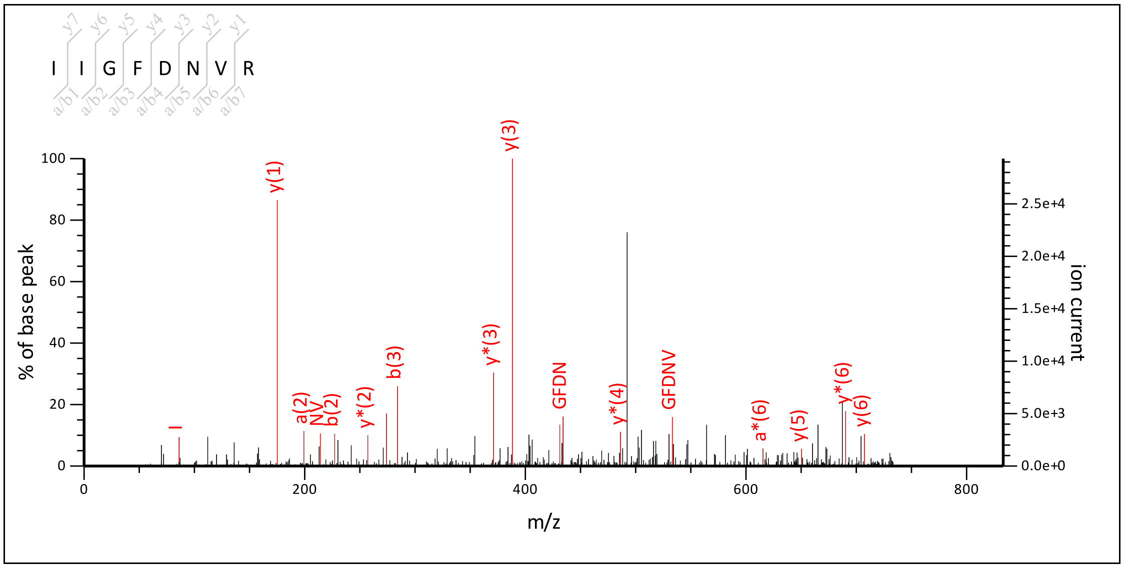
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **IIGFDNVR**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 33: 932.585134 from(933.592410,1+) intensity(0.0000) index(2)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227087, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



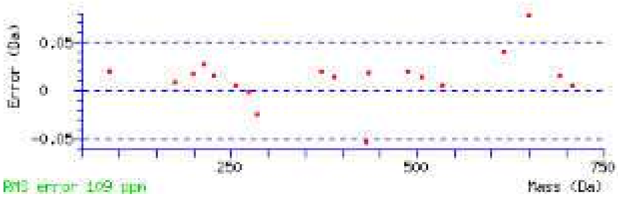
0 to 833.2

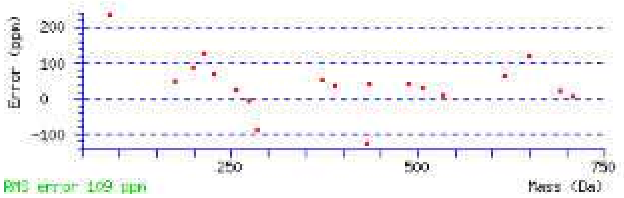
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 932.5080
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 13
Matches : 21/98 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	**86.0964**			114.0913			44.0495		I							8
2	86.0964	**199.1805**			**227.1754**			171.1492	185.1648	I	762.3529	775.3733	789.3890	820.4312	803.4046	802.4206	7
3	30.0338	256.2020			**284.1969**					G				***707.3471***	690.3206	689.3365	6
4	120.0808	403.2704			**431.2653**					F	558.2630			***650.3256***	633.2991	632.3151	5
5	88.0393	518.2973		500.2867	546.2922		528.2817	474.3075		D	443.2361	442.2409		503.2572	486.2307	485.2467	4
6	87.0553	632.3402	615.3137	614.3297	660.3352	643.3086	642.3246	589.3344		N	329.1932	328.1979		***388.2303***	371.2037		3
7	72.0808	731.4087	714.3821	713.3981	759.4036	742.3770	741.3930	717.3930		V	230.1248	243.1452		***274.1874***	257.1608		2
8	129.1135									R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IG	143.1179	171.1128	IGF	290.1863	318.1812	IGFD	405.2132	433.2082
IGFDN	519.2562	547.2511	IGFDNV	618.3246	646.3195	GF	177.1022	205.0972
GFD	292.1292	320.1241	GFDN	406.1721	434.1670	GFDNV	505.2405	533.2354
FD	235.1077	263.1026	FDN	349.1506	377.1456	FDNV	448.2191	476.2140
DN	202.0822	230.0771	DNV	301.1506	329.1456	NV	186.1237	214.1186





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.5	932.5080	0.0772	IIGFDNVR
30.2	932.5444	0.0408	VGTFGAILR
26.7	932.5807	0.0044	KTFGVLLR
26.6	932.5113	0.0738	LLGSMVASR
26.0	932.5807	0.0044	TKFGVLLR
25.0	932.4927	0.0924	ILGDTTSAR
24.7	932.5080	0.0772	LPTSFNVR
24.4	932.5556	0.0296	RTFGALLR
24.0	932.5444	0.0408	AGFTGVLLR
23.9	932.5113	0.0738	LIGMSGALR

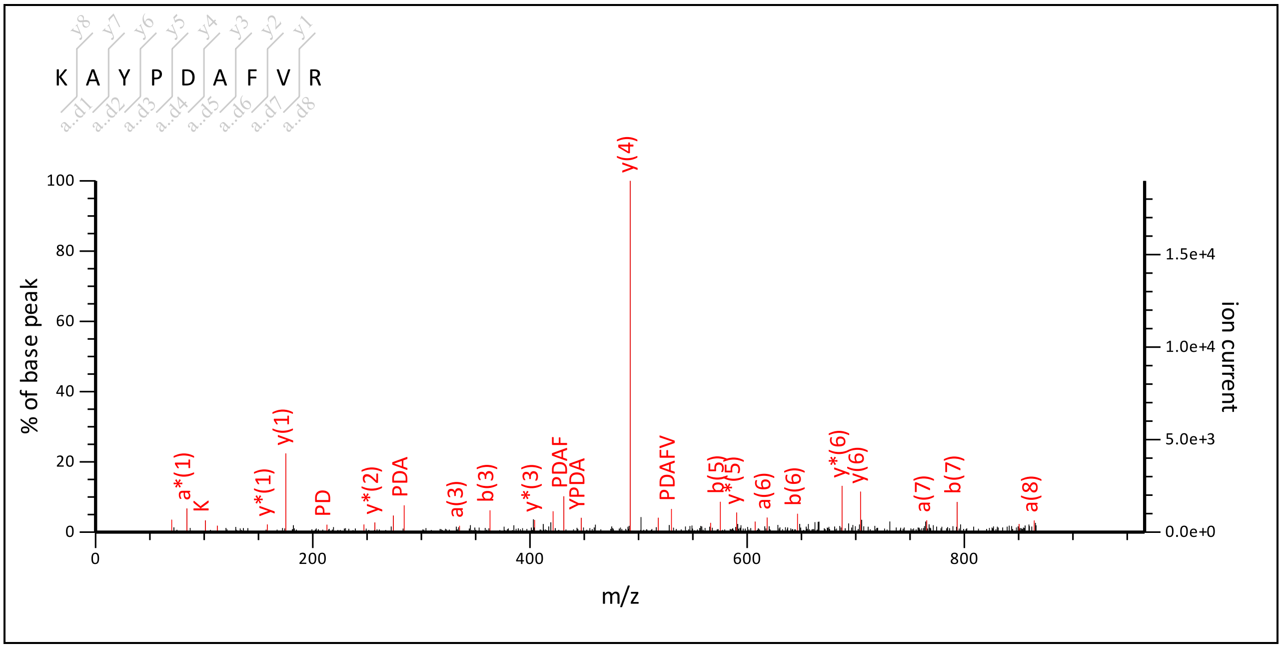
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **KAYPDAFVR**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 91: 1065.665124 from(1066.672400,1+) intensity(0.0000) index(9)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227091, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



0 to 966.02

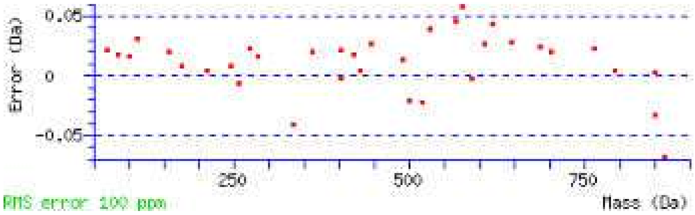
Label all possible matches ○ Label matches used for scoring ●

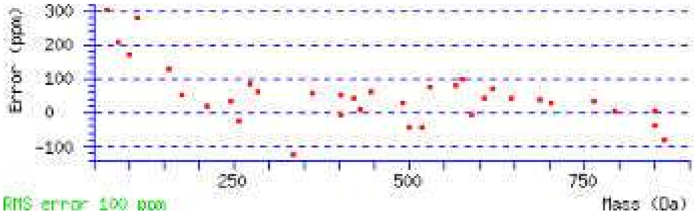
Monoisotopic mass of neutral peptide Mr(calc): 1065.5607
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.13
Matches : 38/125 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	Seq.	v	w	y	y*	y⁰	#
1	101.1073	***101.1073***	84.0808		129.1022	112.0757		44.0495	**K**						9
2	44.0495	172.1444	155.1179		200.1394	183.1128			**A**	922.4417		938.4730	921.4465	920.4625	8
3	136.0757	***335.2078***	318.1812		**363.2027**	346.1761			**Y**	759.3784		867.4359	850.4094	849.4254	7
4	70.0651	432.2605	415.2340		460.2554	443.2289		406.2449	**P**	662.3257	661.3304	***704.3726***	687.3461	686.3620	6
5	88.0393	547.2875	530.2609	529.2769	**575.2824**	558.2558	557.2718	503.2976	**D**	547.2987	546.3035	***607.3198***	590.2933	589.3093	5
6	44.0495	***618.3246***	601.2980	600.3140	**646.3195**	629.2930	628.3089		**A**	476.2616		***492.2929***	475.2663		4
7	120.0808	***765.3930***	748.3665	747.3824	**793.3879**	776.3614	775.3774		**F**	329.1932		***421.2558***	404.2292		3
8	72.0808	***864.4614***	847.4349	846.4509	892.4563	875.4298	874.4458	850.4458	**V**	230.1248	243.1452	***274.1874***	257.1608		2
9	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AY	207.1128	235.1077	**AYP**	304.1656	332.1605	**AYPD**	419.1925	447.1874
AYPDA	490.2296	518.2245	**AYPDAF**	637.2980	665.2930	**YP**	233.1285	261.1234
YPD	348.1554	376.1503	**YPDA**	419.1925	447.1874	**YPDAF**	566.2609	594.2558

YPDAFV	665.3293	693.3243	**PD**	185.0921	213.0870	**PDA**	256.1292	284.1241
PDAF	403.1976	431.1925	**PDAFV**	502.2660	530.2609	**DA**	159.0764	187.0713
DAF	306.1448	334.1397	**DAFV**	405.2132	433.2082	**AF**	191.1179	219.1128
AFV	290.1863	318.1812	**FV**	219.1492	247.1441			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.6	1065.5607	0.1044	KAYPDAFVR
34.9	1065.5641	0.1010	KYVSPAMVR
34.3	1065.5607	0.1044	QSFPVSFVR
32.6	1065.5641	0.1010	MVISQVFAR
31.7	1065.5641	0.1010	MVLQSVFAR
30.9	1065.5641	0.1010	MEAFVKAVR
30.6	1065.5753	0.0898	AFLSRAMVR
29.4	1065.5641	0.1010	KEFAVMAVR
29.2	1065.5971	0.0680	KAIFDAFVR
28.1	1065.5607	0.1044	FKSFDPAVR

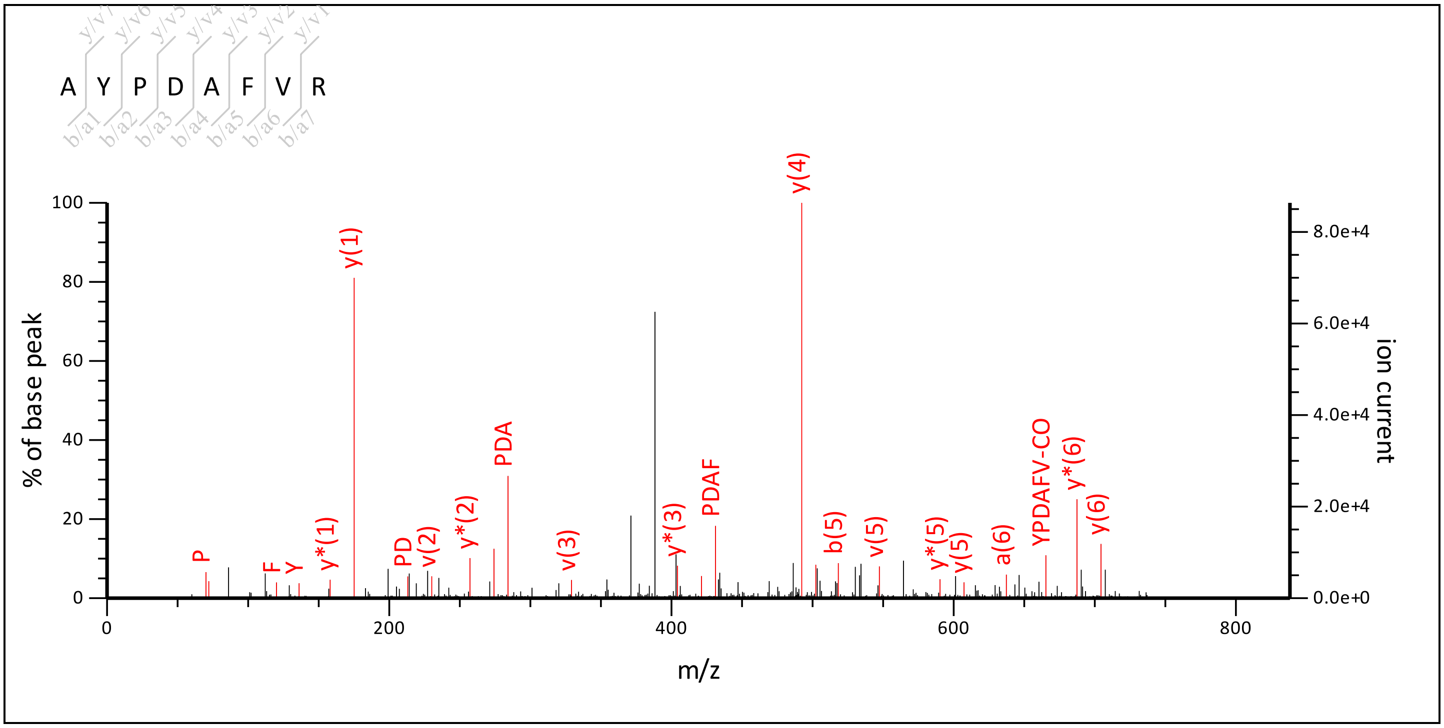
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **AYPDAFVR**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 35: 937.542044 from(938.549320,1+) intensity(0.0000) index(3)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227089, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



0 to 838.29

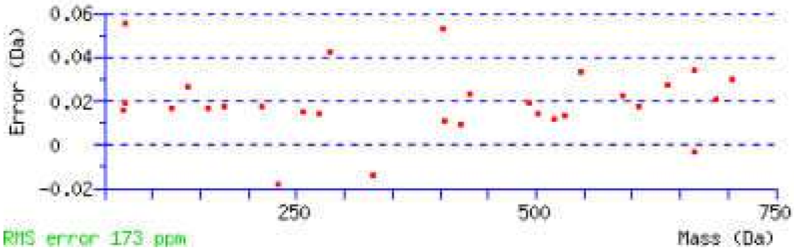
Label all possible matches ○ Label matches used for scoring ●

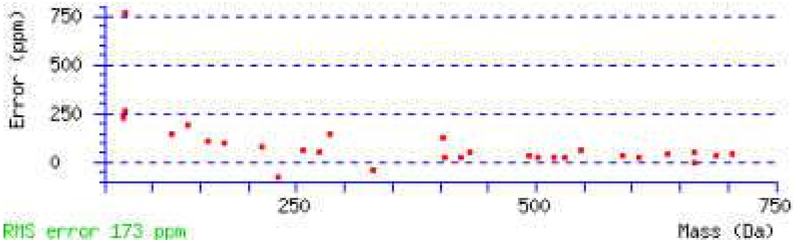
Monoisotopic mass of neutral peptide Mr(calc): 937.4658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 14
Matches : 29/92 fragment ions using 49 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		**72.0444**		44.0495	A						8
2	136.0757	207.1128		235.1077			Y	759.3784		867.4359	850.4094	849.4254	7
3	70.0651	304.1656		332.1605		278.1499	P	662.3257	661.3304	***704.3726***	687.3461	686.3620	6
4	88.0393	419.1925	401.1819	447.1874	429.1769	375.2027	D	547.2987	546.3035	***607.3198***	590.2933	589.3093	5
5	44.0495	490.2296	472.2191	**518.2245**	500.2140		A	476.2616		***492.2929***	475.2663		4
6	120.0808	637.2980	619.2875	**665.2930**	647.2824		F	329.1932		***421.2558***	404.2292		3
7	72.0808	736.3665	718.3559	764.3614	746.3508	722.3508	V	230.1248	243.1452	***274.1874***	257.1608		2

8	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YP	233.1285	261.1234	**YPD**	348.1554	376.1503	**YPDA**	419.1925	447.1874
YPDAF	566.2609	594.2558	**YPDAFV**	665.3293	693.3243	**PD**	185.0921	213.0870
PDA	256.1292	284.1241	**PDAF**	403.1976	431.1925	**PDAFV**	502.2660	530.2609
DA	159.0764	187.0713	**DAF**	306.1448	334.1397	**DAFV**	405.2132	433.2082
AF	191.1179	219.1128	**AFV**	290.1863	318.1812	**FV**	219.1492	247.1441





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.7	937.4658	0.0763	AYPDAFVR
25.9	937.5134	0.0287	HPIGYPVR
25.5	937.5385	0.0035	YALLGFVR
25.4	937.4658	0.0763	YAEGFPVR
25.2	937.5168	0.0253	HPAMIVVR
25.2	937.5168	0.0253	HPAMVIVR
25.2	937.5168	0.0253	HPSMVIVR
25.0	937.4617	0.0803	LSDHDPVR
25.0	937.4617	0.0803	SLDHDPVR
24.8	937.5055	0.0365	SFVLAMVR

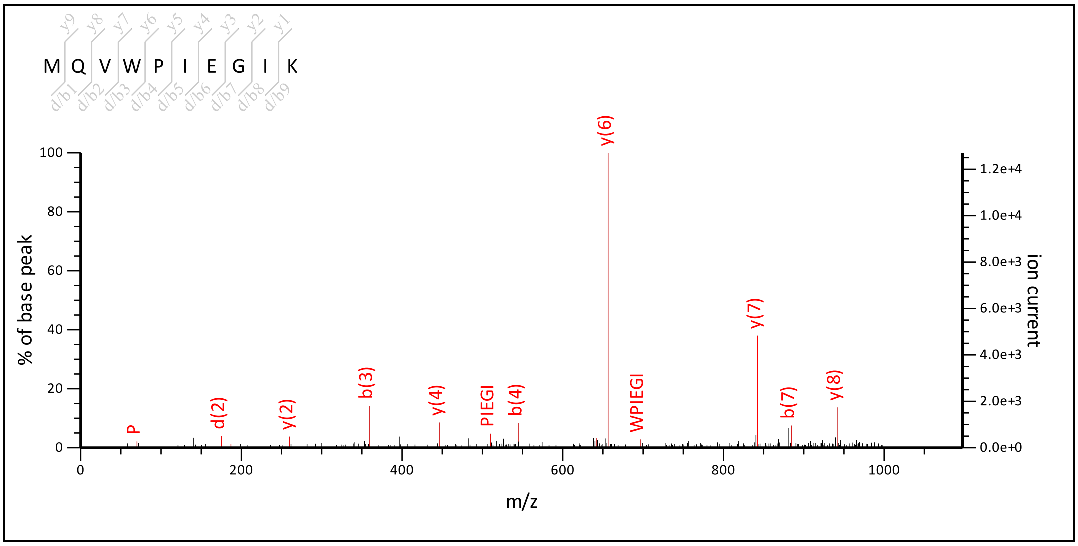
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **MQVWPIEGIK**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 125: 1199.741024 from(1200.748300,1+) intensity(0.0000) index(13)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227093, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



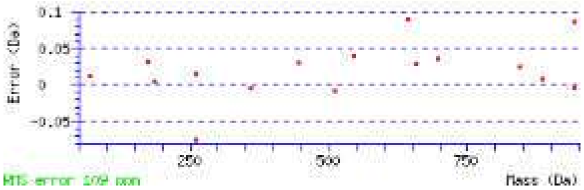
0 to 1097.53

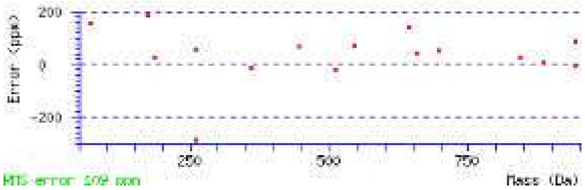
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): `1199.6373`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `46` **Expect:** `0.54`
Matches : `16/148 fragment ions using 20 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0
1	104.0528	104.0528			132.0478			44.0495		**M**						
2	101.0709	232.1114	215.0849		***260.1063***	243.0798		175.0900		**Q**	996.5513	995.5560		1069.6041	1052.5775	1051.5
3	72.0808	331.1798	314.1533		***359.1748***	342.1482		317.1642		**V**	897.4829	910.5033		***941.5455***	924.5189	923.5
4	159.0917	517.2592	500.2326		***545.2541***	528.2275				**W**	711.4036			***842.4771***	825.4505	824.4
5	70.0651	614.3119	597.2854		***642.3068***	625.2803		588.2963		**P**	614.3508	613.3556		***656.3978***	639.3712	638.3
6	86.0964	727.3960	710.3694		755.3909	738.3643		699.3647	713.3803	**I**	501.2667	514.2871	528.3028	559.3450	542.3184	541.3
7	102.0550	856.4386	839.4120	838.4280	***884.4335***	867.4069	866.4229	798.4331		**E**	372.2241	371.2289		***446.2609***	429.2344	428.2
8	30.0338	913.4600	896.4335	895.4495	***941.4550***	924.4284	923.4444			**G**				317.2183	300.1918	
9	86.0964	1026.5441	1009.5176	1008.5335	1054.5390	1037.5125	1036.5285	998.5128	1012.5285	**I**	202.1186	215.1390	229.1547	***260.1969***	243.1703	
10	101.1073									**K**	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QV	200.1394	228.1343	**QVW**	386.2187	414.2136	**QVWP**	483.2714	511.2663
QVWPI	596.3555	624.3504	**VW**	258.1601	286.1550	**VWP**	355.2129	383.2078
VWPI	468.2969	496.2918	**VWPIE**	597.3395	625.3344	**VWPIEG**	654.3610	682.3559
WP	256.1444	284.1394	**WPI**	369.2285	397.2234	**WPIE**	498.2711	526.2660
WPIEG	555.2926	583.2875	**WPIEGI**	668.3766	696.3715	**PI**	183.1492	211.1441
PIE	312.1918	340.1867	**PIEG**	369.2132	397.2082	**PIEGI**	482.2973	510.2922
IE	215.1390	243.1339	**IEG**	272.1605	300.1554	**IEGI**	385.2445	413.2395
EG	159.0764	187.0713	**EGI**	272.1605	300.1554	**GI**	143.1179	171.1128





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.2	1199.6373	0.1038	MQVWPIEGIK
46.2	1199.6373	0.1038	MQVWPIEGIK
43.4	1199.6761	0.0649	ATSVAPEALTIK
40.8	1199.6696	0.0714	MQVVSSPILAR
40.7	1199.6398	0.1013	VSDGSVPDIAIK
40.0	1199.6914	0.0496	ASTVLSPWVLK
37.2	1199.6874	0.0536	TVTGSVPLLASR
32.7	1199.6220	0.1190	AMGVPVEAELGK
31.7	1199.6696	0.0714	LSVVCPVSALR
30.7	1199.6332	0.1078	EGVCVPLLASR

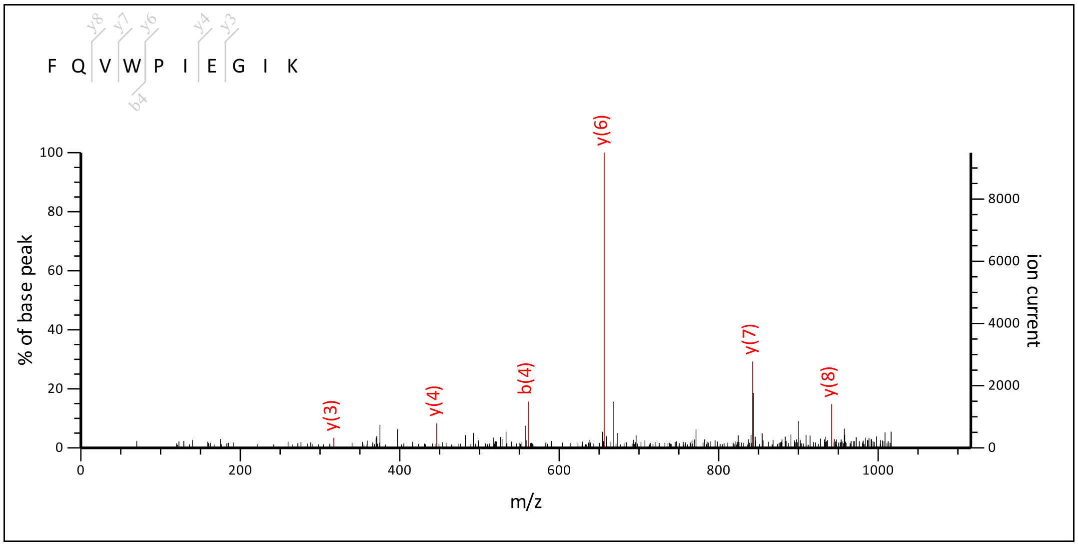
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **FQVWPIEGIK**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 130: 1215.734924 from(1216.742200,1+) intensity(0.0000) index(14)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227094, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



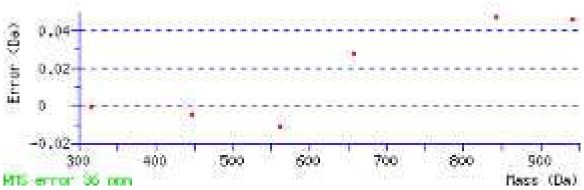
0 to 1116.27

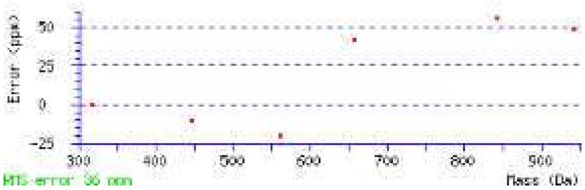
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1215.6652
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 14
Matches : 6/148 fragment ions using 10 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y
1	120.0808	120.0808			148.0757			44.0495		F						
2	101.0709	248.1394	231.1128		276.1343	259.1077		191.1179		Q	996.5513	995.5560		1069.6041	1052.5775	1051.
3	72.0808	347.2078	330.1812		375.2027	358.1761		333.1921		V	897.4829	910.5033		***941.5455***	924.5189	923.
4	159.0917	533.2871	516.2605		**561.2820**	544.2554				W	711.4036			***842.4771***	825.4505	824.
5	70.0651	630.3398	613.3133		658.3348	641.3082		604.3242		P	614.3508	613.3556		***656.3978***	639.3712	638.
6	86.0964	743.4239	726.3974		771.4188	754.3923		715.3926	729.4083	I	501.2667	514.2871	528.3028	559.3450	542.3184	541.
7	102.0550	872.4665	855.4400	854.4559	900.4614	883.4349	882.4509	814.4610		E	372.2241	371.2289		***446.2609***	429.2344	428.
8	30.0338	929.4880	912.4614	911.4774	957.4829	940.4563	939.4723			G				***317.2183***	300.1918	
9	86.0964	1042.5720	1025.5455	1024.5615	1070.5669	1053.5404	1052.5564	1014.5407	1028.5564	I	202.1186	215.1390	229.1547	260.1969	243.1703	
10	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QV	200.1394	228.1343	QVW	386.2187	414.2136	QVWP	483.2714	511.2663
QVWPI	596.3555	624.3504	VW	258.1601	286.1550	VWP	355.2129	383.2078
VWPI	468.2969	496.2918	VWPIE	597.3395	625.3344	VWPIEG	654.3610	682.3559
WP	256.1444	284.1394	WPI	369.2285	397.2234	WPIE	498.2711	526.2660
WPIEG	555.2926	583.2875	WPIEGI	668.3766	696.3715	PI	183.1492	211.1441
PIE	312.1918	340.1867	PIEG	369.2132	397.2082	PIEGI	482.2973	510.2922
IE	215.1390	243.1339	IEG	272.1605	300.1554	IEGI	385.2445	413.2395
EG	159.0764	187.0713	EGI	272.1605	300.1554	GI	143.1179	171.1128





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.7	1215.6652	0.0697	FQVWPIEGIK
32.7	1215.6322	0.1028	MQVWPIEGIK
32.7	1215.6322	0.1028	MQVWPIEGIK
29.6	1215.6281	0.1068	MAALPTLTEGGR
29.6	1215.6506	0.0843	KMGGRPGSLASR
28.5	1215.6459	0.0890	TASDADLLALAR
26.8	1215.6281	0.1068	TASGLMLPEAAR
26.5	1215.6281	0.1068	GMAVTPREVEK
25.5	1215.6645	0.0704	MQVVSSPILAR
25.5	1215.6758	0.0591	AMGVVVKLGNGR

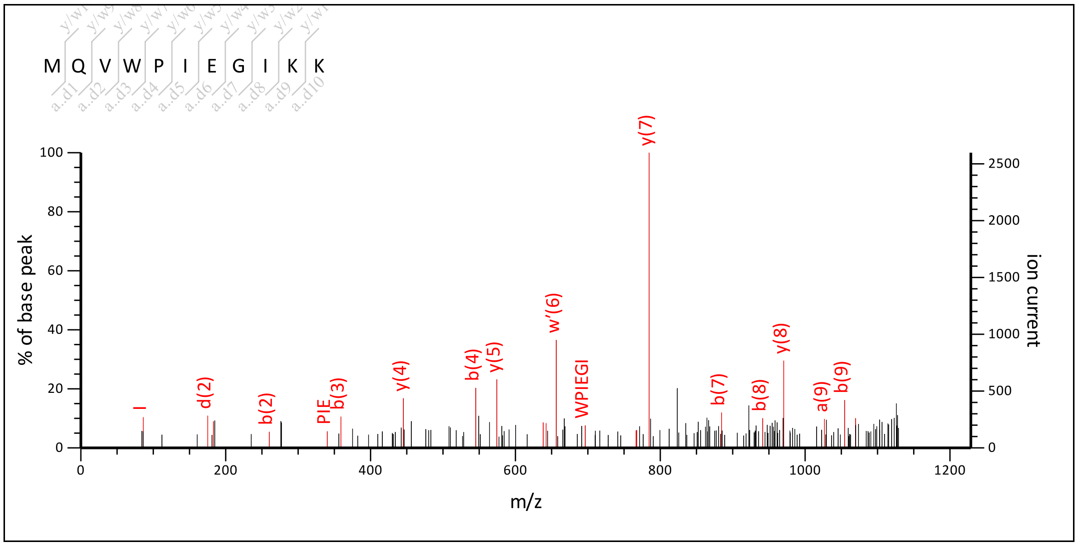
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **MQVWPIEGIKK**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 174: 1327.848024 from(1328.855300,1+) intensity(0.0000) index(19)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227107, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



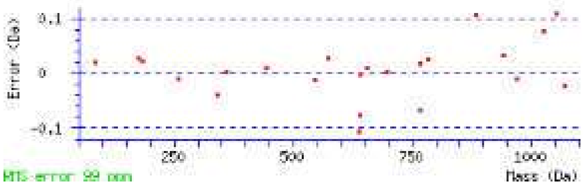
0 to 1228.83

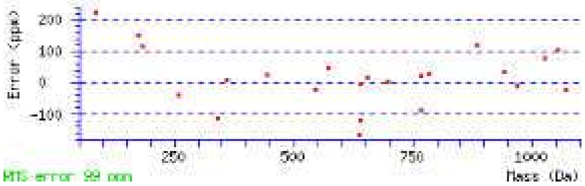
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): `1327.7322`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `27` **Expect:** `22`
Matches : `24/170 fragment ions using 55 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	104.0528	104.0528			132.0478			44.0495		M					
2	101.0709	232.1114	215.0849		***260.1063***	243.0798		175.0900		Q	1124.6463	1123.6510		1197.6990	1180.6725
3	72.0808	331.1798	314.1533		***359.1748***	342.1482		317.1642		V	1025.5778	1038.5982		**1069.6404**	1052.6139
4	159.0917	517.2592	500.2326		***545.2541***	528.2275				W	839.4985			**970.5720**	953.5455
5	70.0651	614.3119	597.2854		***642.3068***	625.2803		588.2963		P	742.4458	741.4505		**784.4927**	767.4662
6	86.0964	727.3960	710.3694		755.3909	738.3643		699.3647	713.3803	I	629.3617	642.3821	656.3978	687.4400	670.4134
7	102.0550	856.4386	839.4120	838.4280	***884.4335***	867.4069	866.4229	798.4331		E	500.3191	499.3239		**574.3559**	557.3293
8	30.0338	913.4600	896.4335	895.4495	***941.4550***	924.4284	923.4444			G				**445.3133**	428.2867
9	86.0964	1026.5441	1009.5176	1008.5335	***1054.5390***	1037.5125	1036.5285	998.5128	1012.5285	I	330.2136	343.2340	357.2496	388.2918	371.2653
10	101.1073	1154.6391	1137.6125	1136.6285	1182.6340	1165.6074	1164.6234	1097.5812		K	202.1186	201.1234		275.2078	258.1812
11	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QV	200.1394	228.1343	**QVW**	386.2187	414.2136	**QVWP**	483.2714	511.2663
QVWPI	596.3555	624.3504	**VW**	258.1601	286.1550	**VWP**	355.2129	383.2078
VWPI	468.2969	496.2918	**VWPIE**	597.3395	625.3344	**VWPIEG**	654.3610	682.3559
WP	256.1444	284.1394	**WPI**	369.2285	397.2234	**WPIE**	498.2711	526.2660
WPIEG	555.2926	583.2875	**WPIEGI**	668.3766	696.3715	**PI**	183.1492	211.1441
PIE	312.1918	340.1867	**PIEG**	369.2132	397.2082	**PIEGI**	482.2973	510.2922
PIEGIK	610.3923	638.3872	**IE**	215.1390	243.1339	**IEG**	272.1605	300.1554
IEGI	385.2445	413.2395	**IEGIK**	513.3395	541.3344	**EG**	159.0764	187.0713
EGI	272.1605	300.1554	**EGIK**	400.2554	428.2504	**GI**	143.1179	171.1128
GIK	271.2129	299.2078	**IK**	214.1914	242.1863			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.4	1327.7322	0.1158	MQVWPIEGIKK
27.4	1327.7322	0.1158	MQVWPIEGIKK
26.9	1327.7459	0.1021	EKTVSPLQSAIR
21.6	1327.7646	0.0835	NCLTIALLALAR
20.2	1327.7646	0.0835	ADMKVGALLAALR
19.5	1327.7646	0.0835	QKMGLLLIGAER
18.4	1327.8340	0.0141	VAVKFKPSLAIR
18.1	1327.7459	0.1021	LTSENKAIISPR
17.9	1327.7572	0.0909	IIGISSIAGERGR
17.9	1327.7572	0.0908	RSDGIILGTGLAR

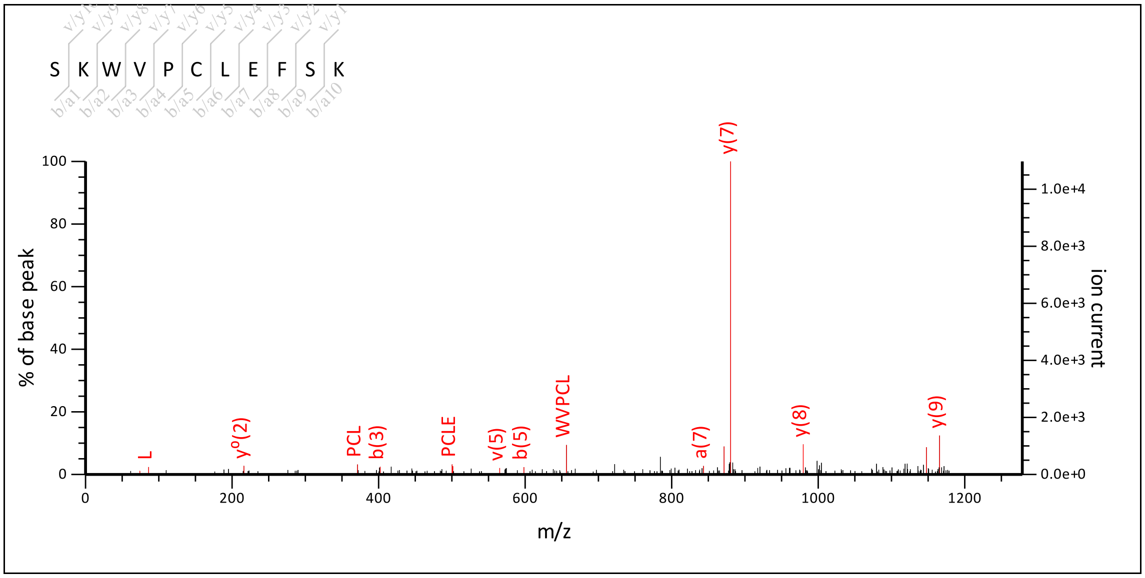
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 8**

MS/MS Fragmentation of **SKWVPCLEFSK**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 183: 1379.818024 from(1380.825300,1+) intensity(0.0000) index(22)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227096, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



0 to 1278.55

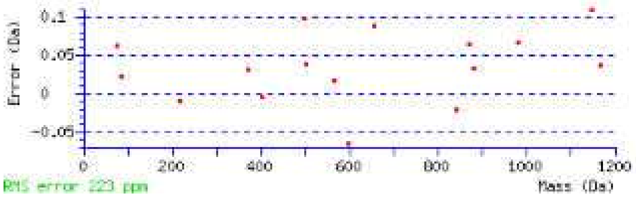
Label all possible matches ○ Label matches used for scoring ●

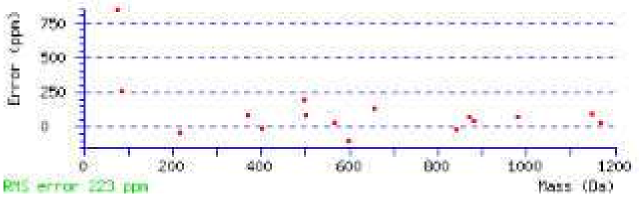
Monoisotopic mass of neutral peptide Mr(calc): 1379.6907
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 77
Matches : 18/176 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495	S						11
2	101.1073	188.1394	171.1128	170.1288	***216.1343***	199.1077	198.1237	131.0815	K	1220.5769	1219.5816	1293.6660	1276.6395	1275.6554	10
3	159.0917	374.2187	357.1921	356.2081	***402.2136***	385.1870	384.2030		W	1034.4975		**1165.5710**	1148.5445	1147.5605	9
4	72.0808	473.2871	456.2605	455.2765	***501.2820***	484.2554	483.2714	459.2714	V	935.4291	948.4495	**979.4917**	962.4652	961.4812	8
5	70.0651	570.3398	553.3133	552.3293	***598.3348***	581.3082	580.3242	544.3242	P	838.3764	837.3811	**880.4233**	863.3968	862.4128	7
6	133.0430	730.3705	713.3439	712.3599	758.3654	741.3389	740.3548	641.3770	C	678.3457	677.3505	783.3706	766.3440	765.3600	6
7	86.0964	843.4546	826.4280	825.4440	***871.4495***	854.4229	853.4389	801.4076	L	565.2617	564.2664	623.3399	606.3134	605.3293	5
8	102.0550	972.4971	955.4706	954.4866	1000.4921	983.4655	982.4815	914.4917	E	436.2191	435.2238	510.2558	493.2293	492.2453	4
9	120.0808	1119.5656	1102.5390	1101.5550	***1147.5605***	1130.5339	1129.5499		F	289.1506		381.2132	364.1867	363.2027	3
10	60.0444	1206.5976	1189.5710	1188.5870	1234.5925	1217.5660	1216.5819	1190.6027	S	202.1186	201.1234	234.1448	217.1183	216.1343	2
11	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KW	287.1866	315.1816	KWV	386.2551	414.2500	KWVP	483.3078	511.3027
KWVPC	643.3385	671.3334	WV	258.1601	286.1550	WVP	355.2129	383.2078
WVPC	515.2435	543.2384	WVPCL	628.3276	656.3225	VP	169.1335	197.1285
VPC	329.1642	357.1591	VPCL	442.2483	470.2432	VPCLE	571.2908	599.2858
PC	230.0958	258.0907	PCL	343.1798	371.1748	PCLE	472.2224	500.2173
PCLEF	619.2908	647.2858	CL	246.1271	274.1220	CLE	375.1697	403.1646

CLEF	522.2381	550.2330	**CLEFS**	609.2701	637.2650	**LE**	215.1390	243.1339
LEF	362.2074	390.2023	**LEFS**	449.2395	477.2344	**EF**	249.1234	277.1183
EFS	336.1554	364.1503	**FS**	207.1128	235.1077			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.4	1379.6907	0.1273	SKWVPCLEFSK
20.9	1379.6867	0.1313	IREEHMIPDPK
20.4	1379.7231	0.0949	LMGFLDGTGAVRK
20.3	1379.7885	0.0295	LTPSERPVVLNR
18.7	1379.6867	0.1313	LREYCDAVQVK
18.7	1379.7343	0.0837	LGIDMQPHVARK
18.6	1379.8249	-0.0068	IVSSLRQIHISK
18.4	1379.7521	0.0659	ADVIERQLAHTK
16.5	1379.8249	-0.0068	AGSVSLLIRISHK
16.4	1379.7674	0.0507	VWIATIHSVAQR

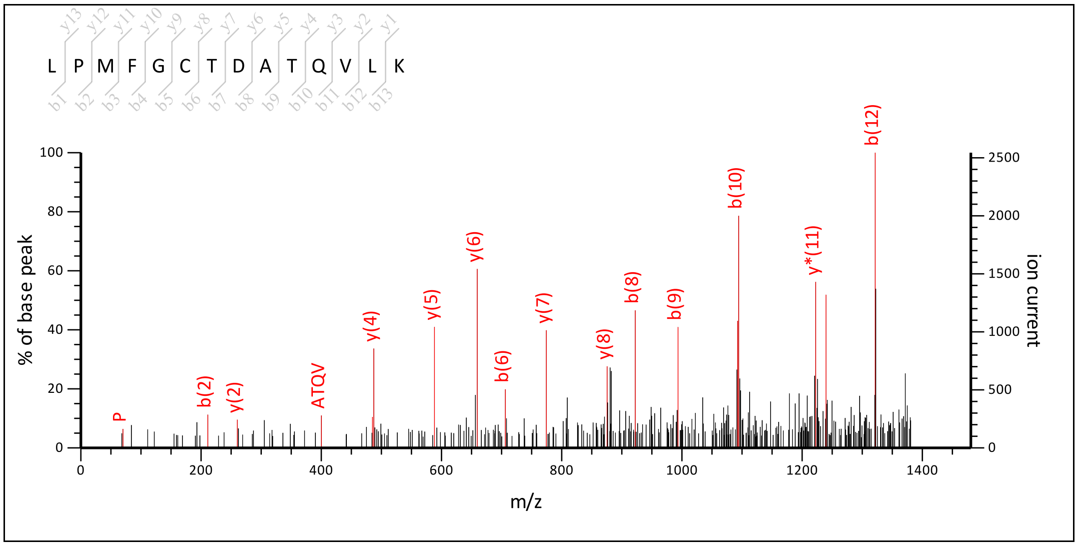
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **LPMFGCTDATQVLK**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 205: 1579.924724 from(1580.932000,1+) intensity(0.0000) index(26)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227100, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



0 to 1480.69

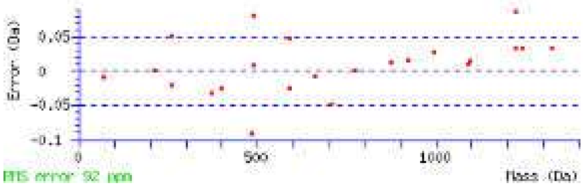
Label all possible matches ○ Label matches used for scoring ●

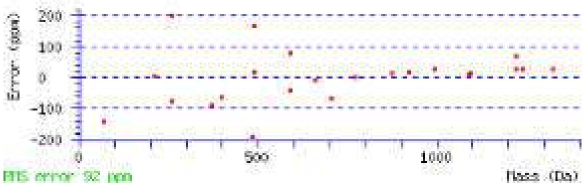
Monoisotopic mass of neutral peptide Mr(calc): 1579.7738
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 0.019
Matches : 24/220 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	86.0964			114.0913			44.0495		**L**						
2	70.0651	183.1492			***211.1441***			157.1335		**P**	1425.6501	1424.6549		1467.6971	1450.6705	14
3	104.0528	314.1897			342.1846			254.1863		**M**	1294.6096	1293.6144		1370.6443	1353.6177	13
4	120.0808	461.2581			489.2530					**F**	1147.5412			***1239.6038***	1222.5773	12
5	30.0338	518.2796			546.2745					**G**				***1092.5354***	1075.5088	10
6	133.0430	678.3102			***706.3051***			589.3167		**C**	930.4891	929.4938		1035.5139	1018.4874	10
7	74.0600	779.3579		761.3473	807.3528		789.3422	763.3630	765.3422	**T**	829.4414	842.4618	844.4411	***875.4833***	858.4567	8
8	88.0393	894.3848		876.3743	***922.3797***		904.3692	850.3950		**D**	714.4145	713.4192		***774.4356***	757.4090	7
9	44.0495	965.4219		947.4114	***993.4169***		975.4063			**A**	643.3774			***659.4087***	642.3821	6
10	74.0600	1066.4696		1048.4591	***1094.4645***		1076.4540	1050.4747	1052.4540	**T**	542.3297	555.3501	557.3293	***588.3715***	571.3450	5
11	101.0709	1194.5282	1177.5016	1176.5176	***1222.5231***	1205.4966	1204.5125	1137.5067		**Q**	414.2711	413.2758		***487.3239***	470.2973	
12	72.0808	1293.5966	1276.5701	1275.5860	***1321.5915***	1304.5650	1303.5810	1279.5810		**V**	315.2027	328.2231		359.2653	342.2387	
13	86.0964	1406.6807	1389.6541	1388.6701	1434.6756	1417.6490	1416.6650	1364.6337		**L**	202.1186	201.1234		***260.1969***	243.1703	
14	101.1073									**K**	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PM	201.1056	229.1005	**PMF**	348.1740	376.1689	**PMFG**	405.1955	433.1904
PMFGC	565.2261	593.2211	**PMFGCT**	666.2738	694.2687	**MF**	251.1213	279.1162
MFG	308.1427	336.1376	**MFGC**	468.1734	496.1683	**MFGCT**	569.2211	597.2160
MFGCTD	684.2480	712.2429	**FG**	177.1022	205.0972	**FGC**	337.1329	365.1278
FGCT	438.1806	466.1755	**FGCTD**	553.2075	581.2024	**FGCTDA**	624.2446	652.2395
GC	190.0645	218.0594	**GCT**	291.1122	319.1071	**GCTD**	406.1391	434.1340
GCTDA	477.1762	505.1711	**GCTDAT**	578.2239	606.2188	**CT**	234.0907	262.0856

CTD	349.1176	377.1125	**CTDA**	420.1547	448.1497	**CTDAT**	521.2024	549.1973
CTDATQ	649.2610	677.2559	**TD**	189.0870	217.0819	**TDA**	260.1241	288.1190
TDAT	361.1718	389.1667	**TDATQ**	489.2304	517.2253	**TDATQV**	588.2988	616.2937
DA	159.0764	187.0713	**DAT**	260.1241	288.1190	**DATQ**	388.1827	416.1776
DATQV	487.2511	515.2460	**DATQVL**	600.3352	628.3301	**AT**	145.0972	173.0921
ATQ	273.1557	301.1506	**ATQV**	372.2241	400.2191	**ATQVL**	485.3082	513.3031
TQ	202.1186	230.1135	**TQV**	301.1870	329.1819	**TQVL**	414.2711	442.2660
QV	200.1394	228.1343	**QVL**	313.2234	341.2183	**VL**	185.1648	213.1598





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.5	1579.7738	0.1509	LPMFGCTDATQVLK
24.4	1579.8756	0.0491	FLLSRMSSATQVLK
23.0	1579.8570	0.0678	LPLPGDLTDAQTALR
21.0	1579.7916	0.1331	QMGFEESLATQLVK
18.3	1579.8029	0.1219	MFDTVAIVGATGAVGR
17.9	1579.8868	0.0379	RMIAEHALATNLIK
17.6	1579.8206	0.1042	ENKLSSDTSFILAR
17.5	1579.7850	0.1397	KQNGMMLFATQSPK
16.3	1579.8643	0.0604	VYTLIMQGATLNLK
16.2	1579.8933	0.0314	ELVQELLPATGAAIR

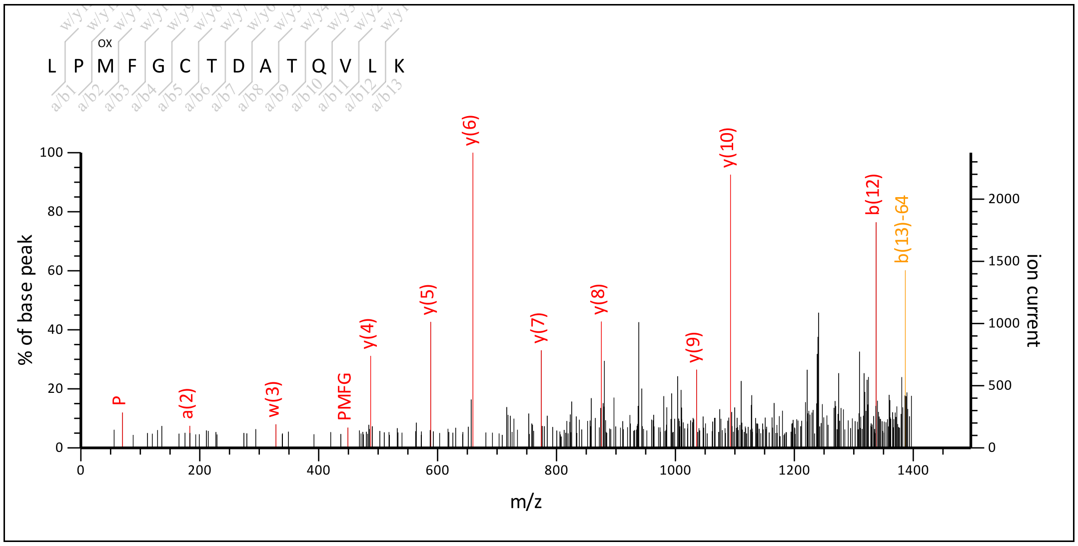
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 8

MS/MS Fragmentation of **LPMFGCTDATQVLK**
Found in **gi|56966763** in **NCBInr**, Chain S, Crystal Structure Of Activated Rice Rubisco Complexed With 2- Carboxyarabinitol-1,5-Bisphosphate

Match to Query 207: 1595.917624 from(1596.924900,1+) intensity(0.0000) index(27)
Title: Label: N9, Spot_Id: 219815, Peak_List_Id: 227095, MSMS Job_Run_Id: 21951, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N9_136868212700.txt



0 to 1496.86

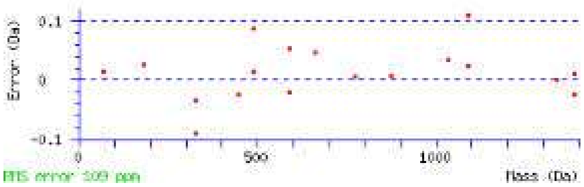
Label all possible matches ○ Label matches used for scoring ●

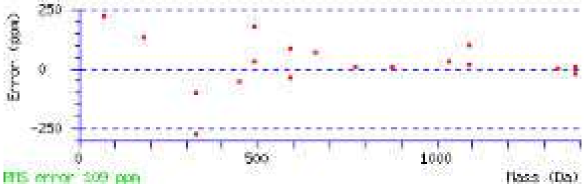
Monoisotopic mass of neutral peptide Mr(calc): 1595.7688
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 74 **Expect:** 0.00091
Matches : 18/295 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	86.0964			114.0913			44.0495		L						
2	70.0651	**183.1492**			211.1441			157.1335		P	1441.6450	1440.6498		1483.6920	1466.6654	146
3	120.0478	330.1846			358.1795			254.1863		M	1294.6096	1293.6144		***1386.6392***	1369.6127	136
4	120.0808	477.2530			505.2479					F	1147.5412			1239.6038	1222.5773	122
5	30.0338	534.2745			562.2694					G				***1092.5354***	1075.5088	107
6	133.0430	694.3051			722.3000			605.3116		C	930.4891	929.4938		***1035.5139***	1018.4874	101
7	74.0600	795.3528		777.3422	823.3477		805.3371	779.3579	781.3371	T	829.4414	842.4618	844.4411	***875.4833***	858.4567	85
8	88.0393	910.3797		892.3692	938.3747		920.3641	866.3899		D	714.4145	713.4192		***774.4356***	757.4090	75
9	44.0495	981.4169		963.4063	1009.4118		991.4012			A	643.3774			***659.4087***	642.3821	64
10	74.0600	1082.4645		1064.4540	1110.4594		1092.4489	1066.4696	1068.4489	T	542.3297	555.3501	557.3293	***588.3715***	571.3450	57
11	101.0709	1210.5231	1193.4966	1192.5125	1238.5180	1221.4915	1220.5075	1153.5016		Q	414.2711	413.2758		***487.3239***	470.2973	
12	72.0808	1309.5915	1292.5650	1291.5810	**1337.5864**	1320.5599	1319.5759	1295.5759		V	315.2027	328.2231		359.2653	342.2387	
13	86.0964	1422.6756	1405.6490	1404.6650	1450.6705	1433.6440	1432.6599	1380.6286		L	202.1186	201.1234		260.1969	243.1703	
14	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PM	217.1005	245.0954	PMF	364.1689	392.1639	PMFG	421.1904	449.1853
PMFGC	581.2211	609.2160	PMFGCT	682.2687	710.2636	MF	267.1162	295.1111
MFG	324.1376	352.1326	MFGC	484.1683	512.1632	MFGCT	585.2160	613.2109
FG	177.1022	205.0972	FGC	337.1329	365.1278	FGCT	438.1806	466.1755
FGCTD	553.2075	581.2024	FGCTDA	624.2446	652.2395	GC	190.0645	218.0594
GCT	291.1122	319.1071	GCTD	406.1391	434.1340	GCTDA	477.1762	505.1711

GCTDAT	578.2239	606.2188	**CT**	234.0907	262.0856	**CTD**	349.1176	377.1125
CTDA	420.1547	448.1497	**CTDAT**	521.2024	549.1973	**CTDATQ**	649.2610	677.2559
TD	189.0870	217.0819	**TDA**	260.1241	288.1190	**TDAT**	361.1718	389.1667
TDATQ	489.2304	517.2253	**TDATQV**	588.2988	616.2937	**DA**	159.0764	187.0713
DAT	260.1241	288.1190	**DATQ**	388.1827	416.1776	**DATQV**	487.2511	515.2460
DATQVL	600.3352	628.3301	**AT**	145.0972	173.0921	**ATQ**	273.1557	301.1506
ATQV	372.2241	400.2191	**ATQVL**	485.3082	513.3031	**TQ**	202.1186	230.1135
TQV	301.1870	329.1819	**TQVL**	414.2711	442.2660	**QV**	200.1394	228.1343
QVL	313.2234	341.2183	**VL**	185.1648	213.1598			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.2	1595.7688	0.1489	LPMFGCTDATQVLK
74.2	1595.7688	0.1489	LPMYGCTDATQVLK
26.0	1595.8276	0.0900	TLLLMVSTCLHHR
24.1	1595.8882	0.0294	VGSSRTAEEPILPLK
16.1	1595.7692	0.1484	HDHPTADALYTSIR
15.8	1595.8379	0.0797	EQRAQLPDATIAQR
15.1	1595.8269	0.0907	VFLDALDVMGYPIK
14.7	1595.7614	0.1562	VCVAGGDVVSSEYVR
14.1	1595.7687	0.1489	EIILMFDMDKPGR
13.9	1595.8415	0.0761	LMMLFGEKSGLNIK

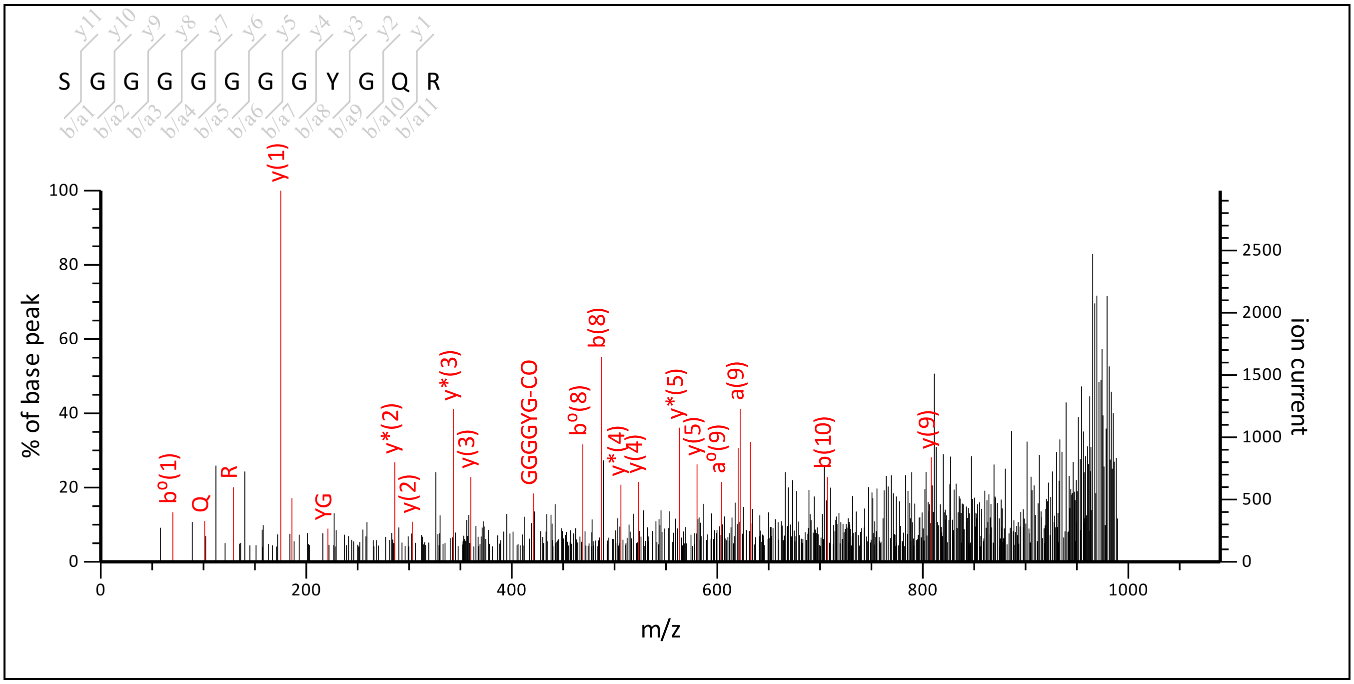
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 10

MS/MS Fragmentation of **SGGGGGGGYGQR**
Found in **gi|18103931** in **NCBInr**, glycine rich RNA binding protein [Oryza sativa Indica Group]

Match to Query 12: 1008.498624 from(1009.505900,1+) intensity(0.0000) index(5)
Title: Label: E6, Spot_Id: 228926, Peak_List_Id: 257517, MSMS Job_Run_Id: 24923, Comment:
Data file ppw_E6_138985130300.txt



0 to 1089.46

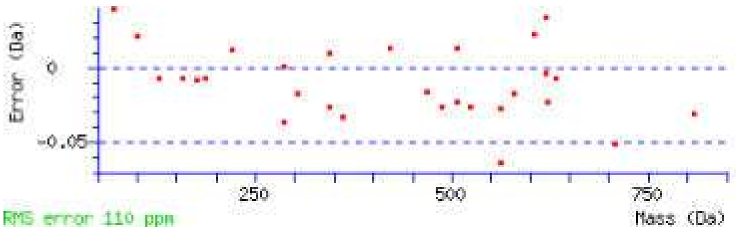
Label all possible matches ○ Label matches used for scoring ●

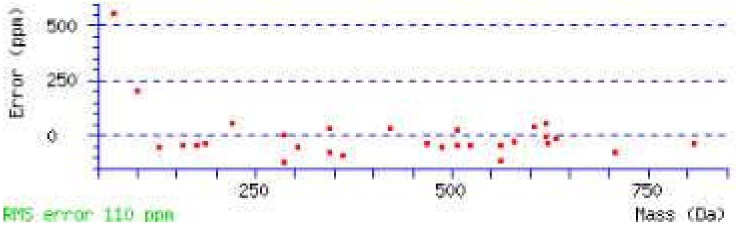
Monoisotopic mass of neutral peptide Mr(calc): 1008.4373
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 50
Matches : 37/175 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495	S					12
2	30.0338	117.0659		99.0553	145.0608		127.0502		G			922.4126	905.3860	11
3	30.0338	174.0873		156.0768	202.0822		184.0717		G			865.3911	848.3646	10
4	30.0338	231.1088		213.0982	259.1037		241.0931		G			***808.3696***	791.3431	9
5	30.0338	288.1302		270.1197	316.1252		298.1146		G			751.3482	734.3216	8
6	30.0338	345.1517		327.1411	373.1466		355.1361		G			694.3267	677.3002	7
7	30.0338	402.1732		384.1626	430.1681		412.1575		G			637.3053	620.2787	6
8	30.0338	459.1946		441.1841	**487.1896**		469.1790		G			***580.2838***	563.2572	5
9	136.0757	622.2580		604.2474	650.2529		632.2423		Y	415.2048		***523.2623***	506.2358	4
10	30.0338	679.2794		661.2689	**707.2743**		689.2638		G			***360.1990***	343.1724	3

11	101.0709	807.3380	790.3115	789.3274	835.3329	818.3064	817.3224	750.3165	**Q**	230.1248	229.1295	***303.1775***	286.1510	**2**
12	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GG	87.0553	115.0502	GGG	144.0768	172.0717	GGGG	201.0982	229.0931
GGGGG	258.1197	286.1146	GGGGGG	315.1411	343.1361	GGGGGGG	372.1626	400.1575
GGGGGGGY	535.2259	563.2209	GGGGGGGYG	592.2474	620.2423	GG	87.0553	115.0502
GGG	144.0768	172.0717	GGGG	201.0982	229.0931	GGGGG	258.1197	286.1146
GGGGGG	315.1411	343.1361	GGGGGGY	478.2045	506.1994	GGGGGGYG	535.2259	563.2209
GGGGGGYGQ	663.2845	691.2794	GG	87.0553	115.0502	GGG	144.0768	172.0717
GGGG	201.0982	229.0931	GGGGG	258.1197	286.1146	GGGGGY	421.1830	449.1779
GGGGGYG	478.2045	506.1994	GGGGGYGQ	606.2631	634.2580	GG	87.0553	115.0502
GGG	144.0768	172.0717	GGGG	201.0982	229.0931	GGGGY	364.1615	392.1565
GGGGYG	421.1830	449.1779	GGGGYGQ	549.2416	577.2365	GG	87.0553	115.0502
GGG	144.0768	172.0717	GGGY	307.1401	335.1350	GGGYG	364.1615	392.1565
GGGYGQ	492.2201	520.2150	GG	87.0553	115.0502	GGY	250.1186	278.1135
GGYG	307.1401	335.1350	GGYGQ	435.1987	463.1936	GY	193.0972	221.0921
GYG	250.1186	278.1135	GYGQ	378.1772	406.1721	YG	193.0972	221.0921
YGQ	321.1557	349.1506	GQ	158.0924	186.0873			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.2	1008.4373	0.0613	SGGGGGGGYGQR
9.2	1008.5352	-0.0366	YGVVSGGSKR
8.6	1008.4413	0.0573	QDWGYANR
8.1	1008.5101	-0.0115	RVGSSYGQR
8.0	1008.4373	0.0613	SGGGGGGGAGYGR
7.4	1008.5716	-0.0730	VVSANPVPAR
7.2	1008.5287	-0.0301	QGAMPPRPR

7.1	1008.4295	0.0692	MASDGDGKGR
6.6	1008.4889	0.0097	RWYNSQR
6.3	1008.5604	-0.0618	KSSLFGGVSK

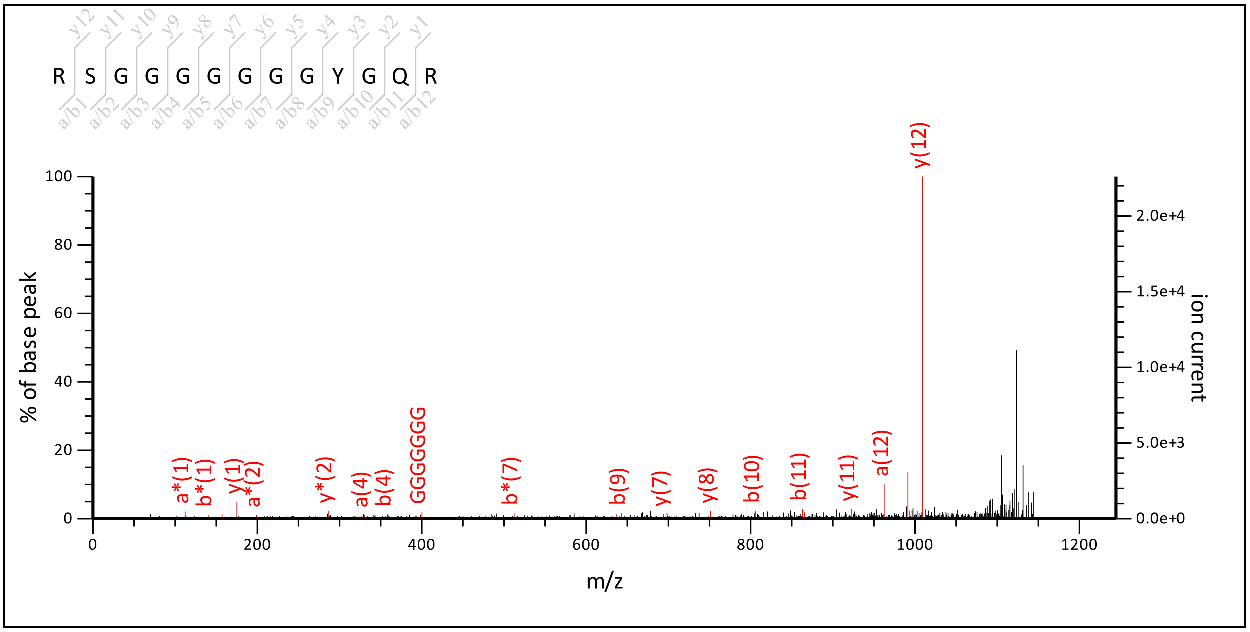
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 10**

MS/MS Fragmentation of **RSGGGGGGGYGQR**
Found in **gi|18103931** in **NCBInr**, glycine rich RNA binding protein [Oryza sativa Indica Group]

Match to Query 22: 1164.605024 from(1165.612300,1+) intensity(0.0000) index(9)
Title: Label: E6, Spot_Id: 228926, Peak_List_Id: 257520, MSMS Job_Run_Id: 24923, Comment:
Data file ppw_E6_138985130300.txt



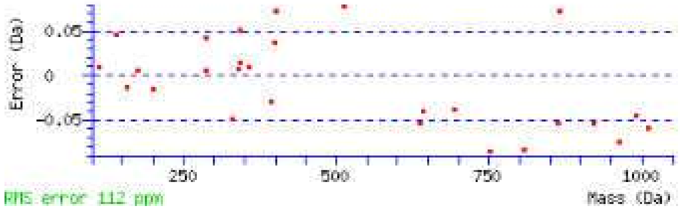
0 to 1244.44

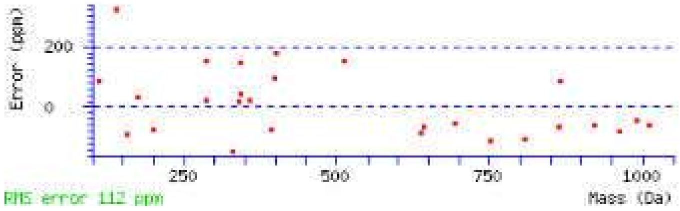
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1164.5385
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 2.6
Matches : 32/223 fragment ions using 77 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	129.1135	129.1135	112.0869		***157.1084***	140.0818		44.0495	R						13
2	60.0444	216.1455	199.1190	198.1349	244.1404	227.1139	226.1298	200.1506	S	977.4184	976.4231	***1009.4446***	992.4181	991.4340	12
3	30.0338	273.1670	256.1404	255.1564	301.1619	284.1353	283.1513		G			***922.4126***	905.3860		11
4	30.0338	**330.1884**	313.1619	312.1779	***358.1833***	341.1568	340.1728		G			***865.3911***	848.3646		10
5	30.0338	387.2099	370.1833	369.1993	415.2048	398.1783	397.1942		G			808.3696	791.3431		9
6	30.0338	444.2314	427.2048	426.2208	472.2263	455.1997	454.2157		G			***751.3482***	734.3216		8
7	30.0338	501.2528	484.2263	483.2423	529.2477	512.2212	511.2372		G			***694.3267***	677.3002		7
8	30.0338	558.2743	541.2477	540.2637	586.2692	569.2427	568.2586		G			***637.3053***	620.2787		6
9	30.0338	615.2957	598.2692	597.2852	***643.2907***	626.2641	625.2801		G			580.2838	563.2572		5
10	136.0757	778.3591	761.3325	760.3485	***806.3540***	789.3274	788.3434		Y	415.2048		523.2623	506.2358		4
11	30.0338	835.3805	818.3540	817.3700	***863.3755***	846.3489	845.3649		G			360.1990	343.1724		3
12	101.0709	**963.4391**	946.4126	945.4286	***991.4340***	974.4075	973.4235	906.4177	Q	230.1248	229.1295	303.1775	286.1510		2
13	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SG	117.0659	145.0608	**SGG**	174.0873	202.0822	**SGGG**	231.1088	259.1037
SGGGG	288.1302	316.1252	**SGGGGG**	345.1517	373.1466	**SGGGGGG**	402.1732	430.1681
SGGGGGGG	459.1946	487.1896	**SGGGGGGGY**	622.2580	650.2529	**SGGGGGGGYG**	679.2794	707.2743
GG	87.0553	115.0502	**GGG**	144.0768	172.0717	**GGGG**	201.0982	229.0931
GGGGG	258.1197	286.1146	**GGGGGG**	315.1411	343.1361	**GGGGGGG**	372.1626	400.1575
GGGGGGGY	535.2259	563.2209	**GGGGGGGYG**	592.2474	620.2423	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGG**	201.0982	229.0931	**GGGGG**	258.1197	286.1146
GGGGGG	315.1411	343.1361	**GGGGGGY**	478.2045	506.1994	**GGGGGGYG**	535.2259	563.2209
GGGGGGYGQ	663.2845	691.2794	**GG**	87.0553	115.0502	**GGG**	144.0768	172.0717
GGGG	201.0982	229.0931	**GGGGG**	258.1197	286.1146	**GGGGGY**	421.1830	449.1779
GGGGGYG	478.2045	506.1994	**GGGGGYGQ**	606.2631	634.2580	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGG**	201.0982	229.0931	**GGGGY**	364.1615	392.1565
GGGGYG	421.1830	449.1779	**GGGGYGQ**	549.2416	577.2365	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGY**	307.1401	335.1350	**GGGYG**	364.1615	392.1565
GGGYGQ	492.2201	520.2150	**GG**	87.0553	115.0502	**GGY**	250.1186	278.1135
GGYG	307.1401	335.1350	**GGYGQ**	435.1987	463.1936	**GY**	193.0972	221.0921
GYG	250.1186	278.1135	**GYGQ**	378.1772	406.1721	**YG**	193.0972	221.0921
YGQ	321.1557	349.1506	**GQ**	158.0924	186.0873			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.3	1164.5385	0.0666	RSGGGGGGGYGQR
19.2	1164.5636	0.0414	VGQDSYRGAGR
19.0	1164.5385	0.0666	RSGGGGGGGAGYGR
15.9	1164.6251	-0.0201	RELVYTAASR
15.9	1164.5974	0.0076	RTLXVSVIXR
14.0	1164.5676	0.0374	RPEDAFFQR
14.0	1164.5709	0.0341	RFIAENEMR
13.9	1164.5128	0.0922	REMMGGNSQR
13.9	1164.6040	0.0011	RENAYFPLR
12.3	1164.6476	-0.0425	RPRVDAAQPR

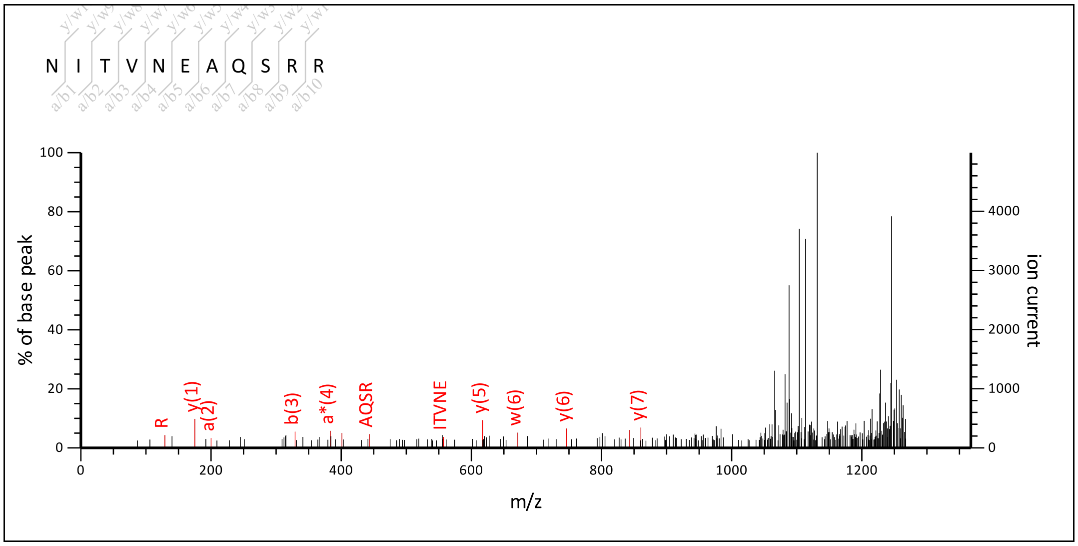
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 10

MS/MS Fragmentation of **NITVNEAQSRR**
Found in **gi|18103931** in **NCBInr**, glycine rich RNA binding protein [Oryza sativa Indica Group]

Match to Query 26: 1286.750124 from(1287.757400,1+) intensity(0.0000) index(11)
Title: Label: E6, Spot_Id: 228926, Peak_List_Id: 257529, MSMS Job_Run_Id: 24923, Comment:
Data file ppw_E6_138985130300.txt



0 to 1367.5

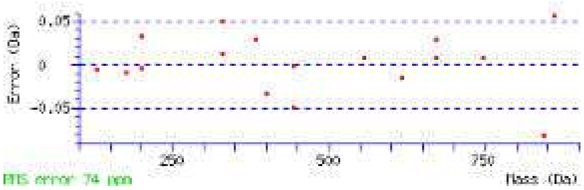
Label all possible matches ○ Label matches used for scoring ●

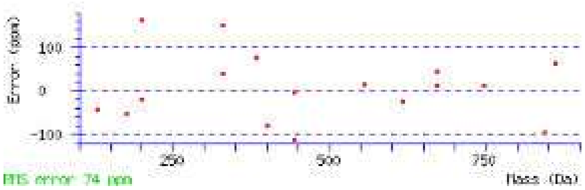
Monoisotopic mass of neutral peptide Mr(calc): 1286.6691
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 10 **Expect:** 1.9e+02
Matches : 18/187 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495		N						
2	86.0964	200.1394	183.1128		228.1343	211.1077		172.1081	186.1237	I	1115.5552	1128.5756	1142.5913	1173.6335	1156.6069	11
3	74.0600	301.1870	284.1605	283.1765	**329.1819**	312.1554	311.1714	285.1921	287.1714	T	1014.5075	1027.5279	1029.5072	1060.5494	1043.5228	104
4	72.0808	400.2554	383.2289	382.2449	428.2504	411.2238	410.2398	386.2398		V	915.4391	928.4595		959.5017	942.4752	94
5	87.0553	514.2984	497.2718	496.2878	542.2933	525.2667	524.2827	471.2926		N	801.3962	800.4009		***860.4333***	843.4068	84
6	102.0550	643.3410	626.3144	625.3304	**671.3359**	654.3093	653.3253	585.3355		E	672.3536	671.3583		***746.3904***	729.3638	72
7	44.0495	714.3781	697.3515	696.3675	742.3730	725.3464	724.3624			A	601.3165			***617.3478***	600.3212	59
8	101.0709	842.4367	825.4101	824.4261	870.4316	853.4050	852.4210	785.4152		Q	473.2579	472.2627		546.3107	529.2841	52
9	60.0444	929.4687	912.4421	911.4581	957.4636	940.4371	939.4530	913.4738		S	386.2259	385.2306		418.2521	401.2255	40
10	129.1135	1085.5698	1068.5432	1067.5592	1113.5647	1096.5382	1095.5541	1000.5058		R	230.1248	229.1295		331.2201	314.1935	
11	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IT	187.1441	215.1390	ITV	286.2125	314.2074	ITVN	400.2554	428.2504
ITVNE	529.2980	557.2930	ITVNEA	600.3352	628.3301	TV	173.1285	201.1234
TVN	287.1714	315.1663	TVNE	416.2140	444.2089	TVNEA	487.2511	515.2460
TVNEAQ	615.3097	643.3046	VN	186.1237	214.1186	VNE	315.1663	343.1612
VNEA	386.2034	414.1983	VNEAQ	514.2620	542.2569	VNEAQS	601.2940	629.2889
NE	216.0979	244.0928	NEA	287.1350	315.1299	NEAQ	415.1936	443.1885
NEAQS	502.2256	530.2205	NEAQSR	658.3267	686.3216	EA	173.0921	201.0870
EAQ	301.1506	329.1456	EAQS	388.1827	416.1776	EAQSR	544.2838	572.2787
AQ	172.1081	200.1030	AQS	259.1401	287.1350	AQSR	415.2412	443.2361

QS		188.1030	216.0979	**QSR**		344.2041	372.1990	**SR**		216.1455	244.1404





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.8	1286.6579	0.0923	RGQSIEVVDER
15.1	1286.6983	0.0519	GVATALNFPLER
14.7	1286.6830	0.0671	RATVNEDEILK
14.5	1286.6731	0.0770	RSPSPAPPPEPR
11.2	1286.6466	0.1035	AIASQLANQDEK
11.0	1286.6830	0.0671	LNEVQSSLLER
10.9	1286.7194	0.0307	KVLGEGSLSLER
10.8	1286.6691	0.0810	QVTVNEAQSRR
10.4	1286.6691	0.0810	NITVNEAQSRR
10.1	1286.6327	0.1174	RQEQESAAAAAR

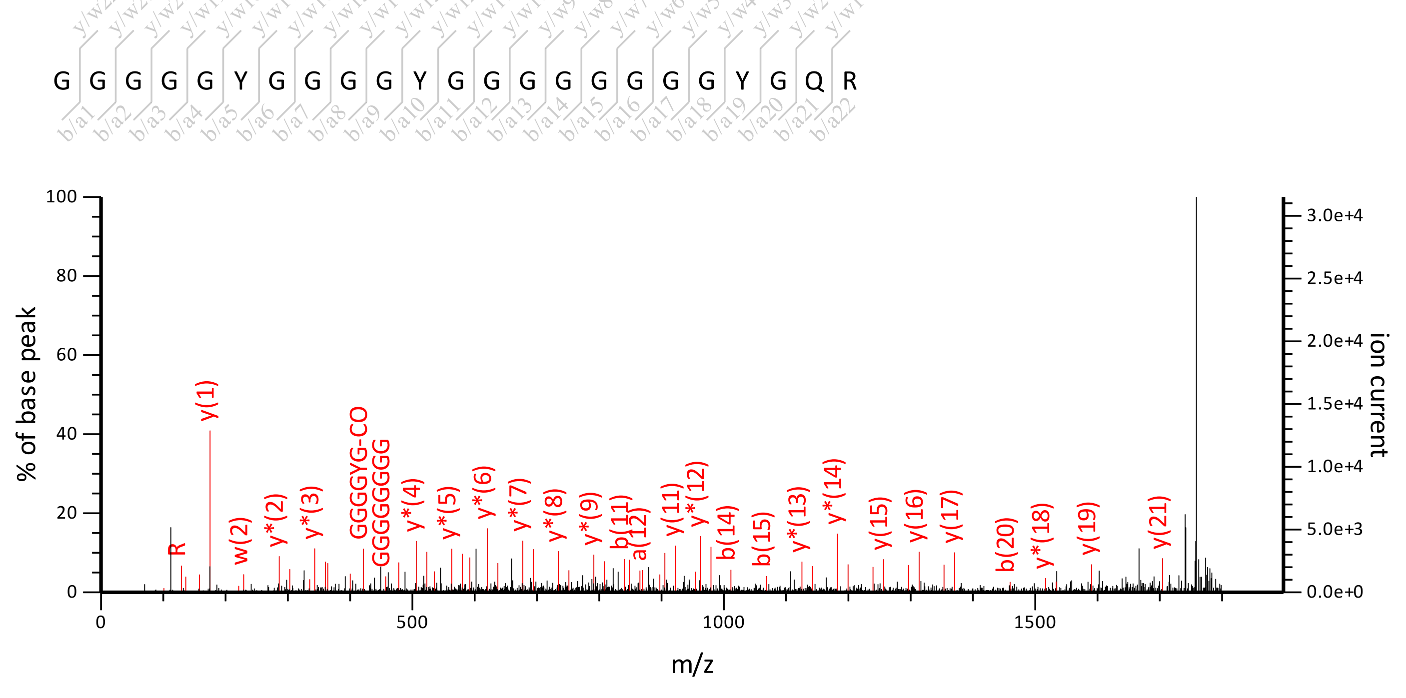
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 10

MS/MS Fragmentation of **GGGGGYGGGGYGGGGGGGGYGQR**
Found in **gi|18103931** in **NCBInr**, glycine rich RNA binding protein [Oryza sativa Indica Group]

Match to Query 46: 1817.858424 from(1818.865700,1+) intensity(0.0000) index(21)
Title: Label: E6, Spot_Id: 228926, Peak_List_Id: 257514, MSMS Job_Run_Id: 24923, Comment:
Data file ppw_E6_138985130300.txt



0 to 1898.59

Label all possible matches ○ Label matches used for scoring ●

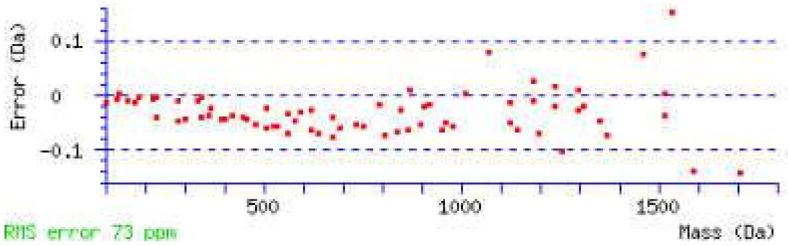
Monoisotopic mass of neutral peptide Mr(calc): 1817.7467
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 124 **Expect:** 8.8e-10
Matches : 207/392 fragment ions using 126 most intense peaks (help)

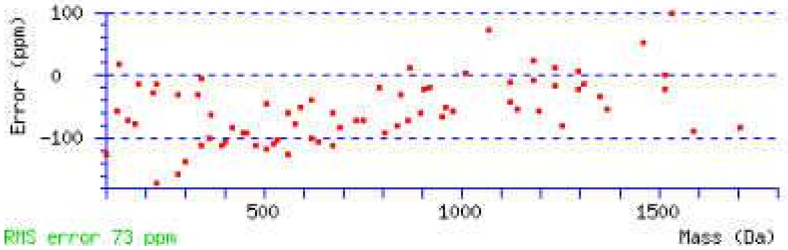
#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	30.0338	30.0338		58.0287		44.0495	G					23
2	30.0338	87.0553		115.0502			G			1761.7324	1744.7059	22
3	30.0338	144.0768		172.0717			G			***1704.7109***	1687.6844	21
4	30.0338	201.0982		**229.0931**			G			1647.6895	1630.6629	20
5	30.0338	258.1197		**286.1146**			G			***1590.6680***	1573.6415	19
6	136.0757	**421.1830**		**449.1779**			Y	1425.5890		***1533.6465***	1516.6200	18
7	30.0338	**478.2045**		**506.1994**			G			***1370.5832***	1353.5567	17
8	30.0338	**535.2259**		**563.2209**			G			***1313.5618***	1296.5352	16

9	30.0338	**592.2474**		**620.2423**			**G**			***1256.5403***	1239.5137	**15**
10	30.0338	649.2689		**677.2638**			**G**			***1199.5188***	1182.4923	**14**
11	136.0757	812.3322		**840.3271**			**Y**	1034.4398		***1142.4974***	1125.4708	**13**
12	30.0338	**869.3537**		**897.3486**			**G**			***979.4340***	962.4075	**12**
13	30.0338	926.3751		**954.3700**			**G**			***922.4126***	905.3860	**11**
14	30.0338	983.3966		**1011.3915**			**G**			***865.3911***	848.3646	**10**
15	30.0338	1040.4181		**1068.4130**			**G**			***808.3696***	791.3431	**9**
16	30.0338	1097.4395		**1125.4344**			**G**			***751.3482***	734.3216	**8**
17	30.0338	1154.4610		**1182.4559**			**G**			***694.3267***	677.3002	**7**
18	30.0338	1211.4824		**1239.4774**			**G**			***637.3053***	620.2787	**6**
19	30.0338	1268.5039		**1296.4988**			**G**			***580.2838***	563.2572	**5**
20	136.0757	1431.5672		**1459.5622**			**Y**	415.2048		***523.2623***	506.2358	**4**
21	30.0338	1488.5887		**1516.5836**			**G**			***360.1990***	343.1724	**3**
22	101.0709	1616.6473	1599.6207	1644.6422	1627.6156	1559.6258	**Q**	230.1248	229.1295	***303.1775***	286.1510	**2**
23	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924	**1**

Seq	**ya**	**yb**	**Seq**	**ya**	**yb**	**Seq**	**ya**	**yb**
GG	87.0553	115.0502	**GGG**	144.0768	172.0717	**GGGG**	201.0982	229.0931
GGGGY	364.1615	392.1565	**GGGGYG**	421.1830	449.1779	**GGGGYGG**	478.2045	506.1994
GGGGYGGG	535.2259	563.2209	**GGGGYGGGG**	592.2474	620.2423	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGY**	307.1401	335.1350	**GGGYG**	364.1615	392.1565
GGGYGG	421.1830	449.1779	**GGGYGGG**	478.2045	506.1994	**GGGYGGGG**	535.2259	563.2209
GGGYGGGGY	698.2893	726.2842	**GG**	87.0553	115.0502	**GGY**	250.1186	278.1135
GGYG	307.1401	335.1350	**GGYGG**	364.1615	392.1565	**GGYGGG**	421.1830	449.1779
GGYGGGG	478.2045	506.1994	**GGYGGGGY**	641.2678	669.2627	**GGYGGGGYG**	698.2893	726.2842
GY	193.0972	221.0921	**GYG**	250.1186	278.1135	**GYGG**	307.1401	335.1350
GYGGG	364.1615	392.1565	**GYGGGG**	421.1830	449.1779	**GYGGGGY**	584.2463	612.2413
GYGGGGYG	641.2678	669.2627	**GYGGGGYGG**	698.2893	726.2842	**YG**	193.0972	221.0921
YGG	250.1186	278.1135	**YGGG**	307.1401	335.1350	**YGGGG**	364.1615	392.1565
YGGGGY	527.2249	555.2198	**YGGGGYG**	584.2463	612.2413	**YGGGGYGG**	641.2678	669.2627
YGGGGYGGG	698.2893	726.2842	**GG**	87.0553	115.0502	**GGG**	144.0768	172.0717
GGGG	201.0982	229.0931	**GGGGY**	364.1615	392.1565	**GGGGYG**	421.1830	449.1779
GGGGYGG	478.2045	506.1994	**GGGGYGGG**	535.2259	563.2209	**GGGGYGGGG**	592.2474	620.2423
GGGGYGGGGG	649.2689	677.2638	**GG**	87.0553	115.0502	**GGG**	144.0768	172.0717
GGGY	307.1401	335.1350	**GGGYG**	364.1615	392.1565	**GGGYGG**	421.1830	449.1779
GGGYGGG	478.2045	506.1994	**GGGYGGGG**	535.2259	563.2209	**GGGYGGGGG**	592.2474	620.2423
GGGYGGGGGG	649.2689	677.2638	**GG**	87.0553	115.0502	**GGY**	250.1186	278.1135
GGYG	307.1401	335.1350	**GGYGG**	364.1615	392.1565	**GGYGGG**	421.1830	449.1779
GGYGGGG	478.2045	506.1994	**GGYGGGGG**	535.2259	563.2209	**GGYGGGGGG**	592.2474	620.2423
GGYGGGGGGG	649.2689	677.2638	**GY**	193.0972	221.0921	**GYG**	250.1186	278.1135
GYGG	307.1401	335.1350	**GYGGG**	364.1615	392.1565	**GYGGGG**	421.1830	449.1779

GYGGGGG	478.2045	506.1994	GYGGGGGG	535.2259	563.2209	GYGGGGGGG	592.2474	620.2423
GYGGGGGGGG	649.2689	677.2638	YG	193.0972	221.0921	YGG	250.1186	278.1135
YGGG	307.1401	335.1350	YGGGG	364.1615	392.1565	YGGGGG	421.1830	449.1779
YGGGGGG	478.2045	506.1994	YGGGGGGG	535.2259	563.2209	YGGGGGGGG	592.2474	620.2423
GG	87.0553	115.0502	GGG	144.0768	172.0717	GGGG	201.0982	229.0931
GGGGG	258.1197	286.1146	GGGGGG	315.1411	343.1361	GGGGGGG	372.1626	400.1575
GGGGGGGG	429.1841	457.1790	GGGGGGGGY	592.2474	620.2423	GGGGGGGGYG	649.2689	677.2638
GG	87.0553	115.0502	GGG	144.0768	172.0717	GGGG	201.0982	229.0931
GGGGG	258.1197	286.1146	GGGGGG	315.1411	343.1361	GGGGGGG	372.1626	400.1575
GGGGGGGY	535.2259	563.2209	GGGGGGGYG	592.2474	620.2423	GG	87.0553	115.0502
GGG	144.0768	172.0717	GGGG	201.0982	229.0931	GGGGG	258.1197	286.1146
GGGGGG	315.1411	343.1361	GGGGGGY	478.2045	506.1994	GGGGGGYG	535.2259	563.2209
GGGGGGYGQ	663.2845	691.2794	GG	87.0553	115.0502	GGG	144.0768	172.0717
GGGG	201.0982	229.0931	GGGGG	258.1197	286.1146	GGGGGY	421.1830	449.1779
GGGGGYG	478.2045	506.1994	GGGGGYGQ	606.2631	634.2580	GG	87.0553	115.0502
GGG	144.0768	172.0717	GGGG	201.0982	229.0931	GGGGY	364.1615	392.1565
GGGGYG	421.1830	449.1779	GGGGYGQ	549.2416	577.2365	GG	87.0553	115.0502
GGG	144.0768	172.0717	GGGY	307.1401	335.1350	GGGYG	364.1615	392.1565
GGGYGQ	492.2201	520.2150	GG	87.0553	115.0502	GGY	250.1186	278.1135
GGYG	307.1401	335.1350	GGYGQ	435.1987	463.1936	GY	193.0972	221.0921
GYG	250.1186	278.1135	GYGQ	378.1772	406.1721	YG	193.0972	221.0921
YGQ	321.1557	349.1506	GQ	158.0924	186.0873			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
123.7	1817.7467	0.1118	GGGGGYGGGGYGGGGGGGGYGQR

115.9	1817.7467	0.1118	GGGGGYGGGGGYGGGGGGGYGQR
17.8	1817.7360	0.1224	GDHGNRGNDEGMNHHR
14.6	1817.7825	0.0759	WVCEGAGPPGGMGESTAR
14.5	1817.9577	-0.0993	QGVIFLTDHGFFPGKR
13.0	1817.8472	0.0112	NFPIYSDGLYTESGQK
12.8	1817.8584	-0.0000	DFIFGVSSSAYQVEGGR
12.6	1817.8730	-0.0146	ASMKEEHSLIGGPGFSR
12.3	1817.7937	0.0647	NNNFTVSAMHGDMPQR
11.1	1817.9247	-0.0663	VLRMHGYEVTPDVFR

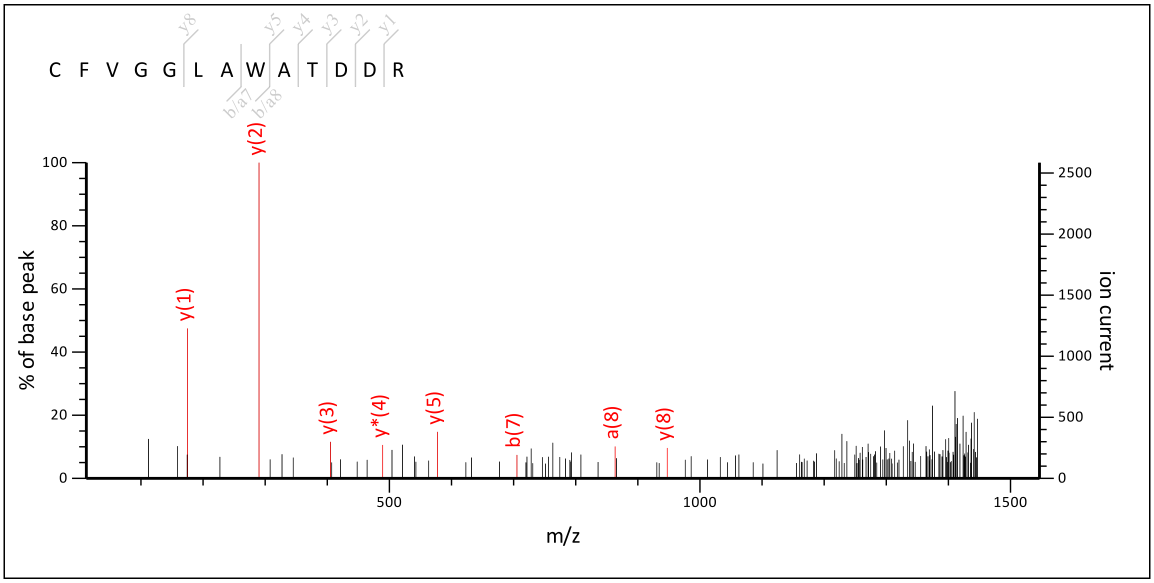
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 10

MS/MS Fragmentation of **CFVGGLAWATDDR**
Found in **gi|18103931** in **NCBInr**, glycine rich RNA binding protein [Oryza sativa Indica Group]

Match to Query 34: 1466.759724 from(1467.767000,1+) intensity(0.0000) index(15)
Title: Label: E6, Spot_Id: 228926, Peak_List_Id: 257530, MSMS Job_Run_Id: 24923, Comment:
Data file ppw_E6_138985130300.txt



12.09 to 1546.66

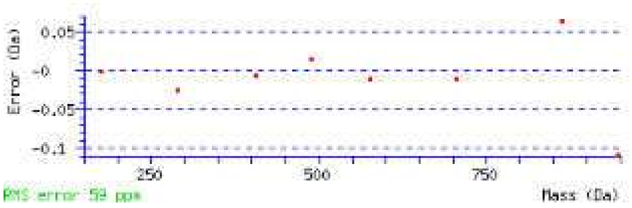
Label all possible matches ○ Label matches used for scoring ●

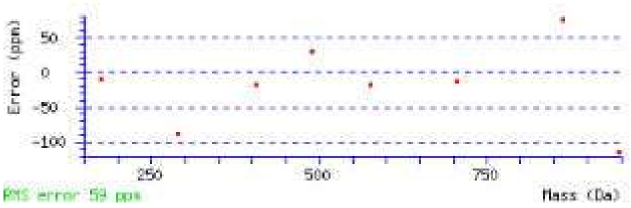
Monoisotopic mass of neutral peptide Mr(calc): 1466.6613
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 7.9
Matches : 8/187 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	133.0430	133.0430		161.0379		44.0495		**C**							**13**
2	120.0808	280.1114		308.1063				**F**	1215.5753			1307.6379	1290.6113	1289.6273	**12**
3	72.0808	379.1798		407.1748		365.1642		**V**	1116.5069	1129.5273		1160.5695	1143.5429	1142.5589	**11**
4	30.0338	436.2013		464.1962				**G**				1061.5011	1044.4745	1043.4905	**10**
5	30.0338	493.2228		521.2177				**G**				1004.4796	987.4530	986.4690	**9**
6	86.0964	606.3068		634.3017		564.2599		**L**	889.3799	888.3846		***947.4581***	930.4316	929.4476	**8**
7	44.0495	677.3439		**705.3389**				**A**	818.3428			834.3741	817.3475	816.3635	**7**
8	159.0917	**863.4233**		891.4182				**W**	632.2634			763.3369	746.3104	745.3264	**6**
9	44.0495	934.4604		962.4553				**A**	561.2263			***577.2576***	560.2311	559.2471	**5**
10	74.0600	1035.5081	1017.4975	1063.5030	1045.4924	1019.5131	1021.4924	**T**	460.1787	473.1991	475.1783	506.2205	489.1940	488.2100	**4**
11	88.0393	1150.5350	1132.5244	1178.5299	1160.5193	1106.5452		**D**	345.1517	344.1565		***405.1728***	388.1463	387.1623	**3**
12	88.0393	1265.5619	1247.5514	1293.5569	1275.5463	1221.5721		**D**	230.1248	229.1295		***290.1459***	273.1193	272.1353	**2**
13	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FV	219.1492	247.1441	**FVG**	276.1707	304.1656	**FVGG**	333.1921	361.1870
FVGGL	446.2762	474.2711	**FVGGLA**	517.3133	545.3082	**VG**	129.1022	157.0972
VGG	186.1237	214.1186	**VGGL**	299.2078	327.2027	**VGGLA**	370.2449	398.2398

VGGLAW	556.3242	584.3191	**VGGLAWA**	627.3613	655.3562	**GG**	87.0553	115.0502
GGL	200.1394	228.1343	**GGLA**	271.1765	299.1714	**GGLAW**	457.2558	485.2507
GGLAWA	528.2929	556.2878	**GGLAWAT**	629.3406	657.3355	**GL**	143.1179	171.1128
GLA	214.1550	242.1499	**GLAW**	400.2343	428.2292	**GLAWA**	471.2714	499.2663
GLAWAT	572.3191	600.3140	**GLAWATD**	687.3461	715.3410	**LA**	157.1335	185.1285
LAW	343.2129	371.2078	**LAWA**	414.2500	442.2449	**LAWAT**	515.2976	543.2926
LAWATD	630.3246	658.3195	**AW**	230.1288	258.1237	**AWA**	301.1659	329.1608
AWAT	402.2136	430.2085	**AWATD**	517.2405	545.2354	**AWATDD**	632.2675	660.2624
WA	230.1288	258.1237	**WAT**	331.1765	359.1714	**WATD**	446.2034	474.1983
WATDD	561.2304	589.2253	**AT**	145.0972	173.0921	**ATD**	260.1241	288.1190
ATDD	375.1510	403.1460	**TD**	189.0870	217.0819	**TDD**	304.1139	332.1088
DD	203.0662	231.0612						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.9	1466.6613	0.0985	CFVGGLAWATDDR
14.9	1466.6274	0.1323	GNVFTADADADTDR
11.0	1466.6638	0.0960	GLVSYGDASPDSGSR
9.2	1466.6903	0.0695	GGQFSRPFSVDDR
9.1	1466.6691	0.0906	GYNAEGWRFPDR
8.1	1466.7551	0.0046	GKQIMFIGDSISR
8.1	1466.6282	0.1315	GLMTSDAEMWNGR
8.1	1466.6686	0.0911	GTPYWMAPEMIR
7.7	1466.6613	0.0985	HGFDVSQDIFMR
7.7	1466.6671	0.0926	KLSMDASTQTDDR

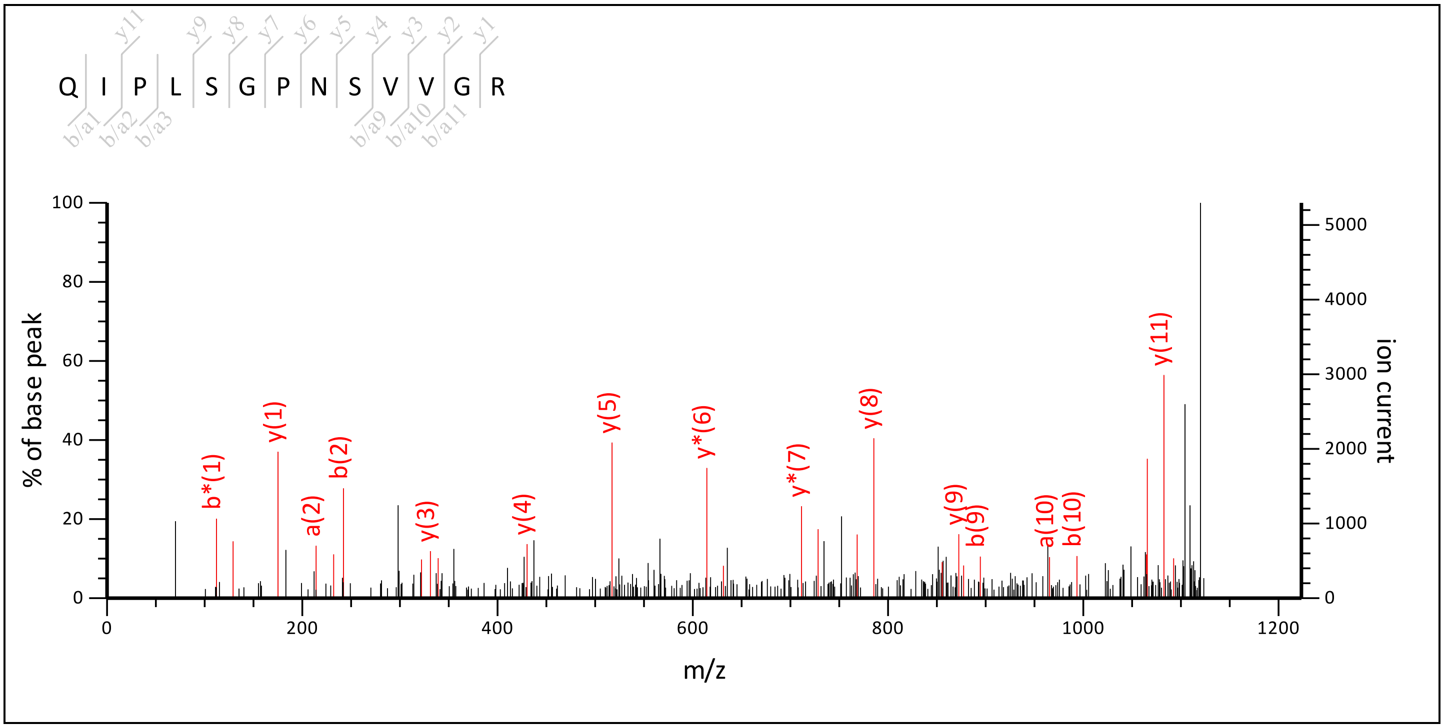
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 13

MS/MS Fragmentation of **QIPLSGPNSVVGR**
Found in **gi|42408425** in **NCBInr**, putative superoxide dismutase [Cu-Zn], chloroplast precursor [Oryza sativa Japonica Group]

Match to Query 216: 1322.758024 from(1323.765300,1+) intensity(0.0000) index(23)
Title: Label: G6, Spot_Id: 219760, Peak_List_Id: 225740, MSMS Job_Run_Id: 21788, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_G6_136842238300.txt



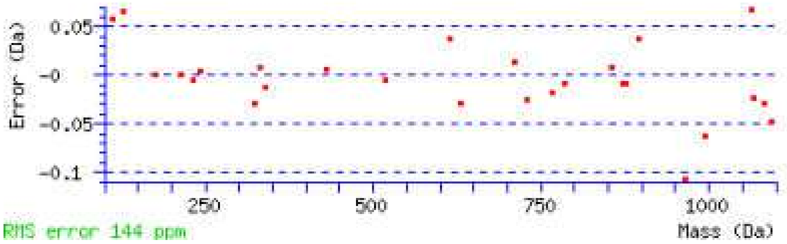
0 to 1223.41

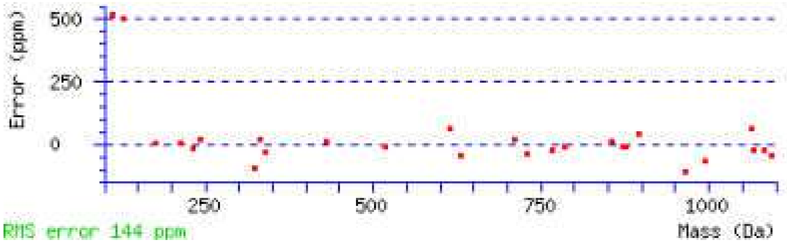
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1322.7307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 0.0022
Matches : 27/72 fragment ions using 55 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	101.0709	84.0444	**129.0659**	112.0393	**Q**			**13**
2	**214.1550**	197.1285	**242.1499**	225.1234	**I**	1195.6793	1178.6528	**12**
3	311.2078	294.1812	**339.2027**	322.1761	**P**	***1082.5953***	1065.5687	**11**
4	424.2918	407.2653	452.2867	435.2602	**L**	985.5425	968.5160	**10**
5	511.3239	494.2973	539.3188	522.2922	**S**	***872.4585***	855.4319	**9**
6	568.3453	551.3188	596.3402	579.3137	**G**	***785.4264***	768.3999	**8**
7	665.3981	648.3715	693.3930	676.3665	**P**	***728.4050***	711.3784	**7**

8	779.4410	762.4145	807.4359	790.4094	**N**	***631.3522***	614.3256	**6**
9	866.4730	849.4465	**894.4680**	877.4414	**S**	***517.3093***	500.2827	**5**
10	**965.5415**	948.5149	**993.5364**	976.5098	**V**	***430.2772***	413.2507	**4**
11	**1064.6099**	1047.5833	**1092.6048**	1075.5782	**V**	***331.2088***	314.1823	**3**
12	1121.6313	1104.6048	1149.6262	1132.5997	**G**	***232.1404***	215.1139	**2**
13					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.8	1322.7307	0.0274	QIPLSGPNSVVGR
12.1	1322.8034	-0.0454	QLPTNVKLALAR
11.9	1322.7207	0.0373	QLPAFLADHRR
10.6	1322.6488	0.1092	MNMHVPPWRR
10.4	1322.6691	0.0889	QLPQERPADGGR
10.2	1322.7921	-0.0341	KLLEELAPIAAR
9.8	1322.8034	-0.0454	KLIALSQPALNR
9.2	1322.7493	0.0088	KLLPSHGTLMAR
8.9	1322.6653	0.0928	QLGEKGLEMFR
8.7	1322.6322	0.1258	KINAMGSMSQQL

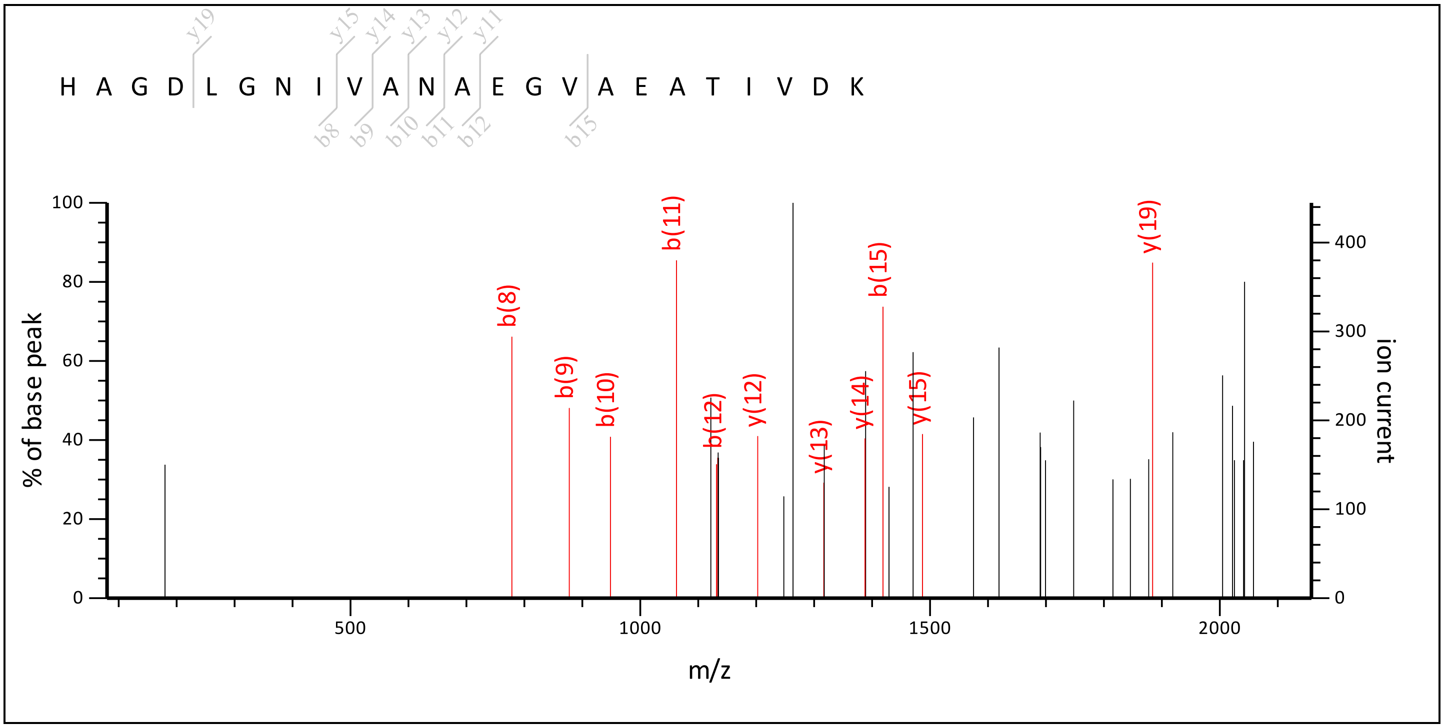
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 13

MS/MS Fragmentation of **HAGDLGNIVANAEGVAEATIVDK**
Found in **gi|42408425** in **NCBInr**, putative superoxide dismutase [Cu-Zn], chloroplast precursor [Oryza sativa Japonica Group]

Match to Query 255: 2263.154124 from(2264.161400,1+) intensity(0.0000) index(30)
Title: Label: G6, Spot_Id: 219760, Peak_List_Id: 225757, MSMS Job_Run_Id: 21788, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_G6_136842238300.txt



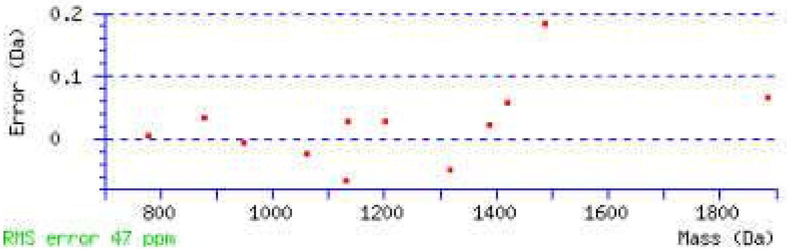
79.92 to 2158.07

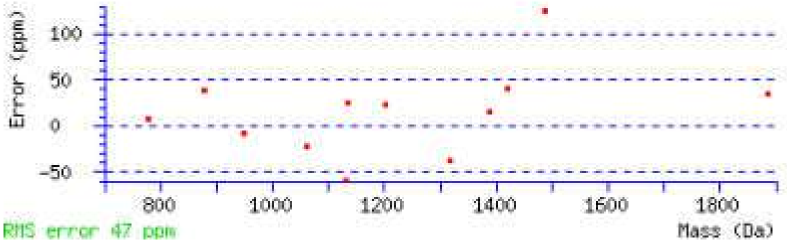
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2263.1444
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 28
Matches : 12/120 fragment ions using 37 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	110.0713		138.0662		H			23
2	181.1084		209.1033		A	2127.0928	2110.0663	22
3	238.1299		266.1248		G	2056.0557	2039.0291	21
4	353.1568		381.1517		D	1999.0342	1982.0077	20
5	466.2409		494.2358		L	***1884.0073***	1866.9807	19
6	523.2623		551.2572		G	1770.9232	1753.8967	18
7	637.3052	620.2787	665.3002	648.2736	N	1713.9018	1696.8752	17

8	750.3893	733.3628	***778.3842***	761.3577	**I**	1599.8588	1582.8323	**16**
9	849.4577	832.4312	***877.4526***	860.4261	**V**	***1486.7748***	1469.7482	**15**
10	920.4948	903.4683	***948.4898***	931.4632	**A**	***1387.7064***	1370.6798	**14**
11	1034.5378	1017.5112	***1062.5327***	1045.5061	**N**	***1316.6692***	1299.6427	**13**
12	1105.5749	1088.5483	***1133.5698***	1116.5432	**A**	***1202.6263***	1185.5998	**12**
13	1234.6175	1217.5909	1262.6124	1245.5858	**E**	***1131.5892***	1114.5626	**11**
14	1291.6389	1274.6124	1319.6339	1302.6073	**G**	1002.5466	985.5201	**10**
15	1390.7074	1373.6808	***1418.7023***	1401.6757	**V**	945.5251	928.4986	**9**
16	1461.7445	1444.7179	1489.7394	1472.7128	**A**	846.4567	829.4302	**8**
17	1590.7871	1573.7605	1618.7820	1601.7554	**E**	775.4196	758.3931	**7**
18	1661.8242	1644.7976	1689.8191	1672.7925	**A**	646.3770	629.3505	**6**
19	1762.8719	1745.8453	1790.8668	1773.8402	**T**	575.3399	558.3134	**5**
20	1875.9559	1858.9294	1903.9508	1886.9243	**I**	474.2922	457.2657	**4**
21	1975.0243	1957.9978	2003.0192	1985.9927	**V**	361.2082	344.1816	**3**
22	2090.0513	2073.0247	2118.0462	2101.0196	**D**	262.1397	245.1132	**2**
23					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.8	2263.1444	0.0097	HAGDLGNIVANAEGVAEATIVDK
3.1	2263.1228	0.0313	QMGLAENQLSIDMLELWLK
1.4	2263.0869	0.0672	FEQSGGWIRTLLEEAENER
0.7	2263.1444	0.0097	NQAEGSFITNNDSKQSALVLK
0.1	2263.1696	-0.0155	TFKSGVEGAGSGGAVLPSSVESIK

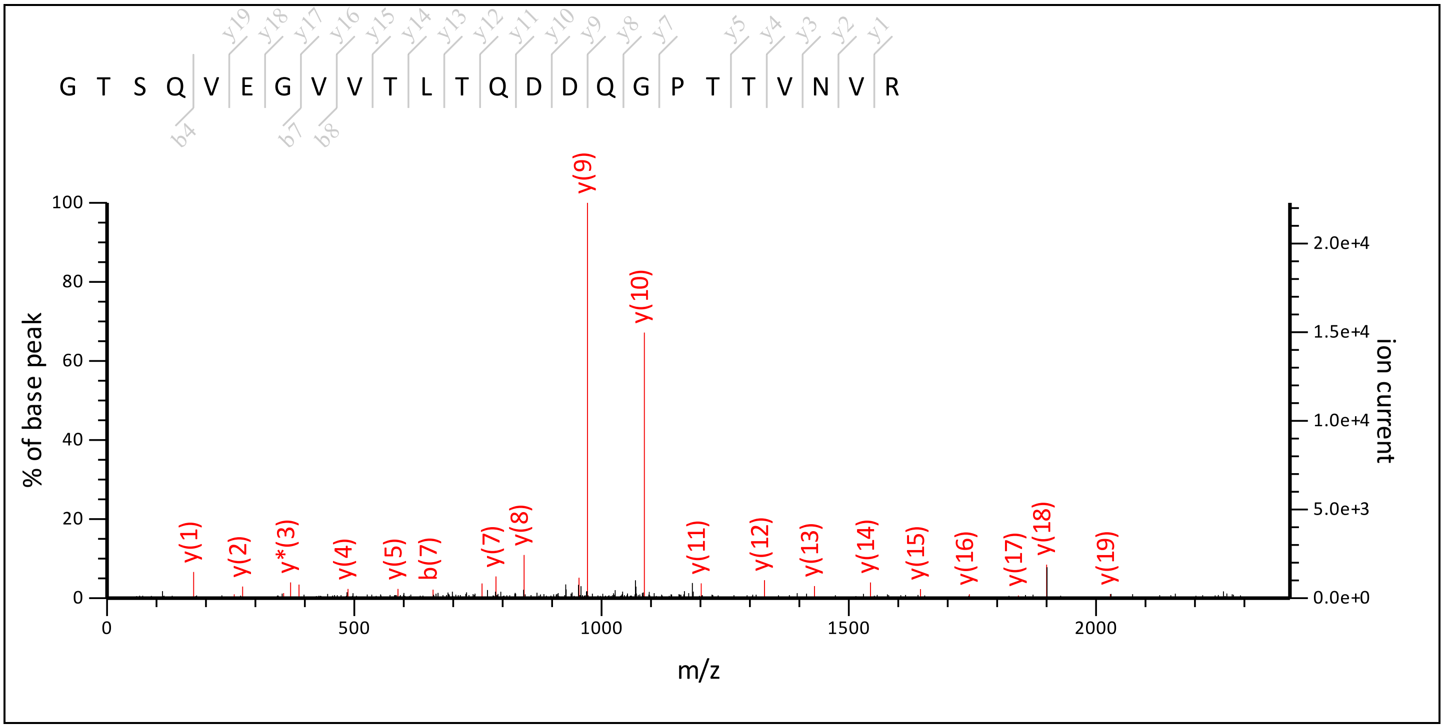
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 13

MS/MS Fragmentation of **GTSQVEGVVTLTQDDQGPTTVNVR**
Found in **gi|42408425** in **NCBInr**, putative superoxide dismutase [Cu-Zn], chloroplast precursor [Oryza sativa Japonica Group]

Match to Query 257: 2500.258824 from(2501.266100,1+) intensity(0.0000) index(31)
Title: Label: G6, Spot_Id: 219760, Peak_List_Id: 225741, MSMS Job_Run_Id: 21788, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_G6_136842238300.txt



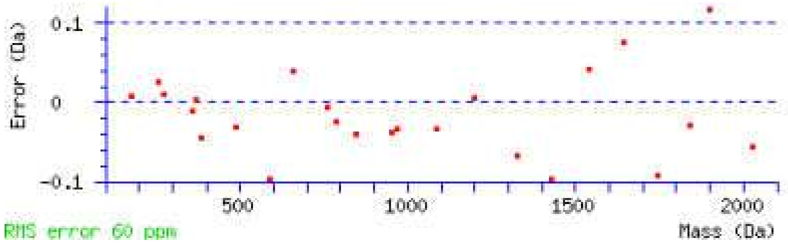
0 to 2392.08

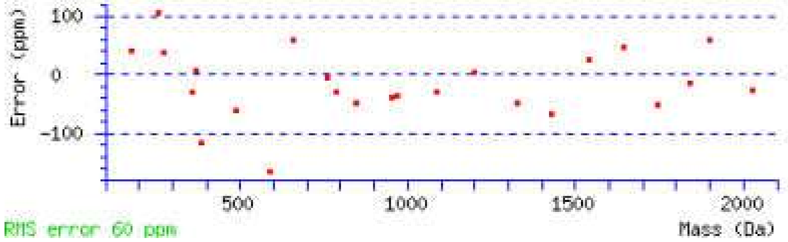
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2500.2406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 129 **Expect:** 1.8e-10
Matches : 24/132 fragment ions using 46 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			24
2	131.0815		159.0764		T	2444.2263	2427.1998	23
3	218.1135		246.1084		S	2343.1787	2326.1521	22
4	346.1721	329.1456	374.1670	357.1405	Q	2256.1466	2239.1201	21
5	445.2405	428.2140	473.2354	456.2089	V	2128.0881	2111.0615	20
6	574.2831	557.2566	602.2780	585.2515	E	***2029.0196***	2011.9931	19
7	631.3046	614.2780	**659.2995**	642.2729	G	***1899.9770***	1882.9505	18

8	730.3730	713.3464	758.3679	741.3414	V	1842.9556	1825.9290	17
9	829.4414	812.4149	857.4363	840.4098	V	1743.8872	1726.8606	16
10	930.4891	913.4625	958.4840	941.4575	T	1644.8188	1627.7922	15
11	1043.5732	1026.5466	1071.5681	1054.5415	L	1543.7711	1526.7445	14
12	1144.6208	1127.5943	1172.6157	1155.5892	T	1430.6870	1413.6605	13
13	1272.6794	1255.6529	1300.6743	1283.6478	Q	1329.6393	1312.6128	12
14	1387.7064	1370.6798	1415.7013	1398.6747	D	1201.5808	1184.5542	11
15	1502.7333	1485.7067	1530.7282	1513.7017	D	1086.5538	1069.5273	10
16	1630.7919	1613.7653	1658.7868	1641.7602	Q	971.5269	954.5003	9
17	1687.8133	1670.7868	1715.8083	1698.7817	G	843.4683	826.4417	8
18	1784.8661	1767.8396	1812.8610	1795.8345	P	786.4468	769.4203	7
19	1885.9138	1868.8872	1913.9087	1896.8821	T	689.3941	672.3675	6
20	1986.9615	1969.9349	2014.9564	1997.9298	T	588.3464	571.3198	5
21	2086.0299	2069.0033	2114.0248	2096.9982	V	487.2987	470.2722	4
22	2200.0728	2183.0463	2228.0677	2211.0412	N	388.2303	371.2037	3
23	2299.1412	2282.1147	2327.1361	2310.1096	V	274.1874	257.1608	2
24					R	175.1190	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
129.3	2500.2406	0.0182	GTSQVEGVVTLTQDDQGPTTVNVR
16.6	2500.2406	0.0183	GNSTVEGVVTLTQENEGPTTVNVR
7.6	2500.2881	-0.0293	SVAVASSRLTSLEQQGAASTSTPPR
6.0	2500.3537	-0.0948	EKTLEIQLLELYGLQEQGAAVR
5.4	2500.1758	0.0830	EDETEFSPFYGIDKGAVLQEAR
5.2	2500.1978	0.0610	YLCVAADLDNESDVVMLLAAFR

5.1	2500.3108	-0.0519	EWVIGVGETLAEAASMLRTQALR
4.2	2500.2647	-0.0058	CLPGIISAYLKLNSYFPCAWK
3.6	2500.3286	-0.0697	AVDENPPLQPVQIEKQVAGVDVR
3.4	2500.1039	0.1549	VVPEFEGLQDFGGSVMHACDYK

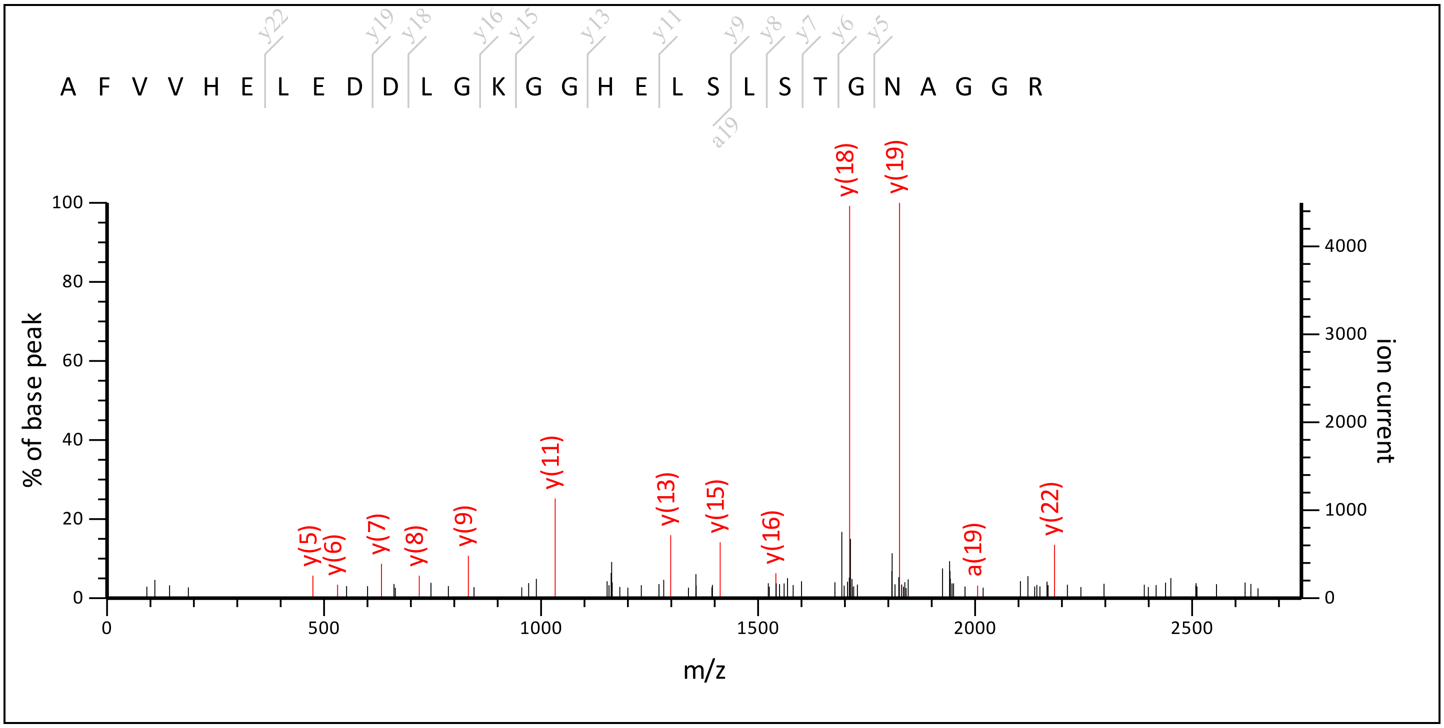
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 13

MS/MS Fragmentation of **AFVVHELEDDLGKGGHELSLSTGNAGGR**
Found in **gi|42408425** in **NCBInr**, putative superoxide dismutase [Cu-Zn], chloroplast precursor [Oryza sativa Japonica Group]

Match to Query 259: 2864.417024 from(2865.424300,1+) intensity(0.0000) index(32)
Title: Label: G6, Spot_Id: 219760, Peak_List_Id: 225744, MSMS Job_Run_Id: 21788, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_G6_136842238300.txt



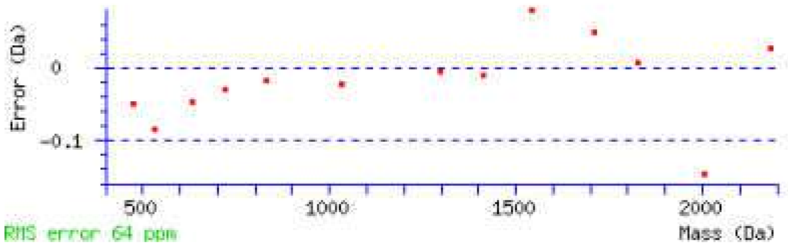
0 to 2751.78

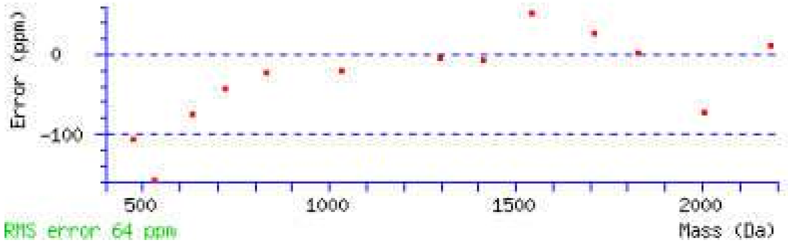
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2864.4053
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 9.8e-05
Matches : 13/138 fragment ions using 24 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			28
2	191.1179		219.1128		F	2794.3755	2777.3489	27
3	290.1863		318.1812		V	2647.3070	2630.2805	26
4	389.2547		417.2496		V	2548.2386	2531.2121	25
5	526.3136		554.3085		H	2449.1702	2432.1437	24
6	655.3562		683.3511		E	2312.1113	2295.0848	23
7	768.4403		796.4352		L	*2183.0687*	2166.0422	22

8	897.4829		925.4778		E	2069.9847	2052.9581	21
9	1012.5098		1040.5047		D	1940.9421	1923.9155	20
10	1127.5368		1155.5317		D	***1825.9151***	1808.8886	19
11	1240.6208		1268.6157		L	***1710.8882***	1693.8616	18
12	1297.6423		1325.6372		G	1597.8041	1580.7776	17
13	1425.7373	1408.7107	1453.7322	1436.7056	K	***1540.7826***	1523.7561	16
14	1482.7587	1465.7322	1510.7536	1493.7271	G	***1412.6877***	1395.6611	15
15	1539.7802	1522.7536	1567.7751	1550.7486	G	1355.6662	1338.6397	14
16	1676.8391	1659.8125	1704.8340	1687.8075	H	***1298.6448***	1281.6182	13
17	1805.8817	1788.8551	1833.8766	1816.8501	E	1161.5858	1144.5593	12
18	1918.9658	1901.9392	1946.9607	1929.9341	L	***1032.5432***	1015.5167	11
19	2005.9978	1988.9712	2033.9927	2016.9661	S	919.4592	902.4326	10
20	2119.0818	2102.0553	2147.0768	2130.0502	L	***832.4272***	815.4006	9
21	2206.1139	2189.0873	2234.1088	2217.0822	S	***719.3431***	702.3165	8
22	2307.1616	2290.1350	2335.1565	2318.1299	T	***632.3111***	615.2845	7
23	2364.1830	2347.1565	2392.1779	2375.1514	G	***531.2634***	514.2368	6
24	2478.2259	2461.1994	2506.2209	2489.1943	N	***474.2419***	457.2154	5
25	2549.2631	2532.2365	2577.2580	2560.2314	A	360.1990	343.1724	4
26	2606.2845	2589.2580	2634.2794	2617.2529	G	289.1619	272.1353	3
27	2663.3060	2646.2794	2691.3009	2674.2744	G	232.1404	215.1139	2
28					R	175.1190	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.0	2864.4053	0.0117	AFVVHELEDDLGKGGHELSLSTGNAGGR
9.1	2864.4879	-0.0709	ALESPAPIANQGVITQLSDQISTLNER

0.9	2864.3022	0.1148	DDSDGGISLAPAGARTHMGHAHHHHHK
0.8	2864.4451	-0.0281	HTQGDGSAVAVLESMGSKGSVLVNGTHVK
0.3	2864.5398	-0.1227	KEKPPLADPDAVYLIPMEWVLTPVK
0.2	2864.1973	0.2198	EVESGMMEDDPINFQQAMKSSNSMK

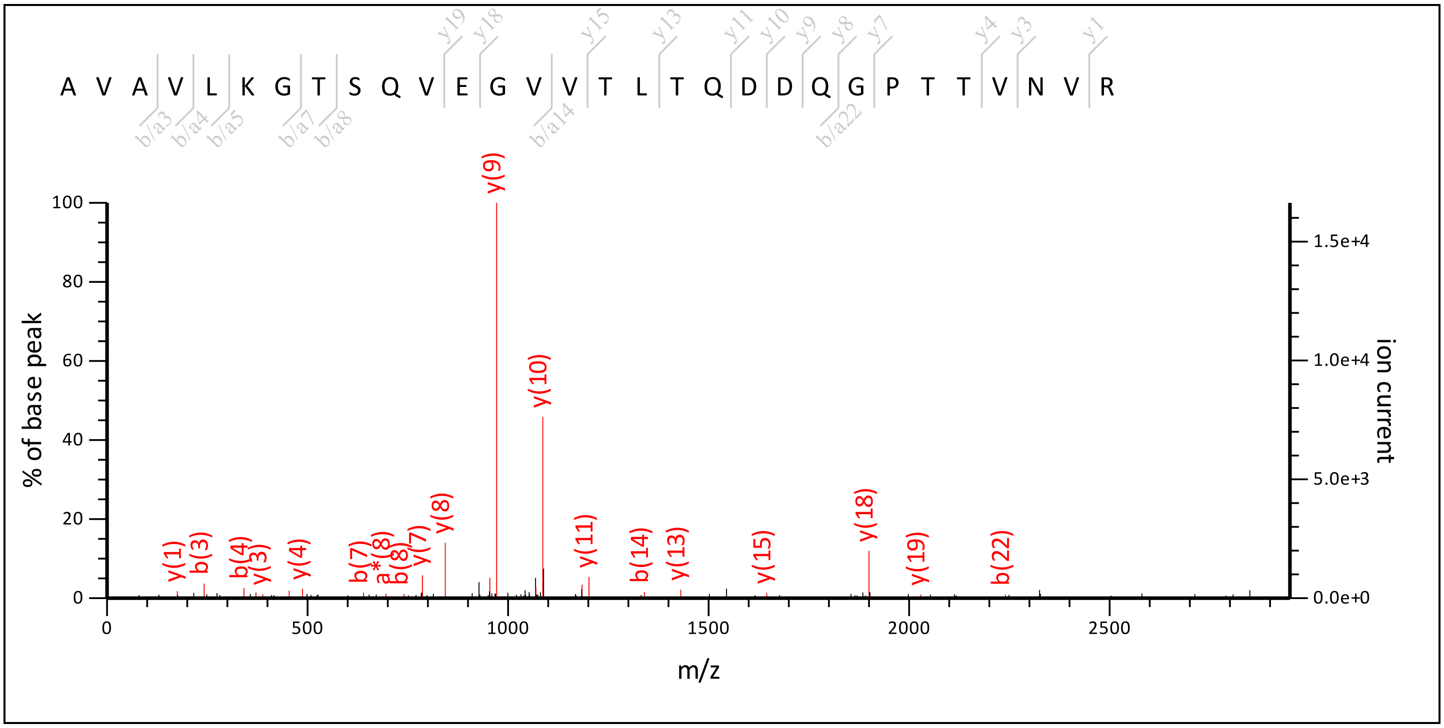
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 13

MS/MS Fragmentation of **AVAVLKGTSQVEGVVTLTQDDQGPTTVNVR**
Found in **gi|42408425** in **NCBInr**, putative superoxide dismutase [Cu-Zn], chloroplast precursor [Oryza sativa Japonica Group]

Match to Query 261: 3081.629924 from(3082.637200,1+) intensity(0.0000) index(33)
Title: Label: G6, Spot_Id: 219760, Peak_List_Id: 225743, MSMS Job_Run_Id: 21788, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_G6_136842238300.txt



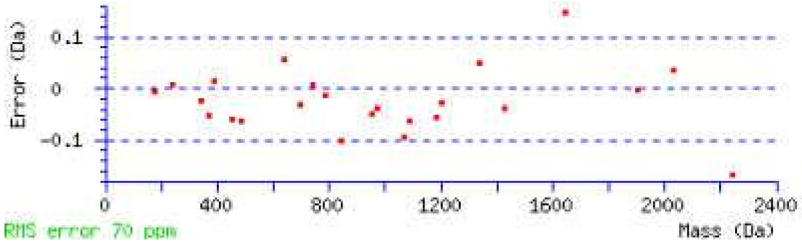
0 to 2949.57

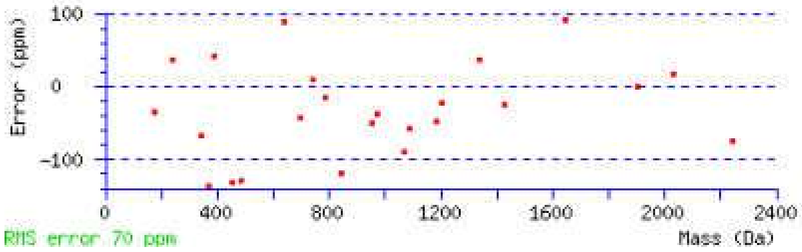
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 3081.6307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 0.0002
Matches : 24/164 fragment ions using 48 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			30
2	143.1179		171.1128		V	3011.6008	2994.5742	29
3	214.1550		*242.1499*		A	2912.5324	2895.5058	28
4	313.2234		*341.2183*		V	2841.4952	2824.4687	27
5	426.3075		*454.3024*		L	2742.4268	2725.4003	26
6	554.4024	537.3759	582.3974	565.3708	K	2629.3428	2612.3162	25
7	611.4239	594.3974	*639.4188*	622.3923	G	2501.2478	2484.2213	24

8	712.4716	695.4450	***740.4665***	723.4400	T	2444.2263	2427.1998	23
9	799.5036	782.4771	827.4985	810.4720	S	2343.1787	2326.1521	22
10	927.5622	910.5356	955.5571	938.5306	Q	2256.1466	2239.1201	21
11	1026.6306	1009.6041	1054.6255	1037.5990	V	2128.0881	2111.0615	20
12	1155.6732	1138.6467	1183.6681	1166.6416	E	***2029.0196***	2011.9931	19
13	1212.6947	1195.6681	1240.6896	1223.6630	G	***1899.9770***	1882.9505	18
14	1311.7631	1294.7365	***1339.7580***	1322.7314	V	1842.9556	1825.9290	17
15	1410.8315	1393.8049	1438.8264	1421.7999	V	1743.8872	1726.8606	16
16	1511.8792	1494.8526	1539.8741	1522.8475	T	***1644.8188***	1627.7922	15
17	1624.9632	1607.9367	1652.9582	1635.9316	L	1543.7711	1526.7445	14
18	1726.0109	1708.9844	1754.0058	1736.9793	T	***1430.6870***	1413.6605	13
19	1854.0695	1837.0429	1882.0644	1865.0379	Q	1329.6393	1312.6128	12
20	1969.0964	1952.0699	1997.0914	1980.0648	D	***1201.5808***	1184.5542	11
21	2084.1234	2067.0968	2112.1183	2095.0917	D	***1086.5538***	1069.5273	10
22	2212.1820	2195.1554	***2240.1769***	2223.1503	Q	***971.5269***	954.5003	9
23	2269.2034	2252.1769	2297.1983	2280.1718	G	***843.4683***	826.4417	8
24	2366.2562	2349.2296	2394.2511	2377.2245	P	***786.4468***	769.4203	7
25	2467.3039	2450.2773	2495.2988	2478.2722	T	689.3941	672.3675	6
26	2568.3515	2551.3250	2596.3465	2579.3199	T	588.3464	571.3198	5
27	2667.4200	2650.3934	2695.4149	2678.3883	V	***487.2987***	470.2722	4
28	2781.4629	2764.4363	2809.4578	2792.4312	N	***388.2303***	371.2037	3
29	2880.5313	2863.5047	2908.5262	2891.4997	V	274.1874	257.1608	2
30					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence

66.2	3081.6307	-0.0007	AVAVLKGTSQVEGVVTLTQDDQGPTTVNVR
12.9	3081.6306	-0.0007	AVAVLKGNSTVEGVVTLTQENEGPTTVNVR
10.7	3081.4834	0.1465	QAAADALMHYSQFAMVCISQGVSPSKLR
6.7	3081.5403	0.0897	LVKLGSPMETVYIAEQATPMVVEWSGSK
5.4	3081.4834	0.1465	QAAADALMHYSQFAMVCISQGVSPSKLR
4.6	3081.3855	0.2444	MEFSMVDHPPCARHLGDDVAIAEAGQGR
4.6	3081.3855	0.2444	MEFSMVDHPPCARHLGDDVAIAEAGQGR
4.5	3081.4615	0.1685	GSFETIHVQDSTGHEFATRMGNVFTIGK
4.3	3081.3891	0.2409	RMPFGLCNAPATFQECMLSIFSDMVK
3.5	3081.4727	0.1572	IRVSDGDGNGETTAGQGGVVGVFFAGCWLR

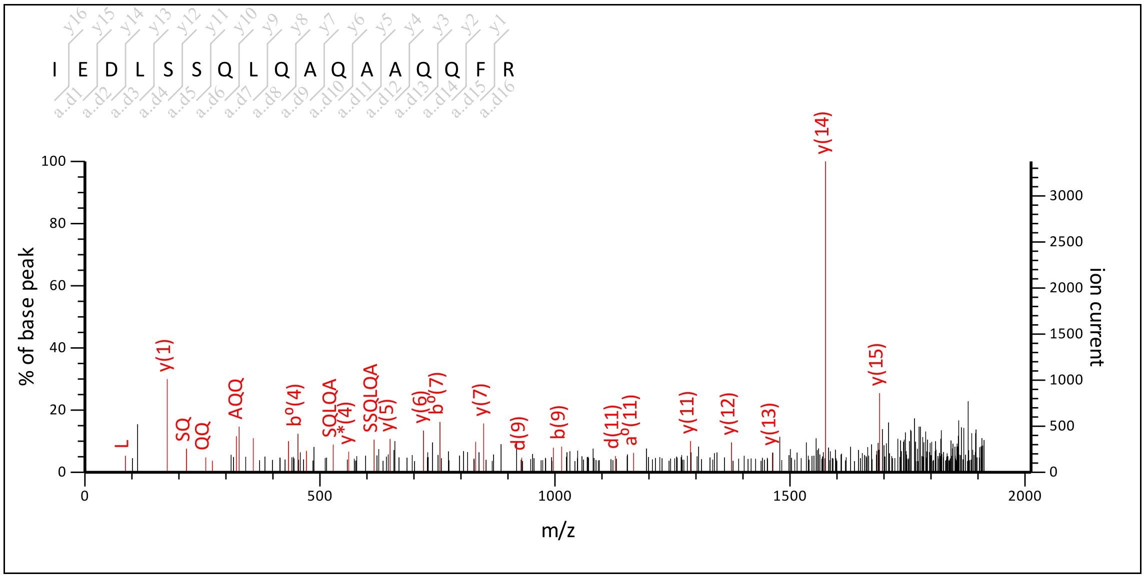
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 41

MS/MS Fragmentation of **IEDLSSQLQAQAAQQFR**
Found in **gi|56784713** in **NCBInr**, alpha NAC-like protein [Oryza sativa Japonica Group]

Match to Query 41: 1932.133724 from(1933.141000,1+) intensity(0.0000) index(14)
Title: Label: L6, Spot_Id: 228933, Peak_List_Id: 257650, MSMS Job_Run_Id: 24929, Comment:
Data file ppw_L6_138985137000.txt



0 to 2012.89

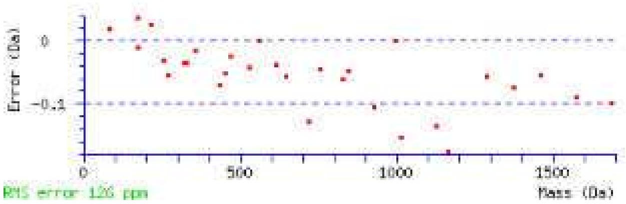
Label all possible matches ○ Label matches used for scoring ●

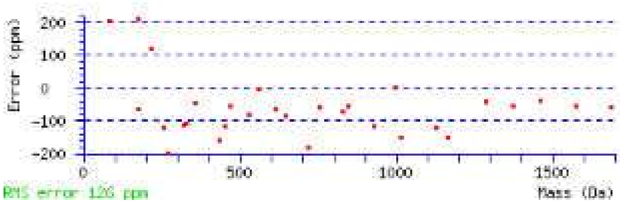
```
Monoisotopic mass of neutral peptide Mr(calc): 1931.9701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.025
Matches : 37/300 fragment ions using 57 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	86.0964	86.0964			114.0913			44.0495	I						17
2	102.0550	215.1390		197.1285	243.1339		225.1234	157.1335	E	1745.8565	1744.8613	1819.8933	1802.8668	1801.8828	16
3	88.0393	330.1660		312.1554	**358.1609**		340.1503	286.1761	D	1630.8296	1629.8343	***1690.8507***	1673.8242	1672.8402	15
4	86.0964	443.2500		425.2395	**471.2449**		453.2344	401.2031	L	1517.7455	1516.7503	***1575.8238***	1558.7972	1557.8132	14
5	60.0444	530.2821		512.2715	558.2770		540.2664	514.2871	S	1430.7135	1429.7183	***1462.7397***	1445.7132	1444.7292	13
6	60.0444	617.3141		599.3035	645.3090		627.2984	601.3192	S	1343.6815	1342.6862	***1375.7077***	1358.6811	1357.6971	12
7	101.0709	745.3727	728.3461	727.3621	773.3676	756.3410	755.3570	688.3512	Q	1215.6229	1214.6276	***1288.6757***	1271.6491		11
8	86.0964	858.4567	841.4302	840.4462	886.4516	869.4251	868.4411	816.4098	L	1102.5388	1101.5436	1160.6171	1143.5905		10
9	101.0709	986.5153	969.4888	968.5047	**1014.5102**	997.4837	996.4997	929.4938	Q	974.4803	973.4850	1047.5330	1030.5065		9
10	44.0495	1057.5524	1040.5259	1039.5419	1085.5473	1068.5208	1067.5368		A	903.4431		919.4744	902.4479		8
11	101.0709	1185.6110	1168.5844	1167.6004	1213.6059	1196.5794	1195.5953	1128.5895	Q	775.3846	774.3893	***848.4373***	831.4108		7
12	44.0495	1256.6481	1239.6216	1238.6375	1284.6430	1267.6165	1266.6325		A	704.3475		***720.3788***	703.3522		6
13	44.0495	1327.6852	1310.6587	1309.6747	1355.6801	1338.6536	1337.6696		A	633.3103		***649.3416***	632.3151		5
14	101.0709	1455.7438	1438.7173	1437.7332	1483.7387	1466.7122	1465.7281	1398.7223	Q	505.2518	504.2565	578.3045	561.2780		4
15	101.0709	1583.8024	1566.7758	1565.7918	1611.7973	1594.7707	1593.7867	1526.7809	Q	377.1932	376.1979	450.2459	433.2194		3
16	120.0808	1730.8708	1713.8442	1712.8602	1758.8657	1741.8392	1740.8551		F	230.1248		***322.1874***	305.1608		2
17	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

ED	217.0819	245.0768	**EDL**	330.1660	358.1609	**EDLS**	417.1980	445.1929
EDLSS	504.2300	532.2249	**EDLSSQ**	632.2886	660.2835	**DL**	201.1234	229.1183
DLS	288.1554	316.1503	**DLSS**	375.1874	403.1823	**DLSSQ**	503.2460	531.2409
DLSSQL	616.3301	644.3250	**LS**	173.1285	201.1234	**LSS**	260.1605	288.1554
LSSQ	388.2191	416.2140	**LSSQL**	501.3031	529.2980	**LSSQLQ**	629.3617	657.3566
SS	147.0764	175.0713	**SSQ**	275.1350	303.1299	**SSQL**	388.2191	416.2140
SSQLQ	516.2776	544.2726	**SSQLQA**	587.3148	615.3097	**SQ**	188.1030	216.0979
SQL	301.1870	329.1819	**SQLQ**	429.2456	457.2405	**SQLQA**	500.2827	528.2776
SQLQAQ	628.3413	656.3362	**SQLQAQA**	699.3784	727.3733	**QL**	214.1550	242.1499
QLQ	342.2136	370.2085	**QLQA**	413.2507	441.2456	**QLQAQ**	541.3093	569.3042
QLQAQA	612.3464	640.3413	**QLQAQAA**	683.3835	711.3784	**LQ**	214.1550	242.1499
LQA	285.1921	313.1870	**LQAQ**	413.2507	441.2456	**LQAQA**	484.2878	512.2827
LQAQAA	555.3249	583.3198	**LQAQAAQ**	683.3835	711.3784	**QA**	172.1081	200.1030
QAQ	300.1666	328.1615	**QAQA**	371.2037	399.1987	**QAQAA**	442.2409	470.2358
QAQAAQ	570.2994	598.2944	**QAQAAQQ**	698.3580	726.3529	**AQ**	172.1081	200.1030
AQA	243.1452	271.1401	**AQAA**	314.1823	342.1772	**AQAAQ**	442.2409	470.2358
AQAAQQ	570.2994	598.2944	**QA**	172.1081	200.1030	**QAA**	243.1452	271.1401
QAAQ	371.2037	399.1987	**QAAQQ**	499.2623	527.2572	**QAAQQF**	646.3307	674.3257
AA	115.0866	143.0815	**AAQ**	243.1452	271.1401	**AAQQ**	371.2037	399.1987
AAQQF	518.2722	546.2671	**AQ**	172.1081	200.1030	**AQQ**	300.1666	328.1615
AQQF	447.2350	475.2300	**QQ**	229.1295	257.1244	**QQF**	376.1979	404.1928
QF	248.1394	276.1343						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.8	1931.9701	0.1636	IEDLSSQLQAQAAQQFR
7.1	1932.0065	0.1273	GQGDASQEELLFLLRTR
3.8	1932.0330	0.1008	QSALAHFTQTKPLHTPR
3.3	1931.9775	0.1562	LFPLGNLDGASITMGSSPR
2.6	1931.9424	0.1913	HRLSIYNHMSDFIQR
2.2	1932.0204	0.1133	GDNGSVFVLIKEGSSLLTP
1.6	1932.0350	0.0988	QKTLVSLNSAESNALVMK
1.5	1931.9734	0.1603	LSMLQRNAEEQEIISR
1.1	1931.9775	0.1562	EILTQVVTMDTAAQAWR
1.0	1931.9926	0.1412	EVKNGHPRPSQDGGLSVR

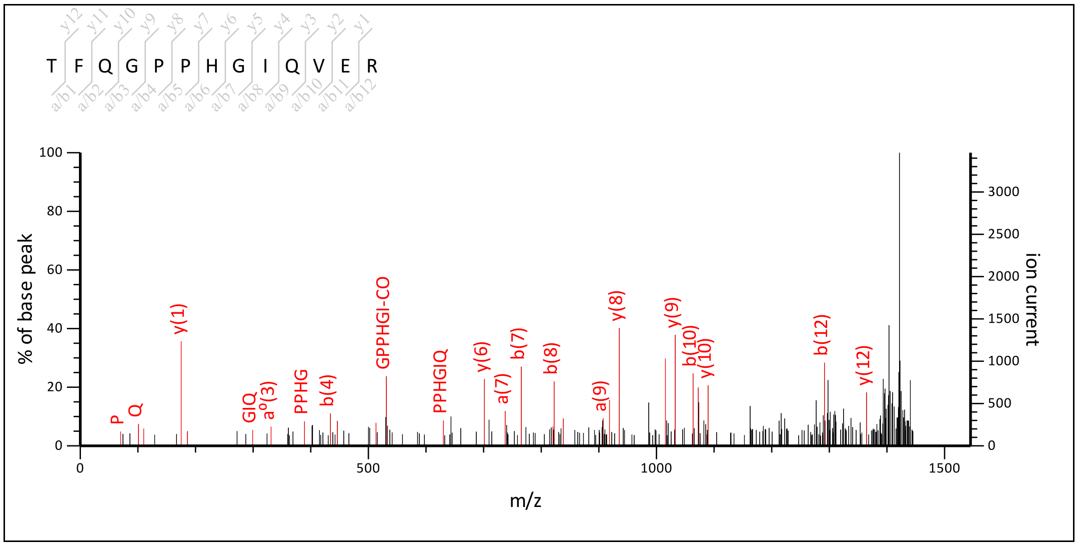
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 42

MS/MS Fragmentation of **TFQGPPHGIQVER**
Found in **gi|2961307** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase [Rondeletia odorata]

Match to Query 83: 1464.871524 from(1465.878800,1+) intensity(0.0000) index(16)
Title: Label: N6, Spot_Id: 228935, Peak_List_Id: 257665, MSMS Job_Run_Id: 24931, Comment:
Data file ppw_N6_138985138100.txt



0 to 1545.05

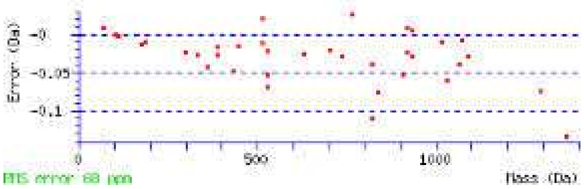
Label all possible matches ○ Label matches used for scoring ●

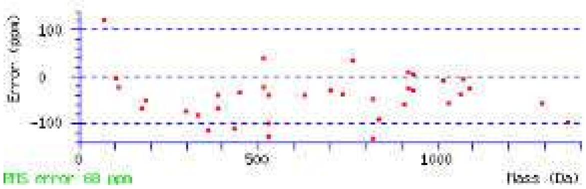
Monoisotopic mass of neutral peptide Mr(calc): 1464.7474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 0.0031
Matches : 40/229 fragment ions using 41 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	120.0808	221.1285		203.1179	249.1234		231.1128			F	1272.6444			***1364.7070***	1347.6804	134
3	101.0709	349.1870	332.1605	331.1765	377.1819	360.1554	359.1714	292.1656		Q	1144.5858	1143.5905		1217.6385	1200.6120	119
4	30.0338	406.2085	389.1819	388.1979	***434.2034***	417.1769	416.1928			G				***1089.5800***	1072.5534	107
5	70.0651	503.2613	486.2347	485.2507	***531.2562***	514.2296	513.2456	477.2456		P	990.5116	989.5163		***1032.5585***	1015.5320	101
6	70.0651	600.3140	583.2875	582.3035	628.3089	611.2824	610.2984	574.2984		P	893.4588	892.4635		***935.5057***	918.4792	91
7	110.0713	**737.3729**	720.3464	719.3624	***765.3679***	748.3413	747.3573			H	756.3999			***838.4530***	821.4264	82
8	30.0338	794.3944	777.3679	776.3838	***822.3893***	805.3628	804.3787			G				***701.3941***	684.3675	68
9	86.0964	**907.4785**	890.4519	889.4679	***935.4734***	918.4468	917.4628	879.4472	893.4628	I	586.2944	599.3148	613.3304	644.3726	627.3461	62
10	101.0709	1035.5370	1018.5105	1017.5265	***1063.5320***	1046.5054	1045.5214	978.5156		Q	458.2358	457.2405		***531.2885***	514.2620	51
11	72.0808	1134.6055	1117.5789	1116.5949	1162.6004	1145.5738	1144.5898	1120.5898		V	359.1674	372.1878		403.2300	386.2034	38
12	102.0550	1263.6480	1246.6215	1245.6375	***1291.6430***	1274.6164	1273.6324	1205.6426		E	230.1248	229.1295		304.1615	287.1350	28
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	**FQG**	305.1608	333.1557	**FQGP**	402.2136	430.2085
FQGPP	499.2663	527.2613	**FQGPPH**	636.3253	664.3202	**FQGPPHG**	693.3467	721.3416
QG	158.0924	186.0873	**QGP**	255.1452	283.1401	**QGPP**	352.1979	380.1928
QGPPH	489.2568	517.2518	**QGPPHG**	546.2783	574.2732	**QGPPHGI**	659.3624	687.3573
GP	127.0866	155.0815	**GPP**	224.1394	252.1343	**GPPH**	361.1983	389.1932
GPPHG	418.2197	446.2146	**GPPHGI**	531.3038	559.2987	**GPPHGIQ**	659.3624	687.3573
PP	167.1179	195.1128	**PPH**	304.1768	332.1717	**PPHG**	361.1983	389.1932

PPHGI	474.2823	502.2772	**PPHGIQ**	602.3409	630.3358	**PH**	207.1240	235.1190
PHG	264.1455	292.1404	**PHGI**	377.2296	405.2245	**PHGIQ**	505.2881	533.2831
PHGIQV	604.3566	632.3515	**HG**	167.0927	195.0877	**HGI**	280.1768	308.1717
HGIQ	408.2354	436.2303	**HGIQV**	507.3038	535.2987	**HGIQVE**	636.3464	664.3413
GI	143.1179	171.1128	**GIQ**	271.1765	299.1714	**GIQV**	370.2449	398.2398
GIQVE	499.2875	527.2824	**IQ**	214.1550	242.1499	**IQV**	313.2234	341.2183
IQVE	442.2660	470.2609	**QV**	200.1394	228.1343	**QVE**	329.1819	357.1769
VE	201.1234	229.1183						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.9	1464.7474	0.1241	TFQGPPHGLQVER
60.9	1464.7474	0.1241	TFQGPPHGLQVER
60.0	1464.7838	0.0878	TFKGPPHGIQVER
60.0	1464.7838	0.0878	TFKGPPHGIQVER
60.0	1464.7838	0.0878	TFQGPPHGIKVER
60.0	1464.7838	0.0878	TFQGPPHGIKVER
60.0	1464.7474	0.1241	TFQGPPHGIQVER
60.0	1464.7474	0.1241	TFQGPPHGIQVER
60.0	1464.7474	0.1241	TFQGPPHGIQVER
60.0	1464.7474	0.1241	TFQGPPHGIQVER

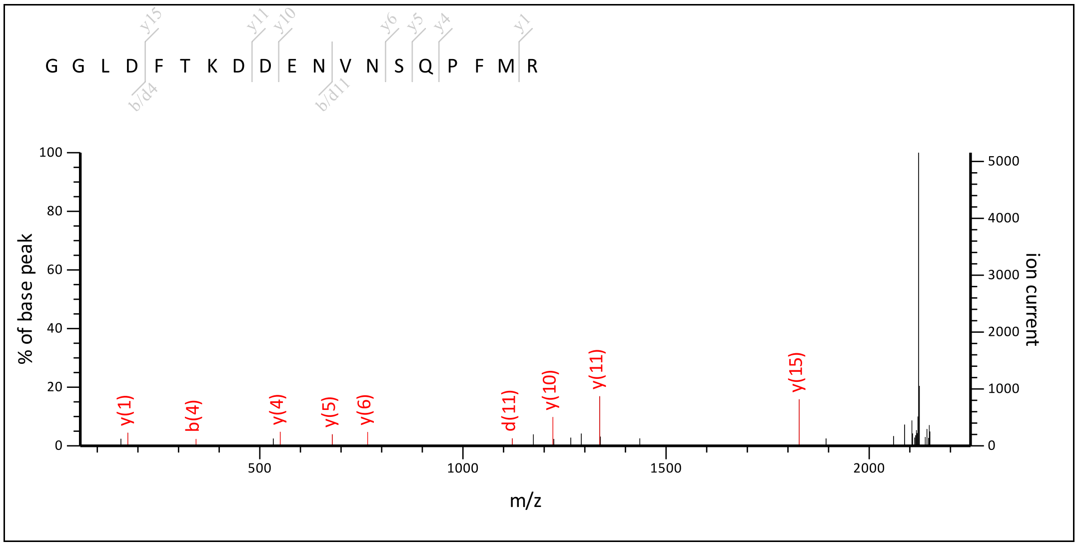
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 42

MS/MS Fragmentation of **GGLDFTKDDENVNSQPFMR**
Found in **gi|2961307** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase [Rondeletia odorata]

Match to Query 113: 2169.179224 from(2170.186500,1+) intensity(0.0000) index(24)
Title: Label: N6, Spot_Id: 228935, Peak_List_Id: 257671, MSMS Job_Run_Id: 24931, Comment:
Data file ppw_N6_138985138100.txt



58.11 to 2249.42

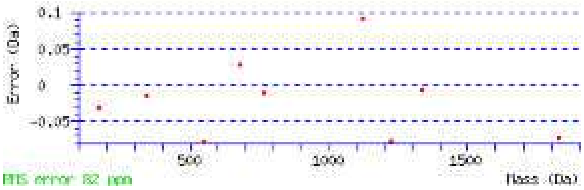
Label all possible matches ○ Label matches used for scoring ●

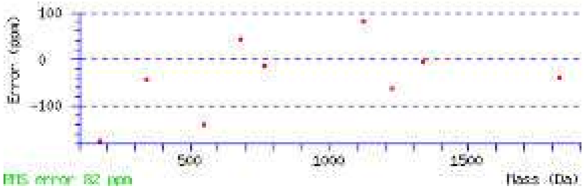
Monoisotopic mass of neutral peptide Mr(calc): 2168.9797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.053
Matches : 10/340 fragment ions using 12 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		**G**					
2	30.0338	87.0553			115.0502					**G**				2112.9655	2095.9389
3	86.0964	200.1394			228.1343			158.0924		**L**	1997.8658	1996.8705		2055.9440	2038.9175
4	88.0393	315.1663		297.1557	**343.1612**		325.1506	271.1765		**D**	1882.8388	1881.8436		1942.8600	1925.8334
5	120.0808	462.2347		444.2241	490.2296		472.2191			**F**	1735.7704			***1827.8330***	1810.8065
6	74.0600	563.2824		545.2718	591.2773		573.2667	547.2875	549.2667	**T**	1634.7227	1647.7431	1649.7224	1680.7646	1663.7381
7	101.1073	691.3774	674.3508	673.3668	719.3723	702.3457	701.3617	634.3195		**K**	1506.6278	1505.6325		1579.7169	1562.6904
8	88.0393	806.4043	789.3777	788.3937	834.3992	817.3727	816.3886	762.4145		**D**	1391.6008	1390.6056		1451.6220	1434.5954
9	88.0393	921.4312	904.4047	903.4207	949.4262	932.3996	931.4156	877.4414		**D**	1276.5739	1275.5786		***1336.5950***	1319.5685
10	102.0550	1050.4738	1033.4473	1032.4633	1078.4687	1061.4422	1060.4582	992.4684		**E**	1147.5313	1146.5361		***1221.5681***	1204.5415
11	87.0553	1164.5168	1147.4902	1146.5062	1192.5117	1175.4851	1174.5011	1121.5109		**N**	1033.4884	1032.4931		1092.5255	1075.4989
12	72.0808	1263.5852	1246.5586	1245.5746	1291.5801	1274.5535	1273.5695	1249.5695		**V**	934.4200	947.4404		978.4826	961.4560
13	87.0553	1377.6281	1360.6016	1359.6175	1405.6230	1388.5965	1387.6124	1334.6223		**N**	820.3770	819.3818		879.4141	862.3876
14	60.0444	1464.6601	1447.6336	1446.6496	1492.6550	1475.6285	1474.6445	1448.6652		**S**	733.3450	732.3498		***765.3712***	748.3447
15	101.0709	1592.7187	1575.6922	1574.7081	1620.7136	1603.6871	1602.7031	1535.6972		**Q**	605.2864	604.2912		***678.3392***	661.3126
16	70.0651	1689.7715	1672.7449	1671.7609	1717.7664	1700.7398	1699.7558	1663.7558		**P**	508.2337	507.2384		***550.2806***	533.2541
17	120.0808	1836.8399	1819.8133	1818.8293	1864.8348	1847.8082	1846.8242			**F**	361.1653			453.2279	436.2013
18	104.0528	1967.8804	1950.8538	1949.8698	1995.8753	1978.8487	1977.8647	1907.8770		**M**	230.1248	229.1295		306.1594	289.1329
19	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	**GLD**	258.1448	286.1397	**GLDF**	405.2132	433.2082

GLDFT	506.2609	534.2558	**GLDFTK**	634.3559	662.3508	**LD**	201.1234	229.1183
LDF	348.1918	376.1867	**LDFT**	449.2395	477.2344	**LDFTK**	577.3344	605.3293
LDFTKD	692.3614	720.3563	**DF**	235.1077	263.1026	**DFT**	336.1554	364.1503
DFTK	464.2504	492.2453	**DFTKD**	579.2773	607.2722	**DFTKDD**	694.3042	722.2992
FT	221.1285	249.1234	**FTK**	349.2234	377.2183	**FTKD**	464.2504	492.2453
FTKDD	579.2773	607.2722	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDD	432.2089	460.2038	**TKDDE**	561.2515	589.2464	**TKDDEN**	675.2944	703.2893
KD	216.1343	244.1292	**KDD**	331.1612	359.1561	**KDDE**	460.2038	488.1987
KDDEN	574.2467	602.2416	**KDDENV**	673.3151	701.3101	**DD**	203.0662	231.0612
DDE	332.1088	360.1038	**DDEN**	446.1518	474.1467	**DDENV**	545.2202	573.2151
DDENVN	659.2631	687.2580	**DE**	217.0819	245.0768	**DEN**	331.1248	359.1197
DENV	430.1932	458.1882	**DENVN**	544.2362	572.2311	**DENVNS**	631.2682	659.2631
EN	216.0979	244.0928	**ENV**	315.1663	343.1612	**ENVN**	429.2092	457.2041
ENVNS	516.2413	544.2362	**ENVNSQ**	644.2998	672.2947	**NV**	186.1237	214.1186
NVN	300.1666	328.1615	**NVNS**	387.1987	415.1936	**NVNSQ**	515.2572	543.2522
NVNSQP	612.3100	640.3049	**VN**	186.1237	214.1186	**VNS**	273.1557	301.1506
VNSQ	401.2143	429.2092	**VNSQP**	498.2671	526.2620	**VNSQPF**	645.3355	673.3304
NS	174.0873	202.0822	**NSQ**	302.1459	330.1408	**NSQP**	399.1987	427.1936
NSQPF	546.2671	574.2620	**NSQPFM**	677.3076	705.3025	**SQ**	188.1030	216.0979
SQP	285.1557	313.1506	**SQPF**	432.2241	460.2191	**SQPFM**	563.2646	591.2595
QP	198.1237	226.1186	**QPF**	345.1921	373.1870	**QPFM**	476.2326	504.2275
PF	217.1335	245.1285	**PFM**	348.1740	376.1689	**FM**	251.1213	279.1162





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.0	2168.9797	0.1995	GGIDFTKDDENVNSQPFMR
48.0	2168.9797	0.1995	GGIDFTKDDENVNSQPFMR
48.0	2169.0161	0.1632	GGLDFTKDDENVNSKPFMR
48.0	2168.9797	0.1995	GGLDFTKDDENVNSQPFMR
48.0	2168.9797	0.1995	GGLDFTKDDENVNSQPFMR
48.0	2168.9797	0.1995	GGLDFTKDDENVNSQPFMR
48.0	2168.9797	0.1995	GGLDFTKDDENVNSQPFMR
48.0	2168.9797	0.1995	GGLDFTKDDENVNSQPFMR
48.0	2168.9797	0.1995	GGLDFTKDDENVNSQPFMR
48.0	2168.9797	0.1995	GGLDFTKDDENVNSQPFMR

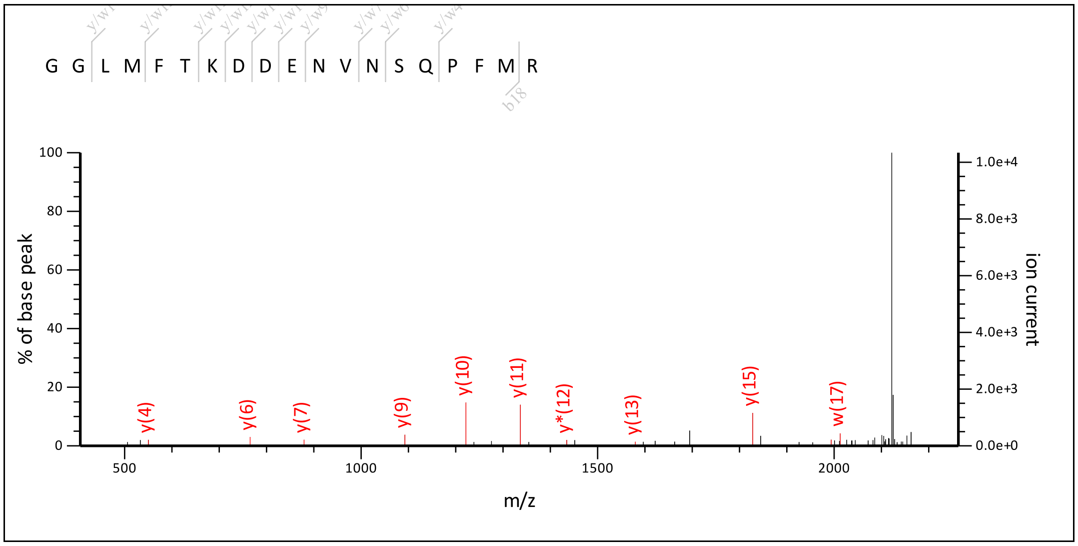
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 42

MS/MS Fragmentation of **GGLMFTKDDENVNSQPFMR**
Found in **gi|2961307** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase [Rondeletia odorata]

Match to Query 115: 2185.160924 from(2186.168200,1+) intensity(0.0000) index(25)
Title: Label: N6, Spot_Id: 228935, Peak_List_Id: 257674, MSMS Job_Run_Id: 24931, Comment:
Data file ppw_N6_138985138100.txt



406.24 to 2262.72

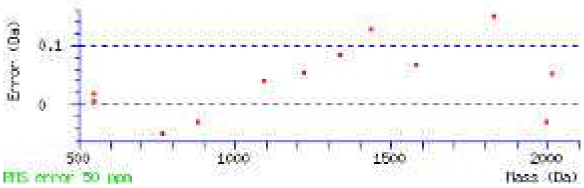
Label all possible matches ○ Label matches used for scoring ●

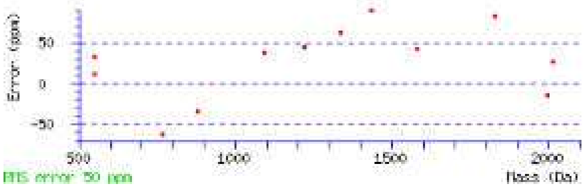
```
Monoisotopic mass of neutral peptide Mr(calc): 2184.9932
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 0.0046
Matches : 12/334 fragment ions using 13 most intense peaks   (help)
```

#	Immon.	a	a*	a^{0}	b	b*	b^{0}	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	30.0338	87.0553			115.0502					G				2128.9790	2111.9525
3	86.0964	200.1394			228.1343			158.0924		L	2013.8793	2012.8841		2071.9576	2054.9310
4	104.0528	331.1798			359.1748			271.1765		M	1882.8388	1881.8436		1958.8735	1941.8470
5	120.0808	478.2483			506.2432					F	1735.7704			***1827.8330***	1810.8065
6	74.0600	579.2959		561.2854	607.2908		589.2803	563.3010	565.2803	T	1634.7227	1647.7431	1649.7224	1680.7646	1663.7381
7	101.1073	707.3909	690.3643	689.3803	735.3858	718.3593	717.3752	650.3330		K	1506.6278	1505.6325		***1579.7169***	1562.6904
8	88.0393	822.4178	805.3913	804.4073	850.4128	833.3862	832.4022	778.4280		D	1391.6008	1390.6056		1451.6220	1434.5954
9	88.0393	937.4448	920.4182	919.4342	965.4397	948.4131	947.4291	893.4550		D	1276.5739	1275.5786		***1336.5950***	1319.5685
10	102.0550	1066.4874	1049.4608	1048.4768	1094.4823	1077.4557	1076.4717	1008.4819		E	1147.5313	1146.5361		***1221.5681***	1204.5415
11	87.0553	1180.5303	1163.5038	1162.5197	1208.5252	1191.4987	1190.5146	1137.5245		N	1033.4884	1032.4931		***1092.5255***	1075.4989
12	72.0808	1279.5987	1262.5722	1261.5881	1307.5936	1290.5671	1289.5831	1265.5831		V	934.4200	947.4404		978.4826	961.4560
13	87.0553	1393.6416	1376.6151	1375.6311	1421.6366	1404.6100	1403.6260	1350.6358		N	820.3770	819.3818		***879.4141***	862.3876
14	60.0444	1480.6737	1463.6471	1462.6631	1508.6686	1491.6420	1490.6580	1464.6788		S	733.3450	732.3498		***765.3712***	748.3447
15	101.0709	1608.7322	1591.7057	1590.7217	1636.7272	1619.7006	1618.7166	1551.7108		Q	605.2864	604.2912		678.3392	661.3126
16	70.0651	1705.7850	1688.7585	1687.7744	1733.7799	1716.7534	1715.7694	1679.7694		P	508.2337	507.2384		***550.2806***	533.2541
17	120.0808	1852.8534	1835.8269	1834.8429	1880.8483	1863.8218	1862.8378			F	361.1653			453.2279	436.2013
18	104.0528	1983.8939	1966.8674	1965.8833	2011.8888	1994.8623	1993.8783	1923.8905		M	230.1248	229.1295		306.1594	289.1329
19	129.1135									R	74.0237	73.0284		175.1190	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	GLM	274.1584	302.1533	GLMF	421.2268	449.2217

GLMFT	522.2745	550.2694	**GLMFTK**	650.3694	678.3643	**LM**	217.1369	245.1318
LMF	364.2053	392.2002	**LMFT**	465.2530	493.2479	**LMFTK**	593.3480	621.3429
MF	251.1213	279.1162	**MFT**	352.1689	380.1639	**MFTK**	480.2639	508.2588
MFTKD	595.2908	623.2858	**FT**	221.1285	249.1234	**FTK**	349.2234	377.2183
FTKD	464.2504	492.2453	**FTKDD**	579.2773	607.2722	**TK**	202.1550	230.1499
TKD	317.1819	345.1769	**TKDD**	432.2089	460.2038	**TKDDE**	561.2515	589.2464
TKDDEN	675.2944	703.2893	**KD**	216.1343	244.1292	**KDD**	331.1612	359.1561
KDDE	460.2038	488.1987	**KDDEN**	574.2467	602.2416	**KDDENV**	673.3151	701.3101
DD	203.0662	231.0612	**DDE**	332.1088	360.1038	**DDEN**	446.1518	474.1467
DDENV	545.2202	573.2151	**DDENVN**	659.2631	687.2580	**DE**	217.0819	245.0768
DEN	331.1248	359.1197	**DENV**	430.1932	458.1882	**DENVN**	544.2362	572.2311
DENVNS	631.2682	659.2631	**EN**	216.0979	244.0928	**ENV**	315.1663	343.1612
ENVN	429.2092	457.2041	**ENVNS**	516.2413	544.2362	**ENVNSQ**	644.2998	672.2947
NV	186.1237	214.1186	**NVN**	300.1666	328.1615	**NVNS**	387.1987	415.1936
NVNSQ	515.2572	543.2522	**NVNSQP**	612.3100	640.3049	**VN**	186.1237	214.1186
VNS	273.1557	301.1506	**VNSQ**	401.2143	429.2092	**VNSQP**	498.2671	526.2620
VNSQPF	645.3355	673.3304	**NS**	174.0873	202.0822	**NSQ**	302.1459	330.1408
NSQP	399.1987	427.1936	**NSQPF**	546.2671	574.2620	**NSQPFM**	677.3076	705.3025
SQ	188.1030	216.0979	**SQP**	285.1557	313.1506	**SQPF**	432.2241	460.2191
SQPFM	563.2646	591.2595	**QP**	198.1237	226.1186	**QPF**	345.1921	373.1870
QPFM	476.2326	504.2275	**PF**	217.1335	245.1285	**PFM**	348.1740	376.1689
FM	251.1213	279.1162						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.7	2184.9932	0.1677	GGLMFTKDDENVNSQPFMR
43.8	2184.9746	0.1863	GGLDYTKDDENVNSQPFMR
28.3	2184.9932	0.1677	GGLDFTKMDENVNSQPFMR
16.8	2185.1201	0.0408	NMLHALLTILEDEGAGGLYR
16.5	2184.9932	0.1677	GGLDFTKDMENVNSQPFMR
11.8	2185.0586	0.1023	LISGYMAQLVEDGGNHGGVPR
11.5	2185.0361	0.1248	HLQIIESGLEEGGDEVWMK
11.5	2185.0262	0.1347	DWLYASGNIRQLYCLQGE
11.4	2185.0725	0.0884	CVATSFVNLNDQLTDIFTK
10.1	2185.0646	0.0963	IYAELCKLETDEMSTAAIK

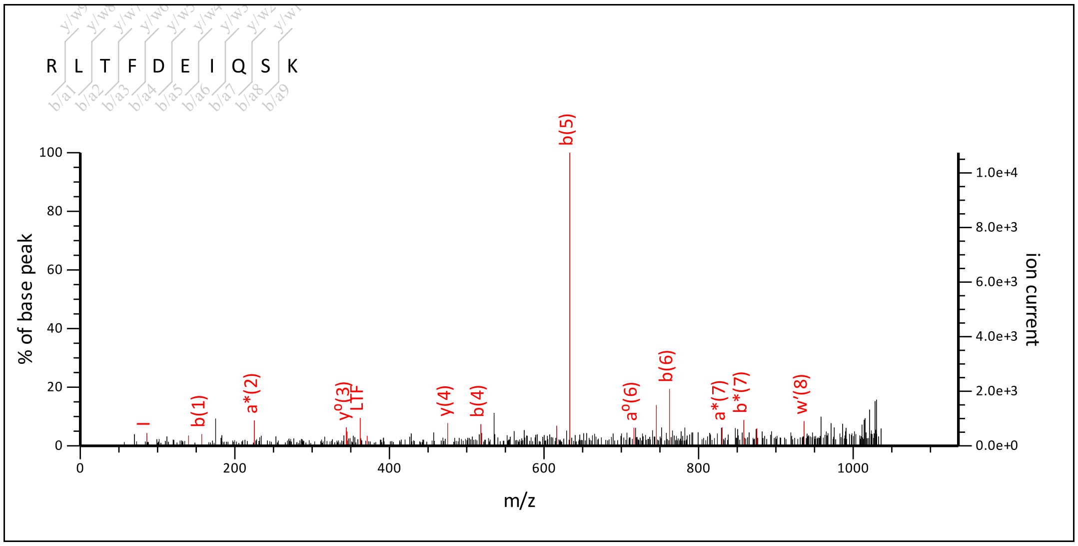
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 45

MS/MS Fragmentation of **RLTFDEIQSK**
Found in **gi|739292** in **NCBInr**, oxygen-evolving complex protein 1

Match to Query 22: 1235.688724 from(1236.696000,1+) intensity(0.0000) index(21)
Title: Label: N3, Spot_Id: 219719, Peak_List_Id: 225482, MSMS Job_Run_Id: 21780, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_N3_136842149300.txt



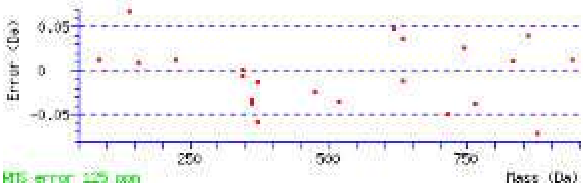
0 to 1136.14

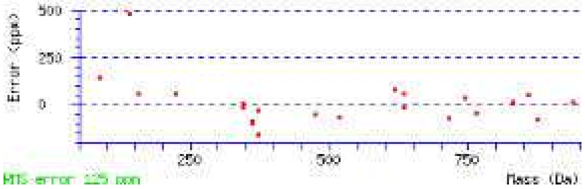
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1235.6510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 1.7
Matches : 23/161 fragment ions using 30 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	129.1135	129.1135	112.0869		***157.1084***	140.0818		44.0495		**R**						
2	86.0964	242.1975	225.1710		270.1925	253.1659		200.1506		**L**	1022.4789	1021.4837		1080.5572	1063.5306	106
3	74.0600	343.2452	326.2187	325.2347	***371.2401***	354.2136	353.2296	327.2503	329.2296	**T**	921.4312	934.4516	936.4309	967.4731	950.4466	94
4	120.0808	490.3136	473.2871	472.3031	***518.3085***	501.2820	500.2980			**F**	774.3628			866.4254	849.3989	84
5	88.0393	605.3406	588.3140	587.3300	***633.3355***	616.3089	615.3249	561.3507		**D**	659.3359	658.3406		719.3570	702.3305	70
6	102.0550	734.3832	717.3566	716.3726	***762.3781***	745.3515	744.3675	676.3777		**E**	530.2933	529.2980		604.3301	587.3035	58
7	86.0964	847.4672	830.4407	829.4567	***875.4621***	858.4356	857.4516	819.4359	833.4516	**I**	417.2092	430.2296	444.2453	**475.2875**	458.2609	45
8	101.0709	975.5258	958.4993	957.5152	1003.5207	986.4942	985.5102	918.5043		**Q**	289.1506	288.1554		**362.2034**	345.1769	34
9	60.0444	1062.5578	1045.5313	1044.5473	1090.5528	1073.5262	1072.5422	1046.5629		**S**	202.1186	201.1234		234.1448	217.1183	21
10	101.1073									**K**	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LT	187.1441	215.1390	**LTF**	334.2125	362.2074	**LTFD**	449.2395	477.2344
LTFDE	578.2821	606.2770	**LTFDEI**	691.3661	719.3610	**TF**	221.1285	249.1234
TFD	336.1554	364.1503	**TFDE**	465.1980	493.1929	**TFDEI**	578.2821	606.2770
FD	235.1077	263.1026	**FDE**	364.1503	392.1452	**FDEI**	477.2344	505.2293
FDEIQ	605.2930	633.2879	**FDEIQS**	692.3250	720.3199	**DE**	217.0819	245.0768
DEI	330.1660	358.1609	**DEIQ**	458.2245	486.2195	**DEIQS**	545.2566	573.2515
EI	215.1390	243.1339	**EIQ**	343.1976	371.1925	**EIQS**	430.2296	458.2245
IQ	214.1550	242.1499	**IQS**	301.1870	329.1819	**QS**	188.1030	216.0979





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.7	1235.6510	0.0377	RLTFDEIQSK
16.8	1235.6007	0.0880	HHSLETDNKR
14.7	1235.5895	0.0993	LQNFTDAQGSR
14.4	1235.6033	0.0854	IFLTEAEEER
14.4	1235.5935	0.0953	LQFNSAENWK
14.1	1235.6106	0.0781	VGSSSGNLSVSSR
13.6	1235.6663	0.0225	YPTLQVVNFR
12.4	1235.5969	0.0919	CVNTEPTFLR
12.2	1235.5968	0.0919	SAYGLAMPSSPR
12.1	1235.6007	0.0880	RFGGGEGGSAVSR

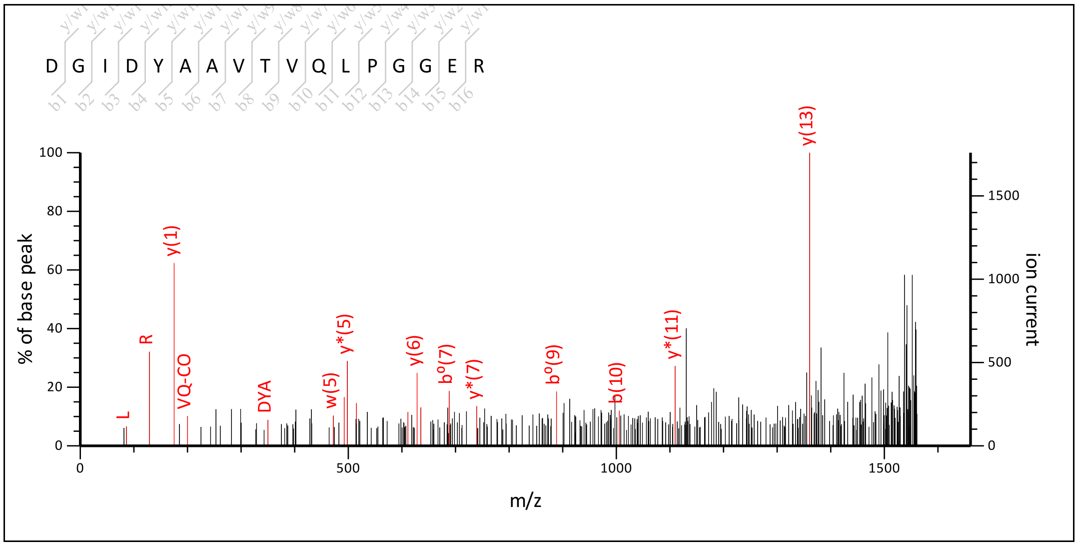
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 45

MS/MS Fragmentation of **DGIDYAAVTVQLPGGER**
Found in **gi|739292** in **NCBInr**, oxygen-evolving complex protein 1

Match to Query 35: 1759.930824 from(1760.938100,1+) intensity(0.0000) index(32)
Title: Label: N3, Spot_Id: 219719, Peak_List_Id: 225497, MSMS Job_Run_Id: 21780, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_N3_136842149300.txt



0 to 1660.79

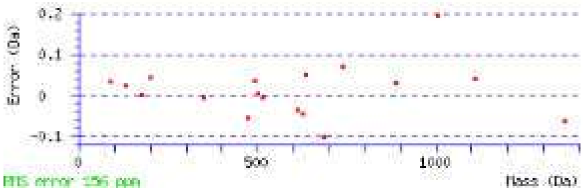
Label all possible matches ○ Label matches used for scoring ●

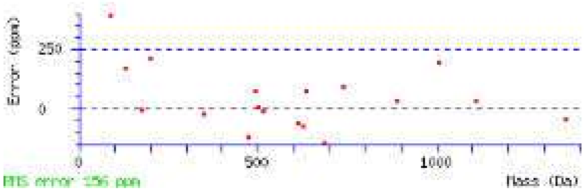
Monoisotopic mass of neutral peptide Mr(calc): 1759.8741
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 4 **Expect:** 6.1e+02
Matches : 20/309 fragment ions using 45 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D					
2	30.0338	145.0608		127.0502	173.0557		155.0451			G				1645.8544	1628.8279
3	86.0964	258.1448		240.1343	286.1397		268.1292	230.1135	244.1292	I	1530.7547	1543.7751	1557.7908	1588.8329	1571.8064
4	88.0393	373.1718		355.1612	401.1667		383.1561	329.1819		D	1415.7278	1414.7325		1475.7489	1458.7223
5	136.0757	536.2351		518.2245	564.2300		546.2195			Y	1252.6644			***1360.7219***	1343.6954
6	44.0495	607.2722		589.2617	**635.2671**		617.2566			A	1181.6273			1197.6586	1180.6321
7	44.0495	678.3093		660.2988	706.3042		688.2937			A	1110.5902			1126.6215	1109.5950
8	72.0808	777.3777		759.3672	805.3727		787.3621	763.3621		V	1011.5218	1024.5422		1055.5844	1038.5578
9	74.0600	878.4254		860.4149	906.4203		888.4098	862.4305	864.4098	T	910.4741	923.4945	925.4738	956.5160	939.4894
10	72.0808	977.4938		959.4833	**1005.4888**		987.4782	963.4782		V	811.4057	824.4261		855.4683	838.4417
11	101.0709	1105.5524	1088.5259	1087.5419	1133.5473	1116.5208	1115.5368	1048.5310		Q	683.3471	682.3519		756.3999	739.3733
12	86.0964	1218.6365	1201.6099	1200.6259	1246.6314	1229.6048	1228.6208	1176.5895		L	570.2631	569.2678		***628.3413***	611.3148
13	70.0651	1315.6892	1298.6627	1297.6787	1343.6842	1326.6576	1325.6736	1289.6736		P	473.2103	472.2150		***515.2572***	498.2307
14	30.0338	1372.7107	1355.6842	1354.7001	1400.7056	1383.6791	1382.6951			G				418.2045	401.1779
15	30.0338	1429.7322	1412.7056	1411.7216	1457.7271	1440.7005	1439.7165			G				361.1830	344.1565
16	102.0550	1558.7748	1541.7482	1540.7642	1586.7697	1569.7431	1568.7591	1500.7693		E	230.1248	229.1295		304.1615	287.1350
17	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GI	143.1179	171.1128	GID	258.1448	286.1397	GIDY	421.2082	449.2031
GIDYA	492.2453	520.2402	GIDYAA	563.2824	591.2773	GIDYAAV	662.3508	690.3457
ID	201.1234	229.1183	IDY	364.1867	392.1816	IDYA	435.2238	463.2187
IDYAA	506.2609	534.2558	IDYAAV	605.3293	633.3243	DY	251.1026	279.0975

DYA	322.1397	350.1347	**DYAA**	393.1769	421.1718	**DYAAV**	492.2453	520.2402
DYAAVT	593.2930	621.2879	**DYAAVTV**	692.3614	720.3563	**YA**	207.1128	235.1077
YAA	278.1499	306.1448	**YAAV**	377.2183	405.2132	**YAAVT**	478.2660	506.2609
YAAVTV	577.3344	605.3293	**AA**	115.0866	143.0815	**AAV**	214.1550	242.1499
AAVT	315.2027	343.1976	**AAVTV**	414.2711	442.2660	**AAVTVQ**	542.3297	570.3246
AAVTVQL	655.4137	683.4087	**AV**	143.1179	171.1128	**AVT**	244.1656	272.1605
AVTV	343.2340	371.2289	**AVTVQ**	471.2926	499.2875	**AVTVQL**	584.3766	612.3715
AVTVQLP	681.4294	709.4243	**VT**	173.1285	201.1234	**VTV**	272.1969	300.1918
VTVQ	400.2554	428.2504	**VTVQL**	513.3395	541.3344	**VTVQLP**	610.3923	638.3872
VTVQLPG	667.4137	695.4087	**TV**	173.1285	201.1234	**TVQ**	301.1870	329.1819
TVQL	414.2711	442.2660	**TVQLP**	511.3239	539.3188	**TVQLPG**	568.3453	596.3402
TVQLPGG	625.3668	653.3617	**VQ**	200.1394	228.1343	**VQL**	313.2234	341.2183
VQLP	410.2762	438.2711	**VQLPG**	467.2976	495.2926	**VQLPGG**	524.3191	552.3140
VQLPGGE	653.3617	681.3566	**QL**	214.1550	242.1499	**QLP**	311.2078	339.2027
QLPG	368.2292	396.2241	**QLPGG**	425.2507	453.2456	**QLPGGE**	554.2933	582.2882
LP	183.1492	211.1441	**LPG**	240.1707	268.1656	**LPGG**	297.1921	325.1870
LPGGE	426.2347	454.2296	**PG**	127.0866	155.0815	**PGG**	184.1081	212.1030
PGGE	313.1506	341.1456	**GG**	87.0553	115.0502	**GGE**	216.0979	244.0928
GE	159.0764	187.0713						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
9.4	1759.8840	0.0469	IVAESTDDVIDGPSSKK
8.9	1759.9026	0.0282	SDLKVINDCLDDLIK
6.8	1759.9316	-0.0007	ISTVETELQKLSQER
6.5	1759.9832	-0.0524	LPASPPVILAAAGTTPER
4.8	1759.8159	0.1149	EEMPQQVASGEQAGKR
4.8	1759.8597	0.0711	GCALLLDLDCNDLIR
4.7	1759.8523	0.0786	AESNPDAASMVDRLLR
4.4	1759.8741	0.0567	DGIDYAAVTVQLPGGER
4.3	1759.9502	-0.0194	LSSIVTGLQMQEVSLR
3.9	1759.9356	-0.0048	AVGVLYAVVDDIIEER

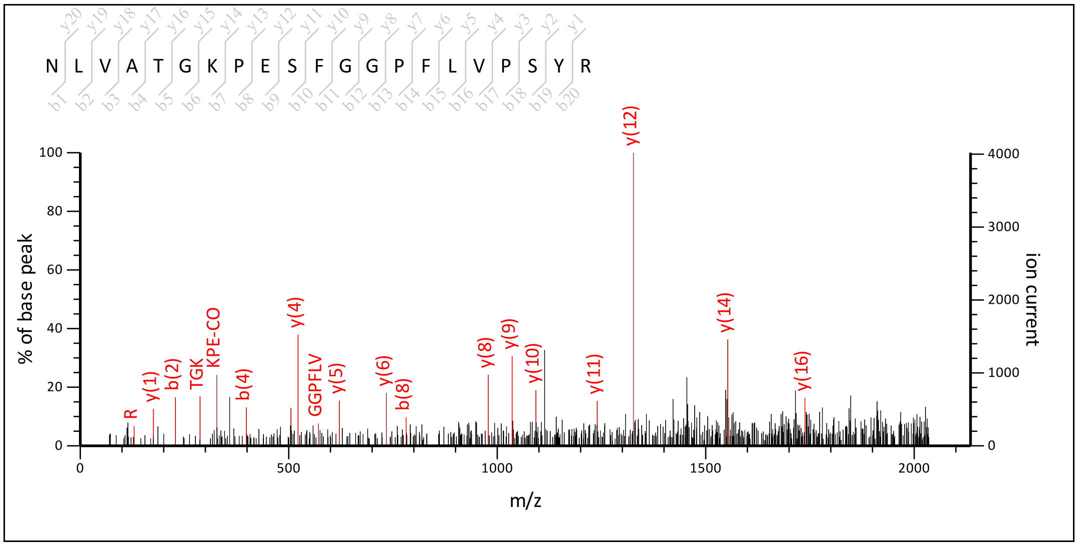
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 45

MS/MS Fragmentation of **NLVATGKPESFGGPFLVPSYR**
Found in **gi|739292** in **NCBInr**, oxygen-evolving complex protein 1

Match to Query 159: 2235.221024 from(2236.228300,1+) intensity(0.0000) index(34)
Title: Label: N3, Spot_Id: 219719, Peak_List_Id: 225485, MSMS Job_Run_Id: 21780, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_N3_136842149300.txt



0 to 2135.14

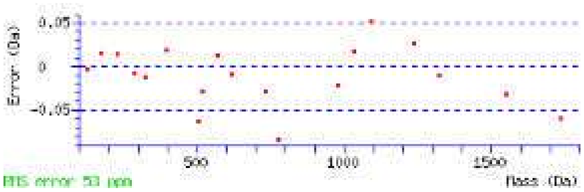
Label all possible matches ○ Label matches used for scoring ●

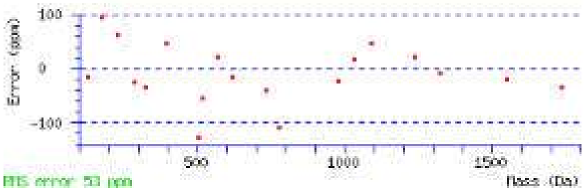
```
Monoisotopic mass of neutral peptide Mr(calc): 2235.1688
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 0.0027
Matches : 20/412 fragment ions using 40 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495		N					
2	86.0964	200.1394	183.1128		**228.1343**	211.1077		158.0924		L	2064.0549	2063.0597		2122.1332	2105.1066
3	72.0808	299.2078	282.1812		**327.2027**	310.1761		285.1921		V	1964.9865	1978.0069		2009.0491	1992.0225
4	44.0495	370.2449	353.2183		**398.2398**	381.2132				A	1893.9494			1909.9807	1892.9541
5	74.0600	471.2926	454.2660	453.2820	499.2875	482.2609	481.2769	455.2976	457.2769	T	1792.9017	1805.9221	1807.9014	1838.9436	1821.9170
6	30.0338	528.3140	511.2875	510.3035	556.3089	539.2824	538.2984			G				***1737.8959***	1720.8693
7	101.1073	656.4090	639.3824	638.3984	684.4039	667.3774	666.3933	599.3511		K	1607.7853	1606.7900		1680.8744	1663.8479
8	70.0651	753.4618	736.4352	735.4512	**781.4567**	764.4301	763.4461	727.4461		P	1510.7325	1509.7373		***1552.7795***	1535.7529
9	102.0550	882.5043	865.4778	864.4938	910.4993	893.4727	892.4887	824.4989		E	1381.6899	1380.6947		1455.7267	1438.7001
10	60.0444	969.5364	952.5098	951.5258	997.5313	980.5047	979.5207	953.5415		S	1294.6579	1293.6626		***1326.6841***	1309.6576
11	120.0808	1116.6048	1099.5782	1098.5942	1144.5997	1127.5732	1126.5891			F	1147.5895			***1239.6521***	1222.6255
12	30.0338	1173.6262	1156.5997	1155.6157	1201.6212	1184.5946	1183.6106			G				***1092.5837***	1075.5571
13	30.0338	1230.6477	1213.6212	1212.6371	1258.6426	1241.6161	1240.6321			G				***1035.5622***	1018.5356
14	70.0651	1327.7005	1310.6739	1309.6899	1355.6954	1338.6688	1337.6848	1301.6848		P	936.4938	935.4985		***978.5407***	961.5142
15	120.0808	1474.7689	1457.7423	1456.7583	1502.7638	1485.7373	1484.7532			F	789.4254			881.4880	864.4614
16	86.0964	1587.8530	1570.8264	1569.8424	1615.8479	1598.8213	1597.8373	1545.8060		L	676.3413	675.3461		***734.4196***	717.3930
17	72.0808	1686.9214	1669.8948	1668.9108	1714.9163	1697.8897	1696.9057	1672.9057		V	577.2729	590.2933		***621.3355***	604.3089
18	70.0651	1783.9741	1766.9476	1765.9636	1811.9690	1794.9425	1793.9585	1757.9585		P	480.2201	479.2249		***522.2671***	505.2405
19	60.0444	1871.0062	1853.9796	1852.9956	1899.0011	1881.9745	1880.9905	1855.0112		S	393.1881	392.1928		425.2143	408.1878
20	136.0757	2034.0695	2017.0429	2016.0589	2062.0644	2045.0379	2044.0538			Y	230.1248			338.1823	321.1557
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

LV	185.1648	213.1598	**LVA**	256.2020	284.1969	**LVAT**	357.2496	385.2445
LVATG	414.2711	442.2660	**LVATGK**	542.3661	570.3610	**LVATGKP**	639.4188	667.4137
VA	143.1179	171.1128	**VAT**	244.1656	272.1605	**VATG**	301.1870	329.1819
VATGK	429.2820	457.2769	**VATGKP**	526.3348	554.3297	**VATGKPE**	655.3774	683.3723
AT	145.0972	173.0921	**ATG**	202.1186	230.1135	**ATGK**	330.2136	358.2085
ATGKP	427.2663	455.2613	**ATGKPE**	556.3089	584.3039	**ATGKPES**	643.3410	671.3359
TG	131.0815	159.0764	**TGK**	259.1765	287.1714	**TGKP**	356.2292	384.2241
TGKPE	485.2718	513.2667	**TGKPES**	572.3039	600.2988	**GK**	158.1288	186.1237
GKP	255.1816	283.1765	**GKPE**	384.2241	412.2191	**GKPES**	471.2562	499.2511
GKPESF	618.3246	646.3195	**GKPESFG**	675.3461	703.3410	**KP**	198.1601	226.1550
KPE	327.2027	355.1976	**KPES**	414.2347	442.2296	**KPESF**	561.3031	589.2980
KPESFG	618.3246	646.3195	**KPESFGG**	675.3461	703.3410	**PE**	199.1077	227.1026
PES	286.1397	314.1347	**PESF**	433.2082	461.2031	**PESFG**	490.2296	518.2245
PESFGG	547.2511	575.2460	**PESFGGP**	644.3039	672.2988	**ES**	189.0870	217.0819
ESF	336.1554	364.1503	**ESFG**	393.1769	421.1718	**ESFGG**	450.1983	478.1932
ESFGGP	547.2511	575.2460	**ESFGGPF**	694.3195	722.3144	**SF**	207.1128	235.1077
SFG	264.1343	292.1292	**SFGG**	321.1557	349.1506	**SFGGP**	418.2085	446.2034
SFGGPF	565.2769	593.2718	**SFGGPFL**	678.3610	706.3559	**FG**	177.1022	205.0972
FGG	234.1237	262.1186	**FGGP**	331.1765	359.1714	**FGGPF**	478.2449	506.2398
FGGPFL	591.3289	619.3239	**FGGPFLV**	690.3974	718.3923	**GG**	87.0553	115.0502
GGP	184.1081	212.1030	**GGPF**	331.1765	359.1714	**GGPFL**	444.2605	472.2554
GGPFLV	543.3289	571.3239	**GGPFLVP**	640.3817	668.3766	**GP**	127.0866	155.0815
GPF	274.1550	302.1499	**GPFL**	387.2391	415.2340	**GPFLV**	486.3075	514.3024
GPFLVP	583.3602	611.3552	**GPFLVPS**	670.3923	698.3872	**PF**	217.1335	245.1285
PFL	330.2176	358.2125	**PFLV**	429.2860	457.2809	**PFLVP**	526.3388	554.3337
PFLVPS	613.3708	641.3657	**FL**	233.1648	261.1598	**FLV**	332.2333	360.2282
FLVP	429.2860	457.2809	**FLVPS**	516.3180	544.3130	**FLVPSY**	679.3814	707.3763
LV	185.1648	213.1598	**LVP**	282.2176	310.2125	**LVPS**	369.2496	397.2445
LVPSY	532.3130	560.3079	**VP**	169.1335	197.1285	**VPS**	256.1656	284.1605
VPSY	419.2289	447.2238	**PS**	157.0972	185.0921	**PSY**	320.1605	348.1554
SY	223.1077	251.1026						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.4	2235.1688	0.0522	NLVATGKPESFGGPFLVPSYR
32.7	2235.1688	0.0522	QLVATGKPDSFGGPFLVPSYR
7.9	2235.0916	0.1295	LAVLVGDYMGGPVVDPDSMLR
5.5	2235.1933	0.0277	KVVISGSAEGVQMANYLLTQK
4.7	2235.1259	0.0951	QPTASAQMFTRPWLALFDR
4.4	2235.0452	0.1758	WKEIPFQSPASDLPNGMMR
4.4	2235.1102	0.1108	MCELETVVGGFVIVATHVMK
4.0	2235.2331	-0.0120	VRVALMMSAGVTTAAVLVLSSK
3.4	2235.1899	0.0311	IIETSFVSVPANAAPQPEPIR
3.1	2235.1859	0.0352	LALGDNALPEAGIGAIASQLADR

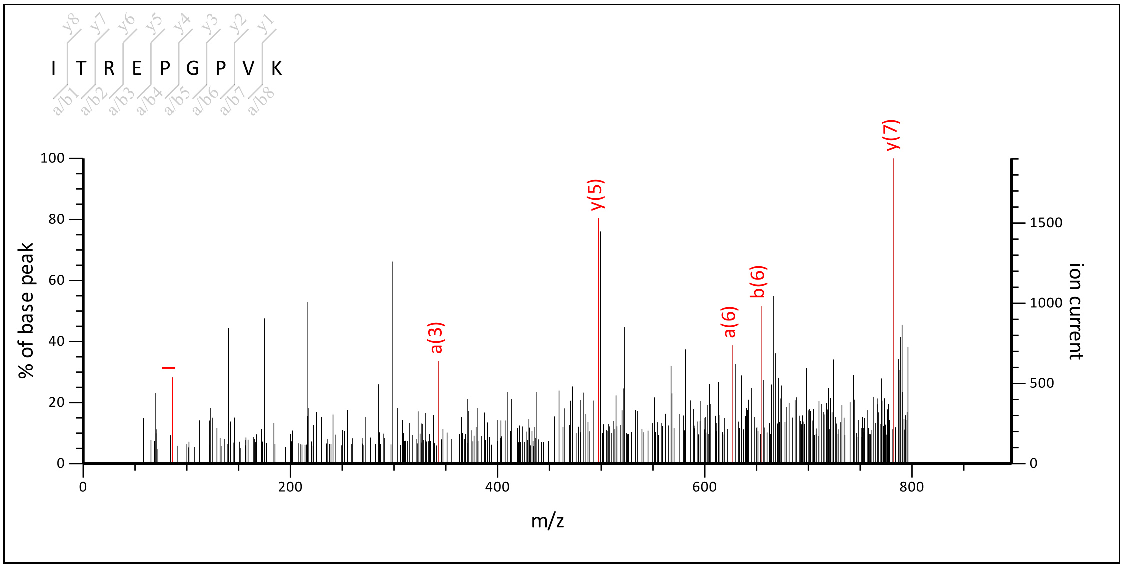
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 47

MS/MS Fragmentation of **ITREPGPVK**
Found in **gi|162461576** in **NCBInr**, glyoxylase1 [Zea mays]

Match to Query 27: 995.564684 from(996.571960,1+) intensity(0.0000) index(7)
Title: Label: M3, Spot_Id: 219718, Peak_List_Id: 225458, MSMS Job_Run_Id: 21779, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_M3_136842147700.txt



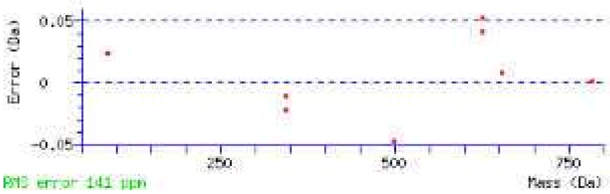
0 to 896.13

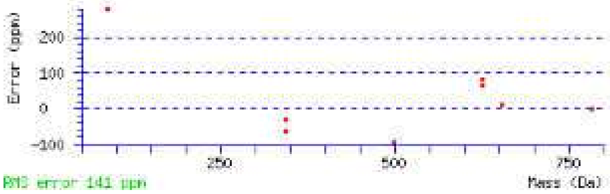
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 995.5764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 12 **Expect:** 1.1e+02
Matches : 9/133 fragment ions using 16 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	***86.0964***			114.0913			44.0495		**I**							9
2	74.0600	187.1441		169.1335	215.1390		197.1285	171.1492	173.1285	**T**	837.4577	850.4781	852.4574	883.4996	866.4730	865.4890	8
3	129.1135	***343.2452***	326.2187	325.2346	371.2401	354.2136	353.2296	258.1812		**R**	681.3566	680.3614		***782.4519***	765.4254	764.4413	7
4	102.0550	472.2878	455.2613	454.2772	500.2827	483.2562	482.2722	414.2823		**E**	552.3140	551.3188		***626.3508***	609.3243	608.3402	6
5	70.0651	569.3406	552.3140	551.3300	597.3355	580.3089	579.3249	543.3249		**P**	455.2613	454.2660		***497.3082***	480.2817		5
6	30.0338	***626.3620***	609.3355	608.3515	654.3570	637.3304	636.3464			**G**				400.2554	383.2289		4
7	70.0651	723.4148	706.3883	705.4042	751.4097	734.3832	733.3992	697.3992		**P**	301.1870	300.1918		***343.2340***	326.2074		3
8	72.0808	822.4832	805.4567	804.4726	850.4781	833.4516	832.4676	808.4676		**V**	202.1186	215.1390		246.1812	229.1547		2
9	101.1073									**K**	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TR	230.1612	258.1561	**TRE**	359.2037	387.1987	**TREP**	456.2565	484.2514
TREPG	513.2780	541.2729	**TREPGP**	610.3307	638.3257	**RE**	258.1561	286.1510
REP	355.2088	383.2037	**REPG**	412.2303	440.2252	**REPGP**	509.2831	537.2780
REPGPV	608.3515	636.3464	**EP**	199.1077	227.1026	**EPG**	256.1292	284.1241
EPGP	353.1819	381.1769	**EPGPV**	452.2504	480.2453	**PG**	127.0866	155.0815
PGP	224.1394	252.1343	**PGPV**	323.2078	351.2027	**GP**	127.0866	155.0815
GPV	226.1550	254.1499	**PV**	169.1335	197.1285			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
12.0	995.5764	-0.0117	ITREPGPVK
10.2	995.6128	-0.0481	VDKGPLLVR
8.6	995.6240	-0.0593	LSAILRAPR
8.3	995.6127	-0.0481	TINLLIPGR
8.2	995.6128	-0.0481	LQTLVVPAR
8.1	995.5764	-0.0117	LLVAAGAEPR
8.1	995.6128	-0.0481	AVQILTVPR
8.1	995.6128	-0.0481	LLVATPVAGR
8.0	995.6240	-0.0593	ILASRLAPR
8.0	995.6240	-0.0593	LLASRLAPR

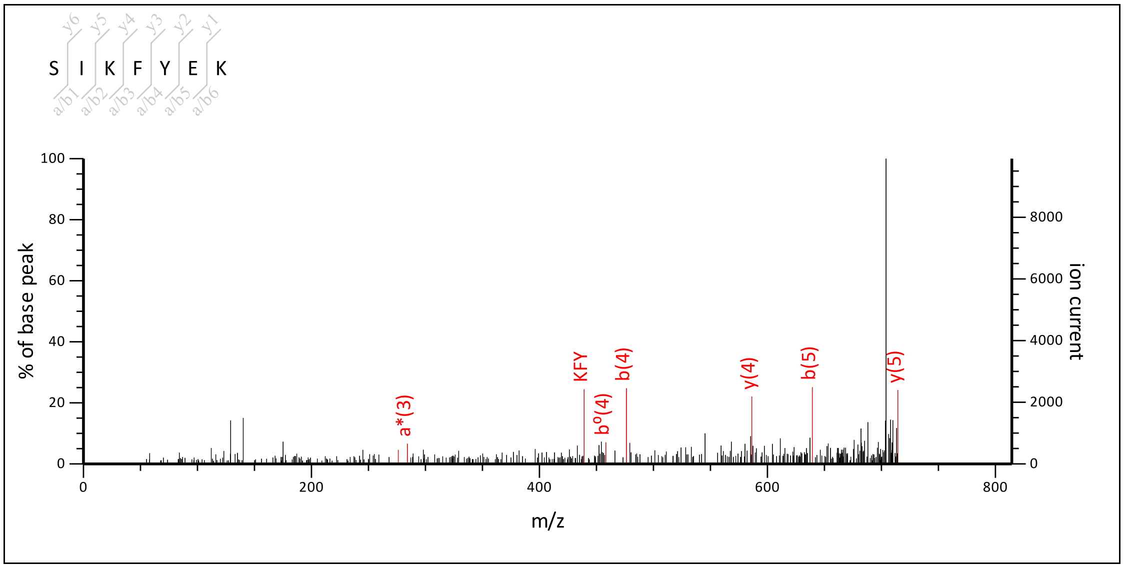
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 47

MS/MS Fragmentation of **SIKFYEK**
Found in **gi|162461576** in **NCBInr**, glyoxylase1 [Zea mays]

Match to Query 11: 913.476614 from(914.483890,1+) intensity(0.0000) index(3)
Title: Label: M3, Spot_Id: 219718, Peak_List_Id: 225455, MSMS Job_Run_Id: 21779, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_M3_136842147700.txt



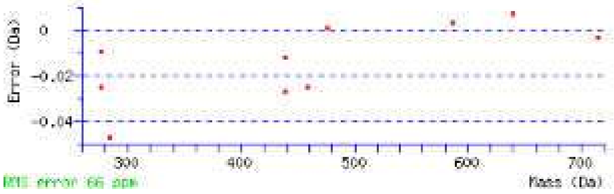
0 to 814.38

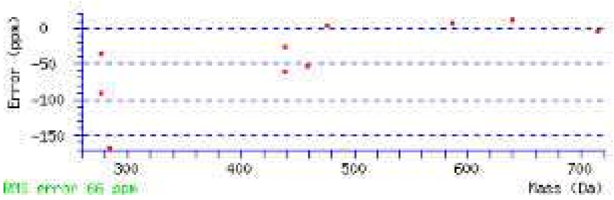
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 913.4909
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 13  Expect: 1.6e+02
Matches : 10/92 fragment ions using 21 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S							7
2	86.0964	173.1285		155.1179	201.1234		183.1128	145.0972	159.1128	I	769.3879	782.4083	796.4240	827.4662	810.4396	809.4556	6
3	101.1073	301.2234	284.1969	283.2129	329.2183	312.1918	311.2078	244.1656		K	641.2930	640.2977		***714.3821***	697.3556	696.3715	5
4	120.0808	448.2918	431.2653	430.2813	**476.2867**	459.2602	458.2762			F	494.2245			***586.2871***	569.2606	568.2766	4
5	136.0757	611.3552	594.3286	593.3446	**639.3501**	622.3235	621.3395			Y	331.1612			***439.2187***	422.1922	421.2082	3
6	102.0550	740.3978	723.3712	722.3872	768.3927	751.3661	750.3821	682.3923		E	202.1186	201.1234		***276.1554***	259.1288	258.1448	2
7	101.1073									K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IK	214.1914	242.1863	IKF	361.2598	389.2547	IKFY	524.3231	552.3180
IKFYE	653.3657	681.3606	KF	248.1757	276.1707	KFY	411.2391	439.2340
KFYE	540.2817	568.2766	FY	283.1441	311.1390	FYE	412.1867	440.1816
YE	265.1183	293.1132						





NCBI **BLAST** search of SIKFYEK

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.8	913.5021	-0.0255	KFYISTR
15.5	913.4691	0.0075	LSMKYTR
14.0	913.4658	0.0109	SIFGAYTR
14.0	913.4505	0.0261	SSTLSYTR
13.9	913.4658	0.0109	ALGSFYTR
13.9	913.4658	0.0109	TNIFYTR
13.0	913.4909	-0.0143	SIKFYEK
12.4	913.4658	0.0109	SLGAYFTR
12.0	913.4658	0.0109	FQYTLSR
12.0	913.4294	0.0472	KFYDDAR

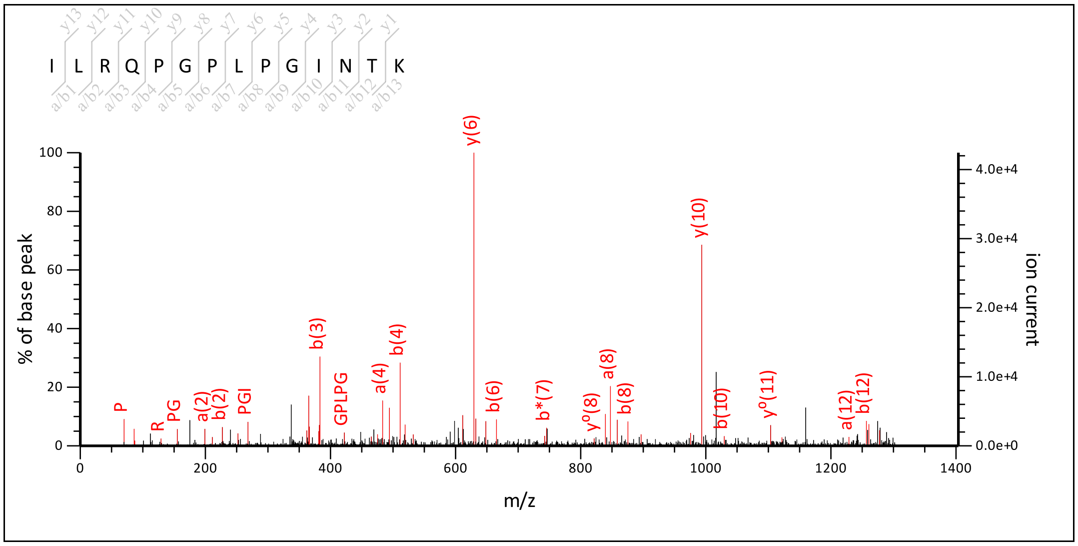
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 47**

MS/MS Fragmentation of **ILRQPGPLPGINTK**
Found in **gi|162461576** in **NCBInr**, glyoxylase1 [Zea mays]

Match to Query 63: 1502.895824 from(1503.903100,1+) intensity(0.0000) index(19)
Title: Label: M3, Spot_Id: 219718, Peak_List_Id: 225450, MSMS Job_Run_Id: 21779, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_M3_136842147700.txt



0 to 1403.8

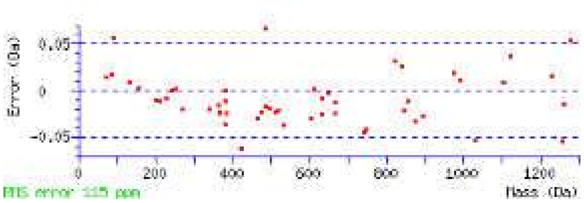
Label all possible matches ○ Label matches used for scoring ●

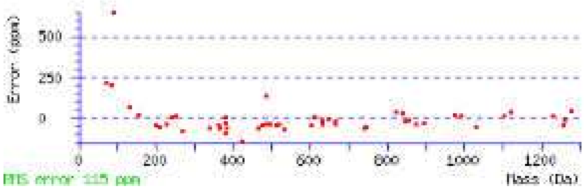
Monoisotopic mass of neutral peptide Mr(calc): 1502.8933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 0.0038
Matches : 69/237 fragment ions using 91 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	**86.0964**			114.0913			44.0495		I						
2	86.0964	**199.1805**			**227.1754**			157.1335		L	1332.7383	1331.7430		1390.8165	1373.7900	13
3	129.1135	355.2816	338.2551		**383.2765**	366.2500		270.2176		R	1176.6372	1175.6419		***1277.7324***	1260.7059	12
4	101.0709	**483.3402**	466.3136		**511.3351**	494.3085		426.3187		Q	1048.5786	1047.5833		***1121.6313***	1104.6048	11
5	70.0651	580.3929	563.3664		608.3879	591.3613		554.3773		P	951.5258	950.5306		***993.5728***	976.5462	9
6	30.0338	637.4144	620.3879		**665.4093**	648.3828				G				***896.5200***	879.4934	8
7	70.0651	734.4672	717.4406		762.4621	745.4355		708.4515		P	797.4516	796.4563		***839.4985***	822.4720	8
8	86.0964	**847.5512**	830.5247		**875.5461**	858.5196		805.5043		L	684.3675	683.3723		***742.4458***	725.4192	7
9	70.0651	944.6040	927.5774		972.5989	955.5724		918.5883		P	587.3148	586.3195		***629.3617***	612.3352	6
10	30.0338	1001.6255	984.5989		**1029.6204**	1012.5938				G				***532.3089***	515.2824	5
11	86.0964	1114.7095	1097.6830		1142.7044	1125.6779		1086.6782	1100.6939	I	417.2092	430.2296	444.2453	***475.2875***	458.2609	4
12	87.0553	**1228.7525**	1211.7259		**1256.7474**	1239.7208		1185.7466		N	303.1663	302.1710		***362.2034***	345.1769	3
13	74.0600	1329.8001	1312.7736	1311.7896	1357.7950	1340.7685	1339.7845	1313.8052	1315.7845	T	202.1186	215.1390	217.1183	248.1605	231.1339	2
14	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LR	242.1975	270.1925	LRQ	370.2561	398.2510	LRQP	467.3089	495.3038
LRQPG	524.3303	552.3253	LRQPGP	621.3831	649.3780	RQ	257.1720	285.1670
RQP	354.2248	382.2197	RQPG	411.2463	439.2412	RQPGP	508.2990	536.2940
RQPGPL	621.3831	649.3780	QP	198.1237	226.1186	QPG	255.1452	283.1401
QPGP	352.1979	380.1928	QPGPL	465.2820	493.2769	QPGPLP	562.3348	590.3297
QPGPLPG	619.3562	647.3511	PG	127.0866	155.0815	PGP	224.1394	252.1343
PGPL	337.2234	365.2183	PGPLP	434.2762	462.2711	PGPLPG	491.2976	519.2926

PGPLPGI	604.3817	632.3766	**GP**	127.0866	155.0815	**GPL**	240.1707	268.1656
GPLP	337.2234	365.2183	**GPLPG**	394.2449	422.2398	**GPLPGI**	507.3289	535.3239
GPLPGIN	621.3719	649.3668	**PL**	183.1492	211.1441	**PLP**	280.2020	308.1969
PLPG	337.2234	365.2183	**PLPGI**	450.3075	478.3024	**PLPGIN**	564.3504	592.3453
PLPGINT	665.3981	693.3930	**LP**	183.1492	211.1441	**LPG**	240.1707	268.1656
LPGI	353.2547	381.2496	**LPGIN**	467.2976	495.2926	**LPGINT**	568.3453	596.3402
PG	127.0866	155.0815	**PGI**	240.1707	268.1656	**PGIN**	354.2136	382.2085
PGINT	455.2613	483.2562	**GI**	143.1179	171.1128	**GIN**	257.1608	285.1557
GINT	358.2085	386.2034	**IN**	200.1394	228.1343	**INT**	301.1870	329.1819
NT	188.1030	216.0979						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.1	1502.8933	0.0025	ILRQPGPLPGINTK
55.1	1502.8933	0.0025	ILRQPGPLPGLNTK
15.9	1502.9548	-0.0590	LPSILLHTKQILK
15.1	1502.8245	0.0713	GPPLGWIPTPEIAR
13.4	1502.8167	0.0791	LIIDAMGNFSPVVK
13.4	1502.8167	0.0791	LLIDAMGNFSPVVK
13.3	1502.8820	0.0138	LLRQAFVESIVTK
13.1	1502.8708	0.0250	ILLPEVIPPDEIR
12.8	1502.7702	0.1256	RRPTPEPSSSHPR
11.4	1502.8430	0.0528	APGRAVLQVHGTAAR

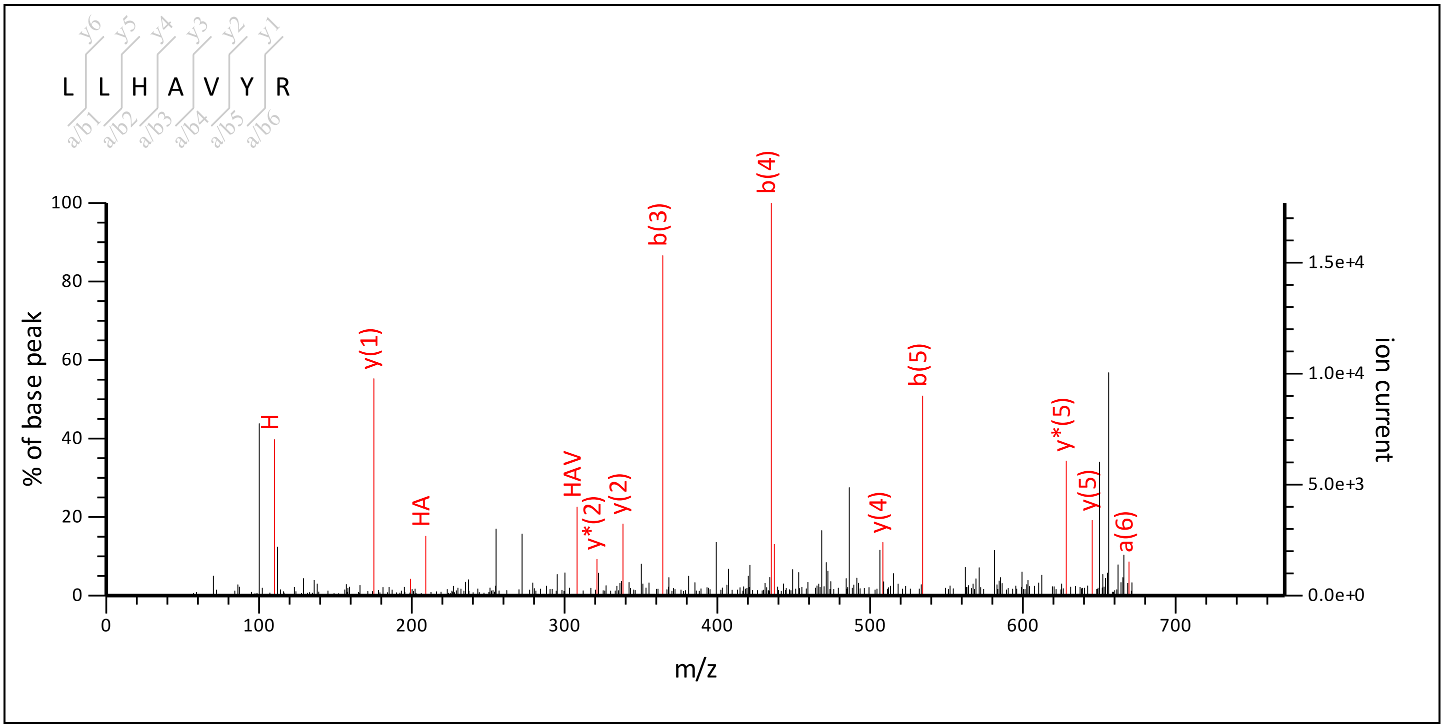
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 48

MS/MS Fragmentation of **LLHAVYR**
Found in **gi|115475151** in **NCBInr**, Os08g0191700 [Oryza sativa Japonica Group]

Match to Query 3: 870.583724 from(871.591000,1+) intensity(0.0000) index(0)
Title: Label: E19, Spot_Id: 219966, Peak_List_Id: 229275, MSMS Job_Run_Id: 22016, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E19_136868347200.txt



0 to 771.37

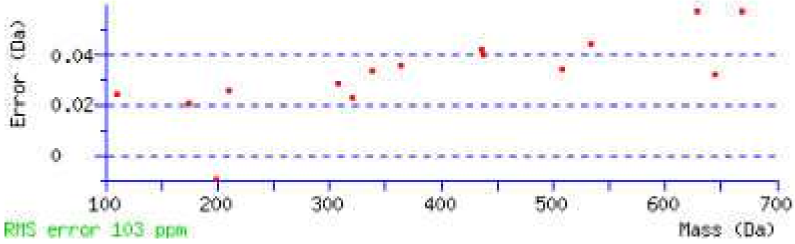
Label all possible matches ○ Label matches used for scoring ●

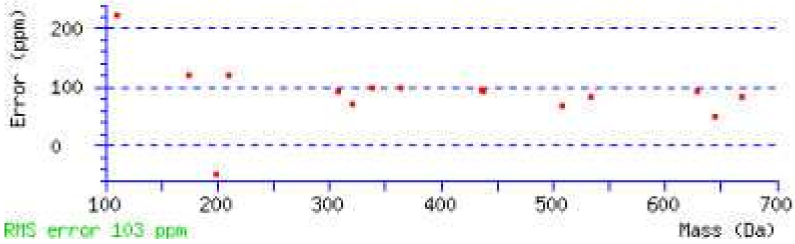
Monoisotopic mass of neutral peptide Mr(calc): 870.5076
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 29
Matches : 15/63 fragment ions using 28 most intense peaks (help)

#	Immon.	a	b	d	Seq.	v	w	y	y*	#
1	86.0964	86.0964	114.0913	44.0495	L					7
2	86.0964	**199.1805**	227.1754	157.1335	L	700.3525	699.3573	758.4308	741.4042	6
3	110.0713	336.2394	**364.2343**		H	563.2936		***645.3467***	628.3202	5
4	44.0495	407.2765	**435.2714**		A	492.2565		***508.2878***	491.2613	4
5	72.0808	506.3449	**534.3398**	492.3293	V	393.1881	406.2085	***437.2507***	420.2241	3
6	136.0757	**669.4083**	697.4032		Y	230.1248		***338.1823***	321.1557	2
7	129.1135				R	74.0237	73.0284	***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

LH	223.1553	251.1503	**LHA**	294.1925	322.1874	**LHAV**	393.2609	421.2558
LHAVY	556.3242	584.3191	**HA**	181.1084	209.1033	**HAV**	280.1768	308.1717
HAVY	443.2401	471.2350	**AV**	143.1179	171.1128	**AVY**	306.1812	334.1761
VY	235.1441	263.1390						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	870.5076	0.0762	ILHAVYR
30.6	870.5076	0.0762	LLHAVYR
27.0	870.5076	0.0762	HVLLAYR
22.9	870.5076	0.0762	LLHVAYR
22.8	870.5076	0.0762	VHLIAYR
22.7	870.5076	0.0762	VHIAIYR
22.6	870.5076	0.0762	VHAILYR
22.6	870.5076	0.0762	VHALLYR
22.4	870.5076	0.0761	VVHVVYR
21.8	870.5076	0.0762	VHLLAYR

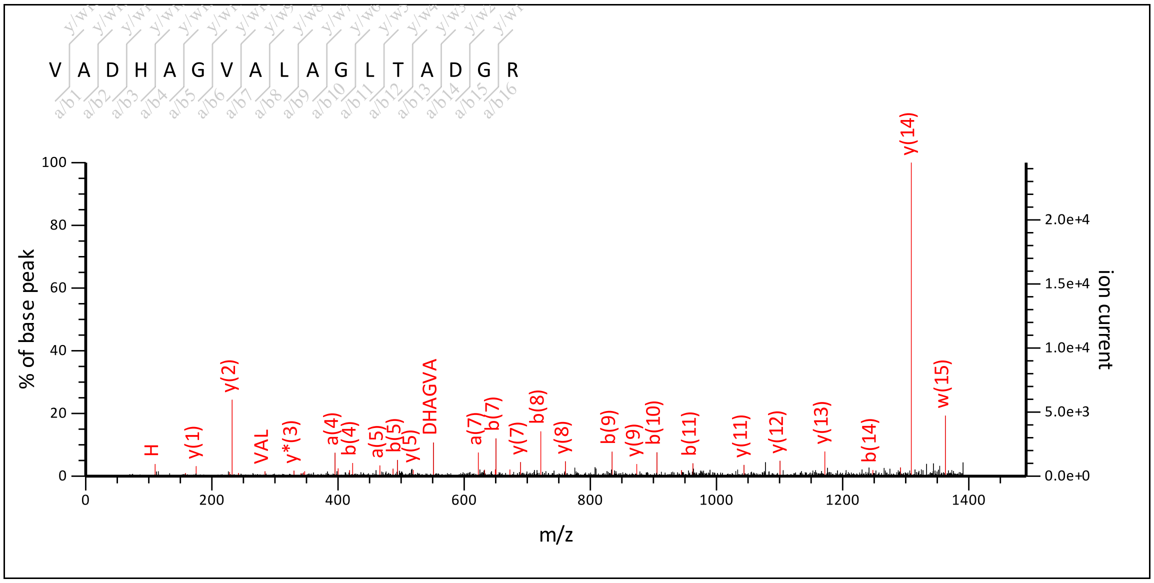
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 48

MS/MS Fragmentation of **VADHAGVALAGLTADGR**
Found in **gi|115444057** in **NCBInr**, Os02g0133800 [Oryza sativa Japonica Group]

Match to Query 159: 1592.901024 from(1593.908300,1+) intensity(0.0000) index(26)
Title: Label: E19, Spot_Id: 219966, Peak_List_Id: 229271, MSMS Job_Run_Id: 22016, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E19_136868347200.txt



0 to 1490.9

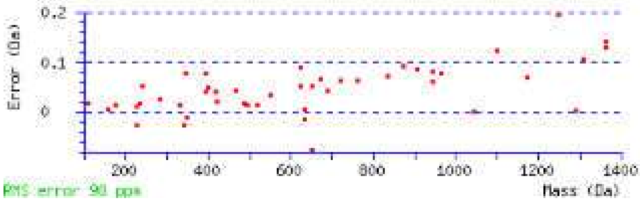
Label all possible matches ○ Label matches used for scoring ●

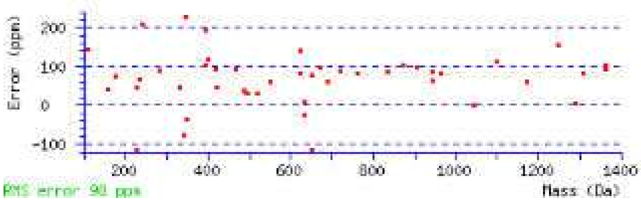
Monoisotopic mass of neutral peptide Mr(calc): 1592.8271
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 0.00021
Matches : 50/301 fragment ions using 84 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495		V							17
2	44.0495	143.1179		171.1128				A	1478.7346			1494.7659	1477.7394	1476.7554	16
3	88.0393	258.1448	240.1343	286.1397	268.1292	214.1550		D	1363.7077	1362.7124		1423.7288	1406.7023	1405.7183	15
4	110.0713	**395.2037**	377.1932	**423.1987**	405.1881			H	1226.6488			***1308.7019***	1291.6753	1290.6913	14
5	44.0495	**466.2409**	448.2303	**494.2358**	476.2252			A	1155.6117			***1171.6430***	1154.6164	1153.6324	13
6	30.0338	523.2623	505.2518	**551.2572**	533.2467			G				***1100.6059***	1083.5793	1082.5953	12
7	72.0808	**622.3307**	604.3202	**650.3257**	632.3151	608.3151		V	999.5218	1012.5422		***1043.5844***	1026.5578	1025.5738	11
8	44.0495	693.3678	675.3573	**721.3628**	703.3522			A	928.4847			***944.5160***	927.4894	926.5054	10
9	86.0964	806.4519	788.4413	**834.4468**	816.4363	764.4050		L	815.4006	814.4054		***873.4789***	856.4523	855.4683	9
10	44.0495	877.4890	859.4785	**905.4839**	887.4734			A	744.3635			***760.3948***	743.3682	742.3842	8
11	30.0338	934.5105	916.4999	**962.5054**	944.4948			G				***689.3577***	672.3311	671.3471	7
12	86.0964	1047.5946	1029.5840	1075.5895	1057.5789	1005.5476		L	574.2580	573.2627		***632.3362***	615.3097	614.3257	6
13	74.0600	1148.6422	1130.6317	1176.6372	1158.6266	1132.6473	1134.6266	T	473.2103	486.2307	488.2100	***519.2522***	502.2256	501.2416	5
14	44.0495	1219.6793	1201.6688	**1247.6743**	1229.6637			A	402.1732			***418.2045***	401.1779	400.1939	4
15	88.0393	1334.7063	1316.6957	**1362.7012**	1344.6906	1290.7165		D	287.1462	286.1510		***347.1674***	330.1408	329.1568	3
16	30.0338	1391.7278	1373.7172	1419.7227	1401.7121			G				***232.1404***	215.1139		2
17	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

AD	159.0764	187.0713	**ADH**	296.1353	324.1302	**ADHA**	367.1724	395.1674
ADHAG	424.1939	452.1888	**ADHAGV**	523.2623	551.2572	**ADHAGVA**	594.2994	622.2944
DH	225.0982	253.0931	**DHA**	296.1353	324.1302	**DHAG**	353.1568	381.1517
DHAGV	452.2252	480.2201	**DHAGVA**	523.2623	551.2572	**DHAGVAL**	636.3464	664.3413
HA	181.1084	209.1033	**HAG**	238.1299	266.1248	**HAGV**	337.1983	365.1932
HAGVA	408.2354	436.2303	**HAGVAL**	521.3194	549.3144	**HAGVALA**	592.3566	620.3515
HAGVALAG	649.3780	677.3729	**AG**	101.0709	129.0659	**AGV**	200.1394	228.1343
AGVA	271.1765	299.1714	**AGVAL**	384.2605	412.2554	**AGVALA**	455.2976	483.2926
AGVALAG	512.3191	540.3140	**AGVALAGL**	625.4032	653.3981	**GV**	129.1022	157.0972
GVA	200.1394	228.1343	**GVAL**	313.2234	341.2183	**GVALA**	384.2605	412.2554
GVALAG	441.2820	469.2769	**GVALAGL**	554.3661	582.3610	**GVALAGLT**	655.4137	683.4087
VA	143.1179	171.1128	**VAL**	256.2020	284.1969	**VALA**	327.2391	355.2340
VALAG	384.2605	412.2554	**VALAGL**	497.3446	525.3395	**VALAGLT**	598.3923	626.3872
VALAGLTA	669.4294	697.4243	**AL**	157.1335	185.1285	**ALA**	228.1707	256.1656
ALAG	285.1921	313.1870	**ALAGL**	398.2762	426.2711	**ALAGLT**	499.3239	527.3188
ALAGLTA	570.3610	598.3559	**ALAGLTAD**	685.3879	713.3828	**LA**	157.1335	185.1285
LAG	214.1550	242.1499	**LAGL**	327.2391	355.2340	**LAGLT**	428.2867	456.2817
LAGLTA	499.3239	527.3188	**LAGLTAD**	614.3508	642.3457	**LAGLTADG**	671.3723	699.3672
AG	101.0709	129.0659	**AGL**	214.1550	242.1499	**AGLT**	315.2027	343.1976
AGLTA	386.2398	414.2347	**AGLTAD**	501.2667	529.2617	**AGLTADG**	558.2882	586.2831
GL	143.1179	171.1128	**GLT**	244.1656	272.1605	**GLTA**	315.2027	343.1976
GLTAD	430.2296	458.2245	**GLTADG**	487.2511	515.2460	**LT**	187.1441	215.1390
LTA	258.1812	286.1761	**LTAD**	373.2082	401.2031	**LTADG**	430.2296	458.2245
TA	145.0972	173.0921	**TAD**	260.1241	288.1190	**TADG**	317.1456	345.1405
AD	159.0764	187.0713	**ADG**	216.0979	244.0928	**DG**	145.0608	173.0557





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
83.9	1592.8271	0.0740	VADHAGVALAGLTADGR
33.4	1592.8131	0.0879	ARHEGIGIEQRDGR
27.3	1592.7794	0.1216	GYDSAGVATVAAGELGR
26.5	1592.8046	0.0964	GYDSAGVALLDGNTLK
25.9	1592.8423	0.0587	FAFGAGVTAIVGRDGR
25.8	1592.9038	-0.0028	GFKFAGIIAGDKNKK
24.0	1592.8383	0.0628	REHQAALVKQEER
24.0	1592.8385	0.0626	ACVYGVAAILWATAK
23.8	1592.8674	0.0336	AFLTGAAGALAAAAYVR
22.9	1592.8133	0.0877	MKFALNIVDWQGR

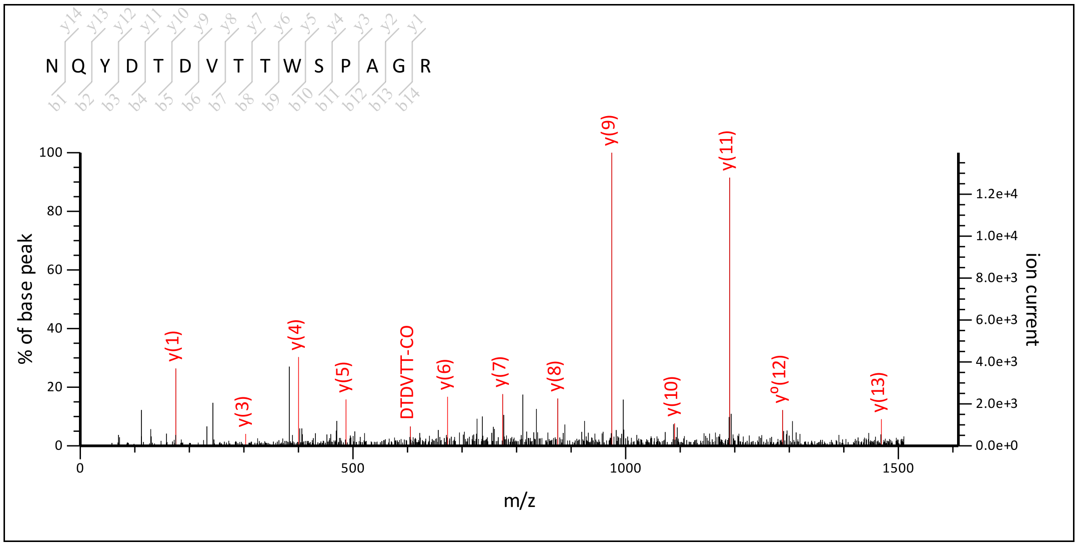
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 48

MS/MS Fragmentation of **NQYDTDVTTWSPAGR**
Found in **gi|115444057** in **NCBInr**, Os02g0133800 [Oryza sativa Japonica Group]

Match to Query 172: 1709.843224 from(1710.850500,1+) intensity(0.0000) index(30)
Title: Label: E19, Spot_Id: 219966, Peak_List_Id: 229270, MSMS Job_Run_Id: 22016, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E19_136868347200.txt



0 to 1610.06

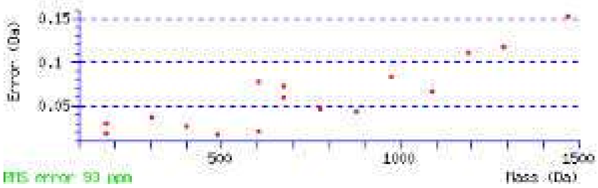
Label all possible matches ○ Label matches used for scoring ●

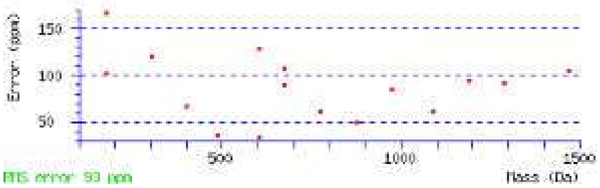
Monoisotopic mass of neutral peptide Mr(calc): 1709.7645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 7.6e-07
Matches : 16/269 fragment ions using 15 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495		N					
2	101.0709	215.1139	198.0873		243.1088	226.0822		158.0924		Q	1523.6761	1522.6809		1596.7289	1579.7023
3	136.0757	378.1772	361.1506		406.1721	389.1456				Y	1360.6128			***1468.6703***	1451.6438
4	88.0393	493.2041	476.1776	475.1936	521.1991	504.1725	503.1885	449.2143		D	1245.5858	1244.5906		1305.6070	1288.5804
5	74.0600	594.2518	577.2253	576.2413	622.2467	605.2202	604.2362	578.2569	580.2362	T	1144.5382	1157.5586	1159.5378	***1190.5800***	1173.5535
6	88.0393	709.2788	692.2522	691.2682	737.2737	720.2471	719.2631	665.2889		D	1029.5112	1028.5160		***1089.5323***	1072.5058
7	72.0808	808.3472	791.3206	790.3366	836.3421	819.3155	818.3315	794.3315		V	930.4428	943.4632		***974.5054***	957.4789
8	74.0600	909.3949	892.3683	891.3843	937.3898	920.3632	919.3792	893.3999	895.3792	T	829.3951	842.4155	844.3948	***875.4370***	858.4104
9	74.0600	1010.4425	993.4160	992.4320	1038.4374	1021.4109	1020.4269	994.4476	996.4269	T	728.3474	741.3678	743.3471	***774.3893***	757.3628
10	159.0917	1196.5218	1179.4953	1178.5113	1224.5168	1207.4902	1206.5062			W	542.2681			***673.3416***	656.3151
11	60.0444	1283.5539	1266.5273	1265.5433	1311.5488	1294.5222	1293.5382	1267.5590		S	455.2361	454.2409		***487.2623***	470.2358
12	70.0651	1380.6066	1363.5801	1362.5961	1408.6016	1391.5750	1390.5910	1354.5910		P	358.1833	357.1881		***400.2303***	383.2037
13	44.0495	1451.6438	1434.6172	1433.6332	1479.6387	1462.6121	1461.6281			A	287.1462			***303.1775***	286.1510
14	30.0338	1508.6652	1491.6387	1490.6546	1536.6601	1519.6336	1518.6496			G				232.1404	215.1139
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QY	264.1343	292.1292	QYD	379.1612	407.1561	QYDT	480.2089	508.2038
QYDTD	595.2358	623.2307	QYDTDV	694.3042	722.2992	YD	251.1026	279.0975
YDT	352.1503	380.1452	YDTD	467.1773	495.1722	YDTDV	566.2457	594.2406
YDTDVT	667.2933	695.2883	DT	189.0870	217.0819	DTD	304.1139	332.1088
DTDV	403.1823	431.1773	DTDVT	504.2300	532.2249	DTDVTT	605.2777	633.2726
TD	189.0870	217.0819	TDV	288.1554	316.1503	TDVT	389.2031	417.1980

TDVTT	490.2508	518.2457	**TDVTTW**	676.3301	704.3250	**DV**	187.1077	215.1026
DVT	288.1554	316.1503	**DVTT**	389.2031	417.1980	**DVTTW**	575.2824	603.2773
DVTTWS	662.3144	690.3093	**VT**	173.1285	201.1234	**VTT**	274.1761	302.1710
VTTW	460.2554	488.2504	**VTTWS**	547.2875	575.2824	**VTTWSP**	644.3402	672.3352
TT	175.1077	203.1026	**TTW**	361.1870	389.1819	**TTWS**	448.2191	476.2140
TTWSP	545.2718	573.2667	**TTWSPA**	616.3089	644.3039	**TTWSPAG**	673.3304	701.3253
TW	260.1394	288.1343	**TWS**	347.1714	375.1663	**TWSP**	444.2241	472.2191
TWSPA	515.2613	543.2562	**TWSPAG**	572.2827	600.2776	**WS**	246.1237	274.1186
WSP	343.1765	371.1714	**WSPA**	414.2136	442.2085	**WSPAG**	471.2350	499.2300
SP	157.0972	185.0921	**SPA**	228.1343	256.1292	**SPAG**	285.1557	313.1506
PA	141.1022	169.0972	**PAG**	198.1237	226.1186	**AG**	101.0709	129.0659





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
108.4	1709.7645	0.0787	NQYDTDVTTWSPAGR
36.2	1709.8883	-0.0450	HKDKLDMVQESPKR
34.9	1709.8809	-0.0377	IHNGVTDVTRNETVR
25.2	1709.8948	-0.0516	KPVVPSEEEIEGNKR
22.1	1709.7719	0.0713	EFMPTFPALNEQDR
22.0	1709.8948	-0.0516	LNVPSEPVTVIGDTNR
21.7	1709.8559	-0.0127	KATVSIGSMVDWFNR
21.7	1709.9536	-0.1104	LAKNLQPARATASVDR
21.6	1709.8566	-0.0134	HKMGAPMNRGKSPGAR
21.4	1709.8696	-0.0264	LEPLAGRAEAAEAEQR

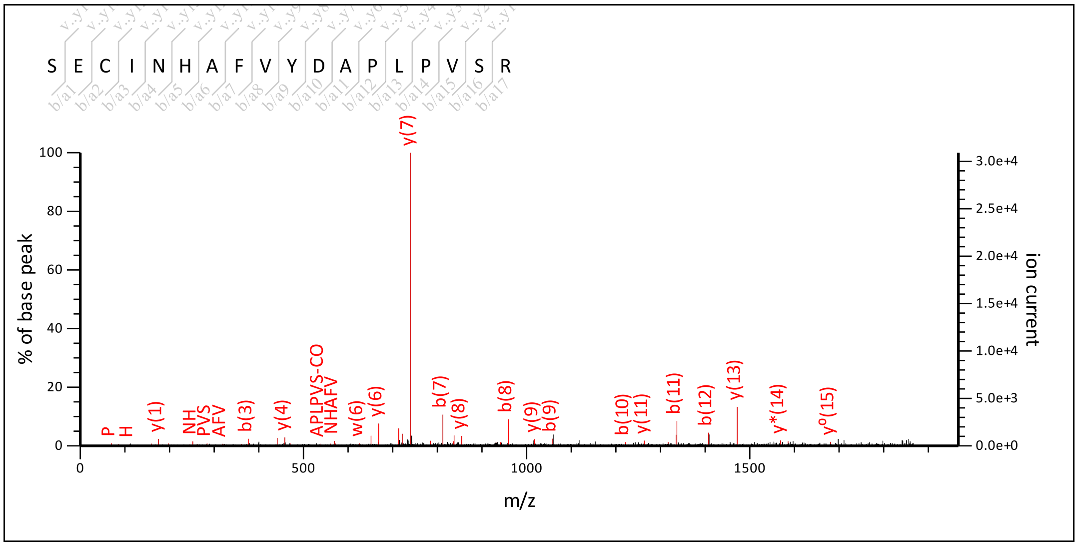
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 48

MS/MS Fragmentation of **SECINHAFVYDAPLPVSR**
Found in **gi|115444057** in **NCBInr**, Os02g0133800 [Oryza sativa Japonica Group]

Match to Query 186: 2074.099124 from(2075.106400,1+) intensity(0.0000) index(32)
Title: Label: E19, Spot_Id: 219966, Peak_List_Id: 229273, MSMS Job_Run_Id: 22016, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E19_136868347200.txt



0 to 1967.39

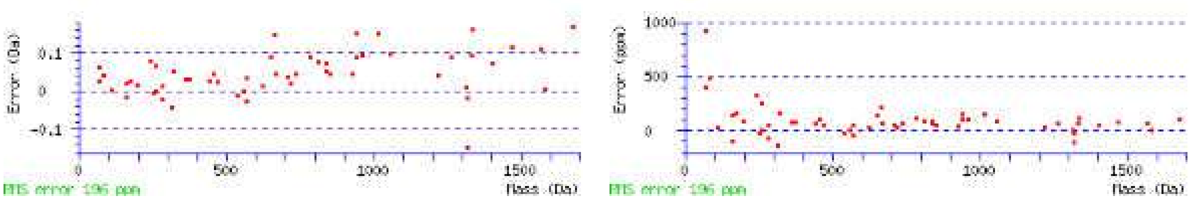
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2073.9942
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 0.0022
Matches : 57/330 fragment ions using 90 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	102.0550	189.0870		171.0764	217.0819		199.0713	131.0815		E	1913.9327	1912.9374		1987.9695	1970.9429
3	133.0430	349.1176		331.1071	**377.1125**		359.1020	260.1241		C	1753.9020	1752.9068		1858.9269	1841.9003
4	86.0964	462.2017		444.1911	490.1966		472.1860	434.1704	448.1860	I	1640.8180	1653.8384	1667.8540	1698.8962	1681.8697
5	87.0553	576.2446	559.2181	558.2341	604.2395	587.2130	586.2290	533.2388		N	1526.7750	1525.7798		***1585.8122***	1568.7856
6	110.0713	**713.3035**	696.2770	695.2930	741.2984	724.2719	723.2879			H	1389.7161			***1471.7692***	1454.7427
7	44.0495	**784.3406**	767.3141	766.3301	**812.3356**	795.3090	794.3250			A	1318.6790			***1334.7103***	1317.6838
8	120.0808	**931.4091**	914.3825	913.3985	**959.4040**	942.3774	941.3934			F	1171.6106			***1263.6732***	1246.6467
9	72.0808	1030.4775	1013.4509	1012.4669	**1058.4724**	1041.4458	1040.4618	1016.4618		V	1072.5422	1085.5626		1116.6048	1099.5782
10	136.0757	1193.5408	1176.5143	1175.5302	**1221.5357**	1204.5092	1203.5252			Y	909.4789			***1017.5364***	1000.5098
11	88.0393	1308.5677	1291.5412	1290.5572	**1336.5627**	1319.5361	1318.5521	1264.5779		D	794.4519	793.4567		***854.4730***	837.4465
12	44.0495	1379.6049	1362.5783	1361.5943	**1407.5998**	1390.5732	1389.5892			A	723.4148			***739.4461***	722.4196
13	70.0651	1476.6576	1459.6311	1458.6471	1504.6525	1487.6260	1486.6420	1450.6420		P	626.3620	625.3668		***668.4090***	651.3824
14	86.0964	1589.7417	1572.7151	1571.7311	1617.7366	1600.7101	1599.7260	1547.6947		L	513.2780	512.2827		***571.3562***	554.3297
15	70.0651	1686.7945	1669.7679	1668.7839	1714.7894	1697.7628	1696.7788	1660.7788		P	416.2252	415.2300		***458.2722***	441.2456
16	72.0808	1785.8629	1768.8363	1767.8523	1813.8578	1796.8312	1795.8472	1771.8472		V	317.1568	330.1772		***361.2194***	344.1928
17	60.0444	1872.8949	1855.8683	1854.8843	1900.8898	1883.8633	1882.8792	1856.9000		S	230.1248	229.1295		***262.1510***	245.1244
18	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
EC	262.0856	290.0805	ECI	375.1697	403.1646	ECIN	489.2126	517.2075
ECINH	626.2715	654.2664	ECINHA	697.3086	725.3035	CI	246.1271	274.1220
CIN	360.1700	388.1649	CINH	497.2289	525.2238	CINHA	568.2660	596.2609

IN	200.1394	228.1343	**INH**	337.1983	365.1932	**INHA**	408.2354	436.2303
INHAF	555.3038	583.2987	**INHAFV**	654.3722	682.3671	**NH**	224.1142	252.1091
NHA	295.1513	323.1462	**NHAF**	442.2197	470.2146	**NHAFV**	541.2881	569.2831
HA	181.1084	209.1033	**HAF**	328.1768	356.1717	**HAFV**	427.2452	455.2401
HAFVY	590.3085	618.3035	**AF**	191.1179	219.1128	**AFV**	290.1863	318.1812
AFVY	453.2496	481.2445	**AFVYD**	568.2766	596.2715	**AFVYDA**	639.3137	667.3086
FV	219.1492	247.1441	**FVY**	382.2125	410.2074	**FVYD**	497.2395	525.2344
FVYDA	568.2766	596.2715	**FVYDAP**	665.3293	693.3243	**VY**	235.1441	263.1390
VYD	350.1710	378.1660	**VYDA**	421.2082	449.2031	**VYDAP**	518.2609	546.2558
VYDAPL	631.3450	659.3399	**YD**	251.1026	279.0975	**YDA**	322.1397	350.1347
YDAP	419.1925	447.1874	**YDAPL**	532.2766	560.2715	**YDAPLP**	629.3293	657.3243
DA	159.0764	187.0713	**DAP**	256.1292	284.1241	**DAPL**	369.2132	397.2082
DAPLP	466.2660	494.2609	**DAPLPV**	565.3344	593.3293	**DAPLPVS**	652.3665	680.3614
AP	141.1022	169.0972	**APL**	254.1863	282.1812	**APLP**	351.2391	379.2340
APLPV	450.3075	478.3024	**APLPVS**	537.3395	565.3344	**PL**	183.1492	211.1441
PLP	280.2020	308.1969	**PLPV**	379.2704	407.2653	**PLPVS**	466.3024	494.2973
LP	183.1492	211.1441	**LPV**	282.2176	310.2125	**LPVS**	369.2496	397.2445
PV	169.1335	197.1285	**PVS**	256.1656	284.1605	**VS**	159.1128	187.1077



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.3	2073.9942	0.1049	SECINHAFVYDAPLPVSR
28.2	2074.1106	-0.0114	METTYGLVLRRAGVSIHR
20.0	2074.1833	-0.0842	KVGGGRIAAHEIMIGIPAIR
20.0	2074.1833	-0.0842	KVGGGRIAAHEIMLGIPAIR
17.5	2074.1833	-0.0842	KIGGGRVAAHEIMIAVPAIR
17.5	2074.1833	-0.0842	KIGGGRVAAHEIMLAVPAIR
16.7	2074.1826	-0.0835	LSIVAALAPVEKAEFVYVR
15.7	2074.1946	-0.0954	MGHDKVADKLAPLLRRVR
15.3	2074.1833	-0.0842	KGIRVNALCPGPVNTPLLR
15.3	2074.1535	-0.0543	ENLLRLVNPTLSGPEIPGR

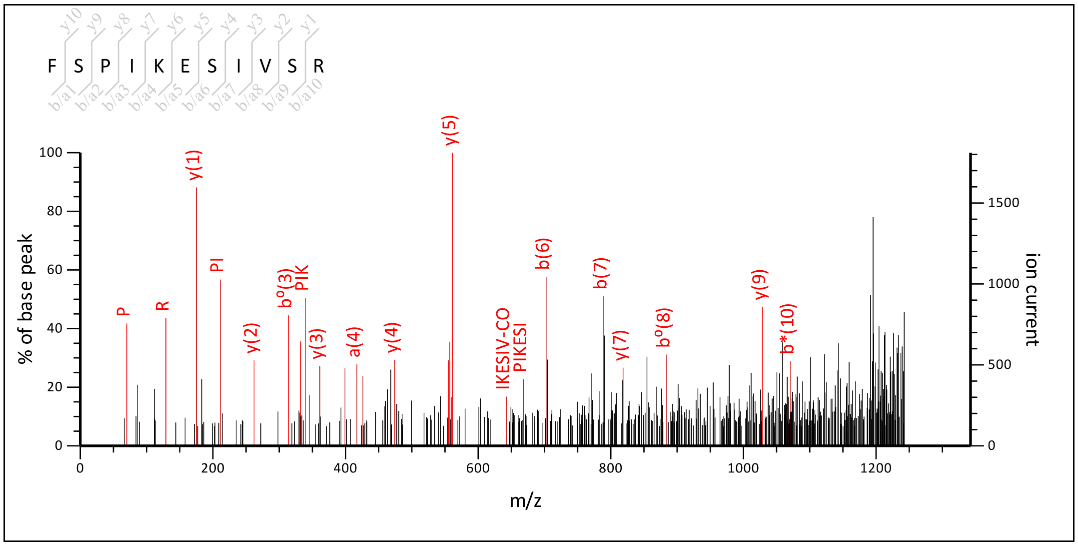
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 49

MS/MS Fragmentation of **FSPIKESIVSR**
Found in **gi|27261025** in **NCBInr**, putative thiamine biosynthesis protein [Oryza sativa Japonica Group]

Match to Query 25: 1261.788524 from(1262.795800,1+) intensity(0.0000) index(11)
Title: Label: H9, Spot_Id: 228977, Peak_List_Id: 257861, MSMS Job_Run_Id: 24940, Comment:
Data file ppw_H9_138985153400.txt



0 to 1342.47

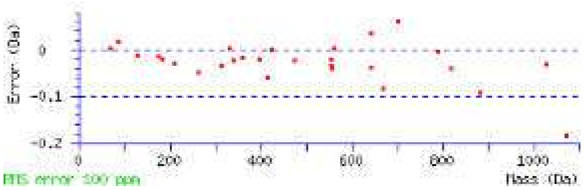
Label all possible matches ○ Label matches used for scoring ●

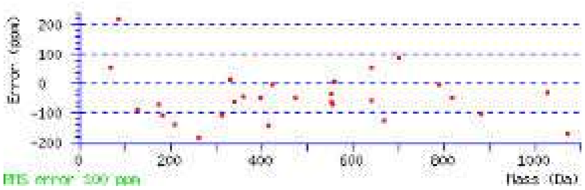
Monoisotopic mass of neutral peptide Mr(calc): 1261.7030
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.52
Matches : 30/184 fragment ions using 48 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	120.0808	120.0808			148.0757			44.0495		F						
2	60.0444	207.1128		189.1022	235.1077		217.0972	191.1179		S	1083.6157	1082.6204		1115.6419	1098.6153	109
3	70.0651	304.1656		286.1550	**332.1605**		314.1499	278.1499		P	986.5629	985.5677		***1028.6099***	1011.5833	101
4	86.0964	417.2496		399.2391	445.2445		427.2340	389.2183	403.2340	I	873.4789	886.4993	900.5149	931.5571	914.5306	91
5	101.1073	545.3446	528.3180	527.3340	573.3395	556.3130	555.3289	488.2867		K	745.3839	744.3886		***818.4730***	801.4465	80
6	102.0550	674.3872	657.3606	656.3766	**702.3821**	685.3556	684.3715	616.3817		E	616.3413	615.3461		690.3781	673.3515	67
7	60.0444	761.4192	744.3927	743.4086	**789.4141**	772.3876	771.4036	745.4243		S	529.3093	528.3140		***561.3355***	544.3089	54
8	86.0964	874.5033	857.4767	856.4927	902.4982	885.4716	884.4876	846.4720	860.4876	I	416.2252	429.2456	443.2613	***474.3035***	457.2769	45
9	72.0808	973.5717	956.5451	955.5611	1001.5666	984.5401	983.5560	959.5560		V	317.1568	330.1772		***361.2194***	344.1928	34
10	60.0444	1060.6037	1043.5772	1042.5932	1088.5986	1071.5721	1070.5881	1044.6088		S	230.1248	229.1295		***262.1510***	245.1244	24
11	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SP	157.0972	185.0921	SPI	270.1812	298.1761	SPIK	398.2762	426.2711
SPIKE	527.3188	555.3137	SPIKES	614.3508	642.3457	PI	183.1492	211.1441
PIK	311.2442	339.2391	PIKE	440.2867	468.2817	PIKES	527.3188	555.3137
PIKESI	640.4028	668.3978	IK	214.1914	242.1863	IKE	343.2340	371.2289
IKES	430.2660	458.2609	IKESI	543.3501	571.3450	IKESIV	642.4185	670.4134
KE	230.1499	258.1448	KES	317.1819	345.1769	KESI	430.2660	458.2609
KESIV	529.3344	557.3293	KESIVS	616.3665	644.3614	ES	189.0870	217.0819
ESI	302.1710	330.1660	ESIV	401.2395	429.2344	ESIVS	488.2715	516.2664
SI	173.1285	201.1234	SIV	272.1969	300.1918	SIVS	359.2289	387.2238

IV	185.1648	213.1598	**IVS**	272.1969	300.1918	**VS**	159.1128	187.1077





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.1	1261.7030	0.0855	FSPIKESIVSR
14.9	1261.6666	0.1219	ALAFASIPETSR
10.1	1261.7030	0.0855	IYNPTLSLVSR
8.7	1261.6779	0.1107	GRLFVESLEGR
8.6	1261.6813	0.1073	MSVIVRTEVGR
8.3	1261.6853	0.1033	YRPGSPMLLTK
8.2	1261.7030	0.0855	AKELFLSLEGR
8.2	1261.6626	0.1259	QNSGSSVTITLR
8.0	1261.6666	0.1219	AFSSSPIVGEIR
7.7	1261.6779	0.1107	AALHDLPQLER

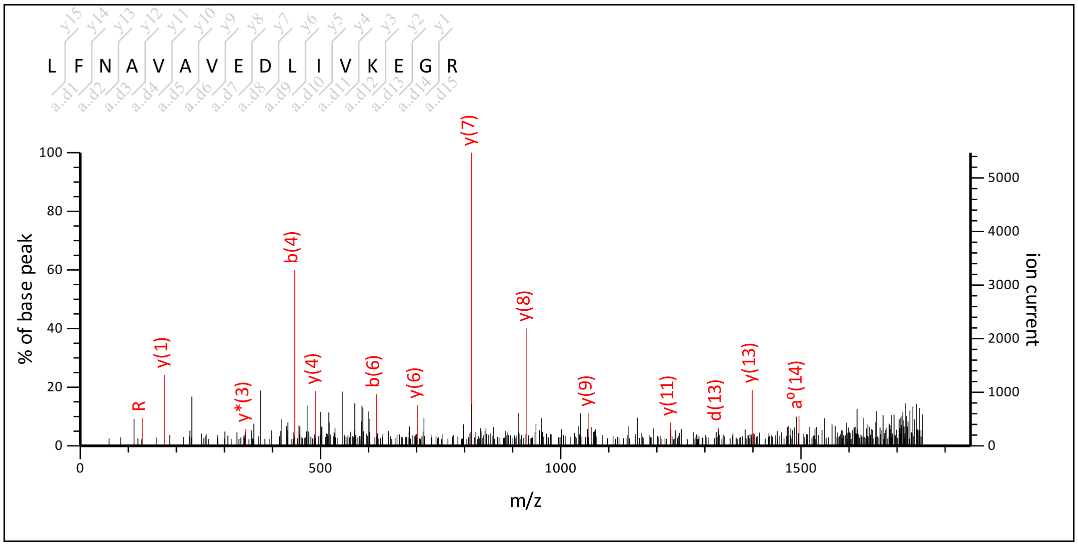
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 49

MS/MS Fragmentation of **LFNAVAVEDLIVKEGR**
Found in **gi|27261025** in **NCBInr**, putative thiamine biosynthesis protein [Oryza sativa Japonica Group]

Match to Query 28: 1772.097624 from(1773.104900,1+) intensity(0.0000) index(12)
Title: Label: H9, Spot_Id: 228977, Peak_List_Id: 257859, MSMS Job_Run_Id: 24940, Comment:
Data file ppw_H9_138985153400.txt



0 to 1852.94

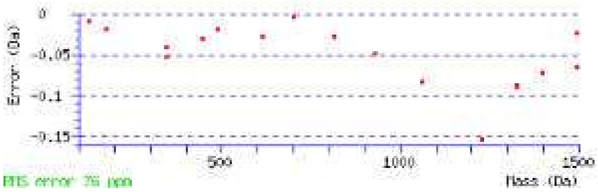
Label all possible matches ○ Label matches used for scoring ●

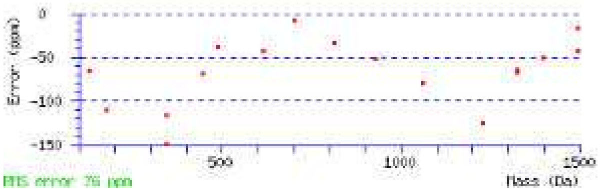
Monoisotopic mass of neutral peptide Mr(calc): 1771.9832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77 **Expect:** 1.5e-05
Matches : 17/283 fragment ions using 17 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	86.0964			114.0913			44.0495		L						
2	120.0808	233.1648			261.1598					F	1567.8438			1659.9064	1642.8799	164
3	87.0553	347.2078	330.1812		375.2027	358.1761		304.2020		N	1453.8009	1452.8057		1512.8380	1495.8115	149
4	44.0495	418.2449	401.2183		**446.2398**	429.2132				A	1382.7638			***1398.7951***	1381.7686	138
5	72.0808	517.3133	500.2867		545.3082	528.2817		503.2976		V	1283.6954	1296.7158		***1327.7580***	1310.7314	13
6	44.0495	588.3504	571.3239		**616.3453**	599.3188				A	1212.6583			***1228.6896***	1211.6630	12
7	72.0808	687.4188	670.3923		715.4137	698.3872		673.4032		V	1113.5899	1126.6103		1157.6525	1140.6259	11
8	102.0550	816.4614	799.4349	798.4508	844.4563	827.4298	826.4458	758.4559		E	984.5473	983.5520		***1058.5840***	1041.5575	10
9	88.0393	931.4884	914.4618	913.4778	959.4833	942.4567	941.4727	887.4985		D	869.5203	868.5251		***929.5415***	912.5149	9
10	86.0964	1044.5724	1027.5459	1026.5619	1072.5673	1055.5408	1054.5568	1002.5255		L	756.4363	755.4410		***814.5145***	797.4880	7
11	86.0964	1157.6565	1140.6299	1139.6459	1185.6514	1168.6249	1167.6408	1129.6252	1143.6408	I	643.3522	656.3726	670.3883	***701.4304***	684.4039	6
12	72.0808	1256.7249	1239.6984	1238.7143	1284.7198	1267.6933	1266.7092	1242.7092		V	544.2838	557.3042		588.3464	571.3198	5
13	101.1073	1384.8199	1367.7933	1366.8093	1412.8148	1395.7882	1394.8042	1327.7620		K	416.1888	415.1936		***489.2780***	472.2514	4
14	102.0550	1513.8625	1496.8359	1495.8519	1541.8574	1524.8308	1523.8468	1455.8570		E	287.1462	286.1510		361.1830	344.1565	3
15	30.0338	1570.8839	1553.8574	1552.8734	1598.8788	1581.8523	1580.8683			G				232.1404	215.1139	
16	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FN	234.1237	262.1186	FNA	305.1608	333.1557	FNAV	404.2292	432.2241
FNAVA	475.2663	503.2613	FNAVAV	574.3348	602.3297	NA	158.0924	186.0873
NAV	257.1608	285.1557	NAVA	328.1979	356.1928	NAVAV	427.2663	455.2613
NAVAVE	556.3089	584.3039	NAVAVED	671.3359	699.3308	AV	143.1179	171.1128

AVA	214.1550	242.1499	**AVAV**	313.2234	341.2183	**AVAVE**	442.2660	470.2609
AVAVED	557.2930	585.2879	**AVAVEDL**	670.3770	698.3719	**VA**	143.1179	171.1128
VAV	242.1863	270.1812	**VAVE**	371.2289	399.2238	**VAVED**	486.2558	514.2508
VAVEDL	599.3399	627.3348	**AV**	143.1179	171.1128	**AVE**	272.1605	300.1554
AVED	387.1874	415.1823	**AVEDL**	500.2715	528.2664	**AVEDLI**	613.3556	641.3505
VE	201.1234	229.1183	**VED**	316.1503	344.1452	**VEDL**	429.2344	457.2293
VEDLI	542.3184	570.3134	**VEDLIV**	641.3869	669.3818	**ED**	217.0819	245.0768
EDL	330.1660	358.1609	**EDLI**	443.2500	471.2449	**EDLIV**	542.3184	570.3134
EDLIVK	670.4134	698.4083	**DL**	201.1234	229.1183	**DLI**	314.2074	342.2023
DLIV	413.2758	441.2708	**DLIVK**	541.3708	569.3657	**DLIVKE**	670.4134	698.4083
LI	199.1805	227.1754	**LIV**	298.2489	326.2438	**LIVK**	426.3439	454.3388
LIVKE	555.3865	583.3814	**LIVKEG**	612.4079	640.4028	**IV**	185.1648	213.1598
IVK	313.2598	341.2547	**IVKE**	442.3024	470.2973	**IVKEG**	499.3239	527.3188
VK	200.1757	228.1707	**VKE**	329.2183	357.2132	**VKEG**	386.2398	414.2347
KE	230.1499	258.1448	**KEG**	287.1714	315.1663	**EG**	159.0764	187.0713





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.5	1771.9832	0.1144	LFNAVAVEDLIVKEGR
19.6	1771.9502	0.1474	RSAMLILGSDSPAVVEK
18.4	1771.9250	0.1726	EMNLRAELISQLEAR
16.4	1771.9581	0.1396	LFNAVAAEDLIIRGDR
16.0	1771.9325	0.1652	QVDEVLLVGGMTRMPK
15.9	1771.9291	0.1685	MARIGSPEEVVVGVWK
14.0	1771.9316	0.1660	DDSKVLLTSPTANGINK
12.7	1771.9693	0.1283	NIFIVRAINEGGNTVR
10.8	1771.9614	0.1362	SCIIADALITAIREAR
10.8	1772.0084	0.0892	LNKILFLDDDIVVQK

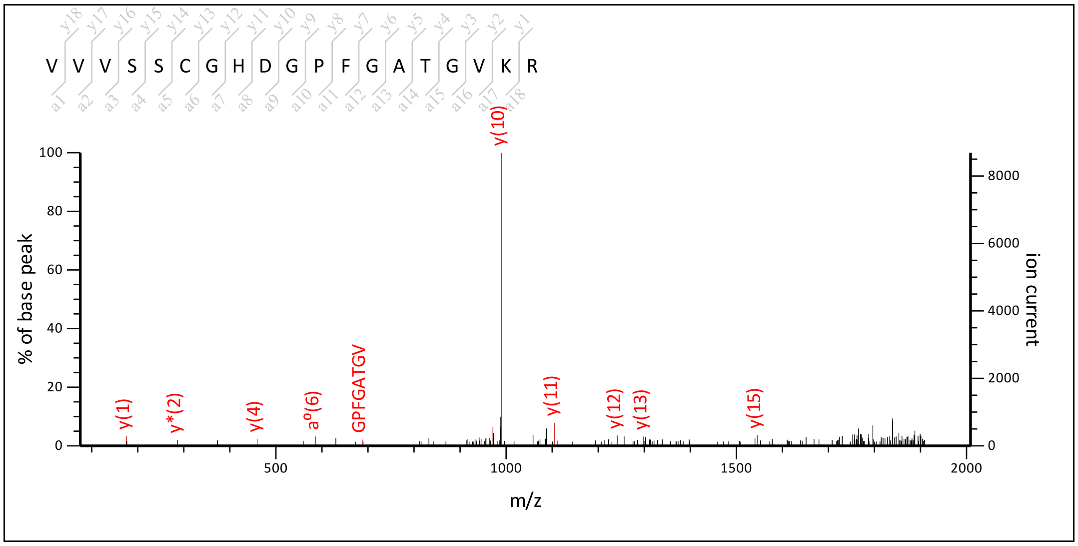
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 49

MS/MS Fragmentation of **VVVSSCGHDGPFGATGVKR**
Found in **gi|27261025** in **NCBInr**, putative thiamine biosynthesis protein [Oryza sativa Japonica Group]

Match to Query 32: 1929.079224 from(1930.086500,1+) intensity(0.0000) index(14)
Title: Label: H9, Spot_Id: 228977, Peak_List_Id: 257872, MSMS Job_Run_Id: 24940, Comment:
Data file ppw_H9_138985153400.txt



75.12 to 2008.65

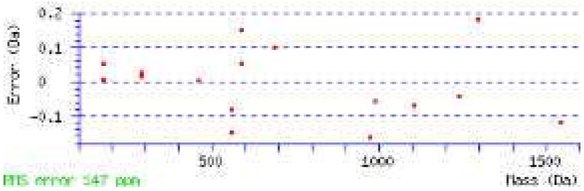
Label all possible matches ○ Label matches used for scoring ●

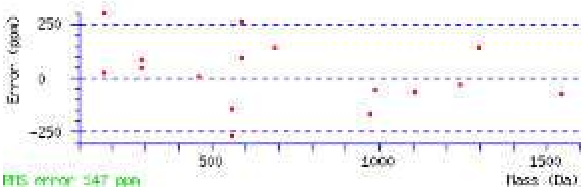
Monoisotopic mass of neutral peptide Mr(calc): 1928.9527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 0.0082
Matches : 16/333 fragment ions using 18 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	72.0808	171.1492			199.1441			157.1335		V	1786.8289	1799.8493		1830.8915	1813.8650
3	72.0808	270.2176			298.2125			256.2020		V	1687.7605	1700.7809		1731.8231	1714.7966
4	60.0444	357.2496		339.2391	385.2445		367.2340	341.2547		S	1600.7285	1599.7333		1632.7547	1615.7282
5	60.0444	444.2817		426.2711	472.2766		454.2660	428.2867		S	1513.6965	1512.7012		***1545.7227***	1528.6961
6	133.0430	604.3123		586.3017	632.3072		614.2967	515.3188		C	1353.6658	1352.6706		1458.6907	1441.6641
7	30.0338	661.3338		643.3232	689.3287		671.3181			G				***1298.6600***	1281.6335
8	110.0713	798.3927		780.3821	826.3876		808.3770			H	1159.5854			***1241.6385***	1224.6120
9	88.0393	913.4196		895.4091	941.4145		923.4040	869.4298		D	1044.5585	1043.5633		***1104.5796***	1087.5531
10	30.0338	970.4411		952.4305	998.4360		980.4254			G				***989.5527***	972.5261
11	70.0651	1067.4939		1049.4833	1095.4888		1077.4782	1041.4782		P	890.4843	889.4890		932.5312	915.5047
12	120.0808	1214.5623		1196.5517	1242.5572		1224.5466			F	743.4159			835.4785	818.4519
13	30.0338	1271.5837		1253.5732	1299.5786		1281.5681			G				688.4100	671.3835
14	44.0495	1342.6208		1324.6103	1370.6158		1352.6052			A	615.3573			631.3886	614.3620
15	74.0600	1443.6685		1425.6580	1471.6634		1453.6529	1427.6736	1429.6529	T	514.3096	527.3300	529.3093	***560.3515***	543.3249
16	30.0338	1500.6900		1482.6794	1528.6849		1510.6743			G				***459.3038***	442.2772
17	72.0808	1599.7584		1581.7478	1627.7533		1609.7428	1585.7428		V	358.2197	371.2401		402.2823	385.2558
18	101.1073	1727.8534	1710.8268	1709.8428	1755.8483	1738.8217	1737.8377	1670.7955		K	230.1248	229.1295		303.2139	286.1874
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VV	171.1492	199.1441	VVS	258.1812	286.1761	VVSS	345.2132	373.2082

VVSSC	505.2439	533.2388	**VVSSCG**	562.2654	590.2603	**VVSSCGH**	699.3243	727.3192
VS	159.1128	187.1077	**VSS**	246.1448	274.1397	**VSSC**	406.1755	434.1704
VSSCG	463.1969	491.1919	**VSSCGH**	600.2559	628.2508	**SS**	147.0764	175.0713
SSC	307.1071	335.1020	**SSCG**	364.1285	392.1234	**SSCGH**	501.1874	529.1824
SSCGHD	616.2144	644.2093	**SSCGHDG**	673.2358	701.2308	**SC**	220.0750	248.0700
SCG	277.0965	305.0914	**SCGH**	414.1554	442.1503	**SCGHD**	529.1824	557.1773
SCGHDG	586.2038	614.1987	**SCGHDGP**	683.2566	711.2515	**CG**	190.0645	218.0594
CGH	327.1234	355.1183	**CGHD**	442.1503	470.1452	**CGHDG**	499.1718	527.1667
CGHDGP	596.2246	624.2195	**GH**	167.0927	195.0877	**GHD**	282.1197	310.1146
GHDG	339.1411	367.1361	**GHDGP**	436.1939	464.1888	**GHDGPF**	583.2623	611.2572
GHDGPFG	640.2838	668.2787	**HD**	225.0982	253.0931	**HDG**	282.1197	310.1146
HDGP	379.1724	407.1674	**HDGPF**	526.2409	554.2358	**HDGPFG**	583.2623	611.2572
HDGPFGA	654.2994	682.2944	**DG**	145.0608	173.0557	**DGP**	242.1135	270.1084
DGPF	389.1819	417.1769	**DGPFG**	446.2034	474.1983	**DGPFGA**	517.2405	545.2354
DGPFGAT	618.2882	646.2831	**DGPFGATG**	675.3097	703.3046	**GP**	127.0866	155.0815
GPF	274.1550	302.1499	**GPFG**	331.1765	359.1714	**GPFGA**	402.2136	430.2085
GPFGAT	503.2613	531.2562	**GPFGATG**	560.2827	588.2776	**GPFGATGV**	659.3511	687.3461
PF	217.1335	245.1285	**PFG**	274.1550	302.1499	**PFGA**	345.1921	373.1870
PFGAT	446.2398	474.2347	**PFGATG**	503.2613	531.2562	**PFGATGV**	602.3297	630.3246
FG	177.1022	205.0972	**FGA**	248.1394	276.1343	**FGAT**	349.1870	377.1819
FGATG	406.2085	434.2034	**FGATGV**	505.2769	533.2718	**FGATGVK**	633.3719	661.3668
GA	101.0709	129.0659	**GAT**	202.1186	230.1135	**GATG**	259.1401	287.1350
GATGV	358.2085	386.2034	**GATGVK**	486.3035	514.2984	**AT**	145.0972	173.0921
ATG	202.1186	230.1135	**ATGV**	301.1870	329.1819	**ATGVK**	429.2820	457.2769
TG	131.0815	159.0764	**TGV**	230.1499	258.1448	**TGVK**	358.2449	386.2398
GV	129.1022	157.0972	**GVK**	257.1972	285.1921	**VK**	200.1757	228.1707





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.0	1928.9527	0.1265	VVVSSCGHDGPFGATGVKR
40.5	1928.9197	0.1595	VVVSSCGHDGPMGATGVKR
9.3	1928.8878	0.1915	FGGNGQQHYTDAPEPRR
6.7	1929.0935	-0.0143	IPILVYELVSNGSLEKR
6.5	1928.9495	0.1297	WVVELSQFDIYFMPR
5.6	1929.0068	0.0724	NAGSKHFTVSLLDTGNLR
4.3	1928.9884	0.0908	SKETAPVIDVTQFGYFK
3.3	1928.9998	0.0794	LCMQRAADALLGICLPK
3.1	1928.9052	0.1740	FVEMTSASIAMSFFAFK
3.0	1928.9076	0.1717	LAESEQAGDLVVGGEGGEGR

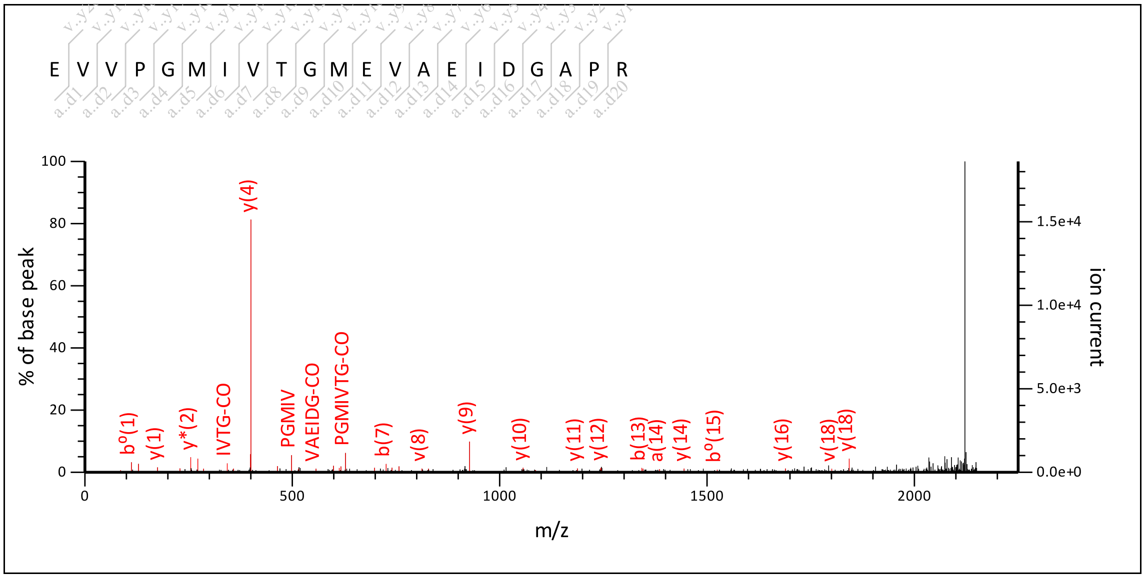
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 49

MS/MS Fragmentation of **EVVPGMIVTGMEVAEIDGAPR**
Found in **gi|27261025** in **NCBInr**, putative thiamine biosynthesis protein [Oryza sativa Japonica Group]

Match to Query 36: 2169.228524 from(2170.235800,1+) intensity(0.0000) index(16)
Title: Label: H9, Spot_Id: 228977, Peak_List_Id: 257865, MSMS Job_Run_Id: 24940, Comment:
Data file ppw_H9_138985153400.txt



0 to 2250.16

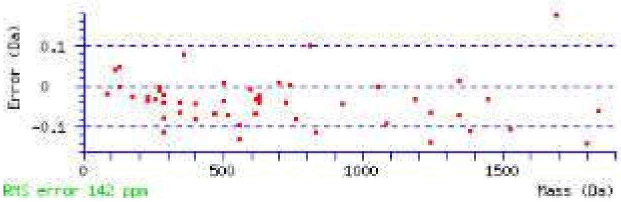
Label all possible matches ○ Label matches used for scoring ●

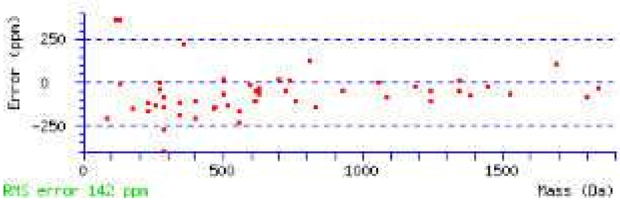
Monoisotopic mass of neutral peptide Mr(calc): 2169.0810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 3.5e-05
Matches : 61/386 fragment ions using 105 most intense peaks (help)

#	Immon.	a	a⁰	b	b⁰	d	d'	Seq.	v	w	w'	y	y*	y⁰	#
1	102.0550	102.0550	84.0444	130.0499	112.0393	44.0495		E							21
2	72.0808	201.1234	183.1128	**229.1183**	211.1077	187.1077		V	1996.9831	2010.0035		2041.0457	2024.0191	2023.0351	20
3	72.0808	300.1918	282.1812	328.1867	310.1761	286.1761		V	1897.9146	1910.9350		1941.9772	1924.9507	1923.9667	19
4	70.0651	397.2445	379.2340	425.2395	407.2289	371.2289		P	1800.8619	1799.8666		***1842.9088***	1825.8823	1824.8983	18
5	30.0338	454.2660	436.2554	482.2609	464.2504			G				1745.8561	1728.8295	1727.8455	17
6	104.0528	585.3065	567.2959	**613.3014**	595.2908	525.3031		M	1612.7999	1611.8047		***1688.8346***	1671.8081	1670.8240	16
7	86.0964	**698.3906**	680.3800	**726.3855**	708.3749	670.3593	684.3749	I	1499.7159	1512.7363	1526.7519	1557.7941	1540.7676	1539.7836	15
8	72.0808	797.4590	779.4484	825.4539	807.4433	783.4433		V	1400.6475	1413.6679		***1444.7101***	1427.6835	1426.6995	14
9	74.0600	898.5067	880.4961	926.5016	908.4910	882.5117	884.4910	T	1299.5998	1312.6202	1314.5994	***1345.6416***	1328.6151	1327.6311	13
10	30.0338	955.5281	937.5176	983.5230	965.5125			G				***1244.5940***	1227.5674	1226.5834	12
11	104.0528	**1086.5686**	1068.5580	1114.5635	1096.5530	1026.5652		M	1111.5378	1110.5426		***1187.5725***	1170.5460	1169.5619	11
12	102.0550	1215.6112	1197.6006	**1243.6061**	1225.5955	1157.6057		E	982.4952	981.5000		***1056.5320***	1039.5055	1038.5215	10
13	72.0808	1314.6796	1296.6690	**1342.6745**	1324.6640	1300.6640		V	883.4268	896.4472		***927.4894***	910.4629	909.4789	9
14	44.0495	**1385.7167**	1367.7062	1413.7116	1395.7011			A	812.3897			***828.4210***	811.3945	810.4104	8
15	102.0550	1514.7593	1496.7488	1542.7542	1524.7437	1456.7538		E	683.3471	682.3519		***757.3839***	740.3573	739.3733	7
16	86.0964	1627.8434	1609.8328	1655.8383	1637.8277	1599.8121	1613.8277	I	570.2631	583.2835	597.2991	***628.3413***	611.3148	610.3307	6
17	88.0393	1742.8703	1724.8598	1770.8652	1752.8547	1698.8805		D	455.2361	454.2409		***515.2572***	498.2307	497.2467	5
18	30.0338	1799.8918	1781.8812	1827.8867	1809.8761			G				***400.2303***	383.2037		4
19	44.0495	1870.9289	1852.9183	1898.9238	1880.9133			A	327.1775			***343.2088***	326.1823		3

20	70.0651	1967.9817	1949.9711	1995.9766	1977.9660	1941.9660		**P**	230.1248	229.1295		***272.1717***	255.1452		**2**
21	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VV	171.1492	199.1441	**VVP**	268.2020	296.1969	**VVPG**	325.2234	353.2183
VVPGM	456.2639	484.2588	**VVPGMI**	569.3480	597.3429	**VVPGMIV**	668.4164	696.4113
VP	169.1335	197.1285	**VPG**	226.1550	254.1499	**VPGM**	357.1955	385.1904
VPGMI	470.2796	498.2745	**VPGMIV**	569.3480	597.3429	**VPGMIVT**	670.3956	698.3906
PG	127.0866	155.0815	**PGM**	258.1271	286.1220	**PGMI**	371.2111	399.2061
PGMIV	470.2796	498.2745	**PGMIVT**	571.3272	599.3221	**PGMIVTG**	628.3487	656.3436
GM	161.0743	189.0692	**GMI**	274.1584	302.1533	**GMIV**	373.2268	401.2217
GMIVT	474.2745	502.2694	**GMIVTG**	531.2959	559.2908	**GMIVTGM**	662.3364	690.3313
MI	217.1369	245.1318	**MIV**	316.2053	344.2002	**MIVT**	417.2530	445.2479
MIVTG	474.2745	502.2694	**MIVTGM**	605.3150	633.3099	**IV**	185.1648	213.1598
IVT	286.2125	314.2074	**IVTG**	343.2340	371.2289	**IVTGM**	474.2745	502.2694
IVTGME	603.3171	631.3120	**VT**	173.1285	201.1234	**VTG**	230.1499	258.1448
VTGM	361.1904	389.1853	**VTGME**	490.2330	518.2279	**VTGMEV**	589.3014	617.2963
VTGMEVA	660.3385	688.3334	**TG**	131.0815	159.0764	**TGM**	262.1220	290.1169
TGME	391.1646	419.1595	**TGMEV**	490.2330	518.2279	**TGMEVA**	561.2701	589.2650
TGMEVAE	690.3127	718.3076	**GM**	161.0743	189.0692	**GME**	290.1169	318.1118
GMEV	389.1853	417.1802	**GMEVA**	460.2224	488.2173	**GMEVAE**	589.2650	617.2599
ME	233.0954	261.0904	**MEV**	332.1639	360.1588	**MEVA**	403.2010	431.1959
MEVAE	532.2436	560.2385	**MEVAEI**	645.3276	673.3225	**EV**	201.1234	229.1183
EVA	272.1605	300.1554	**EVAE**	401.2031	429.1980	**EVAEI**	514.2871	542.2821
EVAEID	629.3141	657.3090	**EVAEIDG**	686.3355	714.3305	**VA**	143.1179	171.1128
VAE	272.1605	300.1554	**VAEI**	385.2445	413.2395	**VAEID**	500.2715	528.2664
VAEIDG	557.2930	585.2879	**VAEIDGA**	628.3301	656.3250	**AE**	173.0921	201.0870
AEI	286.1761	314.1710	**AEID**	401.2031	429.1980	**AEIDG**	458.2245	486.2195
AEIDGA	529.2617	557.2566	**AEIDGAP**	626.3144	654.3093	**EI**	215.1390	243.1339
EID	330.1660	358.1609	**EIDG**	387.1874	415.1823	**EIDGA**	458.2245	486.2195
EIDGAP	555.2773	583.2722	**ID**	201.1234	229.1183	**IDG**	258.1448	286.1397
IDGA	329.1819	357.1769	**IDGAP**	426.2347	454.2296	**DG**	145.0608	173.0557
DGA	216.0979	244.0928	**DGAP**	313.1506	341.1456	**GA**	101.0709	129.0659
GAP	198.1237	226.1186	**AP**	141.1022	169.0972			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.9	2169.0810	0.1475	EVVPGMIVTGMEVAEIDGAPR
7.0	2169.1218	0.1067	GVLEVEIFHGEYNATVKHK
6.1	2169.1389	0.0896	NQIVLVAEDTDGSAIAELRR
6.0	2169.2330	-0.0045	VAEKDLVTVIELLMNELIK
5.1	2169.1001	0.1284	FTVTGRLSVFAVMGDLNNGR

4.6	2169.1688	0.0597	SLMSTARASLRPAAPSSTLPR
4.6	2169.0161	0.2125	ELPNPTNPMASSSNPTPPFR
4.5	2169.1827	0.0458	RLDMLPSLLSENLASLLER
4.4	2169.1389	0.0896	SSQAENIEINTGQILQGVIR
4.4	2169.1165	0.1121	DADQLPKVLEDGVTAAAIESK

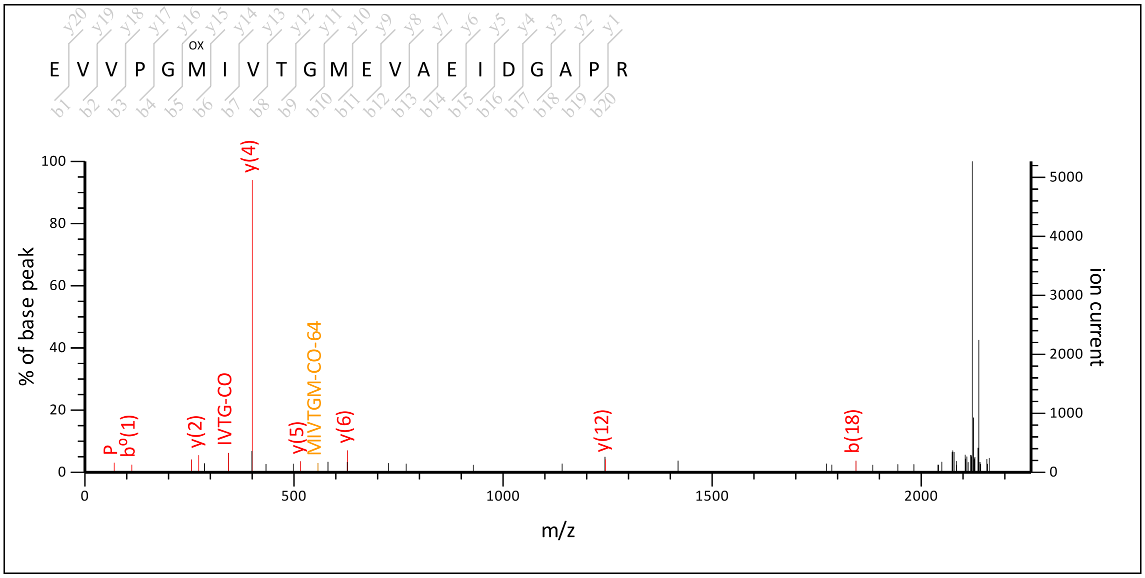
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 49

MS/MS Fragmentation of **EVVPGMIVTGMEVAEIDGAPR**
Found in **gi|27261025** in **NCBInr**, putative thiamine biosynthesis protein [Oryza sativa Japonica Group]

Match to Query 38: 2185.194624 from(2186.201900,1+) intensity(0.0000) index(17)
Title: Label: H9, Spot_Id: 228977, Peak_List_Id: 257876, MSMS Job_Run_Id: 24940, Comment:
Data file ppw_H9_138985153400.txt



0 to 2262.68

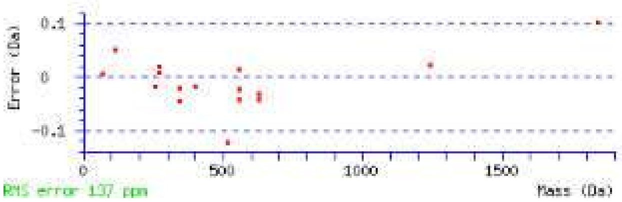
Label all possible matches ○ Label matches used for scoring ●

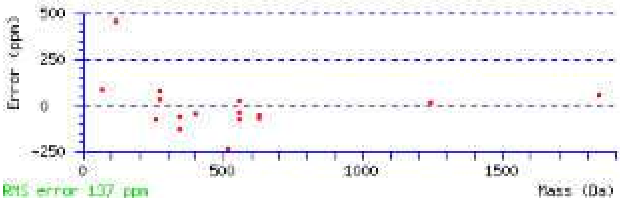
Monoisotopic mass of neutral peptide Mr(calc): 2185.0759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 11
Matches : 18/521 fragment ions using 26 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	102.0550	102.0550	84.0444	130.0499	112.0393	44.0495		E							21
2	72.0808	201.1234	183.1128	229.1183	211.1077	187.1077		V	2012.9780	2025.9984		2057.0406	2040.0140	2039.0300	20
3	72.0808	300.1918	282.1812	328.1867	310.1761	286.1761		V	1913.9096	1926.9300		1957.9722	1940.9456	1939.9616	19
4	70.0651	397.2445	379.2340	425.2395	407.2289	371.2289		P	1816.8568	1815.8616		1858.9037	1841.8772	1840.8932	18
5	30.0338	454.2660	436.2554	482.2609	464.2504			G				1761.8510	1744.8244	1743.8404	17
6	120.0478	601.3014	583.2908	629.2963	611.2858	525.3031		M	1612.7999	1611.8047		1704.8295	1687.8030	1686.8190	16
7	86.0964	714.3855	696.3749	742.3804	724.3698	686.3542	700.3698	I	1499.7159	1512.7363	1526.7519	1557.7941	1540.7676	1539.7836	15
8	72.0808	813.4539	795.4433	841.4488	823.4382	799.4382		V	1400.6475	1413.6679		1444.7101	1427.6835	1426.6995	14
9	74.0600	914.5016	896.4910	942.4965	924.4859	898.5067	900.4859	T	1299.5998	1312.6202	1314.5994	1345.6416	1328.6151	1327.6311	13
10	30.0338	971.5230	953.5125	999.5179	981.5074			G				***1244.5940***	1227.5674	1226.5834	12
11	104.0528	1102.5635	1084.5530	1130.5584	1112.5479	1042.5601		M	1111.5378	1110.5426		1187.5725	1170.5460	1169.5619	11
12	102.0550	1231.6061	1213.5955	1259.6010	1241.5905	1173.6006		E	982.4952	981.5000		1056.5320	1039.5055	1038.5215	10
13	72.0808	1330.6745	1312.6640	1358.6694	1340.6589	1316.6589		V	883.4268	896.4472		927.4894	910.4629	909.4789	9
14	44.0495	1401.7116	1383.7011	1429.7066	1411.6960			A	812.3897			828.4210	811.3945	810.4104	8
15	102.0550	1530.7542	1512.7437	1558.7491	1540.7386	1472.7488		E	683.3471	682.3519		757.3839	740.3573	739.3733	7
16	86.0964	1643.8383	1625.8277	1671.8332	1653.8226	1615.8070	1629.8226	I	570.2631	583.2835	597.2991	***628.3413***	611.3148	610.3307	6
17	88.0393	1758.8652	1740.8547	1786.8602	1768.8496	1714.8754		D	455.2361	454.2409		***515.2572***	498.2307	497.2467	5
18	30.0338	1815.8867	1797.8761	1843.8816	1825.8711			G				***400.2303***	383.2037		4

19	44.0495	1886.9238	1868.9133	1914.9187	1896.9082			A	327.1775			***343.2088***	326.1823		3
20	70.0651	1983.9766	1965.9660	2011.9715	1993.9609	1957.9609		P	230.1248	229.1295		***272.1717***	255.1452		2
21	129.1135							R	74.0237	73.0284		175.1190	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VV	171.1492	199.1441	VVP	268.2020	296.1969	VVPG	325.2234	353.2183
VVPGM	472.2588	500.2537	VVPGMI	585.3429	613.3378	VVPGMIV	684.4113	712.4062
VP	169.1335	197.1285	VPG	226.1550	254.1499	VPGM	373.1904	401.1853
VPGMI	486.2745	514.2694	VPGMIV	585.3429	613.3378	VPGMIVT	686.3906	714.3855
PG	127.0866	155.0815	PGM	274.1220	302.1169	PGMI	387.2061	415.2010
PGMIV	486.2745	514.2694	PGMIVT	587.3221	615.3171	PGMIVTG	644.3436	672.3385
GM	177.0692	205.0641	GMI	290.1533	318.1482	GMIV	389.2217	417.2166
GMIVT	490.2694	518.2643	GMIVTG	547.2908	575.2858	GMIVTGM	678.3313	706.3262
MI	233.1318	261.1267	MIV	332.2002	360.1952	MIVT	433.2479	461.2428
MIVTG	490.2694	518.2643	MIVTGM	621.3099	649.3048	IV	185.1648	213.1598
IVT	286.2125	314.2074	IVTG	343.2340	371.2289	IVTGM	474.2745	502.2694
IVTGME	603.3171	631.3120	VT	173.1285	201.1234	VTG	230.1499	258.1448
VTGM	361.1904	389.1853	VTGME	490.2330	518.2279	VTGMEV	589.3014	617.2963
VTGMEVA	660.3385	688.3334	TG	131.0815	159.0764	TGM	262.1220	290.1169
TGME	391.1646	419.1595	TGMEV	490.2330	518.2279	TGMEVA	561.2701	589.2650
TGMEVAE	690.3127	718.3076	GM	161.0743	189.0692	GME	290.1169	318.1118
GMEV	389.1853	417.1802	GMEVA	460.2224	488.2173	GMEVAE	589.2650	617.2599
ME	233.0954	261.0904	MEV	332.1639	360.1588	MEVA	403.2010	431.1959
MEVAE	532.2436	560.2385	MEVAEI	645.3276	673.3225	EV	201.1234	229.1183
EVA	272.1605	300.1554	EVAE	401.2031	429.1980	EVAEI	514.2871	542.2821
EVAEID	629.3141	657.3090	EVAEIDG	686.3355	714.3305	VA	143.1179	171.1128
VAE	272.1605	300.1554	VAEI	385.2445	413.2395	VAEID	500.2715	528.2664
VAEIDG	557.2930	585.2879	VAEIDGA	628.3301	656.3250	AE	173.0921	201.0870
AEI	286.1761	314.1710	AEID	401.2031	429.1980	AEIDG	458.2245	486.2195
AEIDGA	529.2617	557.2566	AEIDGAP	626.3144	654.3093	EI	215.1390	243.1339
EID	330.1660	358.1609	EIDG	387.1874	415.1823	EIDGA	458.2245	486.2195
EIDGAP	555.2773	583.2722	ID	201.1234	229.1183	IDG	258.1448	286.1397
IDGA	329.1819	357.1769	IDGAP	426.2347	454.2296	DG	145.0608	173.0557
DGA	216.0979	244.0928	DGAP	313.1506	341.1456	GA	101.0709	129.0659
GAP	198.1237	226.1186	AP	141.1022	169.0972			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.5	2185.0759	0.1187	EVVPGMIVTGMEVAEIDGAPR
20.4	2185.0759	0.1187	EVVPGMIVTGMEVAEIDGAPR
12.8	2185.0345	0.1601	FMAVPHYTYIMMKMPGPR
11.8	2185.0345	0.1601	FMAVPHYTYMIMKMPGPR
11.6	2185.0797	0.1149	GDLNNNQVGEAMERVLALDK

10.1	2185.1703	0.0243	VSVGVGGVLTNNNGGISDGITKK
10.1	2185.1703	0.0243	VSVGVGGVLTNNNGGLSDGITKK
9.9	2185.1242	0.0705	VWLNPTGTIEMLLWQGPSK
9.4	2185.1024	0.0923	SLLNLMGVKDNSPMFAPAHK
9.3	2185.0838	0.1109	DGILGTAGAPIHMVAASEGGSFK

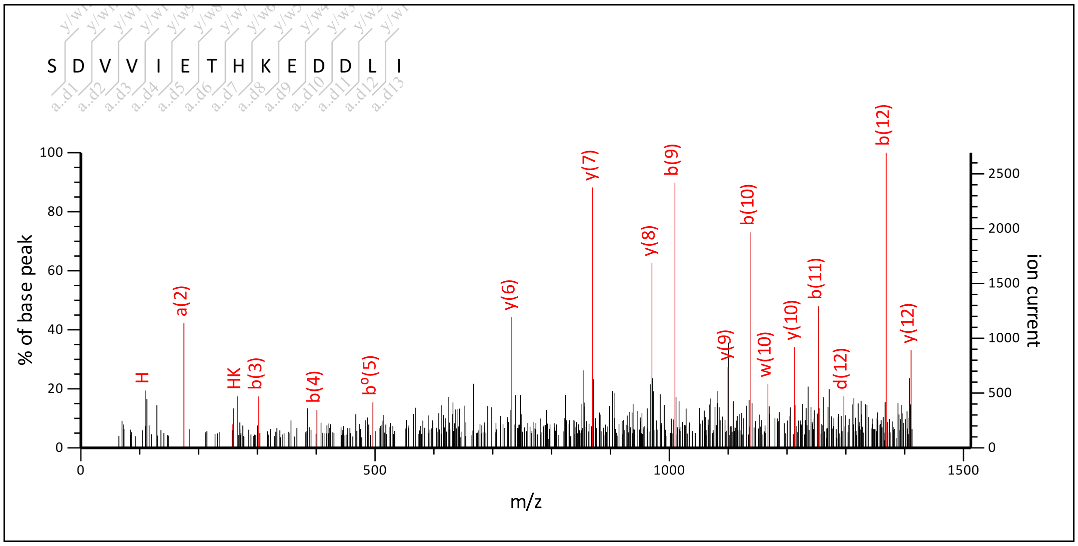
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 16

MS/MS Fragmentation of **SDVVIETHKEDDLI**
Found in **gi|18698985** in **NCBInr**, anti-disease protein 1 [Oryza sativa]

Match to Query 11: 1611.876224 from(1612.883500,1+) intensity(0.0000) index(5)
Title: Label: L7, Spot_Id: 219781, Peak_List_Id: 226463, MSMS Job_Run_Id: 21845, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_L7_136859918200.txt



0 to 1512.48

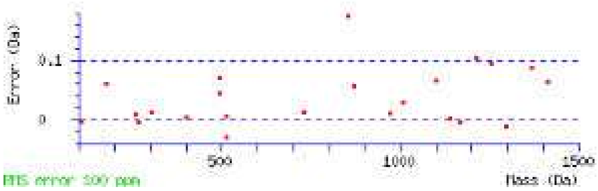
Label all possible matches ○ Label matches used for scoring ●

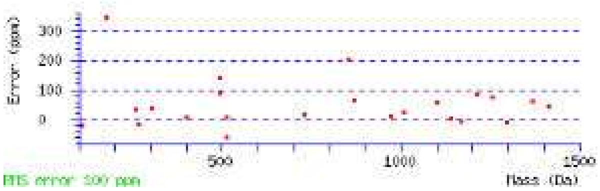
Monoisotopic mass of neutral peptide Mr(calc): 1611.7992
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.99
Matches : 24/231 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S						
2	88.0393	**175.0713**		157.0608	203.0662		185.0557	131.0815		D	1465.7533	1464.7581		1525.7744	1508.7479	15
3	72.0808	274.1397		256.1292	***302.1347***		284.1241	260.1241		V	1366.6849	1379.7053		***1410.7475***	1393.7209	13
4	72.0808	373.2082		355.1976	***401.2031***		383.1925	359.1925		V	1267.6165	1280.6369		1311.6791	1294.6525	12
5	86.0964	486.2922		468.2817	***514.2871***		496.2766	458.2609	472.2766	I	1154.5324	1167.5528	1181.5685	***1212.6107***	1195.5841	11
6	102.0550	615.3348		597.3243	643.3297		625.3192	557.3293		E	1025.4898	1024.4946		***1099.5266***	1082.5000	10
7	74.0600	716.3825		698.3719	744.3774		726.3668	700.3876	702.3668	T	924.4421	937.4625	939.4418	***970.4840***	953.4575	9
8	110.0713	**853.4414**		835.4308	881.4363		863.4258			H	787.3832			***869.4363***	852.4098	8
9	101.1073	981.5364	964.5098	963.5258	***1009.5313***	992.5047	991.5207	924.4785		K	659.2883	658.2930		***732.3774***	715.3509	7
10	102.0550	1110.5790	1093.5524	1092.5684	***1138.5739***	1121.5473	1120.5633	1052.5735		E	530.2457	529.2504		604.2824		5
11	88.0393	1225.6059	1208.5794	1207.5953	***1253.6008***	1236.5743	1235.5903	1181.6161		D	415.2187	414.2235		475.2399		4
12	88.0393	1340.6329	1323.6063	1322.6223	***1368.6278***	1351.6012	1350.6172	1296.6430		D	300.1918	299.1965		360.2129		3
13	86.0964	1453.7169	1436.6904	1435.7063	1481.7118	1464.6853	1463.7013	1411.6700		L	187.1077	186.1125		245.1860		
14	86.0964									I	74.0237	73.0284		132.1019		

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DV	187.1077	215.1026	DVV	286.1761	314.1710	DVVI	399.2602	427.2551
DVVIE	528.3028	556.2977	DVVIET	629.3505	657.3454	VV	171.1492	199.1441
VVI	284.2333	312.2282	VVIE	413.2758	441.2708	VVIET	514.3235	542.3184
VVIETH	651.3824	679.3774	VI	185.1648	213.1598	VIE	314.2074	342.2023
VIET	415.2551	443.2500	VIETH	552.3140	580.3089	VIETHK	680.4090	708.4039
IE	215.1390	243.1339	IET	316.1867	344.1816	IETH	453.2456	481.2405
IETHK	581.3406	609.3355	ET	203.1026	231.0975	ETH	340.1615	368.1565

ETHK	468.2565	496.2514	**ETHKE**	597.2991	625.2940	**TH**	211.1190	239.1139
THK	339.2139	367.2088	**THKE**	468.2565	496.2514	**THKED**	583.2835	611.2784
THKEDD	698.3104	726.3053	**HK**	238.1662	266.1612	**HKE**	367.2088	395.2037
HKED	482.2358	510.2307	**HKEDD**	597.2627	625.2576	**KE**	230.1499	258.1448
KED	345.1769	373.1718	**KEDD**	460.2038	488.1987	**KEDDL**	573.2879	601.2828
ED	217.0819	245.0768	**EDD**	332.1088	360.1038	**EDDL**	445.1929	473.1878
DD	203.0662	231.0612	**DDL**	316.1503	344.1452	**DL**	201.1234	229.1183





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.6	1611.7992	0.0770	SDVVIETHKEDDLI
27.9	1611.8216	0.0546	AEVTIEGTTSAGALHR
20.9	1611.8580	0.0182	NNATLLDGSTGALLPR
20.6	1611.8733	0.0029	ERVLAAFPGLGETPR
18.6	1611.8481	0.0281	RQSDTGVHYALPLR
18.4	1611.7781	0.0982	DEDDVLGSFFSLIR
18.3	1611.8766	-0.0004	AMPLTAGQEVKALQR
17.6	1611.7311	0.1451	GEILEHNPMASENR
17.5	1611.8832	-0.0069	LDATIETLPDLQKR
17.4	1611.9195	-0.0433	ELGITEDKVNIILR

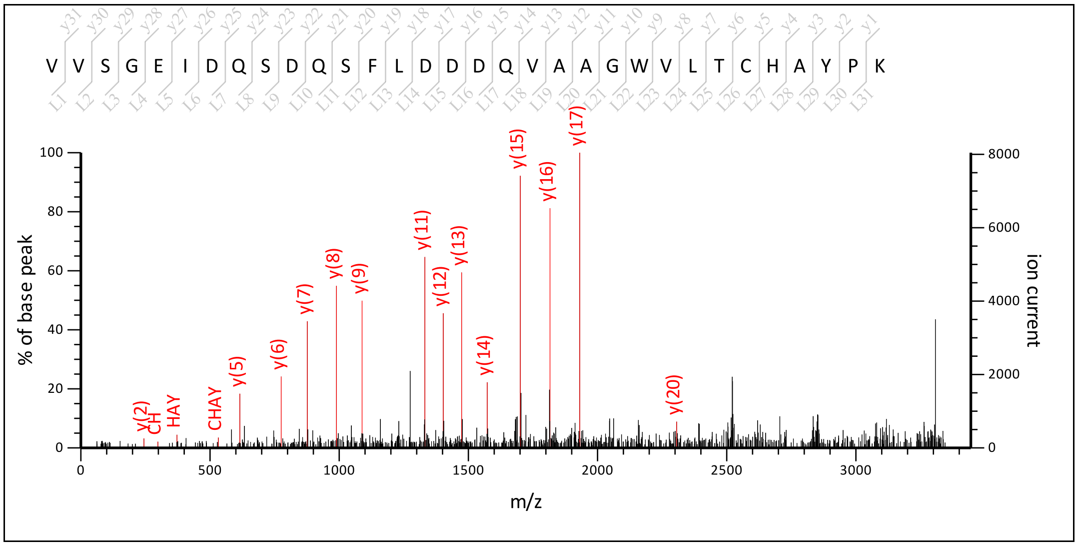
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 16

MS/MS Fragmentation of **VVSGEIDQSDQSFLDDDQVAAGWVLTCHAYPK**
Found in **gi|18698985** in **NCBInr**, anti-disease protein 1 [Oryza sativa]

Match to Query 19: 3549.797124 from(3550.804400,1+) intensity(0.0000) index(9)
Title: Label: L7, Spot_Id: 219781, Peak_List_Id: 226457, MSMS Job_Run_Id: 21845, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_L7_136859918200.txt



0 to 3444.93

Label all possible matches ○ Label matches used for scoring ●

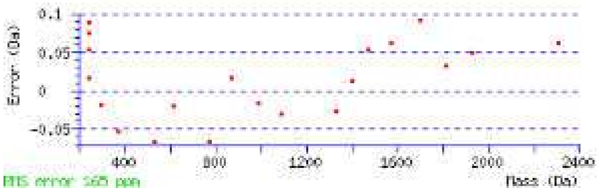
Monoisotopic mass of neutral peptide Mr(calc): 3549.6359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 0.00017
Matches : 22/632 fragment ions using 33 most intense peaks (help)

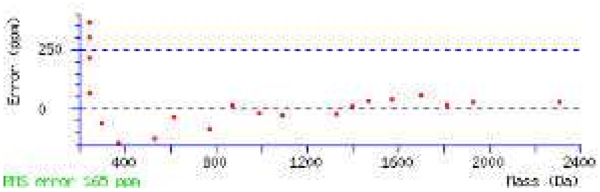
#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	72.0808	171.1492			199.1441			157.1335		V	3407.5121	3420.5325		3451.5747	3434.5481
3	60.0444	258.1812		240.1707	286.1761		268.1656	242.1863		S	3320.4801	3319.4848		3352.5063	3335.4797
4	30.0338	315.2027		297.1921	343.1976		325.1870			G				3265.4743	3248.4477
5	102.0550	444.2453		426.2347	472.2402		454.2296	386.2398		E	3134.4160	3133.4208		3208.4528	3191.4262
6	86.0964	557.3293		539.3188	585.3243		567.3137	529.2980	543.3137	I	3021.3319	3034.3523	3048.3680	3079.4102	3062.3836
7	88.0393	672.3563		654.3457	700.3512		682.3406	628.3665		D	2906.3050	2905.3098		2966.3261	2949.2996
8	101.0709	800.4149	783.3883	782.4043	828.4098	811.3832	810.3992	743.3934		Q	2778.2464	2777.2512		2851.2992	2834.2726
9	60.0444	887.4469	870.4203	869.4363	915.4418	898.4153	897.4312	871.4520		S	2691.2144	2690.2191		2723.2406	2706.2141
10	88.0393	1002.4738	985.4473	984.4633	1030.4687	1013.4422	1012.4582	958.4840		D	2576.1875	2575.1922		2636.2086	2619.1820
11	101.0709	1130.5324	1113.5059	1112.5218	1158.5273	1141.5008	1140.5168	1073.5109		Q	2448.1289	2447.1336		2521.1816	2504.1551
12	60.0444	1217.5644	1200.5379	1199.5539	1245.5594	1228.5328	1227.5488	1201.5695		S	2361.0968	2360.1016		2393.1231	2376.0965
13	120.0808	1364.6329	1347.6063	1346.6223	1392.6278	1375.6012	1374.6172			F	2214.0284			***2306.0910***	2289.0645
14	86.0964	1477.7169	1460.6904	1459.7063	1505.7118	1488.6853	1487.7013	1435.6700		L	2100.9444	2099.9491		2159.0226	2141.9961
15	88.0393	1592.7439	1575.7173	1574.7333	1620.7388	1603.7122	1602.7282	1548.7540		D	1985.9174	1984.9222		2045.9386	2028.9120
16	88.0393	1707.7708	1690.7443	1689.7602	1735.7657	1718.7392	1717.7552	1663.7810		D	1870.8905	1869.8952		***1930.9116***	1913.8851
17	88.0393	1822.7977	1805.7712	1804.7872	1850.7927	1833.7661	1832.7821	1778.8079		D	1755.8635	1754.8683		***1815.8847***	1798.8581
18	101.0709	1950.8563	1933.8298	1932.8458	1978.8512	1961.8247	1960.8407	1893.8349		Q	1627.8050	1626.8097		***1700.8577***	1683.8312
19	72.0808	2049.9247	2032.8982	2031.9142	2077.9196	2060.8931	2059.9091	2035.9091		V	1528.7365	1541.7569		***1572.7991***	1555.7726
20	44.0495	2120.9618	2103.9353	2102.9513	2148.9568	2131.9302	2130.9462			A	1457.6994			***1473.7307***	1456.7042
21	44.0495	2191.9990	2174.9724	2173.9884	2219.9939	2202.9673	2201.9833			A	1386.6623			***1402.6936***	1385.6671
22	30.0338	2249.0204	2231.9939	2231.0099	2277.0153	2259.9888	2259.0048			G				***1331.6565***	1314.6300
23	159.0917	2435.0997	2418.0732	2417.0892	2463.0947	2446.0681	2445.0841			W	1143.5615			1274.6350	1257.6085

24	72.0808	2534.1682	2517.1416	2516.1576	2562.1631	2545.1365	2544.1525	2520.1525		**V**	1044.4931	1057.5135		***1088.5557***	1071.5292
25	86.0964	2647.2522	2630.2257	2629.2417	2675.2471	2658.2206	2657.2366	2605.2053		**L**	931.4091	930.4138		***989.4873***	972.4608
26	74.0600	2748.2999	2731.2733	2730.2893	2776.2948	2759.2683	2758.2842	2732.3050	2734.2842	**T**	830.3614	843.3818	845.3611	***876.4033***	859.3767
27	133.0430	2908.3305	2891.3040	2890.3200	2936.3255	2919.2989	2918.3149	2819.3370		**C**	670.3307	669.3355		***775.3556***	758.3290
28	110.0713	3045.3895	3028.3629	3027.3789	3073.3844	3056.3578	3055.3738			**H**	533.2718			***615.3249***	598.2984
29	44.0495	3116.4266	3099.4000	3098.4160	3144.4215	3127.3949	3126.4109			**A**	462.2347			478.2660	461.2395
30	136.0757	3279.4899	3262.4634	3261.4793	3307.4848	3290.4583	3289.4743			**Y**	299.1714			407.2289	390.2023
31	70.0651	3376.5427	3359.5161	3358.5321	3404.5376	3387.5110	3386.5270	3350.5270		**P**	202.1186	201.1234		***244.1656***	227.1390
32	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VS	159.1128	187.1077	**VSG**	216.1343	244.1292	**VSGE**	345.1769	373.1718
VSGEI	458.2609	486.2558	**VSGEID**	573.2879	601.2828	**SG**	117.0659	145.0608
SGE	246.1084	274.1034	**SGEI**	359.1925	387.1874	**SGEID**	474.2195	502.2144
SGEIDQ	602.2780	630.2729	**SGEIDQS**	689.3101	717.3050	**GE**	159.0764	187.0713
GEI	272.1605	300.1554	**GEID**	387.1874	415.1823	**GEIDQ**	515.2460	543.2409
GEIDQS	602.2780	630.2729	**EI**	215.1390	243.1339	**EID**	330.1660	358.1609
EIDQ	458.2245	486.2195	**EIDQS**	545.2566	573.2515	**EIDQSD**	660.2835	688.2784
ID	201.1234	229.1183	**IDQ**	329.1819	357.1769	**IDQS**	416.2140	444.2089
IDQSD	531.2409	559.2358	**IDQSDQ**	659.2995	687.2944	**DQ**	216.0979	244.0928
DQS	303.1299	331.1248	**DQSD**	418.1569	446.1518	**DQSDQ**	546.2154	574.2103
DQSDQS	633.2475	661.2424	**QS**	188.1030	216.0979	**QSD**	303.1299	331.1248
QSDQ	431.1885	459.1834	**QSDQS**	518.2205	546.2154	**QSDQSF**	665.2889	693.2838
SD	175.0713	203.0662	**SDQ**	303.1299	331.1248	**SDQS**	390.1619	418.1569
SDQSF	537.2304	565.2253	**SDQSFL**	650.3144	678.3093	**DQ**	216.0979	244.0928
DQS	303.1299	331.1248	**DQSF**	450.1983	478.1932	**DQSFL**	563.2824	591.2773
DQSFLD	678.3093	706.3042	**QS**	188.1030	216.0979	**QSF**	335.1714	363.1663
QSFL	448.2554	476.2504	**QSFLD**	563.2824	591.2773	**QSFLDD**	678.3093	706.3042
SF	207.1128	235.1077	**SFL**	320.1969	348.1918	**SFLD**	435.2238	463.2187
SFLDD	550.2508	578.2457	**SFLDDD**	665.2777	693.2726	**FL**	233.1648	261.1598
FLD	348.1918	376.1867	**FLDD**	463.2187	491.2136	**FLDDD**	578.2457	606.2406
LD	201.1234	229.1183	**LDD**	316.1503	344.1452	**LDDD**	431.1773	459.1722
LDDDQ	559.2358	587.2307	**LDDDQV**	658.3042	686.2992	**DD**	203.0662	231.0612
DDD	318.0932	346.0881	**DDDQ**	446.1518	474.1467	**DDDQV**	545.2202	573.2151
DDDQVA	616.2573	644.2522	**DDDQVAA**	687.2944	715.2893	**DD**	203.0662	231.0612
DDQ	331.1248	359.1197	**DDQV**	430.1932	458.1882	**DDQVA**	501.2304	529.2253
DDQVAA	572.2675	600.2624	**DDQVAAG**	629.2889	657.2838	**DQ**	216.0979	244.0928
DQV	315.1663	343.1612	**DQVA**	386.2034	414.1983	**DQVAA**	457.2405	485.2354
DQVAAG	514.2620	542.2569	**QV**	200.1394	228.1343	**QVA**	271.1765	299.1714
QVAA	342.2136	370.2085	**QVAAG**	399.2350	427.2300	**QVAAGW**	585.3144	613.3093
QVAAGWV	684.3828	712.3777	**VA**	143.1179	171.1128	**VAA**	214.1550	242.1499
VAAG	271.1765	299.1714	**VAAGW**	457.2558	485.2507	**VAAGWV**	556.3242	584.3191
VAAGWVL	669.4083	697.4032	**AA**	115.0866	143.0815	**AAG**	172.1081	200.1030
AAGW	358.1874	386.1823	**AAGWV**	457.2558	485.2507	**AAGWVL**	570.3398	598.3348
AAGWVLT	671.3875	699.3824	**AG**	101.0709	129.0659	**AGW**	287.1503	315.1452
AGWV	386.2187	414.2136	**AGWVL**	499.3027	527.2976	**AGWVLT**	600.3504	628.3453
GW	216.1131	244.1081	**GWV**	315.1816	343.1765	**GWVL**	428.2656	456.2605
GWVLT	529.3133	557.3082	**GWVLTC**	689.3439	717.3389	**WV**	258.1601	286.1550
WVL	371.2442	399.2391	**WVLT**	472.2918	500.2867	**WVLTC**	632.3225	660.3174
VL	185.1648	213.1598	**VLT**	286.2125	314.2074	**VLTC**	446.2432	474.2381
VLTCH	583.3021	611.2970	**VLTCHA**	654.3392	682.3341	**LT**	187.1441	215.1390
LTC	347.1748	375.1697	**LTCH**	484.2337	512.2286	**LTCHA**	555.2708	583.2657
TC	234.0907	262.0856	**TCH**	371.1496	399.1445	**TCHA**	442.1867	470.1816
TCHAY	605.2500	633.2450	**CH**	270.1019	298.0968	**CHA**	341.1390	369.1340
CHAY	504.2024	532.1973	**CHAYP**	601.2551	629.2500	**HA**	181.1084	209.1033

HAY	344.1717	372.1666	**HAYP**	441.2245	469.2194	**AY**	207.1128	235.1077
AYP	304.1656	332.1605	**YP**	233.1285	261.1234			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.3	3549.6359	0.1613	VVSGEIDQSDQSFLDDDQVAAGWVLTCHAYPK
14.5	3549.7774	0.0197	SWNRTTVTAVTAAAAVVVACGVTGFLLLGDDGDDK
6.1	3549.9177	-0.1206	GWRWLFIIEGAATVGFAIISLFILPDFPGTSR
5.9	3549.7912	0.0059	EFIKPEDVSAEVVEKEYQVQLDIAMQSGKPK
5.7	3549.7005	0.0966	AATTTAAAVGATTTAAAAGPESTAPDMHQATGPPLSER
5.4	3549.9489	-0.1518	MGFLLLLGGVVGGTLGVQLIMVLRAMGNADFVIK
4.5	3549.8103	-0.0132	KDFIDALHNATSEEHVVELVNTVIHPAPETPK
4.0	3549.8081	-0.0109	SVLIMAHRPAAIAECDMLLVLDHGVRMAFGPK
3.8	3549.8640	-0.0669	MLLSALSAVLSLAGSAAAALTYKGVDWSSVPVEEK
3.5	3549.5525	0.2446	GGNGGGIEACSSAAAAAAVRDACETFAEAFETFER

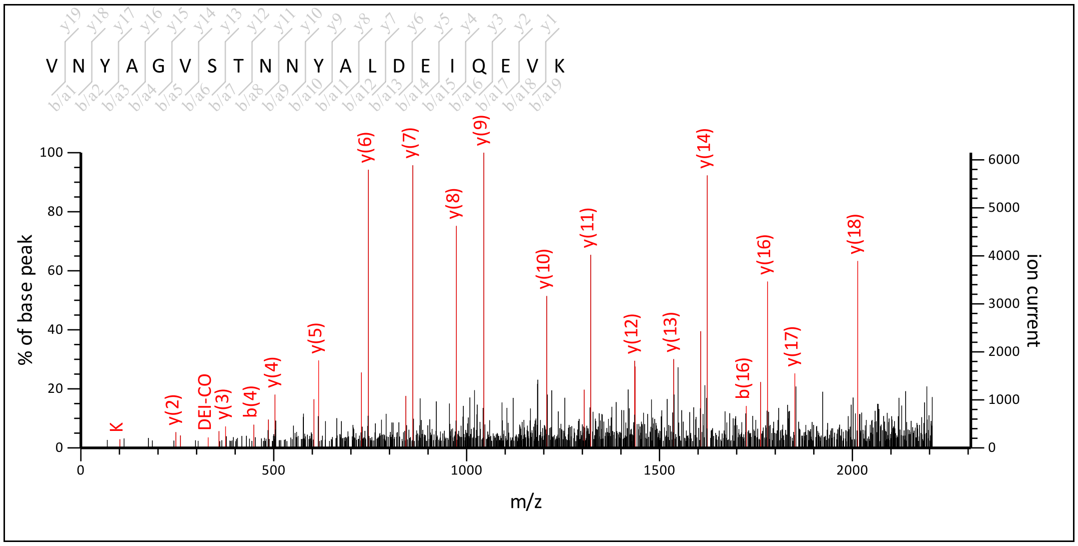
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 17

MS/MS Fragmentation of **VNYAGVSTNNYALDEIQEVK**
Found in **gi|34394725** in **NCBInr**, putative Photosystem I reaction center subunit IV [Oryza sativa Japonica Group]

Match to Query 23: 2226.235424 from(2227.242700,1+) intensity(0.0000) index(9)
Title: Label: O9, Spot_Id: 228984, Peak_List_Id: 257934, MSMS Job_Run_Id: 24944, Comment:
Data file ppw_O9_138985154400.txt



0 to 2307.02

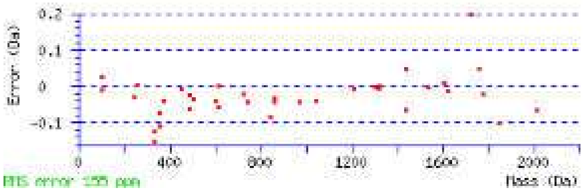
Label all possible matches ○ Label matches used for scoring ●

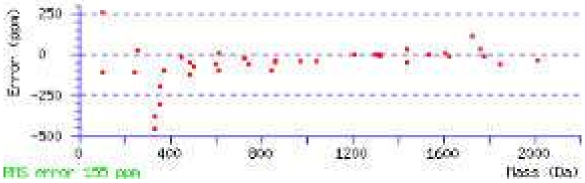
Monoisotopic mass of neutral peptide Mr(calc): 2226.0804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 128 **Expect:** 2.3e-10
Matches : 40/376 fragment ions using 44 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	87.0553	186.1237	169.0972		214.1186	197.0921		143.1179		N	2068.9822	2067.9869		2128.0193	2110.9928
3	136.0757	349.1870	332.1605		377.1819	360.1554				Y	1905.9189			***2013.9764***	1996.9498
4	44.0495	420.2241	403.1976		**448.2191**	431.1925				A	1834.8817			***1850.9130***	1833.8865
5	30.0338	477.2456	460.2191		505.2405	488.2140				G				***1779.8759***	1762.8494
6	72.0808	576.3140	559.2875		**604.3089**	587.2824		562.2984		V	1678.7919	1691.8123		1722.8545	1705.8279
7	60.0444	663.3461	646.3195	645.3355	691.3410	674.3144	673.3304	647.3511		S	1591.7598	1590.7646		***1623.7861***	1606.7595
8	74.0600	764.3937	747.3672	746.3832	792.3886	775.3621	774.3781	748.3988	750.3781	T	1490.7122	1503.7326	1505.7118	***1536.7540***	1519.7275
9	87.0553	878.4367	861.4101	860.4261	906.4316	889.4050	888.4210	835.4308		N	1376.6692	1375.6740		***1435.7063***	1418.6798
10	87.0553	992.4796	975.4530	974.4690	1020.4745	1003.4479	1002.4639	949.4738		N	1262.6263	1261.6311		***1321.6634***	1304.6369
11	136.0757	1155.5429	1138.5164	1137.5323	1183.5378	1166.5113	1165.5273			Y	1099.5630			***1207.6205***	1190.5939
12	44.0495	1226.5800	1209.5535	1208.5695	1254.5749	1237.5484	1236.5644			A	1028.5259			***1044.5572***	1027.5306
13	86.0964	1339.6641	1322.6375	1321.6535	1367.6590	1350.6325	1349.6484	1297.6171		L	915.4418	914.4466		***973.5201***	956.4935
14	88.0393	1454.6910	1437.6645	1436.6805	1482.6859	1465.6594	1464.6754	1410.7012		D	800.4149	799.4196		***860.4360***	843.4094
15	102.0550	1583.7336	1566.7071	1565.7231	1611.7285	1594.7020	1593.7180	1525.7281		E	671.3723	670.3770		***745.4090***	728.3825
16	86.0964	1696.8177	1679.7911	1678.8071	**1724.8126**	1707.7861	1706.8020	1668.7864	1682.8020	I	558.2882	571.3086	585.3243	***616.3665***	599.3399
17	101.0709	1824.8763	1807.8497	1806.8657	1852.8712	1835.8446	1834.8606	1767.8548		Q	430.2296	429.2344		***503.2824***	486.2558
18	102.0550	1953.9189	1936.8923	1935.9083	1981.9138	1964.8872	1963.9032	1895.9134		E	301.1870	300.1918		***375.2238***	358.1973
19	72.0808	2052.9873	2035.9607	2034.9767	2080.9822	2063.9556	2062.9716	2038.9716		V	202.1186	215.1390		***246.1812***	229.1547
20	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NY	250.1186	278.1135	NYA	321.1557	349.1506	NYAG	378.1772	406.1721

NYAGV	477.2456	505.2405	**NYAGVS**	564.2776	592.2726	**NYAGVST**	665.3253	693.3202
YA	207.1128	235.1077	**YAG**	264.1343	292.1292	**YAGV**	363.2027	391.1976
YAGVS	450.2347	478.2296	**YAGVST**	551.2824	579.2773	**YAGVSTN**	665.3253	693.3202
AG	101.0709	129.0659	**AGV**	200.1394	228.1343	**AGVS**	287.1714	315.1663
AGVST	388.2191	416.2140	**AGVSTN**	502.2620	530.2569	**AGVSTNN**	616.3049	644.2998
GV	129.1022	157.0972	**GVS**	216.1343	244.1292	**GVST**	317.1819	345.1769
GVSTN	431.2249	459.2198	**GVSTNN**	545.2678	573.2627	**VS**	159.1128	187.1077
VST	260.1605	288.1554	**VSTN**	374.2034	402.1983	**VSTNN**	488.2463	516.2413
VSTNNY	651.3097	679.3046	**ST**	161.0921	189.0870	**STN**	275.1350	303.1299
STNN	389.1779	417.1728	**STNNY**	552.2413	580.2362	**STNNYA**	623.2784	651.2733
TN	188.1030	216.0979	**TNN**	302.1459	330.1408	**TNNY**	465.2092	493.2041
TNNYA	536.2463	564.2413	**TNNYAL**	649.3304	677.3253	**NN**	201.0982	229.0931
NNY	364.1615	392.1565	**NNYA**	435.1987	463.1936	**NNYAL**	548.2827	576.2776
NNYALD	663.3097	691.3046	**NY**	250.1186	278.1135	**NYA**	321.1557	349.1506
NYAL	434.2398	462.2347	**NYALD**	549.2667	577.2617	**NYALDE**	678.3093	706.3042
YA	207.1128	235.1077	**YAL**	320.1969	348.1918	**YALD**	435.2238	463.2187
YALDE	564.2664	592.2613	**YALDEI**	677.3505	705.3454	**AL**	157.1335	185.1285
ALD	272.1605	300.1554	**ALDE**	401.2031	429.1980	**ALDEI**	514.2871	542.2821
ALDEIQ	642.3457	670.3406	**LD**	201.1234	229.1183	**LDE**	330.1660	358.1609
LDEI	443.2500	471.2449	**LDEIQ**	571.3086	599.3035	**DE**	217.0819	245.0768
DEI	330.1660	358.1609	**DEIQ**	458.2245	486.2195	**DEIQE**	587.2671	615.2620
DEIQEV	686.3355	714.3305	**EI**	215.1390	243.1339	**EIQ**	343.1976	371.1925
EIQE	472.2402	500.2351	**EIQEV**	571.3086	599.3035	**IQ**	214.1550	242.1499
IQE	343.1976	371.1925	**IQEV**	442.2660	470.2609	**QE**	230.1135	258.1084
QEV	329.1819	357.1769	**EV**	201.1234	229.1183			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
127.7	2226.0804	0.1550	VNYAGVSTNNYALDEIQEVK
8.8	2226.0990	0.1364	QMDALGLPFSFLSNKETSNK
8.2	2226.1492	0.0863	ASVSGTLEQIIDKHGDIASASK
7.0	2226.1063	0.1291	LGQCPSNVELHIDTSKSSVR
4.5	2226.1141	0.1213	GAHQQDAAAPPPLVLGQQDSAR
4.4	2226.0382	0.1972	FFYETGIDFSNANSPSFKR
4.2	2226.1128	0.1226	DSEKGSTSNNLVIASTHIPEK
4.1	2226.0725	0.1629	EEEEELVEYILSTSRCLK
4.0	2226.0625	0.1729	VDSSSHSPHANSASLSSRVSSK
3.9	2226.0725	0.1629	YEKILEMISDEDIQSELR

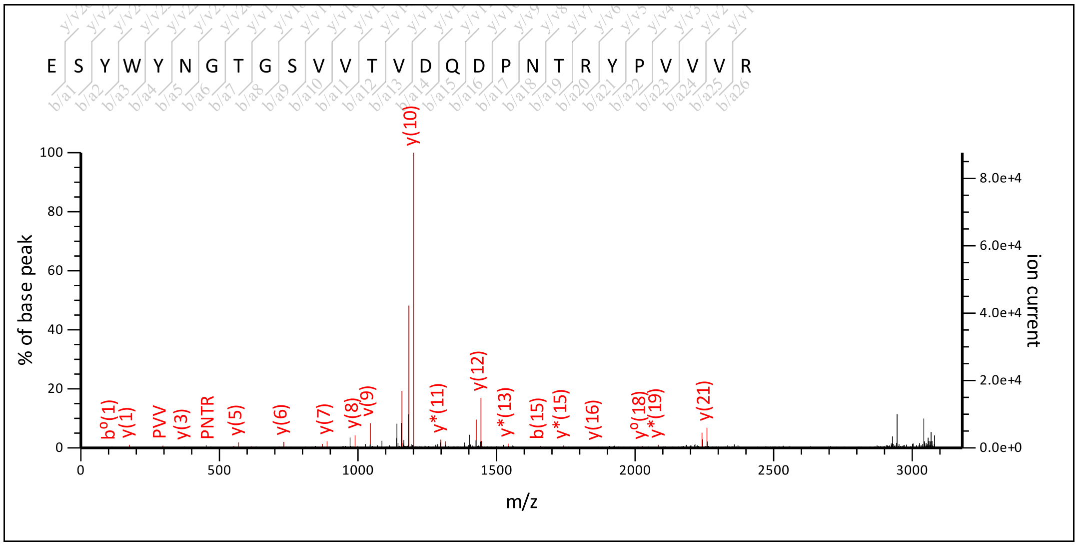
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 17

MS/MS Fragmentation of **ESYWYNGTGSVVTVDQDPNTRYPVVVR**
Found in **gi|34394725** in **NCBInr**, putative Photosystem I reaction center subunit IV [Oryza sativa Japonica Group]

Match to Query 26: 3100.773724 from(3101.781000,1+) intensity(0.0000) index(10)
Title: Label: O9, Spot_Id: 228984, Peak_List_Id: 257937, MSMS Job_Run_Id: 24944, Comment:
Data file ppw_O9_138985154400.txt



0 to 3180.62

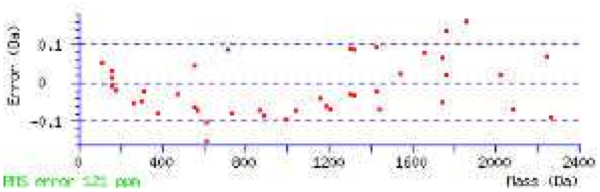
Label all possible matches ○ Label matches used for scoring ●

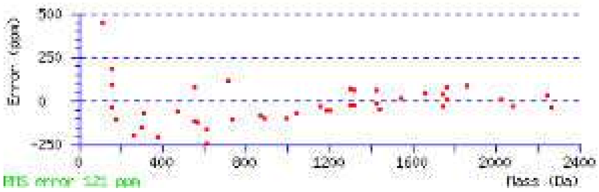
Monoisotopic mass of neutral peptide Mr(calc): 3100.4891
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 0.0033
Matches : 44/532 fragment ions using 62 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	60.0444	189.0870		171.0764	217.0819		199.0713	173.0921		S	2940.4275	2939.4323		2972.4537	2955.4272
3	136.0757	352.1503		334.1397	380.1452		362.1347			Y	2777.3642			2885.4217	2868.3951
4	159.0917	538.2296		520.2191	566.2245		548.2140			W	2591.2849			2722.3584	2705.3318
5	136.0757	701.2930		683.2824	729.2879		711.2773			Y	2428.2215			2536.2790	2519.2525
6	87.0553	815.3359	798.3093	797.3253	843.3308	826.3042	825.3202	772.3301		N	2314.1786	2313.1834		2373.2157	2356.1892
7	30.0338	872.3573	855.3308	854.3468	900.3523	883.3257	882.3417			G				***2259.1728***	2242.1462
8	74.0600	973.4050	956.3785	955.3945	1001.3999	984.3734	983.3894	957.4101	959.3894	T	2156.1095	2169.1299	2171.1091	2202.1513	2185.1248
9	30.0338	1030.4265	1013.3999	1012.4159	1058.4214	1041.3949	1040.4108			G				2101.1036	2084.0771
10	60.0444	1117.4585	1100.4320	1099.4480	1145.4534	1128.4269	1127.4429	1101.4636		S	2012.0560	2011.0607		2044.0822	2027.0556
11	72.0808	1216.5269	1199.5004	1198.5164	1244.5218	1227.4953	1226.5113	1202.5113		V	1912.9876	1926.0080		1957.0502	1940.0236
12	72.0808	**1315.5953**	1298.5688	1297.5848	1343.5903	1326.5637	1325.5797	1301.5797		V	1813.9191	1826.9395		***1857.9817***	1840.9552
13	74.0600	1416.6430	1399.6165	1398.6325	1444.6379	1427.6114	1426.6274	1400.6481	1402.6274	T	1712.8715	1725.8919	1727.8711	***1758.9133***	1741.8868
14	72.0808	1515.7114	1498.6849	1497.7009	1543.7064	1526.6798	1525.6958	1501.6958		V	1613.8030	1626.8234		1657.8656	1640.8391
15	88.0393	1630.7384	1613.7118	1612.7278	1658.7333	1641.7067	1640.7227	1586.7486		D	1498.7761	1497.7809		1558.7972	1541.7707
16	101.0709	**1758.7970**	1741.7704	1740.7864	1786.7919	1769.7653	1768.7813	1701.7755		Q	1370.7175	1369.7223		***1443.7703***	1426.7437
17	88.0393	1873.8239	1856.7974	1855.8133	1901.8188	1884.7923	1883.8083	1829.8341		D	1255.6906	1254.6953		***1315.7117***	1298.6852
18	70.0651	1970.8767	1953.8501	1952.8661	1998.8716	1981.8450	1980.8610	1944.8610		P	1158.6378	1157.6426		***1200.6848***	1183.6582
19	87.0553	2084.9196	2067.8930	2066.9090	2112.9145	2095.8880	2094.9039	2041.9138		N	1044.5949	1043.5996		1103.6320	1086.6055
20	74.0600	2185.9673	2168.9407	2167.9567	2213.9622	2196.9356	2195.9516	2169.9724	2171.9516	T	943.5472	956.5676	958.5469	***989.5891***	972.5625
21	129.1135	2342.0684	2325.0418	2324.0578	2370.0633	2353.0367	2352.0527	2257.0044		R	787.4461	786.4509		***888.5414***	871.5148
22	136.0757	2505.1317	2488.1052	2487.1211	2533.1266	2516.1001	2515.1161			Y	624.3828			***732.4403***	715.4137
23	70.0651	2602.1845	2585.1579	2584.1739	2630.1794	2613.1528	2612.1688	2576.1688		P	527.3300	526.3348		***569.3770***	552.3504

24	72.0808	2701.2529	2684.2263	2683.2423	2729.2478	2712.2213	2711.2372	2687.2372		V	428.2616	441.2820		472.3242	455.2976
25	72.0808	2800.3213	2783.2948	2782.3107	2828.3162	2811.2897	2810.3057	2786.3057		V	329.1932	342.2136		***373.2558***	356.2292
26	72.0808	2899.3897	2882.3632	2881.3792	2927.3846	2910.3581	2909.3741	2885.3741		V	230.1248	243.1452		274.1874	257.1608
27	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SY	223.1077	251.1026	**SYW**	409.1870	437.1819	**SYWY**	572.2504	600.2453
SYWYN	686.2933	714.2882	**YW**	322.1550	350.1499	**YWY**	485.2183	513.2132
YWYN	599.2613	627.2562	**YWYNG**	656.2827	684.2776	**WY**	322.1550	350.1499
WYN	436.1979	464.1928	**WYNG**	493.2194	521.2143	**WYNGT**	594.2671	622.2620
WYNGTG	651.2885	679.2835	**YN**	250.1186	278.1135	**YNG**	307.1401	335.1350
YNGT	408.1878	436.1827	**YNGTG**	465.2092	493.2041	**YNGTGS**	552.2413	580.2362
YNGTGSV	651.3097	679.3046	**NG**	144.0768	172.0717	**NGT**	245.1244	273.1193
NGTG	302.1459	330.1408	**NGTGS**	389.1779	417.1728	**NGTGSV**	488.2463	516.2413
NGTGSVV	587.3148	615.3097	**NGTGSVVT**	688.3624	716.3573	**GT**	131.0815	159.0764
GTG	188.1030	216.0979	**GTGS**	275.1350	303.1299	**GTGSV**	374.2034	402.1983
GTGSVV	473.2718	501.2667	**GTGSVVT**	574.3195	602.3144	**GTGSVVTV**	673.3879	701.3828
TG	131.0815	159.0764	**TGS**	218.1135	246.1084	**TGSV**	317.1819	345.1769
TGSVV	416.2504	444.2453	**TGSVVT**	517.2980	545.2930	**TGSVVTV**	616.3665	644.3614
GS	117.0659	145.0608	**GSV**	216.1343	244.1292	**GSVV**	315.2027	343.1976
GSVVT	416.2504	444.2453	**GSVVTV**	515.3188	543.3137	**GSVVTVD**	630.3457	658.3406
SV	159.1128	187.1077	**SVV**	258.1812	286.1761	**SVVT**	359.2289	387.2238
SVVTV	458.2973	486.2922	**SVVTVD**	573.3243	601.3192	**VV**	171.1492	199.1441
VVT	272.1969	300.1918	**VVTV**	371.2653	399.2602	**VVTVD**	486.2922	514.2871
VVTVDQ	614.3508	642.3457	**VT**	173.1285	201.1234	**VTV**	272.1969	300.1918
VTVD	387.2238	415.2187	**VTVDQ**	515.2824	543.2773	**VTVDQD**	630.3093	658.3042
TV	173.1285	201.1234	**TVD**	288.1554	316.1503	**TVDQ**	416.2140	444.2089
TVDQD	531.2409	559.2358	**TVDQDP**	628.2937	656.2886	**VD**	187.1077	215.1026
VDQ	315.1663	343.1612	**VDQD**	430.1932	458.1882	**VDQDP**	527.2460	555.2409
VDQDPN	641.2889	669.2838	**DQ**	216.0979	244.0928	**DQD**	331.1248	359.1197
DQDP	428.1776	456.1725	**DQDPN**	542.2205	570.2154	**DQDPNT**	643.2682	671.2631
QD	216.0979	244.0928	**QDP**	313.1506	341.1456	**QDPN**	427.1936	455.1885
QDPNT	528.2413	556.2362	**QDPNTR**	684.3424	712.3373	**DP**	185.0921	213.0870
DPN	299.1350	327.1299	**DPNT**	400.1827	428.1776	**DPNTR**	556.2838	584.2787
PN	184.1081	212.1030	**PNT**	285.1557	313.1506	**PNTR**	441.2568	469.2518
PNTRY	604.3202	632.3151	**NT**	188.1030	216.0979	**NTR**	344.2041	372.1990
NTRY	507.2674	535.2623	**NTRYP**	604.3202	632.3151	**TR**	230.1612	258.1561
TRY	393.2245	421.2194	**TRYP**	490.2772	518.2722	**TRYPV**	589.3457	617.3406
TRYPVV	688.4141	716.4090	**RY**	292.1768	320.1717	**RYP**	389.2296	417.2245
RYPV	488.2980	516.2929	**RYPVV**	587.3664	615.3613	**RYPVVV**	686.4348	714.4297
YP	233.1285	261.1234	**YPV**	332.1969	360.1918	**YPVV**	431.2653	459.2602
YPVVV	530.3337	558.3286	**PV**	169.1335	197.1285	**PVV**	268.2020	296.1969
PVVV	367.2704	395.2653	**VV**	171.1492	199.1441	**VVV**	270.2176	298.2125
VV	171.1492	199.1441						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.8	3100.4891	0.2847	ESYWYNGTGSVVTVDQDPNTRYPVVVR
2.4	3100.4648	0.3089	GNPGFGVSEMSGGVGFGWMGRTLVVASAWR
0.9	3100.4949	0.2788	NTSSTSSEFLYLGTIVNSRGGVDELSDPR
0.8	3100.5646	0.2091	VGGTVVMAMNGTVDGGSVVGPVTVNQNVTAVR
0.5	3100.5011	0.2726	FANWRDSLGCSMAPNPPKPENLPTVFR

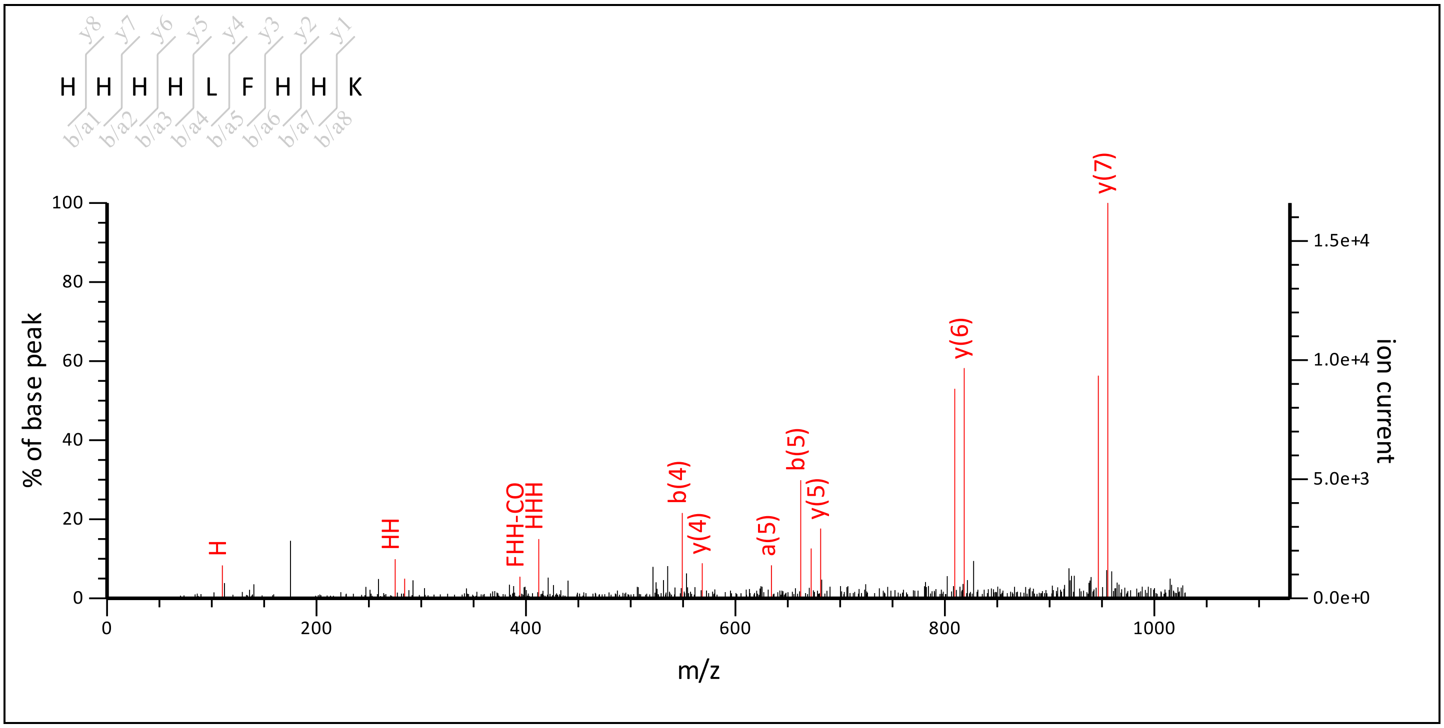
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 18

MS/MS Fragmentation of **HHHHLFHHK**
Found in **gi|15667623** in **NCBInr**, drought inducible 22 kD protein [Saccharum officinarum]

Match to Query 7: 1228.673524 from(1229.680800,1+) intensity(0.0000) index(2)
Title: Label: K8, Spot_Id: 219796, Peak_List_Id: 226437, MSMS Job_Run_Id: 21844, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K8_136859930300.txt



0 to 1129.46

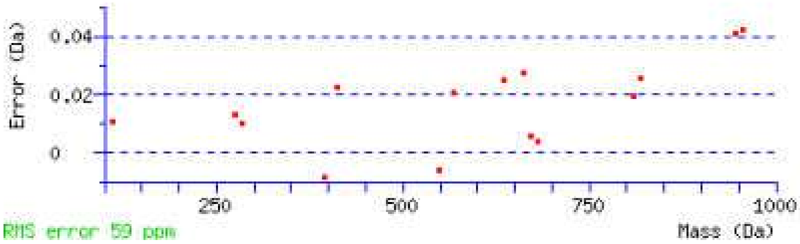
Label all possible matches ○ Label matches used for scoring ●

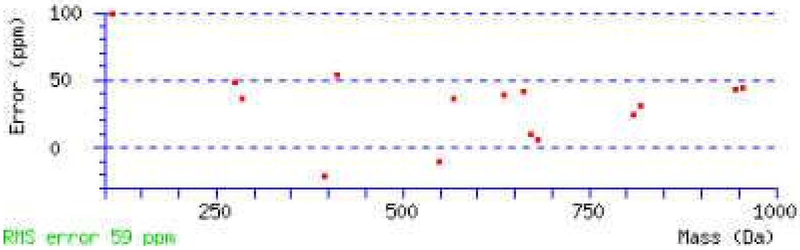
Monoisotopic mass of neutral peptide Mr(calc): 1228.6115
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 1.1
Matches : 27/89 fragment ions using 20 most intense peaks (help)

#	Immon.	a	b	d	Seq.	v	w	y	y*	#
1	110.0713	**110.0713**	138.0662	44.0495	H					9
2	110.0713	247.1302	***275.1251***		H	1010.5067		1092.5598	1075.5333	8
3	110.0713	384.1891	***412.1840***		H	873.4478		**955.5009**	938.4744	7
4	110.0713	521.2480	***549.2429***		H	736.3889		**818.4420**	801.4155	6
5	86.0964	**634.3321**	***662.3270***	592.2851	L	623.3049	622.3096	**681.3831**	664.3566	5
6	120.0808	781.4005	***809.3954***		F	476.2364		**568.2990**	551.2725	4
7	110.0713	918.4594	***946.4543***		H	339.1775		421.2306	404.2041	3
8	110.0713	1055.5183	1083.5132		H	202.1186		**284.1717**	267.1452	2

9	101.1073				K	74.0237	73.0284	147.1128	130.0863	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HH	247.1302	275.1251	HHH	384.1891	412.1840	HHHL	497.2732	525.2681
HHHLF	644.3416	672.3365	HH	247.1302	275.1251	HHL	360.2142	388.2092
HHLF	507.2827	535.2776	HHLFH	644.3416	672.3365	HL	223.1553	251.1503
HLF	370.2238	398.2187	HLFH	507.2827	535.2776	HLFHH	644.3416	672.3365
LF	233.1648	261.1598	LFH	370.2238	398.2187	LFHH	507.2827	535.2776
FH	257.1397	285.1346	FHH	394.1986	422.1935	HH	247.1302	275.1251





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.2	1228.6115	0.0620	HHHHLFHHK
30.6	1228.7153	-0.0417	RAALVAVHHQK
28.6	1228.7292	-0.0557	GLIAGVGLQVFR
27.7	1228.6313	0.0423	GSQEFIRHGAK
27.7	1228.6941	-0.0206	RPWQLHHKK
27.7	1228.6651	0.0084	WMHLLHHKK
27.5	1228.5533	0.1202	HHHHHHMTR
27.5	1228.6075	0.0661	HHHHHQLQR
27.5	1228.6075	0.0661	HHHHQQHLR
24.9	1228.5983	0.0753	ADAGPRLVDCR

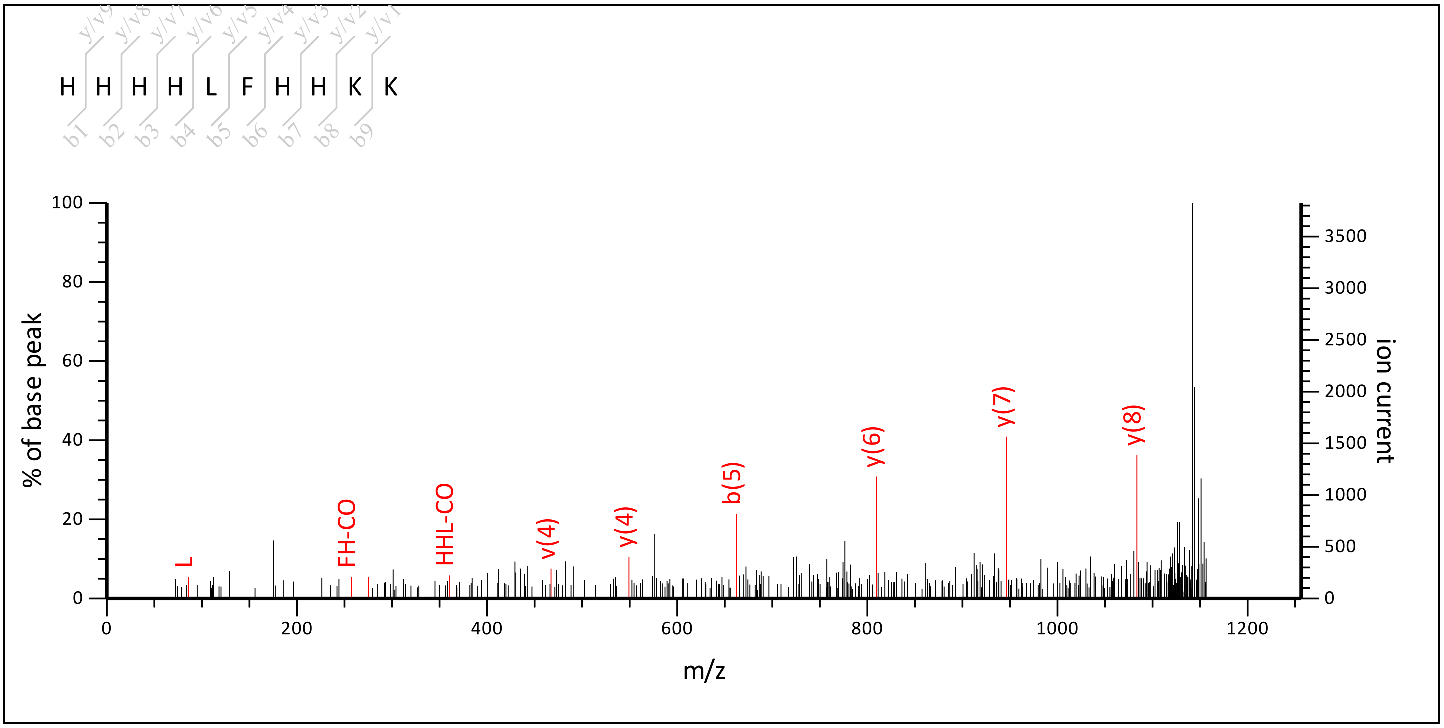
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 18

MS/MS Fragmentation of **HHHHLFHHKK**
Found in **gi|15667623** in **NCBInr**, drought inducible 22 kD protein [Saccharum officinarum]

Match to Query 10: 1356.769724 from(1357.777000,1+) intensity(0.0000) index(4)
Title: Label: K8, Spot_Id: 219796, Peak_List_Id: 226451, MSMS Job_Run_Id: 21844, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K8_136859930300.txt



0 to 1256.32

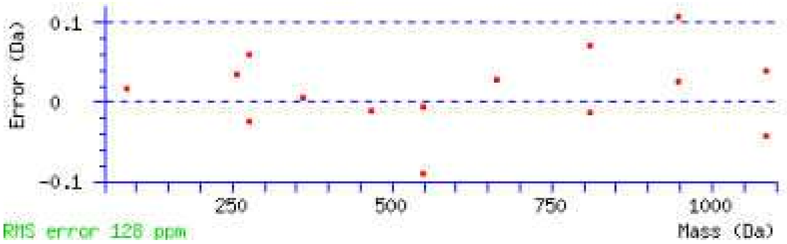
Label all possible matches ○ Label matches used for scoring ●

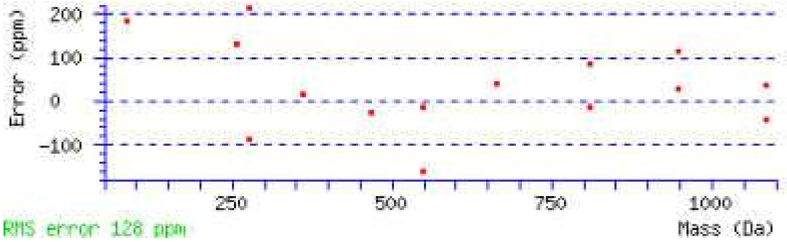
Monoisotopic mass of neutral peptide Mr(calc): 1356.7064
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 6.7e+02
Matches : 18/107 fragment ions using 33 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	110.0713	110.0713		138.0662		44.0495	H					10
2	110.0713	247.1302		***275.1251***			H	1138.6017		1220.6548	1203.6283	9
3	110.0713	384.1891		412.1840			H	1001.5428		**1083.5959**	1066.5693	8
4	110.0713	521.2480		***549.2429***			H	864.4839		**946.5370**	929.5104	7
5	86.0964	634.3321		***662.3270***		592.2851	L	751.3998	750.4046	**809.4781**	792.4515	6
6	120.0808	781.4005		***809.3954***			F	604.3314		696.3940	679.3675	5
7	110.0713	918.4594		***946.4543***			H	467.2725		**549.3256**	532.2990	4
8	110.0713	1055.5183		***1083.5132***			H	330.2136		412.2667	395.2401	3

9	101.1073	1183.6133	1166.5867	1211.6082	1194.5816	1126.5554	K	202.1186	201.1234	**275.2078**	258.1812	2
10	101.1073						K	74.0237	73.0284	147.1128	130.0863	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HH	247.1302	275.1251	**HHH**	384.1891	412.1840	**HHHL**	497.2732	525.2681
HHHLF	644.3416	672.3365	**HH**	247.1302	275.1251	**HHL**	360.2142	388.2092
HHLF	507.2827	535.2776	**HHLFH**	644.3416	672.3365	**HL**	223.1553	251.1503
HLF	370.2238	398.2187	**HLFH**	507.2827	535.2776	**HLFHH**	644.3416	672.3365
LF	233.1648	261.1598	**LFH**	370.2238	398.2187	**LFHH**	507.2827	535.2776
LFHHK	635.3776	663.3725	**FH**	257.1397	285.1346	**FHH**	394.1986	422.1935
FHHK	522.2936	550.2885	**HH**	247.1302	275.1251	**HHK**	375.2251	403.2201
HK	238.1662	266.1612						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.8	1356.8030	-0.0333	ILKGHFLQVFR
20.2	1356.6422	0.1275	AGDAPHFSSLEAR
17.7	1356.6568	0.1129	DPGAAGRALENMR
17.7	1356.8493	-0.0796	IPLATSLLKVFR
17.6	1356.7361	0.0336	IGLQIGNLSGETR
17.0	1356.7302	0.0395	ADPKHLFNFLR
16.7	1356.7064	0.0633	HHHHLFHHKK
16.5	1356.6820	0.0878	SSMRSLFSSSLR
15.6	1356.7184	0.0514	KGAPLPASSGGLMR
15.3	1356.7262	0.0435	AGTQHGLIPAHAGK

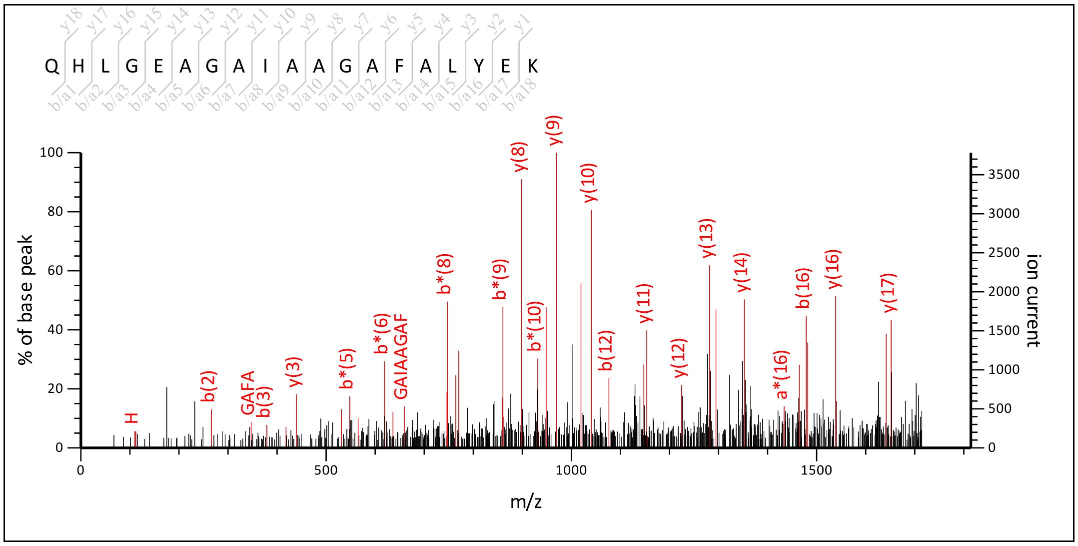
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 18

MS/MS Fragmentation of **QHLGEAGAIAAGAFALYEK**
Found in **gi|15667623** in **NCBInr**, drought inducible 22 kD protein [Saccharum officinarum]

Match to Query 24: 1916.054524 from(1917.061800,1+) intensity(0.0000) index(10)
Title: Label: K8, Spot_Id: 219796, Peak_List_Id: 226444, MSMS Job_Run_Id: 21844, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K8_136859930300.txt



0 to 1814.36

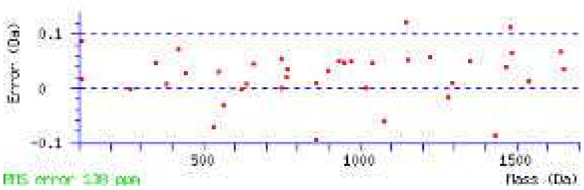
Label all possible matches ○ Label matches used for scoring ●

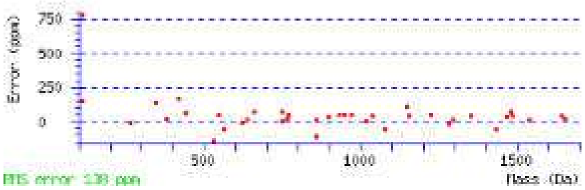
Monoisotopic mass of neutral peptide Mr(calc): 1915.9792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 105 **Expect:** 8.1e-07
Matches : 44/377 fragment ions using 51 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.0709	101.0709	84.0444		129.0659	112.0393		44.0495		Q					
2	110.0713	238.1299	221.1033		***266.1248***	249.0982				H	1706.8748			1788.9279	1771.9014
3	86.0964	351.2139	334.1874		***379.2088***	362.1823		309.1670		L	1593.7908	1592.7955		***1651.8690***	1634.8425
4	30.0338	408.2354	391.2088		436.2303	419.2037				G				***1538.7849***	1521.7584
5	102.0550	537.2780	520.2514	519.2674	***565.2729***	548.2463	547.2623	479.2725		E	1407.7267	1406.7314		***1481.7635***	1464.7369
6	44.0495	608.3151	591.2885	590.3045	***636.3100***	619.2835	618.2994			A	1336.6896			***1352.7209***	1335.6943
7	30.0338	665.3366	648.3100	647.3260	693.3315	676.3049	675.3209			G				***1281.6838***	1264.6572
8	44.0495	736.3737	719.3471	718.3631	***764.3686***	747.3420	746.3580			A	1208.6310			***1224.6623***	1207.6358
9	86.0964	849.4577	832.4312	831.4472	877.4526	860.4261	859.4421	821.4264	835.4421	I	1095.5469	1108.5673	1122.5830	***1153.6252***	1136.5986
10	44.0495	920.4948	903.4683	902.4843	***948.4898***	931.4632	930.4792			A	1024.5098			***1040.5411***	1023.5146
11	44.0495	991.5320	974.5054	973.5214	***1019.5269***	1002.5003	1001.5163			A	953.4727			***969.5040***	952.4775
12	30.0338	1048.5534	1031.5269	1030.5429	***1076.5483***	1059.5218	1058.5378			G				***898.4669***	881.4403
13	44.0495	1119.5905	1102.5640	1101.5800	***1147.5854***	1130.5589	1129.5749			A	825.4141			841.4454	824.4189
14	120.0808	1266.6589	1249.6324	1248.6484	***1294.6539***	1277.6273	1276.6433			F	678.3457			***770.4083***	753.3818
15	44.0495	1337.6961	1320.6695	1319.6855	1365.6910	1348.6644	1347.6804			A	607.3086			623.3399	606.3134
16	86.0964	1450.7801	1433.7536	1432.7696	***1478.7750***	1461.7485	1460.7645	1408.7332		L	494.2245	493.2293		552.3028	535.2762
17	136.0757	1613.8435	1596.8169	1595.8329	***1641.8384***	1624.8118	1623.8278			Y	331.1612			***439.2187***	422.1922
18	102.0550	1742.8860	1725.8595	1724.8755	1770.8810	1753.8544	1752.8704	1684.8806		E	202.1186	201.1234		276.1554	259.1288
19	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HL	223.1553	251.1503	**HLG**	280.1768	308.1717	**HLGE**	409.2194	437.2143
HLGEA	480.2565	508.2514	**HLGEAG**	537.2780	565.2729	**HLGEAGA**	608.3151	636.3100

LG	143.1179	171.1128	**LGE**	272.1605	300.1554	**LGEA**	343.1976	371.1925
LGEAG	400.2191	428.2140	**LGEAGA**	471.2562	499.2511	**LGEAGAI**	584.3402	612.3352
LGEAGAIA	655.3774	683.3723	**GE**	159.0764	187.0713	**GEA**	230.1135	258.1084
GEAG	287.1350	315.1299	**GEAGA**	358.1721	386.1670	**GEAGAI**	471.2562	499.2511
GEAGAIA	542.2933	570.2882	**GEAGAIAA**	613.3304	641.3253	**GEAGAIAAG**	670.3519	698.3468
EA	173.0921	201.0870	**EAG**	230.1135	258.1084	**EAGA**	301.1506	329.1456
EAGAI	414.2347	442.2296	**EAGAIA**	485.2718	513.2667	**EAGAIAA**	556.3089	584.3039
EAGAIAAG	613.3304	641.3253	**EAGAIAAGA**	684.3675	712.3624	**AG**	101.0709	129.0659
AGA	172.1081	200.1030	**AGAI**	285.1921	313.1870	**AGAIA**	356.2292	384.2241
AGAIAA	427.2663	455.2613	**AGAIAAG**	484.2878	512.2827	**AGAIAAGA**	555.3249	583.3198
GA	101.0709	129.0659	**GAI**	214.1550	242.1499	**GAIA**	285.1921	313.1870
GAIAA	356.2292	384.2241	**GAIAAG**	413.2507	441.2456	**GAIAAGA**	484.2878	512.2827
GAIAAGAF	631.3562	659.3511	**AI**	157.1335	185.1285	**AIA**	228.1707	256.1656
AIAA	299.2078	327.2027	**AIAAG**	356.2292	384.2241	**AIAAGA**	427.2663	455.2613
AIAAGAF	574.3348	602.3297	**AIAAGAFA**	645.3719	673.3668	**IA**	157.1335	185.1285
IAA	228.1707	256.1656	**IAAG**	285.1921	313.1870	**IAAGA**	356.2292	384.2241
IAAGAF	503.2976	531.2926	**IAAGAFA**	574.3348	602.3297	**IAAGAFAL**	687.4188	715.4137
AA	115.0866	143.0815	**AAG**	172.1081	200.1030	**AAGA**	243.1452	271.1401
AAGAF	390.2136	418.2085	**AAGAFA**	461.2507	489.2456	**AAGAFAL**	574.3348	602.3297
AG	101.0709	129.0659	**AGA**	172.1081	200.1030	**AGAF**	319.1765	347.1714
AGAFA	390.2136	418.2085	**AGAFAL**	503.2976	531.2926	**AGAFALY**	666.3610	694.3559
GA	101.0709	129.0659	**GAF**	248.1394	276.1343	**GAFA**	319.1765	347.1714
GAFAL	432.2605	460.2554	**GAFALY**	595.3239	623.3188	**AF**	191.1179	219.1128
AFA	262.1550	290.1499	**AFAL**	375.2391	403.2340	**AFALY**	538.3024	566.2973
AFALYE	667.3450	695.3399	**FA**	191.1179	219.1128	**FAL**	304.2020	332.1969
FALY	467.2653	495.2602	**FALYE**	596.3079	624.3028	**AL**	157.1335	185.1285
ALY	320.1969	348.1918	**ALYE**	449.2395	477.2344	**LY**	249.1598	277.1547
LYE	378.2023	406.1973	**YE**	265.1183	293.1132			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
104.9	1915.9792	0.0754	QHLGEAGAIAAGAFALYEK
104.9	1915.9792	0.0754	QHLGEAGALAAGAFALYEK
21.1	1916.0592	-0.0047	LLLTHDAHRITVTVGDR
20.6	1915.8768	0.1778	MDSASMTAAAKALADAGFR
16.1	1916.0150	0.0396	IGDVVTKGQAIALMGNTGR
15.4	1916.0731	-0.0186	TVAVIGGGVSGLAAAKAFAEK
14.7	1915.9534	0.1011	GSGKGGQLQAAMAQIAEAGR
14.6	1915.9561	0.0984	DVMGTDDPLILSLISGDR
14.4	1915.9866	0.0679	DFLLMKPSAYFINVSR
14.2	1915.9064	0.1481	AGDYFSEAGATPATKAFGR

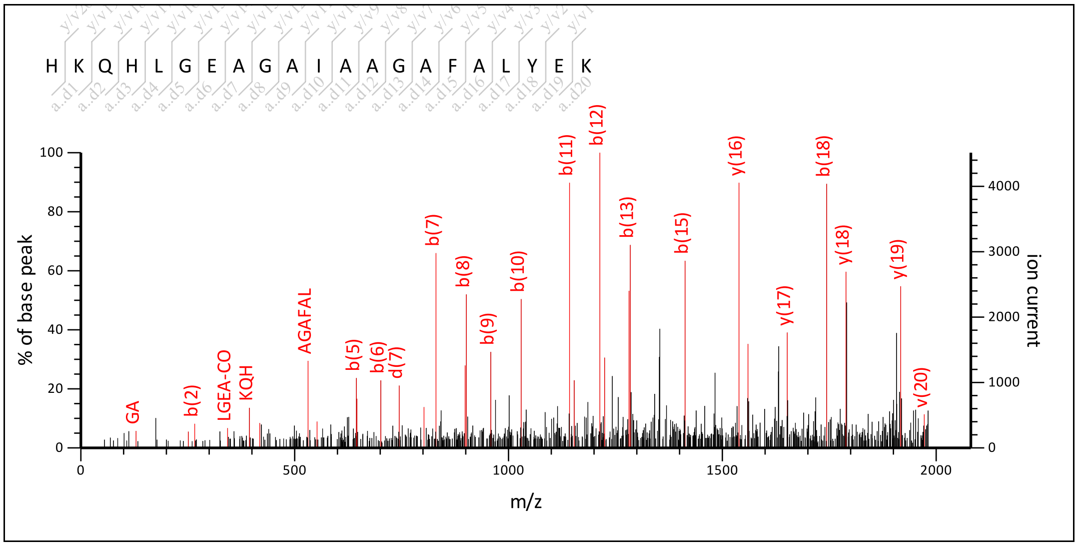
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 18

MS/MS Fragmentation of **HKQHLGEAGAIAAGAFALYEK**
Found in **gi|15667623** in **NCBInr**, drought inducible 22 kD protein [Saccharum officinarum]

Match to Query 26: 2181.221024 from(2182.228300,1+) intensity(0.0000) index(11)
Title: Label: K8, Spot_Id: 219796, Peak_List_Id: 226439, MSMS Job_Run_Id: 21844, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K8_136859930300.txt



0 to 2081.08

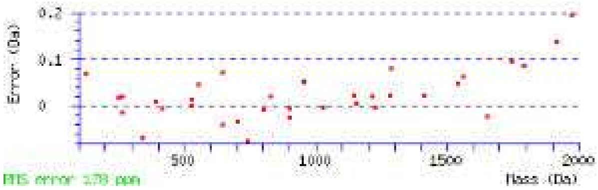
Label all possible matches ○ Label matches used for scoring ●

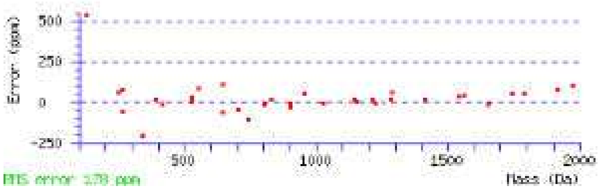
Monoisotopic mass of neutral peptide Mr(calc): 2181.1330
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 131 **Expect:** 1.7e-09
Matches : 40/419 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	110.0713	110.0713			138.0662			44.0495		H					
2	101.1073	238.1662	221.1397		***266.1612***	249.1346		181.1084		K	1971.9923	1970.9971		2045.0815	2028.0549
3	101.0709	366.2248	349.1983		***394.2197***	377.1932		309.2034		Q	1843.9337	1842.9385		**1916.9865**	1899.9599
4	110.0713	503.2837	486.2572		***531.2786***	514.2521				H	1706.8748			**1788.9279**	1771.9014
5	86.0964	616.3678	599.3412		***644.3627***	627.3362		574.3208		L	1593.7908	1592.7955		**1651.8690**	1634.8425
6	30.0338	673.3893	656.3627		***701.3842***	684.3576				G				**1538.7849**	1521.7584
7	102.0550	802.4318	785.4053	784.4213	***830.4268***	813.4002	812.4162	744.4264		E	1407.7267	1406.7314		1481.7635	1464.7369
8	44.0495	873.4690	856.4424	855.4584	***901.4639***	884.4373	883.4533			A	1336.6896			1352.7209	1335.6943
9	30.0338	930.4904	913.4639	912.4799	***958.4853***	941.4588	940.4748			G				**1281.6838**	1264.6572
10	44.0495	1001.5275	984.5010	983.5170	***1029.5225***	1012.4959	1011.5119			A	1208.6310			**1224.6623**	1207.6358
11	86.0964	1114.6116	1097.5851	1096.6010	***1142.6065***	1125.5800	1124.5960	1086.5803	1100.5960	I	1095.5469	1108.5673	1122.5830	**1153.6252**	1136.5986
12	44.0495	1185.6487	1168.6222	1167.6382	***1213.6436***	1196.6171	1195.6331			A	1024.5098			1040.5411	1023.5146
13	44.0495	1256.6858	1239.6593	1238.6753	***1284.6807***	1267.6542	1266.6702			A	953.4727			969.5040	952.4775
14	30.0338	1313.7073	1296.6807	1295.6967	1341.7022	1324.6757	1323.6916			G				**898.4669**	881.4403
15	44.0495	1384.7444	1367.7179	1366.7338	***1412.7393***	1395.7128	1394.7288			A	825.4141			841.4454	824.4189
16	120.0808	1531.8128	1514.7863	1513.8023	***1559.8077***	1542.7812	1541.7972			F	678.3457			770.4083	753.3818
17	44.0495	1602.8499	1585.8234	1584.8394	1630.8449	1613.8183	1612.8343			A	607.3086			623.3399	606.3134
18	86.0964	1715.9340	1698.9075	1697.9234	***1743.9289***	1726.9024	1725.9184	1673.8871		L	494.2245	493.2293		**552.3028**	535.2762
19	136.0757	1878.9973	1861.9708	1860.9868	1906.9922	1889.9657	1888.9817			Y	331.1612			439.2187	422.1922
20	102.0550	2008.0399	1991.0134	1990.0294	2036.0348	2019.0083	2018.0243	1950.0344		E	202.1186	201.1234		276.1554	259.1288
21	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

KQ	229.1659	257.1608	**KQH**	366.2248	394.2197	**KQHL**	479.3089	507.3038
KQHLG	536.3303	564.3253	**KQHLGE**	665.3729	693.3679	**QH**	238.1299	266.1248
QHL	351.2139	379.2088	**QHLG**	408.2354	436.2303	**QHLGE**	537.2780	565.2729
QHLGEA	608.3151	636.3100	**QHLGEAG**	665.3366	693.3315	**HL**	223.1553	251.1503
HLG	280.1768	308.1717	**HLGE**	409.2194	437.2143	**HLGEA**	480.2565	508.2514
HLGEAG	537.2780	565.2729	**HLGEAGA**	608.3151	636.3100	**LG**	143.1179	171.1128
LGE	272.1605	300.1554	**LGEA**	343.1976	371.1925	**LGEAG**	400.2191	428.2140
LGEAGA	471.2562	499.2511	**LGEAGAI**	584.3402	612.3352	**LGEAGAIA**	655.3774	683.3723
GE	159.0764	187.0713	**GEA**	230.1135	258.1084	**GEAG**	287.1350	315.1299
GEAGA	358.1721	386.1670	**GEAGAI**	471.2562	499.2511	**GEAGAIA**	542.2933	570.2882
GEAGAIAA	613.3304	641.3253	**GEAGAIAAG**	670.3519	698.3468	**EA**	173.0921	201.0870
EAG	230.1135	258.1084	**EAGA**	301.1506	329.1456	**EAGAI**	414.2347	442.2296
EAGAIA	485.2718	513.2667	**EAGAIAA**	556.3089	584.3039	**EAGAIAAG**	613.3304	641.3253
EAGAIAAGA	684.3675	712.3624	**AG**	101.0709	129.0659	**AGA**	172.1081	200.1030
AGAI	285.1921	313.1870	**AGAIA**	356.2292	384.2241	**AGAIAA**	427.2663	455.2613
AGAIAAG	484.2878	512.2827	**AGAIAAGA**	555.3249	583.3198	**GA**	101.0709	129.0659
GAI	214.1550	242.1499	**GAIA**	285.1921	313.1870	**GAIAA**	356.2292	384.2241
GAIAAG	413.2507	441.2456	**GAIAAGA**	484.2878	512.2827	**GAIAAGAF**	631.3562	659.3511
AI	157.1335	185.1285	**AIA**	228.1707	256.1656	**AIAA**	299.2078	327.2027
AIAAG	356.2292	384.2241	**AIAAGA**	427.2663	455.2613	**AIAAGAF**	574.3348	602.3297
AIAAGAFA	645.3719	673.3668	**IA**	157.1335	185.1285	**IAA**	228.1707	256.1656
IAAG	285.1921	313.1870	**IAAGA**	356.2292	384.2241	**IAAGAF**	503.2976	531.2926
IAAGAFA	574.3348	602.3297	**IAAGAFAL**	687.4188	715.4137	**AA**	115.0866	143.0815
AAG	172.1081	200.1030	**AAGA**	243.1452	271.1401	**AAGAF**	390.2136	418.2085
AAGAFA	461.2507	489.2456	**AAGAFAL**	574.3348	602.3297	**AG**	101.0709	129.0659
AGA	172.1081	200.1030	**AGAF**	319.1765	347.1714	**AGAFA**	390.2136	418.2085
AGAFAL	503.2976	531.2926	**AGAFALY**	666.3610	694.3559	**GA**	101.0709	129.0659
GAF	248.1394	276.1343	**GAFA**	319.1765	347.1714	**GAFAL**	432.2605	460.2554
GAFALY	595.3239	623.3188	**AF**	191.1179	219.1128	**AFA**	262.1550	290.1499
AFAL	375.2391	403.2340	**AFALY**	538.3024	566.2973	**AFALYE**	667.3450	695.3399
FA	191.1179	219.1128	**FAL**	304.2020	332.1969	**FALY**	467.2653	495.2602
FALYE	596.3079	624.3028	**AL**	157.1335	185.1285	**ALY**	320.1969	348.1918
ALYE	449.2395	477.2344	**LY**	249.1598	277.1547	**LYE**	378.2023	406.1973
YE	265.1183	293.1132						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
130.7	2181.1330	0.0880	HKQHLGEAGAIAAGAFALYEK
130.7	2181.1330	0.0880	HKQHLGEAGALAAGAFALYEK
29.5	2181.2344	-0.0133	MAIGAALGAAVSLALLVVWSPR
25.2	2181.2382	-0.0172	GHTGHLLGGAGALAAVVVLEALR
25.1	2181.1688	0.0522	HIAGMDNTLSLTQVGIRSLR
21.9	2181.2018	0.0192	QHQIASYLGITPTQLSRIR
21.1	2181.0675	0.1535	HQPAPLGPPAQEGGQEGAERR
20.8	2181.2020	0.0190	LFIPYTAVALAGAVNVFLMR
20.6	2181.1100	0.1111	IGDNMLGISQLNDTVHVLDK

20.0	2181.2633	-0.0423	GLGFRLLVLALAAAAAAEVEAR

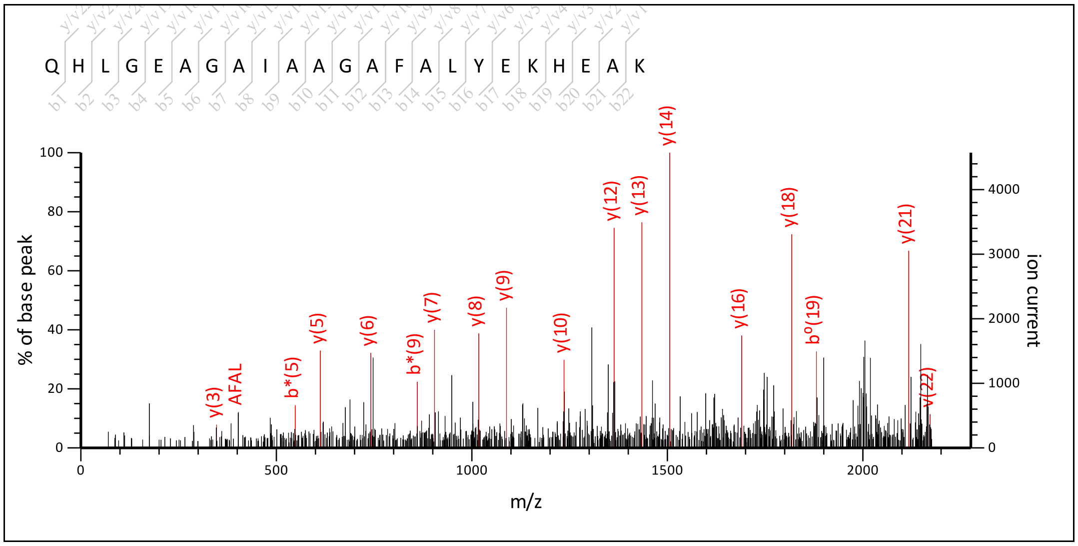
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 18

MS/MS Fragmentation of **QHLGEAGAIAAGAFALYEKHEAK**
Found in **gi|15667623** in **NCBInr**, drought inducible 22 kD protein [Saccharum officinarum]

Match to Query 35: 2381.304724 from(2382.312000,1+) intensity(0.0000) index(15)
Title: Label: K8, Spot_Id: 219796, Peak_List_Id: 226441, MSMS Job_Run_Id: 21844, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K8_136859930300.txt



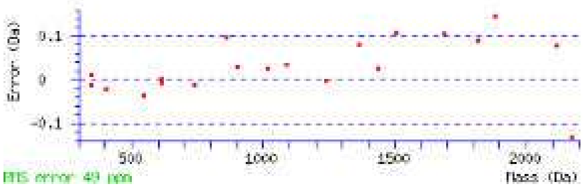
0 to 2276.14

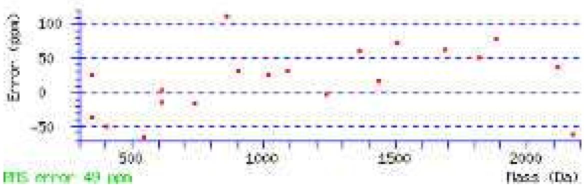
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): `2381.2127`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `100` **Expect:** `1.9e-06`
Matches : `21/456 fragment ions using 22 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.0709	101.0709	84.0444		129.0659	112.0393		44.0495		Q					
2	110.0713	238.1299	221.1033		266.1248	249.0982				H	2172.1084			2254.1615	2237.1349
3	86.0964	351.2139	334.1874		379.2088	362.1823		309.1670		L	2059.0243	2058.0291		***2117.1026***	2100.0760
4	30.0338	408.2354	391.2088		436.2303	419.2037				G				2004.0185	1986.9920
5	102.0550	537.2780	520.2514	519.2674	565.2729	548.2463	547.2623	479.2725		E	1872.9603	1871.9650		1946.9971	1929.9705
6	44.0495	608.3151	591.2885	590.3045	636.3100	619.2835	618.2994			A	1801.9232			***1817.9545***	1800.9279
7	30.0338	665.3366	648.3100	647.3260	693.3315	676.3049	675.3209			G				1746.9173	1729.8908
8	44.0495	736.3737	719.3471	718.3631	764.3686	747.3420	746.3580			A	1673.8646			***1689.8959***	1672.8693
9	86.0964	849.4577	832.4312	831.4472	877.4526	860.4261	859.4421	821.4264	835.4421	I	1560.7805	1573.8009	1587.8166	1618.8588	1601.8322
10	44.0495	920.4948	903.4683	902.4843	948.4898	931.4632	930.4792			A	1489.7434			***1505.7747***	1488.7482
11	44.0495	991.5320	974.5054	973.5214	1019.5269	1002.5003	1001.5163			A	1418.7063			***1434.7376***	1417.7110
12	30.0338	1048.5534	1031.5269	1030.5429	1076.5483	1059.5218	1058.5378			G				***1363.7005***	1346.6739
13	44.0495	1119.5905	1102.5640	1101.5800	1147.5854	1130.5589	1129.5749			A	1290.6477			1306.6790	1289.6525
14	120.0808	1266.6589	1249.6324	1248.6484	1294.6539	1277.6273	1276.6433			F	1143.5793			***1235.6419***	1218.6154
15	44.0495	1337.6961	1320.6695	1319.6855	1365.6910	1348.6644	1347.6804			A	1072.5422			***1088.5735***	1071.5469
16	86.0964	1450.7801	1433.7536	1432.7696	1478.7750	1461.7485	1460.7645	1408.7332		L	959.4581	958.4629		***1017.5364***	1000.5098
17	136.0757	1613.8435	1596.8169	1595.8329	1641.8384	1624.8118	1623.8278			Y	796.3948			***904.4523***	887.4258
18	102.0550	1742.8860	1725.8595	1724.8755	1770.8810	1753.8544	1752.8704	1684.8806		E	667.3522	666.3570		***741.3890***	724.3624
19	101.1073	1870.9810	1853.9545	1852.9704	1898.9759	1881.9494	1880.9654	1813.9232		K	539.2572	538.2620		***612.3464***	595.3198
20	110.0713	2008.0399	1991.0134	1990.0294	2036.0348	2019.0083	2018.0243			H	402.1983			484.2514	467.2249
21	102.0550	2137.0825	2120.0560	2119.0720	2165.0774	2148.0509	2147.0669	2079.0770		E	273.1557	272.1605		***347.1925***	330.1660
22	44.0495	2208.1196	2191.0931	2190.1091	2236.1145	2219.0880	2218.1040			A	202.1186			218.1499	201.1234
23	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HL	223.1553	251.1503	HLG	280.1768	308.1717	HLGE	409.2194	437.2143
HLGEA	480.2565	508.2514	HLGEAG	537.2780	565.2729	HLGEAGA	608.3151	636.3100
LG	143.1179	171.1128	LGE	272.1605	300.1554	LGEA	343.1976	371.1925
LGEAG	400.2191	428.2140	LGEAGA	471.2562	499.2511	LGEAGAI	584.3402	612.3352
LGEAGAIA	655.3774	683.3723	GE	159.0764	187.0713	GEA	230.1135	258.1084
GEAG	287.1350	315.1299	GEAGA	358.1721	386.1670	GEAGAI	471.2562	499.2511
GEAGAIA	542.2933	570.2882	GEAGAIAA	613.3304	641.3253	GEAGAIAAG	670.3519	698.3468
EA	173.0921	201.0870	EAG	230.1135	258.1084	EAGA	301.1506	329.1456
EAGAI	414.2347	442.2296	EAGAIA	485.2718	513.2667	EAGAIAA	556.3089	584.3039
EAGAIAAG	613.3304	641.3253	EAGAIAAGA	684.3675	712.3624	AG	101.0709	129.0659
AGA	172.1081	200.1030	AGAI	285.1921	313.1870	AGAIA	356.2292	384.2241
AGAIAA	427.2663	455.2613	AGAIAAG	484.2878	512.2827	AGAIAAGA	555.3249	583.3198
GA	101.0709	129.0659	GAI	214.1550	242.1499	GAIA	285.1921	313.1870
GAIAA	356.2292	384.2241	GAIAAG	413.2507	441.2456	GAIAAGA	484.2878	512.2827
GAIAAGAF	631.3562	659.3511	AI	157.1335	185.1285	AIA	228.1707	256.1656
AIAA	299.2078	327.2027	AIAAG	356.2292	384.2241	AIAAGA	427.2663	455.2613
AIAAGAF	574.3348	602.3297	AIAAGAFA	645.3719	673.3668	IA	157.1335	185.1285
IAA	228.1707	256.1656	IAAG	285.1921	313.1870	IAAGA	356.2292	384.2241
IAAGAF	503.2976	531.2926	IAAGAFA	574.3348	602.3297	IAAGAFAL	687.4188	715.4137
AA	115.0866	143.0815	AAG	172.1081	200.1030	AAGA	243.1452	271.1401
AAGAF	390.2136	418.2085	AAGAFA	461.2507	489.2456	AAGAFAL	574.3348	602.3297
AG	101.0709	129.0659	AGA	172.1081	200.1030	AGAF	319.1765	347.1714
AGAFA	390.2136	418.2085	AGAFAL	503.2976	531.2926	AGAFALY	666.3610	694.3559
GA	101.0709	129.0659	GAF	248.1394	276.1343	GAFA	319.1765	347.1714
GAFAL	432.2605	460.2554	GAFALY	595.3239	623.3188	AF	191.1179	219.1128
AFA	262.1550	290.1499	AFAL	375.2391	403.2340	AFALY	538.3024	566.2973
AFALYE	667.3450	695.3399	FA	191.1179	219.1128	FAL	304.2020	332.1969
FALY	467.2653	495.2602	FALYE	596.3079	624.3028	AL	157.1335	185.1285
ALY	320.1969	348.1918	ALYE	449.2395	477.2344	ALYEK	577.3344	605.3293
LY	249.1598	277.1547	LYE	378.2023	406.1973	LYEK	506.2973	534.2922
LYEKH	643.3562	671.3511	YE	265.1183	293.1132	YEK	393.2132	421.2082
YEKH	530.2722	558.2671	YEKHE	659.3148	687.3097	EK	230.1499	258.1448
EKH	367.2088	395.2037	EKHE	496.2514	524.2463	EKHEA	567.2885	595.2835
KH	238.1662	266.1612	KHE	367.2088	395.2037	KHEA	438.2459	466.2409
HE	239.1139	267.1088	HEA	310.1510	338.1459	EA	173.0921	201.0870





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.1	2381.2127	0.0920	QHLGEAGAIAAGAFALYEKHEAK
100.1	2381.2127	0.0920	QHLGEAGALAAGAFALYEKHEAK
17.7	2381.1971	0.1077	MSVADLPTTALFQALLSGIMDR
17.1	2381.1436	0.1611	SDIVVMVATLAFFGFACGEFGK
16.4	2381.2664	0.0383	LLEQDYSVQFALALMLKDLR
14.5	2381.1144	0.1903	DVSHPNMGYAFKAVGNGLEMTK

12.9	2381.1719	0.1328	HMNALLSKTATSDEGYVMLIR
11.7	2381.1177	0.1870	HSMAMVGMAAKQLYVGEEAQAK
11.5	2381.1256	0.1791	AQCPDGYVGQFAADVDRMLLR
11.5	2381.1733	0.1314	GGSQTWRVFGAMAGGGCLLATLR

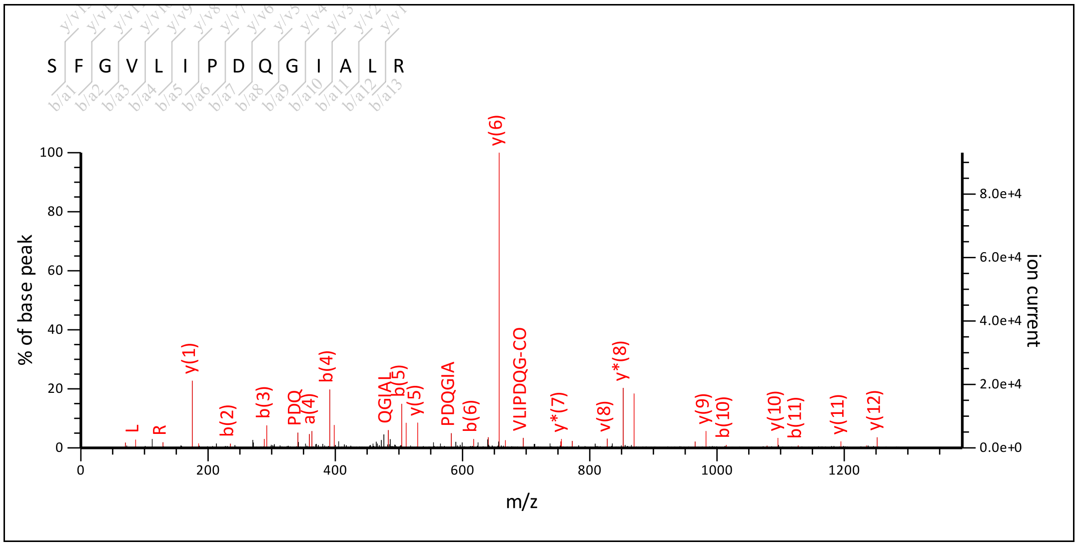
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 19

MS/MS Fragmentation of **SFGVLIPDQGIALR**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 81: 1484.901924 from(1485.909200,1+) intensity(0.0000) index(13)
Title: Label: H17, Spot_Id: 219937, Peak_List_Id: 228919, MSMS Job_Run_Id: 22005, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H17_136868316000.txt



0 to 1385.58

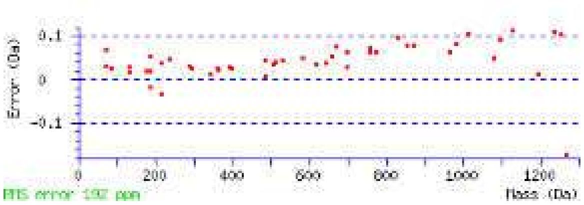
Label all possible matches ○ Label matches used for scoring ●

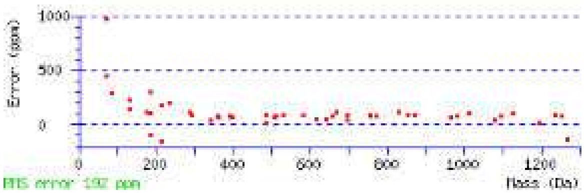
```
Monoisotopic mass of neutral peptide Mr(calc): 1484.8351
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 90  Expect: 1.7e-05
Matches : 56/238 fragment ions using 52 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S						
2	120.0808	207.1128		189.1022	**235.1077**		217.0972			F	1306.7478			1398.8104	1381.7838	13
3	30.0338	264.1343		246.1237	**292.1292**		274.1186			G				***1251.7419***	1234.7154	12
4	72.0808	363.2027		345.1921	**391.1976**		373.1870	349.1870		V	1150.6579	1163.6783		***1194.7205***	1177.6939	11
5	86.0964	476.2867		458.2762	**504.2817**		486.2711	434.2398		L	1037.5738	1036.5786		***1095.6521***	1078.6255	10
6	86.0964	589.3708		571.3602	**617.3657**		599.3552	561.3395	575.3552	I	924.4898	937.5102	951.5258	***982.5680***	965.5415	96
7	70.0651	686.4236		668.4130	714.4185		696.4079	660.4079		P	827.4370	826.4417		***869.4839***	852.4574	8
8	88.0393	801.4505		783.4400	829.4454		811.4349	757.4607		D	712.4100	711.4148		***772.4312***	755.4046	7
9	101.0709	929.5091	912.4825	911.4985	957.5040	940.4775	939.4934	872.4876		Q	584.3515	583.3562		***657.4042***	640.3777	
10	30.0338	986.5306	969.5040	968.5200	**1014.5255**	997.4989	996.5149			G				***529.3457***	512.3191	
11	86.0964	1099.6146	1082.5881	1081.6041	**1127.6095**	1110.5830	1109.5990	1071.5833	1085.5990	I	414.2459	427.2663	441.2820	472.3242	455.2976	
12	44.0495	1170.6517	1153.6252	1152.6412	1198.6467	1181.6201	1180.6361			A	343.2088			***359.2401***	342.2136	
13	86.0964	1283.7358	1266.7093	1265.7252	1311.7307	1294.7042	1293.7201	1241.6889		L	230.1248	229.1295		***288.2030***	271.1765	
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FG	177.1022	205.0972	**FGV**	276.1707	304.1656	**FGVL**	389.2547	417.2496
FGVLI	502.3388	530.3337	**FGVLIP**	599.3915	627.3865	**GV**	129.1022	157.0972
GVL	242.1863	270.1812	**GVLI**	355.2704	383.2653	**GVLIP**	452.3231	480.3180
GVLIPD	567.3501	595.3450	**GVLIPDQ**	695.4087	723.4036	**VL**	185.1648	213.1598
VLI	298.2489	326.2438	**VLIP**	395.3017	423.2966	**VLIPD**	510.3286	538.3235
VLIPDQ	638.3872	666.3821	**VLIPDQG**	695.4087	723.4036	**LI**	199.1805	227.1754
LIP	296.2333	324.2282	**LIPD**	411.2602	439.2551	**LIPDQ**	539.3188	567.3137

LIPDQG	596.3402	624.3352	**IP**	183.1492	211.1441	**IPD**	298.1761	326.1710
IPDQ	426.2347	454.2296	**IPDQG**	483.2562	511.2511	**IPDQGI**	596.3402	624.3352
IPDQGIA	667.3774	695.3723	**PD**	185.0921	213.0870	**PDQ**	313.1506	341.1456
PDQG	370.1721	398.1670	**PDQGI**	483.2562	511.2511	**PDQGIA**	554.2933	582.2882
PDQGIAL	667.3774	695.3723	**DQ**	216.0979	244.0928	**DQG**	273.1193	301.1143
DQGI	386.2034	414.1983	**DQGIA**	457.2405	485.2354	**DQGIAL**	570.3246	598.3195
QG	158.0924	186.0873	**QGI**	271.1765	299.1714	**QGIA**	342.2136	370.2085
QGIAL	455.2976	483.2926	**GI**	143.1179	171.1128	**GIA**	214.1550	242.1499
GIAL	327.2391	355.2340	**IA**	157.1335	185.1285	**IAL**	270.2176	298.2125
AL	157.1335	185.1285						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
90.4	1484.8351	0.0668	SFGVLIPDQGIALR
32.3	1484.8674	0.0345	SSLALAVARLIESR
32.0	1484.7835	0.1185	VTSAIANVLPDETR
30.4	1484.8212	0.0807	FSRIIVSASHVNR
30.4	1484.8576	0.0444	HPRLLTITEHIR
30.4	1484.8212	0.0807	SFRLLSQLTQHR
30.0	1484.8861	0.0158	LSSIAAVRIVAMVR
29.9	1484.7697	0.1322	MSRLFAFLIDEK
29.9	1484.8562	0.0457	LVQIITSNILDTR
27.7	1484.7875	0.1144	FDKILTITYESR

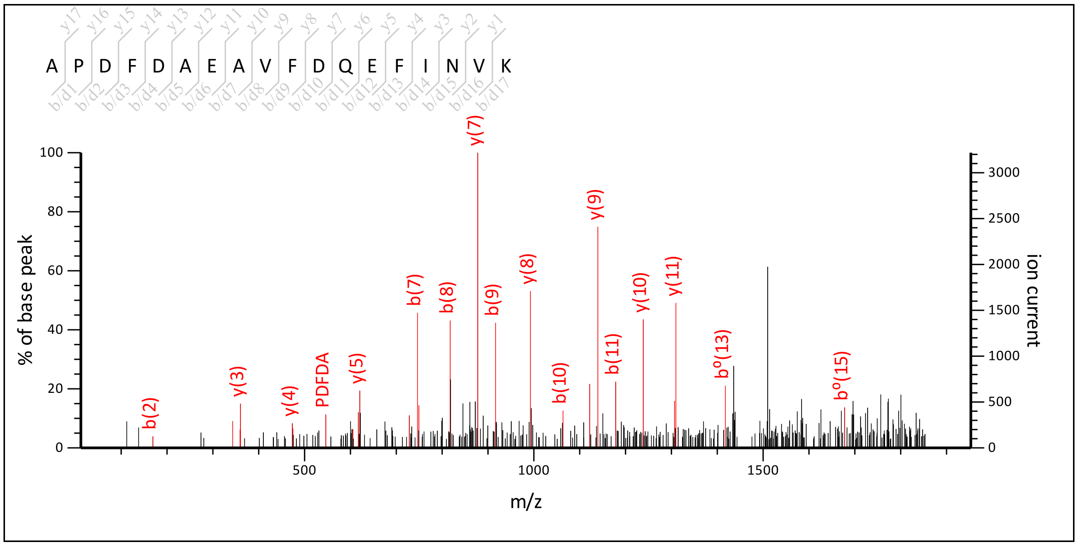
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 19

MS/MS Fragmentation of **APDFDAEAVFDQEFINVK**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 92: 2054.045724 from(2055.053000,1+) intensity(0.0000) index(18)
Title: Label: H17, Spot_Id: 219937, Peak_List_Id: 228922, MSMS Job_Run_Id: 22005, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H17_136868316000.txt



12.11 to 1953.01

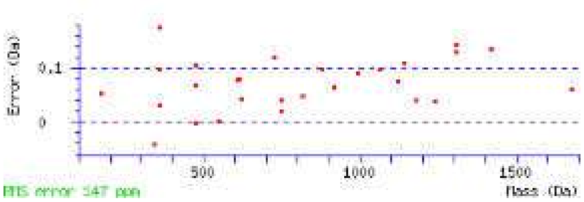
Label all possible matches ○ Label matches used for scoring ●

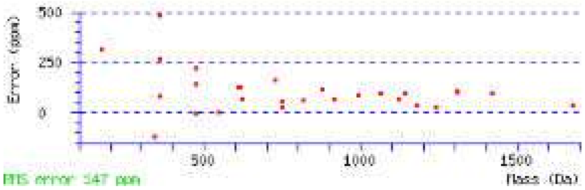
Monoisotopic mass of neutral peptide Mr(calc): 2053.9633
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.28
Matches : 33/305 fragment ions using 53 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	44.0495	44.0495			72.0444			44.0495		A						
2	70.0651	141.1022			***169.0972***			115.0866		P	1941.8865	1940.8913		1983.9335	1966.9069	19
3	88.0393	256.1292		238.1186	284.1241		266.1135	212.1394		D	1826.8596	1825.8643		1886.8807	1869.8541	18
4	120.0808	403.1976		385.1870	431.1925		413.1819			F	1679.7911			1771.8537	1754.8272	17
5	88.0393	518.2245		500.2140	***546.2195***		528.2089	474.2347		D	1564.7642	1563.7690		1624.7853	1607.7588	16
6	44.0495	589.2617		571.2511	***617.2566***		599.2460			A	1493.7271			1509.7584	1492.7318	14
7	102.0550	718.3042		700.2937	***746.2992***		728.2886	660.2988		E	1364.6845	1363.6892		1438.7213	1421.6947	14
8	44.0495	789.3414		771.3308	***817.3363***		799.3257			A	1293.6474			***1309.6787***	1292.6521	12
9	72.0808	888.4098		870.3992	***916.4047***		898.3941	874.3941		V	1194.5790	1207.5994		***1238.6416***	1221.6150	12
10	120.0808	1035.4782		1017.4676	***1063.4731***		1045.4625			F	1047.5106			***1139.5732***	1122.5466	11
11	88.0393	1150.5051		1132.4946	***1178.5000***		1160.4895	1106.5153		D	932.4836	931.4884		***992.5047***	975.4782	9
12	101.0709	1278.5637	1261.5372	1260.5531	***1306.5586***	1289.5321	1288.5481	1221.5422		Q	804.4250	803.4298		***877.4778***	860.4512	8
13	102.0550	1407.6063	1390.5798	1389.5957	1435.6012	1418.5747	1417.5907	1349.6008		E	675.3824	674.3872		***749.4192***	732.3927	7
14	120.0808	1554.6747	1537.6482	1536.6642	1582.6696	1565.6431	1564.6591			F	528.3140			***620.3766***	603.3501	
15	86.0964	1667.7588	1650.7322	1649.7482	1695.7537	1678.7271	1677.7431	1639.7275	1653.7431	I	415.2300	428.2504	442.2660	***473.3082***	456.2817	
16	87.0553	1781.8017	1764.7752	1763.7911	1809.7966	1792.7701	1791.7861	1738.7959		N	301.1870	300.1918		***360.2241***	343.1976	
17	72.0808	1880.8701	1863.8436	1862.8596	1908.8650	1891.8385	1890.8545	1866.8545		V	202.1186	215.1390		246.1812	229.1547	
18	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PD	185.0921	213.0870	PDF	332.1605	360.1554	PDFD	447.1874	475.1823
PDFDA	518.2245	546.2195	PDFDAE	647.2671	675.2620	DF	235.1077	263.1026
DFD	350.1347	378.1296	DFDA	421.1718	449.1667	DFDAE	550.2144	578.2093

DFDAEA	621.2515	649.2464	**FD**	235.1077	263.1026	**FDA**	306.1448	334.1397
FDAE	435.1874	463.1823	**FDAEA**	506.2245	534.2195	**FDAEAV**	605.2930	633.2879
DA	159.0764	187.0713	**DAE**	288.1190	316.1139	**DAEA**	359.1561	387.1510
DAEAV	458.2245	486.2195	**DAEAVF**	605.2930	633.2879	**AE**	173.0921	201.0870
AEA	244.1292	272.1241	**AEAV**	343.1976	371.1925	**AEAVF**	490.2660	518.2609
AEAVFD	605.2930	633.2879	**EA**	173.0921	201.0870	**EAV**	272.1605	300.1554
EAVF	419.2289	447.2238	**EAVFD**	534.2558	562.2508	**EAVFDQ**	662.3144	690.3093
AV	143.1179	171.1128	**AVF**	290.1863	318.1812	**AVFD**	405.2132	433.2082
AVFDQ	533.2718	561.2667	**AVFDQE**	662.3144	690.3093	**VF**	219.1492	247.1441
VFD	334.1761	362.1710	**VFDQ**	462.2347	490.2296	**VFDQE**	591.2773	619.2722
FD	235.1077	263.1026	**FDQ**	363.1663	391.1612	**FDQE**	492.2089	520.2038
FDQEF	639.2773	667.2722	**DQ**	216.0979	244.0928	**DQE**	345.1405	373.1354
DQEF	492.2089	520.2038	**DQEFI**	605.2930	633.2879	**QE**	230.1135	258.1084
QEF	377.1819	405.1769	**QEFI**	490.2660	518.2609	**QEFIN**	604.3089	632.3039
EF	249.1234	277.1183	**EFI**	362.2074	390.2023	**EFIN**	476.2504	504.2453
EFINV	575.3188	603.3137	**FI**	233.1648	261.1598	**FIN**	347.2078	375.2027
FINV	446.2762	474.2711	**IN**	200.1394	228.1343	**INV**	299.2078	327.2027
NV	186.1237	214.1186						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.5	2053.9633	0.0824	APDFDAEAVFDQEFINVK
14.1	2054.0507	-0.0049	ENHLPIIVFDMDTVGNLK
13.6	2054.0029	0.0429	HALTAVAVQTADETTADNAR
12.4	2053.9592	0.0865	VVEYEAATEADFLAQADGR
12.4	2054.0428	0.0030	MDKILEAVMLSSYPTNVK
12.2	2054.0684	-0.0227	SVLDGELSVYENLYLRGK
11.7	2053.9819	0.0638	QNQFDIAVMSALTYFYK
10.8	2054.0652	-0.0195	VPPGLLVCRAMVAELEER
10.3	2053.8964	0.1493	EGSQSGEAFVELESEDDVK
9.7	2053.9482	0.0975	MVEMVTGEKTSLEEMGGAR

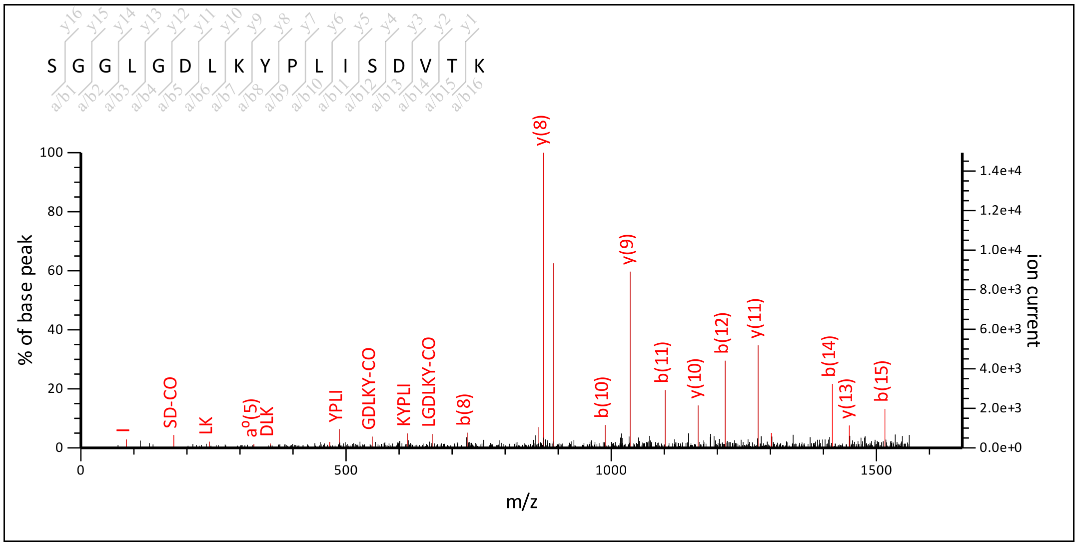
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 19

MS/MS Fragmentation of **SGGLGDLKYPLISDVTK**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 88: 1762.020824 from(1763.028100,1+) intensity(0.0000) index(16)
Title: Label: H17, Spot_Id: 219937, Peak_List_Id: 228921, MSMS Job_Run_Id: 22005, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H17_136868316000.txt



0 to 1661.88

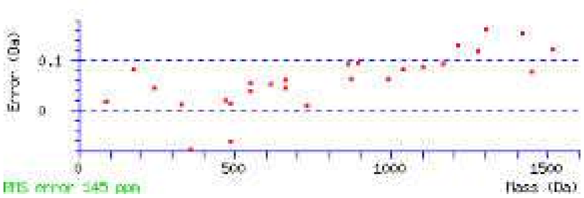
Label all possible matches ○ Label matches used for scoring ●

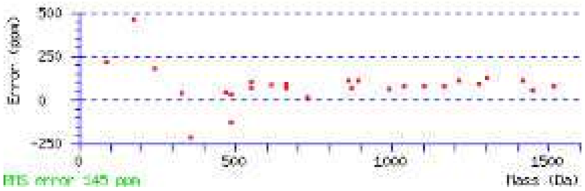
```
Monoisotopic mass of neutral peptide Mr(calc): 1761.9513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71  Expect: 0.0018
Matches : 31/305 fragment ions using 30 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S						
2	30.0338	117.0659		99.0553	145.0608		127.0502			G				1675.9265	1658.9000	16
3	30.0338	174.0873		156.0768	202.0822		184.0717			G				1618.9051	1601.8785	16
4	86.0964	287.1714		269.1608	315.1663		297.1557	245.1244		L	1503.8053	1502.8101		1561.8836	1544.8570	15
5	30.0338	344.1928		326.1823	372.1878		354.1772			G				***1448.7995***	1431.7730	14
6	88.0393	459.2198		441.2092	***487.2147***		469.2041	415.2300		D	1331.7569	1330.7617		1391.7781	1374.7515	13
7	86.0964	572.3039		554.2933	600.2988		582.2882	530.2569		L	1218.6729	1217.6776		***1276.7511***	1259.7246	12
8	101.1073	700.3988	683.3723	682.3882	***728.3937***	711.3672	710.3832	643.3410		K	1090.5779	1089.5827		***1163.6671***	1146.6405	11
9	136.0757	863.4621	846.4356	845.4516	***891.4571***	874.4305	873.4465			Y	927.5146			***1035.5721***	1018.5455	10
10	70.0651	960.5149	943.4884	942.5043	***988.5098***	971.4833	970.4993	934.4993		P	830.4618	829.4666		***872.5088***	855.4822	8
11	86.0964	1073.5990	1056.5724	1055.5884	***1101.5939***	1084.5673	1083.5833	1031.5520		L	717.3777	716.3825		775.4560	758.4294	7
12	86.0964	1186.6830	1169.6565	1168.6725	***1214.6780***	1197.6514	1196.6674	1158.6517	1172.6674	I	604.2937	617.3141	631.3297	***662.3719***	645.3454	6
13	60.0444	1273.7151	1256.6885	1255.7045	***1301.7100***	1284.6834	1283.6994	1257.7201		S	517.2617	516.2664		***549.2879***	532.2613	5
14	88.0393	1388.7420	1371.7155	1370.7314	***1416.7369***	1399.7104	1398.7264	1344.7522		D	402.2347	401.2395		462.2558	445.2293	4
15	72.0808	1487.8104	1470.7839	1469.7999	***1515.8053***	1498.7788	1497.7948	1473.7948		V	303.1663	316.1867		347.2289	330.2023	3
16	74.0600	1588.8581	1571.8316	1570.8475	1616.8530	1599.8265	1598.8425	1572.8632	1574.8425	T	202.1186	215.1390	217.1183	248.1605	231.1339	2
17	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GG	87.0553	115.0502	GGL	200.1394	228.1343	GGLG	257.1608	285.1557
GGLGD	372.1878	400.1827	GGLGDL	485.2718	513.2667	GGLGDLK	613.3668	641.3617
GL	143.1179	171.1128	GLG	200.1394	228.1343	GLGD	315.1663	343.1612
GLGDL	428.2504	456.2453	GLGDLK	556.3453	584.3402	LG	143.1179	171.1128

LGD	258.1448	286.1397	**LGDL**	371.2289	399.2238	**LGDLK**	499.3239	527.3188
LGDLKY	662.3872	690.3821	**GD**	145.0608	173.0557	**GDL**	258.1448	286.1397
GDLK	386.2398	414.2347	**GDLKY**	549.3031	577.2980	**GDLKYP**	646.3559	674.3508
DL	201.1234	229.1183	**DLK**	329.2183	357.2132	**DLKY**	492.2817	520.2766
DLKYP	589.3344	617.3293	**LK**	214.1914	242.1863	**LKY**	377.2547	405.2496
LKYP	474.3075	502.3024	**LKYPL**	587.3915	615.3865	**KY**	264.1707	292.1656
KYP	361.2234	389.2183	**KYPL**	474.3075	502.3024	**KYPLI**	587.3915	615.3865
KYPLIS	674.4236	702.4185	**YP**	233.1285	261.1234	**YPL**	346.2125	374.2074
YPLI	459.2966	487.2915	**YPLIS**	546.3286	574.3235	**YPLISD**	661.3556	689.3505
PL	183.1492	211.1441	**PLI**	296.2333	324.2282	**PLIS**	383.2653	411.2602
PLISD	498.2922	526.2871	**PLISDV**	597.3606	625.3556	**PLISDVT**	698.4083	726.4032
LI	199.1805	227.1754	**LIS**	286.2125	314.2074	**LISD**	401.2395	429.2344
LISDV	500.3079	528.3028	**LISDVT**	601.3556	629.3505	**IS**	173.1285	201.1234
ISD	288.1554	316.1503	**ISDV**	387.2238	415.2187	**ISDVT**	488.2715	516.2664
SD	175.0713	203.0662	**SDV**	274.1397	302.1347	**SDVT**	375.1874	403.1823
DV	187.1077	215.1026	**DVT**	288.1554	316.1503	**VT**	173.1285	201.1234





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.7	1761.9513	0.0696	SGGLGDLKYPLISDVTK
42.3	1761.9149	0.1059	TGGLGDLNYPLISDVTK
39.4	1761.9513	0.0696	SGGLGDLKYPLVSDLTK
24.4	1761.8897	0.1311	IATTQKAWNSLSDAEK
23.4	1761.9447	0.0761	KPLYCDGGSGLTLLLR
22.5	1761.8679	0.1529	AAGMSDTQIQQELAKR
22.0	1761.8614	0.1594	AVGEQLCAAAARGSMVR
19.6	1761.8872	0.1336	GFGQPQLAMIFPLDGR
19.5	1761.9586	0.0622	MLPEEFKIPLTTSIK
19.4	1761.9989	0.0219	TIGSKQLTATLLDFVR

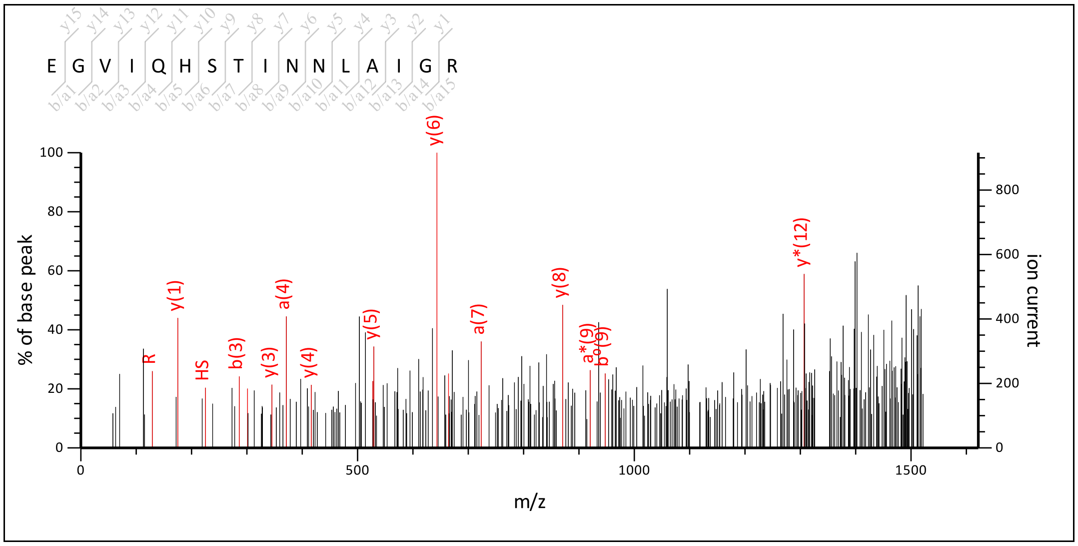
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 19

MS/MS Fragmentation of **EGVIQHSTINNLAIGR**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 86: 1721.003924 from(1722.011200,1+) intensity(0.0000) index(15)
Title: Label: H17, Spot_Id: 219937, Peak_List_Id: 228932, MSMS Job_Run_Id: 22005, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H17_136868316000.txt



0 to 1621.59

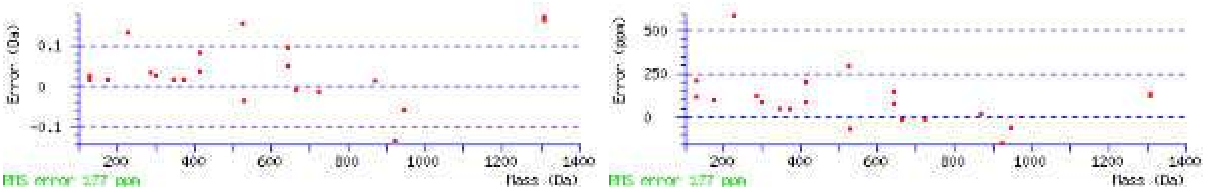
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1720.9220
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 11 **Expect:** 1.5e+03
Matches : 21/292 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	30.0338	159.0764		141.0659	187.0713		169.0608			G				1592.8867	1575.8602
3	72.0808	258.1448		240.1343	***286.1397***		268.1292	244.1292		V	1491.8027	1504.8231		1535.8653	1518.8387
4	86.0964	**371.2289**		353.2183	399.2238		381.2132	343.1976	357.2132	I	1378.7186	1391.7390	1405.7546	1436.7968	1419.7703
5	101.0709	499.2875	482.2609	481.2769	***527.2824***	510.2558	509.2718	442.2660		Q	1250.6600	1249.6648		1323.7128	1306.6862
6	110.0713	636.3464	619.3198	618.3358	***664.3413***	647.3148	646.3307			H	1113.6011			1195.6542	1178.6276
7	60.0444	**723.3784**	706.3519	705.3678	751.3733	734.3468	733.3628	707.3835		S	1026.5691	1025.5738		1058.5953	1041.5687
8	74.0600	824.4261	807.3995	806.4155	852.4210	835.3945	834.4104	808.4312	810.4104	T	925.5214	938.5418	940.5211	971.5633	954.5367
9	86.0964	937.5102	920.4836	919.4996	965.5051	948.4785	947.4945	909.4789	923.4945	I	812.4373	825.4577	839.4734	***870.5156***	853.4890
10	87.0553	1051.5531	1034.5265	1033.5425	1079.5480	1062.5215	1061.5374	1008.5473		N	698.3944	697.3991		757.4315	740.4050
11	87.0553	1165.5960	1148.5695	1147.5854	1193.5909	1176.5644	1175.5804	1122.5902		N	584.3515	583.3562		***643.3886***	626.3620
12	86.0964	1278.6801	1261.6535	1260.6695	***1306.6750***	1289.6484	1288.6644	1236.6331		L	471.2674	470.2722		***529.3457***	512.3191
13	44.0495	1349.7172	1332.6906	1331.7066	1377.7121	1360.6856	1359.7015			A	400.2303			***416.2616***	399.2350
14	86.0964	1462.8013	1445.7747	1444.7907	1490.7962	1473.7696	1472.7856	1434.7700	1448.7856	I	287.1462	300.1666	314.1823	***345.2245***	328.1979
15	30.0338	1519.8227	1502.7962	1501.8122	1547.8176	1530.7911	1529.8071			G				232.1404	215.1139
16	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GV	129.1022	157.0972	GVI	242.1863	270.1812	GVIQ	370.2449	398.2398
GVIQH	507.3038	535.2987	GVIQHS	594.3358	622.3307	GVIQHST	695.3835	723.3784
VI	185.1648	213.1598	VIQ	313.2234	341.2183	VIQH	450.2823	478.2772
VIQHS	537.3144	565.3093	VIQHST	638.3620	666.3570	IQ	214.1550	242.1499
IQH	351.2139	379.2088	IQHS	438.2459	466.2409	IQHST	539.2936	567.2885

IQHSTI	652.3777	680.3726	**QH**	238.1299	266.1248	**QHS**	325.1619	353.1568
QHST	426.2096	454.2045	**QHSTI**	539.2936	567.2885	**QHSTIN**	653.3365	681.3315
HS	197.1033	225.0982	**HST**	298.1510	326.1459	**HSTI**	411.2350	439.2300
HSTIN	525.2780	553.2729	**HSTINN**	639.3209	667.3158	**ST**	161.0921	189.0870
STI	274.1761	302.1710	**STIN**	388.2191	416.2140	**STINN**	502.2620	530.2569
STINNL	615.3460	643.3410	**STINNLA**	686.3832	714.3781	**TI**	187.1441	215.1390
TIN	301.1870	329.1819	**TINN**	415.2300	443.2249	**TINNL**	528.3140	556.3089
TINNLA	599.3511	627.3461	**IN**	200.1394	228.1343	**INN**	314.1823	342.1772
INNL	427.2663	455.2613	**INNLA**	498.3035	526.2984	**INNLAI**	611.3875	639.3824
INNLAIG	668.4090	696.4039	**NN**	201.0982	229.0931	**NNL**	314.1823	342.1772
NNLA	385.2194	413.2143	**NNLAI**	498.3035	526.2984	**NNLAIG**	555.3249	583.3198
NL	200.1394	228.1343	**NLA**	271.1765	299.1714	**NLAI**	384.2605	412.2554
NLAIG	441.2820	469.2769	**LA**	157.1335	185.1285	**LAI**	270.2176	298.2125
LAIG	327.2391	355.2340	**AI**	157.1335	185.1285	**AIG**	214.1550	242.1499
IG	143.1179	171.1128						



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

All matches to this query

Score	**Mr(calc)**	**Delta**	**Sequence**
12.7	1720.9108	0.0932	NANDQLPQKLPSAPTK
11.8	1720.8605	0.1434	RDVSGGVGLAHSAQPDR
11.3	1720.9220	0.0819	EGVIQHSTINNLAIGR
9.2	1720.8566	0.1473	QTFHEMAGLSITKSR
9.1	1720.8488	0.1551	QMVVASVGPTTSEMLR
8.9	1721.0386	-0.0347	VTSIVVRPMLPPLKR
8.5	1720.9624	0.0415	ATGWVLVGPTPANIIGR
8.5	1720.9624	0.0415	AWGTVLVGPTPANIIGR
8.5	1720.9625	0.0414	AWGTVLVGPTPVNVVGR
8.5	1720.9948	0.0091	RTGTVLVGPTPANIIGR

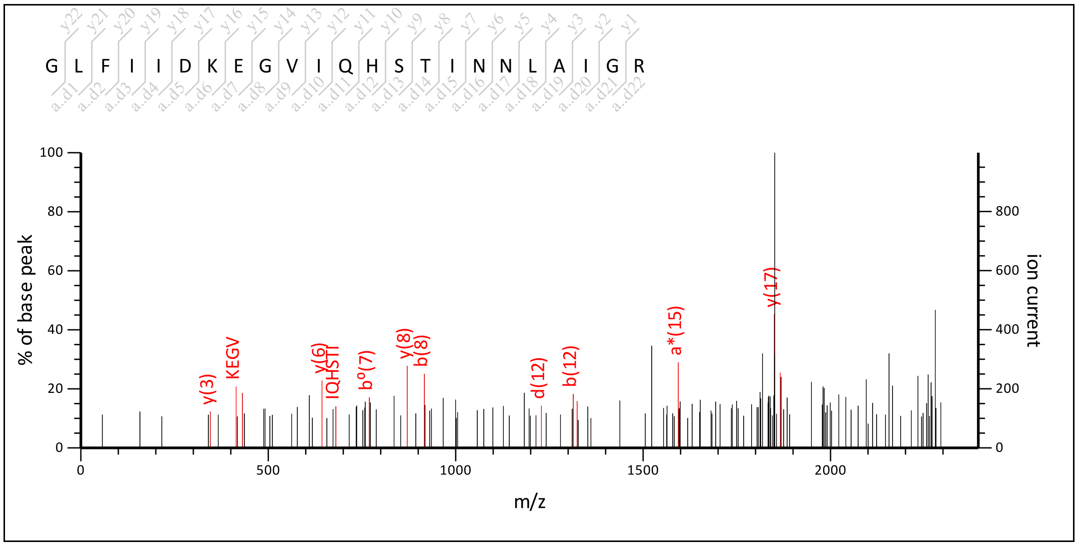
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 19

MS/MS Fragmentation of **GLFIIDKEGVIQHSTINNLAIGR**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 99: 2507.505424 from(2508.512700,1+) intensity(0.0000) index(20)
Title: Label: H17, Spot_Id: 219937, Peak_List_Id: 228929, MSMS Job_Run_Id: 22005, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H17_136868316000.txt



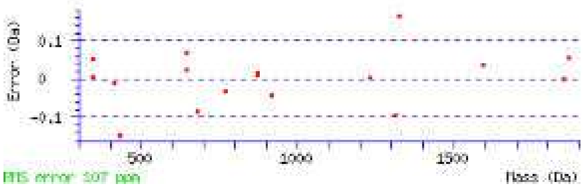
0 to 2394.22

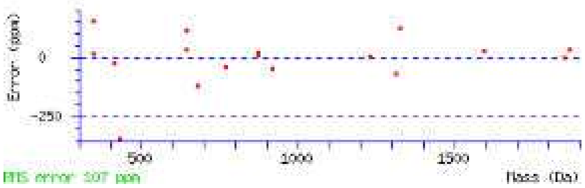
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2507.3860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 6 **Expect:** 2.6e+03
Matches : 17/437 fragment ions using 45 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			101.0709		L	2393.2936	2392.2983		2451.3718	2434.3453
3	120.0808	290.1863			318.1812					F	2246.2252			2338.2878	2321.2612
4	86.0964	403.2704			***431.2653***			375.2391	389.2547	I	2133.1411	2146.1615	2160.1771	2191.2193	2174.1928
5	86.0964	516.3544			544.3493			488.3231	502.3388	I	2020.0570	2033.0774	2047.0931	2078.1353	2061.1087
6	88.0393	631.3814		613.3708	659.3763		641.3657	587.3915		D	1905.0301	1904.0348		1965.0512	1948.0247
7	101.1073	759.4763	742.4498	741.4658	787.4713	770.4447	769.4607	702.4185		K	1776.9351	1775.9399		***1850.0243***	1832.9977
8	102.0550	888.5189	871.4924	870.5084	***916.5138***	899.4873	898.5033	830.5135		E	1647.8925	1646.8973		1721.9293	1704.9028
9	30.0338	945.5404	928.5138	927.5298	973.5353	956.5088	955.5247			G				1592.8867	1575.8602
10	72.0808	1044.6088	1027.5823	1026.5982	1072.6037	1055.5772	1054.5932	1030.5932		V	1491.8027	1504.8231		1535.8653	1518.8387
11	86.0964	1157.6929	1140.6663	1139.6823	1185.6878	1168.6612	1167.6772	1129.6616	1143.6772	I	1378.7186	1391.7390	1405.7546	1436.7968	1419.7703
12	101.0709	1285.7515	1268.7249	1267.7409	***1313.7464***	1296.7198	1295.7358	1228.7300		Q	1250.6600	1249.6648		***1323.7128***	1306.6862
13	110.0713	1422.8104	1405.7838	1404.7998	1450.8053	1433.7787	1432.7947			H	1113.6011			1195.6542	1178.6276
14	60.0444	1509.8424	1492.8158	1491.8318	1537.8373	1520.8108	1519.8267	1493.8475		S	1026.5691	1025.5738		1058.5953	1041.5687
15	74.0600	1610.8901	1593.8635	1592.8795	1638.8850	1621.8584	1620.8744	1594.8952	1596.8744	T	925.5214	938.5418	940.5211	971.5633	954.5367
16	86.0964	1723.9741	1706.9476	1705.9636	1751.9690	1734.9425	1733.9585	1695.9428	1709.9585	I	812.4373	825.4577	839.4734	***870.5156***	853.4890
17	87.0553	1838.0171	1820.9905	1820.0065	***1866.0120***	1848.9854	1848.0014	1795.0112		N	698.3944	697.3992		757.4315	740.4050
18	87.0553	1952.0600	1935.0334	1934.0494	1980.0549	1963.0284	1962.0443	1909.0542		N	584.3515	583.3562		***643.3886***	626.3620
19	86.0964	2065.1441	2048.1175	2047.1335	2093.1390	2076.1124	2075.1284	2023.0971		L	471.2674	470.2722		529.3457	512.3191
20	44.0495	2136.1812	2119.1546	2118.1706	2164.1761	2147.1495	2146.1655			A	400.2303			416.2616	399.2350
21	86.0964	2249.2652	2232.2387	2231.2547	2277.2601	2260.2336	2259.2496	2221.2339	2235.2496	I	287.1462	300.1666	314.1823	***345.2245***	328.1979
22	30.0338	2306.2867	2289.2601	2288.2761	2334.2816	2317.2551	2316.2710			G				232.1404	215.1139
23	129.1135									R	74.0237	73.0284		175.1190	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LF	233.1648	261.1598	**LFI**	346.2489	374.2438	**LFII**	459.3330	487.3279
LFIID	574.3599	602.3548	**FI**	233.1648	261.1598	**FII**	346.2489	374.2438
FIID	461.2758	489.2708	**FIIDK**	589.3708	617.3657	**II**	199.1805	227.1754
IID	314.2074	342.2023	**IIDK**	442.3024	470.2973	**IIDKE**	571.3450	599.3399
IIDKEG	628.3665	656.3614	**ID**	201.1234	229.1183	**IDK**	329.2183	357.2132
IDKE	458.2609	486.2558	**IDKEG**	515.2824	543.2773	**IDKEGV**	614.3508	642.3457
DK	216.1343	244.1292	**DKE**	345.1769	373.1718	**DKEG**	402.1983	430.1932
DKEGV	501.2667	529.2617	**DKEGVI**	614.3508	642.3457	**KE**	230.1499	258.1448
KEG	287.1714	315.1663	**KEGV**	386.2398	414.2347	**KEGVI**	499.3239	527.3188
KEGVIQ	627.3824	655.3774	**EG**	159.0764	187.0713	**EGV**	258.1448	286.1397
EGVI	371.2289	399.2238	**EGVIQ**	499.2875	527.2824	**EGVIQH**	636.3464	664.3413
GV	129.1022	157.0972	**GVI**	242.1863	270.1812	**GVIQ**	370.2449	398.2398
GVIQH	507.3038	535.2987	**GVIQHS**	594.3358	622.3307	**GVIQHST**	695.3835	723.3784
VI	185.1648	213.1598	**VIQ**	313.2234	341.2183	**VIQH**	450.2823	478.2772
VIQHS	537.3144	565.3093	**VIQHST**	638.3620	666.3570	**IQ**	214.1550	242.1499
IQH	351.2139	379.2088	**IQHS**	438.2459	466.2409	**IQHST**	539.2936	567.2885
IQHSTI	652.3777	680.3726	**QH**	238.1299	266.1248	**QHS**	325.1619	353.1568
QHST	426.2096	454.2045	**QHSTI**	539.2936	567.2885	**QHSTIN**	653.3365	681.3315
HS	197.1033	225.0982	**HST**	298.1510	326.1459	**HSTI**	411.2350	439.2300
HSTIN	525.2780	553.2729	**HSTINN**	639.3209	667.3158	**ST**	161.0921	189.0870
STI	274.1761	302.1710	**STIN**	388.2191	416.2140	**STINN**	502.2620	530.2569
STINNL	615.3461	643.3410	**STINNLA**	686.3832	714.3781	**TI**	187.1441	215.1390
TIN	301.1870	329.1819	**TINN**	415.2300	443.2249	**TINNL**	528.3140	556.3089
TINNLA	599.3511	627.3461	**IN**	200.1394	228.1343	**INN**	314.1823	342.1772
INNL	427.2663	455.2613	**INNLA**	498.3035	526.2984	**INNLAI**	611.3875	639.3824
INNLAIG	668.4090	696.4039	**NN**	201.0982	229.0931	**NNL**	314.1823	342.1772
NNLA	385.2194	413.2143	**NNLAI**	498.3035	526.2984	**NNLAIG**	555.3249	583.3198
NL	200.1394	228.1343	**NLA**	271.1765	299.1714	**NLAI**	384.2605	412.2554
NLAIG	441.2820	469.2769	**LA**	157.1335	185.1285	**LAI**	270.2176	298.2125
LAIG	327.2391	355.2340	**AI**	157.1335	185.1285	**AIG**	214.1550	242.1499
IG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
5.6	2507.3860	0.1194	GLFIIDKEGVIQHSTINNLAIGR

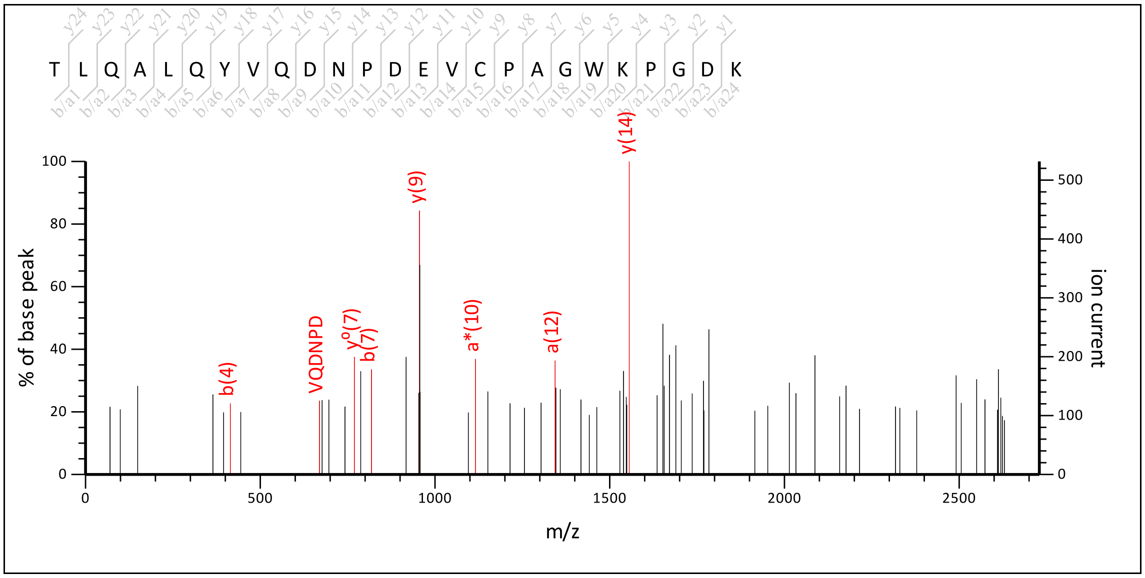
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 19

MS/MS Fragmentation of **TLQALQYVQDNPDEVCPAGWKPGDK**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 101: 2828.457824 from(2829.465100,1+) intensity(0.0000) index(21)
Title: Label: H17, Spot_Id: 219937, Peak_List_Id: 228940, MSMS Job_Run_Id: 22005, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H17_136868316000.txt



0 to 2729.35

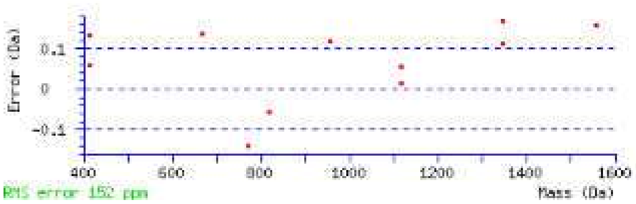
Label all possible matches ○ Label matches used for scoring ●

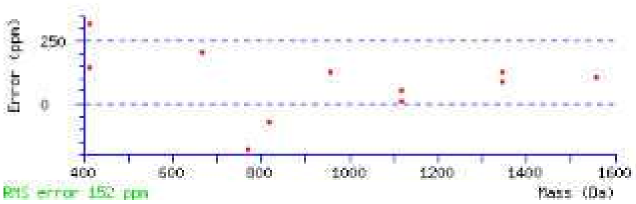
Monoisotopic mass of neutral peptide Mr(calc): 2828.3439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 5 **Expect:** 4.9e+03
Matches : 11/487 fragment ions using 23 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495	T						25
2	86.0964	187.1441		169.1335	215.1390		197.1285	145.0972	L	2670.2253	2669.2300	2728.3035	2711.2770	2710.2930	24
3	101.0709	315.2027	298.1761	297.1921	343.1976	326.1710	325.1870	258.1812	Q	2542.1667	2541.1715	2615.2195	2598.1929	2597.2089	23
4	44.0495	386.2398	369.2132	368.2292	***414.2347***	397.2082	396.2241		A	2471.1296		2487.1609	2470.1344	2469.1503	22
5	86.0964	499.3239	482.2973	481.3133	527.3188	510.2922	509.3082	457.2769	L	2358.0455	2357.0503	2416.1238	2399.0972	2398.1132	21
6	101.0709	627.3824	610.3559	609.3719	655.3774	638.3508	637.3668	570.3610	Q	2229.9870	2228.9917	2303.0397	2286.0132	2285.0292	20
7	136.0757	790.4458	773.4192	772.4352	***818.4407***	801.4141	800.4301		Y	2066.9236		2174.9811	2157.9546	2156.9706	19
8	72.0808	889.5142	872.4876	871.5036	917.5091	900.4825	899.4985	875.4985	V	1967.8552	1980.8756	2011.9178	1994.8913	1993.9073	18
9	101.0709	1017.5728	1000.5462	999.5622	1045.5677	1028.5411	1027.5571	960.5513	Q	1839.7966	1838.8014	1912.8494	1895.8229	1894.8388	17
10	88.0393	1132.5997	1115.5732	1114.5891	1160.5946	1143.5681	1142.5841	1088.6099	D	1724.7697	1723.7744	1784.7908	1767.7643	1766.7803	16
11	87.0553	1246.6426	1229.6161	1228.6321	1274.6375	1257.6110	1256.6270	1203.6368	N	1610.7268	1609.7315	1669.7639	1652.7373	1651.7533	15
12	70.0651	1343.6954	1326.6688	1325.6848	1371.6903	1354.6638	1353.6797	1317.6797	P	1513.6740	1512.6788	***1555.7210***	1538.6944	1537.7104	14
13	88.0393	1458.7223	1441.6958	1440.7118	1486.7173	1469.6907	1468.7067	1414.7325	D	1398.6471	1397.6518	1458.6682	1441.6416	1440.6576	13
14	102.0550	1587.7649	1570.7384	1569.7544	1615.7598	1598.7333	1597.7493	1529.7595	E	1269.6045	1268.6092	***1343.6412***	1326.6147	1325.6307	12
15	72.0808	1686.8333	1669.8068	1668.8228	1714.8283	1697.8017	1696.8177	1672.8177	V	1170.5361	1183.5565	1214.5987	1197.5721	1196.5881	11
16	133.0430	1846.8640	1829.8374	1828.8534	1874.8589	1857.8324	1856.8483	1757.8705	C	1010.5054	1009.5102	***1115.5302***	1098.5037	1097.5197	10
17	70.0651	1943.9168	1926.8902	1925.9062	1971.9117	1954.8851	1953.9011	1917.9011	P	913.4526	912.4574	***955.4996***	938.4730	937.4890	9
18	44.0495	2014.9539	1997.9273	1996.9433	2042.9488	2025.9222	2024.9382		A	842.4155		858.4468	841.4203	840.4363	8
19	30.0338	2071.9753	2054.9488	2053.9648	2099.9702	2082.9437	2081.9597		G			787.4097	770.3832	769.3992	7

20	159.0917	2258.0546	2241.0281	2240.0441	2286.0496	2269.0230	2268.0390		W	599.3148		730.3883	713.3617	712.3777	6
21	101.1073	2386.1496	2369.1231	2368.1390	2414.1445	2397.1180	2396.1340	2329.0918	K	471.2198	470.2245	544.3089	527.2824	526.2984	5
22	70.0651	2483.2024	2466.1758	2465.1918	2511.1973	2494.1707	2493.1867	2457.1867	P	374.1670	373.1718	416.2140	399.1874	398.2034	4
23	30.0338	2540.2238	2523.1973	2522.2133	2568.2188	2551.1922	2550.2082		G			319.1612	302.1347	301.1506	3
24	88.0393	2655.2508	2638.2242	2637.2402	2683.2457	2666.2191	2665.2351	2611.2610	D	202.1186	201.1234	262.1397	245.1132	244.1292	2
25	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LQ	214.1550	242.1499	LQA	285.1921	313.1870	LQAL	398.2762	426.2711
LQALQ	526.3348	554.3297	LQALQY	689.3981	717.3930	QA	172.1081	200.1030
QAL	285.1921	313.1870	QALQ	413.2507	441.2456	QALQY	576.3140	604.3089
QALQYV	675.3824	703.3774	AL	157.1335	185.1285	ALQ	285.1921	313.1870
ALQY	448.2554	476.2504	ALQYV	547.3239	575.3188	ALQYVQ	675.3824	703.3774
LQ	214.1550	242.1499	LQY	377.2183	405.2132	LQYV	476.2867	504.2817
LQYVQ	604.3453	632.3402	QY	264.1343	292.1292	QYV	363.2027	391.1976
QYVQ	491.2613	519.2562	QYVQD	606.2882	634.2831	YV	235.1441	263.1390
YVQ	363.2027	391.1976	YVQD	478.2296	506.2245	YVQDN	592.2726	620.2675
YVQDNP	689.3253	717.3202	VQ	200.1394	228.1343	VQD	315.1663	343.1612
VQDN	429.2092	457.2041	VQDNP	526.2620	554.2569	VQDNPD	641.2889	669.2838
QD	216.0979	244.0928	QDN	330.1408	358.1357	QDNP	427.1936	455.1885
QDNPD	542.2205	570.2154	QDNPDE	671.2631	699.2580	DN	202.0822	230.0771
DNP	299.1350	327.1299	DNPD	414.1619	442.1569	DNPDE	543.2045	571.1994
DNPDEV	642.2729	670.2679	NP	184.1081	212.1030	NPD	299.1350	327.1299
NPDE	428.1776	456.1725	NPDEV	527.2460	555.2409	NPDEVC	687.2767	715.2716
PD	185.0921	213.0870	PDE	314.1347	342.1296	PDEV	413.2031	441.1980
PDEVC	573.2337	601.2286	PDEVCP	670.2865	698.2814	DE	217.0819	245.0768
DEV	316.1503	344.1452	DEVC	476.1810	504.1759	DEVCP	573.2337	601.2286
DEVCPA	644.2708	672.2658	EV	201.1234	229.1183	EVC	361.1540	389.1489
EVCP	458.2068	486.2017	EVCPA	529.2439	557.2388	EVCPAG	586.2654	614.2603
VC	232.1114	260.1063	VCP	329.1642	357.1591	VCPA	400.2013	428.1962
VCPAG	457.2228	485.2177	VCPAGW	643.3021	671.2970	CP	230.0958	258.0907
CPA	301.1329	329.1278	CPAG	358.1544	386.1493	CPAGW	544.2337	572.2286
CPAGWK	672.3286	700.3235	PA	141.1022	169.0972	PAG	198.1237	226.1186
PAGW	384.2030	412.1979	PAGWK	512.2980	540.2929	PAGWKP	609.3507	637.3457
PAGWKPG	666.3722	694.3671	AG	101.0709	129.0659	AGW	287.1503	315.1452
AGWK	415.2452	443.2401	AGWKP	512.2980	540.2929	AGWKPG	569.3194	597.3144
AGWKPGD	684.3464	712.3413	GW	216.1131	244.1081	GWK	344.2081	372.2030
GWKP	441.2609	469.2558	GWKPG	498.2823	526.2772	GWKPGD	613.3093	641.3042
WK	287.1866	315.1816	WKP	384.2394	412.2343	WKPG	441.2609	469.2558
WKPGD	556.2878	584.2827	KP	198.1601	226.1550	KPG	255.1816	283.1765
KPGD	370.2085	398.2034	PG	127.0866	155.0815	PGD	242.1135	270.1084
GD	145.0608	173.0557						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
5.5	2828.3439	0.1139	TLQALQYVQDNPDEVCPAGWKPGDK
4.4	2828.4598	-0.0020	LLVMQMAQQQKLDQQQMDDLLLAK
2.8	2828.4929	-0.0351	DGAVAYPSGHTTLMVVVLGMVILVAGAR
2.5	2828.4531	0.0047	LSWNTVDVVTDAGGVPVMSKTGHAFIK
0.9	2828.3551	0.1027	GSPLNEIFPGESNLSQLMRAHDWSK
0.3	2828.3837	0.0741	ATQIEFLDGPTHIVPVMIGDAATCTR
0.1	2828.3433	0.1145	SQGLSQEPESGTLIQMQGQSKDMPPR

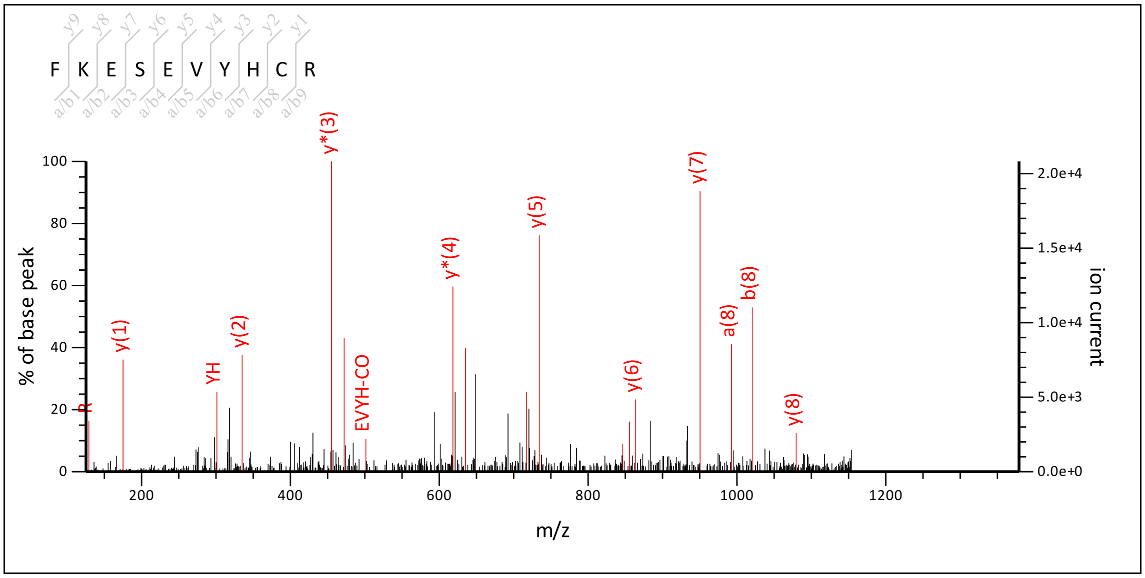
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 20

MS/MS Fragmentation of **FKESEVYHCR**
Found in **gi|115467828** in **NCBInr**, Os06g0320500 [Oryza sativa Japonica Group]

Match to Query 255: 1353.666024 from(1354.673300,1+) intensity(0.0000) index(28)
Title: Label: H13, Spot_Id: 219873, Peak_List_Id: 227935, MSMS Job_Run_Id: 21976, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H13_136868249100.txt



125.37 to 1379.05

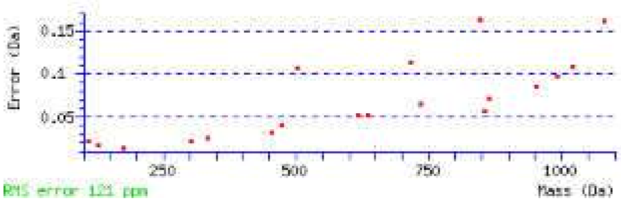
Label all possible matches ○ Label matches used for scoring ●

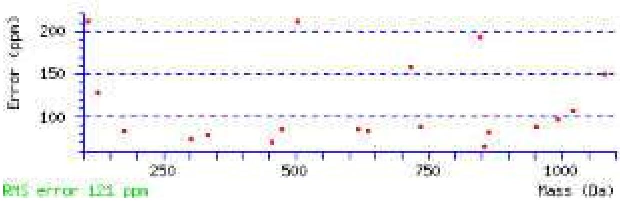
Monoisotopic mass of neutral peptide Mr(calc): 1353.6136
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 0.0034
Matches : 19/147 fragment ions using 22 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	Seq.	v	w	y	y*	y⁰	#
1	120.0808	120.0808			148.0757			44.0495	F						10
2	101.1073	248.1757	231.1492		276.1707	259.1441		191.1179	K	1134.4633	1133.4680	1207.5524	1190.5259	1189.5419	9
3	102.0550	377.2183	360.1918	359.2078	405.2132	388.1867	387.2027	319.2129	E	1005.4207	1004.4254	***1079.4575***	1062.4309	1061.4469	8
4	60.0444	464.2504	447.2238	446.2398	492.2453	475.2187	474.2347	448.2554	S	918.3887	917.3934	***950.4149***	933.3883	932.4043	7
5	102.0550	593.2930	576.2664	575.2824	621.2879	604.2613	603.2773	535.2875	E	789.3461	788.3508	***863.3828***	846.3563	845.3723	6
6	72.0808	692.3614	675.3348	674.3508	720.3563	703.3297	702.3457	678.3457	V	690.2777	703.2981	***734.3403***	717.3137		5
7	136.0757	**855.4247**	838.3981	837.4141	883.4196	866.3931	865.4090		Y	527.2143		***635.2718***	618.2453		4
8	110.0713	**992.4836**	975.4571	974.4730	1020.4785	1003.4520	1002.4680		H	390.1554		***472.2085***	455.1820		3
9	133.0430	1152.5143	1135.4877	1134.5037	1180.5092	1163.4826	1162.4986	1063.5207	C	230.1248	229.1295	***335.1496***	318.1231		2
10	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KE	230.1499	258.1448	**KES**	317.1819	345.1769	**KESE**	446.2245	474.2195
KESEV	545.2930	573.2879	**ES**	189.0870	217.0819	**ESE**	318.1296	346.1245
ESEV	417.1980	445.1929	**ESEVY**	580.2613	608.2562	**SE**	189.0870	217.0819
SEV	288.1554	316.1503	**SEVY**	451.2187	479.2136	**SEVYH**	588.2776	616.2726
EV	201.1234	229.1183	**EVY**	364.1867	392.1816	**EVYH**	501.2456	529.2405
EVYHC	661.2763	689.2712	**VY**	235.1441	263.1390	**VYH**	372.2030	400.1979
VYHC	532.2337	560.2286	**YH**	273.1346	301.1295	**YHC**	433.1653	461.1602

HC	270.1019	298.0968						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.9	1353.6136	0.0525	FKESEVYHCR
32.8	1353.6048	0.0612	QISEAFQSSDDK
27.5	1353.7306	-0.0646	HPKHYVTAVFR
25.9	1353.6161	0.0499	TDTSAPGSQFSTR
25.4	1353.6564	0.0096	KHFSYLSSEEK
24.3	1353.5401	0.1259	RMEMGDANGSDR
23.7	1353.7656	-0.0996	YISKEVYALLR
23.6	1353.6976	-0.0315	IKYIHLDHCR
23.4	1353.6048	0.0612	AYKEELSEDDR
23.3	1353.6381	0.0279	STSMVVVGGGTMGR

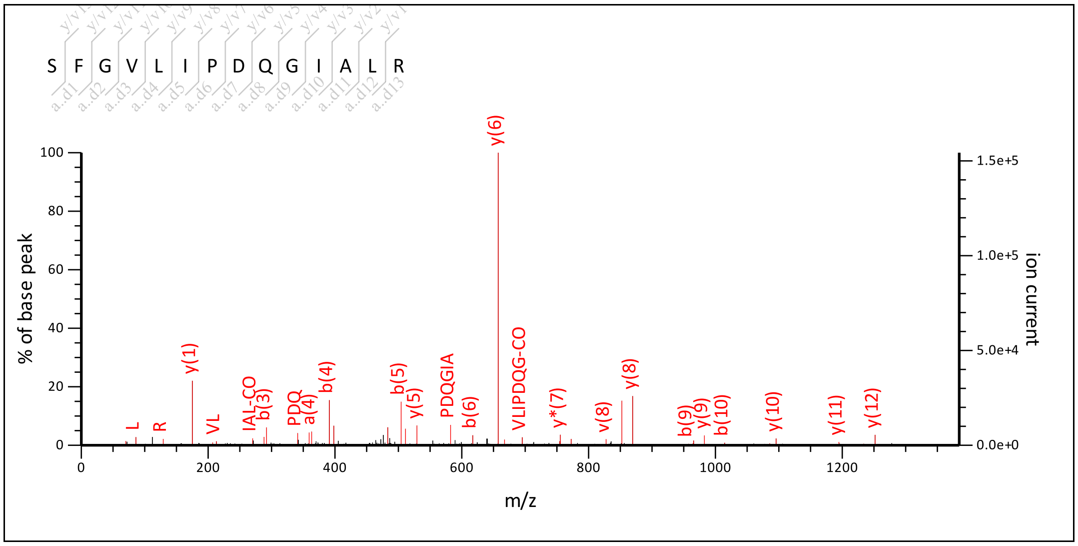
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 21

MS/MS Fragmentation of **SFGVLIPDQGIALR**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 13: 1484.907024 from(1485.914300,1+) intensity(0.0000) index(4)
Title: Label: J7, Spot_Id: 219779, Peak_List_Id: 226419, MSMS Job_Run_Id: 21843, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J7_136859916700.txt



0 to 1384.47

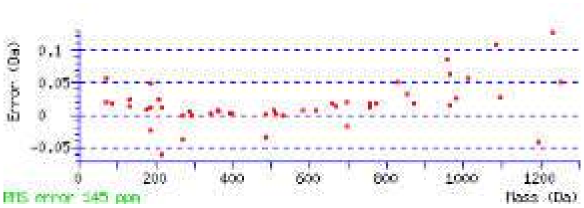
Label all possible matches ○ Label matches used for scoring ●

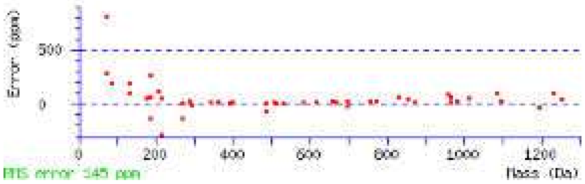
Monoisotopic mass of neutral peptide Mr(calc): 1484.8351
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 6.6e-06
Matches : 57/238 fragment ions using 52 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		**S**					
2	120.0808	**207.1128**		189.1022	235.1077		217.0972			**F**	1306.7478			1398.8104	1381.7838
3	30.0338	264.1343		246.1237	**292.1292**		274.1186			**G**				***1251.7419***	1234.7154
4	72.0808	**363.2027**		345.1921	**391.1976**		373.1870	349.1870		**V**	1150.6579	1163.6783		***1194.7205***	1177.6939
5	86.0964	476.2867		458.2762	**504.2817**		486.2711	434.2398		**L**	1037.5738	1036.5786		***1095.6521***	1078.6255
6	86.0964	589.3708		571.3602	**617.3657**		599.3552	561.3395	575.3552	**I**	924.4898	937.5102	951.5258	***982.5680***	965.5415
7	70.0651	686.4236		668.4130	714.4185		696.4079	660.4079		**P**	827.4370	826.4417		***869.4839***	852.4574
8	88.0393	801.4505		783.4400	829.4454		811.4349	757.4607		**D**	712.4100	711.4148		***772.4312***	755.4046
9	101.0709	929.5091	912.4825	911.4985	**957.5040**	940.4775	939.4934	872.4876		**Q**	584.3515	583.3562		***657.4042***	640.3777
10	30.0338	986.5306	969.5040	968.5200	**1014.5255**	997.4989	996.5149			**G**				***529.3457***	512.3191
11	86.0964	1099.6146	1082.5881	1081.6041	1127.6095	1110.5830	1109.5990	1071.5833	1085.5990	**I**	414.2459	427.2663	441.2820	472.3242	455.2976
12	44.0495	1170.6517	1153.6252	1152.6412	1198.6467	1181.6201	1180.6361			**A**	343.2088			***359.2401***	342.2136
13	86.0964	1283.7358	1266.7093	1265.7252	1311.7307	1294.7042	1293.7201	1241.6889		**L**	230.1248	229.1295		***288.2030***	271.1765
14	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FG	177.1022	205.0972	**FGV**	276.1707	304.1656	**FGVL**	389.2547	417.2496
FGVLI	502.3388	530.3337	**FGVLIP**	599.3915	627.3865	**GV**	129.1022	157.0972
GVL	242.1863	270.1812	**GVLI**	355.2704	383.2653	**GVLIP**	452.3231	480.3180
GVLIPD	567.3501	595.3450	**GVLIPDQ**	695.4087	723.4036	**VL**	185.1648	213.1598
VLI	298.2489	326.2438	**VLIP**	395.3017	423.2966	**VLIPD**	510.3286	538.3235
VLIPDQ	638.3872	666.3821	**VLIPDQG**	695.4087	723.4036	**LI**	199.1805	227.1754
LIP	296.2333	324.2282	**LIPD**	411.2602	439.2551	**LIPDQ**	539.3188	567.3137

LIPDQG	596.3402	624.3352	**IP**	183.1492	211.1441	**IPD**	298.1761	326.1710
IPDQ	426.2347	454.2296	**IPDQG**	483.2562	511.2511	**IPDQGI**	596.3402	624.3352
IPDQGIA	667.3774	695.3723	**PD**	185.0921	213.0870	**PDQ**	313.1506	341.1456
PDQG	370.1721	398.1670	**PDQGI**	483.2562	511.2511	**PDQGIA**	554.2933	582.2882
PDQGIAL	667.3774	695.3723	**DQ**	216.0979	244.0928	**DQG**	273.1193	301.1143
DQGI	386.2034	414.1983	**DQGIA**	457.2405	485.2354	**DQGIAL**	570.3246	598.3195
QG	158.0924	186.0873	**QGI**	271.1765	299.1714	**QGIA**	342.2136	370.2085
QGIAL	455.2976	483.2926	**GI**	143.1179	171.1128	**GIA**	214.1550	242.1499
GIAL	327.2391	355.2340	**IA**	157.1335	185.1285	**IAL**	270.2176	298.2125
AL	157.1335	185.1285						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
94.1	1484.8351	0.0719	SFGVLIPDQGIALR
33.7	1484.8562	0.0508	LVQIITSNILDTR
30.3	1484.8674	0.0396	SSLALAVARLIESR
29.7	1484.7697	0.1373	MSRLFAFLIDEK
29.7	1484.8198	0.0872	ALTSLLVGLNAEER
29.2	1484.8311	0.0759	IVSTTDPSIGARIR
29.2	1484.8311	0.0760	LSEARAGIVIAETR
28.6	1484.8450	0.0620	VLVVKQDDLSIEK
28.6	1484.7947	0.1123	REDVGKPIDITSR
28.2	1484.8311	0.0760	RETVAQALLLSER

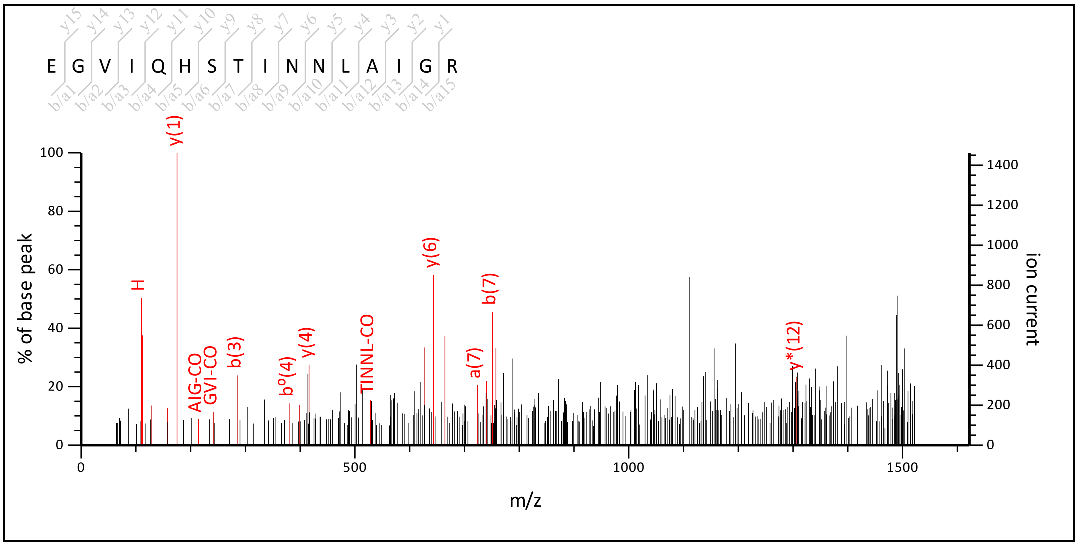
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 21

MS/MS Fragmentation of **EGVIQHSTINNLAIGR**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 21: 1721.009124 from(1722.016400,1+) intensity(0.0000) index(7)
Title: Label: J7, Spot_Id: 219779, Peak_List_Id: 226428, MSMS Job_Run_Id: 21843, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J7_136859916700.txt



0 to 1621.94

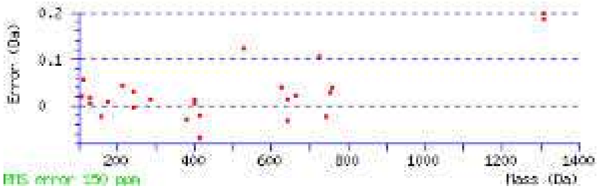
Label all possible matches ○ Label matches used for scoring ●

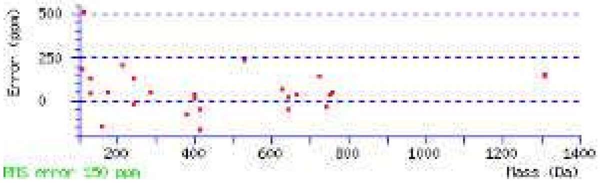
Monoisotopic mass of neutral peptide Mr(calc): 1720.9220
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 10 **Expect:** 1.9e+03
Matches : 28/292 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	30.0338	159.0764		141.0659	187.0713		169.0608			G				1592.8867	1575.8602
3	72.0808	258.1448		240.1343	***286.1397***		268.1292	244.1292		V	1491.8027	1504.8231		1535.8653	1518.8387
4	86.0964	371.2289		353.2183	***399.2238***		381.2132	343.1976	357.2132	I	1378.7186	1391.7390	1405.7546	1436.7968	1419.7703
5	101.0709	499.2875	482.2609	481.2769	527.2824	510.2558	509.2718	442.2660		Q	1250.6600	1249.6648		1323.7128	1306.6862
6	110.0713	636.3464	619.3198	618.3358	***664.3413***	647.3148	646.3307			H	1113.6011			1195.6542	1178.6276
7	60.0444	723.3784	706.3519	705.3678	***751.3733***	734.3468	733.3628	707.3835		S	1026.5691	1025.5738		1058.5953	1041.5687
8	74.0600	824.4261	807.3995	806.4155	852.4210	835.3945	834.4104	808.4312	810.4104	T	925.5214	938.5418	940.5211	971.5633	954.5367
9	86.0964	937.5102	920.4836	919.4996	965.5051	948.4785	947.4945	909.4789	923.4945	I	812.4373	825.4577	839.4734	870.5156	853.4890
10	87.0553	1051.5531	1034.5265	1033.5425	1079.5480	1062.5215	1061.5374	1008.5473		N	698.3944	697.3991		***757.4315***	740.4050
11	87.0553	1165.5960	1148.5695	1147.5854	1193.5909	1176.5644	1175.5804	1122.5902		N	584.3515	583.3562		***643.3886***	626.3620
12	86.0964	1278.6801	1261.6535	1260.6695	***1306.6750***	1289.6484	1288.6644	1236.6331		L	471.2674	470.2722		529.3457	512.3191
13	44.0495	1349.7172	1332.6906	1331.7066	1377.7121	1360.6856	1359.7015			A	400.2303			***416.2616***	399.2350
14	86.0964	1462.8013	1445.7747	1444.7907	1490.7962	1473.7696	1472.7856	1434.7700	1448.7856	I	287.1462	300.1666	314.1823	345.2245	328.1979
15	30.0338	1519.8227	1502.7962	1501.8122	1547.8176	1530.7911	1529.8071			G				232.1404	215.1139
16	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GV	129.1022	157.0972	**GVI**	242.1863	270.1812	**GVIQ**	370.2449	398.2398
GVIQH	507.3038	535.2987	**GVIQHS**	594.3358	622.3307	**GVIQHST**	695.3835	723.3784
VI	185.1648	213.1598	**VIQ**	313.2234	341.2183	**VIQH**	450.2823	478.2772
VIQHS	537.3144	565.3093	**VIQHST**	638.3620	666.3570	**IQ**	214.1550	242.1499
IQH	351.2139	379.2088	**IQHS**	438.2459	466.2409	**IQHST**	539.2936	567.2885

IQHSTI	652.3777	680.3726	**QH**	238.1299	266.1248	**QHS**	325.1619	353.1568
QHST	426.2096	454.2045	**QHSTI**	539.2936	567.2885	**QHSTIN**	653.3365	681.3315
HS	197.1033	225.0982	**HST**	298.1510	326.1459	**HSTI**	411.2350	439.2300
HSTIN	525.2780	553.2729	**HSTINN**	639.3209	667.3158	**ST**	161.0921	189.0870
STI	274.1761	302.1710	**STIN**	388.2191	416.2140	**STINN**	502.2620	530.2569
STINNL	615.3460	643.3410	**STINNLA**	686.3832	714.3781	**TI**	187.1441	215.1390
TIN	301.1870	329.1819	**TINN**	415.2300	443.2249	**TINNL**	528.3140	556.3089
TINNLA	599.3511	627.3461	**IN**	200.1394	228.1343	**INN**	314.1823	342.1772
INNL	427.2663	455.2613	**INNLA**	498.3035	526.2984	**INNLAI**	611.3875	639.3824
INNLAIG	668.4090	696.4039	**NN**	201.0982	229.0931	**NNL**	314.1823	342.1772
NNLA	385.2194	413.2143	**NNLAI**	498.3035	526.2984	**NNLAIG**	555.3249	583.3198
NL	200.1394	228.1343	**NLA**	271.1765	299.1714	**NLAI**	384.2605	412.2554
NLAIG	441.2820	469.2769	**LA**	157.1335	185.1285	**LAI**	270.2176	298.2125
LAIG	327.2391	355.2340	**AI**	157.1335	185.1285	**AIG**	214.1550	242.1499
IG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.9	1720.9472	0.0619	QLVTNSVNTVYSIKR
13.0	1720.8744	0.1348	NAETTGNYLLDNLKR
12.9	1720.9162	0.0930	FPWPSGPPRGLNLAGR
12.8	1720.9359	0.0732	RLEELATGTTFVAVSK
12.0	1720.8937	0.1155	NYHIFYQLLAGAPSK
11.3	1720.9332	0.0759	RGEPAAALQGQVGALGAR
11.1	1720.9334	0.0757	SLLTPCYFGGPILKR
10.3	1720.9049	0.1042	NYHIFYQLLAGLNR
10.3	1720.9220	0.0871	EGVIQHSTINNLAIGR
10.1	1720.9108	0.0983	VDSLISHSADALPIQR

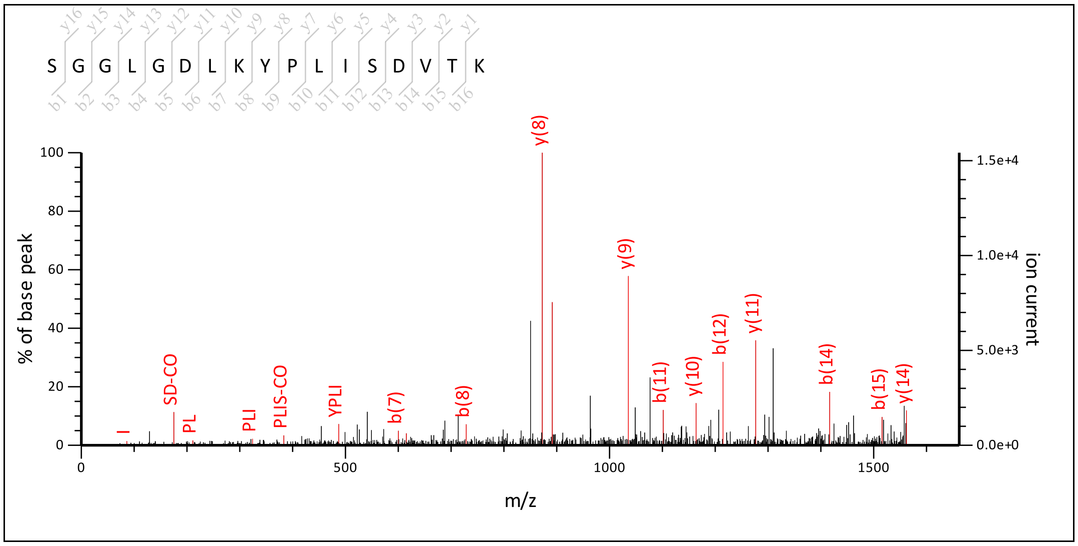
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 21

MS/MS Fragmentation of **SGGLGDLKYPLISDVTK**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 24: 1762.019224 from(1763.026500,1+) intensity(0.0000) index(8)
Title: Label: J7, Spot_Id: 219779, Peak_List_Id: 226422, MSMS Job_Run_Id: 21843, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J7_136859916700.txt



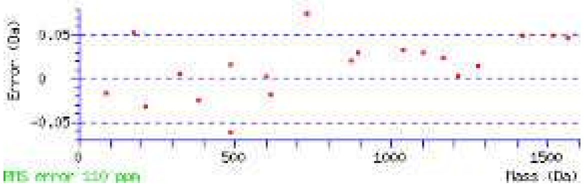
Label all possible matches ○ Label matches used for scoring ●

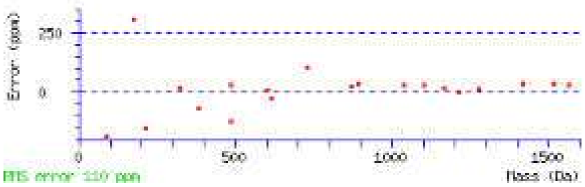
```
Monoisotopic mass of neutral peptide Mr(calc): 1761.9513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33   Expect: 10
Matches : 24/305 fragment ions using 45 most intense peaks    (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	30.0338	117.0659		99.0553	145.0608		127.0502			G				1675.9265	1658.9000
3	30.0338	174.0873		156.0768	202.0822		184.0717			G				1618.9051	1601.8785
4	**86.0964**	287.1714		269.1608	315.1663		297.1557	245.1244		L	1503.8053	1502.8101		**1561.8836**	1544.8570
5	30.0338	344.1928		326.1823	372.1878		354.1772			G				1448.7995	1431.7730
6	88.0393	459.2198		441.2092	***487.2147***		469.2041	415.2300		D	1331.7569	1330.7617		1391.7781	1374.7515
7	**86.0964**	572.3039		554.2933	***600.2988***		582.2882	530.2569		L	1218.6729	1217.6776		**1276.7511**	1259.7246
8	101.1073	700.3988	683.3723	682.3882	***728.3937***	711.3672	710.3832	643.3410		K	1090.5779	1089.5827		**1163.6671**	1146.6405
9	136.0757	863.4621	846.4356	845.4516	***891.4571***	874.4305	873.4465			Y	927.5146			**1035.5721**	1018.5455
10	70.0651	960.5149	943.4884	942.5043	988.5098	971.4833	970.4993	934.4993		P	830.4618	829.4666		**872.5088**	855.4822
11	**86.0964**	1073.5990	1056.5724	1055.5884	***1101.5939***	1084.5673	1083.5833	1031.5520		L	717.3777	716.3825		775.4560	758.4294
12	**86.0964**	1186.6830	1169.6565	1168.6725	***1214.6780***	1197.6514	1196.6674	1158.6517	1172.6674	I	604.2937	617.3141	631.3297	662.3719	645.3454
13	60.0444	1273.7151	1256.6885	1255.7045	1301.7100	1284.6834	1283.6994	1257.7201		S	517.2617	516.2664		549.2879	532.2613
14	88.0393	1388.7420	1371.7155	1370.7314	***1416.7369***	1399.7104	1398.7264	1344.7522		D	402.2347	401.2395		462.2558	445.2293
15	72.0808	1487.8104	1470.7839	1469.7999	***1515.8053***	1498.7788	1497.7948	1473.7948		V	303.1663	316.1867		347.2289	330.2023
16	74.0600	1588.8581	1571.8316	1570.8475	1616.8530	1599.8265	1598.8425	1572.8632	1574.8425	T	202.1186	215.1390	217.1183	248.1605	231.1339
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GG	87.0553	115.0502	GGL	200.1394	228.1343	GGLG	257.1608	285.1557
GGLGD	372.1878	400.1827	GGLGDL	485.2718	513.2667	GGLGDLK	613.3668	641.3617
GL	143.1179	171.1128	GLG	200.1394	228.1343	GLGD	315.1663	343.1612
GLGDL	428.2504	456.2453	GLGDLK	556.3453	584.3402	LG	143.1179	171.1128

LGD	258.1448	286.1397	**LGDL**	371.2289	399.2238	**LGDLK**	499.3239	527.3188
LGDLKY	662.3872	690.3821	**GD**	145.0608	173.0557	**GDL**	258.1448	286.1397
GDLK	386.2398	414.2347	**GDLKY**	549.3031	577.2980	**GDLKYP**	646.3559	674.3508
DL	201.1234	229.1183	**DLK**	329.2183	357.2132	**DLKY**	492.2817	520.2766
DLKYP	589.3344	617.3293	**LK**	214.1914	242.1863	**LKY**	377.2547	405.2496
LKYP	474.3075	502.3024	**LKYPL**	587.3915	615.3865	**KY**	264.1707	292.1656
KYP	361.2234	389.2183	**KYPL**	474.3075	502.3024	**KYPLI**	587.3915	615.3865
KYPLIS	674.4236	702.4185	**YP**	233.1285	261.1234	**YPL**	346.2125	374.2074
YPLI	459.2966	487.2915	**YPLIS**	546.3286	574.3235	**YPLISD**	661.3556	689.3505
PL	183.1492	211.1441	**PLI**	296.2333	324.2282	**PLIS**	383.2653	411.2602
PLISD	498.2922	526.2871	**PLISDV**	597.3606	625.3556	**PLISDVT**	698.4083	726.4032
LI	199.1805	227.1754	**LIS**	286.2125	314.2074	**LISD**	401.2395	429.2344
LISDV	500.3079	528.3028	**LISDVT**	601.3556	629.3505	**IS**	173.1285	201.1234
ISD	288.1554	316.1503	**ISDV**	387.2238	415.2187	**ISDVT**	488.2715	516.2664
SD	175.0713	203.0662	**SDV**	274.1397	302.1347	**SDVT**	375.1874	403.1823
DV	187.1077	215.1026	**DVT**	288.1554	316.1503	**VT**	173.1285	201.1234





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.2	1761.9513	0.0680	SGGLGDLKYPLISDVTK
24.9	1762.0213	-0.0021	TTRQISLLPAASHLVR
23.9	1762.0352	-0.0160	IPEAADPLRLSLQVLK
22.0	1761.8719	0.1473	MQSLPEYNSLLTPNR
21.4	1761.9598	0.0594	ALEVGSRNHALAGSKPR
21.3	1761.9447	0.0745	SSLLNLLMGFIAPSSGR
21.2	1761.9737	0.0455	KPDISTSPLHSLPSRK
20.9	1761.9261	0.0931	QVAATVETLYSLSPQR
20.4	1761.9665	0.0527	QFLNPLESFSLGVLAK
19.1	1761.9513	0.0680	SGGLGDLKYPLVSDLTK

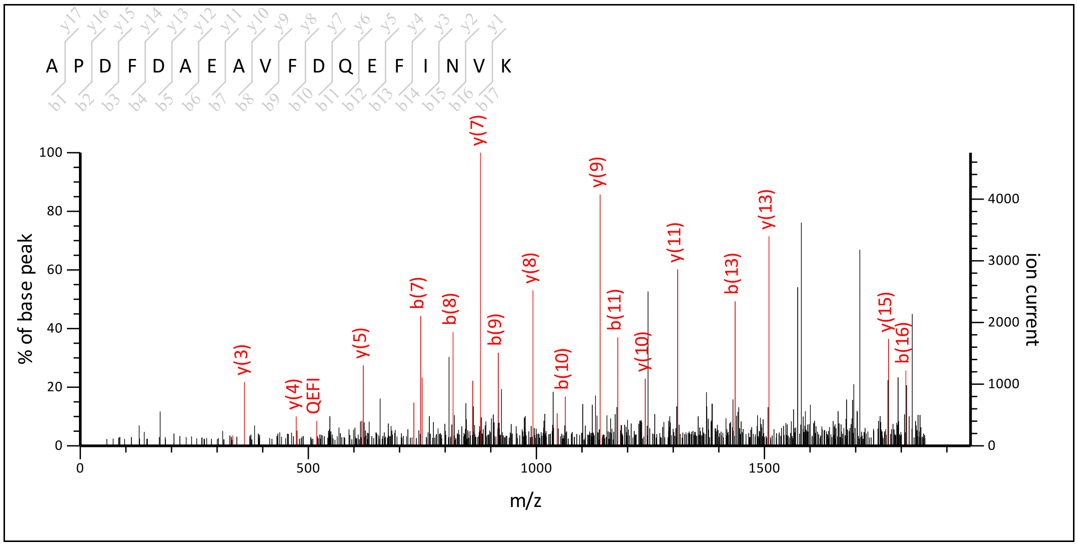
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 21

MS/MS Fragmentation of **APDFDAEAVFDQEFINVK**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 30: 2054.050824 from(2055.058100,1+) intensity(0.0000) index(10)
Title: Label: J7, Spot_Id: 219779, Peak_List_Id: 226423, MSMS Job_Run_Id: 21843, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J7_136859916700.txt



0 to 1951.84

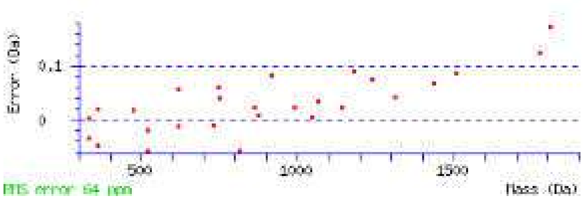
Label all possible matches ○ Label matches used for scoring ●

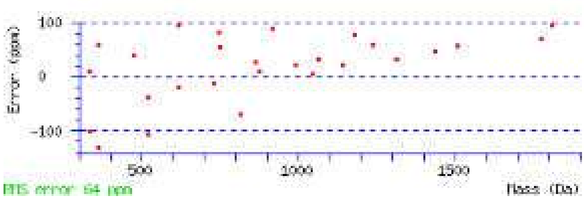
Monoisotopic mass of neutral peptide Mr(calc): 2053.9633
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 0.098
Matches : 29/305 fragment ions using 54 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	70.0651	141.1022			169.0972			115.0866		P	1941.8865	1940.8913		1983.9335	1966.9069
3	88.0393	256.1292		238.1186	284.1241		266.1135	212.1394		D	1826.8596	1825.8643		1886.8807	1869.8541
4	120.0808	403.1976		385.1870	431.1925		413.1819			F	1679.7911			***1771.8537***	1754.8272
5	88.0393	518.2245		500.2140	546.2195		528.2089	474.2347		D	1564.7642	1563.7690		1624.7853	1607.7588
6	44.0495	589.2617		571.2511	**617.2566**		599.2460			A	1493.7271			***1509.7584***	1492.7318
7	102.0550	718.3042		700.2937	**746.2992**		728.2886	660.2988		E	1364.6845	1363.6892		1438.7213	1421.6947
8	44.0495	789.3414		771.3308	**817.3363**		799.3257			A	1293.6474			***1309.6787***	1292.6521
9	72.0808	888.4098		870.3992	**916.4047**		898.3941	874.3941		V	1194.5790	1207.5994		***1238.6416***	1221.6150
10	120.0808	1035.4782		1017.4676	**1063.4731**		1045.4625			F	1047.5106			***1139.5732***	1122.5466
11	88.0393	1150.5051		1132.4946	**1178.5000**		1160.4895	1106.5153		D	932.4836	931.4884		***992.5047***	975.4782
12	101.0709	1278.5637	1261.5372	1260.5531	1306.5586	1289.5321	1288.5481	1221.5422		Q	804.4250	803.4298		***877.4778***	860.4512
13	102.0550	1407.6063	1390.5798	1389.5957	**1435.6012**	1418.5747	1417.5907	1349.6008		E	675.3824	674.3872		***749.4192***	732.3927
14	120.0808	1554.6747	1537.6482	1536.6642	1582.6696	1565.6431	1564.6591			F	528.3140			***620.3766***	603.3501
15	86.0964	1667.7588	1650.7322	1649.7482	1695.7537	1678.7271	1677.7431	1639.7275	1653.7431	I	415.2300	428.2504	442.2660	***473.3082***	456.2817
16	87.0553	1781.8017	1764.7752	1763.7911	**1809.7966**	1792.7701	1791.7861	1738.7959		N	301.1870	300.1918		***360.2241***	343.1976
17	72.0808	1880.8701	1863.8436	1862.8596	1908.8650	1891.8385	1890.8545	1866.8545		V	202.1186	215.1390		246.1812	229.1547
18	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PD	185.0921	213.0870	PDF	332.1605	360.1554	PDFD	447.1874	475.1823
PDFDA	518.2245	546.2195	PDFDAE	647.2671	675.2620	DF	235.1077	263.1026
DFD	350.1347	378.1296	DFDA	421.1718	449.1667	DFDAE	550.2144	578.2093

DFDAEA	621.2515	649.2464	**FD**	235.1077	263.1026	**FDA**	306.1448	334.1397
FDAE	435.1874	463.1823	**FDAEA**	506.2245	534.2195	**FDAEAV**	605.2930	633.2879
DA	159.0764	187.0713	**DAE**	288.1190	316.1139	**DAEA**	359.1561	387.1510
DAEAV	458.2245	486.2195	**DAEAVF**	605.2930	633.2879	**AE**	173.0921	201.0870
AEA	244.1292	272.1241	**AEAV**	343.1976	371.1925	**AEAVF**	490.2660	518.2609
AEAVFD	605.2930	633.2879	**EA**	173.0921	201.0870	**EAV**	272.1605	300.1554
EAVF	419.2289	447.2238	**EAVFD**	534.2558	562.2508	**EAVFDQ**	662.3144	690.3093
AV	143.1179	171.1128	**AVF**	290.1863	318.1812	**AVFD**	405.2132	433.2082
AVFDQ	533.2718	561.2667	**AVFDQE**	662.3144	690.3093	**VF**	219.1492	247.1441
VFD	334.1761	362.1710	**VFDQ**	462.2347	490.2296	**VFDQE**	591.2773	619.2722
FD	235.1077	263.1026	**FDQ**	363.1663	391.1612	**FDQE**	492.2089	520.2038
FDQEF	639.2773	667.2722	**DQ**	216.0979	244.0928	**DQE**	345.1405	373.1354
DQEF	492.2089	520.2038	**DQEFI**	605.2930	633.2879	**QE**	230.1135	258.1084
QEF	377.1819	405.1769	**QEFI**	490.2660	518.2609	**QEFIN**	604.3089	632.3039
EF	249.1234	277.1183	**EFI**	362.2074	390.2023	**EFIN**	476.2504	504.2453
EFINV	575.3188	603.3137	**FI**	233.1648	261.1598	**FIN**	347.2078	375.2027
FINV	446.2762	474.2711	**IN**	200.1394	228.1343	**INV**	299.2078	327.2027
NV	186.1237	214.1186						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.0	2053.9633	0.0875	APDFDAEAVFDQEFINVK
20.8	2054.0029	0.0480	HALTAVAVQTADETTADNAR
19.2	2053.9858	0.0650	TQDQFKPFADPFTGAQTR
18.7	2053.9482	0.1026	MVEMVTGEKTSLEEMGGAR
18.5	2053.9819	0.0689	QNQFDIAVMSALTYFYK
15.5	2054.0255	0.0253	GVQAAAYLAAFVEDMKASGR
15.0	2054.1097	-0.0589	MLVLYLCVFLGDVPLFR
14.0	2054.0657	-0.0149	HAPAAVSDAFTATRLAGVSGR
13.9	2054.1637	-0.1128	RLFTGGNVALTALNGLPGVGK
13.7	2054.0003	0.0505	MNNEIKVFSNNQFGQIR

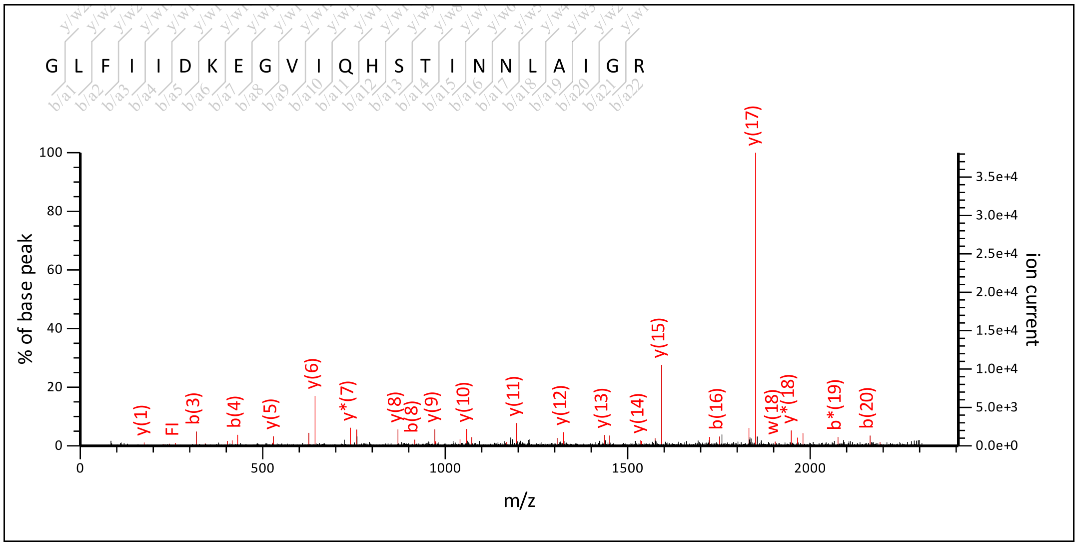
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 21

MS/MS Fragmentation of **GLFIIDKEGVIQHSTINNLAIGR**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 35: 2507.492924 from(2508.500200,1+) intensity(0.0000) index(12)
Title: Label: J7, Spot_Id: 219779, Peak_List_Id: 226420, MSMS Job_Run_Id: 21843, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J7_136859916700.txt



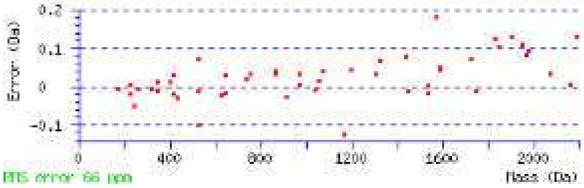
0 to 2406.12

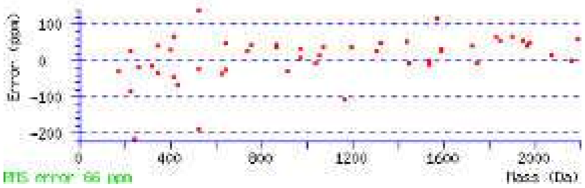
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2507.3860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 110 **Expect:** 1e-07
Matches : 53/437 fragment ions using 69 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			101.0709		L	2393.2936	2392.2983		2451.3718	2434.3453
3	120.0808	290.1863			**318.1812**					F	2246.2252			2338.2878	2321.2612
4	86.0964	**403.2704**			**431.2653**			375.2391	389.2547	I	2133.1411	2146.1615	2160.1771	***2191.2193***	2174.1928
5	86.0964	516.3544			544.3493			488.3231	502.3388	I	2020.0570	2033.0774	2047.0931	2078.1353	2061.1087
6	88.0393	631.3814		613.3708	659.3763		641.3657	587.3915		D	1905.0301	1904.0348		***1965.0512***	1948.0247
7	101.1073	759.4763	742.4498	741.4658	787.4713	770.4447	769.4607	702.4185		K	1776.9351	1775.9399		***1850.0243***	1832.9977
8	102.0550	888.5189	871.4924	870.5084	**916.5138**	899.4873	898.5033	830.5135		E	1647.8925	1646.8973		1721.9293	1704.9028
9	30.0338	945.5404	928.5138	927.5298	**973.5353**	956.5088	955.5247			G				***1592.8867***	1575.8602
10	72.0808	1044.6088	1027.5823	1026.5982	**1072.6037**	1055.5772	1054.5932	1030.5932		V	1491.8027	1504.8231		***1535.8653***	1518.8387
11	86.0964	1157.6929	1140.6663	1139.6823	1185.6878	1168.6612	1167.6772	1129.6616	1143.6772	I	1378.7186	1391.7390	1405.7546	***1436.7968***	1419.7703
12	101.0709	1285.7515	1268.7249	1267.7409	1313.7464	1296.7198	1295.7358	1228.7300		Q	1250.6600	1249.6648		***1323.7128***	1306.6862
13	110.0713	1422.8104	1405.7838	1404.7998	**1450.8053**	1433.7787	1432.7947			H	1113.6011			***1195.6542***	1178.6276
14	60.0444	1509.8424	1492.8158	1491.8318	**1537.8373**	1520.8108	1519.8267	1493.8475		S	1026.5691	1025.5738		***1058.5953***	1041.5687
15	74.0600	1610.8901	1593.8635	1592.8795	1638.8850	1621.8584	1620.8744	1594.8952	1596.8744	T	925.5214	938.5418	940.5211	***971.5633***	954.5367
16	86.0964	**1723.9741**	1706.9476	1705.9636	**1751.9690**	1734.9425	1733.9585	1695.9428	1709.9585	I	812.4373	825.4577	839.4734	***870.5156***	853.4890
17	87.0553	1838.0171	1820.9905	1820.0065	1866.0120	1848.9854	1848.0014	1795.0112		N	698.3944	697.3992		***757.4315***	740.4050
18	87.0553	1952.0600	1935.0334	1934.0494	**1980.0549**	1963.0284	1962.0443	1909.0542		N	584.3515	583.3562		***643.3886***	626.3620
19	86.0964	2065.1441	2048.1175	2047.1335	2093.1390	2076.1124	2075.1284	2023.0971		L	471.2674	470.2722		***529.3457***	512.3191
20	44.0495	2136.1812	2119.1546	2118.1706	**2164.1761**	2147.1495	2146.1655			A	400.2303			***416.2616***	399.2350
21	86.0964	2249.2652	2232.2387	2231.2547	2277.2601	2260.2336	2259.2496	2221.2339	2235.2496	I	287.1462	300.1666	314.1823	345.2245	328.1979
22	30.0338	2306.2867	2289.2601	2288.2761	2334.2816	2317.2551	2316.2710			G				232.1404	215.1139
23	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LF	233.1648	261.1598	LFI	346.2489	374.2438	LFII	459.3330	487.3279
LFIID	574.3599	602.3548	FI	233.1648	261.1598	FII	346.2489	374.2438
FIID	461.2758	489.2708	FIIDK	589.3708	617.3657	II	199.1805	227.1754
IID	314.2074	342.2023	IIDK	442.3024	470.2973	IIDKE	571.3450	599.3399
IIDKEG	628.3665	656.3614	ID	201.1234	229.1183	IDK	329.2183	357.2132
IDKE	458.2609	486.2558	IDKEG	515.2824	543.2773	IDKEGV	614.3508	642.3457
DK	216.1343	244.1292	DKE	345.1769	373.1718	DKEG	402.1983	430.1932
DKEGV	501.2667	529.2617	DKEGVI	614.3508	642.3457	KE	230.1499	258.1448
KEG	287.1714	315.1663	KEGV	386.2398	414.2347	KEGVI	499.3239	527.3188
KEGVIQ	627.3824	655.3774	EG	159.0764	187.0713	EGV	258.1448	286.1397
EGVI	371.2289	399.2238	EGVIQ	499.2875	527.2824	EGVIQH	636.3464	664.3413
GV	129.1022	157.0972	GVI	242.1863	270.1812	GVIQ	370.2449	398.2398
GVIQH	507.3038	535.2987	GVIQHS	594.3358	622.3307	GVIQHST	695.3835	723.3784
VI	185.1648	213.1598	VIQ	313.2234	341.2183	VIQH	450.2823	478.2772
VIQHS	537.3144	565.3093	VIQHST	638.3620	666.3570	IQ	214.1550	242.1499
IQH	351.2139	379.2088	IQHS	438.2459	466.2409	IQHST	539.2936	567.2885
IQHSTI	652.3777	680.3726	QH	238.1299	266.1248	QHS	325.1619	353.1568
QHST	426.2096	454.2045	QHSTI	539.2936	567.2885	QHSTIN	653.3365	681.3315
HS	197.1033	225.0982	HST	298.1510	326.1459	HSTI	411.2350	439.2300
HSTIN	525.2780	553.2729	HSTINN	639.3209	667.3158	ST	161.0921	189.0870
STI	274.1761	302.1710	STIN	388.2191	416.2140	STINN	502.2620	530.2569
STINNL	615.3461	643.3410	STINNLA	686.3832	714.3781	TI	187.1441	215.1390
TIN	301.1870	329.1819	TINN	415.2300	443.2249	TINNL	528.3140	556.3089
TINNLA	599.3511	627.3461	IN	200.1394	228.1343	INN	314.1823	342.1772
INNL	427.2663	455.2613	INNLA	498.3035	526.2984	INNLAI	611.3875	639.3824
INNLAIG	668.4090	696.4039	NN	201.0982	229.0931	NNL	314.1823	342.1772
NNLA	385.2194	413.2143	NNLAI	498.3035	526.2984	NNLAIG	555.3249	583.3198
NL	200.1394	228.1343	NLA	271.1765	299.1714	NLAI	384.2605	412.2554
NLAIG	441.2820	469.2769	LA	157.1335	185.1285	LAI	270.2176	298.2125
LAIG	327.2391	355.2340	AI	157.1335	185.1285	AIG	214.1550	242.1499
IG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
110.2	2507.3860	0.1069	GLFIIDKEGVIQHSTINNLAIGR
72.1	2507.3860	0.1069	GLFIIDKEGVIQHSTIQNLGIGR
13.8	2507.3860	0.1069	GLFIIDKEGIIQHSTINNLGIGR
12.6	2507.2703	0.2226	MPHIRPDGDPVRLTSNFQNGLK
11.9	2507.2512	0.2417	GNQTIQMANFGAGDIVAIMIGNLK
11.1	2507.4111	0.0818	EATAPSRLFLVGAVLPELVEAAVR
10.5	2507.2631	0.2298	WGERPMAFVILTPAAEKEYAGR
9.8	2507.3384	0.1545	TGNYLGQNFGLITGVSEVEIKLR
9.8	2507.2626	0.2303	LPAYMIPSAFVMLSTMPLNPNGK
9.7	2507.2763	0.2166	LGLMEIENRLQSDLAELFLCK

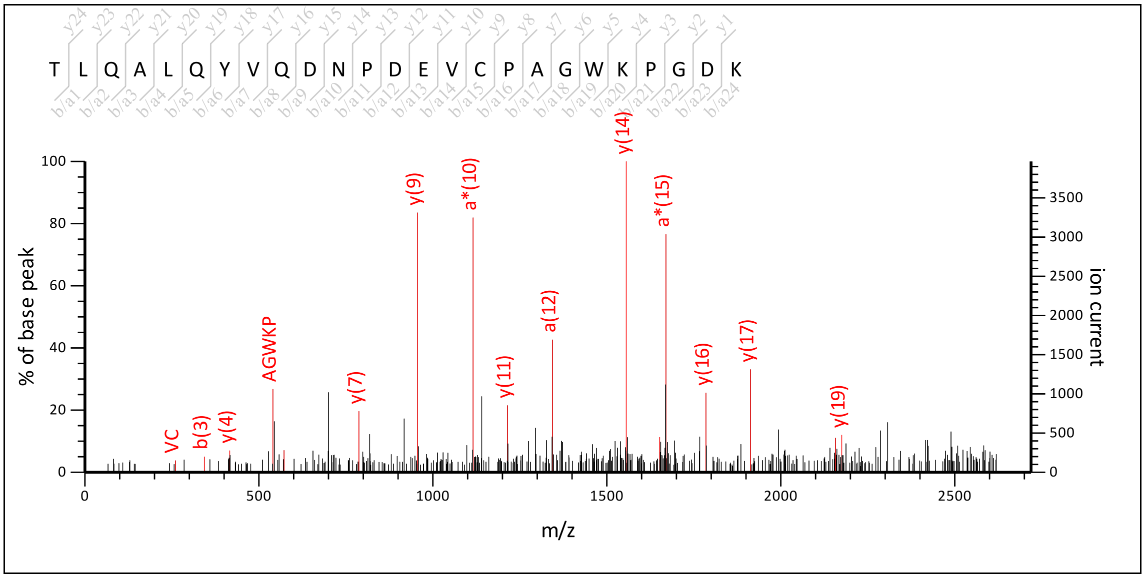
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 21

MS/MS Fragmentation of **TLQALQYVQDNPDEVCPAGWKPGDK**
Found in **gi|115446541** in **NCBInr**, Os02g0537700 [Oryza sativa Japonica Group]

Match to Query 37: 2828.469024 from(2829.476300,1+) intensity(0.0000) index(13)
Title: Label: J7, Spot_Id: 219779, Peak_List_Id: 226427, MSMS Job_Run_Id: 21843, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J7_136859916700.txt



0 to 2719.26

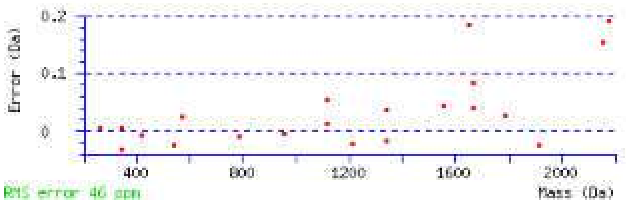
Label all possible matches ○ Label matches used for scoring ●

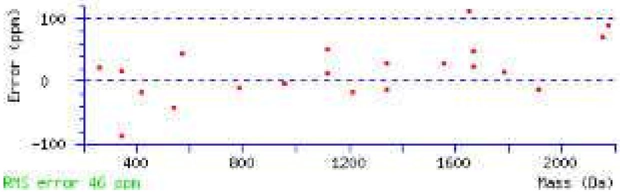
Monoisotopic mass of neutral peptide Mr(calc): 2828.3439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 0.0015
Matches : 22/487 fragment ions using 26 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495	T						25
2	86.0964	187.1441		169.1335	215.1390		197.1285	145.0972	L	2670.2253	2669.2300	2728.3035	2711.2770	2710.2930	24
3	101.0709	315.2027	298.1761	297.1921	343.1976	326.1710	325.1870	258.1812	Q	2542.1667	2541.1715	2615.2195	2598.1929	2597.2089	23
4	44.0495	386.2398	369.2132	368.2292	414.2347	397.2082	396.2241		A	2471.1296		2487.1609	2470.1344	2469.1503	22
5	86.0964	499.3239	482.2973	481.3133	527.3188	510.2922	509.3082	457.2769	L	2358.0455	2357.0503	2416.1238	2399.0972	2398.1132	21
6	101.0709	627.3824	610.3559	609.3719	655.3774	638.3508	637.3668	570.3610	Q	2229.9870	2228.9917	2303.0397	2286.0132	2285.0292	20
7	136.0757	790.4458	773.4192	772.4352	818.4407	801.4141	800.4301		Y	2066.9236		***2174.9811***	2157.9546	2156.9706	19
8	72.0808	889.5142	872.4876	871.5036	917.5091	900.4825	899.4985	875.4985	V	1967.8552	1980.8756	2011.9178	1994.8913	1993.9073	18
9	101.0709	1017.5728	1000.5462	999.5622	1045.5677	1028.5411	1027.5571	960.5513	Q	1839.7966	1838.8014	***1912.8494***	1895.8229	1894.8388	17
10	88.0393	1132.5997	1115.5732	1114.5891	1160.5946	1143.5681	1142.5841	1088.6099	D	1724.7697	1723.7744	***1784.7908***	1767.7643	1766.7803	16
11	87.0553	1246.6426	1229.6161	1228.6321	1274.6375	1257.6110	1256.6270	1203.6368	N	1610.7268	1609.7315	***1669.7639***	1652.7373	1651.7533	15
12	70.0651	1343.6954	1326.6688	1325.6848	1371.6903	1354.6638	1353.6797	1317.6797	P	1513.6740	1512.6788	***1555.7210***	1538.6944	1537.7104	14
13	88.0393	1458.7223	1441.6958	1440.7118	1486.7173	1469.6907	1468.7067	1414.7325	D	1398.6471	1397.6518	1458.6682	1441.6416	1440.6576	13
14	102.0550	1587.7649	1570.7384	1569.7544	1615.7598	1598.7333	1597.7493	1529.7595	E	1269.6045	1268.6092	***1343.6412***	1326.6147	1325.6307	12
15	72.0808	1686.8333	1669.8068	1668.8228	1714.8283	1697.8017	1696.8177	1672.8177	V	1170.5361	1183.5565	***1214.5987***	1197.5721	1196.5881	11
16	133.0430	1846.8640	1829.8374	1828.8534	1874.8589	1857.8324	1856.8483	1757.8705	C	1010.5054	1009.5102	***1115.5302***	1098.5037	1097.5197	10
17	70.0651	1943.9168	1926.8902	1925.9062	1971.9117	1954.8851	1953.9011	1917.9011	P	913.4526	912.4574	***955.4996***	938.4730	937.4890	9
18	44.0495	2014.9539	1997.9273	1996.9433	2042.9488	2025.9222	2024.9382		A	842.4155		858.4468	841.4203	840.4363	8
19	30.0338	2071.9753	2054.9488	2053.9648	2099.9702	2082.9437	2081.9597		G			***787.4097***	770.3832	769.3992	7

20	159.0917	2258.0546	2241.0281	2240.0441	2286.0496	2269.0230	2268.0390		**W**	599.3148		730.3883	713.3617	712.3777	**6**
21	101.1073	2386.1496	2369.1231	2368.1390	2414.1445	2397.1180	2396.1340	2329.0918	**K**	471.2198	470.2245	544.3089	527.2824	526.2984	**5**
22	70.0651	2483.2024	2466.1758	2465.1918	2511.1973	2494.1707	2493.1867	2457.1867	**P**	374.1670	373.1718	***416.2140***	399.1874	398.2034	**4**
23	30.0338	2540.2238	2523.1973	2522.2133	2568.2188	2551.1922	2550.2082		**G**			319.1612	302.1347	301.1506	**3**
24	88.0393	2655.2508	2638.2242	2637.2402	2683.2457	2666.2191	2665.2351	2611.2610	**D**	202.1186	201.1234	262.1397	245.1132	244.1292	**2**
25	101.1073								**K**	74.0237	73.0284	147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LQ	214.1550	242.1499	**LQA**	285.1921	313.1870	**LQAL**	398.2762	426.2711
LQALQ	526.3348	554.3297	**LQALQY**	689.3981	717.3930	**QA**	172.1081	200.1030
QAL	285.1921	313.1870	**QALQ**	413.2507	441.2456	**QALQY**	576.3140	604.3089
QALQYV	675.3824	703.3774	**AL**	157.1335	185.1285	**ALQ**	285.1921	313.1870
ALQY	448.2554	476.2504	**ALQYV**	547.3239	575.3188	**ALQYVQ**	675.3824	703.3774
LQ	214.1550	242.1499	**LQY**	377.2183	405.2132	**LQYV**	476.2867	504.2817
LQYVQ	604.3453	632.3402	**QY**	264.1343	292.1292	**QYV**	363.2027	391.1976
QYVQ	491.2613	519.2562	**QYVQD**	606.2882	634.2831	**YV**	235.1441	263.1390
YVQ	363.2027	391.1976	**YVQD**	478.2296	506.2245	**YVQDN**	592.2726	620.2675
YVQDNP	689.3253	717.3202	**VQ**	200.1394	228.1343	**VQD**	315.1663	343.1612
VQDN	429.2092	457.2041	**VQDNP**	526.2620	554.2569	**VQDNPD**	641.2889	669.2838
QD	216.0979	244.0928	**QDN**	330.1408	358.1357	**QDNP**	427.1936	455.1885
QDNPD	542.2205	570.2154	**QDNPDE**	671.2631	699.2580	**DN**	202.0822	230.0771
DNP	299.1350	327.1299	**DNPD**	414.1619	442.1569	**DNPDE**	543.2045	571.1994
DNPDEV	642.2729	670.2679	**NP**	184.1081	212.1030	**NPD**	299.1350	327.1299
NPDE	428.1776	456.1725	**NPDEV**	527.2460	555.2409	**NPDEVC**	687.2767	715.2716
PD	185.0921	213.0870	**PDE**	314.1347	342.1296	**PDEV**	413.2031	441.1980
PDEVC	573.2337	601.2286	**PDEVCP**	670.2865	698.2814	**DE**	217.0819	245.0768
DEV	316.1503	344.1452	**DEVC**	476.1810	504.1759	**DEVCP**	573.2337	601.2286
DEVCPA	644.2708	672.2658	**EV**	201.1234	229.1183	**EVC**	361.1540	389.1489
EVCP	458.2068	486.2017	**EVCPA**	529.2439	557.2388	**EVCPAG**	586.2654	614.2603
VC	232.1114	260.1063	**VCP**	329.1642	357.1591	**VCPA**	400.2013	428.1962
VCPAG	457.2228	485.2177	**VCPAGW**	643.3021	671.2970	**CP**	230.0958	258.0907
CPA	301.1329	329.1278	**CPAG**	358.1544	386.1493	**CPAGW**	544.2337	572.2286
CPAGWK	672.3286	700.3235	**PA**	141.1022	169.0972	**PAG**	198.1237	226.1186
PAGW	384.2030	412.1979	**PAGWK**	512.2980	540.2929	**PAGWKP**	609.3507	637.3457
PAGWKPG	666.3722	694.3671	**AG**	101.0709	129.0659	**AGW**	287.1503	315.1452
AGWK	415.2452	443.2401	**AGWKP**	512.2980	540.2929	**AGWKPG**	569.3194	597.3144
AGWKPGD	684.3464	712.3413	**GW**	216.1131	244.1081	**GWK**	344.2081	372.2030
GWKP	441.2609	469.2558	**GWKPG**	498.2823	526.2772	**GWKPGD**	613.3093	641.3042
WK	287.1866	315.1816	**WKP**	384.2394	412.2343	**WKPG**	441.2609	469.2558
WKPGD	556.2878	584.2827	**KP**	198.1601	226.1550	**KPG**	255.1816	283.1765
KPGD	370.2085	398.2034	**PG**	127.0866	155.0815	**PGD**	242.1135	270.1084
GD	145.0608	173.0557						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.5	2828.3439	0.1251	TLQALQYVQDNPDEVCPAGWKPGDK
11.4	2828.4630	0.0061	KMVAEEGGVSPEEVILVELYPSGLQR
9.6	2828.4888	-0.0198	MQVVAMASALLSQGPALSQAGSDLLRSK
9.1	2828.3941	0.0750	QGGSDVRANTTTAIPIDDGTYELLGHK
8.3	2828.4234	0.0456	GIPVAAMEIMDEVQMKVVNIGGATAPR
8.3	2828.4234	0.0456	GIPVAAMEIMDEVQMKVVNLGGATAPR
8.2	2828.3076	0.1615	DLFSDHKWNILCAPDGAVSSDPQEK
7.7	2828.3763	0.0927	VLDEVVACAGSGNPADTAGGALAAFTAPAR
7.6	2828.2877	0.1813	AMAQQTEGMDIESEAAALDSKASAMLK
7.6	2828.2877	0.1813	AMAQQTEGMDIESEAAALDSKASAMLK

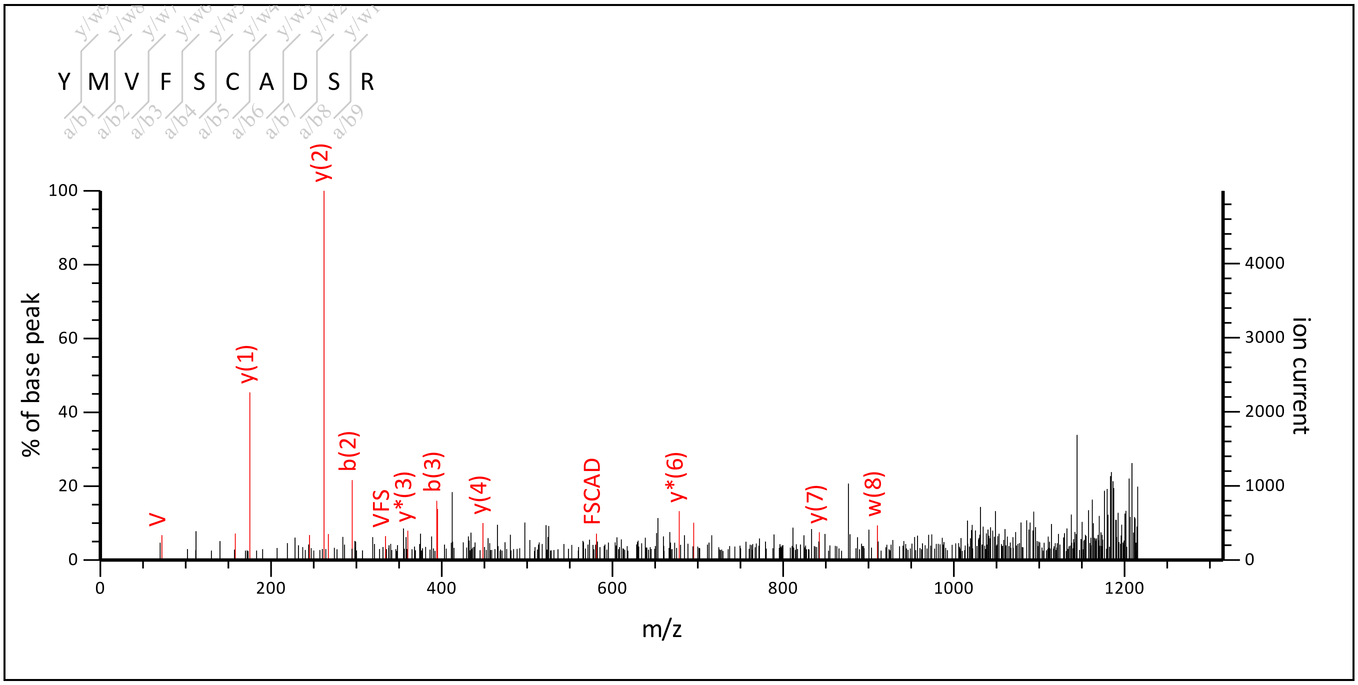
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 23

MS/MS Fragmentation of **YMVFSCADSR**
Found in **gi|3345477** in **NCBInr**, carbonic anhydrase [Oryza sativa]

Match to Query 21: 1234.592824 from(1235.600100,1+) intensity(0.0000) index(9)
Title: Label: G9, Spot_Id: 228976, Peak_List_Id: 257846, MSMS Job_Run_Id: 24939, Comment:
Data file ppw_G9_138985152400.txt



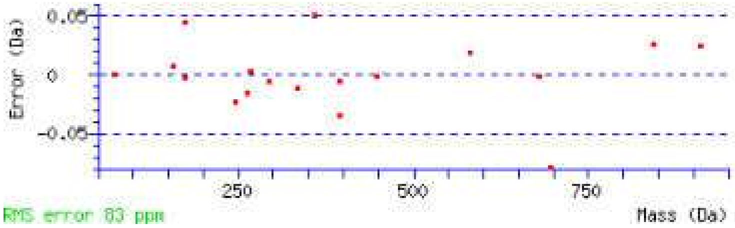
0 to 1315.41

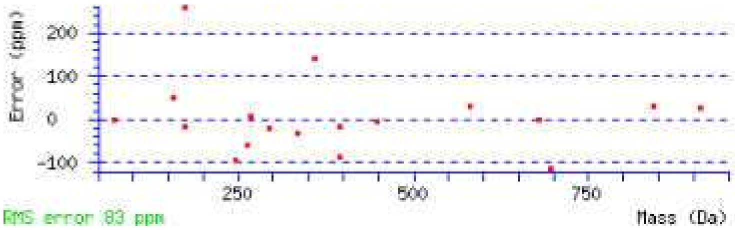
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1234.5111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 10 **Expect:** 2.6e+02
Matches : 18/137 fragment ions using 48 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	136.0757	136.0757		164.0706		44.0495	Y						10
2	104.0528	267.1162		**295.1111**		207.1128	M	996.4204	995.4251	1072.4550	1055.4285	1054.4445	9
3	72.0808	366.1846		**394.1795**		352.1689	V	897.3519	910.3723	941.4145	924.3880	923.4040	8
4	120.0808	513.2530		541.2479			F	750.2835		***842.3461***	825.3196	824.3356	7
5	60.0444	600.2850	582.2745	628.2799	610.2694	584.2901	S	663.2515	662.2563	***695.2777***	678.2512	677.2671	6
6	133.0430	760.3157	742.3051	788.3106	770.3000	671.3221	C	503.2209	502.2256	608.2457	591.2191	590.2351	5
7	44.0495	831.3528	813.3422	859.3477	841.3371		A	432.1837		***448.2150***	431.1885	430.2045	4
8	88.0393	946.3797	928.3692	974.3747	956.3641	902.3899	D	317.1568	316.1615	377.1779	360.1514	359.1674	3
9	60.0444	1033.4118	1015.4012	1061.4067	1043.3961	1017.4169	S	230.1248	229.1295	***262.1510***	245.1244	244.1404	2
10	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
MV	203.1213	231.1162	**MVF**	350.1897	378.1846	**MVFS**	437.2217	465.2166
MVFSC	597.2524	625.2473	**MVFSCA**	668.2895	696.2844	**VF**	219.1492	247.1441
VFS	306.1812	334.1761	**VFSC**	466.2119	494.2068	**VFSCA**	537.2490	565.2439
VFSCAD	652.2759	680.2708	**FS**	207.1128	235.1077	**FSC**	367.1435	395.1384
FSCA	438.1806	466.1755	**FSCAD**	553.2075	581.2024	**FSCADS**	640.2395	668.2345
SC	220.0750	248.0700	**SCA**	291.1122	319.1071	**SCAD**	406.1391	434.1340
SCADS	493.1711	521.1660	**CA**	204.0801	232.0750	**CAD**	319.1071	347.1020
CADS	406.1391	434.1340	**AD**	159.0764	187.0713	**ADS**	246.1084	274.1034
DS	175.0713	203.0662						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
10.4	1234.5111	0.0817	YMVFSCADSR
6.6	1234.6670	-0.0742	VAIQYGTGAISR
6.3	1234.5441	0.0487	FFVFACSDSR
6.3	1234.5111	0.0817	FMVFACSDSR
5.8	1234.6459	-0.0530	VPWGLAGGEPPR
5.5	1234.5111	0.0817	YMVFACSDSR
5.3	1234.6050	-0.0121	IMVGLPSMESR
5.2	1234.6054	-0.0126	ASNEGVRPYSR
5.1	1234.6016	-0.0088	FPDQLIMESR
5.0	1234.6306	-0.0377	IEDAERIFSR

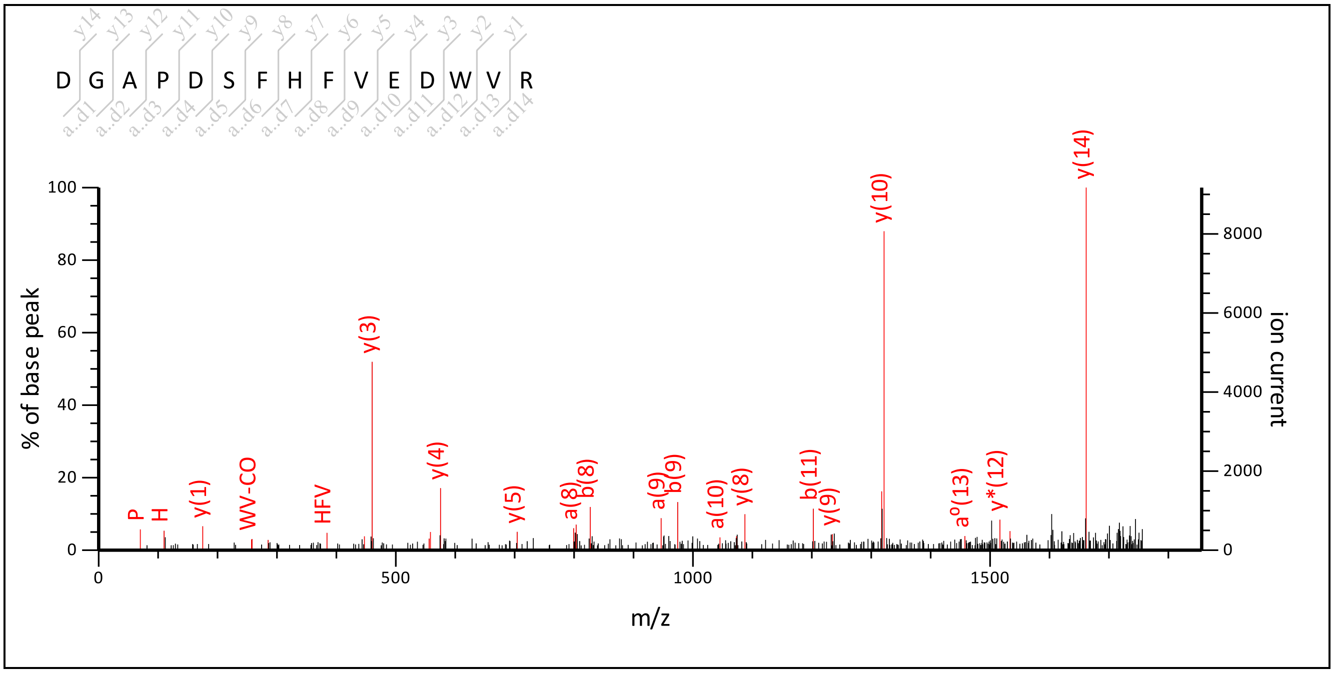
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 23

MS/MS Fragmentation of **DGAPDSFHFVEDWVR**
Found in **gi|3345477** in **NCBInr**, carbonic anhydrase [Oryza sativa]

Match to Query 27: 1775.892724 from(1776.900000,1+) intensity(0.0000) index(12)
Title: Label: G9, Spot_Id: 228976, Peak_List_Id: 257844, MSMS Job_Run_Id: 24939, Comment:
Data file ppw_G9_138985152400.txt



0 to 1856.1

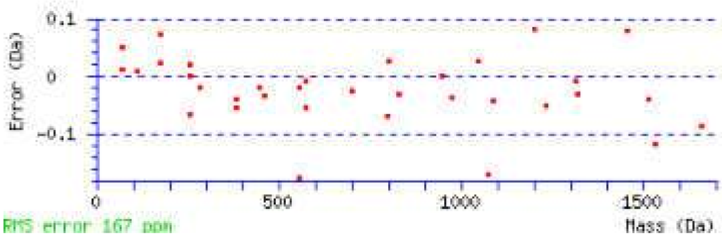
Label all possible matches ○ Label matches used for scoring ●

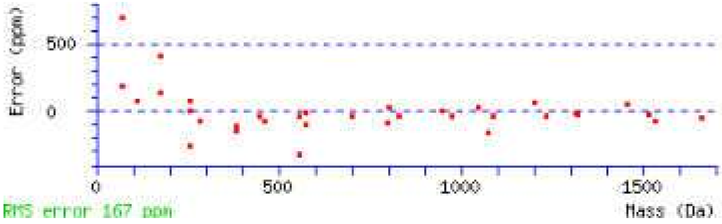
Monoisotopic mass of neutral peptide Mr(calc): 1775.7904
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 0.0023
Matches : 36/228 fragment ions using 51 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	88.0393	88.0393	70.0287	116.0342	98.0237	44.0495	D						15
2	30.0338	145.0608	127.0502	173.0557	155.0451		G			***1661.7707***	1644.7441	1643.7601	14
3	44.0495	216.0979	198.0873	244.0928	226.0822		A	1588.7179		1604.7492	1587.7227	1586.7387	13
4	70.0651	313.1506	295.1401	341.1456	323.1350	287.1350	P	1491.6652	1490.6699	***1533.7121***	1516.6856	1515.7015	12
5	88.0393	428.1776	410.1670	456.1725	438.1619	384.1878	D	1376.6382	1375.6430	1436.6593	1419.6328	1418.6488	11
6	60.0444	515.2096	497.1991	543.2045	525.1940	499.2147	S	1289.6062	1288.6109	***1321.6324***	1304.6058	1303.6218	10
7	120.0808	662.2780	644.2675	690.2729	672.2624		F	1142.5378		***1234.6004***	1217.5738	1216.5898	9
8	110.0713	**799.3369**	781.3264	**827.3319**	809.3213		H	1005.4789		***1087.5320***	1070.5054	1069.5214	8
9	120.0808	**946.4054**	928.3948	**974.4003**	956.3897		F	858.4104		950.4730	933.4465	932.4625	7
10	72.0808	**1045.4738**	1027.4632	**1073.4687**	1055.4581	1031.4581	V	759.3420	772.3624	***803.4046***	786.3781	785.3941	6
11	102.0550	1174.5164	1156.5058	**1202.5113**	1184.5007	1116.5109	E	630.2994	629.3042	***704.3362***	687.3097	686.3257	5

12	88.0393	1289.5433	1271.5327	**1317.5382**	1299.5277	1245.5535	D	515.2725	514.2772	***575.2936***	558.2671	557.2831	4
13	159.0917	1475.6226	1457.6121	1503.6175	1485.6070		W	329.1932		***460.2667***	443.2401		3
14	72.0808	1574.6910	1556.6805	1602.6859	1584.6754	1560.6754	V	230.1248	243.1452	274.1874	257.1608		2
15	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GA	101.0709	129.0659	GAP	198.1237	226.1186	GAPD	313.1506	341.1456
GAPDS	400.1827	428.1776	GAPDSF	547.2511	575.2460	GAPDSFH	684.3100	712.3049
AP	141.1022	169.0972	APD	256.1292	284.1241	APDS	343.1612	371.1561
APDSF	490.2296	518.2245	APDSFH	627.2885	655.2835	PD	185.0921	213.0870
PDS	272.1241	300.1190	PDSF	419.1925	447.1874	PDSFH	556.2514	584.2463
DS	175.0713	203.0662	DSF	322.1397	350.1347	DSFH	459.1987	487.1936
DSFHF	606.2671	634.2620	SF	207.1128	235.1077	SFH	344.1717	372.1666
SFHF	491.2401	519.2350	SFHFV	590.3085	618.3035	FH	257.1397	285.1346
FHF	404.2081	432.2030	FHFV	503.2765	531.2714	FHFVE	632.3191	660.3140
HF	257.1397	285.1346	HFV	356.2081	384.2030	HFVE	485.2507	513.2456
HFVED	600.2776	628.2726	FV	219.1492	247.1441	FVE	348.1918	376.1867
FVED	463.2187	491.2136	FVEDW	649.2980	677.2930	VE	201.1234	229.1183
VED	316.1503	344.1452	VEDW	502.2296	530.2245	VEDWV	601.2980	629.2930
ED	217.0819	245.0768	EDW	403.1612	431.1561	EDWV	502.2296	530.2245
DW	274.1186	302.1135	DWV	373.1870	401.1819	WV	258.1601	286.1550





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.7	1775.7904	0.1023	DGAPDSFHFVEDWVR
15.4	1775.8916	0.0011	EYYSFLKILCGVER
14.8	1775.8074	0.0853	DGFPDAPSSQNNITASR
13.8	1775.8818	0.0110	DPKDMLVSFWHFVR
12.5	1775.8115	0.0812	DDPAGSTVPQADYVWR
11.7	1775.7598	0.1329	DRPSFEESPESDPER

11.7	1775.8672	0.0256	MLSARDLGHMHHISR
10.3	1775.8479	0.0449	DHLNYSVYIPDADVR
9.7	1775.8876	0.0051	DAVKLTGGPAYEVPMGR
9.7	1775.8108	0.0819	DQDQMNVQSLSVEQR

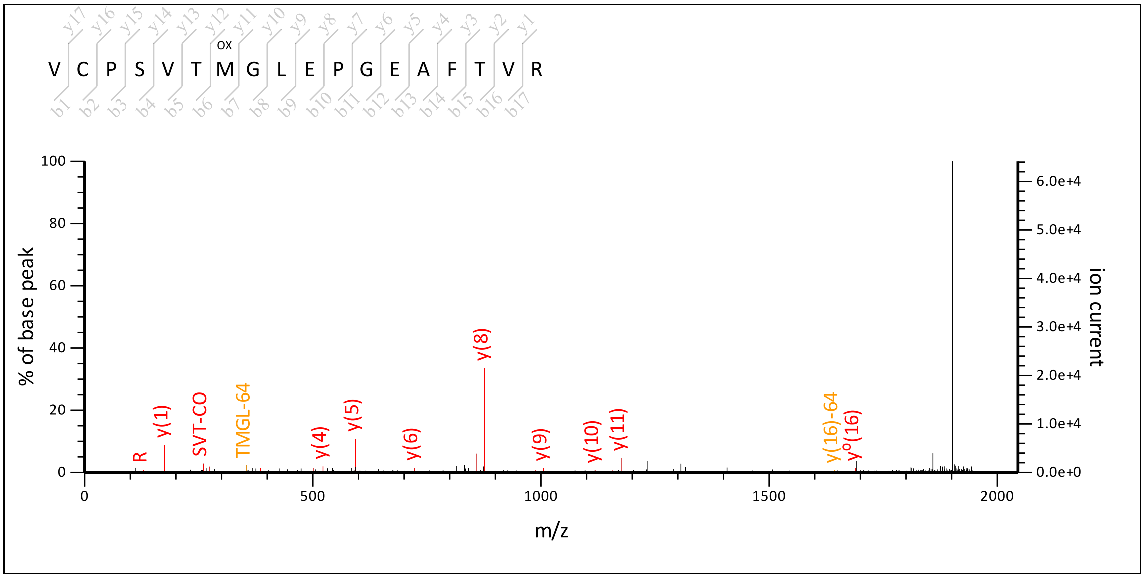
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 23

MS/MS Fragmentation of **VCPSVTMGLEPGEAFTVR**
Found in **gi|3345477** in **NCBInr**, carbonic anhydrase [Oryza sativa]

Match to Query 31: 1965.031224 from(1966.038500,1+) intensity(0.0000) index(14)
Title: Label: G9, Spot_Id: 228976, Peak_List_Id: 257845, MSMS Job_Run_Id: 24939, Comment:
Data file ppw_G9_138985152400.txt



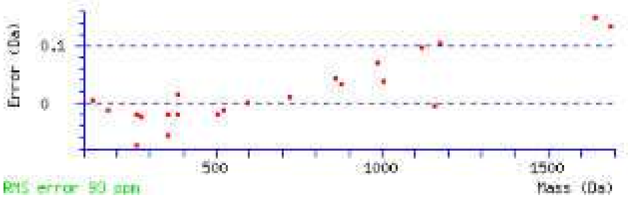
0 to 2045.23

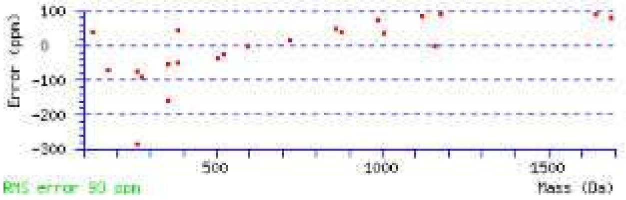
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1964.9336
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 57 **Expect:** 0.0041
Matches : 23/452 fragment ions using 38 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495		V							18
2	133.0430	232.1114		260.1063		143.1179		C	1697.8493	1696.8541		1802.8742	1785.8476	1784.8636	17
3	70.0651	329.1642		357.1591		303.1485		P	1600.7966	1599.8013		***1642.8435***	1625.8170	1624.8329	16
4	60.0444	416.1962	398.1857	444.1911	426.1806	400.2013		S	1513.7645	1512.7693		1545.7908	1528.7642	1527.7802	15
5	72.0808	515.2646	497.2541	543.2595	525.2490	501.2490		V	1414.6961	1427.7165		1458.7587	1441.7322	1440.7482	14
6	74.0600	616.3123	598.3017	644.3072	626.2967	600.3174	602.2967	T	1313.6484	1326.6688	1328.6481	1359.6903	1342.6638	1341.6797	13
7	56.0495	699.3494	681.3389	727.3443	709.3338	687.3494		M	1230.6113	1229.6161		1258.6426	1241.6161	1240.6321	12
8	30.0338	756.3709	738.3603	784.3658	766.3552			G				***1175.6055***	1158.5790	1157.5949	11
9	86.0964	869.4550	851.4444	897.4499	879.4393	827.4080		L	1060.5058	1059.5106		***1118.5841***	1101.5575	1100.5735	10
10	102.0550	998.4975	980.4870	1026.4925	1008.4819	940.4921		E	931.4632	930.4680		***1005.5000***	988.4734	987.4894	9
11	70.0651	1095.5503	1077.5397	1123.5452	1105.5347	1069.5347		P	834.4104	833.4152		***876.4574***	859.4308	858.4468	8
12	30.0338	1152.5718	1134.5612	1180.5667	1162.5561			G				779.4046	762.3781	761.3941	7
13	102.0550	1281.6144	1263.6038	1309.6093	1291.5987	1223.6089		E	648.3464	647.3511		***722.3832***	705.3566	704.3726	6
14	44.0495	1352.6515	1334.6409	1380.6464	1362.6358			A	577.3093			***593.3406***	576.3140	575.3300	5
15	120.0808	1499.7199	1481.7093	1527.7148	1509.7042			F	430.2409			***522.3035***	505.2769	504.2929	4
16	74.0600	1600.7676	1582.7570	1628.7625	1610.7519	1584.7727	1586.7519	T	329.1932	342.2136	344.1928	375.2350	358.2085	357.2245	3
17	72.0808	1699.8360	1681.8254	1727.8309	1709.8203	1685.8203		V	230.1248	243.1452		***274.1874***	257.1608		2
18	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
CP	230.0958	258.0907	**CPS**	317.1278	345.1227	**CPSV**	416.1962	444.1911
CPSVT	517.2439	545.2388	**CPSVTM**	600.2810	628.2759	**CPSVTMG**	657.3025	685.2974
PS	157.0972	185.0921	**PSV**	256.1656	284.1605	**PSVT**	357.2132	385.2082
PSVTM	440.2504	468.2453	**PSVTMG**	497.2718	525.2667	**PSVTMGL**	610.3559	638.3508
SV	159.1128	187.1077	**SVT**	260.1605	288.1554	**SVTM**	343.1976	371.1925
SVTMG	400.2191	428.2140	**SVTMGL**	513.3031	541.2980	**SVTMGLE**	642.3457	670.3406
VT	173.1285	201.1234	**VTM**	256.1656	284.1605	**VTMG**	313.1870	341.1819
VTMGL	426.2711	454.2660	**VTMGLE**	555.3137	583.3086	**VTMGLEP**	652.3665	680.3614
TM	157.0972	185.0921	**TMG**	214.1186	242.1135	**TMGL**	327.2027	355.1976
TMGLE	456.2453	484.2402	**TMGLEP**	553.2980	581.2930	**TMGLEPG**	610.3195	638.3144
MG	113.0709	141.0659	**MGL**	226.1550	254.1499	**MGLE**	355.1976	383.1925
MGLEP	452.2504	480.2453	**MGLEPG**	509.2718	537.2667	**MGLEPGE**	638.3144	666.3093
GL	143.1179	171.1128	**GLE**	272.1605	300.1554	**GLEP**	369.2132	397.2082
GLEPG	426.2347	454.2296	**GLEPGE**	555.2773	583.2722	**GLEPGEA**	626.3144	654.3093
LE	215.1390	243.1339	**LEP**	312.1918	340.1867	**LEPG**	369.2132	397.2082
LEPGE	498.2558	526.2508	**LEPGEA**	569.2930	597.2879	**EP**	199.1077	227.1026
EPG	256.1292	284.1241	**EPGE**	385.1718	413.1667	**EPGEA**	456.2089	484.2038
EPGEAF	603.2773	631.2722	**PG**	127.0866	155.0815	**PGE**	256.1292	284.1241
PGEA	327.1663	355.1612	**PGEAF**	474.2347	502.2296	**PGEAFT**	575.2824	603.2773
PGEAFTV	674.3508	702.3457	**GE**	159.0764	187.0713	**GEA**	230.1135	258.1084
GEAF	377.1819	405.1769	**GEAFT**	478.2296	506.2245	**GEAFTV**	577.2980	605.2930
EA	173.0921	201.0870	**EAF**	320.1605	348.1554	**EAFT**	421.2082	449.2031
EAFTV	520.2766	548.2715	**AF**	191.1179	219.1128	**AFT**	292.1656	320.1605
AFTV	391.2340	419.2289	**FT**	221.1285	249.1234	**FTV**	320.1969	348.1918
TV	173.1285	201.1234						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.7	1964.9336	0.0976	VCPSVTMGLEPGEAFTVR
17.1	1964.9778	0.0534	LKGMGFEQSLHEAAIYR
16.5	1965.0419	-0.0106	VSDLGSTSTLRYLDPTLK
13.4	1964.9183	0.1129	MQEPCEVSIDISVSLSR
12.2	1964.8997	0.1316	VERSSMAVEIADSPSDEK
11.8	1964.9448	0.0864	VASSALGFGPQMAMQVAER
11.8	1965.0030	0.0282	MVGLEGFGLIDQIYGPTR
11.6	1964.9473	0.0839	EVRGSLTDMLNEEVTTR
11.1	1964.9990	0.0322	ILGEGGQGTVYKGMLVDGR
10.4	1964.9051	0.1262	TYVSQYDLHHAEMTVR

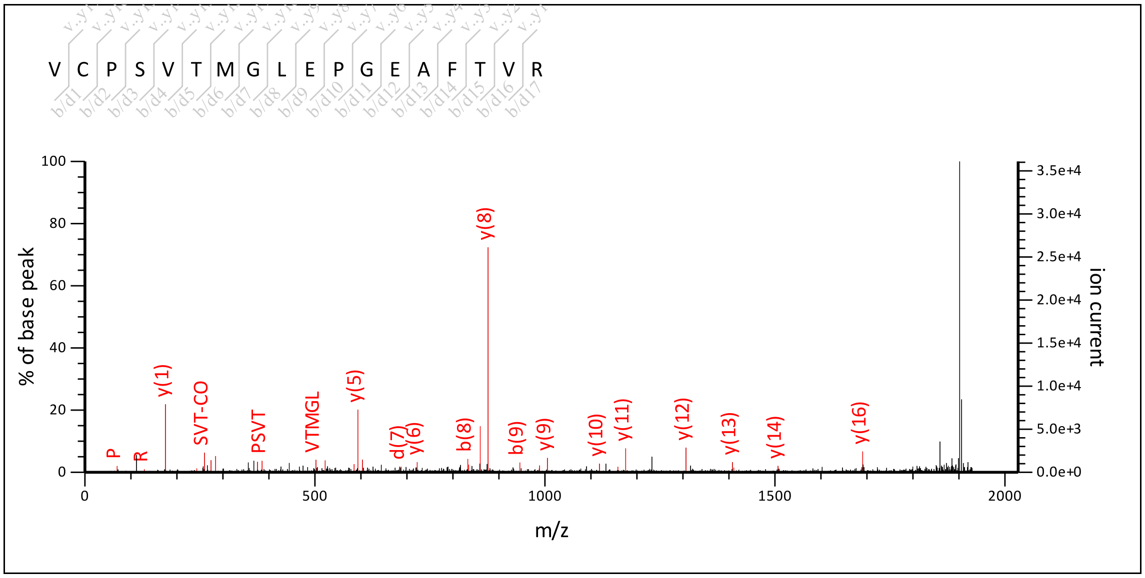
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 23

MS/MS Fragmentation of **VCPSVTMGLEPGEAFTVR**
Found in **gi|3345477** in **NCBInr**, carbonic anhydrase [Oryza sativa]

Match to Query 29: 1949.058124 from(1950.065400,1+) intensity(0.0000) index(13)
Title: Label: G9, Spot_Id: 228976, Peak_List_Id: 257843, MSMS Job_Run_Id: 24939, Comment:
Data file ppw_G9_138985152400.txt



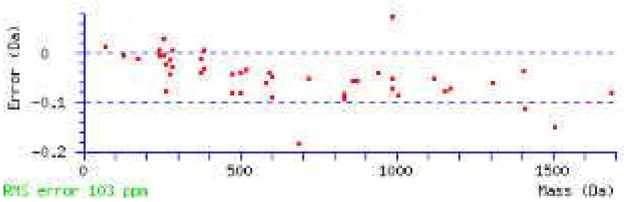
0 to 2028.71

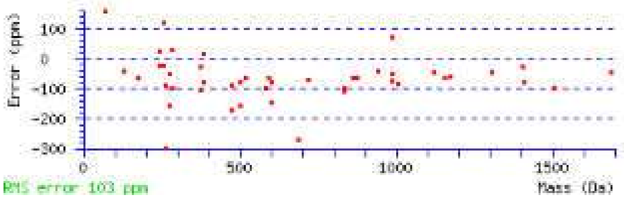
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1948.9387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 101 **Expect:** 1.4e-07
Matches : 49/313 fragment ions using 57 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495		V							18
2	133.0430	232.1114		**260.1063**		143.1179		C	1745.8527	1744.8575		1850.8775	1833.8510	1832.8670	17
3	70.0651	329.1642		357.1591		303.1485		P	1648.7999	1647.8047		***1690.8469***	1673.8203	1672.8363	16
4	60.0444	416.1962	398.1857	444.1911	426.1806	400.2013		S	1561.7679	1560.7727		1593.7941	1576.7676	1575.7836	15
5	72.0808	515.2646	497.2541	543.2595	525.2490	501.2490		V	1462.6995	1475.7199		***1506.7621***	1489.7355	1488.7515	14
6	74.0600	616.3123	598.3017	644.3072	626.2967	600.3174	602.2967	T	1361.6518	1374.6722	1376.6515	***1407.6937***	1390.6671	1389.6831	13
7	104.0528	747.3528	729.3422	775.3477	757.3371	687.3494		M	1230.6113	1229.6161		***1306.6460***	1289.6195	1288.6354	12
8	30.0338	804.3743	786.3637	**832.3692**	814.3586			G				***1175.6055***	1158.5790	1157.5950	11
9	86.0964	917.4583	899.4478	**945.4532**	927.4427	875.4114		L	1060.5058	1059.5106		***1118.5841***	1101.5575	1100.5735	10
10	102.0550	1046.5009	1028.4904	1074.4958	1056.4853	988.4954		E	931.4632	930.4680		***1005.5000***	988.4734	987.4894	9
11	70.0651	1143.5537	1125.5431	1171.5486	1153.5380	1117.5380		P	834.4104	833.4152		***876.4574***	859.4308	858.4468	8
12	30.0338	1200.5751	1182.5646	1228.5701	1210.5595			G				779.4046	762.3781	761.3941	7
13	102.0550	1329.6177	1311.6072	1357.6127	1339.6021	1271.6123		E	648.3464	647.3511		***722.3832***	705.3566	704.3726	6
14	44.0495	1400.6549	1382.6443	1428.6498	1410.6392			A	577.3093			***593.3406***	576.3140	575.3300	5
15	120.0808	1547.7233	1529.7127	1575.7182	1557.7076			F	430.2409			***522.3035***	505.2769	504.2929	4
16	74.0600	1648.7709	1630.7604	1676.7659	1658.7553	1632.7760	1634.7553	T	329.1932	342.2136	344.1928	***375.2350***	358.2085	357.2245	3
17	72.0808	1747.8394	1729.8288	1775.8343	1757.8237	1733.8237		V	230.1248	243.1452		***274.1874***	257.1608		2
18	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
CP	230.0958	258.0907	**CPS**	317.1278	345.1227	**CPSV**	416.1962	444.1911
CPSVT	517.2439	545.2388	**CPSVTM**	648.2844	676.2793	**PS**	157.0972	185.0921
PSV	256.1656	284.1605	**PSVT**	357.2132	385.2082	**PSVTM**	488.2537	516.2486
PSVTMG	545.2752	573.2701	**PSVTMGL**	658.3593	686.3542	**SV**	159.1128	187.1077
SVT	260.1605	288.1554	**SVTM**	391.2010	419.1959	**SVTMG**	448.2224	476.2173
SVTMGL	561.3065	589.3014	**SVTMGLE**	690.3491	718.3440	**VT**	173.1285	201.1234
VTM	304.1689	332.1639	**VTMG**	361.1904	389.1853	**VTMGL**	474.2745	502.2694
VTMGLE	603.3171	631.3120	**TM**	205.1005	233.0954	**TMG**	262.1220	290.1169
TMGL	375.2061	403.2010	**TMGLE**	504.2486	532.2436	**TMGLEP**	601.3014	629.2963
TMGLEPG	658.3229	686.3178	**MG**	161.0743	189.0692	**MGL**	274.1584	302.1533
MGLE	403.2010	431.1959	**MGLEP**	500.2537	528.2486	**MGLEPG**	557.2752	585.2701
MGLEPGE	686.3178	714.3127	**GL**	143.1179	171.1128	**GLE**	272.1605	300.1554
GLEP	369.2132	397.2082	**GLEPG**	426.2347	454.2296	**GLEPGE**	555.2773	583.2722
GLEPGEA	626.3144	654.3093	**LE**	215.1390	243.1339	**LEP**	312.1918	340.1867
LEPG	369.2132	397.2082	**LEPGE**	498.2558	526.2508	**LEPGEA**	569.2930	597.2879
EP	199.1077	227.1026	**EPG**	256.1292	284.1241	**EPGE**	385.1718	413.1667
EPGEA	456.2089	484.2038	**EPGEAF**	603.2773	631.2722	**PG**	127.0866	155.0815
PGE	256.1292	284.1241	**PGEA**	327.1663	355.1612	**PGEAF**	474.2347	502.2296
PGEAFT	575.2824	603.2773	**PGEAFTV**	674.3508	702.3457	**GE**	159.0764	187.0713
GEA	230.1135	258.1084	**GEAF**	377.1819	405.1769	**GEAFT**	478.2296	506.2245
GEAFTV	577.2980	605.2930	**EA**	173.0921	201.0870	**EAF**	320.1605	348.1554
EAFT	421.2082	449.2031	**EAFTV**	520.2766	548.2715	**AF**	191.1179	219.1128
AFT	292.1656	320.1605	**AFTV**	391.2340	419.2289	**FT**	221.1285	249.1234
FTV	320.1969	348.1918	**TV**	173.1285	201.1234			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.5	1948.9387	0.1194	VCPSVTMGLEPGEAFTVR
13.9	1949.0155	0.0427	AMAVAVCEIVWLISFLQ
12.3	1948.8684	0.1897	DGSDADESVEVQVTMPVR
11.8	1948.9928	0.0653	CVGSAEDLIDFVISVLGR
11.2	1949.0027	0.0554	ITKTSIMLGLGESDDELK
10.2	1949.0081	0.0501	LLGEFAELCGPFAGVLTR
9.1	1948.9564	0.1017	PTLTKLYSMEEAATHNK
9.0	1948.9061	0.1520	SRSDSHCDEIIGFVTAR
8.7	1948.9829	0.0752	LKGMGFEQSLHEAAIYR
8.7	1948.9234	0.1347	MQEPCEVSIDISVSLSR

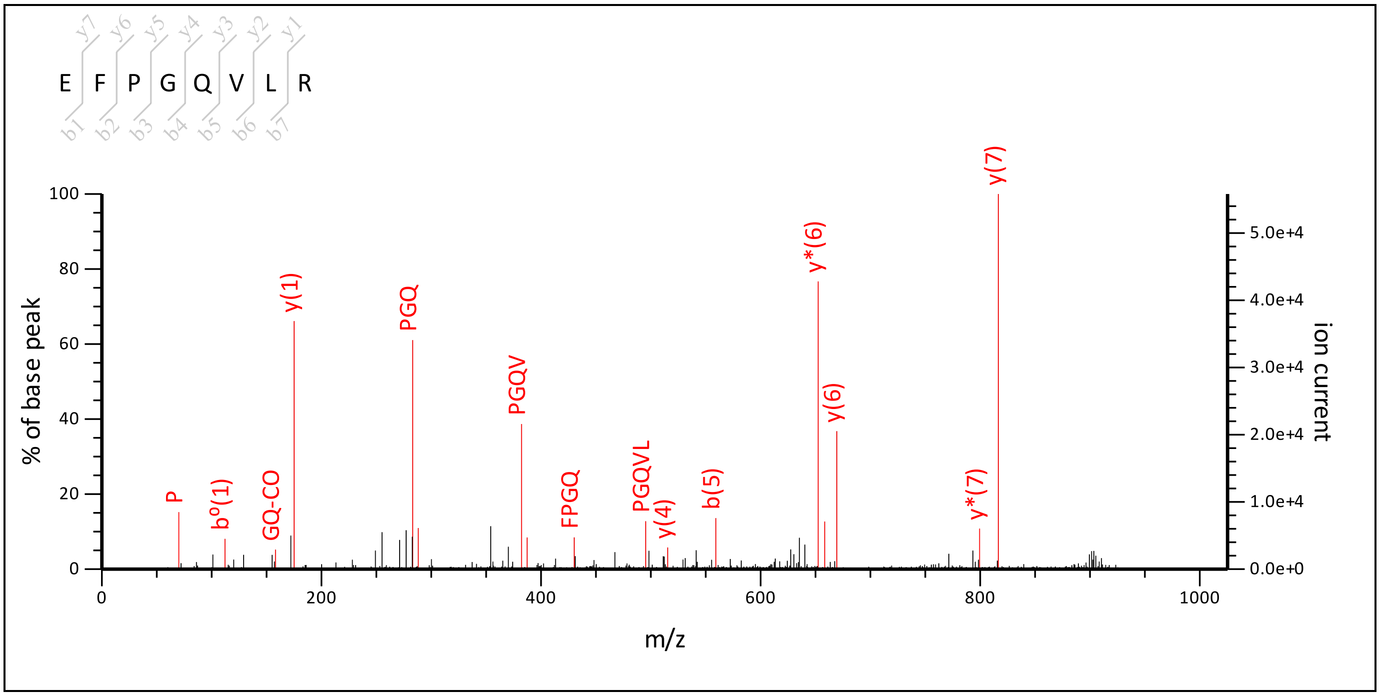
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **EFPGQVLR**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 9: 944.618394 from(945.625670,1+) intensity(0.0000) index(2)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221696, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



0 to 1025.33

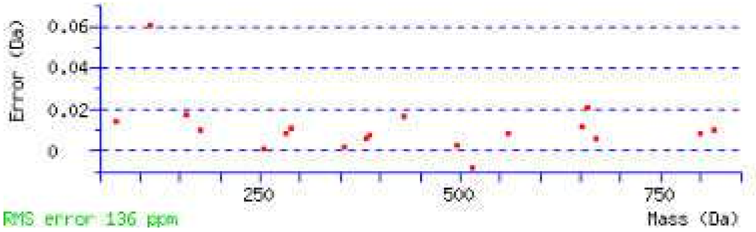
Label all possible matches ○ Label matches used for scoring ●

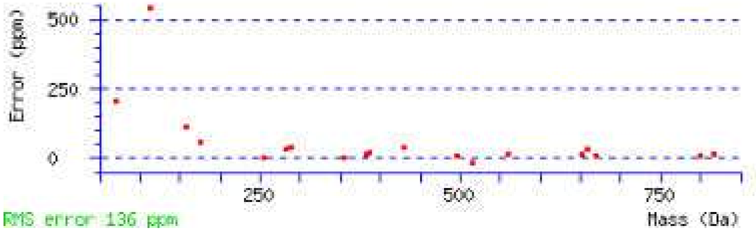
Monoisotopic mass of neutral peptide Mr(calc): 944.5080
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.22
Matches : 20/102 fragment ions using 27 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495	E					8
2	120.0808	249.1234		231.1128	277.1183		259.1077		F	724.4101		***816.4727***	799.4461	7
3	70.0651	346.1761		328.1656	374.1710		356.1605	320.1605	P	627.3573	626.3620	***669.4042***	652.3777	6
4	30.0338	403.1976		385.1870	431.1925		413.1819		G			572.3515	555.3249	5
5	101.0709	531.2562	514.2296	513.2456	**559.2511**	542.2245	541.2405	474.2347	Q	442.2772	441.2820	***515.3300***	498.3035	4
6	72.0808	630.3246	613.2980	612.3140	**658.3195**	641.2930	640.3089	616.3089	V	343.2088	356.2292	***387.2714***	370.2449	3
7	86.0964	743.4087	726.3821	725.3981	771.4036	754.3770	753.3930	701.3617	L	230.1248	229.1295	***288.2030***	271.1765	2
8	129.1135								R	74.0237	73.0284	***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FP	217.1335	245.1285	FPG	274.1550	302.1499	FPGQ	402.2136	430.2085

FPGQV	501.2820	529.2769	**FPGQVL**	614.3661	642.3610	**PG**	127.0866	155.0815
PGQ	255.1452	283.1401	**PGQV**	354.2136	382.2085	**PGQVL**	467.2976	495.2926
GQ	158.0924	186.0873	**GQV**	257.1608	285.1557	**GQVL**	370.2449	398.2398
QV	200.1394	228.1343	**QVL**	313.2234	341.2183	**VL**	185.1648	213.1598





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.8	944.5080	0.1104	EFPGQVLR
26.7	944.5114	0.1070	MTGVGPVLR
25.8	944.4862	0.1322	EMQRPLR
25.2	943.4611	1.1573	QGPLADSEK
25.2	945.5430	-0.9246	NVMAKVLR
23.8	944.4749	0.1435	MEAAPAALR
22.6	944.4927	0.1257	GEEDKVLR
21.7	944.4563	0.1621	EEQEAAIR
21.5	943.4723	1.1461	AGEQEAALR
20.9	943.5239	1.0945	AGFAVNPIR

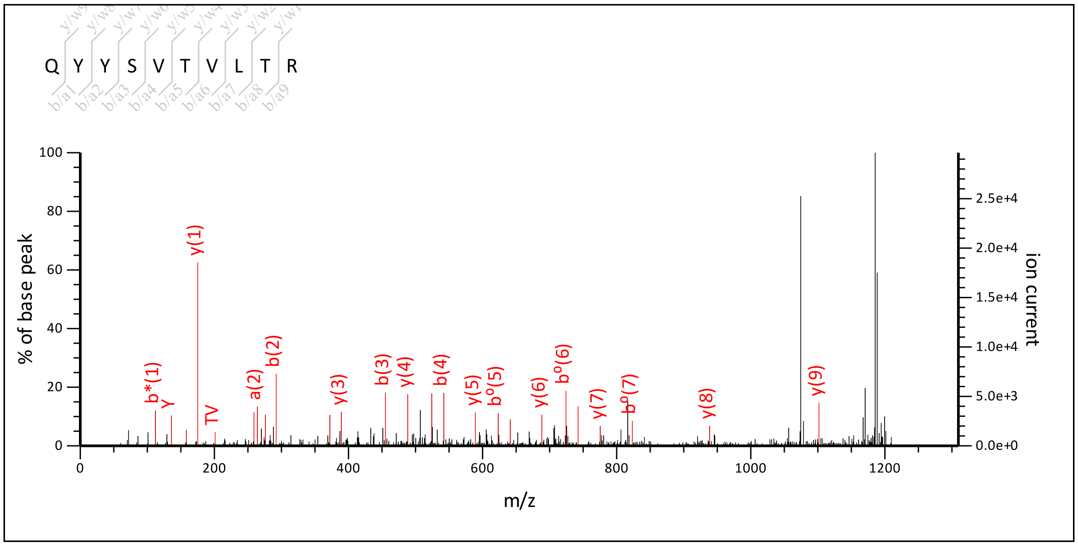
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **QYYSVTVLTR**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 13: 1228.790724 from(1229.798000,1+) intensity(0.0000) index(4)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221697, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



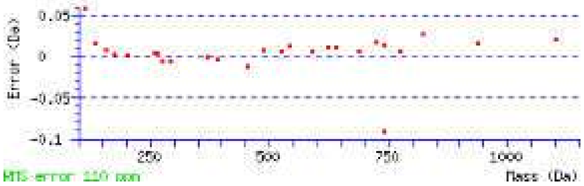
0 to 1309.63

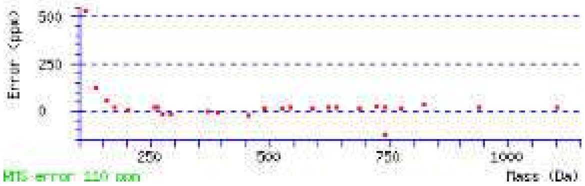
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1228.6452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67   Expect: 0.0012
Matches : 28/160 fragment ions using 36 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y
1	101.0709	101.0709	84.0444		129.0659	112.0393		44.0495		**Q**						
2	136.0757	264.1343	247.1077		**292.1292**	275.1026				**Y**	993.5364			***1101.5939***	1084.5673	1083.
3	136.0757	427.1976	410.1710		**455.1925**	438.1660				**Y**	830.4730			***938.5306***	921.5040	920.
4	60.0444	514.2296	497.2031	496.2191	**542.2245**	525.1980	524.2140	498.2347		**S**	743.4410	742.4458		***775.4672***	758.4407	757.
5	72.0808	613.2980	596.2715	595.2875	**641.2930**	624.2664	623.2824	599.2824		**V**	644.3726	657.3930		***688.4352***	671.4087	670.
6	74.0600	714.3457	697.3192	696.3352	**742.3406**	725.3141	724.3301	698.3508	700.3301	**T**	543.3249	556.3453	558.3246	***589.3668***	572.3402	571.
7	72.0808	813.4141	796.3876	795.4036	841.4090	824.3825	823.3985	799.3985		**V**	444.2565	457.2769		***488.3191***	471.2926	470.
8	86.0964	926.4982	909.4716	908.4876	954.4931	937.4666	936.4825	884.4512		**L**	331.1724	330.1772		***389.2507***	372.2241	371.
9	74.0600	1027.5459	1010.5193	1009.5353	1055.5408	1038.5142	1037.5302	1011.5510	1013.5302	**T**	230.1248	243.1452	245.1244	***276.1666***	259.1401	258.
10	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YY	299.1390	327.1339	**YYS**	386.1710	414.1660	**YYSV**	485.2395	513.2344
YYSVT	586.2871	614.2821	**YYSVTV**	685.3556	713.3505	**YS**	223.1077	251.1026
YSV	322.1761	350.1710	**YSVT**	423.2238	451.2187	**YSVTV**	522.2922	550.2871
YSVTVL	635.3763	663.3712	**SV**	159.1128	187.1077	**SVT**	260.1605	288.1554
SVTV	359.2289	387.2238	**SVTVL**	472.3130	500.3079	**SVTVLT**	573.3606	601.3556
VT	173.1285	201.1234	**VTV**	272.1969	300.1918	**VTVL**	385.2809	413.2758
VTVLT	486.3286	514.3235	**TV**	173.1285	201.1234	**TVL**	286.2125	314.2074
TVLT	387.2602	415.2551	**VL**	185.1648	213.1598	**VLT**	286.2125	314.2074
LT	187.1441	215.1390						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
66.7	1228.6452	0.1455	QYYSVTVLTR
21.7	1227.6572	1.1336	ANPGSNVTVTLR
19.4	1229.6802	-0.8895	ISVPQVIMSTR
17.5	1227.6823	1.1085	LNNEAVEALKK
17.1	1227.6823	1.1084	DIPQSISVITR
16.9	1229.7092	-0.9184	RSVLDALSLTR
16.8	1228.6564	0.1343	SGNWPVSIITR
15.3	1227.7187	1.0721	VALEKLDAITR
14.3	1228.7139	0.0768	KGTIQITEALR
14.0	1228.6160	0.1747	SLVNQAEAQNR

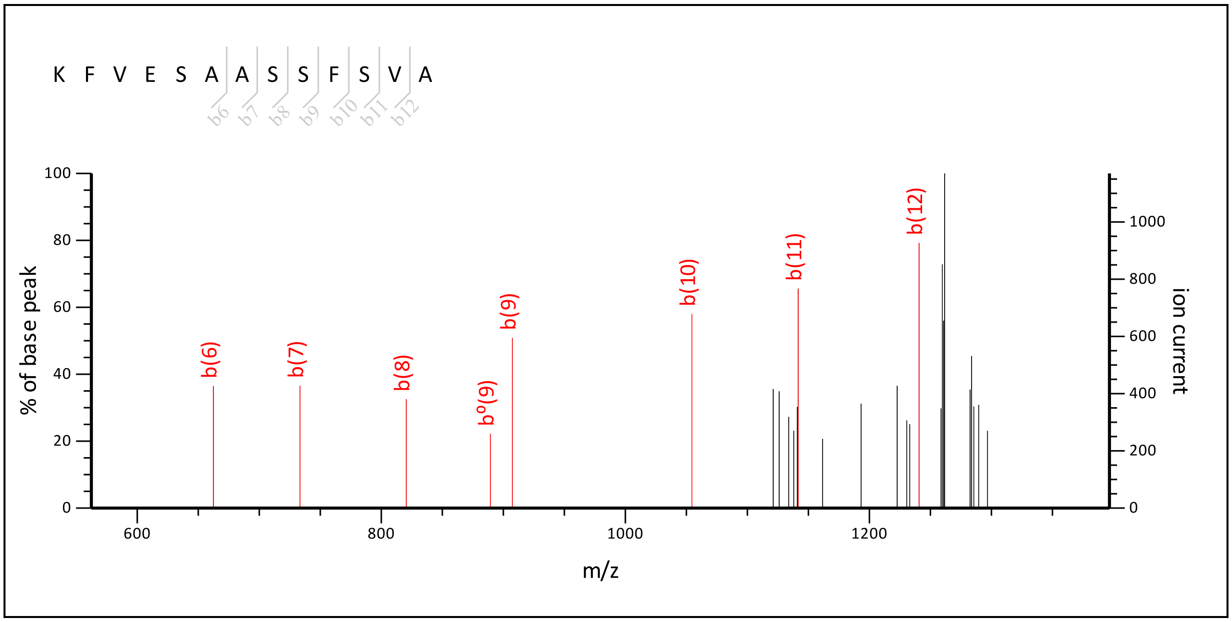
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **KFVESAASSFSVA**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 16: 1328.787024 from(1329.794300,1+) intensity(0.0000) index(5)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221715, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



562.38 to 1396.72

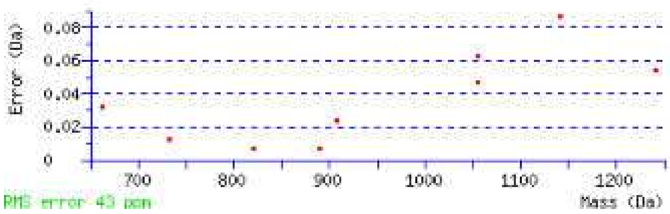
Label all possible matches ○ Label matches used for scoring ●

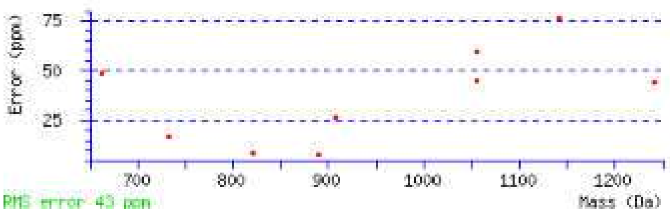
Monoisotopic mass of neutral peptide Mr(calc): 1328.6612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 0.029
Matches : 9/219 fragment ions using 12 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y^0	#
1	101.1073	101.1073	84.0808		129.1022	112.0757		44.0495	K					13
2	120.0808	248.1757	231.1492		276.1707	259.1441			F	1109.5109		1201.5735	1183.5630	12
3	72.0808	347.2442	330.2176		375.2391	358.2125		333.2285	V	1010.4425	1023.4629	1054.5051	1036.4946	11
4	102.0550	476.2867	459.2602	458.2762	504.2817	487.2551	486.2711	418.2813	E	881.3999	880.4047	955.4367	937.4262	10
5	60.0444	563.3188	546.2922	545.3082	591.3137	574.2871	573.3031	547.3239	S	794.3679	793.3727	826.3941	808.3836	9
6	44.0495	634.3559	617.3293	616.3453	***662.3508***	645.3243	644.3402		A	723.3308		739.3621	721.3515	8
7	44.0495	705.3930	688.3665	687.3824	***733.3879***	716.3614	715.3774		A	652.2937		668.3250	650.3144	7
8	60.0444	792.4250	775.3985	774.4145	***820.4199***	803.3934	802.4094	776.4301	S	565.2617	564.2664	597.2879	579.2773	6
9	60.0444	879.4571	862.4305	861.4465	***907.4520***	890.4254	889.4414	863.4621	S	478.2296	477.2344	510.2558	492.2453	5
10	120.0808	1026.5255	1009.4989	1008.5149	***1054.5204***	1037.4938	1036.5098		F	331.1612		423.2238	405.2132	4
11	60.0444	1113.5575	1096.5310	1095.5469	***1141.5524***	1124.5259	1123.5418	1097.5626	S	244.1292	243.1339	276.1554	258.1448	3
12	72.0808	1212.6259	1195.5994	1194.6153	***1240.6208***	1223.5943	1222.6103	1198.6103	V	145.0608	158.0812	189.1234		2
13	44.0495								A	74.0237	73.0284	90.0550		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FV	219.1492	247.1441	FVE	348.1918	376.1867	FVES	435.2238	463.2187

FVESA	506.2609	534.2558	**FVESAA**	577.2980	605.2930	**FVESAAS**	664.3301	692.3250
VE	201.1234	229.1183	**VES**	288.1554	316.1503	**VESA**	359.1925	387.1874
VESAA	430.2296	458.2245	**VESAAS**	517.2617	545.2566	**VESAASS**	604.2937	632.2886
ES	189.0870	217.0819	**ESA**	260.1241	288.1190	**ESAA**	331.1612	359.1561
ESAAS	418.1932	446.1882	**ESAASS**	505.2253	533.2202	**ESAASSF**	652.2937	680.2886
SA	131.0815	159.0764	**SAA**	202.1186	230.1135	**SAAS**	289.1506	317.1456
SAASS	376.1827	404.1776	**SAASSF**	523.2511	551.2460	**SAASSFS**	610.2831	638.2780
AA	115.0866	143.0815	**AAS**	202.1186	230.1135	**AASS**	289.1506	317.1456
AASSF	436.2191	464.2140	**AASSFS**	523.2511	551.2460	**AASSFSV**	622.3195	650.3144
AS	131.0815	159.0764	**ASS**	218.1135	246.1084	**ASSF**	365.1819	393.1769
ASSFS	452.2140	480.2089	**ASSFSV**	551.2824	579.2773	**SS**	147.0764	175.0713
SSF	294.1448	322.1397	**SSFS**	381.1769	409.1718	**SSFSV**	480.2453	508.2402
SF	207.1128	235.1077	**SFS**	294.1448	322.1397	**SFSV**	393.2132	421.2082
FS	207.1128	235.1077	**FSV**	306.1812	334.1761	**SV**	159.1128	187.1077





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.9	1328.6612	0.1258	KFVESAASSFSVA
28.7	1328.6183	0.1687	TARMDWSSFTK
28.7	1328.5997	0.1873	TNASSWNSSFTK
25.5	1327.6806	1.1065	NSISIMASSFKK
24.5	1328.6096	0.1774	TSSFSLQESTDK
20.6	1328.6282	0.1588	ASALNYISSMEK
19.7	1327.6289	1.1581	STLSSEQSSMKK
19.6	1329.7517	-0.9647	AAAIPSSAFARIR
16.8	1327.6554	1.1316	AHNVSTGEAMAIK
16.4	1328.7048	0.0822	TSSESRLSPLPR

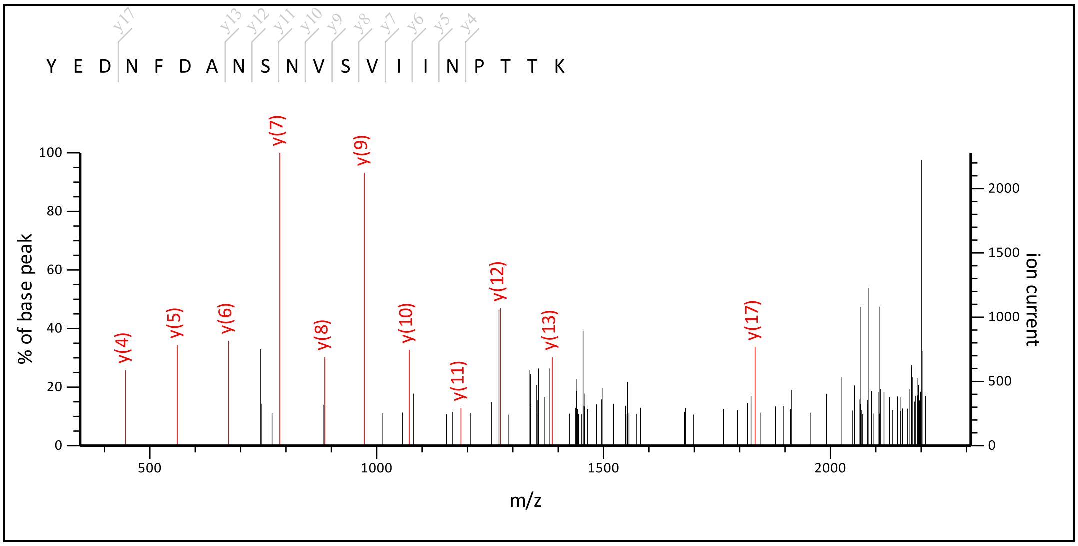
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **YEDNFDANSNVSVIINPTTK**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 28: 2240.296424 from(2241.303700,1+) intensity(0.0000) index(10)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221710, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



346.21 to 2309.31

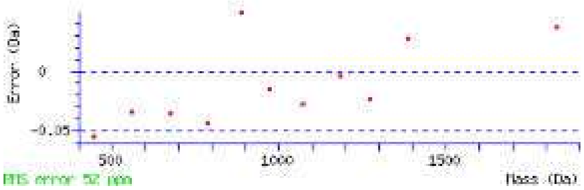
Label all possible matches ○ Label matches used for scoring ●

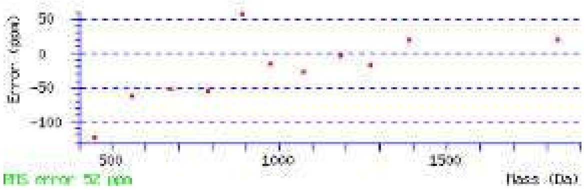
Monoisotopic mass of neutral peptide Mr(calc): 2240.0597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77 **Expect:** 6.3e-05
Matches : 11/401 fragment ions using 18 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	136.0757	136.0757			164.0706			44.0495		Y						
2	102.0550	265.1183		247.1077	293.1132		275.1026	207.1128		E	2003.9669	2002.9716		2078.0037	2060.9771	20
3	88.0393	380.1452		362.1347	408.1401		390.1296	336.1554		D	1888.9399	1887.9447		1948.9611	1931.9345	19
4	87.0553	494.1882	477.1616	476.1776	522.1831	505.1565	504.1725	451.1823		N	1774.8970	1773.9018		***1833.9341***	1816.9076	18
5	120.0808	641.2566	624.2300	623.2460	669.2515	652.2249	651.2409			F	1627.8286			1719.8912	1702.8646	17
6	88.0393	756.2835	739.2570	738.2729	784.2784	767.2519	766.2679	712.2937		D	1512.8016	1511.8064		1572.8228	1555.7962	15
7	44.0495	827.3206	810.2941	809.3101	855.3155	838.2890	837.3050			A	1441.7645			1457.7958	1440.7693	14
8	87.0553	941.3636	924.3370	923.3530	969.3585	952.3319	951.3479	898.3577		N	1327.7216	1326.7264		***1386.7587***	1369.7322	13
9	60.0444	1028.3956	1011.3690	1010.3850	1056.3905	1039.3639	1038.3799	1012.4007		S	1240.6896	1239.6943		***1272.7158***	1255.6892	12
10	87.0553	1142.4385	1125.4120	1124.4279	1170.4334	1153.4069	1152.4229	1099.4327		N	1126.6467	1125.6514		***1185.6838***	1168.6572	11
11	72.0808	1241.5069	1224.4804	1223.4964	1269.5018	1252.4753	1251.4913	1227.4913		V	1027.5782	1040.5986		***1071.6408***	1054.6143	10
12	60.0444	1328.5389	1311.5124	1310.5284	1356.5339	1339.5073	1338.5233	1312.5440		S	940.5462	939.5510		***972.5724***	955.5459	9
13	72.0808	1427.6074	1410.5808	1409.5968	1455.6023	1438.5757	1437.5917	1413.5917		V	841.4778	854.4982		***885.5404***	868.5138	8
14	86.0964	1540.6914	1523.6649	1522.6809	1568.6863	1551.6598	1550.6758	1512.6601	1526.6758	I	728.3937	741.4141	755.4298	***786.4720***	769.4454	7
15	86.0964	1653.7755	1636.7489	1635.7649	1681.7704	1664.7439	1663.7598	1625.7442	1639.7598	I	615.3097	628.3301	642.3457	***673.3879***	656.3614	6
16	87.0553	1767.8184	1750.7919	1749.8079	1795.8133	1778.7868	1777.8028	1724.8126		N	501.2667	500.2715		***560.3039***	543.2773	5
17	70.0651	1864.8712	1847.8446	1846.8606	1892.8661	1875.8395	1874.8555	1838.8555		P	404.2140	403.2187		***446.2609***	429.2344	4
18	74.0600	1965.9189	1948.8923	1947.9083	1993.9138	1976.8872	1975.9032	1949.9239	1951.9032	T	303.1663	316.1867	318.1660	349.2082	332.1816	3
19	74.0600	2066.9665	2049.9400	2048.9560	2094.9615	2077.9349	2076.9509	2050.9716	2052.9509	T	202.1186	215.1390	217.1183	248.1605	231.1339	2
20	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ED	217.0819	245.0768	EDN	331.1248	359.1197	EDNF	478.1932	506.1882

EDNFD	593.2202	621.2151	**EDNFDA**	664.2573	692.2522	**DN**	202.0822	230.0771
DNF	349.1506	377.1456	**DNFD**	464.1776	492.1725	**DNFDA**	535.2147	563.2096
DNFDAN	649.2576	677.2525	**NF**	234.1237	262.1186	**NFD**	349.1506	377.1456
NFDA	420.1878	448.1827	**NFDAN**	534.2307	562.2256	**NFDANS**	621.2627	649.2576
FD	235.1077	263.1026	**FDA**	306.1448	334.1397	**FDAN**	420.1878	448.1827
FDANS	507.2198	535.2147	**FDANSN**	621.2627	649.2576	**DA**	159.0764	187.0713
DAN	273.1193	301.1143	**DANS**	360.1514	388.1463	**DANSN**	474.1943	502.1892
DANSNV	573.2627	601.2576	**DANSNVS**	660.2947	688.2897	**AN**	158.0924	186.0873
ANS	245.1244	273.1193	**ANSN**	359.1674	387.1623	**ANSNV**	458.2358	486.2307
ANSNVS	545.2678	573.2627	**ANSNVSV**	644.3362	672.3311	**NS**	174.0873	202.0822
NSN	288.1302	316.1252	**NSNV**	387.1987	415.1936	**NSNVS**	474.2307	502.2256
NSNVSV	573.2991	601.2940	**NSNVSVI**	686.3832	714.3781	**SN**	174.0873	202.0822
SNV	273.1557	301.1506	**SNVS**	360.1878	388.1827	**SNVSV**	459.2562	487.2511
SNVSVI	572.3402	600.3352	**SNVSVII**	685.4243	713.4192	**NV**	186.1237	214.1186
NVS	273.1557	301.1506	**NVSV**	372.2241	400.2191	**NVSVI**	485.3082	513.3031
NVSVII	598.3923	626.3872	**VS**	159.1128	187.1077	**VSV**	258.1812	286.1761
VSVI	371.2653	399.2602	**VSVII**	484.3493	512.3443	**VSVIIN**	598.3923	626.3872
VSVIINP	695.4450	723.4400	**SV**	159.1128	187.1077	**SVI**	272.1969	300.1918
SVII	385.2809	413.2758	**SVIIN**	499.3239	527.3188	**SVIINP**	596.3766	624.3715
SVIINPT	697.4243	725.4192	**VI**	185.1648	213.1598	**VII**	298.2489	326.2438
VIIN	412.2918	440.2867	**VIINP**	509.3446	537.3395	**VIINPT**	610.3923	638.3872
II	199.1805	227.1754	**IIN**	313.2234	341.2183	**IINP**	410.2762	438.2711
IINPT	511.3239	539.3188	**IINPTT**	612.3715	640.3665	**IN**	200.1394	228.1343
INP	297.1921	325.1870	**INPT**	398.2398	426.2347	**INPTT**	499.2875	527.2824
NP	184.1081	212.1030	**NPT**	285.1557	313.1506	**NPTT**	386.2034	414.1983
PT	171.1128	199.1077	**PTT**	272.1605	300.1554	**TT**	175.1077	203.1026





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.5	2240.0597	0.2367	YEDNFDANSNVSVIINPTTK
62.2	2240.0597	0.2367	YEDNFDANSNVSVIIQPTSK
17.0	2241.0801	-0.7837	YEDNFDATSNLSVIINPTTK
10.7	2241.0437	-0.7473	AEDDELIVEGSISDAYFNVR
8.7	2240.0359	0.2605	NNTSGSLPNSWGGNSKNGFFR
8.6	2241.2077	-0.9113	LTLNIDGSVKASTNNAGIGGALR
5.3	2240.1107	0.1857	GMQVIDTGAPLSEPVGENTLGR
3.3	2240.1722	0.1242	DLLDILMDAAADPAAEVKLTR
3.0	2239.1531	1.1433	AQAAEAMLVDATRHLPATAFR
2.9	2241.2369	-0.9405	FAVEIIQAVVDEIGADKVGIR

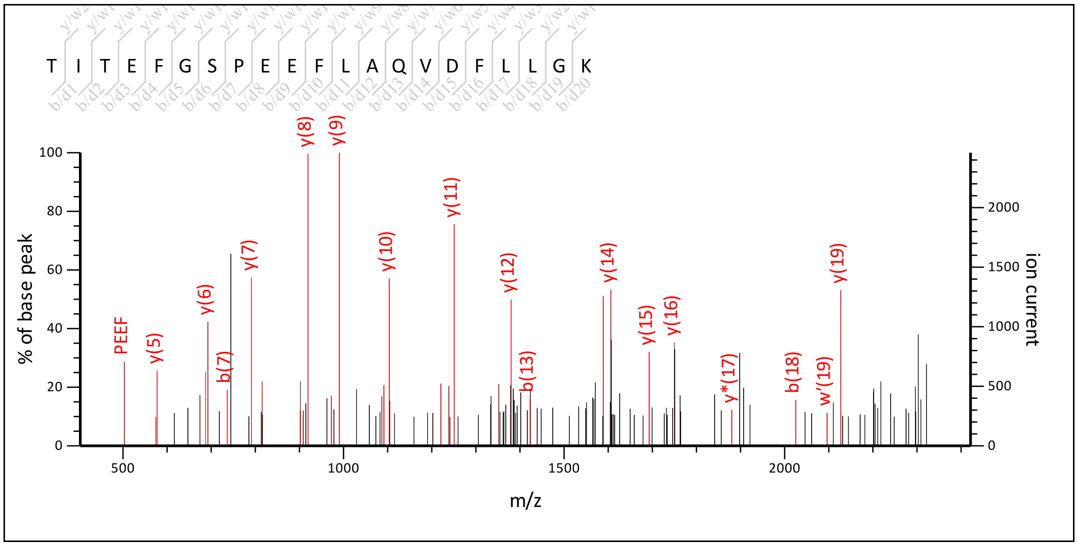
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **TITEFGSPEEFLAQVDFLLGK**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 30: 2340.437524 from(2341.444800,1+) intensity(0.0000) index(11)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221706, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



403.2 to 2421.37

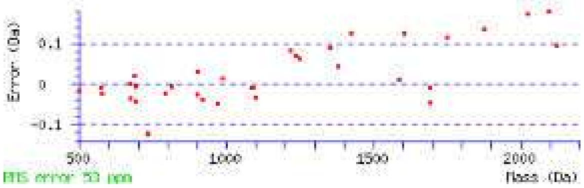
Label all possible matches ○ Label matches used for scoring ●

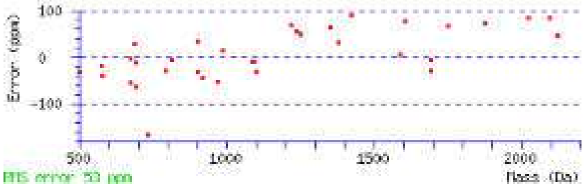
```
Monoisotopic mass of neutral peptide Mr(calc): 2340.1889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67  Expect: 0.00048
Matches : 36/377 fragment ions using 55 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	86.0964	187.1441		169.1335	215.1390		197.1285	159.1128	173.1285	I	2182.0703	2195.0907	2209.1063	2240.1485	2223.1220	22
3	74.0600	288.1918		270.1812	316.1867		298.1761	272.1969	274.1761	T	2081.0226	2094.0430	2096.0223	***2127.0645***	2110.0379	21
4	102.0550	417.2344		399.2238	445.2293		427.2187	359.2289		E	1951.9800	1950.9848		2026.0168	2008.9902	20
5	120.0808	564.3028		546.2922	592.2977		574.2871			F	1804.9116			1896.9742	1879.9476	18
6	30.0338	621.3243		603.3137	649.3192		631.3086			G				***1749.9058***	1732.8792	17
7	60.0444	708.3563		690.3457	**736.3512**		718.3406	692.3614		S	1660.8581	1659.8629		***1692.8843***	1675.8578	16
8	70.0651	805.4090		787.3985	833.4040		815.3934	779.3934		P	1563.8053	1562.8101		***1605.8523***	1588.8257	15
9	102.0550	934.4516		916.4411	962.4466		944.4360	876.4462		E	1434.7627	1433.7675		1508.7995	1491.7730	14
10	102.0550	1063.4942		1045.4837	**1091.4891**		1073.4786	1005.4888		E	1305.7202	1304.7249		***1379.7569***	1362.7304	13
11	120.0808	1210.5626		1192.5521	**1238.5576**		1220.5470			F	1158.6517			***1250.7143***	1233.6878	12
12	86.0964	1323.6467		1305.6361	**1351.6416**		1333.6311	1281.5998		L	1045.5677	1044.5724		***1103.6459***	1086.6194	10
13	44.0495	1394.6838		1376.6733	**1422.6787**		1404.6682			A	974.5306			***990.5619***	973.5353	9
14	101.0709	1522.7424	1505.7159	1504.7318	1550.7373	1533.7108	1532.7268	1465.7209		Q	846.4720	845.4767		***919.5247***	902.4982	9
15	72.0808	1621.8108	1604.7843	1603.8003	1649.8057	1632.7792	1631.7952	1607.7952		V	747.4036	760.4240		***791.4662***	774.4396	7
16	88.0393	1736.8378	1719.8112	1718.8272	1764.8327	1747.8061	1746.8221	1692.8479		D	632.3766	631.3814		***692.3978***	675.3712	6
17	120.0808	1883.9062	1866.8796	1865.8956	1911.9011	1894.8745	1893.8905			F	485.3082			***577.3708***	560.3443	
18	86.0964	1996.9902	1979.9637	1978.9797	**2024.9852**	2007.9586	2006.9746	1954.9433		L	372.2241	371.2289		430.3024	413.2758	
19	86.0964	2110.0743	2093.0478	2092.0637	2138.0692	2121.0427	2120.0587	2068.0274		L	259.1401	258.1448		317.2183	300.1918	
20	30.0338	2167.0958	2150.0692	2149.0852	2195.0907	2178.0641	2177.0801			G				204.1343	187.1077	
21	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

IT	187.1441	215.1390	**ITE**	316.1867	344.1816	**ITEF**	463.2551	491.2500
ITEFG	520.2766	548.2715	**ITEFGS**	607.3086	635.3035	**TE**	203.1026	231.0975
TEF	350.1710	378.1660	**TEFG**	407.1925	435.1874	**TEFGS**	494.2245	522.2195
TEFGSP	591.2773	619.2722	**EF**	249.1234	277.1183	**EFG**	306.1448	334.1397
EFGS	393.1769	421.1718	**EFGSP**	490.2296	518.2245	**EFGSPE**	619.2722	647.2671
FG	177.1022	205.0972	**FGS**	264.1343	292.1292	**FGSP**	361.1870	389.1819
FGSPE	490.2296	518.2245	**FGSPEE**	619.2722	647.2671	**GS**	117.0659	145.0608
GSP	214.1186	242.1135	**GSPE**	343.1612	371.1561	**GSPEE**	472.2038	500.1987
GSPEEF	619.2722	647.2671	**SP**	157.0972	185.0921	**SPE**	286.1397	314.1347
SPEE	415.1823	443.1773	**SPEEF**	562.2508	590.2457	**SPEEFL**	675.3348	703.3297
PE	199.1077	227.1026	**PEE**	328.1503	356.1452	**PEEF**	475.2187	503.2136
PEEFL	588.3028	616.2977	**PEEFLA**	659.3399	687.3348	**EE**	231.0975	259.0925
EEF	378.1660	406.1609	**EEFL**	491.2500	519.2449	**EEFLA**	562.2871	590.2821
EEFLAQ	690.3457	718.3406	**EF**	249.1234	277.1183	**EFL**	362.2074	390.2023
EFLA	433.2445	461.2395	**EFLAQ**	561.3031	589.2980	**EFLAQV**	660.3715	688.3665
FL	233.1648	261.1598	**FLA**	304.2020	332.1969	**FLAQ**	432.2605	460.2554
FLAQV	531.3289	559.3239	**FLAQVD**	646.3559	674.3508	**LA**	157.1335	185.1285
LAQ	285.1921	313.1870	**LAQV**	384.2605	412.2554	**LAQVD**	499.2875	527.2824
LAQVDF	646.3559	674.3508	**AQ**	172.1081	200.1030	**AQV**	271.1765	299.1714
AQVD	386.2034	414.1983	**AQVDF**	533.2718	561.2667	**AQVDFL**	646.3559	674.3508
QV	200.1394	228.1343	**QVD**	315.1663	343.1612	**QVDF**	462.2347	490.2296
QVDFL	575.3188	603.3137	**QVDFLL**	688.4028	716.3978	**VD**	187.1077	215.1026
VDF	334.1761	362.1710	**VDFL**	447.2602	475.2551	**VDFLL**	560.3443	588.3392
VDFLLG	617.3657	645.3606	**DF**	235.1077	263.1026	**DFL**	348.1918	376.1867
DFLL	461.2758	489.2708	**DFLLG**	518.2973	546.2922	**FL**	233.1648	261.1598
FLL	346.2489	374.2438	**FLLG**	403.2704	431.2653	**LL**	199.1805	227.1754
LLG	256.2020	284.1969	**LG**	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
66.8	2340.1889	0.2486	TITEFGSPEEFLAQVDFLLGK
10.1	2341.1413	-0.7037	SEFVEAQEALVQMKDWFLR
8.4	2340.1541	0.2834	LCAVLGGTFAVTGMLDRWMSR
7.8	2340.0991	0.3384	LDGQWSTMALMGGFARIDNNK
6.4	2341.1882	-0.7507	MATSTMPLGGASPSGRVLGPALDR
5.9	2340.1566	0.2809	TVFSTVIKNMGTTLGACGDVNR
5.5	2340.2325	0.2050	LTFPSSSGGLAITRLPFSSTSSK
4.8	2339.9780	0.4595	AVGCNDAACALGSETQCLSDNK
2.9	2341.1606	-0.7231	GHPPNRPVYTMLITMCGRGGK
2.4	2339.2705	1.1670	MLTSRVLNSTTMAIVILYAAR

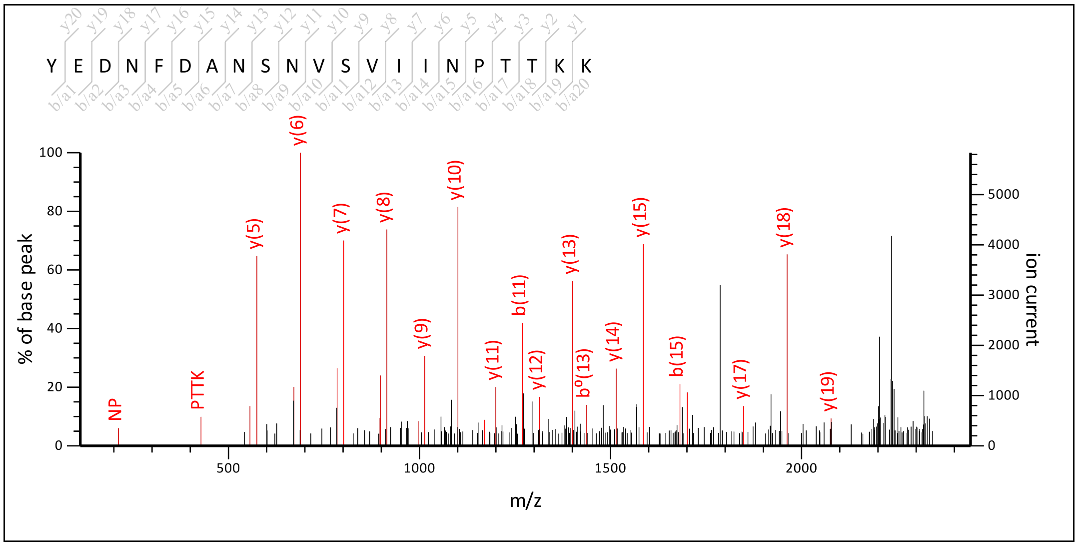
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **YEDNFDANSNVSVIINPTTKK**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 32: 2368.419724 from(2369.427000,1+) intensity(0.0000) index(12)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221707, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



112.11 to 2442.32

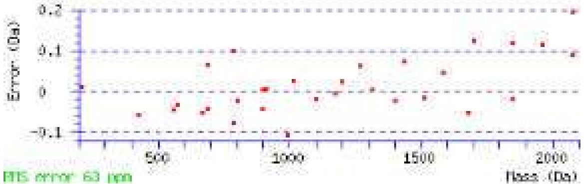
Label all possible matches ○ Label matches used for scoring ●

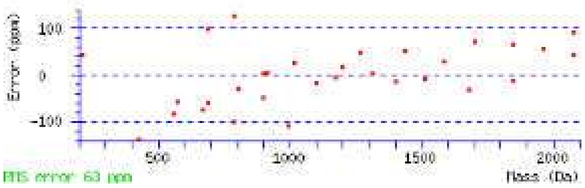
Monoisotopic mass of neutral peptide Mr(calc): 2368.1546
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 116 **Expect:** 6.1e-09
Matches : 31/423 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	136.0757	136.0757			164.0706			44.0495		Y					
2	102.0550	265.1183		247.1077	293.1132		275.1026	207.1128		E	2132.0618	2131.0666		2206.0986	2189.0721
3	88.0393	380.1452		362.1347	408.1401		390.1296	336.1554		D	2017.0349	2016.0396		***2077.0560***	2060.0295
4	87.0553	494.1882	477.1616	476.1776	522.1831	505.1565	504.1725	451.1823		N	1902.9920	1901.9967		***1962.0291***	1945.0025
5	120.0808	641.2566	624.2300	623.2460	669.2515	652.2249	651.2409			F	1755.9236			***1847.9862***	1830.9596
6	88.0393	756.2835	739.2570	738.2729	**784.2784**	767.2519	766.2679	712.2937		D	1640.8966	1639.9014		***1700.9177***	1683.8912
7	44.0495	827.3206	810.2941	809.3101	855.3155	838.2890	837.3050			A	1569.8595			***1585.8908***	1568.8642
8	87.0553	941.3636	924.3370	923.3530	969.3585	952.3319	951.3479	898.3577		N	1455.8166	1454.8213		***1514.8537***	1497.8271
9	60.0444	1028.3956	1011.3690	1010.3850	1056.3905	1039.3639	1038.3799	1012.4007		S	1368.7845	1367.7893		***1400.8108***	1383.7842
10	87.0553	1142.4385	1125.4120	1124.4279	**1170.4334**	1153.4069	1152.4229	1099.4327		N	1254.7416	1253.7464		***1313.7787***	1296.7522
11	72.0808	1241.5069	1224.4804	1223.4964	**1269.5018**	1252.4753	1251.4913	1227.4913		V	1155.6732	1168.6936		***1199.7358***	1182.7093
12	60.0444	1328.5389	1311.5124	1310.5284	1356.5339	1339.5073	1338.5233	1312.5440		S	1068.6412	1067.6459		***1100.6674***	1083.6408
13	72.0808	1427.6074	1410.5808	1409.5968	1455.6023	1438.5757	1437.5917	1413.5917		V	969.5728	982.5932		***1013.6354***	996.6088
14	86.0964	1540.6914	1523.6649	1522.6809	1568.6863	1551.6598	1550.6758	1512.6601	1526.6758	I	856.4887	869.5091	883.5247	***914.5669***	897.5404
15	86.0964	1653.7755	1636.7489	1635.7649	**1681.7704**	1664.7439	1663.7598	1625.7442	1639.7598	I	743.4046	756.4250	770.4407	***801.4829***	784.4563
16	87.0553	1767.8184	1750.7919	1749.8079	1795.8133	1778.7868	1777.8028	1724.8126		N	629.3617	628.3665		***688.3988***	671.3723
17	70.0651	1864.8712	1847.8446	1846.8606	1892.8661	1875.8395	1874.8555	1838.8555		P	532.3089	531.3137		***574.3559***	557.3293
18	74.0600	1965.9189	1948.8923	1947.9083	1993.9138	1976.8872	1975.9032	1949.9239	1951.9032	T	431.2613	444.2817	446.2609	477.3031	460.2766
19	74.0600	2066.9665	2049.9400	2048.9560	2094.9615	2077.9349	2076.9509	2050.9716	2052.9509	T	330.2136	343.2340	345.2132	376.2554	359.2289
20	101.1073	2195.0615	2178.0350	2177.0509	2223.0564	2206.0299	2205.0459	2138.0037		K	202.1186	201.1234		275.2078	258.1812
21	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

ED	217.0819	245.0768	**EDN**	331.1248	359.1197	**EDNF**	478.1932	506.1882
EDNFD	593.2202	621.2151	**EDNFDA**	664.2573	692.2522	**DN**	202.0822	230.0771
DNF	349.1506	377.1456	**DNFD**	464.1776	492.1725	**DNFDA**	535.2147	563.2096
DNFDAN	649.2576	677.2525	**NF**	234.1237	262.1186	**NFD**	349.1506	377.1456
NFDA	420.1878	448.1827	**NFDAN**	534.2307	562.2256	**NFDANS**	621.2627	649.2576
FD	235.1077	263.1026	**FDA**	306.1448	334.1397	**FDAN**	420.1878	448.1827
FDANS	507.2198	535.2147	**FDANSN**	621.2627	649.2576	**DA**	159.0764	187.0713
DAN	273.1193	301.1143	**DANS**	360.1514	388.1463	**DANSN**	474.1943	502.1892
DANSNV	573.2627	601.2576	**DANSNVS**	660.2947	688.2897	**AN**	158.0924	186.0873
ANS	245.1244	273.1193	**ANSN**	359.1674	387.1623	**ANSNV**	458.2358	486.2307
ANSNVS	545.2678	573.2627	**ANSNVSV**	644.3362	672.3311	**NS**	174.0873	202.0822
NSN	288.1302	316.1252	**NSNV**	387.1987	415.1936	**NSNVS**	474.2307	502.2256
NSNVSV	573.2991	601.2940	**NSNVSVI**	686.3832	714.3781	**SN**	174.0873	202.0822
SNV	273.1557	301.1506	**SNVS**	360.1878	388.1827	**SNVSV**	459.2562	487.2511
SNVSVI	572.3402	600.3352	**SNVSVII**	685.4243	713.4192	**NV**	186.1237	214.1186
NVS	273.1557	301.1506	**NVSV**	372.2241	400.2191	**NVSVI**	485.3082	513.3031
NVSVII	598.3923	626.3872	**VS**	159.1128	187.1077	**VSV**	258.1812	286.1761
VSVI	371.2653	399.2602	**VSVII**	484.3493	512.3443	**VSVIIN**	598.3923	626.3872
VSVIINP	695.4450	723.4400	**SV**	159.1128	187.1077	**SVI**	272.1969	300.1918
SVII	385.2809	413.2758	**SVIIN**	499.3239	527.3188	**SVIINP**	596.3766	624.3715
SVIINPT	697.4243	725.4192	**VI**	185.1648	213.1598	**VII**	298.2489	326.2438
VIIN	412.2918	440.2867	**VIINP**	509.3446	537.3395	**VIINPT**	610.3923	638.3872
II	199.1805	227.1754	**IIN**	313.2234	341.2183	**IINP**	410.2762	438.2711
IINPT	511.3239	539.3188	**IINPTT**	612.3715	640.3665	**IN**	200.1394	228.1343
INP	297.1921	325.1870	**INPT**	398.2398	426.2347	**INPTT**	499.2875	527.2824
INPTTK	627.3824	655.3774	**NP**	184.1081	212.1030	**NPT**	285.1557	313.1506
NPTT	386.2034	414.1983	**NPTTK**	514.2984	542.2933	**PT**	171.1128	199.1077
PTT	272.1605	300.1554	**PTTK**	400.2554	428.2504	**TT**	175.1077	203.1026
TTK	303.2027	331.1976	**TK**	202.1550	230.1499			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
115.8	2368.1546	0.2651	YEDNFDANSNVSVIINPTTKK
93.7	2368.1546	0.2651	YEDNFDANSNVSVIIQPTSKK
14.3	2369.1750	-0.7553	YEDNFDATSNLSVIINPTTKK
7.5	2369.2168	-0.7971	GYHRTIEGVGFGFISILNDFK
6.9	2368.1771	0.2426	TTNPWANEDAVVNVSLETPRR
6.8	2368.2461	0.1736	LTDRSDVFSFGVMLLELITGR
6.8	2368.2461	0.1736	LTDRSDVFSFGVMLLELLTGR
6.0	2369.1362	-0.7165	FITHTVPFSEINKAFDNMDK
6.0	2369.1548	-0.7351	FITHTVPFSEINKAFDNMMK
6.0	2369.2955	-0.8757	TPVLRFLTLEGNDLIDLDGLR

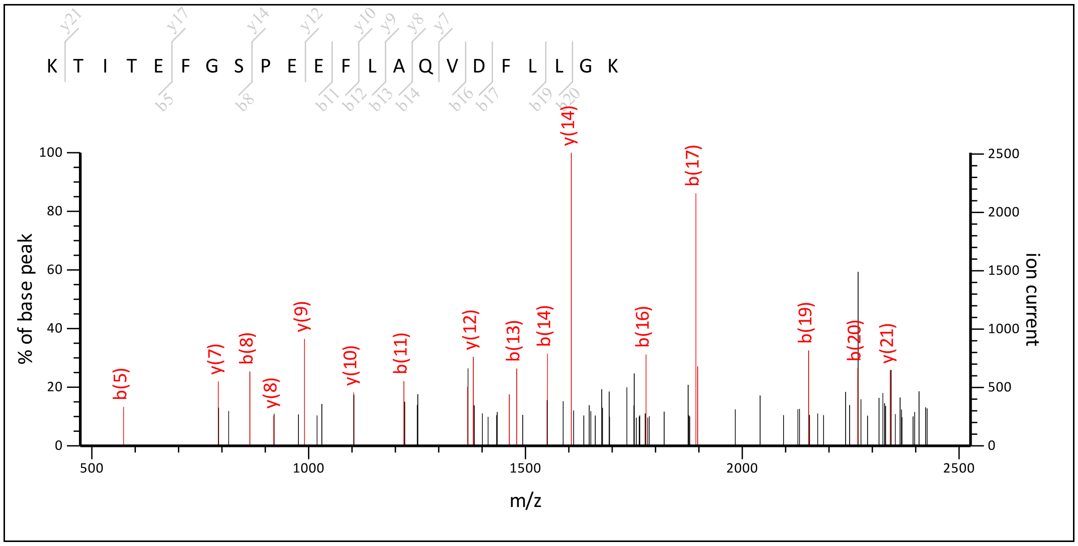
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 24**

MS/MS Fragmentation of **KTITEFGSPEEFLAQVDFLLGK**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 34: 2468.557924 from(2469.565200,1+) intensity(0.0000) index(13)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221708, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



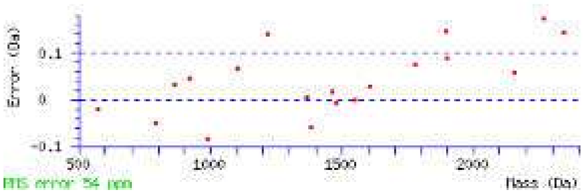
473.3 to 2526.45

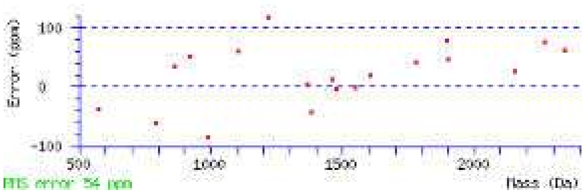
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): `2468.2839`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `60` **Expect:** `0.0022`
Matches : `19/426 fragment ions using 35 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.1073	101.1073	84.0808		129.1022	112.0757		44.0495		**K**					
2	74.0600	202.1550	185.1285	184.1444	230.1499	213.1234	212.1394	186.1601	188.1394	**T**	2295.1543	2308.1747	2310.1540	***2341.1962***	2324.1697
3	86.0964	315.2391	298.2125	297.2285	343.2340	326.2074	325.2234	287.2078	301.2234	**I**	2182.0703	2195.0907	2209.1063	2240.1485	2223.1220
4	74.0600	416.2867	399.2602	398.2762	444.2817	427.2551	426.2711	400.2918	402.2711	**T**	2081.0226	2094.0430	2096.0223	2127.0645	2110.0379
5	102.0550	545.3293	528.3028	527.3188	***573.3243***	556.2977	555.3137	487.3239		**E**	1951.9800	1950.9848		2026.0168	2008.9902
6	120.0808	692.3978	675.3712	674.3872	720.3927	703.3661	702.3821			**F**	1804.9116			***1896.9742***	1879.9476
7	30.0338	749.4192	732.3927	731.4087	777.4141	760.3876	759.4036			**G**				1749.9058	1732.8792
8	60.0444	836.4512	819.4247	818.4407	***864.4462***	847.4196	846.4356	820.4563		**S**	1660.8581	1659.8629		1692.8843	1675.8578
9	70.0651	933.5040	916.4775	915.4934	961.4989	944.4724	943.4884	907.4884		**P**	1563.8053	1562.8101		***1605.8523***	1588.8257
10	102.0550	1062.5466	1045.5201	1044.5360	1090.5415	1073.5150	1072.5310	1004.5411		**E**	1434.7627	1433.7675		1508.7995	1491.7730
11	102.0550	1191.5892	1174.5626	1173.5786	***1219.5841***	1202.5576	1201.5735	1133.5837		**E**	1305.7202	1304.7249		***1379.7569***	1362.7304
12	120.0808	1338.6576	1321.6311	1320.6470	***1366.6525***	1349.6260	1348.6420			**F**	1158.6517			1250.7143	1233.6878
13	86.0964	1451.7417	1434.7151	1433.7311	***1479.7366***	1462.7100	1461.7260	1409.6947		**L**	1045.5677	1044.5724		***1103.6459***	1086.6194
14	44.0495	1522.7788	1505.7522	1504.7682	***1550.7737***	1533.7472	1532.7631			**A**	974.5306			***990.5619***	973.5353
15	101.0709	1650.8374	1633.8108	1632.8268	1678.8323	1661.8057	1660.8217	1593.8159		**Q**	846.4720	845.4767		***919.5247***	902.4982
16	72.0808	1749.9058	1732.8792	1731.8952	***1777.9007***	1760.8741	1759.8901	1735.8901		**V**	747.4036	760.4240		***791.4662***	774.4396
17	88.0393	1864.9327	1847.9062	1846.9222	***1892.9276***	1875.9011	1874.9171	1820.9429		**D**	632.3766	631.3814		692.3978	675.3712
18	120.0808	2012.0011	1994.9746	1993.9906	2039.9961	2022.9695	2021.9855			**F**	485.3082			577.3708	560.3443
19	86.0964	2125.0852	2108.0587	2107.0746	***2153.0801***	2136.0536	2135.0695	2083.0383		**L**	372.2241	371.2289		430.3024	413.2758
20	86.0964	2238.1693	2221.1427	2220.1587	***2266.1642***	2249.1376	2248.1536	2196.1223		**L**	259.1401	258.1448		317.2183	300.1918
21	30.0338	2295.1907	2278.1642	2277.1802	2323.1856	2306.1591	2305.1751			**G**				204.1343	187.1077
22	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TI	187.1441	215.1390	TIT	288.1918	316.1867	TITE	417.2344	445.2293
TITEF	564.3028	592.2977	TITEFG	621.3243	649.3192	IT	187.1441	215.1390
ITE	316.1867	344.1816	ITEF	463.2551	491.2500	ITEFG	520.2766	548.2715
ITEFGS	607.3086	635.3035	TE	203.1026	231.0975	TEF	350.1710	378.1660
TEFG	407.1925	435.1874	TEFGS	494.2245	522.2195	TEFGSP	591.2773	619.2722
EF	249.1234	277.1183	EFG	306.1448	334.1397	EFGS	393.1769	421.1718
EFGSP	490.2296	518.2245	EFGSPE	619.2722	647.2671	FG	177.1022	205.0972
FGS	264.1343	292.1292	FGSP	361.1870	389.1819	FGSPE	490.2296	518.2245
FGSPEE	619.2722	647.2671	GS	117.0659	145.0608	GSP	214.1186	242.1135
GSPE	343.1612	371.1561	GSPEE	472.2038	500.1987	GSPEEF	619.2722	647.2671
SP	157.0972	185.0921	SPE	286.1397	314.1347	SPEE	415.1823	443.1773
SPEEF	562.2508	590.2457	SPEEFL	675.3348	703.3297	PE	199.1077	227.1026
PEE	328.1503	356.1452	PEEF	475.2187	503.2136	PEEFL	588.3028	616.2977
PEEFLA	659.3399	687.3348	EE	231.0975	259.0925	EEF	378.1660	406.1609
EEFL	491.2500	519.2449	EEFLA	562.2871	590.2821	EEFLAQ	690.3457	718.3406
EF	249.1234	277.1183	EFL	362.2074	390.2023	EFLA	433.2445	461.2395
EFLAQ	561.3031	589.2980	EFLAQV	660.3715	688.3665	FL	233.1648	261.1598
FLA	304.2020	332.1969	FLAQ	432.2605	460.2554	FLAQV	531.3289	559.3239
FLAQVD	646.3559	674.3508	LA	157.1335	185.1285	LAQ	285.1921	313.1870
LAQV	384.2605	412.2554	LAQVD	499.2875	527.2824	LAQVDF	646.3559	674.3508
AQ	172.1081	200.1030	AQV	271.1765	299.1714	AQVD	386.2034	414.1983
AQVDF	533.2718	561.2667	AQVDFL	646.3559	674.3508	QV	200.1394	228.1343
QVD	315.1663	343.1612	QVDF	462.2347	490.2296	QVDFL	575.3188	603.3137
QVDFLL	688.4028	716.3978	VD	187.1077	215.1026	VDF	334.1761	362.1710
VDFL	447.2602	475.2551	VDFLL	560.3443	588.3392	VDFLLG	617.3657	645.3606
DF	235.1077	263.1026	DFL	348.1918	376.1867	DFLL	461.2758	489.2708
DFLLG	518.2973	546.2922	FL	233.1648	261.1598	FLL	346.2489	374.2438
FLLG	403.2704	431.2653	LL	199.1805	227.1754	LLG	256.2020	284.1969
LG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.6	2468.2839	0.2740	KTITEFGSPEEFLAQVDFLLGK
10.4	2468.2369	0.3210	QLTSCESLALGDYPVEVRLYR
8.6	2468.2482	0.3097	NDEVLTFELMSQKGQGPHLLGR
7.1	2468.2071	0.3508	NQTDNSSIFPFDVVADAVSTLTK
6.7	2468.1749	0.3830	LADIFLDMALGCMQKQLDDSGK
6.7	2468.1386	0.4194	LADIFLDMALGCMQQQLDDSGK
4.2	2468.1399	0.4180	KIHDMNPGPEHYACMVDLLGR
4.1	2468.1449	0.4130	MATVDGTTAPSSGGKTATVASESGGGR
3.9	2468.1716	0.3864	AKVFMADLEDALSPTWENLMR
3.8	2469.1733	-0.6154	EAYELAVAEGADFIECDVVLTR

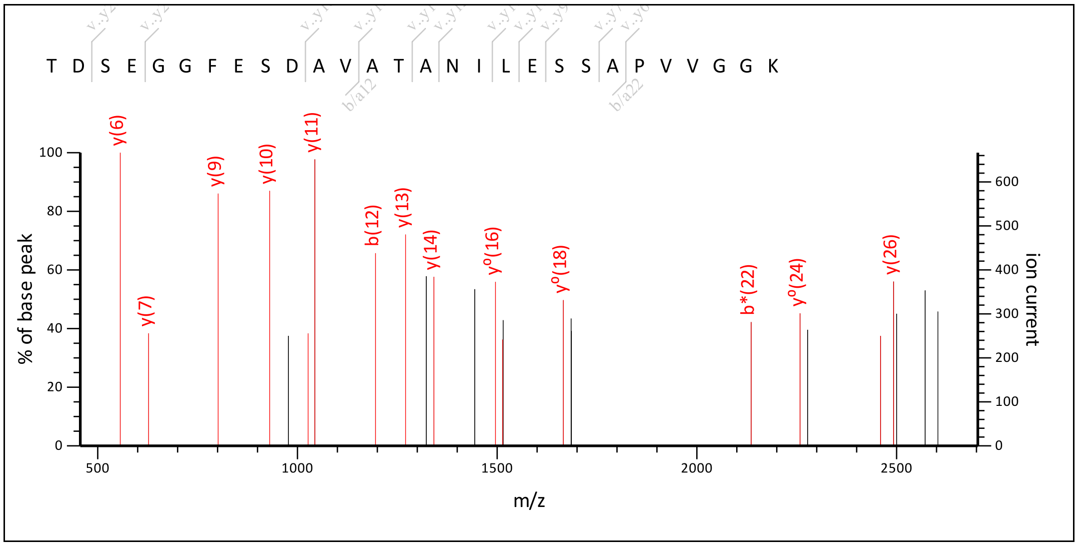
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **TDSEGGFESDAVATANILESSAPVVGGK**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 38: 2707.608424 from(2708.615700,1+) intensity(0.0000) index(15)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221717, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



456.3 to 2703.34

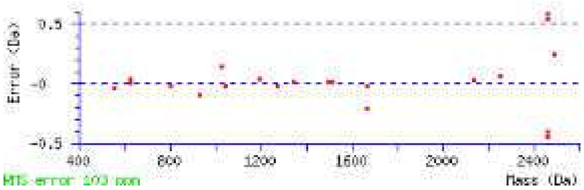
Label all possible matches ○ Label matches used for scoring ●

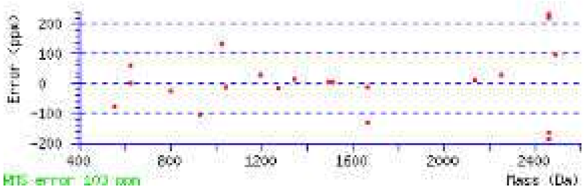
Monoisotopic mass of neutral peptide Mr(calc): 2707.2825
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.017
Matches : 22/561 fragment ions using 26 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	88.0393	189.0870		171.0764	217.0819		199.0713	145.0972		D	2547.2209	2546.2257		2607.2420	2590.2155
3	60.0444	276.1190		258.1084	304.1139		286.1034	260.1241		S	2460.1889	2459.1936		***2492.2151***	2475.1886
4	102.0550	405.1616		387.1510	433.1565		415.1460	347.1561		E	2331.1463	2330.1510		2405.1831	2388.1565
5	30.0338	462.1831		444.1725	490.1780		472.1674			G				2276.1405	2259.1139
6	30.0338	519.2045		501.1940	547.1994		529.1889			G				2219.1190	2202.0925
7	120.0808	666.2729		648.2624	694.2679		676.2573			F	2070.0350			2162.0976	2145.0710
8	102.0550	795.3155		777.3050	823.3105		805.2999	737.3101		E	1940.9924	1939.9971		2015.0291	1998.0026
9	60.0444	882.3476		864.3370	910.3425		892.3319	866.3527		S	1853.9603	1852.9651		1885.9865	1868.9600
10	88.0393	997.3745		979.3639	1025.3694		1007.3589	953.3847		D	1738.9334	1737.9381		1798.9545	1781.9280
11	44.0495	1068.4116		1050.4011	1096.4065		1078.3960			A	1667.8963			1683.9276	1666.9010
12	72.0808	1167.4800		1149.4695	**1195.4750**		1177.4644	1153.4644		V	1568.8279	1581.8483		1612.8905	1595.8639
13	44.0495	1238.5172		1220.5066	1266.5121		1248.5015			A	1497.7907			***1513.8220***	1496.7955
14	74.0600	1339.5648		1321.5543	1367.5597		1349.5492	1323.5699	1325.5492	T	1396.7431	1409.7635	1411.7427	1442.7849	1425.7584
15	44.0495	1410.6019		1392.5914	1438.5969		1420.5863			A	1325.7060			***1341.7373***	1324.7107
16	87.0553	1524.6449	1507.6183	1506.6343	1552.6398	1535.6132	1534.6292	1481.6391		N	1211.6630	1210.6678		***1270.7001***	1253.6736
17	86.0964	1637.7289	1620.7024	1619.7184	**1665.7239**	1648.6973	1647.7133	1609.6976	1623.7133	I	1098.5790	1111.5994	1125.6150	1156.6572	1139.6307
18	86.0964	1750.8130	1733.7865	1732.8024	1778.8079	1761.7814	1760.7973	1708.7660		L	985.4949	984.4997		***1043.5732***	1026.5466
19	102.0550	1879.8556	1862.8290	1861.8450	1907.8505	1890.8240	1889.8399	1821.8501		E	856.4523	855.4571		***930.4891***	913.4625
20	60.0444	1966.8876	1949.8611	1948.8771	1994.8825	1977.8560	1976.8720	1950.8927		S	769.4203	768.4250		***801.4465***	784.4199
21	60.0444	2053.9196	2036.8931	2035.9091	2081.9146	2064.8880	2063.9040	2037.9247		S	682.3883	681.3930		714.4145	697.3879
22	44.0495	2124.9568	2107.9302	2106.9462	2152.9517	2135.9251	2134.9411			A	611.3511			***627.3824***	610.3559
23	70.0651	2222.0095	2204.9830	2203.9990	2250.0044	2232.9779	2231.9939	2195.9939		P	514.2984	513.3031		***556.3453***	539.3188

24	72.0808	2321.0779	2304.0514	2303.0674	2349.0729	2332.0463	2331.0623	2307.0623		**V**	415.2300	428.2504		459.2926	442.2660
25	72.0808	2420.1464	2403.1198	2402.1358	2448.1413	2431.1147	2430.1307	2406.1307		**V**	316.1615	329.1819		360.2241	343.1976
26	30.0338	2477.1678	2460.1413	2459.1573	2505.1627	2488.1362	2487.1522			**G**				261.1557	244.1292
27	30.0338	2534.1893	2517.1627	2516.1787	2562.1842	2545.1576	2544.1736			**G**				204.1343	187.1077
28	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DS	175.0713	203.0662	**DSE**	304.1139	332.1088	**DSEG**	361.1354	389.1303
DSEGG	418.1569	446.1518	**DSEGGF**	565.2253	593.2202	**DSEGGFE**	694.2679	722.2628
SE	189.0870	217.0819	**SEG**	246.1084	274.1034	**SEGG**	303.1299	331.1248
SEGGF	450.1983	478.1932	**SEGGFE**	579.2409	607.2358	**SEGGFES**	666.2729	694.2679
EG	159.0764	187.0713	**EGG**	216.0979	244.0928	**EGGF**	363.1663	391.1612
EGGFE	492.2089	520.2038	**EGGFES**	579.2409	607.2358	**EGGFESD**	694.2679	722.2628
GG	87.0553	115.0502	**GGF**	234.1237	262.1186	**GGFE**	363.1663	391.1612
GGFES	450.1983	478.1932	**GGFESD**	565.2253	593.2202	**GGFESDA**	636.2624	664.2573
GF	177.1022	205.0972	**GFE**	306.1448	334.1397	**GFES**	393.1769	421.1718
GFESD	508.2038	536.1987	**GFESDA**	579.2409	607.2358	**GFESDAV**	678.3093	706.3042
FE	249.1234	277.1183	**FES**	336.1554	364.1503	**FESD**	451.1823	479.1773
FESDA	522.2195	550.2144	**FESDAV**	621.2879	649.2828	**FESDAVA**	692.3250	720.3199
ES	189.0870	217.0819	**ESD**	304.1139	332.1088	**ESDA**	375.1510	403.1460
ESDAV	474.2195	502.2144	**ESDAVA**	545.2566	573.2515	**ESDAVAT**	646.3042	674.2992
SD	175.0713	203.0662	**SDA**	246.1084	274.1034	**SDAV**	345.1769	373.1718
SDAVA	416.2140	444.2089	**SDAVAT**	517.2617	545.2566	**SDAVATA**	588.2988	616.2937
DA	159.0764	187.0713	**DAV**	258.1448	286.1397	**DAVA**	329.1819	357.1769
DAVAT	430.2296	458.2245	**DAVATA**	501.2667	529.2617	**DAVATAN**	615.3097	643.3046
AV	143.1179	171.1128	**AVA**	214.1550	242.1499	**AVAT**	315.2027	343.1976
AVATA	386.2398	414.2347	**AVATAN**	500.2827	528.2776	**AVATANI**	613.3668	641.3617
VA	143.1179	171.1128	**VAT**	244.1656	272.1605	**VATA**	315.2027	343.1976
VATAN	429.2456	457.2405	**VATANI**	542.3297	570.3246	**VATANIL**	655.4137	683.4087
AT	145.0972	173.0921	**ATA**	216.1343	244.1292	**ATAN**	330.1772	358.1721
ATANI	443.2613	471.2562	**ATANIL**	556.3453	584.3402	**ATANILE**	685.3879	713.3828
TA	145.0972	173.0921	**TAN**	259.1401	287.1350	**TANI**	372.2241	400.2191
TANIL	485.3082	513.3031	**TANILE**	614.3508	642.3457	**AN**	158.0924	186.0873
ANI	271.1765	299.1714	**ANIL**	384.2605	412.2554	**ANILE**	513.3031	541.2980
ANILES	600.3352	628.3301	**ANILESS**	687.3672	715.3621	**NI**	200.1394	228.1343
NIL	313.2234	341.2183	**NILE**	442.2660	470.2609	**NILES**	529.2980	557.2930
NILESS	616.3301	644.3250	**NILESSA**	687.3672	715.3621	**IL**	199.1805	227.1754
ILE	328.2231	356.2180	**ILES**	415.2551	443.2500	**ILESS**	502.2871	530.2821
ILESSA	573.3243	601.3192	**ILESSAP**	670.3770	698.3719	**LE**	215.1390	243.1339
LES	302.1710	330.1660	**LESS**	389.2031	417.1980	**LESSA**	460.2402	488.2351
LESSAP	557.2930	585.2879	**LESSAPV**	656.3614	684.3563	**ES**	189.0870	217.0819
ESS	276.1190	304.1139	**ESSA**	347.1561	375.1510	**ESSAP**	444.2089	472.2038
ESSAPV	543.2773	571.2722	**ESSAPVV**	642.3457	670.3406	**ESSAPVVG**	699.3672	727.3621
SS	147.0764	175.0713	**SSA**	218.1135	246.1084	**SSAP**	315.1663	343.1612
SSAPV	414.2347	442.2296	**SSAPVV**	513.3031	541.2980	**SSAPVVG**	570.3246	598.3195
SSAPVVGG	627.3461	655.3410	**SA**	131.0815	159.0764	**SAP**	228.1343	256.1292
SAPV	327.2027	355.1976	**SAPVV**	426.2711	454.2660	**SAPVVG**	483.2926	511.2875
SAPVVGG	540.3140	568.3089	**AP**	141.1022	169.0972	**APV**	240.1707	268.1656
APVV	339.2391	367.2340	**APVVG**	396.2605	424.2554	**APVVGG**	453.2820	481.2769
PV	169.1335	197.1285	**PVV**	268.2020	296.1969	**PVVG**	325.2234	353.2183
PVVGG	382.2449	410.2398	**VV**	171.1492	199.1441	**VVG**	228.1707	256.1656
VVGG	285.1921	313.1870	**VG**	129.1022	157.0972	**VGG**	186.1237	214.1186
GG	87.0553	115.0502						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.7	2707.2825	0.3260	TDSEGGFESDAVATANILESSAPVVGGK
8.6	2708.0980	-0.4896	WGSDGGTMGERWGNDGGTMTTFSGGR
8.0	2707.3925	0.2160	LMTEAELAAMFRDVAIVDEVTVIR
7.9	2707.3541	0.2544	VAVNEGRGIFAVGEGGGVYALAQCWK
5.2	2707.3970	0.2115	AVLGWEPTPFRVVAAALGEAGADADPK
5.1	2707.3925	0.2160	LMTEAELAAMFRDVAIVDEVTVIR
4.8	2708.4095	-0.8011	VIMTLTRVILEGEFQESFPIDGAK
4.6	2707.4466	0.1618	QAMLEPLVDTVEPNQIVTQTQLIK
4.6	2707.4116	0.1969	FNRRPSDGLNLLQVYGDGSMLVIK
4.2	2707.6186	-0.0102	WELRVMVLLSLSLQILLILLGNR

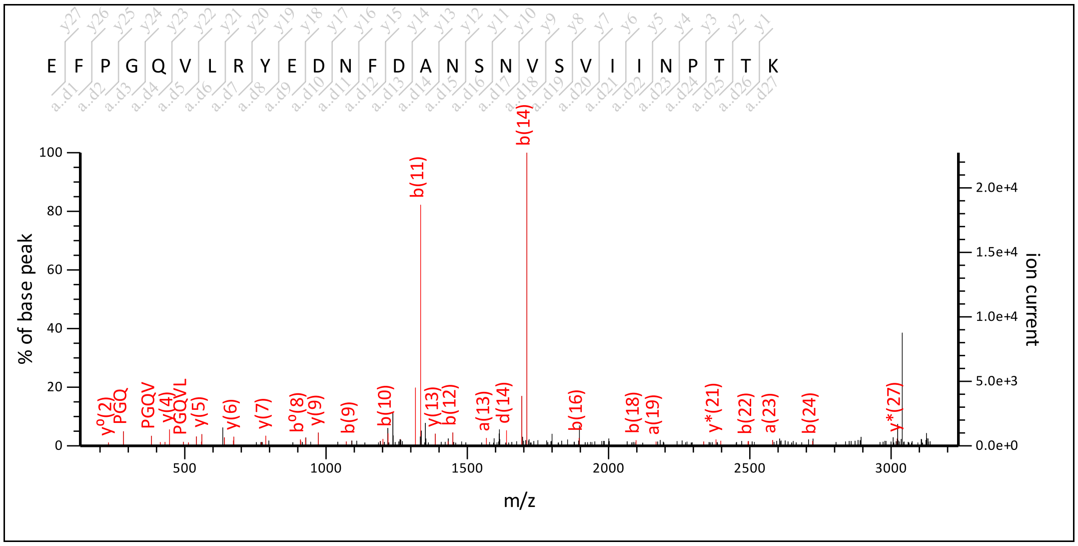
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **EFPGQVLRYEDNFDANSNVSVIINPTTK**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 46: 3166.926324 from(3167.933600,1+) intensity(0.0000) index(19)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221705, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



130.1 to 3238.17

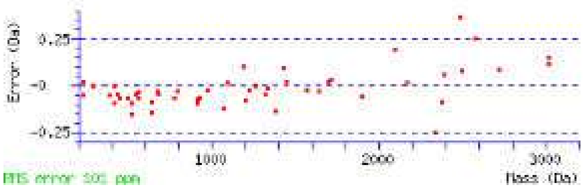
Label all possible matches ○ Label matches used for scoring ●

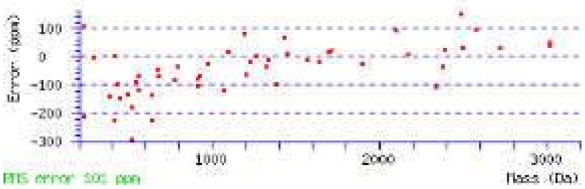
Monoisotopic mass of neutral peptide Mr(calc): 3166.5571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.039
Matches : 51/567 fragment ions using 109 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E						
2	120.0808	249.1234		231.1128	277.1183		259.1077			F	2946.4592			3038.5218	3021.4952	30
3	70.0651	346.1761		328.1656	374.1710		356.1605	320.1605		P	2849.4064	2848.4112		2891.4534	2874.4268	28
4	30.0338	403.1976		385.1870	431.1925		413.1819			G				2794.4006	2777.3741	27
5	101.0709	531.2562	514.2296	513.2456	***559.2511***	542.2245	541.2405	474.2347		Q	2664.3264	2663.3311		2737.3791	2720.3526	27
6	72.0808	630.3246	613.2980	612.3140	658.3195	641.2930	640.3089	616.3089		V	2565.2580	2578.2784		2609.3206	2592.2940	25
7	86.0964	743.4087	726.3821	725.3981	***771.4036***	754.3770	753.3930	701.3617		L	2452.1739	2451.1787		2510.2522	2493.2256	24
8	129.1135	899.5098	882.4832	881.4992	***927.5047***	910.4781	909.4941	814.4458		R	2296.0728	2295.0775		***2397.1681***	2380.1415	23
9	136.0757	1062.5731	1045.5465	1044.5625	***1090.5680***	1073.5415	1072.5574			Y	2133.0095			2241.0670	2224.0404	22
10	102.0550	**1191.6157**	1174.5891	1173.6051	***1219.6106***	1202.5841	1201.6000	1133.6102		E	2003.9669	2002.9716		2078.0037	2060.9771	20
11	88.0393	1306.6426	1289.6161	1288.6321	***1334.6375***	1317.6110	1316.6270	1262.6528		D	1888.9399	1887.9447		1948.9611	1931.9345	19
12	87.0553	1420.6856	1403.6590	1402.6750	***1448.6805***	1431.6539	1430.6699	1377.6797		N	1774.8970	1773.9018		1833.9341	1816.9076	18
13	120.0808	**1567.7540**	1550.7274	1549.7434	1595.7489	1578.7223	1577.7383			F	1627.8286			1719.8912	1702.8646	17
14	88.0393	1682.7809	1665.7544	1664.7703	***1710.7758***	1693.7493	1692.7653	1638.7911		D	1512.8016	1511.8064		1572.8228	1555.7962	15
15	44.0495	1753.8180	1736.7915	1735.8075	1781.8129	1764.7864	1763.8024			A	1441.7645			1457.7958	1440.7693	14
16	87.0553	1867.8610	1850.8344	1849.8504	***1895.8559***	1878.8293	1877.8453	1824.8551		N	1327.7216	1326.7264		***1386.7587***	1369.7322	13
17	60.0444	1954.8930	1937.8664	1936.8824	1982.8879	1965.8613	1964.8773	1938.8981		S	1240.6896	1239.6943		1272.7158	1255.6892	12
18	87.0553	2068.9359	2051.9094	2050.9253	***2096.9308***	2079.9043	2078.9203	2025.9301		N	1126.6467	1125.6514		1185.6838	1168.6572	11
19	72.0808	**2168.0043**	2150.9778	2149.9938	2195.9992	2178.9727	2177.9887	2153.9887		V	1027.5782	1040.5986		***1071.6408***	1054.6143	10
20	60.0444	2255.0363	2238.0098	2237.0258	2283.0313	2266.0047	2265.0207	2239.0414		S	940.5462	939.5510		***972.5724***	955.5459	9
21	72.0808	2354.1048	2337.0782	2336.0942	2382.0997	2365.0731	2364.0891	2340.0891		V	841.4778	854.4982		885.5404	868.5138	8
22	86.0964	2467.1888	2450.1623	2449.1783	***2495.1837***	2478.1572	2477.1732	2439.1575	2453.1732	I	728.3937	741.4141	755.4298	***786.4720***	769.4454	7
23	86.0964	**2580.2729**	2563.2463	2562.2623	2608.2678	2591.2413	2590.2572	2552.2416	2566.2572	I	615.3097	628.3301	642.3457	***673.3879***	656.3614	6

24	87.0553	2694.3158	2677.2893	2676.3053	***2722.3107***	2705.2842	2704.3002	2651.3100		**N**	501.2667	500.2715		***560.3039***	543.2773
25	70.0651	2791.3686	2774.3420	2773.3580	2819.3635	2802.3369	2801.3529	2765.3529		**P**	404.2140	403.2187		***446.2609***	429.2344
26	74.0600	2892.4163	2875.3897	2874.4057	2920.4112	2903.3846	2902.4006	2876.4213	2878.4006	**T**	303.1663	316.1867	318.1660	349.2082	332.1816
27	74.0600	2993.4639	2976.4374	2975.4534	***3021.4589***	3004.4323	3003.4483	2977.4690	2979.4483	**T**	202.1186	215.1390	217.1183	248.1605	231.1339
28	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FP	217.1335	245.1285	**FPG**	274.1550	302.1499	**FPGQ**	402.2136	430.2085
FPGQV	501.2820	529.2769	**FPGQVL**	614.3661	642.3610	**PG**	127.0866	155.0815
PGQ	255.1452	283.1401	**PGQV**	354.2136	382.2085	**PGQVL**	467.2976	495.2926
PGQVLR	623.3988	651.3937	**GQ**	158.0924	186.0873	**GQV**	257.1608	285.1557
GQVL	370.2449	398.2398	**GQVLR**	526.3460	554.3409	**GQVLRY**	689.4093	717.4042
QV	200.1394	228.1343	**QVL**	313.2234	341.2183	**QVLR**	469.3245	497.3194
QVLRY	632.3879	660.3828	**VL**	185.1648	213.1598	**VLR**	341.2659	369.2609
VLRY	504.3293	532.3242	**VLRYE**	633.3719	661.3668	**LR**	242.1975	270.1925
LRY	405.2609	433.2558	**LRYE**	534.3035	562.2984	**LRYED**	649.3304	677.3253
RY	292.1768	320.1717	**RYE**	421.2194	449.2143	**RYED**	536.2463	564.2413
RYEDN	650.2893	678.2842	**YE**	265.1183	293.1132	**YED**	380.1452	408.1401
YEDN	494.1882	522.1831	**YEDNF**	641.2566	669.2515	**ED**	217.0819	245.0768
EDN	331.1248	359.1197	**EDNF**	478.1932	506.1882	**EDNFD**	593.2202	621.2151
EDNFDA	664.2573	692.2522	**DN**	202.0822	230.0771	**DNF**	349.1506	377.1456
DNFD	464.1776	492.1725	**DNFDA**	535.2147	563.2096	**DNFDAN**	649.2576	677.2525
NF	234.1237	262.1186	**NFD**	349.1506	377.1456	**NFDA**	420.1878	448.1827
NFDAN	534.2307	562.2256	**NFDANS**	621.2627	649.2576	**FD**	235.1077	263.1026
FDA	306.1448	334.1397	**FDAN**	420.1878	448.1827	**FDANS**	507.2198	535.2147
FDANSN	621.2627	649.2576	**DA**	159.0764	187.0713	**DAN**	273.1193	301.1143
DANS	360.1514	388.1463	**DANSN**	474.1943	502.1892	**DANSNV**	573.2627	601.2576
DANSNVS	660.2947	688.2897	**AN**	158.0924	186.0873	**ANS**	245.1244	273.1193
ANSN	359.1674	387.1623	**ANSNV**	458.2358	486.2307	**ANSNVS**	545.2678	573.2627
ANSNVSV	644.3362	672.3311	**NS**	174.0873	202.0822	**NSN**	288.1302	316.1252
NSNV	387.1987	415.1936	**NSNVS**	474.2307	502.2256	**NSNVSV**	573.2991	601.2940
NSNVSVI	686.3832	714.3781	**SN**	174.0873	202.0822	**SNV**	273.1557	301.1506
SNVS	360.1878	388.1827	**SNVSV**	459.2562	487.2511	**SNVSVI**	572.3402	600.3352
SNVSVII	685.4243	713.4192	**NV**	186.1237	214.1186	**NVS**	273.1557	301.1506
NVSV	372.2241	400.2191	**NVSVI**	485.3082	513.3031	**NVSVII**	598.3923	626.3872
VS	159.1128	187.1077	**VSV**	258.1812	286.1761	**VSVI**	371.2653	399.2602
VSVII	484.3493	512.3443	**VSVIIN**	598.3923	626.3872	**VSVIINP**	695.4450	723.4400
SV	159.1128	187.1077	**SVI**	272.1969	300.1918	**SVII**	385.2809	413.2758
SVIIN	499.3239	527.3188	**SVIINP**	596.3766	624.3715	**SVIINPT**	697.4243	725.4192
VI	185.1648	213.1598	**VII**	298.2489	326.2438	**VIIN**	412.2918	440.2867
VIINP	509.3446	537.3395	**VIINPT**	610.3923	638.3872	**II**	199.1805	227.1754
IIN	313.2234	341.2183	**IINP**	410.2762	438.2711	**IINPT**	511.3239	539.3188
IINPTT	612.3715	640.3665	**IN**	200.1394	228.1343	**INP**	297.1921	325.1870
INPT	398.2398	426.2347	**INPTT**	499.2875	527.2824	**NP**	184.1081	212.1030
NPT	285.1557	313.1506	**NPTT**	386.2034	414.1983	**PT**	171.1128	199.1077
PTT	272.1605	300.1554	**TT**	175.1077	203.1026			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.5	3166.5571	0.3692	EFPGQVLRYEDNFDANSNVSVIINPTTK
39.2	3166.5571	0.3692	EFPGQVLRYEDNFDANSNVSVIIQPTSK
32.5	3167.5775	-0.6512	EFPGQVLRYEDNFDATSNLSVIINPTTK
5.4	3167.4005	-0.4742	VSSHLFSQGFMPDYYVSYMHGEEQLGK
5.4	3166.6849	0.2414	WIQDEGFIAVGNMSAVDKPNILPLLATVR
3.9	3167.5333	-0.6069	SVVAPPPTDDTRDPEGTPGYMAPELLLGEK
3.8	3167.4630	-0.5366	EIASNEKPSDPEEKPSDPTEKPSDPKDTT
1.5	3166.4165	0.5099	SDQNAAARAVDFMFGWFMGPLTEGEYPK
1.1	3166.6056	0.3207	WRTAVTVAGDNASPMMLWAVEVVPPKPGR
0.7	3166.4403	0.4860	GASEIIVQMCDMMIDGDGNSVPLSEAQRK

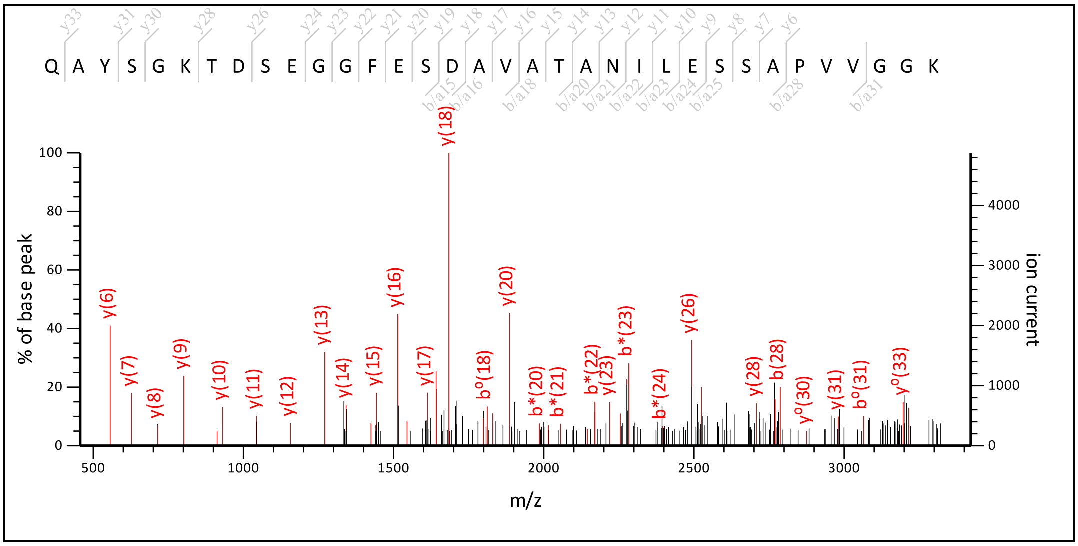
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 24

MS/MS Fragmentation of **QAYSGKTDSEGGFESDAVATANILESSAPVVGGK**
Found in **gi|115470529** in **NCBInr**, Os07g0141400 [Oryza sativa Japonica Group]

Match to Query 50: 3342.033224 from(3343.040500,1+) intensity(0.0000) index(21)
Title: Label: B12, Spot_Id: 216654, Peak_List_Id: 221714, MSMS Job_Run_Id: 21388, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_B12_136117695600.txt



456.31 to 3421.71

Label all possible matches ○ Label matches used for scoring ●

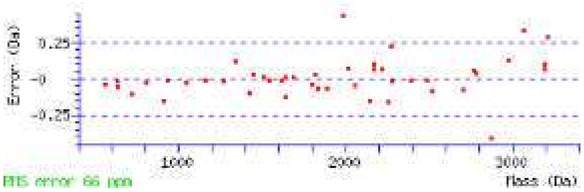
Monoisotopic mass of neutral peptide Mr(calc): 3341.5899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 115 **Expect:** 3.5e-09
Matches : 46/726 fragment ions using 93 most intense peaks (help)

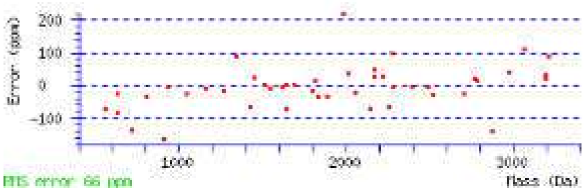
#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.0709	101.0709	84.0444		129.0659	112.0393		44.0495		Q					
2	44.0495	172.1081	155.0815		200.1030	183.0764				A	3198.5073			***3214.5386***	3197.5121
3	136.0757	335.1714	318.1448		363.1663	346.1397				Y	3035.4440			3143.5015	3126.4750
4	60.0444	422.2034	405.1769	404.1928	450.1983	433.1718	432.1878	406.2085		S	2948.4120	2947.4167		***2980.4382***	2963.4116
5	30.0338	479.2249	462.1983	461.2143	507.2198	490.1932	489.2092			G				2893.4062	2876.3796
6	101.1073	607.3198	590.2933	589.3093	635.3148	618.2882	617.3042	550.2620		K	2763.2955	2762.3003		2836.3847	2819.3581
7	74.0600	708.3675	691.3410	690.3570	736.3624	719.3359	718.3519	692.3726	694.3519	T	2662.2479	2675.2683	2677.2475	***2708.2897***	2691.2632
8	88.0393	823.3945	806.3679	805.3839	851.3894	834.3628	833.3788	779.4046		D	2547.2209	2546.2257		2607.2420	2590.2155
9	60.0444	910.4265	893.3999	892.4159	938.4214	921.3949	920.4108	894.4316		S	2460.1889	2459.1936		***2492.2151***	2475.1886
10	102.0550	1039.4691	1022.4425	1021.4585	1067.4640	1050.4374	1049.4534	981.4636		E	2331.1463	2330.1510		2405.1831	2388.1565
11	30.0338	1096.4905	1079.4640	1078.4800	1124.4855	1107.4589	1106.4749			G				***2276.1405***	2259.1139
12	30.0338	1153.5120	1136.4855	1135.5014	1181.5069	1164.4804	1163.4964			G				***2219.1190***	2202.0925
13	120.0808	1300.5804	1283.5539	1282.5699	1328.5753	1311.5488	1310.5648			F	2070.0350			2162.0976	2145.0710
14	102.0550	1429.6230	1412.5965	1411.6124	1457.6179	1440.5914	1439.6074	1371.6175		E	1940.9924	1939.9971		***2015.0291***	1998.0026
15	60.0444	1516.6550	1499.6285	1498.6445	**1544.6500**	1527.6234	1526.6394	1500.6601		S	1853.9603	1852.9651		***1885.9865***	1868.9600
16	88.0393	1631.6820	1614.6554	1613.6714	1659.6769	1642.6504	1641.6663	1587.6922		D	1738.9334	1737.9381		***1798.9545***	1781.9280
17	44.0495	1702.7191	1685.6926	1684.7085	1730.7140	1713.6875	1712.7034			A	1667.8963			***1683.9276***	1666.9010
18	72.0808	1801.7875	1784.7610	1783.7769	**1829.7824**	1812.7559	1811.7719	1787.7719		V	1568.8279	1581.8483		***1612.8905***	1595.8639
19	44.0495	1872.8246	1855.7981	1854.8141	1900.8195	1883.7930	1882.8090			A	1497.7907			***1513.8220***	1496.7955
20	74.0600	1973.8723	1956.8458	1955.8617	2001.8672	1984.8407	1983.8567	1957.8774	1959.8567	T	1396.7431	1409.7635	1411.7427	***1442.7849***	1425.7584
21	44.0495	2044.9094	2027.8829	2026.8989	2072.9043	2055.8778	2054.8938			A	1325.7060			***1341.7373***	1324.7107
22	87.0553	2158.9523	2141.9258	2140.9418	2186.9473	2169.9207	2168.9367	2115.9465		N	1211.6630	1210.6678		***1270.7001***	1253.6736
23	86.0964	2272.0364	2255.0099	2254.0258	2300.0313	2283.0048	2282.0208	2244.0051	2258.0208	I	1098.5790	1111.5994	1125.6150	***1156.6572***	1139.6307

24	86.0964	2385.1205	2368.0939	2367.1099	2413.1154	2396.0888	2395.1048	2343.0735		**L**	985.4949	984.4997		***1043.5732***	1026.5466
25	102.0550	2514.1631	2497.1365	2496.1525	2542.1580	2525.1314	2524.1474	2456.1576		**E**	856.4523	855.4571		***930.4891***	913.4625
26	60.0444	2601.1951	2584.1685	2583.1845	2629.1900	2612.1635	2611.1794	2585.2002		**S**	769.4203	768.4250		***801.4465***	784.4199
27	60.0444	2688.2271	2671.2006	2670.2166	2716.2220	2699.1955	2698.2115	2672.2322		**S**	682.3883	681.3930		***714.4145***	697.3879
28	44.0495	2759.2642	2742.2377	2741.2537	**2787.2592**	2770.2326	2769.2486			**A**	611.3511			***627.3824***	610.3559
29	70.0651	2856.3170	2839.2905	2838.3064	2884.3119	2867.2854	2866.3014	2830.3014		**P**	514.2984	513.3031		***556.3453***	539.3188
30	72.0808	2955.3854	2938.3589	2937.3749	2983.3803	2966.3538	2965.3698	2941.3698		**V**	415.2300	428.2504		459.2926	442.2660
31	72.0808	3054.4538	3037.4273	3036.4433	3082.4487	3065.4222	3064.4382	3040.4382		**V**	316.1615	329.1819		360.2241	343.1976
32	30.0338	3111.4753	3094.4487	3093.4647	3139.4702	3122.4437	3121.4596			**G**				261.1557	244.1292
33	30.0338	3168.4968	3151.4702	3150.4862	**3196.4917**	3179.4651	3178.4811			**G**				204.1343	187.1077
34	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AY	207.1128	235.1077	**AYS**	294.1448	322.1397	**AYSG**	351.1663	379.1612
AYSGK	479.2613	507.2562	**AYSGKT**	580.3089	608.3039	**AYSGKTD**	695.3359	723.3308
YS	223.1077	251.1026	**YSG**	280.1292	308.1241	**YSGK**	408.2241	436.2191
YSGKT	509.2718	537.2667	**YSGKTD**	624.2988	652.2937	**SG**	117.0659	145.0608
SGK	245.1608	273.1557	**SGKT**	346.2085	374.2034	**SGKTD**	461.2354	489.2304
SGKTDS	548.2675	576.2624	**SGKTDSE**	677.3101	705.3050	**GK**	158.1288	186.1237
GKT	259.1765	287.1714	**GKTD**	374.2034	402.1983	**GKTDS**	461.2354	489.2304
GKTDSE	590.2780	618.2729	**GKTDSEG**	647.2995	675.2944	**KT**	202.1550	230.1499
KTD	317.1819	345.1769	**KTDS**	404.2140	432.2089	**KTDSE**	533.2566	561.2515
KTDSEG	590.2780	618.2729	**KTDSEGG**	647.2995	675.2944	**TD**	189.0870	217.0819
TDS	276.1190	304.1139	**TDSE**	405.1616	433.1565	**TDSEG**	462.1831	490.1780
TDSEGG	519.2045	547.1994	**TDSEGGF**	666.2729	694.2679	**DS**	175.0713	203.0662
DSE	304.1139	332.1088	**DSEG**	361.1354	389.1303	**DSEGG**	418.1569	446.1518
DSEGGF	565.2253	593.2202	**DSEGGFE**	694.2679	722.2628	**SE**	189.0870	217.0819
SEG	246.1084	274.1034	**SEGG**	303.1299	331.1248	**SEGGF**	450.1983	478.1932
SEGGFE	579.2409	607.2358	**SEGGFES**	666.2729	694.2679	**EG**	159.0764	187.0713
EGG	216.0979	244.0928	**EGGF**	363.1663	391.1612	**EGGFE**	492.2089	520.2038
EGGFES	579.2409	607.2358	**EGGFESD**	694.2679	722.2628	**GG**	87.0553	115.0502
GGF	234.1237	262.1186	**GGFE**	363.1663	391.1612	**GGFES**	450.1983	478.1932
GGFESD	565.2253	593.2202	**GGFESDA**	636.2624	664.2573	**GF**	177.1022	205.0972
GFE	306.1448	334.1397	**GFES**	393.1769	421.1718	**GFESD**	508.2038	536.1987
GFESDA	579.2409	607.2358	**GFESDAV**	678.3093	706.3042	**FE**	249.1234	277.1183
FES	336.1554	364.1503	**FESD**	451.1823	479.1773	**FESDA**	522.2195	550.2144
FESDAV	621.2879	649.2828	**FESDAVA**	692.3250	720.3199	**ES**	189.0870	217.0819
ESD	304.1139	332.1088	**ESDA**	375.1510	403.1460	**ESDAV**	474.2195	502.2144
ESDAVA	545.2566	573.2515	**ESDAVAT**	646.3042	674.2992	**SD**	175.0713	203.0662
SDA	246.1084	274.1034	**SDAV**	345.1769	373.1718	**SDAVA**	416.2140	444.2089
SDAVAT	517.2617	545.2566	**SDAVATA**	588.2988	616.2937	**DA**	159.0764	187.0713
DAV	258.1448	286.1397	**DAVA**	329.1819	357.1769	**DAVAT**	430.2296	458.2245
DAVATA	501.2667	529.2617	**DAVATAN**	615.3097	643.3046	**AV**	143.1179	171.1128
AVA	214.1550	242.1499	**AVAT**	315.2027	343.1976	**AVATA**	386.2398	414.2347
AVATAN	500.2827	528.2776	**AVATANI**	613.3668	641.3617	**VA**	143.1179	171.1128
VAT	244.1656	272.1605	**VATA**	315.2027	343.1976	**VATAN**	429.2456	457.2405
VATANI	542.3297	570.3246	**VATANIL**	655.4137	683.4087	**AT**	145.0972	173.0921
ATA	216.1343	244.1292	**ATAN**	330.1772	358.1721	**ATANI**	443.2613	471.2562
ATANIL	556.3453	584.3402	**ATANILE**	685.3879	713.3828	**TA**	145.0972	173.0921
TAN	259.1401	287.1350	**TANI**	372.2241	400.2191	**TANIL**	485.3082	513.3031
TANILE	614.3508	642.3457	**AN**	158.0924	186.0873	**ANI**	271.1765	299.1714
ANIL	384.2605	412.2554	**ANILE**	513.3031	541.2980	**ANILES**	600.3352	628.3301
ANILESS	687.3672	715.3621	**NI**	200.1394	228.1343	**NIL**	313.2234	341.2183
NILE	442.2660	470.2609	**NILES**	529.2980	557.2930	**NILESS**	616.3301	644.3250
NILESSA	687.3672	715.3621	**IL**	199.1805	227.1754	**ILE**	328.2231	356.2180

ILES	415.2551	443.2500	**ILESS**	502.2871	530.2821	**ILESSA**	573.3243	601.3192
ILESSAP	670.3770	698.3719	**LE**	215.1390	243.1339	**LES**	302.1710	330.1660
LESS	389.2031	417.1980	**LESSA**	460.2402	488.2351	**LESSAP**	557.2930	585.2879
LESSAPV	656.3614	684.3563	**ES**	189.0870	217.0819	**ESS**	276.1190	304.1139
ESSA	347.1561	375.1510	**ESSAP**	444.2089	472.2038	**ESSAPV**	543.2773	571.2722
ESSAPVV	642.3457	670.3406	**ESSAPVVG**	699.3672	727.3621	**SS**	147.0764	175.0713
SSA	218.1135	246.1084	**SSAP**	315.1663	343.1612	**SSAPV**	414.2347	442.2296
SSAPVV	513.3031	541.2980	**SSAPVVG**	570.3246	598.3195	**SSAPVVGG**	627.3461	655.3410
SA	131.0815	159.0764	**SAP**	228.1343	256.1292	**SAPV**	327.2027	355.1976
SAPVV	426.2711	454.2660	**SAPVVG**	483.2926	511.2875	**SAPVVGG**	540.3140	568.3089
AP	141.1022	169.0972	**APV**	240.1707	268.1656	**APVV**	339.2391	367.2340
APVVG	396.2605	424.2554	**APVVGG**	453.2820	481.2769	**PV**	169.1335	197.1285
PVV	268.2020	296.1969	**PVVG**	325.2234	353.2183	**PVVGG**	382.2449	410.2398
VV	171.1492	199.1441	**VVG**	228.1707	256.1656	**VVGG**	285.1921	313.1870
VG	129.1022	157.0972	**VGG**	186.1237	214.1186	**GG**	87.0553	115.0502





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
115.4	3341.5899	0.4433	QAYSGKTDSEGGFESDAVATANILESSAPVVGGK
1.7	3342.6112	-0.5780	KACSEPISVPTNDANVGAMPTYLSSFSLSGVK
1.2	3342.4301	-0.3969	INMETEVLELFNHAEDNMEKGMDMWER
1.2	3341.7383	0.2949	DYLVKPAQMWWPQNLVQVSLFRTLHEK
0.0	3341.4704	0.5628	DEIQARTDNAVGTYGYMSPEYAMDGVISEK

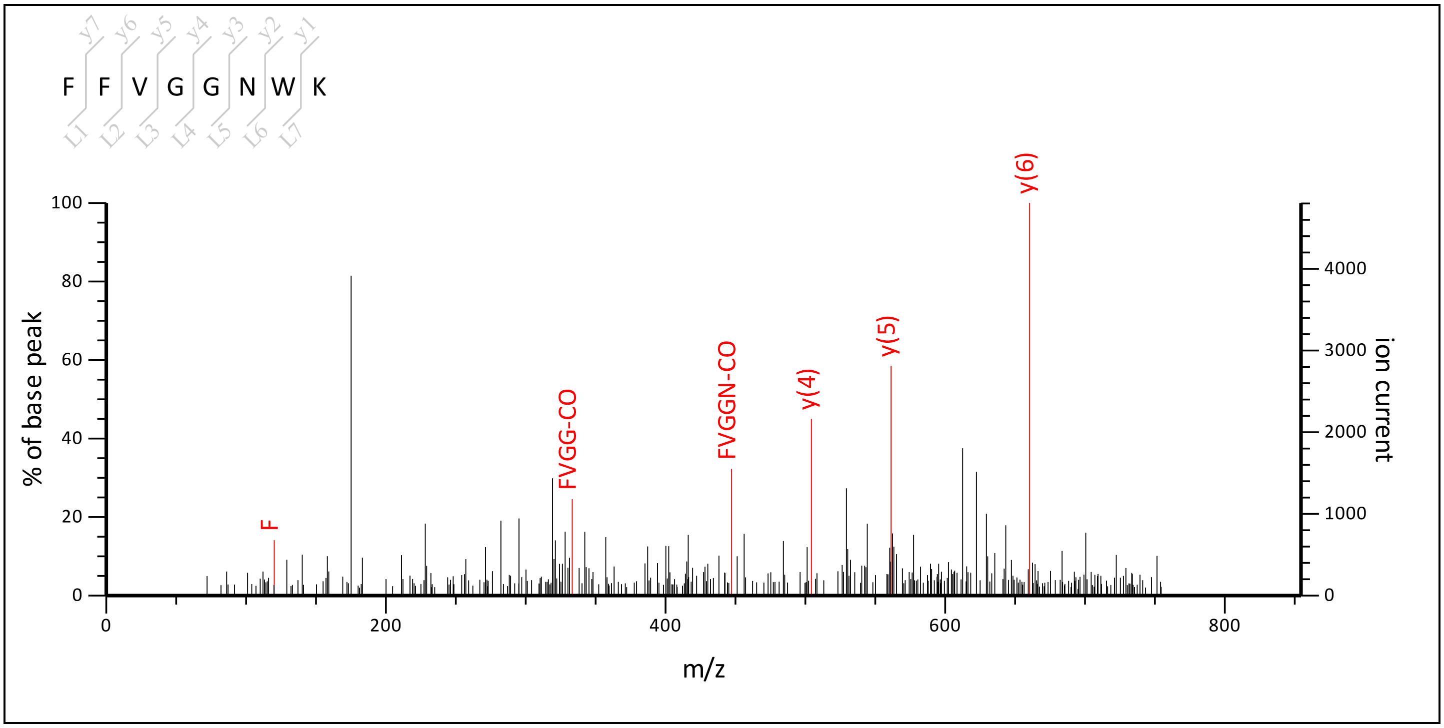
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 28

MS/MS Fragmentation of **FFVGGNWK**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 7: 953.494984 from(954.502260,1+) intensity(0.0000) index(1)
Title: Label: J9, Spot_Id: 219811, Peak_List_Id: 226895, MSMS Job_Run_Id: 21859, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J9_136859946600.txt



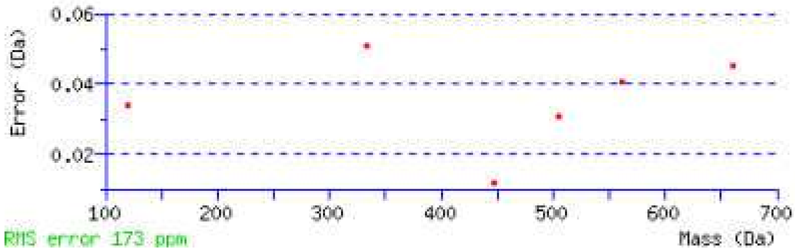
0 to 854.48

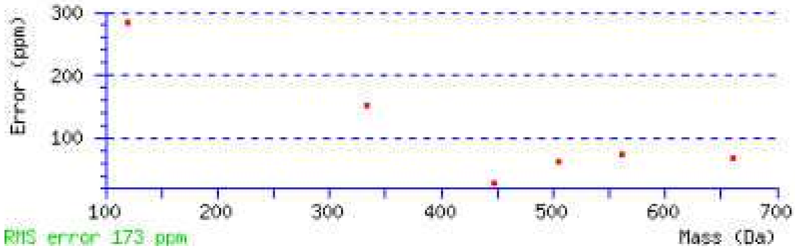
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 953.4760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 83
Matches : 10/81 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	120.0808	**120.0808**		148.0757		44.0495	**F**					8
2	120.0808	267.1492		295.1441			**F**	715.3522		807.4148	790.3883	7
3	72.0808	366.2176		394.2125		352.2020	**V**	616.2838	629.3042	***660.3464***	643.3198	6
4	30.0338	423.2391		451.2340			**G**			***561.2780***	544.2514	5
5	30.0338	480.2605		508.2554			**G**			***504.2565***	487.2300	4
6	87.0553	594.3035	577.2769	622.2984	605.2718	551.2976	**N**	388.1979	387.2027	***447.2350***	430.2085	3
7	159.0917	780.3828	763.3562	808.3777	791.3511		**W**	202.1186		***333.1921***	316.1656	2
8	101.1073						**K**	74.0237	73.0284	147.1128	130.0863	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FV	219.1492	247.1441	**FVG**	276.1707	304.1656	**FVGG**	333.1921	361.1870
FVGGN	447.2350	475.2300	**FVGGNW**	633.3144	661.3093	**VG**	129.1022	157.0972
VGG	186.1237	214.1186	**VGGN**	300.1666	328.1615	**VGGNW**	486.2459	514.2409
GG	87.0553	115.0502	**GGN**	201.0982	229.0931	**GGNW**	387.1775	415.1724
GN	144.0768	172.0717	**GNW**	330.1561	358.1510	**NW**	273.1346	301.1295





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	953.4832	0.0118	FFRGQGSR
28.8	953.4832	0.0118	FFRGQSGR
27.8	953.5083	-0.0133	FFVNGSKR
27.8	953.4389	0.0561	MFVNSANR
27.7	953.4641	0.0309	MFVEIGSR
26.9	953.4641	0.0309	MFVNKDGK
26.5	953.4059	0.0891	MDMNKSGR
26.5	953.4059	0.0891	MDMNKSGR
25.6	953.4760	0.0190	FFVGGNWK
25.6	953.4760	0.0190	FFVGGNWK

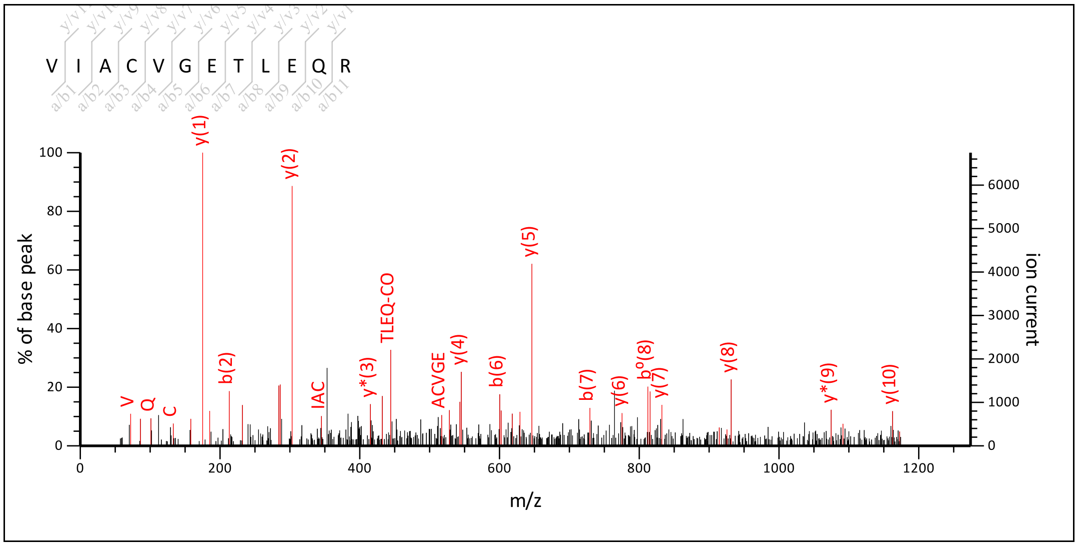
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 28

MS/MS Fragmentation of **VIACVGETLEQR**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 55: 1373.738124 from(1374.745400,1+) intensity(0.0000) index(14)
Title: Label: J9, Spot_Id: 219811, Peak_List_Id: 226893, MSMS Job_Run_Id: 21859, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J9_136859946600.txt



0 to 1274.12

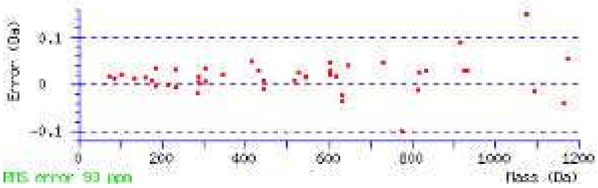
Label all possible matches ○ Label matches used for scoring ●

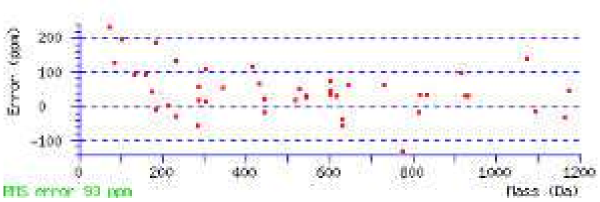
Monoisotopic mass of neutral peptide Mr(calc): 1373.6973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 0.0055
Matches : 48/179 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	**72.0808**			100.0757			44.0495		**V**					
2	86.0964	**185.1648**			**213.1598**			157.1335	171.1492	**I**	1217.5579	1230.5783	1244.5940	1275.6362	1258.6096
3	44.0495	256.2020			**284.1969**					**A**	1146.5208			***1162.5521***	1145.5256
4	133.0430	416.2326			**444.2275**			327.2391		**C**	986.4902	985.4949		***1091.5150***	1074.4884
5	72.0808	515.3010			**543.2959**			501.2854		**V**	887.4217	900.4421		***931.4843***	914.4578
6	30.0338	572.3225			**600.3174**					**G**				***832.4159***	815.3894
7	102.0550	701.3651		683.3545	**729.3600**		711.3494	643.3596		**E**	701.3577	700.3624		***775.3945***	758.3679
8	74.0600	802.4128		784.4022	830.4077		812.3971	786.4178	788.3971	**T**	600.3100	613.3304	615.3097	***646.3519***	629.3253
9	86.0964	915.4968		897.4863	943.4917		925.4812	873.4499		**L**	487.2259	486.2307		***545.3042***	528.2776
10	102.0550	1044.5394		1026.5288	1072.5343		1054.5238	986.5339		**E**	358.1833	357.1881		***432.2201***	415.1936
11	101.0709	**1172.5980**	1155.5714	1154.5874	1200.5929	1183.5664	1182.5823	1115.5765		**Q**	230.1248	229.1295		***303.1775***	286.1510
12	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IA	157.1335	185.1285	**IAC**	317.1642	345.1591	**IACV**	416.2326	444.2275
IACVG	473.2541	501.2490	**IACVGE**	602.2967	630.2916	**AC**	204.0801	232.0750
ACV	303.1485	331.1435	**ACVG**	360.1700	388.1649	**ACVGE**	489.2126	517.2075
ACVGET	590.2603	618.2552	**CV**	232.1114	260.1063	**CVG**	289.1329	317.1278
CVGE	418.1755	446.1704	**CVGET**	519.2232	547.2181	**CVGETL**	632.3072	660.3021
VG	129.1022	157.0972	**VGE**	258.1448	286.1397	**VGET**	359.1925	387.1874
VGETL	472.2766	500.2715	**VGETLE**	601.3192	629.3141	**GE**	159.0764	187.0713
GET	260.1241	288.1190	**GETL**	373.2082	401.2031	**GETLE**	502.2508	530.2457
GETLEQ	630.3093	658.3042	**ET**	203.1026	231.0975	**ETL**	316.1867	344.1816

ETLE	445.2293	473.2242	**ETLEQ**	573.2879	601.2828	**TL**	187.1441	215.1390
TLE	316.1867	344.1816	**TLEQ**	444.2453	472.2402	**LE**	215.1390	243.1339
LEQ	343.1976	371.1925	**EQ**	230.1135	258.1084			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.0	1373.6973	0.0408	VIACVGETLEQR
58.0	1373.6973	0.0408	VIACVGETLQER
39.6	1373.6972	0.0409	QMLAADEAIEKR
37.0	1373.6575	0.0806	NWDIAETELQR
37.0	1373.7701	-0.0319	LVCSGLVTELKR
36.4	1373.7337	0.0044	IVSCADITVLAGR
36.1	1373.6609	0.0772	CVALEGEPGVSTR
35.3	1373.7150	0.0231	AITEQTLSDALGR
33.8	1373.7263	0.0119	ATGITRETLEGAR
33.8	1373.7336	0.0045	DSQIAMIAELKR

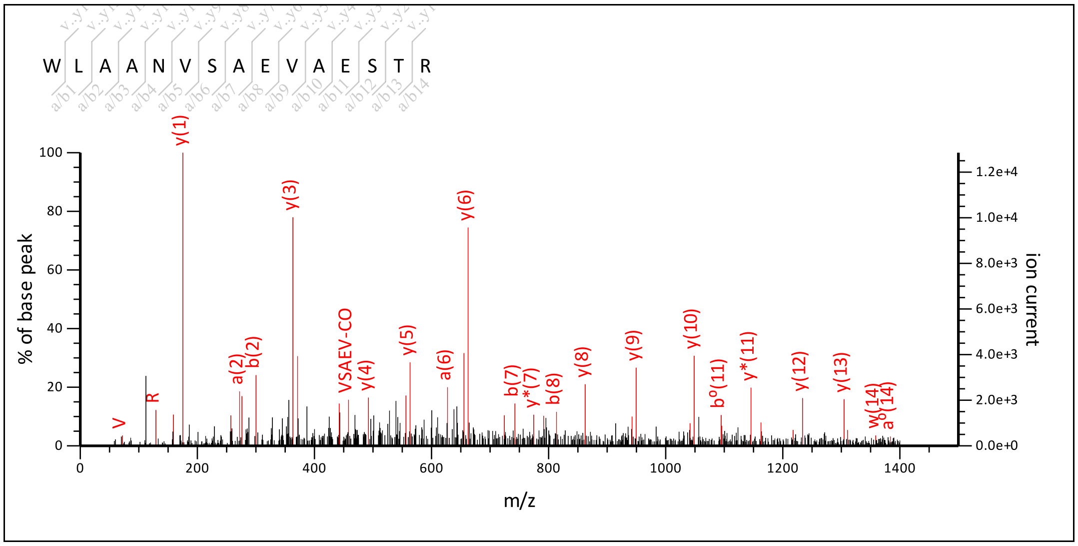
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 28**

MS/MS Fragmentation of **WLAANVSAEVAESTR**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 71: 1602.848324 from(1603.855600,1+) intensity(0.0000) index(20)
Title: Label: J9, Spot_Id: 219811, Peak_List_Id: 226889, MSMS Job_Run_Id: 21859, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J9_136859946600.txt



0 to 1499.97

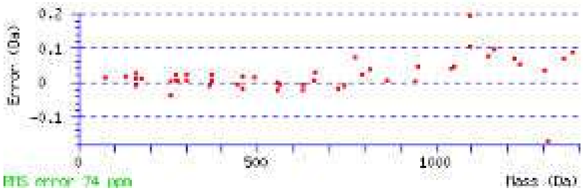
Label all possible matches ○ Label matches used for scoring ●

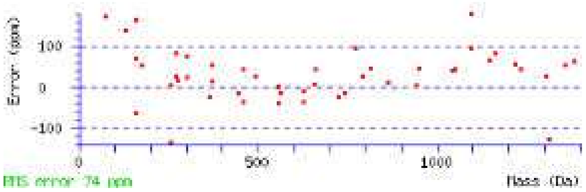
```
Monoisotopic mass of neutral peptide Mr(calc): 1602.8002
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 137  Expect: 6e-10
Matches : 53/270 fragment ions using 42 most intense peaks    (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	159.0917	**159.0917**			187.0866			44.0495		W					
2	86.0964	**272.1757**			**300.1707**			230.1288		L	1359.6499	1358.6546		1417.7281	1400.7016
3	44.0495	343.2129			**371.2078**					A	1288.6128			***1304.6441***	1287.6175
4	44.0495	414.2500			**442.2449**					A	1217.5757			***1233.6070***	1216.5804
5	87.0553	528.2929	511.2663		**556.2878**	539.2613		485.2871		N	1103.5327	1102.5375		***1162.5699***	1145.5433
6	72.0808	**627.3613**	610.3348		**655.3562**	638.3297		613.3457		V	1004.4643	1017.4847		***1048.5269***	1031.5004
7	60.0444	714.3933	697.3668	696.3828	**742.3882**	725.3617	724.3777	698.3984		S	917.4323	916.4371		***949.4585***	932.4320
8	44.0495	785.4304	768.4039	767.4199	**813.4254**	796.3988	795.4148			A	846.3952			***862.4265***	845.3999
9	102.0550	914.4730	897.4465	896.4625	**942.4680**	925.4414	924.4574	856.4676		E	717.3526	716.3573		***791.3894***	774.3628
10	72.0808	1013.5415	996.5149	995.5309	**1041.5364**	1024.5098	1023.5258	999.5258		V	618.2842	631.3046		***662.3468***	645.3202
11	44.0495	1084.5786	1067.5520	1066.5680	1112.5735	1095.5469	1094.5629			A	547.2471			***563.2784***	546.2518
12	102.0550	1213.6212	1196.5946	1195.6106	1241.6161	1224.5895	1223.6055	1155.6157		E	418.2045	417.2092		***492.2413***	475.2147
13	60.0444	1300.6532	1283.6266	1282.6426	1328.6481	1311.6216	1310.6375	1284.6583		S	331.1724	330.1772		***363.1987***	346.1721
14	74.0600	1401.7009	1384.6743	1383.6903	1429.6958	1412.6692	1411.6852	1385.7060	1387.6852	T	230.1248	243.1452	245.1244	***276.1666***	259.1401
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LA	157.1335	185.1285	LAA	228.1707	256.1656	LAAN	342.2136	370.2085
LAANV	441.2820	469.2769	LAANVS	528.3140	556.3089	LAANVSA	599.3511	627.3461
AA	115.0866	143.0815	AAN	229.1295	257.1244	AANV	328.1979	356.1928
AANVS	415.2300	443.2249	AANVSA	486.2671	514.2620	AANVSAE	615.3097	643.3046
AN	158.0924	186.0873	ANV	257.1608	285.1557	ANVS	344.1928	372.1878
ANVSA	415.2300	443.2249	ANVSAE	544.2726	572.2675	ANVSAEV	643.3410	671.3359

NV	186.1237	214.1186	**NVS**	273.1557	301.1506	**NVSA**	344.1928	372.1878
NVSAE	473.2354	501.2304	**NVSAEV**	572.3039	600.2988	**NVSAEVA**	643.3410	671.3359
VS	159.1128	187.1077	**VSA**	230.1499	258.1448	**VSAE**	359.1925	387.1874
VSAEV	458.2609	486.2558	**VSAEVA**	529.2980	557.2930	**VSAEVAE**	658.3406	686.3355
SA	131.0815	159.0764	**SAE**	260.1241	288.1190	**SAEV**	359.1925	387.1874
SAEVA	430.2296	458.2245	**SAEVAE**	559.2722	587.2671	**SAEVAES**	646.3042	674.2992
AE	173.0921	201.0870	**AEV**	272.1605	300.1554	**AEVA**	343.1976	371.1925
AEVAE	472.2402	500.2351	**AEVAES**	559.2722	587.2671	**AEVAEST**	660.3199	688.3148
EV	201.1234	229.1183	**EVA**	272.1605	300.1554	**EVAE**	401.2031	429.1980
EVAES	488.2351	516.2300	**EVAEST**	589.2828	617.2777	**VA**	143.1179	171.1128
VAE	272.1605	300.1554	**VAES**	359.1925	387.1874	**VAEST**	460.2402	488.2351
AE	173.0921	201.0870	**AES**	260.1241	288.1190	**AEST**	361.1718	389.1667
ES	189.0870	217.0819	**EST**	290.1347	318.1296	**ST**	161.0921	189.0870





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
137.3	1602.8002	0.0482	WLAANVSAEVAESTR
34.3	1602.7896	0.0587	GTLDAQGVANRMQAR
34.3	1602.7494	0.0989	MQSEADIAMVHLAR
33.3	1602.8148	0.0336	SVDLAAGRATVEAGMR
33.0	1602.7784	0.0700	TRSPNDAAEMAALTR
33.0	1602.7889	0.0594	DYYVNSSLVLSTSR
32.8	1602.7121	0.1362	LDAAAAADAAEEDSQR
32.7	1602.7889	0.0594	DKPSQVSWLAESEK
30.4	1602.8399	0.0084	KSNILVSAEDMQLR
29.4	1602.7671	0.0812	IAGASEGPSAEVASAMR

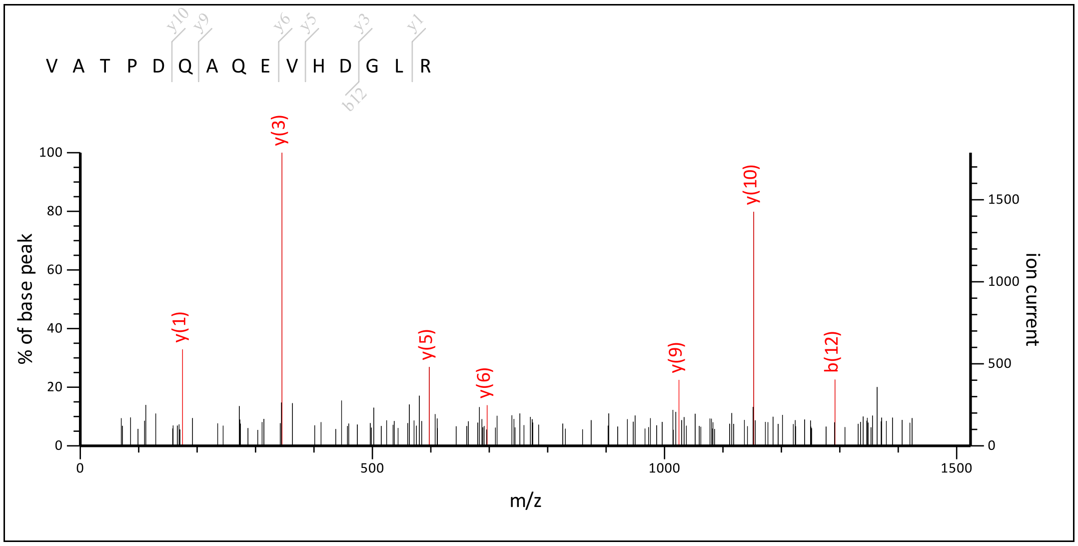
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 28

MS/MS Fragmentation of **VATPDQAQEVHDGLR**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 76: 1634.847224 from(1635.854500,1+) intensity(0.0000) index(21)
Title: Label: J9, Spot_Id: 219811, Peak_List_Id: 226913, MSMS Job_Run_Id: 21859, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J9_136859946600.txt



0 to 1523.75

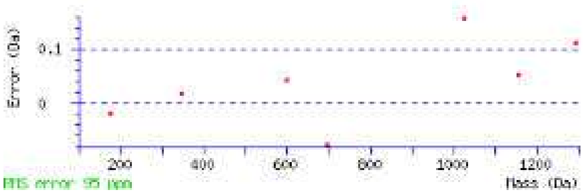
Label all possible matches ○ Label matches used for scoring ●

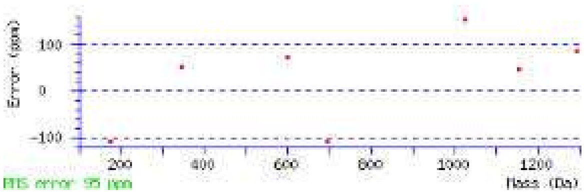
Monoisotopic mass of neutral peptide Mr(calc): 1634.8013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 27
Matches : 7/260 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	44.0495	143.1179			171.1128					A	1520.7088			1536.7401	1519.7136
3	74.0600	244.1656		226.1550	272.1605		254.1499	228.1707	230.1499	T	1419.6611	1432.6815	1434.6608	1465.7030	1448.6764
4	70.0651	341.2183		323.2078	369.2132		351.2027	315.2027		P	1322.6084	1321.6131		1364.6553	1347.6288
5	88.0393	456.2453		438.2347	484.2402		466.2296	412.2554		D	1207.5814	1206.5862		1267.6026	1250.5760
6	101.0709	584.3039	567.2773	566.2933	612.2988	595.2722	594.2882	527.2824		Q	1079.5228	1078.5276		***1152.5756***	1135.5491
7	44.0495	655.3410	638.3144	637.3304	683.3359	666.3093	665.3253			A	1008.4857			***1024.5170***	1007.4905
8	101.0709	783.3995	766.3730	765.3890	811.3945	794.3679	793.3839	726.3781		Q	880.4272	879.4319		953.4799	936.4534
9	102.0550	912.4421	895.4156	894.4316	940.4371	923.4105	922.4265	854.4367		E	751.3846	750.3893		825.4213	808.3948
10	72.0808	1011.5106	994.4840	993.5000	1039.5055	1022.4789	1021.4949	997.4949		V	652.3161	665.3365		***696.3787***	679.3522
11	110.0713	1148.5695	1131.5429	1130.5589	1176.5644	1159.5378	1158.5538			H	515.2572			***597.3103***	580.2838
12	88.0393	1263.5964	1246.5699	1245.5858	**1291.5913**	1274.5648	1273.5808	1219.6066		D	400.2303	399.2350		460.2514	443.2249
13	30.0338	1320.6179	1303.5913	1302.6073	1348.6128	1331.5862	1330.6022			G				***345.2245***	328.1979
14	86.0964	1433.7019	1416.6754	1415.6914	1461.6969	1444.6703	1443.6863	1391.6550		L	230.1248	229.1295		288.2030	271.1765
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AT	145.0972	173.0921	ATP	242.1499	270.1448	ATPD	357.1769	385.1718
ATPDQ	485.2354	513.2304	ATPDQA	556.2726	584.2675	ATPDQAQ	684.3311	712.3260
TP	171.1128	199.1077	TPD	286.1397	314.1347	TPDQ	414.1983	442.1932
TPDQA	485.2354	513.2304	TPDQAQ	613.2940	641.2889	PD	185.0921	213.0870
PDQ	313.1506	341.1456	PDQA	384.1878	412.1827	PDQAQ	512.2463	540.2413
PDQAQE	641.2889	669.2838	DQ	216.0979	244.0928	DQA	287.1350	315.1299

DQAQ	415.1936	443.1885	**DQAQE**	544.2362	572.2311	**DQAQEV**	643.3046	671.2995
QA	172.1081	200.1030	**QAQ**	300.1666	328.1615	**QAQE**	429.2092	457.2041
QAQEV	528.2776	556.2726	**QAQEVH**	665.3366	693.3315	**AQ**	172.1081	200.1030
AQE	301.1506	329.1456	**AQEV**	400.2191	428.2140	**AQEVH**	537.2780	565.2729
AQEVHD	652.3049	680.2998	**QE**	230.1135	258.1084	**QEV**	329.1819	357.1769
QEVH	466.2409	494.2358	**QEVHD**	581.2678	609.2627	**QEVHDG**	638.2893	666.2842
EV	201.1234	229.1183	**EVH**	338.1823	366.1772	**EVHD**	453.2092	481.2041
EVHDG	510.2307	538.2256	**EVHDGL**	623.3148	651.3097	**VH**	209.1397	237.1346
VHD	324.1666	352.1615	**VHDG**	381.1881	409.1830	**VHDGL**	494.2722	522.2671
HD	225.0982	253.0931	**HDG**	282.1197	310.1146	**HDGL**	395.2037	423.1987
DG	145.0608	173.0557	**DGL**	258.1448	286.1397	**GL**	143.1179	171.1128





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1634.8013	0.0460	VATPDQAQEVHDGLR
22.2	1634.8601	-0.0129	QLNQQGLTRHDLGR
14.4	1634.9355	-0.0883	KIQLEQLSVLPPDR
13.9	1634.9104	-0.0632	IDVRPAVDTLPGGIGR
13.7	1635.0083	-0.1611	SLLVAGATALAAPLVLR
13.2	1634.8628	-0.0155	KESQGALILVDGYSR
12.9	1634.8297	0.0175	AALDLMTSLQEKSGR
12.9	1634.9290	-0.0818	KGINAILGPCIGPLGR
12.4	1634.8239	0.0233	LLEQGAVCFSWLGR
12.4	1634.8273	0.0200	ALLWGGATLGVGMAMR

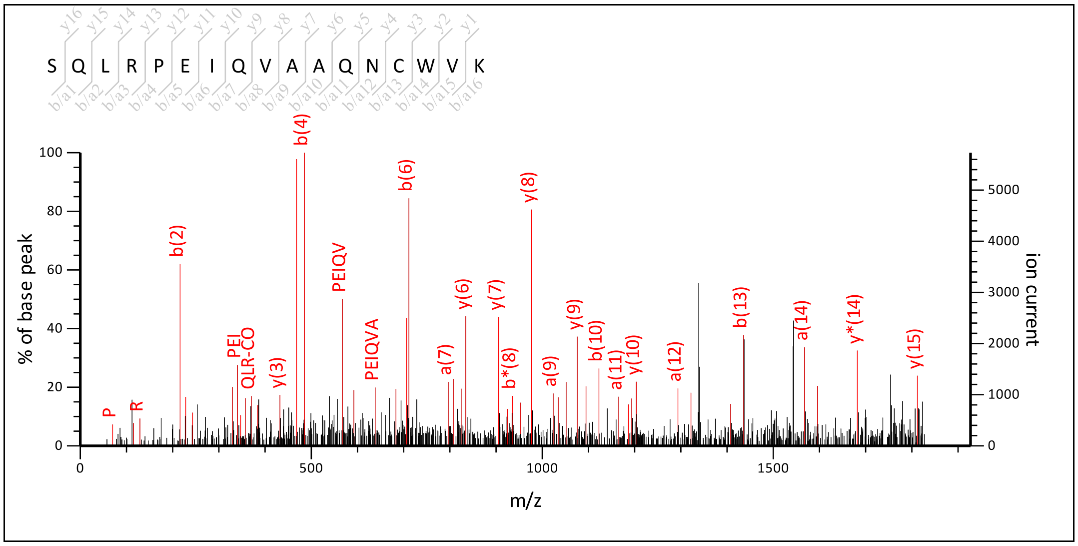
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 28

MS/MS Fragmentation of **SQLRPEIQVAAQNCWVK**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 105: 2026.095624 from(2027.102900,1+) intensity(0.0000) index(30)
Title: Label: J9, Spot_Id: 219811, Peak_List_Id: 226888, MSMS Job_Run_Id: 21859, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J9_136859946600.txt



0 to 1927.01

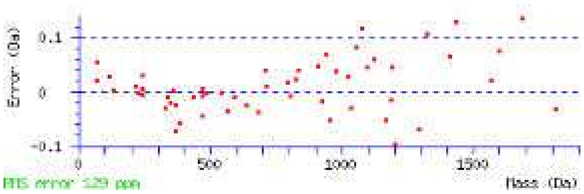
Label all possible matches ○ Label matches used for scoring ●

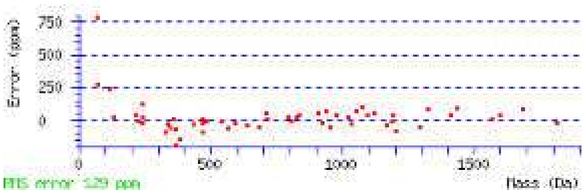
Monoisotopic mass of neutral peptide Mr(calc): 2026.0418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 79 **Expect:** 0.00034
Matches : 57/305 fragment ions using 72 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	101.0709	188.1030	171.0764	170.0924	***216.0979***	199.0713	198.0873	131.0815		Q	1866.9643	1865.9691		1940.0171	1922.9905
3	86.0964	301.1870	284.1605	283.1765	***329.1819***	312.1554	311.1714	259.1401		L	1753.8803	1752.8850		**1811.9585**	1794.9320
4	129.1135	457.2881	440.2616	439.2776	***485.2831***	468.2565	467.2725	372.2241		R	1597.7791	1596.7839		1698.8744	1681.8479
5	70.0651	554.3409	537.3144	536.3303	582.3358	565.3093	564.3253	528.3253		P	1500.7264	1499.7311		1542.7733	1525.7468
6	102.0550	**683.3835**	666.3569	665.3729	***711.3784***	694.3519	693.3678	625.3780		E	1371.6838	1370.6885		1445.7206	1428.6940
7	86.0964	**796.4676**	779.4410	778.4570	***824.4625***	807.4359	806.4519	768.4363	782.4519	I	1258.5997	1271.6201	1285.6358	1316.6780	1299.6514
8	101.0709	**924.5261**	907.4996	906.5156	***952.5211***	935.4945	934.5105	867.5047		Q	1130.5411	1129.5459		**1203.5939**	1186.5674
9	72.0808	**1023.5946**	1006.5680	1005.5840	***1051.5895***	1034.5629	1033.5789	1009.5789		V	1031.4727	1044.4931		**1075.5353**	1058.5088
10	44.0495	**1094.6317**	1077.6051	1076.6211	***1122.6266***	1105.6000	1104.6160			A	960.4356			**976.4669**	959.4404
11	44.0495	**1165.6688**	1148.6422	1147.6582	***1193.6637***	1176.6371	1175.6531			A	889.3985			**905.4298**	888.4033
12	101.0709	**1293.7274**	1276.7008	1275.7168	***1321.7223***	1304.6957	1303.7117	1236.7059		Q	761.3399	760.3447		**834.3927**	817.3661
13	87.0553	**1407.7703**	1390.7437	1389.7597	***1435.7652***	1418.7387	1417.7546	1364.7645		N	647.2970	646.3017		**706.3341**	689.3076
14	133.0430	**1567.8009**	1550.7744	1549.7904	***1595.7959***	1578.7693	1577.7853	1478.8074		C	487.2663	486.2711		**592.2912**	575.2646
15	159.0917	1753.8803	1736.8537	1735.8697	1781.8752	1764.8486	1763.8646			W	301.1870			**432.2605**	415.2340
16	72.0808	1852.9487	1835.9221	1834.9381	1880.9436	1863.9170	1862.9330	1838.9330		V	202.1186	215.1390		246.1812	229.1547
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QL	214.1550	242.1499	QLR	370.2561	398.2510	QLRP	467.3089	495.3038
QLRPE	596.3515	624.3464	LR	242.1975	270.1925	LRP	339.2503	367.2452
LRPE	468.2929	496.2878	LRPEI	581.3770	609.3719	RP	226.1662	254.1612
RPE	355.2088	383.2037	RPEI	468.2929	496.2878	RPEIQ	596.3515	624.3464

RPEIQV	695.4199	723.4148	**PE**	199.1077	227.1026	**PEI**	312.1918	340.1867
PEIQ	440.2504	468.2453	**PEIQV**	539.3188	567.3137	**PEIQVA**	610.3559	638.3508
PEIQVAA	681.3930	709.3879	**EI**	215.1390	243.1339	**EIQ**	343.1976	371.1925
EIQV	442.2660	470.2609	**EIQVA**	513.3031	541.2980	**EIQVAA**	584.3402	612.3352
IQ	214.1550	242.1499	**IQV**	313.2234	341.2183	**IQVA**	384.2605	412.2554
IQVAA	455.2976	483.2926	**IQVAAQ**	583.3562	611.3511	**IQVAAQN**	697.3992	725.3941
QV	200.1394	228.1343	**QVA**	271.1765	299.1714	**QVAA**	342.2136	370.2085
QVAAQ	470.2722	498.2671	**QVAAQN**	584.3151	612.3100	**VA**	143.1179	171.1128
VAA	214.1550	242.1499	**VAAQ**	342.2136	370.2085	**VAAQN**	456.2565	484.2514
VAAQNC	616.2872	644.2821	**AA**	115.0866	143.0815	**AAQ**	243.1452	271.1401
AAQN	357.1881	385.1830	**AAQNC**	517.2187	545.2137	**AQ**	172.1081	200.1030
AQN	286.1510	314.1459	**AQNC**	446.1816	474.1765	**AQNCW**	632.2609	660.2559
QN	215.1139	243.1088	**QNC**	375.1445	403.1394	**QNCW**	561.2238	589.2187
QNCWV	660.2922	688.2872	**NC**	247.0859	275.0809	**NCW**	433.1652	461.1602
NCWV	532.2337	560.2286	**CW**	319.1223	347.1172	**CWV**	418.1907	446.1857
WV	258.1601	286.1550						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.5	2026.0418	0.0538	SQLRPEIQVAAQNCWVK
29.1	2026.1324	-0.0368	DVPAGAVTLAGVAHVPAIGGVR
24.0	2026.1211	-0.0255	VKEINIAPSVNLPPPDAPR
22.3	2026.1146	-0.0190	VVRVLPGMQAAFVDIGQAR
21.9	2026.1575	-0.0619	LILQVAVGSAASSGVFLAAPR
21.4	2025.9136	0.1821	CSPSYGGENVAAQLAEVMK
19.4	2026.0378	0.0578	QSLSLLAVQAMAQSDRHR
19.1	2026.0847	0.0109	RLDPSIPSNAAVFELIER
18.7	2026.1397	-0.0441	LLLRIPQTAPAMAALFER
18.2	2026.1609	-0.0652	LTGGGIALIVGAGMALSAIGRL

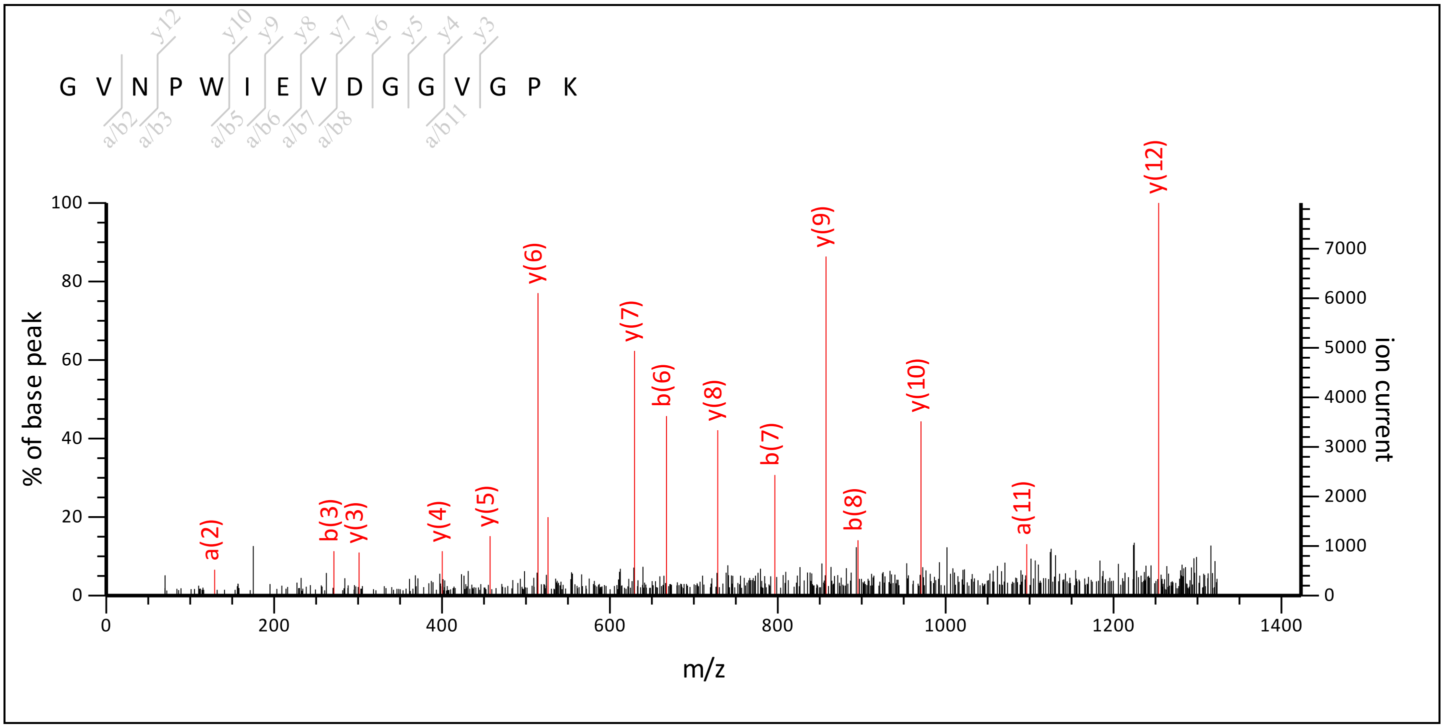
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 29**

MS/MS Fragmentation of **GVNPWIEVDGGVGPK**
Found in **gi|4105561** in **NCBInr**, ribulose-5-phosphate-3-epimerase [Oryza sativa]

Match to Query 77: 1522.849324 from(1523.856600,1+) intensity(0.0000) index(21)
Title: Label: J20, Spot_Id: 219987, Peak_List_Id: 229446, MSMS Job_Run_Id: 22021, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J20_136868359600.txt



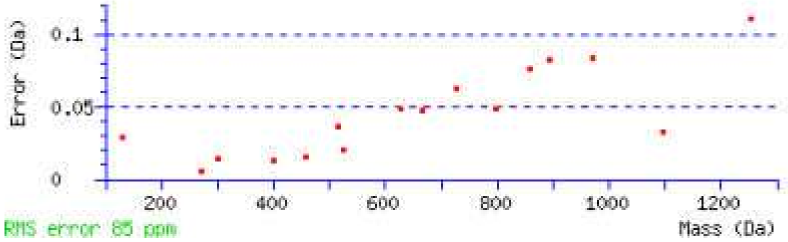
0 to 1423.3

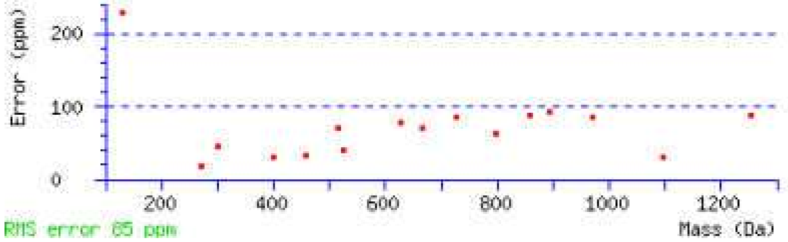
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1522.7780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 0.00085
Matches : 16/80 fragment ions using 26 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			15
2	**129.1022**		157.0972		V	1466.7638	1449.7373	14
3	243.1452	226.1186	**271.1401**	254.1135	N	1367.6954	1350.6688	13
4	340.1979	323.1714	368.1928	351.1663	P	***1253.6525***	1236.6259	12
5	**526.2772**	509.2507	554.2722	537.2456	W	1156.5997	1139.5732	11
6	639.3613	622.3348	**667.3562**	650.3297	I	***970.5204***	953.4938	10
7	768.4039	751.3774	**796.3988**	779.3723	E	***857.4363***	840.4098	9
8	867.4723	850.4458	**895.4672**	878.4407	V	***728.3937***	711.3672	8

9	982.4993	965.4727	1010.4942	993.4676	D	*629.3253*	612.2988	7
10	1039.5207	1022.4942	1067.5156	1050.4891	G	*514.2984*	497.2718	6
11	**1096.5422**	1079.5156	1124.5371	1107.5106	G	*457.2769*	440.2504	5
12	1195.6106	1178.5840	1223.6055	1206.5790	V	*400.2554*	383.2289	4
13	1252.6321	1235.6055	1280.6270	1263.6004	G	*301.1870*	284.1605	3
14	1349.6848	1332.6583	1377.6797	1360.6532	P	244.1656	227.1390	2
15					K	147.1128	130.0863	1





NCBI **BLAST** search of GVNPWIEVDGGVGPK
(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	1522.7780	0.0713	GVNPWIEVDGGVGPK
22.3	1522.8943	-0.0450	NRGLLLEQQIALR
13.6	1522.9096	-0.0603	RGGILGLLLAGWAAR
11.8	1522.7739	0.0754	NTQIGKSQLEYSR
11.7	1522.8944	-0.0450	RIGVGAAGGGVLVLER
9.2	1522.8103	0.0390	QAQLDSITIPQGPR
8.9	1522.7164	0.1329	NLAENSATFGGTWR
8.8	1522.8580	-0.0086	LNILVNNAGTGKPGR
8.5	1522.7052	0.1441	AKVWGDNQEDAYK
7.9	1522.8216	0.0277	RGQDPIVNVIEQR

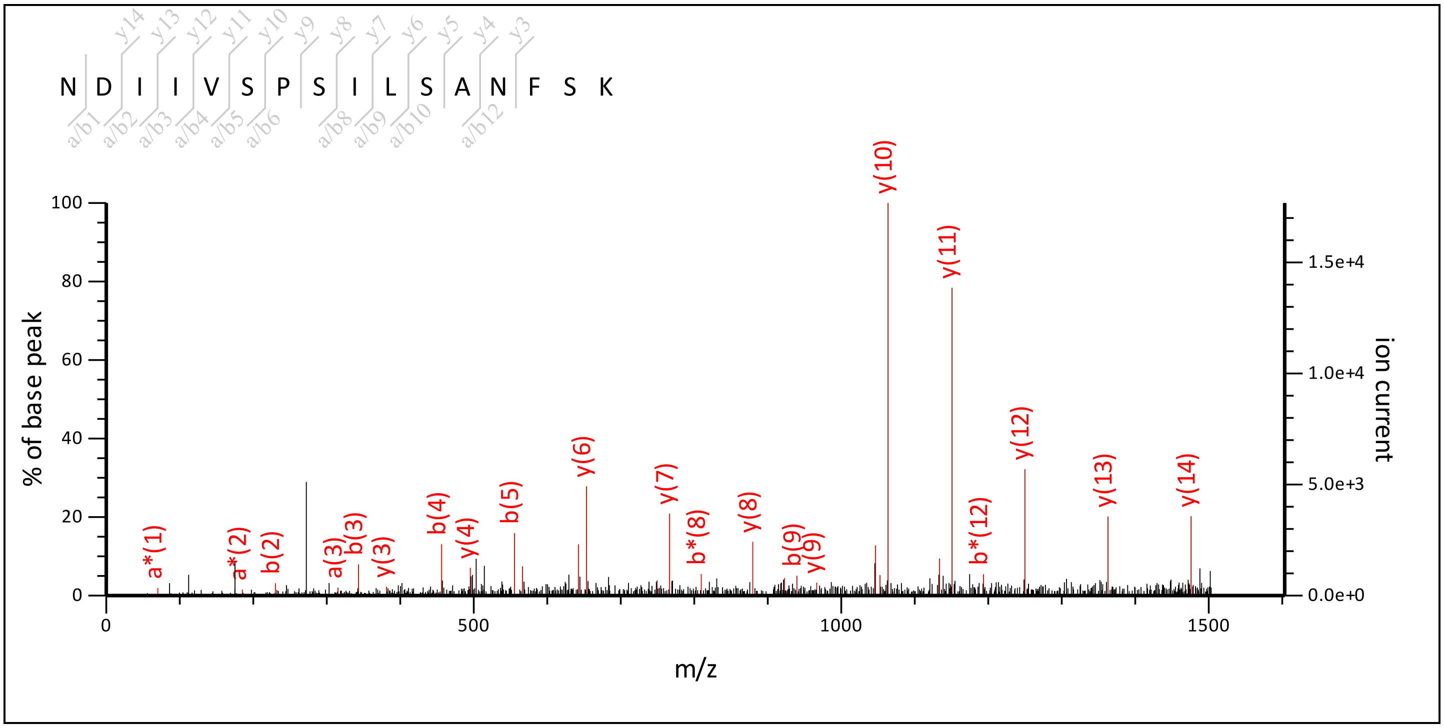
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 29

MS/MS Fragmentation of **NDIIVSPSILSANFSK**
Found in **gi|4105561** in **NCBInr**, ribulose-5-phosphate-3-epimerase [Oryza sativa]

Match to Query 89: 1703.984524 from(1704.991800,1+) intensity(0.0000) index(25)
Title: Label: J20, Spot_Id: 219987, Peak_List_Id: 229444, MSMS Job_Run_Id: 22021, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J20_136868359600.txt



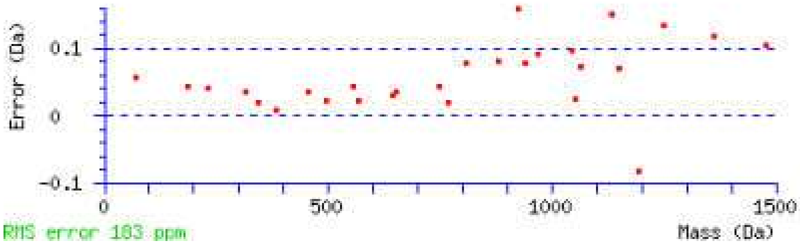
0 to 1603.33

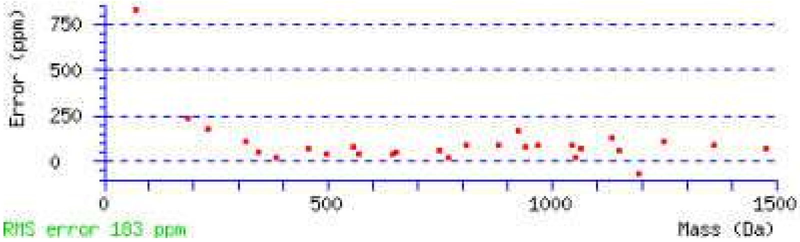
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1703.9094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 0.006
Matches : 28/90 fragment ions using 75 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	87.0553	70.0287	115.0502	98.0237	**N**			**16**
2	202.0822	185.0557	**230.0771**	213.0506	**D**	1590.8737	1573.8472	**15**
3	315.1663	298.1397	**343.1612**	326.1347	**I**	***1475.8468***	1458.8203	**14**
4	428.2504	411.2238	**456.2453**	439.2187	**I**	***1362.7627***	1345.7362	**13**
5	527.3188	510.2922	**555.3137**	538.2871	**V**	***1249.6787***	1232.6521	**12**
6	614.3508	597.3243	**642.3457**	625.3192	**S**	***1150.6103***	1133.5837	**11**
7	711.4036	694.3770	739.3985	722.3719	**P**	***1063.5782***	1046.5517	**10**
8	798.4356	781.4090	826.4305	809.4040	**S**	***966.5255***	949.4989	**9**

9	911.5197	894.4931	**939.5146**	922.4880	**I**	***879.4934***	862.4669	**8**
10	1024.6037	1007.5772	**1052.5986**	1035.5721	**L**	***766.4094***	749.3828	**7**
11	1111.6357	1094.6092	1139.6307	1122.6041	**S**	***653.3253***	636.2988	**6**
12	1182.6729	1165.6463	1210.6678	1193.6412	**A**	***566.2933***	549.2667	**5**
13	1296.7158	1279.6892	1324.7107	1307.6842	**N**	***495.2562***	478.2296	**4**
14	1443.7842	1426.7577	1471.7791	1454.7526	**F**	***381.2132***	364.1867	**3**
15	1530.8162	1513.7897	1558.8111	1541.7846	**S**	234.1448	217.1183	**2**
16					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.5	1703.9094	0.0751	NDIIVSPSILSANFSK
45.9	1703.9458	0.0388	KDVIVSPSILSANFSK
17.5	1703.9682	0.0163	SAALADLIPIRPSGAPR
13.1	1703.9028	0.0817	EEVFRTLIAMNLPR
12.1	1703.9359	0.0486	HLTTSLLSPLSPPWR
11.7	1703.8665	0.1180	GDGGGMYLSAIQAVLPR
11.1	1703.8955	0.0890	GEGGGNAVTVPLGLPPNR
9.1	1703.8168	0.1677	LWVWGQNQGSNYPR
8.6	1703.9795	0.0051	LVQGAPISASQPRPKR
8.6	1703.8512	0.1333	ERLQDALESIVEMR

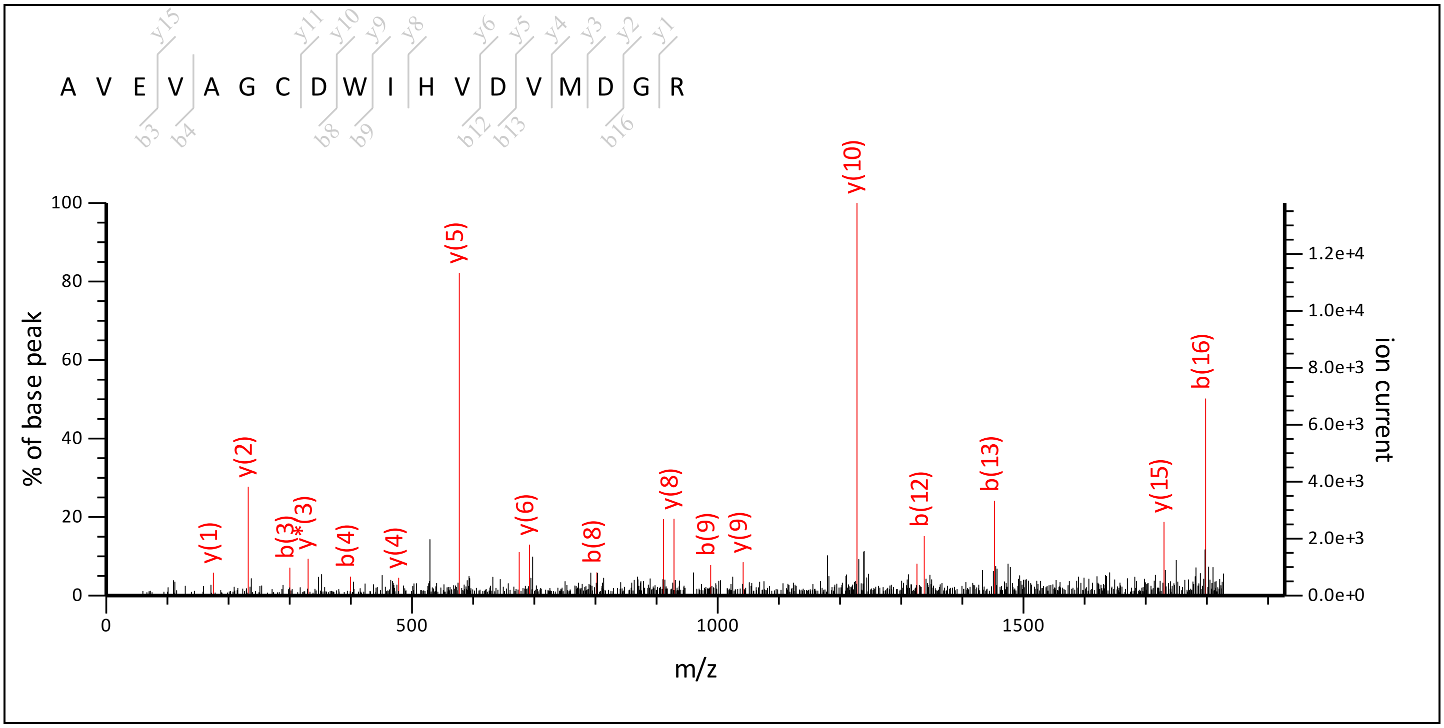
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 29

MS/MS Fragmentation of **AVEVAGCDWIHVDVMDGR**
Found in **gi|4105561** in **NCBInr**, ribulose-5-phosphate-3-epimerase [Oryza sativa]

Match to Query 95: 2028.020924 from(2029.028200,1+) intensity(0.0000) index(27)
Title: Label: J20, Spot_Id: 219987, Peak_List_Id: 229448, MSMS Job_Run_Id: 22021, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J20_136868359600.txt



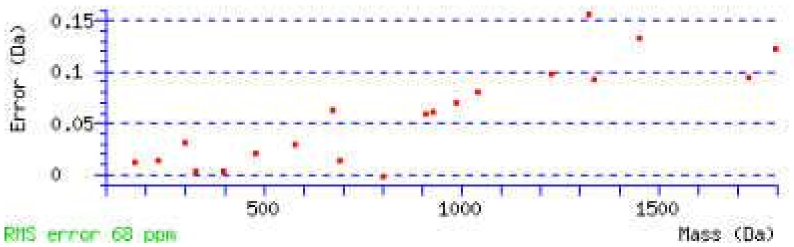
0 to 1927.21

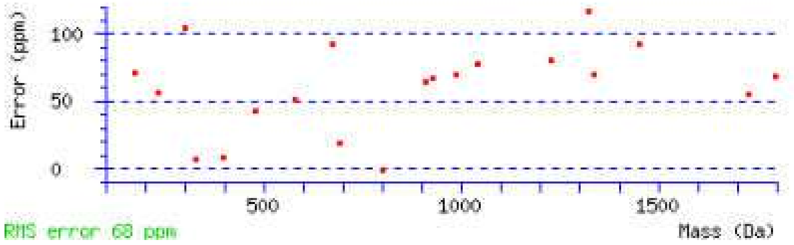
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2027.9194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.018
Matches : 20/68 fragment ions using 36 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	44.0495	72.0444	A			18
2	143.1179	171.1128	V	1957.8895	1940.8629	17
3	272.1605	**300.1554**	E	1858.8211	1841.7945	16
4	371.2289	**399.2238**	V	*1729.7785*	1712.7519	15
5	442.2660	470.2609	A	1630.7101	1613.6835	14
6	499.2875	527.2824	G	1559.6730	1542.6464	13
7	659.3181	687.3130	C	1502.6515	1485.6249	12
8	774.3451	**802.3400**	D	1342.6208	1325.5943	11

9	960.4244	**988.4193**	**W**	***1227.5939***	1210.5674	**10**
10	1073.5084	1101.5034	**I**	***1041.5146***	1024.4880	**9**
11	1210.5674	1238.5623	**H**	***928.4305***	911.4040	**8**
12	1309.6358	**1337.6307**	**V**	791.3716	774.3451	**7**
13	1424.6627	**1452.6576**	**D**	***692.3032***	675.2767	**6**
14	1523.7311	1551.7260	**V**	***577.2763***	560.2497	**5**
15	1654.7716	1682.7665	**M**	***478.2078***	461.1813	**4**
16	1769.7986	**1797.7935**	**D**	347.1674	330.1408	**3**
17	1826.8200	1854.8149	**G**	***232.1404***	215.1139	**2**
18			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.0	2027.9194	0.1016	AVEVAGCDWIHVDVMDGR
22.7	2027.9194	0.1016	AVELAGCDWVHVDVMDGR
7.3	2027.9701	0.0508	KLYGDNGGGVNYVHSGYTK
4.4	2027.9775	0.0434	FVNLMEGHIWIDSEGPGK
2.9	2027.8855	0.1355	ADSFVGDMERGTLAEDSGR
0.9	2027.9185	0.1025	RLLLGDDGSGGGEYEYDGR
0.5	2028.1480	-0.1271	LGDHLRAGALPGVAGVPTSLK
0.4	2027.9377	0.0832	VKDYADVHWEYYQQGK
0.3	2028.0245	-0.0036	VSLLCTQGDPQLRPTMGR
0.1	2027.9872	0.0338	LALAAAATETGADAAAAGENGGR

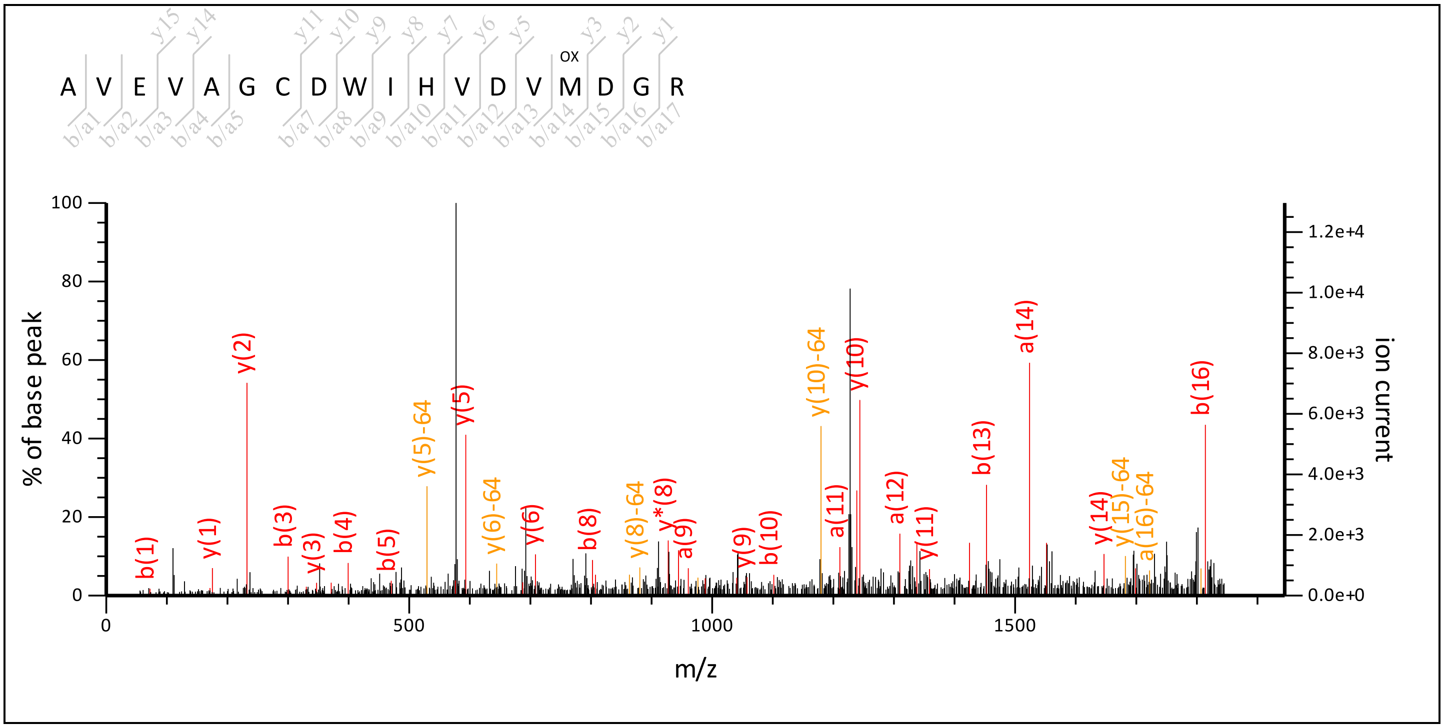
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 29

MS/MS Fragmentation of **AVEVAGCDWIHVDVMDGR**
Found in **gi|4105561** in **NCBInr**, ribulose-5-phosphate-3-epimerase [Oryza sativa]

Match to Query 97: 2044.010324 from(2045.017600,1+) intensity(0.0000) index(28)
Title: Label: J20, Spot_Id: 219987, Peak_List_Id: 229443, MSMS Job_Run_Id: 22021, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J20_136868359600.txt



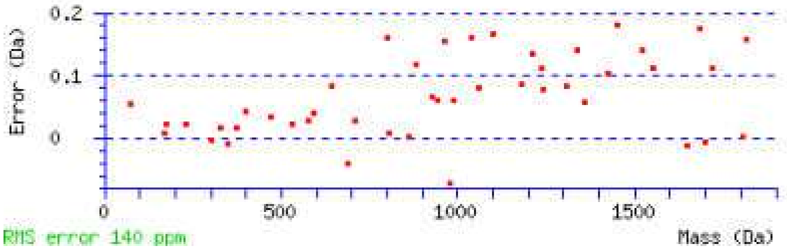
0 to 1944.91

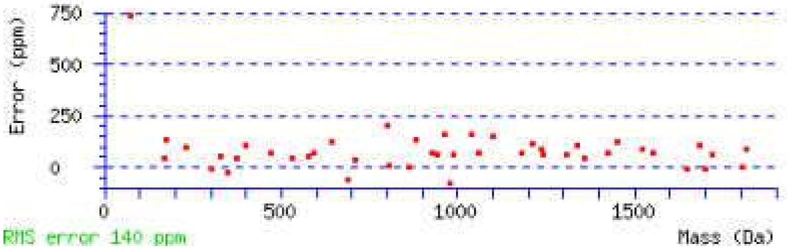
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2043.9143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 **Expect:** 0.088
Matches : 45/102 fragment ions using 180 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	44.0495	***72.0444***	**A**			**18**
2	143.1179	***171.1128***	**V**	1973.8844	1956.8579	**17**
3	272.1605	***300.1554***	**E**	1874.8160	1857.7894	**16**
4	**371.2289**	***399.2238***	**V**	1745.7734	1728.7469	**15**
5	442.2660	***470.2609***	**A**	**1646.7050**	1629.6784	**14**
6	499.2875	527.2824	**G**	1575.6679	1558.6413	**13**
7	659.3181	***687.3130***	**C**	1518.6464	1501.6199	**12**

8	774.3451	***802.3400***	**D**	**1358.6158**	1341.5892	**11**
9	**960.4244**	***988.4193***	**W**	**1243.5888**	1226.5623	**10**
10	1073.5084	***1101.5034***	**I**	**1057.5095**	1040.4830	**9**
11	**1210.5674**	***1238.5623***	**H**	**944.4254**	927.3989	**8**
12	**1309.6358**	***1337.6307***	**V**	**807.3665**	790.3400	**7**
13	**1424.6627**	***1452.6576***	**D**	**708.2981**	691.2716	**6**
14	**1523.7311**	***1551.7260***	**V**	**593.2712**	576.2446	**5**
15	1670.7665	***1698.7614***	**M**	494.2028	477.1762	**4**
16	1785.7935	***1813.7884***	**D**	**347.1674**	330.1408	**3**
17	1842.8149	1870.8098	**G**	**232.1404**	215.1139	**2**
18			**R**	**175.1190**	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.0	2043.9143	0.0960	AVEVAGCDWIHVDVMDGR
16.5	2043.9143	0.0960	AVELAGCDWVHVDVMDGR
7.3	2043.9498	0.0606	GATATSEATRDLYDDVFGR
4.2	2043.9585	0.0518	MYGAAYTGEGAAIVPSHHGR
3.5	2044.0517	-0.0414	HTPEQLELLLYDLFEGK
3.2	2044.0953	-0.0850	DDKLVAGALNLIGGDTLFGR
1.6	2044.0751	-0.0647	HVGMAPFVMAALQVVFATR

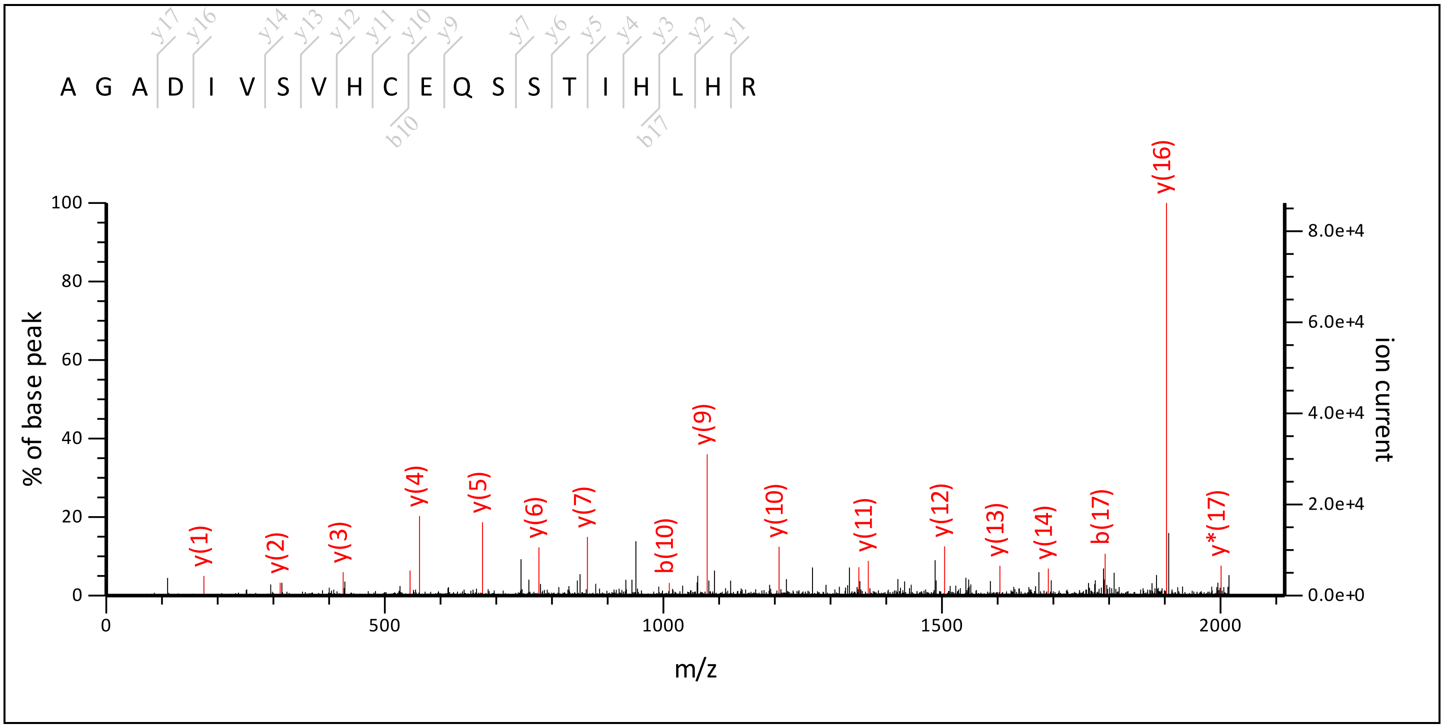
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 29

MS/MS Fragmentation of **AGADIVSVHCEQSSTIHLHR**
Found in **gi|4105561** in **NCBInr**, ribulose-5-phosphate-3-epimerase [Oryza sativa]

Match to Query 106: 2216.185824 from(2217.193100,1+) intensity(0.0000) index(31)
Title: Label: J20, Spot_Id: 219987, Peak_List_Id: 229442, MSMS Job_Run_Id: 22021, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J20_136868359600.txt



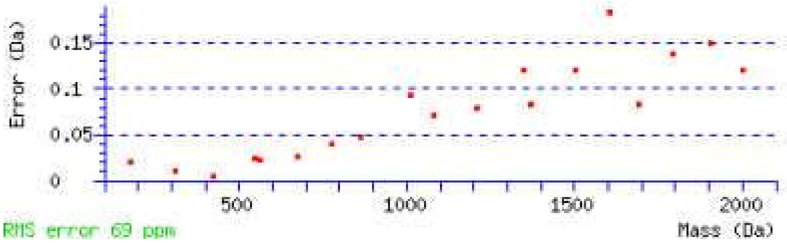
0 to 2115.19

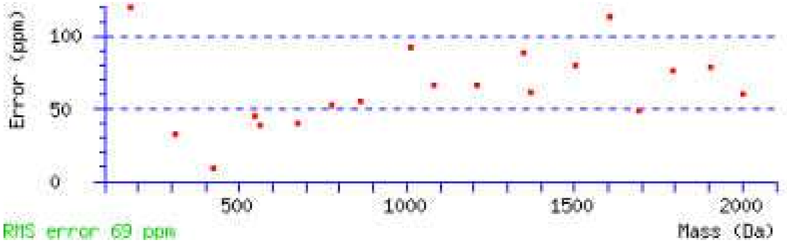
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2216.0757
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 149 **Expect:** 1.7e-12
Matches : 19/92 fragment ions using 20 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			20
2	101.0709		129.0659		G	2146.0458	2129.0193	19
3	172.1081		200.1030		A	2089.0243	2071.9978	18
4	287.1350		315.1299		D	2017.9872	2000.9607	17
5	400.2191		428.2140		I	***1902.9603***	1885.9337	16
6	499.2875		527.2824		V	1789.8762	1772.8497	15
7	586.3195		614.3144		S	***1690.8078***	1673.7813	14
8	685.3879		713.3828		V	***1603.7758***	1586.7492	13

9	822.4468		850.4417		H	1504.7074	1487.6808	12
10	982.4775		1010.4724		C	1367.6485	1350.6219	11
11	1111.5201		1139.5150		E	1207.6178	1190.5913	10
12	1239.5786	1222.5521	1267.5736	1250.5470	Q	1078.5752	1061.5487	9
13	1326.6107	1309.5841	1354.6056	1337.5790	S	950.5166	933.4901	8
14	1413.6427	1396.6162	1441.6376	1424.6111	S	863.4846	846.4581	7
15	1514.6904	1497.6638	1542.6853	1525.6587	T	776.4526	759.4260	6
16	1627.7744	1610.7479	1655.7694	1638.7428	I	675.4049	658.3784	5
17	1764.8334	1747.8068	1792.8283	1775.8017	H	562.3208	545.2943	4
18	1877.9174	1860.8909	1905.9123	1888.8858	L	425.2619	408.2354	3
19	2014.9763	1997.9498	2042.9713	2025.9447	H	312.1779	295.1513	2
20					R	175.1190	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
148.6	2216.0757	0.1102	AGADIVSVHCEQSSTIHLHR
12.5	2216.1524	0.0334	IHGNKLAEMPFIATRPSYR
12.3	2216.0875	0.0983	GTRSTGNPHPIYNFLSYHR
10.5	2216.0929	0.0929	ELIGILNNNPEMSAECKLR
7.5	2216.0202	0.1657	MNYSNIQKVLGCSSTEVDR
4.0	2216.0731	0.1127	VFDIGEMARLCPHEHLHR
3.9	2216.1082	0.0776	GRTFQLTMASLLEMGYQVR
3.9	2216.1082	0.0776	GRTFQLTMASLLEMGYQVR
2.6	2216.1915	-0.0057	YSLVSSKQMVGIFLTIWTK
2.4	2216.0822	0.1037	DAQVALDHLYQRTDIDTSR

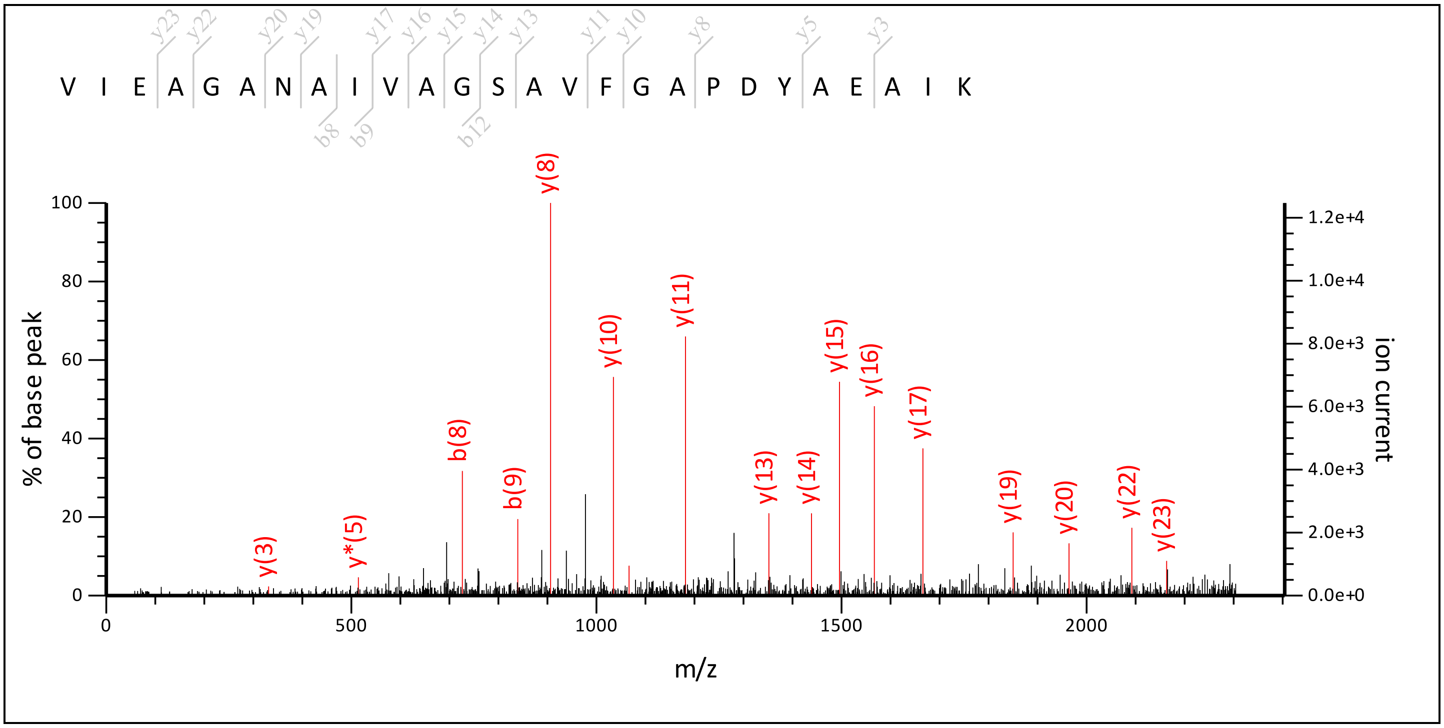
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 29**

MS/MS Fragmentation of **VIEAGANAIVAGSAVFGAPDYAEAIK**
Found in **gi|4105561** in **NCBInr**, ribulose-5-phosphate-3-epimerase [Oryza sativa]

Match to Query 112: 2503.411624 from(2504.418900,1+) intensity(0.0000) index(34)
Title: Label: J20, Spot_Id: 219987, Peak_List_Id: 229447, MSMS Job_Run_Id: 22021, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_J20_136868359600.txt



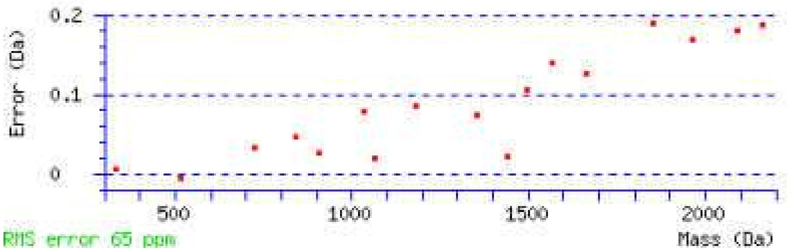
0 to 2404.11

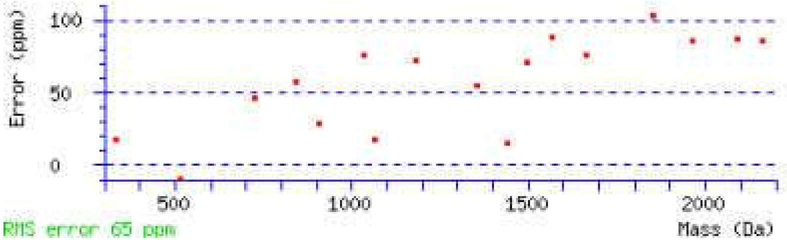
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2503.2958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 102 **Expect:** 5.9e-08
Matches : 17/138 fragment ions using 23 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	72.0808		100.0757		**V**			**26**
2	185.1648		213.1598		**I**	2405.2347	2388.2082	**25**
3	314.2074		342.2023		**E**	2292.1507	2275.1241	**24**
4	385.2445		413.2395		**A**	***2163.1081***	2146.0815	**23**
5	442.2660		470.2609		**G**	***2092.0709***	2075.0444	**22**
6	513.3031		541.2980		**A**	2035.0495	2018.0229	**21**
7	627.3461	610.3195	655.3410	638.3144	**N**	***1964.0124***	1946.9858	**20**
8	698.3832	681.3566	**726.3781**	709.3515	**A**	***1849.9694***	1832.9429	**19**

9	811.4672	794.4407	**839.4621**	822.4356	I	1778.9323	1761.9058	18
10	910.5356	893.5091	938.5306	921.5040	V	***1665.8483***	1648.8217	17
11	981.5728	964.5462	1009.5677	992.5411	A	***1566.7799***	1549.7533	16
12	1038.5942	1021.5677	**1066.5891**	1049.5626	G	***1495.7427***	1478.7162	15
13	1125.6262	1108.5997	1153.6212	1136.5946	S	***1438.7213***	1421.6947	14
14	1196.6634	1179.6368	1224.6583	1207.6317	A	***1351.6892***	1334.6627	13
15	1295.7318	1278.7052	1323.7267	1306.7001	V	1280.6521	1263.6256	12
16	1442.8002	1425.7736	1470.7951	1453.7686	F	***1181.5837***	1164.5572	11
17	1499.8217	1482.7951	1527.8166	1510.7900	G	***1034.5153***	1017.4888	10
18	1570.8588	1553.8322	1598.8537	1581.8271	A	977.4938	960.4673	9
19	1667.9115	1650.8850	1695.9064	1678.8799	P	***906.4567***	889.4302	8
20	1782.9385	1765.9119	1810.9334	1793.9068	D	809.4040	792.3774	7
21	1946.0018	1928.9753	1973.9967	1956.9702	Y	694.3770	677.3505	6
22	2017.0389	2000.0124	2045.0338	2028.0073	A	531.3137	514.2871	5
23	2146.0815	2129.0550	2174.0764	2157.0499	E	460.2766	443.2500	4
24	2217.1186	2200.0921	2245.1135	2228.0870	A	***331.2340***	314.2074	3
25	2330.2027	2313.1761	2358.1976	2341.1711	I	260.1969	243.1703	2
26					K	147.1128	130.0863	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.9	2503.2958	0.1158	VIEAGANAIVAGSAVFGAPDYAEAIK
101.9	2503.2958	0.1158	VIEAGANALVAGSAVFGAPDYAEAIK
11.9	2503.3192	0.0924	LHVPVGGDVAPPPPHMLMLQINR
6.3	2503.3608	0.0508	SPDTLVALIVGVTGMVGFSLAEALK
6.0	2503.2390	0.1726	VSISQENHLGGSNVTAALPWMHR

1.3	2503.3369	0.0747	MQSLQHQLPFTLRPSPLEPLR
1.2	2503.3223	0.0893	LGYVYQDVDIPWLTSKPTPRR
0.2	2503.2410	0.1706	QGITPEIIKELTDCNAMLSSQR
0.0	2503.4373	-0.0257	ITLEVIVLQIDNQIEELLPRR

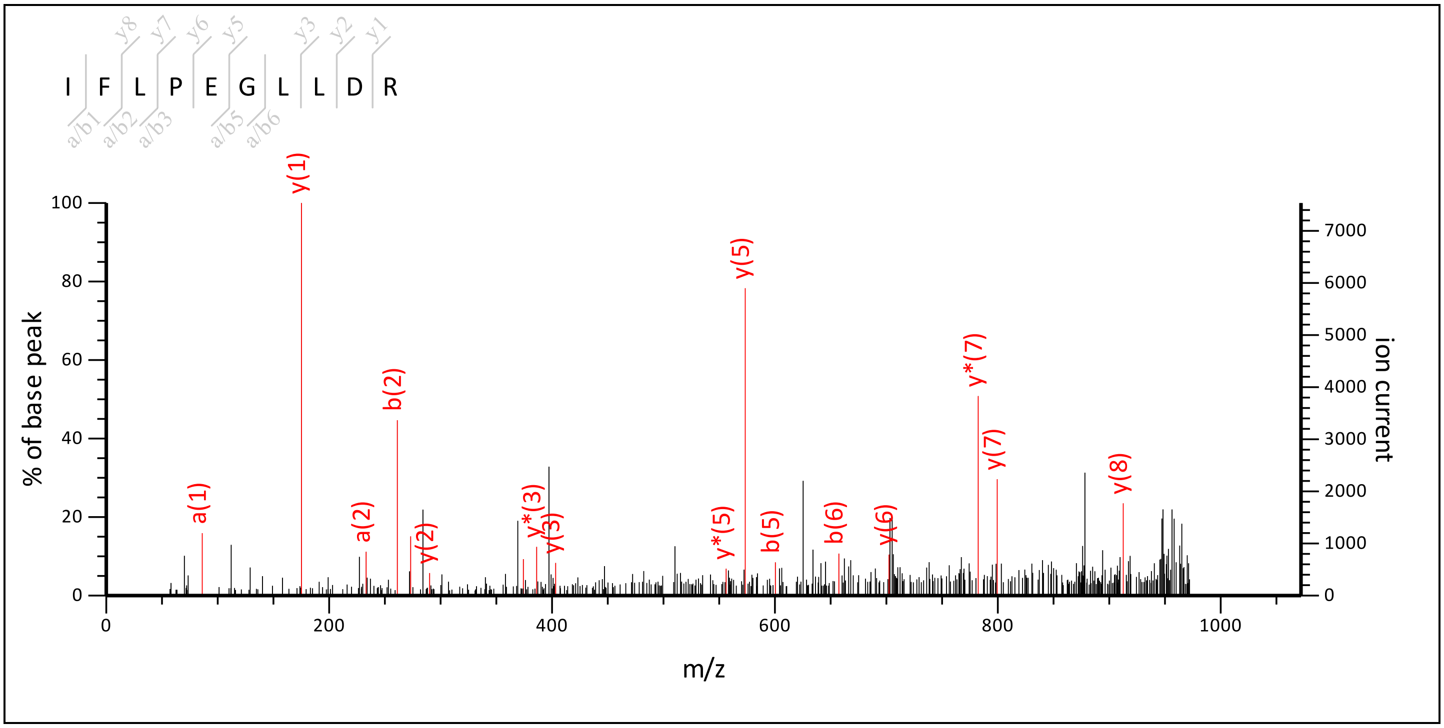
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 30

MS/MS Fragmentation of **IFLPEGLLDR**
Found in **gi|62733870** in **NCBInr**, chlorophyll a/b-binding protein CP26 precursor - maize [Oryza sativa Japonica Group]

Match to Query 120: 1171.732724 from(1172.740000,1+) intensity(0.0000) index(10)
Title: Label: G8, Spot_Id: 219792, Peak_List_Id: 226318, MSMS Job_Run_Id: 21840, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_G8_136859928300.txt



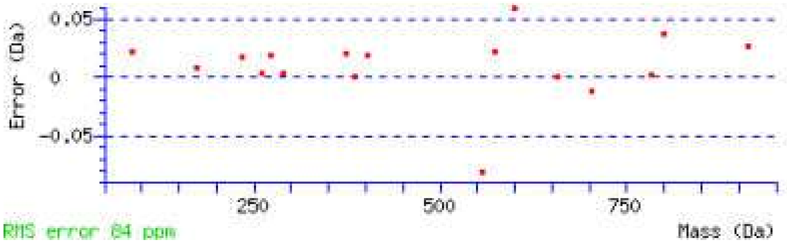
0 to 1072.04

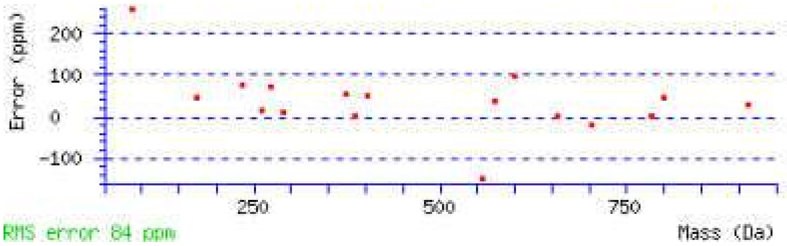
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1171.6601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 50
Matches : 17/36 fragment ions using 50 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	**86.0964**	114.0913	I			10
2	**233.1648**	**261.1598**	F	1059.5833	1042.5568	9
3	346.2489	**374.2438**	L	***912.5149***	895.4884	8
4	443.3017	471.2966	P	***799.4308***	782.4043	7
5	572.3443	**600.3392**	E	***702.3781***	685.3515	6
6	629.3657	**657.3606**	G	***573.3355***	556.3089	5
7	742.4498	770.4447	L	516.3140	499.2875	4
8	855.5339	883.5288	L	***403.2300***	386.2034	3

9	970.5608	998.5557	**D**	***290.1459***	273.1193	**2**
10			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.3	1171.6601	0.0726	IFLPEGLLDR
17.2	1171.7329	-0.0001	LFLLLPLSTR
14.6	1171.7441	-0.0114	LFLLIAGAAKR
13.6	1171.6561	0.0767	IIAATNTNLNK
13.3	1171.6635	0.0693	ILMSLDVLPR
13.2	1171.6423	0.0904	IFLPEPMGLR
13.2	1171.7441	-0.0114	LFILLNGKVR
13.2	1171.7441	-0.0114	LFILLREIR
13.2	1171.6601	0.0726	LFLLIPGDER
13.2	1171.7362	-0.0035	LMLLLLATLR

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

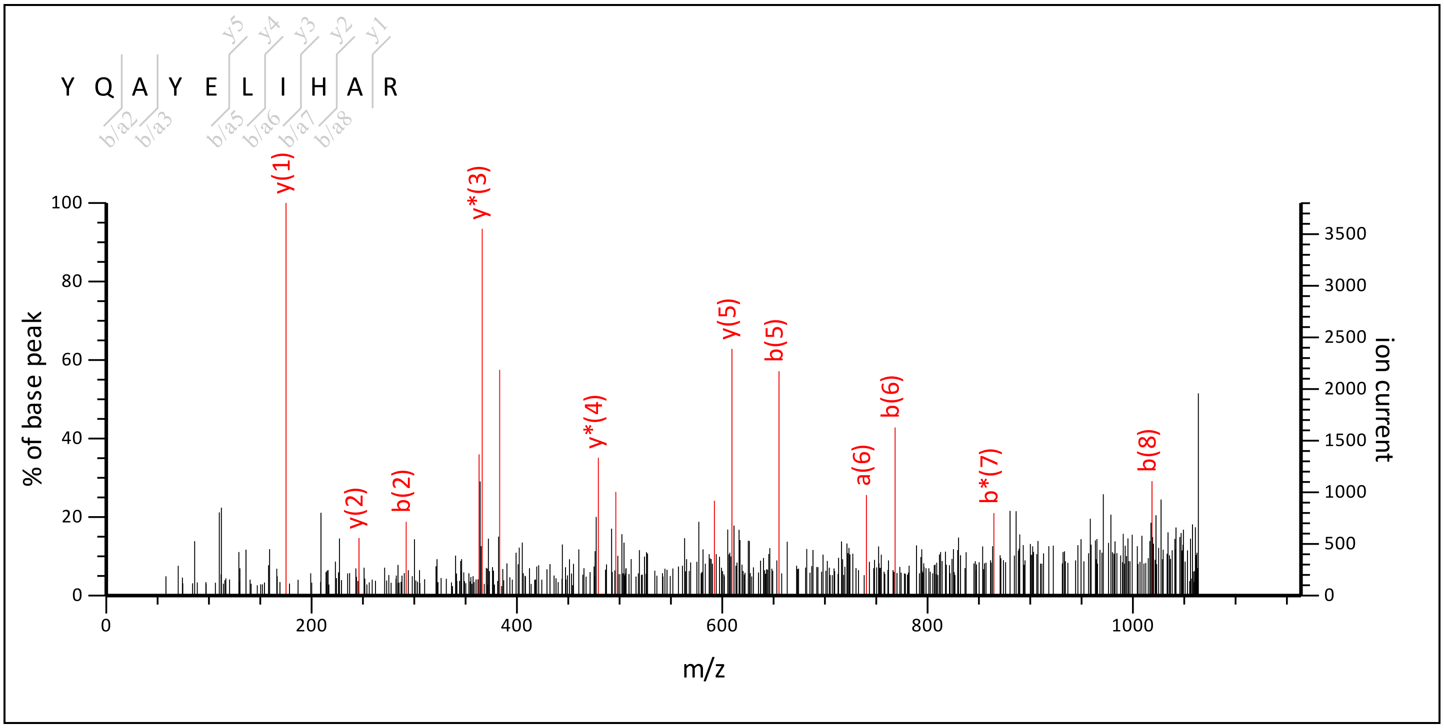
MATRIX SCIENCE

Mascot Search Results

Peptide View Spot no 30

MS/MS Fragmentation of **YQAYELIHAR**
Found in **gi|62733870** in **NCBInr**, chlorophyll a/b-binding protein CP26 precursor - maize [Oryza sativa Japonica Group]

Match to Query 131: 1262.721024 from(1263.728300,1+) intensity(0.0000) index(13)
Title: Label: G8, Spot_Id: 219792, Peak_List_Id: 226319, MSMS Job_Run_Id: 21840, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_G8_136859928300.txt



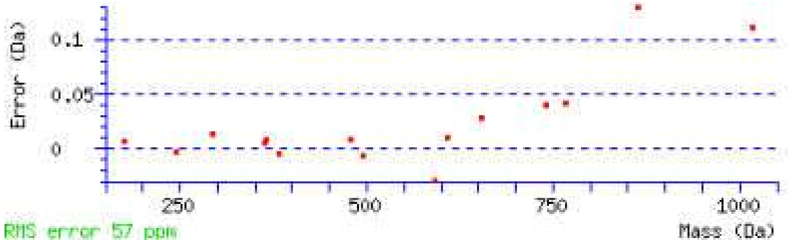
0 to 1163.72

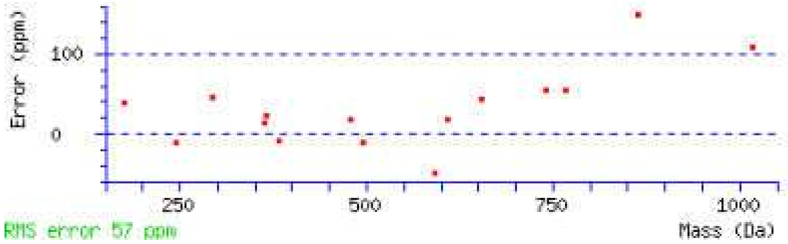
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1262.6407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 1.6e+02
Matches : 15/52 fragment ions using 33 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	136.0757		164.0706		Y			10
2	264.1343	247.1077	***292.1292***	275.1026	Q	1100.5847	1083.5582	9
3	335.1714	318.1448	***363.1663***	346.1397	A	972.5261	955.4996	8
4	498.2347	481.2082	526.2296	509.2031	Y	901.4890	884.4625	7
5	627.2773	610.2508	***655.2722***	638.2457	E	738.4257	721.3992	6
6	740.3614	723.3348	***768.3563***	751.3297	L	***609.3831***	592.3566	5
7	853.4454	836.4189	881.4403	864.4138	I	***496.2990***	479.2725	4
8	990.5043	973.4778	***1018.4993***	1001.4727	H	***383.2150***	366.1884	3

9	1061.5415	1044.5149	1089.5364	1072.5098	**A**	*246.1561*	229.1295	**2**
10					**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.5	1262.6407	0.0803	YQAYELIHAR
17.1	1262.7247	-0.0037	HKEFIIIHAR
17.1	1262.6884	0.0327	HQIFELIHAR
17.1	1262.7207	0.0003	NNVQAKLLHAR
16.1	1262.7247	-0.0037	QHLLYILHAR
15.4	1262.6441	0.0769	LSGSMYLHLAR
15.0	1262.7571	-0.0361	ARVGTAVLHLAR
15.0	1262.7571	-0.0361	GIGRSIALHLAR
14.9	1262.7207	0.0003	AAGVEARLIHAR
14.3	1262.7095	0.0115	LLIEGGANIHAR

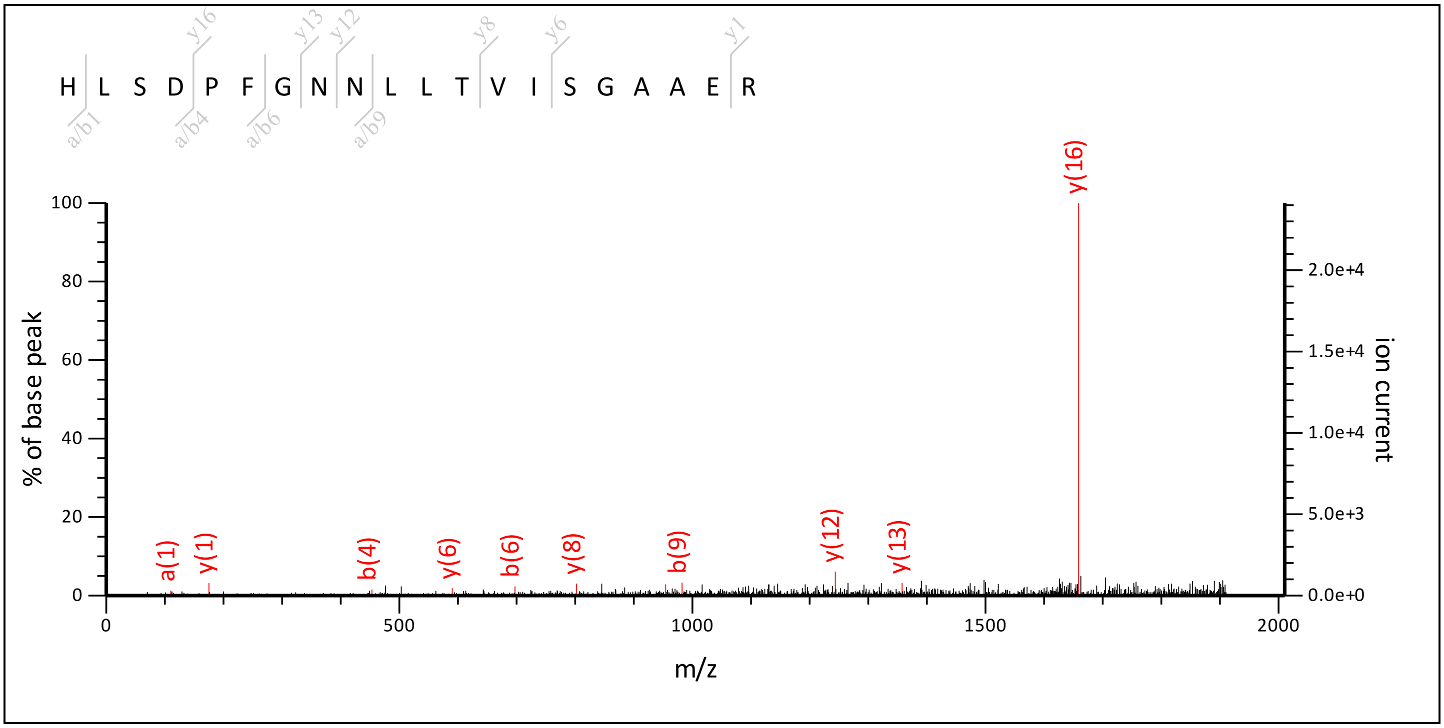
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 30**

MS/MS Fragmentation of **HLSDPFGNNLLTVISGAAER**
Found in **gi|62733870** in **NCBInr**, chlorophyll a/b-binding protein CP26 precursor - maize [Oryza sativa Japonica Group]

Match to Query 251: 2110.183424 from(2111.190700,1+) intensity(0.0000) index(33)
Title: Label: G8, Spot_Id: 219792, Peak_List_Id: 226327, MSMS Job_Run_Id: 21840, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_G8_136859928300.txt



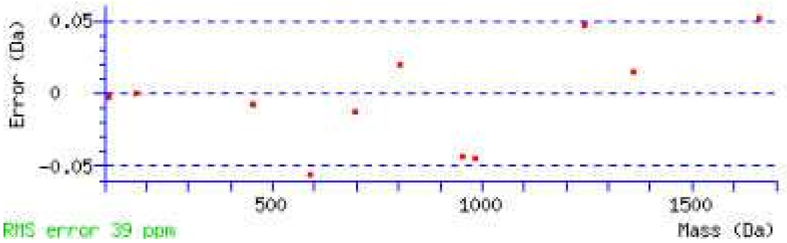
0 to 2010.46

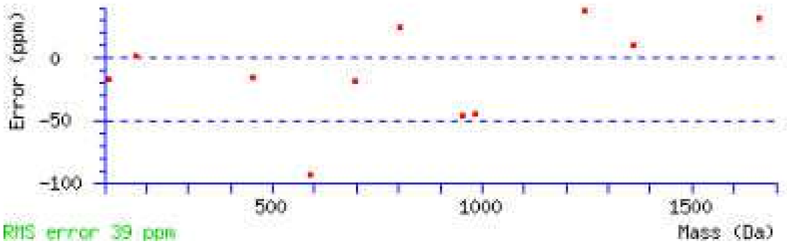
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2110.0807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 26
Matches : 11/100 fragment ions using 19 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**110.0713**		138.0662		**H**			**20**
2	223.1553		251.1503		**L**	1974.0291	1957.0025	**19**
3	310.1874		338.1823		**S**	1860.9450	1843.9185	**18**
4	425.2143		**453.2092**		**D**	1773.9130	1756.8864	**17**
5	522.2671		550.2620		**P**	***1658.8860***	1641.8595	**16**
6	669.3355		**697.3304**		**F**	1561.8333	1544.8067	**15**
7	726.3569		754.3519		**G**	1414.7649	1397.7383	**14**
8	840.3999	823.3733	868.3948	851.3682	**N**	***1357.7434***	1340.7169	**13**

9	**954.4428**	937.4163	**982.4377**	965.4112	**N**	***1243.7005***	1226.6739	**12**
10	1067.5269	1050.5003	1095.5218	1078.4952	**L**	1129.6576	1112.6310	**11**
11	1180.6109	1163.5844	1208.6058	1191.5793	**L**	1016.5735	999.5469	**10**
12	1281.6586	1264.6321	1309.6535	1292.6270	**T**	903.4894	886.4629	**9**
13	1380.7270	1363.7005	1408.7219	1391.6954	**V**	***802.4417***	785.4152	**8**
14	1493.8111	1476.7845	1521.8060	1504.7795	**I**	703.3733	686.3468	**7**
15	1580.8431	1563.8166	1608.8380	1591.8115	**S**	***590.2893***	573.2627	**6**
16	1637.8646	1620.8380	1665.8595	1648.8329	**G**	503.2572	486.2307	**5**
17	1708.9017	1691.8751	1736.8966	1719.8701	**A**	446.2358	429.2092	**4**
18	1779.9388	1762.9123	1807.9337	1790.9072	**A**	375.1987	358.1721	**3**
19	1908.9814	1891.9549	1936.9763	1919.9498	**E**	304.1615	287.1350	**2**
20					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	2110.0807	0.1027	HLSDPFGNNLLTVIAGSAER
28.8	2110.0807	0.1027	HLSDPFGNNLLTVISAGAER
28.8	2110.0807	0.1027	HLSDPFGNNLLTVISGAAER
28.8	2110.0807	0.1027	HLSDPFGNNLLTVLAGSAER
9.2	2110.0192	0.1642	ARQPDWVTASHSLVSEDGR
8.9	2110.0742	0.1092	QHGGNIIVATPGRLEDMFR
6.9	2110.0847	0.0987	ASALELPAASAYRLPFYDR
5.2	2110.0153	0.1681	YSDSMLSEPFSTKAAAHIR
5.0	2110.0551	0.1283	MLQVPGFVASAGAASMLVSSR
5.0	2110.0881	0.0953	LEPLQMTWGTLSPPLGNTR

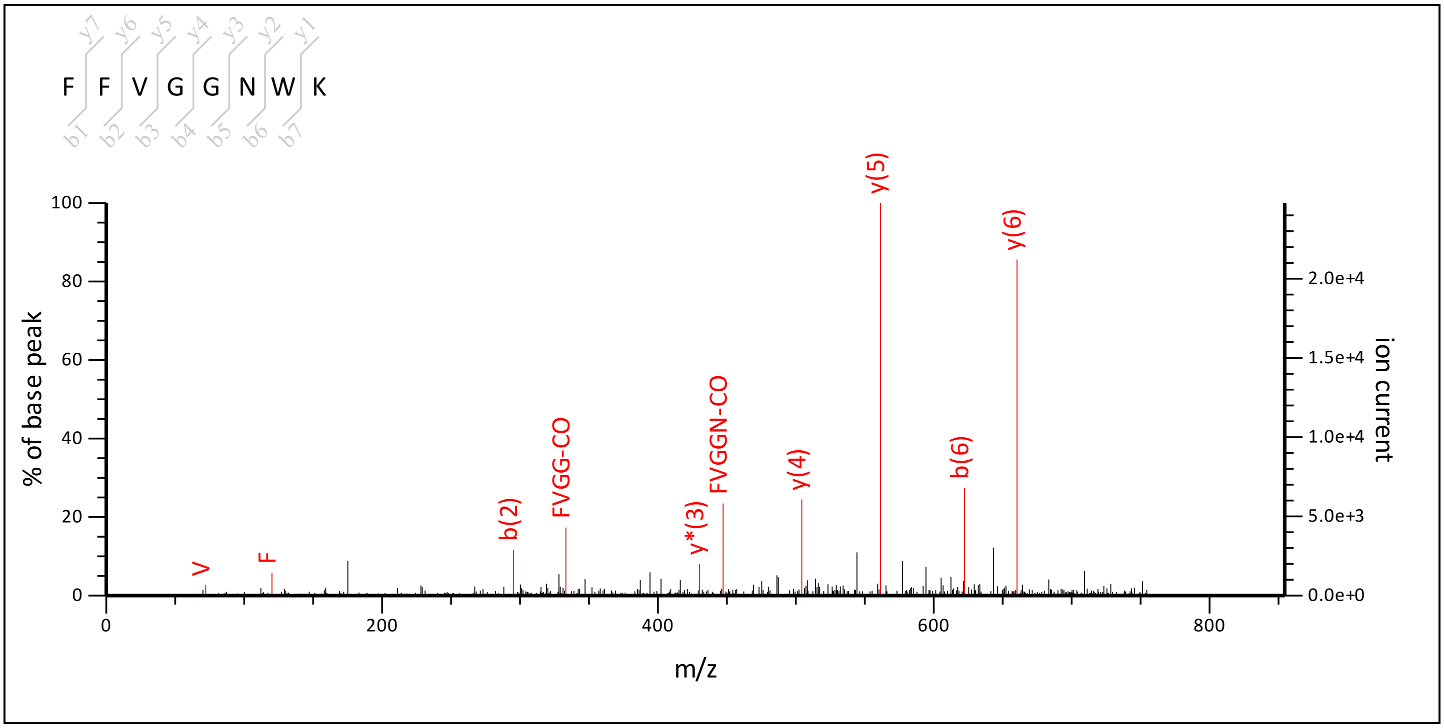
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 32

MS/MS Fragmentation of **FFVGGNWK**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 18: 953.513784 from(954.521060,1+) intensity(0.0000) index(2)
Title: Label: H19, Spot_Id: 219969, Peak_List_Id: 229374, MSMS Job_Run_Id: 22019, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H19_136868348800.txt



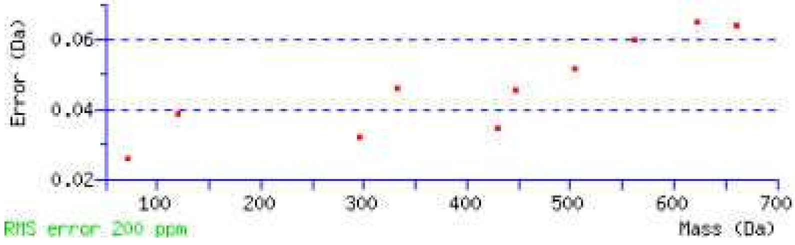
0 to 854.47

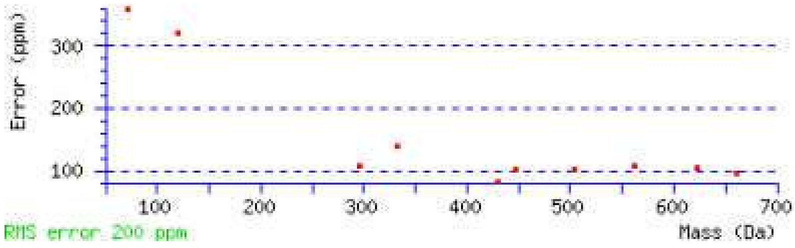
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 953.4760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 3.6
Matches : 14/81 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	120.0808	**120.0808**		148.0757		44.0495	F					8
2	120.0808	267.1492		**295.1441**			F	715.3522		807.4148	790.3883	7
3	72.0808	366.2176		394.2125		352.2020	V	616.2838	629.3042	***660.3464***	643.3198	6
4	30.0338	423.2391		451.2340			G			***561.2780***	544.2514	5
5	30.0338	480.2605		508.2554			G			***504.2565***	487.2300	4
6	87.0553	594.3035	577.2769	**622.2984**	605.2718	551.2976	N	388.1979	387.2027	***447.2350***	430.2085	3
7	159.0917	780.3828	763.3562	808.3777	791.3511		W	202.1186		***333.1921***	316.1656	2
8	101.1073						K	74.0237	73.0284	147.1128	130.0863	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FV	219.1492	247.1441	**FVG**	276.1707	304.1656	**FVGG**	333.1921	361.1870
FVGGN	447.2350	475.2300	**FVGGNW**	633.3144	661.3093	**VG**	129.1022	157.0972
VGG	186.1237	214.1186	**VGGN**	300.1666	328.1615	**VGGNW**	486.2459	514.2409
GG	87.0553	115.0502	**GGN**	201.0982	229.0931	**GGNW**	387.1775	415.1724
GN	144.0768	172.0717	**GNW**	330.1561	358.1510	**NW**	273.1346	301.1295





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.3	953.4760	0.0378	FFVGGNWK
39.3	953.4760	0.0378	FFVGGNWK
39.0	953.4389	0.0749	MFVNSANR
35.4	953.4389	0.0749	VMYGGNASR
34.2	953.5083	0.0055	FFVNGSKR
34.2	953.4641	0.0497	MFVEVASR
30.1	953.4640	0.0497	MYVVESAR
28.9	953.4858	0.0279	FFVDIDAK
28.6	953.4202	0.0935	TYENNSAR
26.2	953.4277	0.0861	FMVGAEER

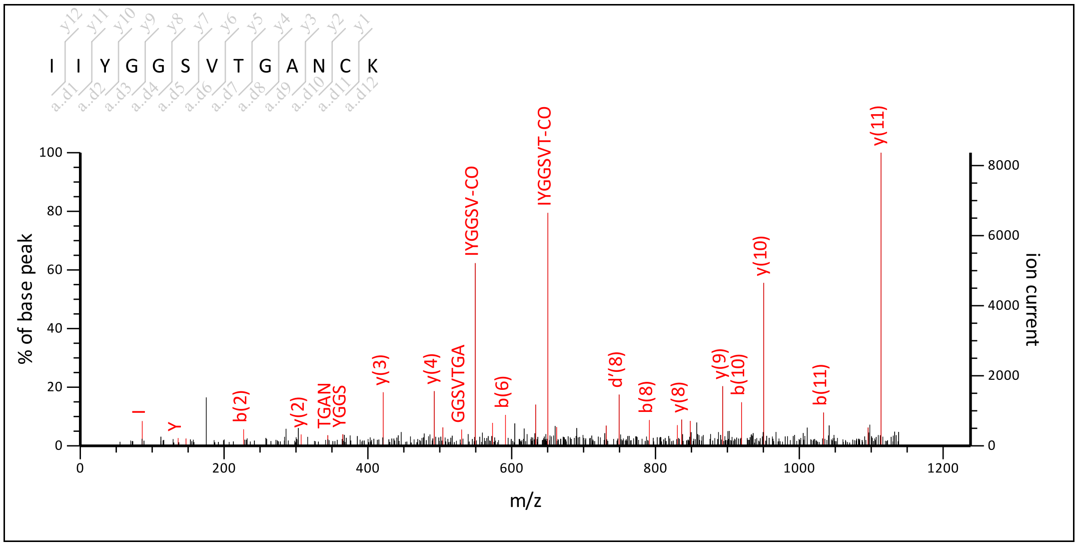
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 32

MS/MS Fragmentation of **IIYGGSVTGANCK**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 81: 1338.724624 from(1339.731900,1+) intensity(0.0000) index(15)
Title: Label: H19, Spot_Id: 219969, Peak_List_Id: 229382, MSMS Job_Run_Id: 22019, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H19_136868348800.txt



0 to 1238.14

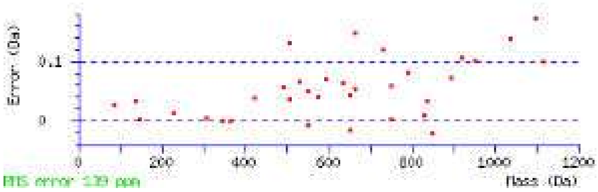
Label all possible matches ○ Label matches used for scoring ●

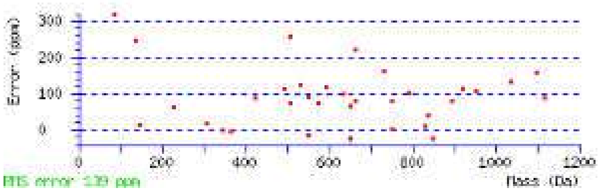
```
Monoisotopic mass of neutral peptide Mr(calc): 1338.6602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 89  Expect: 4e-05
Matches : 37/207 fragment ions using 44 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	**86.0964**			114.0913			44.0495		**I**					
2	86.0964	199.1805			**227.1754**			171.1492	185.1648	**I**	1168.5051	1181.5256	1195.5412	1226.5834	1209.5569
3	136.0757	362.2438			390.2387					**Y**	1005.4418			***1113.4993***	1096.4728
4	30.0338	419.2653			447.2602					**G**				***950.4360***	933.4095
5	30.0338	476.2867			**504.2817**					**G**				***893.4145***	876.3880
6	60.0444	563.3188		545.3082	**591.3137**		573.3031	547.3239		**S**	804.3669	803.3716		***836.3931***	819.3665
7	72.0808	**662.3872**		644.3766	690.3821		672.3715	648.3715		**V**	705.2985	718.3189		***749.3611***	732.3345
8	74.0600	763.4349		745.4243	**791.4298**		773.4192	747.4400	749.4192	**T**	604.2508	617.2712	619.2504	***650.2926***	633.2661
9	30.0338	820.4563		802.4458	**848.4512**		830.4407			**G**				***549.2450***	532.2184
10	44.0495	891.4934		873.4829	**919.4884**		901.4778			**A**	476.1922			***492.2235***	475.1969
11	87.0553	1005.5364	988.5098	987.5258	**1033.5313**	1016.5047	1015.5207	962.5306		**N**	362.1493	361.1540		***421.1864***	404.1598
12	133.0430	1165.5670	1148.5405	1147.5565	1193.5619	1176.5354	1175.5514	1076.5735		**C**	202.1186	201.1234		***307.1435***	290.1169
13	101.1073									**K**	74.0237	73.0284		***147.1128***	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IY	249.1598	277.1547	**IYG**	306.1812	334.1761	**IYGG**	363.2027	391.1976
IYGGS	450.2347	478.2296	**IYGGSV**	549.3031	577.2980	**IYGGSVT**	650.3508	678.3457
YG	193.0972	221.0921	**YGG**	250.1186	278.1135	**YGGS**	337.1506	365.1456
YGGSV	436.2191	464.2140	**YGGSVT**	537.2667	565.2617	**YGGSVTG**	594.2882	622.2831
YGGSVTGA	665.3253	693.3202	**GG**	87.0553	115.0502	**GGS**	174.0873	202.0822
GGSV	273.1557	301.1506	**GGSVT**	374.2034	402.1983	**GGSVTG**	431.2249	459.2198
GGSVTGA	502.2620	530.2569	**GGSVTGAN**	616.3049	644.2998	**GS**	117.0659	145.0608
GSV	216.1343	244.1292	**GSVT**	317.1819	345.1769	**GSVTG**	374.2034	402.1983

GSVTGA	445.2405	473.2354	**GSVTGAN**	559.2835	587.2784	**SV**	159.1128	187.1077
SVT	260.1605	288.1554	**SVTG**	317.1819	345.1769	**SVTGA**	388.2191	416.2140
SVTGAN	502.2620	530.2569	**SVTGANC**	662.2926	690.2876	**VT**	173.1285	201.1234
VTG	230.1499	258.1448	**VTGA**	301.1870	329.1819	**VTGAN**	415.2300	443.2249
VTGANC	575.2606	603.2555	**TG**	131.0815	159.0764	**TGA**	202.1186	230.1135
TGAN	316.1615	344.1565	**TGANC**	476.1922	504.1871	**GA**	101.0709	129.0659
GAN	215.1139	243.1088	**GANC**	375.1445	403.1394	**AN**	158.0924	186.0873
ANC	318.1231	346.1180	**NC**	247.0859	275.0809			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
89.1	1338.6602	0.0644	IIYGGSVTGANCK
89.1	1338.6602	0.0644	ILYGGSVTGANCK
77.7	1338.6602	0.0644	IIYGGSVTAGNCK
77.7	1338.6602	0.0644	ILYGGSVTAGNCK
76.2	1338.6602	0.0645	IIYGGSVSAANCK
76.2	1338.6602	0.0645	ILYGGSVSAANCK
32.8	1338.6714	0.0532	MLENSPHVIQR
30.5	1338.6932	0.0314	IYHYTVNSSKK
29.9	1338.7296	-0.0049	LNYLGETKFVR
29.5	1338.6833	0.0413	NQFNWSIFKR

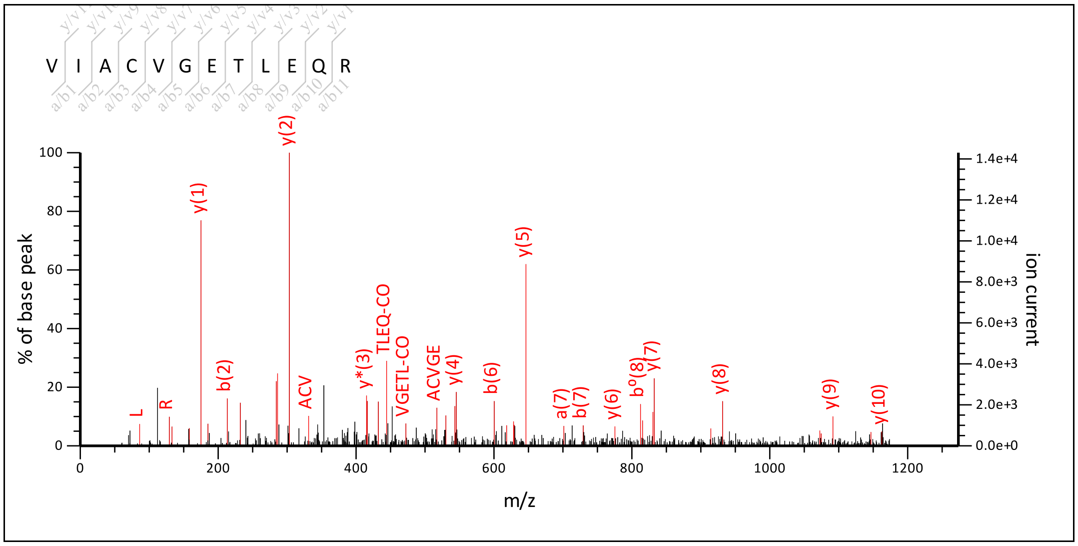
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 32

MS/MS Fragmentation of **VIACVGETLEQR**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 87: 1373.778124 from(1374.785400,1+) intensity(0.0000) index(16)
Title: Label: H19, Spot_Id: 219969, Peak_List_Id: 229376, MSMS Job_Run_Id: 22019, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H19_136868348800.txt



0 to 1273.56

Label all possible matches ○ Label matches used for scoring ●

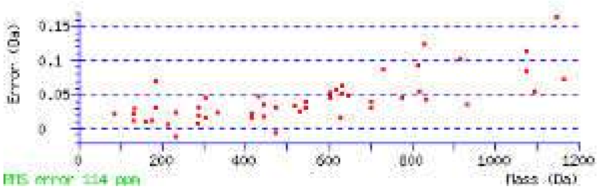
Monoisotopic mass of neutral peptide Mr(calc): 1373.6973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 0.0018
Matches : 53/179 fragment ions using 60 most intense peaks (help)

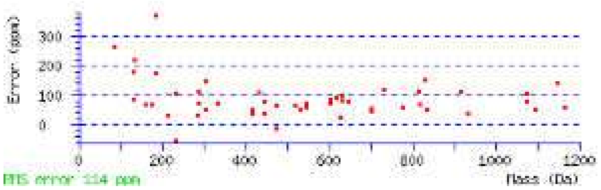
#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		**V**					
2	86.0964	**185.1648**			**213.1598**			157.1335	171.1492	**I**	1217.5579	1230.5783	1244.5940	1275.6362	1258.6096
3	44.0495	256.2020			**284.1969**					**A**	1146.5208			***1162.5521***	1145.5256
4	133.0430	**416.2326**			**444.2275**			327.2391		**C**	986.4902	985.4949		***1091.5150***	1074.4884
5	72.0808	515.3010			**543.2959**			501.2854		**V**	887.4217	900.4421		***931.4843***	914.4578
6	30.0338	572.3225			**600.3174**					**G**				***832.4159***	815.3894
7	102.0550	**701.3651**		683.3545	**729.3600**		711.3494	643.3596		**E**	701.3577	700.3624		***775.3945***	758.3679
8	74.0600	802.4128		784.4022	**830.4077**		812.3971	786.4178	788.3971	**T**	600.3100	613.3304	615.3097	***646.3519***	629.3253
9	86.0964	915.4968		897.4863	943.4917		925.4812	873.4499		**L**	487.2259	486.2307		***545.3042***	528.2776
10	102.0550	1044.5394		1026.5288	**1072.5343**		1054.5238	986.5339		**E**	358.1833	357.1881		***432.2201***	415.1936
11	101.0709	1172.5980	1155.5714	1154.5874	1200.5929	1183.5664	1182.5823	1115.5765		**Q**	230.1248	229.1295		***303.1775***	286.1510
12	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IA	157.1335	185.1285	**IAC**	317.1642	345.1591	**IACV**	416.2326	444.2275
IACVG	473.2541	501.2490	**IACVGE**	602.2967	630.2916	**AC**	204.0801	232.0750
ACV	303.1485	331.1435	**ACVG**	360.1700	388.1649	**ACVGE**	489.2126	517.2075
ACVGET	590.2603	618.2552	**CV**	232.1114	260.1063	**CVG**	289.1329	317.1278
CVGE	418.1755	446.1704	**CVGET**	519.2232	547.2181	**CVGETL**	632.3072	660.3021
VG	129.1022	157.0972	**VGE**	258.1448	286.1397	**VGET**	359.1925	387.1874
VGETL	472.2766	500.2715	**VGETLE**	601.3192	629.3141	**GE**	159.0764	187.0713
GET	260.1241	288.1190	**GETL**	373.2082	401.2031	**GETLE**	502.2508	530.2457
GETLEQ	630.3093	658.3042	**ET**	203.1026	231.0975	**ETL**	316.1867	344.1816

]

ETLE	445.2293	473.2242	**ETLEQ**	573.2879	601.2828	**TL**	187.1441	215.1390
TLE	316.1867	344.1816	**TLEQ**	444.2453	472.2402	**LE**	215.1390	243.1339
LEQ	343.1976	371.1925	**EQ**	230.1135	258.1084			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.3	1373.6973	0.0808	VIACVGETLEQR
58.4	1373.6973	0.0808	VIACVGETLQER
48.9	1373.6722	0.1060	VGGDDVMREQLR
48.0	1373.6973	0.0808	GPGSMVTIAEIAGR
46.5	1373.7085	0.0696	LTNDVMERLAGR
42.5	1373.7489	0.0292	IETAGAWMVLKR
42.5	1373.7085	0.0696	ENGLEGMLARIR
42.2	1373.6787	0.0995	ETTNVDDLAQLR
42.0	1373.7262	0.0519	LTASAAERSALER
40.2	1373.7514	0.0267	LTASAVLSAGITDR

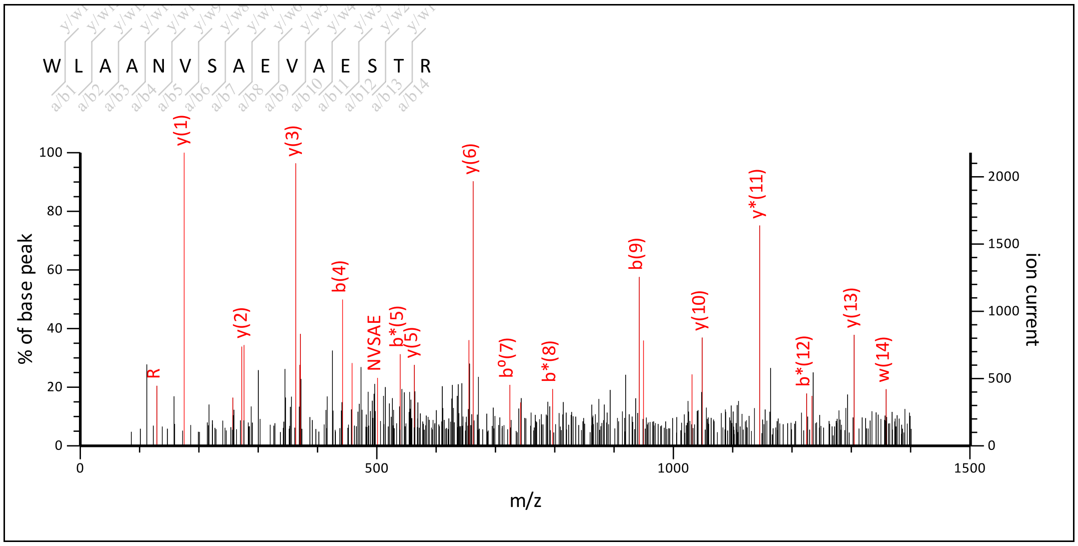
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 32

MS/MS Fragmentation of **WLAANVSAEVAESTR**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 121: 1602.898224 from(1603.905500,1+) intensity(0.0000) index(25)
Title: Label: H19, Spot_Id: 219969, Peak_List_Id: 229381, MSMS Job_Run_Id: 22019, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H19_136868348800.txt



0 to 1501.03

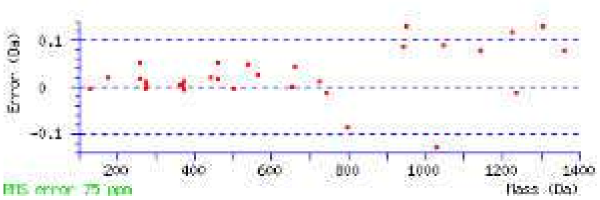
Label all possible matches ○ Label matches used for scoring ●

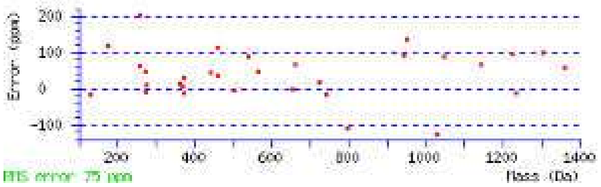
```
Monoisotopic mass of neutral peptide Mr(calc): 1602.8002
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 0.045
Matches : 33/270 fragment ions using 42 most intense peaks   (help)
```

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	159.0917	159.0917			187.0866			44.0495		W						
2	86.0964	272.1757			300.1707			230.1288		L	1359.6499	1358.6546		1417.7281	1400.7016	139
3	44.0495	343.2129			**371.2078**					A	1288.6128			***1304.6441***	1287.6175	128
4	44.0495	414.2500			**442.2449**					A	1217.5757			***1233.6070***	1216.5804	12
5	87.0553	528.2929	511.2663		556.2878	539.2613		485.2871		N	1103.5327	1102.5375		1162.5699	1145.5433	114
6	72.0808	627.3613	610.3348		**655.3562**	638.3297		613.3457		V	1004.4643	1017.4847		***1048.5269***	1031.5004	103
7	60.0444	714.3933	697.3668	696.3828	**742.3882**	725.3617	724.3777	698.3984		S	917.4323	916.4371		***949.4585***	932.4320	93
8	44.0495	785.4304	768.4039	767.4199	813.4254	796.3988	795.4148			A	846.3952			862.4265	845.3999	84
9	102.0550	914.4730	897.4465	896.4625	**942.4680**	925.4414	924.4574	856.4676		E	717.3526	716.3573		791.3894	774.3628	77
10	72.0808	1013.5415	996.5149	995.5309	1041.5364	1024.5098	1023.5258	999.5258		V	618.2842	631.3046		***662.3468***	645.3202	64
11	44.0495	1084.5786	1067.5520	1066.5680	1112.5735	1095.5469	1094.5629			A	547.2471			***563.2784***	546.2518	54
12	102.0550	1213.6212	1196.5946	1195.6106	1241.6161	1224.5895	1223.6055	1155.6157		E	418.2045	417.2092		492.2413	475.2147	47
13	60.0444	1300.6532	1283.6266	1282.6426	1328.6481	1311.6216	1310.6375	1284.6583		S	331.1724	330.1772		***363.1987***	346.1721	34
14	74.0600	1401.7009	1384.6743	1383.6903	1429.6958	1412.6692	1411.6852	1385.7060	1387.6852	T	230.1248	243.1452	245.1244	***276.1666***	259.1401	25
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LA	157.1335	185.1285	LAA	228.1707	256.1656	LAAN	342.2136	370.2085
LAANV	441.2820	469.2769	LAANVS	528.3140	556.3089	LAANVSA	599.3511	627.3461
AA	115.0866	143.0815	AAN	229.1295	257.1244	AANV	328.1979	356.1928
AANVS	415.2300	443.2249	AANVSA	486.2671	514.2620	AANVSAE	615.3097	643.3046
AN	158.0924	186.0873	ANV	257.1608	285.1557	ANVS	344.1928	372.1878
ANVSA	415.2300	443.2249	ANVSAE	544.2726	572.2675	ANVSAEV	643.3410	671.3359

NV	186.1237	214.1186	**NVS**	273.1557	301.1506	**NVSA**	344.1928	372.1878
NVSAE	473.2354	501.2304	**NVSAEV**	572.3039	600.2988	**NVSAEVA**	643.3410	671.3359
VS	159.1128	187.1077	**VSA**	230.1499	258.1448	**VSAE**	359.1925	387.1874
VSAEV	458.2609	486.2558	**VSAEVA**	529.2980	557.2930	**VSAEVAE**	658.3406	686.3355
SA	131.0815	159.0764	**SAE**	260.1241	288.1190	**SAEV**	359.1925	387.1874
SAEVA	430.2296	458.2245	**SAEVAE**	559.2722	587.2671	**SAEVAES**	646.3042	674.2992
AE	173.0921	201.0870	**AEV**	272.1605	300.1554	**AEVA**	343.1976	371.1925
AEVAE	472.2402	500.2351	**AEVAES**	559.2722	587.2671	**AEVAEST**	660.3199	688.3148
EV	201.1234	229.1183	**EVA**	272.1605	300.1554	**EVAE**	401.2031	429.1980
EVAES	488.2351	516.2300	**EVAEST**	589.2828	617.2777	**VA**	143.1179	171.1128
VAE	272.1605	300.1554	**VAES**	359.1925	387.1874	**VAEST**	460.2402	488.2351
AE	173.0921	201.0870	**AES**	260.1241	288.1190	**AEST**	361.1718	389.1667
ES	189.0870	217.0819	**EST**	290.1347	318.1296	**ST**	161.0921	189.0870





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.0	1602.8002	0.0981	WLAANVSAEVAESTR
24.7	1602.8399	0.0583	KSNILVSAEDMQLR
20.6	1602.8213	0.0769	TVVVGGDISNPTTSTR
20.6	1602.8994	-0.0012	VATPAAPRPGFPAVPR
20.4	1602.7962	0.1021	ARADAATSPTTPTSTR
20.4	1602.7784	0.1199	TRSPNDAAEMAALTR
18.9	1602.8253	0.0729	VVPYVTEPGAEVSTR
18.3	1602.8626	0.0356	MVVLPSWICLLTR
17.8	1602.8114	0.0868	AQYEVADSAIPARGR
17.3	1602.7534	0.1448	MSSAVDGFMKYVPR

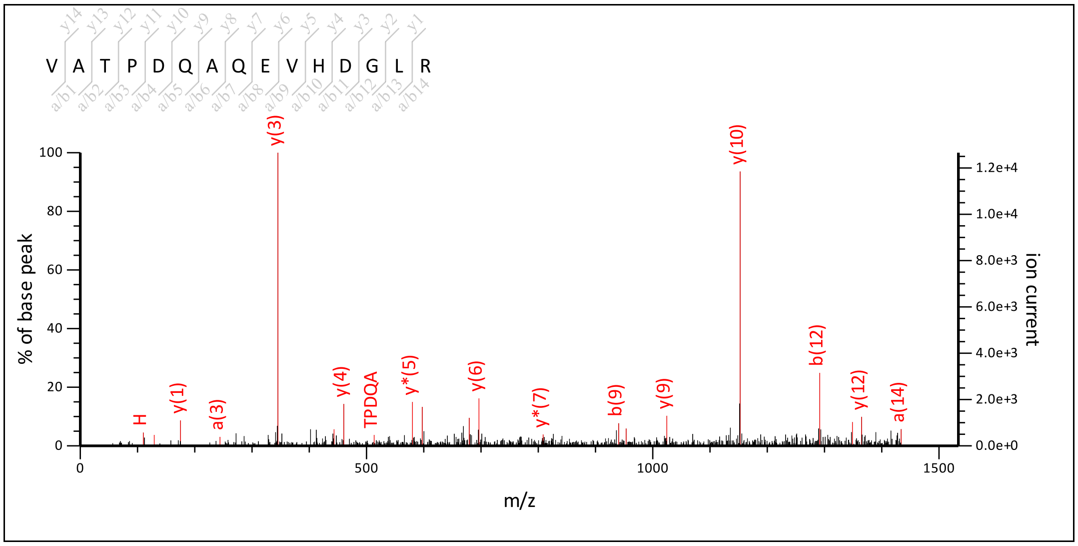
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 32

MS/MS Fragmentation of **VATPDQAQEVHDGLR**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 125: 1634.902224 from(1635.909500,1+) intensity(0.0000) index(26)
Title: Label: H19, Spot_Id: 219969, Peak_List_Id: 229380, MSMS Job_Run_Id: 22019, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H19_136868348800.txt



0 to 1533.87

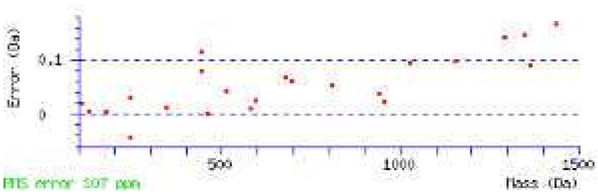
Label all possible matches ○ Label matches used for scoring ●

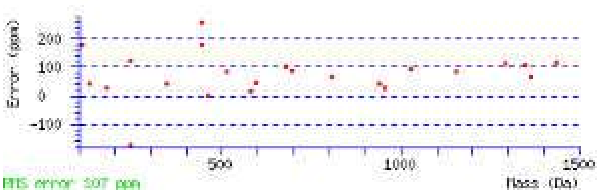
Monoisotopic mass of neutral peptide Mr(calc): 1634.8013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 0.0022
Matches : 24/260 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	44.0495	143.1179			171.1128					A	1520.7088			1536.7401	1519.7136
3	74.0600	**244.1656**		226.1550	272.1605		254.1499	228.1707	230.1499	T	1419.6611	1432.6815	1434.6608	1465.7030	1448.6764
4	70.0651	341.2183		323.2078	369.2132		351.2027	315.2027		P	1322.6084	1321.6131		***1364.6553***	1347.6288
5	88.0393	456.2453		438.2347	484.2402		466.2296	412.2554		D	1207.5814	1206.5862		1267.6026	1250.5760
6	101.0709	584.3039	567.2773	566.2933	612.2988	595.2722	594.2882	527.2824		Q	1079.5228	1078.5276		***1152.5756***	1135.5491
7	44.0495	655.3410	638.3144	637.3304	683.3359	666.3093	665.3253			A	1008.4857			***1024.5170***	1007.4905
8	101.0709	783.3995	766.3730	765.3890	811.3945	794.3679	793.3839	726.3781		Q	880.4272	879.4319		***953.4799***	936.4534
9	102.0550	912.4421	895.4156	894.4316	**940.4371**	923.4105	922.4265	854.4367		E	751.3846	750.3893		825.4213	808.3948
10	72.0808	1011.5106	994.4840	993.5000	1039.5055	1022.4789	1021.4949	997.4949		V	652.3161	665.3365		***696.3787***	679.3522
11	110.0713	1148.5695	1131.5429	1130.5589	1176.5644	1159.5378	1158.5538			H	515.2572			***597.3103***	580.2838
12	88.0393	1263.5964	1246.5699	1245.5858	**1291.5913**	1274.5648	1273.5808	1219.6066		D	400.2303	399.2350		***460.2514***	443.2249
13	30.0338	1320.6179	1303.5913	1302.6073	**1348.6128**	1331.5862	1330.6022			G				***345.2245***	328.1979
14	86.0964	**1433.7019**	1416.6754	1415.6914	1461.6969	1444.6703	1443.6863	1391.6550		L	230.1248	229.1295		288.2030	271.1765
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AT	145.0972	173.0921	**ATP**	242.1499	270.1448	**ATPD**	357.1769	385.1718
ATPDQ	485.2354	513.2304	**ATPDQA**	556.2726	584.2675	**ATPDQAQ**	684.3311	712.3260
TP	171.1128	199.1077	**TPD**	286.1397	314.1347	**TPDQ**	414.1983	442.1932
TPDQA	485.2354	513.2304	**TPDQAQ**	613.2940	641.2889	**PD**	185.0921	213.0870
PDQ	313.1506	341.1456	**PDQA**	384.1878	412.1827	**PDQAQ**	512.2463	540.2413
PDQAQE	641.2889	669.2838	**DQ**	216.0979	244.0928	**DQA**	287.1350	315.1299

DQAQ	415.1936	443.1885	**DQAQE**	544.2362	572.2311	**DQAQEV**	643.3046	671.2995
QA	172.1081	200.1030	**QAQ**	300.1666	328.1615	**QAQE**	429.2092	457.2041
QAQEV	528.2776	556.2726	**QAQEVH**	665.3366	693.3315	**AQ**	172.1081	200.1030
AQE	301.1506	329.1456	**AQEV**	400.2191	428.2140	**AQEVH**	537.2780	565.2729
AQEVHD	652.3049	680.2998	**QE**	230.1135	258.1084	**QEV**	329.1819	357.1769
QEVH	466.2409	494.2358	**QEVHD**	581.2678	609.2627	**QEVHDG**	638.2893	666.2842
EV	201.1234	229.1183	**EVH**	338.1823	366.1772	**EVHD**	453.2092	481.2041
EVHDG	510.2307	538.2256	**EVHDGL**	623.3148	651.3097	**VH**	209.1397	237.1346
VHD	324.1666	352.1615	**VHDG**	381.1881	409.1830	**VHDGL**	494.2722	522.2671
HD	225.0982	253.0931	**HDG**	282.1197	310.1146	**HDGL**	395.2037	423.1987
DG	145.0608	173.0557	**DGL**	258.1448	286.1397	**GL**	143.1179	171.1128





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.2	1634.8013	0.1010	VATPDQAQEVHDGLR
27.3	1634.8601	0.0421	QLNQQGLTRHDLGR
26.5	1634.8264	0.0758	RDIVDDLTYEAGIR
26.3	1634.8740	0.0282	RDIVDHVIDDLVAR
26.3	1634.8814	0.0208	DRLVVEMLYATGIR
26.1	1634.8297	0.0725	IASLVISKDENGMSR
25.6	1634.9832	-0.0810	RDVAIVGTGVVLAPIR
25.5	1634.9104	-0.0082	AVSSPDLRPSALIGPR
25.5	1634.8125	0.0897	RDTGFDSTATVGRPR
25.4	1634.9355	-0.0333	ISAPPKDNLILEGIR

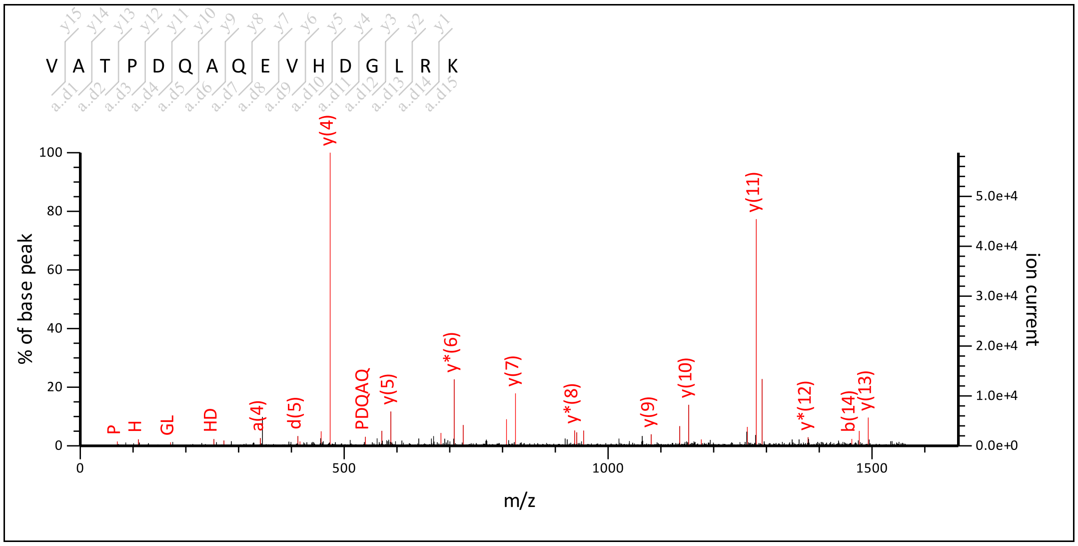
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 32

MS/MS Fragmentation of **VATPDQAQEVHDGLRK**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 137: 1763.004524 from(1764.011800,1+) intensity(0.0000) index(29)
Title: Label: H19, Spot_Id: 219969, Peak_List_Id: 229373, MSMS Job_Run_Id: 22019, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H19_136868348800.txt



0 to 1663.64

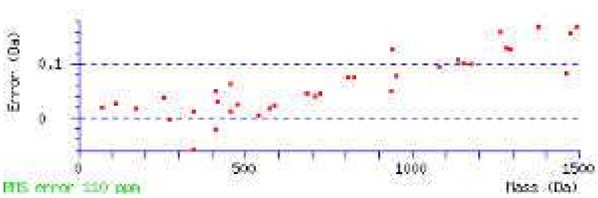
Label all possible matches ○ Label matches used for scoring ●

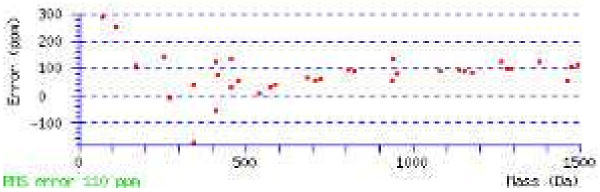
Monoisotopic mass of neutral peptide Mr(calc): 1762.8962
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 0.0029
Matches : 37/282 fragment ions using 48 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	44.0495	143.1179			**171.1128**					A	1648.8038			1664.8351	1647.8085
3	74.0600	244.1656		226.1550	**272.1605**		254.1499	228.1707	230.1499	T	1547.7561	1560.7765	1562.7558	1593.7980	1576.7714
4	70.0651	**341.2183**		323.2078	369.2132		351.2027	315.2027		P	1450.7033	1449.7081		***1492.7503***	1475.7237
5	88.0393	**456.2453**		438.2347	484.2402		466.2296	412.2554		D	1335.6764	1334.6811		1395.6975	1378.6710
6	101.0709	584.3039	567.2773	566.2933	612.2988	595.2722	594.2882	527.2824		Q	1207.6178	1206.6226		***1280.6706***	1263.6440
7	44.0495	655.3410	638.3144	637.3304	**683.3359**	666.3093	665.3253			A	1136.5807			***1152.6120***	1135.5854
8	101.0709	783.3995	766.3730	765.3890	811.3945	794.3679	793.3839	726.3781		Q	1008.5221	1007.5269		***1081.5749***	1064.5483
9	102.0550	912.4421	895.4156	894.4316	**940.4371**	923.4105	922.4265	854.4367		E	879.4795	878.4843		***953.5163***	936.4898
10	72.0808	1011.5106	994.4840	993.5000	1039.5055	1022.4789	1021.4949	997.4949		V	780.4111	793.4315		***824.4737***	807.4472
11	110.0713	1148.5695	1131.5429	1130.5589	**1176.5644**	1159.5378	1158.5538			H	643.3522			***725.4053***	708.3787
12	88.0393	1263.5964	1246.5699	1245.5858	**1291.5913**	1274.5648	1273.5808	1219.6066		D	528.3253	527.3300		***588.3464***	571.3198
13	30.0338	1320.6179	1303.5913	1302.6073	1348.6128	1331.5862	1330.6022			G				***473.3194***	456.2929
14	86.0964	1433.7019	1416.6754	1415.6914	**1461.6969**	1444.6703	1443.6863	1391.6550		L	358.2197	357.2245		***416.2980***	399.2714
15	129.1135	1589.8030	1572.7765	1571.7925	1617.7980	1600.7714	1599.7874	1504.7390		R	202.1186	201.1234		303.2139	286.1874
16	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AT	145.0972	173.0921	ATP	242.1499	270.1448	ATPD	357.1769	385.1718
ATPDQ	485.2354	513.2304	ATPDQA	556.2726	584.2675	ATPDQAQ	684.3311	712.3260
TP	171.1128	199.1077	TPD	286.1397	314.1347	TPDQ	414.1983	442.1932
TPDQA	485.2354	513.2304	TPDQAQ	613.2940	641.2889	PD	185.0921	213.0870
PDQ	313.1506	341.1456	PDQA	384.1878	412.1827	PDQAQ	512.2463	540.2413

PDQAQE	641.2889	669.2838	**DQ**	216.0979	244.0928	**DQA**	287.1350	315.1299
DQAQ	415.1936	443.1885	**DQAQE**	544.2362	572.2311	**DQAQEV**	643.3046	671.2995
QA	172.1081	200.1030	**QAQ**	300.1666	328.1615	**QAQE**	429.2092	457.2041
QAQEV	528.2776	556.2726	**QAQEVH**	665.3366	693.3315	**AQ**	172.1081	200.1030
AQE	301.1506	329.1456	**AQEV**	400.2191	428.2140	**AQEVH**	537.2780	565.2729
AQEVHD	652.3049	680.2998	**QE**	230.1135	258.1084	**QEV**	329.1819	357.1769
QEVH	466.2409	494.2358	**QEVHD**	581.2678	609.2627	**QEVHDG**	638.2893	666.2842
EV	201.1234	229.1183	**EVH**	338.1823	366.1772	**EVHD**	453.2092	481.2041
EVHDG	510.2307	538.2256	**EVHDGL**	623.3148	651.3097	**VH**	209.1397	237.1346
VHD	324.1666	352.1615	**VHDG**	381.1881	409.1830	**VHDGL**	494.2722	522.2671
VHDGLR	650.3733	678.3682	**HD**	225.0982	253.0931	**HDG**	282.1197	310.1146
HDGL	395.2037	423.1987	**HDGLR**	551.3049	579.2998	**DG**	145.0608	173.0557
DGL	258.1448	286.1397	**DGLR**	414.2459	442.2409	**GL**	143.1179	171.1128
GLR	299.2190	327.2139	**LR**	242.1975	270.1925			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.1	1762.8962	0.1083	VATPDQAQEVHDGLRK
32.3	1762.9074	0.0971	RPTEAQQEDRPAIPR
30.7	1762.9400	0.0645	LVCLNQTLPPGDLAPR
29.0	1762.9479	0.0567	KAAGIFHVTNPGSVTHK
27.6	1762.9829	0.0217	LIEQPVEAPNLDGLKK
26.3	1763.0417	-0.0372	VGDLRAVLQLDKPALR
26.1	1762.8594	0.1451	IVVTDIQMPGSMDGLR
25.8	1762.9326	0.0719	ERVAAVGAGLDLPPDQR
25.6	1762.9942	0.0104	AVTQTVDGAPVIIVAGPR
24.7	1762.8850	0.1195	VSVSQTYTDNVNLAPR

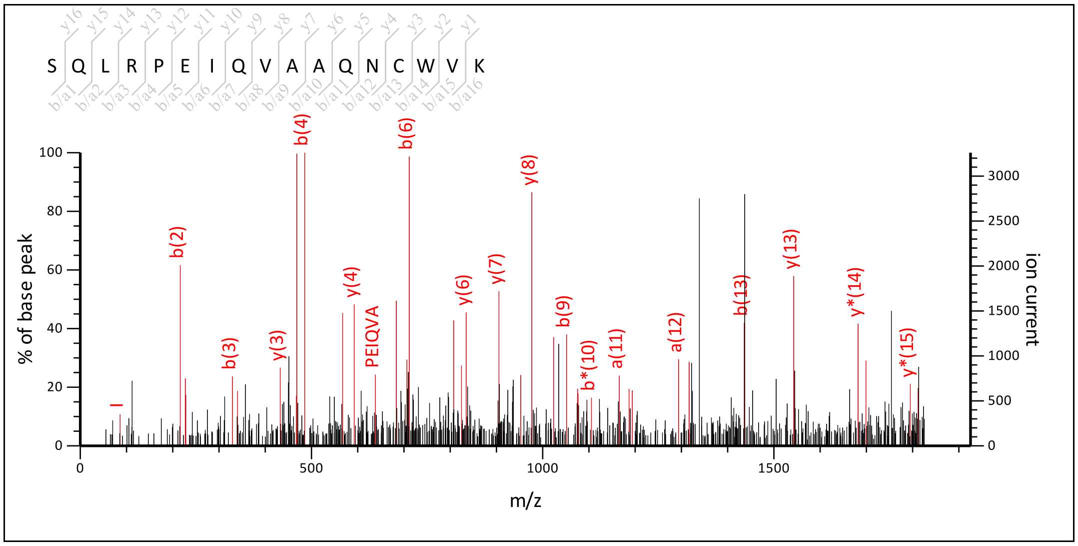
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 32

MS/MS Fragmentation of **SQLRPEIQVAAQNCWVK**
Found in **gi|553107** in **NCBInr**, triosephosphate isomerase, partial [Oryza sativa Japonica Group]

Match to Query 151: 2026.161324 from(2027.168600,1+) intensity(0.0000) index(33)
Title: Label: H19, Spot_Id: 219969, Peak_List_Id: 229378, MSMS Job_Run_Id: 22019, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H19_136868348800.txt



0 to 1925.25

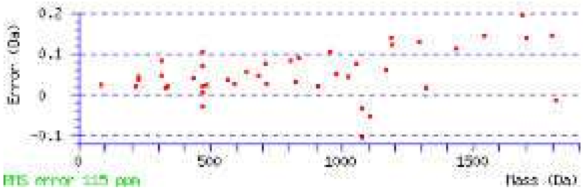
Label all possible matches ○ Label matches used for scoring ●

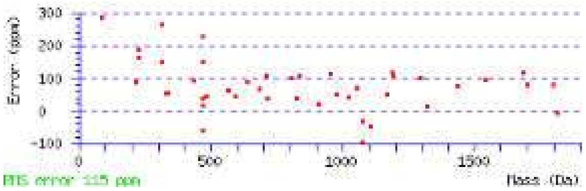
Monoisotopic mass of neutral peptide Mr(calc): 2026.0418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 0.00055
Matches : 45/305 fragment ions using 54 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S						
2	101.0709	188.1030	171.0764	170.0924	**216.0979**	199.0713	198.0873	131.0815		Q	1866.9643	1865.9691		1940.0171	1922.9905	192
3	86.0964	301.1870	284.1605	283.1765	**329.1819**	312.1554	311.1714	259.1401		L	1753.8803	1752.8850		***1811.9585***	1794.9320	179
4	129.1135	457.2881	440.2616	439.2776	**485.2831**	468.2565	467.2725	372.2241		R	1597.7791	1596.7839		***1698.8744***	1681.8479	168
5	70.0651	554.3409	537.3144	536.3303	582.3358	565.3093	564.3253	528.3253		P	1500.7264	1499.7311		***1542.7733***	1525.7468	152
6	102.0550	**683.3835**	666.3569	665.3729	**711.3784**	694.3519	693.3678	625.3780		E	1371.6838	1370.6885		1445.7206	1428.6940	142
7	86.0964	796.4676	779.4410	778.4570	**824.4625**	807.4359	806.4519	768.4363	782.4519	I	1258.5997	1271.6201	1285.6358	***1316.6780***	1299.6514	
8	101.0709	924.5261	907.4996	906.5156	**952.5211**	935.4945	934.5105	867.5047		Q	1130.5411	1129.5459		1203.5939	1186.5674	
9	72.0808	**1023.5946**	1006.5680	1005.5840	**1051.5895**	1034.5629	1033.5789	1009.5789		V	1031.4727	1044.4931		***1075.5353***	1058.5088	
10	44.0495	1094.6317	1077.6051	1076.6211	1122.6266	1105.6000	1104.6160			A	960.4356			***976.4669***	959.4404	
11	44.0495	**1165.6688**	1148.6422	1147.6582	**1193.6637**	1176.6371	1175.6531			A	889.3985			***905.4298***	888.4033	
12	101.0709	**1293.7274**	1276.7008	1275.7168	1321.7223	1304.6957	1303.7117	1236.7059		Q	761.3399	760.3447		***834.3927***	817.3661	
13	87.0553	1407.7703	1390.7437	1389.7597	**1435.7652**	1418.7387	1417.7546	1364.7645		N	647.2970	646.3017		***706.3341***	689.3076	
14	133.0430	1567.8009	1550.7744	1549.7904	1595.7959	1578.7693	1577.7853	1478.8074		C	487.2663	486.2711		***592.2912***	575.2646	
15	159.0917	1753.8803	1736.8537	1735.8697	1781.8752	1764.8486	1763.8646			W	301.1870			***432.2605***	415.2340	
16	72.0808	1852.9487	1835.9221	1834.9381	1880.9436	1863.9170	1862.9330	1838.9330		V	202.1186	215.1390		246.1812	229.1547	
17	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QL	214.1550	242.1499	QLR	370.2561	398.2510	QLRP	467.3089	495.3038
QLRPE	596.3515	624.3464	LR	242.1975	270.1925	LRP	339.2503	367.2452
LRPE	468.2929	496.2878	LRPEI	581.3770	609.3719	RP	226.1662	254.1612
RPE	355.2088	383.2037	RPEI	468.2929	496.2878	RPEIQ	596.3515	624.3464

RPEIQV	695.4199	723.4148	**PE**	199.1077	227.1026	**PEI**	312.1918	340.1867
PEIQ	440.2504	468.2453	**PEIQV**	539.3188	567.3137	**PEIQVA**	610.3559	638.3508
PEIQVAA	681.3930	709.3879	**EI**	215.1390	243.1339	**EIQ**	343.1976	371.1925
EIQV	442.2660	470.2609	**EIQVA**	513.3031	541.2980	**EIQVAA**	584.3402	612.3352
IQ	214.1550	242.1499	**IQV**	313.2234	341.2183	**IQVA**	384.2605	412.2554
IQVAA	455.2976	483.2926	**IQVAAQ**	583.3562	611.3511	**IQVAAQN**	697.3992	725.3941
QV	200.1394	228.1343	**QVA**	271.1765	299.1714	**QVAA**	342.2136	370.2085
QVAAQ	470.2722	498.2671	**QVAAQN**	584.3151	612.3100	**VA**	143.1179	171.1128
VAA	214.1550	242.1499	**VAAQ**	342.2136	370.2085	**VAAQN**	456.2565	484.2514
VAAQNC	616.2872	644.2821	**AA**	115.0866	143.0815	**AAQ**	243.1452	271.1401
AAQN	357.1881	385.1830	**AAQNC**	517.2187	545.2137	**AQ**	172.1081	200.1030
AQN	286.1510	314.1459	**AQNC**	446.1816	474.1765	**AQNCW**	632.2609	660.2559
QN	215.1139	243.1088	**QNC**	375.1445	403.1394	**QNCW**	561.2238	589.2187
QNCWV	660.2922	688.2872	**NC**	247.0859	275.0809	**NCW**	433.1652	461.1602
NCWV	532.2337	560.2286	**CW**	319.1223	347.1172	**CWV**	418.1907	446.1857
WV	258.1601	286.1550						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.5	2026.0418	0.1195	SQLRPEIQVAAQNCWVK
20.3	2026.1324	0.0289	DVPAGAVTLAGVAHVPAIGGVR
18.0	2026.1323	0.0290	LGSAADIRPIGAAATLVFQR
16.3	2026.0636	0.0977	LRPTAVVSQYSNIFEFR
14.5	2026.0517	0.1096	VAEVLPDLDVAAIENRMR
14.2	2026.0259	0.1355	FAGTTLLFTVAAEAAEEASK
13.4	2025.9868	0.1746	QSYAEAIAAAEEDLPRHR
13.0	2026.1171	0.0442	LRPQLVSLGSAALTSQETR
13.0	2026.1184	0.0429	LRQLAENLLLNATHHGAR
12.8	2026.1575	0.0038	LILQVAVGSAASSGVFLAAPR

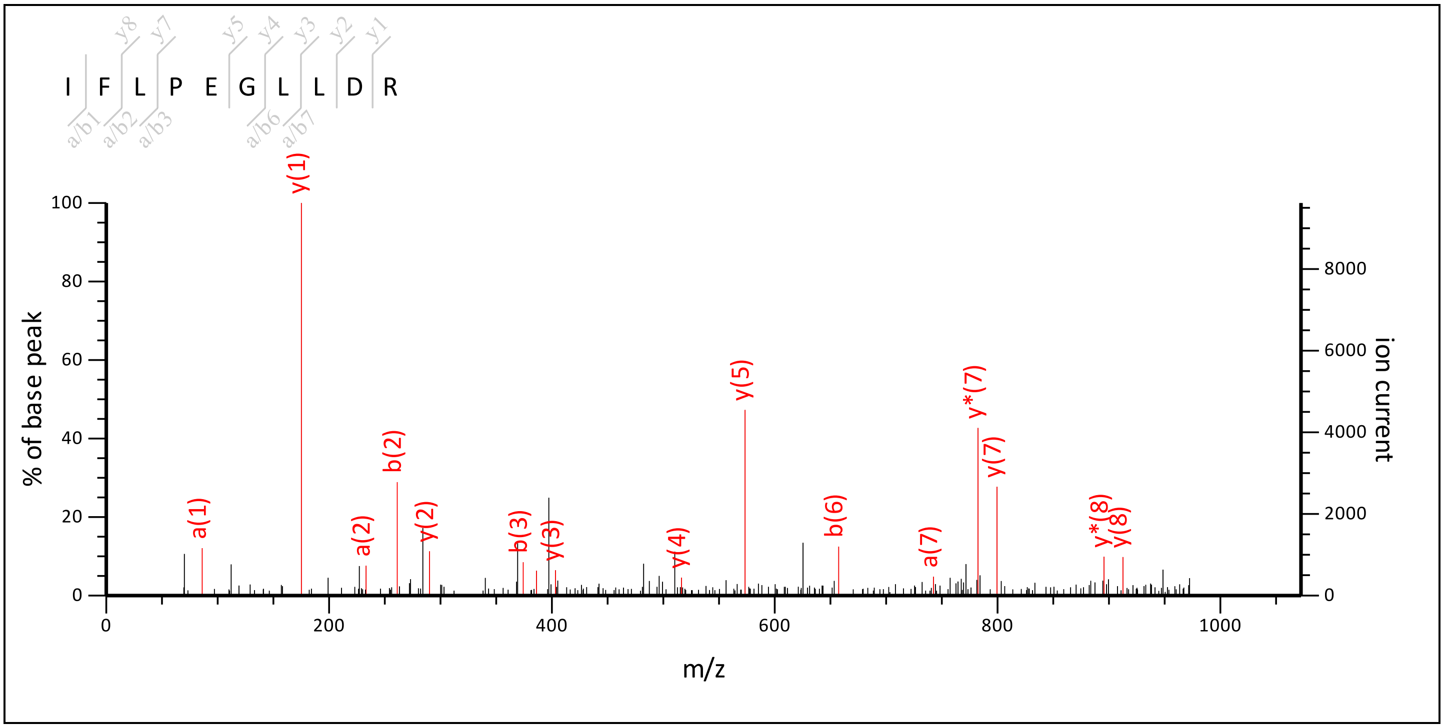
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 34

MS/MS Fragmentation of **IFLPEGLLDR**
Found in **gi|108864186** in **NCBInr**, Chlorophyll A-B binding protein, expressed [Oryza sativa Japonica Group]

Match to Query 115: 1171.705624 from(1172.712900,1+) intensity(0.0000) index(6)
Title: Label: F7, Spot_Id: 219775, Peak_List_Id: 226288, MSMS Job_Run_Id: 21839, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F7_136859913100.txt



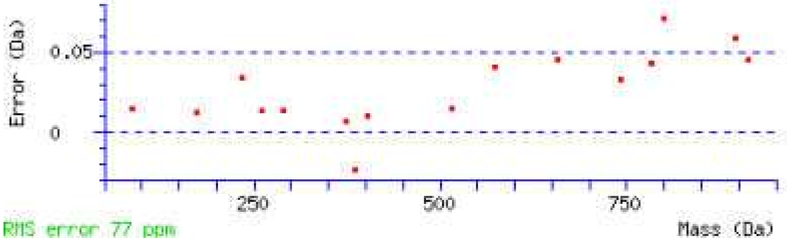
0 to 1072.37

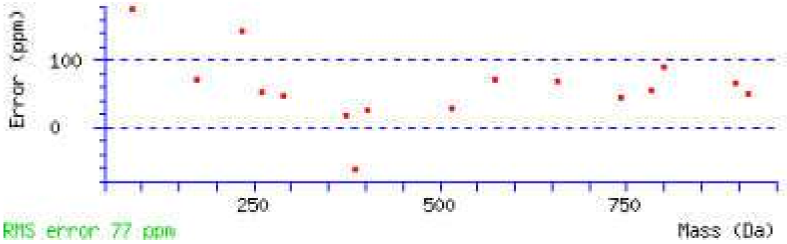
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1171.6601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 9.1
Matches : 16/36 fragment ions using 38 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	**86.0964**	114.0913	I			10
2	**233.1648**	**261.1598**	F	1059.5833	1042.5568	9
3	346.2489	**374.2438**	L	***912.5149***	895.4884	8
4	443.3017	471.2966	P	***799.4308***	782.4043	7
5	572.3443	600.3392	E	702.3781	685.3515	6
6	629.3657	**657.3606**	G	***573.3355***	556.3089	5
7	**742.4498**	770.4447	L	***516.3140***	499.2875	4
8	855.5339	883.5288	L	***403.2300***	386.2034	3

9	970.5608	998.5557	**D**	*290.1459*	273.1193	**2**
10			**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.9	1171.6601	0.0455	IFLPEGLLDR
23.5	1171.6866	0.0190	IFIFGILGHR
23.4	1171.7077	-0.0021	FLLGAAALGLAR
23.3	1171.6965	0.0091	FLLPVSLIDR
23.3	1171.6998	0.0058	MIILGIILDR
22.4	1171.6561	0.0496	LVAILGTNSER
22.2	1171.7441	-0.0385	LFLLIAGAAKR
21.7	1171.6998	0.0058	LMDLLLIVAR
21.3	1171.6495	0.0561	IMIGRSLNPR
21.1	1171.6635	0.0422	VPSLLSMALNK

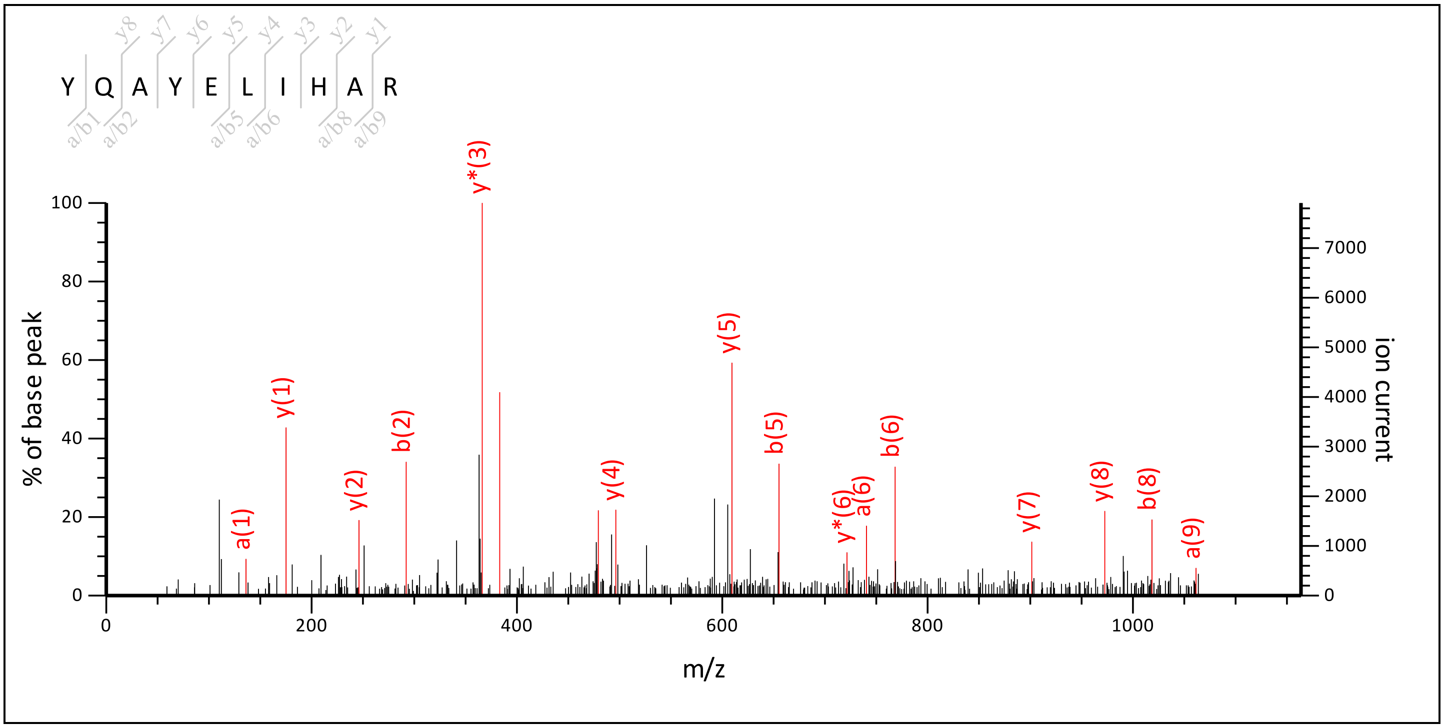
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 34

MS/MS Fragmentation of **YQAYELIHAR**
Found in **gi|108864186** in **NCBInr**, Chlorophyll A-B binding protein, expressed [Oryza sativa Japonica Group]

Match to Query 137: 1262.691324 from(1263.698600,1+) intensity(0.0000) index(8)
Title: Label: F7, Spot_Id: 219775, Peak_List_Id: 226283, MSMS Job_Run_Id: 21839, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F7_136859913100.txt



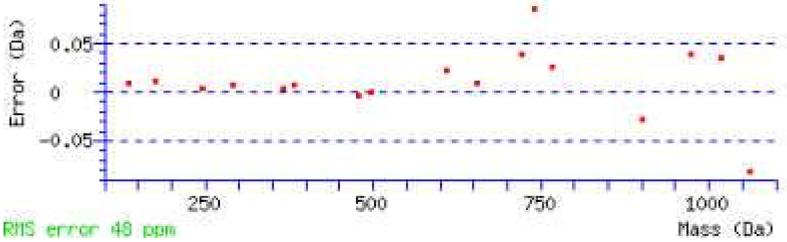
0 to 1163.68

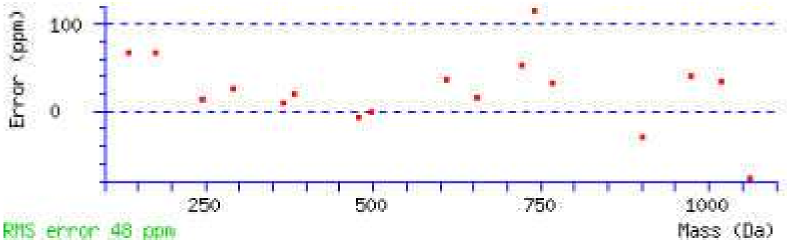
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1262.6407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 0.1
Matches : 17/52 fragment ions using 22 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**136.0757**		164.0706		Y			10
2	264.1343	247.1077	**292.1292**	275.1026	Q	1100.5847	1083.5582	9
3	335.1714	318.1448	363.1663	346.1397	A	***972.5261***	955.4996	8
4	498.2347	481.2082	526.2296	509.2031	Y	***901.4890***	884.4625	7
5	627.2773	610.2508	**655.2722**	638.2457	E	738.4257	721.3992	6
6	**740.3614**	723.3348	**768.3563**	751.3297	L	***609.3831***	592.3566	5
7	853.4454	836.4189	881.4403	864.4138	I	***496.2990***	479.2725	4
8	990.5043	973.4778	**1018.4993**	1001.4727	H	***383.2150***	366.1884	3

9	**1061.5415**	1044.5149	1089.5364	1072.5098	**A**	***246.1561***	229.1295	**2**
10					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.0	1262.6407	0.0506	YQAYELIHAR
28.7	1262.6077	0.0836	YAGLDMTLHAR
28.3	1262.6884	0.0030	HQIFELIHAR
27.4	1262.6077	0.0836	YESVGTMIHAR
26.6	1262.7247	-0.0334	HKEFIIIHAR
26.4	1262.6632	0.0281	FGSGKHPGLHAR
24.9	1262.7207	-0.0294	AAGVEARLIHAR
24.9	1262.6190	0.0724	EVCEHILHAR
24.9	1262.7207	-0.0294	NNVQAKLLHAR
24.9	1262.7247	-0.0334	QHLLYILHAR

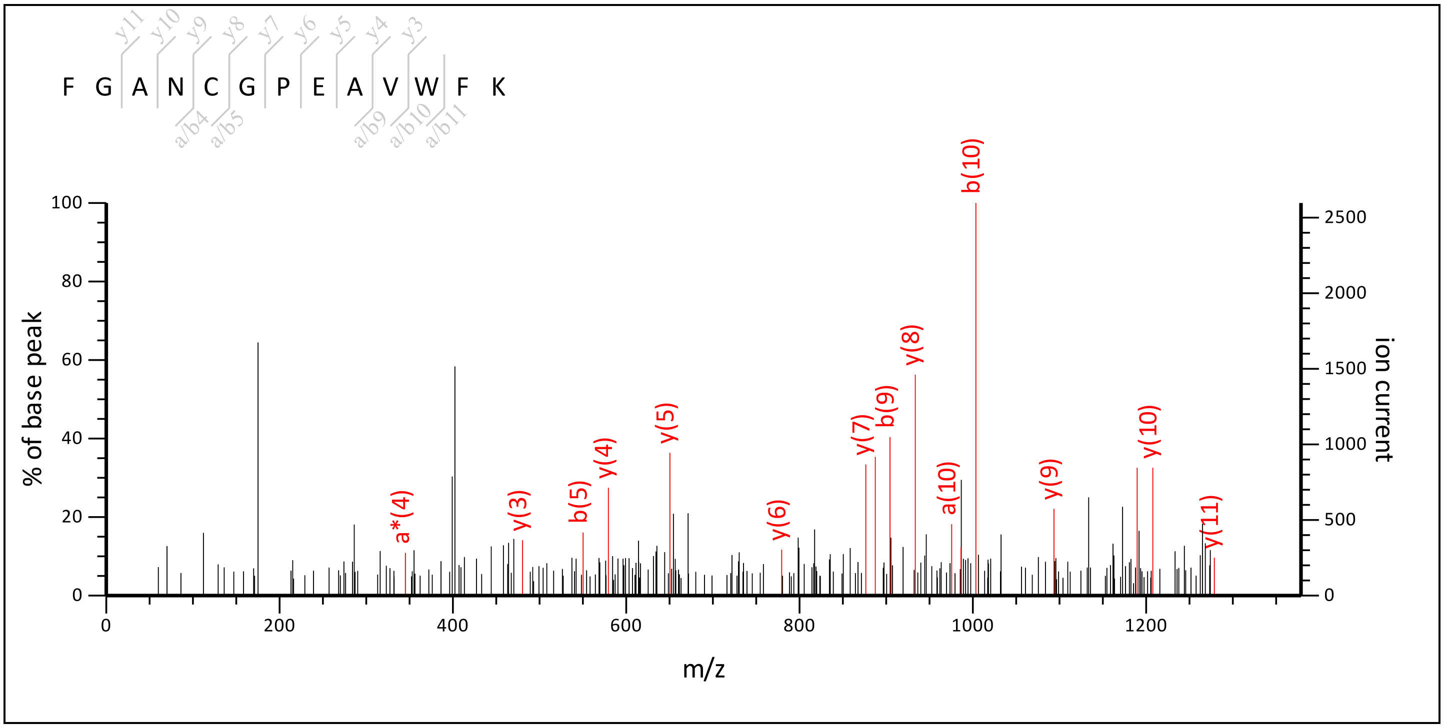
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 34**

MS/MS Fragmentation of **FGANCGPEAVWFK**
Found in **gi|108864186** in **NCBInr**, Chlorophyll A-B binding protein, expressed [Oryza sativa Japonica Group]

Match to Query 204: 1481.717824 from(1482.725100,1+) intensity(0.0000) index(17)
Title: Label: F7, Spot_Id: 219775, Peak_List_Id: 226297, MSMS Job_Run_Id: 21839, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F7_136859913100.txt



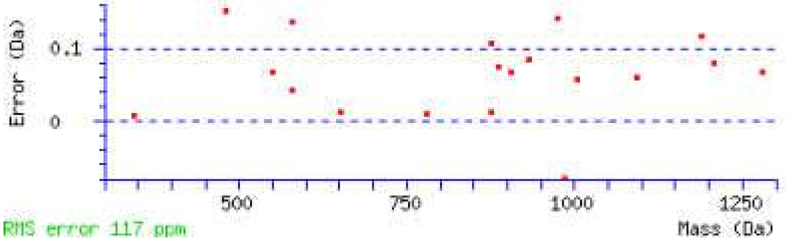
0 to 1378.66

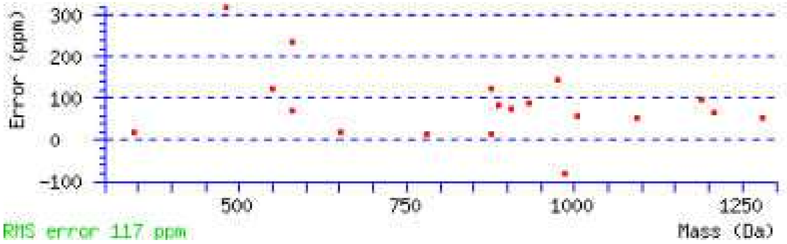
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1481.6762
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 63
Matches : 19/66 fragment ions using 65 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	120.0808		148.0757		F			13
2	177.1022		205.0972		G	1335.6150	1318.5885	12
3	248.1394		276.1343		A	*1278.5936*	1261.5670	11
4	362.1823	345.1557	390.1772	373.1506	N	*1207.5565*	1190.5299	10
5	522.2129	505.1864	**550.2078**	533.1813	C	*1093.5135*	1076.4870	9
6	**579.2344**	562.2078	607.2293	590.2028	G	*933.4829*	916.4563	8
7	676.2872	659.2606	704.2821	687.2555	P	*876.4614*	859.4349	7
8	805.3298	788.3032	833.3247	816.2981	E	*779.4087*	762.3821	6

9	**876.3669**	859.3403	**904.3618**	887.3352	**A**	***650.3661***	633.3395	**5**
10	**975.4353**	958.4087	**1003.4302**	986.4036	**V**	***579.3289***	562.3024	**4**
11	1161.5146	1144.4880	**1189.5095**	1172.4830	**W**	***480.2605***	463.2340	**3**
12	1308.5830	1291.5565	1336.5779	1319.5514	**F**	294.1812	277.1547	**2**
13					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.9	1481.6762	0.0416	FGANCGPEAVWFK
16.5	1481.6789	0.0389	KMNCVPSNITMR
15.7	1481.6966	0.0212	SMDLSMTELGRAR
15.2	1481.7548	-0.0370	TMTTVFDGTPKLR
14.4	1481.7303	-0.0125	RPESIAYDAWFK
13.7	1481.6892	0.0286	QTEVGSSASRAMSR
13.6	1481.7514	-0.0336	DYAISPISAYINR
13.6	1481.7667	-0.0489	VSYISPFTWINR
13.3	1481.7548	-0.0370	LTAISMSLEFAQR
13.2	1481.7184	-0.0006	RTDLMAAEGVEFK

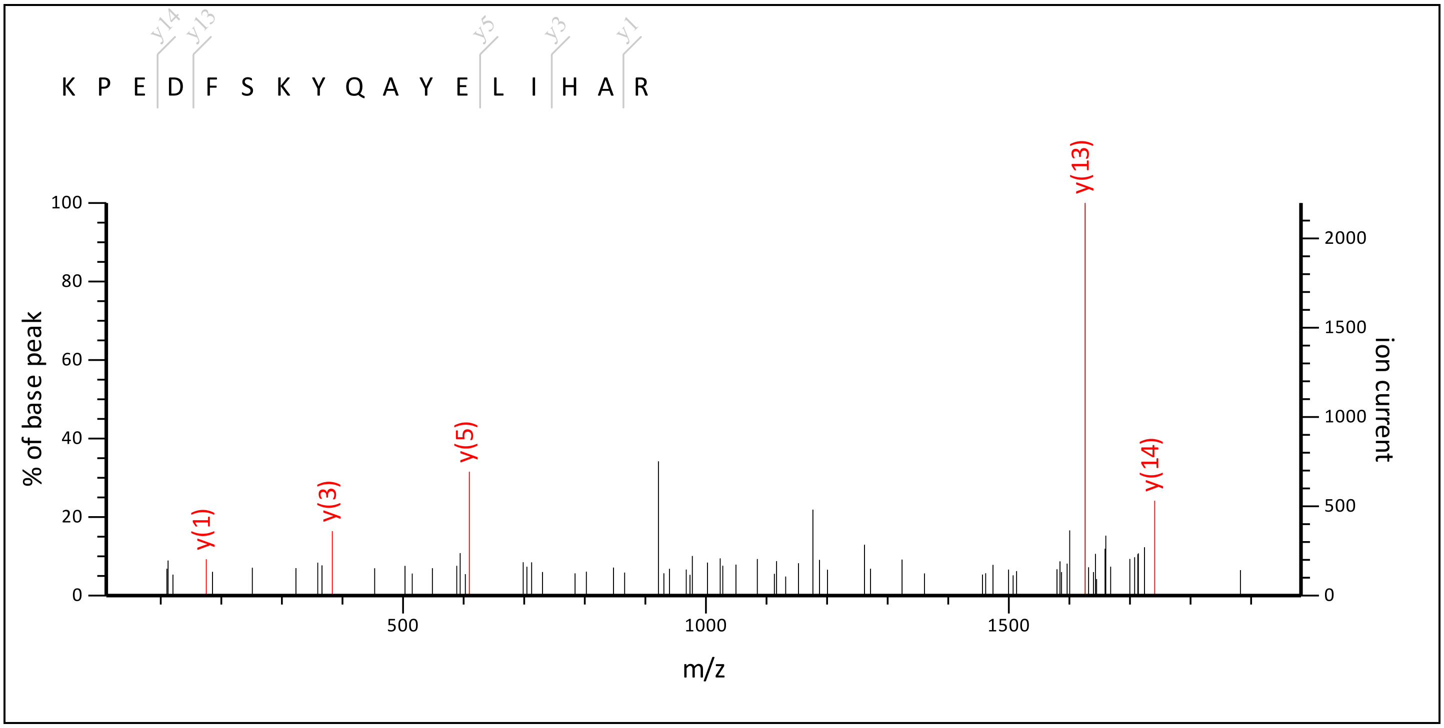
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 34

MS/MS Fragmentation of **KPEDFSKYQAYELIHAR**
Found in **gi|108864186** in **NCBInr**, Chlorophyll A-B binding protein, expressed [Oryza sativa Japonica Group]

Match to Query 302: 2094.141924 from(2095.149200,1+) intensity(0.0000) index(32)
Title: Label: F7, Spot_Id: 219775, Peak_List_Id: 226300, MSMS Job_Run_Id: 21839, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F7_136859913100.txt



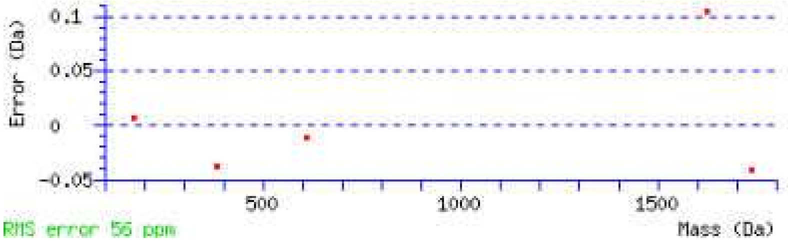
10.07 to 1982.31

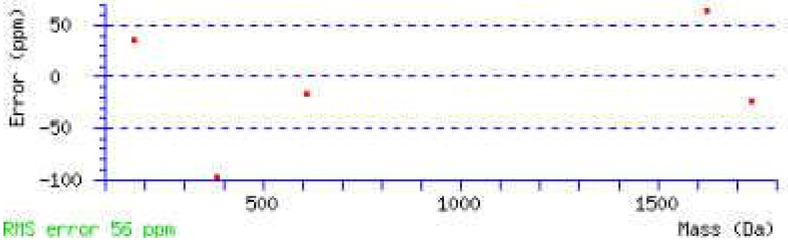
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2094.0534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 12 **Expect:** 1.3e+03
Matches : 5/96 fragment ions using 18 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	101.1073	84.0808	129.1022	112.0757	K			17
2	198.1601	181.1335	226.1550	209.1285	P	1966.9658	1949.9392	16
3	327.2027	310.1761	355.1976	338.1710	E	1869.9130	1852.8864	15
4	442.2296	425.2031	470.2245	453.1980	D	***1740.8704***	1723.8438	14
5	589.2980	572.2715	617.2930	600.2664	F	***1625.8435***	1608.8169	13
6	676.3301	659.3035	704.3250	687.2984	S	1478.7750	1461.7485	12
7	804.4250	787.3985	832.4199	815.3934	K	1391.7430	1374.7165	11
8	967.4884	950.4618	995.4833	978.4567	Y	1263.6480	1246.6215	10

9	1095.5469	1078.5204	1123.5419	1106.5153	**Q**	1100.5847	1083.5582	**9**
10	1166.5841	1149.5575	1194.5790	1177.5524	**A**	972.5261	955.4996	**8**
11	1329.6474	1312.6208	1357.6423	1340.6157	**Y**	901.4890	884.4625	**7**
12	1458.6900	1441.6634	1486.6849	1469.6583	**E**	738.4257	721.3991	**6**
13	1571.7740	1554.7475	1599.7690	1582.7424	**L**	***609.3831***	592.3566	**5**
14	1684.8581	1667.8316	1712.8530	1695.8265	**I**	496.2990	479.2725	**4**
15	1821.9170	1804.8905	1849.9119	1832.8854	**H**	***383.2150***	366.1884	**3**
16	1892.9541	1875.9276	1920.9490	1903.9225	**A**	246.1561	229.1295	**2**
17					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
12.4	2094.0534	0.0885	KPEDFSKYQAYELIHAR
11.8	2094.0528	0.0892	KILDHISDVNMTLSEHAR
9.5	2094.0337	0.1082	LLAVPMTILAASTSDSEGMR
9.0	2094.1249	0.0170	KLLDIGDFIGVEGELFTTK
8.3	2094.0382	0.1038	SINGFDVTDPQKALEAYAR
3.9	2094.0390	0.1029	LVPCNYQWLDTMISKAR
3.3	2093.9726	0.1693	KPDEDAVGSNRVDDVDAHR
3.2	2094.0164	0.1256	IIENNQHDPAEMLAQLSR
3.1	2094.1222	0.0197	TVVVASGASYRKPAVTGFER
3.1	2094.0858	0.0561	KIIDHTSDVNFVLTEHAR

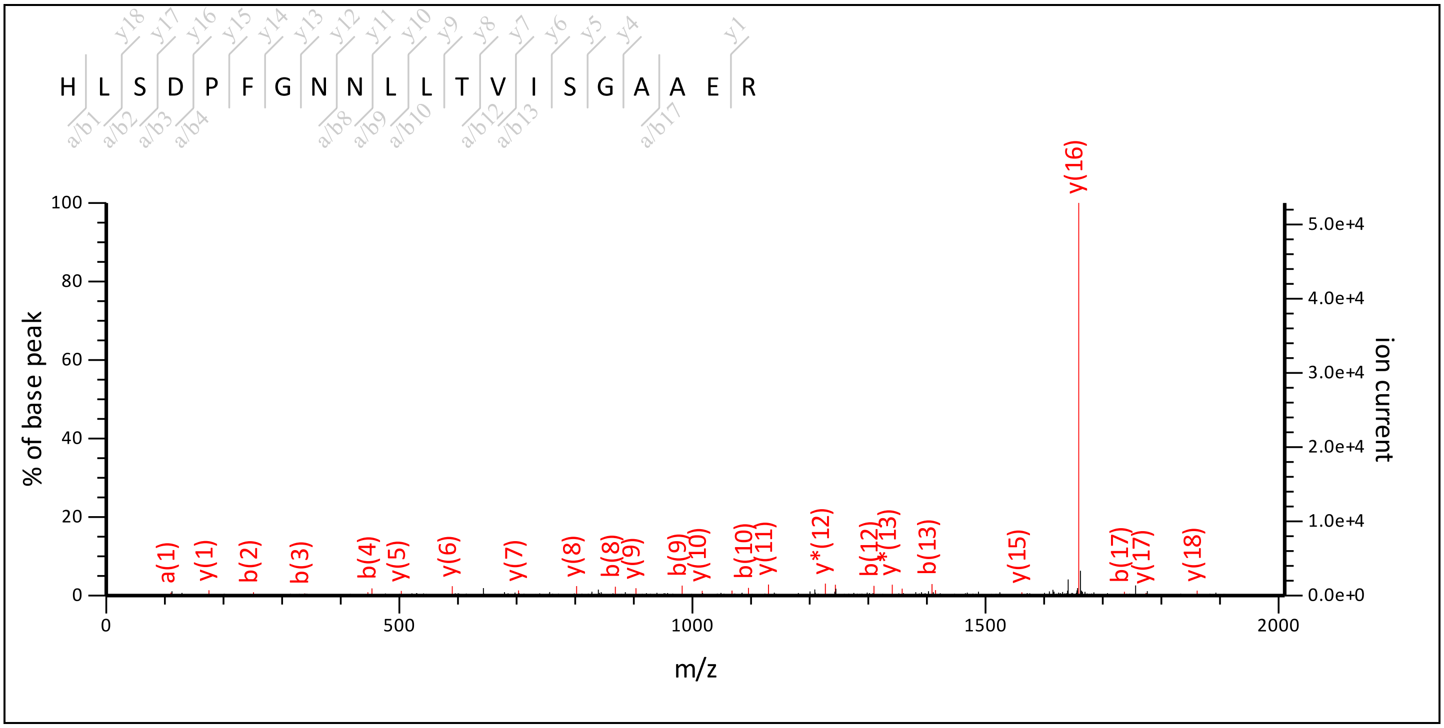
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 34

MS/MS Fragmentation of **HLSDPFGNNLLTVISGAAER**
Found in **gi|108864186** in **NCBInr**, Chlorophyll A-B binding protein, expressed [Oryza sativa Japonica Group]

Match to Query 305: 2110.167524 from(2111.174800,1+) intensity(0.0000) index(33)
Title: Label: F7, Spot_Id: 219775, Peak_List_Id: 226287, MSMS Job_Run_Id: 21839, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F7_136859913100.txt



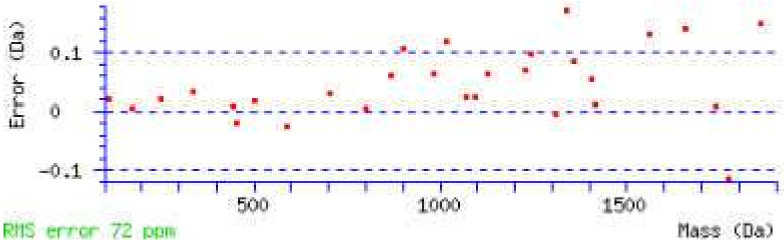
0 to 2010.39

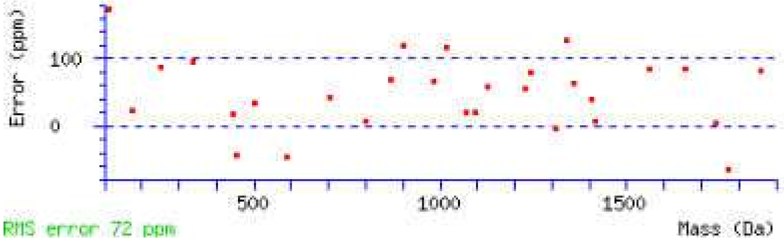
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2110.0807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 110 **Expect:** 2.2e-07
Matches : 29/100 fragment ions using 57 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**110.0713**		138.0662		H			20
2	223.1553		**251.1503**		L	1974.0291	1957.0025	19
3	310.1874		**338.1823**		S	***1860.9450***	1843.9185	18
4	425.2143		**453.2092**		D	***1773.9130***	1756.8864	17
5	522.2671		550.2620		P	***1658.8860***	1641.8595	16
6	669.3355		697.3304		F	***1561.8333***	1544.8067	15
7	726.3569		754.3519		G	***1414.7649***	1397.7383	14
8	840.3999	823.3733	**868.3948**	851.3682	N	***1357.7434***	1340.7169	13

9	954.4428	937.4163	**982.4377**	965.4112	**N**	***1243.7005***	1226.6739	**12**
10	**1067.5269**	1050.5003	**1095.5218**	1078.4952	**L**	***1129.6576***	1112.6310	**11**
11	1180.6109	1163.5844	1208.6058	1191.5793	**L**	***1016.5735***	999.5469	**10**
12	1281.6586	1264.6321	**1309.6535**	1292.6270	**T**	***903.4894***	886.4629	**9**
13	1380.7270	1363.7005	**1408.7219**	1391.6954	**V**	***802.4417***	785.4152	**8**
14	1493.8111	1476.7845	1521.8060	1504.7795	**I**	***703.3733***	686.3468	**7**
15	1580.8431	1563.8166	1608.8380	1591.8115	**S**	***590.2893***	573.2627	**6**
16	1637.8646	1620.8380	1665.8595	1648.8329	**G**	***503.2572***	486.2307	**5**
17	1708.9017	1691.8751	**1736.8966**	1719.8701	**A**	***446.2358***	429.2092	**4**
18	1779.9388	1762.9123	1807.9337	1790.9072	**A**	375.1987	358.1721	**3**
19	1908.9814	1891.9549	1936.9763	1919.9498	**E**	304.1615	287.1350	**2**
20					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
109.8	2110.0807	0.0868	HLSDPFGNNLLTVISGAAER
96.2	2110.0807	0.0868	HLSDPFGNNLLTVISAGAER
83.5	2110.0807	0.0868	HLSDPFGNNLLTVIAGSAER
83.5	2110.0807	0.0868	HLSDPFGNNLLTVLAGSAER
27.2	2110.2626	-0.0951	RFNQIIIPLLSLISINTR
21.0	2110.0980	0.0695	KYPEVVSIIDTVSSMSALR
16.9	2110.1521	0.0154	LEIPASLDIQAISGLSNELK
16.8	2110.0232	0.1443	VGWDSITVDIQHGLHDYR
14.1	2110.2051	-0.0376	LLEPGYLVRPRSPVPVYR
14.1	2110.0775	0.0900	MAHPQALATLLATEGQRMR

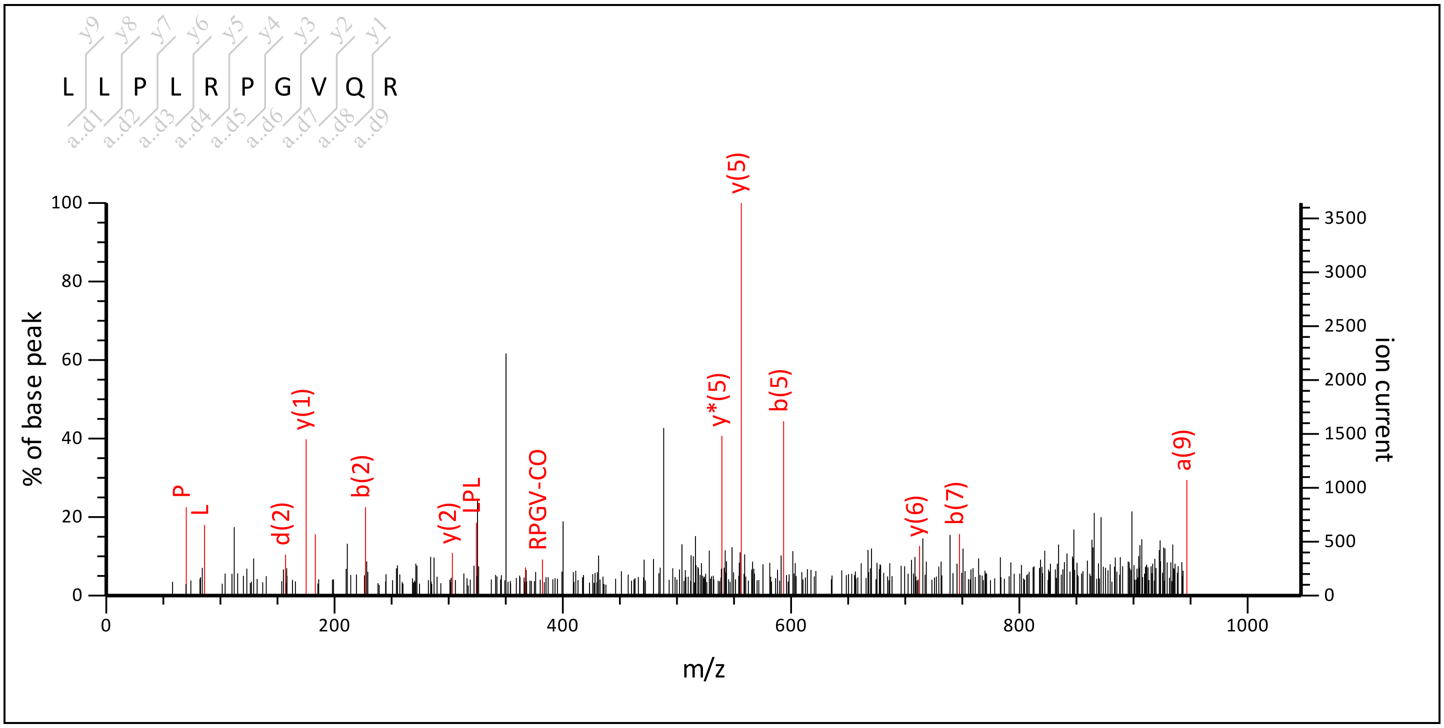
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 36

MS/MS Fragmentation of **LLPLRPGVQR**
Found in **gi|115453797** in **NCBInr**, Os03g0565200 [Oryza sativa Japonica Group]

Match to Query 34: 1147.747824 from(1148.755100,1+) intensity(0.0000) index(8)
Title: Label: I10, Spot_Id: 219826, Peak_List_Id: 226858, MSMS Job_Run_Id: 21858, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I10_136859951300.txt



0 to 1046.73

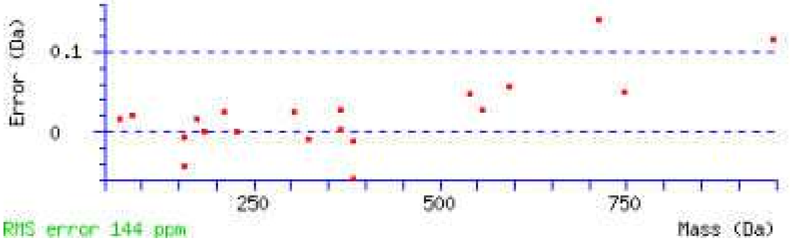
Label all possible matches ○ Label matches used for scoring ●

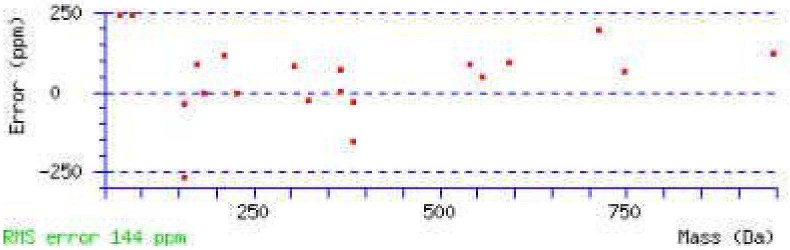
Monoisotopic mass of neutral peptide Mr(calc): 1147.7189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 60
Matches : 28/130 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	86.0964	**86.0964**		114.0913		44.0495	L					10
2	86.0964	199.1805		***227.1754***		157.1335	L	977.5639	976.5687	1035.6422	1018.6156	9
3	70.0651	296.2333		***324.2282***		270.2176	P	880.5112	879.5159	922.5581	905.5316	8
4	86.0964	409.3173		437.3122		367.2704	L	767.4271	766.4318	825.5053	808.4788	7
5	129.1135	565.4184	548.3919	***593.4133***	576.3868	480.3544	R	611.3260	610.3307	***712.4213***	695.3947	6
6	70.0651	662.4712	645.4446	690.4661	673.4396	636.4555	P	514.2732	513.2780	***556.3202***	539.2936	5
7	30.0338	719.4927	702.4661	***747.4876***	730.4610		G			459.2674	442.2409	4
8	72.0808	818.5611	801.5345	846.5560	829.5294	804.5454	V	358.1833	371.2037	402.2459	385.2194	3

9	101.0709	**946.6196**	929.5931	974.6146	957.5880	889.5982	**Q**	230.1248	229.1295	***303.1775***	286.1510	**2**
10	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LP	183.1492	211.1441	**LPL**	296.2333	324.2282	**LPLR**	452.3344	480.3293
LPLRP	549.3871	577.3820	**LPLRPG**	606.4086	634.4035	**PL**	183.1492	211.1441
PLR	339.2503	367.2452	**PLRP**	436.3031	464.2980	**PLRPG**	493.3245	521.3194
PLRPGV	592.3929	620.3879	**LR**	242.1975	270.1925	**LRP**	339.2503	367.2452
LRPG	396.2718	424.2667	**LRPGV**	495.3402	523.3351	**LRPGVQ**	623.3988	651.3937
RP	226.1662	254.1612	**RPG**	283.1877	311.1826	**RPGV**	382.2561	410.2510
RPGVQ	510.3147	538.3096	**PG**	127.0866	155.0815	**PGV**	226.1550	254.1499
PGVQ	354.2136	382.2085	**GV**	129.1022	157.0972	**GVQ**	257.1608	285.1557
VQ	200.1394	228.1343						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.5	1147.7189	0.0289	RVPGIAPAIVR
23.4	1147.6601	0.0877	SDVVFILLSR
22.6	1147.6350	0.1129	QVSIGVYVAGR
21.3	1147.7189	0.0289	LLPLRPGVQR
20.9	1147.6502	0.0976	RVPYPVYVR
19.9	1147.6462	0.1016	IIGTAHGPGAVR
19.8	1147.6462	0.1017	PSPIATAHAKR
19.4	1147.6614	0.0864	LPPVWRPAGR
19.3	1147.6687	0.0792	RTVARPGHVR
19.1	1147.7077	0.0401	ILGPVLGPQVR

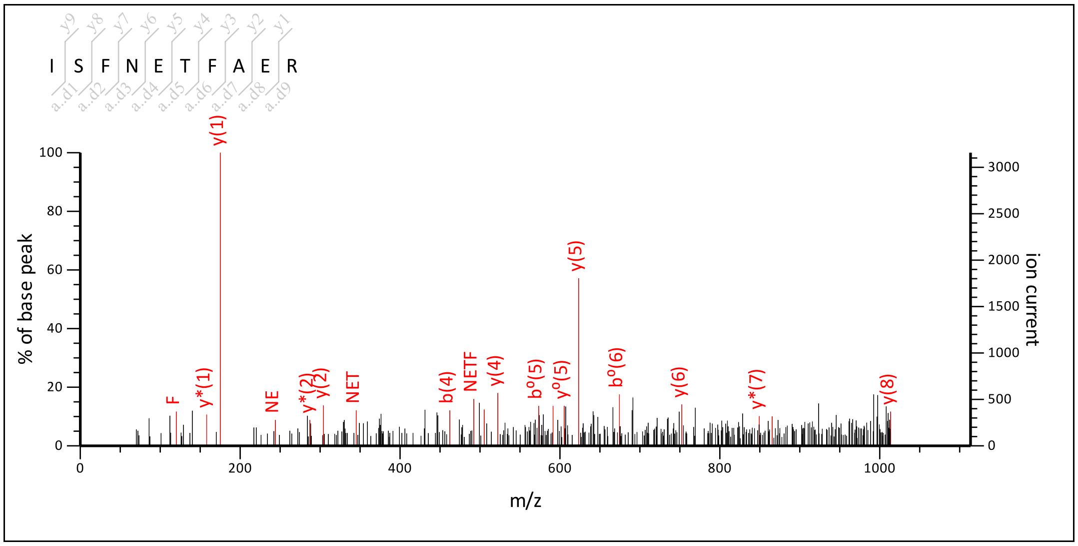
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 36

MS/MS Fragmentation of **ISFNETFAER**
Found in **gi|115453797** in **NCBInr**, Os03g0565200 [Oryza sativa Japonica Group]

Match to Query 41: 1212.614924 from(1213.622200,1+) intensity(0.0000) index(11)
Title: Label: I10, Spot_Id: 219826, Peak_List_Id: 226860, MSMS Job_Run_Id: 21858, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I10_136859951300.txt



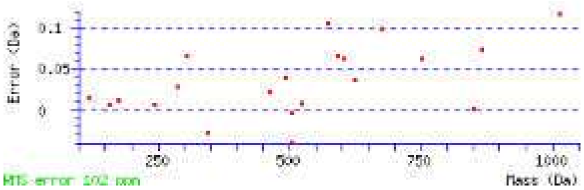
0 to 1113.59

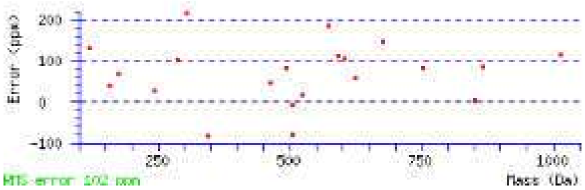
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1212.5775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 88
Matches : 23/153 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0
1	86.0964	86.0964			114.0913			44.0495		I						
2	60.0444	173.1285		155.1179	201.1234		183.1128	157.1335		S	1068.4745	1067.4793		1100.5007	1083.4742	1082.49
3	120.0808	320.1969		302.1863	348.1918		330.1812			F	921.4061			***1013.4687***	996.4421	995.45
4	87.0553	434.2398	417.2132	416.2292	**462.2347**	445.2082	444.2241	391.2340		N	807.3632	806.3679		866.4003	849.3737	848.38
5	102.0550	563.2824	546.2558	545.2718	**591.2773**	574.2508	573.2667	505.2769		E	678.3206	677.3253		***752.3573***	735.3308	734.34
6	74.0600	664.3301	647.3035	646.3195	692.3250	675.2984	674.3144	648.3352	650.3144	T	577.2729	590.2933	592.2726	***623.3148***	606.2882	605.30
7	120.0808	811.3985	794.3719	793.3879	839.3934	822.3668	821.3828			F	430.2045			***522.2671***	505.2405	504.25
8	44.0495	882.4356	865.4090	864.4250	910.4305	893.4040	892.4199			A	359.1674			375.1987	358.1721	357.18
9	102.0550	1011.4782	994.4516	993.4676	1039.4731	1022.4466	1021.4625	953.4727		E	230.1248	229.1295		***304.1615***	287.1350	286.15
10	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SF	207.1128	235.1077	SFN	321.1557	349.1506	SFNE	450.1983	478.1932
SFNET	551.2460	579.2409	SFNETF	698.3144	726.3093	FN	234.1237	262.1186
FNE	363.1663	391.1612	FNET	464.2140	492.2089	FNETF	611.2824	639.2773
FNETFA	682.3195	710.3144	NE	216.0979	244.0928	NET	317.1456	345.1405
NETF	464.2140	492.2089	NETFA	535.2511	563.2460	NETFAE	664.2937	692.2886
ET	203.1026	231.0975	ETF	350.1710	378.1660	ETFA	421.2082	449.2031
ETFAE	550.2508	578.2457	TF	221.1285	249.1234	TFA	292.1656	320.1605
TFAE	421.2082	449.2031	FA	191.1179	219.1128	FAE	320.1605	348.1554
AE	173.0921	201.0870						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.3	1212.5775	0.0374	ISFNETFAER
24.8	1212.5696	0.0453	SEASSTMIFPK
19.4	1212.5921	0.0228	YGSGKMKPSSR
18.9	1212.6172	-0.0023	TAAFSLTMLSR
18.6	1212.6099	0.0051	QPQADTPTISR
18.6	1212.5258	0.0891	SESAFETASER
18.2	1212.5775	0.0374	QDYFPTISSR
17.1	1212.5631	0.0518	MFVEAGAMAVR
17.0	1212.5445	0.0704	LSDSTFADMAR
16.9	1212.5775	0.0374	QDYFPTLSSR

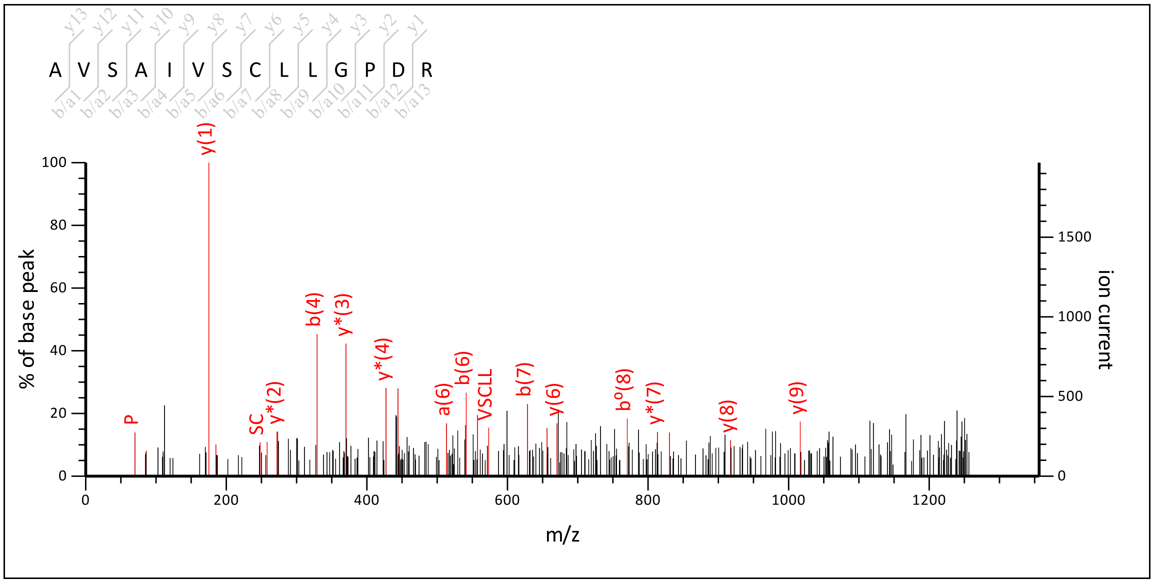
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 36**

MS/MS Fragmentation of **AVSAIVSCLLGPDR**
Found in **gi|115453797** in **NCBInr**, Os03g0565200 [Oryza sativa Japonica Group]

Match to Query 54: 1456.804124 from(1457.811400,1+) intensity(0.0000) index(17)
Title: Label: I10, Spot_Id: 219826, Peak_List_Id: 226864, MSMS Job_Run_Id: 21858, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I10_136859951300.txt



0 to 1356.41

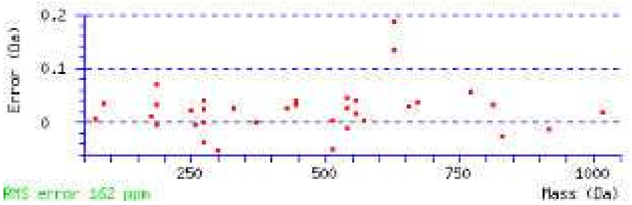
Label all possible matches ○ Label matches used for scoring ●

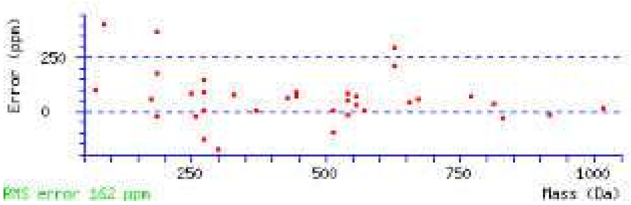
Monoisotopic mass of neutral peptide Mr(calc): 1456.7708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 19
Matches : 40/228 fragment ions using 48 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	44.0495	44.0495		72.0444		44.0495		A							14
2	72.0808	143.1179		171.1128		129.1022		V	1342.6784	1355.6988		1386.7410	1369.7144	1368.7304	13
3	60.0444	230.1499	212.1394	***258.1448***	240.1343	214.1550		S	1255.6463	1254.6511		1287.6725	1270.6460	1269.6620	12
4	44.0495	301.1870	283.1765	***329.1819***	311.1714			A	1184.6092			1200.6405	1183.6140	1182.6300	11
5	86.0964	414.2711	396.2605	442.2660	424.2554	386.2398	400.2554	I	1071.5252	1084.5456	1098.5612	1129.6034	1112.5769	1111.5928	10
6	72.0808	513.3395	495.3289	***541.3344***	523.3239	499.3239		V	972.4567	985.4771		***1016.5193***	999.4928	998.5088	9
7	60.0444	600.3715	582.3610	***628.3665***	610.3559	584.3766		S	885.4247	884.4295		***917.4509***	900.4244	899.4404	8
8	133.0430	760.4022	742.3916	788.3971	770.3865	671.4087		C	725.3941	724.3988		***830.4189***	813.3924	812.4083	7
9	86.0964	873.4863	855.4757	901.4812	883.4706	831.4393		L	612.3100	611.3148		***670.3883***	653.3617	652.3777	6
10	86.0964	986.5703	968.5597	1014.5652	996.5547	944.5234		L	499.2259	498.2307		***557.3042***	540.2776	539.2936	5
11	30.0338	1043.5918	1025.5812	1071.5867	1053.5761			G				***444.2201***	427.1936	426.2096	4
12	70.0651	1140.6445	1122.6340	1168.6395	1150.6289	1114.6289		P	345.1517	344.1565		387.1987	370.1721	369.1881	3
13	88.0393	1255.6715	1237.6609	1283.6664	1265.6558	1211.6817		D	230.1248	229.1295		290.1459	273.1193	272.1353	2
14	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VS	159.1128	187.1077	VSA	230.1499	258.1448	VSAI	343.2340	371.2289
VSAIV	442.3024	470.2973	VSAIVS	529.3344	557.3293	VSAIVSC	689.3651	717.3600
SA	131.0815	159.0764	SAI	244.1656	272.1605	SAIV	343.2340	371.2289

SAIVS	430.2660	458.2609	**SAIVSC**	590.2967	618.2916	**AI**	157.1335	185.1285
AIV	256.2020	284.1969	**AIVS**	343.2340	371.2289	**AIVSC**	503.2646	531.2595
AIVSCL	616.3487	644.3436	**IV**	185.1648	213.1598	**IVS**	272.1969	300.1918
IVSC	432.2275	460.2224	**IVSCL**	545.3116	573.3065	**IVSCLL**	658.3956	686.3906
VS	159.1128	187.1077	**VSC**	319.1435	347.1384	**VSCL**	432.2275	460.2224
VSCLL	545.3116	573.3065	**VSCLLG**	602.3330	630.3280	**VSCLLGP**	699.3858	727.3807
SC	220.0750	248.0700	**SCL**	333.1591	361.1540	**SCLL**	446.2432	474.2381
SCLLG	503.2646	531.2595	**SCLLGP**	600.3174	628.3123	**CL**	246.1271	274.1220
CLL	359.2111	387.2061	**CLLG**	416.2326	444.2275	**CLLGP**	513.2854	541.2803
CLLGPD	628.3123	656.3072	**LL**	199.1805	227.1754	**LLG**	256.2020	284.1969
LLGP	353.2547	381.2496	**LLGPD**	468.2817	496.2766	**LG**	143.1179	171.1128
LGP	240.1707	268.1656	**LGPD**	355.1976	383.1925	**GP**	127.0866	155.0815
GPD	242.1135	270.1084	**PD**	185.0921	213.0870			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.1	1456.7708	0.0333	AVSAIVSCLLGPDR
28.9	1456.8110	-0.0069	ALSGIVSGQNSRLR
24.9	1456.7787	0.0255	FAVAAGPDGVERIR
23.6	1456.7998	0.0044	AAELGDAILSRSVR
23.3	1456.7820	0.0221	TRIVAMASAGVEPR
22.8	1456.7860	0.0181	SLGALMGISVWAPR
21.9	1456.7708	0.0334	QEALADLLMAQVR
21.6	1456.7932	0.0109	RANANAVGVGLMLR
21.4	1456.7708	0.0333	LVDCPLAISDRAK
20.6	1456.7886	0.0155	SSVEVAVTGSGLPVR

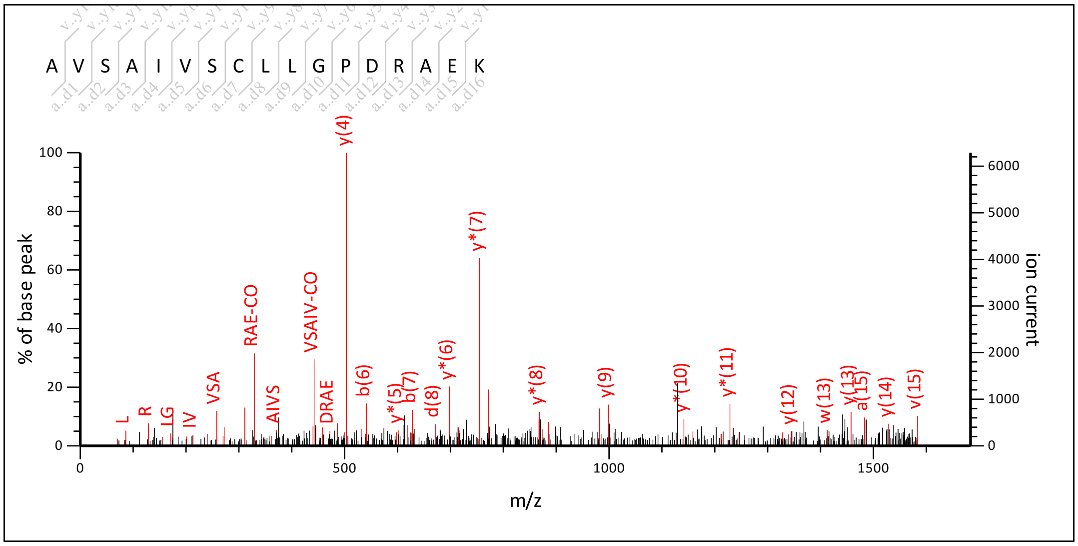
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 36

MS/MS Fragmentation of **AVSAIVSCLLGPDRAEK**
Found in **gi|115453797** in **NCBInr**, Os03g0565200 [Oryza sativa Japonica Group]

Match to Query 72: 1784.986024 from(1785.993300,1+) intensity(0.0000) index(25)
Title: Label: I10, Spot_Id: 219826, Peak_List_Id: 226859, MSMS Job_Run_Id: 21858, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I10_136859951300.txt



0 to 1683.66

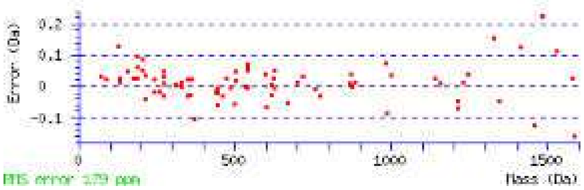
Label all possible matches ○ Label matches used for scoring ●

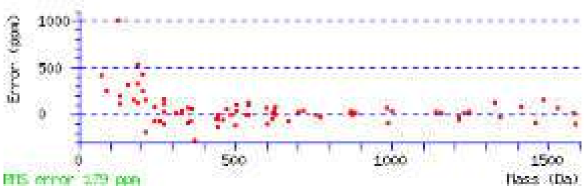
```
Monoisotopic mass of neutral peptide Mr(calc): 1784.9454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 1.3
Matches : 89/296 fragment ions using 158 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	72.0808	143.1179			**171.1128**			129.1022		V	1670.8530	1683.8734		1714.9156	1697.8891
3	60.0444	230.1499		212.1394	**258.1448**		240.1343	214.1550		S	1583.8210	1582.8258		1615.8472	1598.8207
4	44.0495	301.1870		283.1765	**329.1819**		311.1714			A	1512.7839			***1528.8152***	1511.7886
5	86.0964	414.2711		396.2605	**442.2660**		424.2554	386.2398	400.2554	I	1399.6998	1412.7202	1426.7359	***1457.7781***	1440.7515
6	72.0808	513.3395		495.3289	**541.3344**		523.3239	499.3239		V	1300.6314	1313.6518		***1344.6940***	1327.6675
7	60.0444	600.3715		582.3610	**628.3665**		610.3559	584.3766		S	1213.5994	1212.6041		***1245.6256***	1228.5990
8	133.0430	760.4022		742.3916	788.3971		770.3865	671.4087		C	1053.5687	1052.5735		***1158.5936***	1141.5670
9	86.0964	873.4863		855.4757	901.4812		883.4706	831.4393		L	940.4847	939.4894		***998.5629***	981.5364
10	86.0964	986.5703		968.5597	1014.5652		996.5547	944.5234		L	827.4006	826.4054		***885.4789***	868.4523
11	30.0338	1043.5918		1025.5812	1071.5867		1053.5761			G				***772.3948***	755.3682
12	70.0651	1140.6445		1122.6340	1168.6395		1150.6289	1114.6289		P	673.3264	672.3311		***715.3733***	698.3468
13	88.0393	1255.6715		1237.6609	1283.6664		1265.6558	1211.6817		D	558.2994	557.3042		***618.3206***	601.2940
14	129.1135	1411.7726	1394.7460	1393.7620	1439.7675	1422.7410	1421.7569	1326.7086		R	402.1983	401.2031		***503.2936***	486.2671
15	44.0495	1482.8097	1465.7832	1464.7991	1510.8046	1493.7781	1492.7941			A	331.1612			***347.1925***	330.1660
16	102.0550	1611.8523	1594.8258	1593.8417	1639.8472	1622.8207	1621.8367	1553.8468		E	202.1186	201.1234		276.1554	259.1288
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VS	159.1128	187.1077	VSA	230.1499	258.1448	VSAI	343.2340	371.2289
VSAIV	442.3024	470.2973	VSAIVS	529.3344	557.3293	VSAIVSC	689.3651	717.3600
SA	131.0815	159.0764	SAI	244.1656	272.1605	SAIV	343.2340	371.2289
SAIVS	430.2660	458.2609	SAIVSC	590.2967	618.2916	AI	157.1335	185.1285

AIV	256.2020	284.1969	**AIVS**	343.2340	371.2289	**AIVSC**	503.2646	531.2595
AIVSCL	616.3487	644.3436	**IV**	185.1648	213.1598	**IVS**	272.1969	300.1918
IVSC	432.2275	460.2224	**IVSCL**	545.3116	573.3065	**IVSCLL**	658.3956	686.3906
VS	159.1128	187.1077	**VSC**	319.1435	347.1384	**VSCL**	432.2275	460.2224
VSCLL	545.3116	573.3065	**VSCLLG**	602.3330	630.3280	**VSCLLGP**	699.3858	727.3807
SC	220.0750	248.0700	**SCL**	333.1591	361.1540	**SCLL**	446.2432	474.2381
SCLLG	503.2646	531.2595	**SCLLGP**	600.3174	628.3123	**CL**	246.1271	274.1220
CLL	359.2111	387.2061	**CLLG**	416.2326	444.2275	**CLLGP**	513.2854	541.2803
CLLGPD	628.3123	656.3072	**LL**	199.1805	227.1754	**LLG**	256.2020	284.1969
LLGP	353.2547	381.2496	**LLGPD**	468.2817	496.2766	**LLGPDR**	624.3828	652.3777
LLGPDRA	695.4199	723.4148	**LG**	143.1179	171.1128	**LGP**	240.1707	268.1656
LGPD	355.1976	383.1925	**LGPDR**	511.2987	539.2936	**LGPDRA**	582.3358	610.3307
GP	127.0866	155.0815	**GPD**	242.1135	270.1084	**GPDR**	398.2146	426.2096
GPDRA	469.2518	497.2467	**GPDRAE**	598.2944	626.2893	**PD**	185.0921	213.0870
PDR	341.1932	369.1881	**PDRA**	412.2303	440.2252	**PDRAE**	541.2729	569.2678
DR	244.1404	272.1353	**DRA**	315.1775	343.1724	**DRAE**	444.2201	472.2150
RA	200.1506	228.1455	**RAE**	329.1932	357.1881	**AE**	173.0921	201.0870





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.2	1784.9454	0.0406	LNEIVACLLSAKSDPR
43.0	1784.9454	0.0406	AVSAIVSCLLGPDRAEK
33.0	1784.9632	0.0228	TIAASDPELGLSLKNTR
32.8	1784.9156	0.0704	QELAPSEDQASVLTAVK
30.6	1784.9380	0.0480	AGLSLEGEIRDSQAALR
29.2	1784.8839	0.1021	QLDLMAQQNDPQKTR
28.5	1784.9533	0.0327	LDAAAVSFILRHSETR
27.6	1784.9897	-0.0037	FPGTQLRLLTATPSQR
26.6	1784.9632	0.0228	GISAKLSDLLQDLQER
26.6	1784.9057	0.0803	EAGALQQGLPVFSSPER

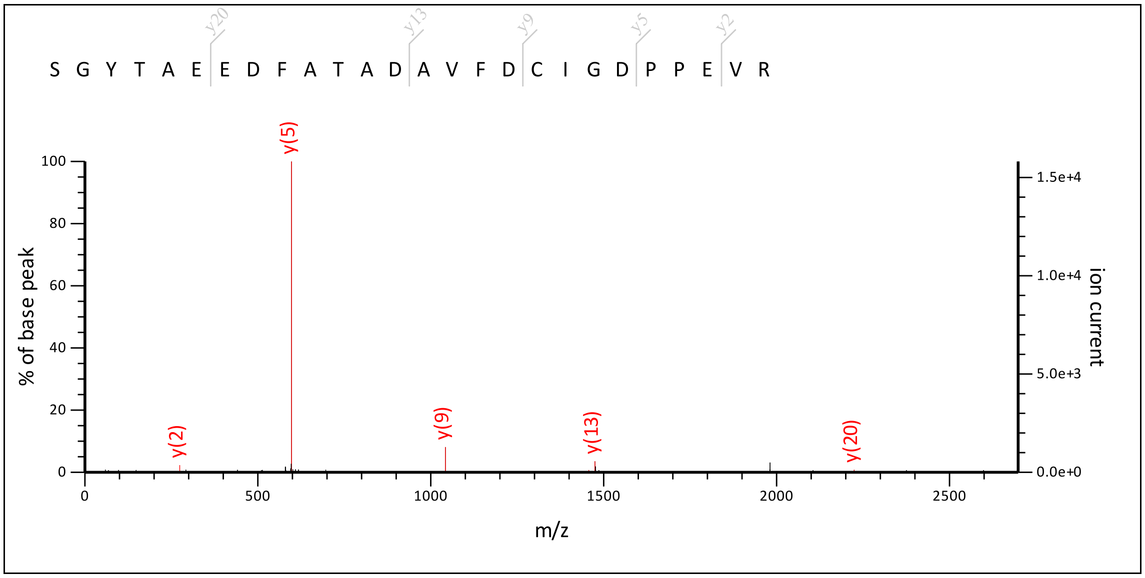
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 36**

MS/MS Fragmentation of **SGYTAEEDFATADAVFDCIGDPPEVR**
Found in **gi|115453797** in **NCBInr**, Os03g0565200 [Oryza sativa Japonica Group]

Match to Query 79: 2831.283024 from(2832.290300,1+) intensity(0.0000) index(27)
Title: Label: I10, Spot_Id: 219826, Peak_List_Id: 226876, MSMS Job_Run_Id: 21858, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I10_136859951300.txt



0 to 2698.47

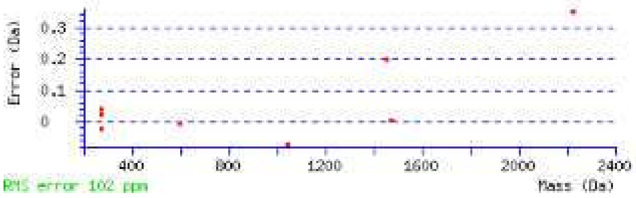
Label all possible matches ○ Label matches used for scoring ●

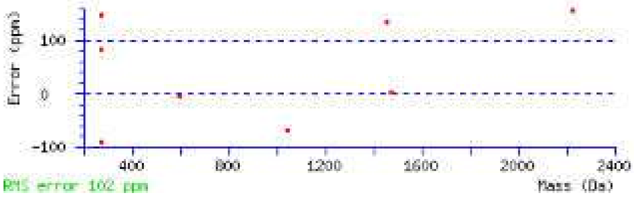
Monoisotopic mass of neutral peptide Mr(calc): 2831.2232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 1.1e+02
Matches : 8/474 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444	42.0338	88.0393	70.0287	44.0495		S							26
2	30.0338	117.0659	99.0553	145.0608	127.0502			G				2745.1985	2728.1719	2727.1879	25
3	136.0757	280.1292	262.1186	308.1241	290.1135			Y	2580.1195			2688.1770	2671.1505	2670.1664	24
4	74.0600	381.1769	363.1663	409.1718	391.1612	365.1819	367.1612	T	2479.0718	2492.0922	2494.0715	2525.1137	2508.0871	2507.1031	23
5	44.0495	452.2140	434.2034	480.2089	462.1983			A	2408.0347			2424.0660	2407.0394	2406.0554	22
6	102.0550	581.2566	563.2460	609.2515	591.2409	523.2511		E	2278.9921	2277.9969		2353.0289	2336.0023	2335.0183	21
7	102.0550	710.2992	692.2886	738.2941	720.2835	652.2937		E	2149.9495	2148.9543		***2223.9863***	2206.9597	2205.9757	20
8	88.0393	825.3261	807.3155	853.3210	835.3105	781.3363		D	2034.9226	2033.9273		2094.9437	2077.9171	2076.9331	19
9	120.0808	972.3945	954.3840	1000.3894	982.3789			F	1887.8542			1979.9168	1962.8902	1961.9062	18
10	44.0495	1043.4316	1025.4211	1071.4265	1053.4160			A	1816.8170			1832.8483	1815.8218	1814.8378	17
11	74.0600	1144.4793	1126.4687	1172.4742	1154.4637	1128.4844	1130.4637	T	1715.7694	1728.7898	1730.7690	1761.8112	1744.7847	1743.8007	16
12	44.0495	1215.5164	1197.5059	1243.5113	1225.5008			A	1644.7322			1660.7635	1643.7370	1642.7530	15
13	88.0393	1330.5434	1312.5328	1358.5383	1340.5277	1286.5535		D	1529.7053	1528.7101		1589.7264	1572.6999	1571.7159	14
14	44.0495	1401.5805	1383.5699	1429.5754	1411.5648			A	1458.6682			***1474.6995***	1457.6729	1456.6889	13
15	72.0808	1500.6489	1482.6383	1528.6438	1510.6332	1486.6332		V	1359.5998	1372.6202		1403.6624	1386.6358	1385.6518	12
16	120.0808	1647.7173	1629.7067	1675.7122	1657.7017			F	1212.5314			1304.5940	1287.5674	1286.5834	11
17	88.0393	1762.7443	1744.7337	1790.7392	1772.7286	1718.7544		D	1097.5044	1096.5092		1157.5255	1140.4990	1139.5150	10
18	133.0430	1922.7749	1904.7643	1950.7698	1932.7593	1833.7814		C	937.4738	936.4785		***1042.4986***	1025.4721	1024.4880	9
19	86.0964	2035.8590	2017.8484	2063.8539	2045.8433	2007.8277	2021.8433	I	824.3897	837.4101	851.4258	882.4680	865.4414	864.4574	8

20	30.0338	2092.8804	2074.8699	2120.8753	2102.8648			**G**				769.3839	752.3573	751.3733		**7**
21	88.0393	2207.9074	2189.8968	2235.9023	2217.8917	2163.9175		**D**	652.3413	651.3461		712.3624	695.3359	694.3519		**6**
22	70.0651	2304.9601	2286.9496	2332.9551	2314.9445	2278.9445		**P**	555.2885	554.2933		***597.3355***	580.3089	579.3249		**5**
23	70.0651	2402.0129	2384.0023	2430.0078	2411.9973	2375.9973		**P**	458.2358	457.2405		500.2827	483.2562	482.2722		**4**
24	102.0550	2531.0555	2513.0449	2559.0504	2541.0398	2473.0500		**E**	329.1932	328.1979		403.2300	386.2034	385.2194		**3**
25	72.0808	2630.1239	2612.1133	2658.1188	2640.1083	2616.1083		**V**	230.1248	243.1452		***274.1874***	257.1608			**2**
26	129.1135							**R**	74.0237	73.0284		175.1190	158.0924			**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GY	193.0972	221.0921	**GYT**	294.1448	322.1397	**GYTA**	365.1819	393.1769
GYTAE	494.2245	522.2195	**GYTAEE**	623.2671	651.2620	**YT**	237.1234	265.1183
YTA	308.1605	336.1554	**YTAE**	437.2031	465.1980	**YTAEE**	566.2457	594.2406
YTAEED	681.2726	709.2675	**TA**	145.0972	173.0921	**TAE**	274.1397	302.1347
TAEE	403.1823	431.1773	**TAEED**	518.2093	546.2042	**TAEEDF**	665.2777	693.2726
AE	173.0921	201.0870	**AEE**	302.1347	330.1296	**AEED**	417.1616	445.1565
AEEDF	564.2300	592.2249	**AEEDFA**	635.2671	663.2620	**EE**	231.0975	259.0925
EED	346.1245	374.1194	**EEDF**	493.1929	521.1878	**EEDFA**	564.2300	592.2249
EEDFAT	665.2777	693.2726	**ED**	217.0819	245.0768	**EDF**	364.1503	392.1452
EDFA	435.1874	463.1823	**EDFAT**	536.2351	564.2300	**EDFATA**	607.2722	635.2671
DF	235.1077	263.1026	**DFA**	306.1448	334.1397	**DFAT**	407.1925	435.1874
DFATA	478.2296	506.2245	**DFATAD**	593.2566	621.2515	**DFATADA**	664.2937	692.2886
FA	191.1179	219.1128	**FAT**	292.1656	320.1605	**FATA**	363.2027	391.1976
FATAD	478.2296	506.2245	**FATADA**	549.2667	577.2617	**FATADAV**	648.3352	676.3301
AT	145.0972	173.0921	**ATA**	216.1343	244.1292	**ATAD**	331.1612	359.1561
ATADA	402.1983	430.1932	**ATADAV**	501.2667	529.2617	**ATADAVF**	648.3352	676.3301
TA	145.0972	173.0921	**TAD**	260.1241	288.1190	**TADA**	331.1612	359.1561
TADAV	430.2296	458.2245	**TADAVF**	577.2980	605.2930	**TADAVFD**	692.3250	720.3199
AD	159.0764	187.0713	**ADA**	230.1135	258.1084	**ADAV**	329.1819	357.1769
ADAVF	476.2504	504.2453	**ADAVFD**	591.2773	619.2722	**DA**	159.0764	187.0713
DAV	258.1448	286.1397	**DAVF**	405.2132	433.2082	**DAVFD**	520.2402	548.2351
DAVFDC	680.2708	708.2658	**AV**	143.1179	171.1128	**AVF**	290.1863	318.1812
AVFD	405.2132	433.2082	**AVFDC**	565.2439	593.2388	**AVFDCI**	678.3280	706.3229
VF	219.1492	247.1441	**VFD**	334.1761	362.1710	**VFDC**	494.2068	522.2017
VFDCI	607.2908	635.2858	**VFDCIG**	664.3123	692.3072	**FD**	235.1077	263.1026
FDC	395.1384	423.1333	**FDCI**	508.2224	536.2173	**FDCIG**	565.2439	593.2388
FDCIGD	680.2708	708.2658	**DC**	248.0700	276.0649	**DCI**	361.1540	389.1489
DCIG	418.1755	446.1704	**DCIGD**	533.2024	561.1973	**DCIGDP**	630.2552	658.2501
CI	246.1271	274.1220	**CIG**	303.1485	331.1435	**CIGD**	418.1755	446.1704
CIGDP	515.2282	543.2232	**CIGDPP**	612.2810	640.2759	**IG**	143.1179	171.1128
IGD	258.1448	286.1397	**IGDP**	355.1976	383.1925	**IGDPP**	452.2504	480.2453
IGDPPE	581.2930	609.2879	**IGDPPEV**	680.3614	708.3563	**GD**	145.0608	173.0557
GDP	242.1135	270.1084	**GDPP**	339.1663	367.1612	**GDPPE**	468.2089	496.2038
GDPPEV	567.2773	595.2722	**DP**	185.0921	213.0870	**DPP**	282.1448	310.1397
DPPE	411.1874	439.1823	**DPPEV**	510.2558	538.2508	**PP**	167.1179	195.1128
PPE	296.1605	324.1554	**PPEV**	395.2289	423.2238	**PE**	199.1077	227.1026
PEV	298.1761	326.1710	**EV**	201.1234	229.1183			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.7	2831.2232	0.0598	SGYTAEEDFATADAVFDCIGDPPEVR
12.5	2831.4388	-0.1558	MSFQPLPPGAAADDAVLVQPETRLHR
12.4	2831.4488	-0.1658	NGAVVGAVQVFDGQEIMLISDQGTLVR
12.3	2831.1181	0.1649	DDYGSSYNYYAMDYWGQGTSVTVSS
11.6	2831.4084	-0.1253	MSTSTTASVSTHILDTSVGRPAGDVAVR
11.5	2831.2894	-0.0064	SMSSAYLEWSSLRASDTAIYYCVR
10.9	2831.2717	0.0113	SFGCMPNAATLGGITPAQWLMEEYR
10.9	2831.2162	0.0668	YAMQEFMILPTGAANFTEAMKMGSE
10.7	2831.4501	-0.1671	MSGQLFDVVQGNSPLIAVALHNGHGVR
10.7	2831.3990	-0.1160	AQANLVVRENYAQVNFYNEISFSR

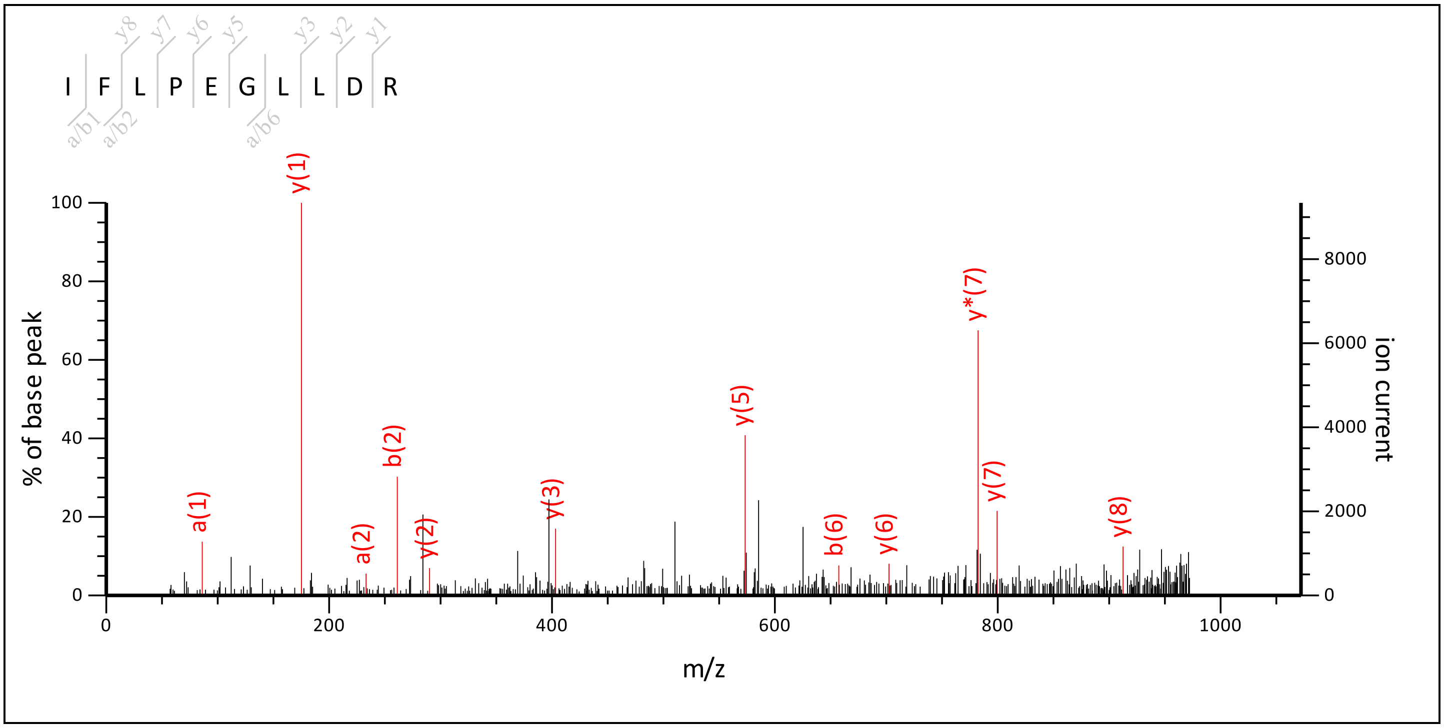
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 37**

MS/MS Fragmentation of **IFLPEGLLDR**
Found in **gi|19184** in **NCBInr**, Type I (26 kD) CP29 polypeptide [Solanum lycopersicum]

Match to Query 175: 1171.674124 from(1172.681400,1+) intensity(0.0000) index(12)
Title: Label: E5, Spot_Id: 219742, Peak_List_Id: 225695, MSMS Job_Run_Id: 21786, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E5_136842184900.txt



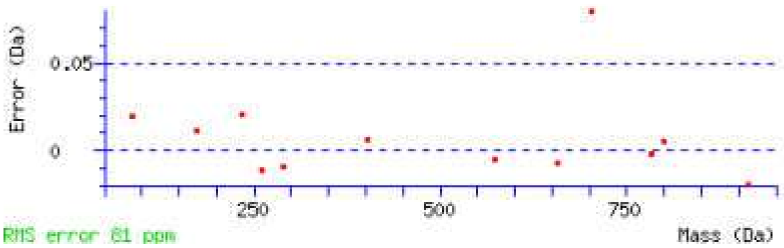
0 to 1072.13

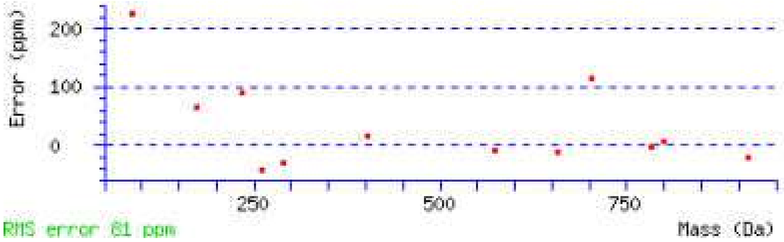
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1171.6601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.64
Matches : 12/36 fragment ions using 30 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	**86.0964**	114.0913	I			10
2	**233.1648**	**261.1598**	F	1059.5833	1042.5568	9
3	346.2489	374.2438	L	***912.5149***	895.4884	8
4	443.3017	471.2966	P	***799.4308***	782.4043	7
5	572.3443	600.3392	E	***702.3781***	685.3515	6
6	629.3657	**657.3606**	G	***573.3355***	556.3089	5
7	742.4498	770.4447	L	516.3140	499.2875	4
8	855.5339	883.5288	L	***403.2300***	386.2034	3

9	970.5608	998.5557	**D**	***290.1459***	273.1193	**2**
10			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.7	1171.6601	0.0140	IFLPEGLLDR
15.3	1171.6462	0.0279	RSGSKPWAVGK
12.8	1171.6999	-0.0257	LMIPTTVILR
12.7	1171.6495	0.0246	IMIGRSLNPR
11.5	1171.5768	0.0973	AATGLQCPAGAR
11.5	1171.7216	-0.0475	IFLPETVLLK
11.5	1171.6713	0.0028	LHPKPEPLNK
11.5	1171.6859	-0.0118	LMLINRAGIR
11.3	1171.6383	0.0358	MEIILNVANR
11.2	1171.5833	0.0908	QNEVEGLIDR

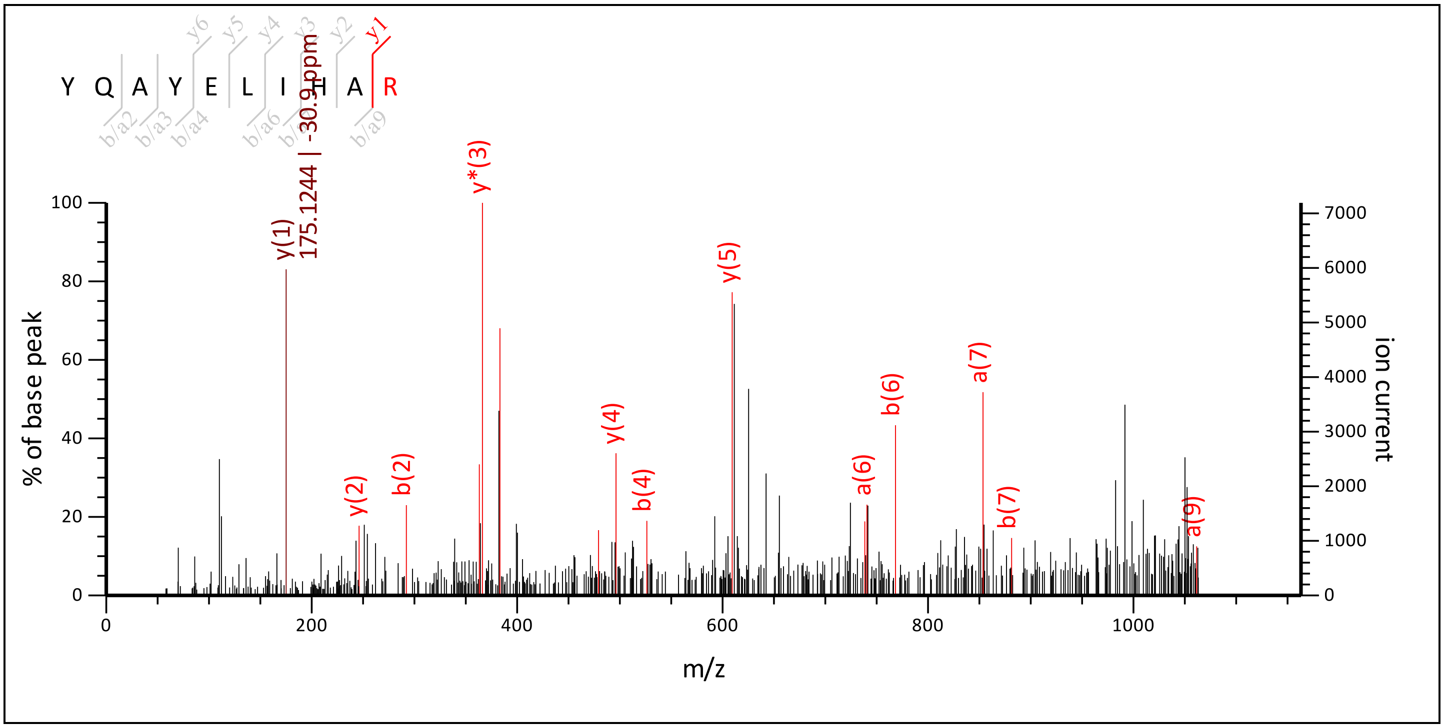
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 37

MS/MS Fragmentation of **YQAYELIHAR**
Found in **gi|19184** in **NCBInr**, Type I (26 kD) CP29 polypeptide [Solanum lycopersicum]

Match to Query 218: 1262.659024 from(1263.666300,1+) intensity(0.0000) index(15)
Title: Label: E5, Spot_Id: 219742, Peak_List_Id: 225693, MSMS Job_Run_Id: 21786, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E5_136842184900.txt



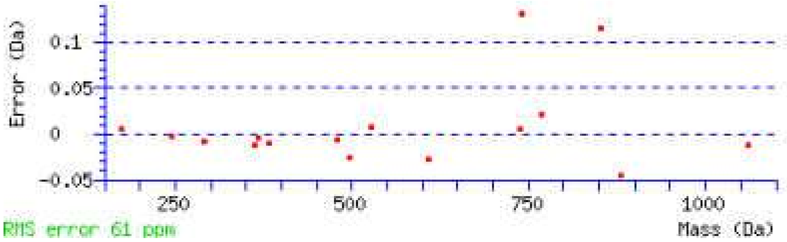
0 to 1163.09

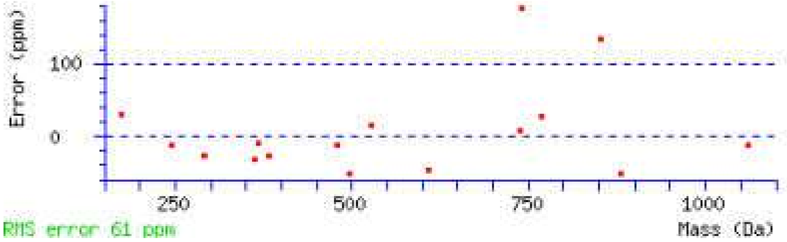
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1262.6407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 11
Matches : 16/52 fragment ions using 44 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	136.0757		164.0706		**Y**			**10**
2	264.1343	247.1077	***292.1292***	275.1026	**Q**	1100.5847	1083.5582	**9**
3	335.1714	318.1448	***363.1663***	346.1397	**A**	972.5261	955.4996	**8**
4	498.2347	481.2082	***526.2296***	509.2031	**Y**	901.4890	884.4625	**7**
5	627.2773	610.2508	655.2722	638.2457	**E**	***738.4257***	721.3992	**6**
6	**740.3614**	723.3348	***768.3563***	751.3297	**L**	***609.3831***	592.3566	**5**
7	**853.4454**	836.4189	***881.4403***	864.4138	**I**	***496.2990***	479.2725	**4**
8	990.5043	973.4778	1018.4993	1001.4727	**H**	***383.2150***	366.1884	**3**

9	**1061.5415**	1044.5149	1089.5364	1072.5098	**A**	*246.1561*	229.1295	**2**
10					**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.3	1262.6407	0.0183	YQAYELIHAR
19.5	1262.6884	-0.0293	HQIFELIHAR
11.1	1262.7057	-0.0466	VLLTIPMSFSR
11.1	1262.6619	-0.0029	LNGLAADISFSR
10.7	1262.6480	0.0110	TGGAPVGVGANHAR
10.0	1262.5527	0.1063	HEDGSELFSSR
9.6	1262.7095	-0.0505	VEALLNQIHAR
8.9	1262.6731	-0.0141	AALRQLDGTYR
8.4	1262.6506	0.0084	APELELYTTAR
8.2	1262.6996	-0.0406	RYHPVVTHVR

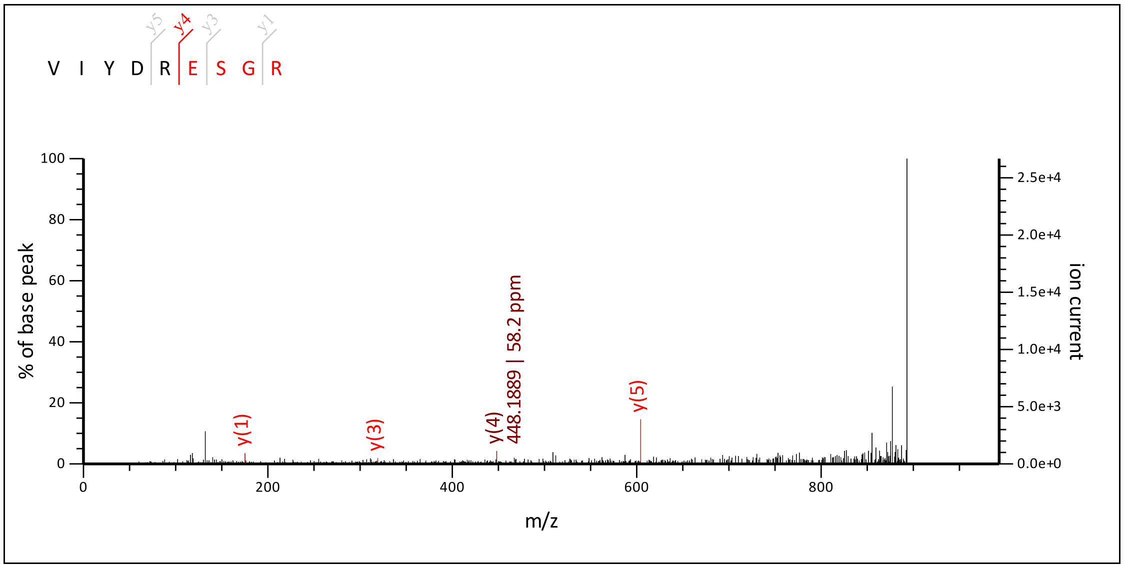
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 38

MS/MS Fragmentation of **VIYDRESGR**
Found in **gi|115473531** in **NCBInr**, Os07g0631900 [Oryza sativa Japonica Group]

Match to Query 149: 1093.530824 from(1094.538100,1+) intensity(0.0000) index(22)
Title: Label: C5, Spot_Id: 219740, Peak_List_Id: 225626, MSMS Job_Run_Id: 21784, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C5_136842183200.txt



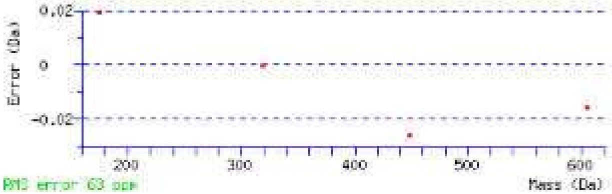
0 to 993.07

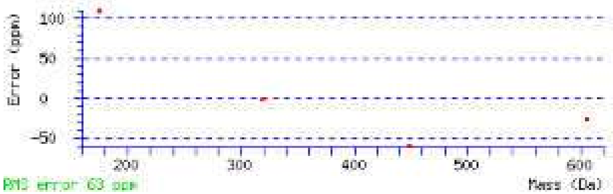
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1093.5516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 13 **Expect:** 1.4e+02
Matches : 4/123 fragment ions using 9 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	72.0808			100.0757			44.0495		V							9
2	86.0964	185.1648			213.1598			157.1335	171.1492	I	937.4122	950.4326	964.4483	995.4905	978.4639	977.4799	8
3	136.0757	348.2282			376.2231					Y	774.3489			882.4064	865.3799	864.3959	7
4	88.0393	463.2551		445.2445	491.2500		473.2395	419.2653		D	659.3220	658.3267		719.3431	702.3165	701.3325	6
5	129.1135	619.3562	602.3297	601.3457	647.3511	630.3246	629.3406	534.2922		R	503.2209	502.2256		***604.3161***	587.2896	586.3056	5
6	102.0550	748.3988	731.3723	730.3883	776.3937	759.3672	758.3832	690.3933		E	374.1783	373.1830		***448.2150***	431.1885	430.2045	4
7	60.0444	835.4308	818.4043	817.4203	863.4258	846.3992	845.4152	819.4359		S	287.1462	286.1510		***319.1724***	302.1459	301.1619	3
8	30.0338	892.4523	875.4258	874.4417	920.4472	903.4207	902.4367			G				232.1404	215.1139		2
9	129.1135									R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IY	249.1598	277.1547	IYD	364.1867	392.1816	IYDR	520.2878	548.2827
IYDRE	649.3304	677.3253	YD	251.1026	279.0975	YDR	407.2037	435.1987
YDRE	536.2463	564.2413	YDRES	623.2784	651.2733	YDRESG	680.2998	708.2947
DR	244.1404	272.1353	DRE	373.1830	401.1779	DRES	460.2150	488.2100
DRESG	517.2365	545.2314	RE	258.1561	286.1510	RES	345.1881	373.1830
RESG	402.2096	430.2045	ES	189.0870	217.0819	ESG	246.1084	274.1034
SG	117.0659	145.0608						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.1	1093.5013	0.0295	EHHSRESGR
13.1	1093.5265	0.0044	FQTNRESGR
13.1	1093.5516	-0.0208	IVYDRESGR
13.1	1093.5516	-0.0208	VIYDRESGR
7.1	1093.4896	0.0412	ISPMMAEGSR
6.5	1093.4975	0.0334	DPYDRAMAR
6.5	1093.5008	0.0300	VMMERDTGR
5.3	1093.5121	0.0188	RSGTGMAMAGR
5.1	1093.4822	0.0486	CASKAEESGR
5.1	1093.5074	0.0235	DGTLMLEGSR

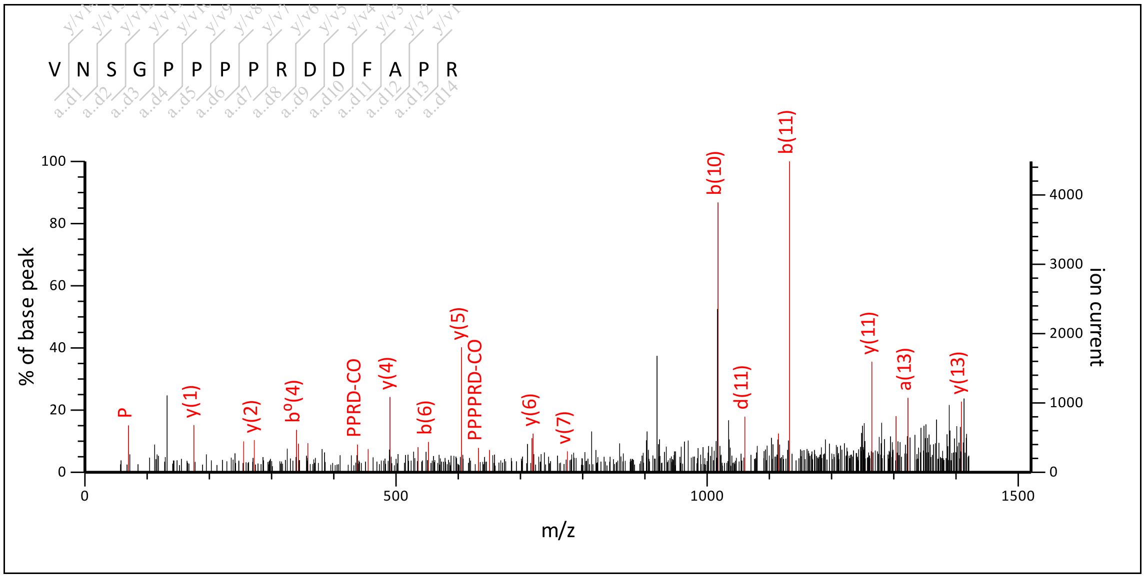
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 38

MS/MS Fragmentation of **VNSGPPPPRDDFAPR**
Found in **gi|115473531** in **NCBInr**, Os07g0631900 [Oryza sativa Japonica Group]

Match to Query 298: 1620.784424 from(1621.791700,1+) intensity(0.0000) index(34)
Title: Label: C5, Spot_Id: 219740, Peak_List_Id: 225628, MSMS Job_Run_Id: 21784, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C5_136842183200.txt



0 to 1520.61

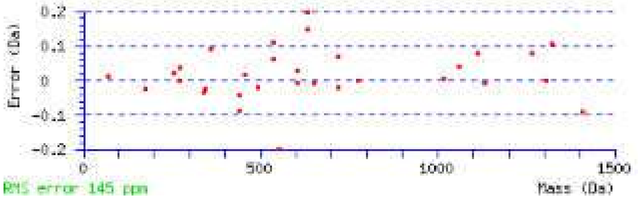
Label all possible matches ○ Label matches used for scoring ●

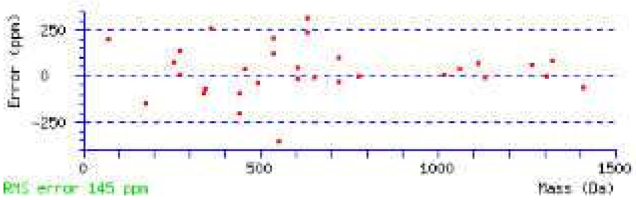
Monoisotopic mass of neutral peptide Mr(calc): 1620.8009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.05
Matches : 36/267 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808			100.0757			44.0495	V						15
2	87.0553	186.1237	169.0972		214.1186	197.0921		143.1179	N	1463.7026	1462.7074	1522.7397	1505.7132	1504.7292	14
3	60.0444	273.1557	256.1292	255.1452	301.1506	284.1241	283.1401	257.1608	S	1376.6706	1375.6753	***1408.6968***	1391.6702	1390.6862	13
4	30.0338	330.1772	313.1506	312.1666	**358.1721**	341.1456	340.1615		G			1321.6648	1304.6382	1303.6542	12
5	70.0651	427.2300	410.2034	409.2194	**455.2249**	438.1983	437.2143	401.2143	P	1222.5963	1221.6011	***1264.6433***	1247.6167	1246.6327	11
6	70.0651	524.2827	507.2562	506.2722	**552.2776**	535.2511	534.2671	498.2671	P	1125.5436	1124.5483	1167.5905	1150.5640	1149.5800	10
7	70.0651	621.3355	604.3089	603.3249	649.3304	632.3039	631.3198	595.3198	P	1028.4908	1027.4956	1070.5378	1053.5112	1052.5272	9
8	70.0651	**718.3883**	701.3617	700.3777	746.3832	729.3566	728.3726	692.3726	P	931.4381	930.4428	973.4850	956.4585	955.4744	8
9	129.1135	874.4894	857.4628	856.4788	902.4843	885.4577	884.4737	789.4254	R	775.3369	774.3417	876.4322	859.4057	858.4217	7
10	88.0393	989.5163	972.4898	971.5057	**1017.5112**	1000.4847	999.5007	945.5265	D	660.3100	659.3148	***720.3311***	703.3046	702.3206	6
11	88.0393	1104.5432	1087.5167	1086.5327	**1132.5382**	1115.5116	1114.5276	1060.5534	D	545.2831	544.2878	***605.3042***	588.2776	587.2936	5
12	120.0808	1251.6117	1234.5851	1233.6011	1279.6066	1262.5800	1261.5960		F	398.2146		***490.2772***	473.2507		4
13	44.0495	**1322.6488**	1305.6222	1304.6382	1350.6437	1333.6171	1332.6331		A	327.1775		***343.2088***	326.1823		3
14	70.0651	1419.7015	1402.6750	1401.6910	1447.6965	1430.6699	1429.6859	1393.6859	P	230.1248	229.1295	***272.1717***	255.1452		2
15	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NS	174.0873	202.0822	NSG	231.1088	259.1037	NSGP	328.1615	356.1565
NSGPP	425.2143	453.2092	NSGPPP	522.2671	550.2620	NSGPPPP	619.3198	647.3148
SG	117.0659	145.0608	SGP	214.1186	242.1135	SGPP	311.1714	339.1663

SGPPP	408.2241	436.2191	**SGPPPP**	505.2769	533.2718	**SGPPPPR**	661.3780	689.3729
GP	127.0866	155.0815	**GPP**	224.1394	252.1343	**GPPP**	321.1921	349.1870
GPPPP	418.2449	446.2398	**GPPPPR**	574.3460	602.3409	**GPPPPRD**	689.3729	717.3679
PP	167.1179	195.1128	**PPP**	264.1707	292.1656	**PPPP**	361.2234	389.2183
PPPPR	517.3245	545.3194	**PPPPRD**	632.3515	660.3464	**PP**	167.1179	195.1128
PPP	264.1707	292.1656	**PPPR**	420.2718	448.2667	**PPPRD**	535.2987	563.2936
PPPRDD	650.3257	678.3206	**PP**	167.1179	195.1128	**PPR**	323.2190	351.2139
PPRD	438.2459	466.2409	**PPRDD**	553.2729	581.2678	**PR**	226.1662	254.1612
PRD	341.1932	369.1881	**PRDD**	456.2201	484.2150	**PRDDF**	603.2885	631.2835
PRDDFA	674.3257	702.3206	**RD**	244.1404	272.1353	**RDD**	359.1674	387.1623
RDDF	506.2358	534.2307	**RDDFA**	577.2729	605.2678	**RDDFAP**	674.3257	702.3206
DD	203.0662	231.0612	**DDF**	350.1347	378.1296	**DDFA**	421.1718	449.1667
DDFAP	518.2245	546.2195	**DF**	235.1077	263.1026	**DFA**	306.1448	334.1397
DFAP	403.1976	431.1925	**FA**	191.1179	219.1128	**FAP**	288.1707	316.1656
AP	141.1022	169.0972						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.7	1620.8009	-0.0164	VNSGPPPPRDDFAPR
16.0	1620.7777	0.0067	SKDMIQNSLDESVR
13.9	1620.6912	0.0932	MPSSSDLYNRTFGM
13.7	1620.7858	-0.0013	MLLFQPEWSDDLK
13.6	1620.6329	0.1516	SSFDFGFNDDDAER
12.9	1620.8141	-0.0297	SAIMTTANNLDNTKK
12.9	1620.8909	-0.1065	SSSIVVMKAAAAPVFK
10.9	1620.7665	0.0179	MEVVVLSDSGDIDSR
10.7	1620.8042	-0.0198	FPCSLLSNGRDSIR
10.4	1620.7678	0.0166	AGDAASARAVFDAMPR

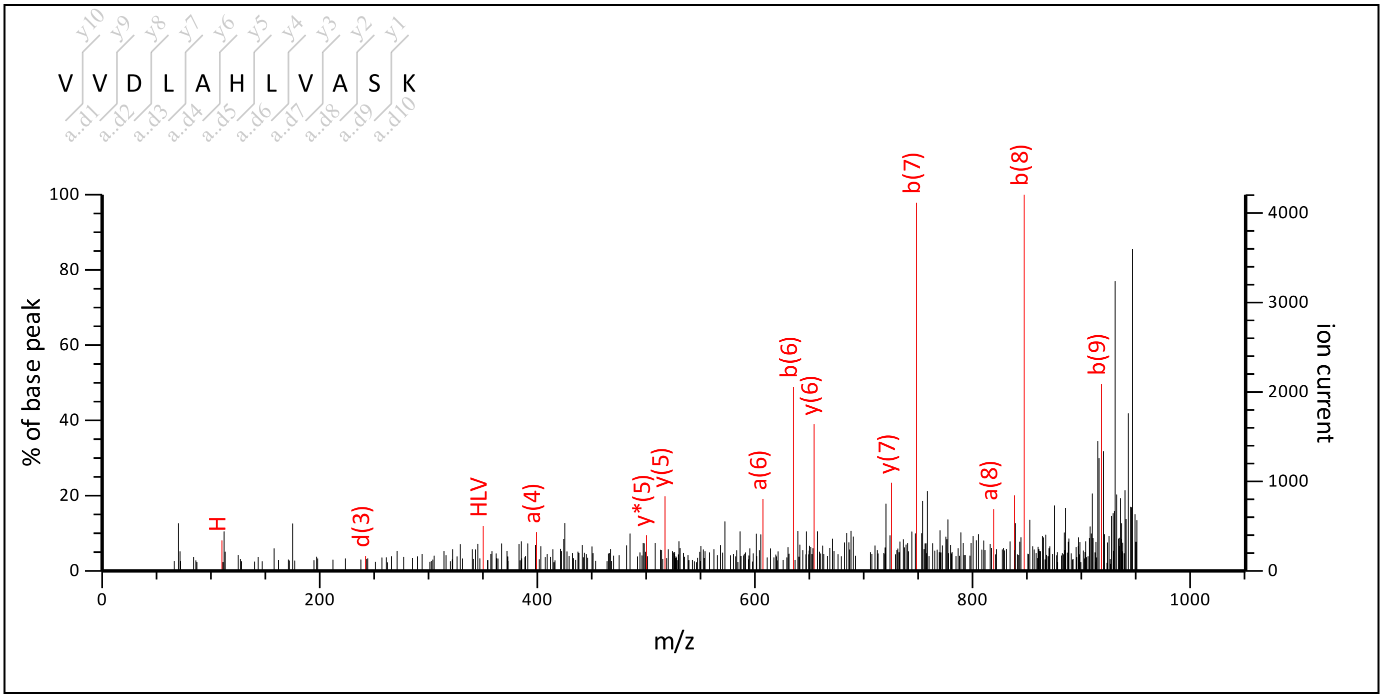
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 39

MS/MS Fragmentation of **VVDLAHLVASK**
Found in **gi|115450493** in **NCBInr**, Os03g0129300 [Oryza sativa Japonica Group]

Match to Query 168: 1150.728824 from(1151.736100,1+) intensity(0.0000) index(15)
Title: Label: H12, Spot_Id: 219857, Peak_List_Id: 227353, MSMS Job_Run_Id: 21959, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H12_136868235200.txt



0 to 1051.06

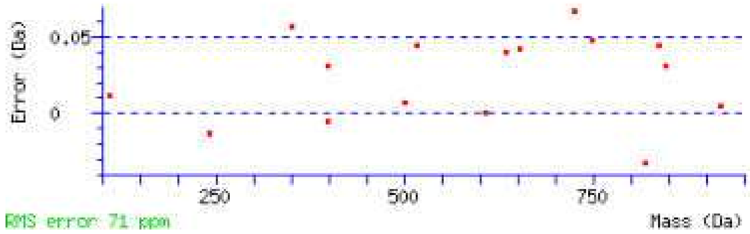
Label all possible matches ○ Label matches used for scoring ●

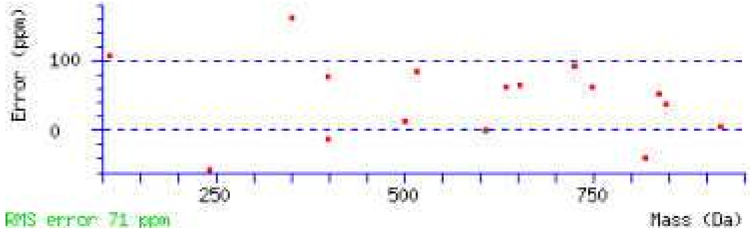
Monoisotopic mass of neutral peptide Mr(calc): 1150.6710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 25
Matches : 16/163 fragment ions using 27 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495	V						11
2	72.0808	171.1492		199.1441		157.1335	V	1008.5473	1021.5677	1052.6099	1035.5833	1034.5993	10
3	88.0393	286.1761	268.1656	314.1710	296.1605	242.1863	D	893.5203	892.5251	953.5415	936.5149	935.5309	9
4	86.0964	**399.2602**	381.2496	427.2551	409.2445	357.2132	L	780.4363	779.4410	***838.5145***	821.4880	820.5039	8
5	44.0495	470.2973	452.2867	498.2922	480.2817		A	709.3991		***725.4304***	708.4039	707.4199	7
6	110.0713	**607.3562**	589.3457	***635.3511***	617.3406		H	572.3402		***654.3933***	637.3668	636.3828	6
7	86.0964	720.4403	702.4297	***748.4352***	730.4246	678.3933	L	459.2562	458.2609	***517.3344***	500.3079	499.3239	5
8	72.0808	**819.5087**	801.4981	***847.5036***	829.4930	805.4930	V	360.1878	373.2082	404.2504	387.2238	386.2398	4
9	44.0495	890.5458	872.5352	***918.5407***	900.5302		A	289.1506		305.1819	288.1554	287.1714	3
10	60.0444	977.5778	959.5673	1005.5728	987.5622	961.5829	S	202.1186	201.1234	234.1448	217.1183	216.1343	2

11	101.1073						**K**	74.0237	73.0284	147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VD	187.1077	215.1026	**VDL**	300.1918	328.1867	**VDLA**	371.2289	399.2238
VDLAH	508.2878	536.2827	**VDLAHL**	621.3719	649.3668	**DL**	201.1234	229.1183
DLA	272.1605	300.1554	**DLAH**	409.2194	437.2143	**DLAHL**	522.3035	550.2984
DLAHLV	621.3719	649.3668	**DLAHLVA**	692.4090	720.4039	**LA**	157.1335	185.1285
LAH	294.1925	322.1874	**LAHL**	407.2765	435.2714	**LAHLV**	506.3449	534.3398
LAHLVA	577.3820	605.3770	**LAHLVAS**	664.4141	692.4090	**AH**	181.1084	209.1033
AHL	294.1925	322.1874	**AHLV**	393.2609	421.2558	**AHLVA**	464.2980	492.2929
AHLVAS	551.3300	579.3249	**HL**	223.1553	251.1503	**HLV**	322.2238	350.2187
HLVA	393.2609	421.2558	**HLVAS**	480.2929	508.2878	**LV**	185.1648	213.1598
LVA	256.2020	284.1969	**LVAS**	343.2340	371.2289	**VA**	143.1179	171.1128
VAS	230.1499	258.1448	**AS**	131.0815	159.0764			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.6	1150.6710	0.0578	VVDLAHLVASK
22.1	1150.6194	0.1095	IKSTSSSGAVSK
21.4	1150.6359	0.0929	HEHLLPLHR
21.4	1150.6458	0.0830	SNTTIPILHR
21.4	1150.6458	0.0830	STQSLPLLHR
20.0	1150.6169	0.1120	GCSVLFSILR
20.0	1150.6169	0.1120	GCSVLFSLLR
18.6	1150.6710	0.0578	ELAAIHVLASK
15.3	1150.6207	0.1082	AEIIAHRDAR
14.6	1150.6532	0.0756	GVHMLPLAVSK

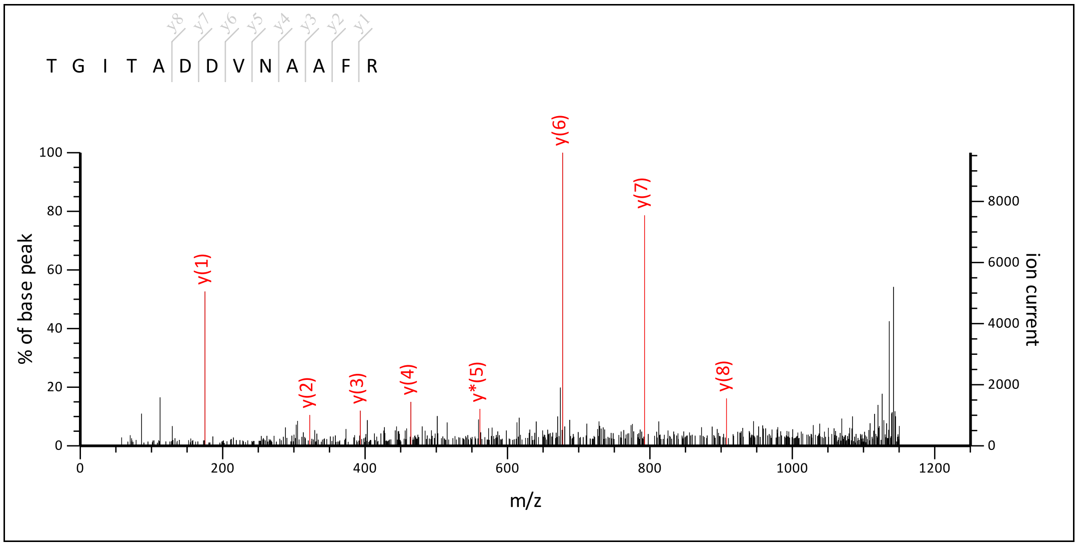
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 39

MS/MS Fragmentation of **TGITADDVNAAFR**
Found in **gi|115450493** in **NCBInr**, Os03g0129300 [Oryza sativa Japonica Group]

Match to Query 273: 1349.752224 from(1350.759500,1+) intensity(0.0000) index(24)
Title: Label: H12, Spot_Id: 219857, Peak_List_Id: 227347, MSMS Job_Run_Id: 21959, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H12_136868235200.txt



0 to 1250.3

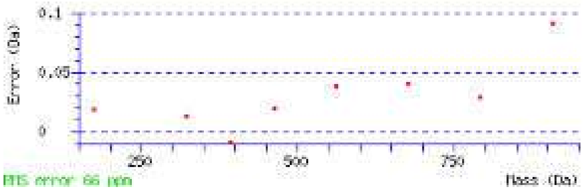
Label all possible matches ○ Label matches used for scoring ●

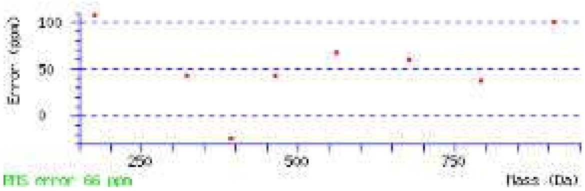
Monoisotopic mass of neutral peptide Mr(calc): 1349.6575
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 0.092
Matches : 8/214 fragment ions using 11 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	30.0338	131.0815		113.0709	159.0764		141.0659			G				1249.6171	1232.5906	123
3	86.0964	244.1656		226.1550	272.1605		254.1499	216.1343	230.1499	I	1134.5174	1147.5378	1161.5535	1192.5957	1175.5691	117
4	74.0600	345.2132		327.2027	373.2082		355.1976	329.2183	331.1976	T	1033.4697	1046.4902	1048.4694	1079.5116	1062.4851	106
5	44.0495	416.2504		398.2398	444.2453		426.2347			A	962.4326			978.4639	961.4374	96
6	88.0393	531.2773		513.2667	559.2722		541.2617	487.2875		D	847.4057	846.4104		***907.4268***	890.4003	88
7	88.0393	646.3042		628.2937	674.2992		656.2886	602.3144		D	732.3787	731.3835		***792.3999***	775.3733	77
8	72.0808	745.3727		727.3621	773.3676		755.3570	731.3570		V	633.3103	646.3307		***677.3729***	660.3464	
9	87.0553	859.4156	842.3890	841.4050	887.4105	870.3840	869.3999	816.4098		N	519.2674	518.2722		578.3045	561.2780	
10	44.0495	930.4527	913.4262	912.4421	958.4476	941.4211	940.4371			A	448.2303			***464.2616***	447.2350	
11	44.0495	1001.4898	984.4633	983.4793	1029.4847	1012.4582	1011.4742			A	377.1932			***393.2245***	376.1979	
12	120.0808	1148.5582	1131.5317	1130.5477	1176.5531	1159.5266	1158.5426			F	230.1248			***322.1874***	305.1608	
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GI	143.1179	171.1128	GIT	244.1656	272.1605	GITA	315.2027	343.1976
GITAD	430.2296	458.2245	GITADD	545.2566	573.2515	GITADDV	644.3250	672.3199
IT	187.1441	215.1390	ITA	258.1812	286.1761	ITAD	373.2082	401.2031
ITADD	488.2351	516.2300	ITADDV	587.3035	615.2984	TA	145.0972	173.0921
TAD	260.1241	288.1190	TADD	375.1510	403.1460	TADDV	474.2195	502.2144
TADDVN	588.2624	616.2573	TADDVNA	659.2995	687.2944	AD	159.0764	187.0713
ADD	274.1034	302.0983	ADDV	373.1718	401.1667	ADDVN	487.2147	515.2096
ADDVNA	558.2518	586.2467	ADDVNAA	629.2889	657.2838	DD	203.0662	231.0612

DDV	302.1347	330.1296	**DDVN**	416.1776	444.1725	**DDVNA**	487.2147	515.2096
DDVNAA	558.2518	586.2467	**DV**	187.1077	215.1026	**DVN**	301.1506	329.1456
DVNA	372.1878	400.1827	**DVNAA**	443.2249	471.2198	**DVNAAF**	590.2933	618.2882
VN	186.1237	214.1186	**VNA**	257.1608	285.1557	**VNAA**	328.1979	356.1928
VNAAF	475.2663	503.2613	**NA**	158.0924	186.0873	**NAA**	229.1295	257.1244
NAAF	376.1979	404.1928	**AA**	115.0866	143.0815	**AAF**	262.1550	290.1499
AF	191.1179	219.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.4	1349.6575	0.0947	TGITADDVNAAFR
33.6	1349.6907	0.0615	RVGMLAATSAAMR
30.5	1349.6874	0.0648	QAIMDGLSRGFR
30.3	1349.6575	0.0947	SDFAQAVTDAGIR
28.1	1349.6687	0.0835	DYNSPSATARLR
27.2	1349.6323	0.1199	DAYAAAAADARER
27.2	1349.6324	0.1199	SEADRDGLNAFR
26.7	1349.6688	0.0835	IENDGSVRSAFR
26.4	1349.6952	0.0570	EFSRNRPAAFR
26.4	1349.7204	0.0318	ERGALFVNAAFR

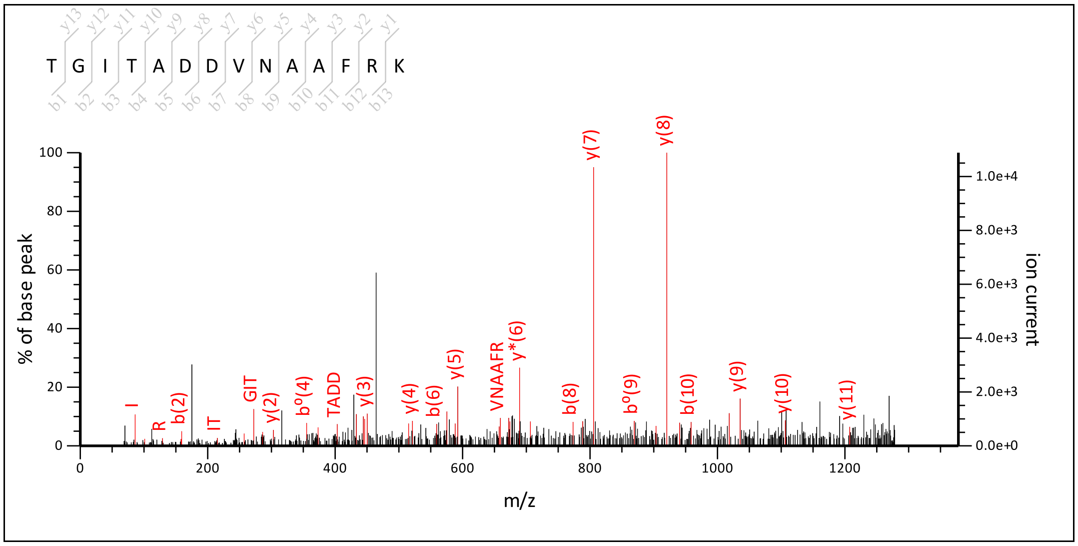
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 39**

MS/MS Fragmentation of **TGITADDVNAAFRK**
Found in **gi|115450493** in **NCBInr**, Os03g0129300 [Oryza sativa Japonica Group]

Match to Query 329: 1477.854824 from(1478.862100,1+) intensity(0.0000) index(27)
Title: Label: H12, Spot_Id: 219857, Peak_List_Id: 227345, MSMS Job_Run_Id: 21959, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H12_136868235200.txt



0 to 1378.08

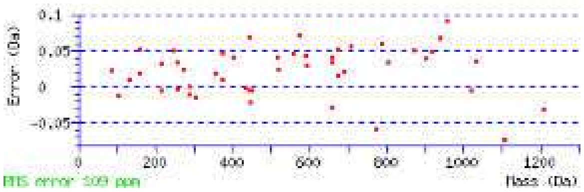
Label all possible matches ○ Label matches used for scoring ●

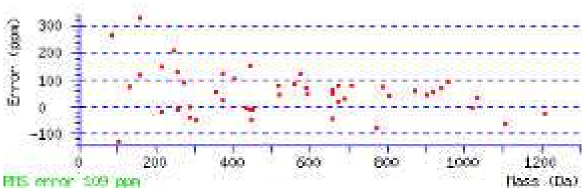
Monoisotopic mass of neutral peptide Mr(calc): 1477.7525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 1.5
Matches : 53/236 fragment ions using 104 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	30.0338	131.0815		113.0709	**159.0764**		141.0659			G				1377.7121	1360.6856
3	86.0964	244.1656		226.1550	**272.1605**		254.1499	216.1343	230.1499	I	1262.6124	1275.6328	1289.6484	1320.6906	1303.6641
4	74.0600	345.2132		327.2027	**373.2082**		355.1976	329.2183	331.1976	T	1161.5647	1174.5851	1176.5644	***1207.6066***	1190.5800
5	44.0495	416.2504		398.2398	**444.2453**		426.2347			A	1090.5276			***1106.5589***	1089.5323
6	88.0393	531.2773		513.2667	**559.2722**		541.2617	487.2875		D	975.5007	974.5054		***1035.5218***	1018.4952
7	88.0393	646.3042		628.2937	**674.2992**		656.2886	602.3144		D	860.4737	859.4785		***920.4948***	903.4683
8	72.0808	745.3727		727.3621	**773.3676**		755.3570	731.3570		V	761.4053	774.4257		***805.4679***	788.4413
9	87.0553	859.4156	842.3890	841.4050	887.4105	870.3840	869.3999	816.4098		N	647.3624	646.3671		***706.3995***	689.3729
10	44.0495	930.4527	913.4262	912.4421	**958.4476**	941.4211	940.4371			A	576.3253			***592.3566***	575.3300
11	44.0495	1001.4898	984.4633	983.4793	1029.4847	1012.4582	1011.4742			A	505.2881			***521.3194***	504.2929
12	120.0808	1148.5582	1131.5317	1130.5477	1176.5531	1159.5266	1158.5426			F	358.2197			***450.2823***	433.2558
13	129.1135	1304.6593	1287.6328	1286.6488	1332.6543	1315.6277	1314.6437	1219.5953		R	202.1186	201.1234		***303.2139***	286.1874
14	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GI	143.1179	171.1128	GIT	244.1656	272.1605	GITA	315.2027	343.1976
GITAD	430.2296	458.2245	GITADD	545.2566	573.2515	GITADDV	644.3250	672.3199
IT	187.1441	215.1390	ITA	258.1812	286.1761	ITAD	373.2082	401.2031
ITADD	488.2351	516.2300	ITADDV	587.3035	615.2984	TA	145.0972	173.0921
TAD	260.1241	288.1190	TADD	375.1510	403.1460	TADDV	474.2195	502.2144
TADDVN	588.2624	616.2573	TADDVNA	659.2995	687.2944	AD	159.0764	187.0713
ADD	274.1034	302.0983	ADDV	373.1718	401.1667	ADDVN	487.2147	515.2096

ADDVNA	558.2518	586.2467	**ADDVNAA**	629.2889	657.2838	**DD**	203.0662	231.0612
DDV	302.1347	330.1296	**DDVN**	416.1776	444.1725	**DDVNA**	487.2147	515.2096
DDVNAA	558.2518	586.2467	**DV**	187.1077	215.1026	**DVN**	301.1506	329.1456
DVNA	372.1878	400.1827	**DVNAA**	443.2249	471.2198	**DVNAAF**	590.2933	618.2882
VN	186.1237	214.1186	**VNA**	257.1608	285.1557	**VNAA**	328.1979	356.1928
VNAAF	475.2663	503.2613	**VNAAFR**	631.3675	659.3624	**NA**	158.0924	186.0873
NAA	229.1295	257.1244	**NAAF**	376.1979	404.1928	**NAAFR**	532.2990	560.2940
AA	115.0866	143.0815	**AAF**	262.1550	290.1499	**AAFR**	418.2561	446.2510
AF	191.1179	219.1128	**AFR**	347.2190	375.2139	**FR**	276.1819	304.1768





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.0	1477.7525	0.1023	TGITADDVNAAFRK
26.9	1477.7381	0.1167	QAIMDGKLTGGMTR
26.6	1477.7599	0.0950	MHSGYIKSDAIIK
26.0	1477.7273	0.1275	YAASVGRDAGQEVR
24.8	1477.7776	0.0772	SDAFAKAAADLIASK
23.6	1477.7307	0.1241	RMSTQGDAGATVIR
23.1	1477.7776	0.0772	LTEGYIQDLTGIR
23.0	1477.7082	0.1466	SGEVTEADMISALR
22.3	1477.7082	0.1466	NKTILMVDDEER
21.7	1477.7373	0.1176	PSTSAASSVVQSTTR

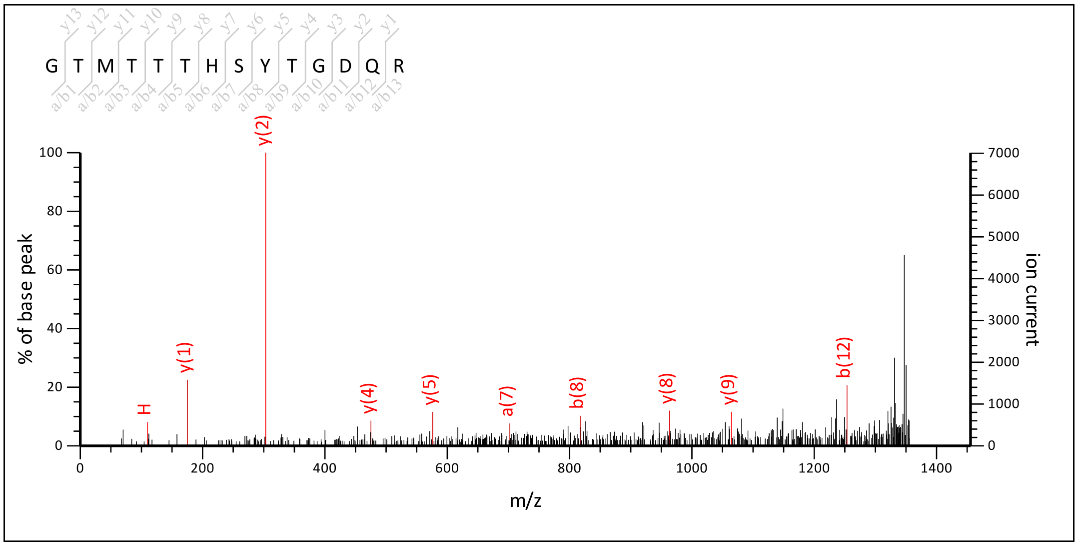
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 39

MS/MS Fragmentation of **GTMTTTHSYTGDQR**
Found in **gi|115450493** in **NCBInr**, Os03g0129300 [Oryza sativa Japonica Group]

Match to Query 354: 1554.784824 from(1555.792100,1+) intensity(0.0000) index(29)
Title: Label: H12, Spot_Id: 219857, Peak_List_Id: 227352, MSMS Job_Run_Id: 21959, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H12_136868235200.txt



0 to 1455.54

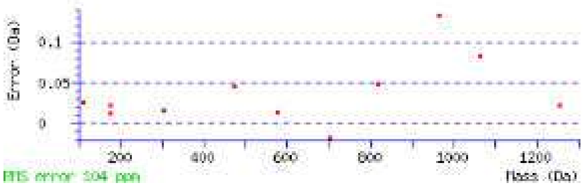
Label all possible matches ○ Label matches used for scoring ●

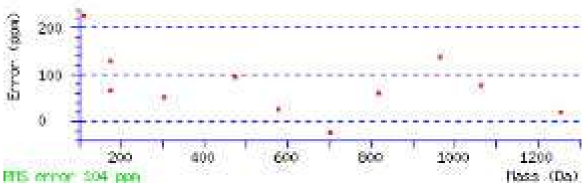
Monoisotopic mass of neutral peptide Mr(calc): 1554.6733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 2.2
Matches : 12/235 fragment ions using 13 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	74.0600	131.0815		113.0709	159.0764		141.0659	115.0866	117.0659	T	1452.6172	1465.6376	1467.6169	1498.6591	1481.6325
3	104.0528	262.1220		244.1114	290.1169		272.1063	202.1186		M	1321.5767	1320.5815		1397.6114	1380.5849
4	74.0600	363.1697		345.1591	391.1646		373.1540	347.1748	349.1540	T	1220.5291	1233.5495	1235.5287	1266.5709	1249.5444
5	74.0600	464.2173		446.2068	492.2123		474.2017	448.2224	450.2017	T	1119.4814	1132.5018	1134.4810	1165.5232	1148.4967
6	74.0600	565.2650		547.2545	593.2599		575.2494	549.2701	551.2494	T	1018.4337	1031.4541	1033.4334	***1064.4756***	1047.4490
7	110.0713	**702.3239**		684.3134	730.3189		712.3083			H	881.3748			***963.4279***	946.4013
8	60.0444	789.3560		771.3454	**817.3509**		799.3403	773.3611		S	794.3428	793.3475		826.3690	809.3424
9	136.0757	952.4193		934.4087	980.4142		962.4036			Y	631.2794			739.3369	722.3104
10	74.0600	1053.4670		1035.4564	1081.4619		1063.4513	1037.4721	1039.4513	T	530.2318	543.2522	545.2314	***576.2736***	559.2471
11	30.0338	1110.4884		1092.4779	1138.4834		1120.4728			G				***475.2259***	458.1994
12	88.0393	1225.5154		1207.5048	**1253.5103**		1235.4997	1181.5256		D	358.1833	357.1881		418.2045	401.1779
13	101.0709	1353.5740	1336.5474	1335.5634	1381.5689	1364.5423	1363.5583	1296.5525		Q	230.1248	229.1295		***303.1775***	286.1510
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TM	205.1005	233.0954	TMT	306.1482	334.1431	TMTT	407.1959	435.1908
TMTTT	508.2436	536.2385	TMTTTH	645.3025	673.2974	MT	205.1005	233.0954
MTT	306.1482	334.1431	MTTT	407.1959	435.1908	MTTTH	544.2548	572.2497
MTTTHS	631.2868	659.2817	TT	175.1077	203.1026	TTT	276.1554	304.1503
TTTH	413.2143	441.2092	TTTHS	500.2463	528.2413	TTTHSY	663.3097	691.3046
TT	175.1077	203.1026	TTH	312.1666	340.1615	TTHS	399.1987	427.1936
TTHSY	562.2620	590.2569	TTHSYT	663.3097	691.3046	TH	211.1190	239.1139

THS	298.1510	326.1459	**THSY**	461.2143	489.2092	**THSYT**	562.2620	590.2569
THSYTG	619.2835	647.2784	**HS**	197.1033	225.0982	**HSY**	360.1666	388.1615
HSYT	461.2143	489.2092	**HSYTG**	518.2358	546.2307	**HSYTGD**	633.2627	661.2576
SY	223.1077	251.1026	**SYT**	324.1554	352.1503	**SYTG**	381.1769	409.1718
SYTGD	496.2038	524.1987	**SYTGDQ**	624.2624	652.2573	**YT**	237.1234	265.1183
YTG	294.1448	322.1397	**YTGD**	409.1718	437.1667	**YTGDQ**	537.2304	565.2253
TG	131.0815	159.0764	**TGD**	246.1084	274.1034	**TGDQ**	374.1670	402.1619
GD	145.0608	173.0557	**GDQ**	273.1193	301.1143	**DQ**	216.0979	244.0928





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.7	1554.6733	0.1115	GTMTTTHSYTGDQR
32.6	1554.8266	-0.0418	YLQSTHAAIPNGKR
28.5	1554.6733	0.1115	GSMTTVHSYTGDQR
23.4	1554.6953	0.0896	MEQSTQMQCIKR
19.6	1554.8188	-0.0340	SFRTTLSTVLMGAR
19.6	1554.6998	0.0851	NDNMFWRTTAQR
18.3	1554.7130	0.0718	TTKATTACGTQCQK
17.4	1554.8267	-0.0418	QGIATPNGKLWSQR
17.4	1554.8631	-0.0782	GVLHKFNALTATQR
17.4	1554.7977	-0.0128	HKLLEMIDSWQR

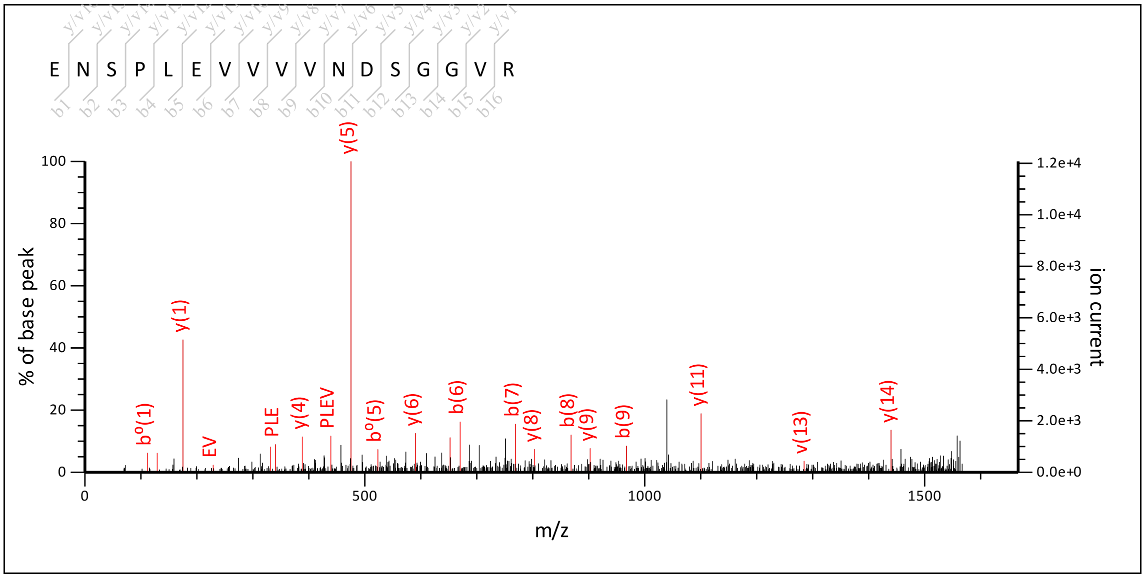
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 39

MS/MS Fragmentation of **ENSPLEVVVVNDSGGVR**
Found in **gi|115450493** in **NCBInr**, Os03g0129300 [Oryza sativa Japonica Group]

Match to Query 377: 1769.017024 from(1770.024300,1+) intensity(0.0000) index(33)
Title: Label: H12, Spot_Id: 219857, Peak_List_Id: 227348, MSMS Job_Run_Id: 21959, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H12_136868235200.txt



0 to 1667.05

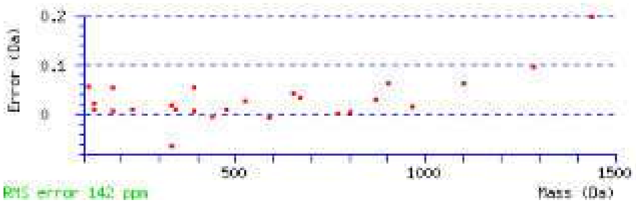
Label all possible matches ○ Label matches used for scoring ●

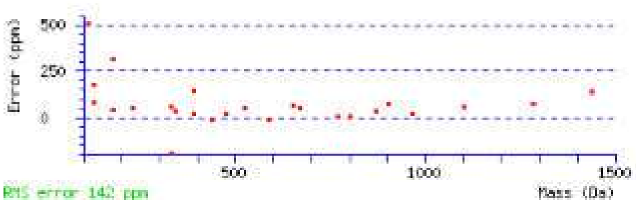
Monoisotopic mass of neutral peptide Mr(calc): 1768.8956
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 0.012
Matches : 26/325 fragment ions using 30 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	Seq.	v	w	y	y*	y⁰	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495	E						17
2	87.0553	216.0979	199.0713	198.0873	244.0928	227.0662	226.0822	173.0921	N	1581.8231	1580.8279	1640.8602	1623.8337	1622.8497	16
3	60.0444	303.1299	286.1034	285.1193	**331.1248**	314.0983	313.1143	287.1350	S	1494.7911	1493.7958	1526.8173	1509.7907	1508.8067	15
4	70.0651	400.1827	383.1561	382.1721	428.1776	411.1510	410.1670	374.1670	P	1397.7383	1396.7431	***1439.7853***	1422.7587	1421.7747	14
5	86.0964	513.2667	496.2402	495.2562	541.2617	524.2351	523.2511	471.2198	L	1284.6543	1283.6590	1342.7325	1325.7060	1324.7219	13
6	102.0550	642.3093	625.2828	624.2988	**670.3042**	653.2777	652.2937	584.3039	E	1155.6117	1154.6164	1229.6484	1212.6219	1211.6379	12
7	72.0808	741.3777	724.3512	723.3672	**769.3727**	752.3461	751.3621	727.3621	V	1056.5432	1069.5636	***1100.6058***	1083.5793	1082.5953	11
8	72.0808	840.4462	823.4196	822.4356	**868.4411**	851.4145	850.4305	826.4305	V	957.4748	970.4952	1001.5374	984.5109	983.5269	10
9	72.0808	939.5146	922.4880	921.5040	**967.5095**	950.4829	949.4989	925.4989	V	858.4064	871.4268	***902.4690***	885.4425	884.4585	9
10	72.0808	1038.5830	1021.5564	1020.5724	1066.5779	1049.5514	1048.5673	1024.5673	V	759.3380	772.3584	***803.4006***	786.3741	785.3900	8
11	87.0553	1152.6259	1135.5994	1134.6153	1180.6208	1163.5943	1162.6103	1109.6201	N	645.2951	644.2998	704.3322	687.3056	686.3216	7
12	88.0393	1267.6529	1250.6263	1249.6423	1295.6478	1278.6212	1277.6372	1223.6630	D	530.2681	529.2729	***590.2893***	573.2627	572.2787	6
13	60.0444	1354.6849	1337.6583	1336.6743	1382.6798	1365.6533	1364.6692	1338.6900	S	443.2361	442.2409	***475.2623***	458.2358	457.2518	5
14	30.0338	1411.7063	1394.6798	1393.6958	1439.7013	1422.6747	1421.6907		G			***388.2303***	371.2037		4
15	30.0338	1468.7278	1451.7013	1450.7172	1496.7227	1479.6962	1478.7122		G			***331.2088***	314.1823		3
16	72.0808	1567.7962	1550.7697	1549.7857	1595.7911	1578.7646	1577.7806	1553.7806	V	230.1248	243.1452	274.1874	257.1608		2
17	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NS	174.0873	202.0822	NSP	271.1401	299.1350	NSPL	384.2241	412.2191

NSPLE	513.2667	541.2617	**NSPLEV**	612.3352	640.3301	**SP**	157.0972	185.0921
SPL	270.1812	298.1761	**SPLE**	399.2238	427.2187	**SPLEV**	498.2922	526.2871
SPLEVV	597.3606	625.3556	**SPLEVVV**	696.4291	724.4240	**PL**	183.1492	211.1441
PLE	312.1918	340.1867	**PLEV**	411.2602	439.2551	**PLEVV**	510.3286	538.3235
PLEVVV	609.3970	637.3919	**LE**	215.1390	243.1339	**LEV**	314.2074	342.2023
LEVV	413.2758	441.2708	**LEVVV**	512.3443	540.3392	**LEVVVV**	611.4127	639.4076
EV	201.1234	229.1183	**EVV**	300.1918	328.1867	**EVVV**	399.2602	427.2551
EVVVV	498.3286	526.3235	**EVVVVN**	612.3715	640.3665	**VV**	171.1492	199.1441
VVV	270.2176	298.2125	**VVVV**	369.2860	397.2809	**VVVVN**	483.3289	511.3239
VVVVND	598.3559	626.3508	**VVVVNDS**	685.3879	713.3828	**VV**	171.1492	199.1441
VVV	270.2176	298.2125	**VVVN**	384.2605	412.2554	**VVVND**	499.2875	527.2824
VVVNDS	586.3195	614.3144	**VVVNDSG**	643.3410	671.3359	**VV**	171.1492	199.1441
VVN	285.1921	313.1870	**VVND**	400.2191	428.2140	**VVNDS**	487.2511	515.2460
VVNDSG	544.2726	572.2675	**VVNDSGG**	601.2940	629.2889	**VN**	186.1237	214.1186
VND	301.1506	329.1456	**VNDS**	388.1827	416.1776	**VNDSG**	445.2041	473.1991
VNDSGG	502.2256	530.2205	**VNDSGGV**	601.2940	629.2889	**ND**	202.0822	230.0771
NDS	289.1143	317.1092	**NDSG**	346.1357	374.1306	**NDSGG**	403.1572	431.1521
NDSGGV	502.2256	530.2205	**DS**	175.0713	203.0662	**DSG**	232.0928	260.0877
DSGG	289.1143	317.1092	**DSGGV**	388.1827	416.1776	**SG**	117.0659	145.0608
SGG	174.0873	202.0822	**SGGV**	273.1557	301.1506	**GG**	87.0553	115.0502
GGV	186.1237	214.1186	**GV**	129.1022	157.0972			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.9	1768.8956	0.1215	ENSPLEVVVVNDSGGVR
28.5	1768.9571	0.0599	KDSPLEVVVINDTGGVK
21.0	1768.9068	0.1103	GSEGTELEVPVNAVGRR
18.4	1768.9207	0.0963	ENSPLEVVVINDTGGVK
18.1	1768.8492	0.1678	EGDPSQYHSVPEIRR
17.6	1768.8778	0.1392	QCVSDAKIHQDELVK
16.9	1768.9544	0.0627	KGGAAGLNAGAGASLVSAAAR
16.1	1768.9571	0.0599	KDSPLDIVVINDTGGVK
16.1	1768.8956	0.1215	AADISDPVVVTTPNASGR
15.9	1768.9757	0.0413	ELPAGSTIVVVLMDGIR

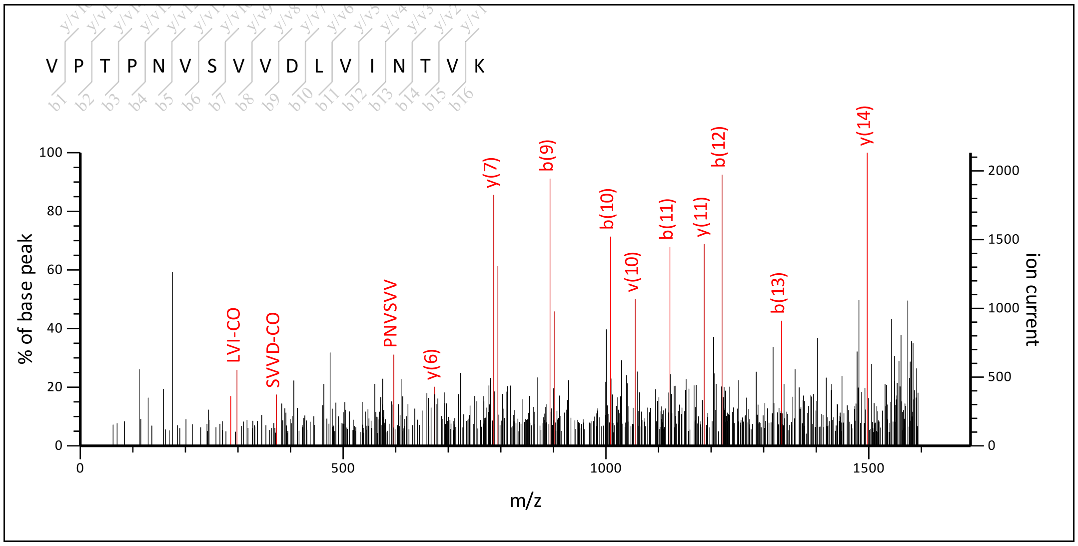
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 39

MS/MS Fragmentation of **VPTPNVSVVDLVINTVK**
Found in **gi|115450493** in **NCBInr**, Os03g0129300 [Oryza sativa Japonica Group]

Match to Query 383: 1793.118824 from(1794.126100,1+) intensity(0.0000) index(34)
Title: Label: H12, Spot_Id: 219857, Peak_List_Id: 227356, MSMS Job_Run_Id: 21959, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_H12_136868235200.txt



0 to 1693.52

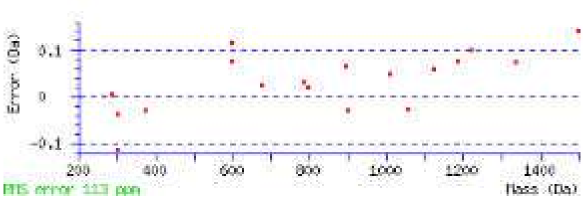
Label all possible matches ○ Label matches used for scoring ●

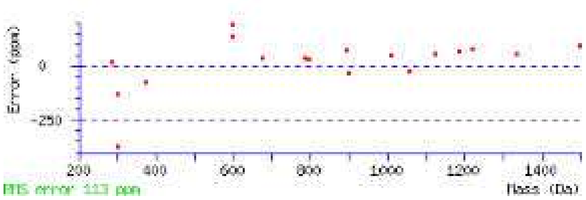
```
Monoisotopic mass of neutral peptide Mr(calc): 1793.0299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 7.6
Matches : 20/329 fragment ions using 32 most intense peaks   (help)
```

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		**V**					
2	70.0651	169.1335			197.1285			143.1179		**P**	1652.9218	1651.9265		1694.9687	1677.9422
3	74.0600	270.1812		252.1707	***298.1761***		280.1656	254.1863	256.1656	**T**	1551.8741	1564.8945	1566.8738	1597.9159	1580.8894
4	70.0651	367.2340		349.2234	395.2289		377.2183	341.2183		**P**	1454.8213	1453.8261		**1496.8683**	1479.8417
5	87.0553	481.2769	464.2504	463.2663	509.2718	492.2453	491.2613	438.2711		**N**	1340.7784	1339.7831		1399.8155	1382.7890
6	72.0808	580.3453	563.3188	562.3348	608.3402	591.3137	590.3297	566.3297		**V**	1241.7100	1254.7304		1285.7726	1268.7460
7	60.0444	667.3774	650.3508	649.3668	695.3723	678.3457	677.3617	651.3824		**S**	1154.6780	1153.6827		**1186.7042**	1169.6776
8	72.0808	766.4458	749.4192	748.4352	***794.4407***	777.4141	776.4301	752.4301		**V**	1055.6095	1068.6299		1099.6721	1082.6456
9	72.0808	865.5142	848.4876	847.5036	***893.5091***	876.4825	875.4985	851.4985		**V**	956.5411	969.5615		1000.6037	983.5772
10	88.0393	980.5411	963.5146	962.5306	***1008.5360***	991.5095	990.5255	936.5513		**D**	841.5142	840.5189		**901.5353**	884.5088
11	86.0964	1093.6252	1076.5986	1075.6146	***1121.6201***	1104.5936	1103.6095	1051.5782		**L**	728.4301	727.4349		**786.5084**	769.4818
12	72.0808	1192.6936	1175.6671	1174.6830	***1220.6885***	1203.6620	1202.6780	1178.6780		**V**	629.3617	642.3821		**673.4243**	656.3978
13	86.0964	1305.7777	1288.7511	1287.7671	***1333.7726***	1316.7460	1315.7620	1277.7464	1291.7620	**I**	516.2776	529.2980	543.3137	574.3559	557.3293
14	87.0553	1419.8206	1402.7940	1401.8100	1447.8155	1430.7890	1429.8049	1376.8148		**N**	402.2347	401.2395		461.2718	444.2453
15	74.0600	1520.8683	1503.8417	1502.8577	1548.8632	1531.8366	1530.8526	1504.8734	1506.8526	**T**	301.1870	314.2074	316.1867	347.2289	330.2023
16	72.0808	1619.9367	1602.9101	1601.9261	1647.9316	1630.9051	1629.9210	1605.9210		**V**	202.1186	215.1390		246.1812	229.1547
17	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PT	171.1128	199.1077	**PTP**	268.1656	296.1605	**PTPN**	382.2085	410.2034
PTPNV	481.2769	509.2718	**PTPNVS**	568.3089	596.3039	**PTPNVSV**	667.3774	695.3723
TP	171.1128	199.1077	**TPN**	285.1557	313.1506	**TPNV**	384.2241	412.2191
TPNVS	471.2562	499.2511	**TPNVSV**	570.3246	598.3195	**TPNVSVV**	669.3930	697.3879

PN	184.1081	212.1030	**PNV**	283.1765	311.1714	**PNVS**	370.2085	398.2034
PNVSV	469.2769	497.2718	**PNVSVV**	568.3453	596.3402	**PNVSVVD**	683.3723	711.3672
NV	186.1237	214.1186	**NVS**	273.1557	301.1506	**NVSV**	372.2241	400.2191
NVSVV	471.2926	499.2875	**NVSVVD**	586.3195	614.3144	**NVSVVDL**	699.4036	727.3985
VS	159.1128	187.1077	**VSV**	258.1812	286.1761	**VSVV**	357.2496	385.2445
VSVVD	472.2766	500.2715	**VSVVDL**	585.3606	613.3556	**VSVVDLV**	684.4291	712.4240
SV	159.1128	187.1077	**SVV**	258.1812	286.1761	**SVVD**	373.2082	401.2031
SVVDL	486.2922	514.2871	**SVVDLV**	585.3606	613.3556	**SVVDLVI**	698.4447	726.4396
VV	171.1492	199.1441	**VVD**	286.1761	314.1710	**VVDL**	399.2602	427.2551
VVDLV	498.3286	526.3235	**VVDLVI**	611.4127	639.4076	**VD**	187.1077	215.1026
VDL	300.1918	328.1867	**VDLV**	399.2602	427.2551	**VDLVI**	512.3443	540.3392
VDLVIN	626.3872	654.3821	**DL**	201.1234	229.1183	**DLV**	300.1918	328.1867
DLVI	413.2758	441.2708	**DLVIN**	527.3188	555.3137	**DLVINT**	628.3665	656.3614
LV	185.1648	213.1598	**LVI**	298.2489	326.2438	**LVIN**	412.2918	440.2867
LVINT	513.3395	541.3344	**LVINTV**	612.4079	640.4028	**VI**	185.1648	213.1598
VIN	299.2078	327.2027	**VINT**	400.2554	428.2504	**VINTV**	499.3239	527.3188
IN	200.1394	228.1343	**INT**	301.1870	329.1819	**INTV**	400.2554	428.2504
NT	188.1030	216.0979	**NTV**	287.1714	315.1663	**TV**	173.1285	201.1234





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1792.9935	0.1253	VPTPNVSVVDLVVNVDK
30.1	1793.0299	0.0889	VPTPNVSVVDLVINTVK
29.1	1793.0299	0.0889	VPTPNVSVVDLVVQISK
29.1	1793.0299	0.0889	VPTPNVSVVDLVVQVTK
24.9	1793.0411	0.0777	VPTPNVSVVDLKAVLSR
23.3	1792.9505	0.1683	MANKLVLIDGNSIAYR
22.7	1793.0411	0.0777	VPTPNVSVVDLTVRLGK
22.5	1792.9935	0.1253	VPTPNVSVVDLVAQVEK
17.2	1793.0451	0.0737	LIAFEIYGTILAKVSR
16.8	1792.9472	0.1716	HPELPVEVVSGGLFTGR

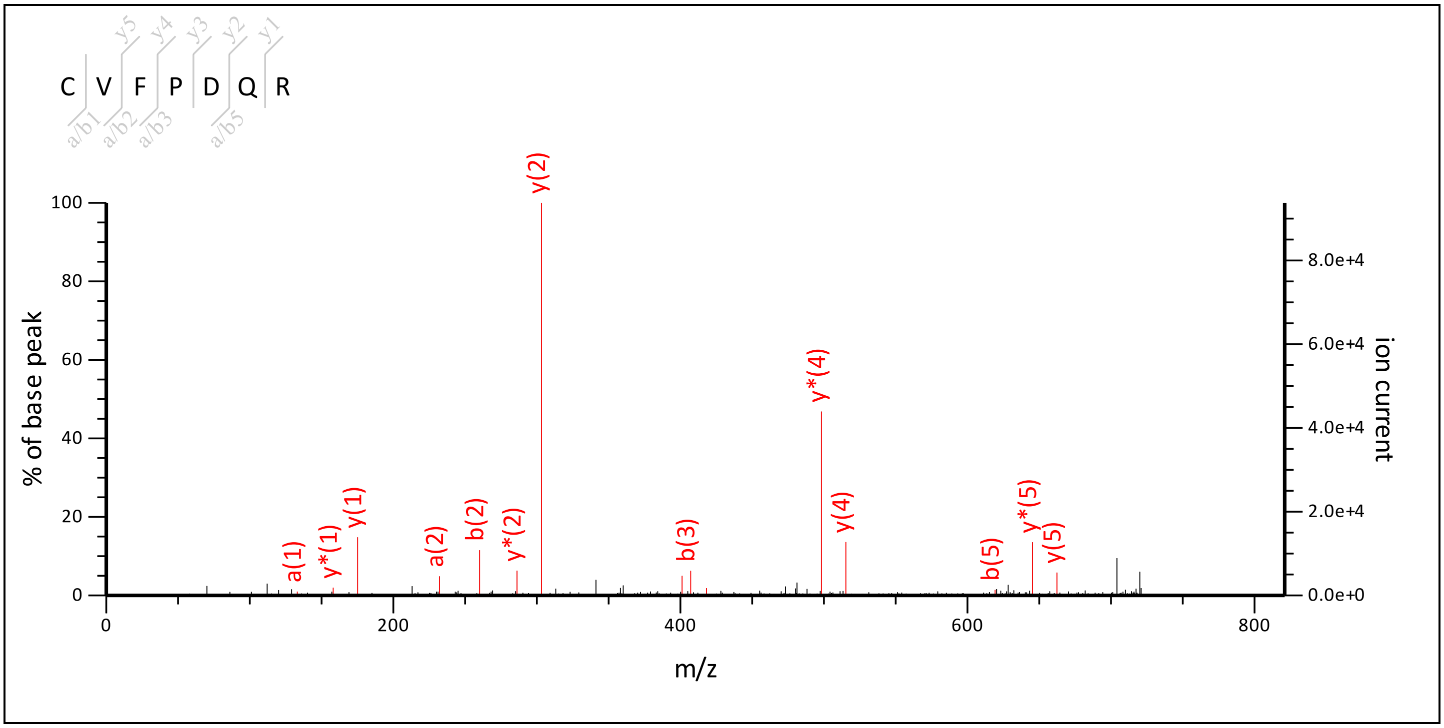
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 40

MS/MS Fragmentation of **CVFPDQR**
Found in **gi|297604125** in **NCBInr**, Os05g0247100 [Oryza sativa Japonica Group]

Match to Query 3: 920.402754 from(921.410030,1+) intensity(0.0000) index(2)
Title: Label: B5, Spot_Id: 219739, Peak_List_Id: 225587, MSMS Job_Run_Id: 21783, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B5_136842181400.txt

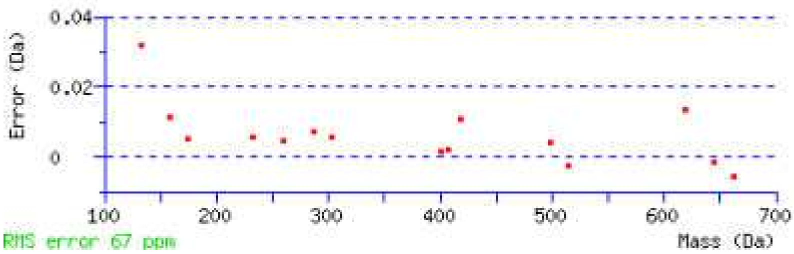


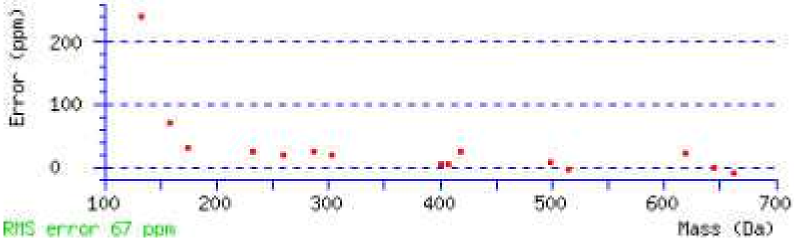
0 to 821.02

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 920.4175
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 9.1
Matches : 15/26 fragment ions using 35 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**133.0430**		161.0379		**C**			**7**
2	**232.1114**		**260.1063**		**V**	761.3941	744.3675	**6**
3	379.1798		**407.1748**		**F**	***662.3257***	645.2991	**5**
4	476.2326		504.2275		**P**	***515.2572***	498.2307	**4**
5	591.2595		**619.2545**		**D**	***418.2045***	401.1779	**3**
6	719.3181	702.2916	747.3130	730.2865	**Q**	***303.1775***	286.1510	**2**
7					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.3	920.4749	-0.0722	KTIEMAGR
23.6	920.4175	-0.0147	CVFPDQR
20.5	920.4749	-0.0722	MTSAVLAGR
19.0	920.4174	-0.0147	QMFPADGR
18.9	920.4936	-0.0908	MKMLVQR
18.9	920.4902	-0.0874	MQFIVQR
18.6	920.4803	-0.0775	XXLALVKR
18.3	920.4385	-0.0358	NDLEMKR
18.1	920.4749	-0.0722	VLMSDGKR
17.9	920.3472	0.0556	SDGEDDAGR

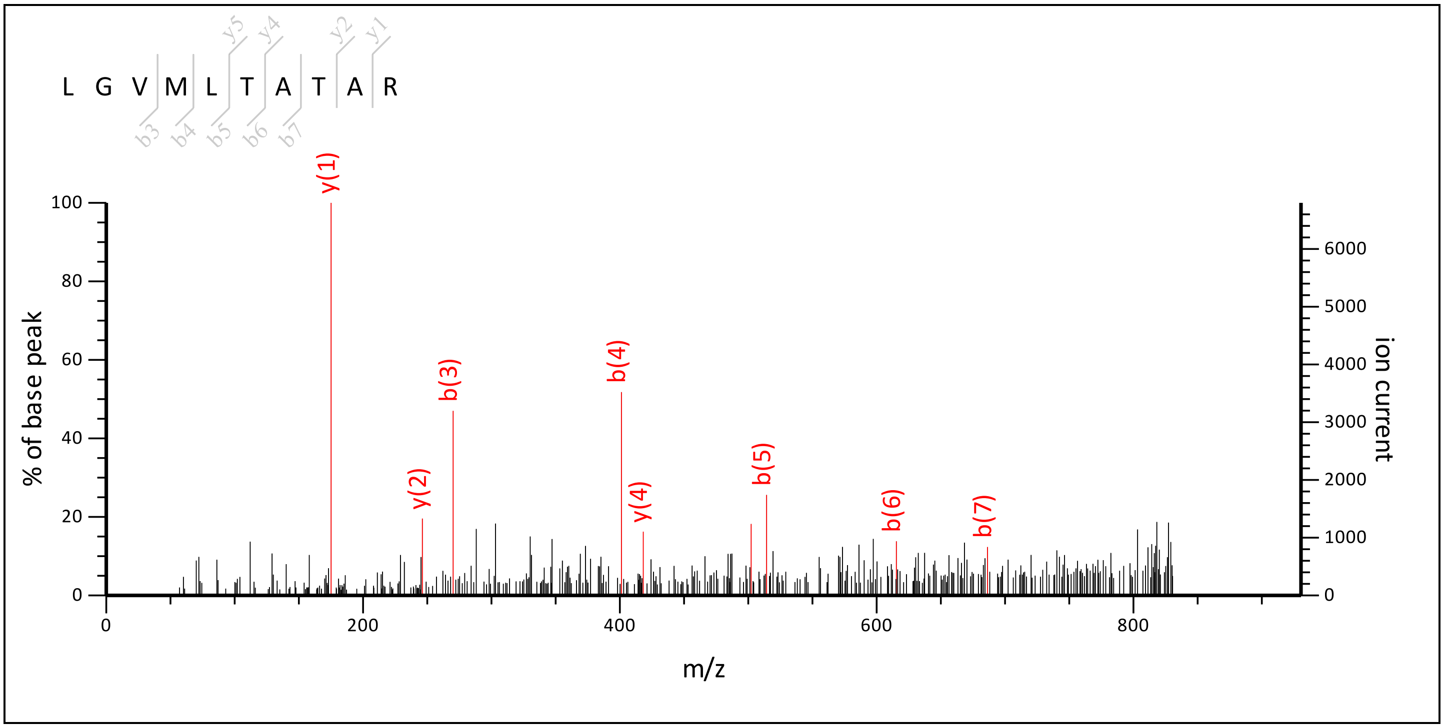
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 40

MS/MS Fragmentation of **LGVMLTATAR**
Found in **gi|297604125** in **NCBInr**, Os05g0247100 [Oryza sativa Japonica Group]

Match to Query 9: 1031.571624 from(1032.578900,1+) intensity(0.0000) index(8)
Title: Label: B5, Spot_Id: 219739, Peak_List_Id: 225593, MSMS Job_Run_Id: 21783, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B5_136842181400.txt



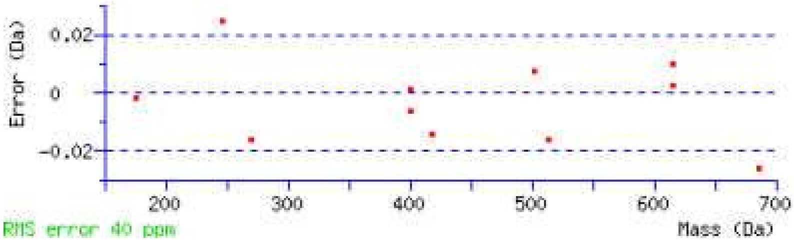
0 to 930.49

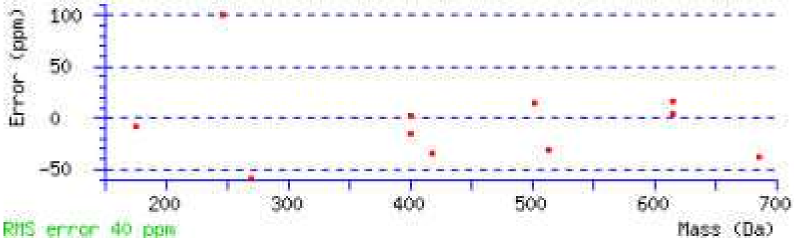
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1031.5797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 1.7
Matches : 11/36 fragment ions using 16 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	86.0964	114.0913	L			10
2	143.1179	171.1128	G	919.5030	902.4764	9
3	242.1863	***270.1812***	V	862.4815	845.4550	8
4	373.2268	***401.2217***	M	763.4131	746.3865	7
5	486.3109	***514.3058***	L	632.3726	615.3461	6
6	587.3585	***615.3534***	T	519.2885	502.2620	5
7	658.3956	***686.3906***	A	***418.2409***	401.2143	4
8	759.4433	787.4382	T	347.2037	330.1772	3

9	830.4804	858.4754	**A**	*246.1561*	229.1295	**2**
10			**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.8	1031.5797	-0.0081	LGVMLTATAR
23.6	1031.5400	0.0316	KFPELADGR
19.6	1031.5433	0.0283	AANDMLIIR
19.6	1031.5797	-0.0081	DQKMLLLR
18.7	1031.5433	0.0283	CEQTLILR
18.7	1031.5910	-0.0193	MNRTIILR
18.2	1031.5508	0.0209	VIGMIPGMAK
18.2	1031.5508	0.0209	VLGMIPGMAK
18.1	1031.5182	0.0534	MTNAGAALGAR
17.5	1031.4996	0.0720	GASGAAVTADGR

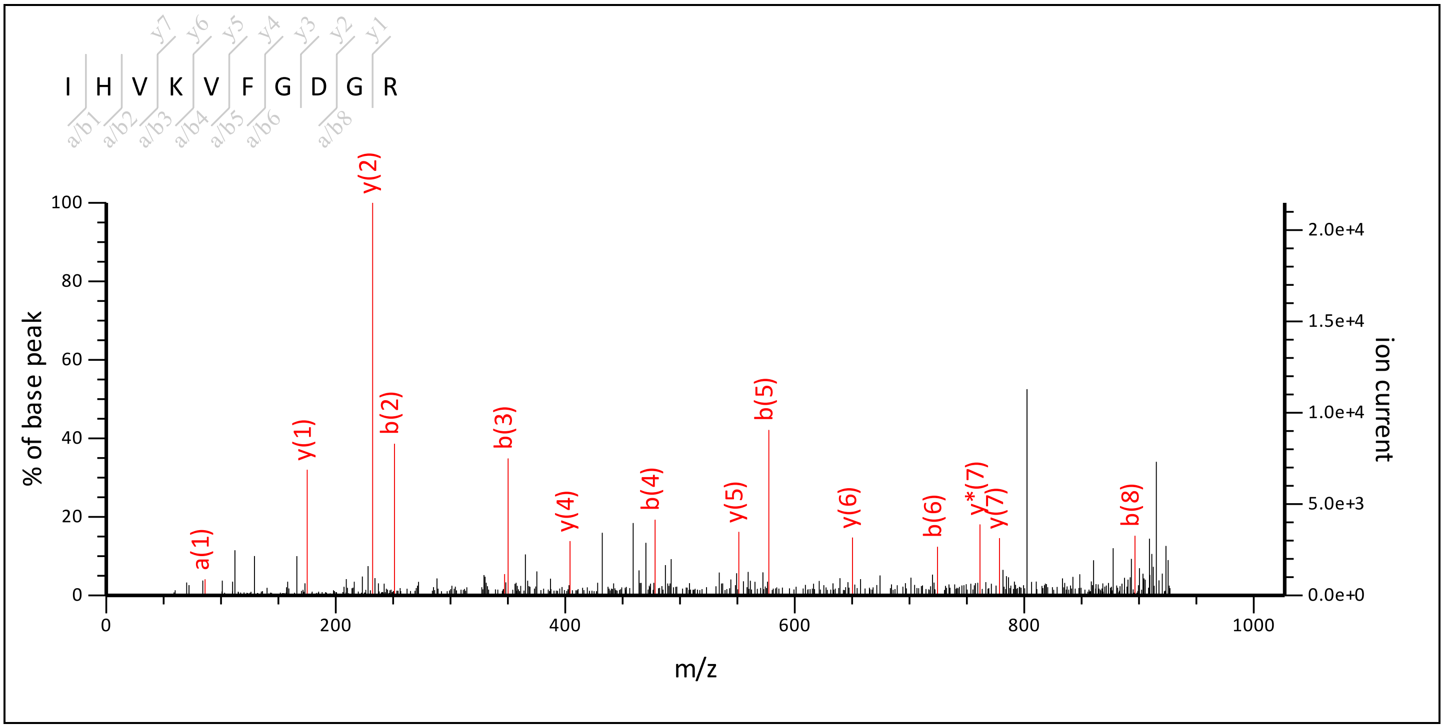
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 40

MS/MS Fragmentation of **IHVKVFGDGR**
Found in **gi|297604125** in **NCBInr**, Os05g0247100 [Oryza sativa Japonica Group]

Match to Query 13: 1126.616524 from(1127.623800,1+) intensity(0.0000) index(12)
Title: Label: B5, Spot_Id: 219739, Peak_List_Id: 225590, MSMS Job_Run_Id: 21783, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B5_136842181400.txt



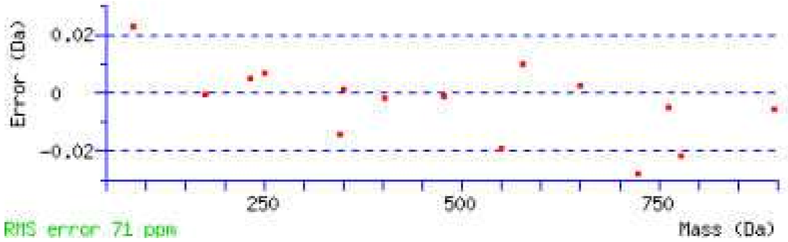
0 to 1026.97

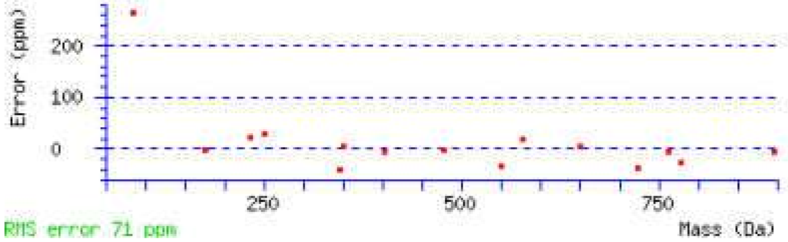
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1126.6247
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.084
Matches : 15/48 fragment ions using 27 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		**I**			**10**
2	223.1553		***251.1503***		**H**	1014.5479	997.5214	**9**
3	322.2238		***350.2187***		**V**	877.4890	860.4625	**8**
4	450.3187	433.2922	***478.3136***	461.2871	**K**	***778.4206***	761.3941	**7**
5	549.3871	532.3606	***577.3820***	560.3555	**V**	***650.3257***	633.2991	**6**
6	696.4555	679.4290	***724.4505***	707.4239	**F**	***551.2572***	534.2307	**5**
7	753.4770	736.4505	781.4719	764.4454	**G**	***404.1888***	387.1623	**4**
8	868.5039	851.4774	***896.4989***	879.4723	**D**	***347.1674***	330.1408	**3**

9	925.5254	908.4989	953.5203	936.4938	**G**	*232.1404*	215.1139	**2**
10					**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.6	1126.6247	-0.0082	IHVKVFGDGR
14.0	1126.5553	0.0612	HTKMLPGDGR
12.6	1126.5619	0.0547	DLPPSTIGDGR
12.5	1126.5441	0.0724	TPAPSPPMTGR
11.4	1126.5376	0.0789	VCSGFVMRR
11.0	1126.5376	0.0790	ARGMMAVGFR
10.6	1126.5515	0.0651	MFNLAMGLSK
10.4	1126.5255	0.0911	IDPTGPAEDGR
9.8	1126.5454	0.0711	RLHGWMDGR
8.2	1126.5441	0.0725	SYVKAMEQR

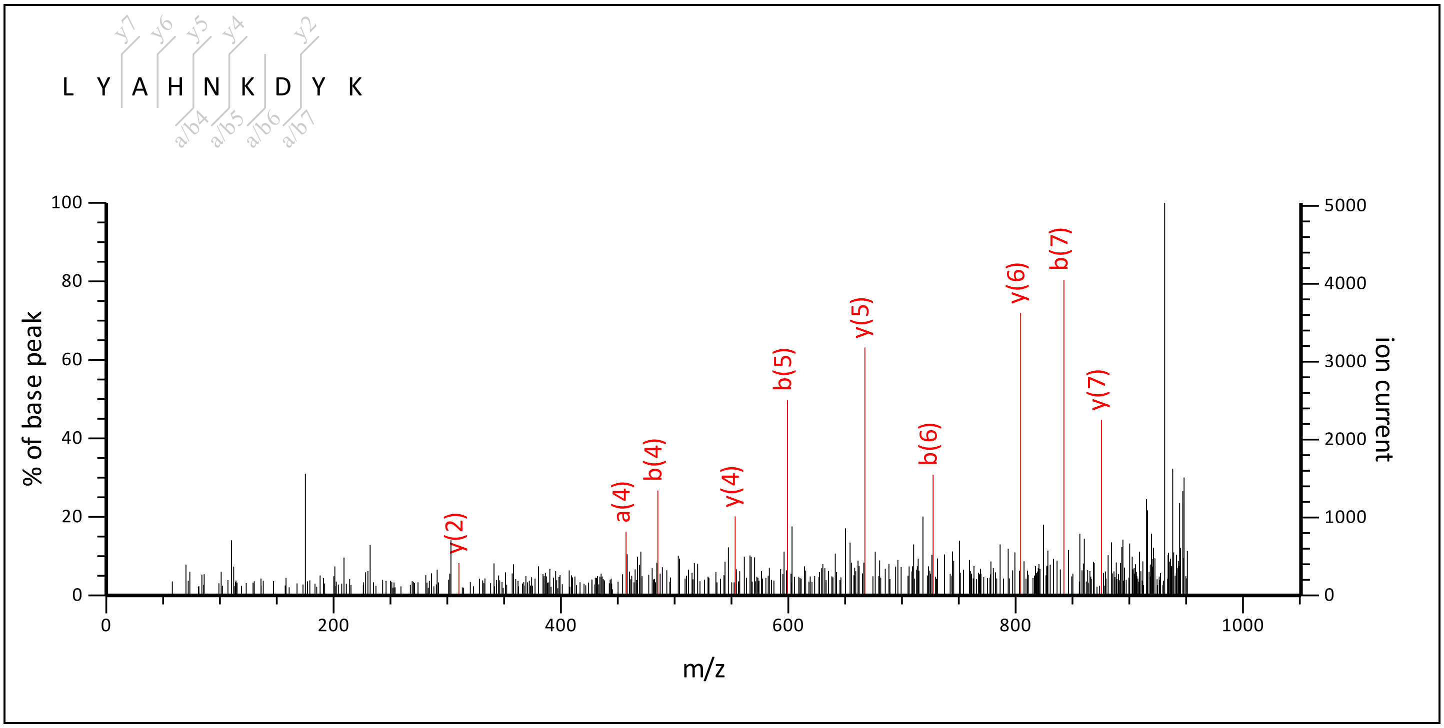
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 40

MS/MS Fragmentation of **LYAHNKDYK**
Found in **gi|297604125** in **NCBInr**, Os05g0247100 [Oryza sativa Japonica Group]

Match to Query 14: 1150.566224 from(1151.573500,1+) intensity(0.0000) index(13)
Title: Label: B5, Spot_Id: 219739, Peak_List_Id: 225597, MSMS Job_Run_Id: 21783, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B5_136842181400.txt



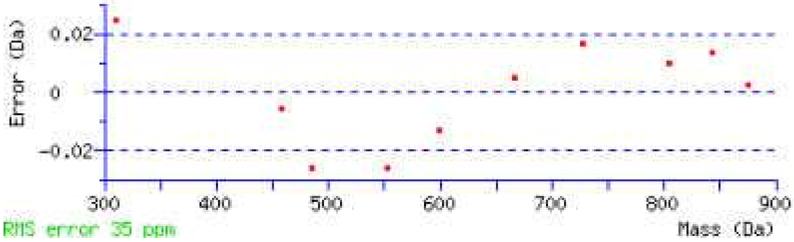
0 to 1051.03

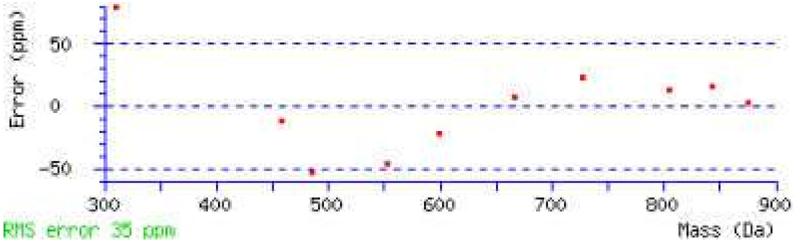
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1150.5771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 6.3
Matches : 10/40 fragment ions using 18 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		L			9
2	249.1598		277.1547		Y	1038.5003	1021.4738	8
3	320.1969		348.1918		A	***875.4370***	858.4104	7
4	457.2558		***485.2507***		H	***804.3999***	787.3733	6
5	571.2987	554.2722	***599.2936***	582.2671	N	***667.3410***	650.3144	5
6	699.3937	682.3671	***727.3886***	710.3620	K	***553.2980***	536.2715	4
7	814.4206	797.3941	***842.4155***	825.3890	D	425.2031	408.1765	3
8	977.4839	960.4574	1005.4789	988.4523	Y	***310.1761***	293.1496	2

9					K	147.1128	130.0863	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.5	1150.5771	-0.0108	LYAHNKDYK
13.7	1150.5587	0.0075	TQMQNMVKR
13.5	1150.5618	0.0044	EELLNYSQR
13.5	1150.5982	-0.0320	IIEENYSKR
13.2	1150.6359	-0.0697	HHPLLPAPNR
8.9	1150.4859	0.0803	NDALACGMQR
8.9	1150.5843	-0.0181	QADAVVGHAQR
8.9	1150.6207	-0.0545	TAQALINHQR
8.9	1150.6571	-0.0909	VSGKIIHGGQR
8.9	1150.5995	-0.0333	YHPSLNHKR

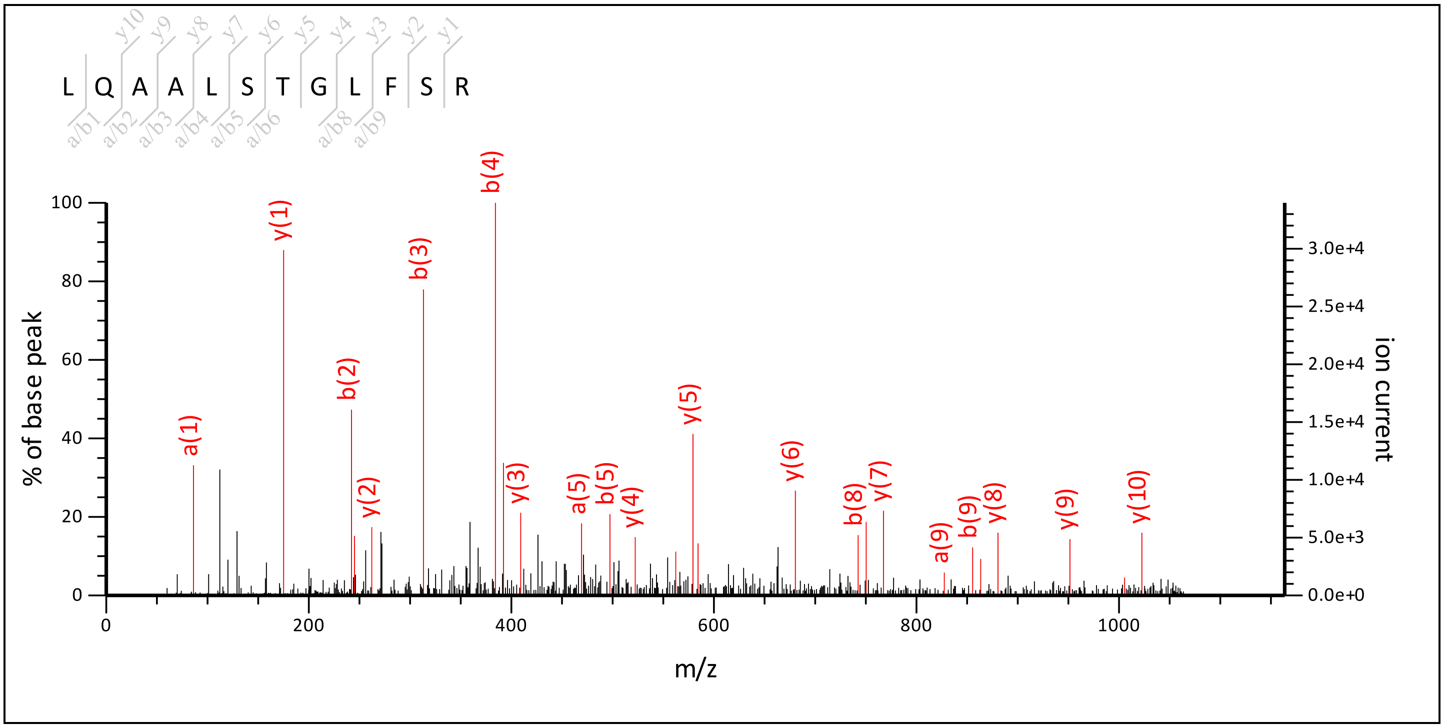
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 40

MS/MS Fragmentation of **LQAALSTGLFSR**
Found in **gi|297604125** in **NCBInr**, Os05g0247100 [Oryza sativa Japonica Group]

Match to Query 20: 1262.689824 from(1263.697100,1+) intensity(0.0000) index(19)
Title: Label: B5, Spot_Id: 219739, Peak_List_Id: 225586, MSMS Job_Run_Id: 21783, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B5_136842181400.txt



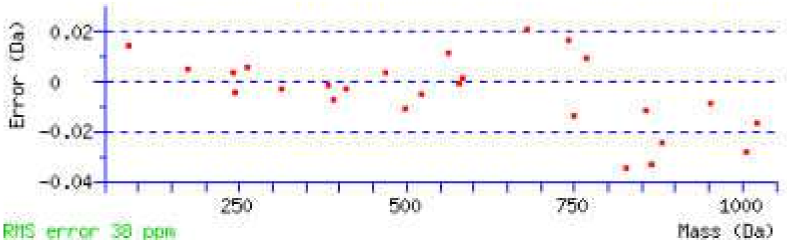
0 to 1163.59

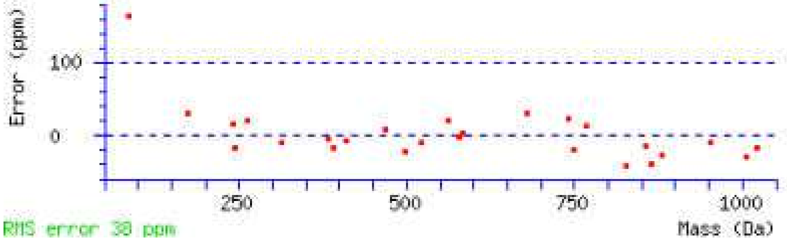
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1262.6983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 93  Expect: 1e-06
Matches : 26/64 fragment ions using 33 most intense peaks   (help)
```

#	a	a*	b	b*	Seq.	y	y*	#
1	**86.0964**		114.0913		L			12
2	214.1550	197.1285	**242.1499**	225.1234	Q	1150.6215	1133.5950	11
3	285.1921	268.1656	**313.1870**	296.1605	A	***1022.5629***	1005.5364	10
4	356.2292	339.2027	**384.2241**	367.1976	A	***951.5258***	934.4993	9
5	**469.3133**	452.2867	**497.3082**	480.2817	L	***880.4887***	863.4621	8
6	556.3453	539.3188	**584.3402**	567.3137	S	***767.4046***	750.3781	7
7	657.3930	640.3665	685.3879	668.3614	T	***680.3726***	663.3461	6
8	714.4145	697.3879	**742.4094**	725.3828	G	***579.3249***	562.2984	5

9	**827.4985**	810.4720	**855.4934**	838.4669	**L**	***522.3035***	505.2769	**4**
10	974.5669	957.5404	1002.5619	985.5353	**F**	***409.2194***	392.1928	**3**
11	1061.5990	1044.5724	1089.5939	1072.5673	**S**	***262.1510***	245.1244	**2**
12					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.0	1262.6983	-0.0084	LQAALSTGLFSR
26.6	1262.7360	-0.0462	LGAAALWHRLR
22.5	1262.6223	0.0675	LRNLDMGLCR
20.4	1262.6553	0.0345	IKAANPEMPHR
20.3	1262.6255	0.0644	LAQAEAAEAAYR
19.9	1262.7247	-0.0349	IQAAFRAFLAR
18.8	1262.6983	-0.0084	AVAAAASYTVAIR
18.4	1262.6982	-0.0084	KGLISIENYAR
17.3	1262.6289	0.0609	LQSGIGEAVMSR
16.4	1262.6553	0.0345	LRHSLSTYMR

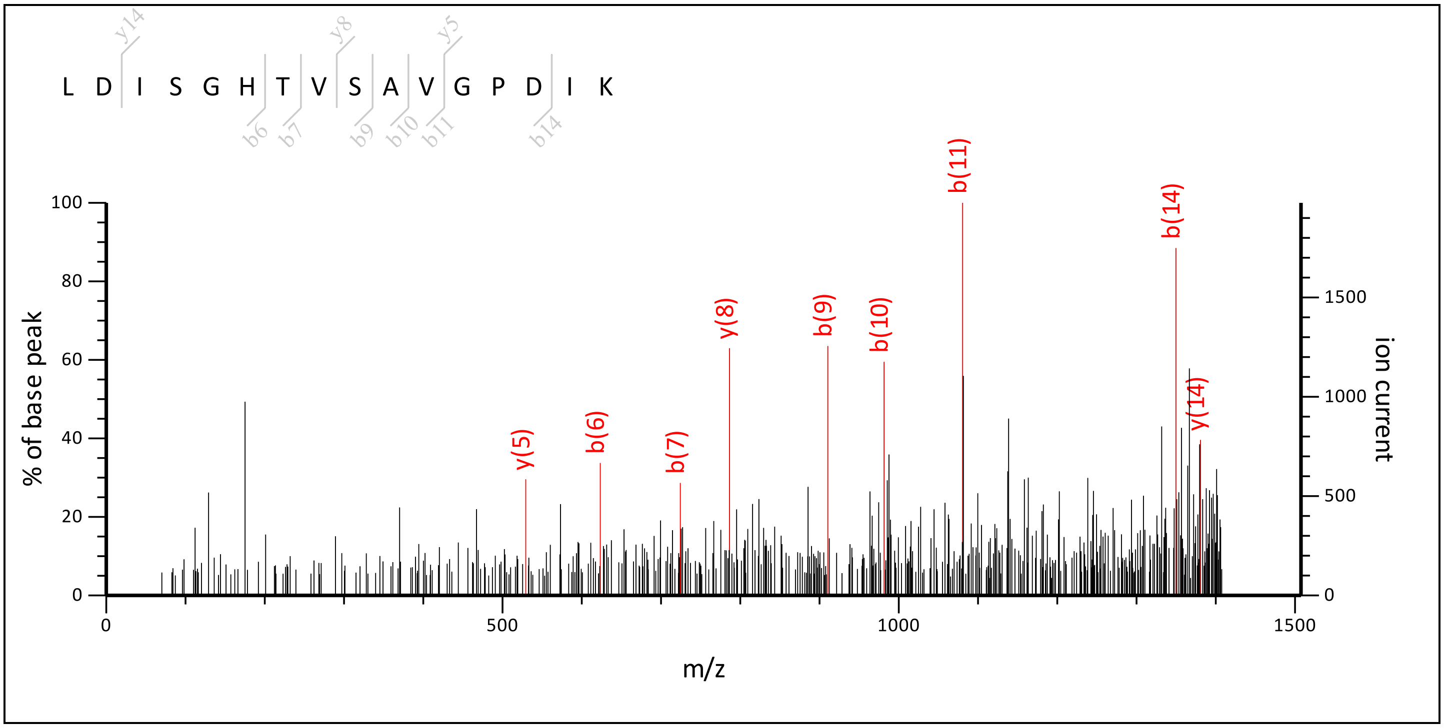
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 40

MS/MS Fragmentation of **LDISGHTVSAVGPDIK**
Found in **gi|297604125** in **NCBInr**, Os05g0247100 [Oryza sativa Japonica Group]

Match to Query 31: 1607.820524 from(1608.827800,1+) intensity(0.0000) index(30)
Title: Label: B5, Spot_Id: 219739, Peak_List_Id: 225604, MSMS Job_Run_Id: 21783, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B5_136842181400.txt



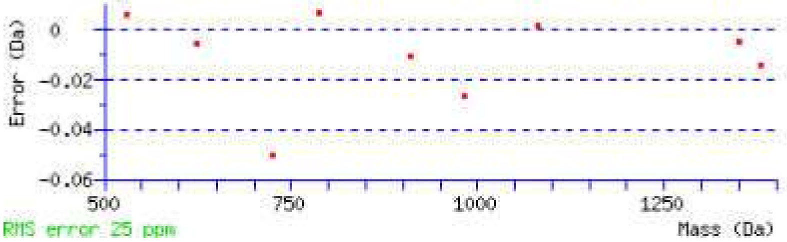
0 to 1507.52

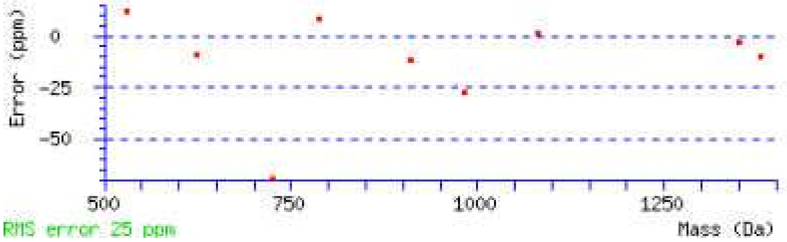
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1607.8519
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.67
Matches : 9/60 fragment ions using 14 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	86.0964	114.0913	L			16
2	201.1234	229.1183	D	1495.7751	1478.7486	15
3	314.2074	342.2023	I	*1380.7482*	1363.7216	14
4	401.2395	429.2344	S	1267.6641	1250.6375	13
5	458.2609	486.2558	G	1180.6321	1163.6055	12
6	595.3198	*623.3148*	H	1123.6106	1106.5841	11
7	696.3675	*724.3624*	T	986.5517	969.5251	10
8	795.4359	823.4308	V	885.5040	868.4775	9

9	882.4680	***910.4629***	**S**	***786.4356***	769.4090	**8**
10	953.5051	***981.5000***	**A**	699.4036	682.3770	**7**
11	1052.5735	***1080.5684***	**V**	628.3665	611.3399	**6**
12	1109.5949	1137.5899	**G**	***529.2980***	512.2715	**5**
13	1206.6477	1234.6426	**P**	472.2766	455.2500	**4**
14	1321.6747	***1349.6696***	**D**	375.2238	358.1973	**3**
15	1434.7587	1462.7536	**I**	260.1969	243.1703	**2**
16			**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.2	1607.8519	-0.0314	LDISGHTVSAVGPDIK
13.5	1607.7210	0.0996	RPSTSVVDESDMGGR
12.8	1607.8128	0.0077	RPGRGVEADGDGLPGR
11.1	1607.8155	0.0050	LDLKSAAYLDEGTGR
10.7	1607.7501	0.0704	YIPDLPSVTDEMGR
8.7	1607.7180	0.1026	KYMMLSMMISGPR
8.7	1607.7097	0.1108	QEASLLGSDEMEQR
7.3	1607.8631	-0.0426	QVAVAAGVDAVVGEAPR
7.1	1607.8784	-0.0579	EVSVIGGSGVFRFVR
6.4	1607.8519	-0.0313	EVPPVDDADARLALK

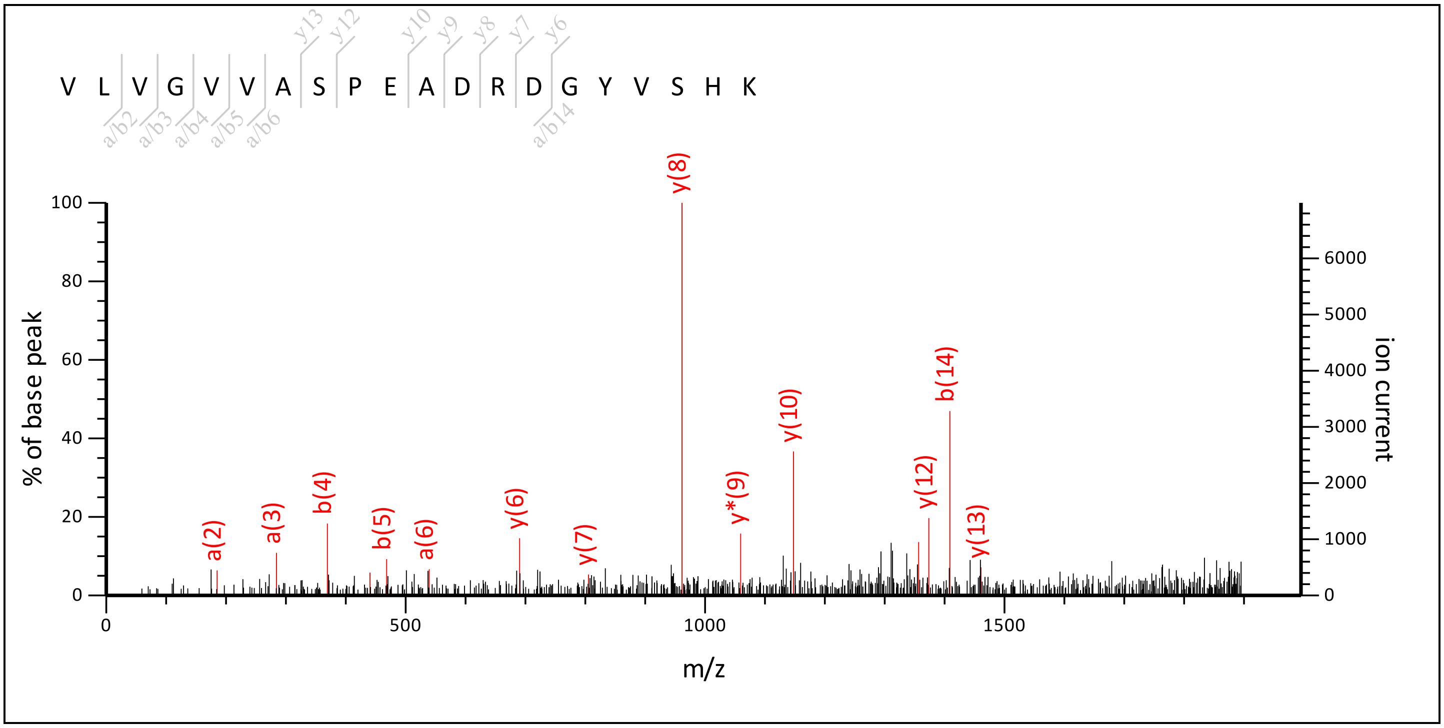
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 40

MS/MS Fragmentation of **VLVGVVASPEADRDGYVSHK**
Found in **gi|297604125** in **NCBInr**, Os05g0247100 [Oryza sativa Japonica Group]

Match to Query 127: 2097.057224 from(2098.064500,1+) intensity(0.0000) index(34)
Title: Label: B5, Spot_Id: 219739, Peak_List_Id: 225596, MSMS Job_Run_Id: 21783, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B5_136842181400.txt



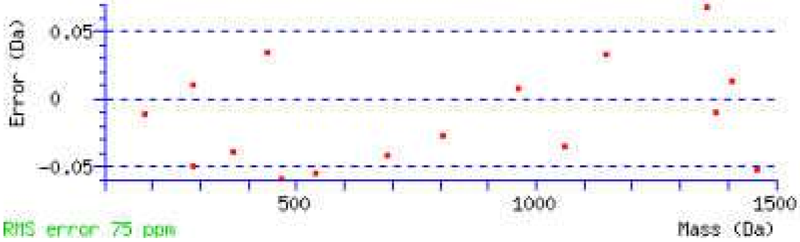
0 to 1995.17

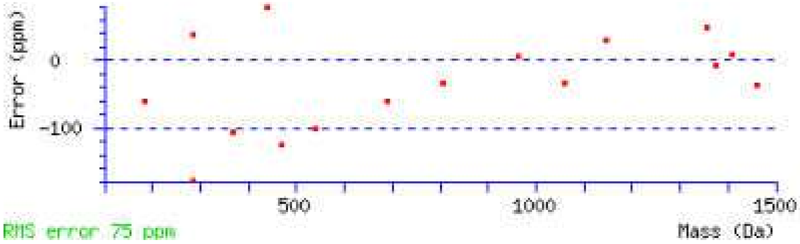
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2097.0855
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 5
Matches : 16/90 fragment ions using 38 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	72.0808		100.0757		V			20
2	*185.1648*		213.1598		L	1999.0243	1981.9978	19
3	*284.2333*		312.2282		V	1885.9403	1868.9137	18
4	341.2547		**369.2496**		G	1786.8719	1769.8453	17
5	*440.3231*		**468.3180**		V	1729.8504	1712.8238	16
6	*539.3915*		567.3865		V	1630.7820	1613.7554	15
7	610.4287		638.4236		A	1531.7136	1514.6870	14
8	697.4607		725.4556		S	*1460.6764*	1443.6499	13

9	794.5135		822.5084		**P**	***1373.6444***	1356.6179	**12**
10	923.5560		951.5510		**E**	1276.5917	1259.5651	**11**
11	994.5932		1022.5881		**A**	***1147.5491***	1130.5225	**10**
12	1109.6201		1137.6150		**D**	1076.5119	1059.4854	**9**
13	1265.7212	1248.6947	1293.7161	1276.6896	**R**	***961.4850***	944.4585	**8**
14	1380.7482	1363.7216	**1408.7431**	1391.7165	**D**	***805.3839***	788.3573	**7**
15	1437.7696	1420.7431	1465.7645	1448.7380	**G**	***690.3570***	673.3304	**6**
16	1600.8329	1583.8064	1628.8279	1611.8013	**Y**	633.3355	616.3089	**5**
17	1699.9014	1682.8748	1727.8963	1710.8697	**V**	470.2722	453.2456	**4**
18	1786.9334	1769.9068	1814.9283	1797.9018	**S**	371.2037	354.1772	**3**
19	1923.9923	1906.9658	1951.9872	1934.9607	**H**	***284.1717***	267.1452	**2**
20					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.5	2097.0855	-0.0283	VLVGVVASPEADRDGYVSHK
5.3	2097.0789	-0.0217	SLMLVHRLLVDGDSSFHR
2.1	2097.0288	0.0284	DPALAHCIPMQLHFLYR
0.8	2096.9440	0.1133	WGIPPSTPDWGADDEELGR

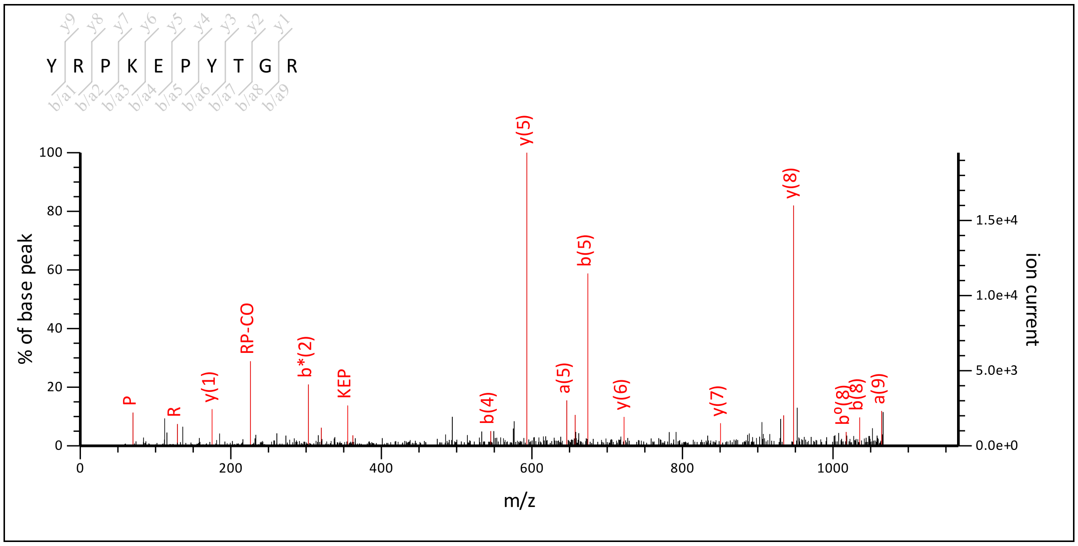
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 50

MS/MS Fragmentation of **YRPKEPYTGR**
Found in **gi|41052915** in **NCBInr**, putative ferredoxin-NADP(H) oxidoreductase [Oryza sativa Japonica Group]

Match to Query 20: 1265.645424 from(1266.652700,1+) intensity(0.0000) index(8)
Title: Label: L3, Spot_Id: 219717, Peak_List_Id: 225433, MSMS Job_Run_Id: 21778, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L3_136842146000.txt



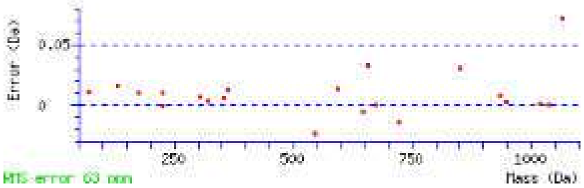
0 to 1166.55

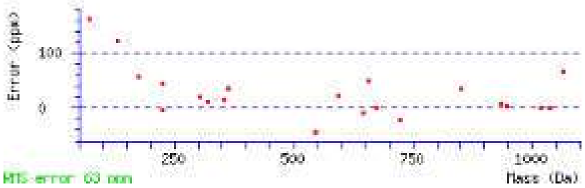
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1265.6516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 1.1
Matches : 25/150 fragment ions using 33 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y
1	136.0757	136.0757			164.0706			44.0495		**Y**						
2	129.1135	292.1768	275.1503		***320.1717***	303.1452		207.1128		**R**	1002.5003	1001.5051		1103.5956	1086.5691	1085.
3	70.0651	389.2296	372.2030		417.2245	400.1979		363.2139		**P**	905.4476	904.4523		***947.4945***	930.4680	929.
4	101.1073	517.3245	500.2980		***545.3194***	528.2929		460.2667		**K**	777.3526	776.3573		***850.4417***	833.4152	832.
5	102.0550	**646.3671**	629.3406	628.3566	***674.3620***	657.3355	656.3515	588.3616		**E**	648.3100	647.3148		***722.3468***	705.3202	704.
6	70.0651	743.4199	726.3933	725.4093	771.4148	754.3883	753.4042	717.4042		**P**	551.2572	550.2620		***593.3042***	576.2776	575.
7	136.0757	906.4832	889.4567	888.4726	***934.4781***	917.4516	916.4676			**Y**	388.1939			496.2514	479.2249	478.
8	74.0600	1007.5309	990.5043	989.5203	***1035.5258***	1018.4993	1017.5152	991.5360	993.5152	**T**	287.1462	300.1666	302.1459	333.1881	316.1615	315.
9	30.0338	**1064.5524**	1047.5258	1046.5418	1092.5473	1075.5207	1074.5367			**G**				232.1404	215.1139	
10	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RP	226.1662	254.1612	**RPK**	354.2612	382.2561	**RPKE**	483.3038	511.2987
RPKEP	580.3566	608.3515	**PK**	198.1601	226.1550	**PKE**	327.2027	355.1976
PKEP	424.2554	452.2504	**PKEPY**	587.3188	615.3137	**PKEPYT**	688.3665	716.3614
KE	230.1499	258.1448	**KEP**	327.2027	355.1976	**KEPY**	490.2660	518.2609
KEPYT	591.3137	619.3086	**KEPYTG**	648.3352	676.3301	**EP**	199.1077	227.1026
EPY	362.1710	390.1660	**EPYT**	463.2187	491.2136	**EPYTG**	520.2402	548.2351
PY	233.1285	261.1234	**PYT**	334.1761	362.1710	**PYTG**	391.1976	419.1925
YT	237.1234	265.1183	**YTG**	294.1448	322.1397	**TG**	131.0815	159.0764





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.9	1265.6516	-0.0062	YRPKEPYTGR
19.7	1265.6000	0.0454	EANSFATSVGAGR
16.3	1265.5888	0.0566	SDNFEEKNGVK
16.1	1265.5968	0.0486	TMAGRAAASMAGR
15.5	1265.5960	0.0494	SNSTGSSSKQQR
15.4	1265.6113	0.0342	SGSGAGAPGPPQAGR
15.2	1265.5524	0.0930	DAADTAEVFGDR
15.1	1265.6364	0.0090	RTYTAEEIQR
15.1	1265.6802	-0.0348	SGGIMVLTFIGR
15.0	1265.6108	0.0346	DAVMKEMATVR

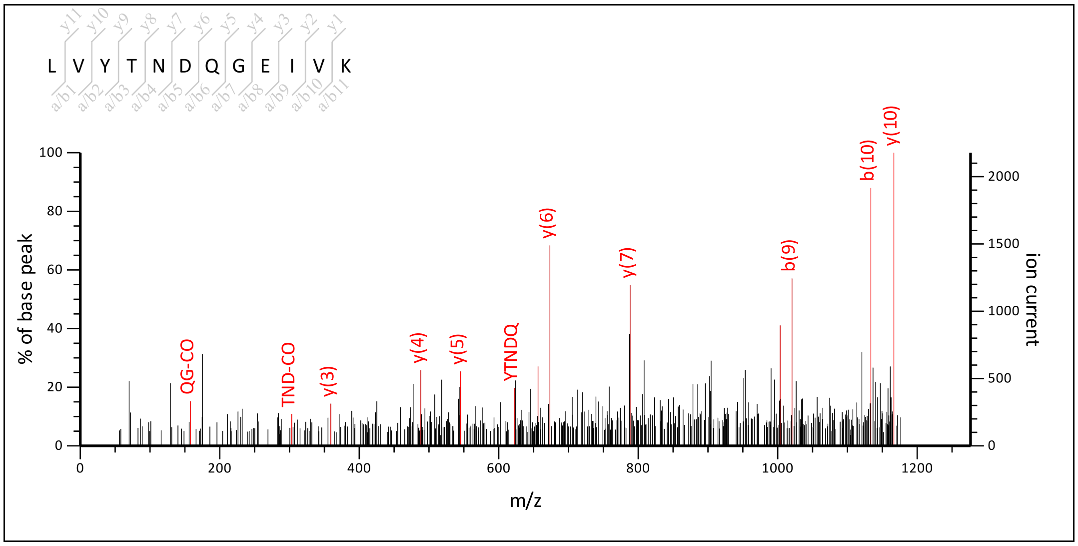
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 50

MS/MS Fragmentation of **LVYTNDQGEIVK**
Found in **gi|41052915** in **NCBInr**, putative ferredoxin-NADP(H) oxidoreductase [Oryza sativa Japonica Group]

Match to Query 28: 1377.684424 from(1378.691700,1+) intensity(0.0000) index(11)
Title: Label: L3, Spot_Id: 219717, Peak_List_Id: 225437, MSMS Job_Run_Id: 21778, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L3_136842146000.txt



0 to 1276.49

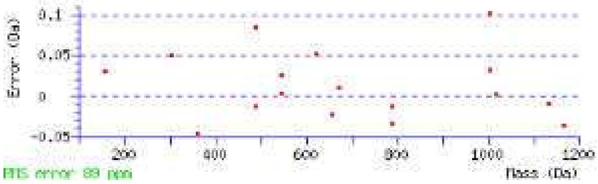
Label all possible matches ○ Label matches used for scoring ●

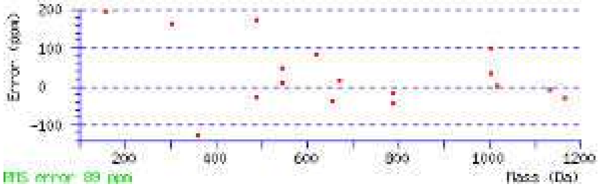
Monoisotopic mass of neutral peptide Mr(calc): 1377.7140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.15
Matches : 17/195 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		L					
2	72.0808	185.1648			213.1598			171.1492		V	1221.5746	1234.5950		1265.6372	1248.6107
3	136.0757	348.2282			376.2231					Y	1058.5113			***1166.5688***	1149.5422
4	74.0600	449.2758		431.2653	477.2708		459.2602	433.2809	435.2602	T	957.4636	970.4840	972.4633	***1003.5055***	986.4789
5	87.0553	563.3188	546.2922	545.3082	591.3137	574.2871	573.3031	520.3130		N	843.4207	842.4254		902.4578	885.4312
6	88.0393	678.3457	661.3192	660.3352	706.3406	689.3141	688.3301	634.3559		D	728.3937	727.3985		***788.4149***	771.3883
7	101.0709	806.4043	789.3777	788.3937	834.3992	817.3727	816.3886	749.3828		Q	600.3352	599.3399		***673.3879***	656.3614
8	30.0338	863.4258	846.3992	845.4152	891.4207	874.3941	873.4101			G				***545.3293***	528.3028
9	102.0550	992.4684	975.4418	974.4578	**1020.4633**	1003.4367	1002.4527	934.4629		E	414.2711	413.2758		***488.3079***	471.2813
10	86.0964	1105.5524	1088.5259	1087.5419	**1133.5473**	1116.5208	1115.5368	1077.5211	1091.5368	I	301.1870	314.2074	328.2231	***359.2653***	342.2387
11	72.0808	1204.6208	1187.5943	1186.6103	1232.6157	1215.5892	1214.6052	1190.6052		V	202.1186	215.1390		246.1812	229.1547
12	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VY	235.1441	263.1390	VYT	336.1918	364.1867	VYTN	450.2347	478.2296
VYTND	565.2617	593.2566	VYTNDQ	693.3202	721.3151	YT	237.1234	265.1183
YTN	351.1663	379.1612	YTND	466.1932	494.1882	YTNDQ	594.2518	622.2467
YTNDQG	651.2733	679.2682	TN	188.1030	216.0979	TND	303.1299	331.1248
TNDQ	431.1885	459.1834	TNDQG	488.2100	516.2049	TNDQGE	617.2525	645.2475
ND	202.0822	230.0771	NDQ	330.1408	358.1357	NDQG	387.1623	415.1572
NDQGE	516.2049	544.1998	NDQGEI	629.2889	657.2838	DQ	216.0979	244.0928
DQG	273.1193	301.1143	DQGE	402.1619	430.1569	DQGEI	515.2460	543.2409
DQGEIV	614.3144	642.3093	QG	158.0924	186.0873	QGE	287.1350	315.1299

QGEI	400.2191	428.2140	**QGEIV**	499.2875	527.2824	**GE**	159.0764	187.0713
GEI	272.1605	300.1554	**GEIV**	371.2289	399.2238	**EI**	215.1390	243.1339
EIV	314.2074	342.2023	**IV**	185.1648	213.1598			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.6	1377.7504	-0.0659	LVYTNDKGEIVK
41.6	1377.7504	-0.0659	LVYTNDKGELVK
41.6	1377.7140	-0.0296	LVYTNDQGEIVK
25.9	1377.7140	-0.0295	LVYTNENGEIVK
25.9	1377.7140	-0.0295	LVYTNENGELVK
19.9	1377.6345	0.0499	AGGGSGSAGRSGGSSAR
18.8	1377.6922	-0.0078	TTLAEGKAVDAMR
17.3	1377.7252	-0.0408	QTEFSLQLEKR
16.5	1377.6380	0.0464	MADAADMKADLAR
15.2	1377.6711	0.0133	VLDFCAEAGIGAR

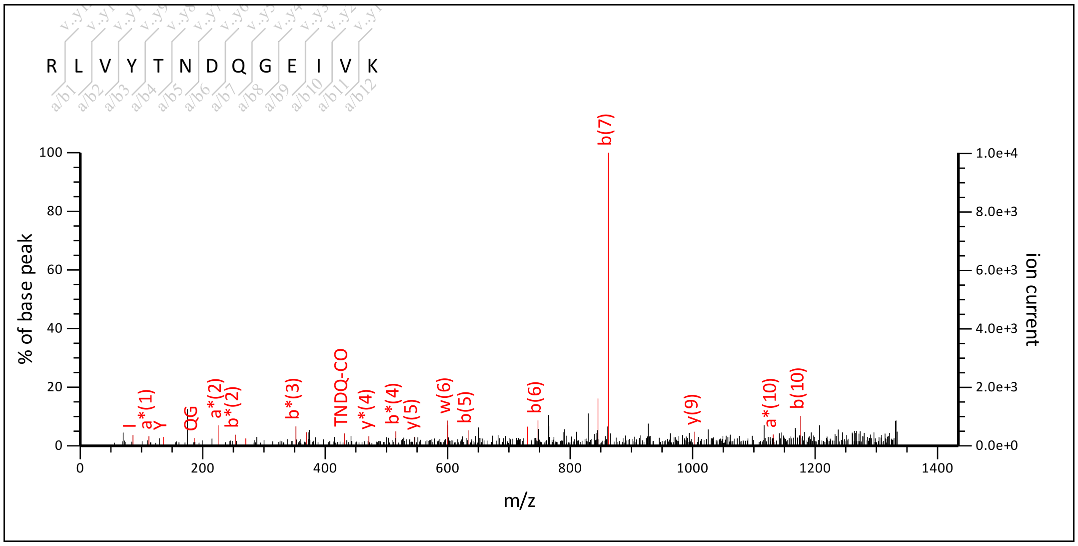
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 50

MS/MS Fragmentation of **RLVYTNDQGEIVK**
Found in **gi|41052915** in **NCBInr**, putative ferredoxin-NADP(H) oxidoreductase [Oryza sativa Japonica Group]

Match to Query 30: 1533.810024 from(1534.817300,1+) intensity(0.0000) index(12)
Title: Label: L3, Spot_Id: 219717, Peak_List_Id: 225436, MSMS Job_Run_Id: 21778, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L3_136842146000.txt



0 to 1433.98

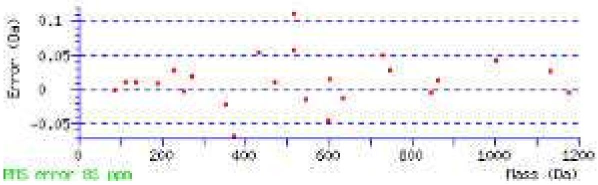
Label all possible matches ○ Label matches used for scoring ●

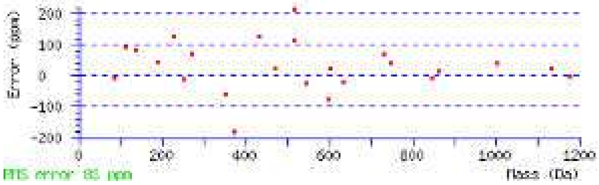
Monoisotopic mass of neutral peptide Mr(calc): 1533.8151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 35
Matches : 25/223 fragment ions using 52 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	129.1135	129.1135	112.0869		157.1084	140.0818		44.0495		R						
2	86.0964	242.1975	225.1710		***270.1925***	253.1659		200.1506		L	1320.6430	1319.6478		1378.7213	1361.6947	136
3	72.0808	341.2660	324.2394		***369.2609***	352.2343		327.2503		V	1221.5746	1234.5950		1265.6372	1248.6107	124
4	136.0757	504.3293	487.3027		532.3242	515.2976				Y	1058.5113			1166.5688	1149.5422	114
5	74.0600	605.3770	588.3504	587.3664	***633.3719***	616.3453	615.3613	589.3820	591.3613	T	957.4636	970.4840	972.4633	**1003.5055**	986.4789	98
6	87.0553	719.4199	702.3933	701.4093	***747.4148***	730.3883	729.4042	676.4141		N	843.4207	842.4254		902.4578	885.4312	88
7	88.0393	834.4468	817.4203	816.4363	***862.4417***	845.4152	844.4312	790.4570		D	728.3937	727.3985		788.4149	771.3883	77
8	101.0709	962.5054	945.4789	944.4948	990.5003	973.4738	972.4898	905.4839		Q	600.3352	599.3399		673.3879	656.3614	65
9	30.0338	1019.5269	1002.5003	1001.5163	1047.5218	1030.4952	1029.5112			G				**545.3293**	528.3028	52
10	102.0550	1148.5695	1131.5429	1130.5589	***1176.5644***	1159.5378	1158.5538	1090.5640		E	414.2711	413.2758		488.3079	471.2813	47
11	86.0964	1261.6535	1244.6270	1243.6430	1289.6484	1272.6219	1271.6379	1233.6222	1247.6379	I	301.1870	314.2074	328.2231	359.2653	342.2387	
12	72.0808	1360.7219	1343.6954	1342.7114	1388.7169	1371.6903	1370.7063	1346.7063		V	202.1186	215.1390		246.1812	229.1547	
13	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LV	185.1648	213.1598	LVY	348.2282	376.2231	LVYT	449.2758	477.2708
LVYTN	563.3188	591.3137	LVYTND	678.3457	706.3406	VY	235.1441	263.1390
VYT	336.1918	364.1867	VYTN	450.2347	478.2296	VYTND	565.2617	593.2566
VYTNDQ	693.3202	721.3151	YT	237.1234	265.1183	YTN	351.1663	379.1612
YTND	466.1932	494.1882	YTNDQ	594.2518	622.2467	YTNDQG	651.2733	679.2682
TN	188.1030	216.0979	TND	303.1299	331.1248	TNDQ	431.1885	459.1834
TNDQG	488.2100	516.2049	TNDQGE	617.2525	645.2475	ND	202.0822	230.0771
NDQ	330.1408	358.1357	NDQG	387.1623	415.1572	NDQGE	516.2049	544.1998

NDQGEI	629.2889	657.2838	**DQ**	216.0979	244.0928	**DQG**	273.1193	301.1143
DQGE	402.1619	430.1569	**DQGEI**	515.2460	543.2409	**DQGEIV**	614.3144	642.3093
QG	158.0924	186.0873	**QGE**	287.1350	315.1299	**QGEI**	400.2191	428.2140
QGEIV	499.2875	527.2824	**GE**	159.0764	187.0713	**GEI**	272.1605	300.1554
GEIV	371.2289	399.2238	**EI**	215.1390	243.1339	**EIV**	314.2074	342.2023
IV	185.1648	213.1598						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.4	1533.8151	-0.0051	RLVYTNDQGEIVK
10.0	1533.8627	-0.0527	ILQHTPDKSINLR
9.9	1533.8159	-0.0059	WTNITGAMKILMR
9.8	1533.7722	0.0379	LARAFGGDAMDAALR
9.7	1533.8047	0.0053	VLELAFPNMTMIR
9.3	1533.7205	0.0895	VANGTLAPNSMSSNR
9.1	1533.8012	0.0089	EFQRTISSARPSR
9.0	1533.7271	0.0829	SSSVSQPDSSPTVTR
8.8	1533.7254	0.0846	YMFTMACGRLIR
8.7	1533.7874	0.0226	ALAWWMSASRALR

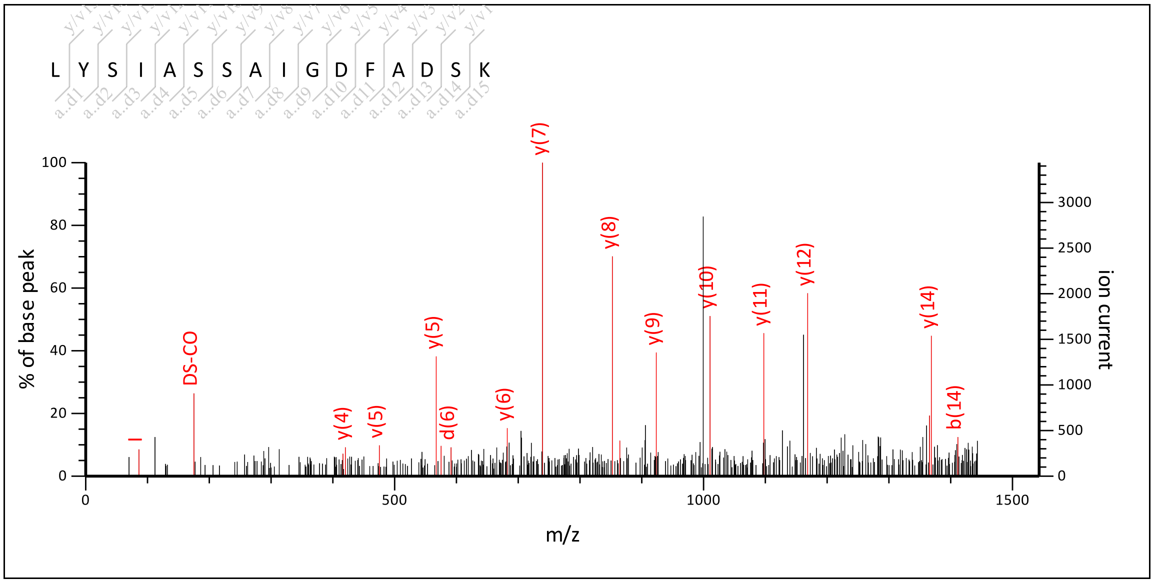
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 50

MS/MS Fragmentation of **LYSIASSAIGDFADSK**
Found in **gi|41052915** in **NCBInr**, putative ferredoxin-NADP(H) oxidoreductase [Oryza sativa Japonica Group]

Match to Query 32: 1643.778324 from(1644.785600,1+) intensity(0.0000) index(13)
Title: Label: L3, Spot_Id: 219717, Peak_List_Id: 225444, MSMS Job_Run_Id: 21778, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L3_136842146000.txt



0 to 1543.16

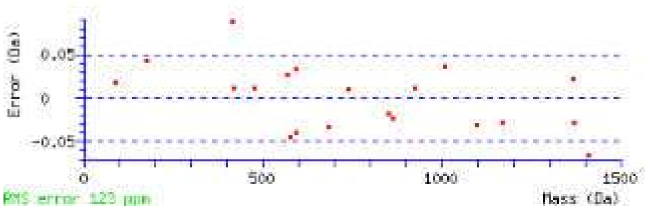
Label all possible matches ○ Label matches used for scoring ●

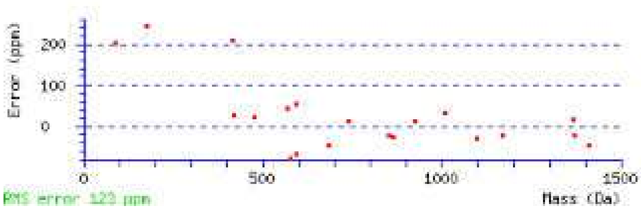
```
Monoisotopic mass of neutral peptide Mr(calc): 1643.8042
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70  Expect: 0.0002
Matches : 26/280 fragment ions using 28 most intense peaks   (help)
```

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		44.0495		**L**							**16**
2	136.0757	249.1598		277.1547				**Y**	1423.6700			1531.7275	1514.7009	1513.7169	**15**
3	60.0444	336.1918	318.1812	364.1867	346.1761	320.1969		**S**	1336.6379	1335.6427		***1368.6642***	1351.6376	1350.6536	**14**
4	86.0964	449.2758	431.2653	477.2708	459.2602	421.2445	435.2602	**I**	1223.5539	1236.5743	1250.5899	1281.6321	1264.6056	1263.6216	**13**
5	44.0495	520.3130	502.3024	548.3079	530.2973			**A**	1152.5168			***1168.5481***	1151.5215	1150.5375	**12**
6	60.0444	607.3450	589.3344	635.3399	617.3293	591.3501		**S**	1065.4847	1064.4895		***1097.5109***	1080.4844	1079.5004	**11**
7	60.0444	694.3770	676.3665	722.3719	704.3614	678.3821		**S**	978.4527	977.4575		***1010.4789***	993.4524	992.4684	**10**
8	44.0495	765.4141	747.4036	793.4090	775.3985			**A**	907.4156			***923.4469***	906.4203	905.4363	**9**
9	86.0964	878.4982	860.4876	906.4931	888.4825	850.4669	864.4825	**I**	794.3315	807.3519	821.3676	***852.4098***	835.3832	834.3992	**8**
10	30.0338	935.5197	917.5091	963.5146	945.5040			**G**				***739.3257***	722.2992	721.3151	**7**
11	88.0393	1050.5466	1032.5360	1078.5415	1060.5310	1006.5568		**D**	622.2831	621.2879		***682.3042***	665.2777	664.2937	**6**
12	120.0808	1197.6150	1179.6045	1225.6099	1207.5994			**F**	475.2147			***567.2773***	550.2508	549.2667	**5**
13	44.0495	1268.6521	1250.6416	1296.6470	1278.6365			**A**	404.1776			***420.2089***	403.1823	402.1983	**4**
14	88.0393	1383.6791	1365.6685	1411.6740	1393.6634	1339.6892		**D**	289.1506	288.1554		349.1718	332.1452	331.1612	**3**
15	60.0444	1470.7111	1452.7005	1498.7060	1480.6955	1454.7162		**S**	202.1186	201.1234		234.1448	217.1183	216.1343	**2**
16	101.1073							**K**	74.0237	73.0284		147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YS	223.1077	251.1026	**YSI**	336.1918	364.1867	**YSIA**	407.2289	435.2238

YSIAS	494.2609	522.2558	**YSIASS**	581.2930	609.2879	**YSIASSA**	652.3301	680.3250
SI	173.1285	201.1234	**SIA**	244.1656	272.1605	**SIAS**	331.1976	359.1925
SIASS	418.2296	446.2245	**SIASSA**	489.2667	517.2617	**SIASSAI**	602.3508	630.3457
SIASSAIG	659.3723	687.3672	**IA**	157.1335	185.1285	**IAS**	244.1656	272.1605
IASS	331.1976	359.1925	**IASSA**	402.2347	430.2296	**IASSAI**	515.3188	543.3137
IASSAIG	572.3402	600.3352	**IASSAIGD**	687.3672	715.3621	**AS**	131.0815	159.0764
ASS	218.1135	246.1084	**ASSA**	289.1506	317.1456	**ASSAI**	402.2347	430.2296
ASSAIG	459.2562	487.2511	**ASSAIGD**	574.2831	602.2780	**SS**	147.0764	175.0713
SSA	218.1135	246.1084	**SSAI**	331.1976	359.1925	**SSAIG**	388.2191	416.2140
SSAIGD	503.2460	531.2409	**SSAIGDF**	650.3144	678.3093	**SA**	131.0815	159.0764
SAI	244.1656	272.1605	**SAIG**	301.1870	329.1819	**SAIGD**	416.2140	444.2089
SAIGDF	563.2824	591.2773	**SAIGDFA**	634.3195	662.3144	**AI**	157.1335	185.1285
AIG	214.1550	242.1499	**AIGD**	329.1819	357.1769	**AIGDF**	476.2504	504.2453
AIGDFA	547.2875	575.2824	**AIGDFAD**	662.3144	690.3093	**IG**	143.1179	171.1128
IGD	258.1448	286.1397	**IGDF**	405.2132	433.2082	**IGDFA**	476.2504	504.2453
IGDFAD	591.2773	619.2722	**IGDFADS**	678.3093	706.3042	**GD**	145.0608	173.0557
GDF	292.1292	320.1241	**GDFA**	363.1663	391.1612	**GDFAD**	478.1932	506.1882
GDFADS	565.2253	593.2202	**DF**	235.1077	263.1026	**DFA**	306.1448	334.1397
DFAD	421.1718	449.1667	**DFADS**	508.2038	536.1987	**FA**	191.1179	219.1128
FAD	306.1448	334.1397	**FADS**	393.1769	421.1718	**AD**	159.0764	187.0713
ADS	246.1084	274.1034	**DS**	175.0713	203.0662			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.6	1643.8042	-0.0259	LYSIASSAIGDFADSK
64.5	1643.8043	-0.0259	LYSIASSALGDFGDTK
20.5	1643.6742	0.1041	CGELDMAGEVFGGMR
15.6	1643.7032	0.0751	RFSGEQDMSSTMPR
14.0	1643.8705	-0.0922	LYTVVYIMDLRSR
10.8	1643.7825	-0.0041	ESIFNASSSSSKCIK
10.4	1643.8242	-0.0459	MRAIFYWSLGTGSR
10.2	1643.8705	-0.0922	YLAVMQAEPVVGVPR
9.7	1643.7766	0.0017	GCTTFEALAAYVWR
9.7	1643.7568	0.0215	LKGMEMALTASAMDK

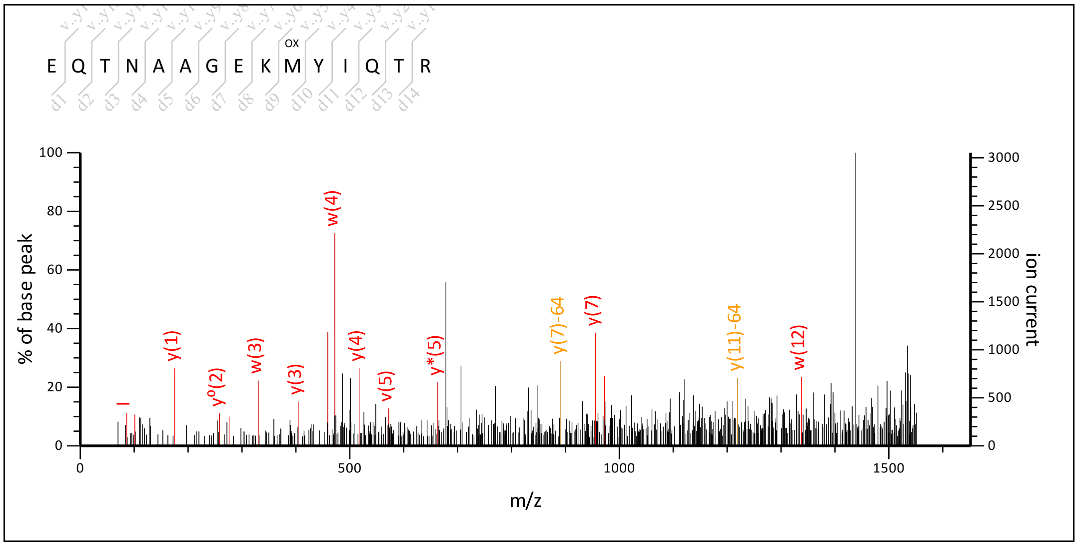
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 50

MS/MS Fragmentation of **EQTNAAGEKMYIQTR**
Found in **gi|41052915** in **NCBInr**, putative ferredoxin-NADP(H) oxidoreductase [Oryza sativa Japonica Group]

Match to Query 34: 1754.808624 from(1755.815900,1+) intensity(0.0000) index(14)
Title: Label: L3, Spot_Id: 219717, Peak_List_Id: 225434, MSMS Job_Run_Id: 21778, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L3_136842146000.txt



0 to 1651.57

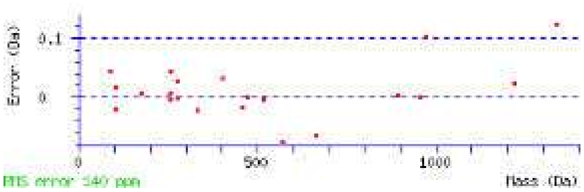
Label all possible matches ○ Label matches used for scoring ●

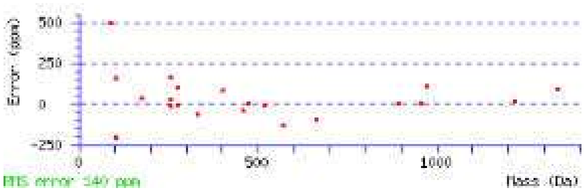
```
Monoisotopic mass of neutral peptide Mr(calc): 1754.8257
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10     : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 20  Expect: 16
Matches : 25/395 fragment ions using 30 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	101.0709	230.1135	213.0870	212.1030	258.1084	241.0819	240.0979	173.0921		Q	1489.7394	1488.7441		1562.7921	1545.7656
3	74.0600	331.1612	314.1347	313.1506	359.1561	342.1296	341.1456	315.1663	317.1456	T	1388.6917	1401.7121	1403.6914	1434.7336	1417.7070
4	87.0553	445.2041	428.1776	427.1936	473.1991	456.1725	455.1885	402.1983		N	1274.6488	1273.6535		1333.6859	1316.6593
5	44.0495	516.2413	499.2147	498.2307	544.2362	527.2096	526.2256			A	1203.6117			***1219.6430***	1202.6164
6	44.0495	587.2784	570.2518	569.2678	615.2733	598.2467	597.2627			A	1132.5746			1148.6059	1131.5793
7	30.0338	644.2998	627.2733	626.2893	672.2947	655.2682	654.2842			G				1077.5687	1060.5422
8	102.0550	773.3424	756.3159	755.3319	801.3373	784.3108	783.3268	715.3369		E	946.5105	945.5152		1020.5473	1003.5207
9	101.1073	901.4374	884.4108	883.4268	929.4323	912.4058	911.4217	844.3795		K	818.4155	817.4203		***891.5047***	874.4781
10	56.0495	984.4745	967.4480	966.4639	1012.4694	995.4429	994.4589	972.4745		M	735.3784	734.3832		763.4097	746.3832
11	136.0757	1147.5378	1130.5113	1129.5273	1175.5327	1158.5062	1157.5222			Y	572.3151			680.3726	663.3461
12	86.0964	1260.6219	1243.5953	1242.6113	1288.6168	1271.5903	1270.6062	1232.5906	1246.6062	I	459.2310	472.2514	486.2671	***517.3093***	500.2827
13	101.0709	1388.6805	1371.6539	1370.6699	1416.6754	1399.6488	1398.6648	1331.6590		Q	331.1724	330.1772		***404.2252***	387.1987
14	74.0600	1489.7282	1472.7016	1471.7176	1517.7231	1500.6965	1499.7125	1473.7332	1475.7125	T	230.1248	243.1452	245.1244	***276.1666***	259.1401
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QT	202.1186	230.1135	QTN	316.1615	344.1565	QTNA	387.1987	415.1936
QTNAA	458.2358	486.2307	QTNAAG	515.2572	543.2522	QTNAAGE	644.2998	672.2947
TN	188.1030	216.0979	TNA	259.1401	287.1350	TNAA	330.1772	358.1721
TNAAG	387.1987	415.1936	TNAAGE	516.2413	544.2362	TNAAGEK	644.3362	672.3311
NA	158.0924	186.0873	NAA	229.1295	257.1244	NAAG	286.1510	314.1459

NAAGE	415.1936	443.1885	**NAAGEK**	543.2885	571.2835	**NAAGEKM**	626.3257	654.3206
AA	115.0866	143.0815	**AAG**	172.1081	200.1030	**AAGE**	301.1506	329.1456
AAGEK	429.2456	457.2405	**AAGEKM**	512.2827	540.2776	**AAGEKMY**	675.3461	703.3410
AG	101.0709	129.0659	**AGE**	230.1135	258.1084	**AGEK**	358.2085	386.2034
AGEKM	441.2456	469.2405	**AGEKMY**	604.3089	632.3039	**GE**	159.0764	187.0713
GEK	287.1714	315.1663	**GEKM**	370.2085	398.2034	**GEKMY**	533.2718	561.2667
GEKMYI	646.3559	674.3508	**EK**	230.1499	258.1448	**EKM**	313.1870	341.1819
EKMY	476.2504	504.2453	**EKMYI**	589.3344	617.3293	**KM**	184.1444	212.1394
KMY	347.2078	375.2027	**KMYI**	460.2918	488.2867	**KMYIQ**	588.3504	616.3453
KMYIQT	689.3981	717.3930	**MY**	219.1128	247.1077	**MYI**	332.1969	360.1918
MYIQ	460.2554	488.2504	**MYIQT**	561.3031	589.2980	**YI**	249.1598	277.1547
YIQ	377.2183	405.2132	**YIQT**	478.2660	506.2609	**IQ**	214.1550	242.1499
IQT	315.2027	343.1976	**QT**	202.1186	230.1135			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.2	1754.8257	-0.0171	EQTNAAGEKMYIQTR
12.8	1754.9389	-0.1303	FLGTCVLTSVYLINR
12.3	1754.8509	-0.0423	AGMVEDDILHLIEER
9.0	1754.7460	0.0626	MGILDAVTEMCACPR
8.9	1754.9567	-0.1481	FAVTGTVDGPLPEIAIR
8.9	1754.8911	-0.0825	LEGTTASTASHAAVNLGR
8.8	1754.8542	-0.0456	SVISSNSGKVTMAAMEK
8.6	1754.8153	-0.0067	IWSAAMEELMSKGMR
8.6	1754.7669	0.0418	EEAEIYEGEAVCTQK
8.3	1754.8509	-0.0423	SSPSICKAFGIESTGSK

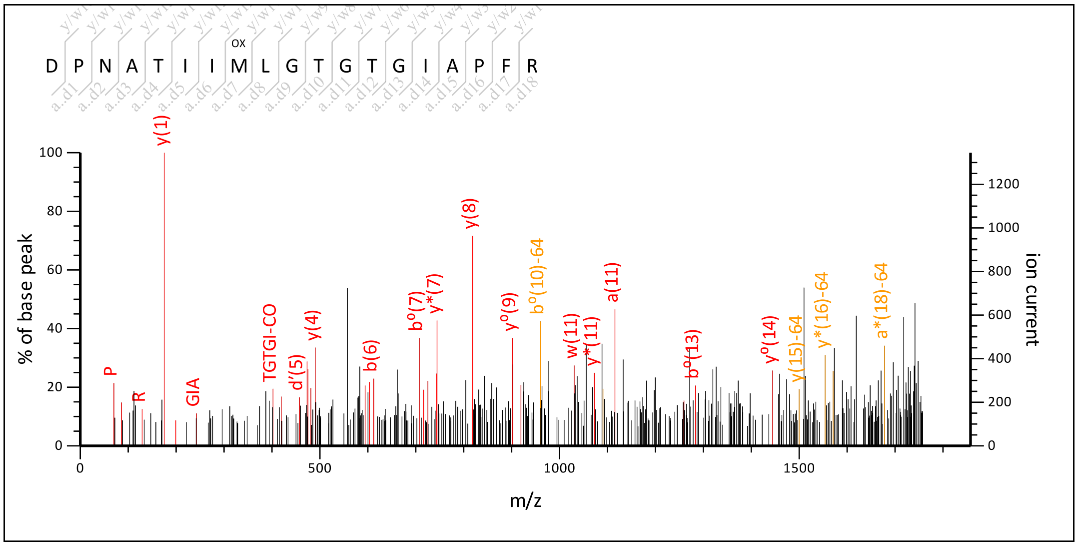
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 50

MS/MS Fragmentation of **DPNATIIMLGTGTGIAPFR**
Found in **gi|41052915** in **NCBInr**, putative ferredoxin-NADP(H) oxidoreductase [Oryza sativa Japonica Group]

Match to Query 37: 1959.991124 from(1960.998400,1+) intensity(0.0000) index(15)
Title: Label: L3, Spot_Id: 219717, Peak_List_Id: 225438, MSMS Job_Run_Id: 21778, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L3_136842146000.txt



0 to 1857.47

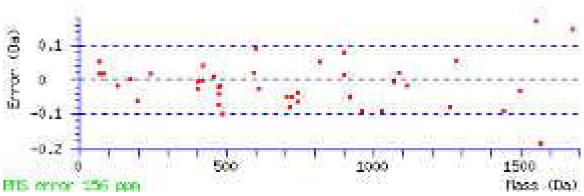
Label all possible matches ○ Label matches used for scoring ●

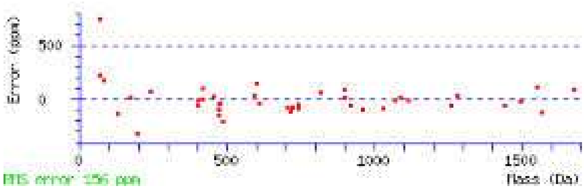
Monoisotopic mass of neutral peptide Mr(calc): 1960.0088
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 17 **Expect:** 31
Matches : 46/558 fragment ions using 85 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D					
2	70.0651	185.0921		167.0815	213.0870		195.0764	159.0764		P	1739.9439	1738.9487		1781.9908	1764.9643
3	87.0553	299.1350	282.1084	281.1244	327.1299	310.1034	309.1193	256.1292		N	1625.9010	1624.9057		1684.9381	1667.9115
4	44.0495	370.1721	353.1456	352.1615	398.1670	381.1405	380.1565			A	1554.8639			***1570.8952***	1553.8686
5	74.0600	471.2198	454.1932	453.2092	499.2147	482.1882	481.2041	455.2249	457.2041	T	1453.8162	1466.8366	1468.8158	***1499.8580***	1482.8315
6	86.0964	584.3039	567.2773	566.2933	**612.2988**	595.2722	594.2882	556.2726	570.2882	I	1340.7321	1353.7525	1367.7682	1398.8104	1381.7838
7	86.0964	697.3879	680.3614	679.3774	**725.3828**	708.3563	707.3723	669.3566	683.3723	I	1227.6481	1240.6685	1254.6841	1285.7263	1268.6998
8	56.0495	780.4250	763.3985	762.4145	808.4199	791.3934	790.4094	768.4250		M	1144.6109	1143.6157		1172.6422	1155.6157
9	86.0964	893.5091	876.4825	875.4985	921.5040	904.4775	903.4934	851.4621		L	1031.5269	1030.5316		1089.6051	1072.5786
10	30.0338	950.5306	933.5040	932.5200	978.5255	961.4989	960.5149			G				976.5211	959.4945
11	74.0600	1051.5782	1034.5517	1033.5677	1079.5732	1062.5466	1061.5626	1035.5833	1037.5626	T	873.4577	886.4781	888.4574	***919.4996***	902.4730
12	30.0338	1108.5997	1091.5732	1090.5891	1136.5946	1119.5681	1118.5841			G				***818.4519***	801.4254
13	74.0600	1209.6474	1192.6208	1191.6368	1237.6423	1220.6157	1219.6317	1193.6525	1195.6317	T	715.3886	728.4090	730.3883	761.4305	744.4039
14	30.0338	1266.6688	1249.6423	1248.6583	1294.6638	1277.6372	1276.6532			G				660.3828	643.3562
15	86.0964	1379.7529	1362.7264	1361.7423	1407.7478	1390.7213	1389.7373	1351.7216	1365.7373	I	545.2831	558.3035	572.3191	***603.3613***	586.3348
16	44.0495	1450.7900	1433.7635	1432.7795	1478.7849	1461.7584	1460.7744			A	474.2459			***490.2772***	473.2507
17	70.0651	1547.8428	1530.8162	1529.8322	1575.8377	1558.8112	1557.8271	1521.8271		P	377.1932	376.1979		***419.2401***	402.2136
18	120.0808	1694.9112	1677.8847	1676.9006	1722.9061	1705.8796	1704.8956			F	230.1248			322.1874	305.1608
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PN	184.1081	212.1030	PNA	255.1452	283.1401	PNAT	356.1928	384.1878

PNATI	469.2769	497.2718	**PNATII**	582.3610	610.3559	**PNATIIM**	665.3981	693.3930
NA	158.0924	186.0873	**NAT**	259.1401	287.1350	**NATI**	372.2241	400.2191
NATII	485.3082	513.3031	**NATIIM**	568.3453	596.3402	**NATIIML**	681.4294	709.4243
AT	145.0972	173.0921	**ATI**	258.1812	286.1761	**ATII**	371.2653	399.2602
ATIIM	454.3024	482.2973	**ATIIML**	567.3865	595.3814	**ATIIMLG**	624.4079	652.4028
TI	187.1441	215.1390	**TII**	300.2282	328.2231	**TIIM**	383.2653	411.2602
TIIML	496.3493	524.3443	**TIIMLG**	553.3708	581.3657	**TIIMLGT**	654.4185	682.4134
II	199.1805	227.1754	**IIM**	282.2176	310.2125	**IIML**	395.3017	423.2966
IIMLG	452.3231	480.3180	**IIMLGT**	553.3708	581.3657	**IIMLGTG**	610.3923	638.3872
IM	169.1335	197.1285	**IML**	282.2176	310.2125	**IMLG**	339.2391	367.2340
IMLGT	440.2867	468.2817	**IMLGTG**	497.3082	525.3031	**IMLGTGT**	598.3559	626.3508
IMLGTGTG	655.3774	683.3723	**ML**	169.1335	197.1285	**MLG**	226.1550	254.1499
MLGT	327.2027	355.1976	**MLGTG**	384.2241	412.2191	**MLGTGT**	485.2718	513.2667
MLGTGTG	542.2933	570.2882	**MLGTGTGI**	655.3774	683.3723	**LG**	143.1179	171.1128
LGT	244.1656	272.1605	**LGTG**	301.1870	329.1819	**LGTGT**	402.2347	430.2296
LGTGTG	459.2562	487.2511	**LGTGTGI**	572.3402	600.3352	**LGTGTGIA**	643.3774	671.3723
GT	131.0815	159.0764	**GTG**	188.1030	216.0979	**GTGT**	289.1506	317.1456
GTGTG	346.1721	374.1670	**GTGTGI**	459.2562	487.2511	**GTGTGIA**	530.2933	558.2882
GTGTGIAP	627.3461	655.3410	**TG**	131.0815	159.0764	**TGT**	232.1292	260.1241
TGTG	289.1506	317.1456	**TGTGI**	402.2347	430.2296	**TGTGIA**	473.2718	501.2667
TGTGIAP	570.3246	598.3195	**GT**	131.0815	159.0764	**GTG**	188.1030	216.0979
GTGI	301.1870	329.1819	**GTGIA**	372.2241	400.2191	**GTGIAP**	469.2769	497.2718
GTGIAPF	616.3453	644.3402	**TG**	131.0815	159.0764	**TGI**	244.1656	272.1605
TGIA	315.2027	343.1976	**TGIAP**	412.2554	440.2504	**TGIAPF**	559.3239	587.3188
GI	143.1179	171.1128	**GIA**	214.1550	242.1499	**GIAP**	311.2078	339.2027
GIAPF	458.2762	486.2711	**IA**	157.1335	185.1285	**IAP**	254.1863	282.1812
IAPF	401.2547	429.2496	**AP**	141.1022	169.0972	**APF**	288.1707	316.1656
PF	217.1335	245.1285						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.2	1960.0088	-0.0177	DPNATIIMLGTGTGIAPFR
11.5	1960.0088	-0.0177	DPNATVIMLATGTGIAPFR
10.8	1960.0088	-0.0177	DPNATIVMLATGTGIAPFR
7.5	1959.9133	0.0778	DSEKNDAEVQAEGVLNSR
4.5	1959.9610	0.0301	GGDNNLATLDATTARVDTR
4.5	1960.0234	-0.0323	VVKPTSVMVELCEARAR
3.9	1960.0485	-0.0574	RLTAMSTVVALPNMLDTK
3.7	1960.0234	-0.0323	AAEILKGMVTLGCKPNSR
3.7	1959.8592	0.1319	QDVCDAVAAAVADGGEGEAR
3.6	1959.9974	-0.0063	VTATTINDGKRPATSSEGR

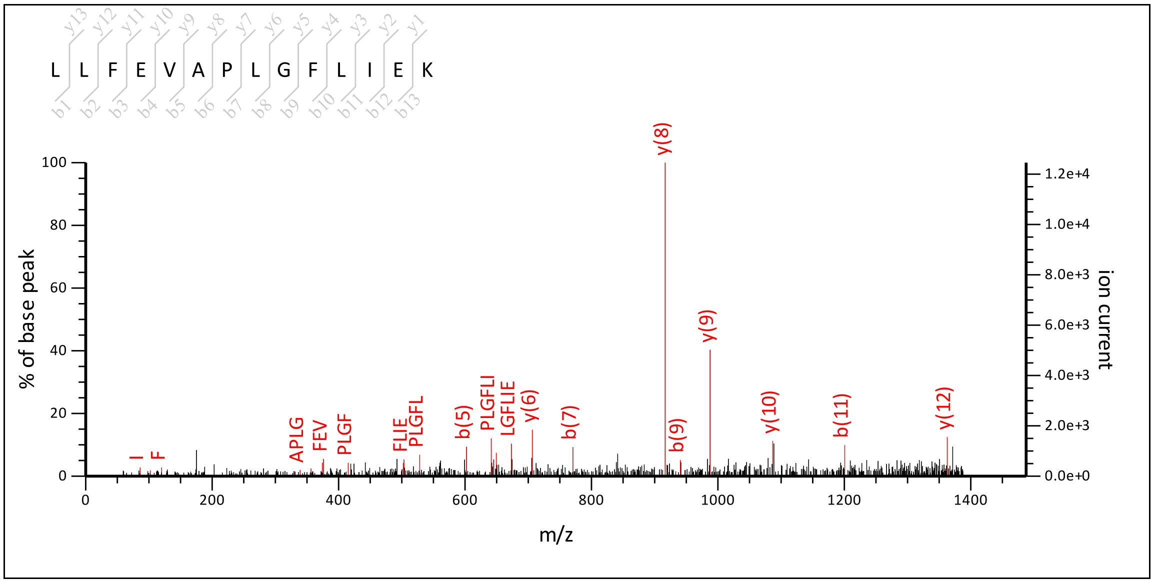
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 53**

MS/MS Fragmentation of **LLFEVAPLGFLIEK**
Found in **gi|118175929** in **NCBInr**, chloroplast sedoheptulose-1,7-bisphosphatase [Morus alba var. multicaulis]

Match to Query 75: 1587.902624 from(1588.909900,1+) intensity(0.0000) index(11)
Title: Label: H4, Spot_Id: 219729, Peak_List_Id: 225332, MSMS Job_Run_Id: 21774, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_H4_136842165600.txt



0 to 1487.58

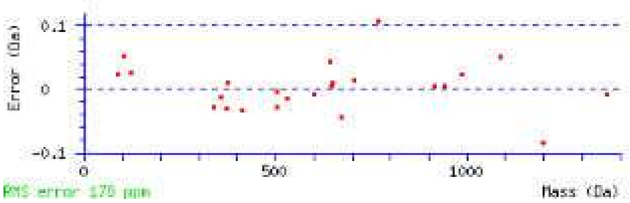
Label all possible matches ○ Label matches used for scoring ●

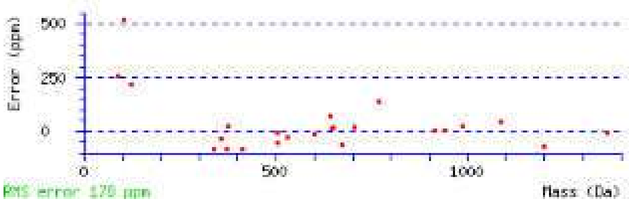
Monoisotopic mass of neutral peptide Mr(calc): 1587.9276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.61
Matches : 35/225 fragment ions using 56 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	**86.0964**		114.0913		44.0495		**L**							**14**
2	86.0964	199.1805		227.1754		157.1335		**L**	1417.7726	1416.7773		1475.8508	1458.8243	1457.8403	**13**
3	120.0808	346.2489		***374.2438***				**F**	1270.7042			***1362.7668***	1345.7402	1344.7562	**12**
4	102.0550	475.2915	457.2809	***503.2864***	485.2758	417.2860		**E**	1141.6616	1140.6663		1215.6984	1198.6718	1197.6878	**11**
5	72.0808	574.3599	556.3493	***602.3548***	584.3443	560.3443		**V**	1042.5932	1055.6136		***1086.6558***	1069.6292	1068.6452	**10**
6	44.0495	**645.3970**	627.3865	***673.3919***	655.3814			**A**	971.5560			***987.5873***	970.5608	969.5768	**9**
7	70.0651	742.4498	724.4392	***770.4447***	752.4341	716.4341		**P**	874.5033	873.5080		***916.5502***	899.5237	898.5397	**8**
8	86.0964	855.5339	837.5233	883.5288	865.5182	813.4869		**L**	761.4192	760.4240		819.4975	802.4709	801.4869	**7**
9	30.0338	912.5553	894.5448	***940.5502***	922.5397			**G**				***706.4134***	689.3869	688.4028	**6**
10	120.0808	1059.6237	1041.6132	1087.6186	1069.6081			**F**	557.3293			***649.3919***	632.3654	631.3814	**5**
11	86.0964	1172.7078	1154.6972	***1200.7027***	1182.6921	1130.6608		**L**	444.2453	443.2500		***502.3235***	485.2970	484.3130	**4**
12	86.0964	1285.7919	1267.7813	1313.7868	1295.7762	1257.7606	1271.7762	**I**	331.1612	344.1816	358.1973	389.2395	372.2129	371.2289	**3**
13	102.0550	1414.8345	1396.8239	1442.8294	1424.8188	1356.8290		**E**	202.1186	201.1234		276.1554	259.1288	258.1448	**2**
14	101.1073							**K**	74.0237	73.0284		147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LF	233.1648	261.1598	**LFE**	362.2074	390.2023	**LFEV**	461.2758	489.2708
LFEVA	532.3130	560.3079	**LFEVAP**	629.3657	657.3606	**FE**	249.1234	277.1183
FEV	348.1918	376.1867	**FEVA**	419.2289	447.2238	**FEVAP**	516.2817	544.2766

FEVAPL	629.3657	657.3606	**FEVAPLG**	686.3872	714.3821	**EV**	201.1234	229.1183
EVA	272.1605	300.1554	**EVAP**	369.2132	397.2082	**EVAPL**	482.2973	510.2922
EVAPLG	539.3188	567.3137	**EVAPLGF**	686.3872	714.3821	**VA**	143.1179	171.1128
VAP	240.1707	268.1656	**VAPL**	353.2547	381.2496	**VAPLG**	410.2762	438.2711
VAPLGF	557.3446	585.3395	**VAPLGFL**	670.4287	698.4236	**AP**	141.1022	169.0972
APL	254.1863	282.1812	**APLG**	311.2078	339.2027	**APLGF**	458.2762	486.2711
APLGFL	571.3602	599.3552	**APLGFLI**	684.4443	712.4392	**PL**	183.1492	211.1441
PLG	240.1707	268.1656	**PLGF**	387.2391	415.2340	**PLGFL**	500.3231	528.3180
PLGFLI	613.4072	641.4021	**LG**	143.1179	171.1128	**LGF**	290.1863	318.1812
LGFL	403.2704	431.2653	**LGFLI**	516.3544	544.3493	**LGFLIE**	645.3970	673.3919
GF	177.1022	205.0972	**GFL**	290.1863	318.1812	**GFLI**	403.2704	431.2653
GFLIE	532.3130	560.3079	**FL**	233.1648	261.1598	**FLI**	346.2489	374.2438
FLIE	475.2915	503.2864	**LI**	199.1805	227.1754	**LIE**	328.2231	356.2180
IE	215.1390	243.1339						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.0	1587.9276	-0.0250	LLFEVAPLGFLIEK
15.5	1587.9276	-0.0250	IVLEAFPAVFLLEK
14.9	1587.8304	0.0723	ATQAIAPMHAAVVHR
14.7	1587.7881	0.1145	WMAGRGWAAGLAWR
14.1	1587.7650	0.1377	INWMKAGMLESHR
13.5	1587.8151	0.0875	MGGAAILLSNRQADR
13.2	1587.8005	0.1021	GFLSINSQPAVNGER
13.1	1587.8654	0.0372	MDLILAQLTTINAR
12.8	1587.7675	0.1352	NMKPDAAAASLNDVR
12.7	1587.7536	0.1490	MGQDAVAANGTAGGGRR

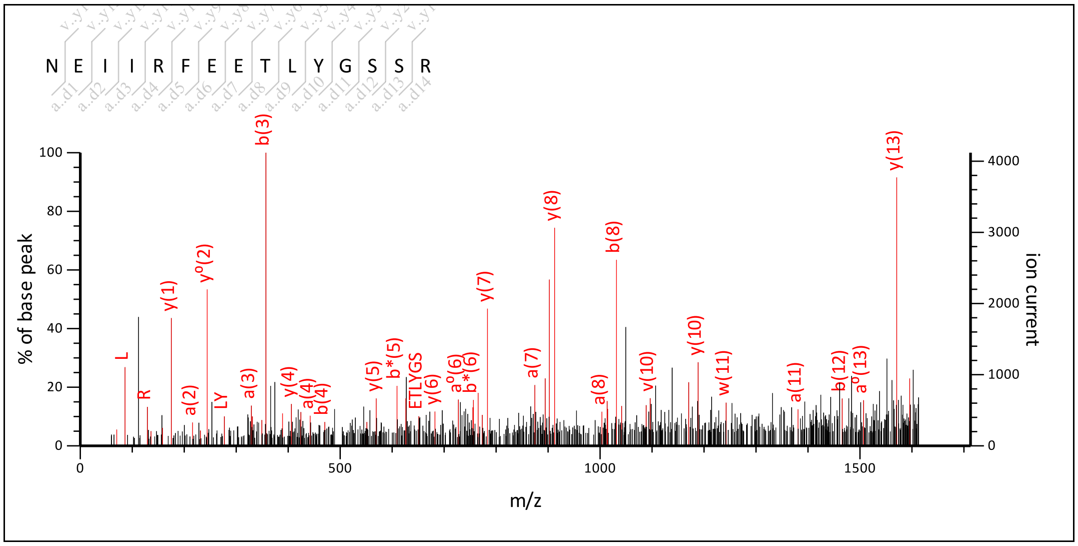
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 53

MS/MS Fragmentation of **NEIIRFEETLYGSSR**
Found in **gi|118175929** in **NCBInr**, chloroplast sedoheptulose-1,7-bisphosphatase [Morus alba var. multicaulis]

Match to Query 82: 1812.887224 from(1813.894500,1+) intensity(0.0000) index(14)
Title: Label: H4, Spot_Id: 219729, Peak_List_Id: 225328, MSMS Job_Run_Id: 21774, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_H4_136842165600.txt



0 to 1712.7

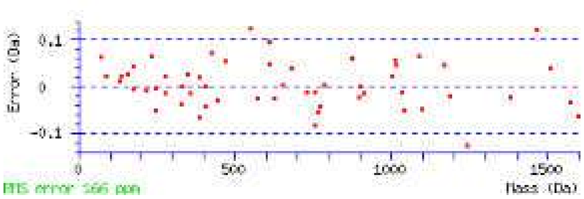
Label all possible matches ○ Label matches used for scoring ●

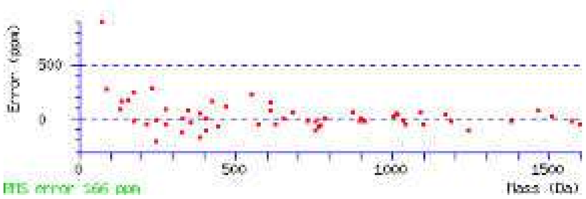
Monoisotopic mass of neutral peptide Mr(calc): 1812.9006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 1.1
Matches : 61/269 fragment ions using 128 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495		**N**					
2	102.0550	**216.0979**	199.0713	198.0873	**244.0928**	227.0662	226.0822	158.0924		**E**	1625.8282	1624.8329		1699.8650	1682.8384
3	86.0964	**329.1819**	312.1554	311.1714	**357.1769**	340.1503	339.1663	301.1506	315.1663	**I**	1512.7441	1525.7645	1539.7802	***1570.8224***	1553.7958
4	86.0964	**442.2660**	425.2395	424.2554	**470.2609**	453.2344	452.2504	414.2347	428.2504	**I**	1399.6601	1412.6805	1426.6961	1457.7383	1440.7118
5	129.1135	598.3671	581.3406	580.3566	**626.3620**	609.3355	608.3515	513.3031		**R**	1243.5590	1242.5637		1344.6543	1327.6277
6	120.0808	745.4355	728.4090	727.4250	**773.4304**	756.4039	755.4199			**F**	1096.4905			***1188.5531***	1171.5266
7	102.0550	**874.4781**	857.4516	856.4676	**902.4730**	885.4465	884.4625	816.4726		**E**	967.4480	966.4527		***1041.4847***	1024.4582
8	102.0550	**1003.5207**	986.4942	985.5102	**1031.5156**	1014.4891	1013.5051	945.5152		**E**	838.4054	837.4101		***912.4421***	895.4156
9	74.0600	1104.5684	1087.5419	1086.5578	1132.5633	1115.5368	1114.5527	1088.5735	1090.5527	**T**	737.3577	750.3781	752.3573	***783.3995***	766.3730
10	86.0964	1217.6525	1200.6259	1199.6419	1245.6474	1228.6208	1227.6368	1175.6055		**L**	624.2736	623.2784		***682.3519***	665.3253
11	136.0757	**1380.7158**	1363.6892	1362.7052	1408.7107	1391.6842	1390.7001			**Y**	461.2103			***569.2678***	552.2413
12	30.0338	1437.7373	1420.7107	1419.7267	**1465.7322**	1448.7056	1447.7216			**G**				***406.2045***	389.1779
13	60.0444	1524.7693	1507.7427	1506.7587	1552.7642	1535.7377	1534.7536	1508.7744		**S**	317.1568	316.1615		***349.1830***	332.1565
14	60.0444	1611.8013	1594.7748	1593.7907	1639.7962	1622.7697	1621.7857	1595.8064		**S**	230.1248	229.1295		262.1510	245.1244
15	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
EI	215.1390	243.1339	**EII**	328.2231	356.2180	**EIIR**	484.3242	512.3191
EIIRF	631.3926	659.3875	**II**	199.1805	227.1754	**IIR**	355.2816	383.2765
IIRF	502.3500	530.3449	**IIRFE**	631.3926	659.3875	**IR**	242.1975	270.1925
IRF	389.2659	417.2609	**IRFE**	518.3085	546.3035	**IRFEE**	647.3511	675.3461
RF	276.1819	304.1768	**RFE**	405.2245	433.2194	**RFEE**	534.2671	562.2620
RFEET	635.3148	663.3097	**FE**	249.1234	277.1183	**FEE**	378.1660	406.1609

FEET	479.2136	507.2086	**FEETL**	592.2977	620.2926	**EE**	231.0975	259.0925
EET	332.1452	360.1401	**EETL**	445.2293	473.2242	**EETLY**	608.2926	636.2875
EETLYG	665.3141	693.3090	**ET**	203.1026	231.0975	**ETL**	316.1867	344.1816
ETLY	479.2500	507.2449	**ETLYG**	536.2715	564.2664	**ETLYGS**	623.3035	651.2984
TL	187.1441	215.1390	**TLY**	350.2074	378.2023	**TLYG**	407.2289	435.2238
TLYGS	494.2609	522.2558	**TLYGSS**	581.2930	609.2879	**LY**	249.1598	277.1547
LYG	306.1812	334.1761	**LYGS**	393.2132	421.2082	**LYGSS**	480.2453	508.2402
YG	193.0972	221.0921	**YGS**	280.1292	308.1241	**YGSS**	367.1612	395.1561
GS	117.0659	145.0608	**GSS**	204.0979	232.0928	**SS**	147.0764	175.0713





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.6	1812.9006	-0.0134	NEIIRFEETLYGSSR
14.8	1812.9330	-0.0457	QDSELAQLRVQEIER
14.5	1812.8755	0.0118	QSLAFILEDGNHEQGR
13.4	1812.9330	-0.0457	QDLSTNEGSKQPAIVAR
10.1	1812.9621	-0.0749	GGETIFPEAEGKLLQPK
9.6	1812.8604	0.0268	RLGSVFLEEFVMEEE
9.4	1812.9523	-0.0651	GVPLNAGRFEWTPVATV
9.1	1812.8014	0.0858	QDITTNSDVGSTEDFGK
8.9	1813.0058	-0.1185	SALLATTDLAGLTRGTPR
8.9	1812.9330	-0.0457	RVVDLEAELSSPTNQR

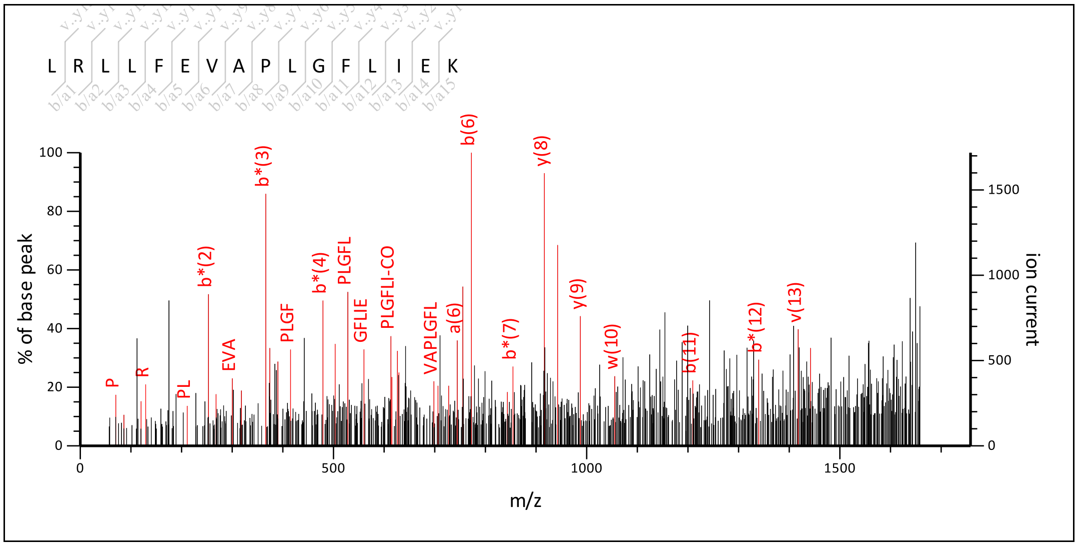
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 53

MS/MS Fragmentation of **LRLLFEVAPLGFLIEK**
Found in **gi|118175929** in **NCBInr**, chloroplast sedoheptulose-1,7-bisphosphatase [Morus alba var. multicaulis]

Match to Query 86: 1857.107224 from(1858.114500,1+) intensity(0.0000) index(16)
Title: Label: H4, Spot_Id: 219729, Peak_List_Id: 225334, MSMS Job_Run_Id: 21774, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_H4_136842165600.txt



0 to 1758.02

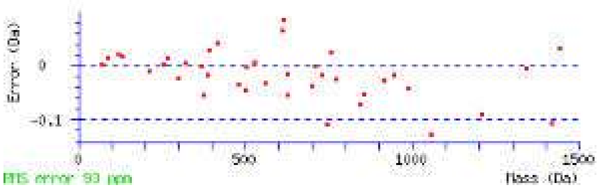
Label all possible matches ○ Label matches used for scoring ●

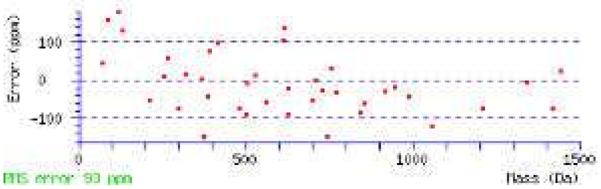
Monoisotopic mass of neutral peptide Mr(calc): 1857.1128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 5 **Expect:** 8.2e+02
Matches : 52/289 fragment ions using 114 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	***86.0964***			114.0913			44.0495		L					
2	129.1135	242.1975	225.1710		270.1925	253.1659		157.1335		R	1643.9407	1642.9455		1745.0360	1728.0095
3	86.0964	355.2816	338.2551		383.2765	366.2500		313.2347		L	1530.8566	1529.8614		1588.9349	1571.9083
4	86.0964	468.3657	451.3391		496.3606	479.3340		426.3187		L	1417.7726	1416.7773		1475.8508	1458.8243
5	120.0808	***615.4341***	598.4075		643.4290	626.4024				F	1270.7042			1362.7668	1345.7402
6	102.0550	***744.4767***	727.4501	726.4661	**772.4716**	755.4450	754.4610	686.4712		E	1141.6616	1140.6663		1215.6984	1198.6718
7	72.0808	***843.5451***	826.5185	825.5345	871.5400	854.5135	853.5294	829.5294		V	1042.5932	1055.6136		1086.6558	1069.6292
8	44.0495	914.5822	897.5557	896.5716	**942.5771**	925.5506	924.5665			A	971.5560			**987.5873**	970.5608
9	70.0651	1011.6350	994.6084	993.6244	1039.6299	1022.6033	1021.6193	985.6193		P	874.5033	873.5080		**916.5502**	899.5237
10	86.0964	1124.7190	1107.6925	1106.7085	1152.7139	1135.6874	1134.7034	1082.6721		L	761.4192	760.4240		819.4975	802.4709
11	30.0338	1181.7405	1164.7139	1163.7299	**1209.7354**	1192.7089	1191.7248			G				**706.4134**	689.3869
12	120.0808	1328.8089	1311.7824	1310.7983	1356.8038	1339.7773	1338.7933			F	557.3293			649.3919	632.3654
13	86.0964	***1441.8930***	1424.8664	1423.8824	1469.8879	1452.8613	1451.8773	1399.8460		L	444.2453	443.2500		502.3235	485.2970
14	86.0964	1554.9770	1537.9505	1536.9665	1582.9719	1565.9454	1564.9614	1526.9457	1540.9614	I	331.1612	344.1816	358.1973	389.2395	372.2129
15	102.0550	1684.0196	1666.9931	1666.0091	1712.0145	1694.9880	1694.0040	1626.0141		E	202.1186	201.1234		276.1554	259.1288
16	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RL	242.1975	270.1925	RLL	355.2816	383.2765	RLLF	502.3500	530.3449
RLLFE	631.3926	659.3875	LL	199.1805	227.1754	LLF	346.2489	374.2438
LLFE	475.2915	503.2864	LLFEV	574.3599	602.3548	LLFEVA	645.3970	673.3919
LF	233.1648	261.1598	LFE	362.2074	390.2023	LFEV	461.2758	489.2708
LFEVA	532.3130	560.3079	LFEVAP	629.3657	657.3606	FE	249.1234	277.1183

FEV	348.1918	376.1867	**FEVA**	419.2289	447.2238	**FEVAP**	516.2817	544.2766
FEVAPL	629.3657	657.3606	**FEVAPLG**	686.3872	714.3821	**EV**	201.1234	229.1183
EVA	272.1605	300.1554	**EVAP**	369.2132	397.2082	**EVAPL**	482.2973	510.2922
EVAPLG	539.3188	567.3137	**EVAPLGF**	686.3872	714.3821	**VA**	143.1179	171.1128
VAP	240.1707	268.1656	**VAPL**	353.2547	381.2496	**VAPLG**	410.2762	438.2711
VAPLGF	557.3446	585.3395	**VAPLGFL**	670.4287	698.4236	**AP**	141.1022	169.0972
APL	254.1863	282.1812	**APLG**	311.2078	339.2027	**APLGF**	458.2762	486.2711
APLGFL	571.3602	599.3552	**APLGFLI**	684.4443	712.4392	**PL**	183.1492	211.1441
PLG	240.1707	268.1656	**PLGF**	387.2391	415.2340	**PLGFL**	500.3231	528.3180
PLGFLI	613.4072	641.4021	**LG**	143.1179	171.1128	**LGF**	290.1863	318.1812
LGFL	403.2704	431.2653	**LGFLI**	516.3544	544.3493	**LGFLIE**	645.3970	673.3919
GF	177.1022	205.0972	**GFL**	290.1863	318.1812	**GFLI**	403.2704	431.2653
GFLIE	532.3130	560.3079	**FL**	233.1648	261.1598	**FLI**	346.2489	374.2438
FLIE	475.2915	503.2864	**LI**	199.1805	227.1754	**LIE**	328.2231	356.2180
IE	215.1390	243.1339						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
6.6	1857.0823	0.0249	SLTLLSLTSVNLTGTIPK
6.0	1857.0281	0.0791	MGLLVKGGDVLESLGEIK
5.1	1857.1128	-0.0055	LRLLFEVAPLGFLIEK
4.2	1856.9605	0.1467	RSQIVGNAVFTGHASASR
4.2	1856.9778	0.1294	LADNMVQLGKEGTLAAAR
4.0	1856.9592	0.1480	ISEDVVIDATERGNIAR
4.0	1857.0030	0.1043	LKMEINGGVATPTASAVAK
4.0	1857.0207	0.0865	RALQETSGVLVISDLEK
4.0	1857.0935	0.0137	VTEVIITTTKLNAVSLR
3.9	1856.9553	0.1519	SLEVPAEGVELMLSDLR

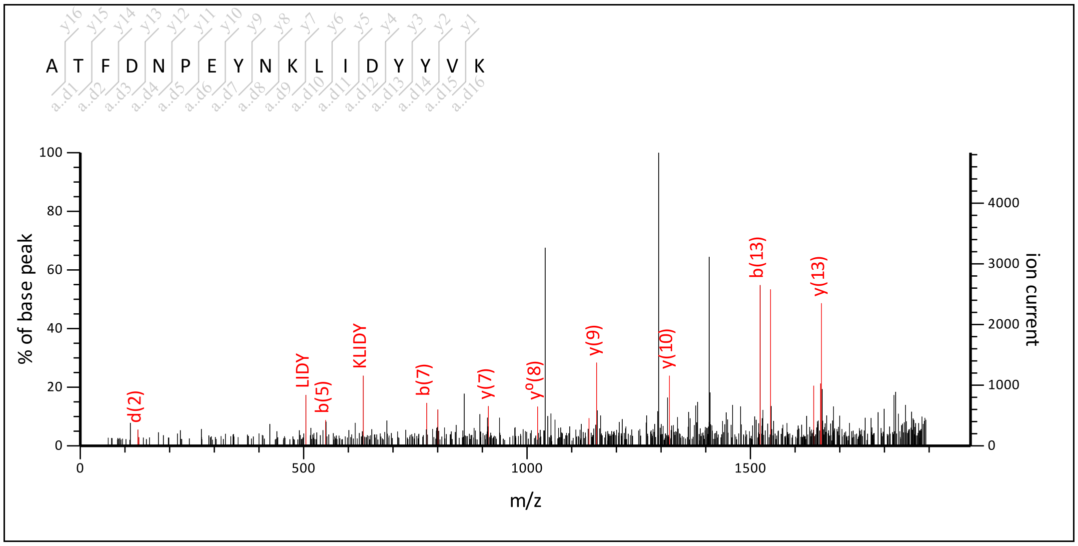
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 53

MS/MS Fragmentation of **ATFDNPEYNKLIDYYVK**
Found in **gi|118175929** in **NCBInr**, chloroplast sedoheptulose-1,7-bisphosphatase [Morus alba var. multicaulis]

Match to Query 90: 2091.987124 from(2092.994400,1+) intensity(0.0000) index(18)
Title: Label: H4, Spot_Id: 219729, Peak_List_Id: 225335, MSMS Job_Run_Id: 21774, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_H4_136842165600.txt



0 to 1992.68

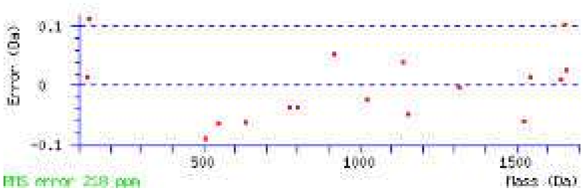
Label all possible matches ○ Label matches used for scoring ●

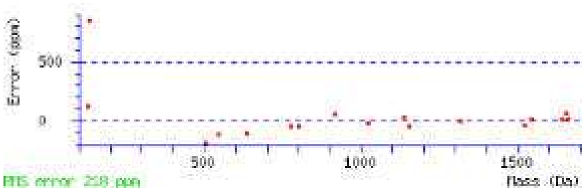
```
Monoisotopic mass of neutral peptide Mr(calc): 2092.0153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 7  Expect: 2.4e+02
Matches : 17/292 fragment ions using 57 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	74.0600	145.0972		127.0866	173.0921		155.0815	129.1022	131.0815	T	1975.9436	1988.9640	1990.9433	2021.9855	2004.9589
3	120.0808	292.1656		274.1550	320.1605		302.1499			F	1828.8752			1920.9378	1903.9113
4	88.0393	407.1925		389.1819	435.1874		417.1769	363.2027		D	1713.8483	1712.8530		1773.8694	1756.8428
5	87.0553	521.2354	504.2089	503.2249	**549.2304**	532.2038	531.2198	478.2296		N	1599.8053	1598.8101		***1658.8425***	1641.8159
6	70.0651	618.2882	601.2617	600.2776	646.2831	629.2566	628.2726	592.2726		P	1502.7526	1501.7573		***1544.7995***	1527.7730
7	102.0550	747.3308	730.3042	729.3202	**775.3257**	758.2992	757.3151	689.3253		E	1373.7100	1372.7147		1447.7468	1430.7202
8	136.0757	910.3941	893.3676	892.3836	938.3890	921.3625	920.3785			Y	1210.6467			***1318.7042***	1301.6776
9	87.0553	1024.4371	1007.4105	1006.4265	1052.4320	1035.4054	1034.4214	981.4312		N	1096.6037	1095.6085		***1155.6408***	1138.6143
10	101.1073	1152.5320	1135.5055	1134.5214	1180.5269	1163.5004	1162.5164	1095.4742		K	968.5088	967.5135		1041.5979	1024.5714
11	86.0964	1265.6161	1248.5895	1247.6055	1293.6110	1276.5844	1275.6004	1223.5691		L	855.4247	854.4294		***913.5029***	896.4764
12	86.0964	1378.7001	1361.6736	1360.6896	1406.6951	1389.6685	1388.6845	1350.6688	1364.6845	I	742.3406	755.3610	769.3767	***800.4189***	783.3923
13	88.0393	1493.7271	1476.7005	1475.7165	**1521.7220**	1504.6955	1503.7114	1449.7373		D	627.3137	626.3184		687.3348	670.3083
14	136.0757	1656.7904	1639.7639	1638.7798	1684.7853	1667.7588	1666.7748			Y	464.2504			572.3079	555.2813
15	136.0757	1819.8537	1802.8272	1801.8432	1847.8487	1830.8221	1829.8381			Y	301.1870			409.2445	392.2180
16	72.0808	1918.9222	1901.8956	1900.9116	1946.9171	1929.8905	1928.9065	1904.9065		V	202.1186	215.1390		246.1812	229.1547
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TF	221.1285	249.1234	TFD	336.1554	364.1503	TFDN	450.1983	478.1932
TFDNP	547.2511	575.2460	TFDNPE	676.2937	704.2886	FD	235.1077	263.1026
FDN	349.1506	377.1456	FDNP	446.2034	474.1983	FDNPE	575.2460	603.2409
DN	202.0822	230.0771	DNP	299.1350	327.1299	DNPE	428.1776	456.1725

DNPEY	591.2409	619.2358	**NP**	184.1081	212.1030	**NPE**	313.1506	341.1456
NPEY	476.2140	504.2089	**NPEYN**	590.2569	618.2518	**PE**	199.1077	227.1026
PEY	362.1710	390.1660	**PEYN**	476.2140	504.2089	**PEYNK**	604.3089	632.3039
EY	265.1183	293.1132	**EYN**	379.1612	407.1561	**EYNK**	507.2562	535.2511
EYNKL	620.3402	648.3352	**YN**	250.1186	278.1135	**YNK**	378.2136	406.2085
YNKL	491.2976	519.2926	**YNKLI**	604.3817	632.3766	**NK**	215.1503	243.1452
NKL	328.2343	356.2292	**NKLI**	441.3184	469.3133	**NKLID**	556.3453	584.3402
KL	214.1914	242.1863	**KLI**	327.2755	355.2704	**KLID**	442.3024	470.2973
KLIDY	605.3657	633.3606	**LI**	199.1805	227.1754	**LID**	314.2074	342.2023
LIDY	477.2708	505.2657	**LIDYY**	640.3341	668.3290	**ID**	201.1234	229.1183
IDY	364.1867	392.1816	**IDYY**	527.2500	555.2449	**IDYYV**	626.3184	654.3134
DY	251.1026	279.0975	**DYY**	414.1660	442.1609	**DYYV**	513.2344	541.2293
YY	299.1390	327.1339	**YYV**	398.2074	426.2023	**YV**	235.1441	263.1390





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.3	2092.0153	-0.0282	ATFDNPEYDKLINYYVK
9.5	2092.0153	-0.0282	ATFDNPDYEKLINYYVK
8.8	2092.0598	-0.0726	MPRVWLDYLQLLMDQR
7.4	2092.0153	-0.0282	ATFDNPEYNKLIDYYVK
4.4	2091.9305	0.0566	QQPSGPGSDGAATSNSTAASSSK
4.1	2092.0623	-0.0752	VIAEDTGIHSTGPSISHLMK
3.0	2091.9618	0.0253	MRFNYNNIGSSIGEFMGR
2.7	2092.1099	-0.1228	RNVSVAMVLSSTPLNVSFR
2.7	2092.0701	-0.0830	DALTPPRLDADELNHFLR
2.5	2092.0636	-0.0765	LNQLKCHTADLLHPYNR

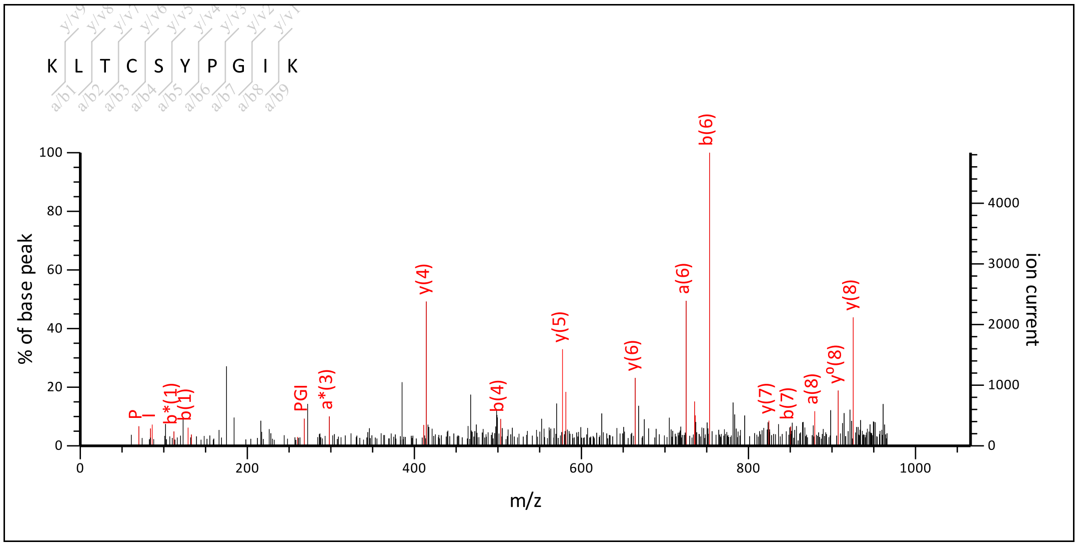
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 56

MS/MS Fragmentation of **KLTCSYPGIK**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 2: 1165.594024 from(1166.601300,1+) intensity(0.0000) index(1)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225358, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



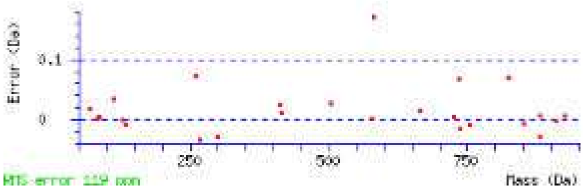
0 to 1065.85

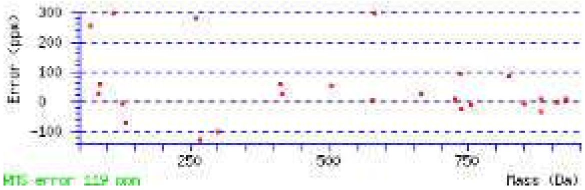
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1165.6165
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 41
Matches : 27/157 fragment ions using 86 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0
1	101.1073	101.1073	84.0808		***129.1022***	112.0757		44.0495		**K**						
2	86.0964	214.1914	197.1648		242.1863	225.1598		172.1444		**L**	980.4506	979.4553		1038.5288	1021.5023	1020.5183
3	74.0600	315.2391	298.2125	297.2285	343.2340	326.2074	325.2234	299.2442	301.2234	**T**	879.4029	892.4233	894.4026	***925.4448***	908.4182	907.4342
4	133.0430	475.2697	458.2432	457.2592	***503.2646***	486.2381	485.2541	386.2762		**C**	719.3723	718.3770		***824.3971***	807.3706	806.3865
5	60.0444	562.3017	545.2752	544.2912	590.2967	573.2701	572.2861	546.3068		**S**	632.3402	631.3450		***664.3665***	647.3399	646.3559
6	136.0757	**725.3651**	708.3385	707.3545	***753.3600***	736.3334	735.3494			**Y**	469.2769			***577.3344***	560.3079	
7	70.0651	822.4178	805.3913	804.4073	***850.4128***	833.3862	832.4022	796.4022		**P**	372.2241	371.2289		***414.2711***	397.2445	
8	30.0338	**879.4393**	862.4128	861.4287	***907.4342***	890.4077	889.4237			**G**				317.2183	300.1918	
9	86.0964	992.5234	975.4968	974.5128	1020.5183	1003.4917	1002.5077	964.4921	978.5077	**I**	202.1186	215.1390	229.1547	***260.1969***	243.1703	
10	101.1073									**K**	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LT	187.1441	215.1390	**LTC**	347.1748	375.1697	**LTCS**	434.2068	462.2017
LTCSY	597.2701	625.2650	**LTCSYP**	694.3229	722.3178	**TC**	234.0907	262.0856
TCS	321.1227	349.1176	**TCSY**	484.1860	512.1810	**TCSYP**	581.2388	609.2337
TCSYPG	638.2603	666.2552	**CS**	220.0750	248.0700	**CSY**	383.1384	411.1333
CSYP	480.1911	508.1860	**CSYPG**	537.2126	565.2075	**CSYPGI**	650.2967	678.2916
SY	223.1077	251.1026	**SYP**	320.1605	348.1554	**SYPG**	377.1819	405.1769
SYPGI	490.2660	518.2609	**YP**	233.1285	261.1234	**YPG**	290.1499	318.1448
YPGI	403.2340	431.2289	**PG**	127.0866	155.0815	**PGI**	240.1707	268.1656
GI	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.6	1165.6819	-0.0878	KILPTEAAAPR
17.3	1165.6165	-0.0225	KLTCSYPGIK
16.3	1165.6026	-0.0086	QLPKCPGNPR
15.9	1165.6819	-0.0879	NDGVGLLLLPR
15.4	1165.6316	-0.0376	LAGSGQRQPPR
15.4	1165.7070	-0.1130	TNLPLITAPVK
14.5	1165.6819	-0.0879	AIGQALEVIPR
14.5	1165.6819	-0.0879	AVAQALEVIPR
14.3	1165.5550	0.0390	MAAAAAGDAVFR
14.2	1165.6819	-0.0879	GAQEAVILLPR

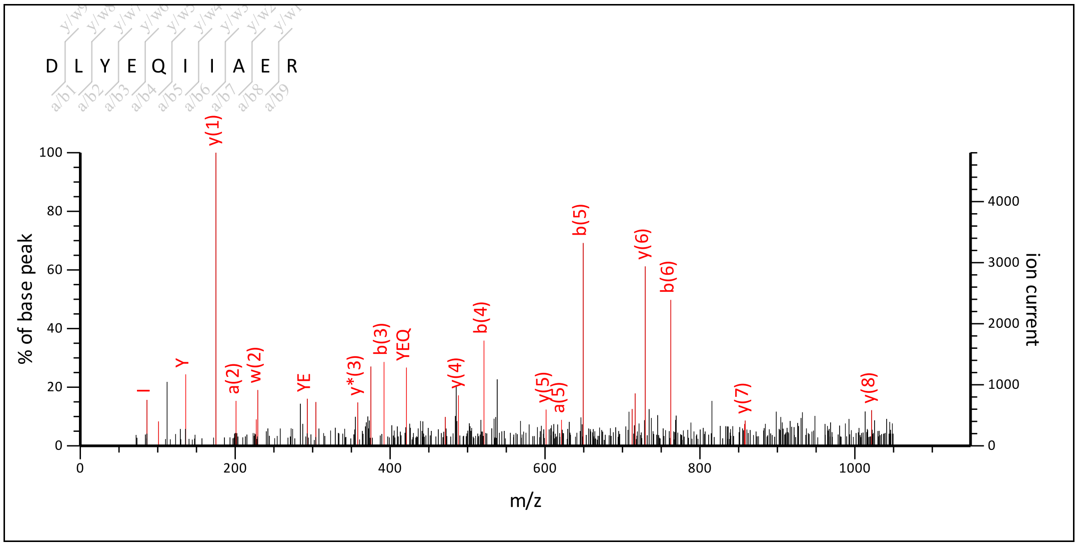
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 56**

MS/MS Fragmentation of **DLYEQIIAER**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 4: 1248.615624 from(1249.622900,1+) intensity(0.0000) index(3)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225357, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



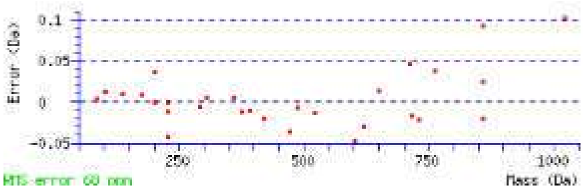
0 to 1149.34

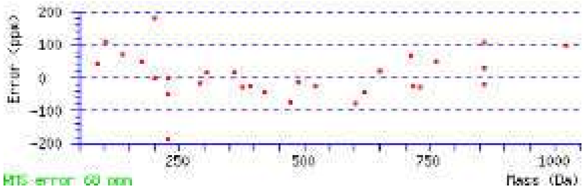
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1248.6350
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 0.0077
Matches : 31/156 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D						
2	86.0964	**201.1234**		183.1128	**229.1183**		211.1077	159.0764		L	1076.5371	1075.5419		1134.6154	1117.5888	1116.
3	136.0757	364.1867		346.1761	**392.1816**		374.1710			Y	913.4738			***1021.5313***	1004.5047	1003.
4	102.0550	493.2293		475.2187	**521.2242**		503.2136	435.2238		E	784.4312	783.4359		***858.4680***	841.4414	840.
5	101.0709	**621.2879**	604.2613	603.2773	**649.2828**	632.2562	631.2722	564.2664		Q	656.3726	655.3774		***729.4254***	712.3988	711.
6	86.0964	734.3719	717.3454	716.3614	**762.3668**	745.3403	744.3563	706.3406	720.3563	I	543.2885	556.3089	570.3246	***601.3668***	584.3402	583.
7	86.0964	847.4560	830.4294	829.4454	875.4509	858.4244	857.4403	819.4247	833.4403	I	430.2045	443.2249	457.2405	***488.2827***	471.2562	470.
8	44.0495	918.4931	901.4666	900.4825	946.4880	929.4615	928.4775			A	359.1674			***375.1987***	358.1721	357.
9	102.0550	1047.5357	1030.5092	1029.5251	1075.5306	1058.5041	1057.5201	989.5302		E	230.1248	229.1295		***304.1615***	287.1350	286.
10	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LY	249.1598	277.1547	**LYE**	378.2023	406.1973	**LYEQ**	506.2609	534.2558
LYEQI	619.3450	647.3399	**YE**	265.1183	293.1132	**YEQ**	393.1769	421.1718
YEQI	506.2609	534.2558	**YEQII**	619.3450	647.3399	**YEQIIA**	690.3821	718.3770
EQ	230.1135	258.1084	**EQI**	343.1976	371.1925	**EQII**	456.2817	484.2766
EQIIA	527.3188	555.3137	**EQIIAE**	656.3614	684.3563	**QI**	214.1550	242.1499
QII	327.2391	355.2340	**QIIA**	398.2762	426.2711	**QIIAE**	527.3188	555.3137
II	199.1805	227.1754	**IIA**	270.2176	298.2125	**IIAE**	399.2602	427.2551
IA	157.1335	185.1285	**IAE**	286.1761	314.1710	**AE**	173.0921	201.0870





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.8	1248.6350	-0.0194	DLYEQIIAER
25.2	1248.6285	-0.0129	LFVQLQEGCR
20.3	1248.6714	-0.0557	LDYLLEKAER
19.8	1248.6714	-0.0557	EYEVKLAELR
18.6	1248.5267	0.0889	IDYCCYTVR
17.2	1248.6649	-0.0492	WTSLLQKMAR
16.1	1248.6132	0.0024	DDMRDLILSR
15.9	1248.6462	-0.0306	DIEYVRGELR
15.9	1248.5834	0.0323	DSSDEDLLISR
15.3	1248.6318	-0.0162	MDMVRLLAER

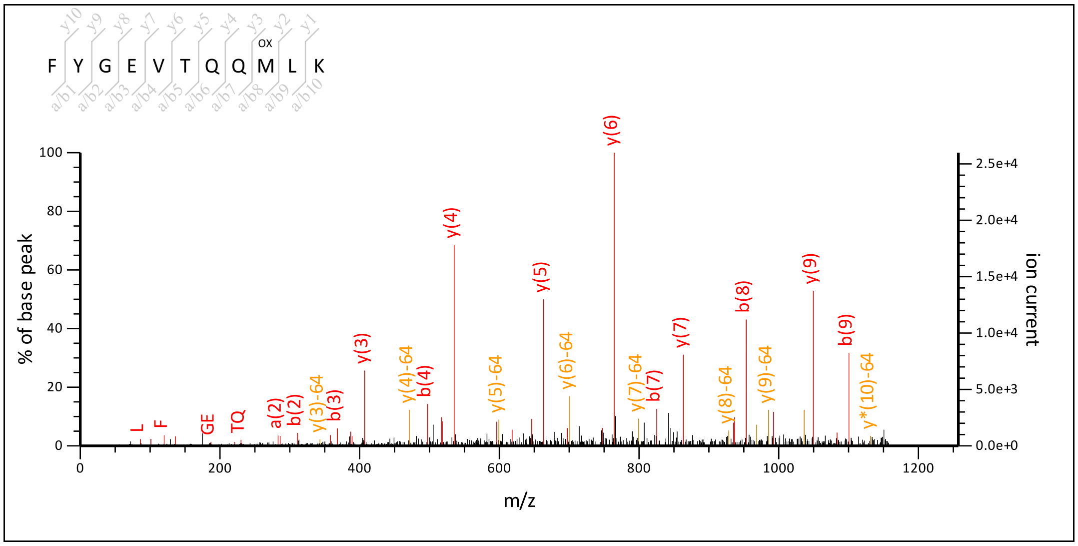
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 56

MS/MS Fragmentation of **FYGEVTQQMLK**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 7: 1358.616524 from(1359.623800,1+) intensity(0.0000) index(6)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225348, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



0 to 1257.23

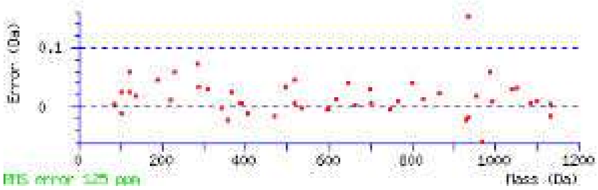
Label all possible matches ○ Label matches used for scoring ●

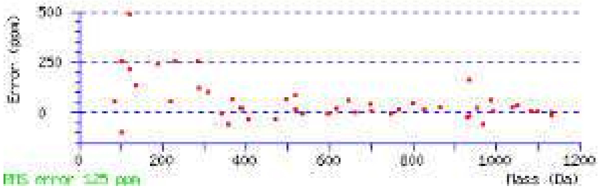
Monoisotopic mass of neutral peptide Mr(calc): 1358.6540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 58 **Expect:** 0.0027
Matches : 50/226 fragment ions using 57 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y
1	120.0808	**120.0808**			148.0757			44.0495		**F**						
2	136.0757	**283.1441**			***311.1390***					**Y**	1104.5354			1212.5929	1195.5664	1194.
3	30.0338	340.1656			***368.1605***					**G**				**1049.5296**	1032.5030	1031.
4	102.0550	469.2082		451.1976	***497.2031***		479.1925	411.2027		**E**	918.4713	917.4761		**992.5081**	975.4816	974.
5	72.0808	568.2766		550.2660	***596.2715***		578.2609	554.2609		**V**	819.4029	832.4233		**863.4655**	846.4390	845.
6	74.0600	669.3243		651.3137	***697.3192***		679.3086	653.3293	655.3086	**T**	718.3552	731.3756	733.3549	**764.3971**	747.3706	746.
7	101.0709	797.3828	780.3563	779.3723	***825.3777***	808.3512	807.3672	740.3614		**Q**	590.2967	589.3014		**663.3494**	646.3229	
8	101.0709	925.4414	908.4149	907.4308	***953.4363***	936.4098	935.4258	868.4199		**Q**	462.2381	461.2428		**535.2908**	518.2643	
9	120.0478	1072.4768	1055.4503	1054.4662	***1100.4717***	1083.4452	1082.4612	996.4785		**M**	315.2027	314.2074		**407.2323**	390.2057	
10	86.0964	1185.5609	1168.5343	1167.5503	1213.5558	1196.5292	1195.5452	1143.5139		**L**	202.1186	201.1234		260.1969	243.1703	
11	101.1073									**K**	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YG	193.0972	221.0921	**YGE**	322.1397	350.1347	**YGEV**	421.2082	449.2031
YGEVT	522.2558	550.2508	**YGEVTQ**	650.3144	678.3093	**GE**	159.0764	187.0713
GEV	258.1448	286.1397	**GEVT**	359.1925	387.1874	**GEVTQ**	487.2511	515.2460
GEVTQQ	615.3097	643.3046	**EV**	201.1234	229.1183	**EVT**	302.1710	330.1660
EVTQ	430.2296	458.2245	**EVTQQ**	558.2882	586.2831	**VT**	173.1285	201.1234
VTQ	301.1870	329.1819	**VTQQ**	429.2456	457.2405	**VTQQM**	576.2810	604.2759
VTQQML	689.3651	717.3600	**TQ**	202.1186	230.1135	**TQQ**	330.1772	358.1721
TQQM	477.2126	505.2075	**TQQML**	590.2967	618.2916	**QQ**	229.1295	257.1244
QQM	376.1649	404.1598	**QQML**	489.2490	517.2439	**QM**	248.1063	276.1013

QML	361.1904	389.1853	**ML**	233.1318	261.1267			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.3	1358.6540	-0.0375	FYGEVTQQMLK
17.7	1358.5674	0.0492	MDGDFEGGRFGR
15.9	1358.6302	-0.0137	CVFSHHGFVNR
15.1	1358.7089	-0.0923	DKPVRTQISCR
14.4	1358.6844	-0.0678	YIHDAPQRFGR
13.8	1358.7041	-0.0876	GQSLEVVEELTR
13.7	1358.6976	-0.0811	LAQIAVEKDCGR
13.4	1358.7095	-0.0930	YTIGYVARGFGR
13.2	1358.6904	-0.0739	WLGIEEPQLMK
13.1	1358.6765	-0.0600	AGTLPHFMERGK

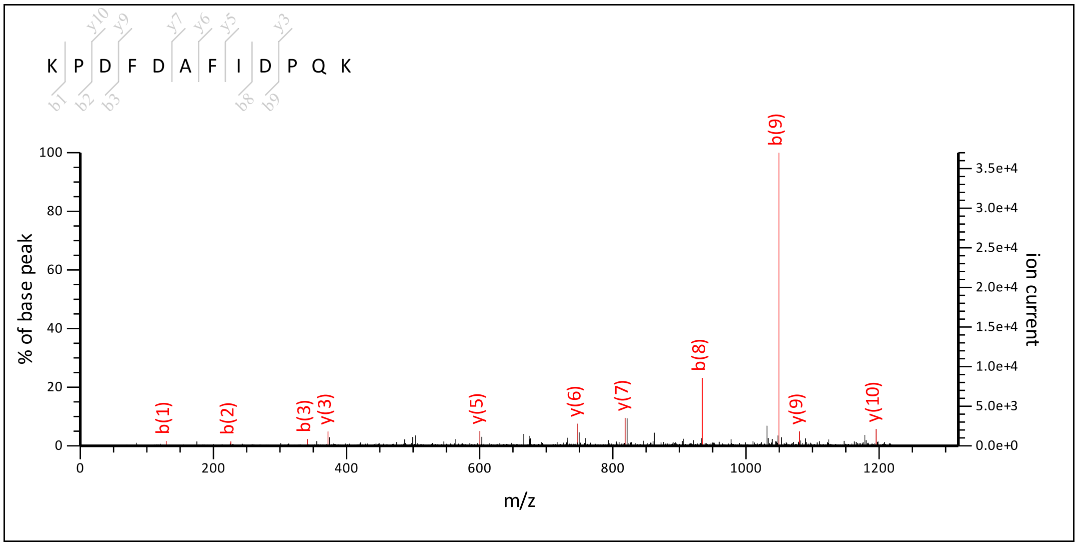
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 56

MS/MS Fragmentation of **KPDFDAFIDPQK**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 8: 1419.661524 from(1420.668800,1+) intensity(0.0000) index(7)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225353, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



0 to 1319.14

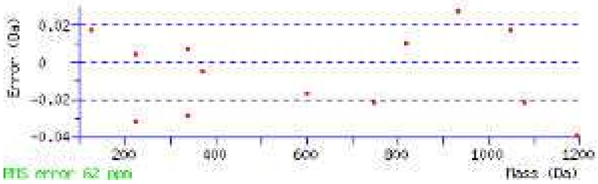
Label all possible matches ○ Label matches used for scoring ●

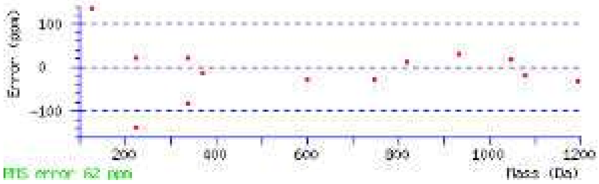
Monoisotopic mass of neutral peptide Mr(calc): 1419.7034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 0.001
Matches : 13/201 fragment ions using 12 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.1073	101.1073	84.0808		***129.1022***	112.0757		44.0495		**K**					
2	70.0651	198.1601	181.1335		***226.1550***	209.1285		172.1444		**P**	1250.5688	1249.5735		1292.6157	1275.5892
3	88.0393	313.1870	296.1605	295.1765	***341.1819***	324.1554	323.1714	269.1972		**D**	1135.5419	1134.5466		***1195.5630***	1178.5364
4	120.0808	460.2554	443.2289	442.2449	488.2504	471.2238	470.2398			**F**	988.4734			***1080.5360***	1063.5095
5	88.0393	575.2824	558.2558	557.2718	603.2773	586.2508	585.2667	531.2926		**D**	873.4465	872.4512		933.4676	916.4411
6	44.0495	646.3195	629.2930	628.3089	674.3144	657.2879	656.3039			**A**	802.4094			***818.4407***	801.4141
7	120.0808	793.3879	776.3614	775.3774	821.3828	804.3563	803.3723			**F**	655.3410			***747.4036***	730.3770
8	86.0964	906.4720	889.4454	888.4614	***934.4669***	917.4403	916.4563	878.4407	892.4563	**I**	542.2569	555.2773	569.2930	***600.3352***	583.3086
9	88.0393	1021.4989	1004.4724	1003.4884	***1049.4938***	1032.4673	1031.4833	977.5091		**D**	427.2300	426.2347		487.2511	470.2245
10	70.0651	1118.5517	1101.5251	1100.5411	1146.5466	1129.5201	1128.5360	1092.5360		**P**	330.1772	329.1819		***372.2241***	355.1976
11	101.0709	1246.6103	1229.5837	1228.5997	1274.6052	1257.5786	1256.5946	1189.5888		**Q**	202.1186	201.1234		275.1714	258.1448
12	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PD	185.0921	213.0870	**PDF**	332.1605	360.1554	**PDFD**	447.1874	475.1823
PDFDA	518.2245	546.2195	**PDFDAF**	665.2930	693.2879	**DF**	235.1077	263.1026
DFD	350.1347	378.1296	**DFDA**	421.1718	449.1667	**DFDAF**	568.2402	596.2351
DFDAFI	681.3243	709.3192	**FD**	235.1077	263.1026	**FDA**	306.1448	334.1397
FDAF	453.2132	481.2082	**FDAFI**	566.2973	594.2922	**FDAFID**	681.3243	709.3192
DA	159.0764	187.0713	**DAF**	306.1448	334.1397	**DAFI**	419.2289	447.2238
DAFID	534.2558	562.2508	**DAFIDP**	631.3086	659.3035	**AF**	191.1179	219.1128
AFI	304.2020	332.1969	**AFID**	419.2289	447.2238	**AFIDP**	516.2817	544.2766
AFIDPQ	644.3402	672.3352	**FI**	233.1648	261.1598	**FID**	348.1918	376.1867

FIDP	445.2445	473.2395	**FIDPQ**	573.3031	601.2980	**ID**	201.1234	229.1183
IDP	298.1761	326.1710	**IDPQ**	426.2347	454.2296	**DP**	185.0921	213.0870
DPQ	313.1506	341.1456	**PQ**	198.1237	226.1186			





NCBI **BLAST** search of KPDFDAFIDPQK
(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	1419.7034	-0.0419	KPDFDAFIDPQK
22.0	1419.6001	0.0614	ELEDLEESDEGR
17.7	1419.7214	-0.0599	AGTAAMNSVVMPKK
15.4	1419.6452	0.0163	ELEDNMWAEKR
15.2	1419.7180	-0.0565	KGGMGTAAGDLAFPK
14.8	1419.7066	-0.0451	SGLNSTSGGESRLR
14.3	1419.6776	-0.0161	RNSSASISDMQPK
14.3	1419.7214	-0.0599	AGTAAMNSVVMPKK
13.5	1419.7027	-0.0412	SVANDLEMELKR
12.8	1419.5862	0.0753	KGGEGGEGGGDEESR

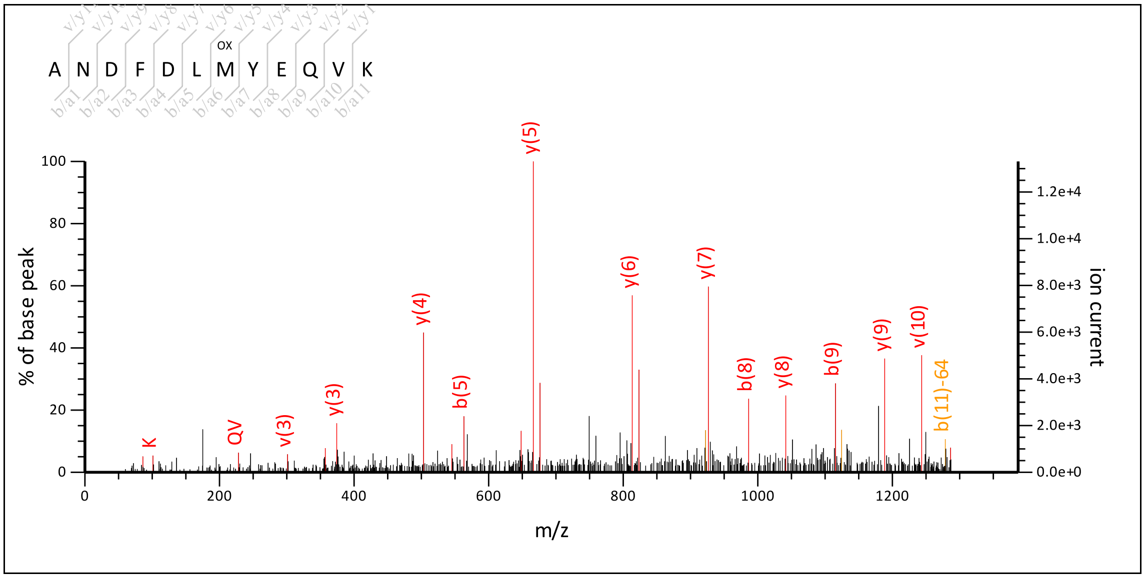
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 56

MS/MS Fragmentation of **ANDFDLMYEQVK**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 10: 1487.624324 from(1488.631600,1+) intensity(0.0000) index(9)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225349, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



0 to 1386.91

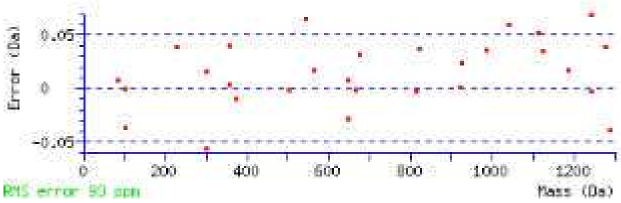
Label all possible matches ○ Label matches used for scoring ●

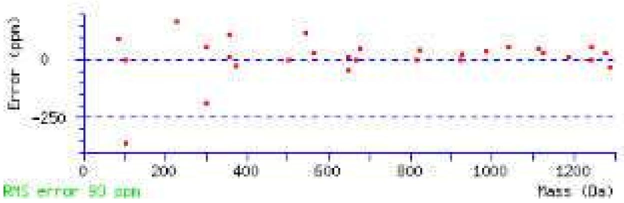
Monoisotopic mass of neutral peptide Mr(calc): 1487.6602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 70 **Expect:** 0.00013
Matches : 29/280 fragment ions using 26 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495			72.0444			44.0495	A						12
2	87.0553	158.0924	141.0659		186.0873	169.0608		115.0866	N	1358.5933	1357.5980	1417.6304	1400.6039	1399.6198	11
3	88.0393	273.1193	256.0928	255.1088	***301.1143***	284.0877	283.1037	229.1295	D	1243.5664	1242.5711	1303.5875	1286.5609	1285.5769	10
4	120.0808	420.1878	403.1612	402.1772	448.1827	431.1561	430.1721		F	1096.4979		***1188.5605***	1171.5340	1170.5500	9
5	88.0393	535.2147	518.1882	517.2041	***563.2096***	546.1831	545.1991	491.2249	D	981.4710	980.4757	***1041.4921***	1024.4656	1023.4816	8
6	86.0964	648.2988	631.2722	630.2882	***676.2937***	659.2671	658.2831	606.2518	L	868.3869	867.3917	***926.4652***	909.4386	908.4546	7
7	120.0478	795.3342	778.3076	777.3236	***823.3291***	806.3025	805.3185	719.3359	M	721.3515	720.3563	***813.3811***	796.3546	795.3706	6
8	136.0757	958.3975	941.3709	940.3869	***986.3924***	969.3659	968.3818		Y	558.2882		***666.3457***	649.3192	648.3352	5
9	102.0550	1087.4401	1070.4135	1069.4295	***1115.4350***	1098.4085	1097.4244	1029.4346	E	429.2456	428.2504	***503.2824***	486.2558	485.2718	4
10	101.0709	1215.4987	1198.4721	1197.4881	***1243.4936***	1226.4670	1225.4830	1158.4772	Q	301.1870	300.1918	***374.2398***	357.2132		3
11	72.0808	1314.5671	1297.5405	1296.5565	1342.5620	1325.5354	1324.5514	1300.5514	V	202.1186	215.1390	246.1812	229.1547		2
12	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ND	202.0822	230.0771	**NDF**	349.1506	377.1456	**NDFD**	464.1776	492.1725
NDFDL	577.2617	605.2566	**DF**	235.1077	263.1026	**DFD**	350.1347	378.1296
DFDL	463.2187	491.2136	**DFDLM**	610.2541	638.2490	**FD**	235.1077	263.1026
FDL	348.1918	376.1867	**FDLM**	495.2272	523.2221	**FDLMY**	658.2905	686.2854

DL	201.1234	229.1183	**DLM**	348.1588	376.1537	**DLMY**	511.2221	539.2170
DLMYE	640.2647	668.2596	**LM**	233.1318	261.1267	**LMY**	396.1952	424.1901
LMYE	525.2377	553.2327	**LMYEQ**	653.2963	681.2912	**MY**	283.1111	311.1060
MYE	412.1537	440.1486	**MYEQ**	540.2123	568.2072	**MYEQV**	639.2807	667.2756
YE	265.1183	293.1132	**YEQ**	393.1769	421.1718	**YEQV**	492.2453	520.2402
EQ	230.1135	258.1084	**EQV**	329.1819	357.1769	**QV**	200.1394	228.1343





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.1	1487.6602	-0.0359	ANDFDLMYEQVK
22.8	1487.7402	-0.1159	DSMVNVPKNLEAR
21.8	1487.6602	-0.0359	AQDFELMYEQAK
19.9	1487.6966	-0.0723	LLEMYFDLGDTR
19.2	1487.7270	-0.1026	SDRFGLFAAHPDR
18.2	1487.7514	-0.1271	NQMEGRIPTSLSR
17.9	1487.7270	-0.1026	LDHHYHSQPQVK
17.9	1487.6899	-0.0656	AREGGAMGAGAGDAAAR
17.1	1487.7402	-0.1159	AGEAQVLVASDAMAR
16.9	1487.7402	-0.1159	AKDTMIPLNDAQR

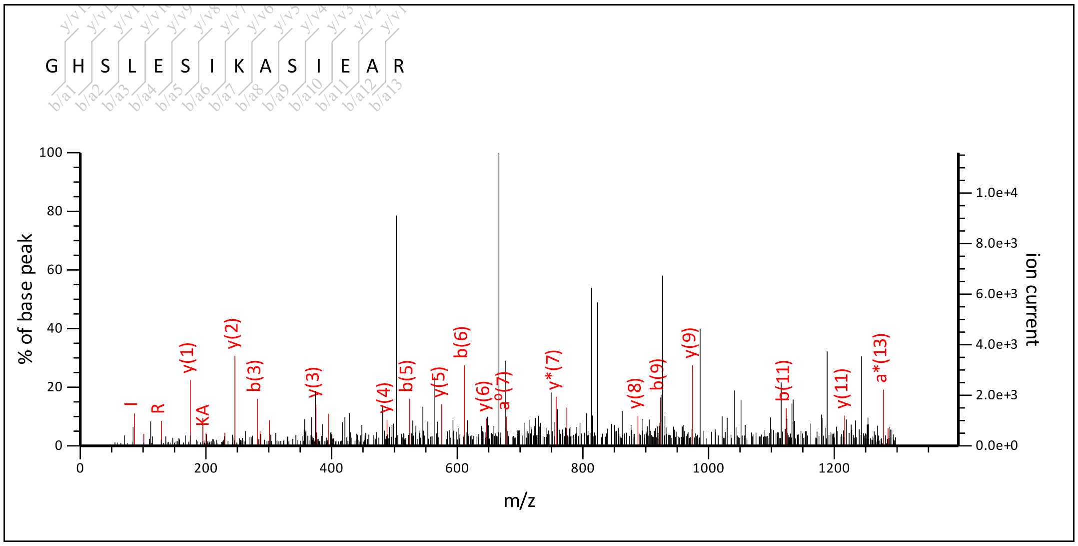
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 56

MS/MS Fragmentation of **GHSLESIKASIEAR**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 11: 1496.772024 from(1497.779300,1+) intensity(0.0000) index(10)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225352, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



0 to 1397.61

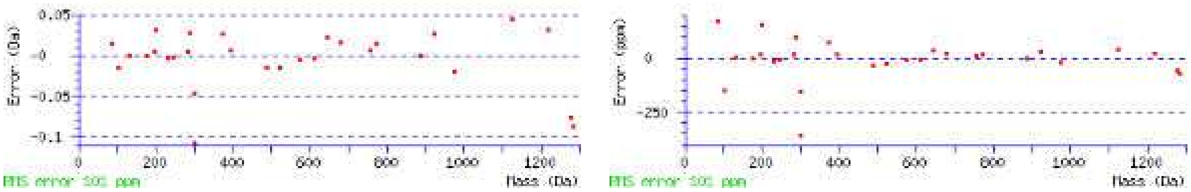
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1496.7947
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.083
Matches : 31/239 fragment ions using 65 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		**G**					
2	110.0713	167.0927			**195.0877**					**H**	1358.7274			1440.7805	1423.7540
3	60.0444	254.1248		236.1142	**282.1197**		264.1091	238.1299		**S**	1271.6954	1270.7001		1303.7216	1286.6951
4	86.0964	367.2088		349.1983	**395.2037**		377.1932	325.1619		**L**	1158.6113	1157.6161		***1216.6896***	1199.6630
5	102.0550	496.2514		478.2409	**524.2463**		506.2358	438.2459		**E**	1029.5687	1028.5735		1103.6055	1086.5790
6	60.0444	583.2835		565.2729	**611.2784**		593.2678	567.2885		**S**	942.5367	941.5415		***974.5629***	957.5364
7	86.0964	696.3675		678.3569	724.3624		706.3519	668.3362	682.3519	**I**	829.4526	842.4730	856.4887	***887.5309***	870.5043
8	101.1073	824.4625	807.4359	806.4519	852.4574	835.4308	834.4468	767.4046		**K**	701.3577	700.3624		***774.4468***	757.4203
9	44.0495	895.4996	878.4730	877.4890	**923.4945**	906.4680	905.4839			**A**	630.3206			***646.3519***	629.3253
10	60.0444	982.5316	965.5051	964.5211	1010.5265	993.5000	992.5160	966.5367		**S**	543.2885	542.2933		***575.3148***	558.2882
11	86.0964	1095.6157	1078.5891	1077.6051	**1123.6106**	1106.5840	1105.6000	1067.5844	1081.6000	**I**	430.2045	443.2249	457.2405	***488.2827***	471.2562
12	102.0550	1224.6583	1207.6317	1206.6477	1252.6532	1235.6266	1234.6426	1166.6528		**E**	301.1619	300.1666		***375.1987***	358.1721
13	44.0495	1295.6954	1278.6688	1277.6848	1323.6903	1306.6638	1305.6797			**A**	230.1248			***246.1561***	229.1295
14	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HS	197.1033	225.0982	**HSL**	310.1874	338.1823	**HSLE**	439.2300	467.2249
HSLES	526.2620	554.2569	**HSLESI**	639.3460	667.3410	**SL**	173.1285	201.1234
SLE	302.1710	330.1660	**SLES**	389.2031	417.1980	**SLESI**	502.2871	530.2821
SLESIK	630.3821	658.3770	**LE**	215.1390	243.1339	**LES**	302.1710	330.1660
LESI	415.2551	443.2500	**LESIK**	543.3501	571.3450	**LESIKA**	614.3872	642.3821
ES	189.0870	217.0819	**ESI**	302.1710	330.1660	**ESIK**	430.2660	458.2609
ESIKA	501.3031	529.2980	**ESIKAS**	588.3352	616.3301	**SI**	173.1285	201.1234

SIK	301.2234	329.2183	**SIKA**	372.2605	400.2554	**SIKAS**	459.2926	487.2875
SIKASI	572.3766	600.3715	**IK**	214.1914	242.1863	**IKA**	285.2285	313.2234
IKAS	372.2605	400.2554	**IKASI**	485.3446	513.3395	**IKASIE**	614.3872	642.3821
IKASIEA	685.4243	713.4192	**KA**	172.1444	200.1394	**KAS**	259.1765	287.1714
KASI	372.2605	400.2554	**KASIE**	501.3031	529.2980	**KASIEA**	572.3402	600.3352
AS	131.0815	159.0764	**ASI**	244.1656	272.1605	**ASIE**	373.2082	401.2031
ASIEA	444.2453	472.2402	**SI**	173.1285	201.1234	**SIE**	302.1710	330.1660
SIEA	373.2082	401.2031	**IE**	215.1390	243.1339	**IEA**	286.1761	314.1710
EA	173.0921	201.0870						



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.6	1496.7947	-0.0226	GHSLESIKASIEAR
34.3	1496.8198	-0.0478	GHSLESIKASIEVK
22.2	1496.7583	0.0137	SPNTDGIHITSSIR
17.3	1496.6718	0.1002	SDAFVMTHGGNFAK
15.5	1496.8351	-0.0631	DPWVLKLAEVTAR
13.4	1496.7583	0.0137	DPVVLASGQQQEAR
12.8	1496.7471	0.0249	VLPQDDPSATVAER
12.7	1496.8497	-0.0777	ICGALGPVVSLRQK
12.6	1496.7471	0.0250	KADADSSFITSSLR
11.9	1496.8861	-0.1140	ICLIARNLLNGLK

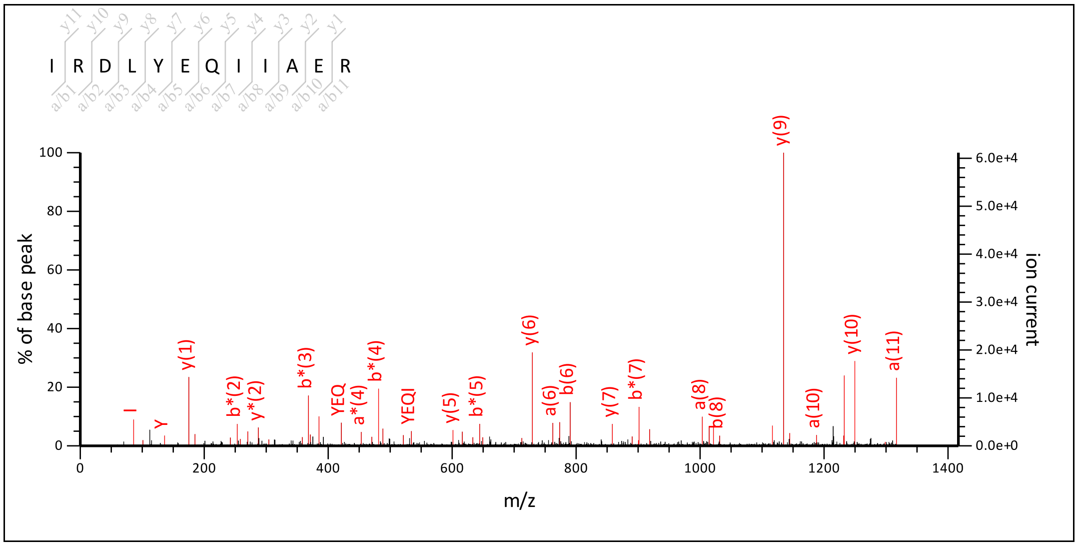
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 56

MS/MS Fragmentation of **IRDLYEQIIAER**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 12: 1517.790924 from(1518.798200,1+) intensity(0.0000) index(11)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225347, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



0 to 1416.73

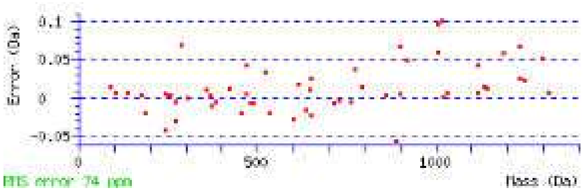
Label all possible matches ○ Label matches used for scoring ●

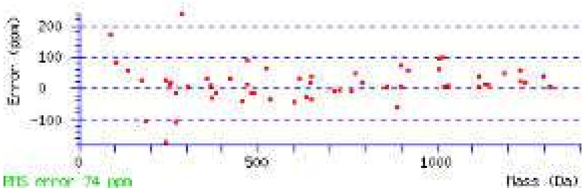
Monoisotopic mass of neutral peptide Mr(calc): 1517.8201
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 3.9e-05
Matches : 62/200 fragment ions using 65 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	***86.0964***			114.0913			44.0495		I						
2	129.1135	***242.1975***	225.1710		**270.1925**	253.1659		157.1335		R	1304.6481	1303.6529		1405.7434	1388.7169	138
3	88.0393	***357.2245***	340.1979	339.2139	**385.2194**	368.1928	367.2088	313.2347		D	1189.6212	1188.6259		**1249.6423**	1232.6157	123
4	86.0964	***470.3085***	453.2820	452.2980	498.3035	481.2769	480.2929	428.2616		L	1076.5371	1075.5419		**1134.6154**	1117.5888	11
5	136.0757	***633.3719***	616.3453	615.3613	661.3668	644.3402	643.3562			Y	913.4738			**1021.5313**	1004.5047	100
6	102.0550	***762.4145***	745.3879	744.4039	**790.4094**	773.3828	772.3988	704.4090		E	784.4312	783.4359		**858.4680**	841.4414	84
7	101.0709	***890.4730***	873.4465	872.4625	**918.4680**	901.4414	900.4574	833.4516		Q	656.3726	655.3774		**729.4254**	712.3988	71
8	86.0964	***1003.5571***	986.5306	985.5465	**1031.5520**	1014.5255	1013.5415	975.5258	989.5415	I	543.2885	556.3089	570.3246	**601.3668**	584.3402	58
9	86.0964	***1116.6412***	1099.6146	1098.6306	**1144.6361**	1127.6095	1126.6255	1088.6099	1102.6255	I	430.2045	443.2249	457.2405	**488.2827**	471.2562	47
10	44.0495	***1187.6783***	1170.6517	1169.6677	1215.6732	1198.6467	1197.6626			A	359.1674			375.1987	358.1721	35
11	102.0550	***1316.7209***	1299.6943	1298.7103	1344.7158	1327.6892	1326.7052	1258.7154		E	230.1248	229.1295		**304.1615**	287.1350	28
12	129.1135									R	74.0237	73.0284		**175.1190**	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RD	244.1404	272.1353	RDL	357.2245	385.2194	RDLY	520.2878	548.2827
RDLYE	649.3304	677.3253	DL	201.1234	229.1183	DLY	364.1867	392.1816
DLYE	493.2293	521.2242	DLYEQ	621.2879	649.2828	LY	249.1598	277.1547
LYE	378.2023	406.1973	LYEQ	506.2609	534.2558	LYEQI	619.3450	647.3399
YE	265.1183	293.1132	YEQ	393.1769	421.1718	YEQI	506.2609	534.2558
YEQII	619.3450	647.3399	YEQIIA	690.3821	718.3770	EQ	230.1135	258.1084
EQI	343.1976	371.1925	EQII	456.2817	484.2766	EQIIA	527.3188	555.3137
EQIIAE	656.3614	684.3563	QI	214.1550	242.1499	QII	327.2391	355.2340
QIIA	398.2762	426.2711	QIIAE	527.3188	555.3137	II	199.1805	227.1754

IIA	270.2176	298.2125	**IIAE**	399.2602	427.2551	**IA**	157.1335	185.1285
IAE	286.1761	314.1710	**AE**	173.0921	201.0870			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
77.8	1517.8201	-0.0292	IRDLYEQIIAER
30.6	1517.7395	0.0514	AMAEEEEKLLEAR
27.4	1517.7950	-0.0041	QYNQQQQLLISR
26.8	1517.8024	-0.0115	IPSSSFKHMISLR
26.7	1517.7474	0.0435	EWSLGALDGSQISR
24.9	1517.8929	-0.1020	ILSAVYSREVIIR
24.4	1517.8202	-0.0292	EVLRQNQYDLLK
23.6	1517.8049	-0.0140	DVSKSETLGNLSLR
23.5	1517.8202	-0.0293	LYVDADLRLDGIR
23.4	1517.6780	0.1129	MAISGPSLDGNEDGR

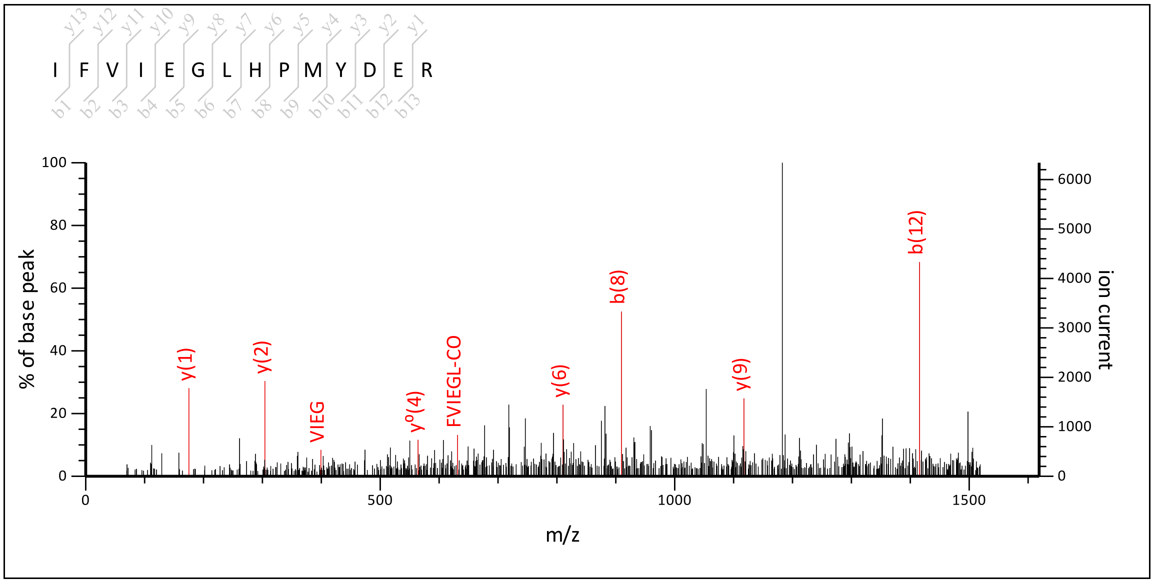
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 56

MS/MS Fragmentation of **IFVIEGLHPMYDER**
Found in **gi|125580** in **NCBInr**, RecName: Full=Phosphoribulokinase, chloroplastic; Short=PRK; Short=PRKase; AltName: Full=Phosphopentokinase; Flags: Precursor

Match to Query 14: 1717.816624 from(1718.823900,1+) intensity(0.0000) index(13)
Title: Label: I4, Spot_Id: 219730, Peak_List_Id: 225350, MSMS Job_Run_Id: 21775, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I4_136842168700.txt



0 to 1618.76

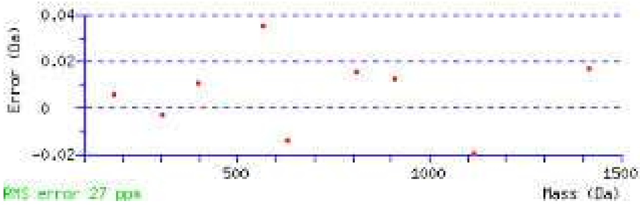
Label all possible matches ○ Label matches used for scoring ●

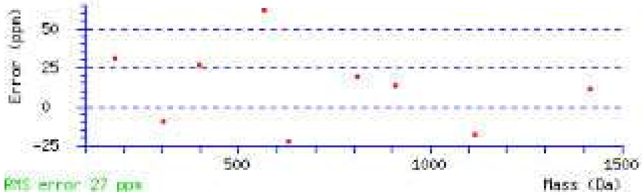
```
Monoisotopic mass of neutral peptide Mr(calc): 1717.8498
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15  Expect: 55
Matches : 10/214 fragment ions using 15 most intense peaks   (help)
```

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		44.0495		I							14
2	120.0808	233.1648		261.1598				F	1513.7104			1605.7730	1588.7464	1587.7624	13
3	72.0808	332.2333		360.2282		318.2176		V	1414.6420	1427.6624		1458.7046	1441.6780	1440.6940	12
4	86.0964	445.3173		473.3122		417.2860	431.3017	I	1301.5579	1314.5783	1328.5940	1359.6362	1342.6096	1341.6256	11
5	102.0550	574.3599	556.3493	602.3548	584.3443	516.3544		E	1172.5153	1171.5201		1246.5521	1229.5256	1228.5415	10
6	30.0338	631.3814	613.3708	659.3763	641.3657			G				***1117.5095***	1100.4830	1099.4989	9
7	86.0964	744.4654	726.4549	772.4604	754.4498	702.4185		L	1002.4098	1001.4145		1060.4880	1043.4615	1042.4775	8
8	110.0713	881.5244	863.5138	**909.5193**	891.5087			H	865.3509			947.4040	930.3774	929.3934	7
9	70.0651	978.5771	960.5665	1006.5720	988.5615	952.5615		P	768.2981	767.3029		***810.3451***	793.3185	792.3345	6
10	104.0528	1109.6176	1091.6070	1137.6125	1119.6019	1049.6142		M	637.2576	636.2624		713.2923	696.2658	695.2817	5
11	136.0757	1272.6809	1254.6704	1300.6758	1282.6653			Y	474.1943			582.2518	565.2253	564.2413	4
12	88.0393	1387.7079	1369.6973	**1415.7028**	1397.6922	1343.7180		D	359.1674	358.1721		419.1885	402.1619	401.1779	3
13	102.0550	1516.7505	1498.7399	1544.7454	1526.7348	1458.7450		E	230.1248	229.1295		***304.1615***	287.1350	286.1510	2
14	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FV	219.1492	247.1441	FVI	332.2333	360.2282	FVIE	461.2758	489.2708
FVIEG	518.2973	546.2922	FVIEGL	631.3814	659.3763	VI	185.1648	213.1598

VIE	314.2074	342.2023	**VIEG**	371.2289	399.2238	**VIEGL**	484.3130	512.3079
VIEGLH	621.3719	649.3668	**IE**	215.1390	243.1339	**IEG**	272.1605	300.1554
IEGL	385.2445	413.2395	**IEGLH**	522.3035	550.2984	**IEGLHP**	619.3562	647.3511
EG	159.0764	187.0713	**EGL**	272.1605	300.1554	**EGLH**	409.2194	437.2143
EGLHP	506.2722	534.2671	**EGLHPM**	637.3126	665.3076	**GL**	143.1179	171.1128
GLH	280.1768	308.1717	**GLHP**	377.2296	405.2245	**GLHPM**	508.2701	536.2650
GLHPMY	671.3334	699.3283	**LH**	223.1553	251.1503	**LHP**	320.2081	348.2030
LHPM	451.2486	479.2435	**LHPMY**	614.3119	642.3068	**HP**	207.1240	235.1190
HPM	338.1645	366.1594	**HPMY**	501.2279	529.2228	**HPMYD**	616.2548	644.2497
PM	201.1056	229.1005	**PMY**	364.1689	392.1639	**PMYD**	479.1959	507.1908
PMYDE	608.2385	636.2334	**MY**	267.1162	295.1111	**MYD**	382.1431	410.1380
MYDE	511.1857	539.1806	**YD**	251.1026	279.0975	**YDE**	380.1452	408.1401
DE	217.0819	245.0768						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.7	1717.8498	-0.0332	IFVIEGLHPMFDER
19.5	1717.8419	-0.0252	MLEYEVKYVMIER
14.9	1717.8498	-0.0331	IFVIEGLHPMYDER
13.1	1717.8167	-0.0001	MLDYETRFVMIER
12.8	1717.8457	-0.0291	MAETLIHYSVNPSTR
12.5	1717.8536	-0.0370	WPEPRGDAAGAPPLER
11.9	1717.8206	-0.0040	IASCLNSSHFQVAER
10.9	1717.8648	-0.0482	GKYLHAAPGASAGPHER
9.7	1717.7036	0.1130	MSGGNSNCTVYIDER
9.4	1717.8496	-0.0330	DHNLGSDVPLRNPER

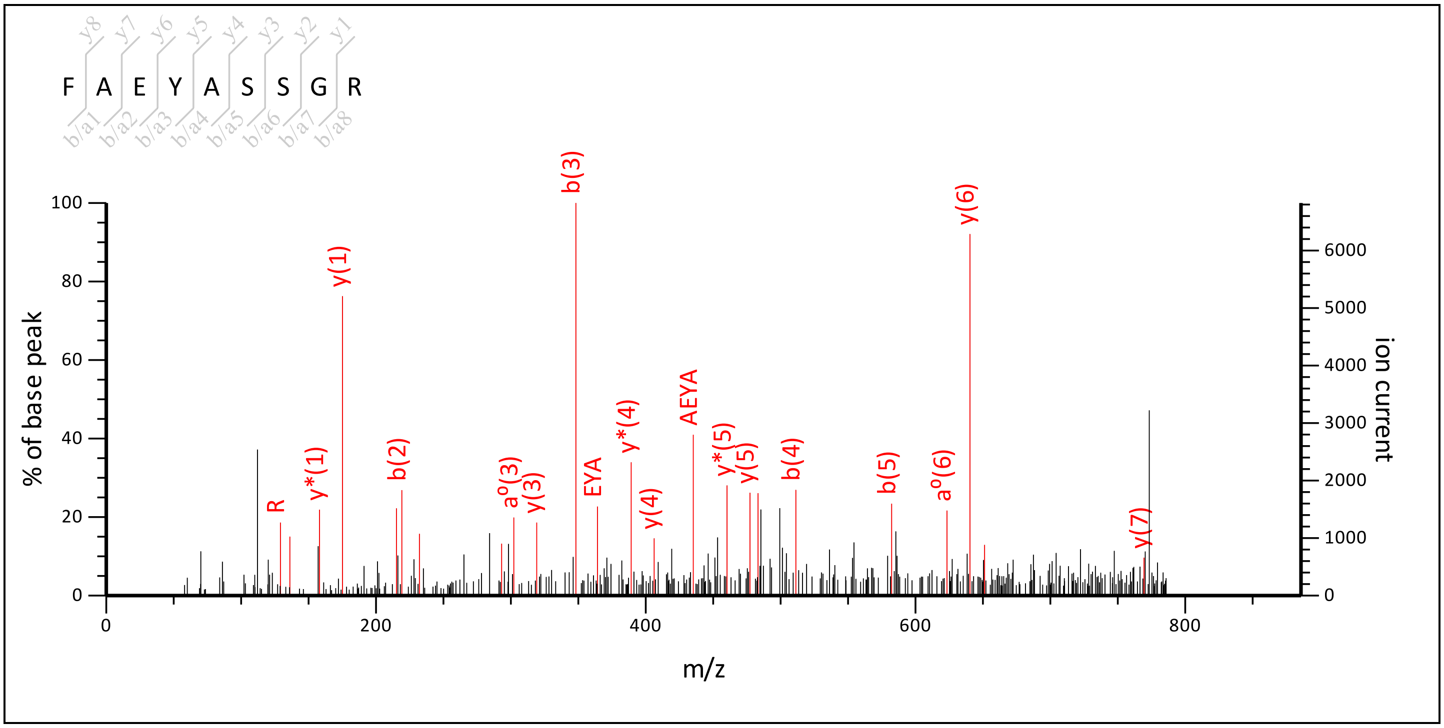
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 57

MS/MS Fragmentation of **FAEYASSGR**
Found in **gi|115471157** in **NCBInr**, Os07g0212200 [Oryza sativa Japonica Group]

Match to Query 58: 986.477164 from(987.484440,1+) intensity(0.0000) index(3)
Title: Label: N11, Spot_Id: 219847, Peak_List_Id: 227553, MSMS Job_Run_Id: 21965, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N11_136868230800.txt



0 to 885.83

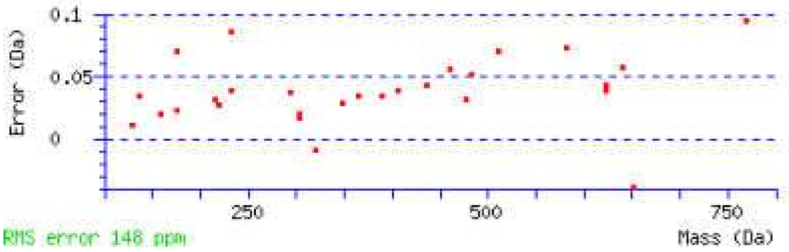
Label all possible matches ○ Label matches used for scoring ●

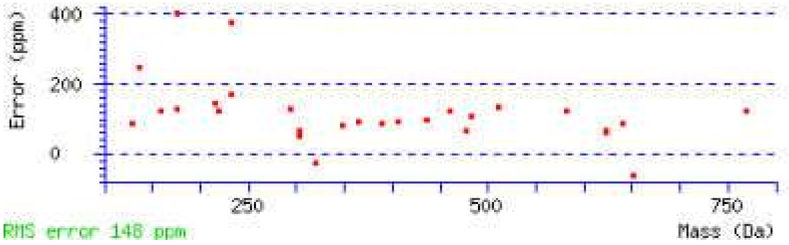
Monoisotopic mass of neutral peptide Mr(calc): 986.4457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.86
Matches : 29/116 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	120.0808	120.0808		148.0757		44.0495	F						9
2	44.0495	191.1179		**219.1128**			A	824.3533		840.3846	823.3581	822.3741	8
3	102.0550	320.1605	302.1499	**348.1554**	330.1448	262.1550	E	695.3107	694.3155	***769.3475***	752.3210	751.3369	7
4	136.0757	483.2238	465.2132	**511.2187**	493.2082		Y	532.2474		***640.3049***	623.2784	622.2944	6
5	44.0495	554.2609	536.2504	**582.2558**	564.2453		A	461.2103		***477.2416***	460.2150	459.2310	5
6	60.0444	641.2930	623.2824	669.2879	651.2773	625.2980	S	374.1783	373.1830	***406.2045***	389.1779	388.1939	4
7	60.0444	728.3250	710.3144	756.3199	738.3093	712.3301	S	287.1462	286.1510	***319.1724***	302.1459	301.1619	3
8	30.0338	785.3464	767.3359	813.3414	795.3308		G			***232.1404***	215.1139		2

9	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AE	173.0921	201.0870	AEY	336.1554	364.1503	AEYA	407.1925	435.1874
AEYAS	494.2245	522.2195	AEYASS	581.2566	609.2515	AEYASSG	638.2780	666.2729
EY	265.1183	293.1132	EYA	336.1554	364.1503	EYAS	423.1874	451.1823
EYASS	510.2195	538.2144	EYASSG	567.2409	595.2358	YA	207.1128	235.1077
YAS	294.1448	322.1397	YASS	381.1769	409.1718	YASSG	438.1983	466.1932
AS	131.0815	159.0764	ASS	218.1135	246.1084	ASSG	275.1350	303.1299
SS	147.0764	175.0713	SSG	204.0979	232.0928	SG	117.0659	145.0608





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.7	986.4457	0.0314	FAEYASSGR
33.6	986.4127	0.0644	ESMYASSGR
25.2	986.3950	0.0822	MAEYMNGR
25.1	986.3950	0.0822	MSEYAACR
24.1	986.4127	0.0644	AEYMASSGR
23.2	986.5073	-0.0301	SSTLAYFAK
22.2	986.4716	0.0056	RPPCASSGR
21.6	986.3983	0.0788	SMMMTSSGR
21.2	986.4821	-0.0050	ALYFSSSGR
20.9	986.5509	-0.0737	ILGAGVTGSGR

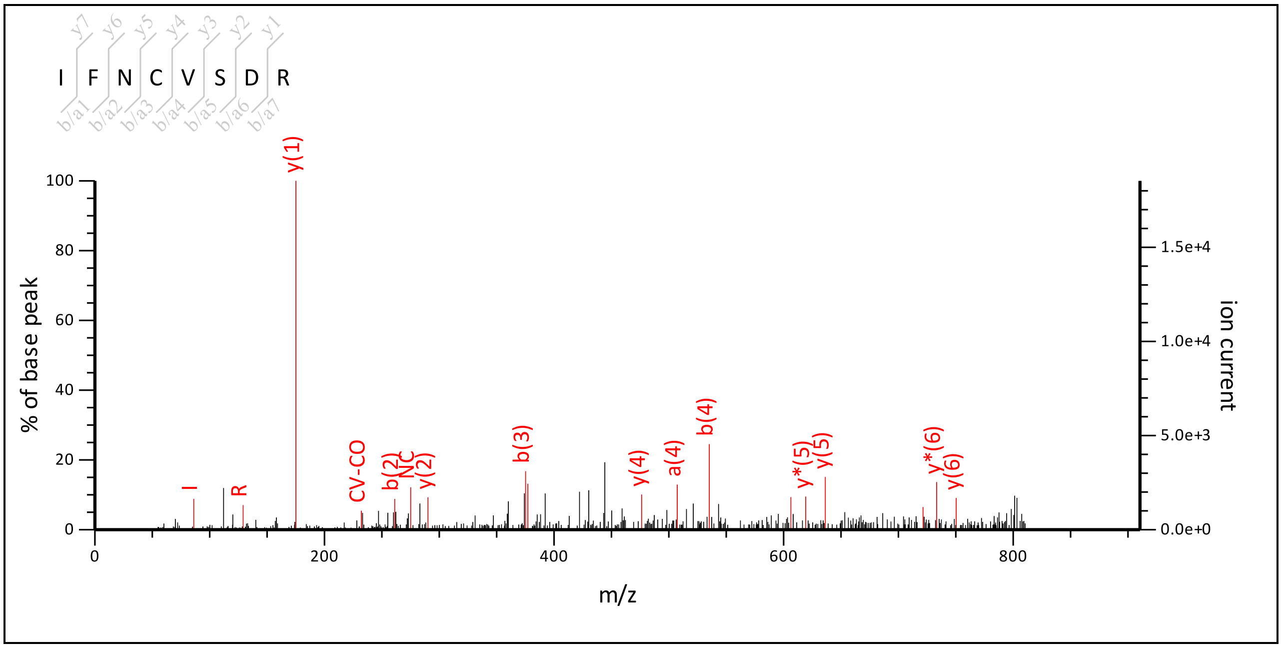
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 57

MS/MS Fragmentation of **IFNCVSDR**
Found in **gi|115471157** in **NCBInr**, Os07g0212200 [Oryza sativa Japonica Group]

Match to Query 73: 1009.493824 from(1010.501100,1+) intensity(0.0000) index(5)
Title: Label: N11, Spot_Id: 219847, Peak_List_Id: 227550, MSMS Job_Run_Id: 21965, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N11_136868230800.txt



0 to 910.45

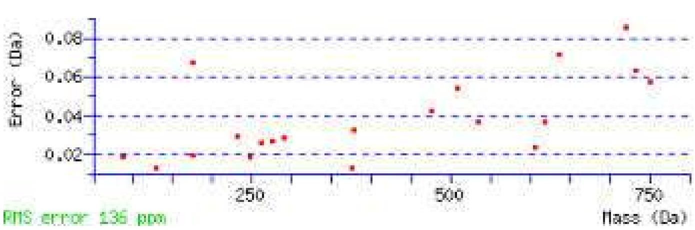
Label all possible matches ○ Label matches used for scoring ●

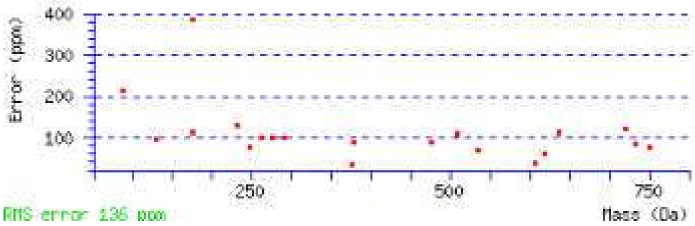
Monoisotopic mass of neutral peptide Mr(calc): 1009.4651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.51
Matches : 21/104 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	86.0964	**86.0964**			114.0913			44.0495	I						8
2	120.0808	233.1648			**261.1598**				F	805.3257		897.3883	880.3618	879.3778	7
3	87.0553	347.2078	330.1812		**375.2027**	358.1761		304.2020	N	691.2828	690.2876	***750.3199***	733.2934	732.3093	6
4	133.0430	**507.2384**	490.2119		**535.2333**	518.2068		418.2449	C	531.2522	530.2569	***636.2770***	619.2504	618.2664	5
5	72.0808	**606.3068**	589.2803		634.3017	617.2752		592.2912	V	432.1837	445.2041	***476.2463***	459.2198	458.2358	4
6	60.0444	693.3389	676.3123	675.3283	**721.3338**	704.3072	703.3232	677.3439	S	345.1517	344.1565	***377.1779***	360.1514	359.1674	3
7	88.0393	808.3658	791.3393	790.3552	836.3607	819.3342	818.3501	764.3760	D	230.1248	229.1295	***290.1459***	273.1193	272.1353	2
8	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FN	234.1237	262.1186	FNC	394.1544	422.1493	FNCV	493.2228	521.2177
FNCVS	580.2548	608.2497	FNCVSD	695.2817	723.2767	NC	247.0859	275.0809
NCV	346.1544	374.1493	NCVS	433.1864	461.1813	NCVSD	548.2133	576.2082
CV	232.1114	260.1063	CVS	319.1435	347.1384	CVSD	434.1704	462.1653

VS	159.1128	187.1077	**VSD**	274.1397	302.1347	**SD**	175.0713	203.0662





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.0	1009.4651	0.0287	IFNCVSDR
34.7	1009.4829	0.0110	LFGSSGAESR
33.1	1009.5015	-0.0077	IFGGTLCSR
31.6	1009.4685	0.0253	MLNCTLSR
30.4	1009.5015	-0.0077	FLNCTLSR
29.4	1009.5094	-0.0155	FIHHVSDR
29.2	1009.4651	0.0287	FLNTCAER
29.1	1009.4498	0.0440	MLGSGSSEAR
28.9	1009.3957	0.0981	MVAGCADDR
28.0	1009.5920	-0.0982	NIPPLTISR

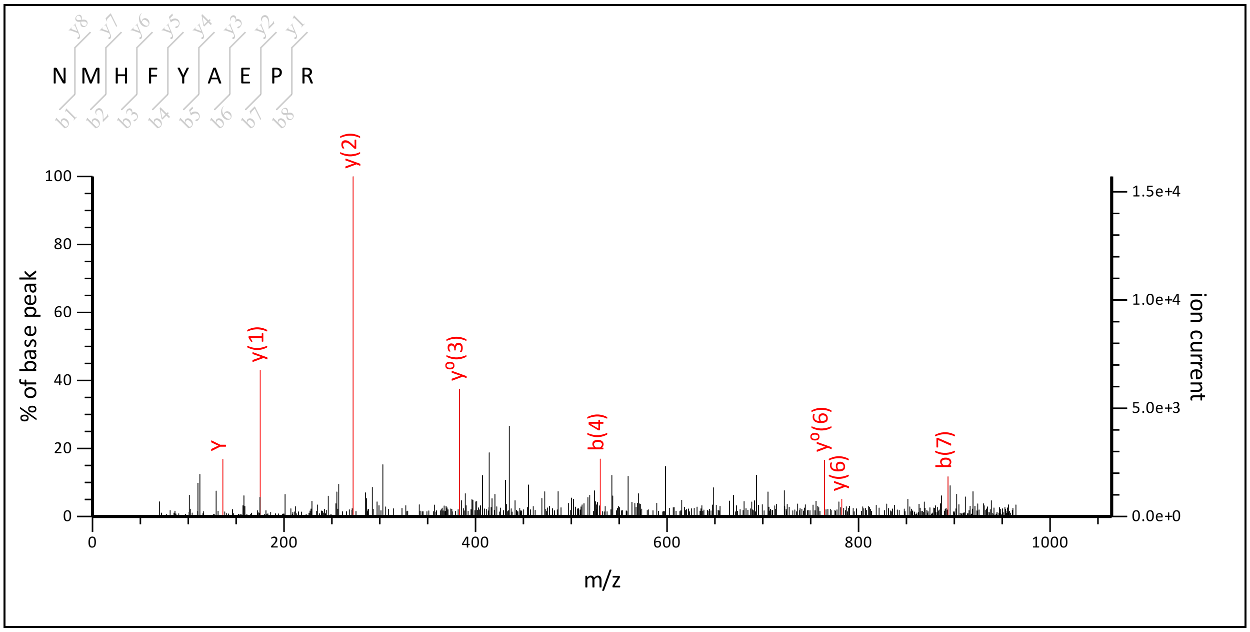
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 57**

MS/MS Fragmentation of **NMHFYAEPR**
Found in **gi|115471157** in **NCBInr**, Os07g0212200 [Oryza sativa Japonica Group]

Match to Query 143: 1163.567524 from(1164.574800,1+) intensity(0.0000) index(13)
Title: Label: N11, Spot_Id: 219847, Peak_List_Id: 227555, MSMS Job_Run_Id: 21965, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N11_136868230800.txt



0 to 1064.32

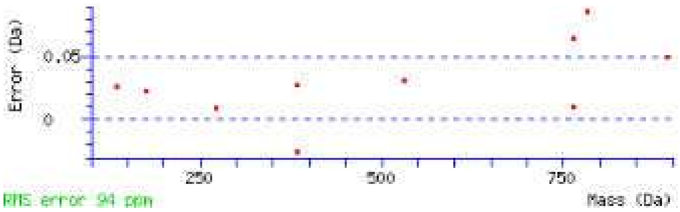
Label all possible matches ○ Label matches used for scoring ●

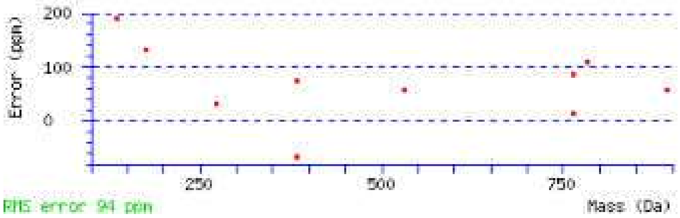
Monoisotopic mass of neutral peptide Mr(calc): 1163.5182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 16
Matches : 10/119 fragment ions using 9 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495	**N**						9
2	104.0528	218.0958	201.0692		246.0907	229.0641		158.0924	**M**	974.4479	973.4526	1050.4826	1033.4560	1032.4720	8
3	110.0713	355.1547	338.1281		***383.1496***	366.1231			**H**	837.3890		919.4421	902.4155	901.4315	7
4	120.0808	502.2231	485.1966		***530.2180***	513.1915			**F**	690.3206		***782.3832***	765.3566	764.3726	6
5	136.0757	665.2864	648.2599		693.2813	676.2548			**Y**	527.2572		635.3148	618.2882	617.3042	5
6	44.0495	736.3235	719.2970		***764.3185***	747.2919			**A**	456.2201		472.2514	455.2249	454.2409	4
7	102.0550	865.3661	848.3396	847.3556	***893.3611***	876.3345	875.3505	807.3607	**E**	327.1775	326.1823	401.2143	384.1878	383.2037	3
8	70.0651	962.4189	945.3924	944.4083	990.4138	973.3873	972.4032	936.4032	**P**	230.1248	229.1295	***272.1717***	255.1452		2
9	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
MH	241.1118	269.1067	**MHF**	388.1802	416.1751	**MHFY**	551.2435	579.2384
MHFYA	622.2806	650.2755	**HF**	257.1397	285.1346	**HFY**	420.2030	448.1979
HFYA	491.2401	519.2350	**HFYAE**	620.2827	648.2776	**FY**	283.1441	311.1390
FYA	354.1812	382.1761	**FYAE**	483.2238	511.2187	**FYAEP**	580.2766	608.2715

YA	207.1128	235.1077	**YAE**	336.1554	364.1503	**YAEP**	433.2082	461.2031
AE	173.0921	201.0870	**AEP**	270.1448	298.1397	**EP**	199.1077	227.1026





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.6	1163.5182	0.0493	NMHFYAEPR
32.5	1163.5935	-0.0259	ITGEAYLNQR
27.5	1163.5683	-0.0008	AAEEAYRQAR
27.5	1163.5934	-0.0259	DREYAEIIR
27.5	1163.5822	-0.0147	GVDEYAELLR
27.5	1163.6186	-0.0511	IASEYAELIR
27.5	1163.5142	0.0534	RDEAYHSMR
27.5	1163.5934	-0.0259	RDEAYIEIR
27.5	1163.5934	-0.0259	SALEYAGNLAR
27.3	1163.5294	0.0381	ASLXTALXNPR

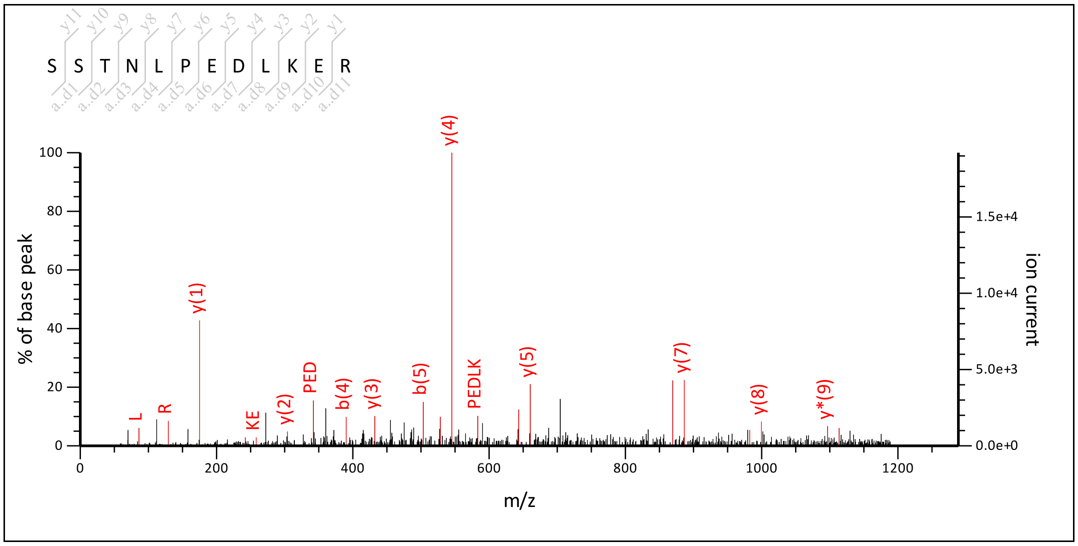
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 57

MS/MS Fragmentation of **SSTNLPEDLKER**
Found in **gi|115471157** in **NCBInr**, Os07g0212200 [Oryza sativa Japonica Group]

Match to Query 203: 1387.755224 from(1388.762500,1+) intensity(0.0000) index(23)
Title: Label: N11, Spot_Id: 219847, Peak_List_Id: 227554, MSMS Job_Run_Id: 21965, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N11_136868230800.txt



0 to 1288.72

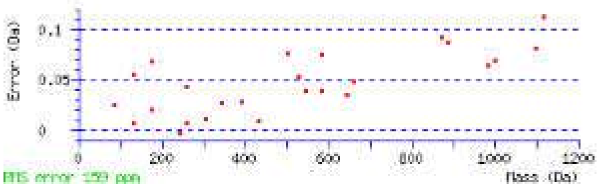
Label all possible matches ○ Label matches used for scoring ●

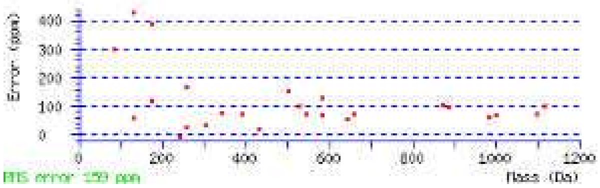
Monoisotopic mass of neutral peptide Mr(calc): 1387.6943
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.34
Matches : 27/208 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	60.0444	147.0764		129.0659	**175.0713**		157.0608	131.0815		S	1269.6434	1268.6481		1301.6696	1284.6430
3	74.0600	248.1241		230.1135	276.1190		258.1084	232.1292	234.1084	T	1168.5957	1181.6161	1183.5953	1214.6375	1197.6110
4	87.0553	362.1670	345.1405	344.1565	**390.1619**	373.1354	372.1514	319.1612		N	1054.5528	1053.5575		***1113.5899***	1096.5633
5	86.0964	475.2511	458.2245	457.2405	**503.2460**	486.2195	485.2354	433.2041		L	941.4687	940.4734		***999.5469***	982.5204
6	70.0651	572.3039	555.2773	554.2933	600.2988	583.2722	582.2882	546.2882		P	844.4159	843.4207		***886.4629***	869.4363
7	102.0550	701.3464	684.3199	683.3359	729.3414	712.3148	711.3308	643.3410		E	715.3733	714.3781		789.4101	772.3836
8	88.0393	816.3734	799.3468	798.3628	844.3683	827.3418	826.3577	772.3836		D	600.3464	599.3511		***660.3675***	643.3410
9	86.0964	929.4575	912.4309	911.4469	957.4524	940.4258	939.4418	887.4105		L	487.2623	486.2671		***545.3406***	528.3140
10	101.1073	1057.5524	1040.5259	1039.5418	1085.5473	1068.5208	1067.5368	1000.4946		K	359.1674	358.1721		***432.2565***	415.2300
11	102.0550	1186.5950	1169.5685	1168.5844	1214.5899	1197.5634	1196.5794	1128.5895		E	230.1248	229.1295		***304.1615***	287.1350
12	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ST	161.0921	189.0870	STN	275.1350	303.1299	STNL	388.2191	416.2140
STNLP	485.2718	513.2667	STNLPE	614.3144	642.3093	TN	188.1030	216.0979
TNL	301.1870	329.1819	TNLP	398.2398	426.2347	TNLPE	527.2824	555.2773
TNLPED	642.3093	670.3042	NL	200.1394	228.1343	NLP	297.1921	325.1870
NLPE	426.2347	454.2296	NLPED	541.2617	569.2566	NLPEDL	654.3457	682.3406
LP	183.1492	211.1441	LPE	312.1918	340.1867	LPED	427.2187	455.2136
LPEDL	540.3028	568.2977	LPEDLK	668.3978	696.3927	PE	199.1077	227.1026
PED	314.1347	342.1296	PEDL	427.2187	455.2136	PEDLK	555.3137	583.3086
PEDLKE	684.3563	712.3512	ED	217.0819	245.0768	EDL	330.1660	358.1609

EDLK	458.2609	486.2558	**EDLKE**	587.3035	615.2984	**DL**	201.1234	229.1183
DLK	329.2183	357.2132	**DLKE**	458.2609	486.2558	**LK**	214.1914	242.1863
LKE	343.2340	371.2289	**KE**	230.1499	258.1448			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.0	1387.6943	0.0609	SSTNLPEDLKER
37.1	1387.6765	0.0787	MQNIEPDKLER
36.1	1387.6943	0.0609	SDDGKLIDLGAER
34.3	1387.6765	0.0787	MKNLPEDDAIAR
33.1	1387.7783	-0.0231	KSGLVINLSSSAGR
29.9	1387.7605	-0.0053	GRAMLDLLLTNR
29.7	1387.7459	0.0093	LFELINALDANR
27.6	1387.6514	0.1038	IDCNINNLQER
27.5	1387.7572	-0.0019	IQFNINNIKER
27.4	1387.6803	0.0749	EAAAAAASSAREGAR

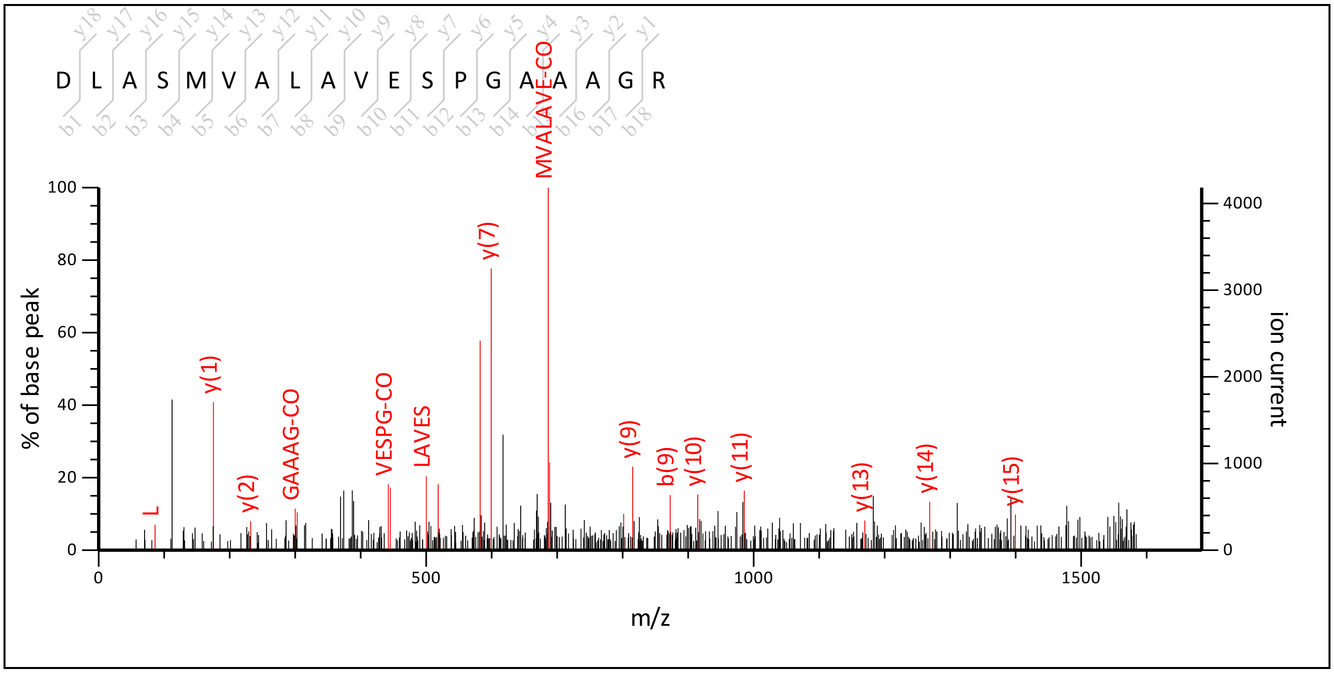
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 57

MS/MS Fragmentation of **DLASMVALAVESPGAAAGR**
Found in **gi|115471157** in **NCBInr**, Os07g0212200 [Oryza sativa Japonica Group]

Match to Query 245: 1784.997524 from(1786.004800,1+) intensity(0.0000) index(30)
Title: Label: N11, Spot_Id: 219847, Peak_List_Id: 227560, MSMS Job_Run_Id: 21965, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N11_136868230800.txt



0 to 1684.04

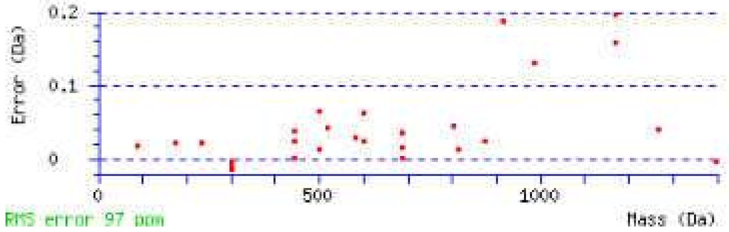
Label all possible matches ○ Label matches used for scoring ●

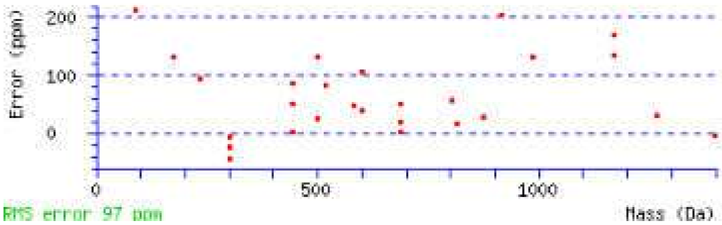
Monoisotopic mass of neutral peptide Mr(calc): 1784.9091
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 3.8e-05
Matches : 30/343 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	88.0393	88.0393	70.0287	116.0342	98.0237	44.0495	D						19
2	86.0964	201.1234	183.1128	229.1183	211.1077	159.0764	L	1612.8112	1611.8159	1670.8894	1653.8629	1652.8789	18
3	44.0495	272.1605	254.1499	**300.1554**	282.1448		A	1541.7741		1557.8054	1540.7788	1539.7948	17
4	60.0444	359.1925	341.1819	387.1874	369.1769	343.1976	S	1454.7420	1453.7468	1486.7682	1469.7417	1468.7577	16
5	104.0528	490.2330	472.2224	**518.2279**	500.2173	430.2296	M	1323.7015	1322.7063	***1399.7362***	1382.7097	1381.7256	15
6	72.0808	589.3014	571.2908	617.2963	599.2858	575.2858	V	1224.6331	1237.6535	***1268.6957***	1251.6692	1250.6852	14
7	44.0495	660.3385	642.3280	**688.3334**	670.3229		A	1153.5960		***1169.6273***	1152.6008	1151.6167	13
8	86.0964	773.4226	755.4120	**801.4175**	783.4069	731.3756	L	1040.5119	1039.5167	1098.5902	1081.5637	1080.5796	12
9	44.0495	844.4597	826.4491	**872.4546**	854.4441		A	969.4748		***985.5061***	968.4796	967.4956	11
10	72.0808	943.5281	925.5175	971.5230	953.5125	929.5125	V	870.4064	883.4268	***914.4690***	897.4425	896.4585	10
11	102.0550	1072.5707	1054.5601	1100.5656	1082.5551	1014.5652	E	741.3638	740.3686	***815.4006***	798.3741	797.3900	9
12	60.0444	1159.6027	1141.5922	1187.5977	1169.5871	1143.6078	S	654.3318	653.3366	***686.3580***	669.3315	668.3474	8

13	70.0651	1256.6555	1238.6449	1284.6504	1266.6399	1230.6399	**P**	557.2790	556.2838	***599.3260***	582.2994		**7**
14	30.0338	1313.6770	1295.6664	1341.6719	1323.6613		**G**			502.2732	485.2467		**6**
15	44.0495	1384.7141	1366.7035	1412.7090	1394.6984		**A**	429.2205		***445.2518***	428.2252		**5**
16	44.0495	1455.7512	1437.7406	1483.7461	1465.7355		**A**	358.1833		374.2146	357.1881		**4**
17	44.0495	1526.7883	1508.7777	1554.7832	1536.7727		**A**	287.1462		***303.1775***	286.1510		**3**
18	30.0338	1583.8098	1565.7992	1611.8047	1593.7941		**G**			***232.1404***	215.1139		**2**
19	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LA	157.1335	185.1285	**LAS**	244.1656	272.1605	**LASM**	375.2061	403.2010
LASMV	474.2745	502.2694	**LASMVA**	545.3116	573.3065	**LASMVAL**	658.3956	686.3906
AS	131.0815	159.0764	**ASM**	262.1220	290.1169	**ASMV**	361.1904	389.1853
ASMVA	432.2275	460.2224	**ASMVAL**	545.3116	573.3065	**ASMVALA**	616.3487	644.3436
SM	191.0849	219.0798	**SMV**	290.1533	318.1482	**SMVA**	361.1904	389.1853
SMVAL	474.2745	502.2694	**SMVALA**	545.3116	573.3065	**SMVALAV**	644.3800	672.3749
MV	203.1213	231.1162	**MVA**	274.1584	302.1533	**MVAL**	387.2424	415.2374
MVALA	458.2796	486.2745	**MVALAV**	557.3480	585.3429	**MVALAVE**	686.3906	714.3855
VA	143.1179	171.1128	**VAL**	256.2020	284.1969	**VALA**	327.2391	355.2340
VALAV	426.3075	454.3024	**VALAVE**	555.3501	583.3450	**VALAVES**	642.3821	670.3770
AL	157.1335	185.1285	**ALA**	228.1707	256.1656	**ALAV**	327.2391	355.2340
ALAVE	456.2817	484.2766	**ALAVES**	543.3137	571.3086	**ALAVESP**	640.3665	668.3614
ALAVESPG	697.3879	725.3828	**LA**	157.1335	185.1285	**LAV**	256.2020	284.1969
LAVE	385.2445	413.2395	**LAVES**	472.2766	500.2715	**LAVESP**	569.3293	597.3243
LAVESPG	626.3508	654.3457	**LAVESPGA**	697.3879	725.3828	**AV**	143.1179	171.1128
AVE	272.1605	300.1554	**AVES**	359.1925	387.1874	**AVESP**	456.2453	484.2402
AVESPG	513.2667	541.2617	**AVESPGA**	584.3039	612.2988	**AVESPGAA**	655.3410	683.3359
VE	201.1234	229.1183	**VES**	288.1554	316.1503	**VESP**	385.2082	413.2031
VESPG	442.2296	470.2245	**VESPGA**	513.2667	541.2617	**VESPGAA**	584.3039	612.2988
VESPGAAA	655.3410	683.3359	**ES**	189.0870	217.0819	**ESP**	286.1397	314.1347
ESPG	343.1612	371.1561	**ESPGA**	414.1983	442.1932	**ESPGAA**	485.2354	513.2304
ESPGAAA	556.2726	584.2675	**ESPGAAAG**	613.2940	641.2889	**SP**	157.0972	185.0921
SPG	214.1186	242.1135	**SPGA**	285.1557	313.1506	**SPGAA**	356.1928	384.1878
SPGAAA	427.2300	455.2249	**SPGAAAG**	484.2514	512.2463	**PG**	127.0866	155.0815
PGA	198.1237	226.1186	**PGAA**	269.1608	297.1557	**PGAAA**	340.1979	368.1928
PGAAAG	397.2194	425.2143	**GA**	101.0709	129.0659	**GAA**	172.1081	200.1030
GAAA	243.1452	271.1401	**GAAAG**	300.1666	328.1615	**AA**	115.0866	143.0815
AAA	186.1237	214.1186	**AAAG**	243.1452	271.1401	**AA**	115.0866	143.0815
AAG	172.1081	200.1030	**AG**	101.0709	129.0659			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.3	1784.9091	0.0885	DLASMVALAVESPGAAAGR
30.8	1784.9454	0.0521	EREIAAMLNLNPSTVK
29.9	1785.0148	-0.0173	ESRAPFIIALAGSVAVGK
29.9	1785.0620	-0.0645	LAMLMGALALLTSLLVR
28.1	1784.8978	0.0997	AGVALPVEAVEVEAMER
26.9	1784.9892	0.0083	IEASLMALAVNKPMVAK
25.4	1784.8978	0.0997	EMIAKLDAIGPEVDER
25.0	1784.9342	0.0633	LELATVSDQMPNGAIVK
24.8	1784.9594	0.0381	ESATLVDLPITVGMPVK
24.8	1784.8918	0.1058	WLSDGAGRAALADAQQR

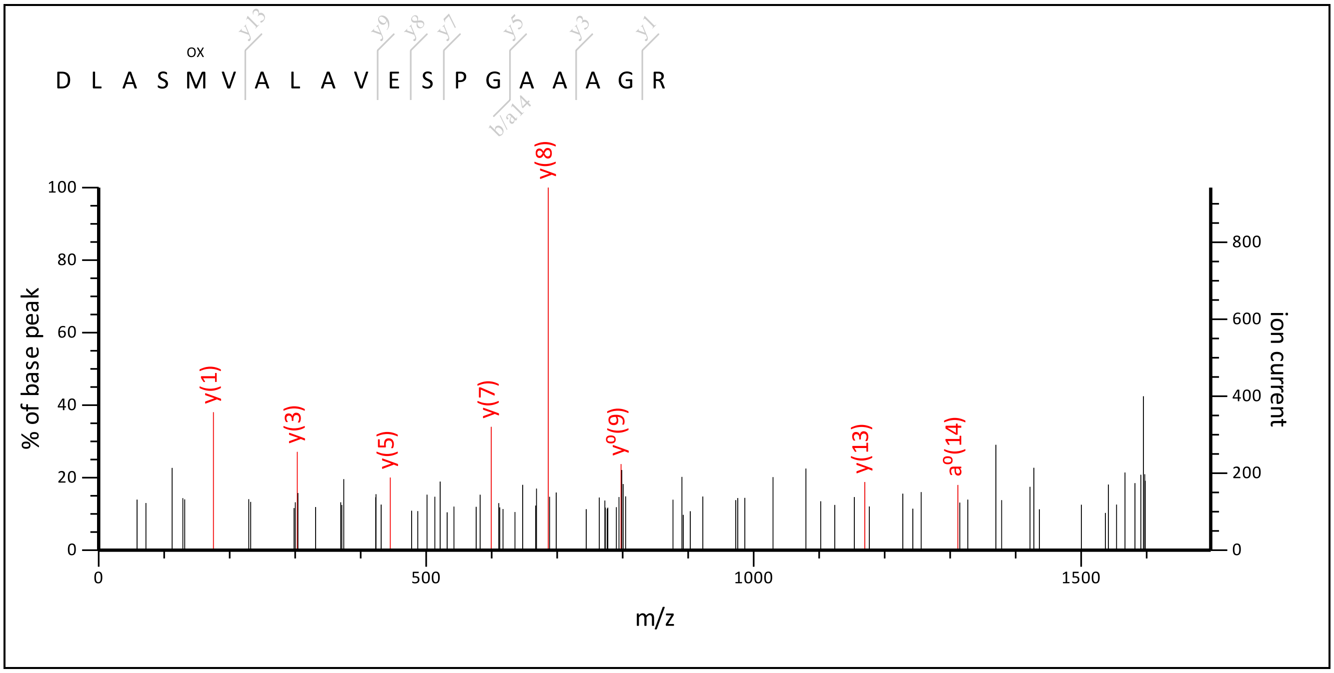
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 57

MS/MS Fragmentation of **DLASMVALAVESPGAAAGR**
Found in **gi|115471157** in **NCBInr**, Os07g0212200 [Oryza sativa Japonica Group]

Match to Query 247: 1800.980924 from(1801.988200,1+) intensity(0.0000) index(31)
Title: Label: N11, Spot_Id: 219847, Peak_List_Id: 227578, MSMS Job_Run_Id: 21965, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N11_136868230800.txt



0 to 1697.79

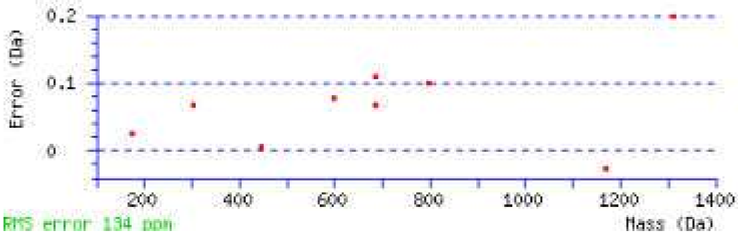
Label all possible matches ○ Label matches used for scoring ●

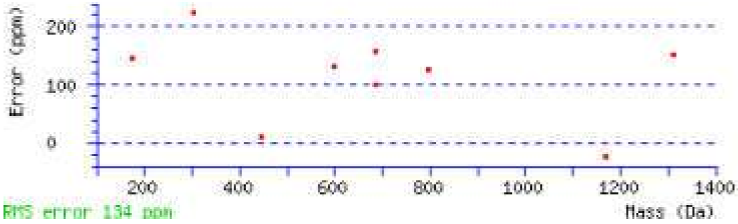
Monoisotopic mass of neutral peptide Mr(calc): 1800.9040
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 1.3e+02
Matches : 9/460 fragment ions using 16 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	88.0393	88.0393	70.0287	116.0342	98.0237	44.0495	D						19
2	86.0964	201.1234	183.1128	229.1183	211.1077	159.0764	L	1628.8061	1627.8108	1686.8843	1669.8578	1668.8738	18
3	44.0495	272.1605	254.1499	300.1554	282.1448		A	1557.7690		1573.8003	1556.7737	1555.7897	17
4	60.0444	359.1925	341.1819	387.1874	369.1769	343.1976	S	1470.7369	1469.7417	1502.7632	1485.7366	1484.7526	16
5	120.0478	506.2279	488.2173	534.2228	516.2123	430.2296	M	1323.7015	1322.7063	1415.7311	1398.7046	1397.7206	15
6	72.0808	605.2963	587.2858	633.2912	615.2807	591.2807	V	1224.6331	1237.6535	1268.6957	1251.6692	1250.6852	14
7	44.0495	676.3334	658.3229	704.3284	686.3178		A	1153.5960		***1169.6273***	1152.6008	1151.6167	13
8	86.0964	789.4175	771.4069	817.4124	799.4019	747.3706	L	1040.5119	1039.5167	1098.5902	1081.5637	1080.5796	12
9	44.0495	860.4546	842.4441	888.4495	870.4390		A	969.4748		985.5061	968.4796	967.4956	11

10	72.0808	959.5230	941.5125	987.5179	969.5074	945.5074	**V**	870.4064	883.4268	914.4690	897.4425	896.4585	**10**
11	102.0550	1088.5656	1070.5551	1116.5605	1098.5500	1030.5601	**E**	741.3638	740.3686	815.4006	798.3741	797.3900	**9**
12	60.0444	1175.5977	1157.5871	1203.5926	1185.5820	1159.6027	**S**	654.3318	653.3366	***686.3580***	669.3315	668.3474	**8**
13	70.0651	1272.6504	1254.6399	1300.6453	1282.6348	1246.6348	**P**	557.2790	556.2838	***599.3260***	582.2994		**7**
14	30.0338	1329.6719	1311.6613	1357.6668	1339.6562		**G**			502.2732	485.2467		**6**
15	44.0495	1400.7090	1382.6984	1428.7039	1410.6933		**A**	429.2205		***445.2518***	428.2252		**5**
16	44.0495	1471.7461	1453.7355	1499.7410	1481.7305		**A**	358.1833		374.2146	357.1881		**4**
17	44.0495	1542.7832	1524.7727	1570.7781	1552.7676		**A**	287.1462		***303.1775***	286.1510		**3**
18	30.0338	1599.8047	1581.7941	1627.7996	1609.7890		**G**			232.1404	215.1139		**2**
19	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LA	157.1335	185.1285	**LAS**	244.1656	272.1605	**LASM**	391.2010	419.1959
LASMV	490.2694	518.2643	**LASMVA**	561.3065	589.3014	**LASMVAL**	674.3906	702.3855
AS	131.0815	159.0764	**ASM**	278.1169	306.1118	**ASMV**	377.1853	405.1802
ASMVA	448.2224	476.2173	**ASMVAL**	561.3065	589.3014	**ASMVALA**	632.3436	660.3385
SM	207.0798	235.0747	**SMV**	306.1482	334.1431	**SMVA**	377.1853	405.1802
SMVAL	490.2694	518.2643	**SMVALA**	561.3065	589.3014	**SMVALAV**	660.3749	688.3698
MV	219.1162	247.1111	**MVA**	290.1533	318.1482	**MVAL**	403.2374	431.2323
MVALA	474.2745	502.2694	**MVALAV**	573.3429	601.3378	**VA**	143.1179	171.1128
VAL	256.2020	284.1969	**VALA**	327.2391	355.2340	**VALAV**	426.3075	454.3024
VALAVE	555.3501	583.3450	**VALAVES**	642.3821	670.3770	**AL**	157.1335	185.1285
ALA	228.1707	256.1656	**ALAV**	327.2391	355.2340	**ALAVE**	456.2817	484.2766
ALAVES	543.3137	571.3086	**ALAVESP**	640.3665	668.3614	**ALAVESPG**	697.3879	725.3828
LA	157.1335	185.1285	**LAV**	256.2020	284.1969	**LAVE**	385.2445	413.2395
LAVES	472.2766	500.2715	**LAVESP**	569.3293	597.3243	**LAVESPG**	626.3508	654.3457
LAVESPGA	697.3879	725.3828	**AV**	143.1179	171.1128	**AVE**	272.1605	300.1554
AVES	359.1925	387.1874	**AVESP**	456.2453	484.2402	**AVESPG**	513.2667	541.2617
AVESPGA	584.3039	612.2988	**AVESPGAA**	655.3410	683.3359	**VE**	201.1234	229.1183
VES	288.1554	316.1503	**VESP**	385.2082	413.2031	**VESPG**	442.2296	470.2245
VESPGA	513.2667	541.2617	**VESPGAA**	584.3039	612.2988	**VESPGAAA**	655.3410	683.3359
ES	189.0870	217.0819	**ESP**	286.1397	314.1347	**ESPG**	343.1612	371.1561
ESPGA	414.1983	442.1932	**ESPGAA**	485.2354	513.2304	**ESPGAAA**	556.2726	584.2675
ESPGAAAG	613.2940	641.2889	**SP**	157.0972	185.0921	**SPG**	214.1186	242.1135
SPGA	285.1557	313.1506	**SPGAA**	356.1928	384.1878	**SPGAAA**	427.2300	455.2249
SPGAAAG	484.2514	512.2463	**PG**	127.0866	155.0815	**PGA**	198.1237	226.1186
PGAA	269.1608	297.1557	**PGAAA**	340.1979	368.1928	**PGAAAG**	397.2194	425.2143
GA	101.0709	129.0659	**GAA**	172.1081	200.1030	**GAAA**	243.1452	271.1401
GAAAG	300.1666	328.1615	**AA**	115.0866	143.0815	**AAA**	186.1237	214.1186
AAAG	243.1452	271.1401	**AA**	115.0866	143.0815	**AAG**	172.1081	200.1030
AG	101.0709	129.0659						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.5	1800.9040	0.0769	DLASMVALAVESPGAAAGR
15.9	1801.0686	-0.0877	KPRLPGPGSLLSKPAQR
14.5	1800.9078	0.0731	SQQLGSATGNTASAKPQR
14.4	1800.8828	0.0981	QLTWGETPELMAAAQR
12.0	1800.9516	0.0294	IMNIQARLETEIAAGR
10.3	1800.8684	0.1125	IESMRALGMYLSMQR
10.2	1800.8101	0.1709	MEPEIDDFHKDAAAGR
10.1	1800.8900	0.0909	MTTAAAAARGAAPESAAQR
9.3	1800.9330	0.0480	ALDASADEILGVRTSAGR
9.2	1800.8966	0.0843	TTALEEQNTQQAAIAGR

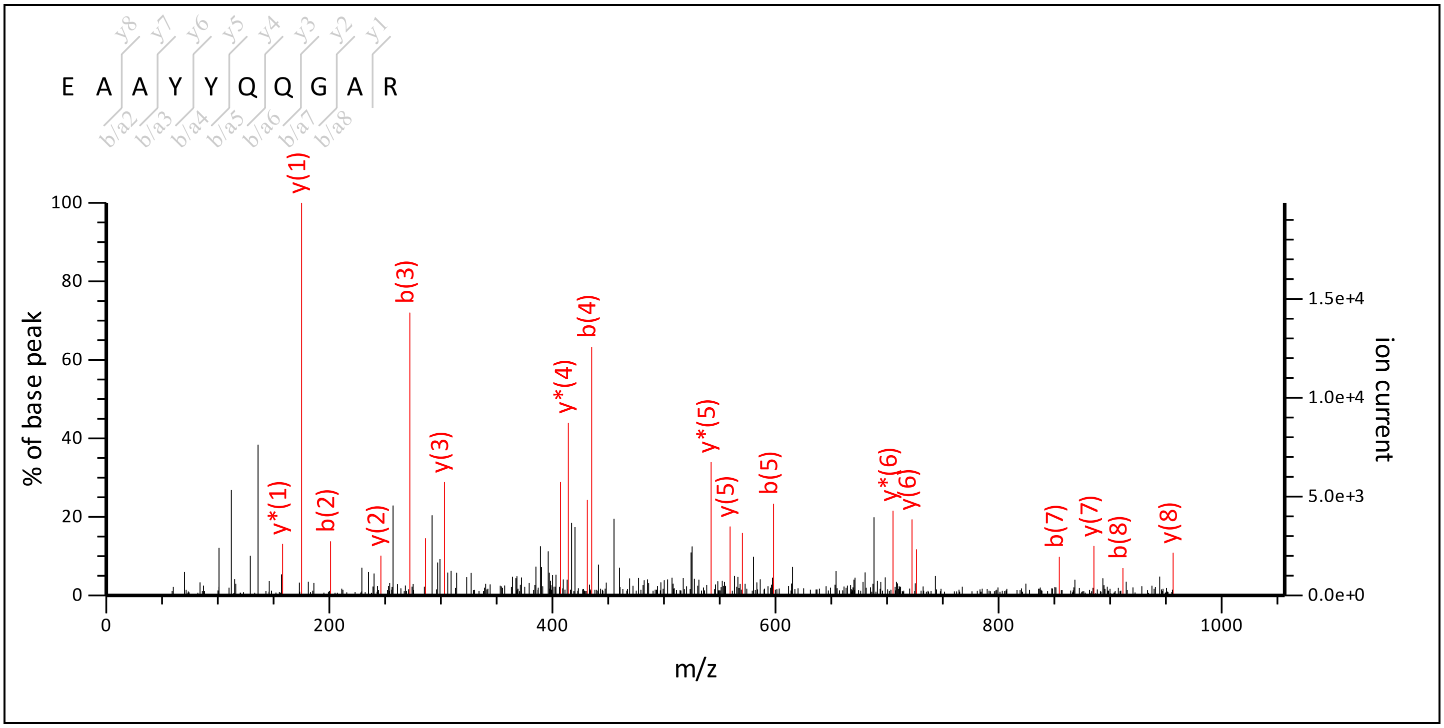
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 58

MS/MS Fragmentation of **EAAYYQQGAR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 82: 1155.571324 from(1156.578600,1+) intensity(0.0000) index(9)
Title: Label: C7, Spot_Id: 219772, Peak_List_Id: 226176, MSMS Job_Run_Id: 21836, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C7_136859909200.txt



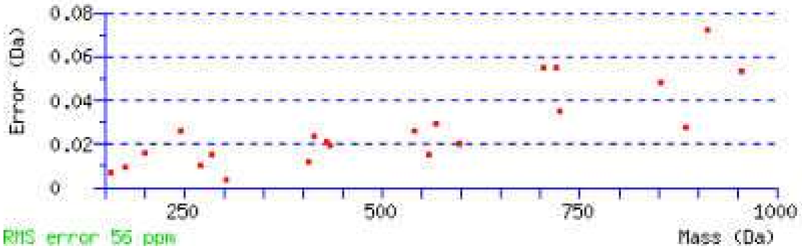
0 to 1056.51

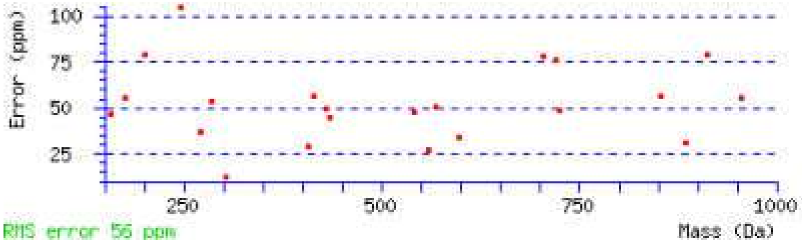
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1155.5309
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 0.086
Matches : 22/44 fragment ions using 36 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	102.0550		130.0499		E			10
2	173.0921		**201.0870**		A	1027.4956	1010.4690	9
3	244.1292		**272.1241**		A	***956.4585***	939.4319	8
4	**407.1925**		**435.1874**		Y	***885.4213***	868.3948	7
5	**570.2558**		**598.2508**		Y	***722.3580***	705.3315	6
6	698.3144	681.2879	**726.3093**	709.2828	Q	***559.2947***	542.2681	5
7	826.3730	809.3464	**854.3679**	837.3414	Q	***431.2361***	414.2096	4

8	883.3945	866.3679	**911.3894**	894.3628	**G**	***303.1775***	286.1510	**3**
9	954.4316	937.4050	982.4265	965.3999	**A**	***246.1561***	229.1295	**2**
10					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.3	1155.5309	0.0405	EAAYYQQGAR
42.3	1155.5672	0.0041	AAEYYKQGAR
35.6	1155.6360	-0.0647	TVAIAAAQQGAR
29.7	1155.5461	0.0252	RDYYTWPR
27.3	1155.5713	0.0001	AYPNLYYPR
27.3	1155.5672	0.0041	DREASYFIR
27.3	1155.5924	-0.0211	ESTLKYYPR
27.3	1155.6110	-0.0397	MKIVSYYPR
27.3	1155.5746	-0.0033	NAILMYYPR
24.7	1155.6360	-0.0647	SIAAAQQALAGR

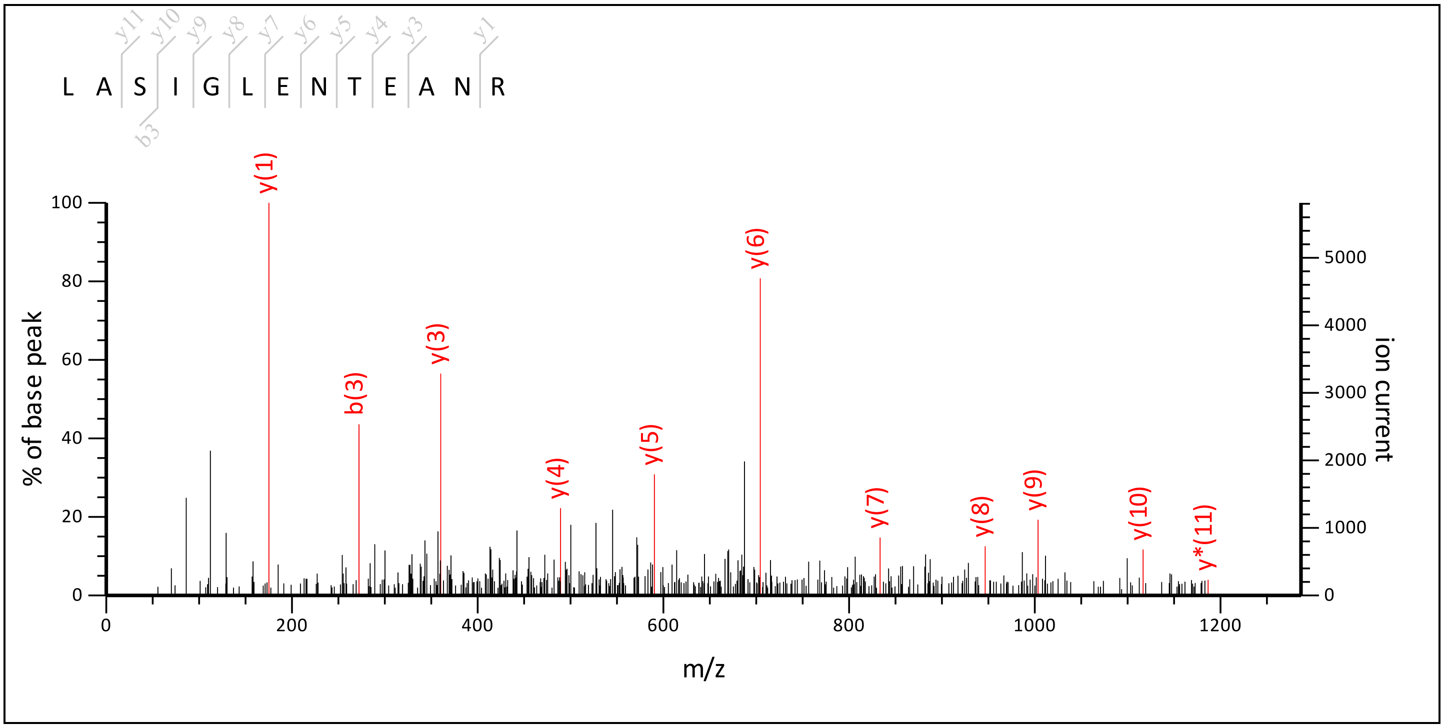
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 58

MS/MS Fragmentation of **LASIGLENTEANR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 134: 1386.757224 from(1387.764500,1+) intensity(0.0000) index(15)
Title: Label: C7, Spot_Id: 219772, Peak_List_Id: 226182, MSMS Job_Run_Id: 21836, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C7_136859909200.txt



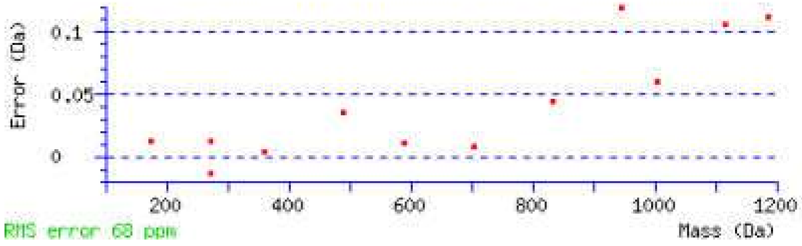
0 to 1286.68

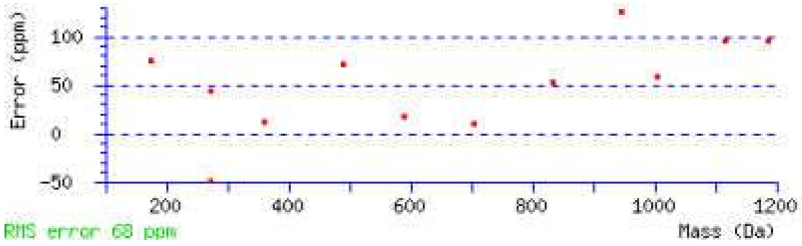
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1386.7103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 2.4e-05
Matches : 12/58 fragment ions using 12 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		L			13
2	157.1335		185.1285		A	1274.6335	1257.6070	12
3	244.1656		**272.1605**		S	1203.5964	1186.5699	11
4	357.2496		385.2445		I	***1116.5644***	1099.5378	10
5	414.2711		442.2660		G	***1003.4803***	986.4538	9
6	527.3552		555.3501		L	***946.4588***	929.4323	8
7	656.3978		684.3927		E	***833.3748***	816.3482	7

8	770.4407	753.4141	798.4356	781.4090	**N**	***704.3322***	687.3056	**6**
9	871.4884	854.4618	899.4833	882.4567	**T**	***590.2893***	573.2627	**5**
10	1000.5310	983.5044	1028.5259	1011.4993	**E**	***489.2416***	472.2150	**4**
11	1071.5681	1054.5415	1099.5630	1082.5364	**A**	***360.1990***	343.1724	**3**
12	1185.6110	1168.5844	1213.6059	1196.5794	**N**	289.1619	272.1353	**2**
13					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.4	1386.7103	0.0470	LASIGLENTEANR
47.2	1386.7619	-0.0047	AAELGLEIRYPR
37.4	1386.7467	0.0106	AVTLLADSKEQGR
36.7	1386.7507	0.0065	VTALFDGELGLPR
34.6	1386.6739	0.0833	SLAAVLGGEDDGAGR
34.2	1386.7177	0.0396	LEARMDEIGIPK
33.9	1386.6375	0.1197	TELPNENTEQGR
33.2	1386.7289	0.0283	TVAAVLEEMRPR
32.1	1386.6449	0.1123	AAELGLAEMDDPR
28.1	1386.7871	-0.0299	LASIFSDVLGLPR

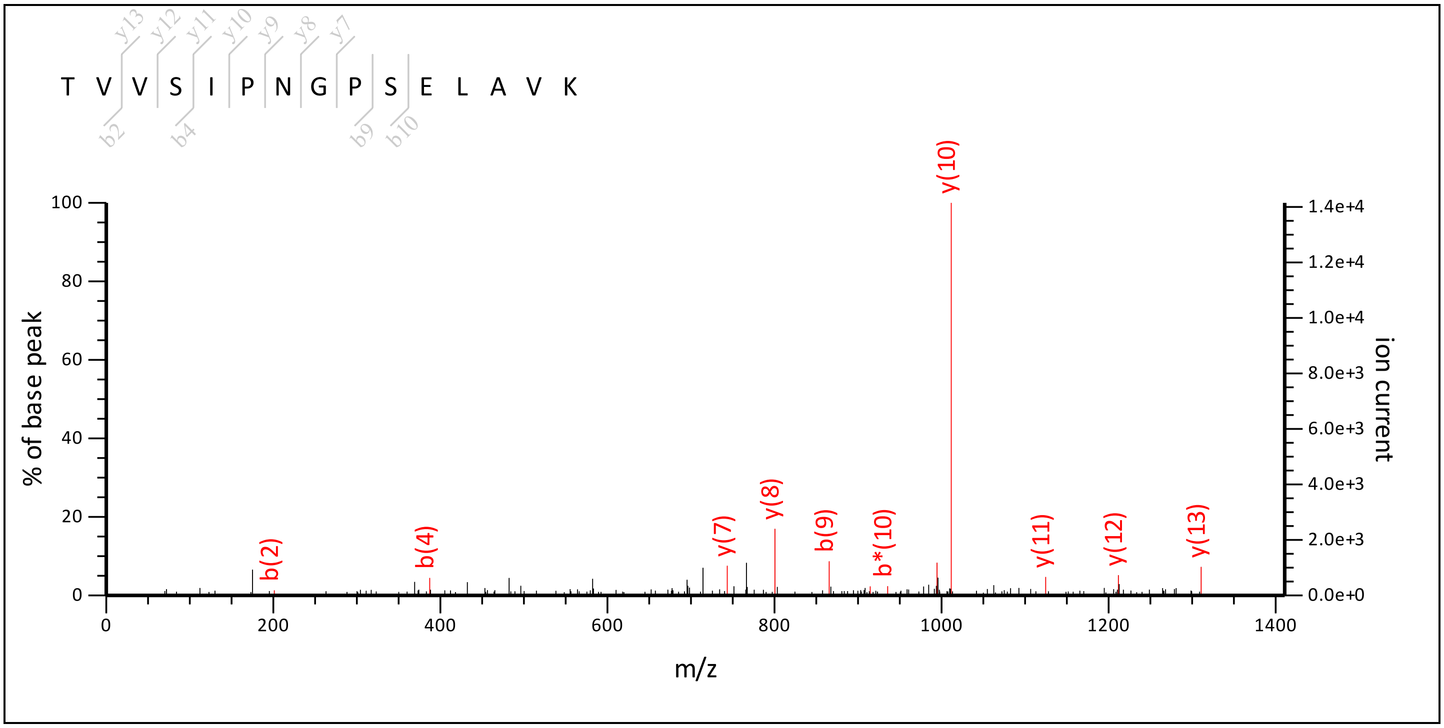
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 58

MS/MS Fragmentation of **TVVSIPNGPSELAVK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 159: 1509.866724 from(1510.874000,1+) intensity(0.0000) index(18)
Title: Label: C7, Spot_Id: 219772, Peak_List_Id: 226201, MSMS Job_Run_Id: 21836, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C7_136859909200.txt



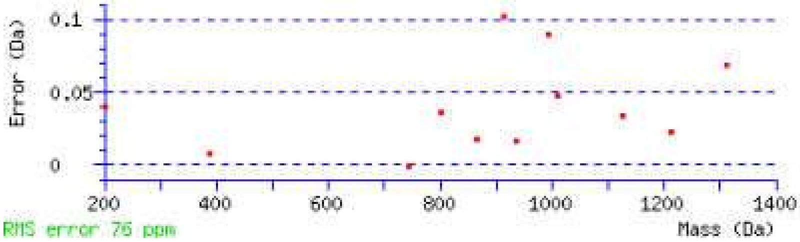
0 to 1410.8

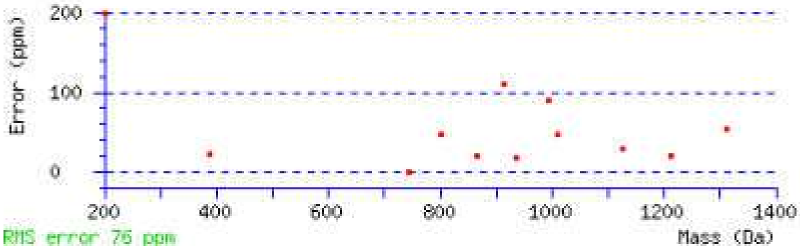
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1509.8403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 7.3
Matches : 12/72 fragment ions using 26 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	74.0600		102.0550		T			15
2	173.1285		**201.1234**		V	1409.7999	1392.7733	14
3	272.1969		300.1918		V	*1310.7314*	1293.7049	13
4	359.2289		**387.2238**		S	*1211.6630*	1194.6365	12
5	472.3130		500.3079		I	*1124.6310*	1107.6045	11
6	569.3657		597.3606		P	*1011.5469*	994.5204	10
7	683.4087	666.3821	711.4036	694.3770	N	*914.4942*	897.4676	9

8	740.4301	723.4036	768.4250	751.3985	**G**	***800.4512***	783.4247	**8**
9	837.4829	820.4563	**865.4778**	848.4512	**P**	***743.4298***	726.4032	**7**
10	924.5149	907.4884	952.5098	935.4833	**S**	646.3770	629.3505	**6**
11	1053.5575	1036.5310	1081.5524	1064.5259	**E**	559.3450	542.3184	**5**
12	1166.6416	1149.6150	1194.6365	1177.6099	**L**	430.3024	413.2758	**4**
13	1237.6787	1220.6521	1265.6736	1248.6470	**A**	317.2183	300.1918	**3**
14	1336.7471	1319.7205	1364.7420	1347.7155	**V**	246.1812	229.1547	**2**
15					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.2	1509.8403	0.0265	TVVSIPNGPSELAVK
30.7	1509.7180	0.1487	AEVSMGAVQRCFR
26.9	1509.8589	0.0079	LSVSLPMPLPSTLR
24.6	1509.8402	0.0265	EAVSLPNPISLKDK
24.2	1509.9395	-0.0728	TVVSLFPLLRLPR
24.2	1509.7675	0.0992	VTVSLDSLSDATFR
24.2	1509.9243	-0.0575	VTVTVSSPKKPVIR
24.1	1509.7787	0.0880	DALSLESAIEAHVR
23.6	1509.7787	0.0880	LSVSLTFSGTGTNAR
23.0	1509.8151	0.0516	EAVSIPIAAAGGLDAR

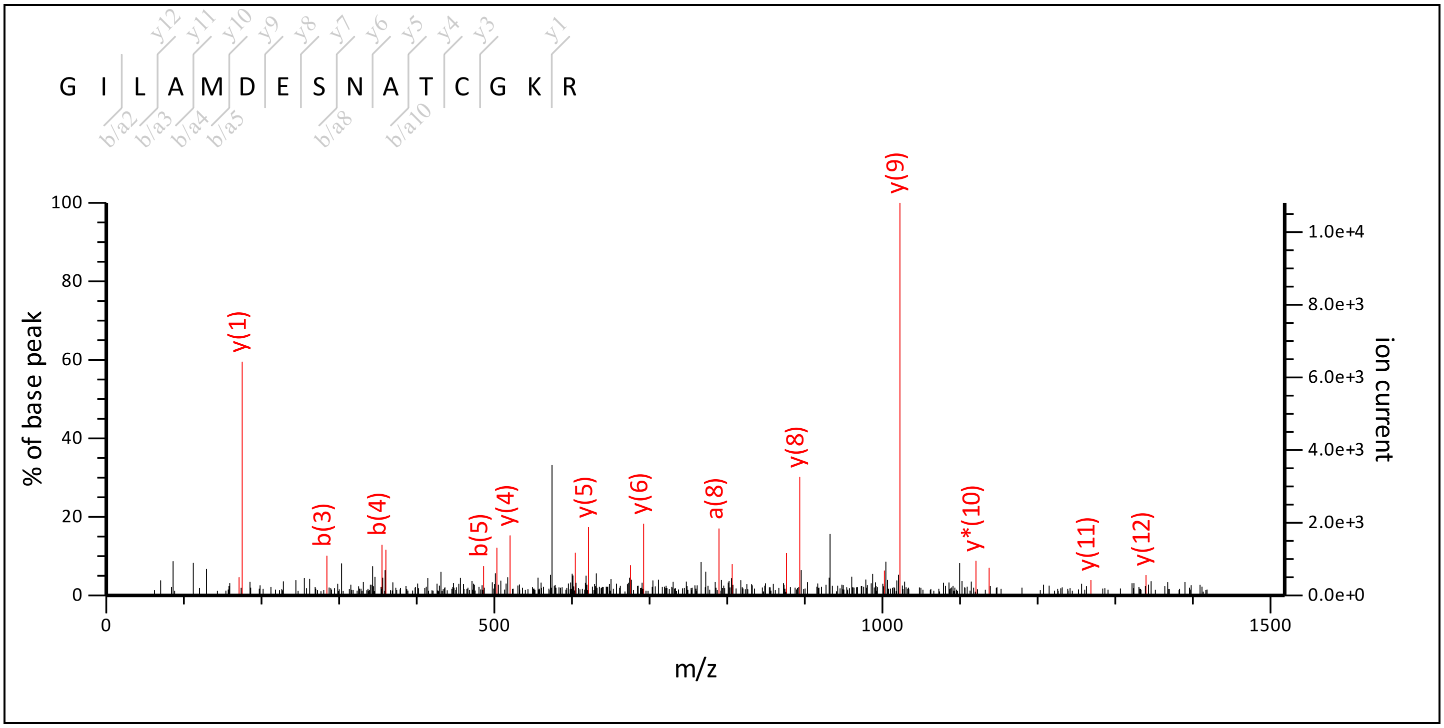
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 58

MS/MS Fragmentation of **GILAMDESNATCGKR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 171: 1621.811924 from(1622.819200,1+) intensity(0.0000) index(20)
Title: Label: C7, Spot_Id: 219772, Peak_List_Id: 226181, MSMS Job_Run_Id: 21836, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C7_136859909200.txt



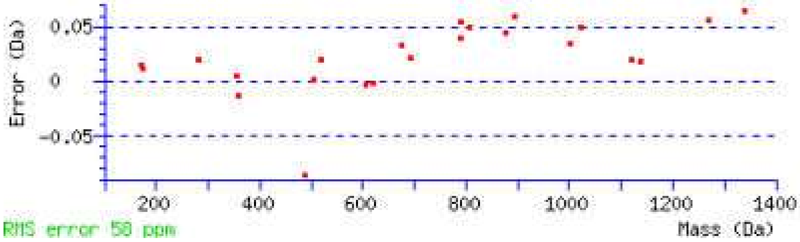
0 to 1518.28

Label all possible matches ○ Label matches used for scoring ●

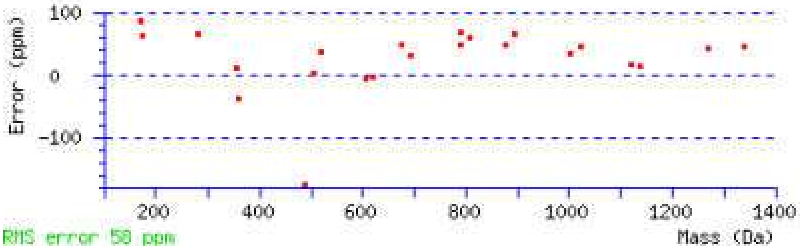
Monoisotopic mass of neutral peptide Mr(calc): 1621.7552
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 0.002
Matches : 23/68 fragment ions using 42 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			15
2	143.1179		**171.1128**		I	1565.7410	1548.7145	14
3	256.2020		**284.1969**		L	1452.6570	1435.6304	13
4	327.2391		**355.2340**		A	*1339.5729*	1322.5464	12
5	458.2796		**486.2745**		M	*1268.5358*	1251.5092	11
6	573.3065		601.3014		D	*1137.4953*	1120.4688	10
7	702.3491		730.3440		E	*1022.4684*	1005.4418	9

8	789.3811		817.3760		S	893.4258	876.3992	8
9	903.4240	886.3975	931.4190	914.3924	N	806.3937	789.3672	7
10	974.4612	957.4346	1002.4561	985.4295	A	692.3508	675.3243	6
11	1075.5088	1058.4823	1103.5038	1086.4772	T	621.3137	604.2872	5
12	1235.5395	1218.5129	1263.5344	1246.5079	C	520.2660	503.2395	4
13	1292.5609	1275.5344	1320.5559	1303.5293	G	360.2354	343.2088	3
14	1420.6559	1403.6294	1448.6508	1431.6243	K	303.2139	286.1874	2
15					R	175.1190	158.0924	1



RMS error 58 ppm



RMS error 58 ppm

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

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.8	1621.7552	0.0567	GILAMDESNATCGKR
32.5	1621.7552	0.0567	GLLAMDESNGTCAKR
16.3	1621.8464	-0.0345	GLIFLGTSGDAATFPR
15.5	1621.8134	-0.0015	TTYGPTAPSMISAAVR
14.9	1621.8610	-0.0491	LVQFLESNRLMTR
13.3	1621.9225	-0.1106	LNPLVEKITVPMPR
13.2	1621.8940	-0.0821	IGLFGLEKLHNPER
13.0	1621.7738	0.0381	ALAVMMSRGMSPPSR
12.2	1621.7657	0.0463	TGTVGTGGTGNTTTGGQR
12.2	1621.8172	-0.0053	LGLDVQAHSAGSAPSGR

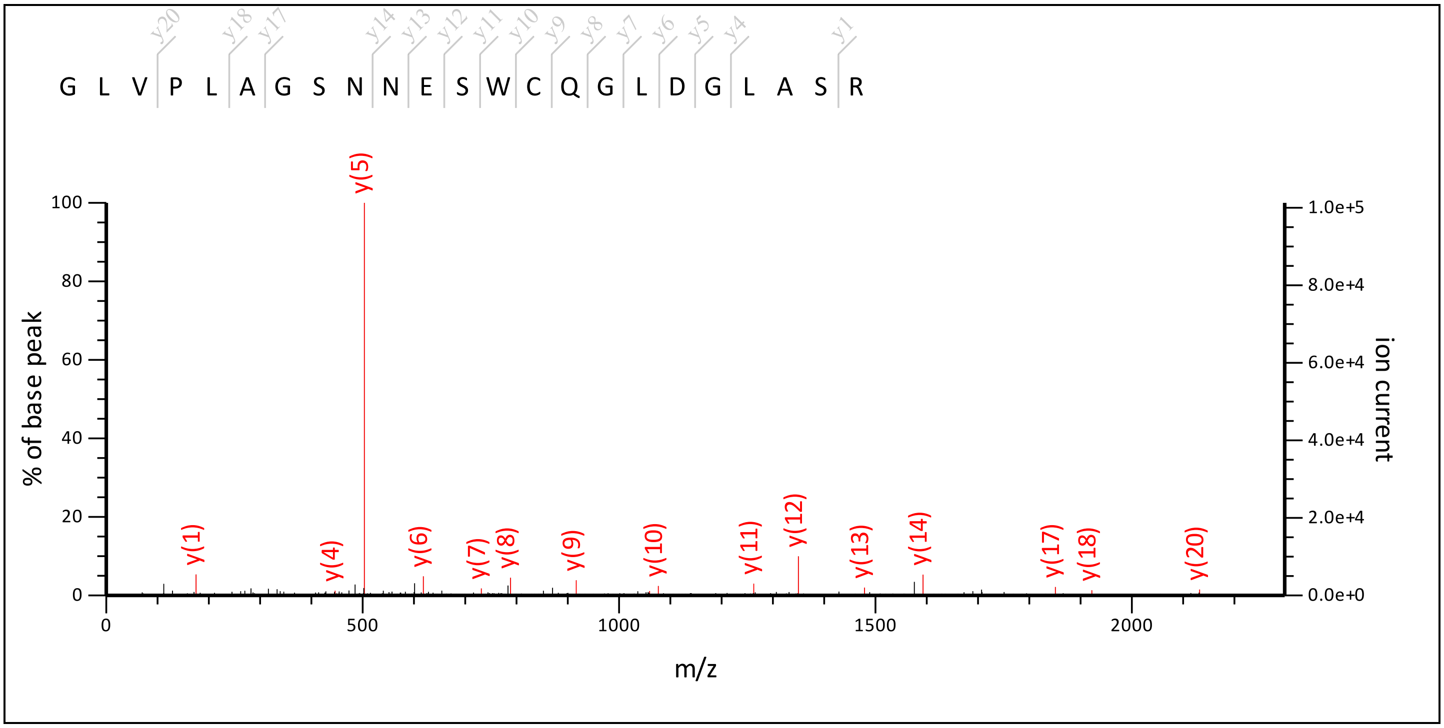
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 58

MS/MS Fragmentation of **GLVPLAGSNNESWCQGLDGLASR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 273: 2400.240524 from(2401.247800,1+) intensity(0.0000) index(32)
Title: Label: C7, Spot_Id: 219772, Peak_List_Id: 226180, MSMS Job_Run_Id: 21836, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C7_136859909200.txt



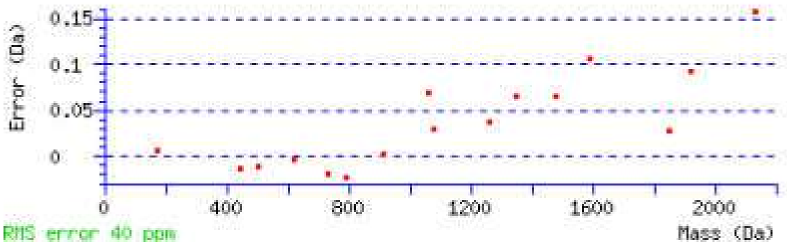
0 to 2298.04

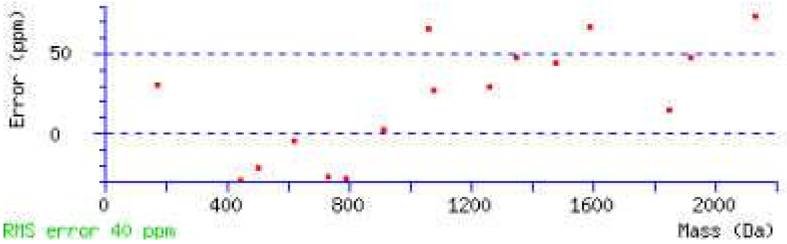
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2400.1492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 132 **Expect:** 1.4e-09
Matches : 16/116 fragment ions using 22 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			23
2	143.1179		171.1128		L	2344.1350	2327.1085	22
3	242.1863		270.1812		V	2231.0510	2214.0244	21
4	339.2391		367.2340		P	*2131.9825*	2114.9560	20
5	452.3231		480.3180		L	2034.9298	2017.9032	19
6	523.3602		551.3552		A	*1921.8457*	1904.8192	18
7	580.3817		608.3766		G	*1850.8086*	1833.7821	17

8	667.4137		695.4087		S	1793.7871	1776.7606	16
9	781.4567	764.4301	809.4516	792.4250	N	1706.7551	1689.7286	15
10	895.4996	878.4730	923.4945	906.4680	N	1592.7122	1575.6856	14
11	1024.5422	1007.5156	1052.5371	1035.5105	E	1478.6693	1461.6427	13
12	1111.5742	1094.5477	1139.5691	1122.5426	S	1349.6267	1332.6001	12
13	1297.6535	1280.6270	1325.6484	1308.6219	W	1262.5946	1245.5681	11
14	1457.6842	1440.6576	1485.6791	1468.6525	C	1076.5153	1059.4888	10
15	1585.7428	1568.7162	1613.7377	1596.7111	Q	916.4847	899.4581	9
16	1642.7642	1625.7377	1670.7591	1653.7326	G	788.4261	771.3995	8
17	1755.8483	1738.8217	1783.8432	1766.8166	L	731.4046	714.3781	7
18	1870.8752	1853.8487	1898.8701	1881.8436	D	618.3206	601.2940	6
19	1927.8967	1910.8701	1955.8916	1938.8651	G	503.2936	486.2671	5
20	2040.9808	2023.9542	2068.9757	2051.9491	L	446.2722	429.2456	4
21	2112.0179	2094.9913	2140.0128	2122.9862	A	333.1881	316.1615	3
22	2199.0499	2182.0233	2227.0448	2210.0183	S	262.1510	245.1244	2
23					R	175.1190	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
131.8	2400.1492	0.0913	GLVPLAGSNNESWCQGLDGLASR
17.6	2400.2649	-0.0243	NPRTGNIVAESFGTIILDENLK
17.1	2400.1890	0.0515	NVMVVELMVGGTGGRPGLDGVDGR
17.1	2400.1890	0.0515	NVMVVELMVGGTGGRPGLDGVDGR
16.9	2400.1193	0.1212	WASSAPATAVAEAEAEALGDGDGVR
12.8	2400.1961	0.0444	RIDLYYGQFGENLTVEGLADK
11.1	2400.1211	0.1194	DSMCGFRVYPLAPCMAILQR

9.7	2400.1591	0.0814	SSASVAQTMGTVSYVGALVGEQSR
9.3	2400.0990	0.1415	GIQTMEAANAWAPSFMTAYNAR
9.2	2400.0335	0.2070	CDTPGCRPYAEEIANGSPHNR

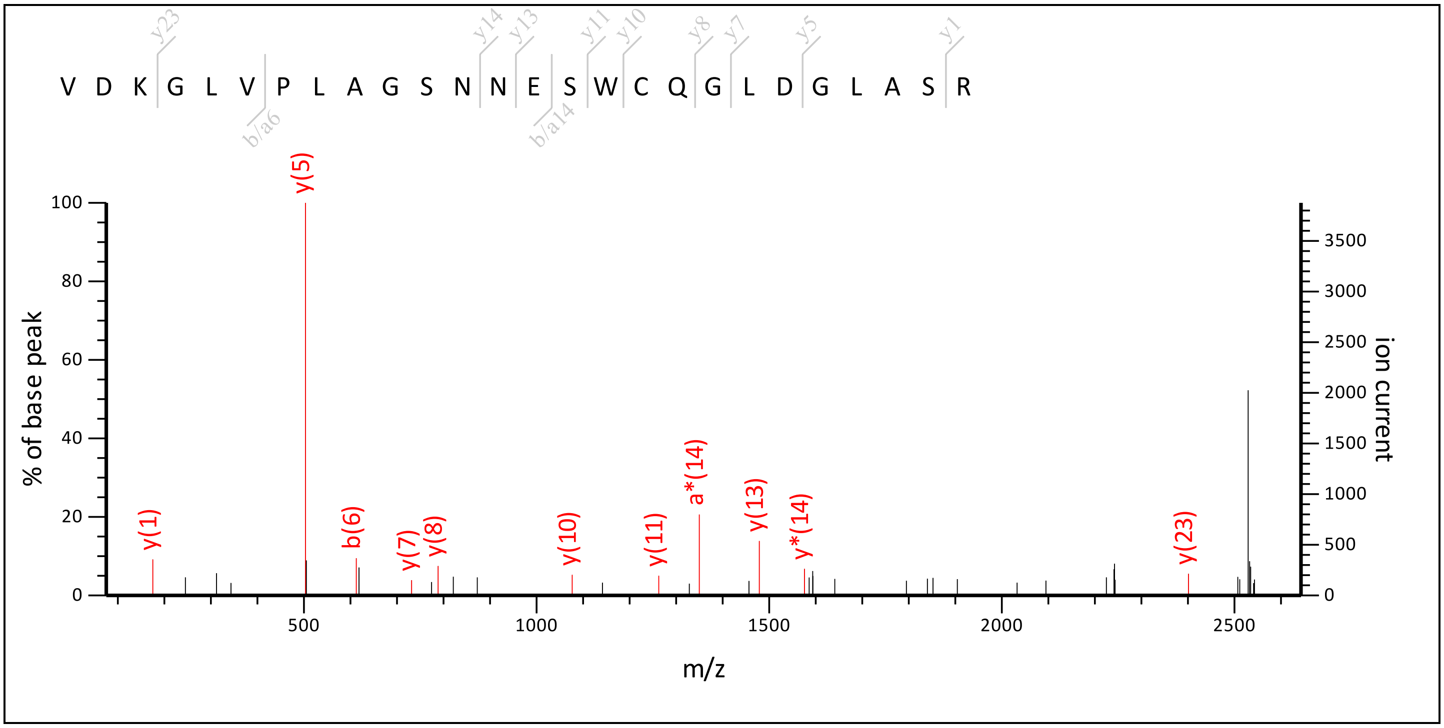
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 58

MS/MS Fragmentation of **VDKGLVPLAGSNNESWCQGLDGLASR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 279: 2742.446624 from(2743.453900,1+) intensity(0.0000) index(33)
Title: Label: C7, Spot_Id: 219772, Peak_List_Id: 226210, MSMS Job_Run_Id: 21836, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C7_136859909200.txt



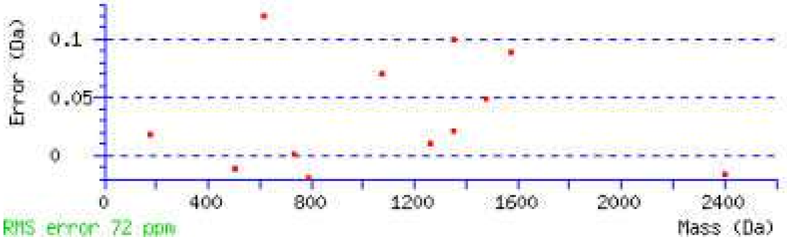
75.14 to 2642.99

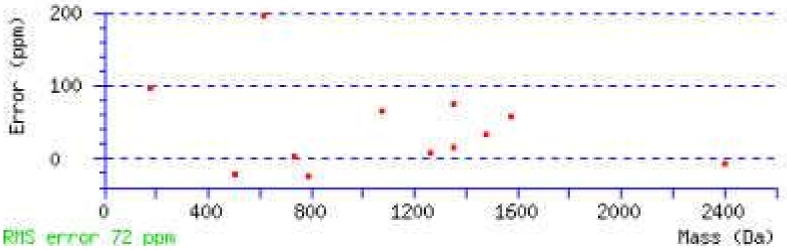
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2742.3395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.17
Matches : 12/146 fragment ions using 19 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	72.0808		100.0757		**V**			**26**
2	187.1077		215.1026		**D**	2644.2784	2627.2518	**25**
3	315.2027	298.1761	343.1976	326.1710	**K**	2529.2514	2512.2249	**24**
4	372.2241	355.1976	400.2191	383.1925	**G**	***2401.1565***	2384.1299	**23**
5	485.3082	468.2817	513.3031	496.2766	**L**	2344.1350	2327.1085	**22**
6	584.3766	567.3501	612.3715	595.3450	**V**	2231.0510	2214.0244	**21**
7	681.4294	664.4028	709.4243	692.3978	**P**	2131.9825	2114.9560	**20**

8	794.5135	777.4869	822.5084	805.4818	L	2034.9298	2017.9032	19
9	865.5506	848.5240	893.5455	876.5189	A	1921.8457	1904.8192	18
10	922.5720	905.5455	950.5669	933.5404	G	1850.8086	1833.7821	17
11	1009.6041	992.5775	1037.5990	1020.5724	S	1793.7871	1776.7606	16
12	1123.6470	1106.6204	1151.6419	1134.6154	N	1706.7551	1689.7286	15
13	1237.6899	1220.6634	1265.6848	1248.6583	N	1592.7122	1575.6856	14
14	1366.7325	1349.7060	1394.7274	1377.7009	E	***1478.6693***	1461.6427	13
15	1453.7645	1436.7380	1481.7594	1464.7329	S	***1349.6267***	1332.6001	12
16	1639.8438	1622.8173	1667.8388	1650.8122	W	***1262.5946***	1245.5681	11
17	1799.8745	1782.8479	1827.8694	1810.8429	C	***1076.5153***	1059.4888	10
18	1927.9331	1910.9065	1955.9280	1938.9014	Q	916.4847	899.4581	9
19	1984.9545	1967.9280	2012.9495	1995.9229	G	***788.4261***	771.3995	8
20	2098.0386	2081.0121	2126.0335	2109.0070	L	***731.4046***	714.3781	7
21	2213.0655	2196.0390	2241.0605	2224.0339	D	618.3206	601.2940	6
22	2270.0870	2253.0605	2298.0819	2281.0554	G	***503.2936***	486.2671	5
23	2383.1711	2366.1445	2411.1660	2394.1394	L	446.2722	429.2456	4
24	2454.2082	2437.1816	2482.2031	2465.1766	A	333.1881	316.1615	3
25	2541.2402	2524.2137	2569.2351	2552.2086	S	262.1510	245.1244	2
26					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.0	2742.3395	0.1071	VDKGLVPLAGSNNESWCQGLDGLASR
11.8	2742.3622	0.0844	AFVVNIGDTFMALTNGIYKSCLHR
10.0	2742.4262	0.0204	LVLTDHDMAPITASVTALFIDVATGR
9.4	2742.3759	0.0707	GQPVAPGLPPVDEHMAASSNSTPSLKR

9.3	2742.2551	0.1916	TGYPVEMLEPGMGMDSDLGIDSIKR
9.0	2742.3422	0.1044	FEPETTGTTIMAVIYDGGLIIGADSR
9.0	2742.3422	0.1044	FEPETTGTTIMAVIYDGGLLIGADSR
8.8	2742.2290	0.2176	DLNVGDPNDPETDVGPMISEEEAKR
8.2	2742.3383	0.1083	MPAPRTLHLNAFLMNAGHHDAAWR
7.6	2742.3978	0.0488	DYPFVKIMDNLEWYLALILNEK

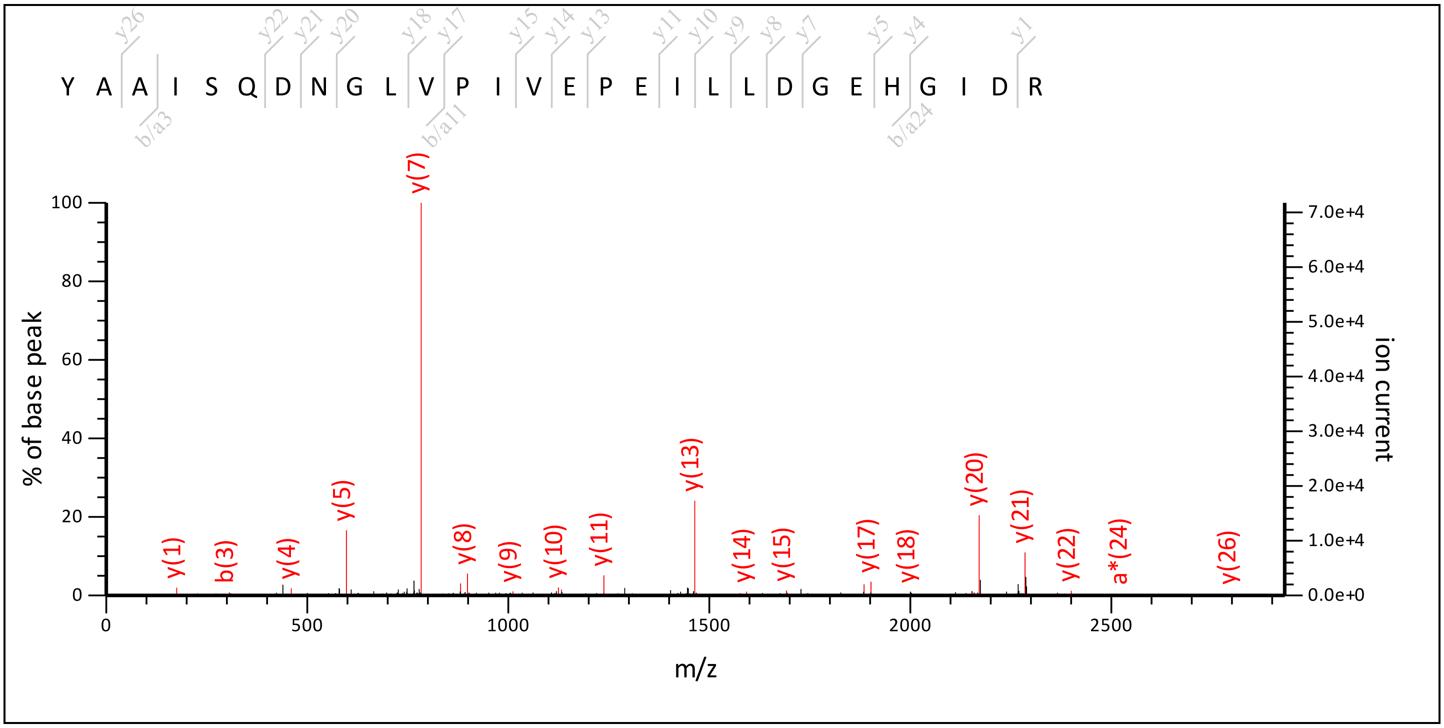
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 58

MS/MS Fragmentation of **YAAISQDNGLVPIVEPEILLDGEHGIDR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 281: 3032.674824 from(3033.682100,1+) intensity(0.0000) index(34)
Title: Label: C7, Spot_Id: 219772, Peak_List_Id: 226185, MSMS Job_Run_Id: 21836, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C7_136859909200.txt



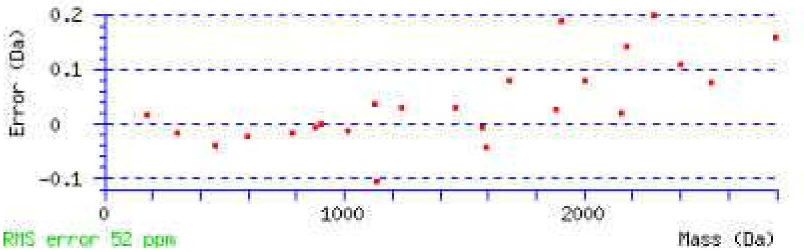
0 to 2931.19

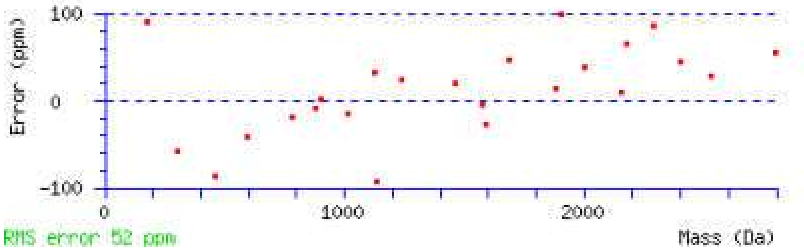
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 3032.5455
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 1e-05
Matches : 24/152 fragment ions using 56 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	136.0757		164.0706		Y			28
2	207.1128		235.1077		A	2870.4894	2853.4629	27
3	278.1499		**306.1448**		A	***2799.4523***	2782.4258	26
4	391.2340		419.2289		I	2728.4152	2711.3887	25
5	478.2660		506.2609		S	2615.3311	2598.3046	24
6	606.3246	589.2980	634.3195	617.2930	Q	2528.2991	2511.2726	23
7	721.3515	704.3250	749.3464	732.3199	D	***2400.2405***	2383.2140	22

8	835.3945	818.3679	863.3894	846.3628	**N**	***2285.2136***	2268.1870	**21**
9	892.4159	875.3894	920.4108	903.3843	**G**	***2171.1707***	2154.1441	**20**
10	1005.5000	988.4734	1033.4949	1016.4684	**L**	2114.1492	2097.1226	**19**
11	1104.5684	1087.5419	**1132.5633**	1115.5368	**V**	***2001.0651***	1984.0386	**18**
12	1201.6212	1184.5946	1229.6161	1212.5895	**P**	***1901.9967***	1884.9702	**17**
13	1314.7052	1297.6787	1342.7001	1325.6736	**I**	1804.9440	1787.9174	**16**
14	1413.7736	1396.7471	1441.7686	1424.7420	**V**	***1691.8599***	1674.8333	**15**
15	1542.8162	1525.7897	1570.8112	1553.7846	**E**	***1592.7915***	1575.7649	**14**
16	1639.8690	1622.8425	1667.8639	1650.8374	**P**	***1463.7489***	1446.7223	**13**
17	1768.9116	1751.8850	1796.9065	1779.8800	**E**	1366.6961	1349.6696	**12**
18	1881.9957	1864.9691	1909.9906	1892.9640	**I**	***1237.6535***	1220.6270	**11**
19	1995.0797	1978.0532	2023.0746	2006.0481	**L**	***1124.5695***	1107.5429	**10**
20	2108.1638	2091.1372	2136.1587	2119.1321	**L**	***1011.4854***	994.4588	**9**
21	2223.1907	2206.1642	2251.1856	2234.1591	**D**	***898.4013***	881.3748	**8**
22	2280.2122	2263.1856	2308.2071	2291.1806	**G**	***783.3744***	766.3478	**7**
23	2409.2548	2392.2282	2437.2497	2420.2231	**E**	726.3529	709.3264	**6**
24	2546.3137	2529.2871	2574.3086	2557.2821	**H**	***597.3103***	580.2838	**5**
25	2603.3352	2586.3086	2631.3301	2614.3035	**G**	***460.2514***	443.2249	**4**
26	2716.4192	2699.3927	2744.4141	2727.3876	**I**	403.2300	386.2034	**3**
27	2831.4462	2814.4196	2859.4411	2842.4145	**D**	290.1459	273.1193	**2**
28					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.1	3032.5455	0.1294	YAAISQDNGLVPIVEPEILLDGEHGIDR
74.2	3032.5455	0.1294	YAAISQDNGLVPIVEPEILLDGDHGIER

19.4	3032.6290	0.0458	GACDVVEDLAKPMPSLLILDILGLPLDR
6.4	3032.5502	0.1246	LGGTARAYYASGGATGVALDGLLDLHQMVR
5.9	3032.9531	-0.2783	TNPLNPLVILGILLVIPMILLAVLLLVR
5.8	3032.4735	0.2013	LQNKIVSDIIQEYAHEPLMWDTMAR
5.5	3032.4590	0.2159	FASMSGGETAQPLADYYVQQWKEIGLK
5.0	3032.5825	0.0923	GIATEVIVATISPADAQAHLRNGLAMGANR
4.9	3032.4558	0.2190	MGFLEDFQASVEALPAMLQRNYSLMR
4.7	3032.4410	0.2338	MTTPPHAAGTPPPGDAAGRASPPDSEPTPPR

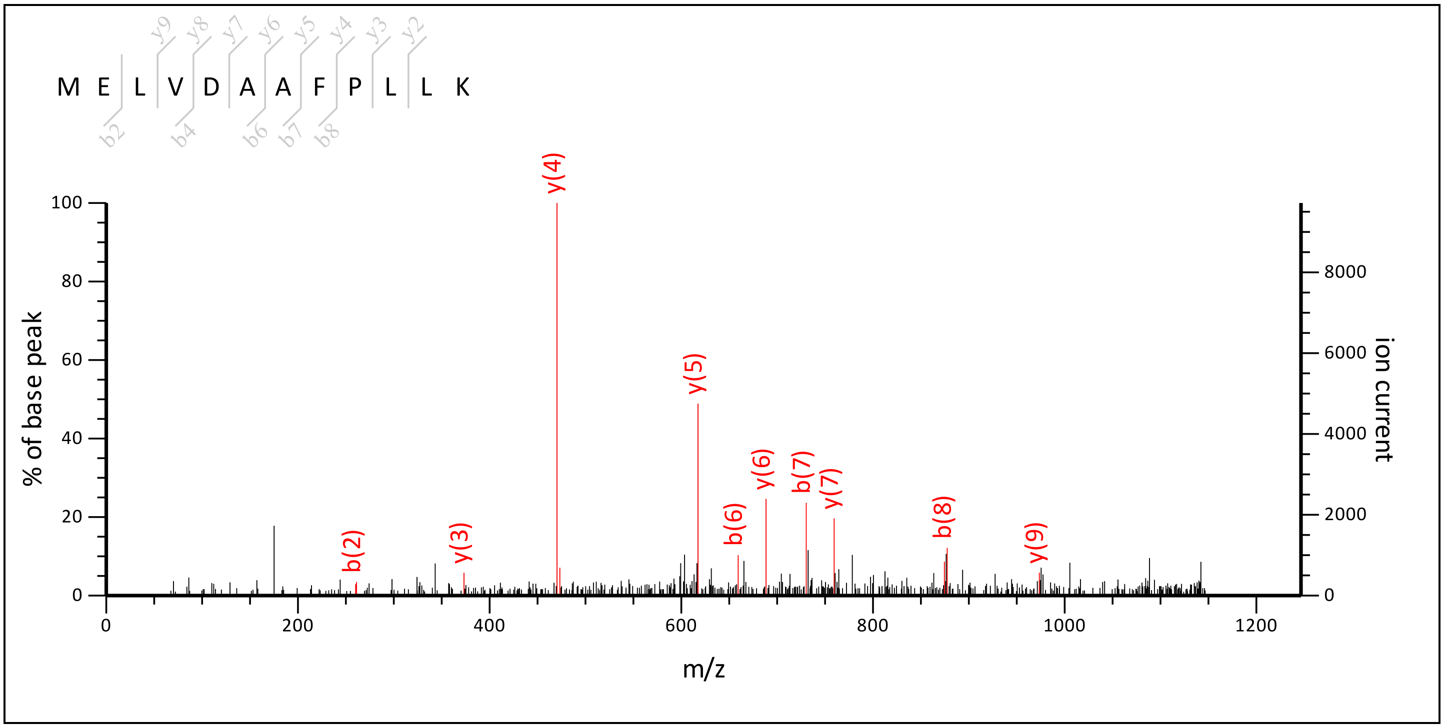
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 60

MS/MS Fragmentation of **MELVDAAFPLLK**
Found in **gi|15982948** in **NCBInr**, NAD-dependent malate dehydrogenase [Prunus persica]

Match to Query 159: 1345.749924 from(1346.757200,1+) intensity(0.0000) index(15)
Title: Label: E10, Spot_Id: 219822, Peak_List_Id: 226724, MSMS Job_Run_Id: 21854, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E10_136859948400.txt



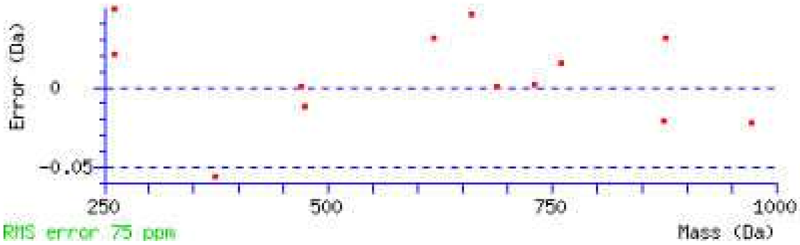
0 to 1246.57

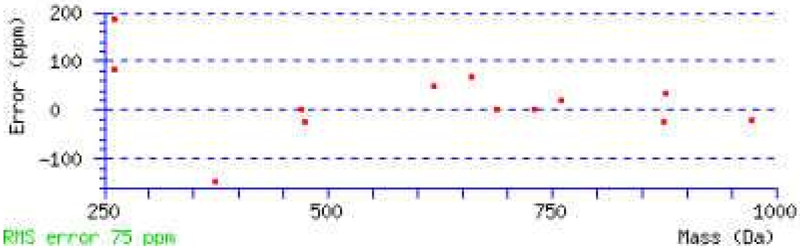
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1345.7315
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 37
Matches : 13/44 fragment ions using 44 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	104.0528	132.0478	M			12
2	233.0954	**261.0904**	E	1215.6984	1198.6718	11
3	346.1795	374.1744	L	1086.6558	1069.6292	10
4	445.2479	**473.2428**	V	***973.5717***	956.5451	9
5	560.2749	588.2698	D	***874.5033***	857.4767	8
6	631.3120	**659.3069**	A	***759.4763***	742.4498	7
7	702.3491	**730.3440**	A	***688.4392***	671.4127	6
8	849.4175	**877.4124**	F	***617.4021***	600.3756	5

9	946.4703	974.4652	**P**	*470.3337*	453.3071	**4**
10	1059.5543	1087.5492	**L**	*373.2809*	356.2544	**3**
11	1172.6384	1200.6333	**L**	*260.1969*	243.1703	**2**
12			**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.6	1345.7315	0.0184	MELVDAAFPLLK
19.9	1345.7354	0.0145	IEGAVVFITGANR
19.5	1345.7969	-0.0470	LASLIFLQLSNK
17.9	1345.7354	0.0146	LVEQFALKENR
17.9	1345.7136	0.0363	ILRSMATAGSAPR
17.9	1345.8373	-0.0874	EVLKFFLPILK
17.8	1345.6772	0.0727	EIVQMAREAGAR
17.8	1345.6626	0.0873	GNSGGPVVDELFR
17.2	1345.7103	0.0397	VRDVFAADQVAR
17.1	1345.6738	0.0761	RSEPLFQQGER

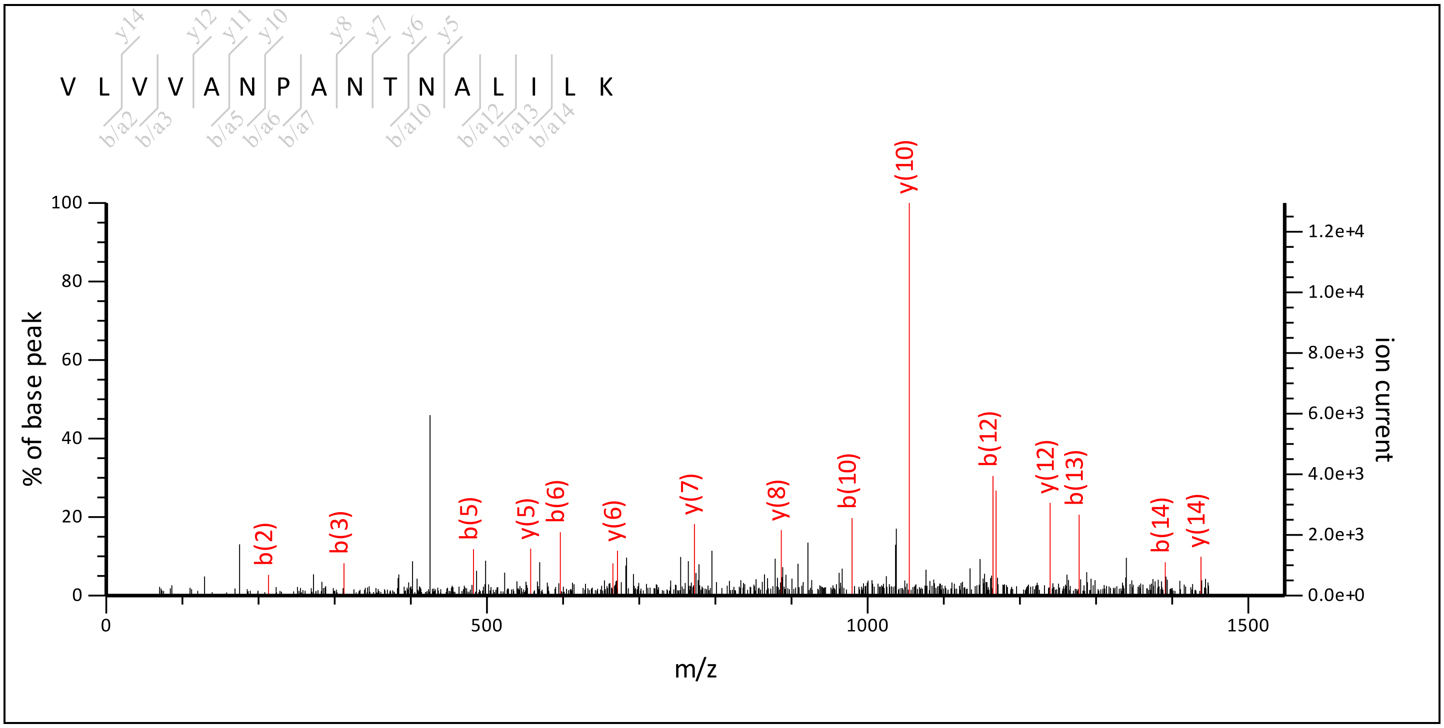
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 60**

MS/MS Fragmentation of **VLVVANPANTNALILK**
Found in **gi|15982948** in **NCBInr**, NAD-dependent malate dehydrogenase [Prunus persica]

Match to Query 207: 1649.011524 from(1650.018800,1+) intensity(0.0000) index(19)
Title: Label: E10, Spot_Id: 219822, Peak_List_Id: 226722, MSMS Job_Run_Id: 21854, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E10_136859948400.txt



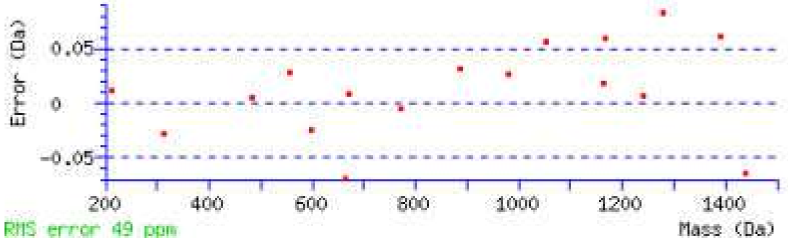
0 to 1547.75

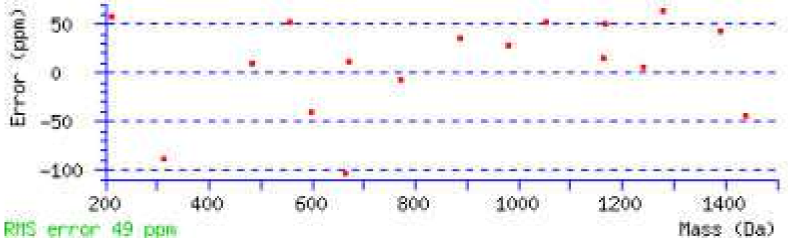
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1648.9876
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 0.0045
Matches : 17/80 fragment ions using 28 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	72.0808		100.0757		**V**			**16**
2	185.1648		*213.1598*		**L**	1550.9265	1533.8999	**15**
3	284.2333		*312.2282*		**V**	*1437.8424*	1420.8158	**14**
4	383.3017		411.2966		**V**	1338.7740	1321.7474	**13**
5	454.3388		*482.3337*		**A**	*1239.7056*	1222.6790	**12**
6	568.3817	551.3552	*596.3766*	579.3501	**N**	*1168.6684*	1151.6419	**11**
7	665.4345	648.4079	693.4294	676.4028	**P**	*1054.6255*	1037.5990	**10**
8	736.4716	719.4450	764.4665	747.4400	**A**	957.5728	940.5462	**9**

9	850.5145	833.4880	878.5094	861.4829	**N**	***886.5356***	869.5091	**8**
10	951.5622	934.5356	***979.5571***	962.5306	**T**	***772.4927***	755.4662	**7**
11	1065.6051	1048.5786	1093.6000	1076.5735	**N**	***671.4450***	654.4185	**6**
12	1136.6422	1119.6157	***1164.6371***	1147.6106	**A**	***557.4021***	540.3756	**5**
13	1249.7263	1232.6997	***1277.7212***	1260.6947	**L**	486.3650	469.3384	**4**
14	1362.8104	1345.7838	***1390.8053***	1373.7787	**I**	373.2809	356.2544	**3**
15	1475.8944	1458.8679	1503.8893	1486.8628	**L**	260.1969	243.1703	**2**
16					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.6	1648.9876	0.0240	VLVVANPANTNALILK
17.9	1648.9875	0.0240	EKDLQQLILLPAIR
17.2	1648.9121	0.0994	LTGAALRTAQANGLHR
16.8	1649.0240	-0.0124	LTGPLNLLVLLTGIGR
16.4	1648.9413	0.0702	LVRIDLLIESWHR
14.8	1648.9624	0.0491	LVLTAAGQTLLSHAVR
14.6	1648.9736	0.0379	STLALGLALSAARLHR
14.4	1648.9261	0.0855	KDITVPVTISNHLGR
14.3	1648.8494	0.1621	VDASIMFNLIEELR
13.5	1648.8896	0.1219	VLVVGSGAAEAAEALHR

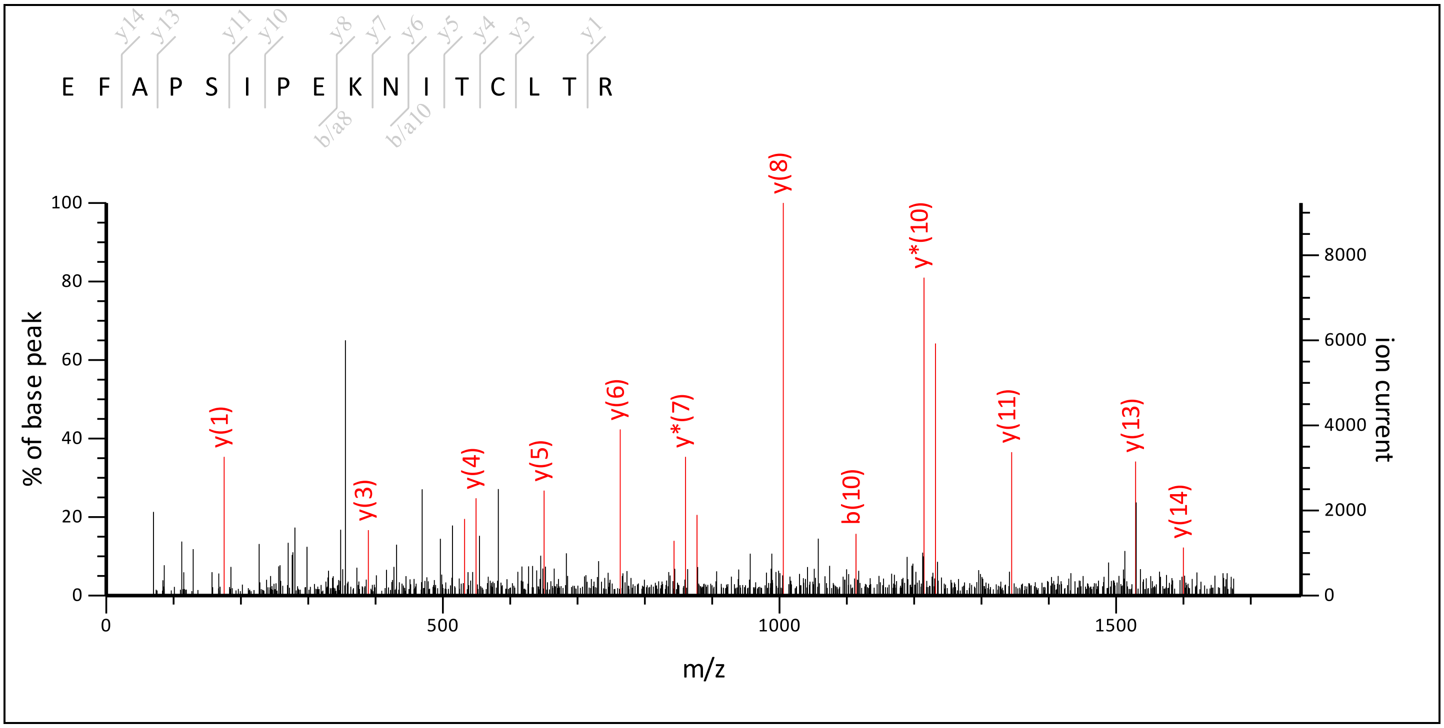
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 60

MS/MS Fragmentation of **EFAPSIPEKNITCLTR**
Found in **gi|15982948** in **NCBInr**, NAD-dependent malate dehydrogenase [Prunus persica]

Match to Query 242: 1875.006224 from(1876.013500,1+) intensity(0.0000) index(23)
Title: Label: E10, Spot_Id: 219822, Peak_List_Id: 226718, MSMS Job_Run_Id: 21854, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E10_136859948400.txt



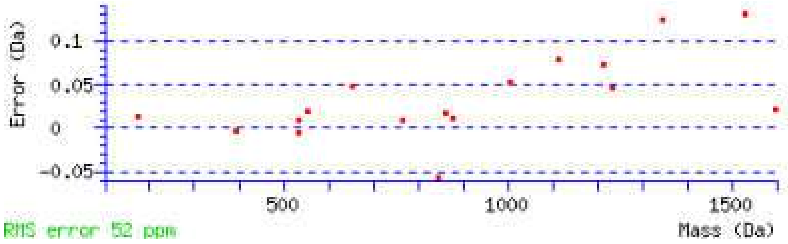
0 to 1774.59

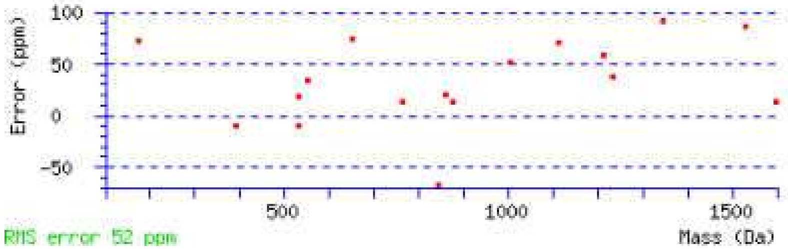
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1874.9560
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 0.013
Matches : 17/74 fragment ions using 34 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	102.0550		130.0499		E			16
2	249.1234		277.1183		F	1746.9207	1729.8942	15
3	320.1605		348.1554		A	***1599.8523***	1582.8258	14
4	417.2132		445.2082		P	***1528.8152***	1511.7886	13
5	504.2453		**532.2402**		S	1431.7624	1414.7359	12
6	617.3293		645.3243		I	***1344.7304***	1327.7038	11
7	714.3821		742.3770		P	***1231.6463***	1214.6198	10
8	843.4247		871.4196		E	1134.5936	1117.5670	9

9	971.5197	954.4931	999.5146	982.4880	K	***1005.5510***	988.5244	8
10	1085.5626	1068.5360	**1113.5575**	1096.5310	N	***877.4560***	860.4295	7
11	1198.6466	1181.6201	1226.6416	1209.6150	I	***763.4131***	746.3865	6
12	1299.6943	1282.6678	1327.6892	1310.6627	T	***650.3290***	633.3025	5
13	1459.7250	1442.6984	1487.7199	1470.6933	C	***549.2813***	532.2548	4
14	1572.8090	1555.7825	1600.8040	1583.7774	L	***389.2507***	372.2241	3
15	1673.8567	1656.8302	1701.8516	1684.8251	T	276.1666	259.1401	2
16					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.2	1874.9560	0.0502	EFAPSIPEKNITCLTR
25.1	1874.9309	0.0753	EFAPSIPDRNVTCLTR
16.5	1874.9117	0.0945	MSESPLLILEQAMEER
15.4	1874.9958	0.0105	MSDMVNINKLILVTER
13.4	1874.8330	0.1732	VPWNDVCQQSTGGSGQR
13.1	1874.9962	0.0100	TAEAARGTLQNGLTVAFR
11.2	1874.9407	0.0655	LENAEISNIEITCTIR
10.4	1874.9295	0.0767	MSEPSAESTLLLEIEAR
10.1	1874.8985	0.1077	MSVYFNEGANTKYVPR
9.9	1874.9519	0.0543	ALMKANEILETQSSNAR

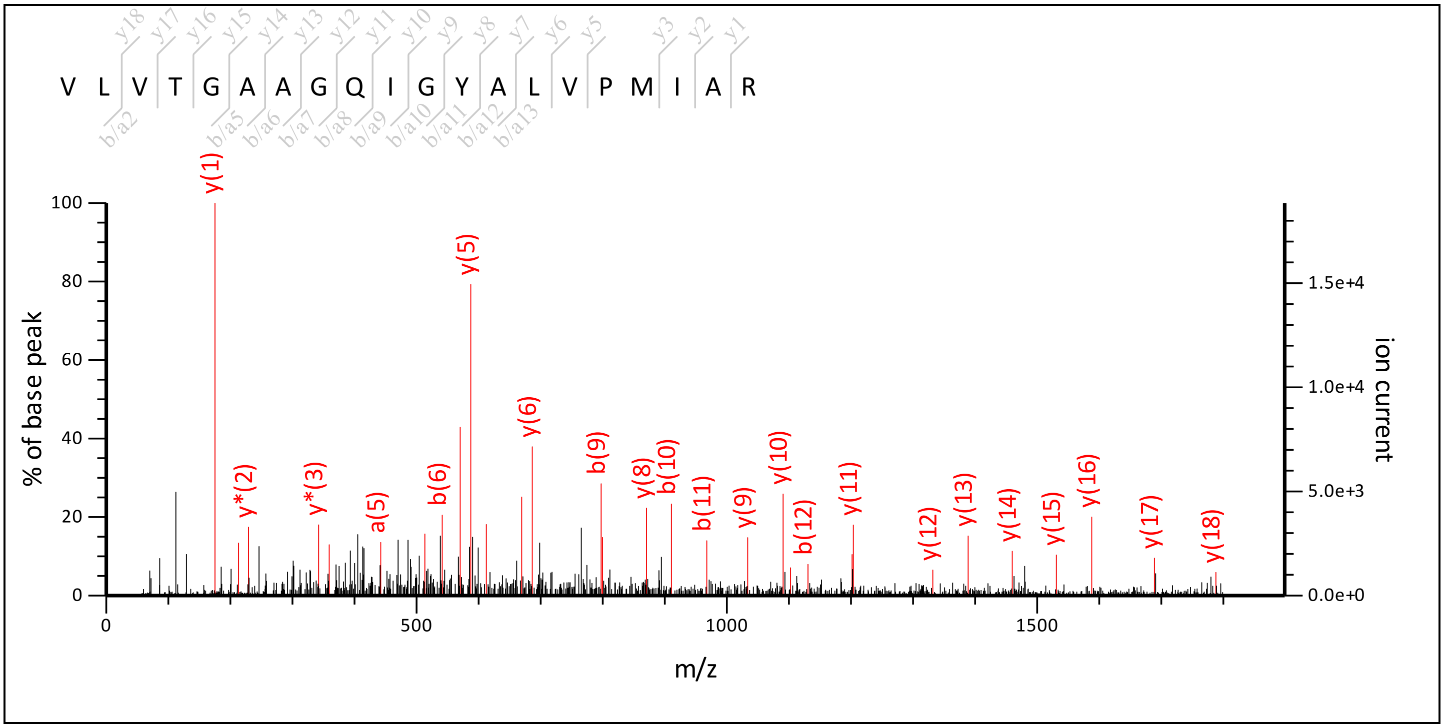
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 60

MS/MS Fragmentation of **VLVTGAAGQIGYALVPMIAR**
Found in **gi|15982948** in **NCBInr**, NAD-dependent malate dehydrogenase [Prunus persica]

Match to Query 254: 1999.182624 from(2000.189900,1+) intensity(0.0000) index(25)
Title: Label: E10, Spot_Id: 219822, Peak_List_Id: 226717, MSMS Job_Run_Id: 21854, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E10_136859948400.txt



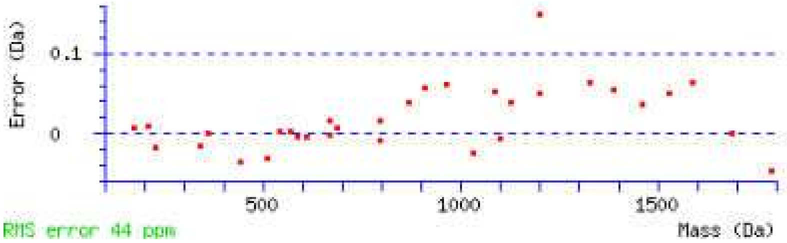
0 to 1898.85

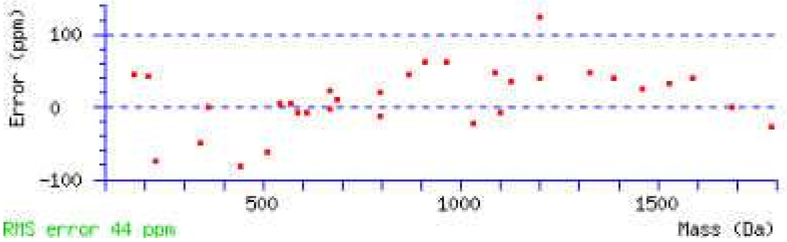
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1999.1288
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 117 **Expect:** 2.9e-08
Matches : 32/98 fragment ions using 54 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	72.0808		100.0757		**V**			**20**
2	185.1648		**213.1598**		**L**	1901.0677	1884.0412	**19**
3	284.2333		312.2282		**V**	***1787.9837***	1770.9571	**18**
4	385.2809		413.2758		**T**	***1688.9152***	1671.8887	**17**
5	**442.3024**		470.2973		**G**	***1587.8676***	1570.8410	**16**
6	**513.3395**		**541.3344**		**A**	***1530.8461***	1513.8195	**15**
7	584.3766		**612.3715**		**A**	***1459.8090***	1442.7824	**14**
8	641.3981		**669.3930**		**G**	***1388.7719***	1371.7453	**13**

9	769.4567	752.4301	797.4516	780.4250	Q	1331.7504	1314.7239	12
10	882.5407	865.5142	910.5356	893.5091	I	1203.6918	1186.6653	11
11	939.5622	922.5356	967.5571	950.5306	G	1090.6078	1073.5812	10
12	1102.6255	1085.5990	1130.6204	1113.5939	Y	1033.5863	1016.5598	9
13	1173.6626	1156.6361	1201.6576	1184.6310	A	870.5230	853.4964	8
14	1286.7467	1269.7202	1314.7416	1297.7151	L	799.4859	782.4593	7
15	1385.8151	1368.7886	1413.8100	1396.7835	V	686.4018	669.3752	6
16	1482.8679	1465.8413	1510.8628	1493.8362	P	587.3334	570.3068	5
17	1613.9084	1596.8818	1641.9033	1624.8767	M	490.2806	473.2541	4
18	1726.9924	1709.9659	1754.9873	1737.9608	I	359.2401	342.2136	3
19	1798.0295	1781.0030	1826.0245	1808.9979	A	246.1561	229.1295	2
20					R	175.1190	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
117.2	1999.1288	0.0538	VLVTGAAGQIGYAIVPMIAR
117.2	1999.1288	0.0538	VLVTGAAGQIGYALVPMIAR
35.3	1999.0521	0.1306	LVSLQQQIASQGGIVMDGR
24.8	1999.1327	0.0499	VRVDAAQGLLHADLGVPLR
24.0	1999.1037	0.0790	NLLAEAGKLAKPGMLGFGGR
22.1	1999.1024	0.0803	IVVDSVLAIGILDQLMER
22.0	1999.1288	0.0538	EKVIASIVHLLQVTFMR
20.9	1999.1215	0.0612	VSVAALAGQGLVAVAKDAFGR
20.9	1999.1003	0.0823	VVAITGAGQGIGLAAAWAFAR
19.2	1999.0963	0.0863	DAVAALKQHGVDSVLIAHR

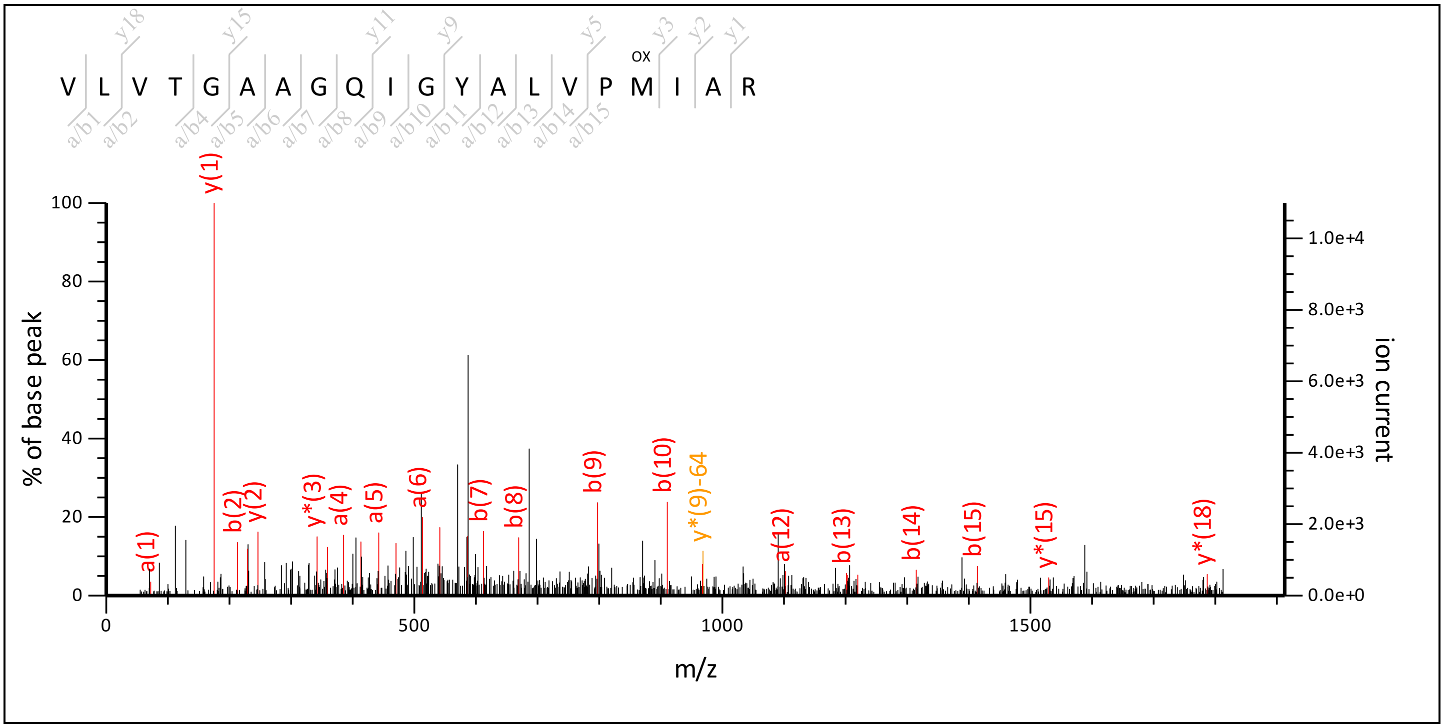
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 60

MS/MS Fragmentation of **VLVTGAAGQIGYALVPMIAR**
Found in **gi|15982948** in **NCBInr**, NAD-dependent malate dehydrogenase [Prunus persica]

Match to Query 256: 2015.162524 from(2016.169800,1+) intensity(0.0000) index(26)
Title: Label: E10, Spot_Id: 219822, Peak_List_Id: 226720, MSMS Job_Run_Id: 21854, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E10_136859948400.txt



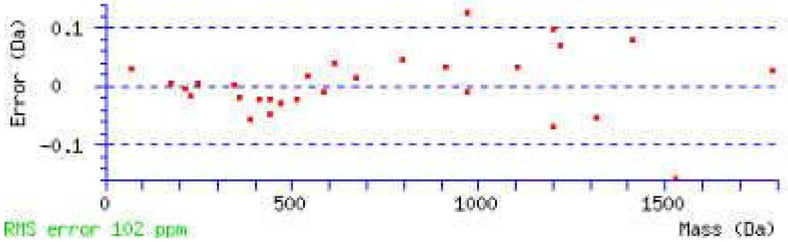
0 to 1912.69

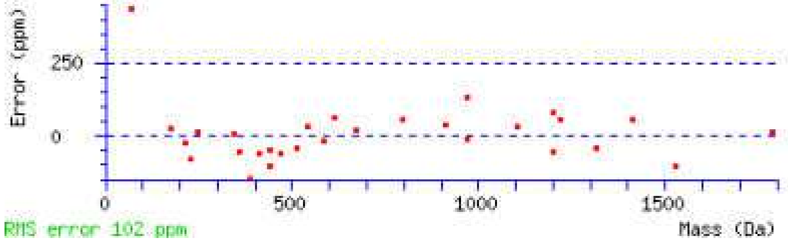
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2015.1238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 **Expect:** 4.1
Matches : 29/142 fragment ions using 90 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**72.0808**		100.0757		**V**			**20**
2	185.1648		***213.1598***		**L**	1917.0626	1900.0361	**19**
3	284.2333		312.2282		**V**	1803.9786	1786.9520	**18**
4	**385.2809**		***413.2758***		**T**	1704.9102	1687.8836	**17**
5	**442.3024**		***470.2973***		**G**	1603.8625	1586.8359	**16**
6	**513.3395**		***541.3344***		**A**	1546.8410	1529.8145	**15**
7	584.3766		***612.3715***		**A**	1475.8039	1458.7774	**14**

8	641.3981		***669.3930***		**G**	1404.7668	1387.7402	**13**
9	769.4567	752.4301	***797.4516***	780.4250	**Q**	1347.7453	1330.7188	**12**
10	882.5407	865.5142	***910.5356***	893.5091	**I**	**1219.6867**	1202.6602	**11**
11	939.5622	922.5356	***967.5571***	950.5306	**G**	1106.6027	1089.5761	**10**
12	**1102.6255**	1085.5990	1130.6204	1113.5939	**Y**	1049.5812	1032.5547	**9**
13	1173.6626	1156.6361	***1201.6576***	1184.6310	**A**	886.5179	869.4913	**8**
14	1286.7467	1269.7202	***1314.7416***	1297.7151	**L**	815.4808	798.4542	**7**
15	1385.8151	1368.7886	***1413.8100***	1396.7835	**V**	702.3967	685.3702	**6**
16	1482.8679	1465.8413	1510.8628	1493.8362	**P**	603.3283	586.3017	**5**
17	1629.9033	1612.8767	1657.8982	1640.8716	**M**	506.2755	489.2490	**4**
18	1742.9873	1725.9608	1770.9823	1753.9557	**I**	**359.2401**	342.2136	**3**
19	1814.0245	1796.9979	1842.0194	1824.9928	**A**	**246.1561**	229.1295	**2**
20					**R**	**175.1190**	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.8	2015.1238	0.0388	VLVTGAAGQIGYAIVPMIAR
36.8	2015.1238	0.0388	VLVTGAAGQIGYALVPMIAR
14.8	2015.0795	0.0831	LMLLDAAKLPAIVEEMAR
12.5	2015.1415	0.0210	ILVSGKVLSPSELQLNYR
12.1	2015.1098	0.0527	AFTCQLAVLAALAVGAGRAR
10.4	2015.0575	0.1050	QAALDELSDYIPIIEVAR
9.1	2015.1891	-0.0266	LSDAGLAKVAAHPVLSVVLR
8.9	2015.0470	0.1156	VSSAVLAGGRPDTAMVIAER
8.8	2015.0800	0.0826	GTKFSSNVNNGLIPVEIAR
8.6	2015.0874	0.0752	IDAFADLMRPLGLIDIAR

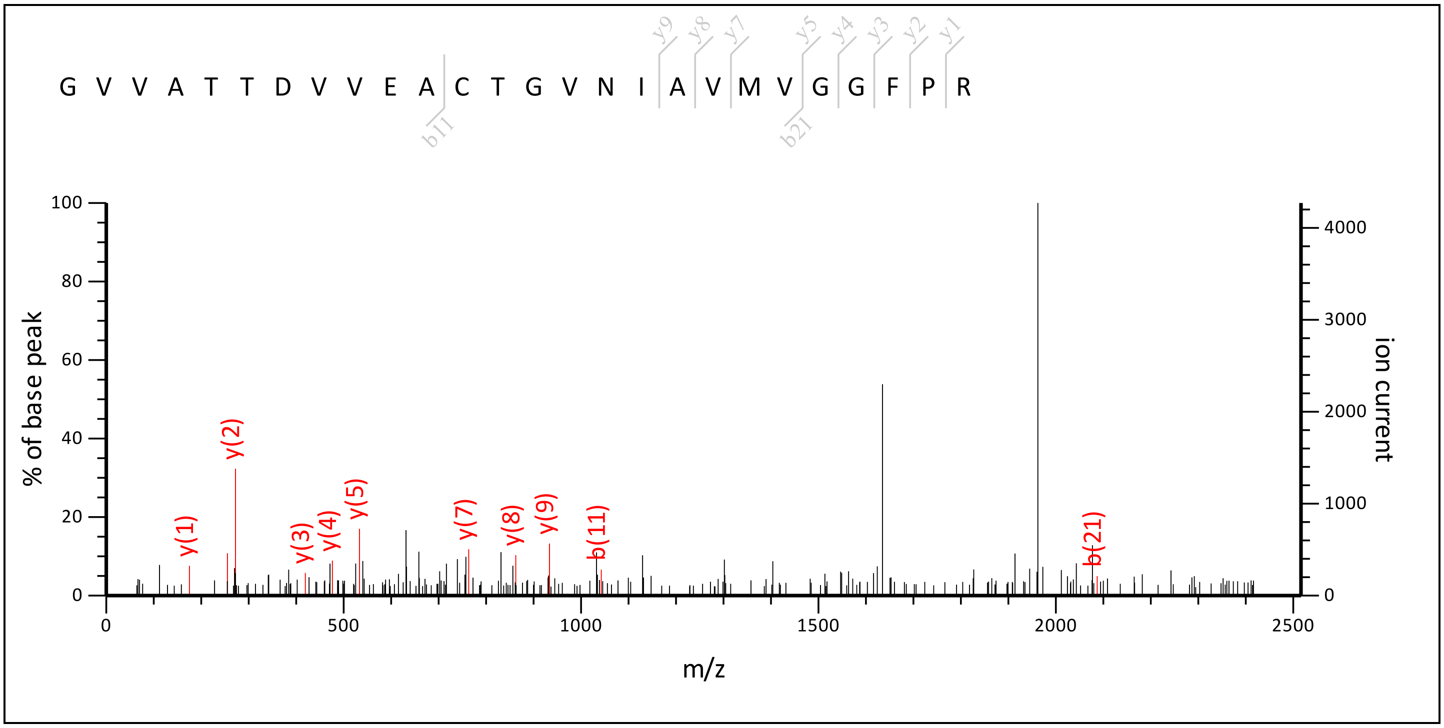
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 60

MS/MS Fragmentation of **GVVATTDVVEACTGVNIAVMVGGFPR**
Found in **gi|15982948** in **NCBInr**, NAD-dependent malate dehydrogenase [Prunus persica]

Match to Query 291: 2618.380924 from(2619.388200,1+) intensity(0.0000) index(33)
Title: Label: E10, Spot_Id: 219822, Peak_List_Id: 226731, MSMS Job_Run_Id: 21854, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E10_136859948400.txt



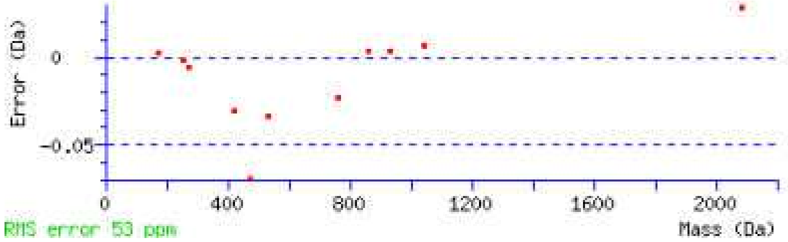
0 to 2516.29

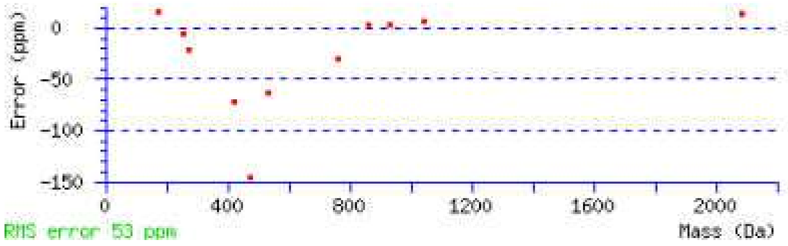
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2618.3197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 10 **Expect:** 1.8e+03
Matches : 11/120 fragment ions using 48 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		**G**			**26**
2	129.1022		157.0972		**V**	2562.3055	2545.2789	**25**
3	228.1707		256.1656		**V**	2463.2370	2446.2105	**24**
4	299.2078		327.2027		**A**	2364.1686	2347.1421	**23**
5	400.2554		428.2504		**T**	2293.1315	2276.1050	**22**
6	501.3031		529.2980		**T**	2192.0838	2175.0573	**21**
7	616.3301		644.3250		**D**	2091.0362	2074.0096	**20**
8	715.3985		743.3934		**V**	1976.0092	1958.9827	**19**

9	814.4669		842.4618		V	1876.9408	1859.9143	18
10	943.5095		971.5044		E	1777.8724	1760.8458	17
11	1014.5466		1042.5415		A	1648.8298	1631.8032	16
12	1174.5773		1202.5722		C	1577.7927	1560.7661	15
13	1275.6249		1303.6198		T	1417.7620	1400.7355	14
14	1332.6464		1360.6413		G	1316.7144	1299.6878	13
15	1431.7148		1459.7097		V	1259.6929	1242.6663	12
16	1545.7577	1528.7312	1573.7527	1556.7261	N	1160.6245	1143.5979	11
17	1658.8418	1641.8153	1686.8367	1669.8102	I	1046.5815	1029.5550	10
18	1729.8789	1712.8524	1757.8738	1740.8473	A	*933.4975*	916.4709	9
19	1828.9473	1811.9208	1856.9422	1839.9157	V	*862.4604*	845.4338	8
20	1959.9878	1942.9613	1987.9827	1970.9562	M	*763.3920*	746.3654	7
21	2059.0562	2042.0297	2087.0511	2070.0246	V	632.3515	615.3249	6
22	2116.0777	2099.0511	2144.0726	2127.0461	G	*533.2831*	516.2565	5
23	2173.0992	2156.0726	2201.0941	2184.0675	G	*476.2616*	459.2350	4
24	2320.1676	2303.1410	2348.1625	2331.1359	F	*419.2401*	402.2136	3
25	2417.2203	2400.1938	2445.2152	2428.1887	P	*272.1717*	255.1452	2
26					R	*175.1190*	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.2	2618.3197	0.0612	GIVATTDVVEACTGVNVAVMVGGFPR
45.0	2618.3197	0.0612	GIVATTDVAEACKGVDVAVMVGGFPR
10.1	2618.3197	0.0612	GVVATTDVVEACTGVNIAVMVGGFPR
7.1	2618.3275	0.0535	WKETLTTALQEHAAANPLAPGMPR
3.5	2618.2040	0.1769	QVGVSCASGLQVWGDVVLCCDGPR

2.7	2618.3309	0.0500	NIGCDIVMIDVNQDVAGFITRLR
2.4	2618.2395	0.1414	MLASGGDDDTVILWDLSDRDRPR
1.2	2618.2283	0.1527	TLCDAGYHVSLETSGALDVSGVDPR
1.2	2618.2039	0.1770	TMLALQSHNMTAWLGSESQNMPR
1.1	2618.2567	0.1242	IASALECSTAVLMSEAESQLAAAAQP

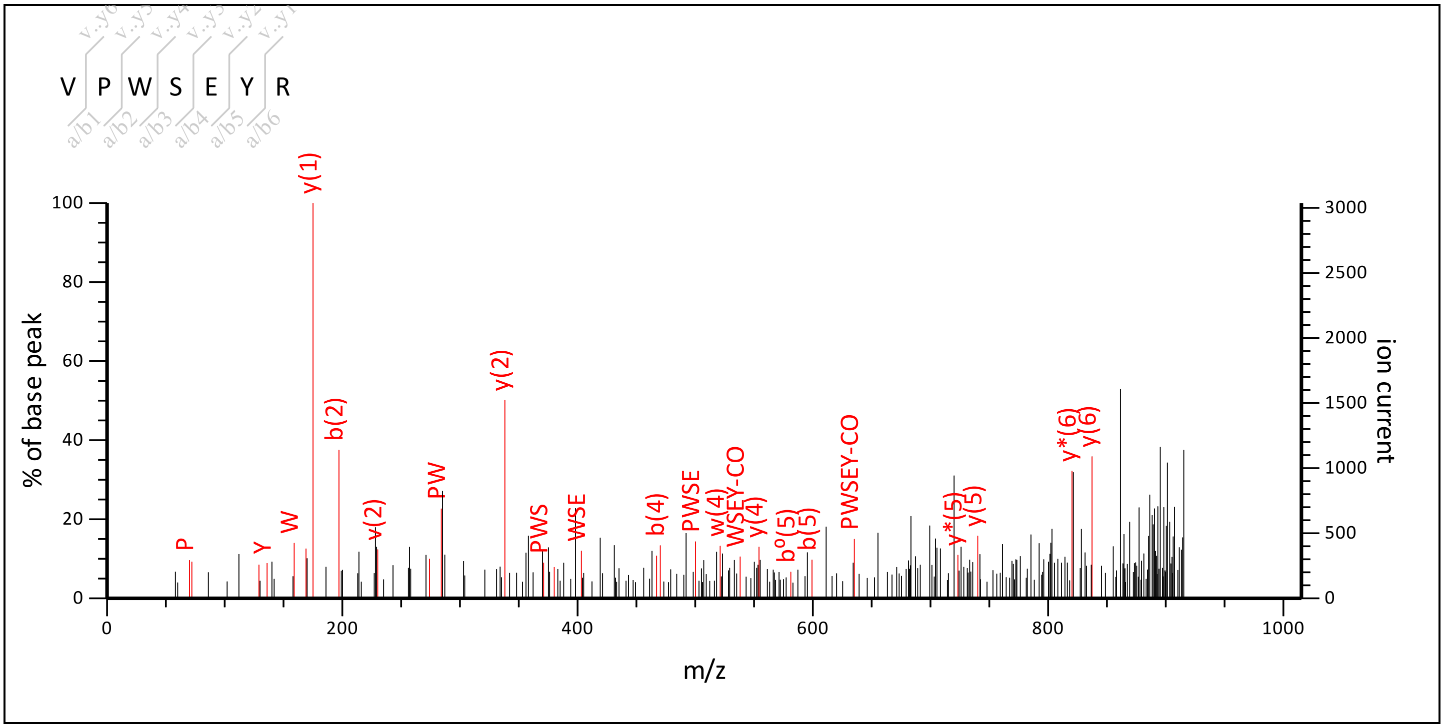
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 64

MS/MS Fragmentation of **VPWSEYR**
Found in **gi|29468084** in **NCBInr**, aspartate aminotransferase [Oryza sativa]

Match to Query 13: 935.521044 from(936.528320,1+) intensity(0.0000) index(2)
Title: Label: K7, Spot_Id: 228948, Peak_List_Id: 257615, MSMS Job_Run_Id: 24928, Comment:
Data file ppw_K7_138985140200.txt



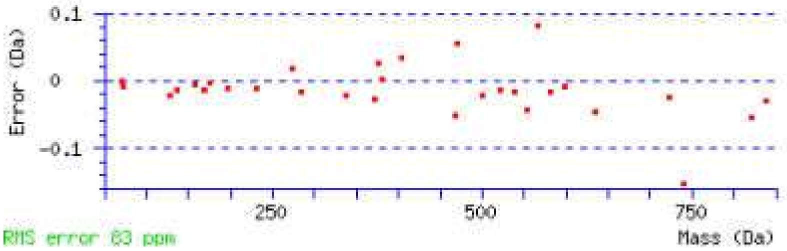
0 to 1015.32

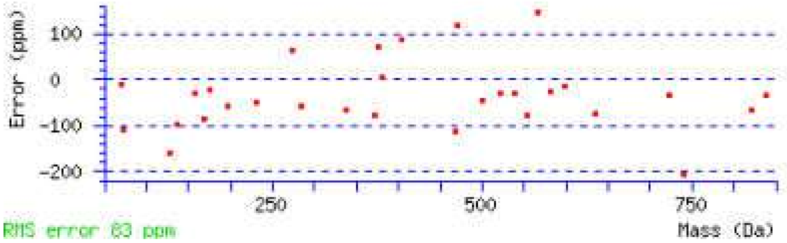
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 935.4501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 29
Matches : 31/75 fragment ions using 90 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	**72.0808**		100.0757		44.0495	**V**						7
2	70.0651	**169.1335**		**197.1285**		143.1179	**P**	795.3420	794.3468	***837.3890***	820.3624	819.3784	6
3	159.0917	355.2129		383.2078			**W**	609.2627		***740.3362***	723.3097	722.3257	5
4	60.0444	442.2449	424.2343	**470.2398**	452.2292	426.2500	**S**	522.2307	521.2354	***554.2569***	537.2304	536.2463	4
5	102.0550	571.2875	553.2769	**599.2824**	581.2718	513.2820	**E**	393.1881	392.1928	***467.2249***	450.1983	449.2143	3
6	136.0757	734.3508	716.3402	762.3457	744.3352		**Y**	230.1248		***338.1823***	321.1557		2
7	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PW	256.1444	284.1394	**PWS**	343.1765	371.1714	**PWSE**	472.2191	500.2140
PWSEY	635.2824	663.2773	**WS**	246.1237	274.1186	**WSE**	375.1663	403.1612
WSEY	538.2296	566.2245	**SE**	189.0870	217.0819	**SEY**	352.1503	380.1452
EY	265.1183	293.1132						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.0	935.4501	0.0709	VPWSEYR
17.1	935.5262	-0.0052	VILCIYR
17.1	935.5076	0.0134	VLIDTGYR
13.0	935.4712	0.0498	DLFSAEVR
12.3	935.5076	0.0134	DLIKEYR
12.3	935.5076	0.0134	DLLKEYR
10.7	935.5188	0.0022	VKNASVYR
10.6	935.4825	0.0386	AANTYIAGR
10.3	935.4825	0.0386	EVHAEPVR
10.2	935.4865	0.0345	VPPASFYR

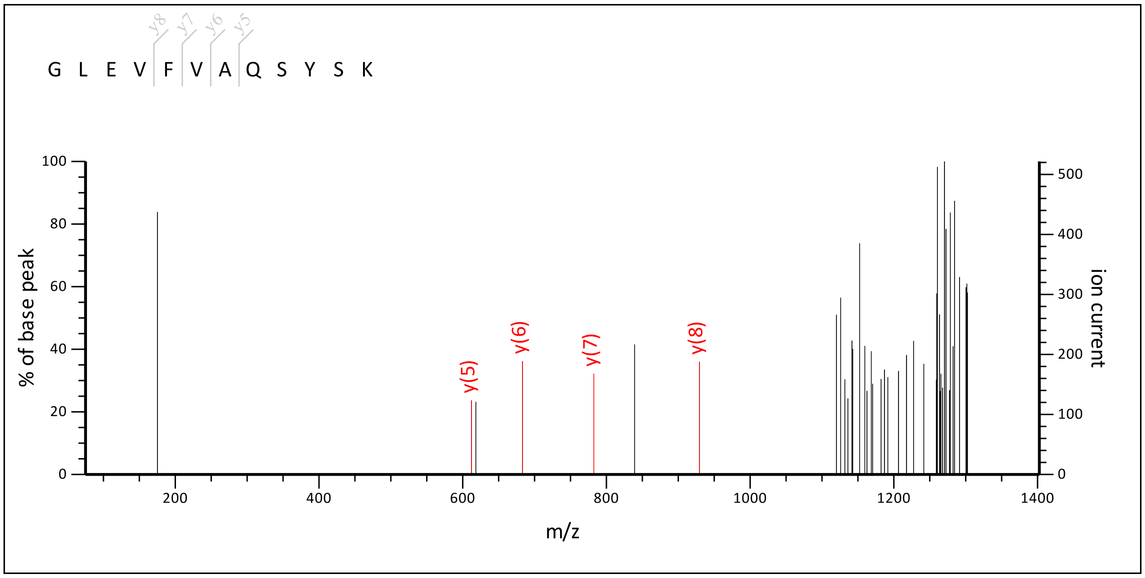
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 64

MS/MS Fragmentation of **GLEVFVAQSYSK**
Found in **gi|29468084** in **NCBInr**, aspartate aminotransferase [Oryza sativa]

Match to Query 45: 1326.763924 from(1327.771200,1+) intensity(0.0000) index(10)
Title: Label: K7, Spot_Id: 228948, Peak_List_Id: 257625, MSMS Job_Run_Id: 24928, Comment:
Data file ppw_K7_138985140200.txt



75.1 to 1402.47

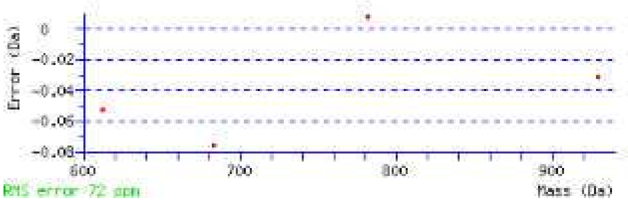
Label all possible matches ○ Label matches used for scoring ●

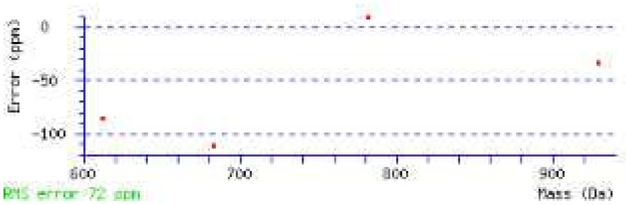
Monoisotopic mass of neutral peptide Mr(calc): 1326.6820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 7 **Expect:** 3.9e+02
Matches : 4/189 fragment ions using 13 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	30.0338	30.0338			58.0287			44.0495	G						12
2	86.0964	143.1179			171.1128			101.0709	L	1212.5895	1211.5943	1270.6678	1253.6412	1252.6572	11
3	102.0550	272.1605		254.1499	300.1554		282.1448	214.1550	E	1083.5469	1082.5517	1157.5837	1140.5572	1139.5732	10
4	72.0808	371.2289		353.2183	399.2238		381.2132	357.2132	V	984.4785	997.4989	1028.5411	1011.5146	1010.5306	9
5	120.0808	518.2973		500.2867	546.2922		528.2817		F	837.4101		***929.4727***	912.4462	911.4621	8
6	72.0808	617.3657		599.3552	645.3606		627.3501	603.3501	V	738.3417	751.3621	***782.4043***	765.3777	764.3937	7
7	44.0495	688.4028		670.3923	716.3978		698.3872		A	667.3046		***683.3359***	666.3093	665.3253	6
8	101.0709	816.4614	799.4349	798.4509	844.4563	827.4298	826.4458	759.4400	Q	539.2460	538.2508	***612.2988***	595.2722	594.2882	5
9	60.0444	903.4934	886.4669	885.4829	931.4884	914.4618	913.4778	887.4985	S	452.2140	451.2187	484.2402	467.2136	466.2296	4
10	136.0757	1066.5568	1049.5302	1048.5462	1094.5517	1077.5251	1076.5411		Y	289.1506		397.2082	380.1816	379.1976	3
11	60.0444	1153.5888	1136.5623	1135.5782	1181.5837	1164.5572	1163.5732	1137.5939	S	202.1186	201.1234	234.1448	217.1183	216.1343	2
12	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LE	215.1390	243.1339	LEV	314.2074	342.2023	LEVF	461.2758	489.2708
LEVFV	560.3443	588.3392	LEVFVA	631.3814	659.3763	EV	201.1234	229.1183
EVF	348.1918	376.1867	EVFV	447.2602	475.2551	EVFVA	518.2973	546.2922
EVFVAQ	646.3559	674.3508	VF	219.1492	247.1441	VFV	318.2176	346.2125
VFVA	389.2547	417.2496	VFVAQ	517.3133	545.3082	VFVAQS	604.3453	632.3402

FV	219.1492	247.1441	**FVA**	290.1863	318.1812	**FVAQ**	418.2449	446.2398
FVAQS	505.2769	533.2718	**FVAQSY**	668.3402	696.3352	**VA**	143.1179	171.1128
VAQ	271.1765	299.1714	**VAQS**	358.2085	386.2034	**VAQSY**	521.2718	549.2667
VAQSYS	608.3039	636.2988	**AQ**	172.1081	200.1030	**AQS**	259.1401	287.1350
AQSY	422.2034	450.1983	**AQSYS**	509.2354	537.2304	**QS**	188.1030	216.0979
QSY	351.1663	379.1612	**QSYS**	438.1983	466.1932	**SY**	223.1077	251.1026
SYS	310.1397	338.1347	**YS**	223.1077	251.1026			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
7.8	1326.6602	0.1038	DSVRVMNLYSK
7.8	1326.6979	0.0660	KVFNRPPPGCR
7.5	1326.6503	0.1136	VMGNLPARFGEH
7.2	1326.6826	0.0813	MATAAPPAASGARR
7.2	1326.6640	0.0999	VGASSSVGHDGAKR
6.7	1326.6820	0.0820	GLEVFVAQSYSK
6.3	1326.6317	0.1323	GGLGFGSNVYNSR
5.8	1326.7408	0.0231	IADVLKASFAHR
5.8	1326.7520	0.0119	VLWRGAGLAQTR
5.6	1326.6891	0.0748	VALEAQVQARNE

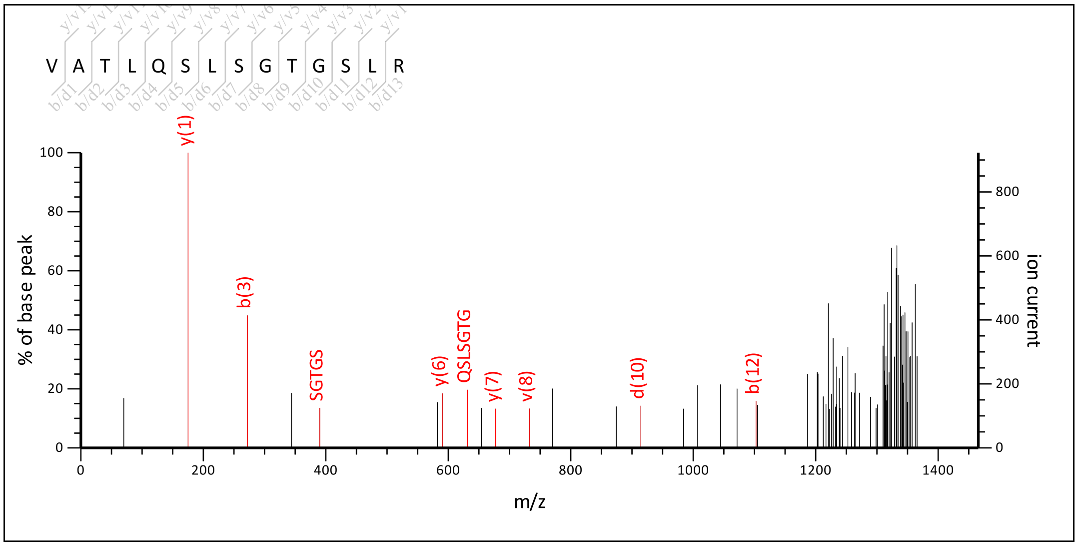
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 64

MS/MS Fragmentation of **VATLQSLSGTGSLR**
Found in **gi|29468084** in **NCBInr**, aspartate aminotransferase [Oryza sativa]

Match to Query 54: 1388.883824 from(1389.891100,1+) intensity(0.0000) index(13)
Title: Label: K7, Spot_Id: 228948, Peak_List_Id: 257621, MSMS Job_Run_Id: 24928, Comment:
Data file ppw_K7_138985140200.txt



0 to 1465.57

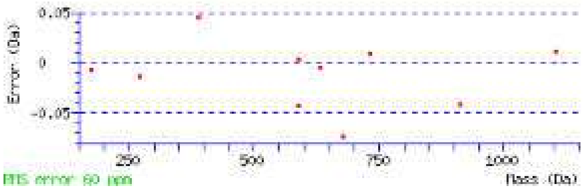
Label all possible matches ○ Label matches used for scoring ●

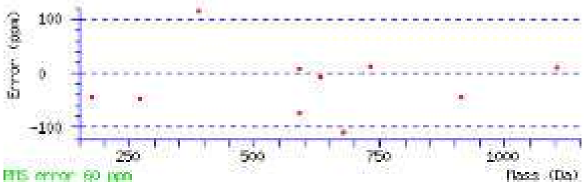
Monoisotopic mass of neutral peptide Mr(calc): 1388.7623
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 8 **Expect:** 1.1e+02
Matches : 10/255 fragment ions using 20 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	44.0495	143.1179			171.1128					A	1274.6699			1290.7012	1273.6747
3	74.0600	244.1656		226.1550	***272.1605***		254.1499	228.1707	230.1499	T	1173.6222	1186.6426	1188.6219	1219.6641	1202.6375
4	86.0964	357.2496		339.2391	385.2445		367.2340	315.2027		L	1060.5382	1059.5429		1118.6164	1101.5899
5	101.0709	485.3082	468.2817	467.2976	513.3031	496.2766	495.2926	428.2867		Q	932.4796	931.4843		1005.5323	988.5058
6	60.0444	572.3402	555.3137	554.3297	600.3352	583.3086	582.3246	556.3453		S	845.4476	844.4523		877.4738	860.4472
7	86.0964	685.4243	668.3978	667.4137	713.4192	696.3927	695.4087	643.3774		L	732.3635	731.3682		790.4417	773.4152
8	60.0444	772.4563	755.4298	754.4458	800.4512	783.4247	782.4407	756.4614		S	645.3315	644.3362		***677.3577***	660.3311
9	30.0338	829.4778	812.4512	811.4672	857.4727	840.4462	839.4621			G				***590.3257***	573.2991
10	74.0600	930.5255	913.4989	912.5149	958.5204	941.4938	940.5098	914.5306	916.5098	T	487.2623	500.2827	502.2620	533.3042	516.2776
11	30.0338	987.5469	970.5204	969.5364	1015.5419	998.5153	997.5313			G				432.2565	415.2300
12	60.0444	1074.5790	1057.5524	1056.5684	***1102.5739***	1085.5473	1084.5633	1058.5841		S	343.2088	342.2136		375.2350	358.2085
13	86.0964	1187.6630	1170.6365	1169.6525	1215.6579	1198.6314	1197.6474	1145.6161		L	230.1248	229.1295		288.2030	271.1765
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AT	145.0972	173.0921	ATL	258.1812	286.1761	ATLQ	386.2398	414.2347
ATLQS	473.2718	501.2667	ATLQSL	586.3559	614.3508	ATLQSLS	673.3879	701.3828
TL	187.1441	215.1390	TLQ	315.2027	343.1976	TLQS	402.2347	430.2296
TLQSL	515.3188	543.3137	TLQSLS	602.3508	630.3457	TLQSLSG	659.3723	687.3672
LQ	214.1550	242.1499	LQS	301.1870	329.1819	LQSL	414.2711	442.2660
LQSLS	501.3031	529.2980	LQSLSG	558.3246	586.3195	LQSLSGT	659.3723	687.3672

QS	188.1030	216.0979	**QSL**	301.1870	329.1819	**QSLS**	388.2191	416.2140
QSLSG	445.2405	473.2354	**QSLSGT**	546.2882	574.2831	**QSLSGTG**	603.3097	631.3046
QSLSGTGS	690.3417	718.3366	**SL**	173.1285	201.1234	**SLS**	260.1605	288.1554
SLSG	317.1819	345.1769	**SLSGT**	418.2296	446.2245	**SLSGTG**	475.2511	503.2460
SLSGTGS	562.2831	590.2780	**SLSGTGSL**	675.3672	703.3621	**LS**	173.1285	201.1234
LSG	230.1499	258.1448	**LSGT**	331.1976	359.1925	**LSGTG**	388.2191	416.2140
LSGTGS	475.2511	503.2460	**LSGTGSL**	588.3352	616.3301	**SG**	117.0659	145.0608
SGT	218.1135	246.1084	**SGTG**	275.1350	303.1299	**SGTGS**	362.1670	390.1619
SGTGSL	475.2511	503.2460	**GT**	131.0815	159.0764	**GTG**	188.1030	216.0979
GTGS	275.1350	303.1299	**GTGSL**	388.2191	416.2140	**TG**	131.0815	159.0764
TGS	218.1135	246.1084	**TGSL**	331.1976	359.1925	**GS**	117.0659	145.0608
GSL	230.1499	258.1448	**SL**	173.1285	201.1234			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
7.8	1388.7623	0.1215	VATIQSLSGTGSLR
7.8	1388.7623	0.1215	VATLQSLSGTGSLR
7.2	1388.7623	0.1215	SSITIETLRNQK
7.0	1388.7452	0.1386	GLIFQEYLPGPR
7.0	1388.7875	0.0963	SDKSISIIQTGLK
6.9	1388.7565	0.1274	GGRIFVYDLPPR
6.9	1388.7663	0.1175	GVLISVYEEKPR
6.5	1388.7452	0.1386	GSSFPLIPPFATR
6.0	1388.7598	0.1240	LKSFQIQCIPR
6.0	1388.7452	0.1386	VTQFLPAPYTPR

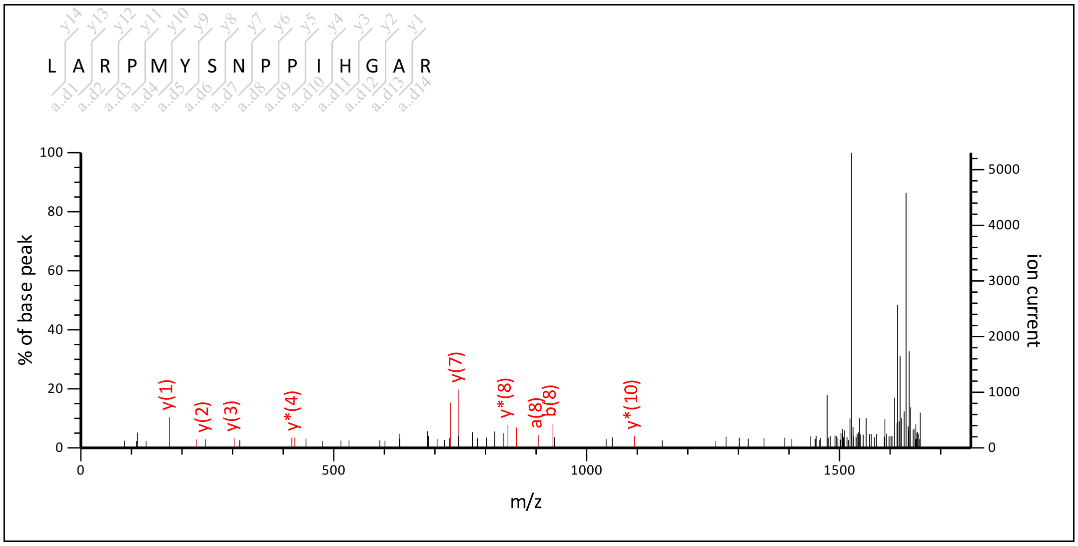
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 64**

MS/MS Fragmentation of **LARPMYSNPPIHGAR**
Found in **gi|29468084** in **NCBInr**, aspartate aminotransferase [Oryza sativa]

Match to Query 73: 1678.996124 from(1680.003400,1+) intensity(0.0000) index(20)
Title: Label: K7, Spot_Id: 228948, Peak_List_Id: 257619, MSMS Job_Run_Id: 24928, Comment:
Data file ppw_K7_138985140200.txt



0 to 1759.61

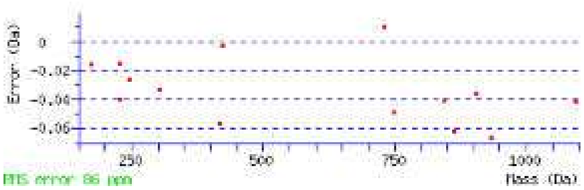
Label all possible matches ○ Label matches used for scoring ●

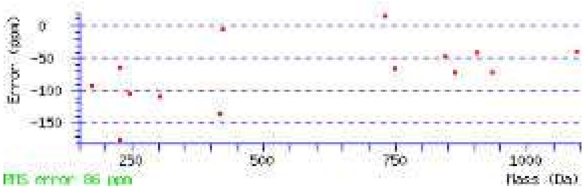
Monoisotopic mass of neutral peptide Mr(calc): 1678.8725
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 8 **Expect:** 1.7e+02
Matches : 14/250 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	86.0964			114.0913			44.0495		**L**						
2	44.0495	157.1335			185.1285					**A**	1550.7645			1566.7958	1549.7692	154
3	129.1135	313.2346	296.2081		341.2296	324.2030		228.1707		**R**	1394.6634	1393.6681		1495.7587	1478.7321	147
4	70.0651	410.2874	393.2609		438.2823	421.2558		384.2718		**P**	1297.6106	1296.6154		1339.6576	1322.6310	132
5	104.0528	541.3279	524.3013		569.3228	552.2963		481.3245		**M**	1166.5701	1165.5749		1242.6048	1225.5783	122
6	136.0757	704.3912	687.3647		732.3861	715.3596				**Y**	1003.5068			1111.5643	1094.5378	109
7	60.0444	791.4233	774.3967	773.4127	819.4182	802.3916	801.4076	775.4283		**S**	916.4748	915.4795		948.5010	931.4744	93
8	87.0553	905.4662	888.4396	887.4556	933.4611	916.4345	915.4505	862.4604		**N**	802.4318	801.4366		***861.4690***	844.4424	
9	70.0651	1002.5189	985.4924	984.5084	1030.5139	1013.4873	1012.5033	976.5033		**P**	705.3791	704.3838		***747.4260***	730.3995	
10	70.0651	1099.5717	1082.5452	1081.5611	1127.5666	1110.5401	1109.5561	1073.5561		**P**	608.3263	607.3311		650.3733	633.3467	
11	86.0964	1212.6558	1195.6292	1194.6452	1240.6507	1223.6241	1222.6401	1184.6245	1198.6401	**I**	495.2423	508.2627	522.2783	553.3205	536.2940	
12	110.0713	1349.7147	1332.6881	1331.7041	1377.7096	1360.6831	1359.6990			**H**	358.1833			440.2364	423.2099	
13	30.0338	1406.7362	1389.7096	1388.7256	1434.7311	1417.7045	1416.7205			**G**				***303.1775***	286.1510	
14	44.0495	1477.7733	1460.7467	1459.7627	1505.7682	1488.7416	1487.7576			**A**	230.1248			***246.1561***	229.1295	
15	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AR	200.1506	228.1455	**ARP**	297.2033	325.1983	**ARPM**	428.2438	456.2387
ARPMY	591.3072	619.3021	**ARPMYS**	678.3392	706.3341	**RP**	226.1662	254.1612
RPM	357.2067	385.2016	**RPMY**	520.2700	548.2650	**RPMYS**	607.3021	635.2970
PM	201.1056	229.1005	**PMY**	364.1689	392.1639	**PMYS**	451.2010	479.1959
PMYSN	565.2439	593.2388	**PMYSNP**	662.2967	690.2916	**MY**	267.1162	295.1111

MYS	354.1482	382.1431	**MYSN**	468.1911	496.1860	**MYSNP**	565.2439	593.2388
MYSNPP	662.2967	690.2916	**YS**	223.1077	251.1026	**YSN**	337.1506	365.1456
YSNP	434.2034	462.1983	**YSNPP**	531.2562	559.2511	**YSNPPI**	644.3402	672.3352
SN	174.0873	202.0822	**SNP**	271.1401	299.1350	**SNPP**	368.1928	396.1878
SNPPI	481.2769	509.2718	**SNPPIH**	618.3358	646.3307	**SNPPIHG**	675.3573	703.3522
NP	184.1081	212.1030	**NPP**	281.1608	309.1557	**NPPI**	394.2449	422.2398
NPPIH	531.3038	559.2987	**NPPIHG**	588.3253	616.3202	**NPPIHGA**	659.3624	687.3573
PP	167.1179	195.1128	**PPI**	280.2020	308.1969	**PPIH**	417.2609	445.2558
PPIHG	474.2823	502.2772	**PPIHGA**	545.3194	573.3144	**PI**	183.1492	211.1441
PIH	320.2081	348.2030	**PIHG**	377.2296	405.2245	**PIHGA**	448.2667	476.2616
IH	223.1553	251.1503	**IHG**	280.1768	308.1717	**IHGA**	351.2139	379.2088
HG	167.0927	195.0877	**HGA**	238.1299	266.1248	**GA**	101.0709	129.0659





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.7	1678.8362	0.1599	RSNCSFWLVGGLGAR
9.8	1678.9114	0.0847	RLLLENPSVGSNGPAR
9.7	1678.8573	0.1388	MVTGDNIHTAKHIAR
9.6	1678.8499	0.1462	RSSSSNHNNIPKPNK
9.2	1678.8322	0.1640	RHVAGAGTPSSAPMGGAR
9.1	1678.8317	0.1644	RIGMSMKPCLELGR
8.9	1678.9036	0.0925	RSTLSTTTTIAIMQR
8.5	1678.8725	0.1236	IARPMYSNPPIHGAR
8.5	1678.8725	0.1236	LARPMYSNPPIHGAR
8.2	1678.8751	0.1210	RGVAVSQSTYTVQQR

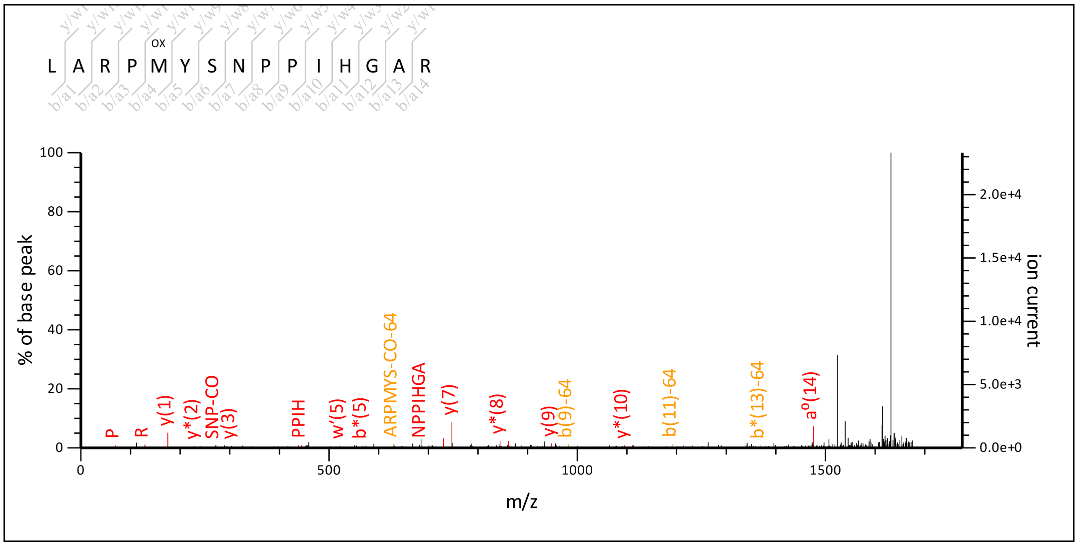
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 64

MS/MS Fragmentation of **LARPMYSNPPIHGAR**
Found in **gi|29468084** in **NCBInr**, aspartate aminotransferase [Oryza sativa]

Match to Query 75: 1694.980024 from(1695.987300,1+) intensity(0.0000) index(21)
Title: Label: K7, Spot_Id: 228948, Peak_List_Id: 257620, MSMS Job_Run_Id: 24928, Comment:
Data file ppw_K7_138985140200.txt



0 to 1775.59

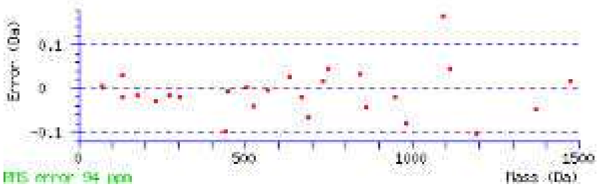
Label all possible matches ○ Label matches used for scoring ●

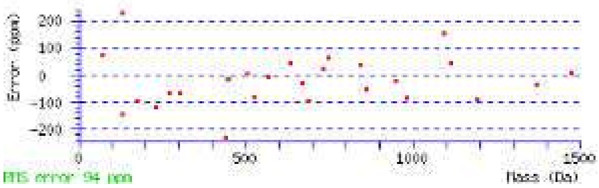
Monoisotopic mass of neutral peptide Mr(calc): 1694.8675
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 13 **Expect:** 82
Matches : 29/365 fragment ions using 77 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	86.0964			114.0913			44.0495		L						
2	44.0495	157.1335			185.1285					A	1502.7611			1518.7924	1501.7659	15
3	129.1135	313.2346	296.2081		341.2296	324.2030		228.1707		R	1346.6600	1345.6648		1447.7553	1430.7288	14
4	70.0651	410.2874	393.2609		**438.2823**	421.2558		384.2718		P	1249.6072	1248.6120		1291.6542	1274.6276	12
5	56.0495	493.3245	476.2980		521.3194	504.2929		481.3245		M	1166.5701	1165.5749		1194.6014	1177.5749	11
6	136.0757	656.3879	639.3613		684.3828	667.3562				Y	1003.5068			***1111.5643***	1094.5378	10
7	60.0444	743.4199	726.3933	725.4093	771.4148	754.3883	753.4042	727.4250		S	916.4748	915.4795		***948.5010***	931.4744	9
8	87.0553	857.4628	840.4363	839.4522	885.4577	868.4312	867.4472	814.4570		N	802.4318	801.4366		***861.4690***	844.4424	
9	70.0651	954.5156	937.4890	936.5050	**982.5105**	965.4839	964.4999	928.4999		P	705.3791	704.3838		***747.4260***	730.3995	
10	70.0651	1051.5683	1034.5418	1033.5578	1079.5633	1062.5367	1061.5527	1025.5527		P	608.3263	607.3311		650.3733	633.3467	
11	86.0964	1164.6524	1147.6259	1146.6418	**1192.6473**	1175.6208	1174.6368	1136.6211	1150.6368	I	495.2423	508.2627	522.2783	553.3205	536.2940	
12	110.0713	1301.7113	1284.6848	1283.7008	1329.7062	1312.6797	1311.6957			H	358.1833			440.2364	423.2099	
13	30.0338	1358.7328	1341.7062	1340.7222	1386.7277	1369.7011	1368.7171			G				***303.1775***	286.1510	
14	44.0495	1429.7699	1412.7433	1411.7593	1457.7648	1440.7383	1439.7542			A	230.1248			246.1561	229.1295	
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AR	200.1506	228.1455	ARP	297.2033	325.1983	ARPM	380.2405	408.2354
ARPMY	543.3038	571.2987	ARPMYS	630.3358	658.3307	RP	226.1662	254.1612
RPM	309.2034	337.1983	RPMY	472.2667	500.2616	RPMYS	559.2987	587.2936
RPMYSN	673.3416	701.3365	PM	153.1022	181.0972	PMY	316.1656	344.1605

PMYS	403.1976	431.1925	**PMYSN**	517.2405	545.2354	**PMYSNP**	614.2933	642.2882
MY	219.1128	247.1077	**MYS**	306.1448	334.1397	**MYSN**	420.1878	448.1827
MYSNP	517.2405	545.2354	**MYSNPP**	614.2933	642.2882	**YS**	223.1077	251.1026
YSN	337.1506	365.1456	**YSNP**	434.2034	462.1983	**YSNPP**	531.2562	559.2511
YSNPPI	644.3402	672.3352	**SN**	174.0873	202.0822	**SNP**	271.1401	299.1350
SNPP	368.1928	396.1878	**SNPPI**	481.2769	509.2718	**SNPPIH**	618.3358	646.3307
SNPPIHG	675.3573	703.3522	**NP**	184.1081	212.1030	**NPP**	281.1608	309.1557
NPPI	394.2449	422.2398	**NPPIH**	531.3038	559.2987	**NPPIHG**	588.3253	616.3202
NPPIHGA	659.3624	687.3573	**PP**	167.1179	195.1128	**PPI**	280.2020	308.1969
PPIH	417.2609	445.2558	**PPIHG**	474.2823	502.2772	**PPIHGA**	545.3194	573.3144
PI	183.1492	211.1441	**PIH**	320.2081	348.2030	**PIHG**	377.2296	405.2245
PIHGA	448.2667	476.2616	**IH**	223.1553	251.1503	**IHG**	280.1768	308.1717
IHGA	351.2139	379.2088	**HG**	167.0927	195.0877	**HGA**	238.1299	266.1248
GA	101.0709	129.0659						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.0	1694.8926	0.0874	RALPHSLNTMVASIW
12.5	1694.8675	0.1126	IARPMYSNPPIHGAR
12.5	1694.8675	0.1126	LARPMYSNPPIHGAR
11.5	1694.9540	0.0260	RTAASGRPLTLPVSNR
11.0	1694.8199	0.1601	GSHGMVYKGVLFNDR
10.0	1694.8886	0.0914	VGESLPLSATHLRCR
10.0	1695.0043	-0.0242	VLDIAAIITRTEKPR
9.7	1694.9540	0.0261	VGAAAILLSNRPSDRR
9.6	1695.0043	-0.0242	RVTEALSSLALPLGLR
9.6	1694.9250	0.0551	RAQLLIHEMAGLTSR

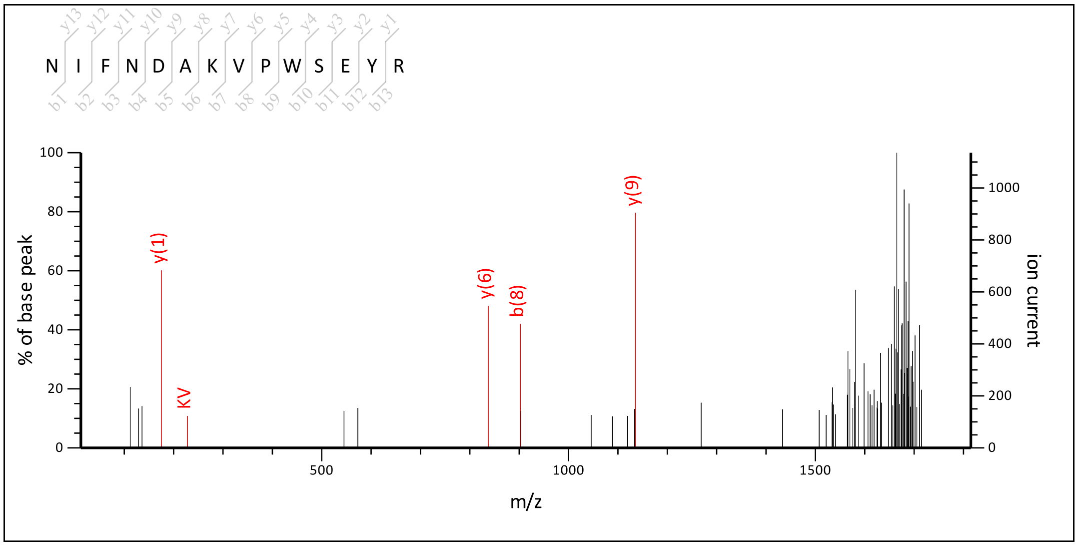
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 64

MS/MS Fragmentation of **NIFNDAKVPWSEYR**
Found in **gi|29468084** in **NCBInr**, aspartate aminotransferase [Oryza sativa]

Match to Query 81: 1737.993624 from(1739.000900,1+) intensity(0.0000) index(23)
Title: Label: K7, Spot_Id: 228948, Peak_List_Id: 257624, MSMS Job_Run_Id: 24928, Comment:
Data file ppw_K7_138985140200.txt



12.09 to 1814.9

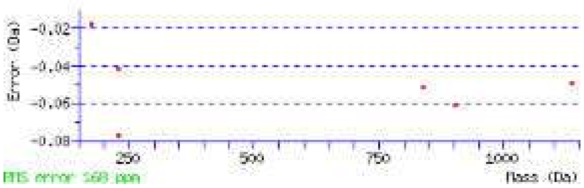
Label all possible matches ○ Label matches used for scoring ●

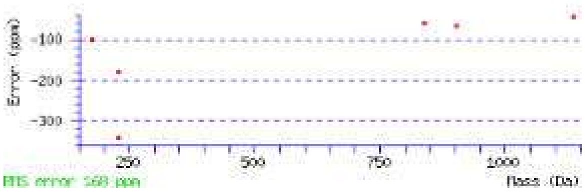
Monoisotopic mass of neutral peptide Mr(calc): 1737.8474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 5 **Expect:** 5.9e+02
Matches : 6/241 fragment ions using 19 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495		N						
2	86.0964	200.1394	183.1128		***228.1343***	211.1077		172.1081	186.1237	I	1566.7336	1579.7540	1593.7696	1624.8118	1607.7853	16
3	120.0808	347.2078	330.1812		375.2027	358.1761				F	1419.6652			1511.7278	1494.7012	14
4	87.0553	461.2507	444.2241		489.2456	472.2191		418.2449		N	1305.6222	1304.6270		1364.6593	1347.6328	13
5	88.0393	576.2776	559.2511	558.2671	604.2726	587.2460	586.2620	532.2878		D	1190.5953	1189.6000		1250.6164	1233.5899	12
6	44.0495	647.3148	630.2882	629.3042	675.3097	658.2831	657.2991			A	1119.5582			***1135.5895***	1118.5629	11
7	101.1073	775.4097	758.3832	757.3991	803.4046	786.3781	785.3941	718.3519		K	991.4632	990.4680		1064.5524	1047.5258	10
8	72.0808	874.4781	857.4516	856.4676	***902.4730***	885.4465	884.4625	860.4625		V	892.3948	905.4152		936.4574	919.4308	9
9	70.0651	971.5309	954.5043	953.5203	999.5258	982.4993	981.5152	945.5152		P	795.3420	794.3468		***837.3890***	820.3624	8
10	159.0917	1157.6102	1140.5837	1139.5996	1185.6051	1168.5786	1167.5946			W	609.2627			740.3362	723.3097	7
11	60.0444	1244.6422	1227.6157	1226.6317	1272.6371	1255.6106	1254.6266	1228.6473		S	522.2307	521.2354		554.2569	537.2304	5
12	102.0550	1373.6848	1356.6583	1355.6743	1401.6797	1384.6532	1383.6692	1315.6793		E	393.1881	392.1928		467.2249	450.1983	4
13	136.0757	1536.7482	1519.7216	1518.7376	1564.7431	1547.7165	1546.7325			Y	230.1248			338.1823	321.1557	
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IF	233.1648	261.1598	IFN	347.2078	375.2027	IFND	462.2347	490.2296
IFNDA	533.2718	561.2667	IFNDAK	661.3668	689.3617	FN	234.1237	262.1186
FND	349.1506	377.1456	FNDA	420.1878	448.1827	FNDAK	548.2827	576.2776
FNDAKV	647.3511	675.3461	ND	202.0822	230.0771	NDA	273.1193	301.1143
NDAK	401.2143	429.2092	NDAKV	500.2827	528.2776	NDAKVP	597.3355	625.3304
DA	159.0764	187.0713	DAK	287.1714	315.1663	DAKV	386.2398	414.2347

DAKVP	483.2926	511.2875	**DAKVPW**	669.3719	697.3668	**AK**	172.1444	200.1394
AKV	271.2129	299.2078	**AKVP**	368.2656	396.2605	**AKVPW**	554.3449	582.3398
AKVPWS	641.3770	669.3719	**KV**	200.1757	228.1707	**KVP**	297.2285	325.2234
KVPW	483.3078	511.3027	**KVPWS**	570.3398	598.3348	**KVPWSE**	699.3824	727.3774
VP	169.1335	197.1285	**VPW**	355.2129	383.2078	**VPWS**	442.2449	470.2398
VPWSE	571.2875	599.2824	**PW**	256.1444	284.1394	**PWS**	343.1765	371.1714
PWSE	472.2191	500.2140	**PWSEY**	635.2824	663.2773	**WS**	246.1237	274.1186
WSE	375.1663	403.1612	**WSEY**	538.2296	566.2245	**SE**	189.0870	217.0819
SEY	352.1503	380.1452	**EY**	265.1183	293.1132			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
8.9	1737.8435	0.1502	HADFIGPVQVADAGEGR
5.5	1737.8257	0.1680	QMVVARSNWEAEFR
5.5	1737.8533	0.1403	QSETTGIQVYSQIER
4.9	1737.8463	0.1473	QVTMDLITCLLEMR
4.5	1737.8474	0.1462	NIFNDAKVPWSEYR
3.9	1737.9058	0.0878	QMKISAMTLLHFFR
3.5	1737.8798	0.1138	GWLDTTYLSRSGNIR
3.5	1737.8798	0.1138	GWLDTTYLSRSGNLR
3.3	1737.8291	0.1646	KVNYVICTMSGSHSR
3.3	1737.8621	0.1316	QLGGVMAYPSPYARGR

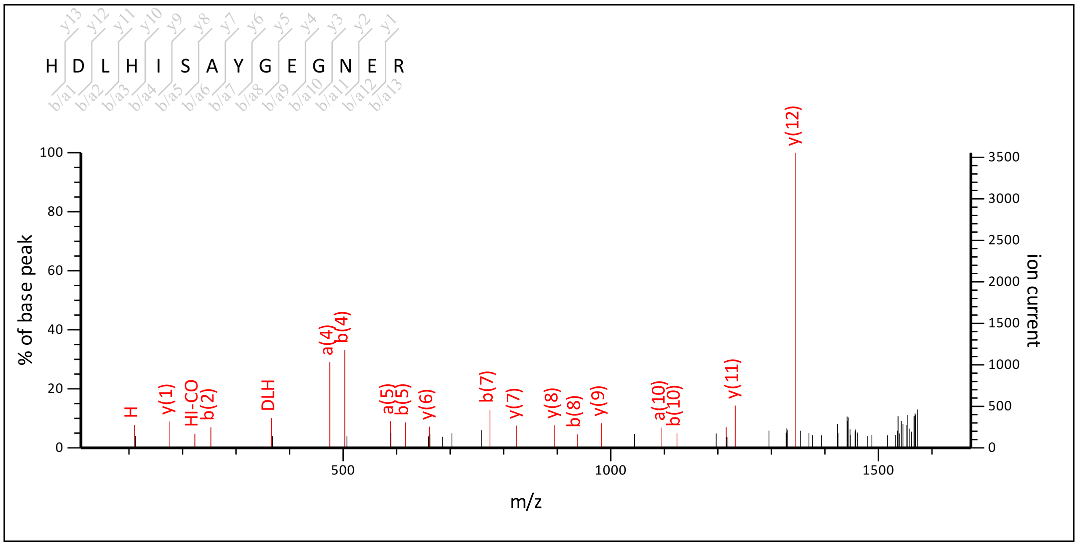
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 66

MS/MS Fragmentation of **HDLHISAYGEGNER**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 69: 1596.843724 from(1597.851000,1+) intensity(0.0000) index(20)
Title: Label: C8, Spot_Id: 228956, Peak_List_Id: 257807, MSMS Job_Run_Id: 24936, Comment:
Data file ppw_C8_138985146000.txt



10.07 to 1672.66

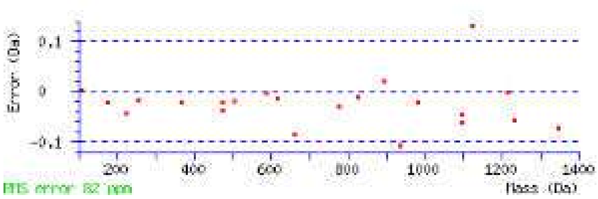
Label all possible matches ○ Label matches used for scoring ●

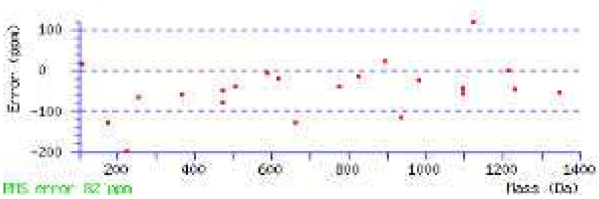
Monoisotopic mass of neutral peptide Mr(calc): 1596.7281
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 0.00069
Matches : 26/230 fragment ions using 30 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	110.0713	**110.0713**			138.0662			44.0495		H					
2	88.0393	225.0982		207.0877	**253.0931**		235.0826	181.1084		D	1400.6553	1399.6601		1460.6764	1443.6499
3	86.0964	338.1823		320.1717	**366.1772**		348.1666	296.1353		L	1287.5713	1286.5760		***1345.6495***	1328.6230
4	110.0713	**475.2412**		457.2306	**503.2361**		485.2255			H	1150.5123			***1232.5654***	1215.5389
5	86.0964	**588.3253**		570.3147	**616.3202**		598.3096	560.2940	574.3096	I	1037.4283	1050.4487	1064.4643	***1095.5065***	1078.4800
6	60.0444	675.3573		657.3467	703.3522		685.3416	659.3624		S	950.3963	949.4010		***982.4225***	965.3959
7	44.0495	746.3944		728.3838	**774.3893**		756.3787			A	879.3591			***895.3904***	878.3639
8	136.0757	909.4577		891.4472	**937.4526**		919.4421			Y	716.2958			***824.3533***	807.3268
9	30.0338	966.4792		948.4686	994.4741		976.4635			G				***661.2900***	644.2634
10	102.0550	**1095.5218**		1077.5112	**1123.5167**		1105.5061	1037.5163		E	530.2317	529.2365		604.2685	587.2420
11	30.0338	1152.5432		1134.5327	1180.5382		1162.5276			G				***475.2259***	458.1994
12	87.0553	1266.5862	1249.5596	1248.5756	1294.5811	1277.5545	1276.5705	1223.5804		N	359.1674	358.1721		418.2045	401.1779
13	102.0550	1395.6288	1378.6022	1377.6182	1423.6237	1406.5971	1405.6131	1337.6233		E	230.1248	229.1295		304.1615	287.1350
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DL	201.1234	229.1183	**DLH**	338.1823	366.1772	**DLHI**	451.2663	479.2613
DLHIS	538.2984	566.2933	**DLHISA**	609.3355	637.3304	**LH**	223.1553	251.1503
LHI	336.2394	364.2343	**LHIS**	423.2714	451.2663	**LHISA**	494.3085	522.3035
LHISAY	657.3719	685.3668	**HI**	223.1553	251.1503	**HIS**	310.1874	338.1823
HISA	381.2245	409.2194	**HISAY**	544.2878	572.2827	**HISAYG**	601.3093	629.3042
IS	173.1285	201.1234	**ISA**	244.1656	272.1605	**ISAY**	407.2289	435.2238
ISAYG	464.2504	492.2453	**ISAYGE**	593.2930	621.2879	**ISAYGEG**	650.3144	678.3093

SA	131.0815	159.0764	**SAY**	294.1448	322.1397	**SAYG**	351.1663	379.1612
SAYGE	480.2089	508.2038	**SAYGEG**	537.2304	565.2253	**SAYGEGN**	651.2733	679.2682
AY	207.1128	235.1077	**AYG**	264.1343	292.1292	**AYGE**	393.1769	421.1718
AYGEG	450.1983	478.1932	**AYGEGN**	564.2413	592.2362	**AYGEGNE**	693.2838	721.2788
YG	193.0972	221.0921	**YGE**	322.1397	350.1347	**YGEG**	379.1612	407.1561
YGEGN	493.2041	521.1991	**YGEGNE**	622.2467	650.2416	**GE**	159.0764	187.0713
GEG	216.0979	244.0928	**GEGN**	330.1408	358.1357	**GEGNE**	459.1834	487.1783
EG	159.0764	187.0713	**EGN**	273.1193	301.1143	**EGNE**	402.1619	430.1569
GN	144.0768	172.0717	**GNE**	273.1193	301.1143	**NE**	216.0979	244.0928





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.1	1596.7281	0.1157	HDLHISAYGEGNER
48.5	1596.7281	0.1157	HEVHISAYGEGNER
48.5	1596.7281	0.1157	HVEHISAYGEGNER
35.9	1596.7644	0.0793	HVEHISSYGLGNER
16.6	1596.8004	0.0434	SFMVECEVLKSIR
11.5	1596.7566	0.0871	VGFTQTTCDLATQR
10.1	1596.7678	0.0759	RMAAGLNGFSSVSER
9.9	1596.7049	0.1388	MENQLSSSSEAASTR
9.5	1596.8493	-0.0056	RCWLLPIARPCR
8.6	1596.7177	0.1260	AKQMWSDMLNWR

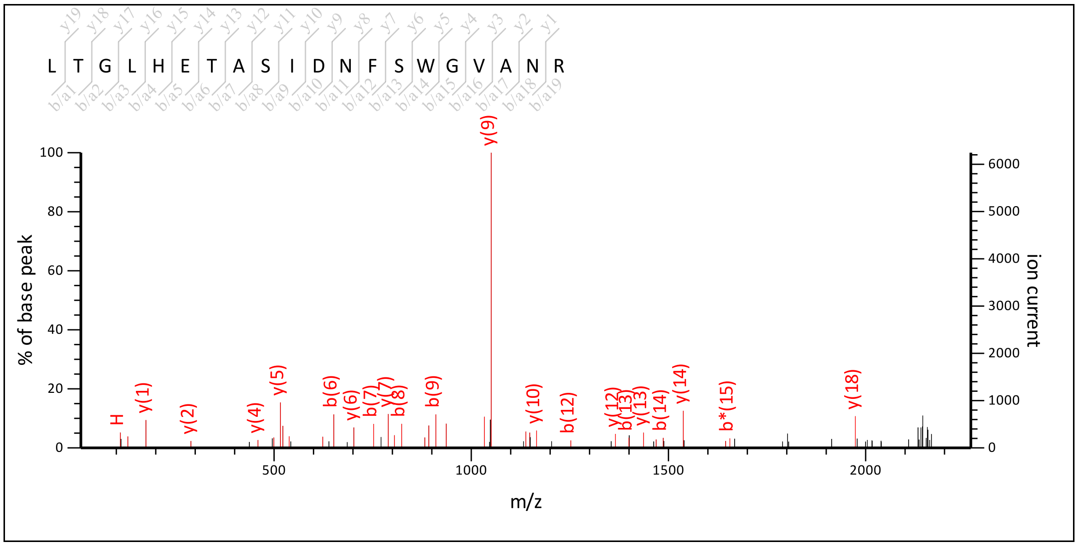
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 66

MS/MS Fragmentation of **LTGLHETASIDNFSWGVANR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 83: 2187.221024 from(2188.228300,1+) intensity(0.0000) index(24)
Title: Label: C8, Spot_Id: 228956, Peak_List_Id: 257806, MSMS Job_Run_Id: 24936, Comment:
Data file ppw_C8_138985146000.txt



10.07 to 2266.76

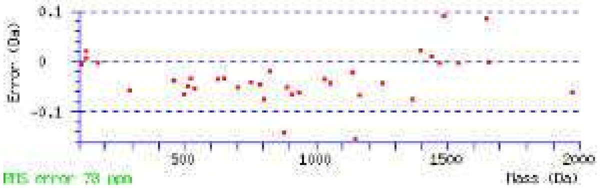
Label all possible matches ○ Label matches used for scoring ●

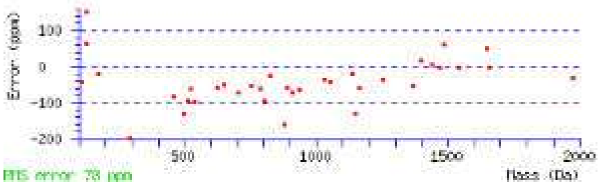
Monoisotopic mass of neutral peptide Mr(calc): 2187.0709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 96 **Expect:** 3.5e-07
Matches : 37/358 fragment ions using 51 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		L					
2	74.0600	187.1441		169.1335	215.1390		197.1285	171.1492	173.1285	T	2028.9522	2041.9726	2043.9519	2074.9941	2057.9675
3	30.0338	244.1656		226.1550	272.1605		254.1499			G				***1973.9464***	1956.9199
4	86.0964	357.2496		339.2391	385.2445		367.2340	315.2027		L	1858.8467	1857.8515		1916.9250	1899.8984
5	110.0713	494.3085		476.2980	**522.3035**		504.2929			H	1721.7878			1803.8409	1786.8143
6	102.0550	**623.3511**		605.3406	**651.3461**		633.3355	565.3457		E	1592.7452	1591.7499		1666.7820	1649.7554
7	74.0600	724.3988		706.3883	**752.3937**		734.3832	708.4039	710.3832	T	1491.6975	1504.7179	1506.6972	***1537.7394***	1520.7128
8	44.0495	795.4359		777.4254	**823.4308**		805.4203			A	1420.6604			***1436.6917***	1419.6652
9	60.0444	**882.4680**		864.4574	**910.4629**		892.4523	866.4730		S	1333.6284	1332.6331		***1365.6546***	1348.6280
10	86.0964	995.5520		977.5415	1023.5469		1005.5364	967.5207	981.5364	I	1220.5443	1233.5647	1247.5804	1278.6226	1261.5960
11	88.0393	1110.5790		1092.5684	**1138.5739**		1120.5633	1066.5891		D	1105.5174	1104.5221		***1165.5385***	1148.5119
12	87.0553	1224.6219	1207.5953	1206.6113	**1252.6168**	1235.5903	1234.6062	1181.6161		N	991.4744	990.4792		***1050.5116***	1033.4850
13	120.0808	1371.6903	1354.6638	1353.6797	**1399.6852**	1382.6587	1381.6747			F	844.4060			***936.4686***	919.4421
14	60.0444	1458.7223	1441.6958	1440.7118	**1486.7172**	1469.6907	1468.7067	1442.7274		S	757.3740	756.3787		***789.4002***	772.3737
15	159.0917	**1644.8016**	1627.7751	1626.7911	1672.7966	1655.7700	1654.7860			W	571.2947			***702.3682***	685.3416
16	30.0338	1701.8231	1684.7966	1683.8125	1729.8180	1712.7915	1711.8075			G				***516.2889***	499.2623
17	72.0808	1800.8915	1783.8650	1782.8810	1828.8864	1811.8599	1810.8759	1786.8759		V	415.2048	428.2252		***459.2674***	442.2409
18	44.0495	1871.9286	1854.9021	1853.9181	1899.9236	1882.8970	1881.9130			A	344.1677			360.1990	343.1724
19	87.0553	1985.9716	1968.9450	1967.9610	2013.9665	1996.9399	1995.9559	1942.9658		N	230.1248	229.1295		***289.1619***	272.1353
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TG	131.0815	159.0764	TGL	244.1656	272.1605	TGLH	381.2245	409.2194

TGLHE	510.2671	538.2620	**TGLHET**	611.3148	639.3097	**TGLHETA**	682.3519	710.3468
GL	143.1179	171.1128	**GLH**	280.1768	308.1717	**GLHE**	409.2194	437.2143
GLHET	510.2671	538.2620	**GLHETA**	581.3042	609.2991	**GLHETAS**	668.3362	696.3311
LH	223.1553	251.1503	**LHE**	352.1979	380.1928	**LHET**	453.2456	481.2405
LHETA	524.2827	552.2776	**LHETAS**	611.3148	639.3097	**HE**	239.1139	267.1088
HET	340.1615	368.1565	**HETA**	411.1987	439.1936	**HETAS**	498.2307	526.2256
HETASI	611.3148	639.3097	**ET**	203.1026	231.0975	**ETA**	274.1397	302.1347
ETAS	361.1718	389.1667	**ETASI**	474.2558	502.2508	**ETASID**	589.2828	617.2777
TA	145.0972	173.0921	**TAS**	232.1292	260.1241	**TASI**	345.2132	373.2082
TASID	460.2402	488.2351	**TASIDN**	574.2831	602.2780	**AS**	131.0815	159.0764
ASI	244.1656	272.1605	**ASID**	359.1925	387.1874	**ASIDN**	473.2354	501.2304
ASIDNF	620.3039	648.2988	**SI**	173.1285	201.1234	**SID**	288.1554	316.1503
SIDN	402.1983	430.1932	**SIDNF**	549.2667	577.2617	**SIDNFS**	636.2988	664.2937
ID	201.1234	229.1183	**IDN**	315.1663	343.1612	**IDNF**	462.2347	490.2296
IDNFS	549.2667	577.2617	**DN**	202.0822	230.0771	**DNF**	349.1506	377.1456
DNFS	436.1827	464.1776	**DNFSW**	622.2620	650.2569	**DNFSWG**	679.2835	707.2784
NF	234.1237	262.1186	**NFS**	321.1557	349.1506	**NFSW**	507.2350	535.2300
NFSWG	564.2565	592.2514	**NFSWGV**	663.3249	691.3198	**FS**	207.1128	235.1077
FSW	393.1921	421.1870	**FSWG**	450.2136	478.2085	**FSWGV**	549.2820	577.2769
FSWGVA	620.3191	648.3140	**SW**	246.1237	274.1186	**SWG**	303.1452	331.1401
SWGV	402.2136	430.2085	**SWGVA**	473.2507	501.2456	**SWGVAN**	587.2936	615.2885
WG	216.1131	244.1081	**WGV**	315.1816	343.1765	**WGVA**	386.2187	414.2136
WGVAN	500.2616	528.2565	**GV**	129.1022	157.0972	**GVA**	200.1394	228.1343
GVAN	314.1823	342.1772	**VA**	143.1179	171.1128	**VAN**	257.1608	285.1557
AN	158.0924	186.0873						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
96.0	2187.0709	0.1501	LTGLHETASIDNFSWGVANR
19.1	2187.0789	0.1421	LRHNCAAVQMPIGLEGEHR
10.7	2187.1834	0.0376	IGVVAAVATATLAAFGCVGAVGGR
10.4	2187.0637	0.1573	FFLENPENFDTLSVVFNR
9.4	2187.0266	0.1944	QMSSPTFLDDATGIGEPLHR
8.9	2187.0392	0.1818	CGAHLGFGYDDTAAARRPPR
8.9	2187.0565	0.1646	KVHCALAANLDSMYVTNHK
7.2	2187.0169	0.2041	MLEGTRALSHLLCSCHMR
7.2	2187.0533	0.1677	MLIGTRALSHLLCSCHMR
7.2	2187.0533	0.1677	MLLGTRALSHLLCSCHMR

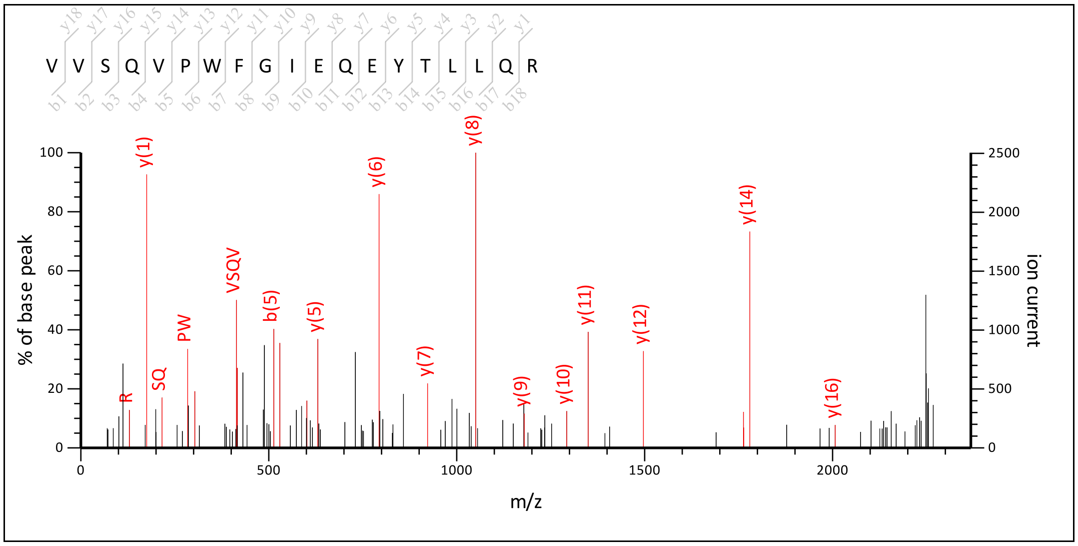
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 66**

MS/MS Fragmentation of **VVSQVPWFGIEQEYTLLQR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 86: 2291.353824 from(2292.361100,1+) intensity(0.0000) index(25)
Title: Label: C8, Spot_Id: 228956, Peak_List_Id: 257805, MSMS Job_Run_Id: 24936, Comment:
Data file ppw_C8_138985146000.txt



0 to 2367.85

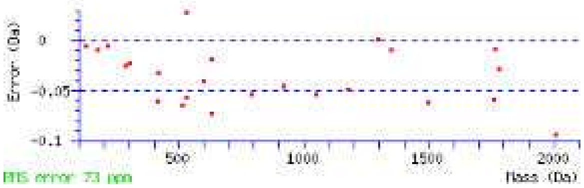
Label all possible matches ○ Label matches used for scoring ●

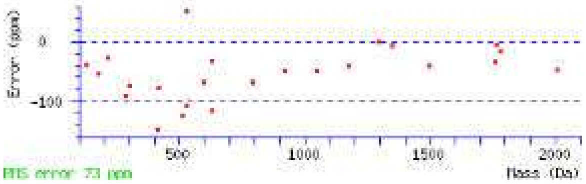
Monoisotopic mass of neutral peptide Mr(calc): 2291.1950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 98 **Expect:** 1.3e-07
Matches : 25/338 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	72.0808	171.1492			199.1441			157.1335		V	2149.0713	2162.0917		2193.1339	2176.1073
3	60.0444	258.1812		240.1707	286.1761		268.1656	242.1863		S	2062.0393	2061.0440		2094.0655	2077.0389
4	101.0709	386.2398	369.2132	368.2292	**414.2347**	397.2082	396.2241	329.2183		Q	1933.9807	1932.9854		***2007.0334***	1990.0069
5	72.0808	485.3082	468.2817	467.2976	**513.3031**	496.2766	495.2926	471.2926		V	1834.9123	1847.9327		1878.9749	1861.9483
6	70.0651	582.3610	565.3344	564.3504	610.3559	593.3293	592.3453	556.3453		P	1737.8595	1736.8643		***1779.9064***	1762.8799
7	159.0917	768.4403	751.4137	750.4297	796.4352	779.4087	778.4246			W	1551.7802			1682.8537	1665.8271
8	120.0808	915.5087	898.4822	897.4981	943.5036	926.4771	925.4930			F	1404.7118			***1496.7744***	1479.7478
9	30.0338	972.5302	955.5036	954.5196	1000.5251	983.4985	982.5145			G				***1349.7060***	1332.6794
10	86.0964	1085.6142	1068.5877	1067.6037	1113.6091	1096.5826	1095.5986	1057.5829	1071.5986	I	1234.6062	1247.6266	1261.6423	***1292.6845***	1275.6579
11	102.0550	1214.6568	1197.6303	1196.6463	1242.6517	1225.6252	1224.6412	1156.6513		E	1105.5637	1104.5684		***1179.6004***	1162.5739
12	101.0709	1342.7154	1325.6889	1324.7048	1370.7103	1353.6838	1352.6997	1285.6939		Q	977.5051	976.5098		***1050.5578***	1033.5313
13	102.0550	1471.7580	1454.7314	1453.7474	1499.7529	1482.7264	1481.7423	1413.7525		E	848.4625	847.4672		***922.4993***	905.4727
14	136.0757	1634.8213	1617.7948	1616.8108	1662.8162	1645.7897	1644.8057			Y	685.3992			***793.4567***	776.4301
15	74.0600	1735.8690	1718.8425	1717.8584	**1763.8639**	1746.8374	1745.8534	1719.8741	1721.8534	T	584.3515	597.3719	599.3511	***630.3933***	613.3668
16	86.0964	1848.9531	1831.9265	1830.9425	1876.9480	1859.9214	1858.9374	1806.9061		L	471.2674	470.2722		***529.3457***	512.3191
17	86.0964	1962.0371	1945.0106	1944.0266	1990.0320	1973.0055	1972.0215	1919.9902		L	358.1833	357.1881		***416.2616***	399.2350
18	101.0709	2090.0957	2073.0692	2072.0851	2118.0906	2101.0641	2100.0801	2033.0742		Q	230.1248	229.1295		***303.1775***	286.1510
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VS	159.1128	187.1077	VSQ	287.1714	315.1663	VSQV	386.2398	414.2347
VSQVP	483.2926	511.2875	VSQVPW	669.3719	697.3668	SQ	188.1030	216.0979

SQV	287.1714	315.1663	**SQVP**	384.2241	412.2191	**SQVPW**	570.3035	598.2984
QV	200.1394	228.1343	**QVP**	297.1921	325.1870	**QVPW**	483.2714	511.2663
QVPWF	630.3398	658.3348	**QVPWFG**	687.3613	715.3562	**VP**	169.1335	197.1285
VPW	355.2129	383.2078	**VPWF**	502.2813	530.2762	**VPWFG**	559.3027	587.2976
VPWFGI	672.3868	700.3817	**PW**	256.1444	284.1394	**PWF**	403.2129	431.2078
PWFG	460.2343	488.2292	**PWFGI**	573.3184	601.3133	**WF**	306.1601	334.1550
WFG	363.1816	391.1765	**WFGI**	476.2656	504.2605	**WFGIE**	605.3082	633.3031
FG	177.1022	205.0972	**FGI**	290.1863	318.1812	**FGIE**	419.2289	447.2238
FGIEQ	547.2875	575.2824	**FGIEQE**	676.3301	704.3250	**GI**	143.1179	171.1128
GIE	272.1605	300.1554	**GIEQ**	400.2191	428.2140	**GIEQE**	529.2617	557.2566
GIEQEY	692.3250	720.3199	**IE**	215.1390	243.1339	**IEQ**	343.1976	371.1925
IEQE	472.2402	500.2351	**IEQEY**	635.3035	663.2984	**EQ**	230.1135	258.1084
EQE	359.1561	387.1510	**EQEY**	522.2195	550.2144	**EQEYT**	623.2671	651.2620
QE	230.1135	258.1084	**QEY**	393.1769	421.1718	**QEYT**	494.2245	522.2195
QEYTL	607.3086	635.3035	**EY**	265.1183	293.1132	**EYT**	366.1660	394.1609
EYTL	479.2500	507.2449	**EYTLL**	592.3341	620.3290	**YT**	237.1234	265.1183
YTL	350.2074	378.2023	**YTLL**	463.2915	491.2864	**YTLLQ**	591.3501	619.3450
TL	187.1441	215.1390	**TLL**	300.2282	328.2231	**TLLQ**	428.2867	456.2817
LL	199.1805	227.1754	**LLQ**	327.2391	355.2340	**LQ**	214.1550	242.1499





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
98.0	2291.1950	0.1588	VVSQVPWFGIEQEYTLLQR
12.3	2291.1645	0.1894	EGDNLVEEAPADIPSLPELKR
9.9	2291.1952	0.1586	RAMPLNMLLTGGLDVQMFLR
9.3	2291.1757	0.1781	EDQHTIETLTHEITDLIKR
8.8	2291.1249	0.2289	MRPEAETLALMSELVTSNQR
8.6	2291.1883	0.1655	QVRPPYLPGGGGGLGGGAAGQAAQR
8.2	2291.2307	0.1231	AAATTICYGPSSIVLGSNLLKR
8.2	2291.2784	0.0755	VEVPAGLQPAMGGITAGLRSIVR
8.1	2291.1952	0.1586	RAMPLNMLLTGGLDVQMFLR
8.0	2291.3287	0.0251	RSSLLVFTILSGVCSILSVLK

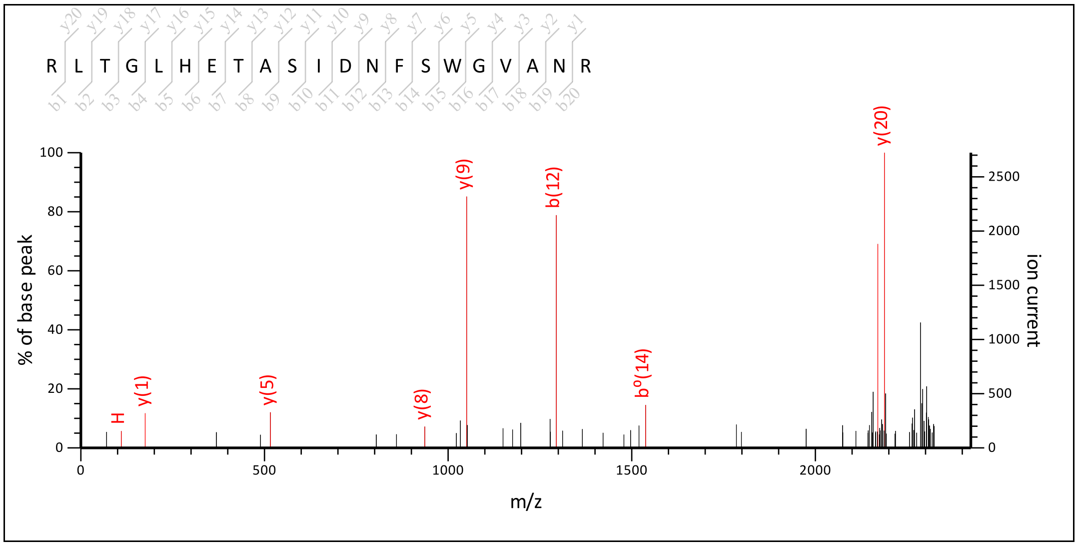
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 66

MS/MS Fragmentation of **RLTGLHETASIDNFSWGVANR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 89: 2343.326224 from(2344.333500,1+) intensity(0.0000) index(26)
Title: Label: C8, Spot_Id: 228956, Peak_List_Id: 257809, MSMS Job_Run_Id: 24936, Comment:
Data file ppw_C8_138985146000.txt



0 to 2423.35

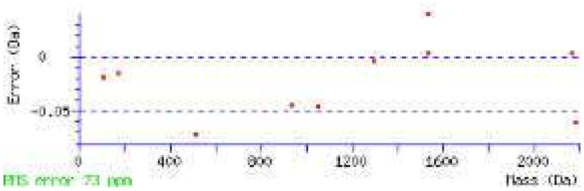
Label all possible matches ○ Label matches used for scoring ●

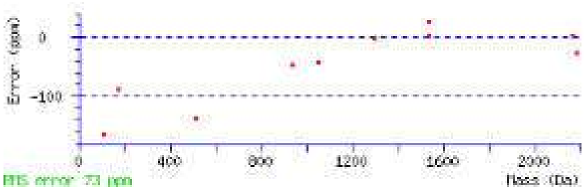
Monoisotopic mass of neutral peptide Mr(calc): 2343.1720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 1.5
Matches : 11/401 fragment ions using 17 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	129.1135	129.1135	112.0869		157.1084	140.0818		44.0495		R					
2	86.0964	242.1975	225.1710		270.1925	253.1659		200.1506		L	2129.9999	2129.0047		***2188.0782***	2171.0516
3	74.0600	343.2452	326.2187	325.2347	371.2401	354.2136	353.2296	327.2503	329.2296	T	2028.9522	2041.9726	2043.9519	2074.9941	2057.9675
4	30.0338	400.2667	383.2401	382.2561	428.2616	411.2350	410.2510			G				1973.9464	1956.9199
5	86.0964	513.3507	496.3242	495.3402	541.3457	524.3191	523.3351	471.3038		L	1858.8467	1857.8515		1916.9250	1899.8984
6	110.0713	650.4097	633.3831	632.3991	678.4046	661.3780	660.3940			H	1721.7878			1803.8409	1786.8143
7	102.0550	779.4522	762.4257	761.4417	807.4472	790.4206	789.4366	721.4468		E	1592.7452	1591.7499		1666.7820	1649.7554
8	74.0600	880.4999	863.4734	862.4894	908.4948	891.4683	890.4843	864.5050	866.4843	T	1491.6975	1504.7179	1506.6972	***1537.7394***	1520.7128
9	44.0495	951.5370	934.5105	933.5265	979.5320	962.5054	961.5214			A	1420.6604			1436.6917	1419.6652
10	60.0444	1038.5691	1021.5425	1020.5585	1066.5640	1049.5374	1048.5534	1022.5742		S	1333.6284	1332.6331		1365.6546	1348.6280
11	86.0964	1151.6531	1134.6266	1133.6426	1179.6480	1162.6215	1161.6375	1123.6218	1137.6375	I	1220.5443	1233.5647	1247.5804	1278.6226	1261.5960
12	88.0393	1266.6801	1249.6535	1248.6695	**1294.6750**	1277.6484	1276.6644	1222.6902		D	1105.5174	1104.5221		1165.5385	1148.5119
13	87.0553	1380.7230	1363.6965	1362.7124	1408.7179	1391.6914	1390.7074	1337.7172		N	991.4744	990.4792		***1050.5116***	1033.4850
14	120.0808	1527.7914	1510.7649	1509.7809	1555.7863	1538.7598	1537.7758			F	844.4060			***936.4686***	919.4421
15	60.0444	1614.8234	1597.7969	1596.8129	1642.8184	1625.7918	1624.8078	1598.8285		S	757.3740	756.3787		789.4002	772.3737
16	159.0917	1800.9028	1783.8762	1782.8922	1828.8977	1811.8711	1810.8871			W	571.2947			702.3682	685.3416
17	30.0338	1857.9242	1840.8977	1839.9137	1885.9191	1868.8926	1867.9086			G				***516.2889***	499.2623
18	72.0808	1956.9926	1939.9661	1938.9821	1984.9876	1967.9610	1966.9770	1942.9770		V	415.2048	428.2252		459.2674	442.2409
19	44.0495	2028.0298	2011.0032	2010.0192	2056.0247	2038.9981	2038.0141			A	344.1677			360.1990	343.1724
20	87.0553	2142.0727	2125.0461	2124.0621	**2170.0676**	2153.0410	2152.0570	2099.0669		N	230.1248	229.1295		289.1619	272.1353
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

LT	187.1441	215.1390	**LTG**	244.1656	272.1605	**LTGL**	357.2496	385.2445
LTGLH	494.3085	522.3035	**LTGLHE**	623.3511	651.3461	**TG**	131.0815	159.0764
TGL	244.1656	272.1605	**TGLH**	381.2245	409.2194	**TGLHE**	510.2671	538.2620
TGLHET	611.3148	639.3097	**TGLHETA**	682.3519	710.3468	**GL**	143.1179	171.1128
GLH	280.1768	308.1717	**GLHE**	409.2194	437.2143	**GLHET**	510.2671	538.2620
GLHETA	581.3042	609.2991	**GLHETAS**	668.3362	696.3311	**LH**	223.1553	251.1503
LHE	352.1979	380.1928	**LHET**	453.2456	481.2405	**LHETA**	524.2827	552.2776
LHETAS	611.3148	639.3097	**HE**	239.1139	267.1088	**HET**	340.1615	368.1565
HETA	411.1987	439.1936	**HETAS**	498.2307	526.2256	**HETASI**	611.3148	639.3097
ET	203.1026	231.0975	**ETA**	274.1397	302.1347	**ETAS**	361.1718	389.1667
ETASI	474.2558	502.2508	**ETASID**	589.2828	617.2777	**TA**	145.0972	173.0921
TAS	232.1292	260.1241	**TASI**	345.2132	373.2082	**TASID**	460.2402	488.2351
TASIDN	574.2831	602.2780	**AS**	131.0815	159.0764	**ASI**	244.1656	272.1605
ASID	359.1925	387.1874	**ASIDN**	473.2354	501.2304	**ASIDNF**	620.3039	648.2988
SI	173.1285	201.1234	**SID**	288.1554	316.1503	**SIDN**	402.1983	430.1932
SIDNF	549.2667	577.2617	**SIDNFS**	636.2988	664.2937	**ID**	201.1234	229.1183
IDN	315.1663	343.1612	**IDNF**	462.2347	490.2296	**IDNFS**	549.2667	577.2617
DN	202.0822	230.0771	**DNF**	349.1506	377.1456	**DNFS**	436.1827	464.1776
DNFSW	622.2620	650.2569	**DNFSWG**	679.2835	707.2784	**NF**	234.1237	262.1186
NFS	321.1557	349.1506	**NFSW**	507.2350	535.2300	**NFSWG**	564.2565	592.2514
NFSWGV	663.3249	691.3198	**FS**	207.1128	235.1077	**FSW**	393.1921	421.1870
FSWG	450.2136	478.2085	**FSWGV**	549.2820	577.2769	**FSWGVA**	620.3191	648.3140
SW	246.1237	274.1186	**SWG**	303.1452	331.1401	**SWGV**	402.2136	430.2085
SWGVA	473.2507	501.2456	**SWGVAN**	587.2936	615.2885	**WG**	216.1131	244.1081
WGV	315.1816	343.1765	**WGVA**	386.2187	414.2136	**WGVAN**	500.2616	528.2565
GV	129.1022	157.0972	**GVA**	200.1394	228.1343	**GVAN**	314.1823	342.1772
VA	143.1179	171.1128	**VAN**	257.1608	285.1557	**AN**	158.0924	186.0873





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.9	2343.1720	0.1542	RLTGLHETASIDNFSWGVANR
17.1	2343.1892	0.1370	LEELNLSHNMLSGLIPASFSR
13.5	2343.1416	0.1846	SSTIYEVGVQMVEIYNEQVR
11.9	2343.3314	-0.0052	IVLKPLPETVGEDRPALFPPR
11.3	2343.1722	0.1541	WAAEHPDMLKVWYVIDQVK
11.2	2343.1940	0.1323	RTPLSELRPMNTMYNIHVR
11.1	2343.1980	0.1282	QMNLSHVISHFSFGMKVLPR
10.6	2343.2086	0.1177	FLSPALFHHFKDPIMITEGK
10.0	2343.1792	0.1471	RAAAAASAHGSGGLGQENAIEHLR
9.7	2343.2838	0.0424	LVNALVSAGKPYELLIFPDER

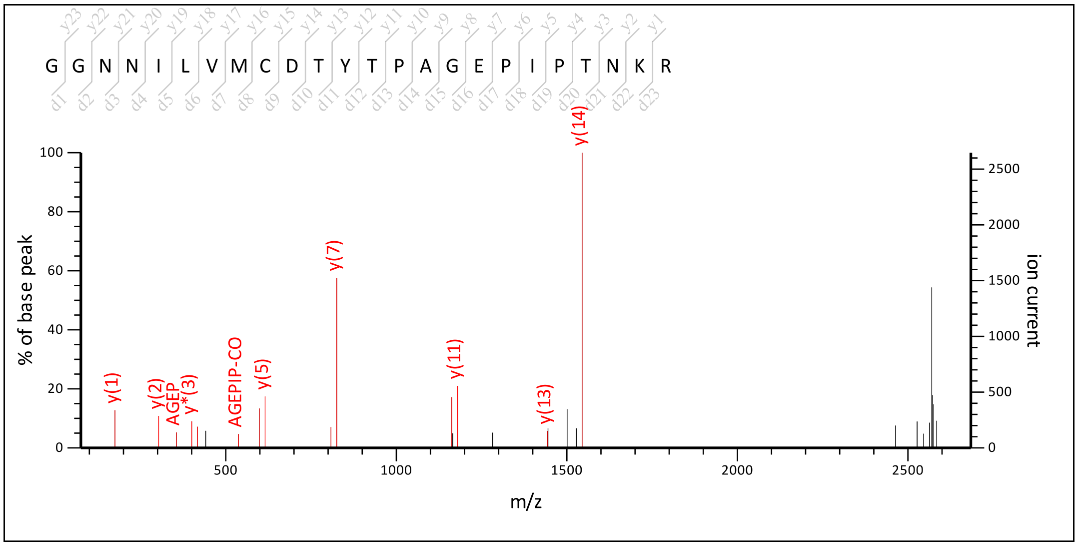
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 66

MS/MS Fragmentation of **GGNNILVMCDTYTPAGEPIPTNKR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 93: 2617.441224 from(2618.448500,1+) intensity(0.0000) index(28)
Title: Label: C8, Spot_Id: 228956, Peak_List_Id: 257811, MSMS Job_Run_Id: 24936, Comment:
Data file ppw_C8_138985146000.txt



75.11 to 2684.47

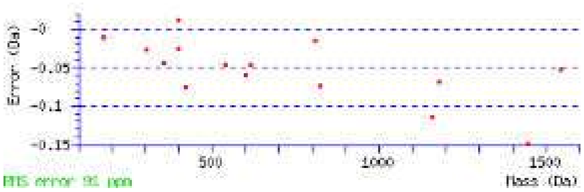
Label all possible matches ○ Label matches used for scoring ●

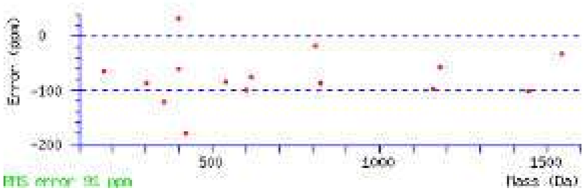
Monoisotopic mass of neutral peptide Mr(calc): 2617.2628
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.019
Matches : 17/464 fragment ions using 22 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	30.0338	87.0553			115.0502					G				2561.2487	2544.2221
3	87.0553	201.0982	184.0717		229.0931	212.0666		158.0924		N	2445.1901	2444.1948		2504.2272	2487.2007
4	87.0553	315.1411	298.1146		343.1361	326.1095		272.1353		N	2331.1472	2330.1519		2390.1843	2373.1577
5	86.0964	428.2252	411.1987		456.2201	439.1936		400.1939	414.2096	I	2218.0631	2231.0835	2245.0992	2276.1414	2259.1148
6	86.0964	541.3093	524.2827		569.3042	552.2776		499.2623		L	2104.9790	2103.9838		2163.0573	2146.0307
7	72.0808	640.3777	623.3511		668.3726	651.3461		626.3620		V	2005.9106	2018.9310		2049.9732	2032.9467
8	104.0528	771.4182	754.3916		799.4131	782.3865		711.4148		M	1874.8701	1873.8749		1950.9048	1933.8783
9	133.0430	931.4488	914.4223		959.4437	942.4172		842.4553		C	1714.8395	1713.8442		1819.8643	1802.8378
10	88.0393	1046.4758	1029.4492	1028.4652	1074.4707	1057.4441	1056.4601	1002.4859		D	1599.8125	1598.8173		1659.8337	1642.8071
11	74.0600	1147.5234	1130.4969	1129.5129	1175.5184	1158.4918	1157.5078	1131.5285	1133.5078	T	1498.7649	1511.7853	1513.7645	***1544.8067***	1527.7802
12	136.0757	1310.5868	1293.5602	1292.5762	1338.5817	1321.5551	1320.5711			Y	1335.7015			***1443.7591***	1426.7325
13	74.0600	1411.6344	1394.6079	1393.6239	1439.6294	1422.6028	1421.6188	1395.6395	1397.6188	T	1234.6539	1247.6743	1249.6535	1280.6957	1263.6692
14	70.0651	1508.6872	1491.6607	1490.6766	1536.6821	1519.6556	1518.6716	1482.6716		P	1137.6011	1136.6058		***1179.6480***	1162.6215
15	44.0495	1579.7243	1562.6978	1561.7138	1607.7192	1590.6927	1589.7087			A	1066.5640			1082.5953	1065.5687
16	30.0338	1636.7458	1619.7192	1618.7352	1664.7407	1647.7142	1646.7301			G				1011.5582	994.5316
17	102.0550	1765.7884	1748.7618	1747.7778	1793.7833	1776.7568	1775.7727	1707.7829		E	880.4999	879.5047		954.5367	937.5102
18	70.0651	1862.8411	1845.8146	1844.8306	1890.8361	1873.8095	1872.8255	1836.8255		P	783.4472	782.4519		***825.4941***	808.4676
19	86.0964	1975.9252	1958.8987	1957.9146	2003.9201	1986.8936	1985.9096	1947.8939	1961.9096	I	670.3631	683.3835	697.3991	728.4413	711.4148
20	70.0651	2072.9780	2055.9514	2054.9674	2100.9729	2083.9463	2082.9623	2046.9623		P	573.3103	572.3151		***615.3573***	598.3307
21	74.0600	2174.0257	2156.9991	2156.0151	2202.0206	2184.9940	2184.0100	2158.0307	2160.0100	T	472.2627	485.2831	487.2623	518.3045	501.2780
22	87.0553	2288.0686	2271.0420	2270.0580	2316.0635	2299.0369	2298.0529	2245.0628		N	358.2197	357.2245		***417.2568***	400.2303
23	101.1073	2416.1635	2399.1370	2398.1530	2444.1585	2427.1319	2426.1479	2359.1057		K	230.1248	229.1295		***303.2139***	286.1874

24	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GN	144.0768	172.0717	**GNN**	258.1197	286.1146	**GNNI**	371.2037	399.1987
GNNIL	484.2878	512.2827	**GNNILV**	583.3562	611.3511	**NN**	201.0982	229.0931
NNI	314.1823	342.1772	**NNIL**	427.2663	455.2613	**NNILV**	526.3348	554.3297
NNILVM	657.3752	685.3702	**NI**	200.1394	228.1343	**NIL**	313.2234	341.2183
NILV	412.2918	440.2867	**NILVM**	543.3323	571.3272	**IL**	199.1805	227.1754
ILV	298.2489	326.2438	**ILVM**	429.2894	457.2843	**ILVMC**	589.3200	617.3150
LV	185.1648	213.1598	**LVM**	316.2053	344.2002	**LVMC**	476.2360	504.2309
LVMCD	591.2629	619.2578	**LVMCDT**	692.3106	720.3055	**VM**	203.1213	231.1162
VMC	363.1519	391.1468	**VMCD**	478.1789	506.1738	**VMCDT**	579.2265	607.2214
MC	264.0835	292.0784	**MCD**	379.1104	407.1054	**MCDT**	480.1581	508.1530
MCDTY	643.2214	671.2164	**CD**	248.0700	276.0649	**CDT**	349.1176	377.1125
CDTY	512.1810	540.1759	**CDTYT**	613.2286	641.2236	**DT**	189.0870	217.0819
DTY	352.1503	380.1452	**DTYT**	453.1980	481.1929	**DTYTP**	550.2508	578.2457
DTYTPA	621.2879	649.2828	**DTYTPAG**	678.3093	706.3042	**TY**	237.1234	265.1183
TYT	338.1710	366.1660	**TYTP**	435.2238	463.2187	**TYTPA**	506.2609	534.2558
TYTPAG	563.2824	591.2773	**TYTPAGE**	692.3250	720.3199	**YT**	237.1234	265.1183
YTP	334.1761	362.1710	**YTPA**	405.2132	433.2082	**YTPAG**	462.2347	490.2296
YTPAGE	591.2773	619.2722	**YTPAGEP**	688.3301	716.3250	**TP**	171.1128	199.1077
TPA	242.1499	270.1448	**TPAG**	299.1714	327.1663	**TPAGE**	428.2140	456.2089
TPAGEP	525.2667	553.2617	**TPAGEPI**	638.3508	666.3457	**PA**	141.1022	169.0972
PAG	198.1237	226.1186	**PAGE**	327.1663	355.1612	**PAGEP**	424.2191	452.2140
PAGEPI	537.3031	565.2980	**PAGEPIP**	634.3559	662.3508	**AG**	101.0709	129.0659
AGE	230.1135	258.1084	**AGEP**	327.1663	355.1612	**AGEPI**	440.2504	468.2453
AGEPIP	537.3031	565.2980	**AGEPIPT**	638.3508	666.3457	**GE**	159.0764	187.0713
GEP	256.1292	284.1241	**GEPI**	369.2132	397.2082	**GEPIP**	466.2660	494.2609
GEPIPT	567.3137	595.3086	**GEPIPTN**	681.3566	709.3515	**EP**	199.1077	227.1026
EPI	312.1918	340.1867	**EPIP**	409.2445	437.2395	**EPIPT**	510.2922	538.2871
EPIPTN	624.3352	652.3301	**PI**	183.1492	211.1441	**PIP**	280.2020	308.1969
PIPT	381.2496	409.2445	**PIPTN**	495.2926	523.2875	**PIPTNK**	623.3875	651.3824
IP	183.1492	211.1441	**IPT**	284.1969	312.1918	**IPTN**	398.2398	426.2347
IPTNK	526.3348	554.3297	**PT**	171.1128	199.1077	**PTN**	285.1557	313.1506
PTNK	413.2507	441.2456	**TN**	188.1030	216.0979	**TNK**	316.1979	344.1928
NK	215.1503	243.1452						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.0	2617.2628	0.1784	GGNNILVMCDTYTPAGEPIPTNKR
11.3	2617.4228	0.0185	QQSSPPLPLPELAPQPLQPSPLQR
7.2	2617.2094	0.2319	DMFGPDIPNATDILVPMWWNNR
5.7	2617.2831	0.1582	KLSEDLEQNATLNTSLSAAAEEQR
5.3	2617.3951	0.0461	SYGPVPMGLLQGRVTHIIWPPQR
5.2	2617.2224	0.2188	SGENLSATLHPSGRDDMSILSMQR
5.1	2617.3026	0.1386	MLPAVSMSGLAPMDVSRTQDVKPR

5.1	2617.3026	0.1386	MLPAVSMSGLAPMDVSRTQDVKPR
4.9	2617.2953	0.1460	VLGLDVCSETVVGNDMLRGVSGGQR
4.7	2617.3751	0.0661	LGVLLEARGESYYNDLIPPTLER

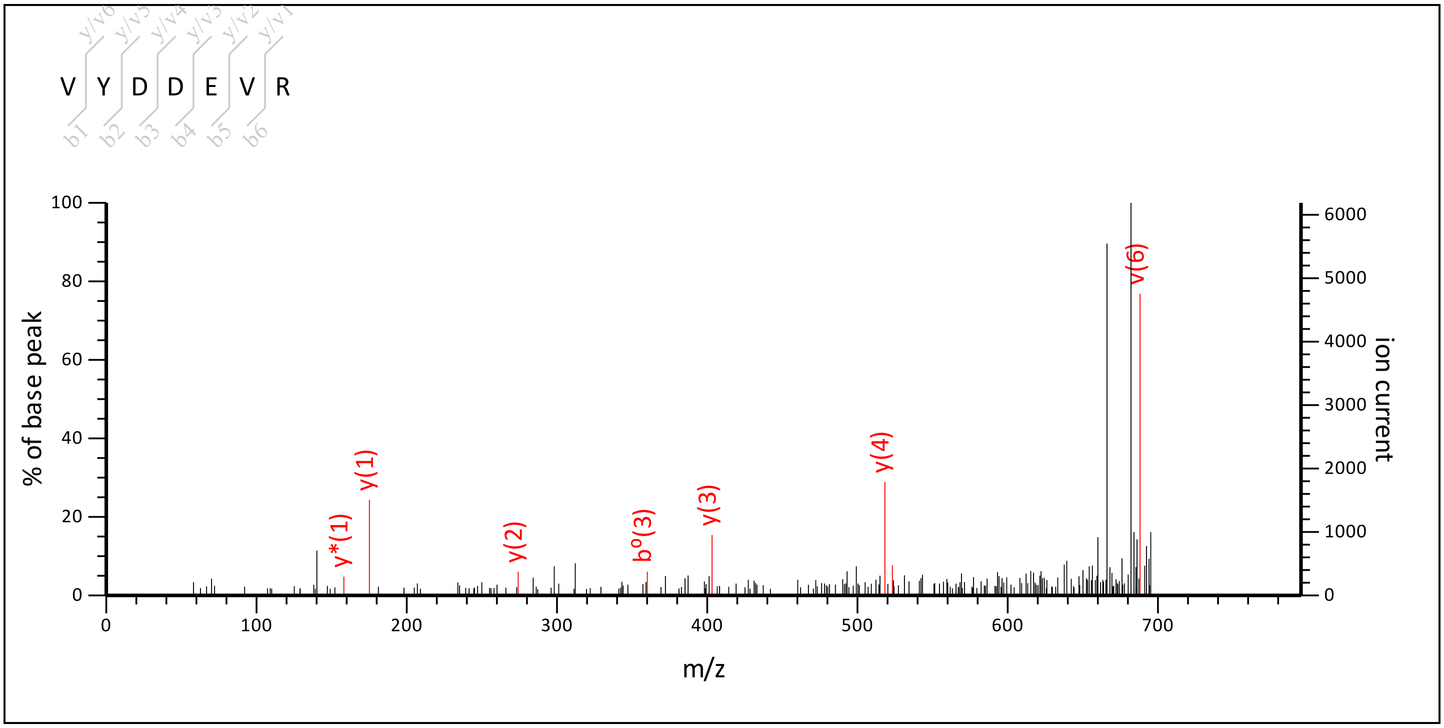
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **VYDDEVR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 4: 894.424424 from(895.431700,1+) intensity(0.0000) index(1)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225233, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



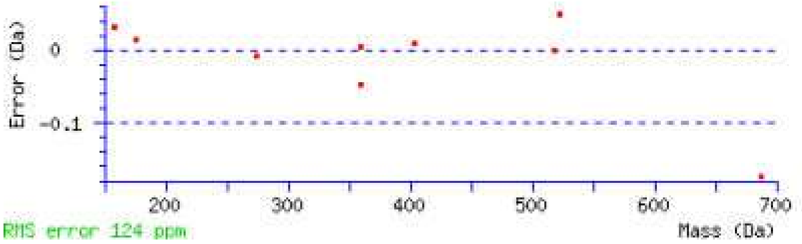
0 to 795.21

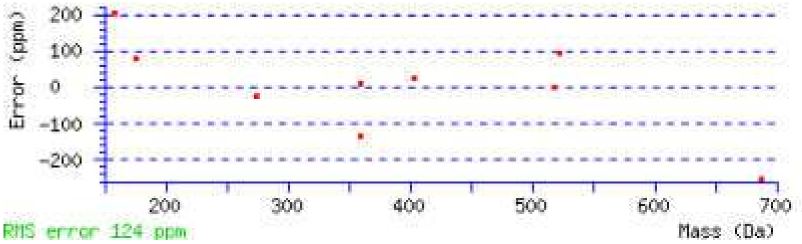
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 894.4083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 71
Matches : 9/79 fragment ions using 21 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495	V						7
2	136.0757	235.1441		263.1390			Y	688.2897		796.3472	779.3206	778.3366	6
3	88.0393	350.1710	332.1605	378.1660	360.1554	306.1812	D	573.2627	572.2675	633.2838	616.2573	615.2733	5
4	88.0393	465.1980	447.1874	493.1929	475.1823	421.2082	D	458.2358	457.2405	***518.2569***	501.2304	500.2463	4
5	102.0550	594.2406	576.2300	622.2355	604.2249	536.2351	E	329.1932	328.1979	***403.2300***	386.2034	385.2194	3
6	72.0808	693.3090	675.2984	721.3039	703.2933	679.2933	V	230.1248	243.1452	***274.1874***	257.1608		2
7	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YD	251.1026	279.0975	**YDD**	366.1296	394.1245	**YDDE**	495.1722	523.1671
YDDEV	594.2406	622.2355	**DD**	203.0662	231.0612	**DDE**	332.1088	360.1038
DDEV	431.1773	459.1722	**DE**	217.0819	245.0768	**DEV**	316.1503	344.1452
EV	201.1234	229.1183						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.5	894.4083	0.0161	VYDDEVR
8.5	894.4633	-0.0389	VDYMIVR
8.2	894.3719	0.0525	DDFDLDR
8.2	894.4083	0.0161	EFTDEVR
8.2	894.4083	0.0161	ETFDDLR
8.2	894.3542	0.0703	FDDDMPR
8.2	894.4447	-0.0203	LYTDVER
8.2	894.3389	0.0855	MDDDDLR
8.2	894.4447	-0.0203	TYLDVER
8.2	894.3905	0.0339	YVDDMPR

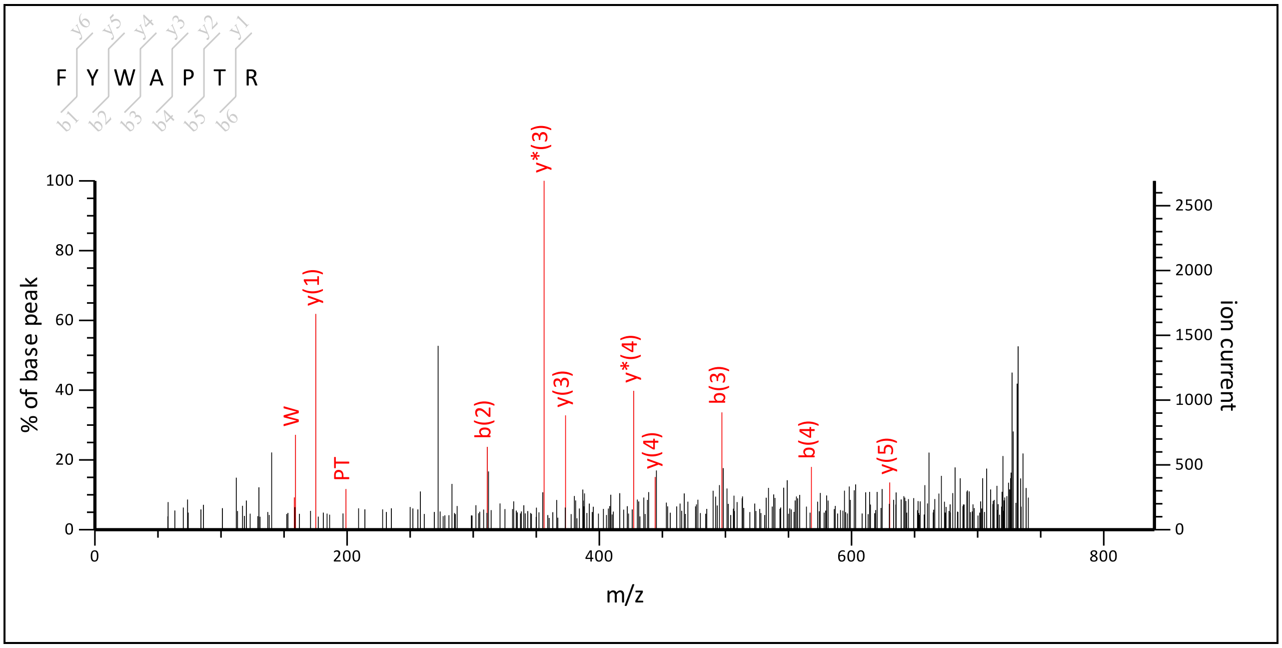
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **FYWAPTR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 7: 939.446334 from(940.453610,1+) intensity(0.0000) index(2)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225224, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



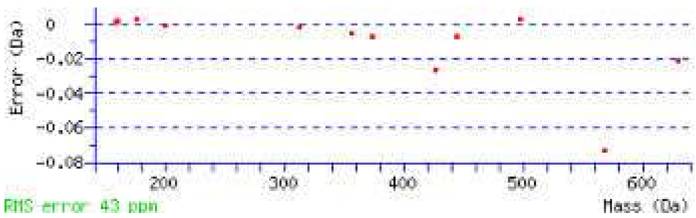
0 to 840.19

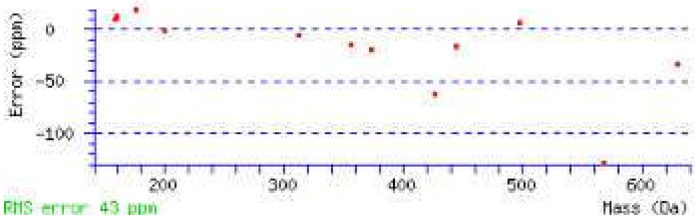
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 939.4603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 70
Matches : 12/72 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	120.0808	120.0808		148.0757		44.0495		**F**							7
2	136.0757	283.1441		**311.1390**				**Y**	685.3416			793.3992	776.3726	775.3886	6
3	159.0917	469.2234		**497.2183**				**W**	499.2623			***630.3358***	613.3093	612.3253	5
4	44.0495	540.2605		**568.2554**				**A**	428.2252			***444.2565***	427.2300	426.2459	4
5	70.0651	637.3133		665.3082		611.2976		**P**	331.1724	330.1772		***373.2194***	356.1928	355.2088	3
6	74.0600	738.3610	720.3504	766.3559	748.3453	722.3661	724.3453	**T**	230.1248	243.1452	245.1244	276.1666	259.1401	258.1561	2
7	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YW	322.1550	350.1499	**YWA**	393.1921	421.1870	**YWAP**	490.2449	518.2398
YWAPT	591.2926	619.2875	**WA**	230.1288	258.1237	**WAP**	327.1816	355.1765
WAPT	428.2292	456.2241	**AP**	141.1022	169.0972	**APT**	242.1499	270.1448
PT	171.1128	199.1077						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.8	939.5362	-0.0899	RGTRPTPR
21.7	939.5250	-0.0787	AAATPRTPR
18.2	939.5138	-0.0674	LTSAAPQPR
16.0	939.4998	-0.0535	RGPDSRPR
14.9	939.5138	-0.0674	LGASAPATPR
14.6	939.5250	-0.0786	AAAPGEIRR
14.6	939.5362	-0.0899	GRPGEIRR
13.9	939.4603	-0.0139	FYWAPTR
13.7	939.4709	-0.0245	HCAKATPR
13.2	939.5250	-0.0787	GRPTSGLPR

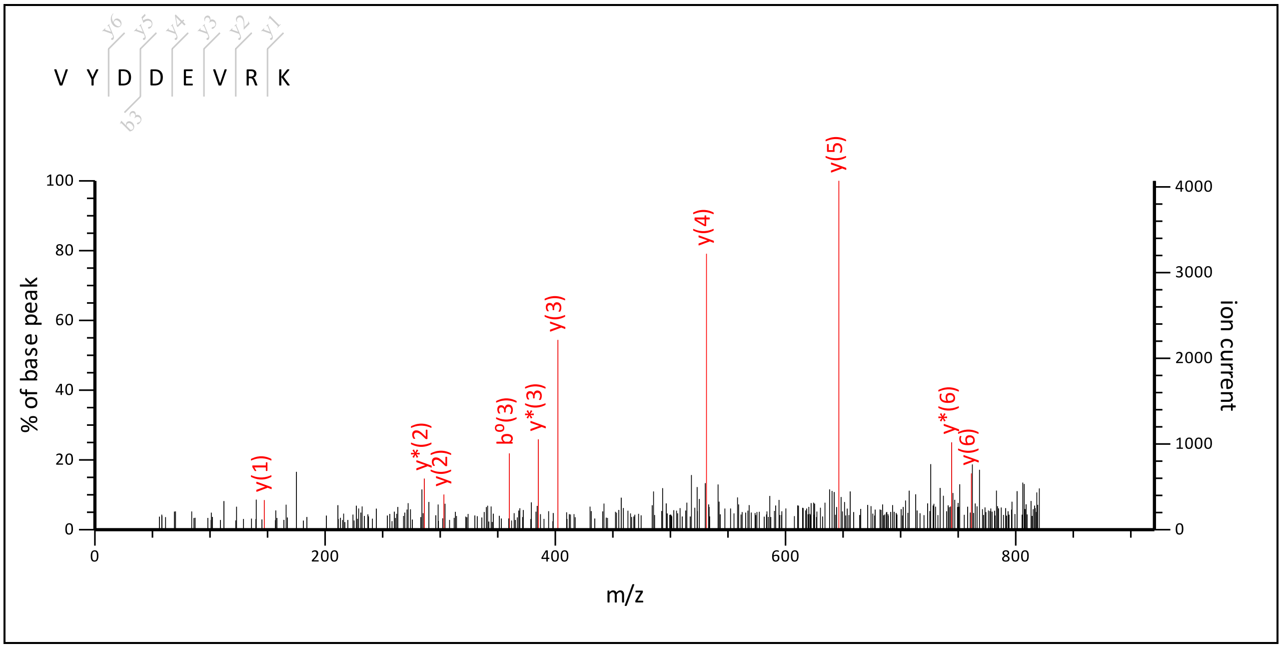
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **VYDDEVRK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 19: 1022.497624 from(1023.504900,1+) intensity(0.0000) index(7)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225220, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



0 to 920.5

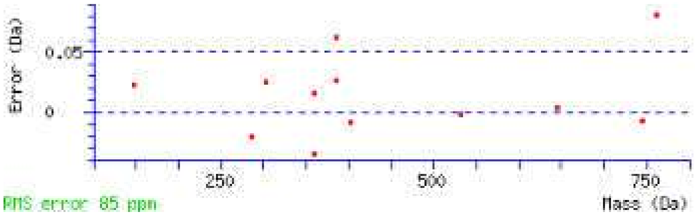
Label all possible matches ○ Label matches used for scoring ●

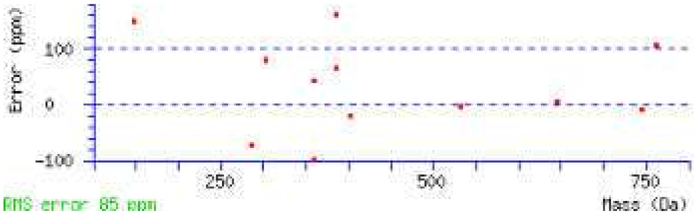
Monoisotopic mass of neutral peptide Mr(calc): 1022.5033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 2.2
Matches : 12/99 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808			100.0757			44.0495	**V**						8
2	136.0757	235.1441			263.1390				**Y**	816.3846		924.4421	907.4156	906.4316	7
3	88.0393	350.1710		332.1605	378.1660		360.1554	306.1812	**D**	701.3577	700.3624	***761.3788***	744.3523	743.3682	6
4	88.0393	465.1980		447.1874	493.1929		475.1823	421.2082	**D**	586.3307	585.3355	***646.3519***	629.3253	628.3413	5
5	102.0550	594.2406		576.2300	622.2355		604.2249	536.2351	**E**	457.2881	456.2929	***531.3249***	514.2984	513.3144	4
6	72.0808	693.3090		675.2984	721.3039		703.2933	679.2933	**V**	358.2197	371.2401	***402.2823***	385.2558		3
7	129.1135	849.4101	832.3836	831.3995	877.4050	860.3785	859.3945	764.3461	**R**	202.1186	201.1234	***303.2139***	286.1874		2
8	101.1073								**K**	74.0237	73.0284	***147.1128***	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YD	251.1026	279.0975	**YDD**	366.1296	394.1245	**YDDE**	495.1722	523.1671
YDDEV	594.2406	622.2355	**DD**	203.0662	231.0612	**DDE**	332.1088	360.1038
DDEV	431.1773	459.1722	**DDEVR**	587.2784	615.2733	**DE**	217.0819	245.0768
DEV	316.1503	344.1452	**DEVR**	472.2514	500.2463	**EV**	201.1234	229.1183

EVR	357.2245	385.2194	**VR**	228.1819	256.1768			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.2	1022.3975	0.1001	DMDDEVQR
30.2	1022.5033	-0.0056	VYDDEVRK
20.9	1022.4702	0.0274	DMTEEVRK
18.4	1022.5145	-0.0169	KDAGEGPPPR
17.4	1022.5734	-0.0757	RVQTHVQR
16.2	1022.4274	0.0703	CTACPTSAR
15.7	1022.5066	-0.0090	KGMITDSGSK
14.4	1022.5145	-0.0169	DYVDRLSR
14.4	1022.5145	-0.0169	EFTDRLSR
14.4	1022.5033	-0.0057	YVDDIVGSR

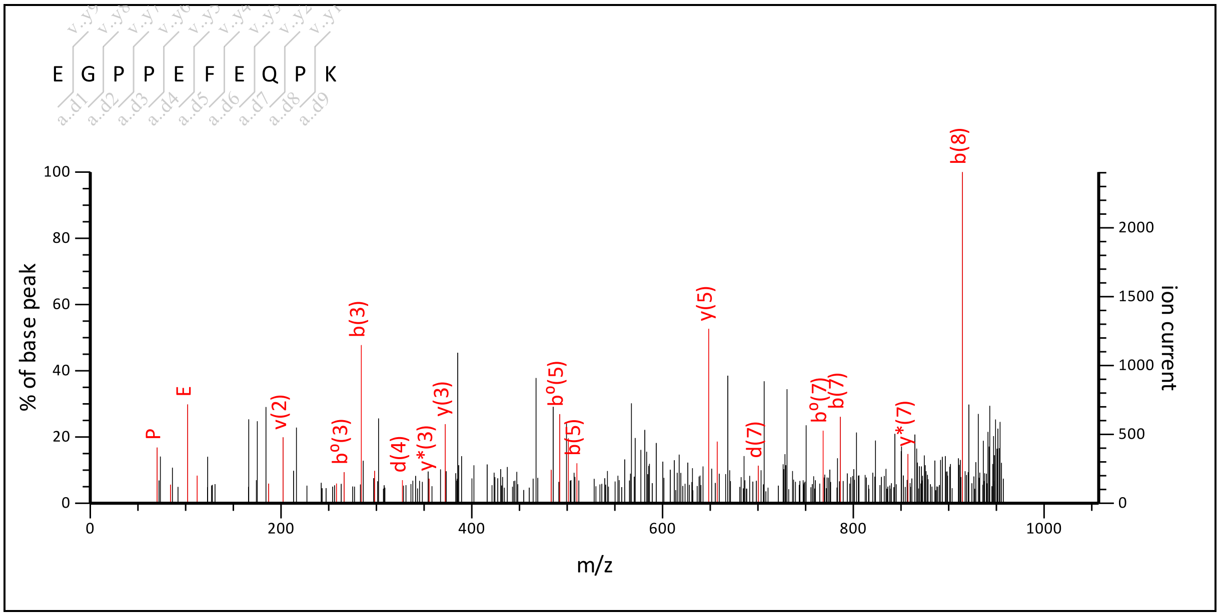
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **EGPPEFEQPK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 37: 1156.524424 from(1157.531700,1+) intensity(0.0000) index(14)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225228, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



0 to 1057.26

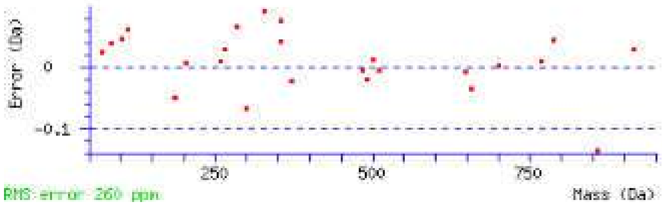
Label all possible matches ○ Label matches used for scoring ●

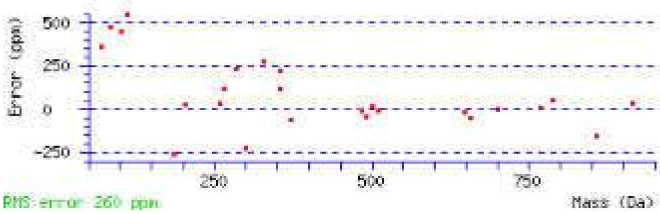
Monoisotopic mass of neutral peptide Mr(calc): 1156.5400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 10 **Expect:** 1.6e+02
Matches : 32/142 fragment ions using 90 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495	E						10
2	30.0338	159.0764		141.0659	***187.0713***		169.0608		G			1028.5047	1011.4782	1010.4942	9
3	70.0651	256.1292		238.1186	***284.1241***		266.1135	230.1135	P	929.4363	928.4411	971.4833	954.4567	953.4727	8
4	70.0651	353.1819		335.1714	381.1769		363.1663	327.1663	P	832.3836	831.3883	874.4305	857.4040	856.4199	7
5	102.0550	482.2245		464.2140	***510.2195***		492.2089	424.2191	E	703.3410	702.3457	777.3777	760.3512	759.3672	6
6	120.0808	629.2930		611.2824	***657.2879***		639.2773		F	556.2726		**648.3352**	631.3086	630.3246	5
7	102.0550	758.3355		740.3250	***786.3305***		768.3199	700.3301	E	427.2300	426.2347	**501.2667**	484.2402	483.2562	4
8	101.0709	886.3941	869.3676	868.3836	***914.3890***	897.3625	896.3785	829.3727	Q	299.1714	298.1761	**372.2241**	355.1976		3
9	70.0651	983.4469	966.4203	965.4363	1011.4418	994.4153	993.4312	957.4312	P	202.1186	201.1234	244.1656	227.1390		2
10	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPE	353.1819	381.1769
GPPEF	500.2504	528.2453	GPPEFE	629.2930	657.2879	PP	167.1179	195.1128
PPE	296.1605	324.1554	PPEF	443.2289	471.2238	PPEFE	572.2715	600.2664
PE	199.1077	227.1026	PEF	346.1761	374.1710	PEFE	475.2187	503.2136

PEFEQ	603.2773	631.2722	**EF**	249.1234	277.1183	**EFE**	378.1660	406.1609
EFEQ	506.2245	534.2195	**EFEQP**	603.2773	631.2722	**FE**	249.1234	277.1183
FEQ	377.1819	405.1769	**FEQP**	474.2347	502.2296	**EQ**	230.1135	258.1084
EQP	327.1663	355.1612	**QP**	198.1237	226.1186			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.8	1156.6088	-0.0844	EKDGAVQVSPK
14.8	1156.5585	-0.0340	EQGADSPAARR
13.3	1156.5989	-0.0745	QSVGLYTHPR
12.4	1156.5811	-0.0567	GWAGLQCIPR
12.2	1156.5877	-0.0632	AWDQSPTPKK
10.9	1156.6200	-0.0956	TALSKGNNQPK
10.4	1156.4852	0.0392	MNKSGGGEMSK
10.3	1156.5400	-0.0156	EGPPEFEQPK
10.2	1156.5546	-0.0302	LMDPEGPNLR
9.7	1156.6200	-0.0956	AVSGGLAEGLQR

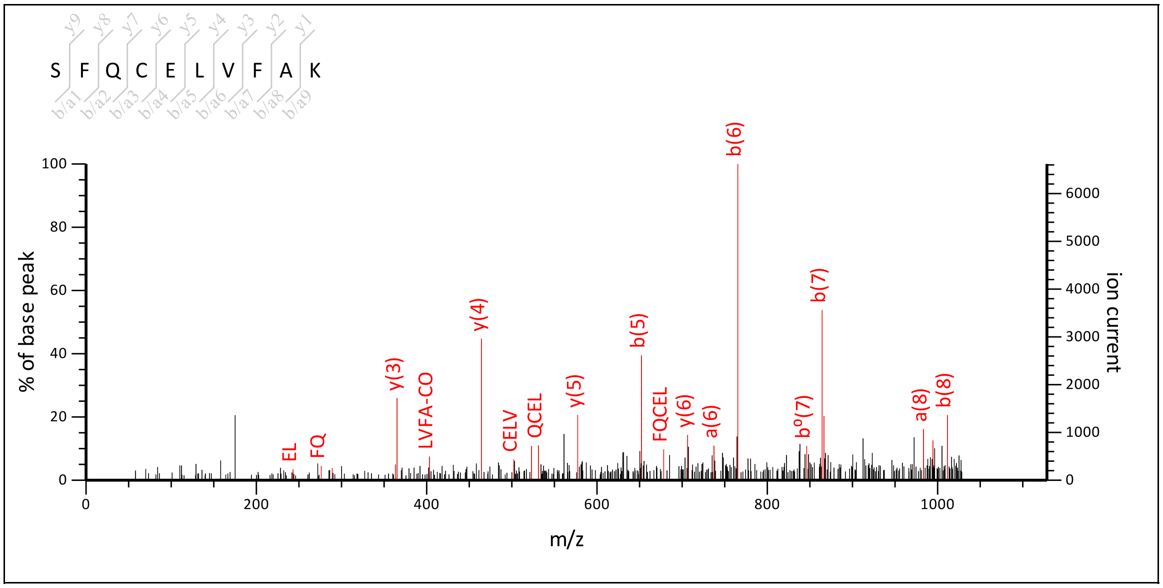
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **SFQCELVFAK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 45: 1227.577724 from(1228.585000,1+) intensity(0.0000) index(17)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225215, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



0 to 1128.36

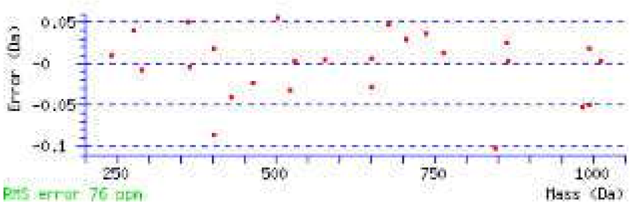
Label all possible matches ○ Label matches used for scoring ●

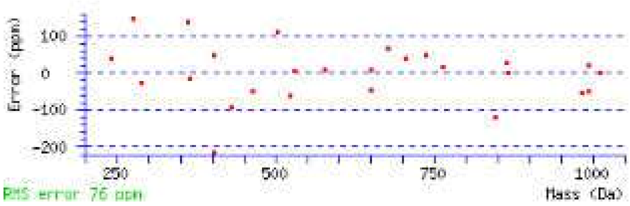
Monoisotopic mass of neutral peptide Mr(calc): 1227.5958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.48
Matches : 26/148 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495	S						10
2	120.0808	207.1128		189.1022	235.1077		217.0972		F	1049.5084		1141.5710	1124.5445	1123.5605	9
3	101.0709	335.1714	318.1448	317.1608	***363.1663***	346.1397	345.1557	278.1499	Q	921.4499	920.4546	***994.5026***	977.4761	976.4921	8
4	133.0430	495.2020	478.1755	477.1915	***523.1969***	506.1704	505.1864	406.2085	C	761.4192	760.4240	***866.4441***	849.4175	848.4335	7
5	102.0550	624.2446	607.2181	606.2341	***652.2395***	635.2130	634.2290	566.2391	E	632.3766	631.3814	***706.4134***	689.3869	688.4028	6
6	86.0964	**737.3287**	720.3021	719.3181	***765.3236***	748.2971	747.3130	695.2817	L	519.2926	518.2973	***577.3708***	560.3443		5
7	72.0808	836.3971	819.3706	818.3865	***864.3920***	847.3655	846.3815	822.3815	V	420.2241	433.2445	***464.2867***	447.2602		4
8	120.0808	**983.4655**	966.4390	965.4549	***1011.4604***	994.4339	993.4499		F	273.1557		***365.2183***	348.1918		3
9	44.0495	1054.5026	1037.4761	1036.4921	1082.4975	1065.4710	1064.4870		A	202.1186		218.1499	201.1234		2
10	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQC	408.1700	436.1649	FQCE	537.2126	565.2075
FQCEL	650.2967	678.2916	QC	261.1016	289.0965	QCE	390.1442	418.1391
QCEL	503.2282	531.2232	QCELV	602.2967	630.2916	CE	262.0856	290.0805
CEL	375.1697	403.1646	CELV	474.2381	502.2330	CELVF	621.3065	649.3014
CELVFA	692.3436	720.3385	EL	215.1390	243.1339	ELV	314.2074	342.2023
ELVF	461.2758	489.2708	ELVFA	532.3130	560.3079	LV	185.1648	213.1598
LVF	332.2333	360.2282	LVFA	403.2704	431.2653	VF	219.1492	247.1441

VFA	290.1863	318.1812	**FA**	191.1179	219.1128			





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

All matches to this query

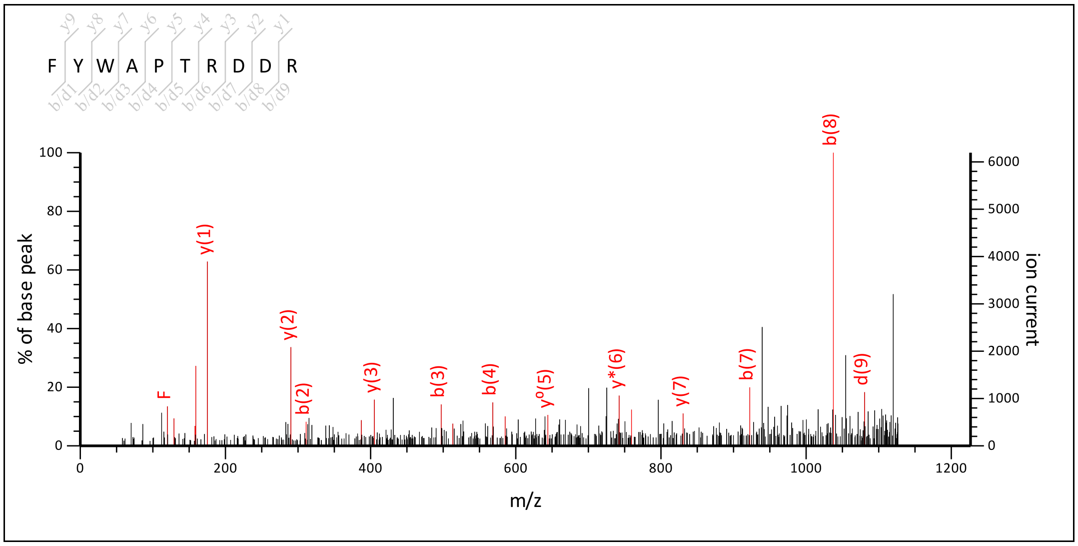
Score	Mr(calc)	Delta	Sequence
37.4	1227.5628	0.0149	SFQCELVMAK
36.1	1227.5958	-0.0181	SFQCELVFAK
36.0	1227.6208	-0.0430	KVHPESSTSTR
29.6	1227.5628	0.0149	SFQCELVMSK
29.4	1227.5376	0.0401	FGCVSTMASPR
24.2	1227.5992	-0.0214	GCFVIKTEMK
23.3	1227.6248	-0.0470	HKPTSESPFAK
23.2	1227.4860	0.0917	ECSSLTSECR
20.8	1227.5488	0.0289	RDCYGLAMAR
20.1	1227.6499	-0.0722	KFSVDISYAAK

Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **FYWAPTRDDR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 58: 1325.603924 from(1326.611200,1+) intensity(0.0000) index(20)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225217, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



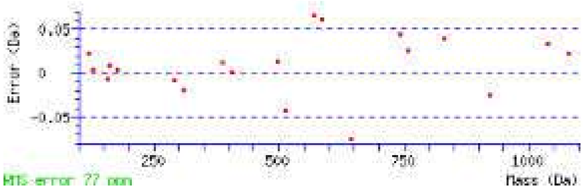
0 to 1226.51

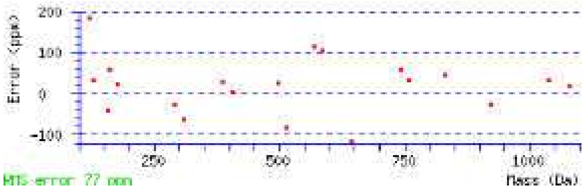
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1325.6153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 3.7
Matches : 23/138 fragment ions using 33 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y
1	120.0808	120.0808			148.0757			44.0495		F						
2	136.0757	283.1441			***311.1390***					Y	1071.4966			1179.5541	1162.5276	1161.
3	159.0917	469.2234			***497.2183***					W	885.4173			1016.4908	999.4643	998.
4	44.0495	540.2605			***568.2554***					A	814.3802			***830.4115***	813.3850	812.
5	70.0651	637.3133			665.3082			611.2976		P	717.3274	716.3322		***759.3744***	742.3478	741.
6	74.0600	738.3610		720.3504	766.3559		748.3453	722.3661	724.3453	T	616.2798	629.3002	631.2794	662.3216	645.2951	644.
7	129.1135	894.4621	877.4355	876.4515	***922.4570***	905.4305	904.4464	809.3981		R	460.1787	459.1834		561.2739	544.2474	543.
8	88.0393	1009.4890	992.4625	991.4785	***1037.4839***	1020.4574	1019.4734	965.4992		D	345.1517	344.1565		***405.1728***	388.1463	387.
9	88.0393	1124.5160	1107.4894	1106.5054	1152.5109	1135.4843	1134.5003	1080.5261		D	230.1248	229.1295		***290.1459***	273.1193	272.
10	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YW	322.1550	350.1499	**YWA**	393.1921	421.1870	**YWAP**	490.2449	518.2398
YWAPT	591.2926	619.2875	**WA**	230.1288	258.1237	**WAP**	327.1816	355.1765
WAPT	428.2292	456.2241	**WAPTR**	584.3303	612.3253	**WAPTRD**	699.3573	727.3522
AP	141.1022	169.0972	**APT**	242.1499	270.1448	**APTR**	398.2510	426.2459
APTRD	513.2780	541.2729	**APTRDD**	628.3049	656.2998	**PT**	171.1128	199.1077
PTR	327.2139	355.2088	**PTRD**	442.2409	470.2358	**PTRDD**	557.2678	585.2627
TR	230.1612	258.1561	**TRD**	345.1881	373.1830	**TRDD**	460.2150	488.2100
RD	244.1404	272.1353	**RDD**	359.1674	387.1623	**DD**	203.0662	231.0612





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.9	1325.6153	-0.0114	FYWAPTRDDR
16.2	1325.5710	0.0329	MQVWVDYDDR
15.2	1325.5921	0.0118	KMETPPSSYDR
15.1	1325.6186	-0.0147	MWAYNDVAKGR
14.7	1325.6252	-0.0212	GIPYLNTYDDR
14.0	1325.6649	-0.0610	METIKVTSFDR
13.8	1325.7052	-0.1012	TPDAAVLGRSPSR
13.7	1325.6616	-0.0576	TLFLVNAYDDR
13.1	1325.6954	-0.0915	FFMWLALKDR
12.5	1325.7092	-0.1053	VFALHADAVLDR

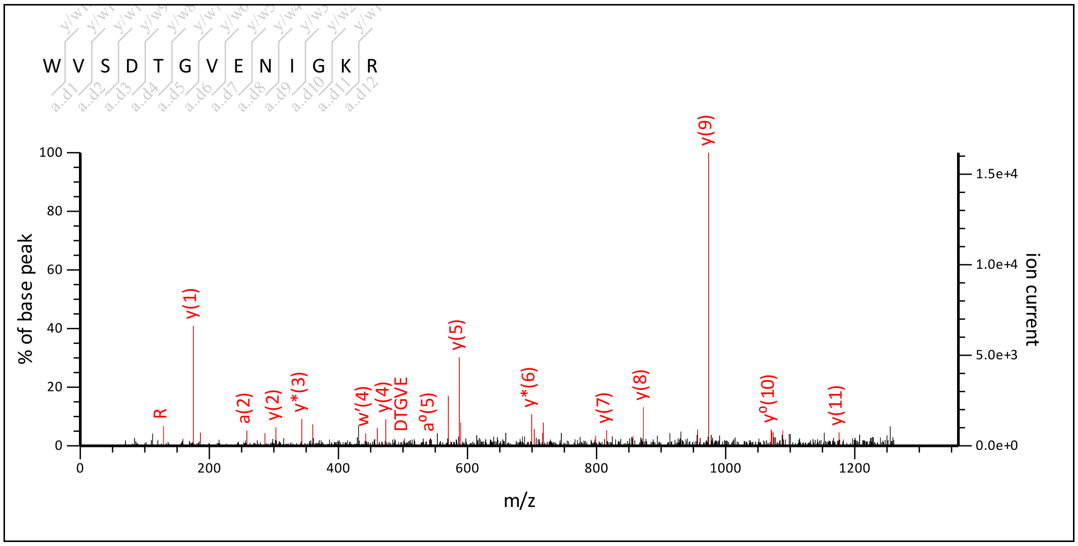
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **WVSDTGVENIGKR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 69: 1459.736224 from(1460.743500,1+) intensity(0.0000) index(24)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225216, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



0 to 1360.59

Label all possible matches ○ Label matches used for scoring ●

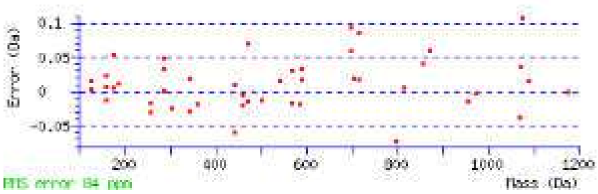
Monoisotopic mass of neutral peptide Mr(calc): 1459.7419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 85 **Expect:** 6.9e-06
Matches : 49/217 fragment ions using 48 most intense peaks (help)

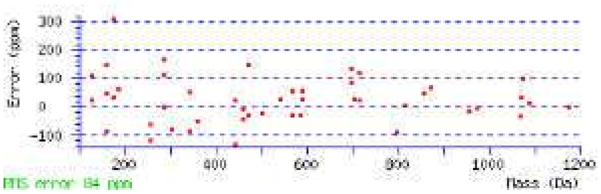
#0000FF>13

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	159.0917	**159.0917**			187.0866			44.0495		**W**					
2	72.0808	**258.1601**			**286.1550**			244.1444		**V**	1230.6073	1243.6277		1274.6699	1257.6434
3	60.0444	345.1921		327.1816	373.1870		355.1765	329.1972		**S**	1143.5753	1142.5800		***1175.6015***	1158.5749
4	88.0393	**460.2191**		442.2085	488.2140		470.2034	416.2292		**D**	1028.5483	1027.5531		***1088.5695***	1071.5429
5	74.0600	561.2667		543.2562	**589.2617**		571.2511	545.2718	547.2511	**T**	927.5007	940.5211	942.5003	***973.5425***	956.5160
6	30.0338	618.2882		600.2776	646.2831		628.2726			**G**				***872.4948***	855.4683
7	72.0808	**717.3566**		699.3461	745.3515		727.3410	703.3410		**V**	771.4108	784.4312		***815.4734***	798.4468
8	102.0550	846.3992		828.3886	874.3941		856.3836	788.3937		**E**	642.3682	641.3729		***716.4050***	699.3784
9	87.0553	960.4421	943.4156	942.4316	988.4371	971.4105	970.4265	917.4363		**N**	528.3253	527.3300		***587.3624***	570.3358
10	86.0964	**1073.5262**	1056.4997	1055.5156	1101.5211	1084.4946	1083.5105	1045.4949	1059.5105	**I**	415.2412	129.1135			

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb									
VS	159.1128	187.1077	**VSD**	274.1397	302.1347	**VSDT**	375.1874	403.1823									
VSDTG	432.2089	460.2038	**VSDTGV**	531.2773	559.2722	**VSDTGVE**	660.3199	688.3148	428.2616	442.2772	***473.3194***	456.2929		**4**			
11	30.0338	1130.5477	1113.5211	1112.5371	1158.5426	1141.5160	1140.5320			**G**				***360.2354***	343.2088		**3**
12	101.1073	1258.6426	1241.6161	1240.6321	1286.6375	1269.6110	1268.6270	1201.5848		**K**	230.1248	229.1295		***303.2139***	286.1874		**2**
SD	175.0713	203.0662	**SDT**	276.1190	304.1139	**SDTG**	333.1405	361.1354									
SDTGV	432.2089	460.2038	**SDTGVE**	561.2515	589.2464	**SDTGVEN**	675.2944	703.2893									
DT	189.0870	217.0819	**DTG**	246.1084	274.1034	**DTGV**	345.1769	373.1718									
DTGVE	474.2195	502.2144	**DTGVEN**	588.2624	616.2573	**TG**	131.0815	159.0764									
TGV	230.1499	258.1448	**TGVE**	359.1925	387.1874	**TGVEN**	473.2354	501.2304									
TGVENI	586.3195	614.3144	**TGVENIG**	643.3410	671.3359	**GV**	129.1022	157.0972									

GVE	258.1448	286.1397	**GVEN**	372.1878	400.1827	**GVENI**	485.2718	513.2667
GVENIG	542.2933	570.2882	**GVENIGK**	670.3882	698.3832	**VE**	201.1234	229.1183
VEN	315.1663	343.1612	**VENI**	428.2504	456.2453	**VENIG**	485.2718	513.2667
VENIGK	613.3668	641.3617	**EN**	216.0979	244.0928	**ENI**	329.1819	357.1769
ENIG	386.2034	414.1983	**ENIGK**	514.2984	542.2933	**NI**	200.1394	228.1343
NIG	257.1608	285.1557	**NIGK**	385.2558	413.2507	**IG**	143.1179	171.1128
IGK	271.2129	299.2078	**GK**	158.1288	186.1237			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.9	1459.7419	-0.0057	WVSDTGVENIGKR
30.6	1459.6652	0.0711	TDEAGGVNQTGAGGAR
30.5	1459.7783	-0.0421	WVTSTGIENIGKR
25.6	1459.6653	0.0709	YYPTTSPLSMER
21.4	1459.7267	0.0095	ATDITINGGGTIDGR
21.3	1459.7630	-0.0268	TALSDVKLNESQR
20.0	1459.6903	0.0459	GNNTDSGVDLEAIR
19.9	1459.7419	-0.0057	ERYVGAPVDLEGR
19.1	1459.7089	0.0273	ADVLAQQAGMDIGR
18.9	1459.6539	0.0823	EADEGANAGADSVVR

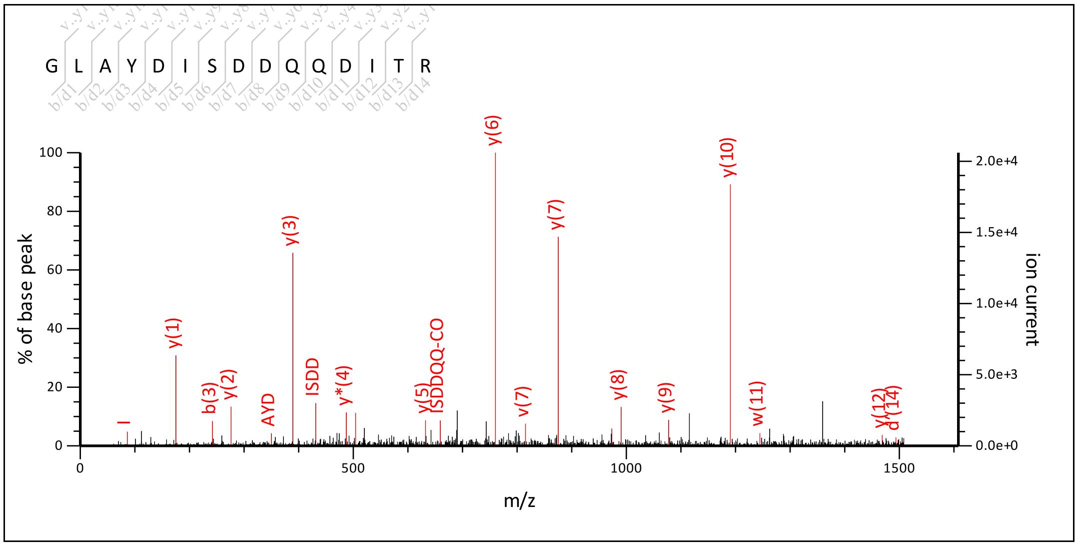
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **GLAYDISDDQQDITR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 79: 1708.780824 from(1709.788100,1+) intensity(0.0000) index(27)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225214, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



0 to 1608.15

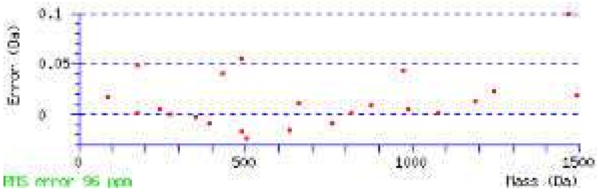
Label all possible matches ○ Label matches used for scoring ●

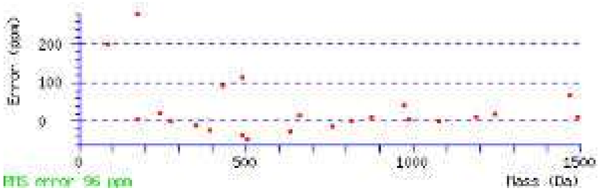
```
Monoisotopic mass of neutral peptide Mr(calc): 1708.7904
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 87  Expect: 3.4e-06
Matches : 27/255 fragment ions using 30 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			101.0709		L	1594.6980	1593.7027		1652.7762	1635.7497
3	44.0495	214.1550			242.1499					A	1523.6609			1539.6922	1522.6656
4	136.0757	377.2183			405.2132					Y	1360.5975			***1468.6550***	1451.6285
5	88.0393	492.2453		474.2347	520.2402		502.2296	448.2554		D	1245.5706	1244.5753		1305.5917	1288.5652
6	86.0964	605.3293		587.3188	633.3243		615.3137	577.2980	591.3137	I	1132.4865	1145.5069	1159.5226	***1190.5648***	1173.5382
7	60.0444	692.3614		674.3508	720.3563		702.3457	676.3665		S	1045.4545	1044.4592		***1077.4807***	1060.4542
8	88.0393	807.3883		789.3777	835.3832		817.3727	763.3985		D	930.4276	929.4323		***990.4487***	973.4221
9	88.0393	922.4153		904.4047	950.4102		932.3996	878.4254		D	815.4006	814.4054		***875.4217***	858.3952
10	101.0709	1050.4738	1033.4473	1032.4633	1078.4687	1061.4422	1060.4582	993.4524		Q	687.3420	686.3468		***760.3948***	743.3682
11	101.0709	1178.5324	1161.5059	1160.5218	1206.5273	1189.5008	1188.5168	1121.5109		Q	559.2835	558.2882		***632.3362***	615.3097
12	88.0393	1293.5594	1276.5328	1275.5488	1321.5543	1304.5277	1303.5437	1249.5695		D	444.2565	443.2613		***504.2776***	487.2511
13	86.0964	1406.6434	1389.6169	1388.6329	1434.6383	1417.6118	1416.6278	1378.6121	1392.6278	I	331.1724	344.1928	358.2085	***389.2507***	372.2241
14	74.0600	1507.6911	1490.6645	1489.6805	1535.6860	1518.6595	1517.6754	1491.6962	1493.6754	T	230.1248	243.1452	245.1244	***276.1666***	259.1401
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LA	157.1335	185.1285	LAY	320.1969	348.1918	LAYD	435.2238	463.2187
LAYDI	548.3079	576.3028	LAYDIS	635.3399	663.3348	AY	207.1128	235.1077
AYD	322.1397	350.1347	AYDI	435.2238	463.2187	AYDIS	522.2558	550.2508
AYDISD	637.2828	665.2777	YD	251.1026	279.0975	YDI	364.1867	392.1816
YDIS	451.2187	479.2136	YDISD	566.2457	594.2406	YDISDD	681.2726	709.2675
DI	201.1234	229.1183	DIS	288.1554	316.1503	DISD	403.1823	431.1773

DISDD	518.2093	546.2042	**DISDDQ**	646.2679	674.2628	**IS**	173.1285	201.1234
ISD	288.1554	316.1503	**ISDD**	403.1823	431.1773	**ISDDQ**	531.2409	559.2358
ISDDQQ	659.2995	687.2944	**SD**	175.0713	203.0662	**SDD**	290.0983	318.0932
SDDQ	418.1569	446.1518	**SDDQQ**	546.2154	574.2103	**SDDQQD**	661.2424	689.2373
DD	203.0662	231.0612	**DDQ**	331.1248	359.1197	**DDQQ**	459.1834	487.1783
DDQQD	574.2103	602.2053	**DDQQDI**	687.2944	715.2893	**DQ**	216.0979	244.0928
DQQ	344.1565	372.1514	**DQQD**	459.1834	487.1783	**DQQDI**	572.2675	600.2624
DQQDIT	673.3151	701.3101	**QQ**	229.1295	257.1244	**QQD**	344.1565	372.1514
QQDI	457.2405	485.2354	**QQDIT**	558.2882	586.2831	**QD**	216.0979	244.0928
QDI	329.1819	357.1769	**QDIT**	430.2296	458.2245	**DI**	201.1234	229.1183
DIT	302.1710	330.1660	**IT**	187.1441	215.1390			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.8	1708.7904	-0.0096	GLAYDISDDQQDITR
66.9	1708.7540	0.0268	GLAFDESDDQQDITR
38.6	1708.7978	-0.0170	GLSTDSLMEAGYPGAPK
18.6	1708.8302	-0.0493	MSDGITVTESISQIGR
18.2	1708.7760	0.0048	LDVMSNGATMEAAVER
18.2	1708.9009	-0.1201	ANIHALSGAWGDKLTR
17.3	1708.8679	-0.0871	SHIQKAGLDMSHTIR
14.7	1708.8784	-0.0976	FSNGANFAIVGSSTLPK
14.6	1708.8203	-0.0394	AYAMVRLEADGQVDR
14.6	1708.8600	-0.0792	VASTSDLMSLMRLNR

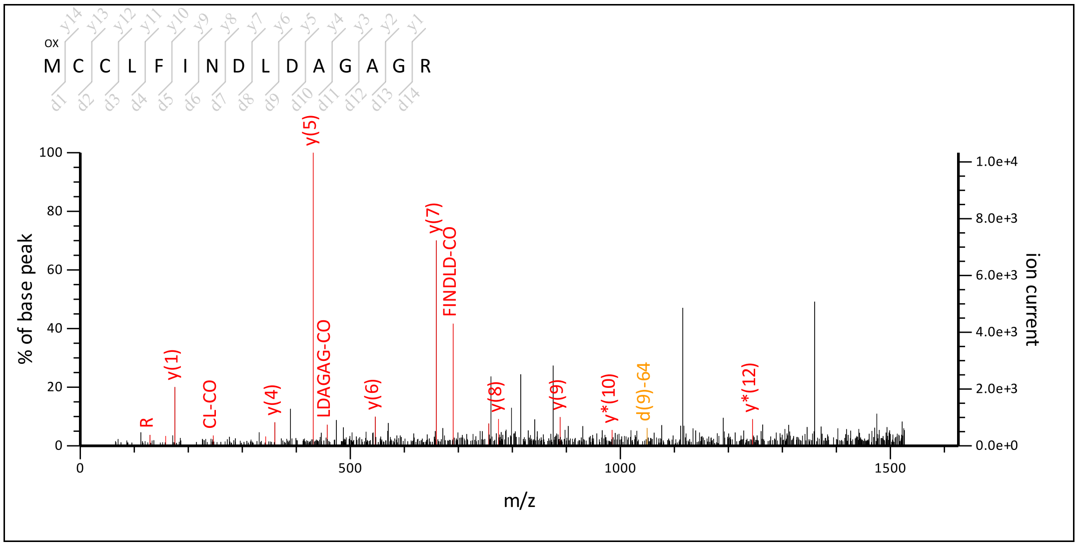
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **MCCLFINDLDAGAGR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 82: 1727.720424 from(1728.727700,1+) intensity(0.0000) index(28)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225219, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



0 to 1625.91

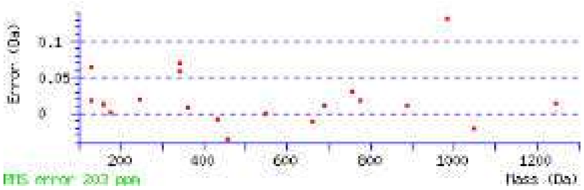
Label all possible matches ○ Label matches used for scoring ●

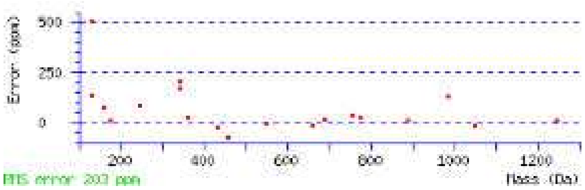
```
Monoisotopic mass of neutral peptide Mr(calc): 1727.7430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 22  Expect: 6.5
Matches : 23/311 fragment ions using 45 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	56.0495	56.0495			84.0444			44.0495		M						
2	133.0430	216.0801			244.0750			127.0866		C	1476.6900	1475.6947		1581.7148	1564.6883	156
3	133.0430	376.1108			404.1057			287.1172		C	1316.6593	1315.6641		1421.6842	1404.6576	140
4	86.0964	489.1948			517.1898			447.1479		L	1203.5753	1202.5800		1261.6535	1244.6270	124
5	120.0808	636.2633			664.2582					F	1056.5069			1148.5695	1131.5429	113
6	86.0964	749.3473			777.3422			721.3160	735.3317	I	943.4228	956.4432	970.4588	1001.5010	984.4745	98
7	87.0553	863.3902	846.3637		891.3852	874.3586		820.3844		N	829.3799	828.3846		***888.4170***	871.3904	87
8	88.0393	978.4172	961.3906	960.4066	1006.4121	989.3856	988.4015	934.4274		D	714.3529	713.3577		***774.3741***	757.3475	75
9	86.0964	1091.5013	1074.4747	1073.4907	1119.4962	1102.4696	1101.4856	1049.4543		L	601.2689	600.2736		***659.3471***	642.3206	64
10	88.0393	1206.5282	1189.5016	1188.5176	1234.5231	1217.4966	1216.5125	1162.5384		D	486.2419	485.2467		***546.2631***	529.2365	52
11	44.0495	1277.5653	1260.5388	1259.5547	1305.5602	1288.5337	1287.5497			A	415.2048			***431.2361***	414.2096	
12	30.0338	1334.5868	1317.5602	1316.5762	1362.5817	1345.5551	1344.5711			G				***360.1990***	343.1724	
13	44.0495	1405.6239	1388.5973	1387.6133	1433.6188	1416.5923	1415.6082			A	287.1462			303.1775	286.1510	
14	30.0338	1462.6453	1445.6188	1444.6348	1490.6403	1473.6137	1472.6297			G				232.1404	215.1139	
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
CC	293.0737	321.0686	CCL	406.1577	434.1526	CCLF	553.2261	581.2211
CCLFI	666.3102	694.3051	CL	246.1271	274.1220	CLF	393.1955	421.1904
CLFI	506.2796	534.2745	CLFIN	620.3225	648.3174	LF	233.1648	261.1598

LFI	346.2489	374.2438	**LFIN**	460.2918	488.2867	**LFIND**	575.3188	603.3137
LFINDL	688.4028	716.3978	**FI**	233.1648	261.1598	**FIN**	347.2078	375.2027
FIND	462.2347	490.2296	**FINDL**	575.3188	603.3137	**FINDLD**	690.3457	718.3406
IN	200.1394	228.1343	**IND**	315.1663	343.1612	**INDL**	428.2504	456.2453
INDLD	543.2773	571.2722	**INDLDA**	614.3144	642.3093	**INDLDAG**	671.3359	699.3308
ND	202.0822	230.0771	**NDL**	315.1663	343.1612	**NDLD**	430.1932	458.1882
NDLDA	501.2304	529.2253	**NDLDAG**	558.2518	586.2467	**NDLDAGA**	629.2889	657.2838
NDLDAGAG	686.3104	714.3053	**DL**	201.1234	229.1183	**DLD**	316.1503	344.1452
DLDA	387.1874	415.1823	**DLDAG**	444.2089	472.2038	**DLDAGA**	515.2460	543.2409
DLDAGAG	572.2675	600.2624	**LD**	201.1234	229.1183	**LDA**	272.1605	300.1554
LDAG	329.1819	357.1769	**LDAGA**	400.2191	428.2140	**LDAGAG**	457.2405	485.2354
DA	159.0764	187.0713	**DAG**	216.0979	244.0928	**DAGA**	287.1350	315.1299
DAGAG	344.1565	372.1514	**AG**	101.0709	129.0659	**AGA**	172.1081	200.1030
AGAG	229.1295	257.1244	**GA**	101.0709	129.0659	**GAG**	158.0924	186.0873
AG	101.0709	129.0659						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.1	1727.8559	-0.1355	GHVMMLNDRIQSVGR
22.4	1727.7430	-0.0225	MCCLFINDLDAGAGR
17.8	1727.8559	-0.1355	GHVMMLNDRIQSVGR
17.2	1727.8559	-0.1355	GHVMMLNDRVQSLGR
14.3	1727.8269	-0.1065	ASLCALMAPVGGHAAMR
12.4	1727.7832	-0.0627	MAPAGGGDSPCASARAPR
12.3	1727.7607	-0.0403	EEELDMFCRNITR
11.8	1727.7780	-0.0576	IMDDESVMPTTKMSK
11.6	1727.8764	-0.1559	GSNIELMLDVPNEGLK
11.2	1727.8070	-0.0866	SPGTTGSVKTGMTMTEK

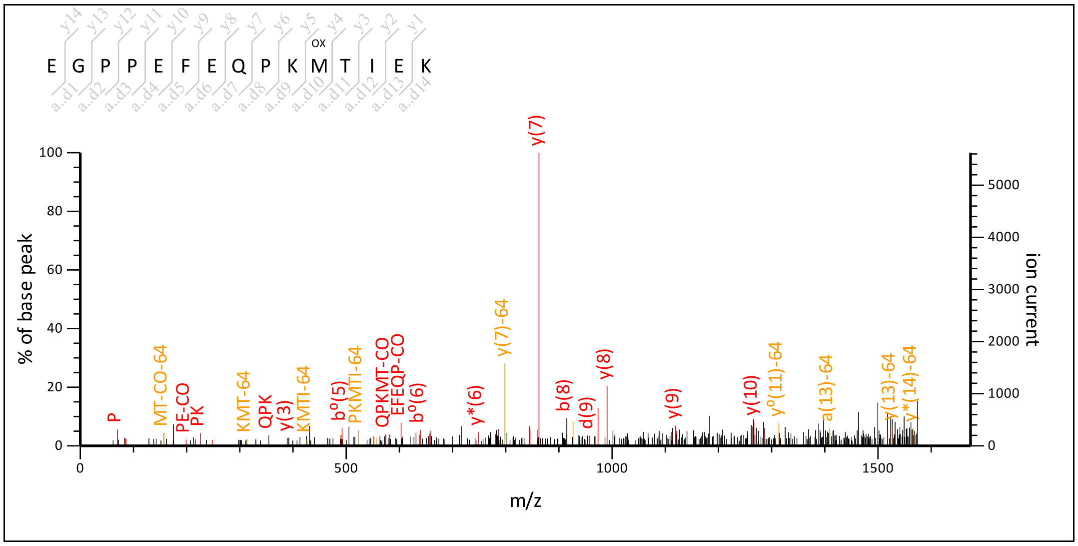
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 67

MS/MS Fragmentation of **EGPPEFEQPKMTIEK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 84: 1774.819624 from(1775.826900,1+) intensity(0.0000) index(29)
Title: Label: D4, Spot_Id: 219725, Peak_List_Id: 225223, MSMS Job_Run_Id: 21770, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D4_136842162200.txt



0 to 1674

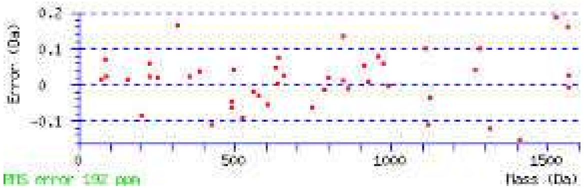
Label all possible matches ○ Label matches used for scoring ●

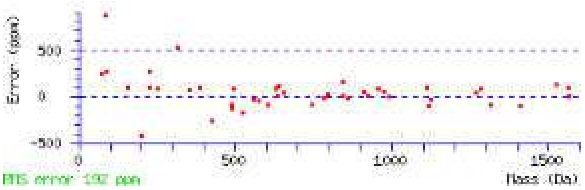
Monoisotopic mass of neutral peptide Mr(calc): 1774.8447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 9 **Expect:** 2e+02
Matches : 50/358 fragment ions using 128 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	30.0338	159.0764		141.0659	187.0713		169.0608			G				1646.8094	1629.7829
3	70.0651	256.1292		238.1186	284.1241		266.1135	230.1135		P	1547.7410	1546.7458		1589.7880	1572.7614
4	70.0651	353.1819		335.1714	381.1769		363.1663	327.1663		P	1450.6883	1449.6930		1492.7352	1475.7087
5	102.0550	482.2245		464.2140	510.2195		492.2089	424.2191		E	1321.6457	1320.6504		1395.6824	1378.6559
6	120.0808	629.2930		611.2824	**657.2879**		639.2773			F	1174.5773			***1266.6399***	1249.6133
7	102.0550	758.3355		740.3250	**786.3305**		768.3199	700.3301		E	1045.5347	1044.5394		***1119.5714***	1102.5449
8	101.0709	886.3941	869.3676	868.3836	**914.3890**	897.3625	896.3785	829.3727		Q	917.4761	916.4808		***990.5288***	973.5023
9	70.0651	983.4469	966.4203	965.4363	1011.4418	994.4153	993.4312	957.4312		P	820.4233	819.4281		***862.4703***	845.4437
10	101.1073	1111.5419	1094.5153	1093.5313	1139.5368	1122.5102	1121.5262	1054.4840		K	692.3284	691.3331		765.4175	748.3910
11	120.0478	1258.5773	1241.5507	1240.5667	**1286.5722**	1269.5456	1268.5616	1182.5790		M	545.2930	544.2977		***637.3225***	620.2960
12	74.0600	1359.6249	1342.5984	1341.6144	1387.6198	1370.5933	1369.6093	1343.6300	1345.6093	T	444.2453	457.2657	459.2449	***490.2871***	473.2606
13	86.0964	1472.7090	1455.6824	1454.6984	1500.7039	1483.6774	1482.6933	1444.6777	1458.6933	I	331.1612	344.1816	358.1973	***389.2395***	372.2129
14	102.0550	1601.7516	1584.7250	1583.7410	1629.7465	1612.7200	1611.7359	1543.7461		E	202.1186	201.1234		276.1554	259.1288
15	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GP	127.0866	155.0815	**GPP**	224.1394	252.1343	**GPPE**	353.1819	381.1769
GPPEF	500.2504	528.2453	**GPPEFE**	629.2930	657.2879	**PP**	167.1179	195.1128
PPE	296.1605	324.1554	**PPEF**	443.2289	471.2238	**PPEFE**	572.2715	600.2664

PE	199.1077	227.1026	**PEF**	346.1761	374.1710	**PEFE**	475.2187	503.2136
PEFEQ	603.2773	631.2722	**EF**	249.1234	277.1183	**EFE**	378.1660	406.1609
EFEQ	506.2245	534.2195	**EFEQP**	603.2773	631.2722	**FE**	249.1234	277.1183
FEQ	377.1819	405.1769	**FEQP**	474.2347	502.2296	**FEQPK**	602.3297	630.3246
EQ	230.1135	258.1084	**EQP**	327.1663	355.1612	**EQPK**	455.2613	483.2562
EQPKM	602.2967	630.2916	**QP**	198.1237	226.1186	**QPK**	326.2187	354.2136
QPKM	473.2541	501.2490	**QPKMT**	574.3017	602.2967	**QPKMTI**	687.3858	715.3807
PK	198.1601	226.1550	**PKM**	345.1955	373.1904	**PKMT**	446.2432	474.2381
PKMTI	559.3272	587.3221	**PKMTIE**	688.3698	716.3647	**KM**	248.1427	276.1376
KMT	349.1904	377.1853	**KMTI**	462.2745	490.2694	**KMTIE**	591.3171	619.3120
MT	221.0954	249.0904	**MTI**	334.1795	362.1744	**MTIE**	463.2221	491.2170
TI	187.1441	215.1390	**TIE**	316.1867	344.1816	**IE**	215.1390	243.1339





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
12.5	1774.7138	0.1058	DSNVMYLDKDCEDR
10.8	1774.9829	-0.1633	SLELDKDLSVALLGFR
9.2	1774.9550	-0.1354	VQGPRAALPQAQAAQGGR
9.1	1774.8447	-0.0251	EGPPEFEQPKMTIEK
8.2	1774.9326	-0.1130	TTNYIRIQATGTPSPR
8.2	1774.9260	-0.1064	FTAEAMVRPQLRANR
7.0	1774.9108	-0.0912	VGQMNGSSTRLLTAQGR
6.8	1774.9287	-0.1091	KPNELGFKELGMTPAK
6.8	1774.9552	-0.1356	LWIRTFPDKPVTMR
6.6	1774.9413	-0.1217	ALGTIHSHPVWMVRR

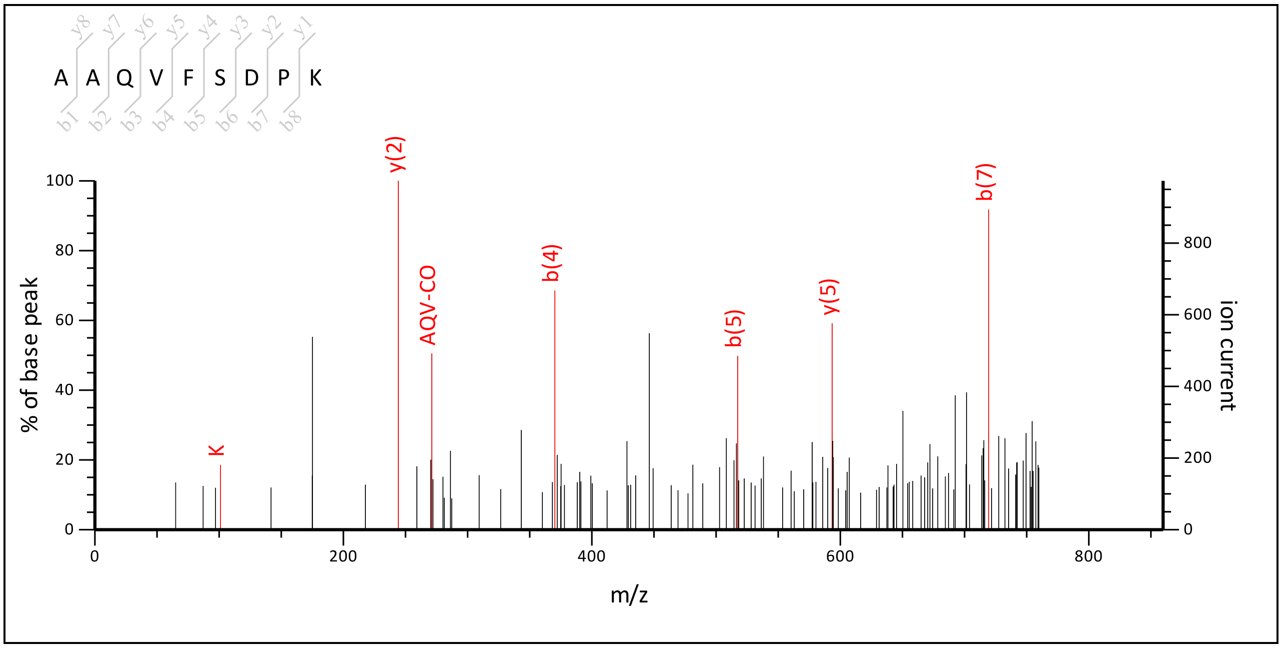
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **AAQVFSDPK**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 15: 961.498704 from(962.505980,1+) intensity(0.0000) index(2)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229185, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 859.79

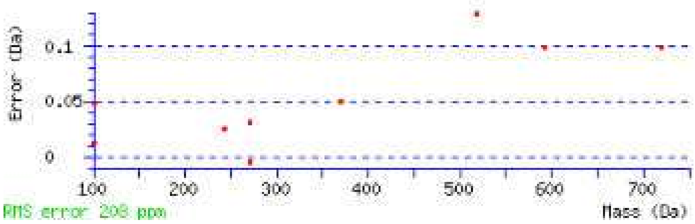
Label all possible matches ○ Label matches used for scoring ●

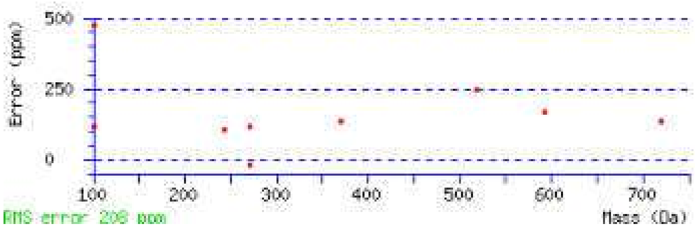
Monoisotopic mass of neutral peptide Mr(calc): 961.4869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 9.9
Matches : 9/125 fragment ions using 7 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495			72.0444			44.0495	A						9
2	44.0495	115.0866			143.0815				A	875.4258		891.4571	874.4305	873.4465	8
3	101.0709	243.1452	226.1186		***271.1401***	254.1135		186.1237	Q	747.3672	746.3719	820.4199	803.3934	802.4094	7
4	72.0808	342.2136	325.1870		***370.2085***	353.1819		328.1979	V	648.2988	661.3192	692.3614	675.3348	674.3508	6
5	120.0808	489.2820	472.2554		***517.2769***	500.2504			F	501.2304		**593.2930**	576.2664	575.2824	5
6	60.0444	576.3140	559.2875	558.3035	604.3089	587.2824	586.2984	560.3191	S	414.1983	413.2031	446.2245	429.1980	428.2140	4
7	88.0393	691.3410	674.3144	673.3304	***719.3359***	702.3093	701.3253	647.3511	D	299.1714	298.1761	359.1925	342.1660	341.1819	3
8	70.0651	788.3937	771.3672	770.3832	816.3886	799.3621	798.3781	762.3781	P	202.1186	201.1234	**244.1656**	227.1390		2
9	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AQ	172.1081	200.1030	AQV	271.1765	299.1714	AQVF	418.2449	446.2398
AQVFS	505.2769	533.2718	AQVFSD	620.3039	648.2988	QV	200.1394	228.1343
QVF	347.2078	375.2027	QVFS	434.2398	462.2347	QVFSD	549.2667	577.2617

QVFSDP	646.3195	674.3144	**VF**	219.1492	247.1441	**VFS**	306.1812	334.1761
VFSD	421.2082	449.2031	**VFSDP**	518.2609	546.2558	**FS**	207.1128	235.1077
FSD	322.1397	350.1347	**FSDP**	419.1925	447.1874	**SD**	175.0713	203.0662
SDP	272.1241	300.1190	**DP**	185.0921	213.0870			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.5	961.4869	0.0118	AAQVFSDPK
36.5	961.5233	-0.0246	AKAVFSDPK
31.2	961.5709	-0.0722	KGLVFVSGR
31.2	961.5709	-0.0722	KVAVFGVSR
31.2	961.5345	-0.0358	QAVVFRDK
31.2	961.5267	-0.0280	QAVVMLGTK
31.2	961.5597	-0.0610	QGLVFAVTK
31.2	961.4981	0.0006	QVAVFQDR
31.2	961.5345	-0.0358	QVAVFSGVR
30.2	961.5345	-0.0358	AGAVVFGVSR

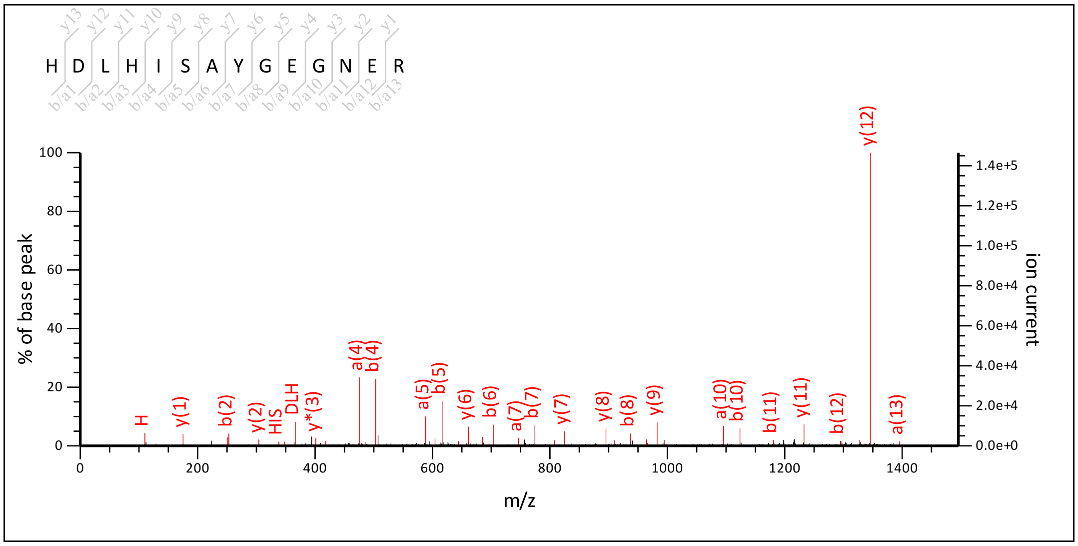
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **HDLHISAYGEGNER**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 112: 1596.776124 from(1597.783400,1+) intensity(0.0000) index(14)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229164, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 1495.79

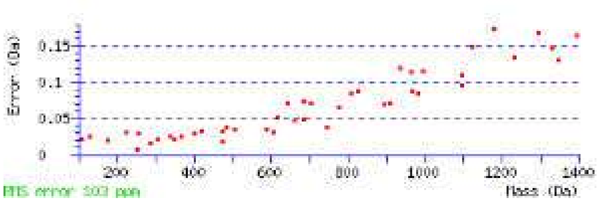
Label all possible matches ○ Label matches used for scoring ●

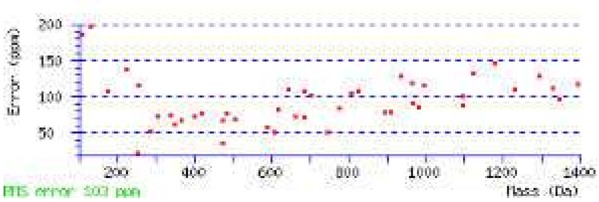
Monoisotopic mass of neutral peptide Mr(calc): 1596.7281
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 1.5e-06
Matches : 52/230 fragment ions using 56 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	110.0713	**110.0713**			138.0662			44.0495		**H**					
2	88.0393	225.0982		207.0877	**253.0931**		235.0826	181.1084		**D**	1400.6553	1399.6601		1460.6764	1443.6499
3	86.0964	**338.1823**		320.1717	**366.1772**		348.1666	296.1353		**L**	1287.5713	1286.5760		***1345.6495***	1328.6230
4	110.0713	**475.2412**		457.2306	**503.2361**		485.2255			**H**	1150.5123			***1232.5654***	1215.5389
5	86.0964	**588.3253**		570.3147	**616.3202**		598.3096	560.2940	574.3096	**I**	1037.4283	1050.4487	1064.4643	***1095.5065***	1078.4800
6	60.0444	675.3573		657.3467	**703.3522**		685.3416	659.3624		**S**	950.3963	949.4010		***982.4225***	965.3959
7	44.0495	**746.3944**		728.3838	**774.3893**		756.3787			**A**	879.3591			***895.3904***	878.3639
8	136.0757	**909.4577**		891.4472	**937.4526**		919.4421			**Y**	716.2958			***824.3533***	807.3268
9	30.0338	**966.4792**		948.4686	**994.4741**		976.4635			**G**				***661.2900***	644.2634
10	102.0550	**1095.5218**		1077.5112	**1123.5167**		1105.5061	1037.5163		**E**	530.2317	529.2365		***604.2685***	587.2420
11	30.0338	1152.5432		1134.5327	**1180.5382**		1162.5276			**G**				***475.2259***	458.1994
12	87.0553	1266.5862	1249.5596	1248.5756	**1294.5811**	1277.5545	1276.5705	1223.5804		**N**	359.1674	358.1721		***418.2045***	401.1779
13	102.0550	**1395.6288**	1378.6022	1377.6182	1423.6237	1406.5971	1405.6131	1337.6233		**E**	230.1248	229.1295		***304.1615***	287.1350
14	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DL	201.1234	229.1183	**DLH**	338.1823	366.1772	**DLHI**	451.2663	479.2613
DLHIS	538.2984	566.2933	**DLHISA**	609.3355	637.3304	**LH**	223.1553	251.1503
LHI	336.2394	364.2343	**LHIS**	423.2714	451.2663	**LHISA**	494.3085	522.3035
LHISAY	657.3719	685.3668	**HI**	223.1553	251.1503	**HIS**	310.1874	338.1823
HISA	381.2245	409.2194	**HISAY**	544.2878	572.2827	**HISAYG**	601.3093	629.3042
IS	173.1285	201.1234	**ISA**	244.1656	272.1605	**ISAY**	407.2289	435.2238
ISAYG	464.2504	492.2453	**ISAYGE**	593.2930	621.2879	**ISAYGEG**	650.3144	678.3093

SA	131.0815	159.0764	**SAY**	294.1448	322.1397	**SAYG**	351.1663	379.1612
SAYGE	480.2089	508.2038	**SAYGEG**	537.2304	565.2253	**SAYGEGN**	651.2733	679.2682
AY	207.1128	235.1077	**AYG**	264.1343	292.1292	**AYGE**	393.1769	421.1718
AYGEG	450.1983	478.1932	**AYGEGN**	564.2413	592.2362	**AYGEGNE**	693.2838	721.2788
YG	193.0972	221.0921	**YGE**	322.1397	350.1347	**YGEG**	379.1612	407.1561
YGEGN	493.2041	521.1991	**YGEGNE**	622.2467	650.2416	**GE**	159.0764	187.0713
GEG	216.0979	244.0928	**GEGN**	330.1408	358.1357	**GEGNE**	459.1834	487.1783
EG	159.0764	187.0713	**EGN**	273.1193	301.1143	**EGNE**	402.1619	430.1569
GN	144.0768	172.0717	**GNE**	273.1193	301.1143	**NE**	216.0979	244.0928





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
103.1	1596.7281	0.0481	HDLHISAYGEGNER
85.3	1596.7281	0.0481	HVEHISAYGEGNER
84.8	1596.7281	0.0481	HEVHISAYGEGNER
70.5	1596.6917	0.0845	HDEHIAAYGEGNER
51.4	1596.7644	0.0117	HVEHISSYGLGNER
33.5	1596.7653	0.0108	HPHMLSVSNCFIR
29.6	1596.7427	0.0335	HDCAPARDSIASAAR
29.3	1596.6991	0.0771	EKNMIDYNDHYR
28.6	1596.7276	0.0485	SMYVPSMVDLGNER
27.4	1596.8293	-0.0532	EMELASLAHLSQLR

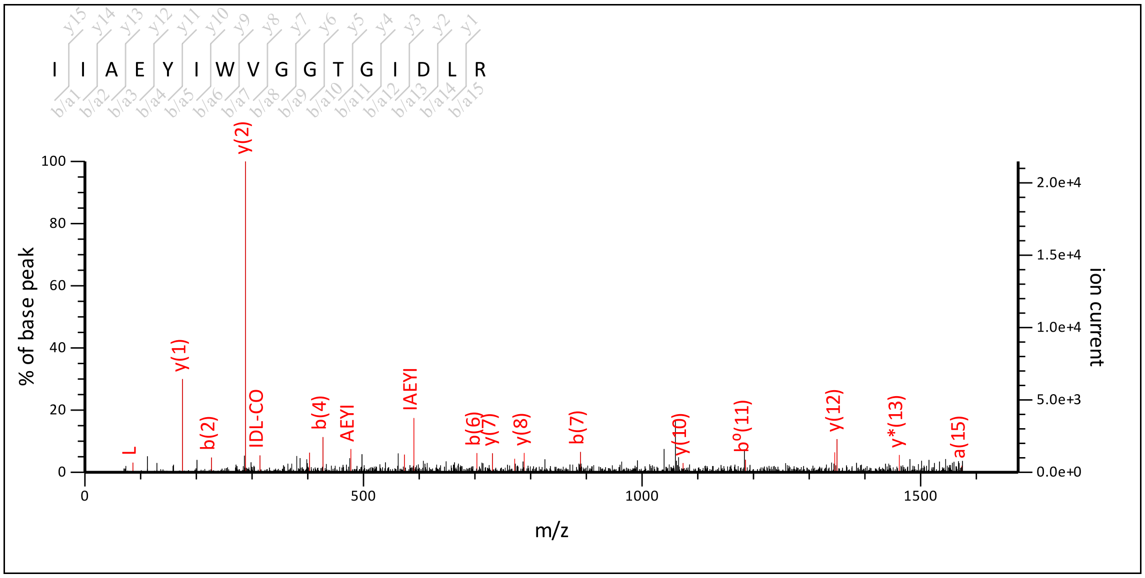
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **IIAEYIWVGGTGIDLR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 143: 1775.011524 from(1776.018800,1+) intensity(0.0000) index(18)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229172, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 1675.04

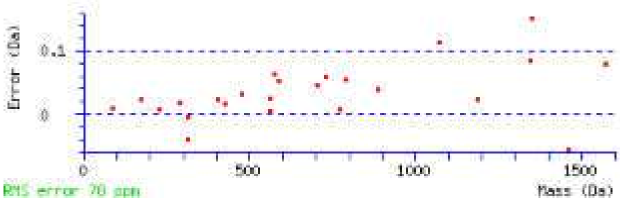
Label all possible matches ○ Label matches used for scoring ●

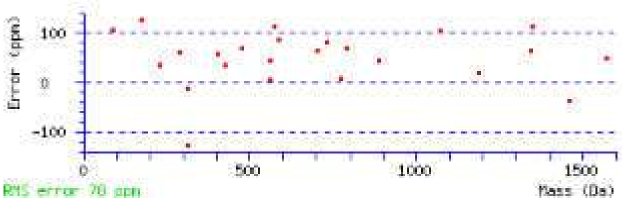
Monoisotopic mass of neutral peptide Mr(calc): 1774.9618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 0.046
Matches : 32/264 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	**86.0964**		114.0913		44.0495		I							16
2	86.0964	199.1805		***227.1754***		171.1492	185.1648	I	1604.8067	1617.8271	1631.8428	1662.8850	1645.8584	1644.8744	15
3	44.0495	270.2176		298.2125				A	1533.7696			1549.8009	1532.7744	1531.7904	14
4	102.0550	399.2602	381.2496	***427.2551***	409.2445	341.2547		E	1404.7270	1403.7318		1478.7638	1461.7373	1460.7532	13
5	136.0757	**562.3235**	544.3130	***590.3184***	572.3079			Y	1241.6637			***1349.7212***	1332.6947	1331.7106	12
6	86.0964	675.4076	657.3970	***703.4025***	685.3919	647.3763	661.3919	I	1128.5796	1141.6000	1155.6157	1186.6579	1169.6313	1168.6473	11
7	159.0917	861.4869	843.4763	***889.4818***	871.4713			W	942.5003			***1073.5738***	1056.5473	1055.5633	10
8	72.0808	960.5553	942.5448	988.5502	970.5397	946.5397		V	843.4319	856.4523		887.4945	870.4680	869.4839	9
9	30.0338	1017.5768	999.5662	1045.5717	1027.5611			G				***788.4261***	771.3995	770.4155	8
10	30.0338	1074.5982	1056.5877	1102.5932	1084.5826			G				***731.4046***	714.3781	713.3941	7
11	74.0600	1175.6459	1157.6354	1203.6408	1185.6303	1159.6510	1161.6303	T	628.3413	641.3617	643.3410	674.3832	657.3566	656.3726	6
12	30.0338	1232.6674	1214.6568	1260.6623	1242.6517			G				***573.3355***	556.3089	555.3249	5
13	86.0964	**1345.7515**	1327.7409	1373.7464	1355.7358	1317.7202	1331.7358	I	458.2358	471.2562	485.2718	516.3140	499.2875	498.3035	4
14	88.0393	1460.7784	1442.7678	1488.7733	1470.7627	1416.7886		D	343.2088	342.2136		***403.2300***	386.2034	385.2194	3
15	86.0964	**1573.8625**	1555.8519	1601.8574	1583.8468	1531.8155		L	230.1248	229.1295		***288.2030***	271.1765		2
16	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IA	157.1335	185.1285	IAE	286.1761	314.1710	IAEY	449.2395	477.2344

IAEYI	562.3235	590.3184	**AE**	173.0921	201.0870	**AEY**	336.1554	364.1503
AEYI	449.2395	477.2344	**AEYIW**	635.3188	663.3137	**EY**	265.1183	293.1132
EYI	378.2023	406.1973	**EYIW**	564.2817	592.2766	**EYIWV**	663.3501	691.3450
YI	249.1598	277.1547	**YIW**	435.2391	463.2340	**YIWV**	534.3075	562.3024
YIWVG	591.3289	619.3239	**YIWVGG**	648.3504	676.3453	**IW**	272.1757	300.1707
IWV	371.2442	399.2391	**IWVG**	428.2656	456.2605	**IWVGG**	485.2871	513.2820
IWVGGT	586.3348	614.3297	**IWVGGTG**	643.3562	671.3511	**WV**	258.1601	286.1550
WVG	315.1816	343.1765	**WVGG**	372.2030	400.1979	**WVGGT**	473.2507	501.2456
WVGGTG	530.2722	558.2671	**WVGGTGI**	643.3562	671.3511	**VG**	129.1022	157.0972
VGG	186.1237	214.1186	**VGGT**	287.1714	315.1663	**VGGTG**	344.1928	372.1878
VGGTGI	457.2769	485.2718	**VGGTGID**	572.3039	600.2988	**VGGTGIDL**	685.3879	713.3828
GG	87.0553	115.0502	**GGT**	188.1030	216.0979	**GGTG**	245.1244	273.1193
GGTGI	358.2085	386.2034	**GGTGID**	473.2354	501.2304	**GGTGIDL**	586.3195	614.3144
GT	131.0815	159.0764	**GTG**	188.1030	216.0979	**GTGI**	301.1870	329.1819
GTGID	416.2140	444.2089	**GTGIDL**	529.2980	557.2930	**TG**	131.0815	159.0764
TGI	244.1656	272.1605	**TGID**	359.1925	387.1874	**TGIDL**	472.2766	500.2715
GI	143.1179	171.1128	**GID**	258.1448	286.1397	**GIDL**	371.2289	399.2238
ID	201.1234	229.1183	**IDL**	314.2074	342.2023	**DL**	201.1234	229.1183





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.0	1774.9618	0.0498	IIAEYIWVGGTGIDLR
45.7	1774.9617	0.0498	IIAEYIWIGGSGIDIR
45.7	1774.9617	0.0498	IIAEYIWIGGSGIDLR
45.7	1774.9617	0.0498	IIAEYIWIGGSGLDLR
45.7	1774.9617	0.0498	IIAEYLWIGGSGLDIR
37.5	1774.9618	0.0498	IIAEYVWIGGTGIDLR
26.3	1774.9135	0.0980	ILAEMEITGITVDAQR
26.1	1774.8638	0.1477	NSLSWEAWVLPSSSGR
23.7	1774.9618	0.0498	IIAEYIWIGGTGIDVR
23.3	1774.8962	0.1153	LERVGFNSPTLSDGQR

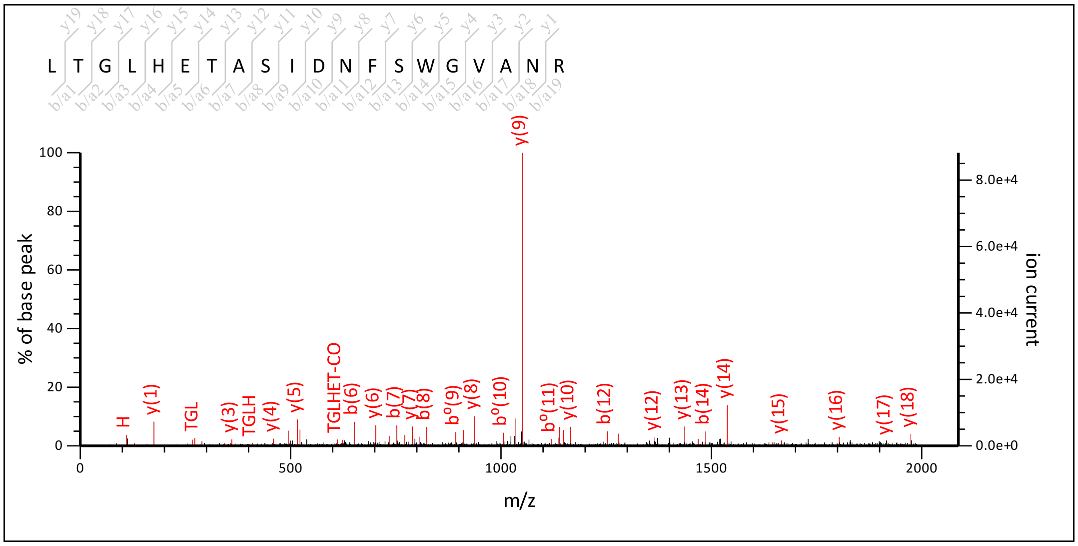
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **LTGLHETASIDNFSWGVANR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 179: 2187.135524 from(2188.142800,1+) intensity(0.0000) index(22)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229165, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 2087.21

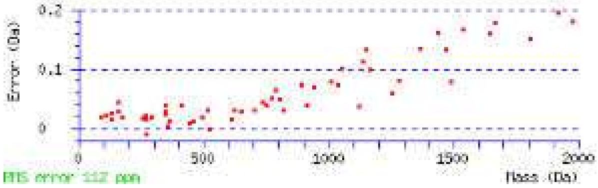
Label all possible matches ○ Label matches used for scoring ●

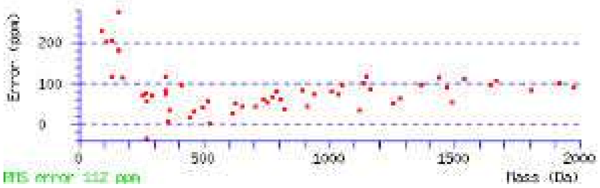
Monoisotopic mass of neutral peptide Mr(calc): 2187.0709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 143 **Expect:** 1.1e-10
Matches : 66/358 fragment ions using 80 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	**86.0964**			114.0913			44.0495		L					
2	74.0600	187.1441		169.1335	215.1390		197.1285	171.1492	173.1285	T	2028.9522	2041.9726	2043.9519	2074.9941	2057.9675
3	30.0338	244.1656		226.1550	**272.1605**		254.1499			G				***1973.9464***	1956.9199
4	86.0964	**357.2496**		339.2391	385.2445		367.2340	315.2027		L	1858.8467	1857.8515		***1916.9250***	1899.8984
5	110.0713	**494.3085**		476.2980	**522.3035**		504.2929			H	1721.7878			***1803.8409***	1786.8143
6	102.0550	**623.3511**		605.3406	**651.3461**		633.3355	565.3457		E	1592.7452	1591.7499		***1666.7820***	1649.7554
7	74.0600	724.3988		706.3883	**752.3937**		734.3832	708.4039	710.3832	T	1491.6975	1504.7179	1506.6972	***1537.7394***	1520.7128
8	44.0495	795.4359		777.4254	**823.4308**		805.4203			A	1420.6604			***1436.6917***	1419.6652
9	60.0444	882.4680		864.4574	**910.4629**		892.4523	866.4730		S	1333.6284	1332.6331		***1365.6546***	1348.6280
10	86.0964	995.5520		977.5415	1023.5469		1005.5364	967.5207	981.5364	I	1220.5443	1233.5647	1247.5804	***1278.6226***	1261.5960
11	88.0393	1110.5790		1092.5684	**1138.5739**		1120.5633	1066.5891		D	1105.5174	1104.5221		***1165.5385***	1148.5119
12	87.0553	1224.6219	1207.5953	1206.6113	**1252.6168**	1235.5903	1234.6062	1181.6161		N	991.4744	990.4792		***1050.5116***	1033.4850
13	120.0808	1371.6903	1354.6638	1353.6797	1399.6852	1382.6587	1381.6747			F	844.4060			***936.4686***	919.4421
14	60.0444	1458.7223	1441.6958	1440.7118	**1486.7172**	1469.6907	1468.7067	1442.7274		S	757.3740	756.3787		***789.4002***	772.3737
15	159.0917	**1644.8016**	1627.7751	1626.7911	1672.7966	1655.7700	1654.7860			W	571.2947			***702.3682***	685.3416
16	30.0338	1701.8231	1684.7966	1683.8125	1729.8180	1712.7915	1711.8075			G				***516.2889***	499.2623
17	72.0808	1800.8915	1783.8650	1782.8810	1828.8864	1811.8599	1810.8759	1786.8759		V	415.2048	428.2252		***459.2674***	442.2409
18	44.0495	1871.9286	1854.9021	1853.9181	1899.9236	1882.8970	1881.9130			A	344.1677			***360.1990***	343.1724
19	87.0553	1985.9716	1968.9450	1967.9610	2013.9665	1996.9399	1995.9559	1942.9658		N	230.1248	229.1295		***289.1619***	272.1353
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TG	131.0815	159.0764	TGL	244.1656	272.1605	TGLH	381.2245	409.2194

TGLHE	510.2671	538.2620	**TGLHET**	611.3148	639.3097	**TGLHETA**	682.3519	710.3468
GL	143.1179	171.1128	**GLH**	280.1768	308.1717	**GLHE**	409.2194	437.2143
GLHET	510.2671	538.2620	**GLHETA**	581.3042	609.2991	**GLHETAS**	668.3362	696.3311
LH	223.1553	251.1503	**LHE**	352.1979	380.1928	**LHET**	453.2456	481.2405
LHETA	524.2827	552.2776	**LHETAS**	611.3148	639.3097	**HE**	239.1139	267.1088
HET	340.1615	368.1565	**HETA**	411.1987	439.1936	**HETAS**	498.2307	526.2256
HETASI	611.3148	639.3097	**ET**	203.1026	231.0975	**ETA**	274.1397	302.1347
ETAS	361.1718	389.1667	**ETASI**	474.2558	502.2508	**ETASID**	589.2828	617.2777
TA	145.0972	173.0921	**TAS**	232.1292	260.1241	**TASI**	345.2132	373.2082
TASID	460.2402	488.2351	**TASIDN**	574.2831	602.2780	**AS**	131.0815	159.0764
ASI	244.1656	272.1605	**ASID**	359.1925	387.1874	**ASIDN**	473.2354	501.2304
ASIDNF	620.3039	648.2988	**SI**	173.1285	201.1234	**SID**	288.1554	316.1503
SIDN	402.1983	430.1932	**SIDNF**	549.2667	577.2617	**SIDNFS**	636.2988	664.2937
ID	201.1234	229.1183	**IDN**	315.1663	343.1612	**IDNF**	462.2347	490.2296
IDNFS	549.2667	577.2617	**DN**	202.0822	230.0771	**DNF**	349.1506	377.1456
DNFS	436.1827	464.1776	**DNFSW**	622.2620	650.2569	**DNFSWG**	679.2835	707.2784
NF	234.1237	262.1186	**NFS**	321.1557	349.1506	**NFSW**	507.2350	535.2300
NFSWG	564.2565	592.2514	**NFSWGV**	663.3249	691.3198	**FS**	207.1128	235.1077
FSW	393.1921	421.1870	**FSWG**	450.2136	478.2085	**FSWGV**	549.2820	577.2769
FSWGVA	620.3191	648.3140	**SW**	246.1237	274.1186	**SWG**	303.1452	331.1401
SWGV	402.2136	430.2085	**SWGVA**	473.2507	501.2456	**SWGVAN**	587.2936	615.2885
WG	216.1131	244.1081	**WGV**	315.1816	343.1765	**WGVA**	386.2187	414.2136
WGVAN	500.2616	528.2565	**GV**	129.1022	157.0972	**GVA**	200.1394	228.1343
GVAN	314.1823	342.1772	**VA**	143.1179	171.1128	**VAN**	257.1608	285.1557
AN	158.0924	186.0873						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
143.3	2187.0709	0.0646	LTGLHETASIDNFSWGVANR
28.0	2187.1775	-0.0420	LTHWIKVFLFNVAQMNAR
20.8	2187.1648	-0.0292	ITGSKIHSIEVSFNVSNISR
20.1	2187.1939	-0.0584	TIGIIIPDISNQFYPEIVR
20.1	2187.1939	-0.0584	TIGILLPDISNQFYPEIVR
19.9	2187.1067	0.0288	LDPIAKNAMPLMELYESPR
19.8	2187.1436	-0.0081	LVGNRPDAAAVEITFGPASFR
19.7	2187.1647	-0.0292	KAQLIIDQIDLGGANNVYSR
19.3	2187.2627	-0.1271	LPAVLEAESLPPRLVSVIER
18.7	2187.2627	-0.1271	LPAVLEAESLPPRLVSVLER

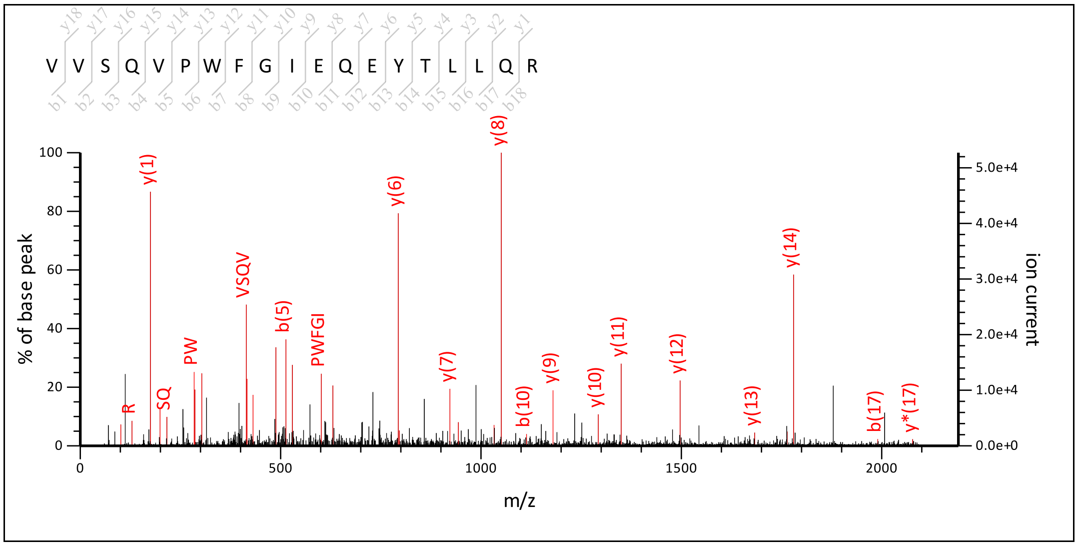
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **VVSQVPWFGIEQEYTLLQR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 199: 2291.265224 from(2292.272500,1+) intensity(0.0000) index(24)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229163, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 2191.39

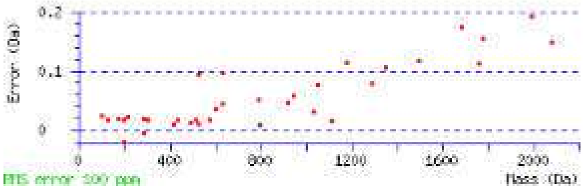
Label all possible matches ○ Label matches used for scoring ●

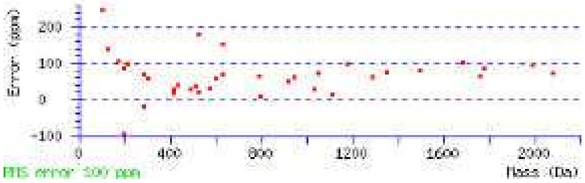
Monoisotopic mass of neutral peptide Mr(calc): 2291.1950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 8.7e-05
Matches : 40/338 fragment ions using 63 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	72.0808	171.1492			**199.1441**			157.1335		V	2149.0713	2162.0917		2193.1339	2176.1073
3	60.0444	258.1812		240.1707	**286.1761**		268.1656	242.1863		S	2062.0393	2061.0440		2094.0655	2077.0389
4	101.0709	386.2398	369.2132	368.2292	**414.2347**	397.2082	396.2241	329.2183		Q	1933.9807	1932.9854		2007.0334	1990.0069
5	72.0808	485.3082	468.2817	467.2976	**513.3031**	496.2766	495.2926	471.2926		V	1834.9123	1847.9327		1878.9749	1861.9483
6	70.0651	582.3610	565.3344	564.3504	610.3559	593.3293	592.3453	556.3453		P	1737.8595	1736.8643		***1779.9064***	1762.8799
7	159.0917	768.4403	751.4137	750.4297	**796.4352**	779.4087	778.4246			W	1551.7802			***1682.8537***	1665.8271
8	120.0808	915.5087	898.4822	897.4981	**943.5036**	926.4771	925.4930			F	1404.7118			***1496.7744***	1479.7478
9	30.0338	972.5302	955.5036	954.5196	1000.5251	983.4985	982.5145			G				***1349.7060***	1332.6794
10	86.0964	1085.6142	1068.5877	1067.6037	**1113.6091**	1096.5826	1095.5986	1057.5829	1071.5986	I	1234.6062	1247.6266	1261.6423	***1292.6845***	1275.6579
11	102.0550	1214.6568	1197.6303	1196.6463	1242.6517	1225.6252	1224.6412	1156.6513		E	1105.5637	1104.5684		***1179.6004***	1162.5739
12	101.0709	1342.7154	1325.6889	1324.7048	1370.7103	1353.6838	1352.6997	1285.6939		Q	977.5051	976.5098		***1050.5578***	1033.5313
13	102.0550	1471.7580	1454.7314	1453.7474	1499.7529	1482.7264	1481.7423	1413.7525		E	848.4625	847.4672		***922.4993***	905.4727
14	136.0757	1634.8213	1617.7948	1616.8108	1662.8162	1645.7897	1644.8057			Y	685.3992			***793.4567***	776.4301
15	74.0600	1735.8690	1718.8425	1717.8584	**1763.8639**	1746.8374	1745.8534	1719.8741	1721.8534	T	584.3515	597.3719	599.3511	***630.3933***	613.3668
16	86.0964	1848.9531	1831.9265	1830.9425	1876.9480	1859.9214	1858.9374	1806.9061		L	471.2674	470.2722		***529.3457***	512.3191
17	86.0964	1962.0371	1945.0106	1944.0266	**1990.0320**	1973.0055	1972.0215	1919.9902		L	358.1833	357.1881		***416.2616***	399.2350
18	101.0709	2090.0957	2073.0692	2072.0851	2118.0906	2101.0641	2100.0801	2033.0742		Q	230.1248	229.1295		***303.1775***	286.1510
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VS	159.1128	187.1077	VSQ	287.1714	315.1663	VSQV	386.2398	414.2347
VSQVP	483.2926	511.2875	VSQVPW	669.3719	697.3668	SQ	188.1030	216.0979

SQV	287.1714	315.1663	**SQVP**	384.2241	412.2191	**SQVPW**	570.3035	598.2984
QV	200.1394	228.1343	**QVP**	297.1921	325.1870	**QVPW**	483.2714	511.2663
QVPWF	630.3398	658.3348	**QVPWFG**	687.3613	715.3562	**VP**	169.1335	197.1285
VPW	355.2129	383.2078	**VPWF**	502.2813	530.2762	**VPWFG**	559.3027	587.2976
VPWFGI	672.3868	700.3817	**PW**	256.1444	284.1394	**PWF**	403.2129	431.2078
PWFG	460.2343	488.2292	**PWFGI**	573.3184	601.3133	**WF**	306.1601	334.1550
WFG	363.1816	391.1765	**WFGI**	476.2656	504.2605	**WFGIE**	605.3082	633.3031
FG	177.1022	205.0972	**FGI**	290.1863	318.1812	**FGIE**	419.2289	447.2238
FGIEQ	547.2875	575.2824	**FGIEQE**	676.3301	704.3250	**GI**	143.1179	171.1128
GIE	272.1605	300.1554	**GIEQ**	400.2191	428.2140	**GIEQE**	529.2617	557.2566
GIEQEY	692.3250	720.3199	**IE**	215.1390	243.1339	**IEQ**	343.1976	371.1925
IEQE	472.2402	500.2351	**IEQEY**	635.3035	663.2984	**EQ**	230.1135	258.1084
EQE	359.1561	387.1510	**EQEY**	522.2195	550.2144	**EQEYT**	623.2671	651.2620
QE	230.1135	258.1084	**QEY**	393.1769	421.1718	**QEYT**	494.2245	522.2195
QEYTL	607.3086	635.3035	**EY**	265.1183	293.1132	**EYT**	366.1660	394.1609
EYTL	479.2500	507.2449	**EYTLL**	592.3341	620.3290	**YT**	237.1234	265.1183
YTL	350.2074	378.2023	**YTLL**	463.2915	491.2864	**YTLLQ**	591.3501	619.3450
TL	187.1441	215.1390	**TLL**	300.2282	328.2231	**TLLQ**	428.2867	456.2817
LL	199.1805	227.1754	**LLQ**	327.2391	355.2340	**LQ**	214.1550	242.1499





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
83.8	2291.1950	0.0702	VVSQVPWFGIEQEYTLLQR
26.9	2291.2750	-0.0098	TPLVLNGTFGAPKGGLQAGPLAGR
25.3	2291.1402	0.1250	GWVVAVLSMVMAASAVAQENSR
21.5	2291.2386	0.0266	ERLPNYGLAVEVLHLSQTPR
18.4	2291.1508	0.1145	QFMELEKGYTVLNTIFNTK
17.9	2291.2712	-0.0059	VAIESPVPVVMVKPEGFVAPAR
16.5	2291.4821	-0.2169	IRVATVIGALLVVAIVAFVLVR
15.5	2291.3187	-0.0535	INLRLLMYGVAATIIFAIAGR
15.2	2291.1944	0.0709	IVAMDDPGRALPPGEVGEIAIR
14.8	2291.2273	0.0379	LLQSEAQLTEYIRSFPIGAR

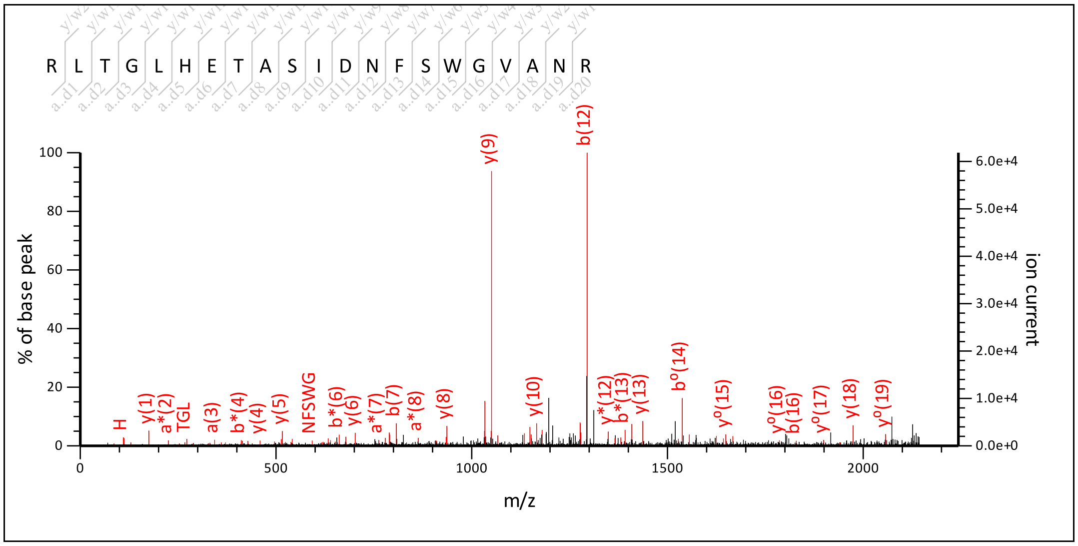
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **RLTGLHETASIDNFSWGVANR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 220: 2343.231724 from(2344.239000,1+) intensity(0.0000) index(27)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229166, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 2243.19

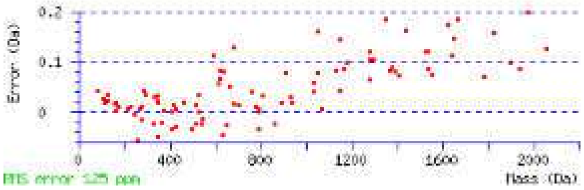
Label all possible matches ○ Label matches used for scoring ●

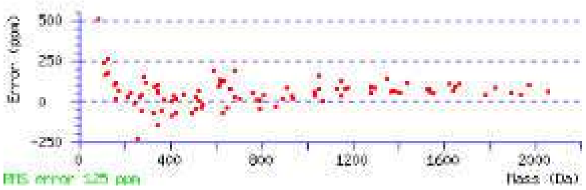
Monoisotopic mass of neutral peptide Mr(calc): 2343.1720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 3.1e-05
Matches : 106/401 fragment ions using 147 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	129.1135	**129.1135**	112.0869		157.1084	140.0818		44.0495		R					
2	86.0964	**242.1975**	225.1710		270.1925	253.1659		200.1506		L	2129.9999	2129.0047		2188.0782	2171.0516
3	74.0600	**343.2452**	326.2187	325.2347	**371.2401**	354.2136	353.2296	327.2503	329.2296	T	2028.9522	2041.9726	2043.9519	2074.9941	2057.9675
4	30.0338	400.2667	383.2401	382.2561	**428.2616**	411.2350	410.2510			G				***1973.9464***	1956.9199
5	86.0964	**513.3507**	496.3242	495.3402	**541.3457**	524.3191	523.3351	471.3038		L	1858.8467	1857.8515		1916.9250	1899.8984
6	110.0713	650.4097	633.3831	632.3991	**678.4046**	661.3780	660.3940			H	1721.7878			1803.8409	1786.8143
7	102.0550	**779.4522**	762.4257	761.4417	**807.4472**	790.4206	789.4366	721.4468		E	1592.7452	1591.7499		***1666.7820***	1649.7554
8	74.0600	880.4999	863.4734	862.4894	**908.4948**	891.4683	890.4843	864.5050	866.4843	T	1491.6975	1504.7179	1506.6972	***1537.7394***	1520.7128
9	44.0495	951.5370	934.5105	933.5265	979.5320	962.5054	961.5214			A	1420.6604			***1436.6917***	1419.6652
10	60.0444	1038.5691	1021.5425	1020.5585	**1066.5640**	1049.5374	1048.5534	1022.5742		S	1333.6284	1332.6331		***1365.6546***	1348.6280
11	86.0964	**1151.6531**	1134.6266	1133.6426	**1179.6480**	1162.6215	1161.6375	1123.6218	1137.6375	I	1220.5443	1233.5647	1247.5804	***1278.6226***	1261.5960
12	88.0393	1266.6801	1249.6535	1248.6695	**1294.6750**	1277.6484	1276.6644	1222.6902		D	1105.5174	1104.5221		***1165.5385***	1148.5119
13	87.0553	**1380.7230**	1363.6965	1362.7124	**1408.7179**	1391.6914	1390.7074	1337.7172		N	991.4744	990.4792		***1050.5116***	1033.4850
14	120.0808	**1527.7914**	1510.7649	1509.7809	**1555.7863**	1538.7598	1537.7758			F	844.4060			***936.4686***	919.4421
15	60.0444	1614.8234	1597.7969	1596.8129	**1642.8184**	1625.7918	1624.8078	1598.8285		S	757.3740	756.3787		***789.4002***	772.3737
16	159.0917	1800.9028	1783.8762	1782.8922	**1828.8977**	1811.8711	1810.8871			W	571.2947			***702.3682***	685.3416
17	30.0338	1857.9242	1840.8977	1839.9137	1885.9191	1868.8926	1867.9086			G				***516.2889***	499.2623
18	72.0808	1956.9926	1939.9661	1938.9821	1984.9876	1967.9610	1966.9770	1942.9770		V	415.2048	428.2252		***459.2674***	442.2409
19	44.0495	2028.0298	2011.0032	2010.0192	2056.0247	2038.9981	2038.0141			A	344.1677			***360.1990***	343.1724
20	87.0553	2142.0727	2125.0461	2124.0621	2170.0676	2153.0410	2152.0570	2099.0669		N	230.1248	229.1295		***289.1619***	272.1353
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

LT	187.1441	215.1390	**LTG**	244.1656	272.1605	**LTGL**	357.2496	385.2445
LTGLH	494.3085	522.3035	**LTGLHE**	623.3511	651.3461	**TG**	131.0815	159.0764
TGL	244.1656	272.1605	**TGLH**	381.2245	409.2194	**TGLHE**	510.2671	538.2620
TGLHET	611.3148	639.3097	**TGLHETA**	682.3519	710.3468	**GL**	143.1179	171.1128
GLH	280.1768	308.1717	**GLHE**	409.2194	437.2143	**GLHET**	510.2671	538.2620
GLHETA	581.3042	609.2991	**GLHETAS**	668.3362	696.3311	**LH**	223.1553	251.1503
LHE	352.1979	380.1928	**LHET**	453.2456	481.2405	**LHETA**	524.2827	552.2776
LHETAS	611.3148	639.3097	**HE**	239.1139	267.1088	**HET**	340.1615	368.1565
HETA	411.1987	439.1936	**HETAS**	498.2307	526.2256	**HETASI**	611.3148	639.3097
ET	203.1026	231.0975	**ETA**	274.1397	302.1347	**ETAS**	361.1718	389.1667
ETASI	474.2558	502.2508	**ETASID**	589.2828	617.2777	**TA**	145.0972	173.0921
TAS	232.1292	260.1241	**TASI**	345.2132	373.2082	**TASID**	460.2402	488.2351
TASIDN	574.2831	602.2780	**AS**	131.0815	159.0764	**ASI**	244.1656	272.1605
ASID	359.1925	387.1874	**ASIDN**	473.2354	501.2304	**ASIDNF**	620.3039	648.2988
SI	173.1285	201.1234	**SID**	288.1554	316.1503	**SIDN**	402.1983	430.1932
SIDNF	549.2667	577.2617	**SIDNFS**	636.2988	664.2937	**ID**	201.1234	229.1183
IDN	315.1663	343.1612	**IDNF**	462.2347	490.2296	**IDNFS**	549.2667	577.2617
DN	202.0822	230.0771	**DNF**	349.1506	377.1456	**DNFS**	436.1827	464.1776
DNFSW	622.2620	650.2569	**DNFSWG**	679.2835	707.2784	**NF**	234.1237	262.1186
NFS	321.1557	349.1506	**NFSW**	507.2350	535.2300	**NFSWG**	564.2565	592.2514
NFSWGV	663.3249	691.3198	**FS**	207.1128	235.1077	**FSW**	393.1921	421.1870
FSWG	450.2136	478.2085	**FSWGV**	549.2820	577.2769	**FSWGVA**	620.3191	648.3140
SW	246.1237	274.1186	**SWG**	303.1452	331.1401	**SWGV**	402.2136	430.2085
SWGVA	473.2507	501.2456	**SWGVAN**	587.2936	615.2885	**WG**	216.1131	244.1081
WGV	315.1816	343.1765	**WGVA**	386.2187	414.2136	**WGVAN**	500.2616	528.2565
GV	129.1022	157.0972	**GVA**	200.1394	228.1343	**GVAN**	314.1823	342.1772
VA	143.1179	171.1128	**VAN**	257.1608	285.1557	**AN**	158.0924	186.0873





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.5	2343.1720	0.0597	RLTGLHETASIDNFSWGVANR
21.9	2343.2659	-0.0341	SNLIASHTEPEAGIVAPLNVRR
21.3	2343.0875	0.1442	MVYDAATGQPITGSLMDYAAPR
18.3	2343.2910	-0.0593	IGLSATQKPIDAVSRFLVGTDR
18.3	2343.1648	0.0669	AEAAKFDAVFFADGPALPDHVR
16.9	2343.3275	-0.0957	DPGVVPEIGSVVTVQVLRINPR
16.2	2343.3242	-0.0925	KFTSAFIILGSIIYYEPILR
15.5	2343.2910	-0.0593	SAIDSLPPLREVIDTHQLLAR
15.5	2343.2448	-0.0130	TLRAHFVRPTSPSSDFGLSIR
14.8	2343.2508	-0.0191	ADIIVLAMKPQDVFAALDELR

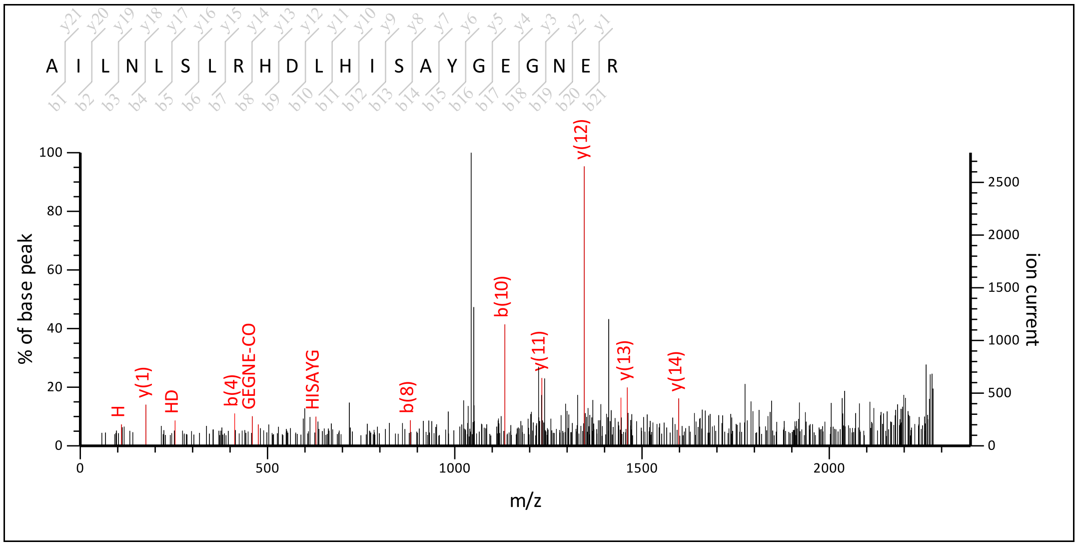
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **AILNLSLRHDLHISAYGEGNER**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 229: 2477.348724 from(2478.356000,1+) intensity(0.0000) index(29)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229180, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



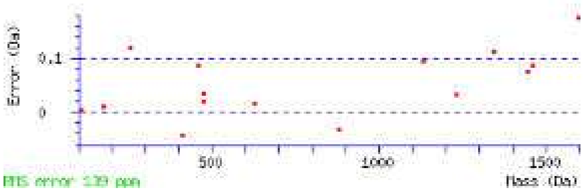
0 to 2377.19

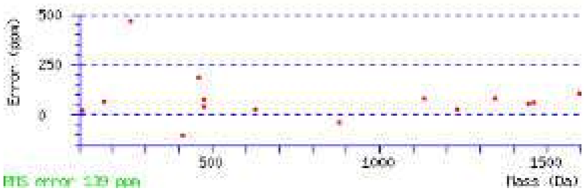
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2477.2775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 6 **Expect:** 4.4e+03
Matches : 16/414 fragment ions using 46 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	86.0964	157.1335			185.1285			129.1022	143.1179	I	2349.1694	2362.1898	2376.2055	2407.2477	2390.2211
3	86.0964	270.2176			298.2125			228.1707		L	2236.0854	2235.0901		2294.1636	2277.1371
4	87.0553	384.2605	367.2340		**412.2554**	395.2289		341.2547		N	2122.0424	2121.0472		2181.0796	2164.0530
5	86.0964	497.3446	480.3180		525.3395	508.3130		455.2976		L	2008.9584	2007.9631		2067.0366	2050.0101
6	60.0444	584.3766	567.3501	566.3661	612.3715	595.3450	594.3610	568.3817		S	1921.9263	1920.9311		1953.9526	1936.9260
7	86.0964	697.4607	680.4341	679.4501	725.4556	708.4291	707.4450	655.4137		L	1808.8423	1807.8470		1866.9205	1849.8940
8	129.1135	853.5618	836.5352	835.5512	**881.5567**	864.5302	863.5461	768.4978		R	1652.7412	1651.7459		1753.8365	1736.8099
9	110.0713	990.6207	973.5942	972.6101	1018.6156	1001.5891	1000.6051			H	1515.6823			***1597.7354***	1580.7088
10	88.0393	1105.6477	1088.6211	1087.6371	**1133.6426**	1116.6160	1115.6320	1061.6578		D	1400.6553	1399.6601		***1460.6764***	1443.6499
11	86.0964	1218.7317	1201.7052	1200.7212	1246.7266	1229.7001	1228.7161	1176.6848		L	1287.5713	1286.5760		***1345.6495***	1328.6230
12	110.0713	1355.7906	1338.7641	1337.7801	1383.7855	1366.7590	1365.7750			H	1150.5123			***1232.5654***	1215.5389
13	86.0964	1468.8747	1451.8481	1450.8641	1496.8696	1479.8431	1478.8590	1440.8434	1454.8590	I	1037.4283	1050.4487	1064.4643	1095.5065	1078.4800
14	60.0444	1555.9067	1538.8802	1537.8962	1583.9016	1566.8751	1565.8911	1539.9118		S	950.3962	949.4010		982.4225	965.3959
15	44.0495	1626.9438	1609.9173	1608.9333	1654.9387	1637.9122	1636.9282			A	879.3591			895.3904	878.3639
16	136.0757	1790.0072	1772.9806	1771.9966	1818.0021	1800.9755	1799.9915			Y	716.2958			824.3533	807.3268
17	30.0338	1847.0286	1830.0021	1829.0181	1875.0235	1857.9970	1857.0130			G				661.2900	644.2634
18	102.0550	1976.0712	1959.0447	1958.0607	2004.0661	1987.0396	1986.0556	1918.0657		E	530.2317	529.2365		604.2685	587.2420
19	30.0338	2033.0927	2016.0661	2015.0821	2061.0876	2044.0610	2043.0770			G				***475.2259***	458.1994
20	87.0553	2147.1356	2130.1091	2129.1250	2175.1305	2158.1040	2157.1200	2104.1298		N	359.1674	358.1721		418.2045	401.1779
21	102.0550	2276.1782	2259.1517	2258.1676	2304.1731	2287.1466	2286.1626	2218.1727		E	230.1248	229.1295		304.1615	287.1350
22	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IL	199.1805	227.1754	**ILN**	313.2234	341.2183	**ILNL**	426.3075	454.3024
ILNLS	513.3395	541.3344	**ILNLSL**	626.4236	654.4185	**LN**	200.1394	228.1343
LNL	313.2234	341.2183	**LNLS**	400.2554	428.2504	**LNLSL**	513.3395	541.3344
LNLSLR	669.4406	697.4355	**NL**	200.1394	228.1343	**NLS**	287.1714	315.1663
NLSL	400.2554	428.2504	**NLSLR**	556.3566	584.3515	**NLSLRH**	693.4155	721.4104
LS	173.1285	201.1234	**LSL**	286.2125	314.2074	**LSLR**	442.3136	470.3085
LSLRH	579.3725	607.3675	**LSLRHD**	694.3995	722.3944	**SL**	173.1285	201.1234
SLR	329.2296	357.2245	**SLRH**	466.2885	494.2834	**SLRHD**	581.3154	609.3103
SLRHDL	694.3995	722.3944	**LR**	242.1975	270.1925	**LRH**	379.2564	407.2514
LRHD	494.2834	522.2783	**LRHDL**	607.3675	635.3624	**RH**	266.1724	294.1673
RHD	381.1993	409.1942	**RHDL**	494.2834	522.2783	**RHDLH**	631.3423	659.3372
HD	225.0982	253.0931	**HDL**	338.1823	366.1772	**HDLH**	475.2412	503.2361
HDLHI	588.3253	616.3202	**HDLHIS**	675.3573	703.3522	**DL**	201.1234	229.1183
DLH	338.1823	366.1772	**DLHI**	451.2663	479.2613	**DLHIS**	538.2984	566.2933
DLHISA	609.3355	637.3304	**LH**	223.1553	251.1503	**LHI**	336.2394	364.2343
LHIS	423.2714	451.2663	**LHISA**	494.3085	522.3035	**LHISAY**	657.3719	685.3668
HI	223.1553	251.1503	**HIS**	310.1874	338.1823	**HISA**	381.2245	409.2194
HISAY	544.2878	572.2827	**HISAYG**	601.3093	629.3042	**IS**	173.1285	201.1234
ISA	244.1656	272.1605	**ISAY**	407.2289	435.2238	**ISAYG**	464.2504	492.2453
ISAYGE	593.2930	621.2879	**ISAYGEG**	650.3144	678.3093	**SA**	131.0815	159.0764
SAY	294.1448	322.1397	**SAYG**	351.1663	379.1612	**SAYGE**	480.2089	508.2038
SAYGEG	537.2304	565.2253	**SAYGEGN**	651.2733	679.2682	**AY**	207.1128	235.1077
AYG	264.1343	292.1292	**AYGE**	393.1769	421.1718	**AYGEG**	450.1983	478.1932
AYGEGN	564.2413	592.2362	**AYGEGNE**	693.2838	721.2788	**YG**	193.0972	221.0921
YGE	322.1397	350.1347	**YGEG**	379.1612	407.1561	**YGEGN**	493.2041	521.1991
YGEGNE	622.2467	650.2416	**GE**	159.0764	187.0713	**GEG**	216.0979	244.0928
GEGN	330.1408	358.1357	**GEGNE**	459.1834	487.1783	**EG**	159.0764	187.0713
EGN	273.1193	301.1143	**EGNE**	402.1619	430.1569	**GN**	144.0768	172.0717
GNE	273.1193	301.1143	**NE**	216.0979	244.0928			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
8.8	2477.1719	0.1768	YTMTGVGGLFMGNDSIGSILSWR
8.0	2477.3082	0.0405	ILGVWAFALIWTIAPMFGWNR
6.3	2477.2775	0.0713	AILNLSLRHDLHISAYGEGNER
5.5	2477.2737	0.0751	LEKTYQCPLLVDHNPLGEVPR
4.8	2477.2836	0.0652	SLGNATIFNQDVLDSLLKEICK
4.5	2477.2551	0.0937	GGSGTPGLPVIKPDPDADAKHFSSK
3.3	2477.2914	0.0573	GFAHATLYKTLVEGISANETLSR
3.1	2477.3173	0.0314	HASSVGTIGSHVMILNTGSIKNVR
3.0	2477.3087	0.0400	KSSAILDEYIGMIVTDANLAIPK
2.5	2477.1881	0.1606	SNTGVGSTPAISADSGSTAEAEILSR

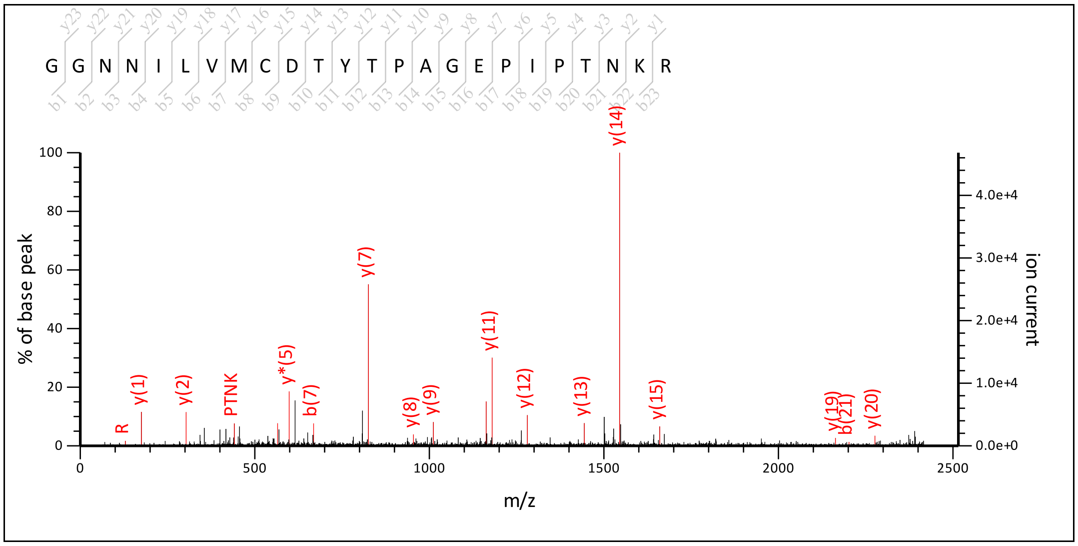
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **GGNNILVMCDTYTPAGEPIPTNKR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 234: 2617.339424 from(2618.346700,1+) intensity(0.0000) index(30)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229168, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 2515.52

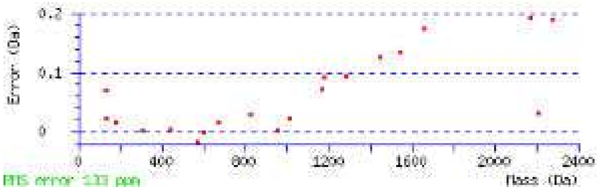
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2617.2628
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 97 **Expect:** 3.6e-06
Matches : 21/464 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	30.0338	87.0553			115.0502					G				2561.2487	2544.2221
3	87.0553	201.0982	184.0717		229.0931	212.0666		158.0924		N	2445.1901	2444.1948		2504.2272	2487.2007
4	87.0553	315.1411	298.1146		343.1361	326.1095		272.1353		N	2331.1472	2330.1519		2390.1843	2373.1577
5	86.0964	428.2252	411.1987		456.2201	439.1936		400.1939	414.2096	I	2218.0631	2231.0835	2245.0992	***2276.1414***	2259.1148
6	86.0964	541.3093	524.2827		569.3042	552.2776		499.2623		L	2104.9790	2103.9838		***2163.0573***	2146.0307
7	72.0808	640.3777	623.3511		**668.3726**	651.3461		626.3620		V	2005.9106	2018.9310		2049.9732	2032.9467
8	104.0528	771.4182	754.3916		799.4131	782.3865		711.4148		M	1874.8701	1873.8749		1950.9048	1933.8783
9	133.0430	931.4488	914.4223		959.4437	942.4172		842.4553		C	1714.8395	1713.8442		1819.8643	1802.8378
10	88.0393	1046.4758	1029.4492	1028.4652	1074.4707	1057.4441	1056.4601	1002.4859		D	1599.8125	1598.8173		***1659.8337***	1642.8071
11	74.0600	1147.5234	1130.4969	1129.5129	1175.5184	1158.4918	1157.5078	1131.5285	1133.5078	T	1498.7649	1511.7853	1513.7645	***1544.8067***	1527.7802
12	136.0757	1310.5868	1293.5602	1292.5762	1338.5817	1321.5551	1320.5711			Y	1335.7015			***1443.7591***	1426.7325
13	74.0600	1411.6344	1394.6079	1393.6239	1439.6294	1422.6028	1421.6188	1395.6395	1397.6188	T	1234.6539	1247.6743	1249.6535	***1280.6957***	1263.6692
14	70.0651	1508.6872	1491.6607	1490.6766	1536.6821	1519.6556	1518.6716	1482.6716		P	1137.6011	1136.6058		***1179.6480***	1162.6215
15	44.0495	1579.7243	1562.6978	1561.7138	1607.7192	1590.6927	1589.7087			A	1066.5640			1082.5953	1065.5687
16	30.0338	1636.7458	1619.7192	1618.7352	1664.7407	1647.7142	1646.7301			G				***1011.5582***	994.5316
17	102.0550	1765.7884	1748.7618	1747.7778	1793.7833	1776.7568	1775.7727	1707.7829		E	880.4999	879.5047		***954.5367***	937.5102
18	70.0651	1862.8411	1845.8146	1844.8306	1890.8361	1873.8095	1872.8255	1836.8255		P	783.4472	782.4519		***825.4941***	808.4676
19	86.0964	1975.9252	1958.8987	1957.9146	2003.9201	1986.8936	1985.9096	1947.8939	1961.9096	I	670.3631	683.3835	697.3991	728.4413	711.4148
20	70.0651	2072.9780	2055.9514	2054.9674	2100.9729	2083.9463	2082.9623	2046.9623		P	573.3103	572.3151		615.3573	598.3307
21	74.0600	2174.0257	2156.9991	2156.0151	**2202.0206**	2184.9940	2184.0100	2158.0307	2160.0100	T	472.2627	485.2831	487.2623	518.3045	501.2780
22	87.0553	2288.0686	2271.0420	2270.0580	2316.0635	2299.0369	2298.0529	2245.0628		N	358.2197	357.2245		417.2568	400.2303

23	101.1073	2416.1635	2399.1370	2398.1530	2444.1585	2427.1319	2426.1479	2359.1057		**K**	230.1248	229.1295		***303.2139***	286.1874	
24	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GN	144.0768	172.0717	**GNN**	258.1197	286.1146	**GNNI**	371.2037	399.1987
GNNIL	484.2878	512.2827	**GNNILV**	583.3562	611.3511	**NN**	201.0982	229.0931
NNI	314.1823	342.1772	**NNIL**	427.2663	455.2613	**NNILV**	526.3348	554.3297
NNILVM	657.3752	685.3702	**NI**	200.1394	228.1343	**NIL**	313.2234	341.2183
NILV	412.2918	440.2867	**NILVM**	543.3323	571.3272	**IL**	199.1805	227.1754
ILV	298.2489	326.2438	**ILVM**	429.2894	457.2843	**ILVMC**	589.3200	617.3150
LV	185.1648	213.1598	**LVM**	316.2053	344.2002	**LVMC**	476.2360	504.2309
LVMCD	591.2629	619.2578	**LVMCDT**	692.3106	720.3055	**VM**	203.1213	231.1162
VMC	363.1519	391.1468	**VMCD**	478.1789	506.1738	**VMCDT**	579.2265	607.2214
MC	264.0835	292.0784	**MCD**	379.1104	407.1054	**MCDT**	480.1581	508.1530
MCDTY	643.2214	671.2164	**CD**	248.0700	276.0649	**CDT**	349.1176	377.1125
CDTY	512.1810	540.1759	**CDTYT**	613.2286	641.2236	**DT**	189.0870	217.0819
DTY	352.1503	380.1452	**DTYT**	453.1980	481.1929	**DTYTP**	550.2508	578.2457
DTYTPA	621.2879	649.2828	**DTYTPAG**	678.3093	706.3042	**TY**	237.1234	265.1183
TYT	338.1710	366.1660	**TYTP**	435.2238	463.2187	**TYTPA**	506.2609	534.2558
TYTPAG	563.2824	591.2773	**TYTPAGE**	692.3250	720.3199	**YT**	237.1234	265.1183
YTP	334.1761	362.1710	**YTPA**	405.2132	433.2082	**YTPAG**	462.2347	490.2296
YTPAGE	591.2773	619.2722	**YTPAGEP**	688.3301	716.3250	**TP**	171.1128	199.1077
TPA	242.1499	270.1448	**TPAG**	299.1714	327.1663	**TPAGE**	428.2140	456.2089
TPAGEP	525.2667	553.2617	**TPAGEPI**	638.3508	666.3457	**PA**	141.1022	169.0972
PAG	198.1237	226.1186	**PAGE**	327.1663	355.1612	**PAGEP**	424.2191	452.2140
PAGEPI	537.3031	565.2980	**PAGEPIP**	634.3559	662.3508	**AG**	101.0709	129.0659
AGE	230.1135	258.1084	**AGEP**	327.1663	355.1612	**AGEPI**	440.2504	468.2453
AGEPIP	537.3031	565.2980	**AGEPIPT**	638.3508	666.3457	**GE**	159.0764	187.0713
GEP	256.1292	284.1241	**GEPI**	369.2132	397.2082	**GEPIP**	466.2660	494.2609
GEPIPT	567.3137	595.3086	**GEPIPTN**	681.3566	709.3515	**EP**	199.1077	227.1026
EPI	312.1918	340.1867	**EPIP**	409.2445	437.2395	**EPIPT**	510.2922	538.2871
EPIPTN	624.3352	652.3301	**PI**	183.1492	211.1441	**PIP**	280.2020	308.1969
PIPT	381.2496	409.2445	**PIPTN**	495.2926	523.2875	**PIPTNK**	623.3875	651.3824
IP	183.1492	211.1441	**IPT**	284.1969	312.1918	**IPTN**	398.2398	426.2347
IPTNK	526.3348	554.3297	**PT**	171.1128	199.1077	**PTN**	285.1557	313.1506
PTNK	413.2507	441.2456	**TN**	188.1030	216.0979	**TNK**	316.1979	344.1928
NK	215.1503	243.1452						



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
97.3	2617.2628	0.0766	GGNNILVMCDTYTPAGEPIPTNKR
25.6	2617.3284	0.0110	TSFHIIFLDTYTTMDTLIAMKR
15.2	2617.5604	-0.2210	AGLLPLGLGTLALLVALSMALSAPLAR
14.7	2617.3785	-0.0391	QTYTQTLLAAVPKLGAMQGSDLPAK
14.7	2617.4010	-0.0616	TIIVQLNESVKITCVRPYSNQR
14.5	2617.3924	-0.0530	IEQLMLKILPEYTVGDPSLETTK

13.4	2617.5128	-0.1734	LEIMKDSAIGTYGVLALILSLLIR
12.2	2617.3612	-0.0218	LPREATPAQHVQYINELSDLPAR
11.9	2617.3210	0.0184	FGGDEFVVILGGSPPQEMIAAIAQR
11.0	2617.3758	-0.0364	TAISVQDAAAAHMAATPGASVVPRLGR

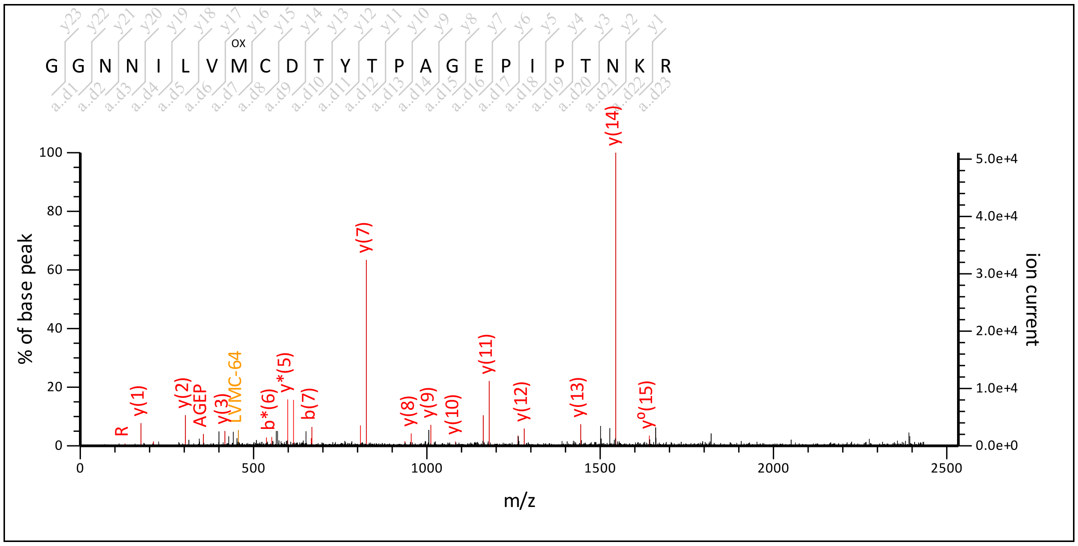
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **GGNNILVMCDTYTPAGEPIPTNKR**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 237: 2633.335024 from(2634.342300,1+) intensity(0.0000) index(31)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229174, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 2533.53

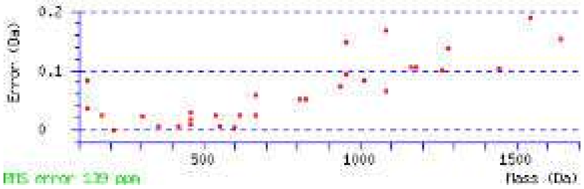
Label all possible matches ○ Label matches used for scoring ●

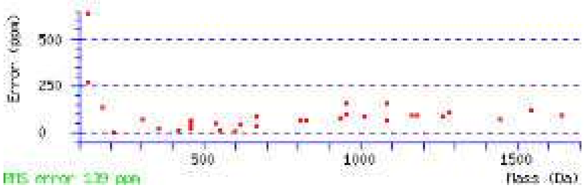
Monoisotopic mass of neutral peptide Mr(calc): 2633.2578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 66 **Expect:** 0.0043
Matches : 35/632 fragment ions using 48 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	30.0338	87.0553			115.0502					G				2577.2436	2560.2170
3	87.0553	201.0982	184.0717		229.0931	212.0666		158.0924		N	2461.1850	2460.1898		2520.2221	2503.1956
4	87.0553	315.1411	298.1146		343.1361	326.1095		272.1353		N	2347.1421	2346.1468		2406.1792	2389.1526
5	86.0964	428.2252	411.1987		**456.2201**	439.1936		400.1939	414.2096	I	2234.0580	2247.0784	2261.0941	2292.1363	2275.1097
6	86.0964	541.3093	524.2827		569.3042	552.2776		499.2623		L	2120.9740	2119.9787		2179.0522	2162.0257
7	72.0808	640.3777	623.3511		**668.3726**	651.3461		626.3620		V	2021.9055	2034.9259		2065.9681	2048.9416
8	120.0478	787.4131	770.3865		815.4080	798.3815		711.4148		M	1874.8701	1873.8749		1966.8997	1949.8732
9	133.0430	947.4437	930.4172		975.4386	958.4121		858.4502		C	1714.8395	1713.8442		1819.8643	1802.8378
10	88.0393	1062.4707	1045.4441	1044.4601	1090.4656	1073.4390	1072.4550	1018.4808		D	1599.8125	1598.8173		1659.8337	1642.8071
11	74.0600	1163.5184	1146.4918	1145.5078	1191.5133	1174.4867	1173.5027	1147.5234	1149.5027	T	1498.7649	1511.7853	1513.7645	***1544.8067***	1527.7802
12	136.0757	1326.5817	1309.5551	1308.5711	1354.5766	1337.5501	1336.5660			Y	1335.7015			***1443.7591***	1426.7325
13	74.0600	1427.6294	1410.6028	1409.6188	1455.6243	1438.5977	1437.6137	1411.6344	1413.6137	T	1234.6539	1247.6743	1249.6535	***1280.6957***	1263.6692
14	70.0651	1524.6821	1507.6556	1506.6716	1552.6770	1535.6505	1534.6665	1498.6665		P	1137.6011	1136.6058		***1179.6480***	1162.6215
15	44.0495	1595.7192	1578.6927	1577.7087	1623.7142	1606.6876	1605.7036			A	1066.5640			***1082.5953***	1065.5687
16	30.0338	1652.7407	1635.7142	1634.7301	1680.7356	1663.7091	1662.7251			G				***1011.5582***	994.5316
17	102.0550	1781.7833	1764.7568	1763.7727	1809.7782	1792.7517	1791.7676	1723.7778		E	880.4999	879.5047		***954.5367***	937.5102
18	70.0651	1878.8361	1861.8095	1860.8255	1906.8310	1889.8044	1888.8204	1852.8204		P	783.4472	782.4519		***825.4941***	808.4676
19	86.0964	1991.9201	1974.8936	1973.9096	2019.9150	2002.8885	2001.9045	1963.8888	1977.9045	I	670.3631	683.3835	697.3991	728.4413	711.4148
20	70.0651	2088.9729	2071.9463	2070.9623	2116.9678	2099.9413	2098.9572	2062.9572		P	573.3103	572.3151		***615.3573***	598.3307
21	74.0600	2190.0206	2172.9940	2172.0100	2218.0155	2200.9889	2200.0049	2174.0257	2176.0049	T	472.2627	485.2831	487.2623	518.3045	501.2780

22	87.0553	2304.0635	2287.0369	2286.0529	2332.0584	2315.0319	2314.0478	2261.0577		N	358.2197	357.2245		*417.2568*	400.2303
23	101.1073	2432.1585	2415.1319	2414.1479	2460.1534	2443.1268	2442.1428	2375.1006		K	230.1248	229.1295		*303.2139*	286.1874
24	129.1135									R	74.0237	73.0284		*175.1190*	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GN	144.0768	172.0717	**GNN**	258.1197	286.1146	**GNNI**	371.2037	399.1987
GNNIL	484.2878	512.2827	**GNNILV**	583.3562	611.3511	**NN**	201.0982	229.0931
NNI	314.1823	342.1772	**NNIL**	427.2663	455.2613	**NNILV**	526.3348	554.3297
NNILVM	673.3702	701.3651	**NI**	200.1394	228.1343	**NIL**	313.2234	341.2183
NILV	412.2918	440.2867	**NILVM**	559.3272	587.3221	**IL**	199.1805	227.1754
ILV	298.2489	326.2438	**ILVM**	445.2843	473.2792	**ILVMC**	605.3150	633.3099
LV	185.1648	213.1598	**LVM**	332.2002	360.1952	**LVMC**	492.2309	520.2258
LVMCD	607.2578	635.2527	**VM**	219.1162	247.1111	**VMC**	379.1468	407.1417
VMCD	494.1738	522.1687	**VMCDT**	595.2214	623.2164	**MC**	280.0784	308.0733
MCD	395.1054	423.1003	**MCDT**	496.1530	524.1479	**MCDTY**	659.2164	687.2113
CD	248.0700	276.0649	**CDT**	349.1176	377.1125	**CDTY**	512.1810	540.1759
CDTYT	613.2286	641.2236	**DT**	189.0870	217.0819	**DTY**	352.1503	380.1452
DTYT	453.1980	481.1929	**DTYTP**	550.2508	578.2457	**DTYTPA**	621.2879	649.2828
DTYTPAG	678.3093	706.3042	**TY**	237.1234	265.1183	**TYT**	338.1710	366.1660
TYTP	435.2238	463.2187	**TYTPA**	506.2609	534.2558	**TYTPAG**	563.2824	591.2773
TYTPAGE	692.3250	720.3199	**YT**	237.1234	265.1183	**YTP**	334.1761	362.1710
YTPA	405.2132	433.2082	**YTPAG**	462.2347	490.2296	**YTPAGE**	591.2773	619.2722
YTPAGEP	688.3301	716.3250	**TP**	171.1128	199.1077	**TPA**	242.1499	270.1448
TPAG	299.1714	327.1663	**TPAGE**	428.2140	456.2089	**TPAGEP**	525.2667	553.2617
TPAGEPI	638.3508	666.3457	**PA**	141.1022	169.0972	**PAG**	198.1237	226.1186
PAGE	327.1663	355.1612	**PAGEP**	424.2191	452.2140	**PAGEPI**	537.3031	565.2980
PAGEPIP	634.3559	662.3508	**AG**	101.0709	129.0659	**AGE**	230.1135	258.1084
AGEP	327.1663	355.1612	**AGEPI**	440.2504	468.2453	**AGEPIP**	537.3031	565.2980
AGEPIPT	638.3508	666.3457	**GE**	159.0764	187.0713	**GEP**	256.1292	284.1241
GEPI	369.2132	397.2082	**GEPIP**	466.2660	494.2609	**GEPIPT**	567.3137	595.3086
GEPIPTN	681.3566	709.3515	**EP**	199.1077	227.1026	**EPI**	312.1918	340.1867
EPIP	409.2445	437.2395	**EPIPT**	510.2922	538.2871	**EPIPTN**	624.3352	652.3301
PI	183.1492	211.1441	**PIP**	280.2020	308.1969	**PIPT**	381.2496	409.2445
PIPTN	495.2926	523.2875	**PIPTNK**	623.3875	651.3824	**IP**	183.1492	211.1441
IPT	284.1969	312.1918	**IPTN**	398.2398	426.2347	**IPTNK**	526.3348	554.3297
PT	171.1128	199.1077	**PTN**	285.1557	313.1506	**PTNK**	413.2507	441.2456
TN	188.1030	216.0979	**TNK**	316.1979	344.1928	**NK**	215.1503	243.1452





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
66.3	2633.2578	0.0773	GGNNILVMCDTYTPAGEPIPTNKR
18.6	2633.3912	-0.0561	IELDISGSKFTNLSTQLLAALDER
14.8	2633.4323	-0.0972	MAQQLLPASAAPSAPRAASVNVVLGSK
14.7	2633.4575	-0.1224	ALGLDVVATGLAMSVGPAISALAGVPAGR
11.0	2633.3521	-0.0171	ALGLPSSVGQEARSLGQDPAGVSAPGGR
9.8	2633.2863	0.0487	GKPPKADPLLGDTAMQISTDIMMR

9.7	2633.3211	0.0139	HAESFRHFPDQASLADIRPLGNR
9.5	2633.4323	-0.0973	LPVSSIKGAIGHSLGAASAIEAAVCVR
8.4	2633.5852	-0.2502	MIVALAVAPVVLITLAIGLRGVAAMR
8.2	2633.5052	-0.1702	KILPLFLTLAMIFALVGCSNIATK

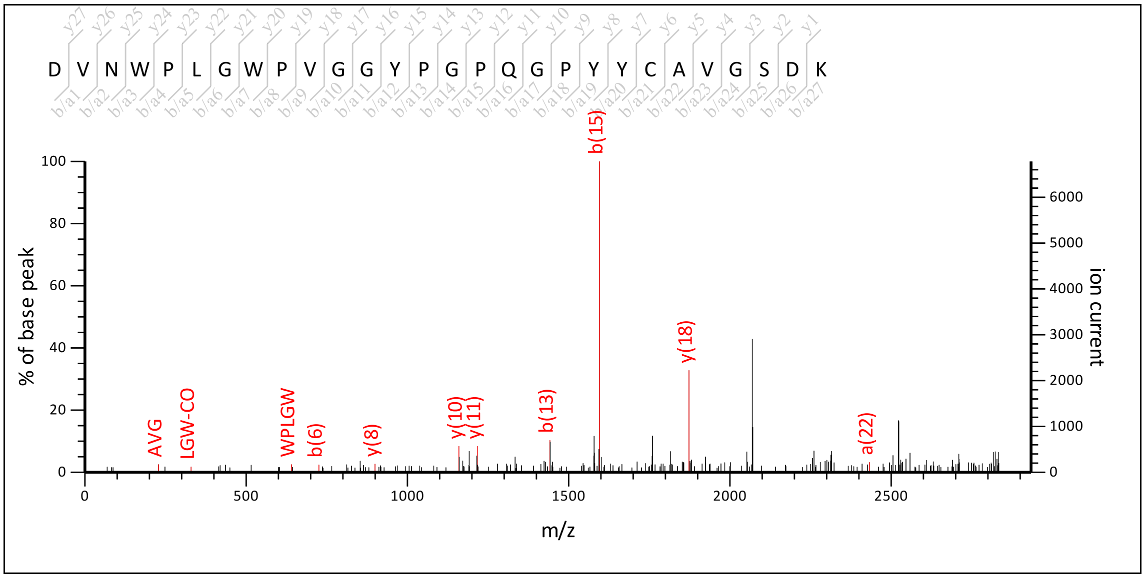
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 69

MS/MS Fragmentation of **DVNWPLGWPVGGYPGPQGPYYCAVGSDK**
Found in **gi|19387272** in **NCBInr**, putative precursor chloroplastic glutamine synthetase [Oryza sativa Japonica Group]

Match to Query 240: 3035.488824 from(3036.496100,1+) intensity(0.0000) index(32)
Title: Label: B19, Spot_Id: 219963, Peak_List_Id: 229184, MSMS Job_Run_Id: 22013, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B19_136868333300.txt



0 to 2933.75

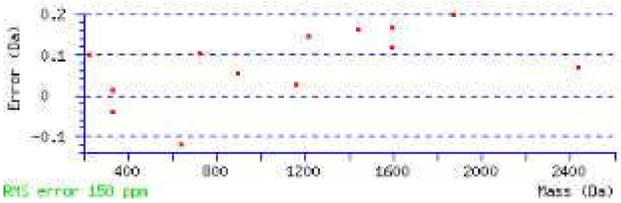
Label all possible matches ○ Label matches used for scoring ●

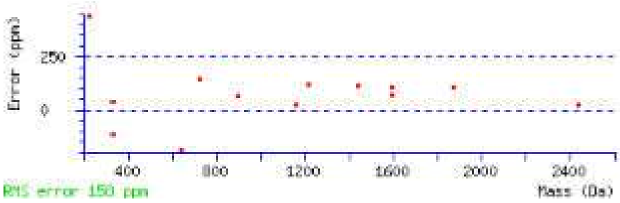
Monoisotopic mass of neutral peptide Mr(calc): 3035.3913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 11 **Expect:** 1.1e+03
Matches : 13/554 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495	D						28
2	72.0808	187.1077		169.0972	215.1026		197.0921	173.0921	V	2877.3090	2890.3294	2921.3716	2904.3450	2903.3610	27
3	87.0553	301.1506	284.1241	283.1401	***329.1456***	312.1190	311.1350	258.1448	N	2763.2660	2762.2708	2822.3032	2805.2766	2804.2926	26
4	159.0917	487.2300	470.2034	469.2194	515.2249	498.1983	497.2143		W	2577.1867		2708.2602	2691.2337	2690.2497	25
5	70.0651	584.2827	567.2562	566.2722	612.2776	595.2511	594.2671	558.2671	P	2480.1340	2479.1387	2522.1809	2505.1544	2504.1703	24
6	86.0964	697.3668	680.3402	679.3562	***725.3617***	708.3352	707.3511	655.3198	L	2367.0499	2366.0546	2425.1281	2408.1016	2407.1176	23
7	30.0338	754.3883	737.3617	736.3777	782.3832	765.3566	764.3726		G			2312.0441	2295.0175	2294.0335	22
8	159.0917	940.4676	923.4410	922.4570	968.4625	951.4359	950.4519		W	2123.9491		2255.0226	2237.9961	2237.0121	21
9	70.0651	1037.5203	1020.4938	1019.5098	1065.5152	1048.4887	1047.5047	1011.5047	P	2026.8964	2025.9011	2068.9433	2051.9168	2050.9327	20
10	72.0808	1136.5887	1119.5622	1118.5782	1164.5837	1147.5571	1146.5731	1122.5731	V	1927.8279	1940.8483	1971.8905	1954.8640	1953.8800	19
11	30.0338	1193.6102	1176.5837	1175.5996	1221.6051	1204.5786	1203.5946		G			***1872.8221***	1855.7956	1854.8116	18
12	30.0338	1250.6317	1233.6051	1232.6211	1278.6266	1261.6000	1260.6160		G			1815.8007	1798.7741	1797.7901	17
13	136.0757	1413.6950	1396.6684	1395.6844	***1441.6899***	1424.6634	1423.6793		Y	1650.7217		1758.7792	1741.7527	1740.7686	16
14	70.0651	1510.7478	1493.7212	1492.7372	1538.7427	1521.7161	1520.7321	1484.7321	P	1553.6689	1552.6737	***1595.7159***	1578.6893	1577.7053	15
15	30.0338	1567.7692	1550.7427	1549.7587	***1595.7641***	1578.7376	1577.7536		G			1498.6631	1481.6366	1480.6525	14
16	70.0651	1664.8220	1647.7954	1646.8114	1692.8169	1675.7904	1674.8063	1638.8063	P	1399.5947	1398.5994	1441.6416	1424.6151	1423.6311	13
17	101.0709	1792.8806	1775.8540	1774.8700	1820.8755	1803.8489	1802.8649	1735.8591	Q	1271.5361	1270.5409	1344.5889	1327.5623	1326.5783	12
18	30.0338	1849.9020	1832.8755	1831.8915	1877.8969	1860.8704	1859.8864		G			***1216.5303***	1199.5038	1198.5197	11
19	70.0651	1946.9548	1929.9282	1928.9442	1974.9497	1957.9232	1956.9391	1920.9391	P	1117.4619	1116.4666	***1159.5088***	1142.4823	1141.4983	10

20	136.0757	2110.0181	2092.9916	2092.0076	2138.0130	2120.9865	2120.0025		**Y**	954.3986		1062.4561	1045.4295	1044.4455	**9**
21	136.0757	2273.0815	2256.0549	2255.0709	2301.0764	2284.0498	2283.0658		**Y**	791.3352		***899.3927***	882.3662	881.3822	**8**
22	133.0430	2433.1121	2416.0856	2415.1015	2461.1070	2444.0805	2443.0965	2344.1186	**C**	631.3046	630.3093	736.3294	719.3029	718.3189	**7**
23	44.0495	2504.1492	2487.1227	2486.1387	2532.1441	2515.1176	2514.1336		**A**	560.2675		576.2988	559.2722	558.2882	**6**
24	72.0808	2603.2176	2586.1911	2585.2071	2631.2125	2614.1860	2613.2020	2589.2020	**V**	461.1991	474.2195	505.2617	488.2351	487.2511	**5**
25	30.0338	2660.2391	2643.2125	2642.2285	2688.2340	2671.2075	2670.2234		**G**			406.1932	389.1667	388.1827	**4**
26	60.0444	2747.2711	2730.2446	2729.2606	2775.2660	2758.2395	2757.2555	2731.2762	**S**	317.1456	316.1503	349.1718	332.1452	331.1612	**3**
27	88.0393	2862.2981	2845.2715	2844.2875	2890.2930	2873.2664	2872.2824	2818.3082	**D**	202.1186	201.1234	262.1397	245.1132	244.1292	**2**
28	101.1073								**K**	74.0237	73.0284	147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VN	186.1237	214.1186	**VNW**	372.2030	400.1979	**VNWP**	469.2558	497.2507
VNWPL	582.3398	610.3348	**VNWPLG**	639.3613	667.3562	**NW**	273.1346	301.1295
NWP	370.1874	398.1823	**NWPL**	483.2714	511.2663	**NWPLG**	540.2929	568.2878
WP	256.1444	284.1394	**WPL**	369.2285	397.2234	**WPLG**	426.2500	454.2449
WPLGW	612.3293	640.3242	**PL**	183.1492	211.1441	**PLG**	240.1707	268.1656
PLGW	426.2500	454.2449	**PLGWP**	523.3027	551.2976	**PLGWPV**	622.3711	650.3661
PLGWPVG	679.3926	707.3875	**LG**	143.1179	171.1128	**LGW**	329.1972	357.1921
LGWP	426.2500	454.2449	**LGWPV**	525.3184	553.3133	**LGWPVG**	582.3398	610.3348
LGWPVGG	639.3613	667.3562	**GW**	216.1131	244.1081	**GWP**	313.1659	341.1608
GWPV	412.2343	440.2292	**GWPVG**	469.2558	497.2507	**GWPVGG**	526.2772	554.2722
GWPVGGY	689.3406	717.3355	**WP**	256.1444	284.1394	**WPV**	355.2129	383.2078
WPVG	412.2343	440.2292	**WPVGG**	469.2558	497.2507	**WPVGGY**	632.3191	660.3140
PV	169.1335	197.1285	**PVG**	226.1550	254.1499	**PVGG**	283.1765	311.1714
PVGGY	446.2398	474.2347	**PVGGYP**	543.2926	571.2875	**PVGGYPG**	600.3140	628.3089
PVGGYPGP	697.3668	725.3617	**VG**	129.1022	157.0972	**VGG**	186.1237	214.1186
VGGY	349.1870	377.1819	**VGGYP**	446.2398	474.2347	**VGGYPG**	503.2613	531.2562
VGGYPGP	600.3140	628.3089	**GG**	87.0553	115.0502	**GGY**	250.1186	278.1135
GGYP	347.1714	375.1663	**GGYPG**	404.1928	432.1878	**GGYPGP**	501.2456	529.2405
GGYPGPQ	629.3042	657.2991	**GGYPGPQG**	686.3257	714.3206	**GY**	193.0972	221.0921
GYP	290.1499	318.1448	**GYPG**	347.1714	375.1663	**GYPGP**	444.2241	472.2191
GYPGPQ	572.2827	600.2776	**GYPGPQG**	629.3042	657.2991	**YP**	233.1285	261.1234
YPG	290.1499	318.1448	**YPGP**	387.2027	415.1976	**YPGPQ**	515.2613	543.2562
YPGPQG	572.2827	600.2776	**YPGPQGP**	669.3355	697.3304	**PG**	127.0866	155.0815
PGP	224.1394	252.1343	**PGPQ**	352.1979	380.1928	**PGPQG**	409.2194	437.2143
PGPQGP	506.2722	534.2671	**PGPQGPY**	669.3355	697.3304	**GP**	127.0866	155.0815
GPQ	255.1452	283.1401	**GPQG**	312.1666	340.1615	**GPQGP**	409.2194	437.2143
GPQGPY	572.2827	600.2776	**PQ**	198.1237	226.1186	**PQG**	255.1452	283.1401
PQGP	352.1979	380.1928	**PQGPY**	515.2613	543.2562	**PQGPYY**	678.3246	706.3195
QG	158.0924	186.0873	**QGP**	255.1452	283.1401	**QGPY**	418.2085	446.2034
QGPYY	581.2718	609.2667	**GP**	127.0866	155.0815	**GPY**	290.1499	318.1448
GPYY	453.2132	481.2082	**GPYYC**	613.2439	641.2388	**GPYYCA**	684.2810	712.2759
PY	233.1285	261.1234	**PYY**	396.1918	424.1867	**PYYC**	556.2224	584.2173
PYYCA	627.2595	655.2545	**YY**	299.1390	327.1339	**YYC**	459.1697	487.1646
YYCA	530.2068	558.2017	**YYCAV**	629.2752	657.2701	**YYCAVG**	686.2967	714.2916
YC	296.1063	324.1013	**YCA**	367.1435	395.1384	**YCAV**	466.2119	494.2068
YCAVG	523.2333	551.2282	**YCAVGS**	610.2654	638.2603	**CA**	204.0801	232.0750
CAV	303.1485	331.1435	**CAVG**	360.1700	388.1649	**CAVGS**	447.2020	475.1969
CAVGSD	562.2290	590.2239	**AV**	143.1179	171.1128	**AVG**	200.1394	228.1343
AVGS	287.1714	315.1663	**AVGSD**	402.1983	430.1932	**VG**	129.1022	157.0972
VGS	216.1343	244.1292	**VGSD**	331.1612	359.1561	**GS**	117.0659	145.0608
GSD	232.0928	260.0877	**SD**	175.0713	203.0662			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
11.3	3035.3913	0.0976	DVNWPLGWPVGGYPGPQGPYYCAVGSDK

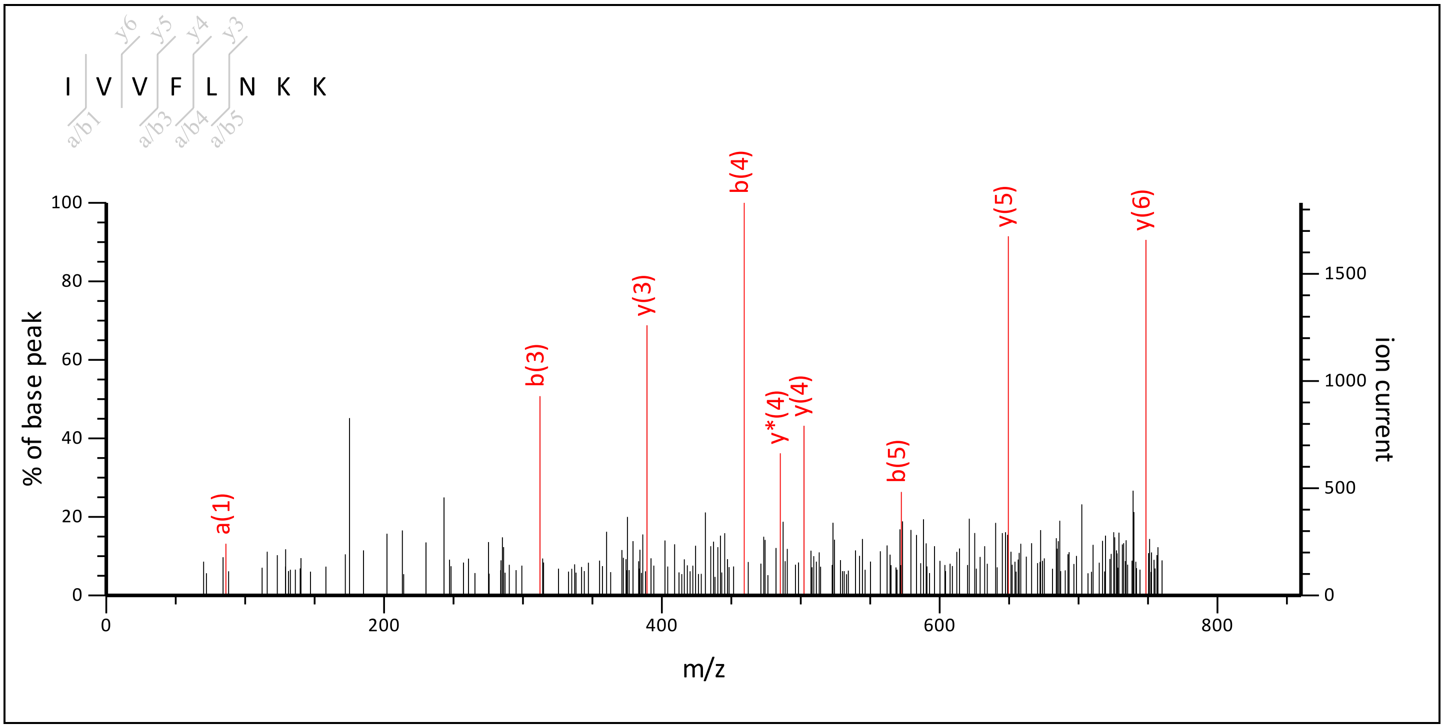
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **IVVFLNKK**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 8: 959.596854 from(960.604130,1+) intensity(0.0000) index(3)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225190, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt

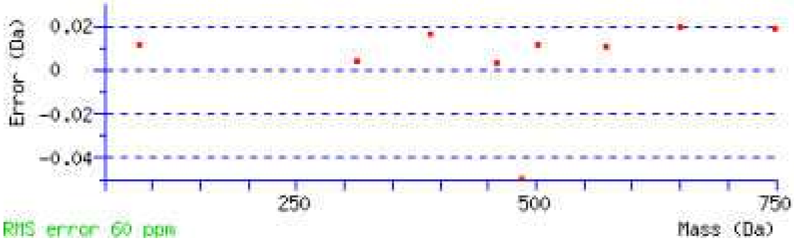


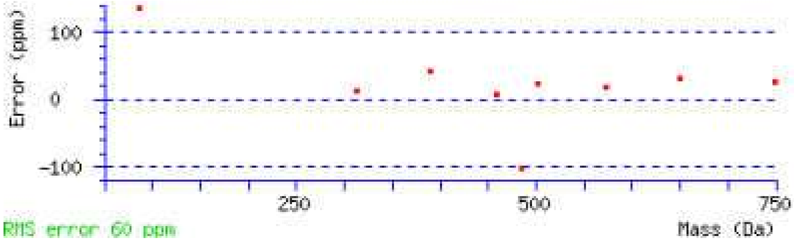
0 to 860.14

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 959.6168
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 5.7
Matches : 9/32 fragment ions using 14 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**86.0964**		114.0913		I			8
2	185.1648		213.1598		V	847.5400	830.5135	7
3	284.2333		**312.2282**		V	***748.4716***	731.4450	6
4	431.3017		**459.2966**		F	***649.4032***	632.3766	5
5	544.3857		**572.3806**		L	***502.3348***	485.3082	4
6	658.4287	641.4021	686.4236	669.3970	N	***389.2507***	372.2241	3
7	786.5236	769.4971	814.5185	797.4920	K	275.2078	258.1812	2
8					K	147.1128	130.0863	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.9	959.5804	0.0164	LVVFVLDR
32.1	959.5804	0.0164	VIVFDLVR
32.1	959.5341	0.0627	VLAFAFHR
24.2	959.6168	-0.0199	IVVFLNKK
23.8	959.5341	0.0627	LQFLFHR
23.8	959.5110	0.0859	LTPMLVDR
21.8	959.5188	0.0780	SSHFIKNK
21.6	959.5341	0.0627	IGAFIFHR
20.1	959.5705	0.0264	IFLKFHR
20.1	959.5341	0.0627	IFLQFHR

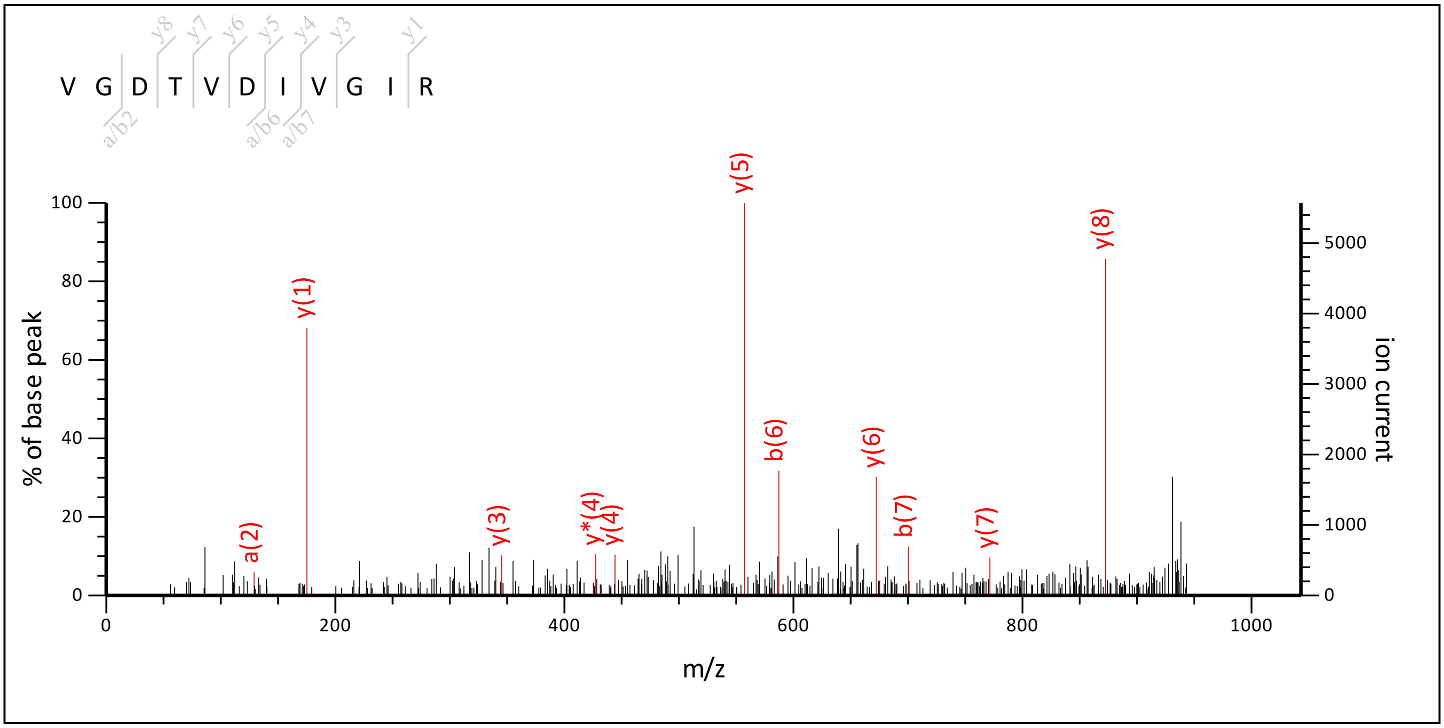
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **VGDTVDIVGIR**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 22: 1142.627224 from(1143.634500,1+) intensity(0.0000) index(9)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225183, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



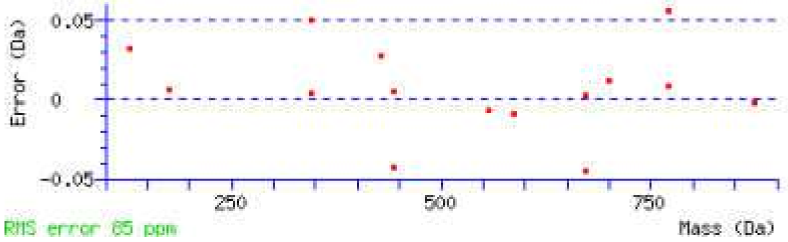
0 to 1043.2

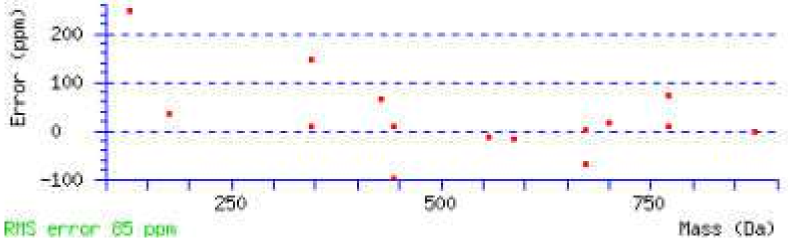
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1142.6296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.48
Matches : 15/40 fragment ions using 27 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	72.0808	100.0757	V			11
2	**129.1022**	157.0972	G	1044.5684	1027.5419	10
3	244.1292	272.1241	D	987.5469	970.5204	9
4	**345.1769**	373.1718	T	***872.5200***	855.4934	8
5	**444.2453**	472.2402	V	***771.4723***	754.4458	7
6	559.2722	**587.2671**	D	***672.4039***	655.3774	6
7	**672.3563**	**700.3512**	I	***557.3770***	540.3504	5
8	**771.4247**	799.4196	V	***444.2929***	427.2663	4

9	828.4462	856.4411	**G**	***345.2245***	328.1979	**3**
10	941.5302	969.5251	**I**	288.2030	271.1765	**2**
11			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.5	1142.6296	-0.0023	VGDTVDIVGIR
26.8	1142.6084	0.0188	WADDVLVGIR
24.6	1142.6044	0.0228	DRTVLDPATR
20.4	1142.6408	-0.0135	SVEGVDLLRR
18.6	1142.6118	0.0155	LGAMIVDPATR
18.6	1142.6659	-0.0387	LGLSESLVLGR
18.6	1142.6746	-0.0474	LWMRLVGLR
18.5	1142.6659	-0.0387	KISDLVDVVR
18.5	1142.6295	-0.0023	SSPAITTLTPR
18.4	1142.6156	0.0116	RSADGAAAVGLR

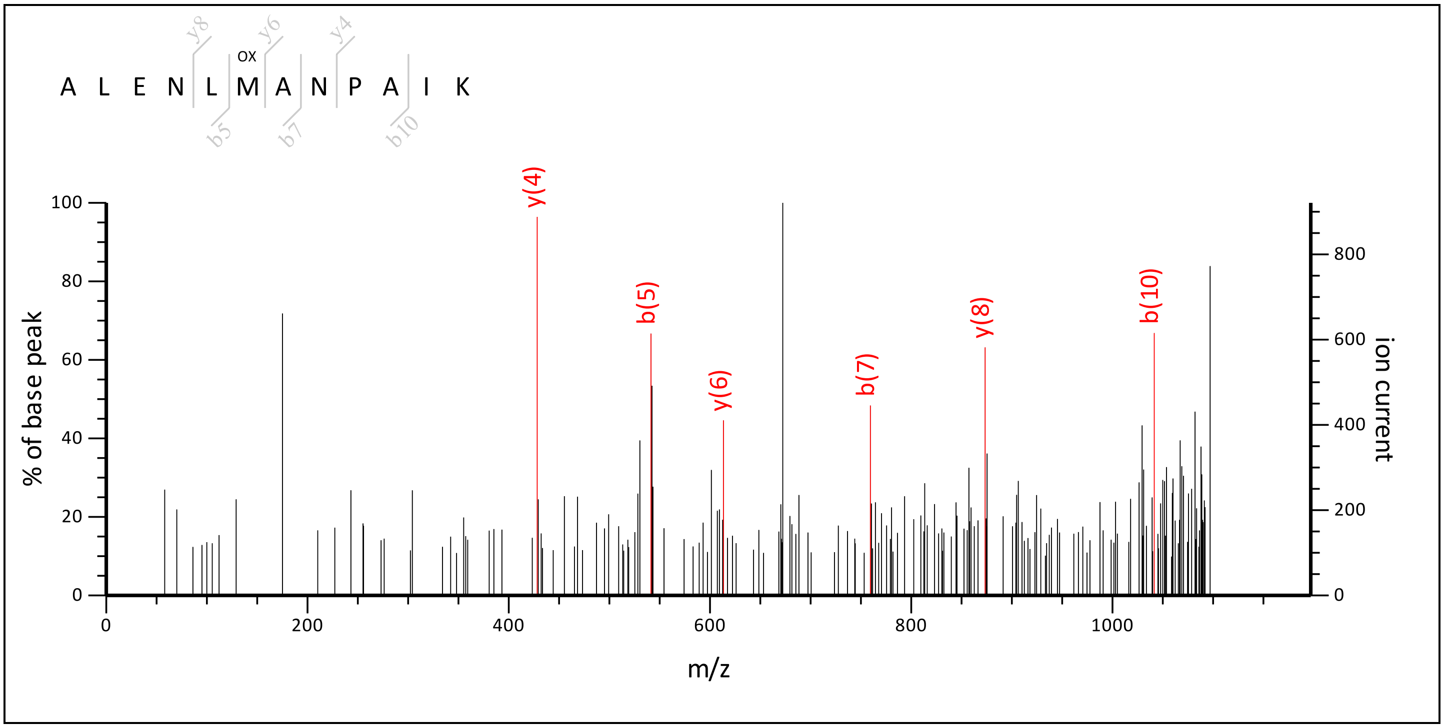
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **ALENLMANPAIK**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 27: 1299.653824 from(1300.661100,1+) intensity(0.0000) index(11)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225185, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



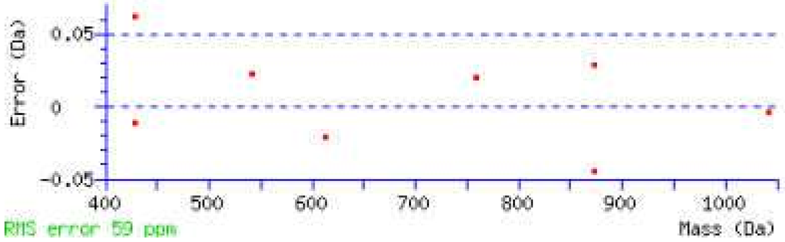
0 to 1197.05

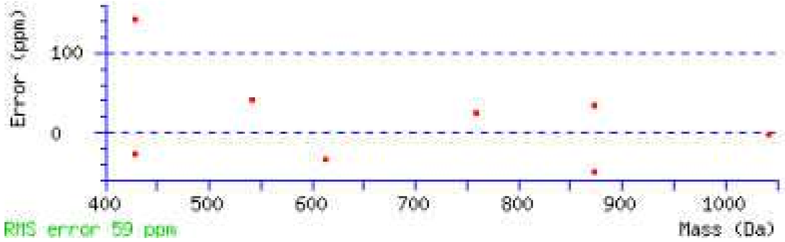
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1299.6856
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 6.5
Matches : 8/94 fragment ions using 11 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			12
2	157.1335		185.1285		L	1229.6558	1212.6293	11
3	286.1761		314.1710		E	1116.5718	1099.5452	10
4	400.2191	383.1925	***428.2140***	411.1874	N	987.5292	970.5026	9
5	513.3031	496.2766	***541.2980***	524.2715	L	**873.4863**	856.4597	8
6	660.3385	643.3120	688.3334	671.3069	M	760.4022	743.3756	7

7	731.3756	714.3491	*759.3706*	742.3440	**A**	**613.3668**	596.3402	**6**
8	845.4186	828.3920	*873.4135*	856.3869	**N**	542.3297	525.3031	**5**
9	942.4713	925.4448	970.4662	953.4397	**P**	**428.2867**	411.2602	**4**
10	1013.5084	996.4819	*1041.5034*	1024.4768	**A**	331.2340	314.2074	**3**
11	1126.5925	1109.5660	1154.5874	1137.5609	**I**	260.1969	243.1703	**2**
12					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.4	1299.6856	-0.0318	ALENLMANPAIK
21.4	1299.6354	0.0184	GAGEKVCGNGVPR
15.7	1299.6895	-0.0357	RASVAGASSPLER
15.5	1299.6782	-0.0244	LQGENSAEIIAR
14.9	1299.6870	-0.0332	GGPGIACFIPRR
14.8	1299.7220	-0.0682	KAIDLMQPQIK
14.8	1299.7220	-0.0682	KALDLMQPQIK
14.8	1299.6857	-0.0318	QALDLMQPQIK
14.1	1299.7663	-0.1124	KLWNSLSLLAR
14.1	1299.7048	-0.0509	NLVTNSPPFRR

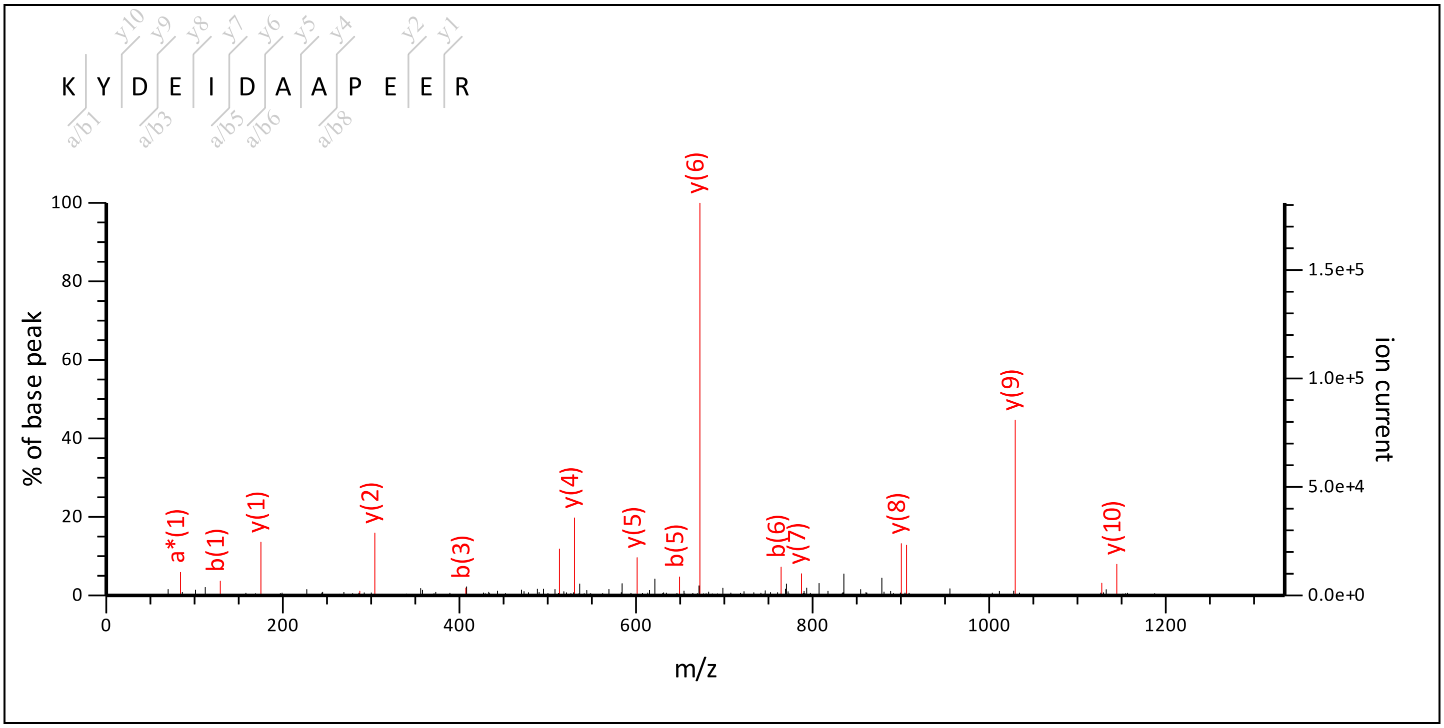
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **KYDEIDAAPEER**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 34: 1434.649024 from(1435.656300,1+) intensity(0.0000) index(14)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225168, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



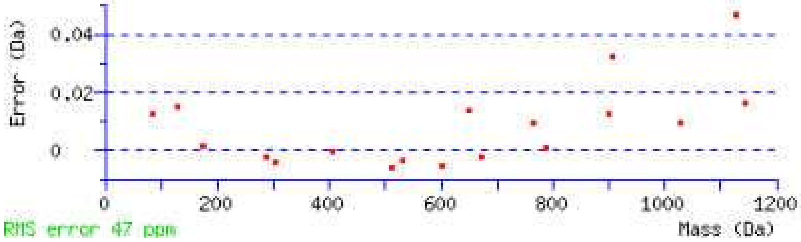
0 to 1334.71

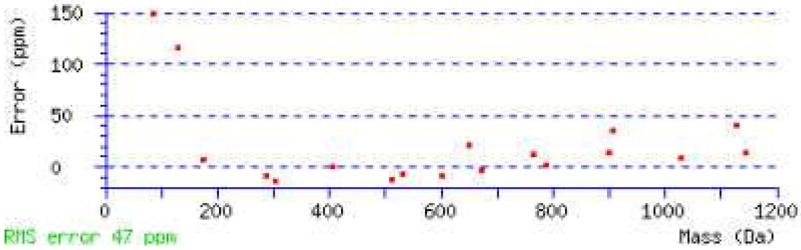
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1434.6626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 5e-05
Matches : 18/66 fragment ions using 24 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	101.1073	84.0808	**129.1022**	112.0757	**K**			**12**
2	264.1707	247.1441	292.1656	275.1390	**Y**	1307.5750	1290.5485	**11**
3	379.1976	362.1710	**407.1925**	390.1660	**D**	***1144.5117***	1127.4851	**10**
4	508.2402	491.2136	536.2351	519.2086	**E**	***1029.4847***	1012.4582	**9**
5	621.3243	604.2977	**649.3192**	632.2926	**I**	***900.4421***	883.4156	**8**
6	736.3512	719.3246	**764.3461**	747.3196	**D**	***787.3581***	770.3315	**7**
7	807.3883	790.3618	835.3832	818.3567	**A**	***672.3311***	655.3046	**6**
8	878.4254	861.3989	**906.4203**	889.3938	**A**	***601.2940***	584.2675	**5**

9	975.4782	958.4516	1003.4731	986.4466	**P**	***530.2569***	513.2304	**4**
10	1104.5208	1087.4942	1132.5157	1115.4891	**E**	433.2041	416.1776	**3**
11	1233.5634	1216.5368	1261.5583	1244.5317	**E**	***304.1615***	287.1350	**2**
12					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.7	1434.6626	-0.0136	KYDEIDAAPEER
27.4	1434.7541	-0.1050	YMTGPTLAALIER
24.9	1434.6626	-0.0136	RYDEIDAAPEEK
17.4	1434.6966	-0.0475	WGYEMPVDVLAR
17.2	1434.6739	-0.0249	ENAKSAGFTPEER
17.0	1434.7354	-0.0864	QEDSIVFSLIER
16.6	1434.6462	0.0028	HMSYHYALQNR
14.3	1434.6991	-0.0500	GVSYEDPSVQLNK
13.7	1434.6661	-0.0170	TMVDSSVVEEAPR
11.8	1434.6959	-0.0469	VKDEVCMGNVIR

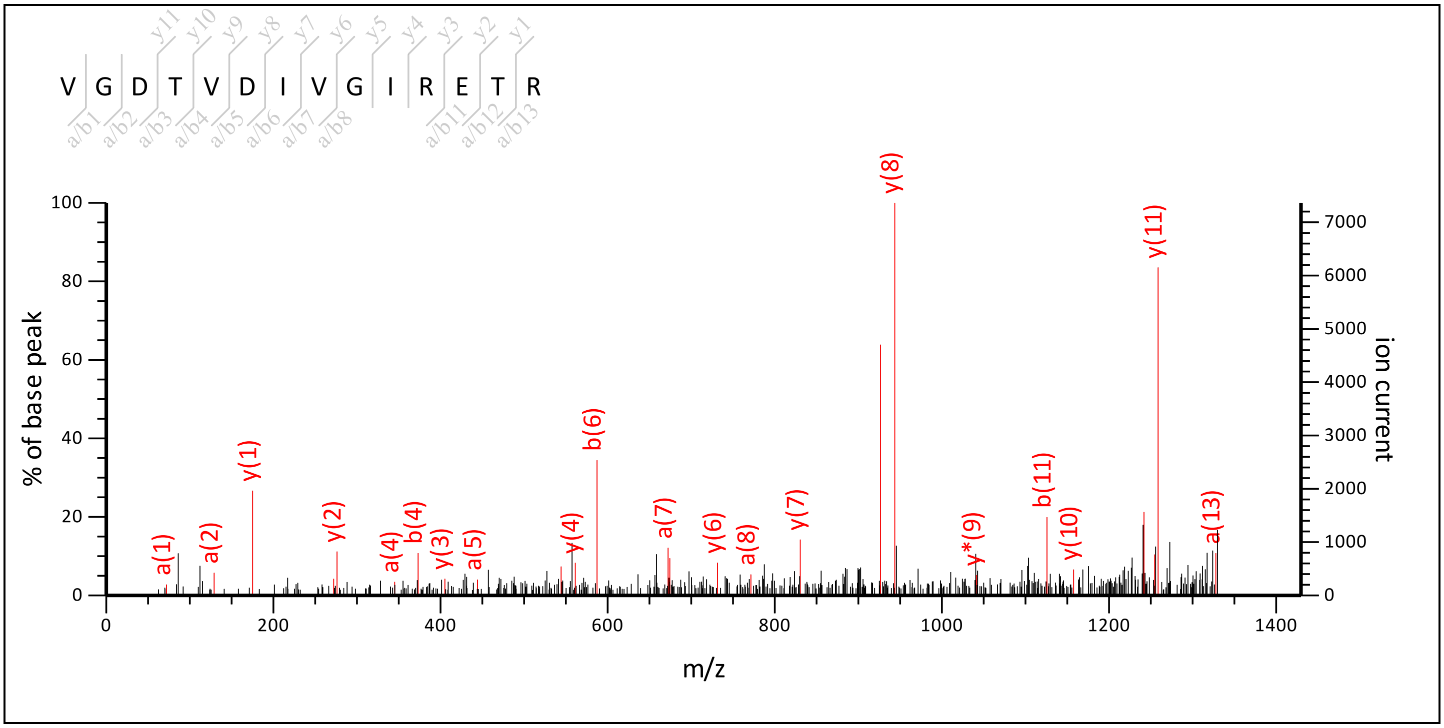
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **VGDTVDIVGIRETR**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 40: 1528.806224 from(1529.813500,1+) intensity(0.0000) index(16)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225172, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



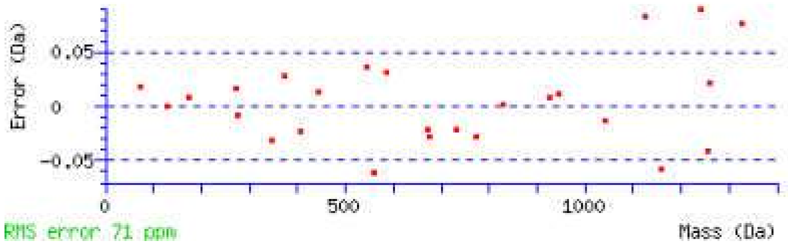
0 to 1429.7

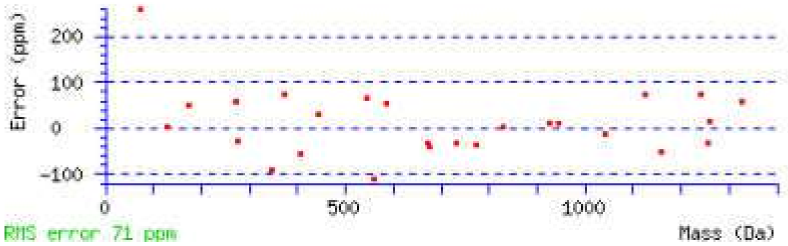
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1528.8209
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.061
Matches : 26/58 fragment ions using 78 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	***72.0808***		100.0757		**V**			**14**
2	***129.1022***		157.0972		**G**	1430.7598	1413.7332	**13**
3	244.1292		**272.1241**		**D**	1373.7383	1356.7118	**12**
4	***345.1769***		**373.1718**		**T**	***1258.7114***	1241.6848	**11**
5	***444.2453***		472.2402		**V**	***1157.6637***	1140.6371	**10**
6	559.2722		**587.2671**		**D**	1058.5953	1041.5687	**9**
7	***672.3563***		700.3512		**I**	***943.5683***	926.5418	**8**
8	***771.4247***		799.4196		**V**	***830.4843***	813.4577	**7**

9	828.4462		856.4411		G	***731.4159***	714.3893	6
10	941.5302		969.5251		I	***674.3944***	657.3679	5
11	1097.6313	1080.6048	**1125.6263**	1108.5997	R	***561.3103***	544.2838	4
12	1226.6739	1209.6474	**1254.6688**	1237.6423	E	***405.2092***	388.1827	3
13	***1327.7216***	1310.6951	1355.7165	1338.6900	T	***276.1666***	259.1401	2
14					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.8	1528.8209	-0.0147	VGDTVDIVGIRETR
27.6	1528.7555	0.0507	ISAAMPVHSKDTEK
23.1	1528.7310	0.0752	EQWVEAISWEPR
21.8	1528.8097	-0.0034	ISDGALVEAAILSDR
21.5	1528.7668	0.0394	MPQAQGGTAVSLTPR
20.7	1528.7482	0.0581	AVSSNGSPSPSPVTSR
20.5	1528.8209	-0.0147	VGDTVEIVGVRETR
18.8	1528.7555	0.0507	EAAELAADSPMGVLR
17.3	1528.8283	-0.0221	MATIPAAITTPSISR
16.5	1528.7780	0.0283	EMVNLLRNNSSPR

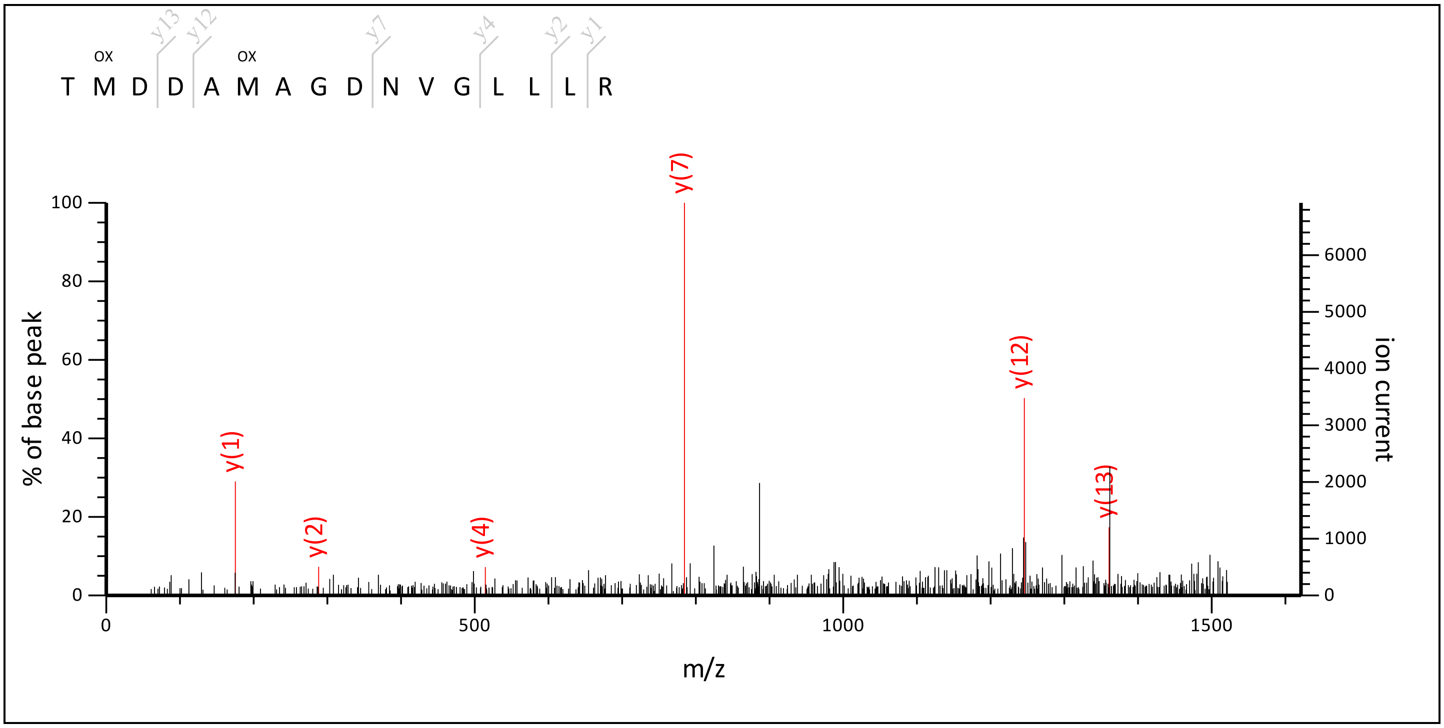
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **TMDDAMAGDNVGLLLR**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 45: 1722.761524 from(1723.768800,1+) intensity(0.0000) index(18)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225171, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



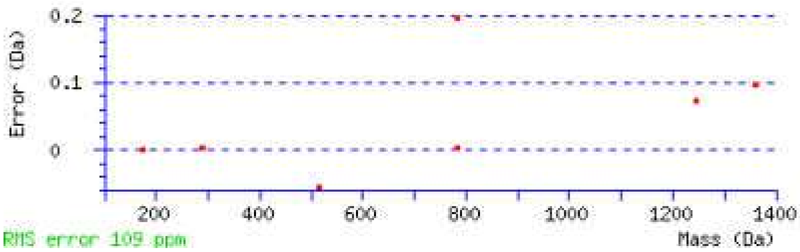
0 to 1621.14

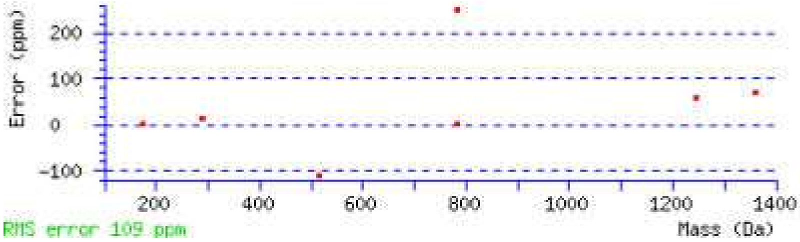
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1722.7917
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 4.3
Matches : 7/122 fragment ions using 15 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	74.0600		102.0550		T			16
2	221.0954		249.0904		M	1622.7513	1605.7247	15
3	336.1224		364.1173		D	1475.7159	1458.6893	14
4	451.1493		479.1442		D	*1360.6889*	1343.6624	13
5	522.1864		550.1814		A	*1245.6620*	1228.6354	12
6	669.2218		697.2168		M	1174.6249	1157.5983	11

7	740.2590		768.2539		A	1027.5895	1010.5629	10
8	797.2804		825.2753		G	956.5524	939.5258	9
9	912.3074		940.3023		D	899.5309	882.5043	8
10	1026.3503	1009.3237	1054.3452	1037.3187	N	***784.5039***	767.4774	7
11	1125.4187	1108.3922	1153.4136	1136.3871	V	670.4610	653.4345	6
12	1182.4402	1165.4136	1210.4351	1193.4085	G	571.3926	554.3661	5
13	1295.5242	1278.4977	1323.5191	1306.4926	L	***514.3711***	497.3446	4
14	1408.6083	1391.5817	1436.6032	1419.5767	L	401.2871	384.2605	3
15	1521.6924	1504.6658	1549.6873	1532.6607	L	***288.2030***	271.1765	2
16					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.2	1722.7917	-0.0301	TMDDAMAGDNVGLLLR
10.9	1722.8862	-0.1247	ESFMELKTDELILR
3.5	1722.7640	-0.0025	WIDMRELPMNCSR
3.0	1722.8424	-0.0809	KSSSSEEAPASFVEIR
2.0	1722.8901	-0.1285	QVITESDLTPNHTLR
1.8	1722.7155	0.0460	DSVIPADPNDSDYCR
1.7	1722.9264	-0.1649	KGPSSGNLPAALDVEIR
1.6	1722.8247	-0.0631	DIADNSMPNLIYVSR
1.5	1722.7784	-0.0169	ASGFMGWTSHSASLER
1.4	1722.9125	-0.1510	LLDHSRTVGGSQQGIR

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

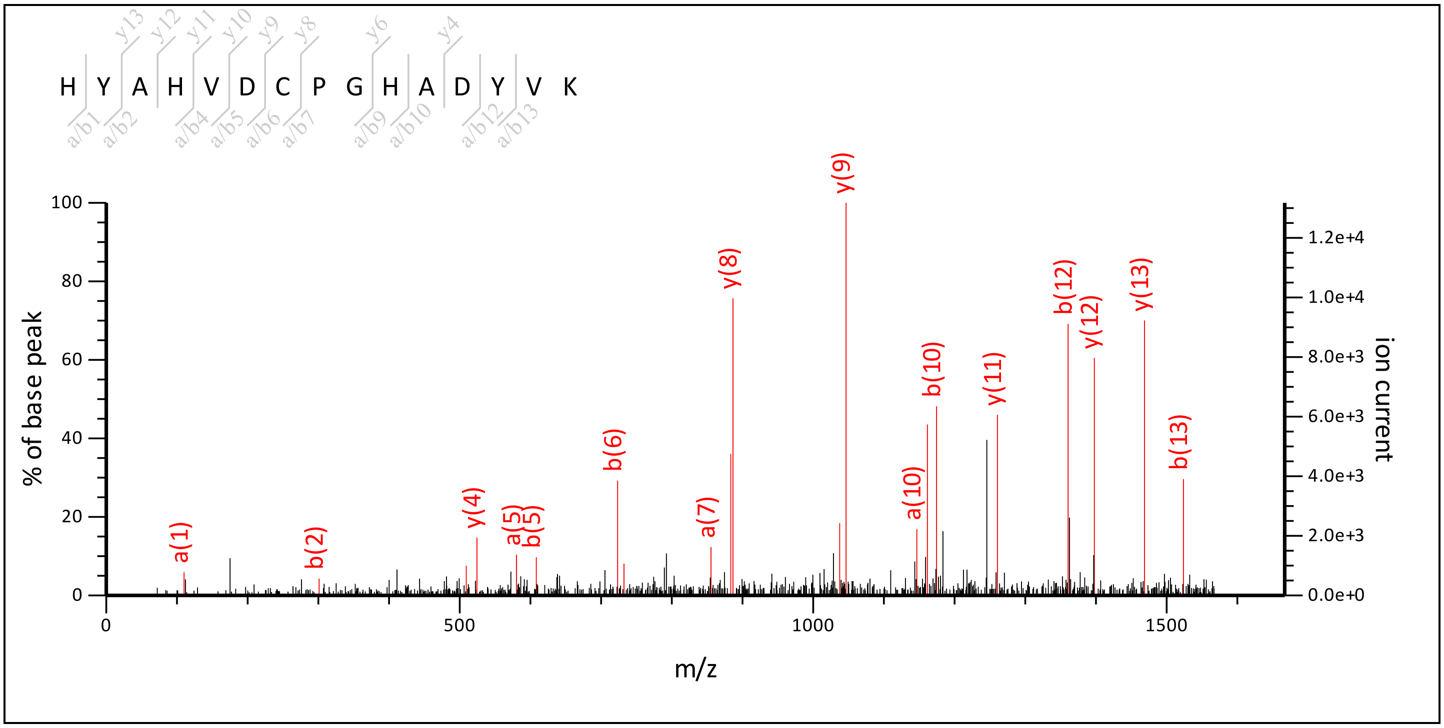
MATRIX SCIENCE

Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **HYAHVDCPGHADYVK**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 47: 1767.754124 from(1768.761400,1+) intensity(0.0000) index(19)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225169, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



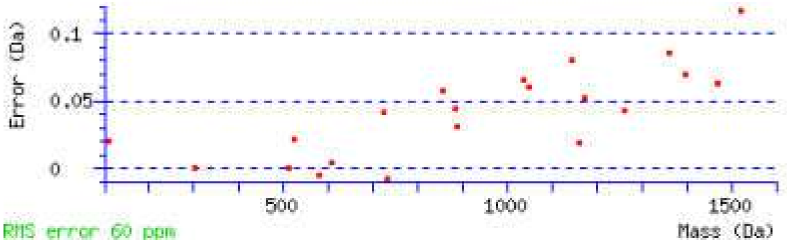
0 to 1666.98

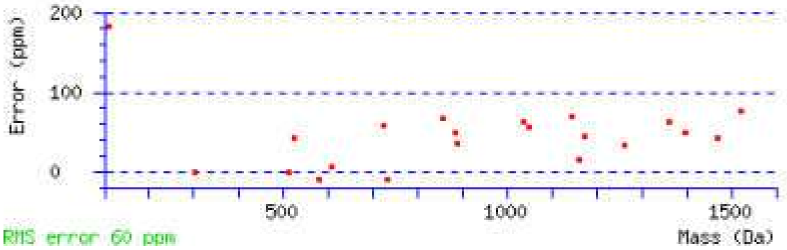
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1767.7787
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 8e-05
Matches : 21/56 fragment ions using 30 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	**110.0713**	138.0662	H			15
2	273.1346	***301.1295***	Y	1631.7271	1614.7006	14
3	344.1717	372.1666	A	***1468.6638***	1451.6372	13
4	481.2306	***509.2255***	H	***1397.6267***	1380.6001	12
5	**580.2990**	***608.2940***	V	***1260.5678***	1243.5412	11
6	695.3260	***723.3209***	D	***1161.4993***	1144.4728	10
7	**855.3566**	***883.3515***	C	***1046.4724***	1029.4458	9
8	952.4094	980.4043	P	***886.4417***	869.4152	8

9	1009.4309	***1037.4258***	**G**	789.3890	772.3624	**7**
10	**1146.4898**	***1174.4847***	**H**	***732.3675***	715.3410	**6**
11	1217.5269	1245.5218	**A**	595.3086	578.2821	**5**
12	1332.5538	***1360.5487***	**D**	***524.2715***	507.2449	**4**
13	1495.6172	***1523.6121***	**Y**	409.2445	392.2180	**3**
14	1594.6856	1622.6805	**V**	246.1812	229.1547	**2**
15			**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.6	1767.7787	-0.0246	HYAHVDCPGHADYVK
9.2	1767.8652	-0.1111	HSVDVANYNHSIVSAR
7.8	1767.8441	-0.0900	HINKDGPHFNEAAYR
7.8	1767.8077	-0.0536	HINQDGPHFNEAAYR
7.7	1767.8760	-0.1219	INTPALICHNMIEAR
5.5	1767.8839	-0.1297	HVREHGVQYMLEVR
5.2	1767.8944	-0.1403	NLDLVAEKYQSWFR
5.2	1767.7291	0.0250	EGEEGMVDQAQATMEK
4.8	1767.8072	-0.0531	SVMEYLCEFNHLAR
4.8	1767.8219	-0.0678	HVYVCATTGGKLCMR

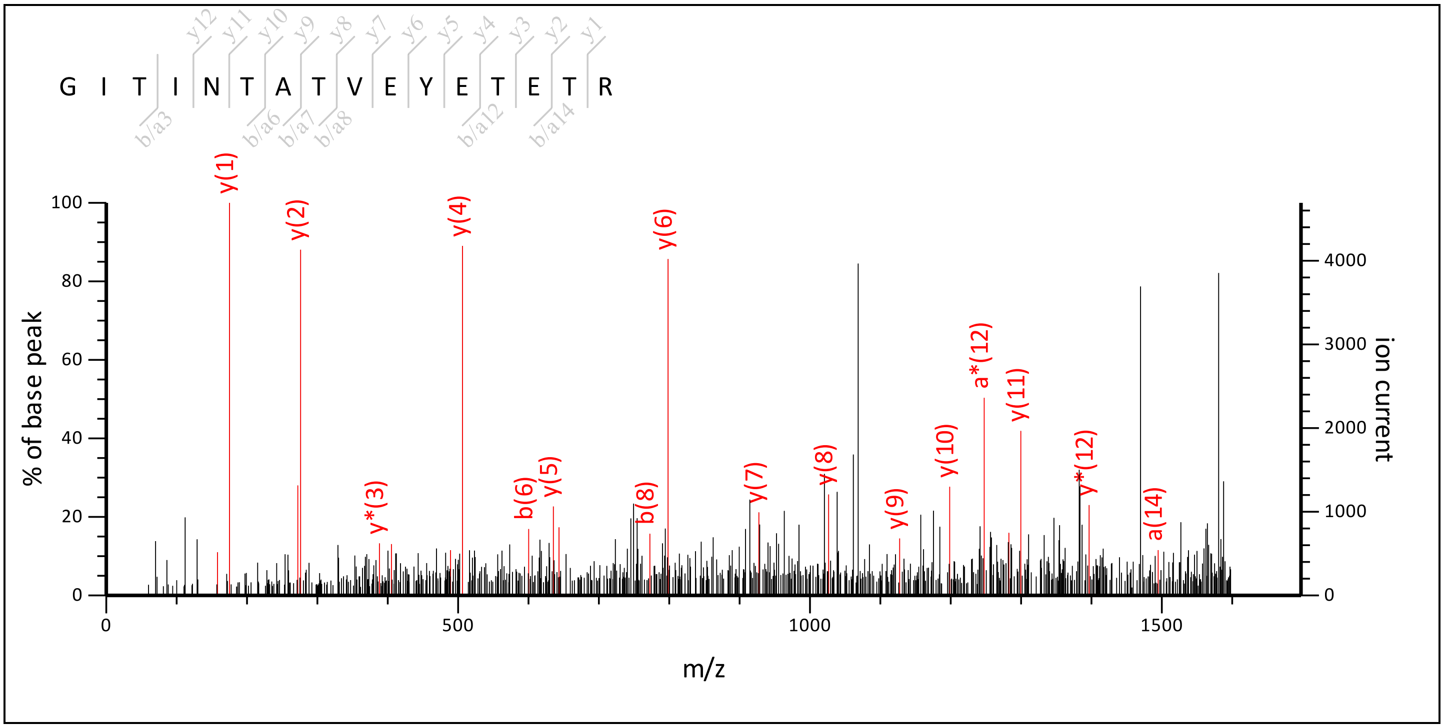
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **GITINTATVEYETETR**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 51: 1796.863524 from(1797.870800,1+) intensity(0.0000) index(21)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225177, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



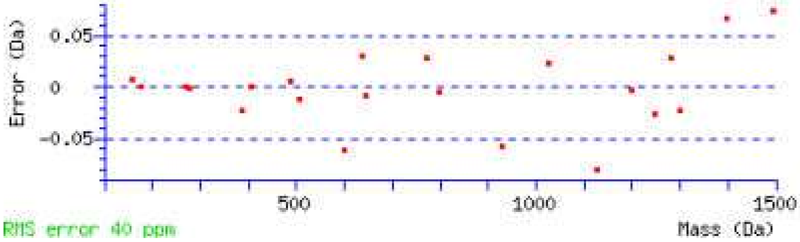
0 to 1697.75

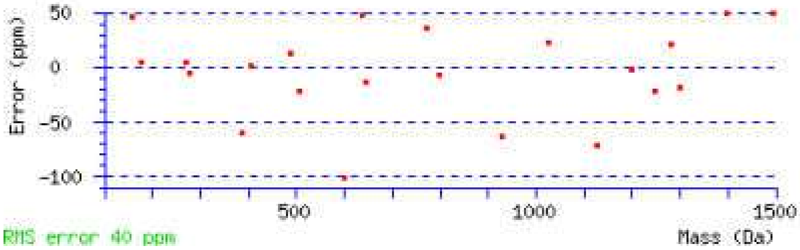
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): `1796.8792`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `44` **Expect:** `0.068`
Matches : `22/82 fragment ions using 64 most intense peaks` (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			16
2	143.1179		171.1128		I	1740.8650	1723.8385	15
3	244.1656		**272.1605**		T	1627.7810	1610.7544	14
4	357.2496		385.2445		I	1526.7333	1509.7067	13
5	471.2926	454.2660	499.2875	482.2609	N	1413.6492	1396.6227	12
6	572.3402	555.3137	**600.3352**	583.3086	T	***1299.6063***	1282.5798	11
7	**643.3774**	626.3508	671.3723	654.3457	A	***1198.5586***	1181.5321	10
8	744.4250	727.3985	**772.4199**	755.3934	T	***1127.5215***	1110.4950	9

9	843.4934	826.4669	871.4884	854.4618	V	***1026.4738***	1009.4473	8
10	972.5360	955.5095	1000.5310	983.5044	E	***927.4054***	910.3789	7
11	1135.5994	1118.5728	1163.5943	1146.5677	Y	***798.3628***	781.3363	6
12	1264.6420	1247.6154	1292.6369	1275.6103	E	***635.2995***	618.2729	5
13	1365.6896	1348.6631	1393.6846	1376.6580	T	***506.2569***	489.2304	4
14	**1494.7322**	1477.7057	1522.7271	1505.7006	E	***405.2092***	388.1827	3
15	1595.7799	1578.7534	1623.7748	1606.7483	T	***276.1666***	259.1401	2
16					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.8	1796.8792	-0.0157	GITINTATVEYETETR
7.7	1796.7119	0.1516	SGSPMREDGETDDETR
7.1	1796.9203	-0.0568	ISQSMASTKPYTRATR
4.8	1796.9380	-0.0745	SLSNPTSSLPRISEGPR
3.6	1796.9203	-0.0568	GVDGSGANHLGTLLMSIR
3.5	1796.8776	-0.0141	KFEFMGLLCCHVLK
3.4	1796.8549	0.0086	RFDDALSLMENLMSR
3.3	1796.9342	-0.0707	QFETSNKALASTLIMK
3.2	1796.8358	0.0277	AMVAEMESLAKDMVEK
2.6	1796.8529	0.0106	HFMNPRTYDLGPHGR

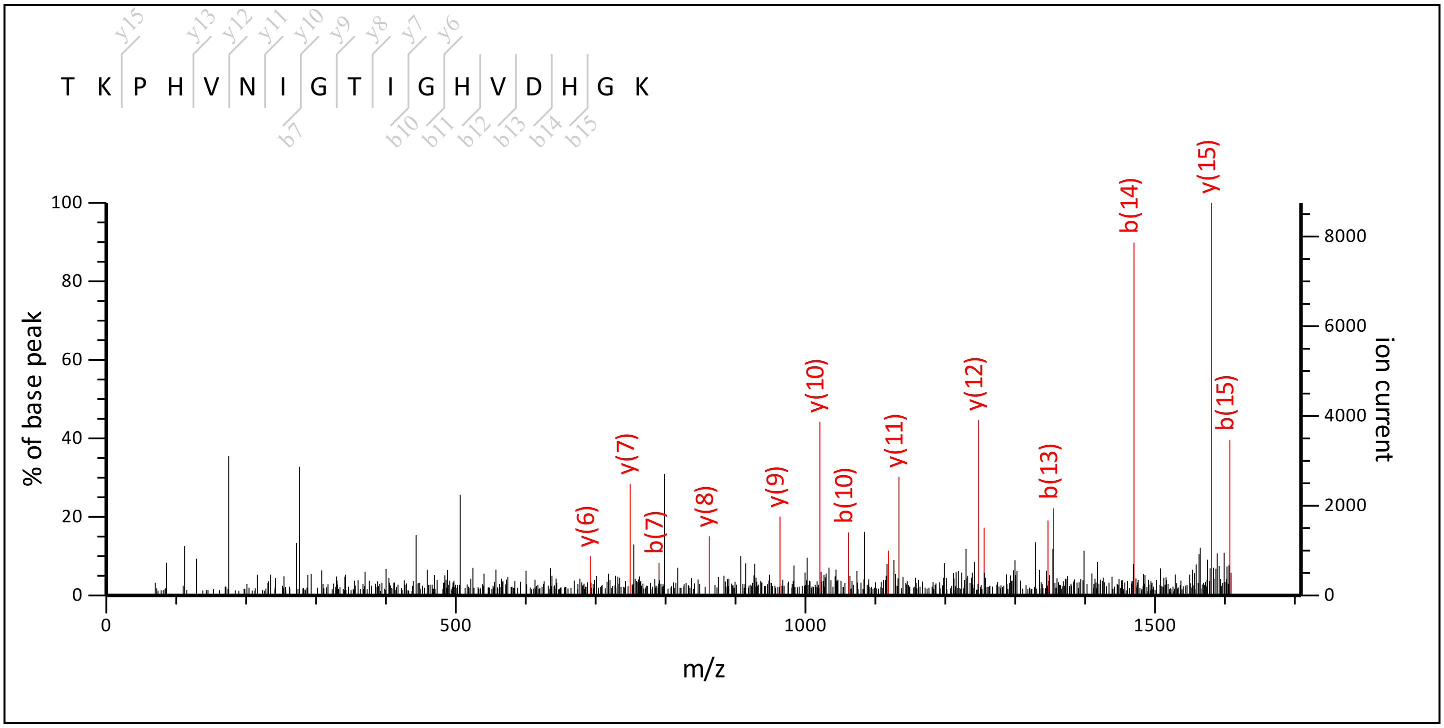
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 71

MS/MS Fragmentation of **TKPHVNIGTIGHVDHGK**
Found in **gi|6525065** in **NCBInr**, chloroplast translational elongation factor Tu [Oryza sativa Japonica Group]

Match to Query 53: 1808.939124 from(1809.946400,1+) intensity(0.0000) index(22)
Title: Label: B3, Spot_Id: 219707, Peak_List_Id: 225174, MSMS Job_Run_Id: 21768, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_B3_136842116600.txt



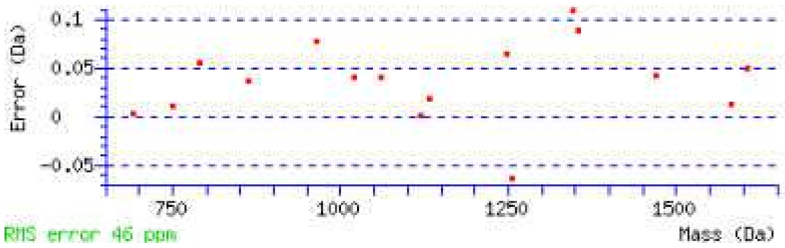
0 to 1708.78

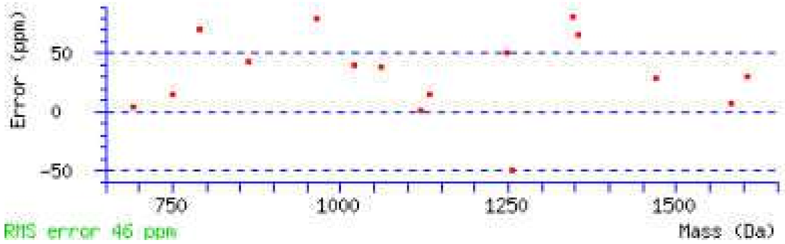
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1808.9646
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.19
Matches : 16/94 fragment ions using 48 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	74.0600		102.0550		T			17
2	202.1550	185.1285	230.1499	213.1234	K	1708.9242	1691.8976	16
3	299.2078	282.1812	327.2027	310.1761	P	*1580.8292*	1563.8027	15
4	436.2667	419.2401	464.2616	447.2350	H	1483.7764	1466.7499	14
5	535.3351	518.3085	563.3300	546.3035	V	*1346.7175*	1329.6910	13
6	649.3780	632.3515	677.3729	660.3464	N	*1247.6491*	1230.6226	12
7	762.4621	745.4355	*790.4570*	773.4304	I	*1133.6062*	1116.5796	11
8	819.4835	802.4570	847.4785	830.4519	G	*1020.5221*	1003.4956	10

9	920.5312	903.5047	948.5261	931.4996	**T**	***963.5007***	946.4741	**9**
10	1033.6153	1016.5887	***1061.6102***	1044.5837	**I**	***862.4530***	845.4264	**8**
11	1090.6368	1073.6102	***1118.6317***	1101.6051	**G**	***749.3689***	732.3424	**7**
12	1227.6957	1210.6691	***1255.6906***	1238.6640	**H**	***692.3474***	675.3209	**6**
13	1326.7641	1309.7375	***1354.7590***	1337.7324	**V**	555.2885	538.2620	**5**
14	1441.7910	1424.7645	***1469.7859***	1452.7594	**D**	456.2201	439.1936	**4**
15	1578.8499	1561.8234	***1606.8449***	1589.8183	**H**	341.1932	324.1666	**3**
16	1635.8714	1618.8449	1663.8663	1646.8398	**G**	204.1343	187.1077	**2**
17					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.4	1808.9646	-0.0255	TKPHVNIGTIGHVDHGK
28.3	1809.0010	-0.0618	KKPHVSIGTIGHVDHGK
27.5	1808.9646	-0.0255	TKPHLNVGTIGHVDHGK
11.5	1808.9594	-0.0202	MATTELKSDAIFELLK
7.4	1808.8781	0.0611	IVYPFGIGRGCYHDR
7.0	1808.8211	0.1180	SLPMQVTSNSVSGDDTR
6.9	1808.8476	0.0916	HSVSFSTTRGMLDDTR
5.2	1808.9394	-0.0003	GSYREVQSIHRPQPR
4.7	1809.0624	-0.1233	KHLALGNTLLNILYAR
4.5	1808.9758	-0.0367	HNIRNISVIAHVDHGK

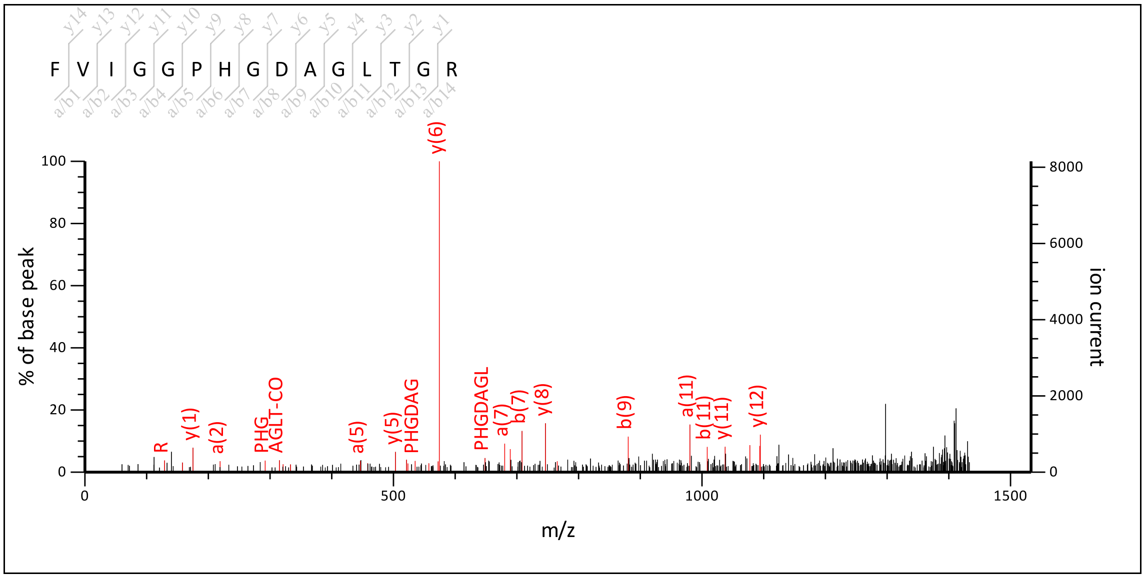
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 72

MS/MS Fragmentation of **FVIGGPHGDAGLTGR**
Found in **gi|127046** in **NCBInr**, RecName: Full=S-adenosylmethionine synthase 2; Short=AdoMet synthase 2; AltName: Full=Methionine adenosyltransferase 2; Short=MAT 2

Match to Query 8: 1452.810224 from(1453.817500,1+) intensity(0.0000) index(3)
Title: Label: F9, Spot_Id: 228975, Peak_List_Id: 257839, MSMS Job_Run_Id: 24938, Comment:
Data file ppw_F9_138985151700.txt



0 to 1533.27

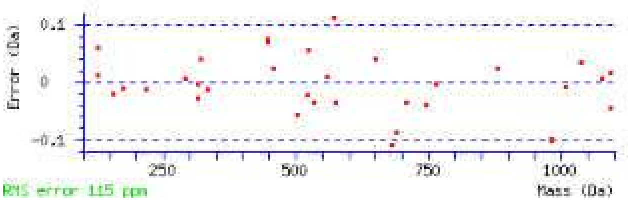
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1452.7474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.058
Matches : 37/241 fragment ions using 70 most intense peaks (help)

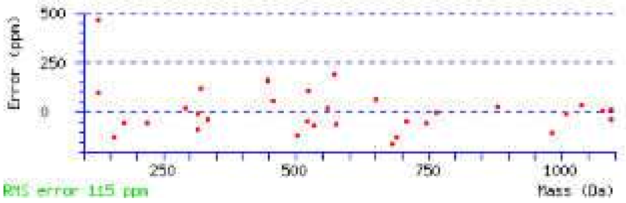
#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	120.0808	120.0808		148.0757		44.0495		F							15
2	72.0808	**219.1492**		247.1441		205.1335		V	1262.6236	1275.6440		1306.6862	1289.6597	1288.6757	14
3	86.0964	332.2333		360.2282		304.2020	318.2176	I	1149.5396	1162.5600	1176.5756	1207.6178	1190.5913	1189.6072	13
4	30.0338	389.2547		417.2496				G				***1094.5337***	1077.5072	1076.5232	12
5	30.0338	**446.2762**		474.2711				G				***1037.5123***	1020.4857	1019.5017	11
6	70.0651	543.3289		571.3239		517.3133		P	938.4439	937.4486		***980.4908***	963.4643	962.4803	10
7	110.0713	**680.3879**		**708.3828**				H	801.3850			883.4381	866.4115	865.4275	9
8	30.0338	737.4093		**765.4042**				G				***746.3791***	729.3526	728.3686	8
9	88.0393	852.4363	834.4257	**880.4312**	862.4206	808.4464		D	629.3366	628.3413		***689.3577***	672.3311	671.3471	7
10	44.0495	923.4734	905.4628	951.4683	933.4577			A	558.2994			***574.3307***	557.3042	556.3202	6
11	30.0338	**980.4948**	962.4843	**1008.4898**	990.4792			G				***503.2936***	486.2671	485.2831	5
12	86.0964	**1093.5789**	1075.5683	1121.5738	1103.5633	1051.5320		L	388.1939	387.1987		***446.2722***	429.2456	428.2616	4
13	74.0600	1194.6266	1176.6160	1222.6215	1204.6109	1178.6317	1180.6109	T	287.1462	300.1666	302.1459	***333.1881***	316.1615	315.1775	3
14	30.0338	1251.6480	1233.6375	1279.6430	1261.6324			G				232.1404	215.1139		2
15	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VI	185.1648	213.1598	VIG	242.1863	270.1812	VIGG	299.2078	327.2027
VIGGP	396.2605	424.2554	VIGGPH	533.3194	561.3144	VIGGPHG	590.3409	618.3358

IG	143.1179	171.1128	**IGG**	200.1394	228.1343	**IGGP**	297.1921	325.1870
IGGPH	434.2510	462.2459	**IGGPHG**	491.2725	519.2674	**IGGPHGD**	606.2994	634.2944
IGGPHGDA	677.3365	705.3315	**GG**	87.0553	115.0502	**GGP**	184.1081	212.1030
GGPH	321.1670	349.1619	**GGPHG**	378.1884	406.1833	**GGPHGD**	493.2154	521.2103
GGPHGDA	564.2525	592.2474	**GGPHGDAG**	621.2740	649.2689	**GP**	127.0866	155.0815
GPH	264.1455	292.1404	**GPHG**	321.1670	349.1619	**GPHGD**	436.1939	464.1888
GPHGDA	507.2310	535.2259	**GPHGDAG**	564.2525	592.2474	**GPHGDAGL**	677.3365	705.3315
PH	207.1240	235.1190	**PHG**	264.1455	292.1404	**PHGD**	379.1724	407.1674
PHGDA	450.2096	478.2045	**PHGDAG**	507.2310	535.2259	**PHGDAGL**	620.3151	648.3100
HG	167.0927	195.0877	**HGD**	282.1197	310.1146	**HGDA**	353.1568	381.1517
HGDAG	410.1783	438.1732	**HGDAGL**	523.2623	551.2572	**HGDAGLT**	624.3100	652.3049
HGDAGLTG	681.3315	709.3264	**GD**	145.0608	173.0557	**GDA**	216.0979	244.0928
GDAG	273.1193	301.1143	**GDAGL**	386.2034	414.1983	**GDAGLT**	487.2511	515.2460
GDAGLTG	544.2726	572.2675	**DA**	159.0764	187.0713	**DAG**	216.0979	244.0928
DAGL	329.1819	357.1769	**DAGLT**	430.2296	458.2245	**DAGLTG**	487.2511	515.2460
AG	101.0709	129.0659	**AGL**	214.1550	242.1499	**AGLT**	315.2027	343.1976
AGLTG	372.2241	400.2191	**GL**	143.1179	171.1128	**GLT**	244.1656	272.1605
GLTG	301.1870	329.1819	**LT**	187.1441	215.1390	**LTG**	244.1656	272.1605
TG	131.0815	159.0764						



RMS error 115 ppm



RMS error 115 ppm

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

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.6	1452.7474	0.0628	FVIGGPHGDAGLTGR
45.6	1452.7474	0.0628	FVIGGPHGDAGLTGR
16.8	1452.7586	0.0516	GVWLGAQPAADRGR
14.0	1452.7209	0.0894	TSDLYKGDANTLR
12.7	1452.7143	0.0959	RFSSTTLSAPACR
12.7	1452.8161	-0.0058	RLLLAGQQAAAADR
12.7	1452.7950	0.0153	RPPYPAPTAATRR
12.7	1452.7950	0.0153	RPSGQQLLAAAWR
12.3	1452.7433	0.0669	SSNAPAAPSPATARR
11.2	1452.6966	0.1137	DRAMQLMTAFNR

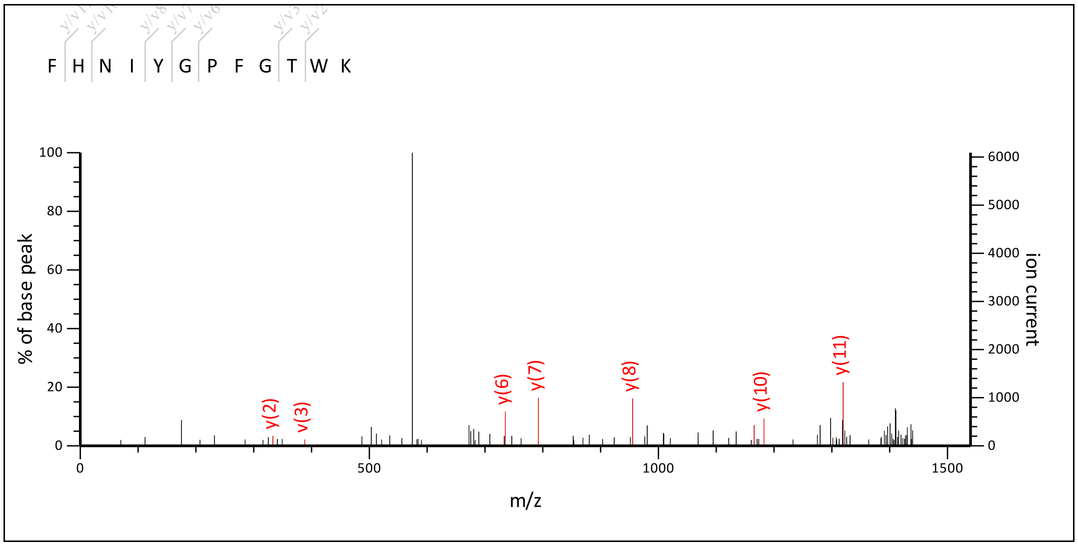
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 73

MS/MS Fragmentation of **FHNIYGPFGTWK**
Found in **gi|110289082** in **NCBInr**, NAD dependent epimerase/dehydratase family protein, expressed [Oryza sativa Japonica Group]

Match to Query 57: 1465.807224 from(1466.814500,1+) intensity(0.0000) index(18)
Title: Label: P7, Spot_Id: 228953, Peak_List_Id: 257728, MSMS Job_Run_Id: 24933, Comment:
Data file ppw_P7_138985142500.txt



0 to 1539.84

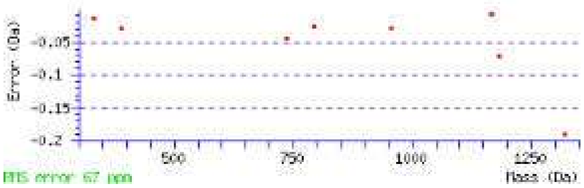
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1465.7143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 1.1
Matches : 8/180 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	120.0808	120.0808			148.0757			44.0495		F					
2	110.0713	257.1397			285.1346					H	1237.6000			***1319.6531***	1302.6266
3	87.0553	371.1826	354.1561		399.1775	382.1510		328.1768		N	1123.5571	1122.5619		***1182.5942***	1165.5677
4	86.0964	484.2667	467.2401		512.2616	495.2350		456.2354	470.2510	I	1010.4730	1023.4934	1037.5091	1068.5513	1051.5247
5	136.0757	647.3300	630.3035		675.3249	658.2984				Y	847.4097			***955.4672***	938.4407
6	30.0338	704.3515	687.3249		732.3464	715.3198				G				***792.4039***	775.3774
7	70.0651	801.4042	784.3777		829.3992	812.3726		775.3886		P	693.3355	692.3402		***735.3824***	718.3559
8	120.0808	948.4726	931.4461		976.4676	959.4410				F	546.2671			638.3297	621.3031
9	30.0338	1005.4941	988.4676		1033.4890	1016.4625				G				491.2613	474.2347
10	74.0600	1106.5418	1089.5152	1088.5312	1134.5367	1117.5102	1116.5261	1090.5469	1092.5261	T	388.1979	401.2183	403.1976	434.2398	417.2132
11	159.0917	1292.6211	1275.5946	1274.6105	1320.6160	1303.5895	1302.6055			W	202.1186			***333.1921***	316.1656
12	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HN	224.1142	252.1091	HNI	337.1983	365.1932	HNIY	500.2616	528.2565
HNIYG	557.2831	585.2780	HNIYGP	654.3358	682.3307	NI	200.1394	228.1343
NIY	363.2027	391.1976	NIYG	420.2241	448.2191	NIYGP	517.2769	545.2718
NIYGPF	664.3453	692.3402	IY	249.1598	277.1547	IYG	306.1812	334.1761
IYGP	403.2340	431.2289	IYGPF	550.3024	578.2973	IYGPFG	607.3239	635.3188
YG	193.0972	221.0921	YGP	290.1499	318.1448	YGPF	437.2183	465.2132
YGPFG	494.2398	522.2347	YGPFGT	595.2875	623.2824	GP	127.0866	155.0815
GPF	274.1550	302.1499	GPFG	331.1765	359.1714	GPFGT	432.2241	460.2191
GPFGTW	618.3035	646.2984	PF	217.1335	245.1285	PFG	274.1550	302.1499

PFGT	375.2027	403.1976	**PFGTW**	561.2820	589.2769	**FG**	177.1022	205.0972
FGT	278.1499	306.1448	**FGTW**	464.2292	492.2241	**GT**	131.0815	159.0764
GTW	317.1608	345.1557	**TW**	260.1394	288.1343			



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.4	1465.7143	0.0929	FHNIYGPFGTWK
21.9	1465.6766	0.1306	MTAERACGAVAGTR
16.5	1465.8188	-0.0115	AGGVCVLHVAISKR
14.9	1465.6871	0.1201	GYLPPMDESKSAR
14.6	1465.8001	0.0071	TSLPLPEGRQVNR
13.5	1465.6797	0.1275	DSLGDYNKDANVR
12.9	1465.6983	0.1089	EIKCAAFNAEGTR
12.7	1465.7096	0.0976	GINSDRAFGTCLR
10.9	1465.8113	-0.0041	RPRLSGPEALGTGR
10.5	1465.7565	0.0507	GVKDSLYTELWR

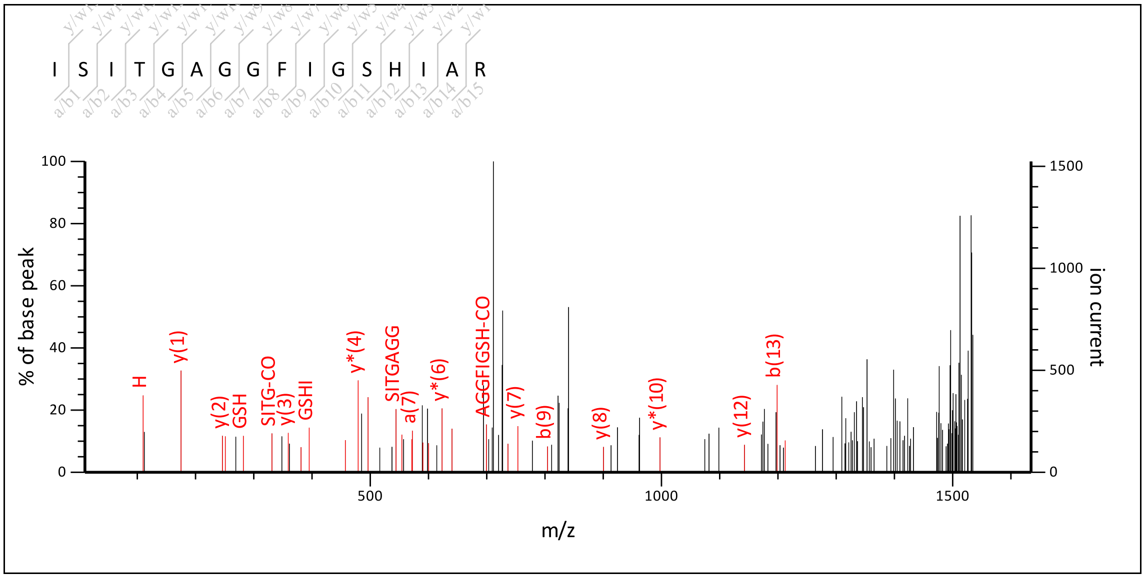
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 73

MS/MS Fragmentation of **ISITGAGGFIGSHIAR**
Found in **gi|110289082** in **NCBInr**, NAD dependent epimerase/dehydratase family protein, expressed [Oryza sativa Japonica Group]

Match to Query 66: 1555.982824 from(1556.990100,1+) intensity(0.0000) index(20)
Title: Label: P7, Spot_Id: 228953, Peak_List_Id: 257722, MSMS Job_Run_Id: 24933, Comment:
Data file ppw_P7_138985142500.txt



10.08 to 1634.59

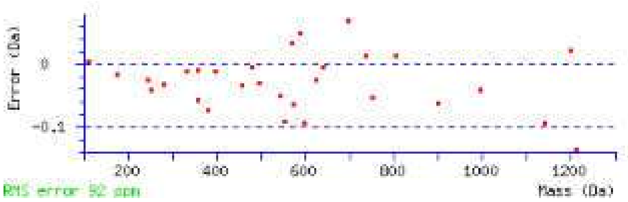
Label all possible matches ○ Label matches used for scoring ●

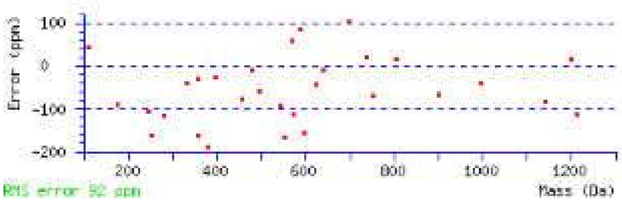
Monoisotopic mass of neutral peptide Mr(calc): 1555.8471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 22
Matches : 31/280 fragment ions using 96 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		44.0495		I							16
2	60.0444	173.1285	155.1179	201.1234	183.1128	157.1335		S	1411.7441	1410.7488		1443.7703	1426.7437	1425.7597	15
3	86.0964	286.2125	268.2020	314.2074	296.1969	258.1812	272.1969	I	1298.6600	1311.6804	1325.6961	1356.7383	1339.7117	1338.7277	14
4	74.0600	387.2602	369.2496	415.2551	397.2445	371.2653	373.2445	T	1197.6123	1210.6327	1212.6120	1243.6542	1226.6276	1225.6436	13
5	30.0338	444.2817	426.2711	472.2766	454.2660			G				***1142.6065***	1125.5800	1124.5960	12
6	44.0495	515.3188	497.3082	543.3137	525.3031			A	1069.5538			1085.5851	1068.5585	1067.5745	11
7	30.0338	572.3402	554.3297	**600.3352**	582.3246			G				1014.5479	997.5214	996.5374	10
8	30.0338	629.3617	611.3511	657.3566	639.3461			G				957.5265	940.4999	939.5159	9
9	120.0808	776.4301	758.4196	**804.4250**	786.4145			F	808.4424			***900.5050***	883.4785	882.4944	8
10	86.0964	889.5142	871.5036	917.5091	899.4985	861.4829	875.4985	I	695.3583	708.3787	722.3944	***753.4366***	736.4100	735.4260	7
11	30.0338	946.5356	928.5251	974.5306	956.5200			G				***640.3525***	623.3260	622.3420	6
12	60.0444	1033.5677	1015.5571	1061.5626	1043.5520	1017.5728		S	551.3049	550.3096		583.3311	566.3045	565.3205	5
13	110.0713	1170.6266	1152.6160	**1198.6215**	1180.6109			H	414.2459			***496.2990***	479.2725		4
14	86.0964	1283.7106	1265.7001	1311.7056	1293.6950	1255.6793	1269.6950	I	301.1619	314.1823	328.1979	***359.2401***	342.2136		3
15	44.0495	1354.7478	1336.7372	1382.7427	1364.7321			A	230.1248			***246.1561***	229.1295		2
16	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SI	173.1285	201.1234	SIT	274.1761	302.1710	SITG	331.1976	359.1925
SITGA	402.2347	430.2296	SITGAG	459.2562	487.2511	SITGAGG	516.2776	544.2726

SITGAGGF	663.3461	691.3410	**IT**	187.1441	215.1390	**ITG**	244.1656	272.1605
ITGA	315.2027	343.1976	**ITGAG**	372.2241	400.2191	**ITGAGG**	429.2456	457.2405
ITGAGGF	576.3140	604.3089	**ITGAGGFI**	689.3981	717.3930	**TG**	131.0815	159.0764
TGA	202.1186	230.1135	**TGAG**	259.1401	287.1350	**TGAGG**	316.1615	344.1565
TGAGGF	463.2300	491.2249	**TGAGGFI**	576.3140	604.3089	**TGAGGFIG**	633.3355	661.3304
GA	101.0709	129.0659	**GAG**	158.0924	186.0873	**GAGG**	215.1139	243.1088
GAGGF	362.1823	390.1772	**GAGGFI**	475.2663	503.2613	**GAGGFIG**	532.2878	560.2827
GAGGFIGS	619.3198	647.3148	**AG**	101.0709	129.0659	**AGG**	158.0924	186.0873
AGGF	305.1608	333.1557	**AGGFI**	418.2449	446.2398	**AGGFIG**	475.2663	503.2613
AGGFIGS	562.2984	590.2933	**AGGFIGSH**	699.3573	727.3522	**GG**	87.0553	115.0502
GGF	234.1237	262.1186	**GGFI**	347.2078	375.2027	**GGFIG**	404.2292	432.2241
GGFIGS	491.2613	519.2562	**GGFIGSH**	628.3202	656.3151	**GF**	177.1022	205.0972
GFI	290.1863	318.1812	**GFIG**	347.2078	375.2027	**GFIGS**	434.2398	462.2347
GFIGSH	571.2987	599.2936	**GFIGSHI**	684.3828	712.3777	**FI**	233.1648	261.1598
FIG	290.1863	318.1812	**FIGS**	377.2183	405.2132	**FIGSH**	514.2772	542.2722
FIGSHI	627.3613	655.3562	**FIGSHIA**	698.3984	726.3933	**IG**	143.1179	171.1128
IGS	230.1499	258.1448	**IGSH**	367.2088	395.2037	**IGSHI**	480.2929	508.2878
IGSHIA	551.3300	579.3249	**GS**	117.0659	145.0608	**GSH**	254.1248	282.1197
GSHI	367.2088	395.2037	**GSHIA**	438.2459	466.2409	**SH**	197.1033	225.0982
SHI	310.1874	338.1823	**SHIA**	381.2245	409.2194	**HI**	223.1553	251.1503
HIA	294.1925	322.1874	**IA**	157.1335	185.1285			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.0	1555.8471	0.1357	ISITGAGGFIGSHIAR
13.6	1555.8504	0.1324	TGSLRIMSLPPASAR
6.8	1555.8331	0.1497	HIPHIQITDRNGR
5.3	1555.8430	0.1398	SSALNAATLGVSGPRR
5.1	1555.8457	0.1371	DSSVSIQIEIVPAAK
5.0	1555.8947	0.0881	VLGHDGGVPPRLLAR
4.0	1555.8293	0.1535	VMGLAPGLEATWRR
3.2	1555.8471	0.1358	TKGSLVNYTPLHAR
3.2	1555.8293	0.1536	MHKYSPNLNLLAR
3.1	1555.8471	0.1357	VSITGAGGFIASHIAR

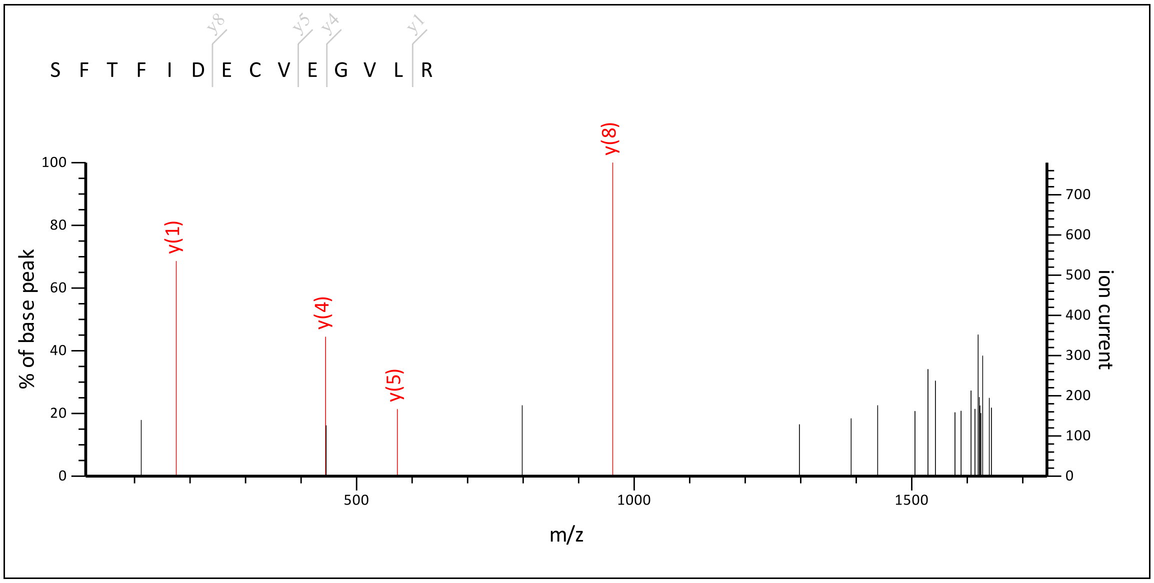
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 73

MS/MS Fragmentation of **SFTFIDECVEGVLR**
Found in **gi|110289082** in **NCBInr**, NAD dependent epimerase/dehydratase family protein, expressed [Oryza sativa Japonica Group]

Match to Query 72: 1670.932624 from(1671.939900,1+) intensity(0.0000) index(23)
Title: Label: P7, Spot_Id: 228953, Peak_List_Id: 257730, MSMS Job_Run_Id: 24933, Comment:
Data file ppw_P7_138985142500.txt



12.07 to 1743.53

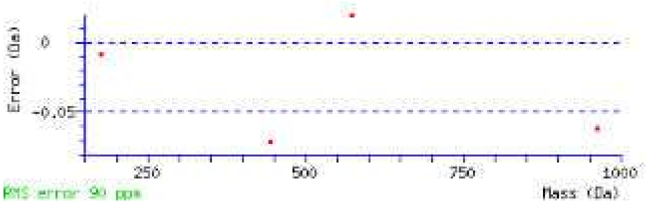
Label all possible matches ○ Label matches used for scoring ●

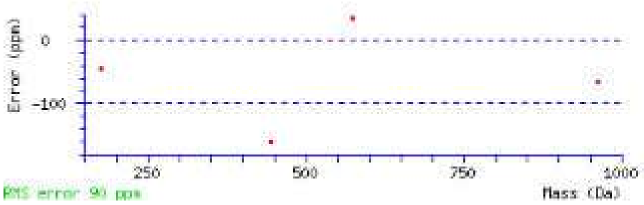
Monoisotopic mass of neutral peptide Mr(calc): 1670.7974
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 58
Matches : 4/219 fragment ions using 10 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444	42.0338	88.0393	70.0287	44.0495		S							14
2	120.0808	207.1128	189.1022	235.1077	217.0972			F	1492.7101			1584.7727	1567.7461	1566.7621	13
3	74.0600	308.1605	290.1499	336.1554	318.1448	292.1656	294.1448	T	1391.6624	1404.6828	1406.6620	1437.7042	1420.6777	1419.6937	12
4	120.0808	455.2289	437.2183	483.2238	465.2132			F	1244.5940			1336.6566	1319.6300	1318.6460	11
5	86.0964	568.3130	550.3024	596.3079	578.2973	540.2817	554.2973	I	1131.5099	1144.5303	1158.5460	1189.5881	1172.5616	1171.5776	10
6	88.0393	683.3399	665.3293	711.3348	693.3243	639.3501		D	1016.4830	1015.4877		1076.5041	1059.4775	1058.4935	9
7	102.0550	812.3825	794.3719	840.3774	822.3668	754.3770		E	887.4404	886.4451		***961.4771***	944.4506	943.4666	8
8	133.0430	972.4131	954.4026	1000.4081	982.3975	883.4196		C	727.4097	726.4145		832.4345	815.4080	814.4240	7
9	72.0808	1071.4816	1053.4710	1099.4765	1081.4659	1057.4659		V	628.3413	641.3617		672.4039	655.3774	654.3933	6
10	102.0550	1200.5242	1182.5136	1228.5191	1210.5085	1142.5187		E	499.2987	498.3035		***573.3355***	556.3089	555.3249	5
11	30.0338	1257.5456	1239.5351	1285.5405	1267.5300			G				***444.2929***	427.2663		4
12	72.0808	1356.6140	1338.6035	1384.6089	1366.5984	1342.5984		V	343.2088	356.2292		387.2714	370.2449		3
13	86.0964	1469.6981	1451.6875	1497.6930	1479.6824	1427.6511		L	230.1248	229.1295		288.2030	271.1765		2
14	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FT	221.1285	249.1234	FTF	368.1969	396.1918	FTFI	481.2809	509.2758
FTFID	596.3079	624.3028	TF	221.1285	249.1234	TFI	334.2125	362.2074
TFID	449.2395	477.2344	TFIDE	578.2821	606.2770	FI	233.1648	261.1598

FID	348.1918	376.1867	**FIDE**	477.2344	505.2293	**FIDEC**	637.2650	665.2599
ID	201.1234	229.1183	**IDE**	330.1660	358.1609	**IDEC**	490.1966	518.1915
IDECV	589.2650	617.2599	**DE**	217.0819	245.0768	**DEC**	377.1125	405.1075
DECV	476.1810	504.1759	**DECVE**	605.2236	633.2185	**DECVEG**	662.2450	690.2399
EC	262.0856	290.0805	**ECV**	361.1540	389.1489	**ECVE**	490.1966	518.1915
ECVEG	547.2181	575.2130	**ECVEGV**	646.2865	674.2814	**CV**	232.1114	260.1063
CVE	361.1540	389.1489	**CVEG**	418.1755	446.1704	**CVEGV**	517.2439	545.2388
CVEGVL	630.3280	658.3229	**VE**	201.1234	229.1183	**VEG**	258.1448	286.1397
VEGV	357.2132	385.2082	**VEGVL**	470.2973	498.2922	**EG**	159.0764	187.0713
EGV	258.1448	286.1397	**EGVL**	371.2289	399.2238	**GV**	129.1022	157.0972
GVL	242.1863	270.1812	**VL**	185.1648	213.1598			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.4	1670.7974	0.1352	SFTFIDECVEGVLR
10.9	1670.9315	0.0011	RAVVATLSVIGDDVTR
10.4	1670.8773	0.0553	KPMSEPKNTITAQAR
10.2	1670.9104	0.0223	KFVNLPEISAAGQAAR
9.5	1670.9468	-0.0141	KSANLSSWKPLVVSR
9.3	1670.8886	0.0440	MGQIGVLTGNAGEIRR
8.7	1670.8773	0.0553	KPMAEPKNTITAQAR
6.7	1670.7900	0.1426	YSYEPASRVDEISR
6.1	1670.9032	0.0294	LFPSKDSVFYILSR
6.1	1670.7835	0.1492	MPSSYEIFQQNRR

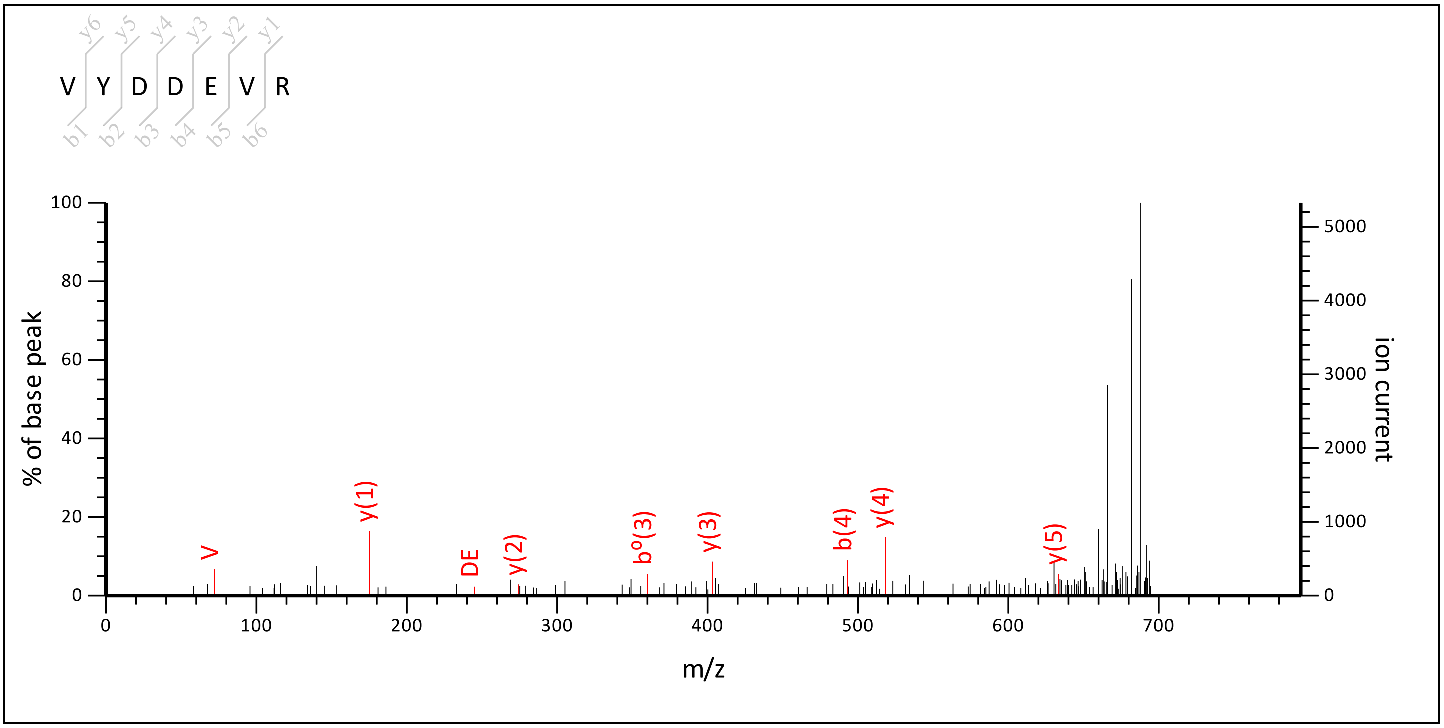
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **VYDDEVR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 2: 894.452744 from(895.460020,1+) intensity(0.0000) index(0)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225099, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



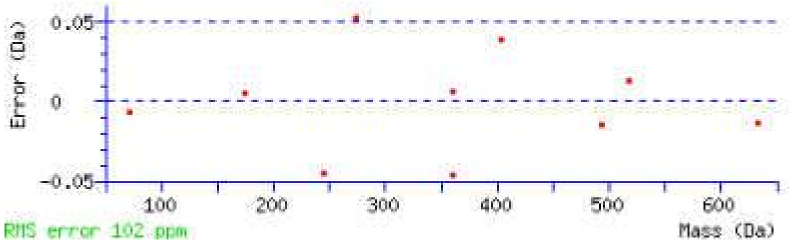
0 to 794.45

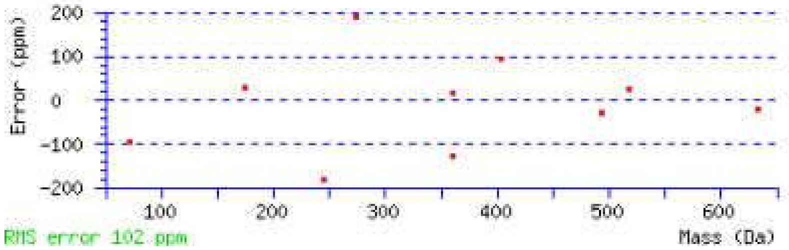
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 894.4083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 14 **Expect:** 88
Matches : 12/79 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495	V						7
2	136.0757	235.1441		263.1390			Y	688.2897		796.3472	779.3206	778.3366	6
3	88.0393	350.1710	332.1605	378.1660	360.1554	306.1812	D	573.2627	572.2675	***633.2838***	616.2573	615.2733	5
4	88.0393	465.1980	447.1874	493.1929	475.1823	421.2082	D	458.2358	457.2405	***518.2569***	501.2304	500.2463	4
5	102.0550	594.2406	576.2300	622.2355	604.2249	536.2351	E	329.1932	328.1979	***403.2300***	386.2034	385.2194	3
6	72.0808	693.3090	675.2984	721.3039	703.2933	679.2933	V	230.1248	243.1452	***274.1874***	257.1608		2
7	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YD	251.1026	279.0975	**YDD**	366.1296	394.1245	**YDDE**	495.1722	523.1671
YDDEV	594.2406	622.2355	**DD**	203.0662	231.0612	**DDE**	332.1088	360.1038
DDEV	431.1773	459.1722	**DE**	217.0819	245.0768	**DEV**	316.1503	344.1452
EV	201.1234	229.1183						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.9	894.3905	0.0622	YVDDMPR
14.0	894.4083	0.0444	VYDDEVR
8.9	894.3719	0.0808	FDDEDVR
7.1	894.4269	0.0258	FDVMDLR
6.9	894.3719	0.0808	DDFDLDR
6.9	894.4083	0.0444	EFTDEVR
6.9	894.4083	0.0444	ETFDDLR
6.9	894.4447	0.0081	LYTDVER
6.9	894.4447	0.0081	TYLDVER
6.3	894.4083	0.0444	DFETEVR

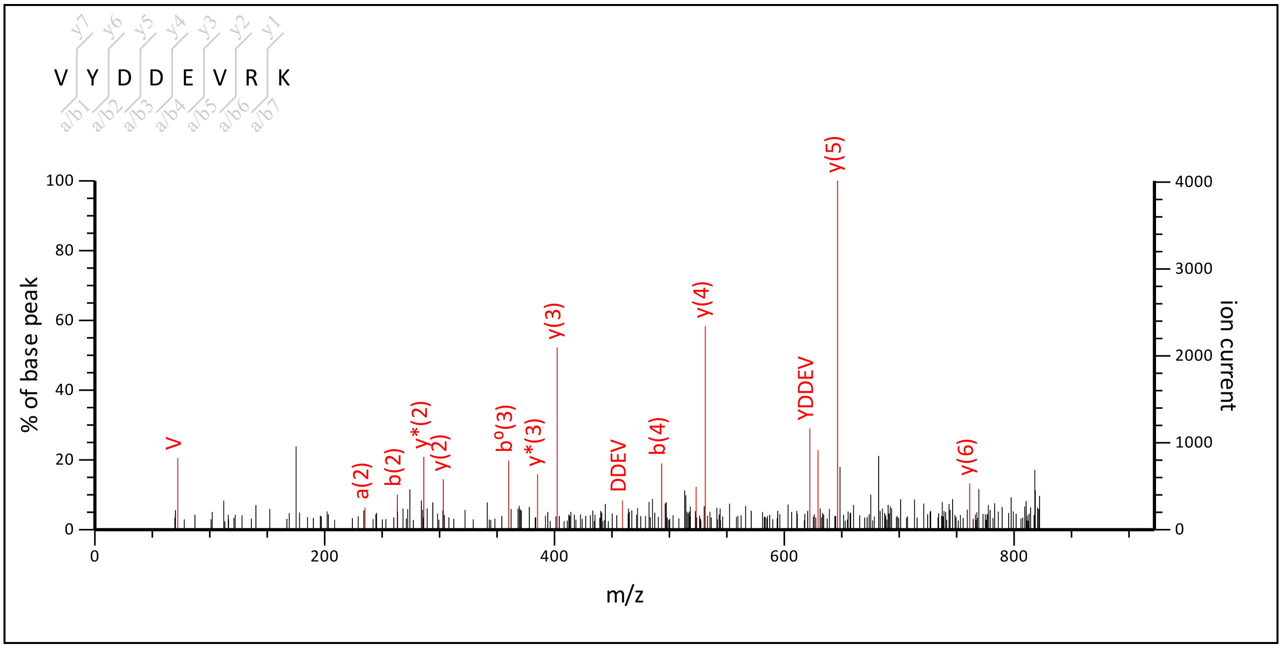
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **VYDDEVRK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 14: 1022.514624 from(1023.521900,1+) intensity(0.0000) index(5)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225084, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



0 to 922.13

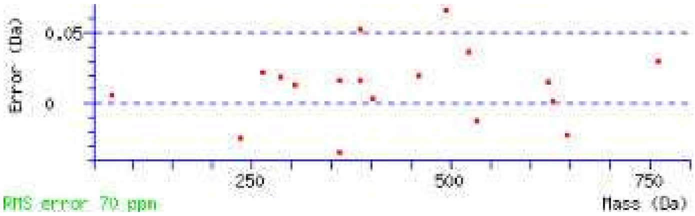
Label all possible matches ○ Label matches used for scoring ●

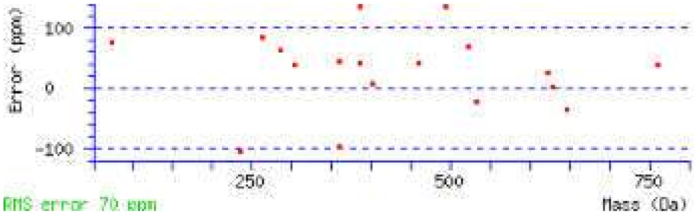
Monoisotopic mass of neutral peptide Mr(calc): 1022.5033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 1.7
Matches : 21/99 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	**72.0808**			100.0757			44.0495	**V**						8
2	136.0757	**235.1441**			**263.1390**				**Y**	816.3846		924.4421	907.4156	906.4316	7
3	88.0393	350.1710		332.1605	378.1660		360.1554	306.1812	**D**	701.3577	700.3624	***761.3788***	744.3523	743.3682	6
4	88.0393	465.1980		447.1874	**493.1929**		475.1823	421.2082	**D**	586.3307	585.3355	***646.3519***	629.3253	628.3413	5
5	102.0550	594.2406		576.2300	**622.2355**		604.2249	536.2351	**E**	457.2881	456.2929	***531.3249***	514.2984	513.3144	4
6	72.0808	693.3090		675.2984	721.3039		703.2933	679.2933	**V**	358.2197	371.2401	***402.2823***	385.2558		3
7	129.1135	849.4101	832.3836	831.3995	877.4050	860.3785	859.3945	764.3461	**R**	202.1186	201.1234	***303.2139***	286.1874		2
8	101.1073								**K**	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YD	251.1026	279.0975	**YDD**	366.1296	394.1245	**YDDE**	495.1722	523.1671
YDDEV	594.2406	622.2355	**DD**	203.0662	231.0612	**DDE**	332.1088	360.1038
DDEV	431.1773	459.1722	**DDEVR**	587.2784	615.2733	**DE**	217.0819	245.0768
DEV	316.1503	344.1452	**DEVR**	472.2514	500.2463	**EV**	201.1234	229.1183

EVR	357.2245	385.2194	**VR**	228.1819	256.1768			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.4	1022.5033	0.0114	VYDDEVRK
19.7	1022.4669	0.0477	YVDDAVEGR
19.7	1022.5185	-0.0039	VYDPFLNR
19.6	1022.5033	0.0113	YVDDIVGSR
17.9	1022.5873	-0.0726	LIHEEVKR
17.8	1022.5145	0.0001	QDTGYGVKR
16.4	1022.5075	0.0071	MMMLVVQR
16.0	1022.4702	0.0444	DMTEEVRK
15.1	1022.5185	-0.0039	VYPFDNLR
14.5	1022.4637	0.0509	ANKDMICR

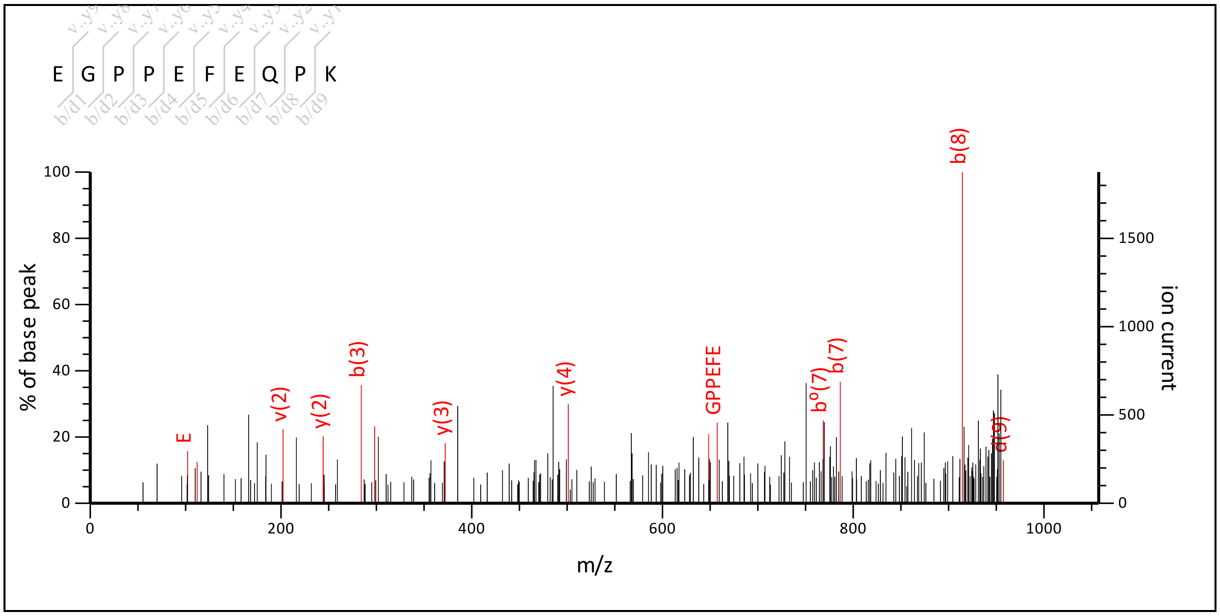
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **EGPPEFEQPK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 25: 1156.536524 from(1157.543800,1+) intensity(0.0000) index(9)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225091, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



0 to 1057.39

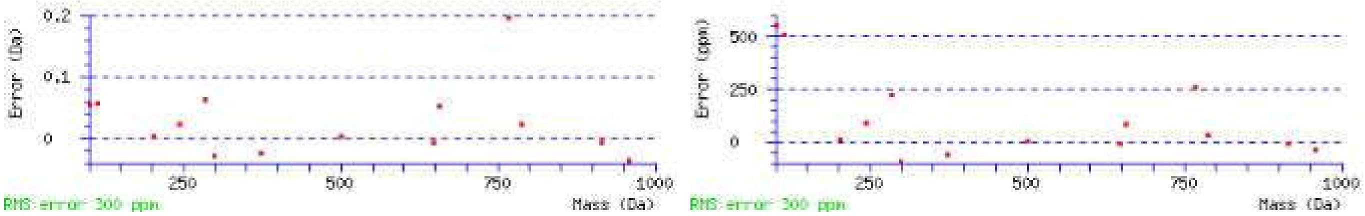
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1156.5400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 16 **Expect:** 45
Matches : 18/142 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495	E						10
2	30.0338	159.0764		141.0659	187.0713		169.0608		G			1028.5047	1011.4782	1010.4942	9
3	70.0651	256.1292		238.1186	***284.1241***		266.1135	230.1135	P	929.4363	928.4411	971.4833	954.4567	953.4727	8
4	70.0651	353.1819		335.1714	381.1769		363.1663	327.1663	P	832.3836	831.3883	874.4305	857.4040	856.4199	7
5	102.0550	482.2245		464.2140	510.2195		492.2089	424.2191	E	703.3410	702.3457	777.3777	760.3512	759.3672	6
6	120.0808	629.2930		611.2824	***657.2879***		639.2773		F	556.2726		***648.3352***	631.3086	630.3246	5
7	102.0550	758.3355		740.3250	***786.3305***		768.3199	700.3301	E	427.2300	426.2347	***501.2667***	484.2402	483.2562	4
8	101.0709	886.3941	869.3676	868.3836	***914.3890***	897.3625	896.3785	829.3727	Q	299.1714	298.1761	***372.2241***	355.1976		3
9	70.0651	983.4469	966.4203	965.4363	1011.4418	994.4153	993.4312	957.4312	P	202.1186	201.1234	***244.1656***	227.1390		2
10	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPE	353.1819	381.1769
GPPEF	500.2504	528.2453	GPPEFE	629.2930	657.2879	PP	167.1179	195.1128
PPE	296.1605	324.1554	PPEF	443.2289	471.2238	PPEFE	572.2715	600.2664
PE	199.1077	227.1026	PEF	346.1761	374.1710	PEFE	475.2187	503.2136

PEFEQ	603.2773	631.2722	**EF**	249.1234	277.1183	**EFE**	378.1660	406.1609
EFEQ	506.2245	534.2195	**EFEQP**	603.2773	631.2722	**FE**	249.1234	277.1183
FEQ	377.1819	405.1769	**FEQP**	474.2347	502.2296	**EQ**	230.1135	258.1084
EQP	327.1663	355.1612	**QP**	198.1237	226.1186			



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
16.2	1156.5400	-0.0035	EGPPEFEQPK
15.1	1156.5910	-0.0545	SLPSCAAVQPK
13.2	1156.6200	-0.0835	TALSKGNNQPK
13.0	1156.5910	-0.0545	THLQSTVMPK
11.9	1156.6063	-0.0698	IHQFMEKPK
11.7	1156.5611	-0.0246	EEINELDAPK
11.3	1156.5949	-0.0583	EATGAATARGPR
11.2	1156.5335	0.0030	HAEMKDWPK
11.2	1156.5585	-0.0219	RSQNGNQEPK
11.0	1156.6200	-0.0835	ENKQATNKPK

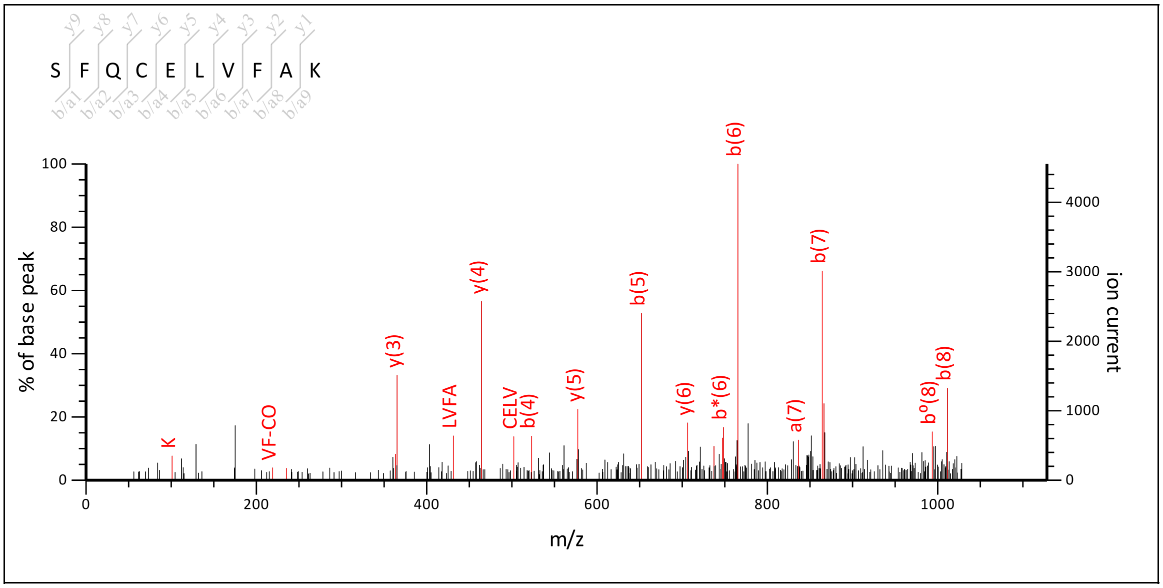
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **SFQCELVFAK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 31: 1227.593924 from(1228.601200,1+) intensity(0.0000) index(12)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225081, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



0 to 1128.23

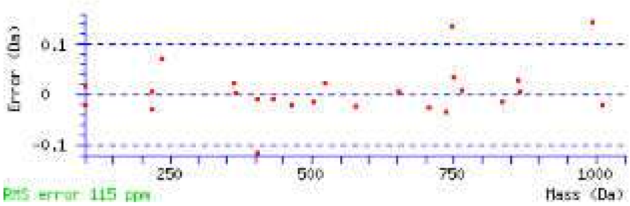
Label all possible matches ○ Label matches used for scoring ●

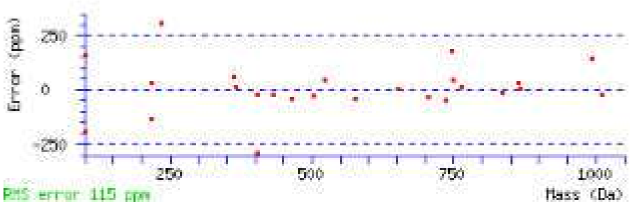
Monoisotopic mass of neutral peptide Mr(calc): 1227.5958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.19
Matches : 25/148 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495	S						10
2	120.0808	207.1128		189.1022	***235.1077***		217.0972		F	1049.5084		1141.5710	1124.5445	1123.5605	9
3	101.0709	335.1714	318.1448	317.1608	***363.1663***	346.1397	345.1557	278.1499	Q	921.4499	920.4546	994.5026	977.4761	976.4921	8
4	133.0430	495.2020	478.1755	477.1915	***523.1969***	506.1704	505.1864	406.2085	C	761.4192	760.4240	**866.4441**	849.4175	848.4335	7
5	102.0550	624.2446	607.2181	606.2341	***652.2395***	635.2130	634.2290	566.2391	E	632.3766	631.3814	**706.4134**	689.3869	688.4028	6
6	86.0964	**737.3287**	720.3021	719.3181	***765.3236***	748.2971	747.3130	695.2817	L	519.2926	518.2973	**577.3708**	560.3443		5
7	72.0808	**836.3971**	819.3706	818.3865	***864.3920***	847.3655	846.3815	822.3815	V	420.2241	433.2445	**464.2867**	447.2602		4
8	120.0808	983.4655	966.4390	965.4549	***1011.4604***	994.4339	993.4499		F	273.1557		**365.2183**	348.1918		3
9	44.0495	1054.5026	1037.4761	1036.4921	1082.4975	1065.4710	1064.4870		A	202.1186		218.1499	201.1234		2
10	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQC	408.1700	436.1649	FQCE	537.2126	565.2075
FQCEL	650.2967	678.2916	QC	261.1016	289.0965	QCE	390.1442	418.1391
QCEL	503.2282	531.2232	QCELV	602.2967	630.2916	CE	262.0856	290.0805
CEL	375.1697	403.1646	CELV	474.2381	502.2330	CELVF	621.3065	649.3014
CELVFA	692.3436	720.3385	EL	215.1390	243.1339	ELV	314.2074	342.2023
ELVF	461.2758	489.2708	ELVFA	532.3130	560.3079	LV	185.1648	213.1598
LVF	332.2333	360.2282	LVFA	403.2704	431.2653	VF	219.1492	247.1441

VFA	290.1863	318.1812	**FA**	191.1179	219.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.5	1227.5958	-0.0019	SFQCELVFAK
40.5	1227.5628	0.0311	SFQCELVMAK
39.0	1227.5628	0.0311	SFQCELVMSK
24.5	1227.5992	-0.0052	GCFVIKTEMK
20.6	1227.4860	0.1079	ECSSLTSECR
19.9	1227.5376	0.0563	FGCVSTMASPR
19.2	1227.6208	-0.0268	KVHPESSTSTR
18.7	1227.6248	-0.0308	HKPTSESPFAK
16.7	1227.6612	-0.0672	YTKALTTFQR
15.9	1227.6499	-0.0560	KFSVDISYAAK

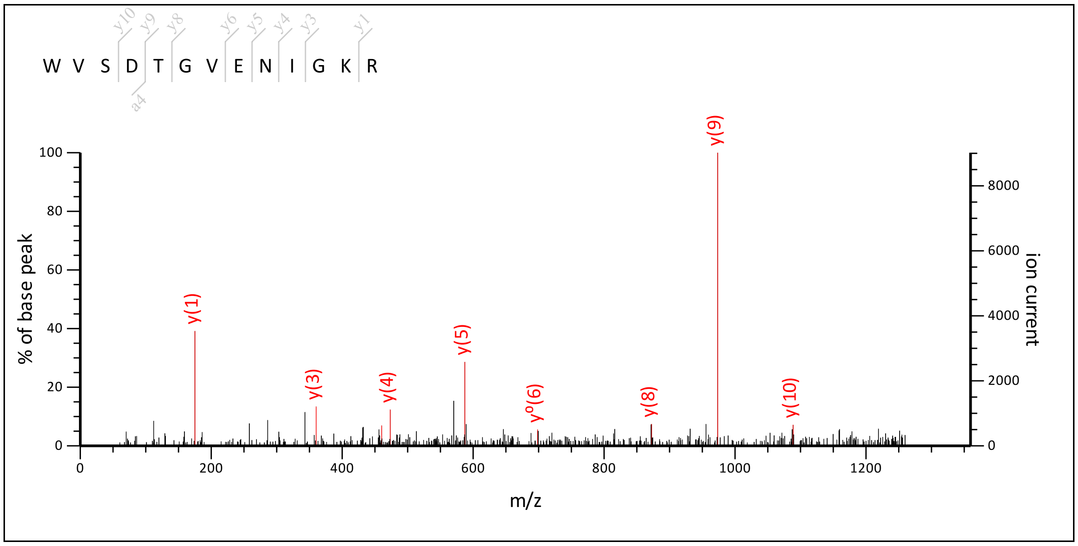
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **WVSDTGVENIGKR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 43: 1459.774424 from(1460.781700,1+) intensity(0.0000) index(16)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225085, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



0 to 1359.64

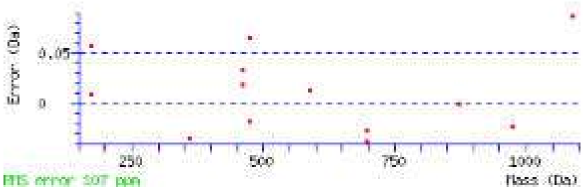
Label all possible matches ○ Label matches used for scoring ●

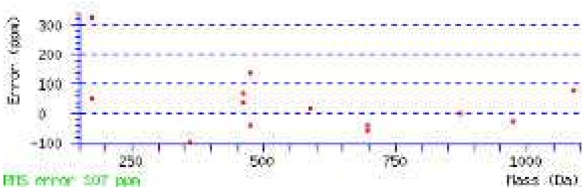
```
Monoisotopic mass of neutral peptide Mr(calc): 1459.7419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55   Expect: 0.0064
Matches : 14/217 fragment ions using 12 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	159.0917	159.0917			187.0866			44.0495		**W**					
2	72.0808	258.1601			286.1550			244.1444		**V**	1230.6073	1243.6277		1274.6699	1257.6434
3	60.0444	345.1921		327.1816	373.1870		355.1765	329.1972		**S**	1143.5753	1142.5800		1175.6015	1158.5749
4	88.0393	**460.2191**		442.2085	488.2140		470.2034	416.2292		**D**	1028.5483	1027.5531		***1088.5695***	1071.5429
5	74.0600	561.2667		543.2562	589.2617		571.2511	545.2718	547.2511	**T**	927.5007	940.5211	942.5003	***973.5425***	956.5160
6	30.0338	618.2882		600.2776	646.2831		628.2726			**G**				***872.4948***	855.4683
7	72.0808	717.3566		699.3461	745.3515		727.3410	703.3410		**V**	771.4108	784.4312		815.4734	798.4468
8	102.0550	846.3992		828.3886	874.3941		856.3836	788.3937		**E**	642.3682	641.3729		716.4050	699.3784
9	87.0553	960.4421	943.4156	942.4316	988.4371	971.4105	970.4265	917.4363		**N**	528.3253	527.3300		***587.3624***	570.3358
10	86.0964	1073.5262	1056.4997	1055.5156	1101.5211	1084.4946	1083.5105	1045.4949	1059.5105	**I**	415.2412	428.2616	442.2772	***473.3194***	456.2929
11	30.0338	1130.5477	1113.5211	1112.5371	1158.5426	1141.5160	1140.5320			**G**				***360.2354***	343.2088
12	101.1073	1258.6426	1241.6161	1240.6321	1286.6375	1269.6110	1268.6270	1201.5848		**K**	230.1248	229.1295		303.2139	286.1874
13	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VS	159.1128	187.1077	**VSD**	274.1397	302.1347	**VSDT**	375.1874	403.1823
VSDTG	432.2089	460.2038	**VSDTGV**	531.2773	559.2722	**VSDTGVE**	660.3199	688.3148
SD	175.0713	203.0662	**SDT**	276.1190	304.1139	**SDTG**	333.1405	361.1354
SDTGV	432.2089	460.2038	**SDTGVE**	561.2515	589.2464	**SDTGVEN**	675.2944	703.2893
DT	189.0870	217.0819	**DTG**	246.1084	274.1034	**DTGV**	345.1769	373.1718
DTGVE	474.2195	502.2144	**DTGVEN**	588.2624	616.2573	**TG**	131.0815	159.0764
TGV	230.1499	258.1448	**TGVE**	359.1925	387.1874	**TGVEN**	473.2354	501.2304
TGVENI	586.3195	614.3144	**TGVENIG**	643.3410	671.3359	**GV**	129.1022	157.0972

GVE	258.1448	286.1397	**GVEN**	372.1878	400.1827	**GVENI**	485.2718	513.2667
GVENIG	542.2933	570.2882	**GVENIGK**	670.3882	698.3832	**VE**	201.1234	229.1183
VEN	315.1663	343.1612	**VENI**	428.2504	456.2453	**VENIG**	485.2718	513.2667
VENIGK	613.3668	641.3617	**EN**	216.0979	244.0928	**ENI**	329.1819	357.1769
ENIG	386.2034	414.1983	**ENIGK**	514.2984	542.2933	**NI**	200.1394	228.1343
NIG	257.1608	285.1557	**NIGK**	385.2558	413.2507	**IG**	143.1179	171.1128
IGK	271.2129	299.2078	**GK**	158.1288	186.1237			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.1	1459.7419	0.0325	WVSDTGVENIGKR
31.3	1459.7024	0.0720	CLQMGAGVGVGAGAGR
24.8	1459.7089	0.0655	ADVLAQQAGMDIGR
22.0	1459.6950	0.0794	AAARCGTSPSAAGAGR
21.6	1459.7453	0.0291	QSSVAPGASSMAVLR
21.1	1459.6903	0.0841	GNNTDSGVDLEAIR
20.0	1459.6652	0.1093	TDEAGGVNQTGAGGAR
19.5	1459.7783	-0.0039	WVTSTGIENIGKR
19.4	1459.6539	0.1205	EENDVVSQQEQR
19.3	1459.8035	-0.0291	LALGADGFVETLVR

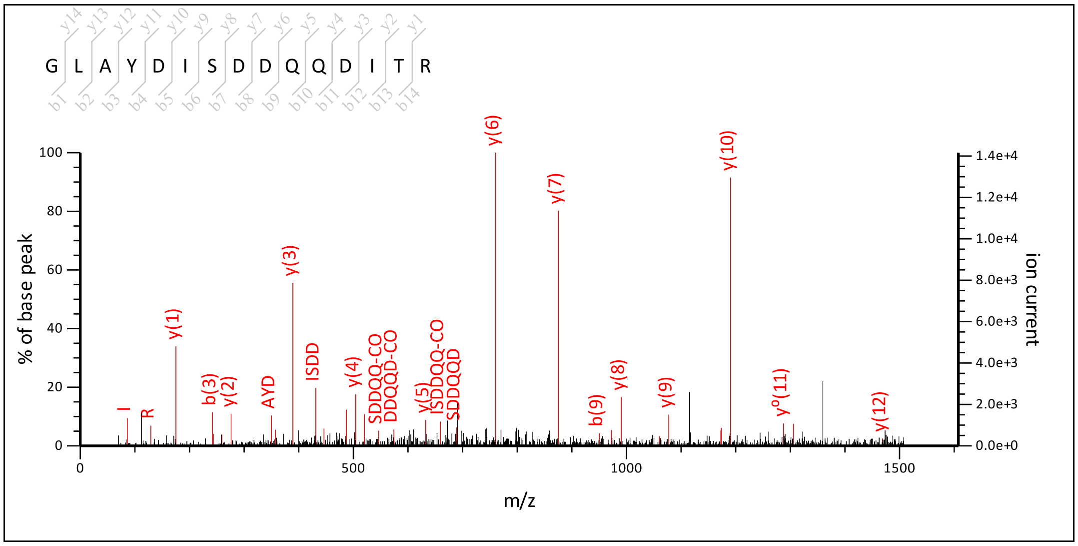
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **GLAYDISDDQQDITR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 51: 1708.823924 from(1709.831200,1+) intensity(0.0000) index(19)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225079, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



0 to 1607.7

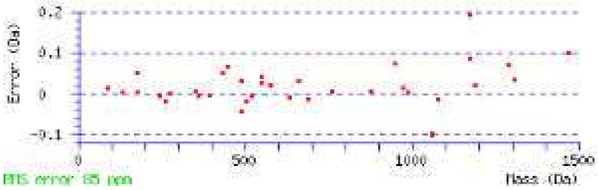
Label all possible matches ○ Label matches used for scoring ●

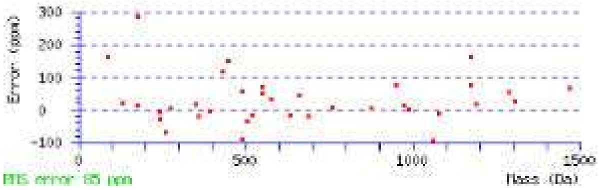
Monoisotopic mass of neutral peptide Mr(calc): 1708.7904
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 78 **Expect:** 3.1e-05
Matches : 43/255 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			101.0709		L	1594.6980	1593.7027		1652.7762	1635.7497
3	44.0495	214.1550			**242.1499**					A	1523.6609			1539.6922	1522.6656
4	136.0757	377.2183			405.2132					Y	1360.5975			***1468.6550***	1451.6285
5	88.0393	492.2453		474.2347	**520.2402**		502.2296	448.2554		D	1245.5706	1244.5753		***1305.5917***	1288.5652
6	86.0964	605.3293		587.3188	633.3243		615.3137	577.2980	591.3137	I	1132.4865	1145.5069	1159.5226	***1190.5648***	1173.5382
7	60.0444	692.3614		674.3508	720.3563		702.3457	676.3665		S	1045.4545	1044.4592		***1077.4807***	1060.4542
8	88.0393	807.3883		789.3777	835.3832		817.3727	763.3985		D	930.4276	929.4323		***990.4487***	973.4221
9	88.0393	922.4153		904.4047	**950.4102**		932.3996	878.4254		D	815.4006	814.4054		***875.4217***	858.3952
10	101.0709	1050.4738	1033.4473	1032.4633	1078.4687	1061.4422	1060.4582	993.4524		Q	687.3420	686.3468		***760.3948***	743.3682
11	101.0709	1178.5324	1161.5059	1160.5218	1206.5273	1189.5008	1188.5168	1121.5109		Q	559.2835	558.2882		***632.3362***	615.3097
12	88.0393	1293.5594	1276.5328	1275.5488	1321.5543	1304.5277	1303.5437	1249.5695		D	444.2565	443.2613		***504.2776***	487.2511
13	86.0964	1406.6434	1389.6169	1388.6329	1434.6383	1417.6118	1416.6278	1378.6121	1392.6278	I	331.1724	344.1928	358.2085	***389.2507***	372.2241
14	74.0600	1507.6911	1490.6645	1489.6805	1535.6860	1518.6595	1517.6754	1491.6962	1493.6754	T	230.1248	243.1452	245.1244	***276.1666***	259.1401
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LA	157.1335	185.1285	**LAY**	320.1969	348.1918	**LAYD**	435.2238	463.2187
LAYDI	548.3079	576.3028	**LAYDIS**	635.3399	663.3348	**AY**	207.1128	235.1077
AYD	322.1397	350.1347	**AYDI**	435.2238	463.2187	**AYDIS**	522.2558	550.2508
AYDISD	637.2828	665.2777	**YD**	251.1026	279.0975	**YDI**	364.1867	392.1816
YDIS	451.2187	479.2136	**YDISD**	566.2457	594.2406	**YDISDD**	681.2726	709.2675
DI	201.1234	229.1183	**DIS**	288.1554	316.1503	**DISD**	403.1823	431.1773

DISDD	518.2093	546.2042	**DISDDQ**	646.2679	674.2628	**IS**	173.1285	201.1234
ISD	288.1554	316.1503	**ISDD**	403.1823	431.1773	**ISDDQ**	531.2409	559.2358
ISDDQQ	659.2995	687.2944	**SD**	175.0713	203.0662	**SDD**	290.0983	318.0932
SDDQ	418.1569	446.1518	**SDDQQ**	546.2154	574.2103	**SDDQQD**	661.2424	689.2373
DD	203.0662	231.0612	**DDQ**	331.1248	359.1197	**DDQQ**	459.1834	487.1783
DDQQD	574.2103	602.2053	**DDQQDI**	687.2944	715.2893	**DQ**	216.0979	244.0928
DQQ	344.1565	372.1514	**DQQD**	459.1834	487.1783	**DQQDI**	572.2675	600.2624
DQQDIT	673.3151	701.3101	**QQ**	229.1295	257.1244	**QQD**	344.1565	372.1514
QQDI	457.2405	485.2354	**QQDIT**	558.2882	586.2831	**QD**	216.0979	244.0928
QDI	329.1819	357.1769	**QDIT**	430.2296	458.2245	**DI**	201.1234	229.1183
DIT	302.1710	330.1660	**IT**	187.1441	215.1390			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
77.5	1708.7904	0.0335	GLAYDISDDQQDITR
51.6	1708.7540	0.0699	GLAFDESDDQQDITR
21.9	1708.8897	-0.0658	AGIDKFGVPVPGDPGGAR
19.3	1708.7023	0.1216	SSEQNLESDGEEETR
18.9	1708.7978	0.0261	GLSTDSLMEAGYPGAPK
16.9	1708.8315	-0.0076	DMQVRSGQSIVNYGR
16.4	1708.8931	-0.0691	MVRFAQVVSSLDTTR
15.5	1708.7397	0.0843	CSLADCDDGLVDITR
15.3	1708.8753	-0.0514	LQGMVASMSRIPTFR
15.1	1708.9009	-0.0770	ANIHALSGAWGDKLTR

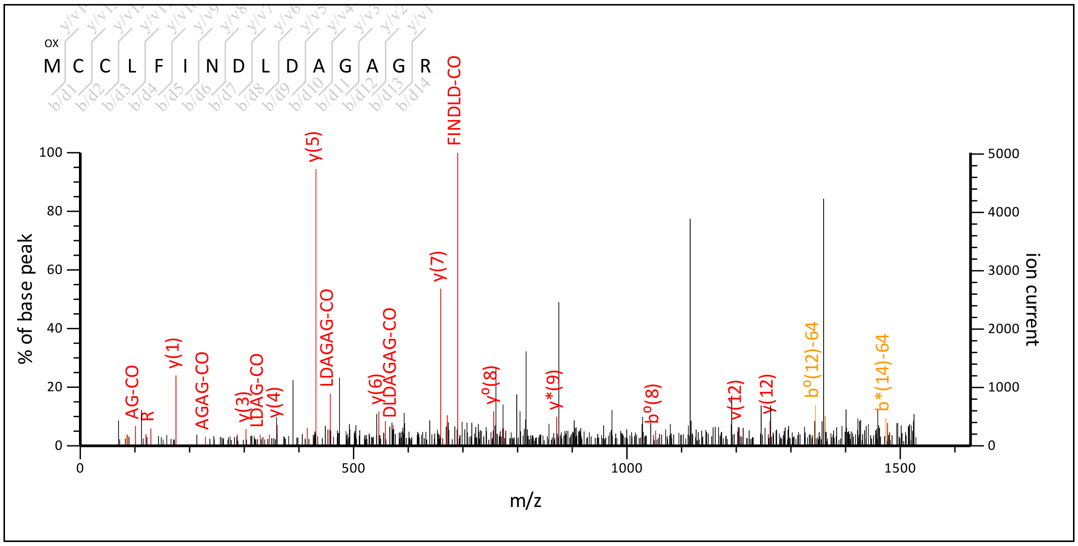
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **MCCLFINDLDAGAGR**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 54: 1727.764324 from(1728.771600,1+) intensity(0.0000) index(20)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225086, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



0 to 1628.57

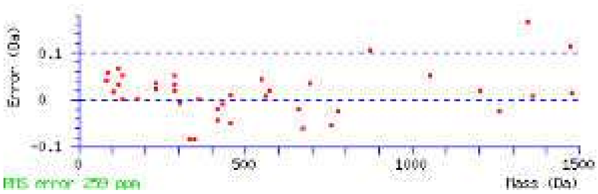
Label all possible matches ○ Label matches used for scoring ●

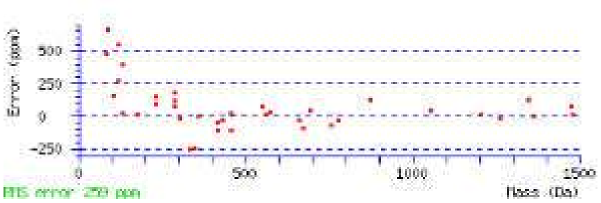
```
Monoisotopic mass of neutral peptide Mr(calc): 1727.7430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 16  Expect: 39
Matches : 46/311 fragment ions using 105 most intense peaks    (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	56.0495	56.0495			**84.0444**			44.0495		M						
2	133.0430	216.0801			244.0750			127.0866		C	1476.6900	1475.6947		1581.7148	1564.6883	156
3	133.0430	376.1108			404.1057			287.1172		C	1316.6593	1315.6641		1421.6842	1404.6576	140
4	86.0964	489.1948			517.1898			447.1479		L	1203.5753	1202.5800		***1261.6535***	1244.6270	124
5	120.0808	636.2633			664.2582					F	1056.5069			1148.5695	1131.5429	113
6	86.0964	749.3473			777.3422			721.3160	735.3317	I	943.4228	956.4432	970.4588	1001.5010	984.4745	98
7	87.0553	863.3902	846.3637		891.3852	874.3586		820.3844		N	829.3799	828.3846		888.4170	871.3904	87
8	88.0393	978.4172	961.3906	960.4066	1006.4121	989.3856	988.4015	934.4274		D	714.3529	713.3577		***774.3741***	757.3475	75
9	86.0964	1091.5013	1074.4747	1073.4907	1119.4962	1102.4696	1101.4856	1049.4543		L	601.2689	600.2736		***659.3471***	642.3206	64
10	88.0393	1206.5282	1189.5016	1188.5176	1234.5231	1217.4966	1216.5125	1162.5384		D	486.2419	485.2467		***546.2631***	529.2365	52
11	44.0495	1277.5653	1260.5388	1259.5547	1305.5602	1288.5337	1287.5497			A	415.2048			***431.2361***	414.2096	
12	30.0338	1334.5868	1317.5602	1316.5762	**1362.5817**	1345.5551	1344.5711			G				***360.1990***	343.1724	
13	44.0495	1405.6239	1388.5973	1387.6133	1433.6188	1416.5923	1415.6082			A	287.1462			***303.1775***	286.1510	
14	30.0338	1462.6453	1445.6188	1444.6348	1490.6403	1473.6137	1472.6297			G				232.1404	215.1139	
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
CC	293.0737	321.0686	CCL	406.1577	434.1526	CCLF	553.2261	581.2211
CCLFI	666.3102	694.3051	CL	246.1271	274.1220	CLF	393.1955	421.1904
CLFI	506.2796	534.2745	CLFIN	620.3225	648.3174	LF	233.1648	261.1598

LFI	346.2489	374.2438	**LFIN**	460.2918	488.2867	**LFIND**	575.3188	603.3137
LFINDL	688.4028	716.3978	**FI**	233.1648	261.1598	**FIN**	347.2078	375.2027
FIND	462.2347	490.2296	**FINDL**	575.3188	603.3137	**FINDLD**	690.3457	718.3406
IN	200.1394	228.1343	**IND**	315.1663	343.1612	**INDL**	428.2504	456.2453
INDLD	543.2773	571.2722	**INDLDA**	614.3144	642.3093	**INDLDAG**	671.3359	699.3308
ND	202.0822	230.0771	**NDL**	315.1663	343.1612	**NDLD**	430.1932	458.1882
NDLDA	501.2304	529.2253	**NDLDAG**	558.2518	586.2467	**NDLDAGA**	629.2889	657.2838
NDLDAGAG	686.3104	714.3053	**DL**	201.1234	229.1183	**DLD**	316.1503	344.1452
DLDA	387.1874	415.1823	**DLDAG**	444.2089	472.2038	**DLDAGA**	515.2460	543.2409
DLDAGAG	572.2675	600.2624	**LD**	201.1234	229.1183	**LDA**	272.1605	300.1554
LDAG	329.1819	357.1769	**LDAGA**	400.2191	428.2140	**LDAGAG**	457.2405	485.2354
DA	159.0764	187.0713	**DAG**	216.0979	244.0928	**DAGA**	287.1350	315.1299
DAGAG	344.1565	372.1514	**AG**	101.0709	129.0659	**AGA**	172.1081	200.1030
AGAG	229.1295	257.1244	**GA**	101.0709	129.0659	**GAG**	158.0924	186.0873
AG	101.0709	129.0659						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.8	1727.7430	0.0214	MCCLFINDLDAGAGR
15.8	1727.8261	-0.0617	QQKVNDDDAMKPPSR
15.0	1727.9352	-0.1709	IPTMDLARLIASQGAR
13.7	1727.8002	-0.0359	YFLVSDEESAQTPSR
11.9	1727.8942	-0.1298	QQIDETQVIVTTPEK
9.5	1727.8842	-0.1199	PSFVANANQQTDVLPK
9.0	1727.9107	-0.1464	RNGFGGPAPSFPLGNIK
8.2	1727.8414	-0.0770	EPDLGGWAVGGCVKQR
8.2	1727.9166	-0.1523	VGNVSVRDVLEGLSER
8.0	1727.7785	-0.0141	QEVMIGYSDSGKDAGR

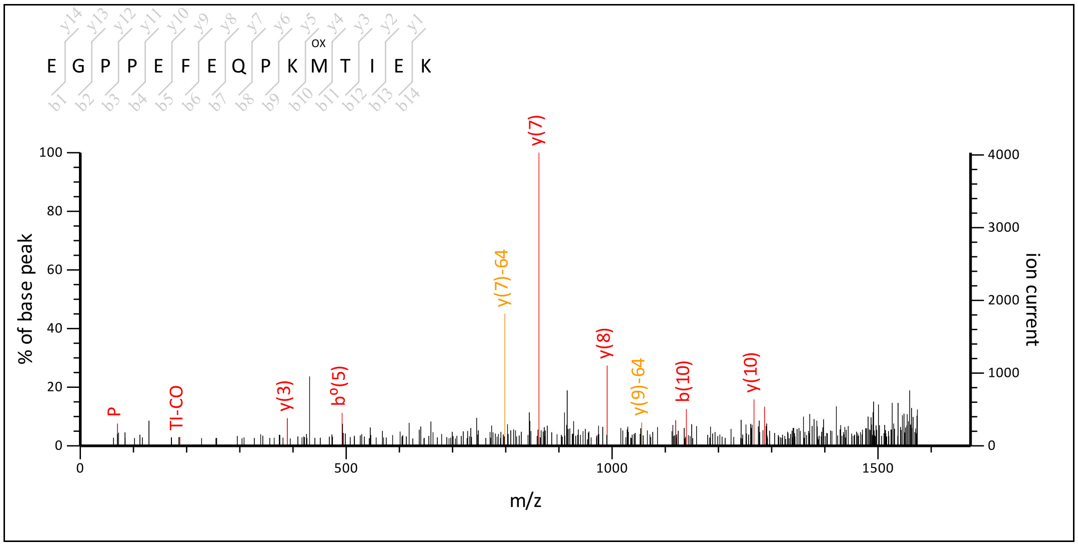
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **EGPPEFEQPKMTIEK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 58: 1774.860424 from(1775.867700,1+) intensity(0.0000) index(22)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225087, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



0 to 1673.97

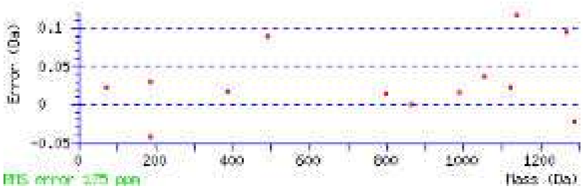
Label all possible matches ○ Label matches used for scoring ●

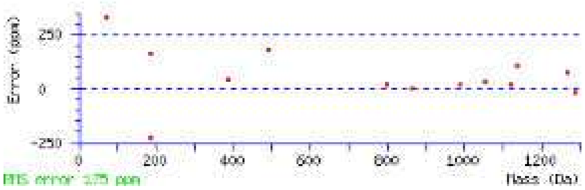
```
Monoisotopic mass of neutral peptide Mr(calc): 1774.8447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 17  Expect: 33
Matches : 15/358 fragment ions using 32 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E						
2	30.0338	159.0764		141.0659	***187.0713***		169.0608			G				1646.8094	1629.7829	162
3	70.0651	256.1292		238.1186	284.1241		266.1135	230.1135		P	1547.7410	1546.7458		1589.7880	1572.7614	15
4	70.0651	353.1819		335.1714	381.1769		363.1663	327.1663		P	1450.6883	1449.6930		1492.7352	1475.7087	14
5	102.0550	482.2245		464.2140	510.2195		492.2089	424.2191		E	1321.6457	1320.6504		1395.6824	1378.6559	13
6	120.0808	629.2930		611.2824	657.2879		639.2773			F	1174.5773			***1266.6399***	1249.6133	124
7	102.0550	758.3355		740.3250	786.3305		768.3199	700.3301		E	1045.5347	1044.5394		***1119.5714***	1102.5449	11
8	101.0709	886.3941	869.3676	868.3836	914.3890	897.3625	896.3785	829.3727		Q	917.4761	916.4808		***990.5288***	973.5023	9
9	70.0651	983.4469	966.4203	965.4363	1011.4418	994.4153	993.4312	957.4312		P	820.4233	819.4281		***862.4703***	845.4437	84
10	101.1073	1111.5419	1094.5153	1093.5313	***1139.5368***	1122.5102	1121.5262	1054.4840		K	692.3284	691.3331		765.4175	748.3910	74
11	120.0478	1258.5773	1241.5507	1240.5667	***1286.5722***	1269.5456	1268.5616	1182.5790		M	545.2930	544.2977		637.3225	620.2960	6
12	74.0600	1359.6249	1342.5984	1341.6144	1387.6198	1370.5933	1369.6093	1343.6300	1345.6093	T	444.2453	457.2657	459.2449	490.2871	473.2606	4
13	86.0964	1472.7090	1455.6824	1454.6984	1500.7039	1483.6774	1482.6933	1444.6777	1458.6933	I	331.1612	344.1816	358.1973	***389.2395***	372.2129	3
14	102.0550	1601.7516	1584.7250	1583.7410	1629.7465	1612.7200	1611.7359	1543.7461		E	202.1186	201.1234		276.1554	259.1288	2
15	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPE	353.1819	381.1769
GPPEF	500.2504	528.2453	GPPEFE	629.2930	657.2879	PP	167.1179	195.1128
PPE	296.1605	324.1554	PPEF	443.2289	471.2238	PPEFE	572.2715	600.2664

PE	199.1077	227.1026	**PEF**	346.1761	374.1710	**PEFE**	475.2187	503.2136
PEFEQ	603.2773	631.2722	**EF**	249.1234	277.1183	**EFE**	378.1660	406.1609
EFEQ	506.2245	534.2195	**EFEQP**	603.2773	631.2722	**FE**	249.1234	277.1183
FEQ	377.1819	405.1769	**FEQP**	474.2347	502.2296	**FEQPK**	602.3297	630.3246
EQ	230.1135	258.1084	**EQP**	327.1663	355.1612	**EQPK**	455.2613	483.2562
EQPKM	602.2967	630.2916	**QP**	198.1237	226.1186	**QPK**	326.2187	354.2136
QPKM	473.2541	501.2490	**QPKMT**	574.3017	602.2967	**QPKMTI**	687.3858	715.3807
PK	198.1601	226.1550	**PKM**	345.1955	373.1904	**PKMT**	446.2432	474.2381
PKMTI	559.3272	587.3221	**PKMTIE**	688.3698	716.3647	**KM**	248.1427	276.1376
KMT	349.1904	377.1853	**KMTI**	462.2745	490.2694	**KMTIE**	591.3171	619.3120
MT	221.0954	249.0904	**MTI**	334.1795	362.1744	**MTIE**	463.2221	491.2170
TI	187.1441	215.1390	**TIE**	316.1867	344.1816	**IE**	215.1390	243.1339





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.2	1774.8447	0.0157	EGPPEFEQPKMTIEK
6.2	1775.0067	-0.1463	AGIPGAAARPAGWRGVLR
5.5	1774.8784	-0.0180	KNSTNMVAELFNVHR
4.8	1774.8355	0.0249	QHMTHAQTRIMSFR
4.8	1774.8771	-0.0167	MATETEVVVAPVSNGGSK
4.8	1774.8905	-0.0301	RPHPPVAAPPMMMRR
4.8	1774.8957	-0.0353	QMDPINVETSLLLMR
4.2	1774.9591	-0.0987	VVFINERPQSRQFR
4.1	1774.9247	-0.0643	QMLEKVAELLASSNAR
4.0	1774.9434	-0.0829	VIGMIPGMGKVSSAQIR

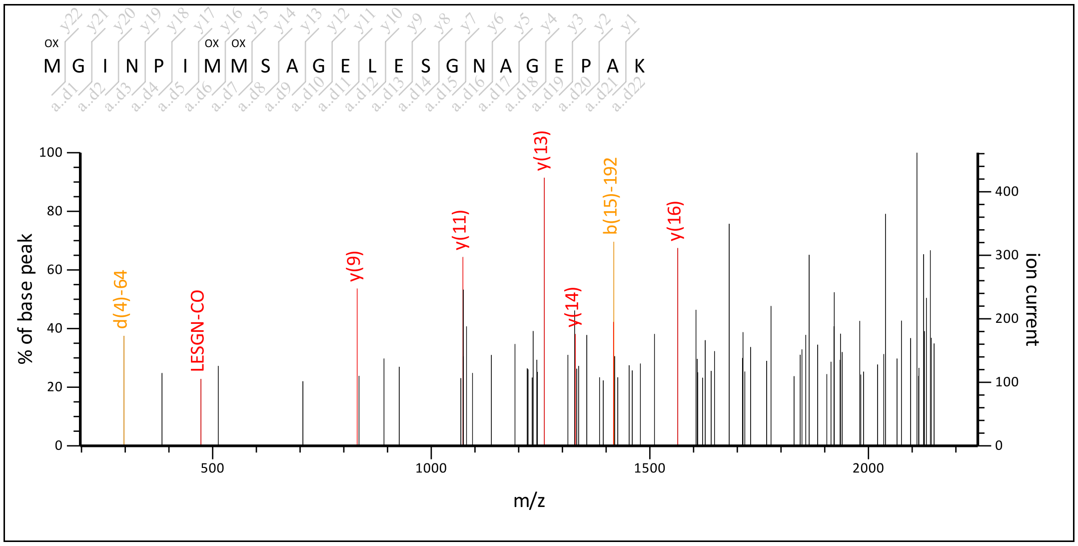
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 74

MS/MS Fragmentation of **MGINPIMMSAGELESGNAGEPAK**
Found in **gi|8918361** in **NCBInr**, RuBisCO activase small isoform precursor [Oryza sativa]

Match to Query 62: 2351.097424 from(2352.104700,1+) intensity(0.0000) index(24)
Title: Label: L1, Spot_Id: 219685, Peak_List_Id: 225097, MSMS Job_Run_Id: 21764, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_L1_136842039200.txt



197.22 to 2250.15

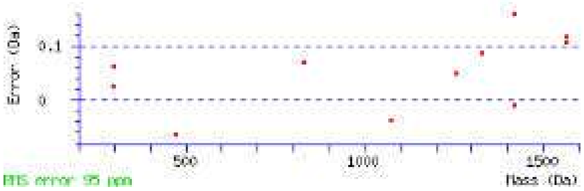
Label all possible matches ○ Label matches used for scoring ●

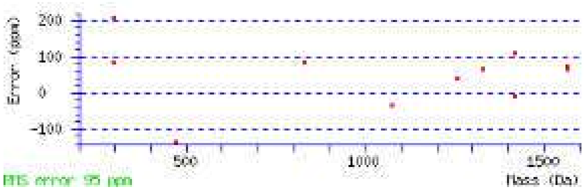
Monoisotopic mass of neutral peptide Mr(calc): 2351.0443
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 9 **Expect:** 1.6e+02
Matches : 13/653 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	120.0478	120.0478			148.0427			44.0495		M						
2	30.0338	177.0692			205.0641					G				2205.0162	2187.9897	218
3	86.0964	290.1533			318.1482			262.1220	276.1376	I	2089.9165	2102.9369	2116.9525	2147.9947	2130.9682	212
4	87.0553	404.1962	387.1697		432.1911	415.1646		361.1904		N	1975.8736	1974.8783		2034.9107	2017.8841	20
5	70.0651	501.2490	484.2224		529.2439	512.2173		475.2333		P	1878.8208	1877.8256		1920.8678	1903.8412	19
6	86.0964	614.3330	597.3065		642.3280	625.3014		586.3017	600.3174	I	1765.7367	1778.7571	1792.7728	1823.8150	1806.7884	18
7	120.0478	761.3684	744.3419		789.3634	772.3368		685.3702		M	1618.7013	1617.7061		1710.7309	1693.7044	16
8	120.0478	908.4038	891.3773		936.3988	919.3722		832.4056		M	1471.6659	1470.6707		***1563.6955***	1546.6690	15
9	60.0444	995.4359	978.4093	977.4253	1023.4308	1006.4042	1005.4202	979.4410		S	1384.6339	1383.6387		***1416.6601***	1399.6336	13
10	44.0495	1066.4730	1049.4464	1048.4624	1094.4679	1077.4414	1076.4573			A	1313.5968			***1329.6281***	1312.6016	13
11	30.0338	1123.4944	1106.4679	1105.4839	1151.4894	1134.4628	1133.4788			G				***1258.5910***	1241.5644	12
12	102.0550	1252.5370	1235.5105	1234.5265	1280.5320	1263.5054	1262.5214	1194.5316		E	1127.5327	1126.5375		1201.5695	1184.5430	11
13	86.0964	1365.6211	1348.5946	1347.6105	1393.6160	1376.5895	1375.6055	1323.5742		L	1014.4487	1013.4534		***1072.5269***	1055.5004	10
14	102.0550	1494.6637	1477.6372	1476.6531	1522.6586	1505.6321	1504.6480	1436.6582		E	885.4061	884.4108		959.4429	942.4163	9
15	60.0444	1581.6957	1564.6692	1563.6852	1609.6906	1592.6641	1591.6801	1565.7008		S	798.3741	797.3788		***830.4003***	813.3737	8
16	30.0338	1638.7172	1621.6906	1620.7066	1666.7121	1649.6856	1648.7015			G				743.3682	726.3417	7
17	87.0553	1752.7601	1735.7336	1734.7496	1780.7550	1763.7285	1762.7445	1709.7543		N	627.3097	626.3144		686.3468	669.3202	6
18	44.0495	1823.7972	1806.7707	1805.7867	1851.7921	1834.7656	1833.7816			A	556.2726			572.3039	555.2773	5
19	30.0338	1880.8187	1863.7921	1862.8081	1908.8136	1891.7871	1890.8030			G				501.2667	484.2402	4
20	102.0550	2009.8613	1992.8347	1991.8507	2037.8562	2020.8297	2019.8456	1951.8558		E	370.2085	369.2132		444.2453	427.2187	4

21	70.0651	2106.9141	2089.8875	2088.9035	2134.9090	2117.8824	2116.8984	2080.8984		P	273.1557	272.1605		315.2027	298.1761
22	44.0495	2177.9512	2160.9246	2159.9406	2205.9461	2188.9195	2187.9355			A	202.1186			218.1499	201.1234
23	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GI	143.1179	171.1128	GIN	257.1608	285.1557	GINP	354.2136	382.2085
GINPI	467.2976	495.2926	GINPIM	614.3330	642.3280	IN	200.1394	228.1343
INP	297.1921	325.1870	INPI	410.2762	438.2711	INPIM	557.3116	585.3065
NP	184.1081	212.1030	NPI	297.1921	325.1870	NPIM	444.2275	472.2224
NPIMM	591.2629	619.2578	NPIMMS	678.2949	706.2899	PI	183.1492	211.1441
PIM	330.1846	358.1795	PIMM	477.2200	505.2149	PIMMS	564.2520	592.2469
PIMMSA	635.2891	663.2840	PIMMSAG	692.3106	720.3055	IM	233.1318	261.1267
IMM	380.1672	408.1621	IMMS	467.1993	495.1942	IMMSA	538.2364	566.2313
IMMSAG	595.2578	623.2527	MM	267.0832	295.0781	MMS	354.1152	382.1101
MMSA	425.1523	453.1472	MMSAG	482.1738	510.1687	MMSAGE	611.2164	639.2113
MS	207.0798	235.0747	MSA	278.1169	306.1118	MSAG	335.1384	363.1333
MSAGE	464.1810	492.1759	MSAGEL	577.2650	605.2599	SA	131.0815	159.0764
SAG	188.1030	216.0979	SAGE	317.1456	345.1405	SAGEL	430.2296	458.2245
SAGELE	559.2722	587.2671	SAGELES	646.3042	674.2992	AG	101.0709	129.0659
AGE	230.1135	258.1084	AGEL	343.1976	371.1925	AGELE	472.2402	500.2351
AGELES	559.2722	587.2671	AGELESG	616.2937	644.2886	GE	159.0764	187.0713
GEL	272.1605	300.1554	GELE	401.2031	429.1980	GELES	488.2351	516.2300
GELESG	545.2566	573.2515	GELESGN	659.2995	687.2944	EL	215.1390	243.1339
ELE	344.1816	372.1765	ELES	431.2136	459.2086	ELESG	488.2351	516.2300
ELESGN	602.2780	630.2729	ELESGNA	673.3151	701.3101	LE	215.1390	243.1339
LES	302.1710	330.1660	LESG	359.1925	387.1874	LESGN	473.2354	501.2304
LESGNA	544.2726	572.2675	LESGNAG	601.2940	629.2889	ES	189.0870	217.0819
ESG	246.1084	274.1034	ESGN	360.1514	388.1463	ESGNA	431.1885	459.1834
ESGNAG	488.2100	516.2049	ESGNAGE	617.2525	645.2475	SG	117.0659	145.0608
SGN	231.1088	259.1037	SGNA	302.1459	330.1408	SGNAG	359.1674	387.1623
SGNAGE	488.2100	516.2049	SGNAGEP	585.2627	613.2576	SGNAGEPA	656.2998	684.2947
GN	144.0768	172.0717	GNA	215.1139	243.1088	GNAG	272.1353	300.1302
GNAGE	401.1779	429.1728	GNAGEP	498.2307	526.2256	GNAGEPA	569.2678	597.2627
NA	158.0924	186.0873	NAG	215.1139	243.1088	NAGE	344.1565	372.1514
NAGEP	441.2092	469.2041	NAGEPA	512.2463	540.2413	AG	101.0709	129.0659
AGE	230.1135	258.1084	AGEP	327.1663	355.1612	AGEPA	398.2034	426.1983
GE	159.0764	187.0713	GEP	256.1292	284.1241	GEPA	327.1663	355.1612
EP	199.1077	227.1026	EPA	270.1448	298.1397	PA	141.1022	169.0972





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
10.3	2351.0807	0.0168	MGINLIMMSAGELESGNAGEPAK
8.8	2351.0443	0.0531	MGINPIMMSAGELESGNAGEPAK
3.2	2351.0807	0.0168	MGINLIMMSAGELESGNAGEPAK
1.8	2351.0807	0.0168	MGINLIMMSAGELESGNAGEPAK

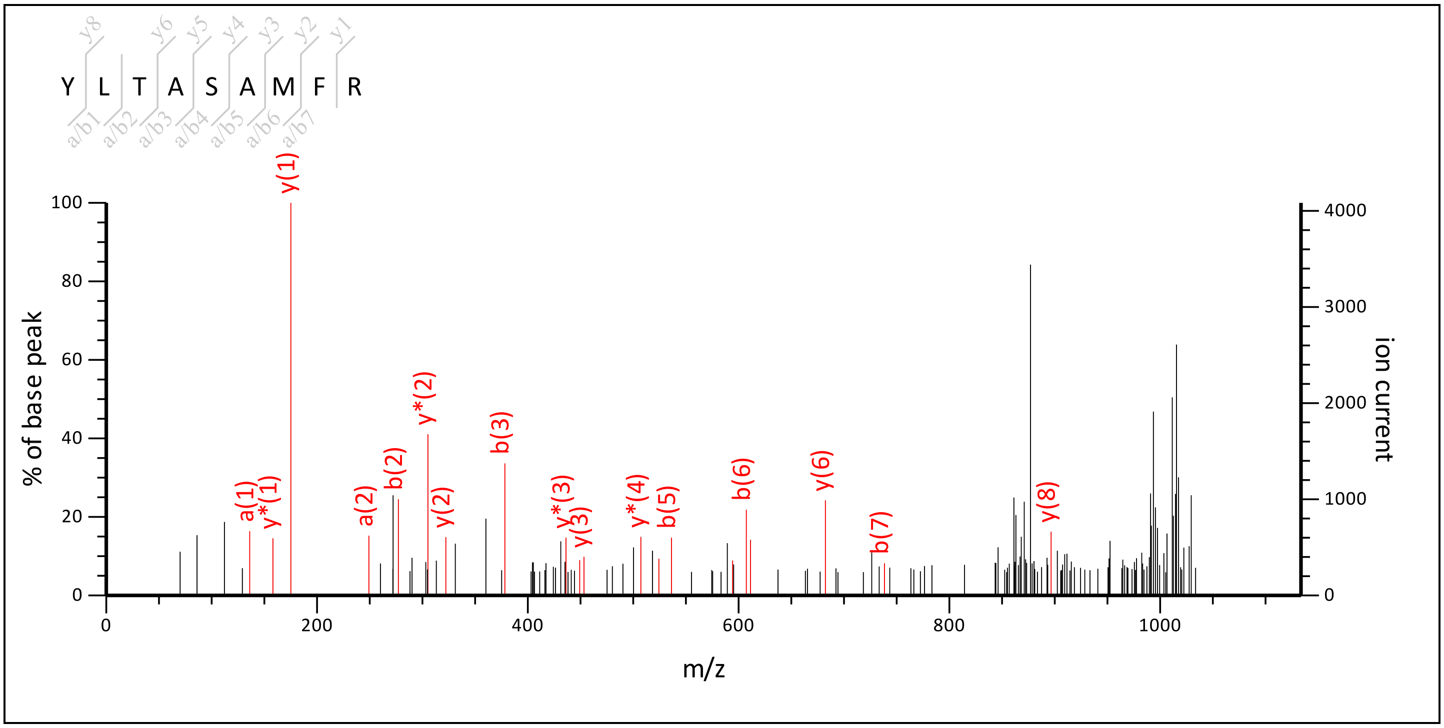
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **YLTASAMFR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 3: 1058.621524 from(1059.628800,1+) intensity(0.0000) index(0)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221751, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



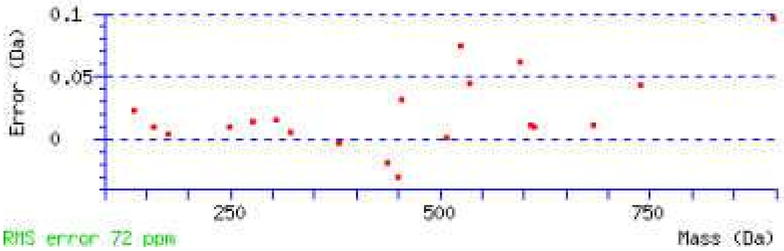
0 to 1133.64

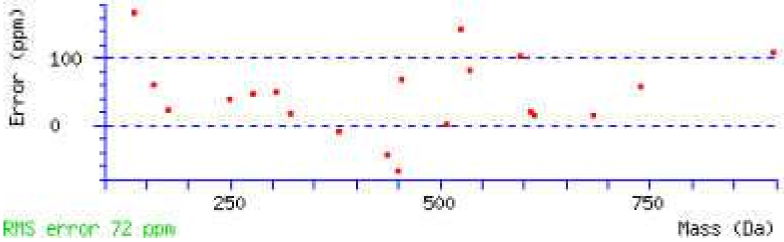
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1058.5219
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 7.9
Matches : 20/32 fragment ions using 48 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	136.0757	164.0706	Y			9
2	249.1598	**277.1547**	L	***896.4659***	879.4393	8
3	350.2074	**378.2023**	T	783.3818	766.3552	7
4	421.2445	**449.2395**	A	***682.3341***	665.3076	6
5	508.2766	**536.2715**	S	***611.2970***	594.2704	5
6	579.3137	**607.3086**	A	***524.2650***	507.2384	4
7	710.3542	**738.3491**	M	***453.2279***	436.2013	3
8	857.4226	885.4175	F	***322.1874***	305.1608	2

9			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.1	1058.5219	0.0996	YLTASAMFR
9.8	1057.5080	1.1135	YIETGAYGGK
7.9	1059.6223	-1.0007	AILRVSVMR
7.9	1059.5495	-0.9280	SPIRTPSMR
6.1	1058.5873	0.0343	YLTSALVHR
5.7	1058.5185	0.1030	YDVFVNFR
5.7	1058.5549	0.0666	YTLVFNFR
5.7	1058.5219	0.0996	YITMNFVR
5.4	1059.5349	-0.9134	SPPPSEPPPR
5.4	1058.5873	0.0343	IYTSVAHLR

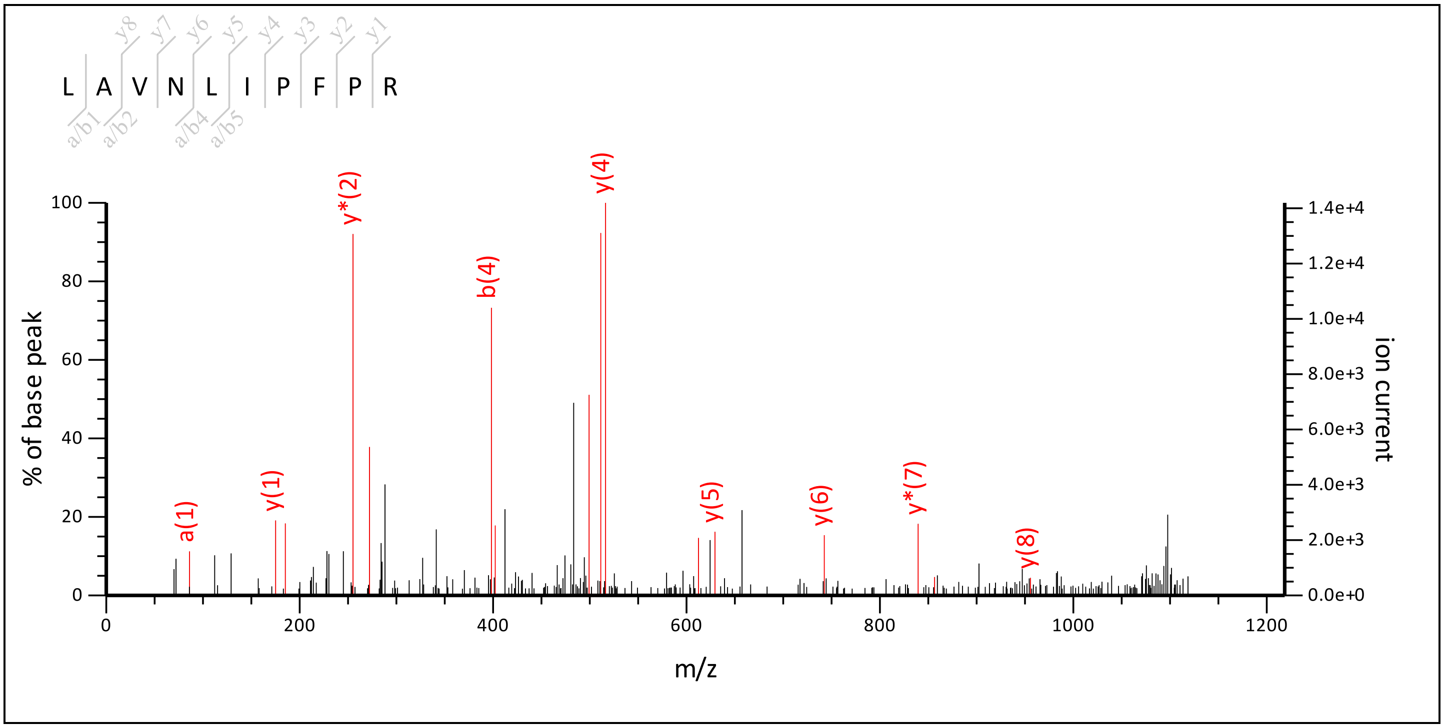
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **LAVNLIPFPR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 8: 1138.786824 from(1139.794100,1+) intensity(0.0000) index(2)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221744, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



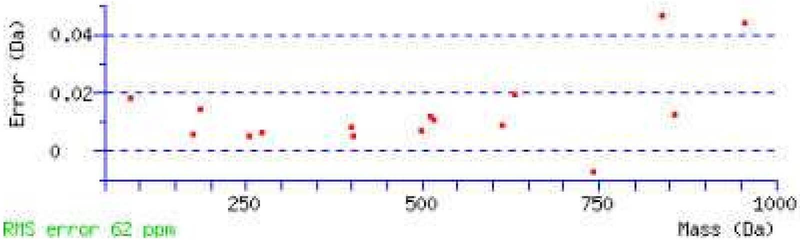
0 to 1218.55

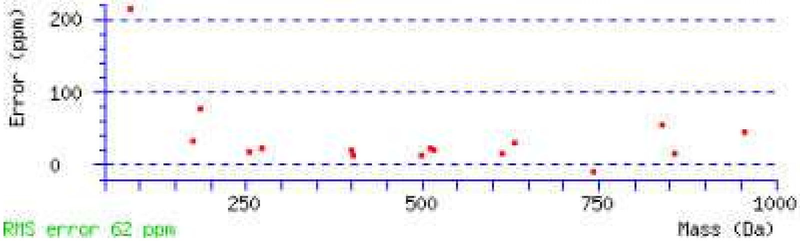
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1138.6862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.81
Matches : 16/48 fragment ions using 33 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		L			10
2	157.1335		**185.1285**		A	1026.6095	1009.5829	9
3	256.2020		284.1969		V	***955.5724***	938.5458	8
4	370.2449	353.2183	**398.2398**	381.2132	N	***856.5039***	839.4774	7
5	483.3289	466.3024	**511.3239**	494.2973	L	***742.4610***	725.4345	6
6	596.4130	579.3865	624.4079	607.3814	I	***629.3770***	612.3504	5
7	693.4658	676.4392	721.4607	704.4341	P	***516.2929***	499.2663	4
8	840.5342	823.5076	868.5291	851.5026	F	419.2401	402.2136	3

9	937.5870	920.5604	965.5819	948.5553	**P**	*272.1717*	255.1452	**2**
10					**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.3	1138.6862	0.1006	IAVNLIPFPR
37.3	1138.6862	0.1006	LAVNLIPFPR
26.0	1138.7074	0.0794	GVLQILLDLR
23.7	1138.6935	0.0934	ARGILLNGAVR
21.7	1137.6618	1.1250	RALASSAIPPR
19.5	1138.6281	0.1587	RSPAVLMPPR
18.3	1137.6658	1.1210	LVWKTAAPPR
18.1	1137.6870	1.0998	LVSQVLLNPR
17.6	1137.7274	1.0594	LAVILIPFPR
16.7	1138.6281	0.1588	RAADPLPMLR

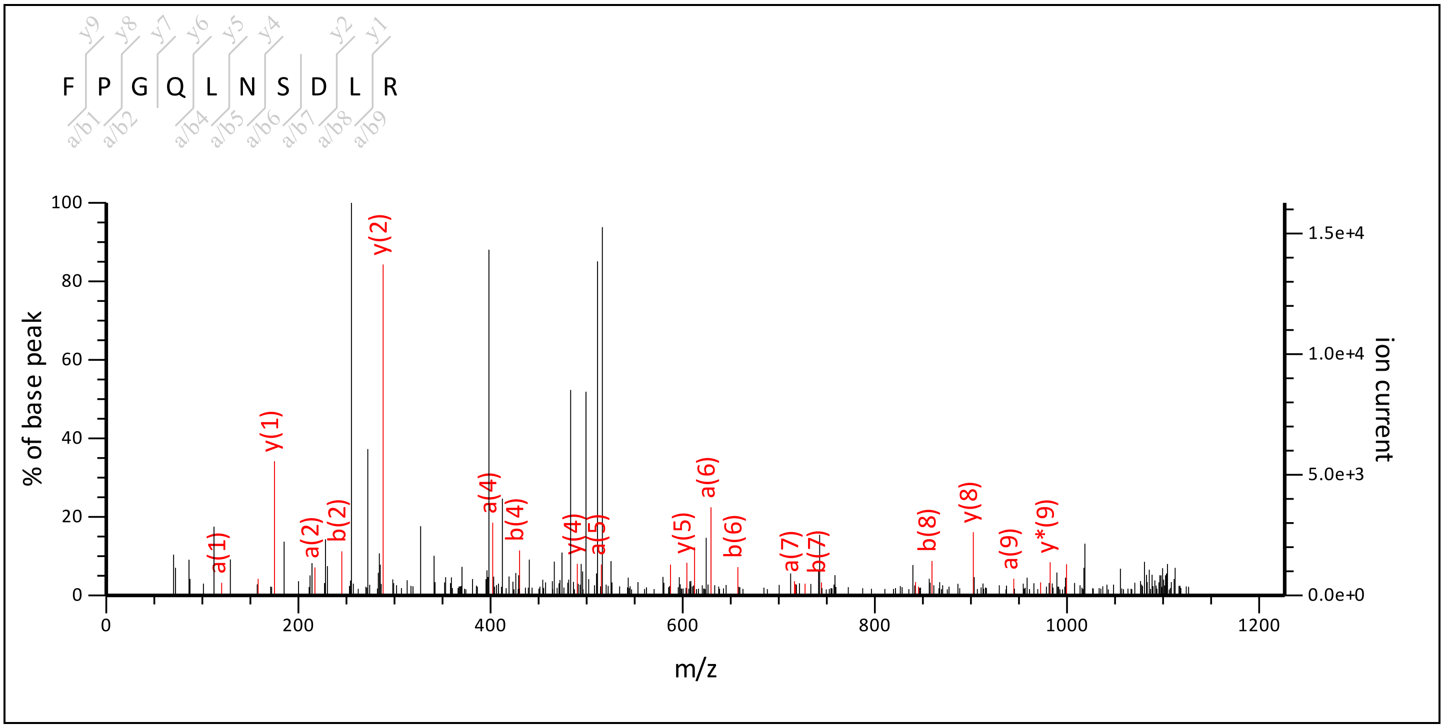
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **FPGQLNSDLR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 10: 1145.690824 from(1146.698100,1+) intensity(0.0000) index(3)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221745, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



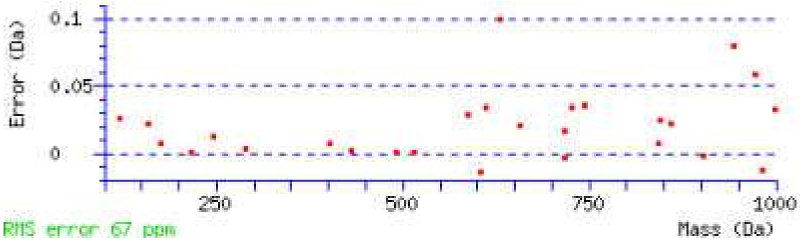
0 to 1226.58

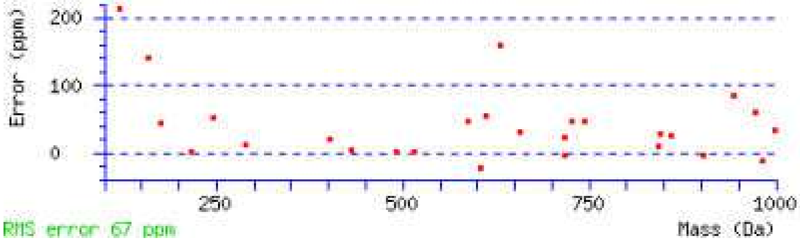
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1145.5829
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 1e+02
Matches : 27/48 fragment ions using 110 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**120.0808**		148.0757		F			10
2	**217.1335**		**245.1285**		P	***999.5218***	982.4952	9
3	274.1550		302.1499		G	***902.4690***	885.4425	8
4	**402.2136**	385.1870	**430.2085**	413.1819	Q	***845.4476***	828.4210	7
5	**515.2976**	498.2711	543.2926	526.2660	L	***717.3890***	700.3624	6
6	**629.3406**	612.3140	**657.3355**	640.3089	N	***604.3049***	587.2784	5
7	**716.3726**	699.3461	**744.3675**	727.3410	S	***490.2620***	473.2354	4
8	831.3995	814.3730	**859.3945**	842.3679	D	403.2300	386.2034	3

9	**944.4836**	927.4571	**972.4785**	955.4520	**L**	***288.2030***	271.1765	**2**
10					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.1	1145.5750	0.1158	EDCLLEVLR
17.9	1145.6193	0.0715	FPGKLNSDLR
17.9	1145.5829	0.1079	FPGQLNSDLR
16.8	1144.5611	1.1297	LAALGGEEEEK
16.1	1144.6386	1.0522	AIVRAISQCK
15.9	1144.5975	1.0933	IAGAVVEETEK
15.1	1145.6114	0.0794	MGEALLVELR
14.4	1144.6452	1.0456	GAVVLATAGGTTK
13.9	1145.6768	0.0140	KLLQSSTTIR
13.4	1146.5161	-0.8253	EDCLNMLPR

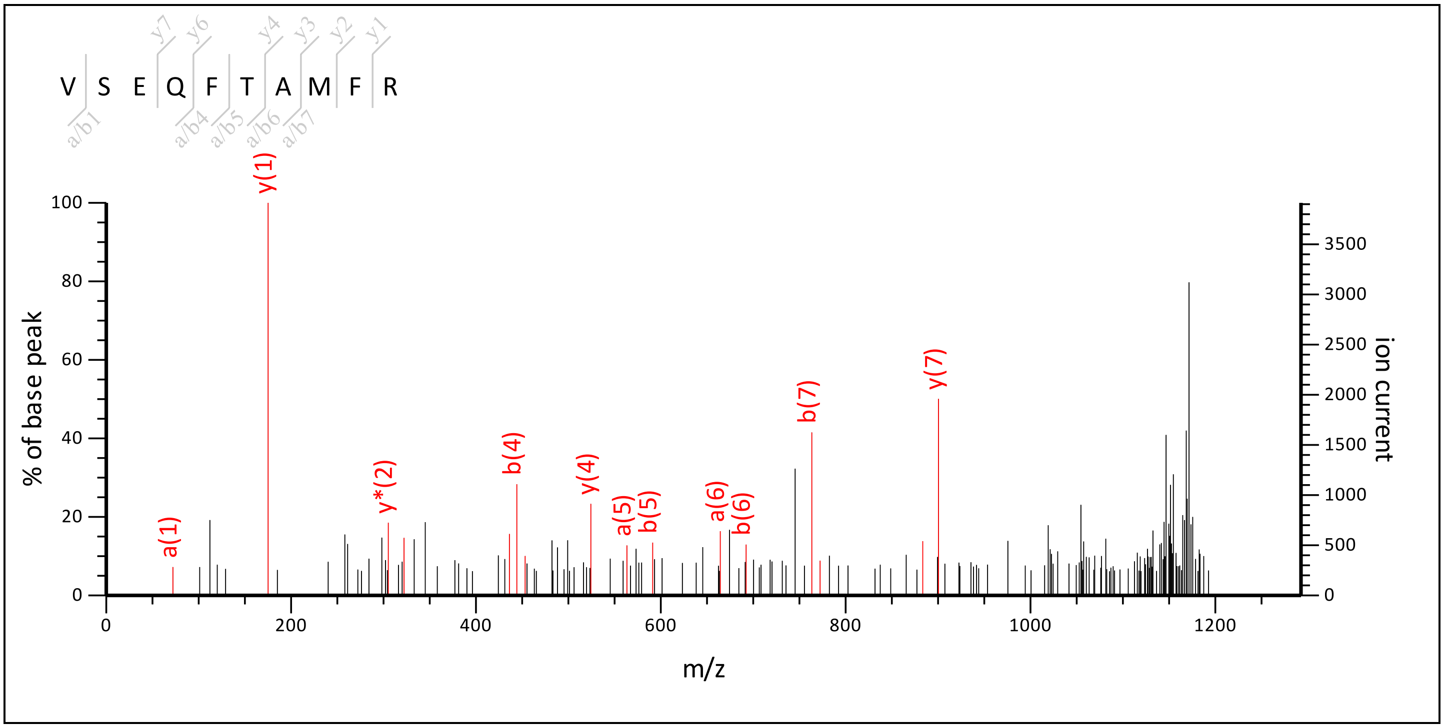
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **VSEQFTAMFR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 15: 1214.687224 from(1215.694500,1+) intensity(0.0000) index(5)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221749, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



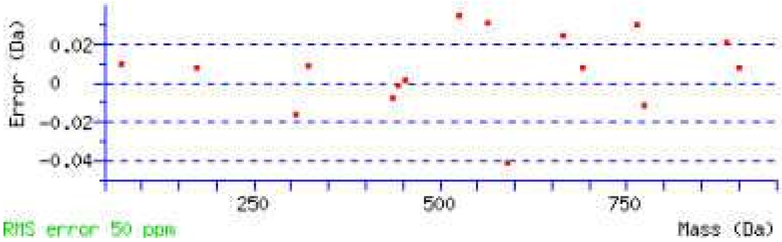
0 to 1292.69

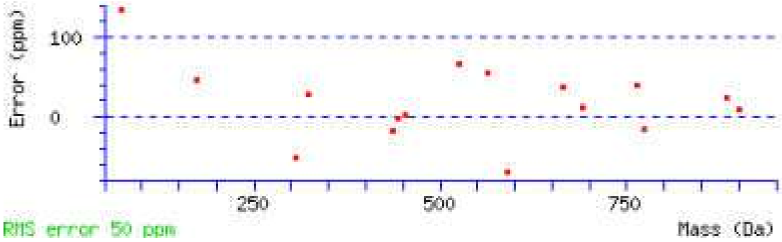
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1214.5754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 91
Matches : 16/48 fragment ions using 48 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	***72.0808***		100.0757		V			10
2	159.1128		187.1077		S	1116.5143	1099.4877	9
3	288.1554		316.1503		E	1029.4822	1012.4557	8
4	416.2140	399.1874	**444.2089**	427.1823	Q	***900.4396***	883.4131	7
5	***563.2824***	546.2558	**591.2773**	574.2508	F	***772.3811***	755.3545	6
6	***664.3301***	647.3035	**692.3250**	675.2984	T	625.3126	608.2861	5
7	735.3672	718.3406	**763.3621**	746.3355	A	***524.2650***	507.2384	4
8	866.4077	849.3811	894.4026	877.3760	M	***453.2279***	436.2013	3

9	1013.4761	996.4495	1041.4710	1024.4444	**F**	***322.1874***	305.1608	**2**
10					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.7	1213.6568	1.0305	GSIGHAFTVGIR
18.4	1214.6118	0.0755	VSEKFTAMFR
18.4	1214.5754	0.1118	VSEQFTAMFR
10.3	1213.5696	1.1176	MGSCVGYLRR
8.4	1215.6030	-0.9158	RESVSMTPGPR
7.3	1213.5509	1.1363	MANSKGSSNFR
7.3	1214.6996	-0.0124	NLHQAKVHLR
7.3	1214.6924	-0.0052	YKLTWVHIR
7.0	1214.6230	0.0642	LYQMYGRLR
6.8	1214.5390	0.1482	GFAFEDGMGIR

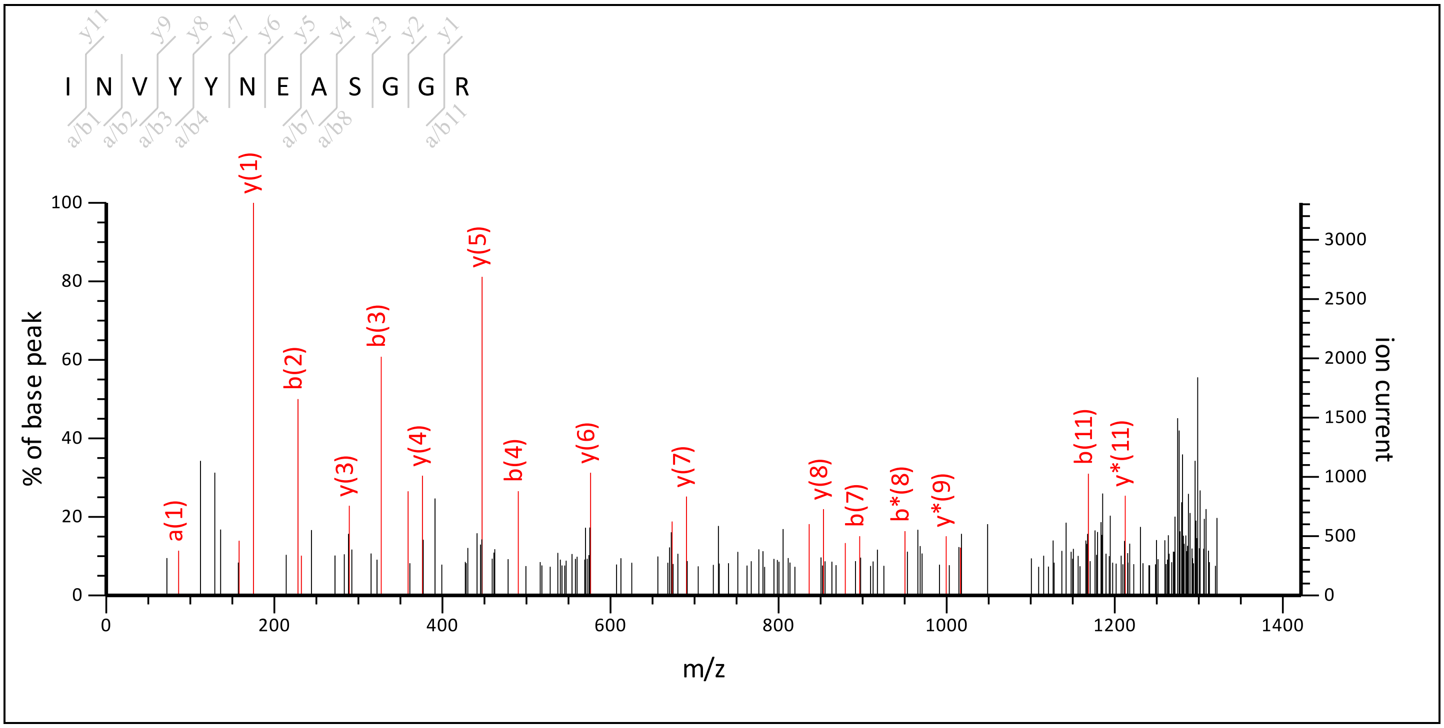
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **INVYYNEASGGR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 24: 1341.751424 from(1342.758700,1+) intensity(0.0000) index(8)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221750, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



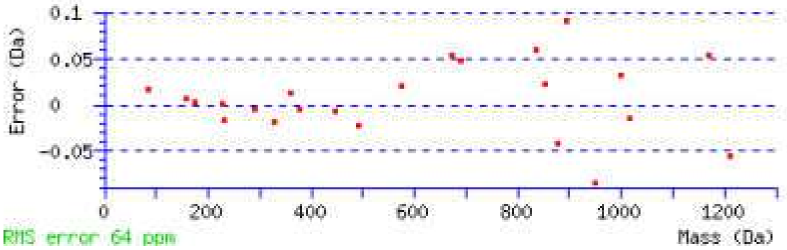
0 to 1421.59

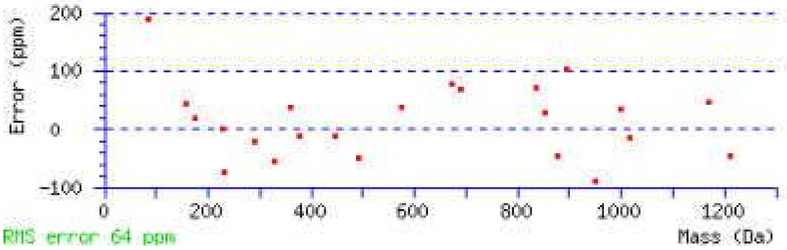
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1341.6313
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 1.5
Matches : 23/64 fragment ions using 65 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		I			12
2	200.1394	183.1128	**228.1343**	211.1077	N	1229.5545	1212.5280	11
3	299.2078	282.1812	**327.2027**	310.1761	V	1115.5116	1098.4851	10
4	462.2711	445.2445	**490.2660**	473.2395	Y	***1016.4432***	999.4167	9
5	625.3344	608.3079	653.3293	636.3028	Y	***853.3799***	836.3533	8
6	739.3774	722.3508	767.3723	750.3457	N	***690.3165***	673.2900	7
7	868.4199	851.3934	**896.4149**	879.3883	E	***576.2736***	559.2471	6
8	939.4571	922.4305	967.4520	950.4254	A	***447.2310***	430.2045	5

9	1026.4891	1009.4625	1054.4840	1037.4575	**S**	***376.1939***	359.1674	**4**
10	1083.5105	1066.4840	1111.5055	1094.4789	**G**	***289.1619***	272.1353	**3**
11	1140.5320	1123.5055	**1168.5269**	1151.5004	**G**	***232.1404***	215.1139	**2**
12					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.5	1341.6313	0.1201	INVYYNEASGGR
35.5	1341.6313	0.1201	LNVYYNEASGGR
26.8	1342.6153	-0.8639	IDVYYNEASGGR
14.0	1342.7027	-0.9513	QVVDQIAVNAMR
12.6	1341.6499	0.1015	QVVYMYPRDR
9.6	1341.6612	0.0902	KVQHCLSEWR
8.9	1340.7776	0.9739	QAATALLLALSNR
8.8	1341.5877	0.1637	YYYYLTGDER
8.1	1341.7115	0.0399	RVVDYFTALMK
8.0	1341.5904	0.1610	DSNASEMAKMVK

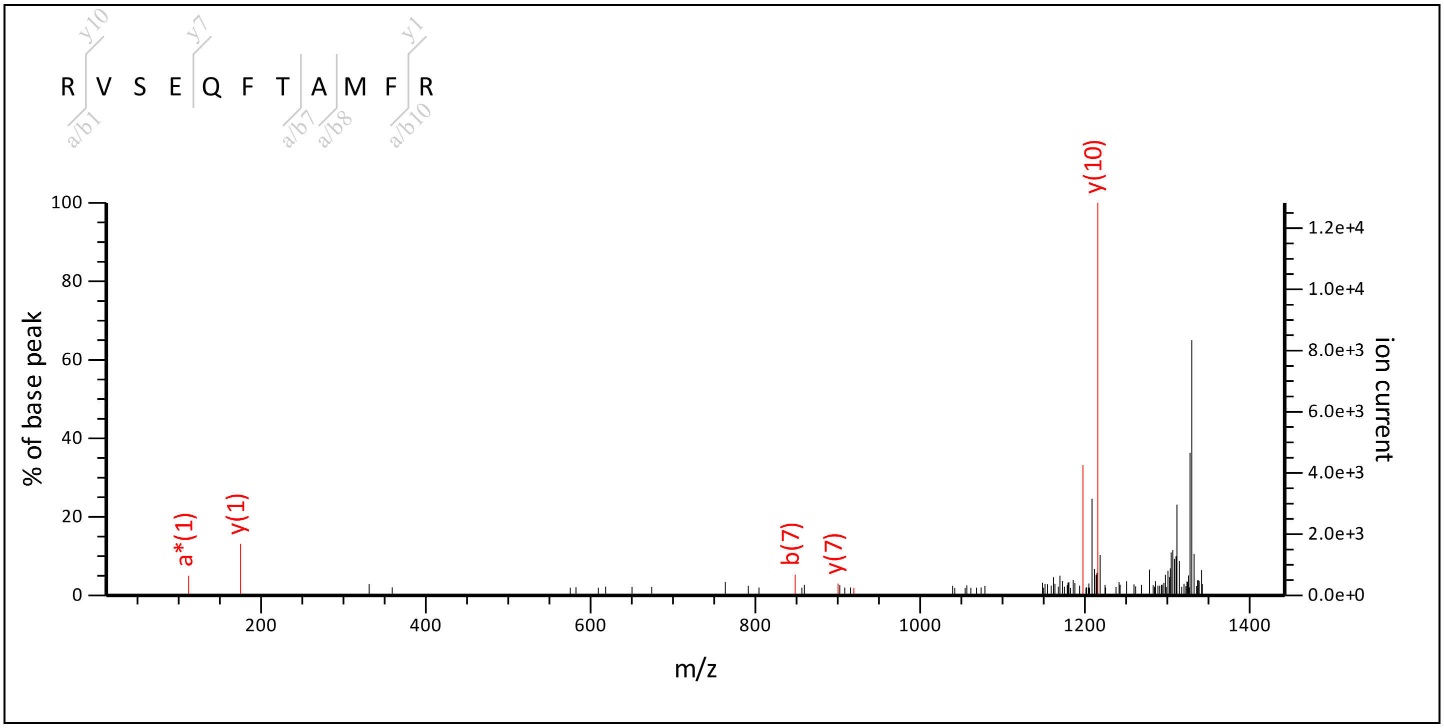
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **RVSEQFTAMFR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 26: 1370.797124 from(1371.804400,1+) intensity(0.0000) index(9)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221754, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



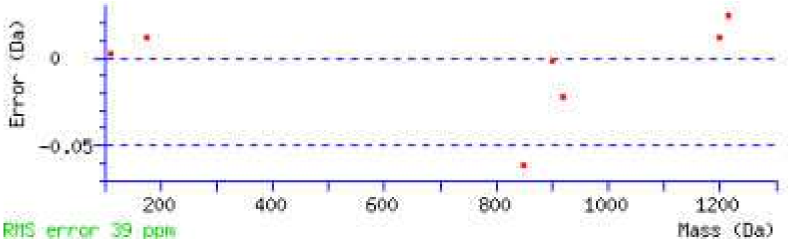
12.09 to 1442.5

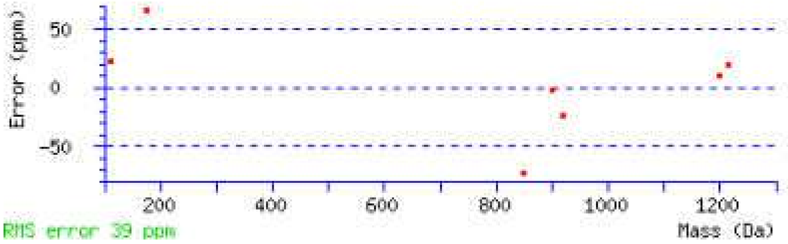
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1370.6765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 7 **Expect:** 1e+03
Matches : 7/60 fragment ions using 22 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	129.1135	112.0869	157.1084	140.0818	R			11
2	228.1819	211.1553	256.1768	239.1503	V	***1215.5827***	1198.5561	10
3	315.2139	298.1874	343.2088	326.1823	S	1116.5143	1099.4877	9
4	444.2565	427.2300	472.2514	455.2249	E	1029.4822	1012.4557	8
5	572.3151	555.2885	600.3100	583.2835	Q	***900.4396***	883.4131	7
6	719.3835	702.3569	747.3784	730.3519	F	772.3811	755.3545	6
7	820.4312	803.4046	***848.4261***	831.3995	T	625.3126	608.2861	5
8	891.4683	874.4417	***919.4632***	902.4367	A	524.2650	507.2384	4

9	1022.5088	1005.4822	1050.5037	1033.4771	**M**	453.2279	436.2013	**3**
10	1169.5772	1152.5506	***1197.5721***	1180.5456	**F**	322.1874	305.1608	**2**
11					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
14.8	1370.6799	0.1173	RMAFTMTATGIR
10.6	1370.6361	0.1610	RSSTSVGFCTNR
8.3	1370.7168	0.0804	VGPRPDTFGGGRR
8.2	1370.7266	0.0705	RGIIEQGLSDQR
8.2	1370.7266	0.0705	RLLGQSVGEEQR
7.8	1370.7419	0.0553	RHTEGTALALFR
7.3	1370.6765	0.1206	RVSEQFTAMFR
6.8	1370.8431	-0.0460	SSLALVMRLIIR
6.4	1370.7571	0.0400	GVRWFQNPVLR
6.4	1370.7419	0.0552	VGVEPQFRNGLR

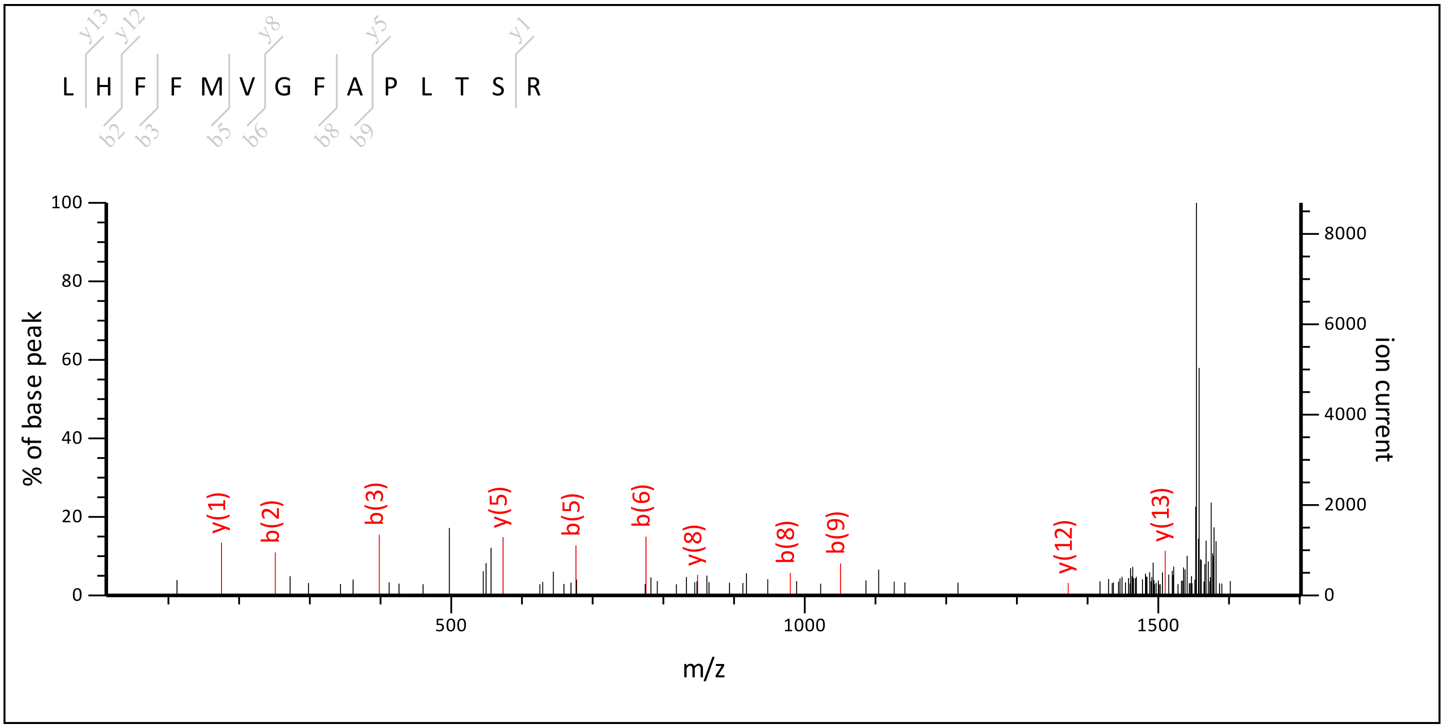
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **LHFFMVGFAPLTSR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 46: 1621.986824 from(1622.994100,1+) intensity(0.0000) index(18)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221756, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



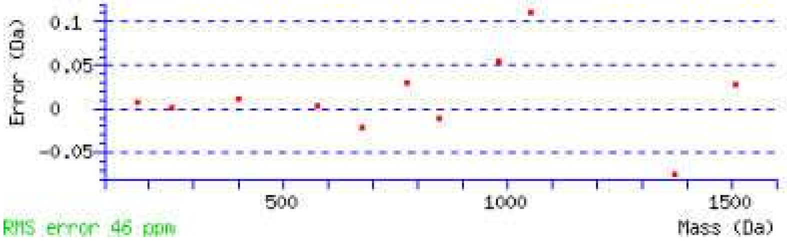
12.1 to 1701.81

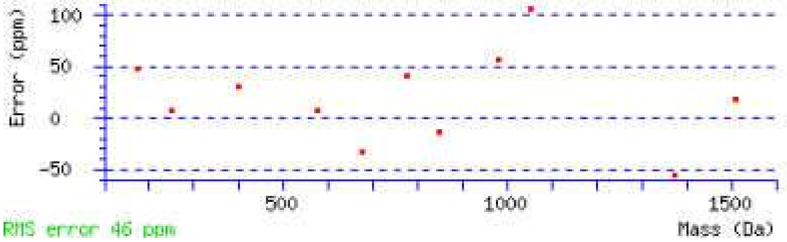
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1621.8439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.14
Matches : 11/52 fragment ions using 15 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	86.0964	114.0913	**L**			**14**
2	223.1553	***251.1503***	**H**	***1509.7671***	1492.7406	**13**
3	370.2238	***398.2187***	**F**	***1372.7082***	1355.6817	**12**
4	517.2922	545.2871	**F**	1225.6398	1208.6132	**11**
5	648.3326	***676.3276***	**M**	1078.5714	1061.5448	**10**
6	747.4011	***775.3960***	**V**	947.5309	930.5043	**9**
7	804.4225	832.4174	**G**	***848.4625***	831.4359	**8**
8	951.4909	***979.4859***	**F**	791.4410	774.4145	**7**

9	1022.5281	*1050.5230*	A	644.3726	627.3461	6
10	1119.5808	1147.5757	P	*573.3355*	556.3089	5
11	1232.6649	1260.6598	L	476.2827	459.2562	4
12	1333.7126	1361.7075	T	363.1987	346.1721	3
13	1420.7446	1448.7395	S	262.1510	245.1244	2
14			R	*175.1190*	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.8	1621.8439	0.1429	LHFFMVGFAPLTSR
11.7	1622.7649	-0.7780	NHGAPEVSGVSDEGLR
11.3	1621.7518	0.2350	LTIDGMQGNQNYPR
9.9	1621.8075	0.1793	LHPAMKPYEYAFR
8.6	1621.9668	0.0200	HLIALGFKVAVIEGR
6.3	1621.7276	0.2593	LHRCYMASMQGPR
6.3	1621.7590	0.2278	LASSNGSSAGNGGRMTR
6.1	1621.7121	0.2747	EEKWDSSTSHFNR
5.7	1622.8013	-0.8144	GGHSSLPPVDGSTAVSR
5.2	1621.7804	0.2065	LLAKMMTTAGADPDR

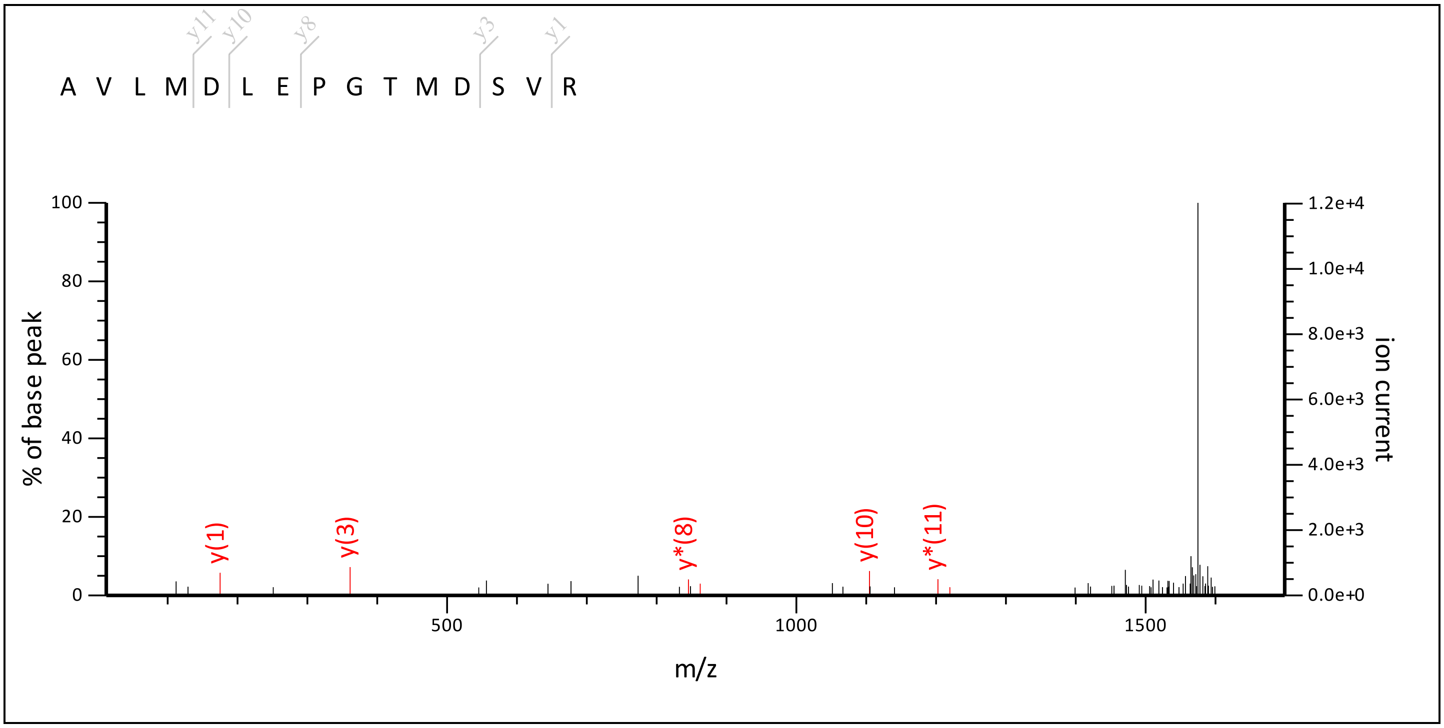
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 81

MS/MS Fragmentation of **AVLMDLEPGTMDSVR**
Found in **gi|493725** in **NCBInr**, beta tubulin [Oryza sativa Japonica Group]

Match to Query 48: 1632.939624 from(1633.946900,1+) intensity(0.0000) index(19)
Title: Label: E13, Spot_Id: 216673, Peak_List_Id: 221764, MSMS Job_Run_Id: 21390, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_E13_136117700900.txt



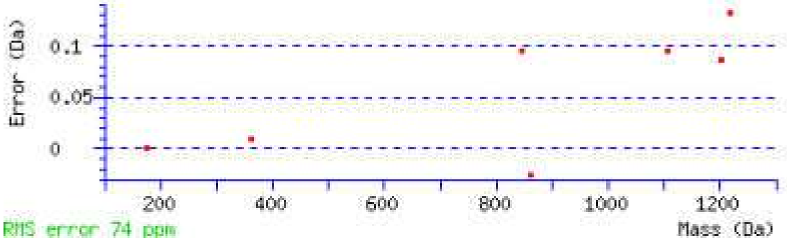
12.11 to 1699.05

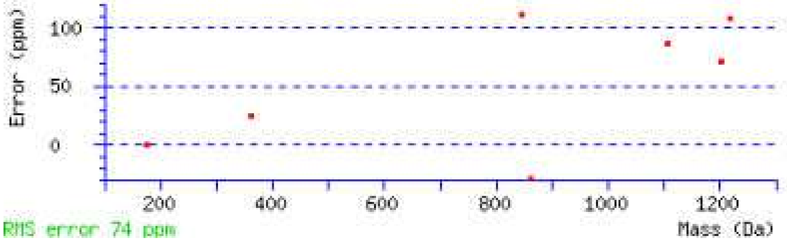
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1632.7851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 11 **Expect:** 3.5e+02
Matches : 7/56 fragment ions using 21 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	44.0495	72.0444	A			15
2	143.1179	171.1128	V	1562.7553	1545.7287	14
3	256.2020	284.1969	L	1463.6869	1446.6603	13
4	387.2424	415.2374	M	1350.6028	1333.5763	12
5	502.2694	530.2643	D	***1219.5623***	1202.5358	11
6	615.3534	643.3484	L	***1104.5354***	1087.5088	10
7	744.3960	772.3910	E	991.4513	974.4248	9
8	841.4488	869.4437	P	***862.4087***	845.3822	8

9	898.4703	926.4652	**G**	765.3560	748.3294	**7**
10	999.5179	1027.5129	**T**	708.3345	691.3080	**6**
11	1130.5584	1158.5533	**M**	607.2868	590.2603	**5**
12	1245.5854	1273.5803	**D**	476.2463	459.2198	**4**
13	1332.6174	1360.6123	**S**	***361.2194***	344.1928	**3**
14	1431.6858	1459.6807	**V**	274.1874	257.1608	**2**
15			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
11.1	1632.7851	0.1545	AVLMDLEPGTMDSVR
11.1	1632.7851	0.1545	AVLMDLEPGTMDSVR
11.1	1632.7851	0.1545	GILMDLEPGTMDSVR
9.4	1632.6396	0.3000	QTGDMMFVSEDGER
8.0	1633.8069	-0.8672	VRCDMALPFGLPSR
7.8	1633.7042	-0.7646	EKASDAAGEYGSYMR
6.3	1631.8202	1.1194	EAVQTCVLSQRWR
6.1	1633.8147	-0.8751	RILFGWANECVNR
6.1	1633.7817	-0.8421	RILMGWANECVNR
5.7	1632.7566	0.1830	SDQELVEMFDKHR

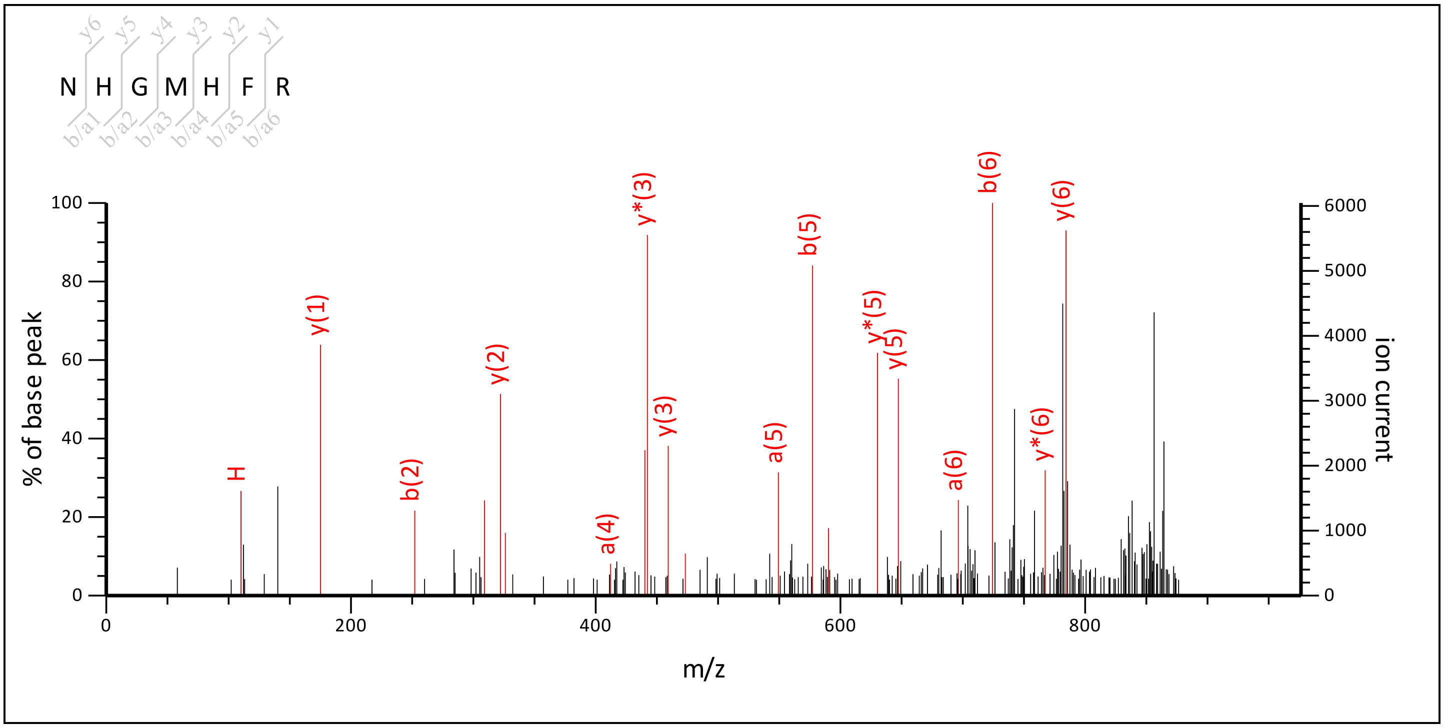
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **NHGMHFR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 2: 897.475204 from(898.482480,1+) intensity(0.0000) index(0)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221214, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



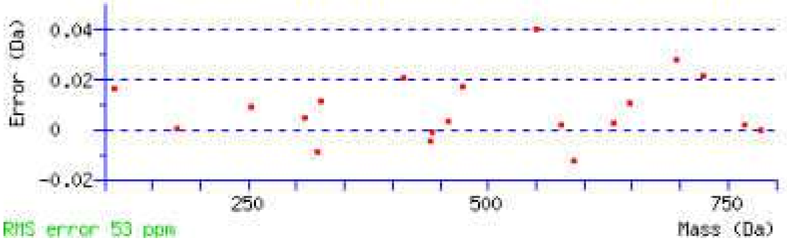
0 to 976.39

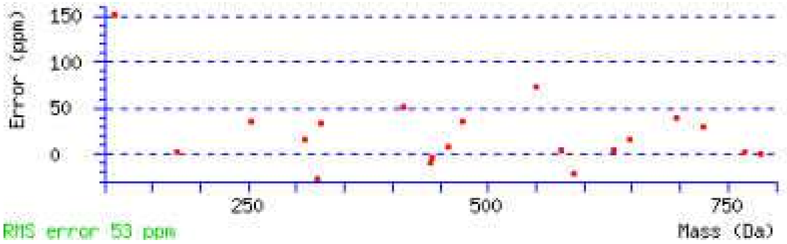
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 897.4028
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.83
Matches : 22/72 fragment ions using 35 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	87.0553	87.0553	70.0287	115.0502	98.0237	44.0495	N					7
2	110.0713	224.1142	207.0877	**252.1091**	235.0826		H	702.3140		***784.3671***	767.3406	6
3	30.0338	281.1357	264.1091	**309.1306**	292.1040		G			***647.3082***	630.2817	5
4	104.0528	**412.1761**	395.1496	**440.1711**	423.1445	352.1728	M	514.2521	513.2568	***590.2868***	573.2602	4
5	110.0713	**549.2351**	532.2085	**577.2300**	560.2034		H	377.1932		***459.2463***	442.2197	3
6	120.0808	**696.3035**	679.2769	**724.2984**	707.2718		F	230.1248		***322.1874***	305.1608	2
7	129.1135						R	74.0237	73.0284	***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HG	167.0927	195.0877	**HGM**	298.1332	326.1281	**HGMH**	435.1921	463.1870
HGMHF	582.2605	610.2555	**GM**	161.0743	189.0692	**GMH**	298.1332	326.1281
GMHF	445.2016	473.1966	**MH**	241.1118	269.1067	**MHF**	388.1802	416.1751
HF	257.1397	285.1346						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.9	897.4028	0.0724	NHGMHFR
38.9	897.4028	0.0724	NHGMHFR
38.9	897.4028	0.0724	NHGMHFR
38.9	897.4028	0.0724	NHGMHFR
38.9	897.4028	0.0724	NHGMHFR
38.9	897.4028	0.0724	NHGMHFR
38.9	897.4028	0.0724	NHGMHFR
38.9	897.3698	0.1054	NHGMHMR
25.7	898.3868	-0.9116	DHGMHFR
25.7	898.3868	-0.9116	DHGMHFR

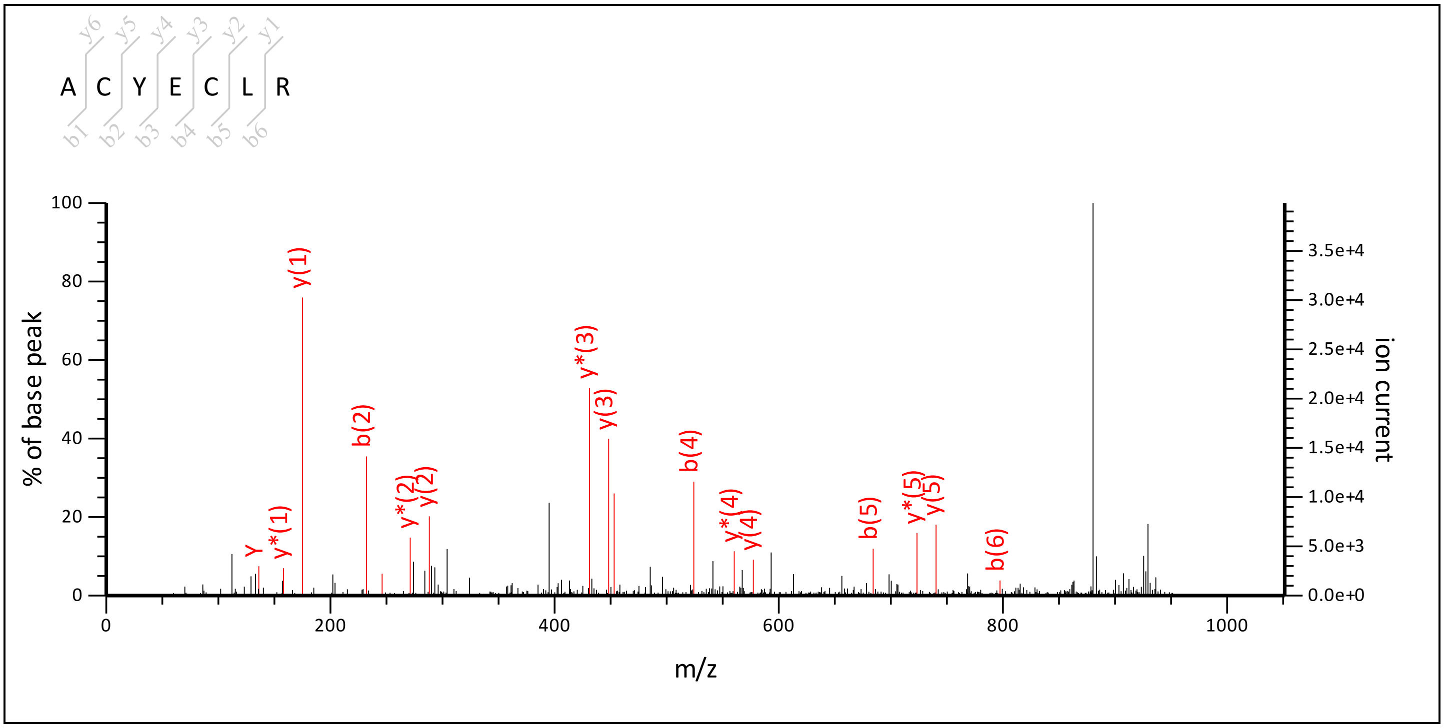
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **ACYECLR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 6: 970.475084 from(971.482360,1+) intensity(0.0000) index(3)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221202, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



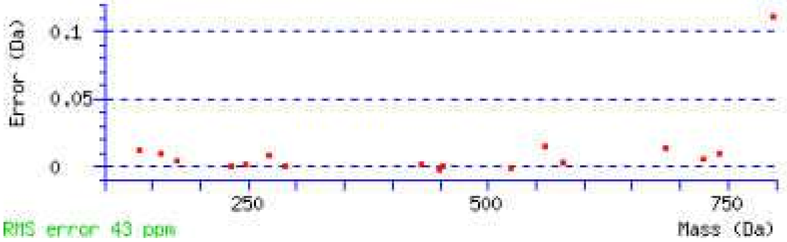
0 to 1051.37

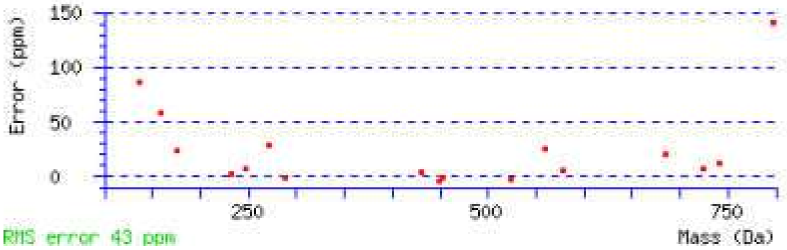
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 970.4001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 6
Matches : 18/75 fragment ions using 27 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		72.0444		44.0495	A						7
2	133.0430	204.0801		**232.0750**		115.0866	C	795.3454	794.3502	900.3702	883.3437	882.3597	6
3	136.0757	367.1435		395.1384			Y	632.2821		***740.3396***	723.3130	722.3290	5
4	102.0550	496.1860	478.1755	**524.1810**	506.1704	438.1806	E	503.2395	502.2442	***577.2763***	560.2497	559.2657	4
5	133.0430	656.2167	638.2061	**684.2116**	666.2010	567.2232	C	343.2088	342.2136	***448.2337***	431.2071		3
6	86.0964	769.3008	751.2902	**797.2957**	779.2851	727.2538	L	230.1248	229.1295	***288.2030***	271.1765		2
7	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
CY	296.1063	324.1013	**CYE**	425.1489	453.1438	**CYEC**	585.1796	613.1745
CYECL	698.2636	726.2586	**YE**	265.1183	293.1132	**YEC**	425.1489	453.1438
YECL	538.2330	566.2279	**EC**	262.0856	290.0805	**ECL**	375.1697	403.1646
CL	246.1271	274.1220						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.4	970.4001	0.0750	ACYECIR
30.4	970.4001	0.0750	ACYECLR
30.4	970.4001	0.0750	ACYECLR
30.4	970.4001	0.0750	ACYECLR
30.4	970.4001	0.0750	ACYECLR
25.8	969.4412	1.0339	MVYECLR
25.4	970.4794	-0.0043	CVYTSTIK
24.5	970.4113	0.0638	RMCADYR
22.9	970.5382	-0.0631	LANPKCLR
20.9	969.5252	0.9499	MAMLVHIR

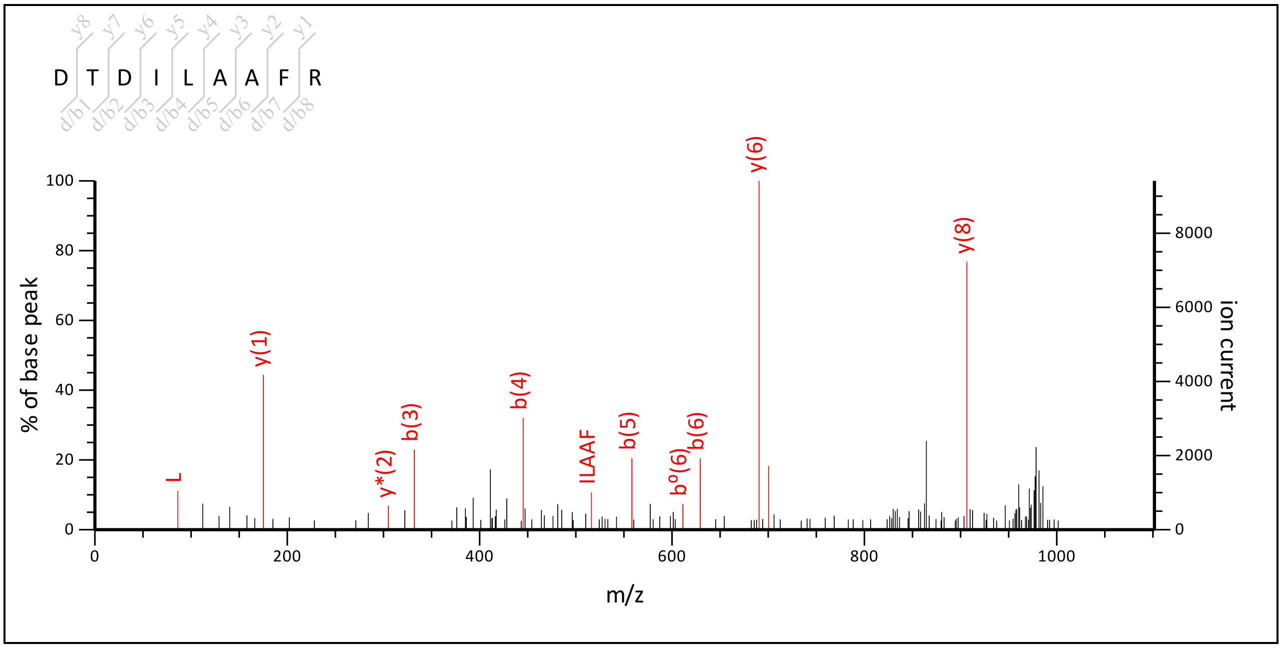
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **DTDILAAFR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 9: 1020.604024 from(1021.611300,1+) intensity(0.0000) index(5)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221223, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1101.53

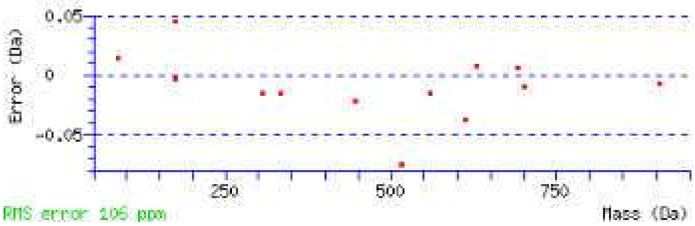
Label all possible matches ○ Label matches used for scoring ●

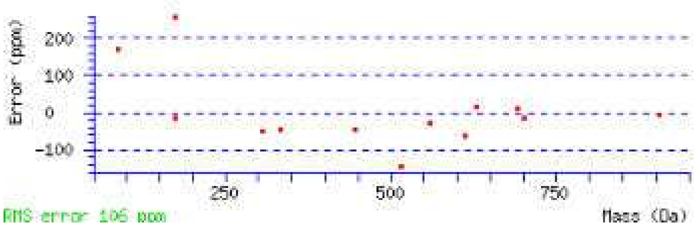
Monoisotopic mass of neutral peptide Mr(calc): 1020.5240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 4.2
Matches : 14/121 fragment ions using 20 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	88.0393	88.0393	70.0287	116.0342	98.0237	44.0495		**D**							9
2	74.0600	189.0870	171.0764	217.0819	199.0713	173.0921	175.0713	**T**	860.4625	873.4829	875.4621	***906.5043***	889.4778	888.4938	8
3	88.0393	304.1139	286.1034	***332.1088***	314.0983	260.1241		**D**	745.4355	744.4403		805.4567	788.4301	787.4461	7
4	86.0964	417.1980	399.1874	***445.1929***	427.1823	389.1667	403.1823	**I**	632.3515	645.3719	659.3875	***690.4297***	673.4032		6
5	86.0964	530.2821	512.2715	***558.2770***	540.2664	488.2351		**L**	519.2674	518.2722		577.3457	560.3191		5
6	44.0495	601.3192	583.3086	***629.3141***	611.3035			**A**	448.2303			464.2616	447.2350		4
7	44.0495	672.3563	654.3457	***700.3512***	682.3406			**A**	377.1932			393.2245	376.1979		3
8	120.0808	819.4247	801.4141	847.4196	829.4090			**F**	230.1248			322.1874	305.1608		2
9	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TD	189.0870	217.0819	**TDI**	302.1710	330.1660	**TDIL**	415.2551	443.2500
TDILA	486.2922	514.2871	**TDILAA**	557.3293	585.3243	**DI**	201.1234	229.1183
DIL	314.2074	342.2023	**DILA**	385.2445	413.2395	**DILAA**	456.2817	484.2766

DILAAF	603.3501	631.3450	**IL**	199.1805	227.1754	**ILA**	270.2176	298.2125
ILAA	341.2547	369.2496	**ILAAF**	488.3231	516.3180	**LA**	157.1335	185.1285
LAA	228.1707	256.1656	**LAAF**	375.2391	403.2340	**AA**	115.0866	143.0815
AAF	262.1550	290.1499	**AF**	191.1179	219.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.0	1020.5240	0.0800	DTDIIAAFR
33.0	1020.5240	0.0800	DTDIIAAFR
33.0	1020.5240	0.0800	DTDILAAFR
33.0	1020.5240	0.0800	DTDILAAFR
33.0	1020.5240	0.0800	DTDILAAFR
33.0	1020.5240	0.0800	DTDILAAFR
33.0	1020.5240	0.0800	DTDILAAFR
33.0	1020.5240	0.0800	DTDILAAFR
33.0	1020.5240	0.0800	DTDILAAFR
33.0	1020.5240	0.0800	DTDILAAFR

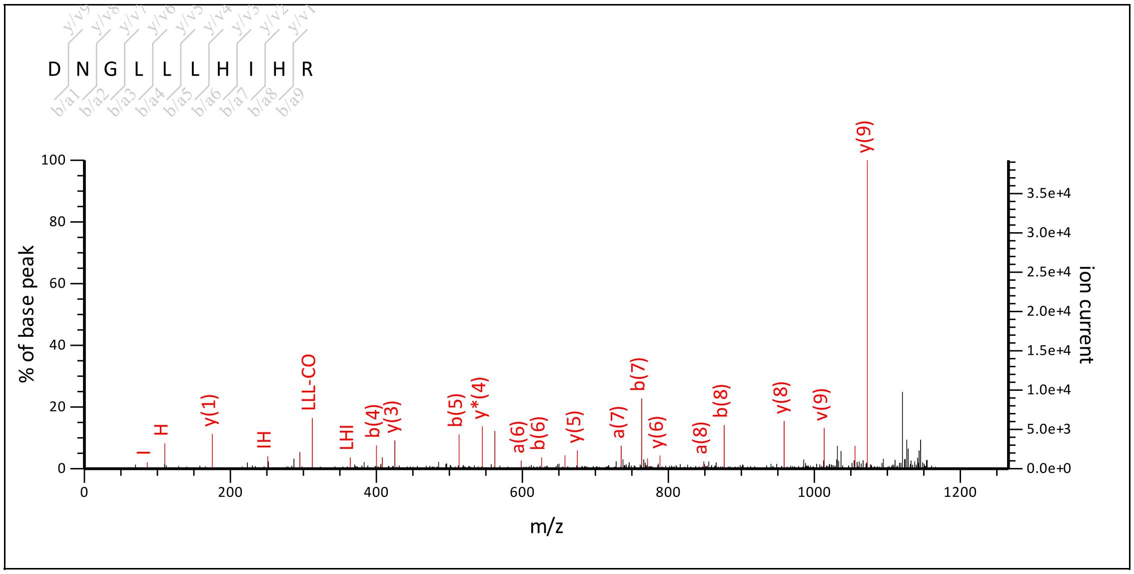
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **DNGLLLHIHR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 14: 1186.746424 from(1187.753700,1+) intensity(0.0000) index(8)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221215, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1265.95

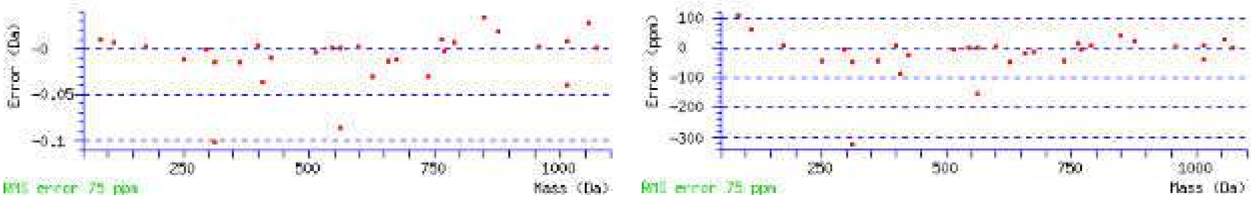
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1186.6571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 75 **Expect:** 0.0002
Matches : 37/151 fragment ions using 33 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	#
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		**D**						**10**
2	87.0553	202.0822	185.0557	184.0717	230.0771	213.0506	212.0666	159.0764		**N**	1013.6003	1012.6051		***1072.6374***	1055.6109	**9**
3	30.0338	259.1037	242.0771	241.0931	287.0986	270.0721	269.0880			**G**				***958.5945***	941.5679	**8**
4	86.0964	372.1878	355.1612	354.1772	**400.1827**	383.1561	382.1721	330.1408		**L**	843.4948	842.4995		901.5730	884.5465	**7**
5	86.0964	485.2718	468.2453	467.2613	**513.2667**	496.2402	495.2562	443.2249		**L**	730.4107	729.4155		***788.4890***	771.4624	**6**
6	86.0964	**598.3559**	581.3293	580.3453	**626.3508**	609.3243	608.3402	556.3089		**L**	617.3267	616.3314		***675.4049***	658.3784	**5**
7	110.0713	**735.4148**	718.3882	717.4042	**763.4097**	746.3832	745.3991			**H**	480.2677			***562.3208***	545.2943	**4**
8	86.0964	**848.4989**	831.4723	830.4883	**876.4938**	859.4672	858.4832	820.4676	834.4832	**I**	367.1837	380.2041	394.2197	***425.2619***	408.2354	**3**
9	110.0713	985.5578	968.5312	967.5472	**1013.5527**	996.5261	995.5421			**H**	230.1248			***312.1779***	295.1513	**2**
10	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NG	144.0768	172.0717	**NGL**	257.1608	285.1557	**NGLL**	370.2449	398.2398
NGLLL	483.3289	511.3239	**NGLLLH**	620.3879	648.3828	**GL**	143.1179	171.1128
GLL	256.2020	284.1969	**GLLL**	369.2860	397.2809	**GLLLH**	506.3449	534.3398
GLLLHI	619.4290	647.4239	**LL**	199.1805	227.1754	**LLL**	312.2646	340.2595
LLLH	449.3235	477.3184	**LLLHI**	562.4075	590.4024	**LLLHIH**	699.4664	727.4614
LL	199.1805	227.1754	**LLH**	336.2394	364.2343	**LLHI**	449.3235	477.3184
LLHIH	586.3824	614.3773	**LH**	223.1553	251.1503	**LHI**	336.2394	364.2343
LHIH	473.2983	501.2932	**HI**	223.1553	251.1503	**HIH**	360.2142	388.2092

IH	223.1553	251.1503						



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
75.5	1186.6571	0.0893	DNGILIHIHR
75.5	1186.6571	0.0893	DNGILLHIHR
75.5	1186.6571	0.0893	DNGILLHIHR
75.5	1186.6571	0.0893	DNGILLHIHR
75.5	1186.6571	0.0893	DNGLILHIHR
75.5	1186.6571	0.0893	DNGLILHIHR
75.5	1186.6571	0.0893	DNGLLIHIHR
75.5	1186.6571	0.0893	DNGLLIHIHR
75.5	1186.6571	0.0893	DNGLLLHIHR
75.5	1186.6571	0.0893	DNGLLLHIHR

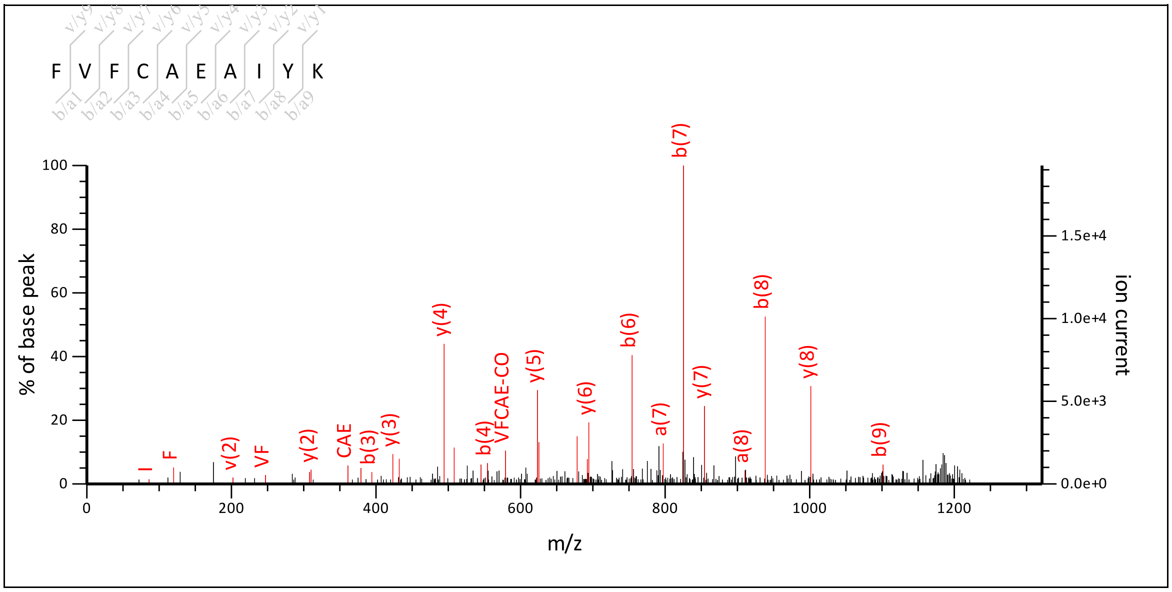
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **FVFCAEAIYK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 16: 1246.683724 from(1247.691000,1+) intensity(0.0000) index(9)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221211, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1321.38

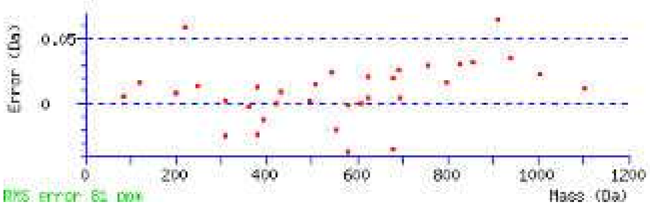
Label all possible matches ○ Label matches used for scoring ●

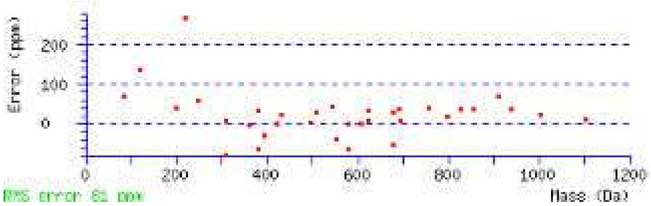
Monoisotopic mass of neutral peptide Mr(calc): 1246.6056
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 0.026
Matches : 38/129 fragment ions using 48 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	120.0808	**120.0808**		148.0757		44.0495		**F**							**10**
2	72.0808	**219.1492**		***247.1441***		205.1335		**V**	1056.4819	1069.5023		1100.5445	1083.5179	1082.5339	**9**
3	120.0808	366.2176		***394.2125***				**F**	909.4135			**1001.4761**	984.4495	983.4655	**8**
4	133.0430	526.2483		***554.2432***		437.2547		**C**	749.3828	748.3876		**854.4077**	837.3811	836.3971	**7**
5	44.0495	597.2854		***625.2803***				**A**	678.3457			**694.3770**	677.3505	676.3665	**6**
6	102.0550	726.3280	708.3174	***754.3229***	736.3123	668.3225		**E**	549.3031	548.3079		**623.3399**	606.3134	605.3293	**5**
7	44.0495	**797.3651**	779.3545	***825.3600***	807.3494			**A**	478.2660			**494.2973**	477.2708		**4**
8	86.0964	**910.4491**	892.4386	***938.4441***	920.4335	882.4178	896.4335	**I**	365.1819	378.2023	392.2180	**423.2602**	406.2336		**3**
9	136.0757	1073.5125	1055.5019	***1101.5074***	1083.4968			**Y**	202.1186			**310.1761**	293.1496		**2**
10	101.1073							**K**	74.0237	73.0284		147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VF	219.1492	247.1441	**VFC**	379.1798	407.1748	**VFCA**	450.2170	478.2119
VFCAE	579.2595	607.2545	**VFCAEA**	650.2967	678.2916	**FC**	280.1114	308.1063
FCA	351.1485	379.1435	**FCAE**	480.1911	508.1860	**FCAEA**	551.2282	579.2232
FCAEAI	664.3123	692.3072	**CA**	204.0801	232.0750	**CAE**	333.1227	361.1176
CAEA	404.1598	432.1547	**CAEAI**	517.2439	545.2388	**CAEAIY**	680.3072	708.3021
AE	173.0921	201.0870	**AEA**	244.1292	272.1241	**AEAI**	357.2132	385.2082

AEAIY	520.2766	548.2715	**EA**	173.0921	201.0870	**EAI**	286.1761	314.1710
EAIY	449.2395	477.2344	**AI**	157.1335	185.1285	**AIY**	320.1969	348.1918
IY	249.1598	277.1547						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.9	1246.6056	0.0781	FVFCAEAIYK
53.9	1246.6056	0.0781	FVFCAEAIYK
53.9	1246.6056	0.0781	FVFCAEAIYK
53.9	1246.6056	0.0781	FVFCAEAIYK
53.9	1246.6056	0.0781	FVFCAEAIYK
53.9	1246.6056	0.0781	FVFCAEAIYK
53.9	1246.6056	0.0781	FVFCAEAIYK
53.9	1246.6056	0.0781	FVFCAEALYK
53.9	1246.6056	0.0781	FVFCAEALYK
53.9	1246.6056	0.0781	FVFCAEALYK

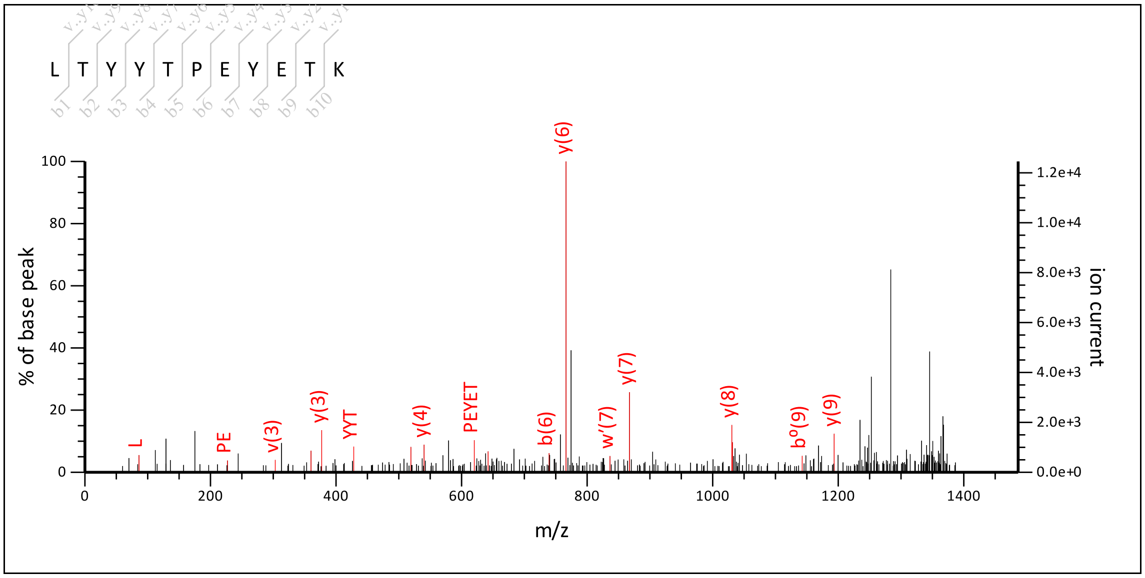
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **LTYYTPEYETK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 18: 1406.744524 from(1407.751800,1+) intensity(0.0000) index(11)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221218, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1486.6

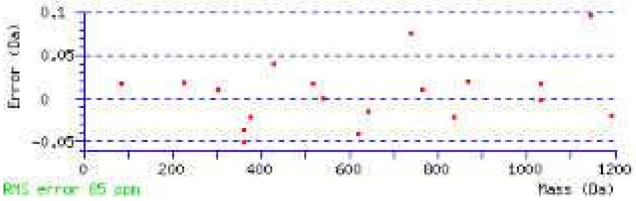
Label all possible matches ○ Label matches used for scoring ●

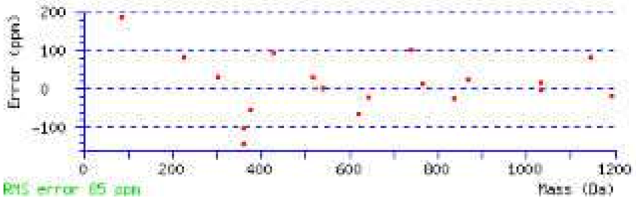
Monoisotopic mass of neutral peptide Mr(calc): 1406.6605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 58
Matches : 22/161 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		44.0495		L							11
2	74.0600	187.1441	169.1335	215.1390	197.1285	171.1492	173.1285	T	1248.5419	1261.5623	1263.5416	1294.5838	1277.5572	1276.5732	10
3	136.0757	350.2074	332.1969	378.2023	360.1918			Y	1085.4786			***1193.5361***	1176.5096	1175.5255	9
4	136.0757	513.2708	495.2602	541.2657	523.2551			Y	922.4153			***1030.4728***	1013.4462	1012.4622	8
5	74.0600	614.3184	596.3079	**642.3134**	624.3028	598.3235	600.3028	T	821.3676	834.3880	836.3672	***867.4094***	850.3829	849.3989	7
6	70.0651	711.3712	693.3606	**739.3661**	721.3556	685.3556		P	724.3148	723.3196		***766.3618***	749.3352	748.3512	6
7	102.0550	840.4138	822.4032	868.4087	850.3981	782.4083		E	595.2722	594.2770		669.3090	652.2824	651.2984	5
8	136.0757	1003.4771	985.4666	**1031.4720**	1013.4615			Y	432.2089			***540.2664***	523.2399	522.2558	4
9	102.0550	1132.5197	1114.5092	1160.5146	1142.5041	1074.5142		E	303.1663	302.1710		***377.2031***	360.1765	359.1925	3
10	74.0600	1233.5674	1215.5568	1261.5623	1243.5517	1217.5725	1219.5517	T	202.1186	215.1390	217.1183	248.1605	231.1339	230.1499	2
11	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TY	237.1234	265.1183	TYY	400.1867	428.1816	TYYT	501.2344	529.2293
TYYTP	598.2871	626.2821	YY	299.1390	327.1339	YYT	400.1867	428.1816
YYTP	497.2395	525.2344	YYTPE	626.2821	654.2770	YT	237.1234	265.1183
YTP	334.1761	362.1710	YTPE	463.2187	491.2136	YTPEY	626.2821	654.2770
TP	171.1128	199.1077	TPE	300.1554	328.1503	TPEY	463.2187	491.2136
TPEYE	592.2613	620.2562	TPEYET	693.3090	721.3039	PE	199.1077	227.1026

PEY	362.1710	390.1660	**PEYE**	491.2136	519.2086	**PEYET**	592.2613	620.2562
EY	265.1183	293.1132	**EYE**	394.1609	422.1558	**EYET**	495.2086	523.2035
YE	265.1183	293.1132	**YET**	366.1660	394.1609	**ET**	203.1026	231.0975





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.3	1406.1685	0.5760	LTYYTPEYZTK
20.1	1406.6605	0.0840	ITYYTPEYETK
20.1	1406.6605	0.0840	ITYYTPEYETK
20.1	1406.6605	0.0840	LTYYTPEYETK
20.1	1406.6605	0.0840	LTYYTPEYETK
20.1	1406.6605	0.0840	LTYYTPEYETK
20.1	1406.6605	0.0840	LTYYTPEYETK
20.1	1406.6605	0.0840	LTYYTPEYETK
20.1	1406.6605	0.0840	LTYYTPEYETK
20.1	1406.6605	0.0840	LTYYTPEYETK

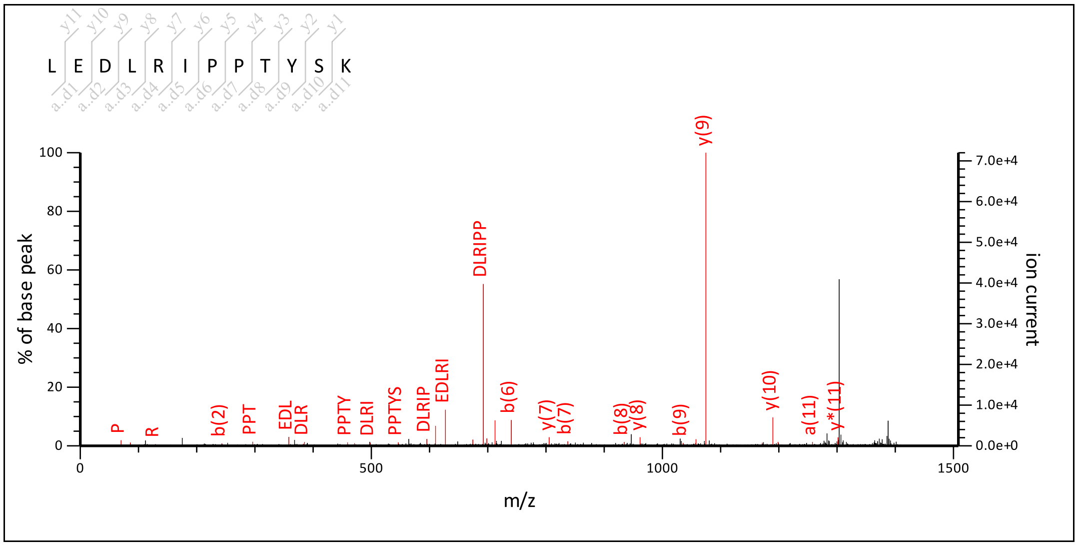
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **LEDLRIPPTYSK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 20: 1430.873124 from(1431.880400,1+) intensity(0.0000) index(12)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221216, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1508.44

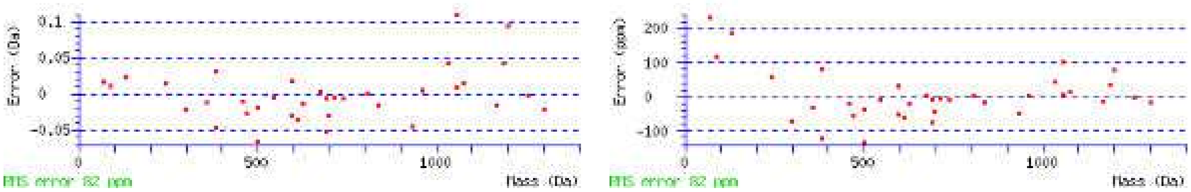
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1430.7769
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.12
Matches : 42/202 fragment ions using 70 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	**86.0964**			114.0913			44.0495		L						
2	102.0550	215.1390		197.1285	***243.1339***		225.1234	157.1335		E	1244.6634	1243.6681		1318.7001	1301.6736	130
3	88.0393	330.1660		312.1554	***358.1609***		340.1503	286.1761		D	1129.6364	1128.6412		**1189.6576**	1172.6310	117
4	86.0964	443.2500		425.2395	***471.2449***		453.2344	401.2031		L	1016.5524	1015.5571		**1074.6306**	1057.6041	105
5	129.1135	599.3511	582.3246	581.3406	***627.3461***	610.3195	609.3355	514.2871		R	860.4512	859.4560		**961.5465**	944.5200	94
6	86.0964	**712.4352**	695.4087	694.4246	***740.4301***	723.4036	722.4196	684.4039	698.4196	I	747.3672	760.3876	774.4032	**805.4454**	788.4189	78
7	70.0651	809.4880	792.4614	791.4774	***837.4829***	820.4563	819.4723	783.4723		P	650.3144	649.3192		**692.3614**	675.3348	67
8	70.0651	906.5407	889.5142	888.5302	***934.5356***	917.5091	916.5251	880.5251		P	553.2617	552.2664		**595.3086**	578.2821	57
9	74.0600	1007.5884	990.5619	989.5778	***1035.5833***	1018.5568	1017.5728	991.5935	993.5728	T	452.2140	465.2344	467.2136	**498.2558**	481.2293	48
10	136.0757	1170.6517	1153.6252	1152.6412	***1198.6467***	1181.6201	1180.6361			Y	289.1506			397.2082	380.1816	37
11	60.0444	**1257.6838**	1240.6572	1239.6732	1285.6787	1268.6521	1267.6681	1241.6889		S	202.1186	201.1234		234.1448	217.1183	21
12	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ED	217.0819	245.0768	**EDL**	330.1660	358.1609	**EDLR**	486.2671	514.2620
EDLRI	599.3511	627.3461	**EDLRIP**	696.4039	724.3988	**DL**	201.1234	229.1183
DLR	357.2245	385.2194	**DLRI**	470.3085	498.3035	**DLRIP**	567.3613	595.3562
DLRIPP	664.4141	692.4090	**LR**	242.1975	270.1925	**LRI**	355.2816	383.2765
LRIP	452.3344	480.3293	**LRIPP**	549.3871	577.3820	**LRIPPT**	650.4348	678.4297
RI	242.1975	270.1925	**RIP**	339.2503	367.2452	**RIPP**	436.3031	464.2980
RIPPT	537.3507	565.3457	**IP**	183.1492	211.1441	**IPP**	280.2020	308.1969
IPPT	381.2496	409.2445	**IPPTY**	544.3130	572.3079	**IPPTYS**	631.3450	659.3399
PP	167.1179	195.1128	**PPT**	268.1656	296.1605	**PPTY**	431.2289	459.2238

PPTYS	518.2609	546.2558	**PT**	171.1128	199.1077	**PTY**	334.1761	362.1710
PTYS	421.2082	449.2031	**TY**	237.1234	265.1183	**TYS**	324.1554	352.1503
YS	223.1077	251.1026						



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.7	1430.7769	0.0962	LEDIRIPPTYSK
46.7	1430.7769	0.0962	LEDLRIPPTYSK
46.7	1430.7769	0.0962	LEDLRIPPTYSK
46.7	1430.7769	0.0962	LEDLRIPPTYSK
46.7	1430.7769	0.0962	LEDLRIPPTYSK
37.7	1430.7769	0.0962	LEDLRIPTPYSK
30.5	1430.7374	0.1358	EPMRLLQEMIR
30.3	1430.7769	0.0962	LEDIRIPPSYTK
30.3	1430.7769	0.0962	LEDIRIPPSYTK
30.3	1430.7769	0.0962	LEDLRIPPSYTK

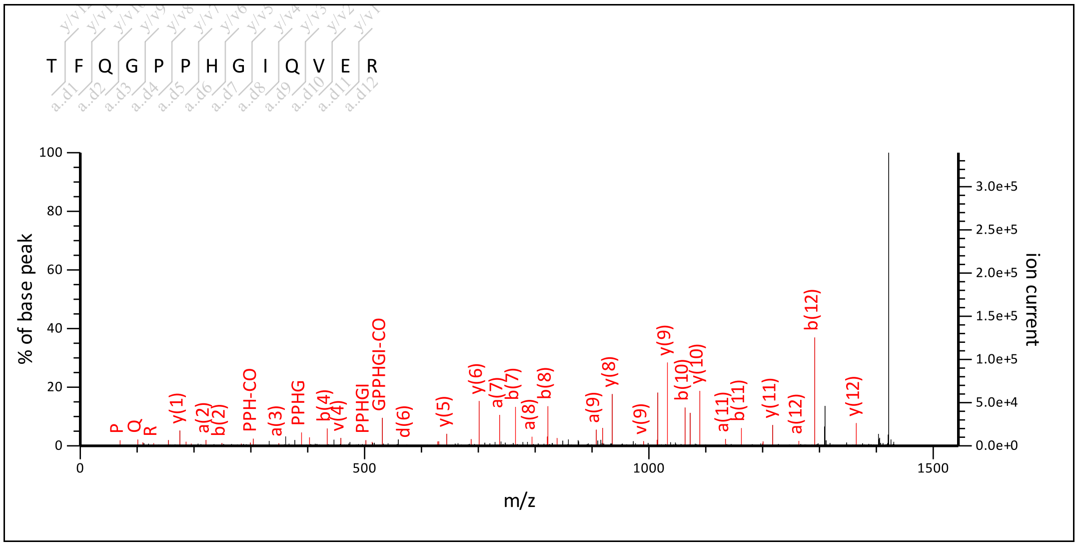
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **TFQGPPHGIQVER**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 22: 1464.842824 from(1465.850100,1+) intensity(0.0000) index(13)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221197, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1544.27

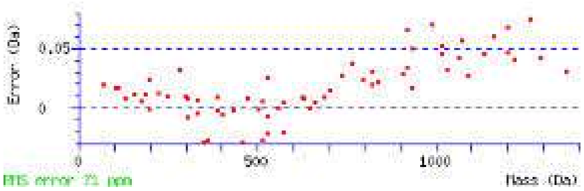
Label all possible matches ○ Label matches used for scoring ●

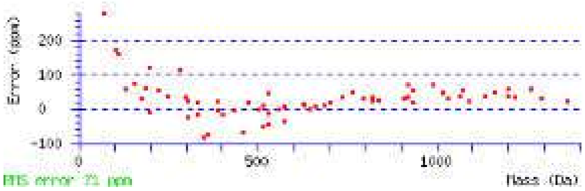
Monoisotopic mass of neutral peptide Mr(calc): 1464.7474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 104 **Expect:** 2.8e-07
Matches : 72/229 fragment ions using 70 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	120.0808	**221.1285**		203.1179	**249.1234**		231.1128			F	1272.6444			***1364.7070***	1347.6804	134
3	101.0709	**349.1870**	332.1605	331.1765	377.1819	360.1554	359.1714	292.1656		Q	1144.5858	1143.5905		***1217.6385***	1200.6120	119
4	30.0338	406.2085	389.1819	388.1979	**434.2034**	417.1769	416.1928			G				***1089.5800***	1072.5534	107
5	70.0651	503.2613	486.2347	485.2507	**531.2562**	514.2296	513.2456	477.2456		P	990.5116	989.5163		***1032.5585***	1015.5320	101
6	70.0651	600.3140	583.2875	582.3035	**628.3089**	611.2824	610.2984	574.2984		P	893.4588	892.4635		***935.5057***	918.4792	91
7	110.0713	**737.3729**	720.3464	719.3624	**765.3679**	748.3413	747.3573			H	756.3999			***838.4530***	821.4264	82
8	30.0338	**794.3944**	777.3679	776.3838	**822.3893**	805.3628	804.3787			G				***701.3941***	684.3675	68
9	86.0964	**907.4785**	890.4519	889.4679	**935.4734**	918.4468	917.4628	879.4472	893.4628	I	586.2944	599.3148	613.3304	***644.3726***	627.3461	62
10	101.0709	1035.5370	1018.5105	1017.5265	**1063.5320**	1046.5054	1045.5214	978.5156		Q	458.2358	457.2405		***531.2885***	514.2620	51
11	72.0808	**1134.6055**	1117.5789	1116.5949	**1162.6004**	1145.5738	1144.5898	1120.5898		V	359.1674	372.1878		***403.2300***	386.2034	38
12	102.0550	**1263.6480**	1246.6215	1245.6375	**1291.6430**	1274.6164	1273.6324	1205.6426		E	230.1248	229.1295		***304.1615***	287.1350	28
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQG	305.1608	333.1557	FQGP	402.2136	430.2085
FQGPP	499.2663	527.2613	FQGPPH	636.3253	664.3202	FQGPPHG	693.3467	721.3416
QG	158.0924	186.0873	QGP	255.1452	283.1401	QGPP	352.1979	380.1928
QGPPH	489.2568	517.2518	QGPPHG	546.2783	574.2732	QGPPHGI	659.3624	687.3573
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPH	361.1983	389.1932
GPPHG	418.2197	446.2146	GPPHGI	531.3038	559.2987	GPPHGIQ	659.3624	687.3573
PP	167.1179	195.1128	PPH	304.1768	332.1717	PPHG	361.1983	389.1932
PPHGI	474.2823	502.2772	PPHGIQ	602.3409	630.3358	PH	207.1240	235.1190

PHG	264.1455	292.1404	**PHGI**	377.2296	405.2245	**PHGIQ**	505.2881	533.2831
PHGIQV	604.3566	632.3515	**HG**	167.0927	195.0877	**HGI**	280.1768	308.1717
HGIQ	408.2354	436.2303	**HGIQV**	507.3038	535.2987	**HGIQVE**	636.3464	664.3413
GI	143.1179	171.1128	**GIQ**	271.1765	299.1714	**GIQV**	370.2449	398.2398
GIQVE	499.2875	527.2824	**IQ**	214.1550	242.1499	**IQV**	313.2234	341.2183
IQVE	442.2660	470.2609	**QV**	200.1394	228.1343	**QVE**	329.1819	357.1769
VE	201.1234	229.1183						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
104.1	1464.7838	0.0591	TFKGPPHGIQVER
104.1	1464.7838	0.0591	TFKGPPHGIQVER
104.1	1464.7838	0.0591	TFQGPPHGIKVER
104.1	1464.7838	0.0591	TFQGPPHGIKVER
104.1	1464.7474	0.0954	TFQGPPHGIQVER
104.1	1464.7474	0.0954	TFQGPPHGIQVER
104.1	1464.7474	0.0954	TFQGPPHGIQVER
104.1	1464.7474	0.0954	TFQGPPHGIQVER
104.1	1464.7474	0.0954	TFQGPPHGIQVER
104.1	1464.7474	0.0954	TFQGPPHGIQVER

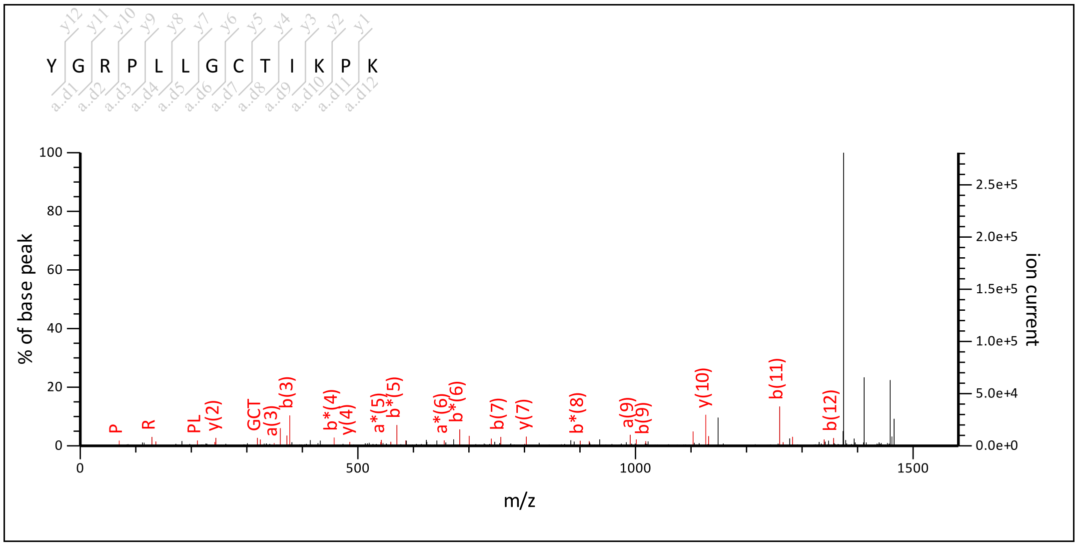
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of YGRPLLGCTIKPK
Found in gi|11466795 in NCBInr, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 24: 1501.935024 from(1502.942300,1+) intensity(0.0000) index(14)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221198, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



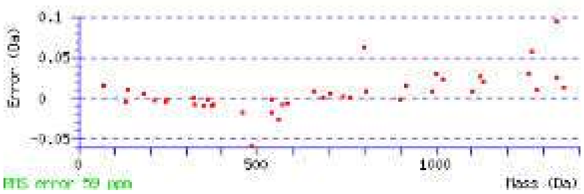
Label all possible matches ○ Label matches used for scoring ●

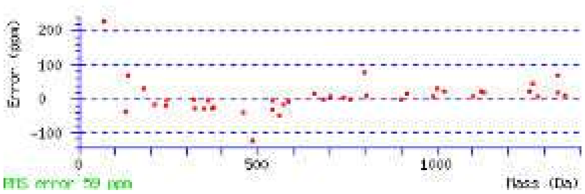
Monoisotopic mass of neutral peptide Mr(calc): 1501.8439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 0.014
Matches : 43/211 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	136.0757	**136.0757**			164.0706			44.0495		Y						
2	30.0338	193.0972			221.0921					G				***1339.7879***	1322.7613	132
3	129.1135	**349.1983**	332.1717		***377.1932***	360.1666		264.1343		R	1181.6711	1180.6758		***1282.7664***	1265.7398	126
4	70.0651	446.2510	429.2245		474.2459	457.2194		420.2354		P	1084.6183	1083.6231		***1126.6653***	1109.6387	110
5	86.0964	**559.3351**	542.3085		587.3300	570.3035		517.2881		L	971.5343	970.5390		1029.6125	1012.5860	101
6	86.0964	672.4192	655.3926		***700.4141***	683.3875		630.3722		L	858.4502	857.4550		***916.5285***	899.5019	89
7	30.0338	729.4406	712.4141		***757.4355***	740.4090				G				***803.4444***	786.4178	78
8	133.0430	889.4713	872.4447		917.4662	900.4396		800.4777		C	641.3981	640.4028		746.4229	729.3964	72
9	74.0600	**990.5189**	973.4924	972.5084	***1018.5139***	1001.4873	1000.5033	974.5240	976.5033	T	540.3504	553.3708	555.3501	***586.3923***	569.3657	56
10	86.0964	**1103.6030**	1086.5765	1085.5924	***1131.5979***	1114.5714	1113.5874	1075.5717	1089.5874	I	427.2663	440.2867	454.3024	***485.3446***	468.3180	
11	101.1073	1231.6980	1214.6714	1213.6874	***1259.6929***	1242.6663	1241.6823	1174.6401		K	299.1714	298.1761		***372.2605***	355.2340	
12	70.0651	1328.7507	1311.7242	1310.7402	***1356.7457***	1339.7191	1338.7351	1302.7351		P	202.1186	201.1234		***244.1656***	227.1390	
13	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GR	186.1349	214.1299	**GRP**	283.1877	311.1826	**GRPL**	396.2718	424.2667
GRPLL	509.3558	537.3507	**GRPLLG**	566.3773	594.3722	**RP**	226.1662	254.1612
RPL	339.2503	367.2452	**RPLL**	452.3344	480.3293	**RPLLG**	509.3558	537.3507
RPLLGC	669.3865	697.3814	**PL**	183.1492	211.1441	**PLL**	296.2333	324.2282
PLLG	353.2547	381.2496	**PLLGC**	513.2854	541.2803	**PLLGCT**	614.3330	642.3280
LL	199.1805	227.1754	**LLG**	256.2020	284.1969	**LLGC**	416.2326	444.2275
LLGCT	517.2803	545.2752	**LLGCTI**	630.3643	658.3593	**LG**	143.1179	171.1128
LGC	303.1485	331.1435	**LGCT**	404.1962	432.1911	**LGCTI**	517.2803	545.2752

LGCTIK	645.3752	673.3702	**GC**	190.0645	218.0594	**GCT**	291.1122	319.1071
GCTI	404.1962	432.1911	**GCTIK**	532.2912	560.2861	**GCTIKP**	629.3439	657.3389
CT	234.0907	262.0856	**CTI**	347.1748	375.1697	**CTIK**	475.2697	503.2646
CTIKP	572.3225	600.3174	**TI**	187.1441	215.1390	**TIK**	315.2391	343.2340
TIKP	412.2918	440.2867	**IK**	214.1914	242.1863	**IKP**	311.2442	339.2391
KP	198.1601	226.1550						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.7	1501.8439	0.0911	YGRPILGCTIKPK
56.7	1501.8439	0.0911	YGRPILGCTIKPK
56.7	1501.8439	0.0911	YGRPLIGCTIKPK
56.7	1501.8439	0.0911	YGRPLLGCTIKPK
56.7	1501.8439	0.0911	YGRPLLGCTIKPK
56.7	1501.8439	0.0911	YGRPLLGCTIKPK
56.7	1501.8439	0.0911	YGRPLLGCTIKPK
56.7	1501.8439	0.0911	YGRPLLGCTIKPK
56.7	1501.8439	0.0911	YGRPLLGCTIKPK
56.7	1501.8439	0.0911	YGRPLLGCTIKPK

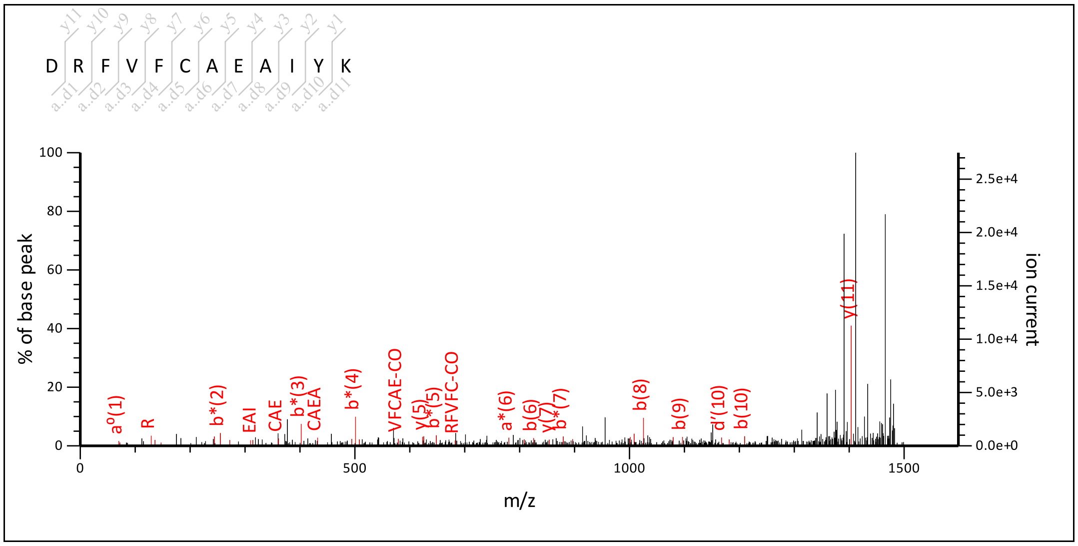
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **DRFVFCAEAIYK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 25: 1517.831024 from(1518.838300,1+) intensity(0.0000) index(15)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221222, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1598.83

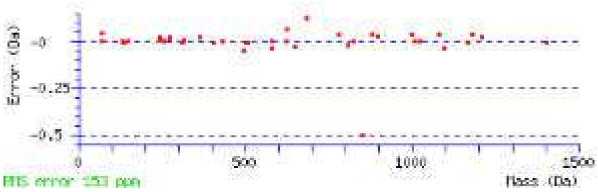
Label all possible matches ○ Label matches used for scoring ●

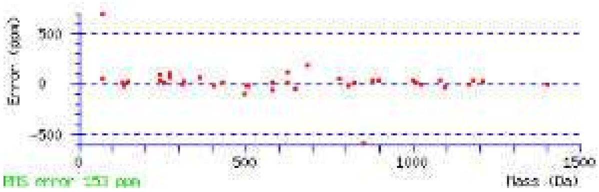
Monoisotopic mass of neutral peptide Mr(calc): 1517.7337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 1.8e+02
Matches : 39/194 fragment ions using 120 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D					
2	129.1135	244.1404	227.1139	226.1299	***272.1353***	255.1088	254.1248	159.0764		R	1302.6187	1301.6235		***1403.7140***	1386.6875
3	120.0808	391.2088	374.1823	373.1983	419.2037	402.1772	401.1932			F	1155.5503			1247.6129	1230.5864
4	72.0808	490.2772	473.2507	472.2667	518.2722	501.2456	500.2616	476.2616		V	1056.4819	1069.5023		1100.5445	1083.5179
5	120.0808	637.3457	620.3191	619.3351	665.3406	648.3140	647.3300			F	909.4135			***1001.4761***	984.4495
6	133.0430	797.3763	780.3498	779.3657	***825.3712***	808.3447	807.3607	708.3828		C	749.3828	748.3876		***854.4077***	837.3811
7	44.0495	868.4134	851.3869	850.4029	***896.4083***	879.3818	878.3978			A	678.3457			694.3770	677.3505
8	102.0550	997.4560	980.4295	979.4454	***1025.4509***	1008.4244	1007.4404	939.4505		E	549.3031	548.3079		***623.3399***	606.3134
9	44.0495	1068.4931	1051.4666	1050.4826	***1096.4880***	1079.4615	1078.4775			A	478.2660			***494.2973***	477.2708
10	86.0964	1181.5772	1164.5506	1163.5666	***1209.5721***	1192.5456	1191.5615	1153.5459	1167.5615	I	365.1819	378.2023	392.2180	423.2602	406.2336
11	136.0757	1344.6405	1327.6140	1326.6300	1372.6354	1355.6089	1354.6249			Y	202.1186			***310.1761***	293.1496
12	101.1073									K	74.0237	73.0284		***147.1128***	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RF	276.1819	304.1768	**RFV**	375.2503	403.2452	**RFVF**	522.3187	550.3136
RFVFC	682.3494	710.3443	**FV**	219.1492	247.1441	**FVF**	366.2176	394.2125
FVFC	526.2483	554.2432	**FVFCA**	597.2854	625.2803	**VF**	219.1492	247.1441
VFC	379.1798	407.1748	**VFCA**	450.2170	478.2119	**VFCAE**	579.2595	607.2545
VFCAEA	650.2967	678.2916	**FC**	280.1114	308.1063	**FCA**	351.1485	379.1435
FCAE	480.1911	508.1860	**FCAEA**	551.2282	579.2232	**FCAEAI**	664.3123	692.3072
CA	204.0801	232.0750	**CAE**	333.1227	361.1176	**CAEA**	404.1598	432.1547
CAEAI	517.2439	545.2388	**CAEAIY**	680.3072	708.3021	**AE**	173.0921	201.0870
AEA	244.1292	272.1241	**AEAI**	357.2132	385.2082	**AEAIY**	520.2766	548.2715

EA	173.0921	201.0870	**EAI**	286.1761	314.1710	**EAIY**	449.2395	477.2344
AI	157.1335	185.1285	**AIY**	320.1969	348.1918	**IY**	249.1598	277.1547





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.9	1517.7007	0.1304	DRFVMCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.9	1517.7337	0.0974	DRFVFCAEAIYK
14.3	1517.7337	0.0974	DRFVFCAEALYK

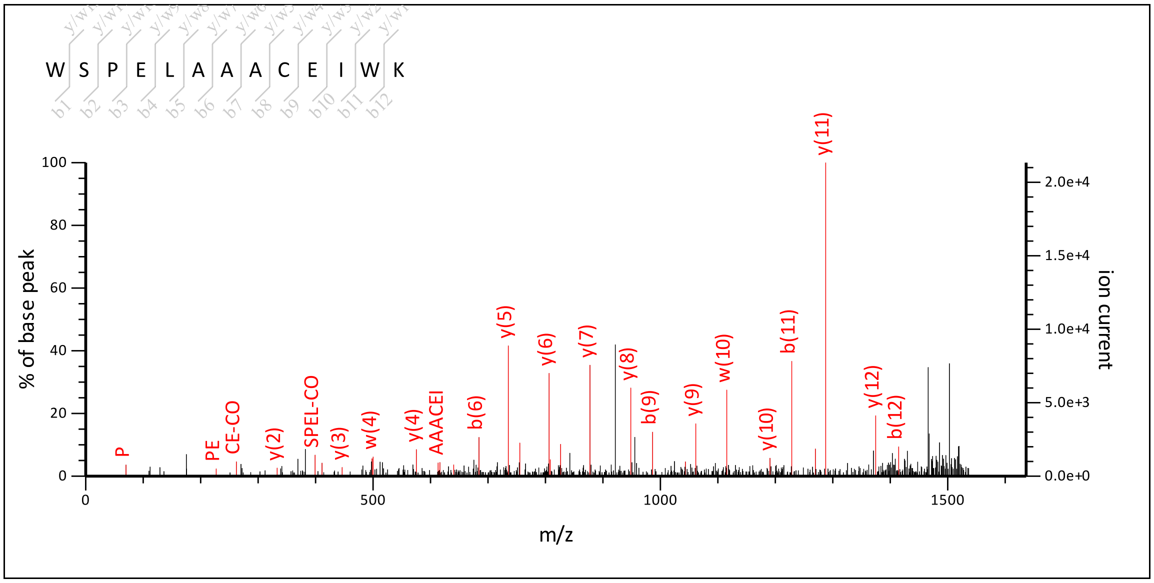
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 82**

MS/MS Fragmentation of **WSPELAAACEIWK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 27: 1559.830624 from(1560.837900,1+) intensity(0.0000) index(16)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221213, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1636.45

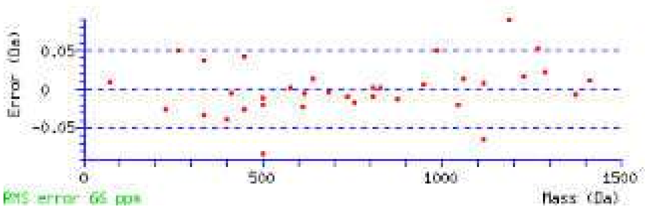
Label all possible matches ○ Label matches used for scoring ●

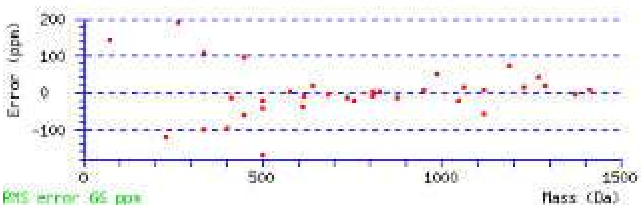
Monoisotopic mass of neutral peptide Mr(calc): 1559.7442
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 0.0017
Matches : 37/203 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	159.0917	159.0917		187.0866		44.0495		W							13
2	60.0444	246.1237	228.1131	274.1186	256.1081	230.1288		S	1342.6460	1341.6508		***1374.6722***	1357.6457	1356.6616	12
3	70.0651	343.1765	325.1659	371.1714	353.1608	317.1608		P	1245.5932	1244.5980		***1287.6402***	1270.6136	1269.6296	11
4	102.0550	472.2191	454.2085	**500.2140**	482.2034	414.2136		E	1116.5506	1115.5554		***1190.5874***	1173.5609	1172.5769	10
5	86.0964	585.3031	567.2926	**613.2980**	595.2875	543.2562		L	1003.4666	1002.4713		***1061.5448***	1044.5183	1043.5343	9
6	44.0495	656.3402	638.3297	**684.3352**	666.3246			A	932.4295			***948.4608***	931.4342	930.4502	8
7	44.0495	727.3774	709.3668	**755.3723**	737.3617			A	861.3924			***877.4237***	860.3971	859.4131	7
8	44.0495	798.4145	780.4039	**826.4094**	808.3988			A	790.3552			***806.3865***	789.3600	788.3760	6
9	133.0430	958.4451	940.4345	**986.4400**	968.4295	869.4516		C	630.3246	629.3293		***735.3494***	718.3229	717.3389	5
10	102.0550	1087.4877	1069.4771	**1115.4826**	1097.4721	1029.4822		E	501.2820	500.2867		***575.3188***	558.2922	557.3082	4
11	86.0964	1200.5718	1182.5612	**1228.5667**	1210.5561	1172.5405	1186.5561	I	388.1979	401.2183	415.2340	***446.2762***	429.2496		3
12	159.0917	1386.6511	1368.6405	**1414.6460**	1396.6354			W	202.1186			***333.1921***	316.1656		2
13	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SP	157.0972	185.0921	SPE	286.1397	314.1347	SPEL	399.2238	427.2187
SPELA	470.2609	498.2558	SPELAA	541.2980	569.2930	SPELAAA	612.3352	640.3301
PE	199.1077	227.1026	PEL	312.1918	340.1867	PELA	383.2289	411.2238
PELAA	454.2660	482.2609	PELAAA	525.3031	553.2980	PELAAAC	685.3338	713.3287

EL	215.1390	243.1339	**ELA**	286.1761	314.1710	**ELAA**	357.2132	385.2082
ELAAA	428.2504	456.2453	**ELAAAC**	588.2810	616.2759	**LA**	157.1335	185.1285
LAA	228.1707	256.1656	**LAAA**	299.2078	327.2027	**LAAAC**	459.2384	487.2333
LAAACE	588.2810	616.2759	**AA**	115.0866	143.0815	**AAA**	186.1237	214.1186
AAAC	346.1544	374.1493	**AAACE**	475.1969	503.1919	**AAACEI**	588.2810	616.2759
AA	115.0866	143.0815	**AAC**	275.1172	303.1122	**AACE**	404.1598	432.1547
AACEI	517.2439	545.2388	**AC**	204.0801	232.0750	**ACE**	333.1227	361.1176
ACEI	446.2068	474.2017	**ACEIW**	632.2861	660.2810	**CE**	262.0856	290.0805
CEI	375.1697	403.1646	**CEIW**	561.2490	589.2439	**EI**	215.1390	243.1339
EIW	401.2183	429.2132	**IW**	272.1757	300.1707			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.7	1559.7442	0.0864	WSPEIAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK
64.7	1559.7442	0.0864	WSPELAAACEIWK

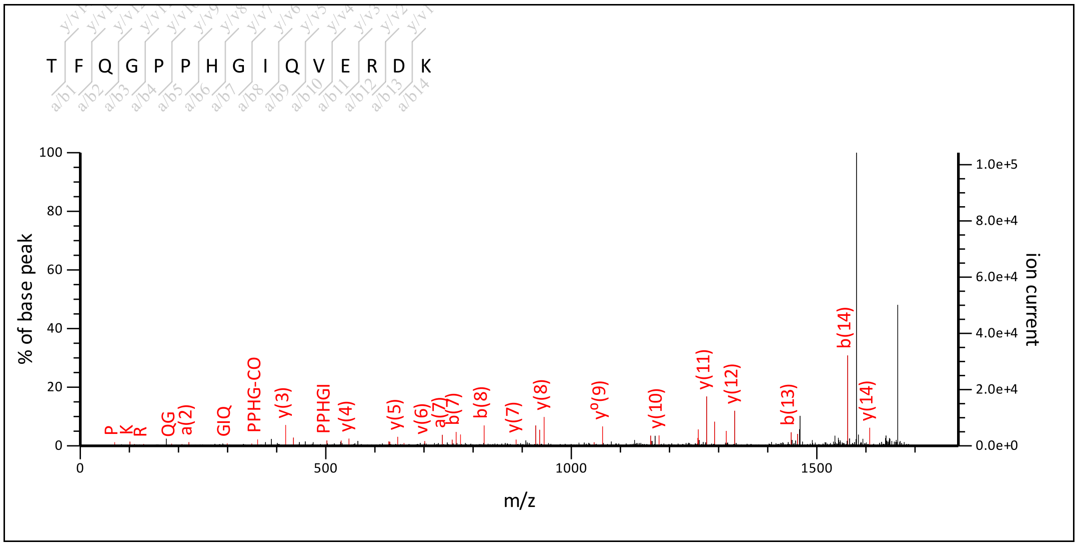
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **TFQGPPHGIQVERDK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 31: 1707.967824 from(1708.975100,1+) intensity(0.0000) index(18)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221209, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 1788.28

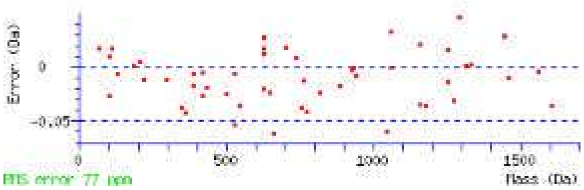
Label all possible matches ○ Label matches used for scoring ●

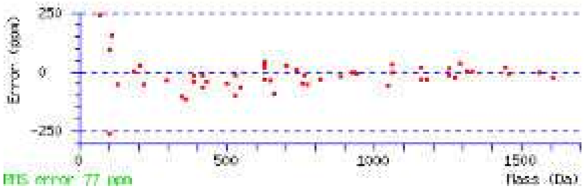
```
Monoisotopic mass of neutral peptide Mr(calc): 1707.8693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 86  Expect: 1.5e-05
Matches : 57/273 fragment ions using 68 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	120.0808	**221.1285**		203.1179	249.1234		231.1128			F	1515.7663			***1607.8289***	1590.8023	158
3	101.0709	**349.1870**	332.1605	331.1765	377.1819	360.1554	359.1714	292.1656		Q	1387.7077	1386.7124		***1460.7605***	1443.7339	144
4	30.0338	406.2085	389.1819	388.1979	***434.2034***	417.1769	416.1928			G				***1332.7019***	1315.6753	131
5	70.0651	503.2613	486.2347	485.2507	***531.2562***	514.2296	513.2456	477.2456		P	1233.6335	1232.6382		***1275.6804***	1258.6539	125
6	70.0651	600.3140	583.2875	582.3035	***628.3089***	611.2824	610.2984	574.2984		P	1136.5807	1135.5854		***1178.6276***	1161.6011	116
7	110.0713	**737.3729**	720.3464	719.3624	***765.3679***	748.3413	747.3573			H	999.5218			1081.5749	1064.5483	106
8	30.0338	794.3944	777.3679	776.3838	***822.3893***	805.3628	804.3787			G				***944.5160***	927.4894	92
9	86.0964	907.4785	890.4519	889.4679	***935.4734***	918.4468	917.4628	879.4472	893.4628	I	829.4163	842.4367	856.4523	***887.4945***	870.4680	86
10	101.0709	1035.5370	1018.5105	1017.5265	***1063.5320***	1046.5054	1045.5214	978.5156		Q	701.3577	700.3624		***774.4104***	757.3839	75
11	72.0808	1134.6055	1117.5789	1116.5949	***1162.6004***	1145.5738	1144.5898	1120.5898		V	602.2893	615.3097		***646.3519***	629.3253	62
12	102.0550	1263.6480	1246.6215	1245.6375	***1291.6430***	1274.6164	1273.6324	1205.6426		E	473.2467	472.2514		***547.2835***	530.2569	52
13	129.1135	1419.7492	1402.7226	1401.7386	***1447.7441***	1430.7175	1429.7335	1334.6852		R	317.1456	316.1503		***418.2409***	401.2143	40
14	88.0393	1534.7761	1517.7496	1516.7655	***1562.7710***	1545.7445	1544.7605	1490.7863		D	202.1186	201.1234		262.1397	245.1132	24
15	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQG	305.1608	333.1557	FQGP	402.2136	430.2085
FQGPP	499.2663	527.2613	FQGPPH	636.3253	664.3202	FQGPPHG	693.3467	721.3416
QG	158.0924	186.0873	QGP	255.1452	283.1401	QGPP	352.1979	380.1928
QGPPH	489.2568	517.2518	QGPPHG	546.2783	574.2732	QGPPHGI	659.3624	687.3573
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPH	361.1983	389.1932
GPPHG	418.2197	446.2146	GPPHGI	531.3038	559.2987	GPPHGIQ	659.3624	687.3573

PP	167.1179	195.1128	**PPH**	304.1768	332.1717	**PPHG**	361.1983	389.1932
PPHGI	474.2823	502.2772	**PPHGIQ**	602.3409	630.3358	**PH**	207.1240	235.1190
PHG	264.1455	292.1404	**PHGI**	377.2296	405.2245	**PHGIQ**	505.2881	533.2831
PHGIQV	604.3566	632.3515	**HG**	167.0927	195.0877	**HGI**	280.1768	308.1717
HGIQ	408.2354	436.2303	**HGIQV**	507.3038	535.2987	**HGIQVE**	636.3464	664.3413
GI	143.1179	171.1128	**GIQ**	271.1765	299.1714	**GIQV**	370.2449	398.2398
GIQVE	499.2875	527.2824	**GIQVER**	655.3886	683.3835	**IQ**	214.1550	242.1499
IQV	313.2234	341.2183	**IQVE**	442.2660	470.2609	**IQVER**	598.3671	626.3620
QV	200.1394	228.1343	**QVE**	329.1819	357.1769	**QVER**	485.2831	513.2780
QVERD	600.3100	628.3049	**VE**	201.1234	229.1183	**VER**	357.2245	385.2194
VERD	472.2514	500.2463	**ER**	258.1561	286.1510	**ERD**	373.1830	401.1779
RD	244.1404	272.1353						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
90.9	1707.8805	0.0873	TFQGPPHGIQVERSR
87.4	1707.8363	0.1316	TMQGPPHGIQVERDK
87.4	1707.8693	0.0985	TFQGPPHGLQVERDK
87.4	1707.8693	0.0985	TFQGPPHGLQVERDK
85.9	1707.8693	0.0985	TFQGPPHGIQVERDK
85.9	1707.8693	0.0985	TFQGPPHGIQVERDK
85.9	1707.8693	0.0985	TFQGPPHGIQVERDK
85.9	1707.8693	0.0985	TFQGPPHGIQVERDK
85.9	1707.8693	0.0985	TFQGPPHGIQVERDK
85.9	1707.8693	0.0985	TFQGPPHGIQVERDK

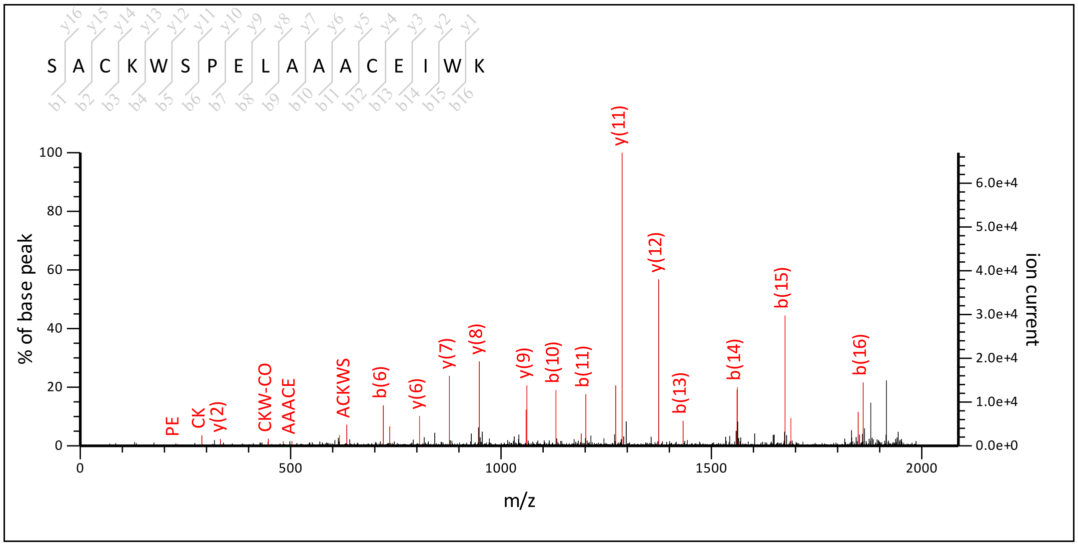
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **SACKWSPELAAACEIWK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 35: 2006.040424 from(2007.047700,1+) intensity(0.0000) index(20)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221203, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 2087.04

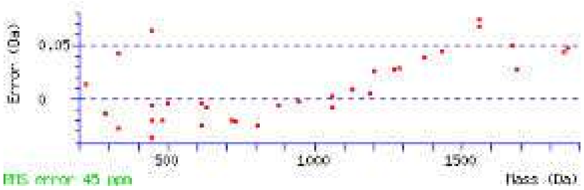
Label all possible matches ○ Label matches used for scoring ●

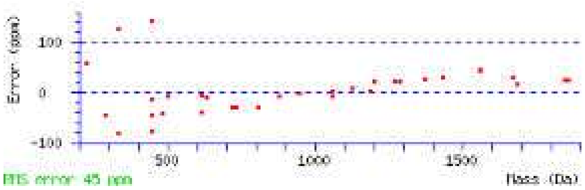
Monoisotopic mass of neutral peptide Mr(calc): 2005.9390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 111 **Expect:** 3.3e-08
Matches : 36/305 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S						
2	44.0495	131.0815		113.0709	159.0764		141.0659			A	1903.8830			1919.9143	1902.8877	19
3	133.0430	291.1122		273.1016	319.1071		301.0965	202.1186		C	1743.8523	1742.8571		***1848.8771***	1831.8506	18
4	101.1073	419.2071	402.1806	401.1966	***447.2020***	430.1755	429.1915	362.1493		K	1615.7573	1614.7621		***1688.8465***	1671.8199	16
5	159.0917	605.2864	588.2599	587.2759	***633.2813***	616.2548	615.2708			W	1429.6780			***1560.7515***	1543.7250	15
6	60.0444	692.3185	675.2919	674.3079	***720.3134***	703.2868	702.3028	676.3235		S	1342.6460	1341.6508		***1374.6722***	1357.6457	13
7	70.0651	789.3712	772.3447	771.3607	817.3661	800.3396	799.3556	763.3556		P	1245.5932	1244.5980		***1287.6402***	1270.6136	12
8	102.0550	918.4138	901.3873	900.4032	946.4087	929.3822	928.3982	860.4083		E	1116.5506	1115.5554		***1190.5874***	1173.5609	11
9	86.0964	1031.4979	1014.4713	1013.4873	***1059.4928***	1042.4662	1041.4822	989.4509		L	1003.4666	1002.4713		***1061.5448***	1044.5183	10
10	44.0495	1102.5350	1085.5084	1084.5244	***1130.5299***	1113.5034	1112.5193			A	932.4295			***948.4608***	931.4342	9
11	44.0495	1173.5721	1156.5456	1155.5615	***1201.5670***	1184.5405	1183.5565			A	861.3924			***877.4237***	860.3971	8
12	44.0495	1244.6092	1227.5827	1226.5987	***1272.6041***	1255.5776	1254.5936			A	790.3552			***806.3865***	789.3600	7
13	133.0430	1404.6399	1387.6133	1386.6293	***1432.6348***	1415.6082	1414.6242	1315.6463		C	630.3246	629.3293		***735.3494***	718.3229	7
14	102.0550	1533.6825	1516.6559	1515.6719	***1561.6774***	1544.6508	1543.6668	1475.6770		E	501.2820	500.2867		575.3188	558.2922	5
15	86.0964	1646.7665	1629.7400	1628.7560	***1674.7614***	1657.7349	1656.7509	1618.7352	1632.7509	I	388.1979	401.2183	415.2340	***446.2762***	429.2496	
16	159.0917	1832.8458	1815.8193	1814.8353	***1860.8408***	1843.8142	1842.8302			W	202.1186			***333.1921***	316.1656	
17	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AC	204.0801	232.0750	ACK	332.1751	360.1700	ACKW	518.2544	546.2493
ACKWS	605.2864	633.2813	CK	261.1380	289.1329	CKW	447.2173	475.2122
CKWS	534.2493	562.2442	CKWSP	631.3021	659.2970	KW	287.1866	315.1816
KWS	374.2187	402.2136	KWSP	471.2714	499.2663	KWSPE	600.3140	628.3089

WS	246.1237	274.1186	**WSP**	343.1765	371.1714	**WSPE**	472.2191	500.2140
WSPEL	585.3031	613.2980	**WSPELA**	656.3402	684.3352	**SP**	157.0972	185.0921
SPE	286.1397	314.1347	**SPEL**	399.2238	427.2187	**SPELA**	470.2609	498.2558
SPELAA	541.2980	569.2930	**SPELAAA**	612.3352	640.3301	**PE**	199.1077	227.1026
PEL	312.1918	340.1867	**PELA**	383.2289	411.2238	**PELAA**	454.2660	482.2609
PELAAA	525.3031	553.2980	**PELAAAC**	685.3338	713.3287	**EL**	215.1390	243.1339
ELA	286.1761	314.1710	**ELAA**	357.2132	385.2082	**ELAAA**	428.2504	456.2453
ELAAAC	588.2810	616.2759	**LA**	157.1335	185.1285	**LAA**	228.1707	256.1656
LAAA	299.2078	327.2027	**LAAAC**	459.2384	487.2333	**LAAACE**	588.2810	616.2759
AA	115.0866	143.0815	**AAA**	186.1237	214.1186	**AAAC**	346.1544	374.1493
AAACE	475.1969	503.1919	**AAACEI**	588.2810	616.2759	**AA**	115.0866	143.0815
AAC	275.1172	303.1122	**AACE**	404.1598	432.1547	**AACEI**	517.2439	545.2388
AC	204.0801	232.0750	**ACE**	333.1227	361.1176	**ACEI**	446.2068	474.2017
ACEIW	632.2861	660.2810	**CE**	262.0856	290.0805	**CEI**	375.1697	403.1646
CEIW	561.2490	589.2439	**EI**	215.1390	243.1339	**EIW**	401.2183	429.2132
IW	272.1757	300.1707						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
110.6	2005.9390	0.1015	SACKWSPELAAACEIWK
79.8	2006.8866	-0.8462	SACKWSPELAAACEIWE
66.8	2004.9615	1.0790	ETSKWSPELAAACEIWK
64.9	2006.8866	-0.8462	EACSWSPELAAACEIWK
27.4	2004.9977	1.0428	NSSRSYHIIAASESQSLR
22.7	2007.0380	-0.9976	MVSLLLETMSVDVAITNR
19.4	2005.0819	0.9585	AAPFGFLLKIVECLQSGR
18.5	2005.9844	0.0560	KDDDDDLLISSSGLSIWK
14.6	2006.0334	0.0071	QKTGASFILPASAQHGHEK
14.3	2005.9449	0.0956	SGVGCKMEIVPETEQGSAK

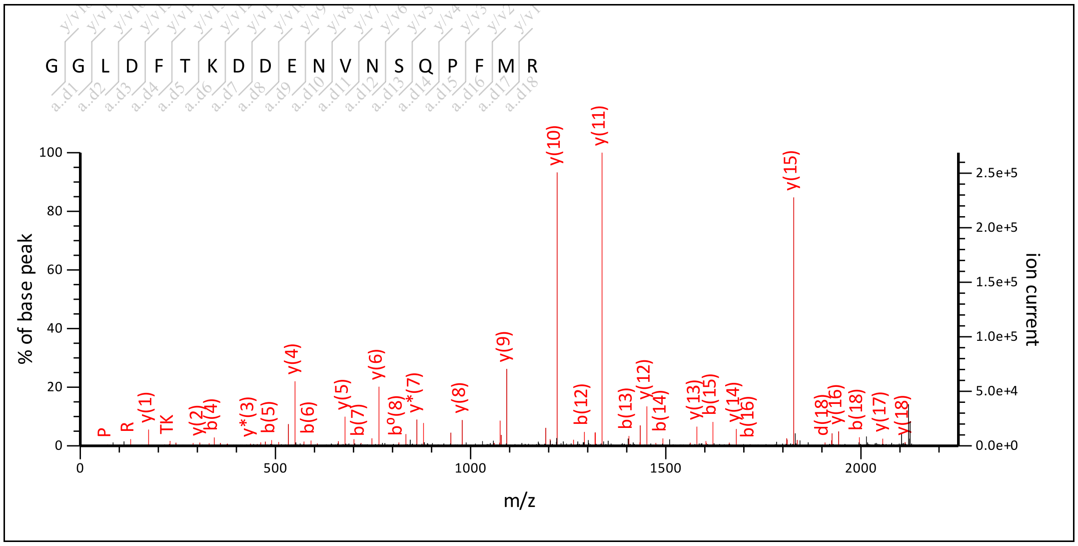
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 82

MS/MS Fragmentation of **GGLDFTKDDENVNSQPFMR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 39: 2169.091824 from(2170.099100,1+) intensity(0.0000) index(22)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221200, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 2249.63

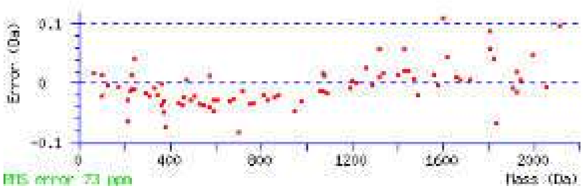
Label all possible matches ○ Label matches used for scoring ●

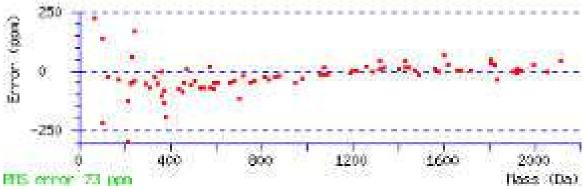
Monoisotopic mass of neutral peptide Mr(calc): 2168.9797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 144 **Expect:** 2.3e-11
Matches : 87/340 fragment ions using 105 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		**G**					
2	30.0338	87.0553			115.0502					**G**				***2112.9655***	2095.9389
3	86.0964	200.1394			**228.1343**			158.0924		**L**	1997.8658	1996.8705		***2055.9440***	2038.9175
4	88.0393	315.1663		297.1557	**343.1612**		325.1506	271.1765		**D**	1882.8388	1881.8436		***1942.8600***	1925.8334
5	120.0808	462.2347		444.2241	**490.2296**		472.2191			**F**	1735.7704			***1827.8330***	1810.8065
6	74.0600	563.2824		545.2718	**591.2773**		573.2667	547.2875	549.2667	**T**	1634.7227	1647.7431	1649.7224	***1680.7646***	1663.7381
7	101.1073	691.3774	674.3508	673.3668	**719.3723**	702.3457	701.3617	634.3195		**K**	1506.6278	1505.6325		***1579.7169***	1562.6904
8	88.0393	806.4043	789.3777	788.3937	**834.3992**	817.3727	816.3886	762.4145		**D**	1391.6008	1390.6056		***1451.6220***	1434.5954
9	88.0393	921.4312	904.4047	903.4207	**949.4262**	932.3996	931.4156	877.4414		**D**	1276.5739	1275.5786		***1336.5950***	1319.5685
10	102.0550	1050.4738	1033.4473	1032.4633	**1078.4687**	1061.4422	1060.4582	992.4684		**E**	1147.5313	1146.5361		***1221.5681***	1204.5415
11	87.0553	1164.5168	1147.4902	1146.5062	**1192.5117**	1175.4851	1174.5011	1121.5109		**N**	1033.4884	1032.4931		***1092.5255***	1075.4989
12	72.0808	1263.5852	1246.5586	1245.5746	**1291.5801**	1274.5535	1273.5695	1249.5695		**V**	934.4200	947.4404		***978.4826***	961.4560
13	87.0553	1377.6281	1360.6016	1359.6175	**1405.6230**	1388.5965	1387.6124	1334.6223		**N**	820.3770	819.3818		***879.4141***	862.3876
14	60.0444	1464.6601	1447.6336	1446.6496	**1492.6550**	1475.6285	1474.6445	1448.6652		**S**	733.3450	732.3498		***765.3712***	748.3447
15	101.0709	1592.7187	1575.6922	1574.7081	**1620.7136**	1603.6871	1602.7031	1535.6972		**Q**	605.2864	604.2912		***678.3392***	661.3126
16	70.0651	1689.7715	1672.7449	1671.7609	**1717.7664**	1700.7398	1699.7558	1663.7558		**P**	508.2337	507.2384		***550.2806***	533.2541
17	120.0808	1836.8399	1819.8133	1818.8293	1864.8348	1847.8082	1846.8242			**F**	361.1653			***453.2279***	436.2013
18	104.0528	1967.8804	1950.8538	1949.8698	**1995.8753**	1978.8487	1977.8647	1907.8770		**M**	230.1248	229.1295		***306.1594***	289.1329
19	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	**GLD**	258.1448	286.1397	**GLDF**	405.2132	433.2082
GLDFT	506.2609	534.2558	**GLDFTK**	634.3559	662.3508	**LD**	201.1234	229.1183

LDF	348.1918	376.1867	**LDFT**	449.2395	477.2344	**LDFTK**	577.3344	605.3293
LDFTKD	692.3614	720.3563	**DF**	235.1077	263.1026	**DFT**	336.1554	364.1503
DFTK	464.2504	492.2453	**DFTKD**	579.2773	607.2722	**DFTKDD**	694.3042	722.2992
FT	221.1285	249.1234	**FTK**	349.2234	377.2183	**FTKD**	464.2504	492.2453
FTKDD	579.2773	607.2722	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDD	432.2089	460.2038	**TKDDE**	561.2515	589.2464	**TKDDEN**	675.2944	703.2893
KD	216.1343	244.1292	**KDD**	331.1612	359.1561	**KDDE**	460.2038	488.1987
KDDEN	574.2467	602.2416	**KDDENV**	673.3151	701.3101	**DD**	203.0662	231.0612
DDE	332.1088	360.1038	**DDEN**	446.1518	474.1467	**DDENV**	545.2202	573.2151
DDENVN	659.2631	687.2580	**DE**	217.0819	245.0768	**DEN**	331.1248	359.1197
DENV	430.1932	458.1882	**DENVN**	544.2362	572.2311	**DENVNS**	631.2682	659.2631
EN	216.0979	244.0928	**ENV**	315.1663	343.1612	**ENVN**	429.2092	457.2041
ENVNS	516.2413	544.2362	**ENVNSQ**	644.2998	672.2947	**NV**	186.1237	214.1186
NVN	300.1666	328.1615	**NVNS**	387.1987	415.1936	**NVNSQ**	515.2572	543.2522
NVNSQP	612.3100	640.3049	**VN**	186.1237	214.1186	**VNS**	273.1557	301.1506
VNSQ	401.2143	429.2092	**VNSQP**	498.2671	526.2620	**VNSQPF**	645.3355	673.3304
NS	174.0873	202.0822	**NSQ**	302.1459	330.1408	**NSQP**	399.1987	427.1936
NSQPF	546.2671	574.2620	**NSQPFM**	677.3076	705.3025	**SQ**	188.1030	216.0979
SQP	285.1557	313.1506	**SQPF**	432.2241	460.2191	**SQPFM**	563.2646	591.2595
QP	198.1237	226.1186	**QPF**	345.1921	373.1870	**QPFM**	476.2326	504.2275
PF	217.1335	245.1285	**PFM**	348.1740	376.1689	**FM**	251.1213	279.1162





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
144.9	2168.4877	0.6041	GGLDFTKDBENVNSQPFMR
143.5	2168.9797	0.1121	GGIDFTKDDENVNSQPFMR
143.5	2168.9797	0.1121	GGIDFTKDDENVNSQPFMR
143.5	2169.0161	0.0758	GGLDFTKDDENVNSKPFMR
143.5	2168.9797	0.1121	GGLDFTKDDENVNSQPFMR
143.5	2168.9797	0.1121	GGLDFTKDDENVNSQPFMR
143.5	2168.9797	0.1121	GGLDFTKDDENVNSQPFMR
143.5	2168.9797	0.1121	GGLDFTKDDENVNSQPFMR
143.5	2168.9797	0.1121	GGLDFTKDDENVNSQPFMR
143.5	2168.9797	0.1121	GGLDFTKDDENVNSQPFMR

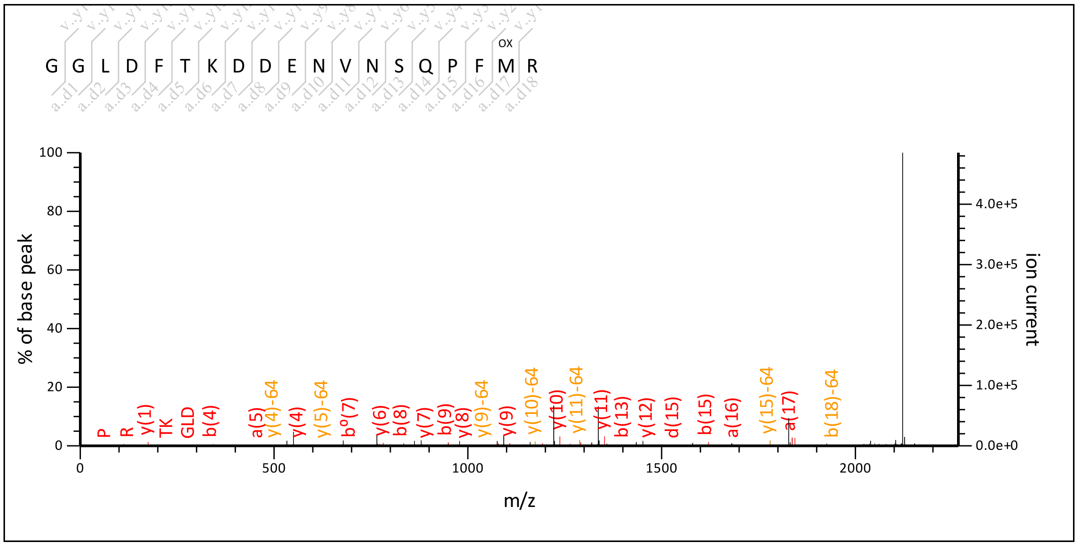
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 82**

MS/MS Fragmentation of **GGLDFTKDDENVNSQPFMR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 41: 2185.077224 from(2186.084500,1+) intensity(0.0000) index(23)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221210, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 2265.68

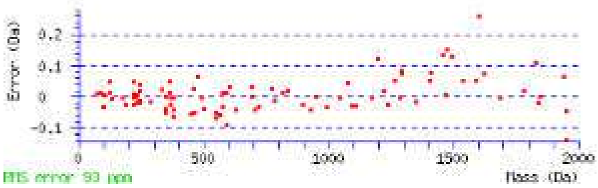
Label all possible matches ○ Label matches used for scoring ●

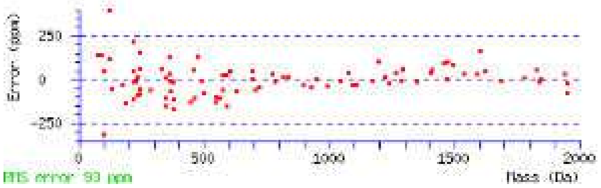
Monoisotopic mass of neutral peptide Mr(calc): 2184.9746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M18 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 42 **Expect:** 0.28
Matches : 94/434 fragment ions using 175 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	30.0338	87.0553			115.0502					G				2064.9621	2047.9356
3	86.0964	200.1394			***228.1343***			158.0924		L	1949.8624	1948.8672		2007.9407	1990.9141
4	88.0393	315.1663		297.1557	***343.1612***		325.1506	271.1765		D	1834.8355	1833.8402		1894.8566	1877.8300
5	120.0808	**462.2347**		444.2241	***490.2296***		472.2191			F	1687.7671			**1779.8297**	1762.8031
6	74.0600	563.2824		545.2718	***591.2773***		573.2667	547.2875	549.2667	T	1586.7194	1599.7398	1601.7190	1632.7612	1615.7347
7	101.1073	691.3774	674.3508	673.3668	719.3723	702.3457	701.3617	634.3195		K	1458.6244	1457.6292		1531.7136	1514.6870
8	88.0393	806.4043	789.3777	788.3937	***834.3992***	817.3727	816.3886	762.4145		D	1343.5975	1342.6022		1403.6186	1386.5920
9	88.0393	921.4312	904.4047	903.4207	***949.4262***	932.3996	931.4156	877.4414		D	1228.5705	1227.5753		**1288.5917**	1271.5651
10	102.0550	1050.4738	1033.4473	1032.4633	***1078.4687***	1061.4422	1060.4582	992.4684		E	1099.5279	1098.5327		**1173.5647**	1156.5382
11	87.0553	1164.5168	1147.4902	1146.5062	***1192.5117***	1175.4851	1174.5011	1121.5109		N	985.4850	984.4898		**1044.5221**	1027.4956
12	72.0808	**1263.5852**	1246.5586	1245.5746	***1291.5801***	1274.5535	1273.5695	1249.5695		V	886.4166	899.4370		**930.4792**	913.4526
13	87.0553	1377.6281	1360.6016	1359.6175	***1405.6230***	1388.5965	1387.6124	1334.6223		N	772.3737	771.3784		831.4108	814.3842
14	60.0444	1464.6601	1447.6336	1446.6496	***1492.6550***	1475.6285	1474.6445	1448.6652		S	685.3416	684.3464		**717.3679**	700.3413
15	101.0709	**1592.7187**	1575.6922	1574.7081	***1620.7136***	1603.6871	1602.7031	1535.6972		Q	557.2831	556.2878		**630.3358**	613.3093
16	70.0651	**1689.7715**	1672.7449	1671.7609	1717.7664	1700.7398	1699.7558	1663.7558		P	460.2303	459.2350		**502.2772**	485.2507
17	120.0808	**1836.8399**	1819.8133	1818.8293	1864.8348	1847.8082	1846.8242			F	313.1619			405.2245	388.1979
18	56.0495	1919.8770	1902.8504	1901.8664	***1947.8719***	1930.8454	1929.8613	1907.8770		M	230.1248	229.1295		258.1561	241.1295
19	129.1135									R	74.0237	73.0284		**175.1190**	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	GLD	258.1448	286.1397	GLDF	405.2132	433.2082

GLDFT	506.2609	534.2558	**GLDFTK**	634.3559	662.3508	**LD**	201.1234	229.1183
LDF	348.1918	376.1867	**LDFT**	449.2395	477.2344	**LDFTK**	577.3344	605.3293
LDFTKD	692.3614	720.3563	**DF**	235.1077	263.1026	**DFT**	336.1554	364.1503
DFTK	464.2504	492.2453	**DFTKD**	579.2773	607.2722	**DFTKDD**	694.3042	722.2992
FT	221.1285	249.1234	**FTK**	349.2234	377.2183	**FTKD**	464.2504	492.2453
FTKDD	579.2773	607.2722	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDD	432.2089	460.2038	**TKDDE**	561.2515	589.2464	**TKDDEN**	675.2944	703.2893
KD	216.1343	244.1292	**KDD**	331.1612	359.1561	**KDDE**	460.2038	488.1987
KDDEN	574.2467	602.2416	**KDDENV**	673.3151	701.3101	**DD**	203.0662	231.0612
DDE	332.1088	360.1038	**DDEN**	446.1518	474.1467	**DDENV**	545.2202	573.2151
DDENVN	659.2631	687.2580	**DE**	217.0819	245.0768	**DEN**	331.1248	359.1197
DENV	430.1932	458.1882	**DENVN**	544.2362	572.2311	**DENVNS**	631.2682	659.2631
EN	216.0979	244.0928	**ENV**	315.1663	343.1612	**ENVN**	429.2092	457.2041
ENVNS	516.2413	544.2362	**ENVNSQ**	644.2998	672.2947	**NV**	186.1237	214.1186
NVN	300.1666	328.1615	**NVNS**	387.1987	415.1936	**NVNSQ**	515.2572	543.2522
NVNSQP	612.3100	640.3049	**VN**	186.1237	214.1186	**VNS**	273.1557	301.1506
VNSQ	401.2143	429.2092	**VNSQP**	498.2671	526.2620	**VNSQPF**	645.3355	673.3304
NS	174.0873	202.0822	**NSQ**	302.1459	330.1408	**NSQP**	399.1987	427.1936
NSQPF	546.2671	574.2620	**NSQPFM**	629.3042	657.2991	**SQ**	188.1030	216.0979
SQP	285.1557	313.1506	**SQPF**	432.2241	460.2191	**SQPFM**	515.2613	543.2562
QP	198.1237	226.1186	**QPF**	345.1921	373.1870	**QPFM**	428.2292	456.2241
PF	217.1335	245.1285	**PFM**	300.1707	328.1656	**FM**	203.1179	231.1128





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.7	2184.9382	0.1390	GGEDFTKDDENVNSQPFMR
93.7	2183.9542	1.1230	GGQDFTKDDENVNSQPFMR
91.4	2184.9932	0.0840	GGLMFTKDDENVNSQPFMR
75.7	2184.9746	0.1026	GGLDYTKDDENVNSQPFMR
59.2	2184.9932	0.0840	GGLDFTKMDENVNSQPFMR
49.7	2184.9932	0.0840	GGLDFTKDMENVNSQPFMR
42.5	2184.9746	0.1026	GGIDFTKDDENVNSQPFMR
42.5	2184.9746	0.1026	GGIDFTKDDENVNSQPFMR
42.5	2185.0110	0.0662	GGLDFTKDDENVNSKPFMR
42.5	2184.9746	0.1026	GGLDFTKDDENVNSQPFMR

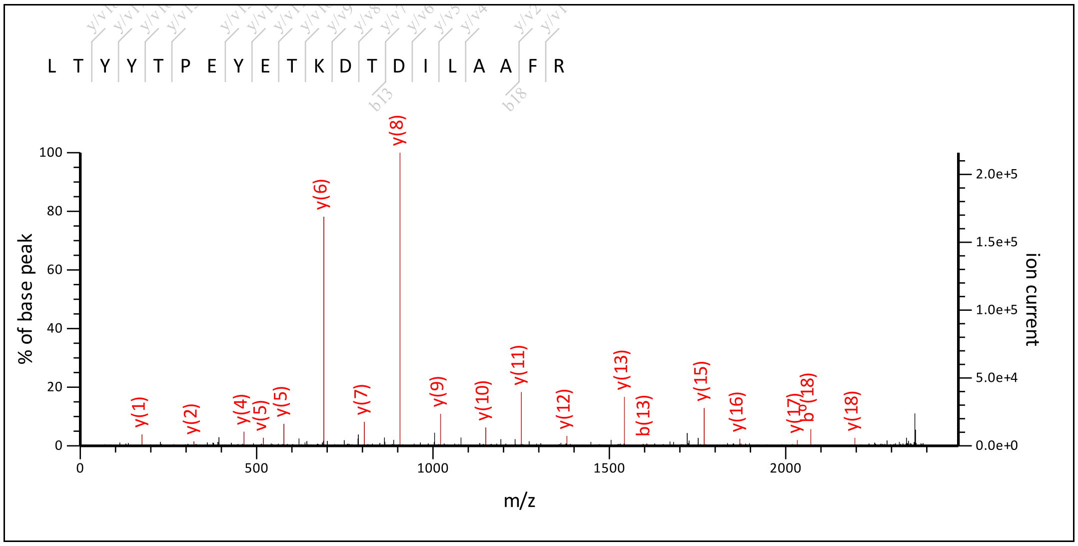
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTYYTPEYETKDTDILAAFR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 46: 2409.289324 from(2410.296600,1+) intensity(0.0000) index(26)
Title: Label: C11, Spot_Id: 216639, Peak_List_Id: 221199, MSMS Job_Run_Id: 21345, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_C11_135997697400.txt



0 to 2489.58

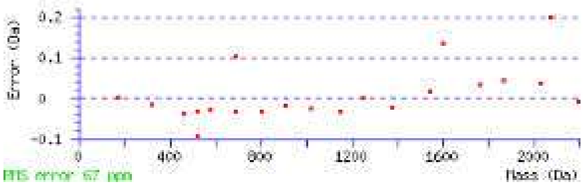
Label all possible matches ○ Label matches used for scoring ●

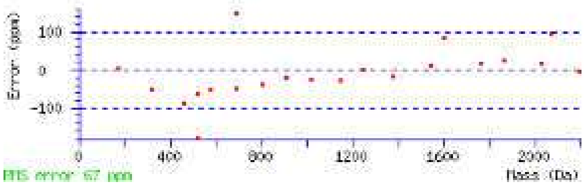
Monoisotopic mass of neutral peptide Mr(calc): 2409.1740
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 143 **Expect:** 1.8e-11
Matches : 21/356 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		L					
2	74.0600	187.1441		169.1335	215.1390		197.1285	171.1492	173.1285	T	2251.0554	2264.0758	2266.0550	2297.0972	2280.0707
3	136.0757	350.2074		332.1969	378.2023		360.1918			Y	2087.9920			***2196.0495***	2179.0230
4	136.0757	513.2708		495.2602	541.2657		523.2551			Y	1924.9287			***2032.9862***	2015.9597
5	74.0600	614.3184		596.3079	642.3134		624.3028	598.3235	600.3028	T	1823.8810	1836.9014	1838.8807	***1869.9229***	1852.8963
6	70.0651	711.3712		693.3606	739.3661		721.3556	685.3556		P	1726.8283	1725.8330		***1768.8752***	1751.8487
7	102.0550	840.4138		822.4032	868.4087		850.3981	782.4083		E	1597.7857	1596.7904		1671.8224	1654.7959
8	136.0757	1003.4771		985.4666	1031.4720		1013.4615			Y	1434.7223			***1542.7799***	1525.7533
9	102.0550	1132.5197		1114.5092	1160.5146		1142.5041	1074.5142		E	1305.6797	1304.6845		***1379.7165***	1362.6900
10	74.0600	1233.5674		1215.5568	1261.5623		1243.5517	1217.5725	1219.5517	T	1204.6321	1217.6525	1219.6317	***1250.6739***	1233.6474
11	101.1073	1361.6624	1344.6358	1343.6518	1389.6573	1372.6307	1371.6467	1304.6045		K	1076.5371	1075.5419		***1149.6262***	1132.5997
12	88.0393	1476.6893	1459.6628	1458.6787	1504.6842	1487.6577	1486.6737	1432.6995		D	961.5102	960.5149		***1021.5313***	1004.5047
13	74.0600	1577.7370	1560.7104	1559.7264	1605.7319	1588.7054	1587.7213	1561.7421	1563.7213	T	860.4625	873.4829	875.4621	***906.5043***	889.4778
14	88.0393	1692.7639	1675.7374	1674.7534	1720.7588	1703.7323	1702.7483	1648.7741		D	745.4355	744.4403		***805.4567***	788.4301
15	86.0964	1805.8480	1788.8214	1787.8374	1833.8429	1816.8164	1815.8323	1777.8167	1791.8323	I	632.3515	645.3719	659.3875	***690.4297***	673.4032
16	86.0964	1918.9321	1901.9055	1900.9215	1946.9270	1929.9004	1928.9164	1876.8851		L	519.2674	518.2722		***577.3457***	560.3191
17	44.0495	1989.9692	1972.9426	1971.9586	2017.9641	2000.9375	1999.9535			A	448.2303			***464.2616***	447.2350
18	44.0495	2061.0063	2043.9797	2042.9957	2089.0012	2071.9746	2070.9906			A	377.1932			393.2245	376.1979
19	120.0808	2208.0747	2191.0481	2190.0641	2236.0696	2219.0431	2218.0590			F	230.1248			***322.1874***	305.1608
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TY	237.1234	265.1183	TYY	400.1867	428.1816	TYYT	501.2344	529.2293

TYYTP	598.2871	626.2821	**YY**	299.1390	327.1339	**YYT**	400.1867	428.1816
YYTP	497.2395	525.2344	**YYTPE**	626.2821	654.2770	**YT**	237.1234	265.1183
YTP	334.1761	362.1710	**YTPE**	463.2187	491.2136	**YTPEY**	626.2821	654.2770
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPEY**	463.2187	491.2136
TPEYE	592.2613	620.2562	**TPEYET**	693.3090	721.3039	**PE**	199.1077	227.1026
PEY	362.1710	390.1660	**PEYE**	491.2136	519.2086	**PEYET**	592.2613	620.2562
EY	265.1183	293.1132	**EYE**	394.1609	422.1558	**EYET**	495.2086	523.2035
EYETK	623.3035	651.2984	**YE**	265.1183	293.1132	**YET**	366.1660	394.1609
YETK	494.2609	522.2558	**YETKD**	609.2879	637.2828	**ET**	203.1026	231.0975
ETK	331.1976	359.1925	**ETKD**	446.2245	474.2195	**ETKDT**	547.2722	575.2671
ETKDTD	662.2992	690.2941	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDT	418.2296	446.2245	**TKDTD**	533.2566	561.2515	**TKDTDI**	646.3406	674.3355
KD	216.1343	244.1292	**KDT**	317.1819	345.1769	**KDTD**	432.2089	460.2038
KDTDI	545.2930	573.2879	**KDTDIL**	658.3770	686.3719	**DT**	189.0870	217.0819
DTD	304.1139	332.1088	**DTDI**	417.1980	445.1929	**DTDIL**	530.2821	558.2770
DTDILA	601.3192	629.3141	**DTDILAA**	672.3563	700.3512	**TD**	189.0870	217.0819
TDI	302.1710	330.1660	**TDIL**	415.2551	443.2500	**TDILA**	486.2922	514.2871
TDILAA	557.3293	585.3243	**DI**	201.1234	229.1183	**DIL**	314.2074	342.2023
DILA	385.2445	413.2395	**DILAA**	456.2817	484.2766	**DILAAF**	603.3501	631.3450
IL	199.1805	227.1754	**ILA**	270.2176	298.2125	**ILAA**	341.2547	369.2496
ILAAF	488.3231	516.3180	**LA**	157.1335	185.1285	**LAA**	228.1707	256.1656
LAAF	375.2391	403.2340	**AA**	115.0866	143.0815	**AAF**	262.1550	290.1499
AF	191.1179	219.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
142.9	2408.6820	0.6073	ITYYTPEYETKDTBILAAFR
142.9	2409.1740	0.1153	ITYYTPEYETKDTDILAAFR
142.9	2409.1740	0.1153	ITYYTPEYETKDTDILAAFR
142.9	2408.6820	0.6073	LTYYTPEYETKDTBILAAFR
142.9	2409.1740	0.1153	LTYYTPEYETKDTDIIAAFR
142.9	2409.1740	0.1153	LTYYTPEYETKDTDILAAFR
142.9	2409.1740	0.1153	LTYYTPEYETKDTDILAAFR
142.9	2409.1740	0.1153	LTYYTPEYETKDTDILAAFR
142.9	2409.1740	0.1153	LTYYTPEYETKDTDILAAFR
142.9	2409.1740	0.1153	LTYYTPEYETKDTDILAAFR

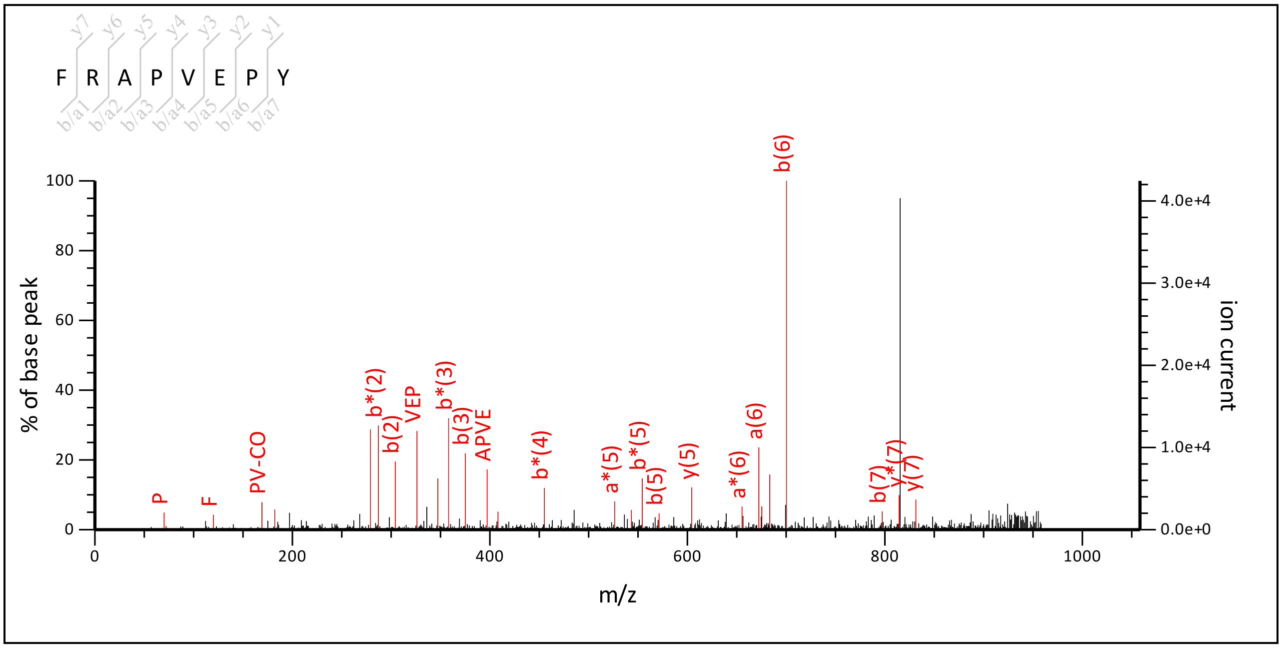
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 84

MS/MS Fragmentation of **FRAPVEPY**
Found in **gi|780372** in **NCBInr**, enolase [Oryza sativa Japonica Group]

Match to Query 18: 977.573844 from(978.581120,1+) intensity(0.0000) index(5)
Title: Label: J6, Spot_Id: 228931, Peak_List_Id: 257585, MSMS Job_Run_Id: 24927, Comment:
Data file ppw_J6_138985135600.txt



0 to 1058.34

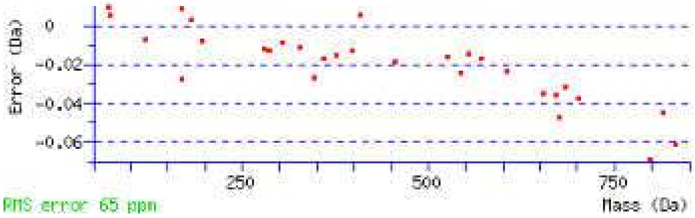
Label all possible matches ○ Label matches used for scoring ●

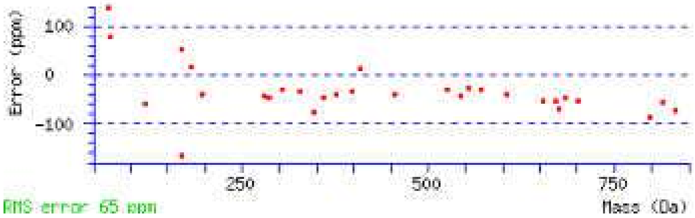
Monoisotopic mass of neutral peptide Mr(calc): 977.4971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.4
Matches : 33/100 fragment ions using 47 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	120.0808	**120.0808**			148.0757			44.0495	F						8
2	129.1135	276.1819	259.1553		**304.1768**	287.1503		191.1179	R	730.3406	729.3454	***831.4359***	814.4094	813.4254	7
3	44.0495	**347.2190**	330.1925		**375.2139**	358.1874			A	659.3035		***675.3348***		657.3243	6
4	70.0651	444.2718	427.2452		472.2667	455.2401		418.2561	P	562.2508	561.2555	***604.2977***		586.2871	5
5	72.0808	**543.3402**	526.3136		**571.3351**	554.3085		529.3245	V	463.1823	476.2027	507.2449		489.2344	4
6	102.0550	**672.3828**	655.3562	654.3722	**700.3777**	683.3511	682.3671	614.3773	E	334.1397	333.1445	***408.1765***		390.1660	3
7	70.0651	769.4355	752.4090	751.4250	**797.4305**	780.4039	779.4199	743.4199	P	237.0870	236.0917	***279.1339***			2
8	136.0757								Y	74.0237	73.0284	***182.0812***			1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RA	200.1506	228.1455	**RAP**	297.2034	325.1983	**RAPV**	396.2718	424.2667
RAPVE	525.3144	553.3093	**RAPVEP**	622.3671	650.3620	**AP**	141.1022	169.0972
APV	240.1707	268.1656	**APVE**	369.2132	397.2082	**APVEP**	466.2660	494.2609

PV	169.1335	197.1285	**PVE**	298.1761	326.1710	**PVEP**	395.2289	423.2238
VE	201.1234	229.1183	**VEP**	298.1761	326.1710	**EP**	199.1077	227.1026





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.8	977.4971	0.0768	FRAPVEPY
21.6	977.5004	0.0734	FMEPVISR
16.6	977.5334	0.0404	YPFPVLSR
15.5	977.5182	0.0557	NATAFVLDK
11.4	977.4818	0.0920	YPEVDLSR
11.3	977.5004	0.0734	MYIVPAER
10.7	977.5004	0.0734	FMEPLVSR
10.5	977.4865	0.0873	MRAGWVSR
10.4	977.5433	0.0305	YDLVLDLK
9.8	977.5328	0.0411	RASAMVLSK

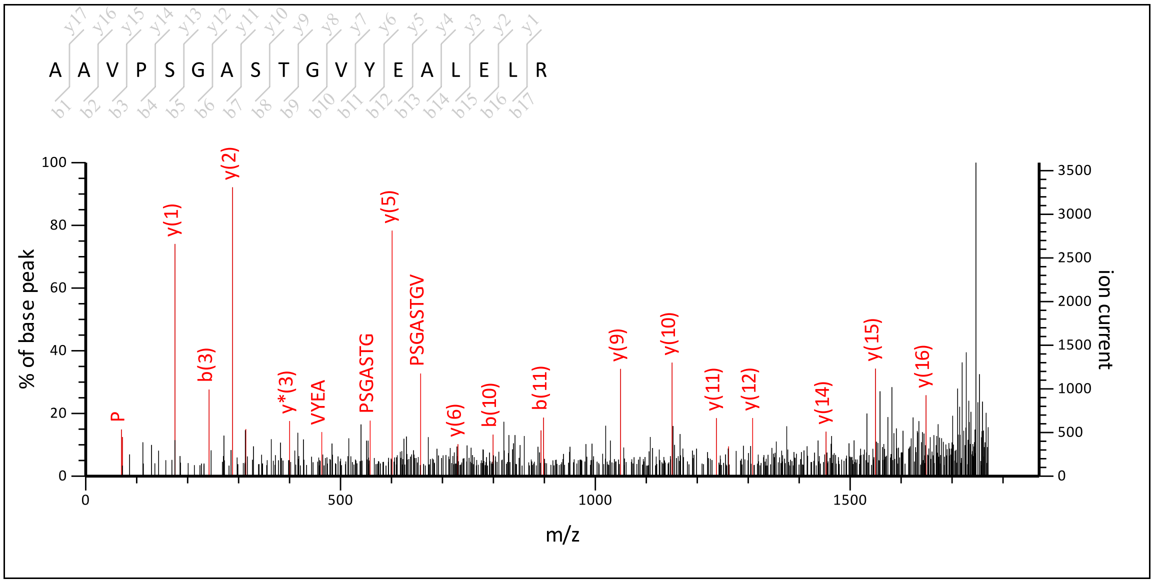
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 84

MS/MS Fragmentation of **AAVPSGASTGVYEALELR**
Found in **gi|780372** in **NCBInr**, enolase [Oryza sativa Japonica Group]

Match to Query 65: 1790.074624 from(1791.081900,1+) intensity(0.0000) index(21)
Title: Label: J6, Spot_Id: 228931, Peak_List_Id: 257588, MSMS Job_Run_Id: 24927, Comment:
Data file ppw_J6_138985135600.txt



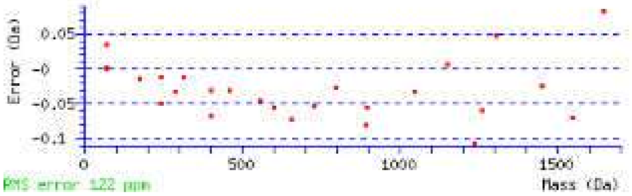
0 to 1870.88

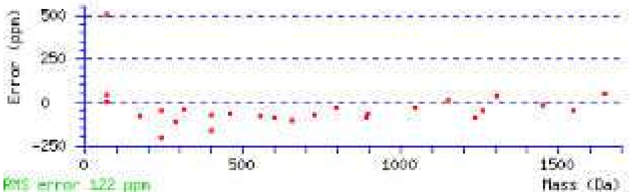
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1789.9210
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 1.7e-06
Matches : 29/313 fragment ions using 35 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	44.0495	44.0495		**72.0444**		44.0495		A							18
2	44.0495	115.0866		143.0815				A	1703.8599			1719.8912	1702.8646	1701.8806	17
3	72.0808	214.1550		**242.1499**		200.1394		V	1604.7915	1617.8119		***1648.8541***	1631.8275	1630.8435	16
4	70.0651	311.2078		339.2027		285.1921		P	1507.7387	1506.7435		***1549.7857***	1532.7591	1531.7751	15
5	60.0444	398.2398	380.2292	426.2347	408.2241	382.2449		S	1420.7067	1419.7114		***1452.7329***	1435.7064	1434.7223	14
6	30.0338	455.2613	437.2507	483.2562	465.2456			G				1365.7009	1348.6743	1347.6903	13
7	44.0495	526.2984	508.2878	554.2933	536.2827			A	1292.6481			***1308.6794***	1291.6529	1290.6688	12
8	60.0444	613.3304	595.3198	641.3253	623.3148	597.3355		S	1205.6161	1204.6208		***1237.6423***	1220.6157	1219.6317	11
9	74.0600	714.3781	696.3675	742.3730	724.3624	698.3832	700.3624	T	1104.5684	1117.5888	1119.5681	***1150.6103***	1133.5837	1132.5997	10
10	30.0338	771.3995	753.3890	**799.3945**	781.3839			G				***1049.5626***	1032.5360	1031.5520	9
11	72.0808	870.4680	852.4574	**898.4629**	880.4523	856.4523		V	948.4785	961.4989		992.5411	975.5146	974.5306	8
12	136.0757	1033.5313	1015.5207	1061.5262	1043.5156			Y	785.4152			***893.4727***	876.4462	875.4621	7
13	102.0550	1162.5739	1144.5633	1190.5688	1172.5582	1104.5684		E	656.3726	655.3774		***730.4094***	713.3828	712.3988	6
14	44.0495	1233.6110	1215.6004	**1261.6059**	1243.5953			A	585.3355			***601.3668***	584.3402	583.3562	5
15	86.0964	1346.6951	1328.6845	1374.6900	1356.6794	1304.6481		L	472.2514	471.2562		530.3297	513.3031	512.3191	4
16	102.0550	1475.7377	1457.7271	1503.7326	1485.7220	1417.7322		E	343.2088	342.2136		417.2456	400.2191	399.2350	3
17	86.0964	1588.8217	1570.8111	1616.8166	1598.8061	1546.7748		L	230.1248	229.1295		***288.2030***	271.1765		2
18	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AV	143.1179	171.1128	**AVP**	240.1707	268.1656	**AVPS**	327.2027	355.1976
AVPSG	384.2241	412.2191	**AVPSGA**	455.2613	483.2562	**AVPSGAS**	542.2933	570.2882
AVPSGAST	643.3410	671.3359	**VP**	169.1335	197.1285	**VPS**	256.1656	284.1605
VPSG	313.1870	341.1819	**VPSGA**	384.2241	412.2191	**VPSGAS**	471.2562	499.2511
VPSGAST	572.3039	600.2988	**VPSGASTG**	629.3253	657.3202	**PS**	157.0972	185.0921
PSG	214.1186	242.1135	**PSGA**	285.1557	313.1506	**PSGAS**	372.1878	400.1827
PSGAST	473.2354	501.2304	**PSGASTG**	530.2569	558.2518	**PSGASTGV**	629.3253	657.3202
SG	117.0659	145.0608	**SGA**	188.1030	216.0979	**SGAS**	275.1350	303.1299
SGAST	376.1827	404.1776	**SGASTG**	433.2041	461.1991	**SGASTGV**	532.2726	560.2675
SGASTGVY	695.3359	723.3308	**GA**	101.0709	129.0659	**GAS**	188.1030	216.0979
GAST	289.1506	317.1456	**GASTG**	346.1721	374.1670	**GASTGV**	445.2405	473.2354
GASTGVY	608.3039	636.2988	**AS**	131.0815	159.0764	**AST**	232.1292	260.1241
ASTG	289.1506	317.1456	**ASTGV**	388.2191	416.2140	**ASTGVY**	551.2824	579.2773
ASTGVYE	680.3250	708.3199	**ST**	161.0921	189.0870	**STG**	218.1135	246.1084
STGV	317.1819	345.1769	**STGVY**	480.2453	508.2402	**STGVYE**	609.2879	637.2828
STGVYEA	680.3250	708.3199	**TG**	131.0815	159.0764	**TGV**	230.1499	258.1448
TGVY	393.2132	421.2082	**TGVYE**	522.2558	550.2508	**TGVYEA**	593.2930	621.2879
GV	129.1022	157.0972	**GVY**	292.1656	320.1605	**GVYE**	421.2082	449.2031
GVYEA	492.2453	520.2402	**GVYEAL**	605.3293	633.3243	**VY**	235.1441	263.1390
VYE	364.1867	392.1816	**VYEA**	435.2238	463.2187	**VYEAL**	548.3079	576.3028
VYEALE	677.3505	705.3454	**YE**	265.1183	293.1132	**YEA**	336.1554	364.1503
YEAL	449.2395	477.2344	**YEALE**	578.2821	606.2770	**YEALEL**	691.3661	719.3610
EA	173.0921	201.0870	**EAL**	286.1761	314.1710	**EALE**	415.2187	443.2136
EALEL	528.3028	556.2977	**AL**	157.1335	185.1285	**ALE**	286.1761	314.1710
ALEL	399.2602	427.2551	**LE**	215.1390	243.1339	**LEL**	328.2231	356.2180
EL	215.1390	243.1339						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.3	1789.9210	0.1536	AAVPSGASTGVYEALELR
56.6	1789.9210	0.1536	AAVPSGASTGIYEAVELR
19.9	1789.9071	0.1675	EEGHVDEPVVARGAGLR
14.7	1789.9210	0.1536	GAVPSGASTGIYEALELR
13.8	1789.9687	0.1060	DSLVDVIPHTLQGQIR
11.4	1789.9951	0.0795	VLLHHLYSRAPSELR
9.9	1790.0050	0.0696	QQLLATTVPPGPSAAAIR
8.7	1789.9032	0.1714	AAVEDSVMPAYAALINR
8.3	1790.0526	0.0220	QLKLAGGPQQLQLLQR
8.3	1789.9183	0.1563	AAAGGGSGAGRGTFLGAAVSR

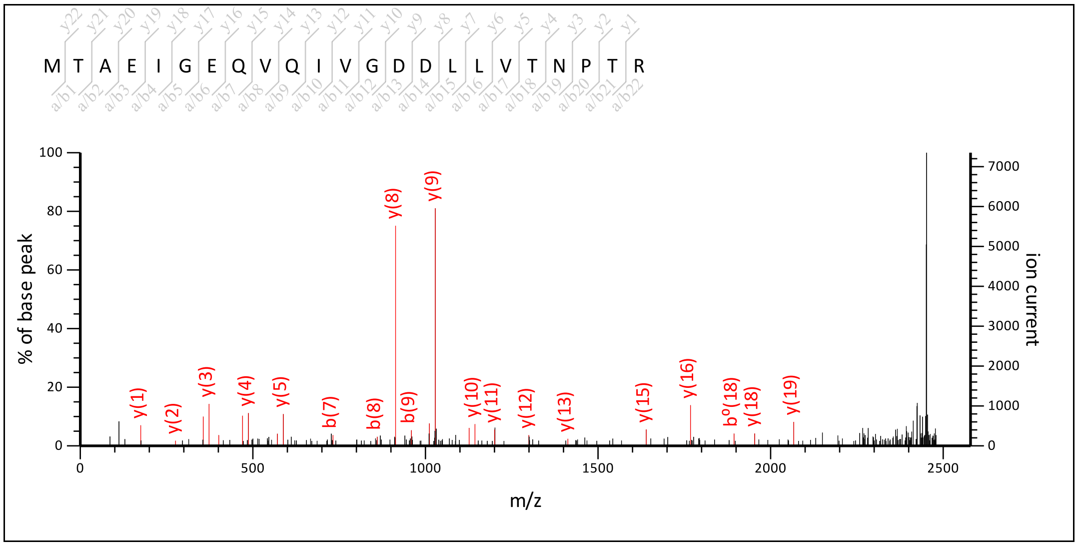
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 84

MS/MS Fragmentation of **MTAEIGEQVQIVGDDLLVTNPTR**
Found in **gi|780372** in **NCBInr**, enolase [Oryza sativa Japonica Group]

Match to Query 80: 2498.474124 from(2499.481400,1+) intensity(0.0000) index(26)
Title: Label: J6, Spot_Id: 228931, Peak_List_Id: 257593, MSMS Job_Run_Id: 24927, Comment:
Data file ppw_J6_138985135600.txt



0 to 2579.21

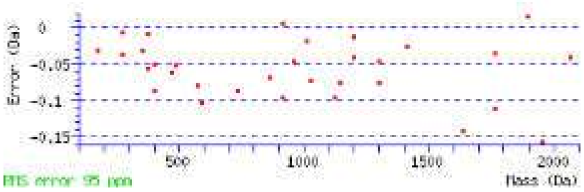
Label all possible matches ○ Label matches used for scoring ●

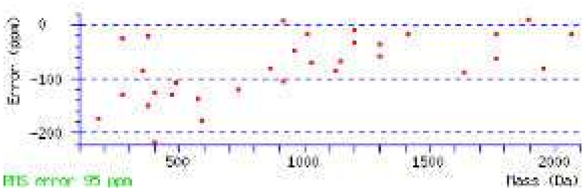
Monoisotopic mass of neutral peptide Mr(calc): 2498.2687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 96 **Expect:** 2.3e-07
Matches : 33/457 fragment ions using 47 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	104.0528	104.0528			132.0478			44.0495		M					
2	74.0600	205.1005		187.0900	233.0954		215.0849	189.1056	191.0849	T	2322.1936	2335.2140	2337.1932	2368.2354	2351.2089
3	44.0495	276.1376		258.1271	304.1326		286.1220			A	2251.1565			2267.1878	2250.1612
4	102.0550	405.1802		387.1697	433.1751		415.1646	347.1748		E	2122.1139	2121.1186		2196.1507	2179.1241
5	86.0964	518.2643		500.2537	546.2592		528.2486	490.2330	504.2486	I	2009.0298	2022.0502	2036.0659	***2067.1081***	2050.0815
6	30.0338	575.2858		557.2752	603.2807		585.2701			G				***1954.0240***	1936.9974
7	102.0550	704.3284		686.3178	**732.3233**		714.3127	646.3229		E	1822.9658	1821.9705		1897.0025	1879.9760
8	101.0709	832.3869	815.3604	814.3764	**860.3818**	843.3553	842.3713	775.3655		Q	1694.9072	1693.9119		***1767.9599***	1750.9334
9	72.0808	931.4553	914.4288	913.4448	**959.4503**	942.4237	941.4397	917.4397		V	1595.8388	1608.8592		***1639.9014***	1622.8748
10	101.0709	1059.5139	1042.4874	1041.5034	1087.5088	1070.4823	1069.4983	1002.4925		Q	1467.7802	1466.7849		1540.8329	1523.8064
11	86.0964	1172.5980	1155.5714	1154.5874	**1200.5929**	1183.5664	1182.5823	1144.5667	1158.5823	I	1354.6961	1367.7165	1381.7322	***1412.7744***	1395.7478
12	72.0808	1271.6664	1254.6399	1253.6558	**1299.6613**	1282.6348	1281.6508	1257.6508		V	1255.6277	1268.6481		***1299.6903***	1282.6638
13	30.0338	1328.6879	1311.6613	1310.6773	1356.6828	1339.6562	1338.6722			G				***1200.6219***	1183.5953
14	88.0393	1443.7148	1426.6883	1425.7042	1471.7097	1454.6832	1453.6992	1399.7250		D	1083.5793	1082.5841		***1143.6004***	1126.5739
15	88.0393	1558.7418	1541.7152	1540.7312	1586.7367	1569.7101	1568.7261	1514.7519		D	968.5524	967.5571		***1028.5735***	1011.5469
16	86.0964	1671.8258	1654.7993	1653.8152	1699.8207	1682.7942	1681.8102	1629.7789		L	855.4683	854.4730		***913.5465***	896.5200
17	86.0964	1784.9099	1767.8833	1766.8993	1812.9048	1795.8782	1794.8942	1742.8629		L	742.3842	741.3890		800.4625	783.4359
18	72.0808	1883.9783	1866.9517	1865.9677	1911.9732	1894.9467	1893.9626	1869.9626		V	643.3158	656.3362		687.3784	670.3519
19	74.0600	1985.0260	1967.9994	1967.0154	2013.0209	1995.9943	1995.0103	1969.0311	1971.0103	T	542.2681	555.2885	557.2678	***588.3100***	571.2835
20	87.0553	2099.0689	2082.0423	2081.0583	2127.0638	2110.0373	2109.0532	2056.0631		N	428.2252	427.2300		***487.2623***	470.2358
21	70.0651	2196.1217	2179.0951	2178.1111	2224.1166	2207.0900	2206.1060	2170.1060		P	331.1724	330.1772		***373.2194***	356.1928
22	74.0600	2297.1693	2280.1428	2279.1588	2325.1643	2308.1377	2307.1537	2281.1744	2283.1537	T	230.1248	243.1452	245.1244	***276.1666***	259.1401

23	129.1135									R	74.0237	73.0284		*175.1190*	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TA	145.0972	173.0921	**TAE**	274.1397	302.1347	**TAEI**	387.2238	415.2187
TAEIG	444.2453	472.2402	**TAEIGE**	573.2879	601.2828	**AE**	173.0921	201.0870
AEI	286.1761	314.1710	**AEIG**	343.1976	371.1925	**AEIGE**	472.2402	500.2351
AEIGEQ	600.2988	628.2937	**AEIGEQV**	699.3672	727.3621	**EI**	215.1390	243.1339
EIG	272.1605	300.1554	**EIGE**	401.2031	429.1980	**EIGEQ**	529.2617	557.2566
EIGEQV	628.3301	656.3250	**IG**	143.1179	171.1128	**IGE**	272.1605	300.1554
IGEQ	400.2191	428.2140	**IGEQV**	499.2875	527.2824	**IGEQVQ**	627.3461	655.3410
GE	159.0764	187.0713	**GEQ**	287.1350	315.1299	**GEQV**	386.2034	414.1983
GEQVQ	514.2620	542.2569	**GEQVQI**	627.3461	655.3410	**EQ**	230.1135	258.1084
EQV	329.1819	357.1769	**EQVQ**	457.2405	485.2354	**EQVQI**	570.3246	598.3195
EQVQIV	669.3930	697.3879	**QV**	200.1394	228.1343	**QVQ**	328.1979	356.1928
QVQI	441.2820	469.2769	**QVQIV**	540.3504	568.3453	**QVQIVG**	597.3719	625.3668
VQ	200.1394	228.1343	**VQI**	313.2234	341.2183	**VQIV**	412.2918	440.2867
VQIVG	469.3133	497.3082	**VQIVGD**	584.3402	612.3352	**VQIVGDD**	699.3672	727.3621
QI	214.1550	242.1499	**QIV**	313.2234	341.2183	**QIVG**	370.2449	398.2398
QIVGD	485.2718	513.2667	**QIVGDD**	600.2988	628.2937	**IV**	185.1648	213.1598
IVG	242.1863	270.1812	**IVGD**	357.2132	385.2082	**IVGDD**	472.2402	500.2351
IVGDDL	585.3243	613.3192	**IVGDDLL**	698.4083	726.4032	**VG**	129.1022	157.0972
VGD	244.1292	272.1241	**VGDD**	359.1561	387.1510	**VGDDL**	472.2402	500.2351
VGDDLL	585.3243	613.3192	**VGDDLLV**	684.3927	712.3876	**GD**	145.0608	173.0557
GDD	260.0877	288.0826	**GDDL**	373.1718	401.1667	**GDDLL**	486.2558	514.2508
GDDLLV	585.3243	613.3192	**GDDLLVT**	686.3719	714.3668	**DD**	203.0662	231.0612
DDL	316.1503	344.1452	**DDLL**	429.2344	457.2293	**DDLLV**	528.3028	556.2977
DDLLVT	629.3505	657.3454	**DL**	201.1234	229.1183	**DLL**	314.2074	342.2023
DLLV	413.2758	441.2708	**DLLVT**	514.3235	542.3184	**DLLVTN**	628.3665	656.3614
LL	199.1805	227.1754	**LLV**	298.2489	326.2438	**LLVT**	399.2966	427.2915
LLVTN	513.3395	541.3344	**LLVTNP**	610.3923	638.3872	**LV**	185.1648	213.1598
LVT	286.2125	314.2074	**LVTN**	400.2554	428.2504	**LVTNP**	497.3082	525.3031
LVTNPT	598.3559	626.3508	**VT**	173.1285	201.1234	**VTN**	287.1714	315.1663
VTNP	384.2241	412.2191	**VTNPT**	485.2718	513.2667	**TN**	188.1030	216.0979
TNP	285.1557	313.1506	**TNPT**	386.2034	414.1983	**NP**	184.1081	212.1030
NPT	285.1557	313.1506	**PT**	171.1128	199.1077			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
95.7	2498.2687	0.2055	MTAEIGEQVQIVGDDLLVTNPTR
8.3	2498.3063	0.1678	DTAISDEKPARIMAARPPPPPPR
8.0	2498.3493	0.1248	QGLLERSGVFVVEGDINDAVLLR
5.0	2498.3163	0.1579	LSTNATASAPAATAASPGVVDVLMKR
1.7	2498.2919	0.1822	VAMFGGSILLDIYIYDYFVKR
0.6	2498.2289	0.2452	RLAEAGYVPDVSSVLHDIGDEEK
0.3	2498.2911	0.1830	MRELVSSSTSSPTAALVAAGHAALR

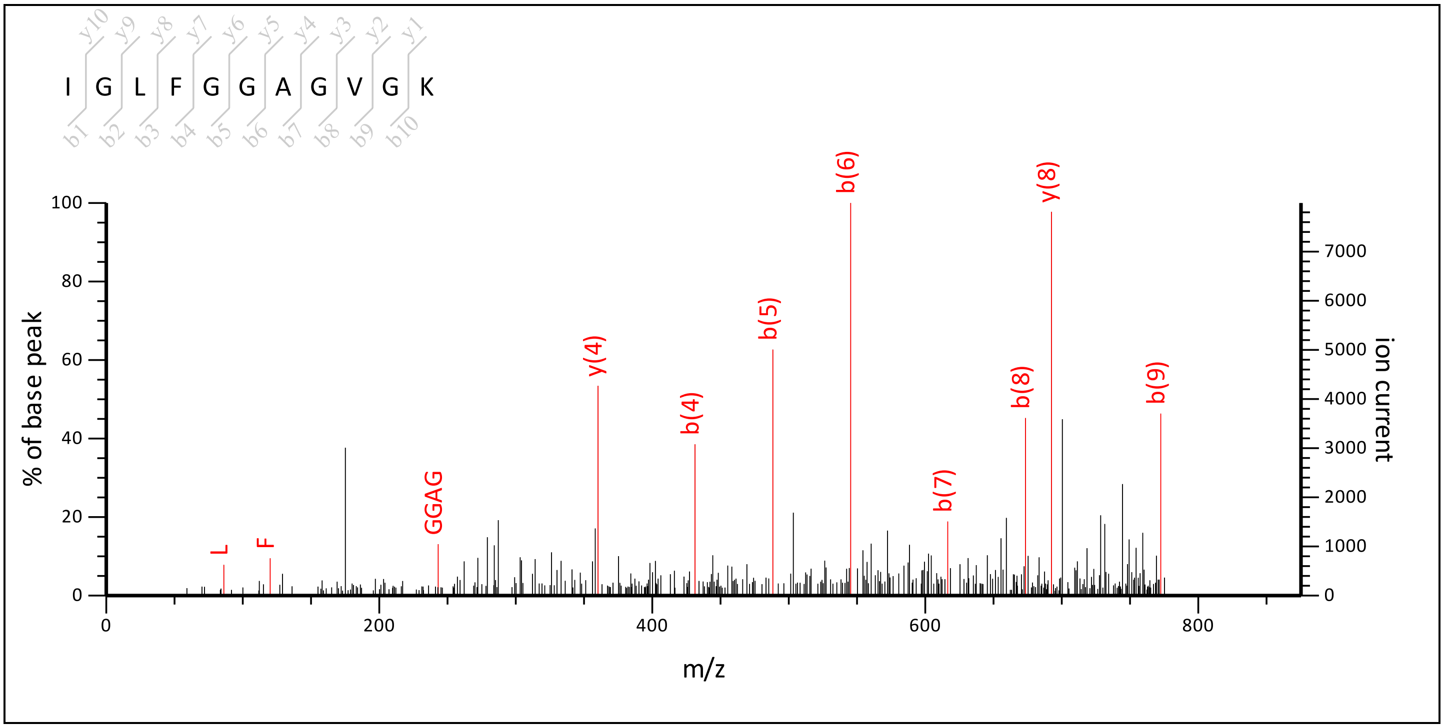
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **IGLFGGAGVGK**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 63: 974.560904 from(975.568180,1+) intensity(0.0000) index(3)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228328, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 875.25

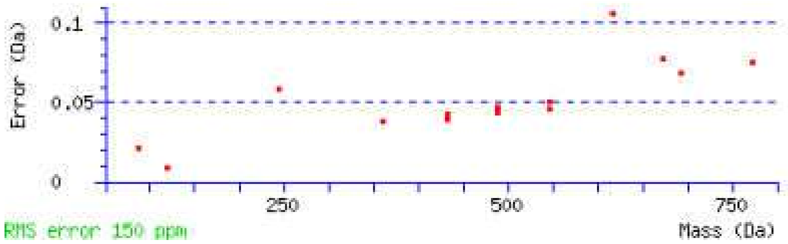
Label all possible matches ○ Label matches used for scoring ●

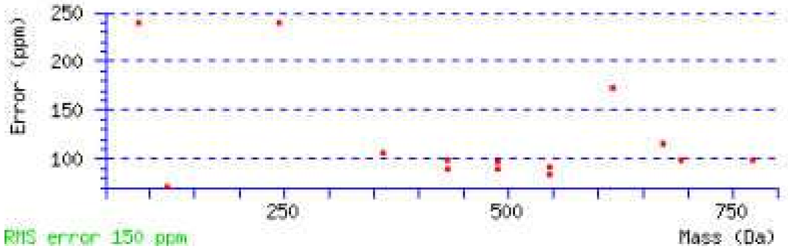
Monoisotopic mass of neutral peptide Mr(calc): 974.5549
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 1
Matches : 16/133 fragment ions using 16 most intense peaks (help)

#	Immon.	a	b	d	Seq.	v	w	y	y*	#
1	86.0964	86.0964	114.0913	44.0495	I					11
2	30.0338	143.1179	171.1128		G			862.4781	845.4516	10
3	86.0964	256.2020	284.1969	214.1550	L	747.3784	746.3832	805.4567	788.4301	9
4	120.0808	403.2704	***431.2653***		F	600.3100		***692.3726***	675.3461	8
5	30.0338	460.2918	***488.2867***		G			***545.3042***	528.2776	7
6	30.0338	517.3133	***545.3082***		G			***488.2827***	471.2562	6
7	44.0495	588.3504	***616.3453***		A	415.2300		***431.2613***	414.2347	5
8	30.0338	645.3719	***673.3668***		G			***360.2241***	343.1976	4

9	72.0808	744.4403	772.4352	730.4246	V	259.1401	272.1605	303.2027	286.1761	3
10	30.0338	801.4618	829.4567		G			204.1343	187.1077	2
11	101.1073				K	74.0237	73.0284	147.1128	130.0863	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	**GLF**	290.1863	318.1812	**GLFG**	347.2078	375.2027
GLFGG	404.2292	432.2241	**GLFGGA**	475.2663	503.2613	**GLFGGAG**	532.2878	560.2827
GLFGGAGV	631.3562	659.3511	**GLFGGAGVG**	688.3777	716.3726	**LF**	233.1648	261.1598
LFG	290.1863	318.1812	**LFGG**	347.2078	375.2027	**LFGGA**	418.2449	446.2398
LFGGAG	475.2663	503.2613	**LFGGAGV**	574.3348	602.3297	**LFGGAGVG**	631.3562	659.3511
FG	177.1022	205.0972	**FGG**	234.1237	262.1186	**FGGA**	305.1608	333.1557
FGGAG	362.1823	390.1772	**FGGAGV**	461.2507	489.2456	**FGGAGVG**	518.2722	546.2671
GG	87.0553	115.0502	**GGA**	158.0924	186.0873	**GGAG**	215.1139	243.1088
GGAGV	314.1823	342.1772	**GGAGVG**	371.2037	399.1987	**GA**	101.0709	129.0659
GAG	158.0924	186.0873	**GAGV**	257.1608	285.1557	**GAGVG**	314.1823	342.1772
AG	101.0709	129.0659	**AGV**	200.1394	228.1343	**AGVG**	257.1608	285.1557
GV	129.1022	157.0972	**GVG**	186.1237	214.1186	**VG**	129.1022	157.0972





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.9	974.5549	0.0060	IAVFGGAGVGK
46.9	974.5549	0.0060	IGIFGGAGVGK
46.9	974.5549	0.0060	IGIFGGAGVGK
46.9	974.5219	0.0390	IGIMGGAGVGK
46.9	974.5549	0.0060	LGIFGGAGVGK
46.3	974.5549	0.0060	IGLFGGAGVGK
46.3	974.5549	0.0060	IGLFGGAGVGK

46.3	974.5549	0.0060	IGLFGGAGVGK
46.3	974.5549	0.0060	IGLFGGAGVGK
46.3	974.5549	0.0060	IGLFGGAGVGK

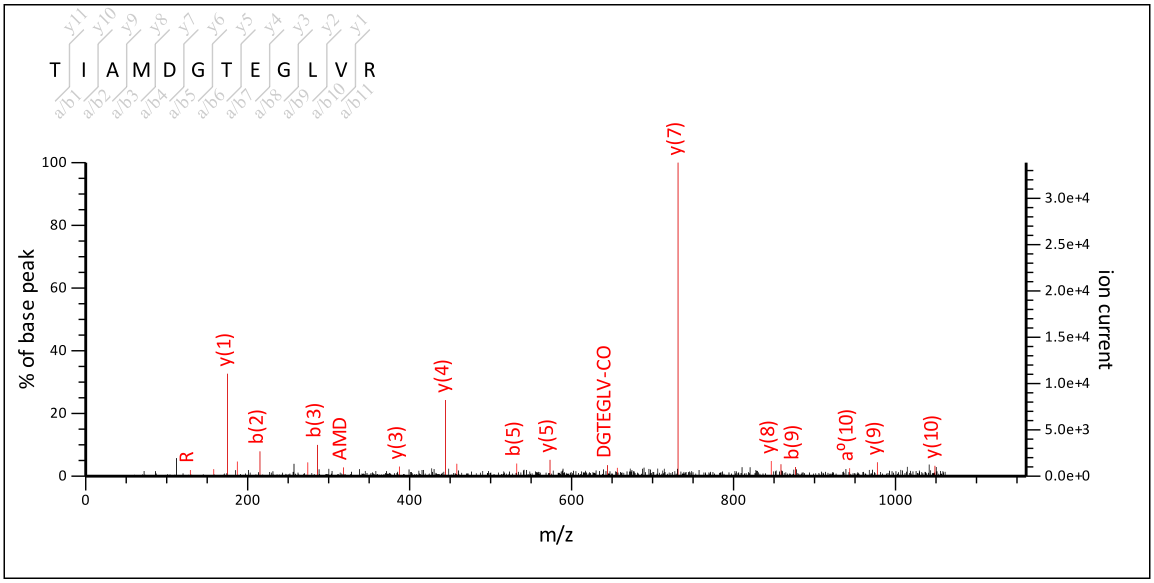
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **TIAMDGTEGLVR**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 175: 1261.664924 from(1262.672200,1+) intensity(0.0000) index(13)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228326, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 1161.31

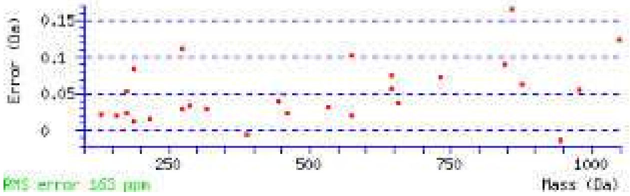
Label all possible matches ○ Label matches used for scoring ●

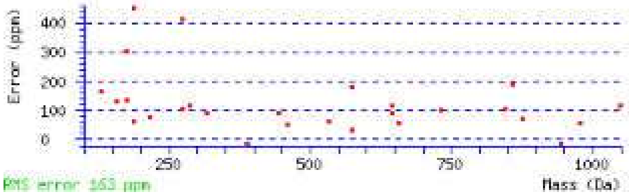
Monoisotopic mass of neutral peptide Mr(calc): 1261.6336
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 0.0023
Matches : 27/190 fragment ions using 31 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	74.0600	74.0600	56.0495	102.0550	84.0444	44.0495		**T**							**12**
2	86.0964	187.1441	169.1335	**215.1390**	197.1285	159.1128	173.1285	**I**	1103.5150	1116.5354	1130.5510	1161.5932	1144.5667	1143.5827	**11**
3	44.0495	258.1812	240.1707	**286.1761**	268.1656			**A**	1032.4779			***1048.5092***	1031.4826	1030.4986	**10**
4	104.0528	389.2217	371.2111	417.2166	399.2061	329.2183		**M**	901.4374	900.4421		***977.4721***	960.4455	959.4615	**9**
5	88.0393	504.2486	486.2381	**532.2436**	514.2330	460.2588		**D**	786.4104	785.4152		***846.4316***	829.4050	828.4210	**8**
6	30.0338	561.2701	543.2595	589.2650	571.2545			**G**				***731.4046***	714.3781	713.3941	**7**
7	74.0600	662.3178	644.3072	690.3127	672.3021	646.3229	648.3021	**T**	628.3413	641.3617	643.3410	674.3832	657.3566	656.3726	**6**
8	102.0550	791.3604	773.3498	819.3553	801.3447	733.3549		**E**	499.2987	498.3035		***573.3355***	556.3089	555.3249	**5**
9	30.0338	848.3818	830.3713	**876.3768**	858.3662			**G**				***444.2929***	427.2663		**4**
10	86.0964	961.4659	943.4553	989.4608	971.4503	919.4190		**L**	329.1932	328.1979		***387.2714***	370.2449		**3**
11	72.0808	1060.5343	1042.5238	1088.5292	1070.5187	1046.5187		**V**	230.1248	243.1452		***274.1874***	257.1608		**2**
12	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IA	157.1335	185.1285	**IAM**	288.1740	316.1689	**IAMD**	403.2010	431.1959
IAMDG	460.2224	488.2173	**IAMDGT**	561.2701	589.2650	**IAMDGTE**	690.3127	718.3076
AM	175.0900	203.0849	**AMD**	290.1169	318.1118	**AMDG**	347.1384	375.1333
AMDGT	448.1860	476.1810	**AMDGTE**	577.2286	605.2236	**AMDGTEG**	634.2501	662.2450
MD	219.0798	247.0747	**MDG**	276.1013	304.0962	**MDGT**	377.1489	405.1438

MDGTE	506.1915	534.1864	**MDGTEG**	563.2130	591.2079	**MDGTEGL**	676.2971	704.2920
DG	145.0608	173.0557	**DGT**	246.1084	274.1034	**DGTE**	375.1510	403.1460
DGTEG	432.1725	460.1674	**DGTEGL**	545.2566	573.2515	**DGTEGLV**	644.3250	672.3199
GT	131.0815	159.0764	**GTE**	260.1241	288.1190	**GTEG**	317.1456	345.1405
GTEGL	430.2296	458.2245	**GTEGLV**	529.2980	557.2930	**TE**	203.1026	231.0975
TEG	260.1241	288.1190	**TEGL**	373.2082	401.2031	**TEGLV**	472.2766	500.2715
EG	159.0764	187.0713	**EGL**	272.1605	300.1554	**EGLV**	371.2289	399.2238
GL	143.1179	171.1128	**GLV**	242.1863	270.1812	**LV**	185.1648	213.1598





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.2	1261.6336	0.0313	TIAMDGTEGLVR
72.2	1261.6336	0.0313	TIAMDGTEGLVR
60.1	1261.6336	0.0313	TIAMDATDGLVR
43.9	1261.6336	0.0313	TIAMDGTDGLIR
43.1	1261.6336	0.0313	AIAMEGTEGLVR
43.0	1261.6336	0.0313	TIAMEGTDGLVR
38.7	1261.6159	0.0491	VDADMAAMAVLR
37.5	1261.7143	-0.0493	ITAIHPGEGIVR
35.6	1261.5721	0.0928	SVVMDGAAADGNR
34.5	1261.6667	-0.0017	GSFLVDAEGIVR

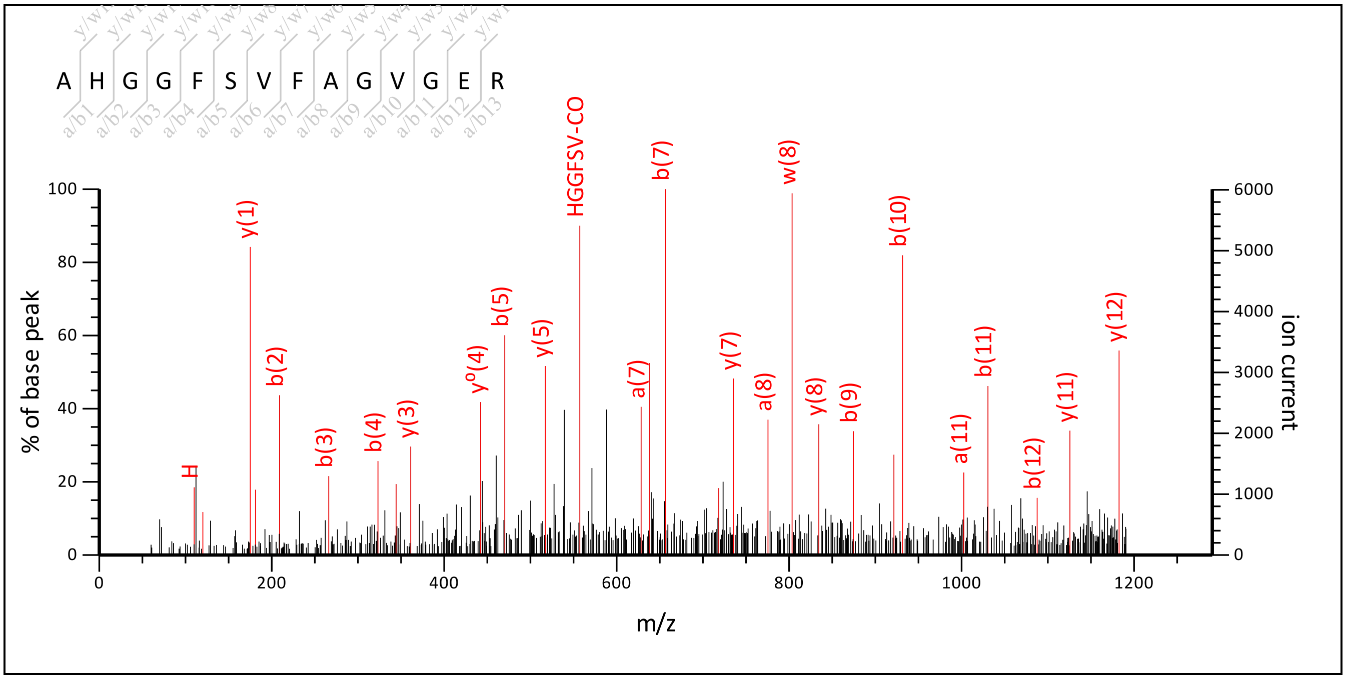
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **AHGGFSVFAGVGER**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 200: 1389.721024 from(1390.728300,1+) intensity(0.0000) index(17)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228324, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 1290.69

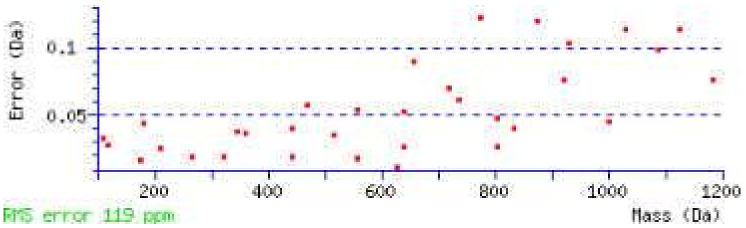
Label all possible matches ○ Label matches used for scoring ●

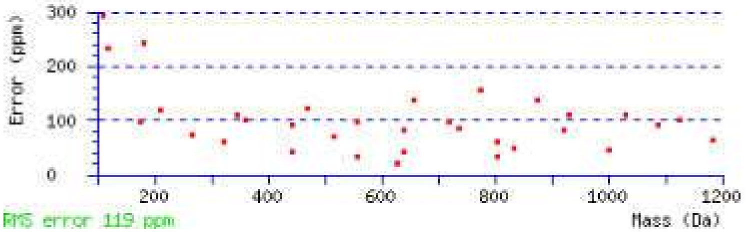
Monoisotopic mass of neutral peptide Mr(calc): 1389.6790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 101 **Expect:** 2.9e-06
Matches : 35/213 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		72.0444		44.0495	A						14
2	110.0713	**181.1084**		***209.1033***			H	1237.5960		1319.6491	1302.6226	1301.6385	13
3	30.0338	238.1299		***266.1248***			G			**1182.5902**	1165.5636	1164.5796	12
4	30.0338	295.1513		***323.1462***			G			**1125.5687**	1108.5422	1107.5582	11
5	120.0808	**442.2197**		***470.2146***			F	976.4847		1068.5473	1051.5207	1050.5367	10
6	60.0444	529.2518	511.2412	***557.2467***	539.2361	513.2568	S	889.4526	888.4574	**921.4789**	904.4523	903.4683	9
7	72.0808	**628.3202**	610.3096	***656.3151***	638.3045	614.3045	V	790.3842	803.4046	**834.4468**	817.4203	816.4363	8
8	120.0808	**775.3886**	757.3780	***803.3835***	785.3729		F	643.3158		**735.3784**	718.3519	717.3678	7
9	44.0495	846.4257	828.4151	***874.4206***	856.4100		A	572.2787		588.3100	571.2835	570.2994	6
10	30.0338	903.4472	885.4366	***931.4421***	913.4315		G			**517.2729**	500.2463	499.2623	5
11	72.0808	**1002.5156**	984.5050	***1030.5105***	1012.4999	988.4999	V	416.1888	429.2092	460.2514	443.2249	442.2409	4

12	30.0338	1059.5370	1041.5265	***1087.5320***	1069.5214		G			**361.1830**	344.1565	343.1724	3
13	102.0550	1188.5796	1170.5691	1216.5745	1198.5640	1130.5742	E	230.1248	229.1295	304.1615	287.1350	286.1510	2
14	129.1135						R	74.0237	73.0284	**175.1190**	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HG	167.0927	195.0877	HGG	224.1142	252.1091	HGGF	371.1826	399.1775
HGGFS	458.2146	486.2096	HGGFSV	557.2831	585.2780	GG	87.0553	115.0502
GGF	234.1237	262.1186	GGFS	321.1557	349.1506	GGFSV	420.2241	448.2191
GGFSVF	567.2926	595.2875	GGFSVFA	638.3297	666.3246	GGFSVFAG	695.3511	723.3461
GF	177.1022	205.0972	GFS	264.1343	292.1292	GFSV	363.2027	391.1976
GFSVF	510.2711	538.2660	GFSVFA	581.3082	609.3031	GFSVFAG	638.3297	666.3246
FS	207.1128	235.1077	FSV	306.1812	334.1761	FSVF	453.2496	481.2445
FSVFA	524.2867	552.2817	FSVFAG	581.3082	609.3031	FSVFAGV	680.3766	708.3715
SV	159.1128	187.1077	SVF	306.1812	334.1761	SVFA	377.2183	405.2132
SVFAG	434.2398	462.2347	SVFAGV	533.3082	561.3031	SVFAGVG	590.3297	618.3246
VF	219.1492	247.1441	VFA	290.1863	318.1812	VFAG	347.2078	375.2027
VFAGV	446.2762	474.2711	VFAGVG	503.2976	531.2926	VFAGVGE	632.3402	660.3352
FA	191.1179	219.1128	FAG	248.1394	276.1343	FAGV	347.2078	375.2027
FAGVG	404.2292	432.2241	FAGVGE	533.2718	561.2667	AG	101.0709	129.0659
AGV	200.1394	228.1343	AGVG	257.1608	285.1557	AGVGE	386.2034	414.1983
GV	129.1022	157.0972	GVG	186.1237	214.1186	GVGE	315.1663	343.1612
VG	129.1022	157.0972	VGE	258.1448	286.1397	GE	159.0764	187.0713





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
101.0	1389.6790	0.0421	AHGGFSVFAGVGER
85.1	1389.6790	0.0421	QHGFSVFAGVGER
82.5	1389.6790	0.0421	AHGGYAVFAGVGER
45.6	1389.6459	0.0751	AHGGYSVMAGVGER
40.6	1389.7405	-0.0195	AIFAGQFVDVPAR

36.9	1389.6922	0.0288	ENILVSMGAVGER
31.6	1389.7075	0.0135	MNDVPVFIVSNR
31.2	1389.6381	0.0829	CPADLAVMGVDAR
31.1	1389.7616	-0.0406	VITKVDFQVDAR
30.8	1389.6790	0.0421	GFPSAQTGQGVWR

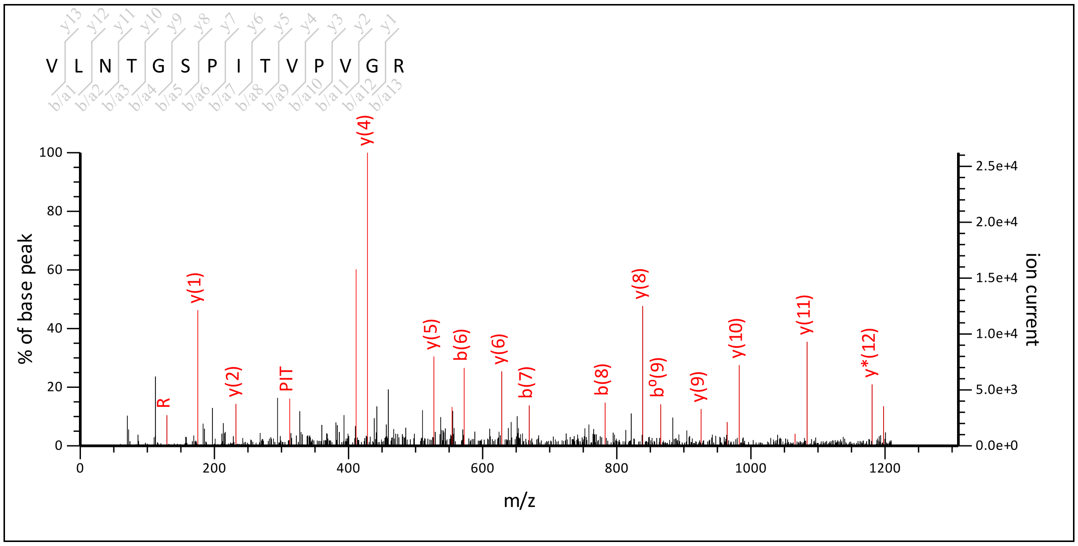
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **VLNTGSPITVPVGR**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 204: 1408.845824 from(1409.853100,1+) intensity(0.0000) index(19)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228322, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 1309.38

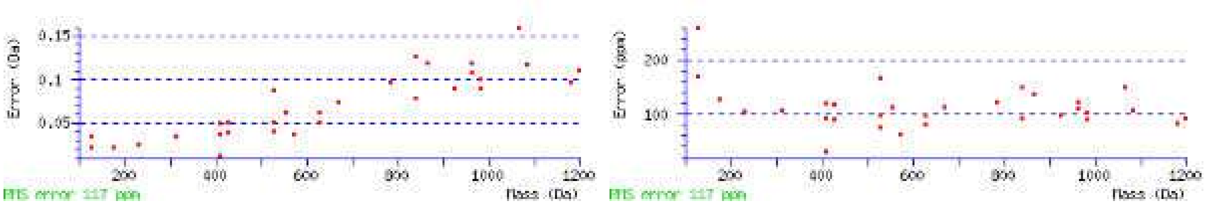
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1408.8038
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 98 **Expect:** 3.1e-06
Matches : 34/257 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	72.0808	72.0808			100.0757			44.0495		V						
2	86.0964	185.1648			213.1598			143.1179		L	1252.6644	1251.6692		1310.7427	1293.7161	129
3	87.0553	299.2078	282.1812		327.2027	310.1761		256.2020		N	1138.6215	1137.6263		***1197.6586***	1180.6321	11
4	74.0600	400.2554	383.2289	382.2449	**428.2504**	411.2238	410.2398	384.2605	386.2398	T	1037.5738	1050.5942	1052.5735	***1083.6157***	1066.5891	10
5	30.0338	457.2769	440.2504	439.2663	485.2718	468.2453	467.2613			G				***982.5680***	965.5415	9
6	60.0444	544.3089	527.2824	526.2984	**572.3039**	555.2773	554.2933	528.3140		S	893.5203	892.5251		***925.5465***	908.5200	9
7	70.0651	641.3617	624.3352	623.3511	**669.3566**	652.3301	651.3461	615.3461		P	796.4676	795.4723		***838.5145***	821.4880	8
8	86.0964	754.4458	737.4192	736.4352	**782.4407**	765.4141	764.4301	726.4145	740.4301	I	683.3835	696.4039	710.4196	741.4618	724.4352	7
9	74.0600	855.4934	838.4669	837.4829	883.4884	866.4618	865.4778	839.4985	841.4778	T	582.3358	595.3562	597.3355	***628.3777***	611.3511	6
10	72.0808	954.5619	937.5353	936.5513	**982.5568**	965.5302	964.5462	940.5462		V	483.2674	496.2878		***527.3300***	510.3035	
11	70.0651	1051.6146	1034.5881	1033.6041	1079.6095	1062.5830	1061.5990	1025.5990		P	386.2146	385.2194		***428.2616***	411.2350	
12	72.0808	1150.6830	1133.6565	1132.6725	1178.6780	1161.6514	1160.6674	1136.6674		V	287.1462	300.1666		331.2088	314.1823	
13	30.0338	1207.7045	1190.6780	1189.6939	1235.6994	1218.6729	1217.6889			G				***232.1404***	215.1139	
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LN	200.1394	228.1343	LNT	301.1870	329.1819	LNTG	358.2085	386.2034
LNTGS	445.2405	473.2354	LNTGSP	542.2933	570.2882	LNTGSPI	655.3774	683.3723
NT	188.1030	216.0979	NTG	245.1244	273.1193	NTGS	332.1565	360.1514
NTGSP	429.2092	457.2041	NTGSPI	542.2933	570.2882	NTGSPIT	643.3410	671.3359
TG	131.0815	159.0764	TGS	218.1135	246.1084	TGSP	315.1663	343.1612
TGSPI	428.2504	456.2453	TGSPIT	529.2980	557.2930	TGSPITV	628.3665	656.3614
GS	117.0659	145.0608	GSP	214.1186	242.1135	GSPI	327.2027	355.1976

GSPIT	428.2504	456.2453	**GSPITV**	527.3188	555.3137	**GSPITVP**	624.3715	652.3665
SP	157.0972	185.0921	**SPI**	270.1812	298.1761	**SPIT**	371.2289	399.2238
SPITV	470.2973	498.2922	**SPITVP**	567.3501	595.3450	**SPITVPV**	666.4185	694.4134
PI	183.1492	211.1441	**PIT**	284.1969	312.1918	**PITV**	383.2653	411.2602
PITVP	480.3180	508.3130	**PITVPV**	579.3865	607.3814	**PITVPVG**	636.4079	664.4028
IT	187.1441	215.1390	**ITV**	286.2125	314.2074	**ITVP**	383.2653	411.2602
ITVPV	482.3337	510.3286	**ITVPVG**	539.3552	567.3501	**TV**	173.1285	201.1234
TVP	270.1812	298.1761	**TVPV**	369.2496	397.2445	**TVPVG**	426.2711	454.2660
VP	169.1335	197.1285	**VPV**	268.2020	296.1969	**VPVG**	325.2234	353.2183
PV	169.1335	197.1285	**PVG**	226.1550	254.1499	**VG**	129.1022	157.0972



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
97.7	1408.8038	0.0420	VLNTGSPITVPVGR
38.9	1408.8038	0.0420	IAEGALTAALAVPGR
37.1	1408.7675	0.0784	AVDTGQPITVPVGR
36.5	1408.7463	0.0995	GTNWLPLDALPGR
34.5	1408.8038	0.0420	LGEKGSPLISPGVR
32.9	1408.7787	0.0672	ATSAPVEARVPVGR
31.8	1408.8402	0.0056	RSIAGLALPLSVVN
31.4	1408.8554	-0.0096	WLKSLLQLVPGR
30.7	1408.8263	0.0196	TQPTATRLLRPR
30.6	1408.8402	0.0056	QLDALSPLKVLGR

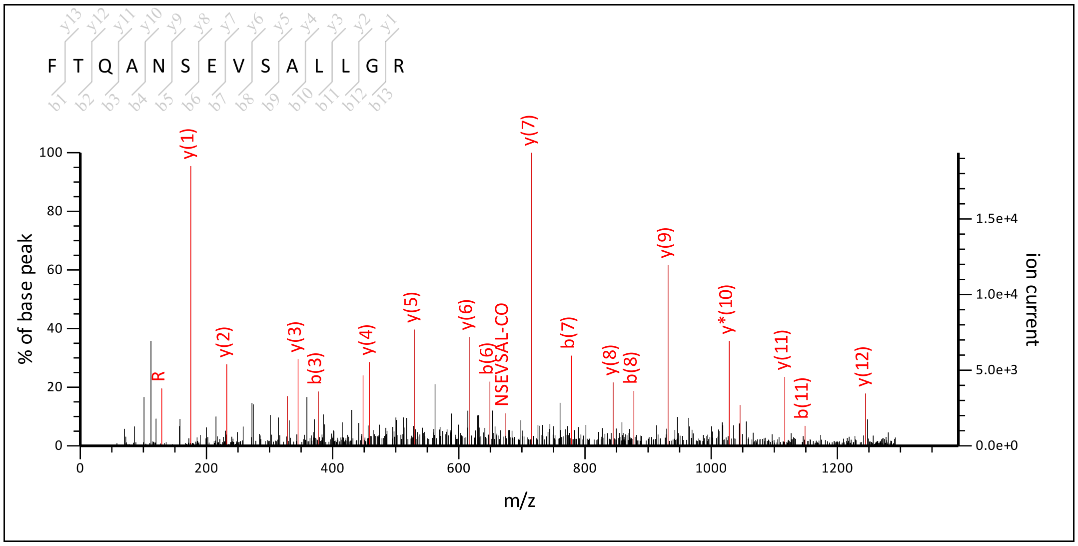
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **FTQANSEVSALLGR**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 223: 1491.812224 from(1492.819500,1+) intensity(0.0000) index(22)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228321, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 1391.82

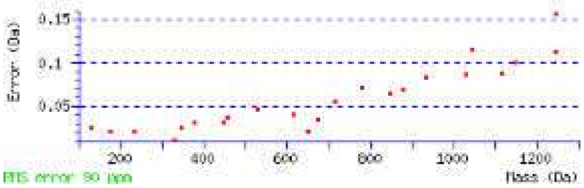
Label all possible matches ○ Label matches used for scoring ●

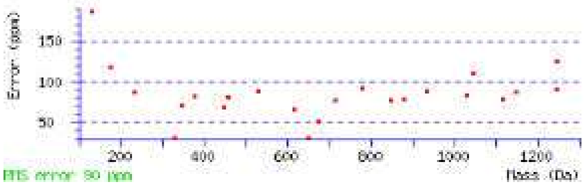
Monoisotopic mass of neutral peptide Mr(calc): 1491.7681
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 123 **Expect:** 1.5e-08
Matches : 23/251 fragment ions using 26 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	120.0808	120.0808			148.0757			44.0495		F					
2	74.0600	221.1285		203.1179	249.1234		231.1128	205.1335	207.1128	T	1299.6652	1312.6856	1314.6648	1345.7070	1328.6805
3	101.0709	349.1870	332.1605	331.1765	**377.1819**	360.1554	359.1714	292.1656		Q	1171.6066	1170.6113		***1244.6593***	1227.6328
4	44.0495	420.2241	403.1976	402.2136	**448.2191**	431.1925	430.2085			A	1100.5695			***1116.6008***	1099.5742
5	87.0553	534.2671	517.2405	516.2565	562.2620	545.2354	544.2514	491.2613		N	986.5265	985.5313		***1045.5636***	1028.5371
6	60.0444	621.2991	604.2726	603.2885	**649.2940**	632.2675	631.2835	605.3042		S	899.4945	898.4993		***931.5207***	914.4942
7	102.0550	750.3417	733.3151	732.3311	**778.3366**	761.3101	760.3260	692.3362		E	770.4519	769.4567		***844.4887***	827.4621
8	72.0808	849.4101	832.3836	831.3995	**877.4050**	860.3785	859.3945	835.3945		V	671.3835	684.4039		***715.4461***	698.4196
9	60.0444	936.4421	919.4156	918.4316	964.4371	947.4105	946.4265	920.4472		S	584.3515	583.3562		***616.3777***	599.3511
10	44.0495	1007.4792	990.4527	989.4687	1035.4742	1018.4476	1017.4636			A	513.3144			***529.3457***	512.3191
11	86.0964	1120.5633	1103.5368	1102.5527	**1148.5582**	1131.5317	1130.5477	1078.5164		L	400.2303	399.2350		***458.3085***	441.2820
12	86.0964	1233.6474	1216.6208	1215.6368	1261.6423	1244.6157	1243.6317	1191.6004		L	287.1462	286.1510		***345.2245***	328.1979
13	30.0338	1290.6688	1273.6423	1272.6583	1318.6638	1301.6372	1300.6532			G				***232.1404***	215.1139
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TQ	202.1186	230.1135	TQA	273.1557	301.1506	TQAN	387.1987	415.1936
TQANS	474.2307	502.2256	TQANSE	603.2733	631.2682	QA	172.1081	200.1030
QAN	286.1510	314.1459	QANS	373.1830	401.1779	QANSE	502.2256	530.2205
QANSEV	601.2940	629.2889	QANSEVS	688.3260	716.3210	AN	158.0924	186.0873
ANS	245.1244	273.1193	ANSE	374.1670	402.1619	ANSEV	473.2354	501.2304
ANSEVS	560.2675	588.2624	ANSEVSA	631.3046	659.2995	NS	174.0873	202.0822
NSE	303.1299	331.1248	NSEV	402.1983	430.1932	NSEVS	489.2304	517.2253

NSEVSA	560.2675	588.2624	**NSEVSAL**	673.3515	701.3464	**SE**	189.0870	217.0819
SEV	288.1554	316.1503	**SEVS**	375.1874	403.1823	**SEVSA**	446.2245	474.2195
SEVSAL	559.3086	587.3035	**SEVSALL**	672.3927	700.3876	**EV**	201.1234	229.1183
EVS	288.1554	316.1503	**EVSA**	359.1925	387.1874	**EVSAL**	472.2766	500.2715
EVSALL	585.3606	613.3556	**EVSALLG**	642.3821	670.3770	**VS**	159.1128	187.1077
VSA	230.1499	258.1448	**VSAL**	343.2340	371.2289	**VSALL**	456.3180	484.3130
VSALLG	513.3395	541.3344	**SA**	131.0815	159.0764	**SAL**	244.1656	272.1605
SALL	357.2496	385.2445	**SALLG**	414.2711	442.2660	**AL**	157.1335	185.1285
ALL	270.2176	298.2125	**ALLG**	327.2391	355.2340	**LL**	199.1805	227.1754
LLG	256.2020	284.1969	**LG**	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
123.1	1491.7681	0.0441	FTQANSEVSALLGR
84.3	1491.7834	0.0288	FTQAGSWVSALLGR
48.3	1491.8297	-0.0175	YTLAVTEVSALLGR
39.4	1491.6987	0.1135	MEATAEEVDRAVR
36.1	1491.7794	0.0329	FTQAGSEISARLGR
34.8	1491.7318	0.0805	STSTAQSDWLAAVR
34.7	1491.7529	0.0593	ITGSGSLGATTDSLGR
32.0	1491.7967	0.0155	KTTGIDTSAAVAVMK
31.4	1491.7351	0.0771	LAVSEAKGGSAMAER
31.0	1491.7100	0.1022	VGETASRGMDNLAR

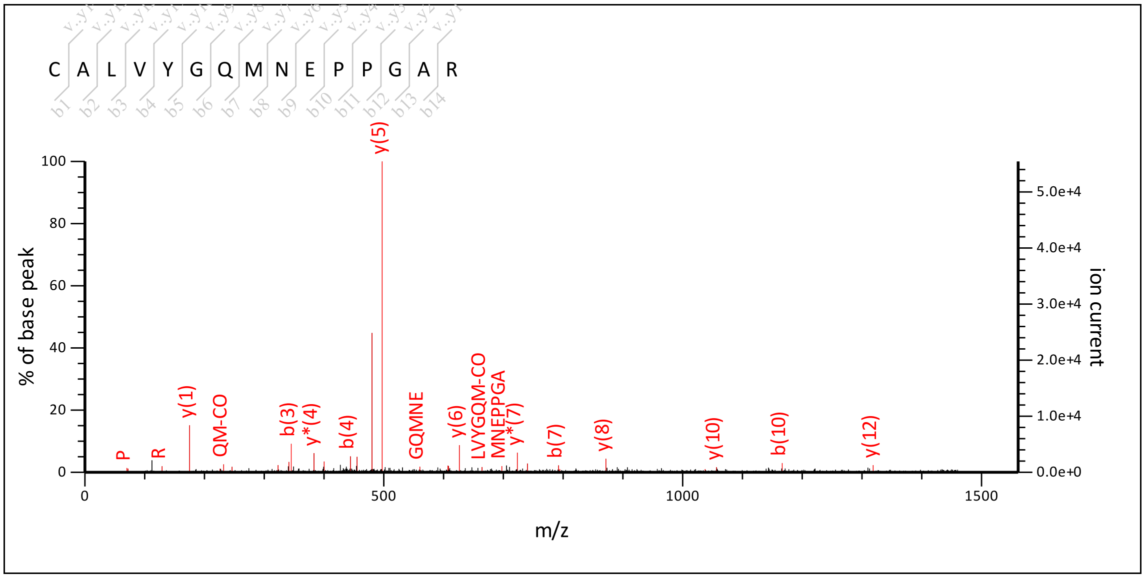
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **CALVYGQMNEPPGAR**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 235: 1661.814424 from(1662.821700,1+) intensity(0.0000) index(24)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228325, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 1561.27

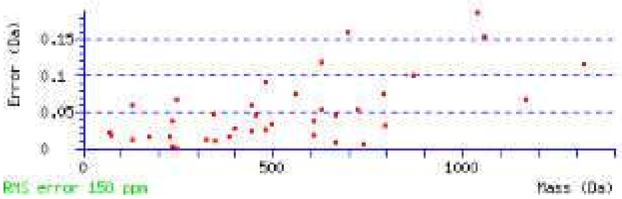
Label all possible matches ○ Label matches used for scoring ●

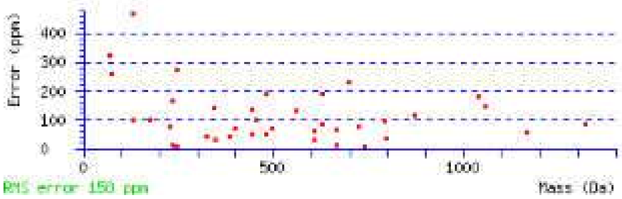
Monoisotopic mass of neutral peptide Mr(calc): 1661.7654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 0.034
Matches : 40/237 fragment ions using 56 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	133.0430	133.0430			161.0379			44.0495	C						15
2	44.0495	204.0801			***232.0750***				A	1486.7107		1502.7420	1485.7155	1484.7315	14
3	86.0964	317.1642			***345.1591***			275.1172	L	1373.6267	1372.6314	1431.7049	1414.6784	1413.6943	13
4	72.0808	416.2326			***444.2275***			402.2170	V	1274.5582	1287.5786	***1318.6208***	1301.5943	1300.6103	12
5	136.0757	579.2959			***607.2908***				Y	1111.4949		1219.5524	1202.5259	1201.5419	11
6	30.0338	636.3174			***664.3123***				G			***1056.4891***	1039.4626	1038.4785	10
7	101.0709	764.3760	747.3494		***792.3709***	775.3443		707.3545	Q	926.4149	925.4196	999.4676	982.4411	981.4571	9
8	104.0528	895.4165	878.3899		923.4114	906.3848		835.4131	M	795.3744	794.3791	***871.4091***	854.3825	853.3985	8
9	87.0553	1009.4594	992.4328		***1037.4543***	1020.4278		966.4536	N	681.3315	680.3362	***740.3686***	723.3420	722.3580	7
10	102.0550	1138.5020	1121.4754	1120.4914	***1166.4969***	1149.4703	1148.4863	1080.4965	E	552.2889	551.2936	***626.3257***	609.2991	608.3151	6
11	70.0651	1235.5547	1218.5282	1217.5442	1263.5497	1246.5231	1245.5391	1209.5391	P	455.2361	454.2409	***497.2831***	480.2565		5
12	70.0651	1332.6075	1315.5810	1314.5969	1360.6024	1343.5759	1342.5919	1306.5919	P	358.1833	357.1881	***400.2303***	383.2037		4
13	30.0338	1389.6290	1372.6024	1371.6184	1417.6239	1400.5973	1399.6133		G			303.1775	286.1510		3
14	44.0495	1460.6661	1443.6395	1442.6555	1488.6610	1471.6345	1470.6504		A	230.1248		***246.1561***	229.1295		2
15	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AL	157.1335	185.1285	ALV	256.2020	284.1969	ALVY	419.2653	447.2602
ALVYG	476.2867	504.2817	ALVYGQ	604.3453	632.3402	LV	185.1648	213.1598
LVY	348.2282	376.2231	LVYG	405.2496	433.2445	LVYGQ	533.3082	561.3031

LVYGQM	664.3487	692.3436	**VY**	235.1441	263.1390	**VYG**	292.1656	320.1605
VYGQ	420.2241	448.2191	**VYGQM**	551.2646	579.2595	**VYGQMN**	665.3076	693.3025
YG	193.0972	221.0921	**YGQ**	321.1557	349.1506	**YGQM**	452.1962	480.1911
YGQMN	566.2391	594.2341	**YGQMNE**	695.2817	723.2767	**GQ**	158.0924	186.0873
GQM	289.1329	317.1278	**GQMN**	403.1758	431.1707	**GQMNE**	532.2184	560.2133
GQMNEP	629.2712	657.2661	**QM**	232.1114	260.1063	**QMN**	346.1544	374.1493
QMNE	475.1969	503.1919	**QMNEP**	572.2497	600.2446	**QMNEPP**	669.3025	697.2974
MN	218.0958	246.0907	**MNE**	347.1384	375.1333	**MNEP**	444.1911	472.1860
MNEPP	541.2439	569.2388	**MNEPPG**	598.2654	626.2603	**MNEPPGA**	669.3025	697.2974
NE	216.0979	244.0928	**NEP**	313.1506	341.1456	**NEPP**	410.2034	438.1983
NEPPG	467.2249	495.2198	**NEPPGA**	538.2620	566.2569	**EP**	199.1077	227.1026
EPP	296.1605	324.1554	**EPPG**	353.1819	381.1769	**EPPGA**	424.2191	452.2140
PP	167.1179	195.1128	**PPG**	224.1394	252.1343	**PPGA**	295.1765	323.1714
PG	127.0866	155.0815	**PGA**	198.1237	226.1186	**GA**	101.0709	129.0659





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.3	1661.7654	0.0490	ACLVYGQMNEPPGAR
59.4	1661.7654	0.0490	CALVYGQMNEPPGAR
59.4	1661.7654	0.0490	CALVYGQMNEPPGAR
42.1	1661.7654	0.0490	VALCYGQMNEPPGAR
42.1	1661.7654	0.0490	VALCYGQMNEPPGAR
39.3	1661.7654	0.0490	CSLVFGQMNEPPGAR
29.6	1661.7654	0.0490	CALVFGQMNEPPGAR
28.9	1661.8737	-0.0592	QPGDGELKVIEPAPGR
27.3	1661.8373	-0.0229	QPGDGELNIIEPAPGR
26.1	1661.9213	-0.1068	QPKGSQLLAAAPSPAAR

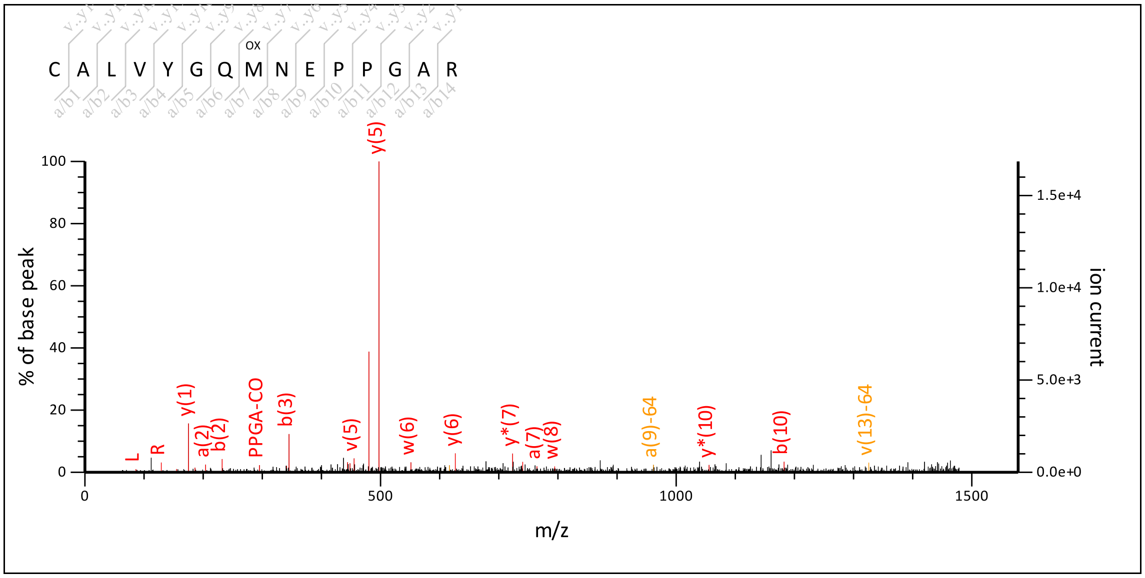
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **CALVYGQMNEPPGAR**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 238: 1677.802324 from(1678.809600,1+) intensity(0.0000) index(25)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228336, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 1578.39

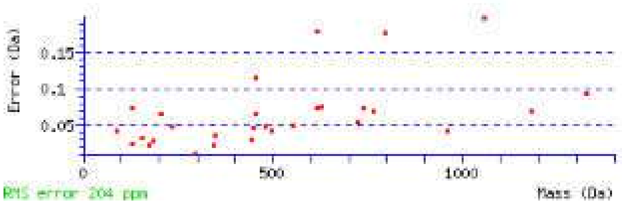
Label all possible matches ○ Label matches used for scoring ●

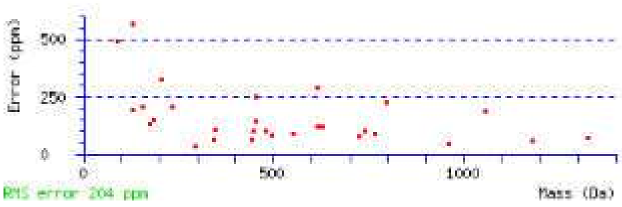
```
Monoisotopic mass of neutral peptide Mr(calc): 1677.7603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 13  Expect: 1.3e+03
Matches : 29/340 fragment ions using 60 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	133.0430	133.0430			161.0379			44.0495	C						15
2	44.0495	**204.0801**			***232.0750***				A	1502.7056		1518.7369	1501.7104	1500.7264	14
3	86.0964	317.1642			***345.1591***			275.1172	L	1389.6216	1388.6263	1447.6998	1430.6733	1429.6893	13
4	72.0808	416.2326			***444.2275***			402.2170	V	1290.5532	1303.5736	1334.6158	1317.5892	1316.6052	12
5	136.0757	579.2959			607.2908				Y	1127.4898		1235.5473	1218.5208	1217.5368	11
6	30.0338	636.3174			664.3123				G			1072.4840	1055.4575	1054.4735	10
7	101.0709	**764.3760**	747.3494		792.3709	775.3443		707.3545	Q	942.4098	941.4145	1015.4626	998.4360	997.4520	9
8	120.0478	911.4114	894.3848		939.4063	922.3797		835.4131	M	795.3744	794.3791	887.4040	870.3774	869.3934	8
9	87.0553	1025.4543	1008.4278		1053.4492	1036.4227		982.4485	N	681.3315	680.3362	***740.3686***	723.3420	722.3580	7
10	102.0550	1154.4969	1137.4703	1136.4863	***1182.4918***	1165.4653	1164.4812	1096.4914	E	552.2889	551.2936	***626.3257***	609.2991	608.3151	6
11	70.0651	1251.5497	1234.5231	1233.5391	1279.5446	1262.5180	1261.5340	1225.5340	P	455.2361	454.2409	***497.2831***	480.2565		5
12	70.0651	1348.6024	1331.5759	1330.5919	1376.5973	1359.5708	1358.5868	1322.5868	P	358.1833	357.1881	400.2303	383.2037		4
13	30.0338	1405.6239	1388.5973	1387.6133	1433.6188	1416.5923	1415.6082		G			303.1775	286.1510		3
14	44.0495	1476.6610	1459.6345	1458.6504	1504.6559	1487.6294	1486.6453		A	230.1248		246.1561	229.1295		2
15	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

AL	157.1335	185.1285	**ALV**	256.2020	284.1969	**ALVY**	419.2653	447.2602
ALVYG	476.2867	504.2817	**ALVYGQ**	604.3453	632.3402	**LV**	185.1648	213.1598
LVY	348.2282	376.2231	**LVYG**	405.2496	433.2445	**LVYGQ**	533.3082	561.3031
LVYGQM	680.3436	708.3385	**VY**	235.1441	263.1390	**VYG**	292.1656	320.1605
VYGQ	420.2241	448.2191	**VYGQM**	567.2595	595.2545	**VYGQMN**	681.3025	709.2974
YG	193.0972	221.0921	**YGQ**	321.1557	349.1506	**YGQM**	468.1911	496.1860
YGQMN	582.2341	610.2290	**GQ**	158.0924	186.0873	**GQM**	305.1278	333.1227
GQMN	419.1707	447.1656	**GQMNE**	548.2133	576.2082	**GQMNEP**	645.2661	673.2610
QM	248.1063	276.1013	**QMN**	362.1493	390.1442	**QMNE**	491.1919	519.1868
QMNEP	588.2446	616.2395	**QMNEPP**	685.2974	713.2923	**MN**	234.0907	262.0856
MNE	363.1333	391.1282	**MNEP**	460.1860	488.1810	**MNEPP**	557.2388	585.2337
MNEPPG	614.2603	642.2552	**MNEPPGA**	685.2974	713.2923	**NE**	216.0979	244.0928
NEP	313.1506	341.1456	**NEPP**	410.2034	438.1983	**NEPPG**	467.2249	495.2198
NEPPGA	538.2620	566.2569	**EP**	199.1077	227.1026	**EPP**	296.1605	324.1554
EPPG	353.1819	381.1769	**EPPGA**	424.2191	452.2140	**PP**	167.1179	195.1128
PPG	224.1394	252.1343	**PPGA**	295.1765	323.1714	**PG**	127.0866	155.0815
PGA	198.1237	226.1186	**GA**	101.0709	129.0659			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.3	1677.8951	-0.0927	AAERPEPGIPTAKWR
14.8	1677.8760	-0.0737	TTMFSSDLPLPKIGR
14.3	1677.8694	-0.0671	MAAQKAQFPIALMAR
14.3	1677.9678	-0.1655	QALKLPYAALLHQGR
14.2	1677.8911	-0.0887	TNALPERATVTVNHR
14.1	1677.7087	0.0936	SMMPSSSSEPTVHGGR
13.7	1677.9050	-0.1026	TATAVPLPEDPAKNVR
13.5	1677.7603	0.0420	ACLVYGQMNEPPGAR
13.5	1677.7603	0.0420	CALVYGQMNEPPGAR
13.5	1677.7603	0.0420	CALVYGQMNEPPGAR

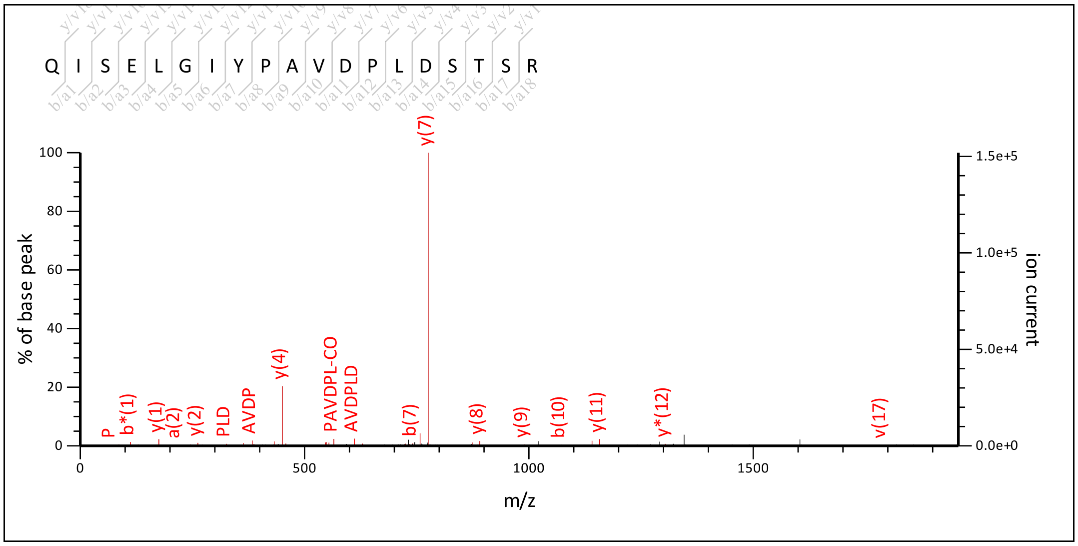
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **QISELGIYPAVDPLDSTSR**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 260: 2060.106524 from(2061.113800,1+) intensity(0.0000) index(31)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228327, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 1957.3

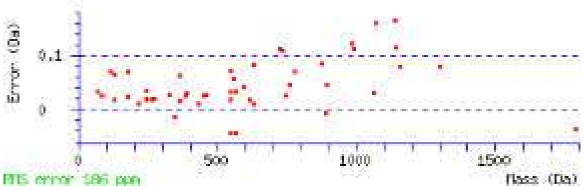
Label all possible matches ○ Label matches used for scoring ●

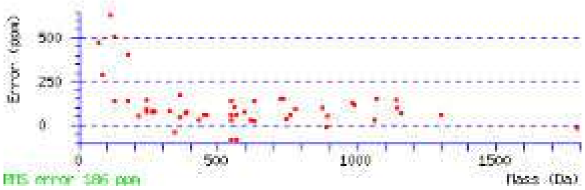
Monoisotopic mass of neutral peptide Mr(calc): 2060.0426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 0.11
Matches : 58/375 fragment ions using 92 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	101.0709	101.0709	84.0444		***129.0659***	112.0393		44.0495		Q						
2	86.0964	214.1550	197.1285		***242.1499***	225.1234		186.1237	200.1394	I	1874.9130	1887.9335	1901.9491	1932.9913	1915.9648	19
3	60.0444	301.1870	284.1605	283.1765	329.1819	312.1554	311.1714	285.1921		S	1787.8810	1786.8858		1819.9072	1802.8807	18
4	102.0550	430.2296	413.2031	412.2191	***458.2245***	441.1980	440.2140	372.2241		E	1658.8384	1657.8432		1732.8752	1715.8487	17
5	86.0964	543.3137	526.2871	525.3031	571.3086	554.2821	553.2980	501.2667		L	1545.7544	1544.7591		1603.8326	1586.8061	15
6	30.0338	600.3352	583.3086	582.3246	***628.3301***	611.3035	610.3195			G				1490.7486	1473.7220	14
7	86.0964	713.4192	696.3927	695.4087	***741.4141***	724.3876	723.4036	685.3879	699.4036	I	1375.6488	1388.6692	1402.6849	1433.7271	1416.7005	14
8	136.0757	876.4825	859.4560	858.4720	904.4775	887.4509	886.4669			Y	1212.5855			1320.6430	1303.6165	13
9	70.0651	973.5353	956.5088	955.5247	1001.5302	984.5037	983.5197	947.5197		P	1115.5327	1114.5375		***1157.5797***	1140.5531	11
10	44.0495	1044.5724	1027.5459	1026.5619	***1072.5673***	1055.5408	1054.5568			A	1044.4956			***1060.5269***	1043.5004	10
11	72.0808	1143.6408	1126.6143	1125.6303	1171.6358	1154.6092	1153.6252	1129.6252		V	945.4272	958.4476		***989.4898***	972.4633	9
12	88.0393	1258.6678	1241.6412	1240.6572	1286.6627	1269.6361	1268.6521	1214.6780		D	830.4003	829.4050		***890.4214***	873.3949	8
13	70.0651	1355.7205	1338.6940	1337.7100	1383.7155	1366.6889	1365.7049	1329.7049		P	733.3475	732.3523		***775.3945***	758.3679	7
14	86.0964	1468.8046	1451.7781	1450.7940	1496.7995	1479.7730	1478.7890	1426.7577		L	620.2634	619.2682		678.3417	661.3151	6
15	88.0393	1583.8316	1566.8050	1565.8210	1611.8265	1594.7999	1593.8159	1539.8417		D	505.2365	504.2413		***565.2576***	548.2311	5
16	60.0444	1670.8636	1653.8370	1652.8530	1698.8585	1681.8319	1680.8479	1654.8687		S	418.2045	417.2092		***450.2307***	433.2041	4
17	74.0600	1771.9113	1754.8847	1753.9007	1799.9062	1782.8796	1781.8956	1755.9163	1757.8956	T	317.1568	330.1772	332.1565	***363.1987***	346.1721	3
18	60.0444	1858.9433	1841.9167	1840.9327	1886.9382	1869.9117	1868.9276	1842.9484		S	230.1248	229.1295		***262.1510***	245.1244	2
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IS	173.1285	201.1234	ISE	302.1710	330.1660	ISEL	415.2551	443.2500
ISELG	472.2766	500.2715	ISELGI	585.3606	613.3556	SE	189.0870	217.0819

SEL	302.1710	330.1660	**SELG**	359.1925	387.1874	**SELGI**	472.2766	500.2715
SELGIY	635.3399	663.3348	**EL**	215.1390	243.1339	**ELG**	272.1605	300.1554
ELGI	385.2445	413.2395	**ELGIY**	548.3079	576.3028	**ELGIYP**	645.3606	673.3556
LG	143.1179	171.1128	**LGI**	256.2020	284.1969	**LGIY**	419.2653	447.2602
LGIYP	516.3180	544.3130	**LGIYPA**	587.3552	615.3501	**LGIYPAV**	686.4236	714.4185
GI	143.1179	171.1128	**GIY**	306.1812	334.1761	**GIYP**	403.2340	431.2289
GIYPA	474.2711	502.2660	**GIYPAV**	573.3395	601.3344	**GIYPAVD**	688.3665	716.3614
IY	249.1598	277.1547	**IYP**	346.2125	374.2074	**IYPA**	417.2496	445.2445
IYPAV	516.3180	544.3130	**IYPAVD**	631.3450	659.3399	**YP**	233.1285	261.1234
YPA	304.1656	332.1605	**YPAV**	403.2340	431.2289	**YPAVD**	518.2609	546.2558
YPAVDP	615.3137	643.3086	**PA**	141.1022	169.0972	**PAV**	240.1707	268.1656
PAVD	355.1976	383.1925	**PAVDP**	452.2504	480.2453	**PAVDPL**	565.3344	593.3293
PAVDPLD	680.3614	708.3563	**AV**	143.1179	171.1128	**AVD**	258.1448	286.1397
AVDP	355.1976	383.1925	**AVDPL**	468.2817	496.2766	**AVDPLD**	583.3086	611.3035
AVDPLDS	670.3406	698.3355	**VD**	187.1077	215.1026	**VDP**	284.1605	312.1554
VDPL	397.2445	425.2395	**VDPLD**	512.2715	540.2664	**VDPLDS**	599.3035	627.2984
DP	185.0921	213.0870	**DPL**	298.1761	326.1710	**DPLD**	413.2031	441.1980
DPLDS	500.2351	528.2300	**DPLDST**	601.2828	629.2777	**DPLDSTS**	688.3148	716.3097
PL	183.1492	211.1441	**PLD**	298.1761	326.1710	**PLDS**	385.2082	413.2031
PLDST	486.2558	514.2508	**PLDSTS**	573.2879	601.2828	**LD**	201.1234	229.1183
LDS	288.1554	316.1503	**LDST**	389.2031	417.1980	**LDSTS**	476.2351	504.2300
DS	175.0713	203.0662	**DST**	276.1190	304.1139	**DSTS**	363.1510	391.1460
ST	161.0921	189.0870	**STS**	248.1241	276.1190	**TS**	161.0921	189.0870





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.3	2060.0790	0.0276	KISELGIYPAVDPLDSTSR
53.3	2060.0426	0.0639	QISELGIYPAVDPLDSTSR
38.8	2060.0426	0.0640	QISELGIYPAVDPLESSSR
26.9	2060.0208	0.0857	LINLMDGDIAVDSQAGLGSR
26.1	2060.0426	0.0639	QIAELGIYPSVDPLDSTSR
16.7	2060.0902	0.0163	ISDGVHIALEPDGTLLASPR
13.0	2060.0724	0.0341	IDAIYDRAALIALPDQMR
12.9	2060.0071	0.0994	MTNPPVFDVPALLEQMSR
12.7	2060.0224	0.0842	FLPFNKGGVMDFMSILGR
12.7	2060.0579	0.0486	DTSGPLVDGFLAISWVDLR

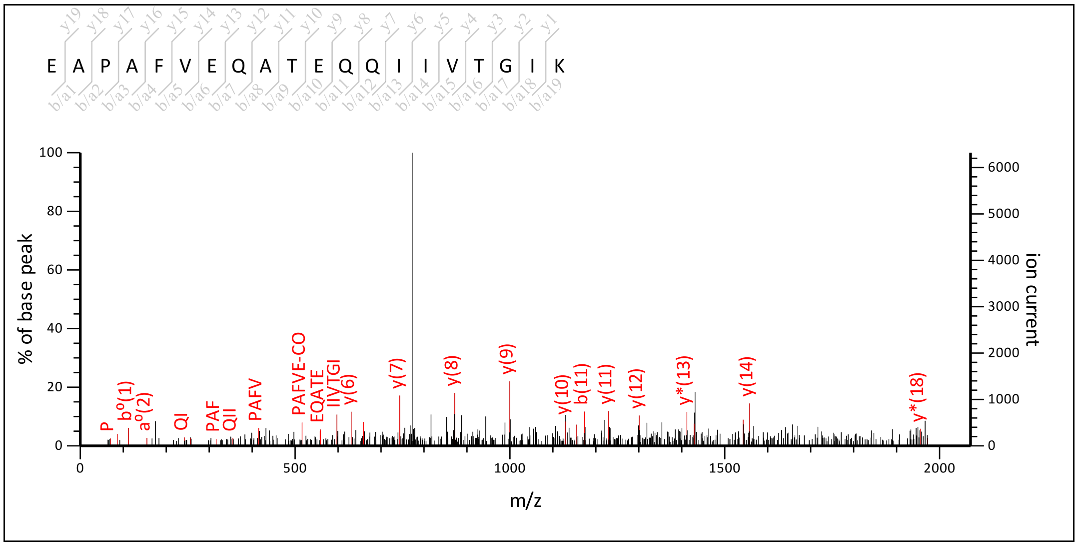
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **EAPAFVEQATEQQIIVTGIK**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 263: 2171.210724 from(2172.218000,1+) intensity(0.0000) index(32)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228335, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 2072.01

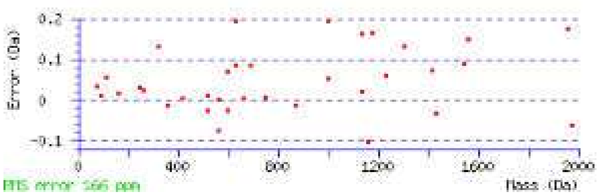
Label all possible matches ○ Label matches used for scoring ●

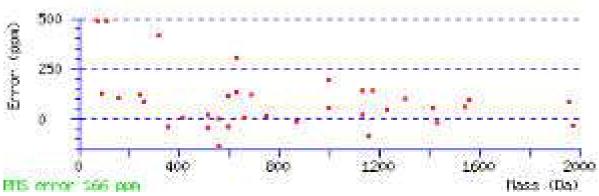
Monoisotopic mass of neutral peptide Mr(calc): 2171.1474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 23
Matches : 38/379 fragment ions using 79 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	44.0495	173.0921		155.0815	201.0870		183.0764			A	2027.0808			2043.1121	2026.0855
3	70.0651	270.1448		252.1343	298.1397		280.1292	244.1292		P	1930.0280	1929.0328		***1972.0750***	1955.0484
4	44.0495	341.1819		323.1714	369.1769		351.1663			A	1858.9909			1875.0222	1857.9957
5	120.0808	488.2504		470.2398	**516.2453**		498.2347			F	1711.9225			1803.9851	1786.9585
6	72.0808	587.3188		569.3082	615.3137		597.3031	573.3031		V	1612.8541	1625.8745		1656.9167	1639.8901
7	102.0550	716.3614		698.3508	744.3563		726.3457	658.3559		E	1483.8115	1482.8162		***1557.8483***	1540.8217
8	101.0709	844.4199	827.3934	826.4094	872.4149	855.3883	854.4043	787.3985		Q	1355.7529	1354.7577		***1428.8057***	1411.7791
9	44.0495	915.4571	898.4305	897.4465	943.4520	926.4254	925.4414			A	1284.7158			***1300.7471***	1283.7205
10	74.0600	1016.5047	999.4782	998.4942	1044.4997	1027.4731	1026.4891	1000.5098	1002.4891	T	1183.6681	1196.6885	1198.6678	***1229.7100***	1212.6834
11	102.0550	1145.5473	1128.5208	1127.5368	**1173.5422**	1156.5157	1155.5317	1087.5419		E	1054.6255	1053.6303		***1128.6623***	1111.6358
12	101.0709	1273.6059	1256.5794	1255.5953	1301.6008	1284.5743	1283.5903	1216.5844		Q	926.5669	925.5717		***999.6197***	982.5932
13	101.0709	1401.6645	1384.6379	1383.6539	1429.6594	1412.6329	1411.6488	1344.6430		Q	798.5084	797.5131		***871.5611***	854.5346
14	86.0964	1514.7486	1497.7220	1496.7380	**1542.7435**	1525.7169	1524.7329	1486.7173	1500.7329	I	685.4243	698.4447	712.4604	***743.5026***	726.4760
15	86.0964	1627.8326	1610.8061	1609.8220	1655.8275	1638.8010	1637.8170	1599.8013	1613.8170	I	572.3402	585.3606	599.3763	***630.4185***	613.3919
16	72.0808	1726.9010	1709.8745	1708.8905	1754.8959	1737.8694	1736.8854	1712.8854		V	473.2718	486.2922		517.3344	500.3079
17	74.0600	1827.9487	1810.9222	1809.9381	1855.9436	1838.9171	1837.9331	1811.9538	1813.9331	T	372.2241	385.2445	387.2238	418.2660	401.2395
18	30.0338	1884.9702	1867.9436	1866.9596	1912.9651	1895.9385	1894.9545			G				317.2183	300.1918
19	86.0964	1998.0542	1981.0277	1980.0437	2026.0492	2009.0226	2008.0386	1970.0229	1984.0386	I	202.1186	215.1390	229.1547	260.1969	243.1703
20	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AP	141.1022	169.0972	APA	212.1394	240.1343	APAF	359.2078	387.2027

APAFV	458.2762	486.2711	**APAFVE**	587.3188	615.3137	**PA**	141.1022	169.0972
PAF	288.1707	316.1656	**PAFV**	387.2391	415.2340	**PAFVE**	516.2817	544.2766
PAFVEQ	644.3402	672.3352	**AF**	191.1179	219.1128	**AFV**	290.1863	318.1812
AFVE	419.2289	447.2238	**AFVEQ**	547.2875	575.2824	**AFVEQA**	618.3246	646.3195
FV	219.1492	247.1441	**FVE**	348.1918	376.1867	**FVEQ**	476.2504	504.2453
FVEQA	547.2875	575.2824	**FVEQAT**	648.3352	676.3301	**VE**	201.1234	229.1183
VEQ	329.1819	357.1769	**VEQA**	400.2191	428.2140	**VEQAT**	501.2667	529.2617
VEQATE	630.3093	658.3042	**EQ**	230.1135	258.1084	**EQA**	301.1506	329.1456
EQAT	402.1983	430.1932	**EQATE**	531.2409	559.2358	**EQATEQ**	659.2995	687.2944
QA	172.1081	200.1030	**QAT**	273.1557	301.1506	**QATE**	402.1983	430.1932
QATEQ	530.2569	558.2518	**QATEQQ**	658.3155	686.3104	**AT**	145.0972	173.0921
ATE	274.1397	302.1347	**ATEQ**	402.1983	430.1932	**ATEQQ**	530.2569	558.2518
ATEQQI	643.3410	671.3359	**TE**	203.1026	231.0975	**TEQ**	331.1612	359.1561
TEQQ	459.2198	487.2147	**TEQQI**	572.3039	600.2988	**TEQQII**	685.3879	713.3828
EQ	230.1135	258.1084	**EQQ**	358.1721	386.1670	**EQQI**	471.2562	499.2511
EQQII	584.3402	612.3352	**EQQIIV**	683.4087	711.4036	**QQ**	229.1295	257.1244
QQI	342.2136	370.2085	**QQII**	455.2976	483.2926	**QQIIV**	554.3661	582.3610
QQIIVT	655.4137	683.4087	**QI**	214.1550	242.1499	**QII**	327.2391	355.2340
QIIV	426.3075	454.3024	**QIIVT**	527.3552	555.3501	**QIIVTG**	584.3766	612.3715
QIIVTGI	697.4607	725.4556	**II**	199.1805	227.1754	**IIV**	298.2489	326.2438
IIVT	399.2966	427.2915	**IIVTG**	456.3180	484.3130	**IIVTGI**	569.4021	597.3970
IV	185.1648	213.1598	**IVT**	286.2125	314.2074	**IVTG**	343.2340	371.2289
IVTGI	456.3180	484.3130	**VT**	173.1285	201.1234	**VTG**	230.1499	258.1448
VTGI	343.2340	371.2289	**TG**	131.0815	159.0764	**TGI**	244.1656	272.1605
GI	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.6	2171.1474	0.0633	EAPAFVEQATEQQIIVTGIK
29.6	2171.1474	0.0633	EAPAFVEQATEQQILVTGIK
18.6	2171.2752	-0.0644	LMALAAVIIFPTLSLITNVR
16.2	2171.2413	-0.0305	QLKSTTLENIISTIEILQK
15.7	2171.1004	0.1103	MTAAQQDNALQVTGLAALEAR
15.6	2171.1474	0.0633	EAPAFVEQETAQQILVTGIK
15.4	2171.2170	-0.0063	ICKTSIMLIIAGALGNLIDR
14.9	2171.0970	0.1137	EWLSSQAELQEQIVARER
13.0	2171.1223	0.0885	IPSAVGYQPTLGTDLGGLQER
12.8	2171.1182	0.0925	DSTGRLLTVLNDDINQLER

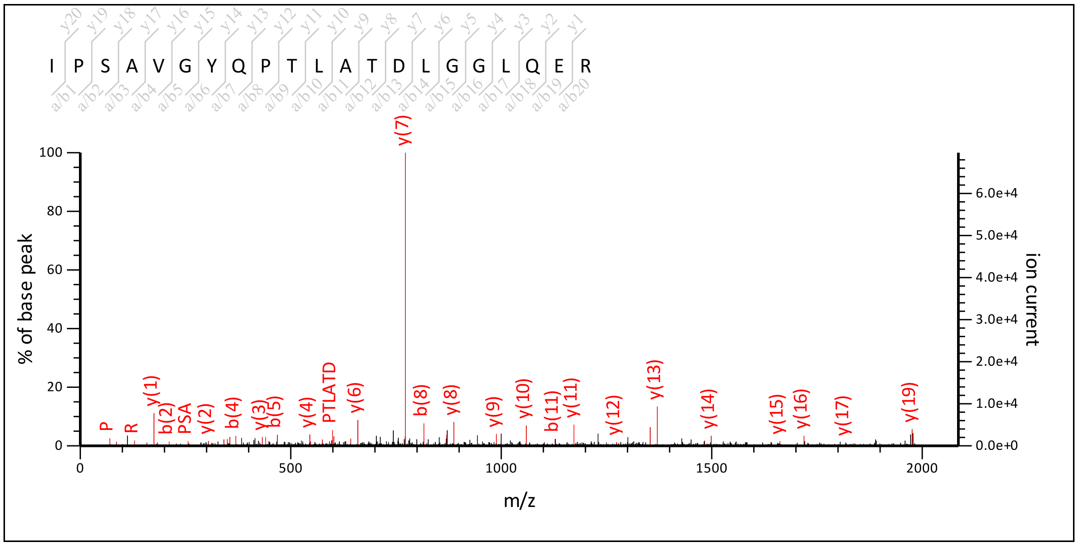
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 85

MS/MS Fragmentation of **IPSAVGYQPTLATDLGGLQER**
Found in **gi|3676294** in **NCBInr**, mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Match to Query 265: 2185.212424 from(2186.219700,1+) intensity(0.0000) index(33)
Title: Label: F15, Spot_Id: 219903, Peak_List_Id: 228323, MSMS Job_Run_Id: 21987, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_F15_136868277600.txt



0 to 2085.93

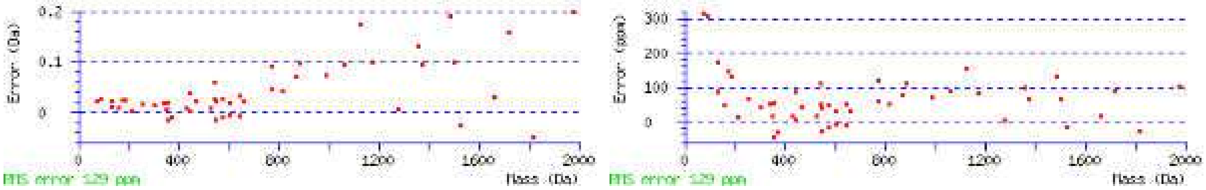
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2185.1379
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 125 **Expect:** 6.1e-09
Matches : 56/405 fragment ions using 80 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	**86.0964**			114.0913			44.0495		I					
2	70.0651	**183.1492**			**211.1441**			157.1335		P	2031.0142	2030.0189		2073.0611	2056.0346
3	60.0444	270.1812		252.1707	298.1761		280.1656	254.1863		S	1943.9821	1942.9869		***1976.0083***	1958.9818
4	44.0495	**341.2183**		323.2078	**369.2132**		351.2027			A	1872.9450			1888.9763	1871.9498
5	72.0808	**440.2867**		422.2762	**468.2817**		450.2711	426.2711		V	1773.8766	1786.8970		***1817.9392***	1800.9127
6	30.0338	497.3082		479.2976	**525.3031**		507.2926			G				***1718.8708***	1701.8442
7	136.0757	660.3715		642.3610	688.3665		670.3559			Y	1553.7918			***1661.8493***	1644.8228
8	101.0709	788.4301	771.4036	770.4196	**816.4250**	799.3985	798.4145	731.4087		Q	1425.7332	1424.7380		***1498.7860***	1481.7595
9	70.0651	885.4829	868.4563	867.4723	913.4778	896.4512	895.4672	859.4672		P	1328.6805	1327.6852		***1370.7274***	1353.7009
10	74.0600	986.5306	969.5040	968.5200	1014.5255	997.4989	996.5149	970.5356	972.5149	T	1227.6328	1240.6532	1242.6325	***1273.6747***	1256.6481
11	86.0964	1099.6146	1082.5881	1081.6041	**1127.6095**	1110.5830	1109.5990	1057.5677		L	1114.5487	1113.5535		***1172.6270***	1155.6004
12	44.0495	1170.6517	1153.6252	1152.6412	1198.6467	1181.6201	1180.6361			A	1043.5116			***1059.5429***	1042.5164
13	74.0600	1271.6994	1254.6729	1253.6889	1299.6943	1282.6678	1281.6838	1255.7045	1257.6838	T	942.4639	955.4843	957.4636	***988.5058***	971.4793
14	88.0393	1386.7264	1369.6998	1368.7158	1414.7213	1397.6947	1396.7107	1342.7365		D	827.4370	826.4417		***887.4581***	870.4316
15	86.0964	1499.8104	1482.7839	1481.7999	**1527.8053**	1510.7788	1509.7948	1457.7635		L	714.3529	713.3577		***772.4312***	755.4046
16	30.0338	1556.8319	1539.8053	1538.8213	1584.8268	1567.8003	1566.8162			G				***659.3471***	642.3206
17	30.0338	1613.8534	1596.8268	1595.8428	1641.8483	1624.8217	1623.8377			G				***602.3257***	585.2991
18	86.0964	1726.9374	1709.9109	1708.9268	1754.9323	1737.9058	1736.9218	1684.8905		L	487.2259	486.2307		***545.3042***	528.2776
19	101.0709	1854.9960	1837.9694	1836.9854	1882.9909	1865.9644	1864.9803	1797.9745		Q	359.1674	358.1721		***432.2201***	415.1936
20	102.0550	1984.0386	1967.0120	1966.0280	2012.0335	1995.0070	1994.0229	1926.0331		E	230.1248	229.1295		***304.1615***	287.1350
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

PS	157.0972	185.0921	**PSA**	228.1343	256.1292	**PSAV**	327.2027	355.1976
PSAVG	384.2241	412.2191	**PSAVGY**	547.2875	575.2824	**PSAVGYQ**	675.3461	703.3410
SA	131.0815	159.0764	**SAV**	230.1499	258.1448	**SAVG**	287.1714	315.1663
SAVGY	450.2347	478.2296	**SAVGYQ**	578.2933	606.2882	**SAVGYQP**	675.3461	703.3410
AV	143.1179	171.1128	**AVG**	200.1394	228.1343	**AVGY**	363.2027	391.1976
AVGYQ	491.2613	519.2562	**AVGYQP**	588.3140	616.3089	**AVGYQPT**	689.3617	717.3566
VG	129.1022	157.0972	**VGY**	292.1656	320.1605	**VGYQ**	420.2241	448.2191
VGYQP	517.2769	545.2718	**VGYQPT**	618.3246	646.3195	**GY**	193.0972	221.0921
GYQ	321.1557	349.1506	**GYQP**	418.2085	446.2034	**GYQPT**	519.2562	547.2511
GYQPTL	632.3402	660.3352	**YQ**	264.1343	292.1292	**YQP**	361.1870	389.1819
YQPT	462.2347	490.2296	**YQPTL**	575.3188	603.3137	**YQPTLA**	646.3559	674.3508
QP	198.1237	226.1186	**QPT**	299.1714	327.1663	**QPTL**	412.2554	440.2504
QPTLA	483.2926	511.2875	**QPTLAT**	584.3402	612.3352	**QPTLATD**	699.3672	727.3621
PT	171.1128	199.1077	**PTL**	284.1969	312.1918	**PTLA**	355.2340	383.2289
PTLAT	456.2817	484.2766	**PTLATD**	571.3086	599.3035	**PTLATDL**	684.3927	712.3876
TL	187.1441	215.1390	**TLA**	258.1812	286.1761	**TLAT**	359.2289	387.2238
TLATD	474.2558	502.2508	**TLATDL**	587.3399	615.3348	**TLATDLG**	644.3614	672.3563
LA	157.1335	185.1285	**LAT**	258.1812	286.1761	**LATD**	373.2082	401.2031
LATDL	486.2922	514.2871	**LATDLG**	543.3137	571.3086	**LATDLGG**	600.3352	628.3301
AT	145.0972	173.0921	**ATD**	260.1241	288.1190	**ATDL**	373.2082	401.2031
ATDLG	430.2296	458.2245	**ATDLGG**	487.2511	515.2460	**ATDLGGL**	600.3352	628.3301
TD	189.0870	217.0819	**TDL**	302.1710	330.1660	**TDLG**	359.1925	387.1874
TDLGG	416.2140	444.2089	**TDLGGL**	529.2980	557.2930	**TDLGGLQ**	657.3566	685.3515
DL	201.1234	229.1183	**DLG**	258.1448	286.1397	**DLGG**	315.1663	343.1612
DLGGL	428.2504	456.2453	**DLGGLQ**	556.3089	584.3039	**DLGGLQE**	685.3515	713.3464
LG	143.1179	171.1128	**LGG**	200.1394	228.1343	**LGGL**	313.2234	341.2183
LGGLQ	441.2820	469.2769	**LGGLQE**	570.3246	598.3195	**GG**	87.0553	115.0502
GGL	200.1394	228.1343	**GGLQ**	328.1979	356.1928	**GGLQE**	457.2405	485.2354
GL	143.1179	171.1128	**GLQ**	271.1765	299.1714	**GLQE**	400.2191	428.2140
LQ	214.1550	242.1499	**LQE**	343.1976	371.1925	**QE**	230.1135	258.1084



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
125.4	2185.1379	0.0745	IPSAVGYQPTLATDLGGLQER
95.5	2185.1379	0.0745	IPSAVGYQPTLATDVGALQER
68.4	2185.1379	0.0745	IPSAVGYQPTLASDLGALQER
23.3	2185.0909	0.1215	QLAAMQGDVEQQVARLQER
21.0	2185.2219	-0.0095	VLLAAQLAIGFTTAVDGRVDR
15.9	2185.0610	0.1514	ESAGRADEEEILNQVEQLR
15.0	2185.1895	0.0229	IPTAYIKTFQGPPAGIQVER
14.3	2185.2219	-0.0095	VALIAFTGSVAGGLAVQKAAADR
14.3	2185.1967	0.0157	APSLPHQAIDLNAKVASIGQR
14.2	2185.1855	0.0269	KLVHIPQALLEGDDAPGAVSR

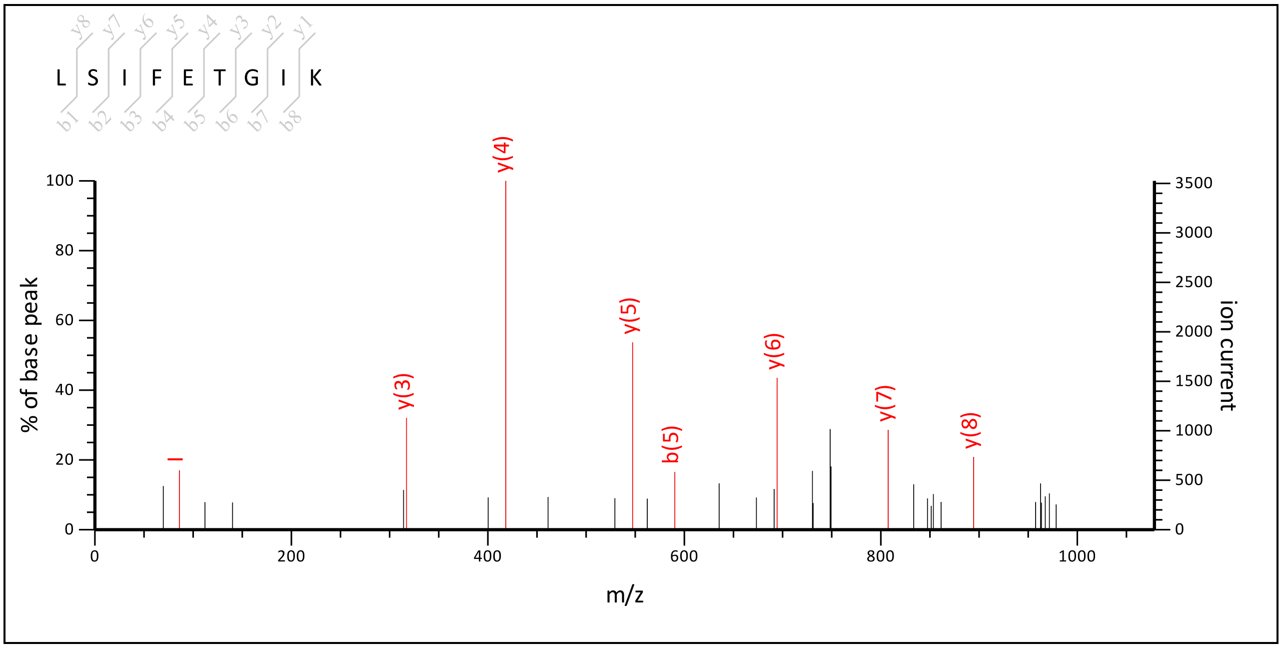
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **LSIFETGIK**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 3: 1006.647224 from(1007.654500,1+) intensity(0.0000) index(1)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221245, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1078.49

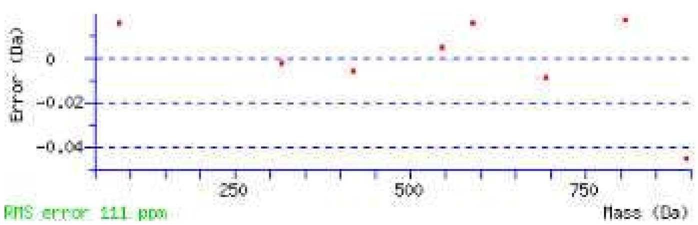
Label all possible matches ○ Label matches used for scoring ●

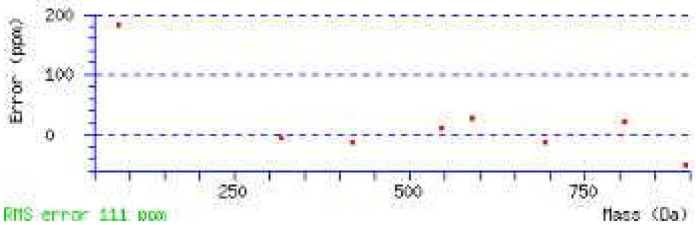
Monoisotopic mass of neutral peptide Mr(calc): `1006.5699`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `53` **Expect:** `0.03`
Matches : `11/125 fragment ions using 9 most intense peaks` (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		44.0495		**L**							**9**
2	60.0444	173.1285	155.1179	201.1234	183.1128	157.1335		**S**	862.4669	861.4716		***894.4931***	877.4666	876.4825	**8**
3	86.0964	286.2125	268.2020	314.2074	296.1969	258.1812	272.1969	**I**	749.3828	762.4032	776.4189	***807.4611***	790.4345	789.4505	**7**
4	120.0808	433.2809	415.2704	461.2758	443.2653			**F**	602.3144			***694.3770***	677.3505	676.3665	**6**
5	102.0550	562.3235	544.3130	590.3184	572.3079	504.3180		**E**	473.2718	472.2766		***547.3086***	530.2821	529.2980	**5**
6	74.0600	663.3712	645.3606	691.3661	673.3556	647.3763	649.3556	**T**	372.2241	385.2445	387.2238	***418.2660***	401.2395	400.2554	**4**
7	30.0338	720.3927	702.3821	748.3876	730.3770			**G**				***317.2183***	300.1918		**3**
8	86.0964	833.4767	815.4662	861.4716	843.4611	805.4454	819.4611	**I**	202.1186	215.1390	229.1547	260.1969	243.1703		**2**
9	101.1073							**K**	74.0237	73.0284		147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SI	173.1285	201.1234	**SIF**	320.1969	348.1918	**SIFE**	449.2395	477.2344
SIFET	550.2871	578.2821	**SIFETG**	607.3086	635.3035	**IF**	233.1648	261.1598
IFE	362.2074	390.2023	**IFET**	463.2551	491.2500	**IFETG**	520.2766	548.2715

IFETGI	633.3606	661.3556	**FE**	249.1234	277.1183	**FET**	350.1710	378.1660
FETG	407.1925	435.1874	**FETGI**	520.2766	548.2715	**ET**	203.1026	231.0975
ETG	260.1241	288.1190	**ETGI**	373.2082	401.2031	**TG**	131.0815	159.0764
TGI	244.1656	272.1605	**GI**	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.5	1006.5699	0.0773	LSIFETGIK
53.5	1006.5699	0.0773	LSIFETGIK
53.5	1006.5699	0.0773	LSIFETGIK
53.5	1006.5699	0.0773	LSIFETGIK
53.5	1006.5699	0.0773	LSIFETGIK
53.5	1006.5699	0.0773	LSIFETGIK
53.5	1006.5699	0.0773	LSIFETGIK
53.5	1006.5699	0.0773	LSIFETGLK
53.5	1006.5699	0.0773	LSIFETGLK
53.5	1006.5369	0.1104	LSIMETGIK

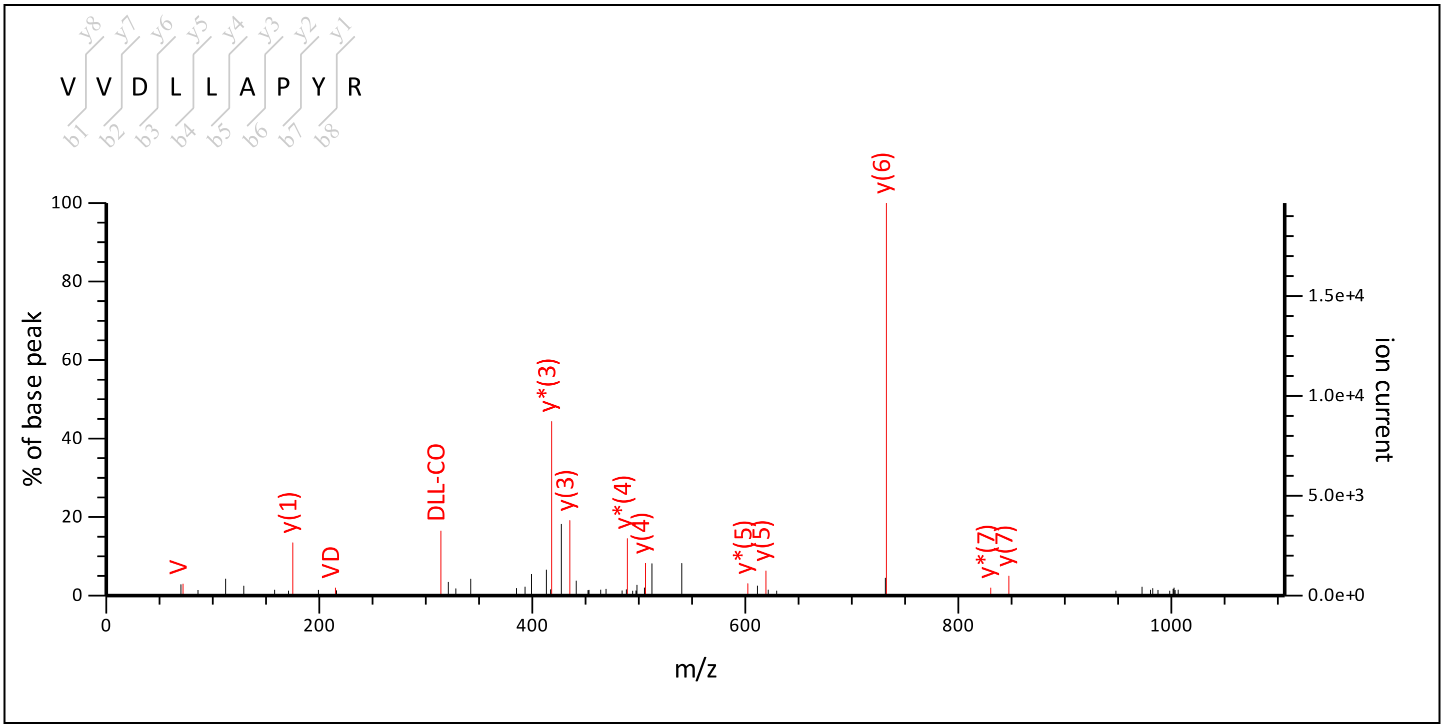
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **VVDLLAPYR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 5: 1044.673224 from(1045.680500,1+) intensity(0.0000) index(2)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221238, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1106.43

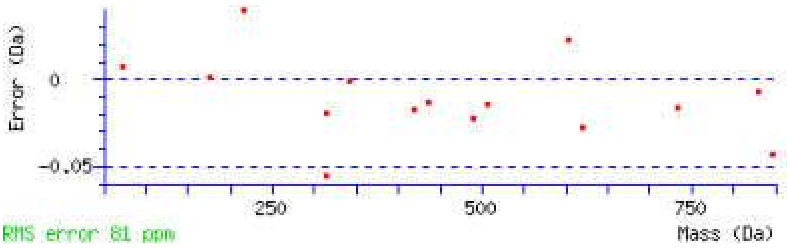
Label all possible matches ○ Label matches used for scoring ●

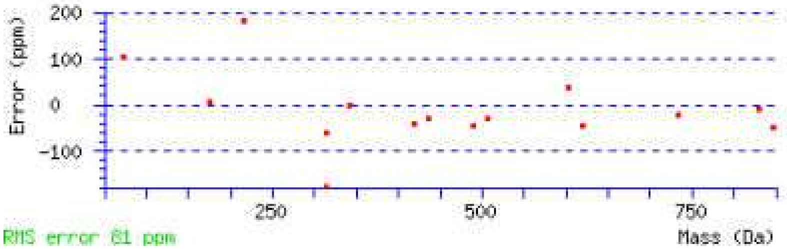
Monoisotopic mass of neutral peptide Mr(calc): 1044.5968
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.11
Matches : 17/115 fragment ions using 19 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495	**V**						**9**
2	72.0808	171.1492		199.1441		157.1335	**V**	902.4730	915.4934	946.5356	929.5091	928.5251	**8**
3	88.0393	286.1761	268.1656	314.1710	296.1605	242.1863	**D**	787.4461	786.4509	***847.4672***	830.4407	829.4567	**7**
4	86.0964	399.2602	381.2496	427.2551	409.2445	357.2132	**L**	674.3620	673.3668	***732.4403***	715.4137		**6**
5	86.0964	512.3443	494.3337	540.3392	522.3286	470.2973	**L**	561.2780	560.2827	***619.3562***	602.3297		**5**
6	44.0495	583.3814	565.3708	611.3763	593.3657		**A**	490.2409		***506.2722***	489.2456		**4**
7	70.0651	680.4341	662.4236	708.4291	690.4185	654.4185	**P**	393.1881	392.1928	***435.2350***	418.2085		**3**
8	136.0757	843.4975	825.4869	871.4924	853.4818		**Y**	230.1248		338.1823	321.1557		**2**

9	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VD	187.1077	215.1026	**VDL**	300.1918	328.1867	**VDLL**	413.2758	441.2708
VDLLA	484.3130	512.3079	**VDLLAP**	581.3657	609.3606	**DL**	201.1234	229.1183
DLL	314.2074	342.2023	**DLLA**	385.2445	413.2395	**DLLAP**	482.2973	510.2922
DLLAPY	645.3606	673.3556	**LL**	199.1805	227.1754	**LLA**	270.2176	298.2125
LLAP	367.2704	395.2653	**LLAPY**	530.3337	558.3286	**LA**	157.1335	185.1285
LAP	254.1863	282.1812	**LAPY**	417.2496	445.2445	**AP**	141.1022	169.0972
APY	304.1656	332.1605	**PY**	233.1285	261.1234			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.0	1044.1048	0.5685	VVBLLAPYR
48.0	1044.5968	0.0765	VVDILAPYR
48.0	1044.5968	0.0765	VVDLIAPYR
48.0	1044.5968	0.0765	VVDLLAPYR
48.0	1044.5968	0.0765	VVDLLAPYR
48.0	1044.5968	0.0765	VVDLLAPYR
48.0	1044.5968	0.0765	VVDLLAPYR
48.0	1044.5968	0.0765	VVDLLAPYR
48.0	1044.5968	0.0765	VVDLLAPYR
48.0	1044.5968	0.0765	VVDLLAPYR

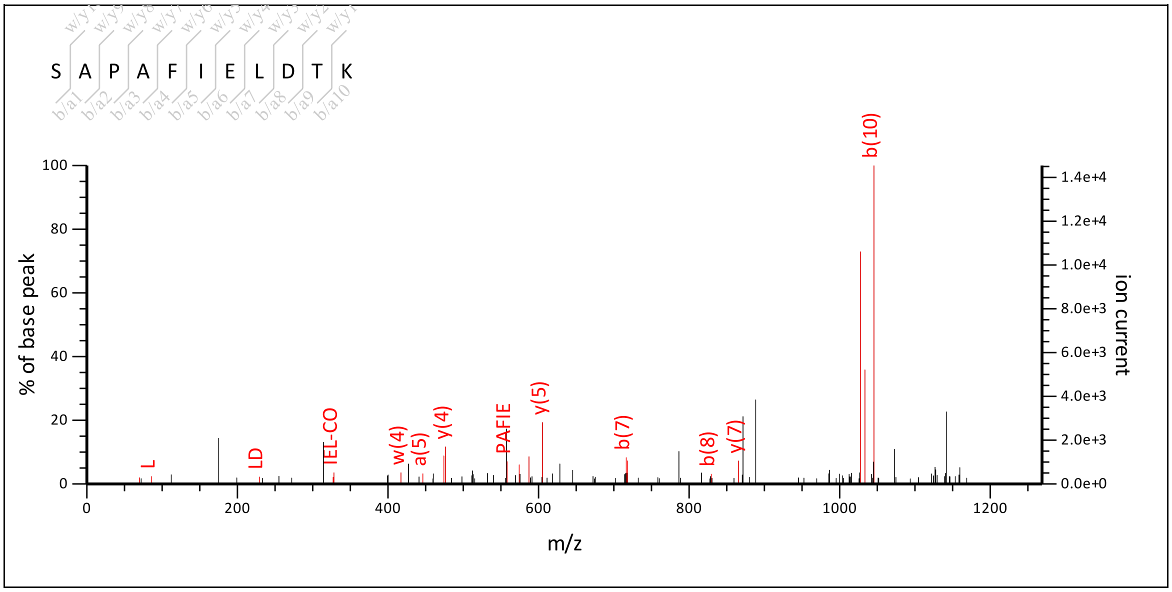
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **SAPAFIELDTK**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 6: 1190.709524 from(1191.716800,1+) intensity(0.0000) index(3)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221243, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1268.77

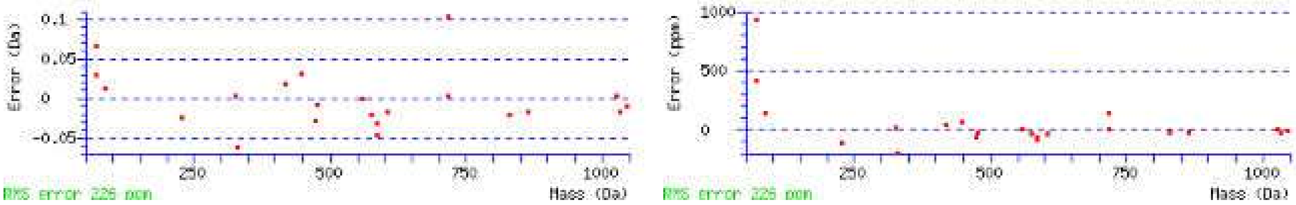
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1190.6183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 11
Matches : 23/167 fragment ions using 44 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444	42.0338	88.0393	70.0287	44.0495		S							11
2	44.0495	131.0815	113.0709	159.0764	141.0659			A	1088.5623			1104.5936	1087.5670	1086.5830	10
3	70.0651	228.1343	210.1237	256.1292	238.1186	202.1186		P	991.5095	990.5142		***1033.5564***	1016.5299	1015.5459	9
4	44.0495	299.1714	281.1608	***327.1663***	309.1557			A	920.4724			936.5037	919.4771	918.4931	8
5	120.0808	446.2398	428.2292	***474.2347***	456.2241			F	773.4040			***865.4666***	848.4400	847.4560	7
6	86.0964	559.3239	541.3133	***587.3188***	569.3082	531.2926	545.3082	I	660.3199	673.3403	687.3559	***718.3981***	701.3716	700.3876	6
7	102.0550	688.3665	670.3559	***716.3614***	698.3508	630.3610		E	531.2773	530.2821		***605.3141***	588.2875	587.3035	5
8	86.0964	801.4505	783.4400	***829.4454***	811.4349	759.4036		L	418.1932	417.1980		***476.2715***	459.2449	458.2609	4
9	88.0393	916.4775	898.4669	944.4724	926.4618	872.4876		D	303.1663	302.1710		363.1874	346.1609	345.1769	3
10	74.0600	1017.5251	999.5146	***1045.5201***	1027.5095	1001.5302	1003.5095	T	202.1186	215.1390	217.1183	248.1605	231.1339	230.1499	2
11	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AP	141.1022	169.0972	APA	212.1394	240.1343	APAF	359.2078	387.2027
APAFI	472.2918	500.2867	APAFIE	601.3344	629.3293	PA	141.1022	169.0972
PAF	288.1707	316.1656	PAFI	401.2547	429.2496	PAFIE	530.2973	558.2922
PAFIEL	643.3814	671.3763	AF	191.1179	219.1128	AFI	304.2020	332.1969
AFIE	433.2445	461.2395	AFIEL	546.3286	574.3235	AFIELD	661.3556	689.3505

FI	233.1648	261.1598	**FIE**	362.2074	390.2023	**FIEL**	475.2915	503.2864
FIELD	590.3184	618.3134	**FIELDT**	691.3661	719.3610	**IE**	215.1390	243.1339
IEL	328.2231	356.2180	**IELD**	443.2500	471.2449	**IELDT**	544.2977	572.2926
EL	215.1390	243.1339	**ELD**	330.1660	358.1609	**ELDT**	431.2136	459.2086
LD	201.1234	229.1183	**LDT**	302.1710	330.1660	**DT**	189.0870	217.0819



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.3	1190.6183	0.0912	SAPAFIELDTK
27.3	1190.6183	0.0912	SAPAFIELDTK
27.3	1190.6183	0.0912	SAPAFIELDTK
27.1	1190.5931	0.1164	SAPAFIQNDTK
26.6	1190.5462	0.1633	MVGGDAGQERR
23.9	1189.6740	1.0355	VVQKMIETVK
23.3	1190.5779	0.1316	ATAESPASTQTK
22.0	1189.6190	1.0905	LLSGGLSSEEAK
20.7	1190.6030	0.1065	GTTESEIVIDK
20.4	1189.6343	1.0752	AAPSFIQLDTK

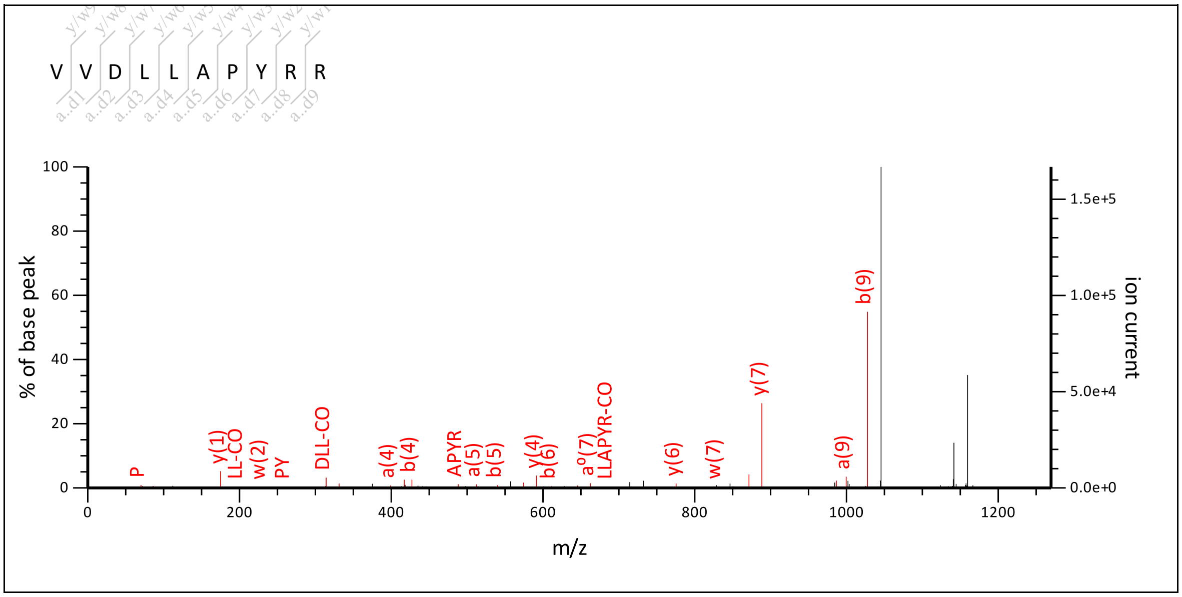
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **VVDLLAPYRR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 8: 1200.762624 from(1201.769900,1+) intensity(0.0000) index(4)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221234, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1269.64

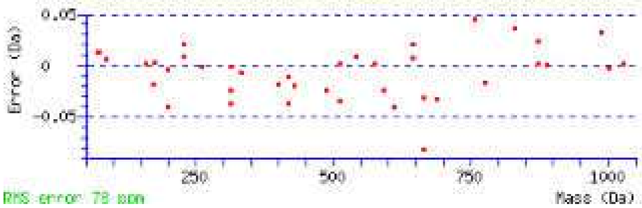
Label all possible matches ○ Label matches used for scoring ●

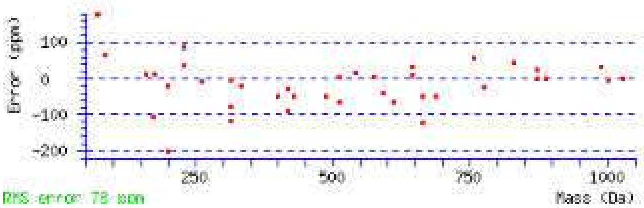
Monoisotopic mass of neutral peptide Mr(calc): 1200.6979
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 1.1
Matches : 44/136 fragment ions using 55 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	**72.0808**			100.0757			44.0495	**V**						**10**
2	72.0808	**171.1492**			***199.1441***			157.1335	**V**	1058.5742	1071.5946	1102.6368	1085.6102	1084.6262	**9**
3	88.0393	286.1761		268.1656	***314.1710***		296.1605	242.1863	**D**	943.5472	942.5520	1003.5683	986.5418	985.5578	**8**
4	86.0964	**399.2602**		381.2496	***427.2551***		409.2445	357.2132	**L**	830.4631	829.4679	**888.5414**	871.5148		**7**
5	86.0964	**512.3443**		494.3337	***540.3392***		522.3286	470.2973	**L**	717.3791	716.3838	**775.4573**	758.4308		**6**
6	44.0495	583.3814		565.3708	***611.3763***		593.3657		**A**	646.3420		**662.3733**	645.3467		**5**
7	70.0651	680.4341		662.4236	708.4291		690.4185	654.4185	**P**	549.2892	548.2940	**591.3362**	574.3096		**4**
8	136.0757	843.4975		825.4869	***871.4924***		853.4818		**Y**	386.2259		494.2834	477.2568		**3**
9	129.1135	**999.5986**	982.5720	981.5880	***1027.5935***	1010.5669	1009.5829	914.5346	**R**	230.1248	229.1295	**331.2201**	314.1935		**2**
10	129.1135								**R**	74.0237	73.0284	**175.1190**	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VD	187.1077	215.1026	**VDL**	300.1918	328.1867	**VDLL**	413.2758	441.2708
VDLLA	484.3130	512.3079	**VDLLAP**	581.3657	609.3606	**DL**	201.1234	229.1183
DLL	314.2074	342.2023	**DLLA**	385.2445	413.2395	**DLLAP**	482.2973	510.2922
DLLAPY	645.3606	673.3556	**LL**	199.1805	227.1754	**LLA**	270.2176	298.2125
LLAP	367.2704	395.2653	**LLAPY**	530.3337	558.3286	**LLAPYR**	686.4348	714.4297
LA	157.1335	185.1285	**LAP**	254.1863	282.1812	**LAPY**	417.2496	445.2445

LAPYR	573.3507	601.3457	**AP**	141.1022	169.0972	**APY**	304.1656	332.1605
APYR	460.2667	488.2616	**PY**	233.1285	261.1234	**PYR**	389.2296	417.2245
YR	292.1768	320.1717						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.7	1200.2059	0.5568	VVBLLAPYRR
38.3	1200.6979	0.0647	VVDLIAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR
37.4	1200.6979	0.0647	VVDLLAPYRR

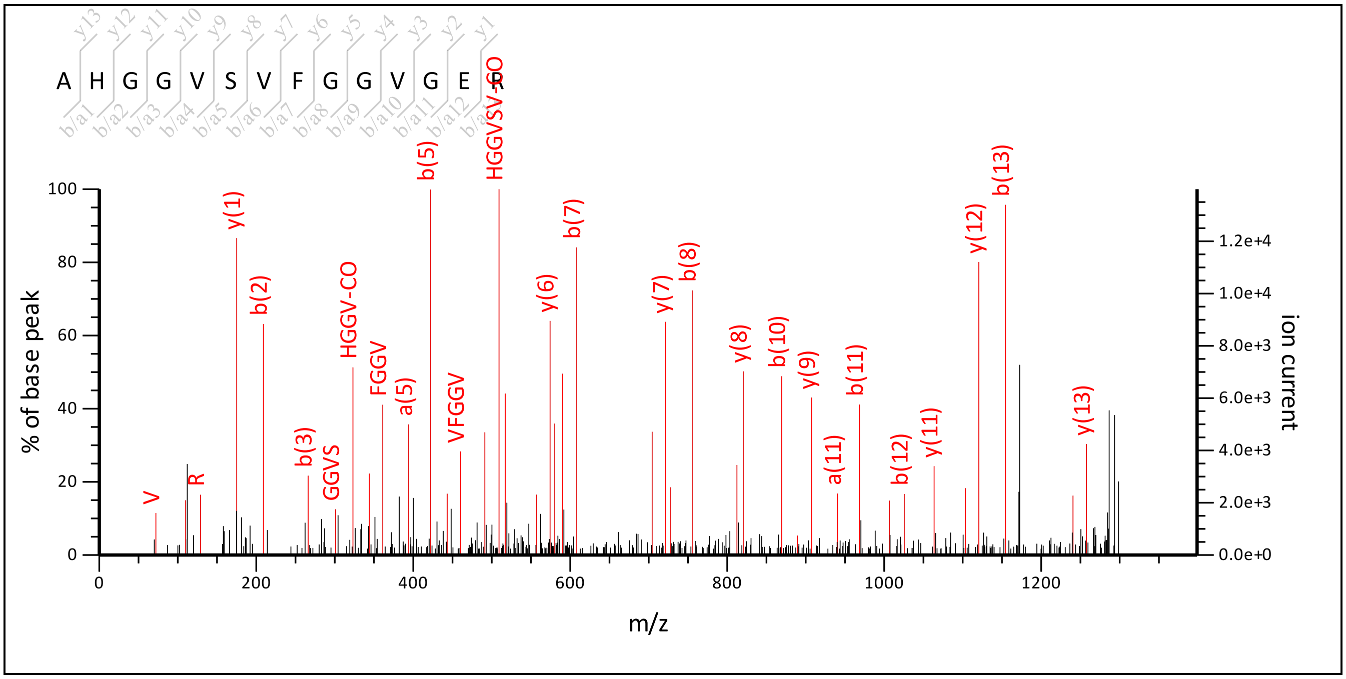
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 87**

MS/MS Fragmentation of **AHGGVSVFGGVGER**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 10: 1327.745924 from(1328.753200,1+) intensity(0.0000) index(5)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221228, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1398.59

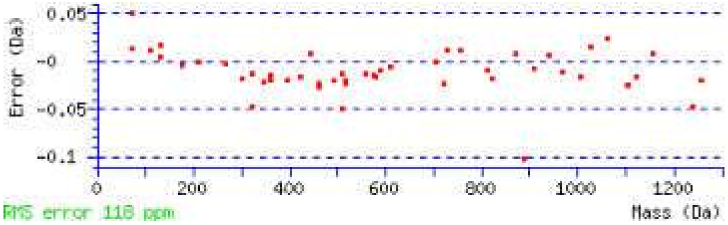
Label all possible matches ○ Label matches used for scoring ●

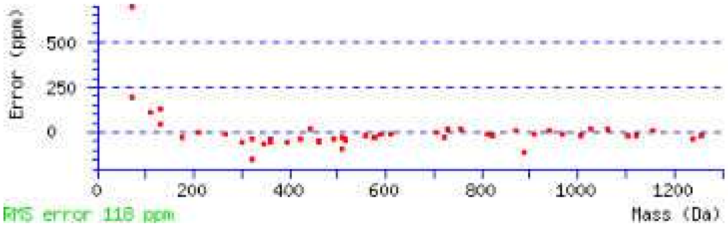
Monoisotopic mass of neutral peptide Mr(calc): 1327.6633
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 128 **Expect:** 8.9e-10
Matches : 53/220 fragment ions using 52 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		***72.0444***		44.0495	A						14
2	110.0713	181.1084		***209.1033***			H	1175.5804		**1257.6335**	1240.6069	1239.6229	13
3	30.0338	238.1299		***266.1248***			G			**1120.5745**	1103.5480	1102.5640	12
4	30.0338	295.1513		***323.1462***			G			**1063.5531**	1046.5265	1045.5425	11
5	72.0808	**394.2197**		***422.2146***		380.2041	V	962.4690	975.4894	**1006.5316**	989.5051	988.5211	10
6	60.0444	481.2518	463.2412	***509.2467***	491.2361	465.2568	S	875.4370	874.4417	**907.4632**	890.4367	889.4526	9
7	72.0808	**580.3202**	562.3096	***608.3151***	590.3045	566.3045	V	776.3686	789.3890	**820.4312**	803.4046	802.4206	8
8	120.0808	**727.3886**	709.3780	***755.3835***	737.3729		F	629.3002		**721.3628**	704.3362	703.3522	7
9	30.0338	784.4100	766.3995	***812.4050***	794.3944		G			**574.2944**	557.2678	556.2838	6
10	30.0338	841.4315	823.4209	***869.4264***	851.4159		G			**517.2729**	500.2463	499.2623	5
11	72.0808	**940.4999**	922.4894	***968.4948***	950.4843	926.4843	V	416.1888	429.2092	**460.2514**	443.2249	442.2409	4

12	30.0338	997.5214	979.5108	***1025.5163***	1007.5057		G			**361.1830**	344.1565	343.1724	3
13	102.0550	1126.5640	1108.5534	***1154.5589***	1136.5483	1068.5585	E	230.1248	229.1295	304.1615	287.1350	286.1510	2
14	129.1135						R	74.0237	73.0284	**175.1190**	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HG	167.0927	195.0877	**HGG**	224.1142	252.1091	**HGGV**	323.1826	351.1775
HGGVS	410.2146	438.2096	**HGGVSV**	509.2831	537.2780	**HGGVSVF**	656.3515	684.3464
GG	87.0553	115.0502	**GGV**	186.1237	214.1186	**GGVS**	273.1557	301.1506
GGVSV	372.2241	400.2191	**GGVSVF**	519.2926	547.2875	**GGVSVFG**	576.3140	604.3089
GGVSVFGG	633.3355	661.3304	**GV**	129.1022	157.0972	**GVS**	216.1343	244.1292
GVSV	315.2027	343.1976	**GVSVF**	462.2711	490.2660	**GVSVFG**	519.2926	547.2875
GVSVFGG	576.3140	604.3089	**GVSVFGGV**	675.3824	703.3774	**VS**	159.1128	187.1077
VSV	258.1812	286.1761	**VSVF**	405.2496	433.2445	**VSVFG**	462.2711	490.2660
VSVFGG	519.2926	547.2875	**VSVFGGV**	618.3610	646.3559	**VSVFGGVG**	675.3824	703.3774
SV	159.1128	187.1077	**SVF**	306.1812	334.1761	**SVFG**	363.2027	391.1976
SVFGG	420.2241	448.2191	**SVFGGV**	519.2926	547.2875	**SVFGGVG**	576.3140	604.3089
VF	219.1492	247.1441	**VFG**	276.1707	304.1656	**VFGG**	333.1921	361.1870
VFGGV	432.2605	460.2554	**VFGGVG**	489.2820	517.2769	**VFGGVGE**	618.3246	646.3195
FG	177.1022	205.0972	**FGG**	234.1237	262.1186	**FGGV**	333.1921	361.1870
FGGVG	390.2136	418.2085	**FGGVGE**	519.2562	547.2511	**GG**	87.0553	115.0502
GGV	186.1237	214.1186	**GGVG**	243.1452	271.1401	**GGVGE**	372.1878	400.1827
GV	129.1022	157.0972	**GVG**	186.1237	214.1186	**GVGE**	315.1663	343.1612
VG	129.1022	157.0972	**VGE**	258.1448	286.1397	**GE**	159.0764	187.0713





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER

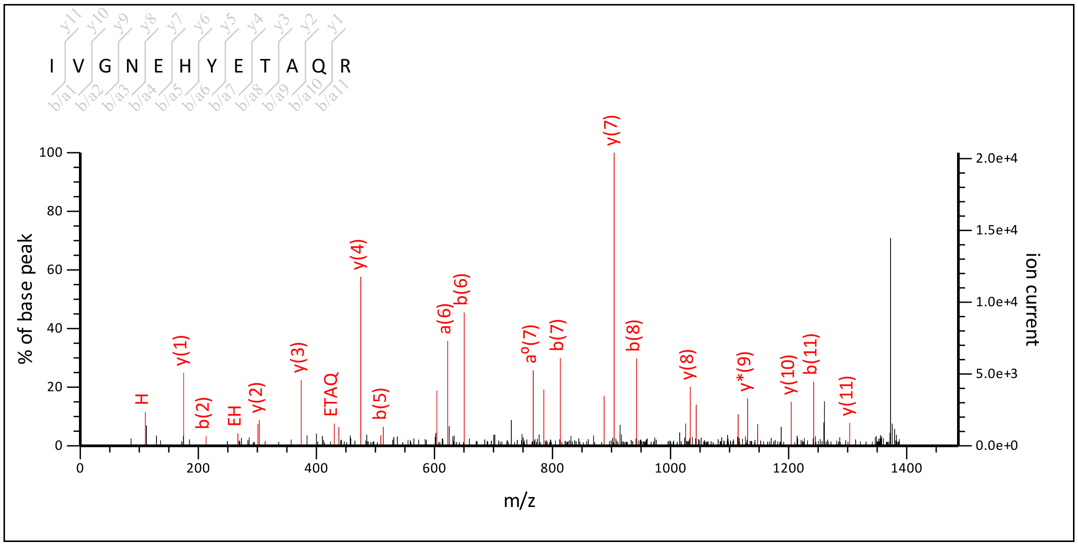
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER
127.9	1327.6633	0.0826	AHGGVSVFGGVGER

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **IVGNEHYETAQR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 12: 1415.766024 from(1416.773300,1+) intensity(0.0000) index(6)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221230, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1487.61

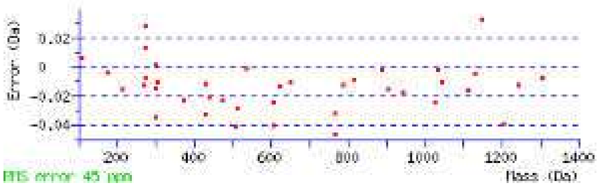
Label all possible matches ○ Label matches used for scoring ●

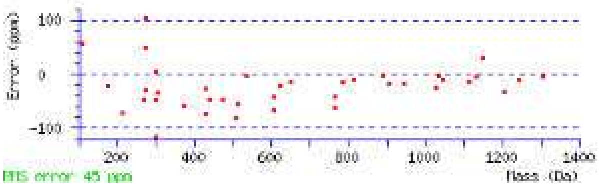
Monoisotopic mass of neutral peptide Mr(calc): 1415.6793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 95 **Expect:** 1.7e-06
Matches : 40/181 fragment ions using 41 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	86.0964			114.0913			44.0495		I						
2	72.0808	185.1648			**213.1598**			171.1492		V	1259.5400	1272.5604		***1303.6026***	1286.5760	12
3	30.0338	242.1863			270.1812					G				***1204.5341***	1187.5076	11
4	87.0553	356.2292	339.2027		384.2241	367.1976		313.2234		N	1088.4756	1087.4803		***1147.5127***	1130.4861	11
5	102.0550	485.2718	468.2453	467.2613	**513.2667**	496.2402	495.2562	427.2663		E	959.4330	958.4377		***1033.4697***	1016.4432	10
6	110.0713	622.3307	605.3042	604.3202	**650.3256**	633.2991	632.3151			H	822.3741			***904.4272***	887.4006	8
7	136.0757	785.3941	768.3675	767.3835	**813.3890**	796.3624	795.3784			Y	659.3107			***767.3682***	750.3417	7
8	102.0550	914.4367	897.4101	896.4261	**942.4316**	925.4050	924.4210	856.4312		E	530.2681	529.2729		***604.3049***	587.2784	5
9	74.0600	1015.4843	998.4578	997.4738	**1043.4793**	1026.4527	1025.4687	999.4894	1001.4687	T	429.2205	442.2409	444.2201	***475.2623***	458.2358	4
10	44.0495	1086.5214	1069.4949	1068.5109	**1114.5164**	1097.4898	1096.5058			A	358.1833			***374.2146***	357.1881	
11	101.0709	1214.5800	1197.5535	1196.5695	**1242.5749**	1225.5484	1224.5644	1157.5586		Q	230.1248	229.1295		***303.1775***	286.1510	
12	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VG	129.1022	157.0972	VGN	243.1452	271.1401	VGNE	372.1878	400.1827
VGNEH	509.2467	537.2416	VGNEHY	672.3100	700.3049	GN	144.0768	172.0717
GNE	273.1193	301.1143	GNEH	410.1783	438.1732	GNEHY	573.2416	601.2365
NE	216.0979	244.0928	NEH	353.1568	381.1517	NEHY	516.2201	544.2150
NEHYE	645.2627	673.2576	EH	239.1139	267.1088	EHY	402.1772	430.1721
EHYE	531.2198	559.2147	EHYET	632.2675	660.2624	HY	273.1346	301.1295
HYE	402.1772	430.1721	HYET	503.2249	531.2198	HYETA	574.2620	602.2569
YE	265.1183	293.1132	YET	366.1660	394.1609	YETA	437.2031	465.1980
YETAQ	565.2617	593.2566	ET	203.1026	231.0975	ETA	274.1397	302.1347

ETAQ	402.1983	430.1932	**TA**	145.0972	173.0921	**TAQ**	273.1557	301.1506
AQ	172.1081	200.1030						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
95.3	1415.6793	0.0867	IVGNEHYETAQR
95.3	1415.6793	0.0867	IVGNEHYETAQR
78.0	1415.7157	0.0503	IVGDKHYETAQR
78.0	1415.7157	0.0503	IVGDKHYETAQR
78.0	1415.6793	0.0867	IVGDQHYETAQR
78.0	1415.6793	0.0867	IVGENHYETAQR
78.0	1415.6793	0.0867	IVGENHYETAQR
78.0	1415.7157	0.0503	IVGKDHYETAQR
78.0	1415.7157	0.0503	IVGKDHYETAQR
39.4	1416.6633	-0.8973	IVGDEHYETAQR

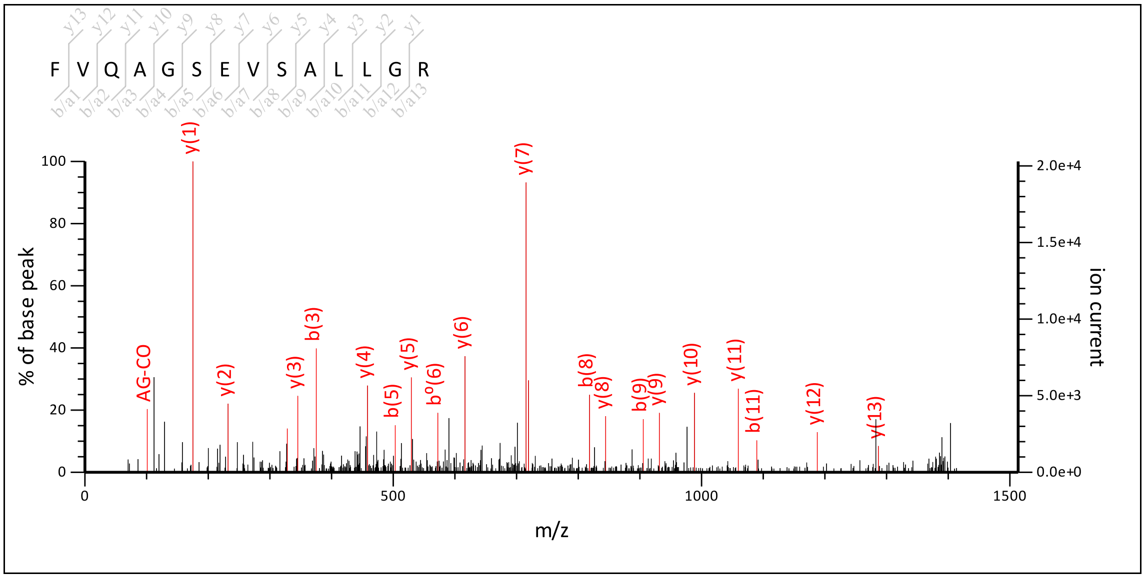
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **FVQAGSEVSALLGR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 14: 1432.848424 from(1433.855700,1+) intensity(0.0000) index(7)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221233, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1513.41

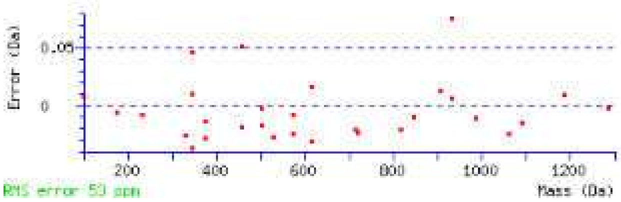
Label all possible matches ○ Label matches used for scoring ●

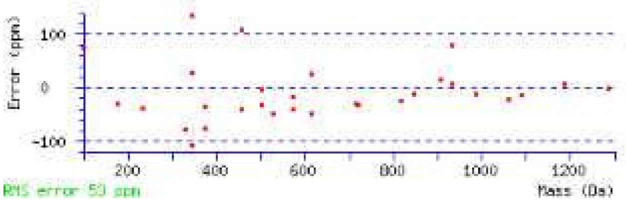
Monoisotopic mass of neutral peptide Mr(calc): 1432.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 131 **Expect:** 4.9e-10
Matches : 34/243 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	120.0808	120.0808			148.0757			44.0495	F						14
2	72.0808	219.1492			247.1441			205.1335	V	1242.6437	1255.6641	***1286.7063***	1269.6797	1268.6957	13
3	101.0709	347.2078	330.1812		**375.2027**	358.1761		290.1863	Q	1114.5851	1113.5899	***1187.6379***	1170.6113	1169.6273	12
4	44.0495	418.2449	401.2183		446.2398	429.2132			A	1043.5480		***1059.5793***	1042.5527	1041.5687	11
5	30.0338	475.2663	458.2398		**503.2613**	486.2347			G			***988.5422***	971.5156	970.5316	10
6	60.0444	562.2984	545.2718	544.2878	590.2933	573.2667	572.2827	546.3035	S	899.4945	898.4993	***931.5207***	914.4942	913.5102	9
7	102.0550	691.3410	674.3144	673.3304	**719.3359**	702.3093	701.3253	633.3355	E	770.4519	769.4567	***844.4887***	827.4621	826.4781	8
8	72.0808	790.4094	773.3828	772.3988	**818.4043**	801.3777	800.3937	776.3937	V	671.3835	684.4039	***715.4461***	698.4196	697.4355	7
9	60.0444	877.4414	860.4149	859.4308	**905.4363**	888.4098	887.4258	861.4465	S	584.3515	583.3562	***616.3777***	599.3511	598.3671	6
10	44.0495	948.4785	931.4520	930.4680	976.4734	959.4469	958.4629		A	513.3144		***529.3457***	512.3191		5
11	86.0964	1061.5626	1044.5360	1043.5520	**1089.5575**	1072.5310	1071.5469	1019.5156	L	400.2303	399.2350	***458.3085***	441.2820		4
12	86.0964	1174.6466	1157.6201	1156.6361	1202.6416	1185.6150	1184.6310	1132.5997	L	287.1462	286.1510	***345.2245***	328.1979		3
13	30.0338	1231.6681	1214.6416	1213.6575	1259.6630	1242.6365	1241.6525		G			***232.1404***	215.1139		2
14	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VQ	200.1394	228.1343	VQA	271.1765	299.1714	VQAG	328.1979	356.1928
VQAGS	415.2300	443.2249	VQAGSE	544.2726	572.2675	VQAGSEV	643.3410	671.3359
QA	172.1081	200.1030	QAG	229.1295	257.1244	QAGS	316.1615	344.1565
QAGSE	445.2041	473.1991	QAGSEV	544.2726	572.2675	QAGSEVS	631.3046	659.2995

AG	101.0709	129.0659	**AGS**	188.1030	216.0979	**AGSE**	317.1456	345.1405
AGSEV	416.2140	444.2089	**AGSEVS**	503.2460	531.2409	**AGSEVSA**	574.2831	602.2780
AGSEVSAL	687.3672	715.3621	**GS**	117.0659	145.0608	**GSE**	246.1084	274.1034
GSEV	345.1769	373.1718	**GSEVS**	432.2089	460.2038	**GSEVSA**	503.2460	531.2409
GSEVSAL	616.3301	644.3250	**SE**	189.0870	217.0819	**SEV**	288.1554	316.1503
SEVS	375.1874	403.1823	**SEVSA**	446.2245	474.2195	**SEVSAL**	559.3086	587.3035
SEVSALL	672.3927	700.3876	**EV**	201.1234	229.1183	**EVS**	288.1554	316.1503
EVSA	359.1925	387.1874	**EVSAL**	472.2766	500.2715	**EVSALL**	585.3606	613.3556
EVSALLG	642.3821	670.3770	**VS**	159.1128	187.1077	**VSA**	230.1499	258.1448
VSAL	343.2340	371.2289	**VSALL**	456.3180	484.3130	**VSALLG**	513.3395	541.3344
SA	131.0815	159.0764	**SAL**	244.1656	272.1605	**SALL**	357.2496	385.2445
SALLG	414.2711	442.2660	**AL**	157.1335	185.1285	**ALL**	270.2176	298.2125
ALLG	327.2391	355.2340	**LL**	199.1805	227.1754	**LLG**	256.2020	284.1969
LG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
130.8	1432.7674	0.0810	FVQAGSEVSAILGR
130.8	1432.7674	0.0810	FVQAGSEVSALIGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR
130.8	1432.7674	0.0810	FVQAGSEVSALLGR

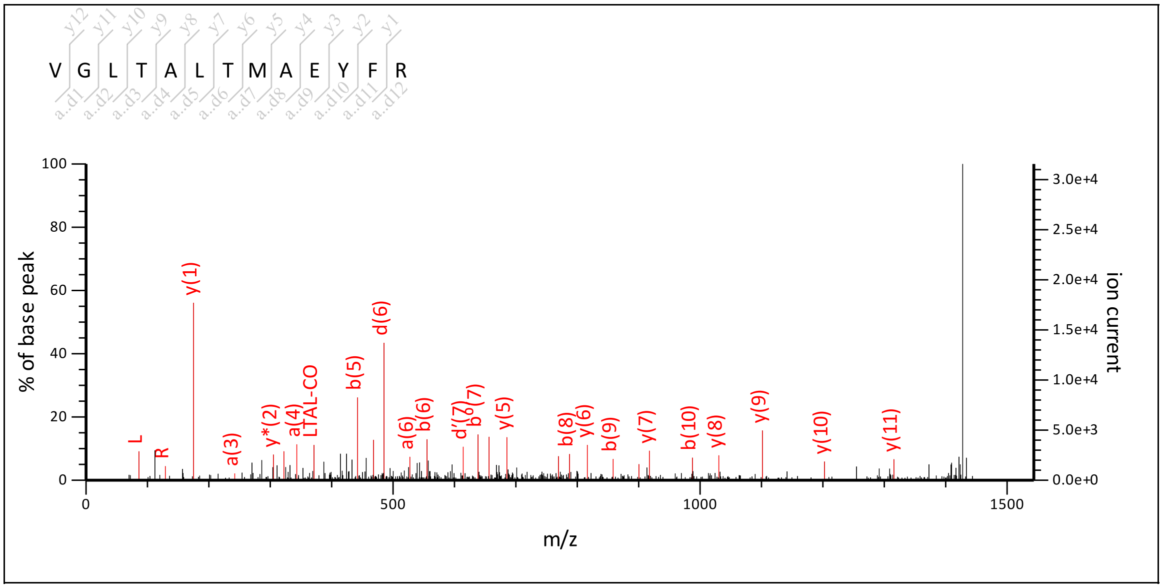
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **VGLTALTMAEYFR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 16: 1470.840124 from(1471.847400,1+) intensity(0.0000) index(8)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221227, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1543.55

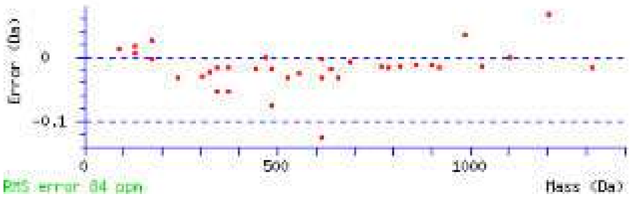
Label all possible matches ○ Label matches used for scoring ●

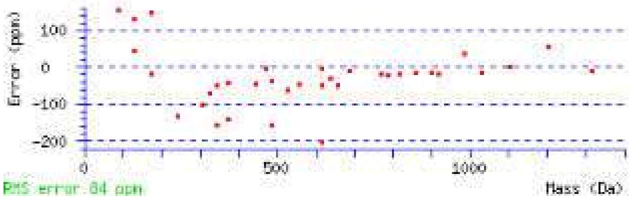
Monoisotopic mass of neutral peptide Mr(calc): 1470.7541
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 9.3e-06
Matches : 36/198 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495		V							13
2	30.0338	**129.1022**		157.0972				G				1372.6930	1355.6664	1354.6824	12
3	86.0964	**242.1863**		270.1812		200.1394		L	1257.5932	1256.5980		***1315.6715***	1298.6449	1297.6609	11
4	74.0600	**343.2340**	325.2234	**371.2289**	353.2183	327.2391	329.2183	T	1156.5456	1169.5660	1171.5452	***1202.5874***	1185.5609	1184.5769	10
5	44.0495	414.2711	396.2605	**442.2660**	424.2554			A	1085.5084			***1101.5397***	1084.5132	1083.5292	9
6	86.0964	**527.3552**	509.3446	**555.3501**	537.3395	485.3082		L	972.4244	971.4291		***1030.5026***	1013.4761	1012.4921	8
7	74.0600	628.4028	610.3923	**656.3978**	638.3872	612.4079	614.3872	T	871.3767	884.3971	886.3764	***917.4186***	900.3920	899.4080	7
8	104.0528	759.4433	741.4328	**787.4382**	769.4277	699.4400		M	740.3362	739.3410		***816.3709***	799.3443	798.3603	6
9	44.0495	830.4804	812.4699	**858.4754**	840.4648			A	669.2991			***685.3304***	668.3039	667.3198	5
10	102.0550	959.5230	941.5125	**987.5179**	969.5074	901.5176		E	540.2565	539.2613		***614.2933***	597.2667	596.2827	4
11	136.0757	1122.5864	1104.5758	1150.5813	1132.5707			Y	377.1932			***485.2507***	468.2241		3
12	120.0808	1269.6548	1251.6442	1297.6497	1279.6391			F	230.1248			***322.1874***	305.1608		2
13	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	GLT	244.1656	272.1605	GLTA	315.2027	343.1976
GLTAL	428.2867	456.2817	GLTALT	529.3344	557.3293	GLTALTM	660.3749	688.3698
LT	187.1441	215.1390	LTA	258.1812	286.1761	LTAL	371.2653	399.2602
LTALT	472.3130	500.3079	LTALTM	603.3534	631.3484	LTALTMA	674.3906	702.3855

TA	145.0972	173.0921	**TAL**	258.1812	286.1761	**TALT**	359.2289	387.2238
TALTM	490.2694	518.2643	**TALTMA**	561.3065	589.3014	**TALTMAE**	690.3491	718.3440
AL	157.1335	185.1285	**ALT**	258.1812	286.1761	**ALTM**	389.2217	417.2166
ALTMA	460.2588	488.2537	**ALTMAE**	589.3014	617.2963	**LT**	187.1441	215.1390
LTM	318.1846	346.1795	**LTMA**	389.2217	417.2166	**LTMAE**	518.2643	546.2592
LTMAEY	681.3276	709.3225	**TM**	205.1005	233.0954	**TMA**	276.1376	304.1326
TMAE	405.1802	433.1751	**TMAEY**	568.2436	596.2385	**MA**	175.0900	203.0849
MAE	304.1326	332.1275	**MAEY**	467.1959	495.1908	**MAEYF**	614.2643	642.2592
AE	173.0921	201.0870	**AEY**	336.1554	364.1503	**AEYF**	483.2238	511.2187
EY	265.1183	293.1132	**EYF**	412.1867	440.1816	**YF**	283.1441	311.1390





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.0	1470.7541	0.0861	VGITALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR
88.0	1470.7541	0.0861	VGLTALTMAEYFR

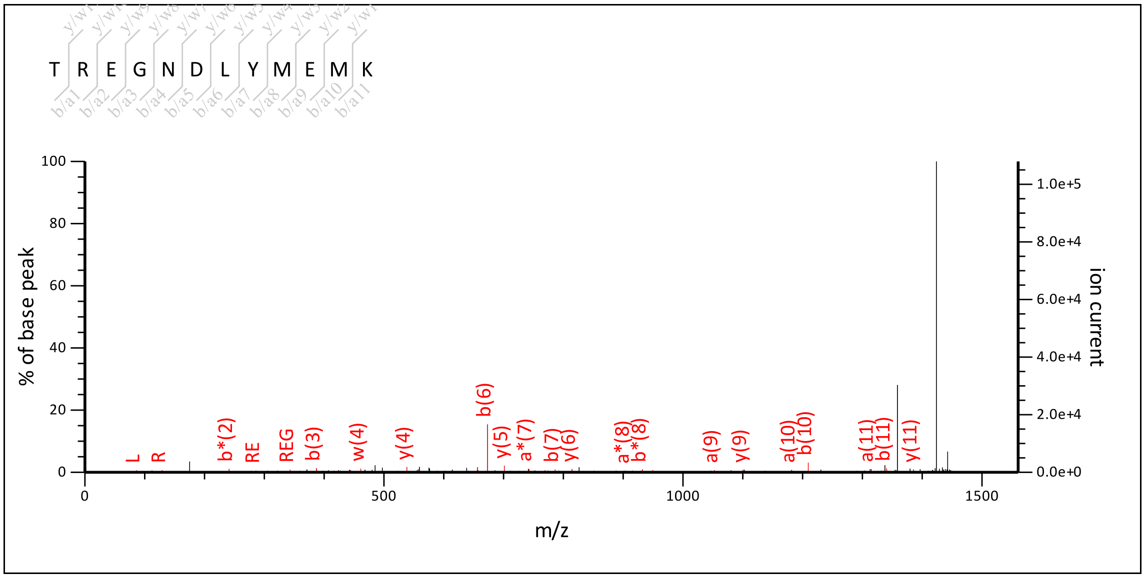
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **TREGNDLYMEMK**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 18: 1485.767524 from(1486.774800,1+) intensity(0.0000) index(9)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221236, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1560.45

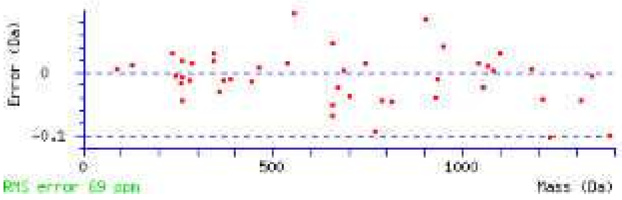
Label all possible matches ○ Label matches used for scoring ●

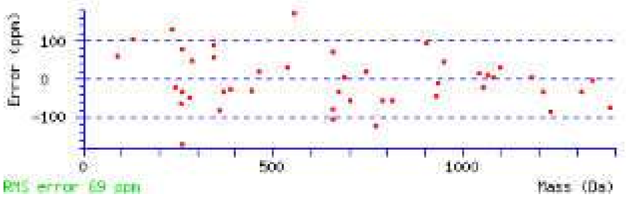
Monoisotopic mass of neutral peptide Mr(calc): 1485.6592
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.41
Matches : 47/201 fragment ions using 95 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495	T						12
2	129.1135	230.1612	213.1346	212.1506	***258.1561***	241.1295	240.1455	145.0972	R	1284.5235	1283.5283	***1385.6188***	1368.5922	1367.6082	11
3	102.0550	**359.2037**	342.1772	341.1932	***387.1987***	370.1721	369.1881	301.1983	E	1155.4809	1154.4857	***1229.5177***	1212.4911	1211.5071	10
4	30.0338	416.2252	399.1987	398.2146	***444.2201***	427.1936	426.2096		G			***1100.4751***	1083.4485	1082.4645	9
5	87.0553	530.2681	513.2416	512.2576	558.2631	541.2365	540.2525	487.2623	N	984.4165	983.4213	***1043.4536***	1026.4271	1025.4431	8
6	88.0393	645.2951	628.2685	627.2845	***673.2900***	656.2634	655.2794	601.3052	D	869.3896	868.3943	***929.4107***	912.3842	911.4001	7
7	86.0964	758.3791	741.3526	740.3686	***786.3741***	769.3475	768.3635	716.3322	L	756.3055	755.3103	***814.3838***	797.3572	796.3732	6
8	136.0757	921.4425	904.4159	903.4319	***949.4374***	932.4108	931.4268		Y	593.2422		***701.2997***	684.2731	683.2891	5
9	104.0528	**1052.4830**	1035.4564	1034.4724	***1080.4779***	1063.4513	1062.4673	992.4796	M	462.2017	461.2064	***538.2364***	521.2098	520.2258	4
10	102.0550	**1181.5255**	1164.4990	1163.5150	***1209.5205***	1192.4939	1191.5099	1123.5201	E	333.1591	332.1639	407.1959	390.1693	389.1853	3
11	104.0528	**1312.5660**	1295.5395	1294.5555	***1340.5609***	1323.5344	1322.5504	1252.5627	M	202.1186	201.1234	***278.1533***	261.1267		2
12	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RE	258.1561	286.1510	REG	315.1775	343.1724	REGN	429.2205	457.2154
REGND	544.2474	572.2423	REGNDL	657.3315	685.3264	EG	159.0764	187.0713
EGN	273.1193	301.1143	EGND	388.1463	416.1412	EGNDL	501.2304	529.2253
EGNDLY	664.2937	692.2886	GN	144.0768	172.0717	GND	259.1037	287.0986
GNDL	372.1878	400.1827	GNDLY	535.2511	563.2460	GNDLYM	666.2916	694.2865
ND	202.0822	230.0771	NDL	315.1663	343.1612	NDLY	478.2296	506.2245

NDLYM	609.2701	637.2650	**DL**	201.1234	229.1183	**DLY**	364.1867	392.1816
DLYM	495.2272	523.2221	**DLYME**	624.2698	652.2647	**LY**	249.1598	277.1547
LYM	380.2002	408.1952	**LYME**	509.2428	537.2377	**LYMEM**	640.2833	668.2782
YM	267.1162	295.1111	**YME**	396.1588	424.1537	**YMEM**	527.1993	555.1942
ME	233.0954	261.0904	**MEM**	364.1359	392.1308	**EM**	233.0954	261.0904





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
41.7	1485.6592	0.1084	TREGNDLYMEMK
35.4	1485.6262	0.1414	TREGNDLMMEMK

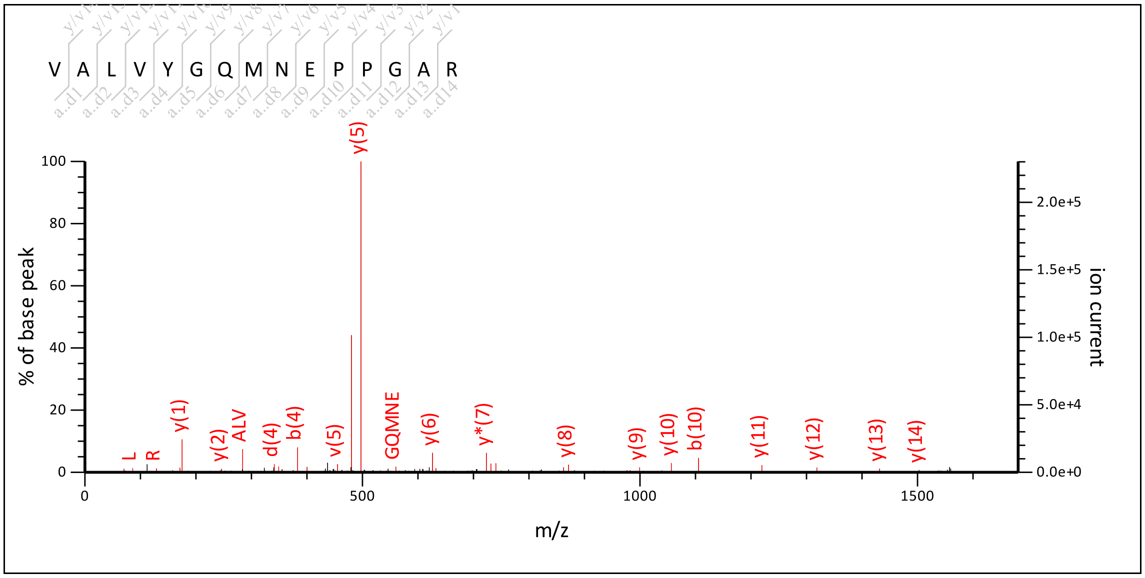
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **VALVYGQMNEPPGAR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 20: 1600.889724 from(1601.897000,1+) intensity(0.0000) index(10)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221229, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1681.32

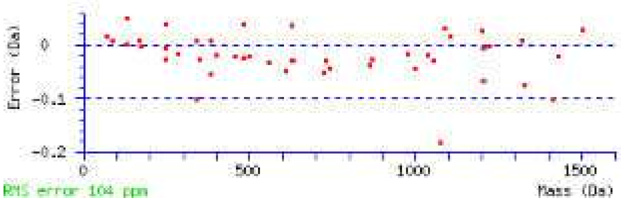
Label all possible matches ○ Label matches used for scoring ●

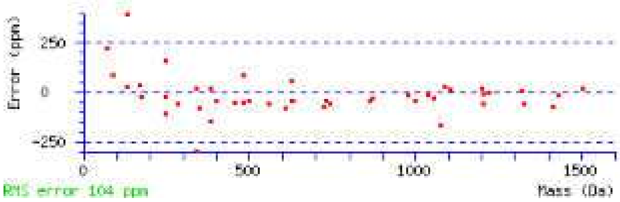
Monoisotopic mass of neutral peptide Mr(calc): 1600.8031
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 5.6e-07
Matches : 48/237 fragment ions using 61 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808			100.0757			44.0495	**V**						**15**
2	44.0495	143.1179			**171.1128**				**A**	1486.7107		***1502.7420***	1485.7155	1484.7315	**14**
3	86.0964	256.2020			**284.1969**			214.1550	**L**	1373.6267	1372.6314	***1431.7049***	1414.6784	1413.6943	**13**
4	72.0808	355.2704			**383.2653**			341.2547	**V**	1274.5582	1287.5786	***1318.6208***	1301.5943	1300.6103	**12**
5	136.0757	518.3337			546.3286				**Y**	1111.4949		***1219.5524***	1202.5259	1201.5419	**11**
6	30.0338	575.3552			603.3501				**G**			***1056.4891***	1039.4626	1038.4785	**10**
7	101.0709	703.4137	686.3872		**731.4087**	714.3821		646.3923	**Q**	926.4149	925.4196	***999.4676***	982.4411	981.4571	**9**
8	104.0528	834.4542	817.4277		**862.4491**	845.4226		774.4509	**M**	795.3744	794.3791	***871.4091***	854.3825	853.3985	**8**
9	87.0553	948.4972	931.4706		**976.4921**	959.4655		905.4913	**N**	681.3315	680.3362	***740.3686***	723.3420	722.3580	**7**
10	102.0550	1077.5397	1060.5132	1059.5292	**1105.5347**	1088.5081	1087.5241	1019.5343	**E**	552.2889	551.2936	***626.3257***	609.2991	608.3151	**6**
11	70.0651	1174.5925	1157.5660	1156.5819	**1202.5874**	1185.5609	1184.5769	1148.5769	**P**	455.2361	454.2409	***497.2831***	480.2565		**5**
12	70.0651	1271.6453	1254.6187	1253.6347	1299.6402	1282.6136	1281.6296	1245.6296	**P**	358.1833	357.1881	***400.2303***	383.2037		**4**
13	30.0338	1328.6667	1311.6402	1310.6562	1356.6617	1339.6351	1338.6511		**G**			303.1775	286.1510		**3**
14	44.0495	1399.7038	1382.6773	1381.6933	1427.6988	1410.6722	1409.6882		**A**	230.1248		***246.1561***	229.1295		**2**
15	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AL	157.1335	185.1285	**ALV**	256.2020	284.1969	**ALVY**	419.2653	447.2602
ALVYG	476.2867	504.2817	**ALVYGQ**	604.3453	632.3402	**LV**	185.1648	213.1598
LVY	348.2282	376.2231	**LVYG**	405.2496	433.2445	**LVYGQ**	533.3082	561.3031

LVYGQM	664.3487	692.3436	**VY**	235.1441	263.1390	**VYG**	292.1656	320.1605
VYGQ	420.2241	448.2191	**VYGQM**	551.2646	579.2595	**VYGQMN**	665.3076	693.3025
YG	193.0972	221.0921	**YGQ**	321.1557	349.1506	**YGQM**	452.1962	480.1911
YGQMN	566.2391	594.2341	**YGQMNE**	695.2817	723.2767	**GQ**	158.0924	186.0873
GQM	289.1329	317.1278	**GQMN**	403.1758	431.1707	**GQMNE**	532.2184	560.2133
GQMNEP	629.2712	657.2661	**QM**	232.1114	260.1063	**QMN**	346.1544	374.1493
QMNE	475.1969	503.1919	**QMNEP**	572.2497	600.2446	**QMNEPP**	669.3025	697.2974
MN	218.0958	246.0907	**MNE**	347.1384	375.1333	**MNEP**	444.1911	472.1860
MNEPP	541.2439	569.2388	**MNEPPG**	598.2654	626.2603	**MNEPPGA**	669.3025	697.2974
NE	216.0979	244.0928	**NEP**	313.1506	341.1456	**NEPP**	410.2034	438.1983
NEPPG	467.2249	495.2198	**NEPPGA**	538.2620	566.2569	**EP**	199.1077	227.1026
EPP	296.1605	324.1554	**EPPG**	353.1819	381.1769	**EPPGA**	424.2191	452.2140
PP	167.1179	195.1128	**PPG**	224.1394	252.1343	**PPGA**	295.1765	323.1714
PG	127.0866	155.0815	**PGA**	198.1237	226.1186	**GA**	101.0709	129.0659





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
99.6	1600.8031	0.0866	VAIVYGQMNEPPGAR
99.6	1600.8031	0.0866	VAIVYGQMNEPPGAR
99.6	1600.8395	0.0502	VALVYGKMNEPPGAR
99.6	1600.8031	0.0866	VALVYGQMNEPPGAR
99.6	1600.8031	0.0866	VALVYGQMNEPPGAR
99.6	1600.8031	0.0866	VALVYGQMNEPPGAR
99.6	1600.8031	0.0866	VALVYGQMNEPPGAR
99.6	1600.8031	0.0866	VALVYGQMNEPPGAR
99.6	1600.8031	0.0866	VALVYGQMNEPPGAR
99.6	1600.8031	0.0866	VALVYGQMNEPPGAR

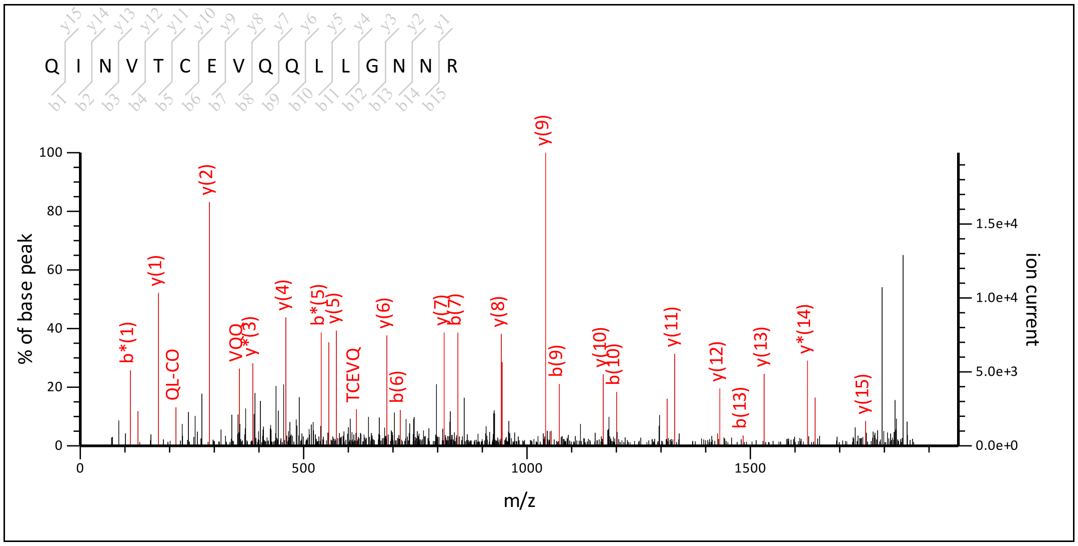
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **QINVTCEVQQLLGNNR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 23: 1885.043724 from(1886.051000,1+) intensity(0.0000) index(12)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221231, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 1965.69

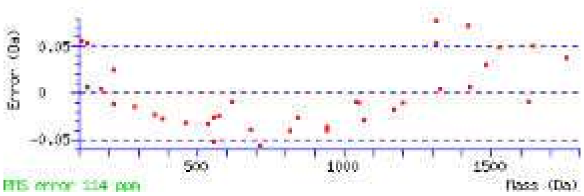
Label all possible matches ○ Label matches used for scoring ●

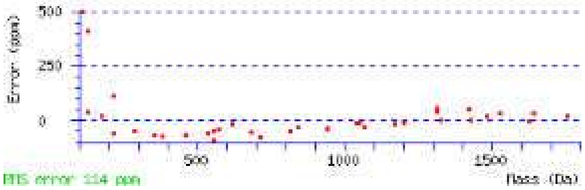
Monoisotopic mass of neutral peptide Mr(calc): 1884.9476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 143 **Expect:** 1.9e-11
Matches : 38/282 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.0709	101.0709	84.0444		**129.0659**	112.0393		44.0495		Q					
2	86.0964	214.1550	197.1285		242.1499	225.1234		186.1237	200.1394	I	1699.8180	1712.8384	1726.8541	***1757.8963***	1740.8697
3	87.0553	328.1979	311.1714		**356.1928**	339.1663		285.1921		N	1585.7751	1584.7799		***1644.8122***	1627.7857
4	72.0808	427.2663	410.2398		455.2613	438.2347		413.2507		V	1486.7067	1499.7271		***1530.7693***	1513.7428
5	74.0600	528.3140	511.2875	510.3035	**556.3089**	539.2824	538.2984	512.3191	514.2984	T	1385.6590	1398.6794	1400.6587	***1431.7009***	1414.6743
6	133.0430	688.3447	671.3181	670.3341	**716.3396**	699.3130	698.3290	599.3511		C	1225.6284	1224.6331		***1330.6532***	1313.6267
7	102.0550	817.3873	800.3607	799.3767	**845.3822**	828.3556	827.3716	759.3818		E	1096.5858	1095.5905		***1170.6226***	1153.5960
8	72.0808	916.4557	899.4291	898.4451	**944.4506**	927.4240	926.4400	902.4400		V	997.5174	1010.5378		***1041.5800***	1024.5534
9	101.0709	1044.5143	1027.4877	1026.5037	**1072.5092**	1055.4826	1054.4986	987.4928		Q	869.4588	868.4635		***942.5116***	925.4850
10	101.0709	1172.5728	1155.5463	1154.5623	**1200.5678**	1183.5412	1182.5572	1115.5514		Q	741.4002	740.4050		***814.4530***	797.4264
11	86.0964	1285.6569	1268.6304	1267.6463	**1313.6518**	1296.6253	1295.6412	1243.6099		L	628.3161	627.3209		***686.3944***	669.3678
12	86.0964	1398.7410	1381.7144	1380.7304	**1426.7359**	1409.7093	1408.7253	1356.6940		L	515.2321	514.2368		***573.3103***	556.2838
13	30.0338	1455.7624	1438.7359	1437.7519	**1483.7573**	1466.7308	1465.7468			G				***460.2263***	443.1997
14	87.0553	1569.8054	1552.7788	1551.7948	1597.8003	1580.7737	1579.7897	1526.7995		N	344.1677	343.1724		403.2048	386.1783
15	87.0553	1683.8483	1666.8217	1665.8377	1711.8432	1694.8166	1693.8326	1640.8425		N	230.1248	229.1295		***289.1619***	272.1353
16	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IN	200.1394	228.1343	INV	299.2078	327.2027	INVT	400.2554	428.2504
INVTC	560.2861	588.2810	INVTCE	689.3287	717.3236	NV	186.1237	214.1186
NVT	287.1714	315.1663	NVTC	447.2020	475.1969	NVTCE	576.2446	604.2395
NVTCEV	675.3130	703.3080	VT	173.1285	201.1234	VTC	333.1591	361.1540
VTCE	462.2017	490.1966	VTCEV	561.2701	589.2650	VTCEVQ	689.3287	717.3236

TC	234.0907	262.0856	**TCE**	363.1333	391.1282	**TCEV**	462.2017	490.1966
TCEVQ	590.2603	618.2552	**CE**	262.0856	290.0805	**CEV**	361.1540	389.1489
CEVQ	489.2126	517.2075	**CEVQQ**	617.2712	645.2661	**EV**	201.1234	229.1183
EVQ	329.1819	357.1769	**EVQQ**	457.2405	485.2354	**EVQQL**	570.3246	598.3195
EVQQLL	683.4087	711.4036	**VQ**	200.1394	228.1343	**VQQ**	328.1979	356.1928
VQQL	441.2820	469.2769	**VQQLL**	554.3661	582.3610	**VQQLLG**	611.3875	639.3824
QQ	229.1295	257.1244	**QQL**	342.2136	370.2085	**QQLL**	455.2976	483.2926
QQLLG	512.3191	540.3140	**QQLLGN**	626.3620	654.3570	**QL**	214.1550	242.1499
QLL	327.2391	355.2340	**QLLG**	384.2605	412.2554	**QLLGN**	498.3035	526.2984
QLLGNN	612.3464	640.3413	**LL**	199.1805	227.1754	**LLG**	256.2020	284.1969
LLGN	370.2449	398.2398	**LLGNN**	484.2878	512.2827	**LG**	143.1179	171.1128
LGN	257.1608	285.1557	**LGNN**	371.2037	399.1987	**GN**	144.0768	172.0717
GNN	258.1197	286.1146	**NN**	201.0982	229.0931			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
143.3	1884.9840	0.0598	KINVTCEVQQLLGNNR
143.3	1884.9476	0.0961	QINVTCEVQQLLGNNR
122.8	1885.9316	-0.8879	EINVTCEVQQLLGNNR
30.0	1884.8927	0.1510	AGLNSILQFDCEVYEK
24.2	1885.9105	-0.8667	EGPTFSNIVQEMHKNR
24.1	1886.0448	-1.0010	RISGMTLAIVEAPYIPR
19.0	1885.9996	-0.9559	AISEEVESVKQLDAQLK
17.8	1885.0673	-0.0236	IVGPISFRVDSGIAVDLK
17.3	1883.9701	1.0736	KQLEQGLEGGTAVGDLNR
16.1	1884.9905	0.0533	IQANGLTSGGAEELLKER

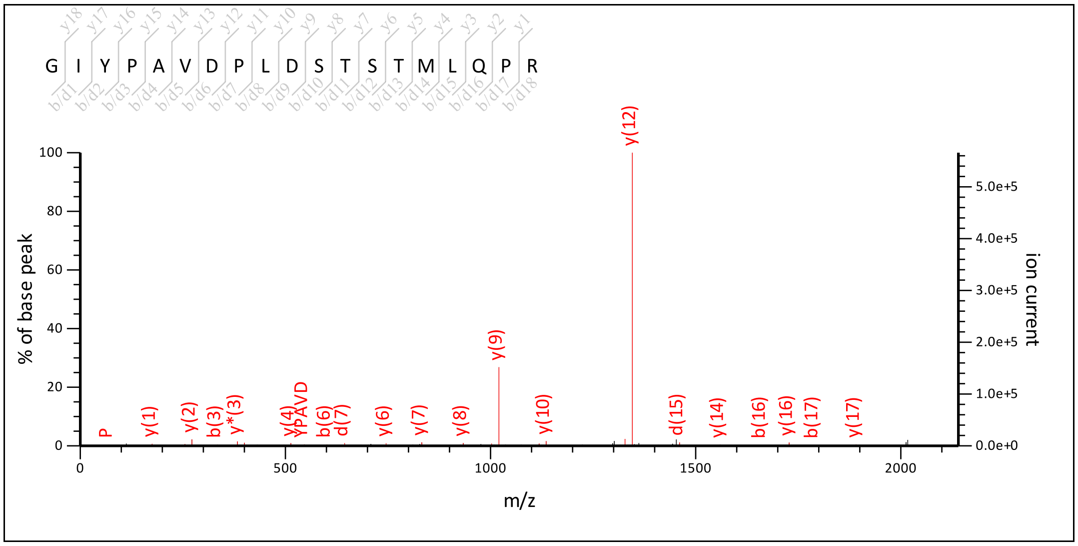
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **GIYPAVDPLDSTSTMLQPR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 27: 2060.121624 from(2061.128900,1+) intensity(0.0000) index(14)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221232, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 2140.33

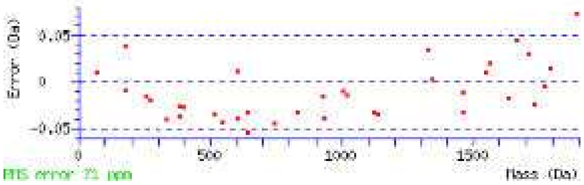
Label all possible matches ○ Label matches used for scoring ●

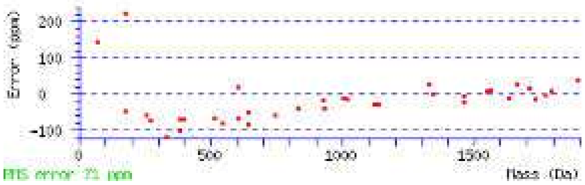
Monoisotopic mass of neutral peptide Mr(calc): 2060.0248
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 152 **Expect:** 2.5e-12
Matches : 40/333 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			115.0866	129.1022	I	1945.9324	1958.9528	1972.9685	2004.0107	1986.9841
3	136.0757	306.1812			**334.1761**					Y	1782.8691			***1890.9266***	1873.9000
4	70.0651	403.2340			431.2289			377.2183		P	1685.8163	1684.8211		***1727.8633***	1710.8367
5	44.0495	474.2711			502.2660					A	1614.7792			***1630.8105***	1613.7840
6	72.0808	573.3395			**601.3344**			559.3239		V	1515.7108	1528.7312		***1559.7734***	1542.7468
7	88.0393	688.3665		670.3559	716.3614		698.3508	644.3766		D	1400.6838	1399.6886		***1460.7050***	1443.6784
8	70.0651	785.4192		767.4087	813.4141		795.4036	759.4036		P	1303.6311	1302.6358		***1345.6780***	1328.6515
9	86.0964	898.5033		880.4927	**926.4982**		908.4876	856.4563		L	1190.5470	1189.5518		1248.6253	1231.5987
10	88.0393	1013.5302		995.5197	1041.5251		1023.5146	969.5404		D	1075.5201	1074.5248		***1135.5412***	1118.5147
11	60.0444	1100.5623		1082.5517	1128.5572		1110.5466	1084.5673		S	988.4880	987.4928		***1020.5143***	1003.4877
12	74.0600	1201.6099		1183.5994	1229.6048		1211.5943	1185.6150	1187.5943	T	887.4404	900.4608	902.4400	***933.4822***	916.4557
13	60.0444	1288.6420		1270.6314	1316.6369		1298.6263	1272.6470		S	800.4083	799.4131		***832.4345***	815.4080
14	74.0600	1389.6896		1371.6791	1417.6846		1399.6740	1373.6947	1375.6740	T	699.3607	712.3811	714.3603	***745.4025***	728.3760
15	104.0528	1520.7301		1502.7196	**1548.7250**		1530.7145	1460.7268		M	568.3202	567.3249		***644.3548***	627.3283
16	86.0964	1633.8142		1615.8036	**1661.8091**		1643.7985	1591.7672		L	455.2361	454.2409		***513.3144***	496.2878
17	101.0709	1761.8728	1744.8462	1743.8622	**1789.8677**	1772.8411	1771.8571	1704.8513		Q	327.1775	326.1823		***400.2303***	383.2037
18	70.0651	1858.9255	1841.8990	1840.9150	1886.9204	1869.8939	1868.9099	1832.9099		P	230.1248	229.1295		***272.1717***	255.1452
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IY	249.1598	277.1547	IYP	346.2125	374.2074	IYPA	417.2496	445.2445
IYPAV	516.3180	544.3130	IYPAVD	631.3450	659.3399	YP	233.1285	261.1234

YPA	304.1656	332.1605	**YPAV**	403.2340	431.2289	**YPAVD**	518.2609	546.2558
YPAVDP	615.3137	643.3086	**PA**	141.1022	169.0972	**PAV**	240.1707	268.1656
PAVD	355.1976	383.1925	**PAVDP**	452.2504	480.2453	**PAVDPL**	565.3344	593.3293
PAVDPLD	680.3614	708.3563	**AV**	143.1179	171.1128	**AVD**	258.1448	286.1397
AVDP	355.1976	383.1925	**AVDPL**	468.2817	496.2766	**AVDPLD**	583.3086	611.3035
AVDPLDS	670.3406	698.3355	**VD**	187.1077	215.1026	**VDP**	284.1605	312.1554
VDPL	397.2445	425.2395	**VDPLD**	512.2715	540.2664	**VDPLDS**	599.3035	627.2984
DP	185.0921	213.0870	**DPL**	298.1761	326.1710	**DPLD**	413.2031	441.1980
DPLDS	500.2351	528.2300	**DPLDST**	601.2828	629.2777	**DPLDSTS**	688.3148	716.3097
PL	183.1492	211.1441	**PLD**	298.1761	326.1710	**PLDS**	385.2082	413.2031
PLDST	486.2558	514.2508	**PLDSTS**	573.2879	601.2828	**PLDSTST**	674.3355	702.3305
LD	201.1234	229.1183	**LDS**	288.1554	316.1503	**LDST**	389.2031	417.1980
LDSTS	476.2351	504.2300	**LDSTST**	577.2828	605.2777	**DS**	175.0713	203.0662
DST	276.1190	304.1139	**DSTS**	363.1510	391.1460	**DSTST**	464.1987	492.1936
DSTSTM	595.2392	623.2341	**ST**	161.0921	189.0870	**STS**	248.1241	276.1190
STST	349.1718	377.1667	**STSTM**	480.2123	508.2072	**STSTML**	593.2963	621.2912
TS	161.0921	189.0870	**TST**	262.1397	290.1347	**TSTM**	393.1802	421.1751
TSTML	506.2643	534.2592	**TSTMLQ**	634.3229	662.3178	**ST**	161.0921	189.0870
STM	292.1326	320.1275	**STML**	405.2166	433.2115	**STMLQ**	533.2752	561.2701
STMLQP	630.3280	658.3229	**TM**	205.1005	233.0954	**TML**	318.1846	346.1795
TMLQ	446.2432	474.2381	**TMLQP**	543.2959	571.2908	**ML**	217.1369	245.1318
MLQ	345.1955	373.1904	**MLQP**	442.2483	470.2432	**LQ**	214.1550	242.1499
LQP	311.2078	339.2027	**QP**	198.1237	226.1186			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMIQPR
151.7	2060.0612	0.0604	GIYPAVDPLDSTSTMLKPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR
151.7	2060.0248	0.0968	GIYPAVDPLDSTSTMLQPR

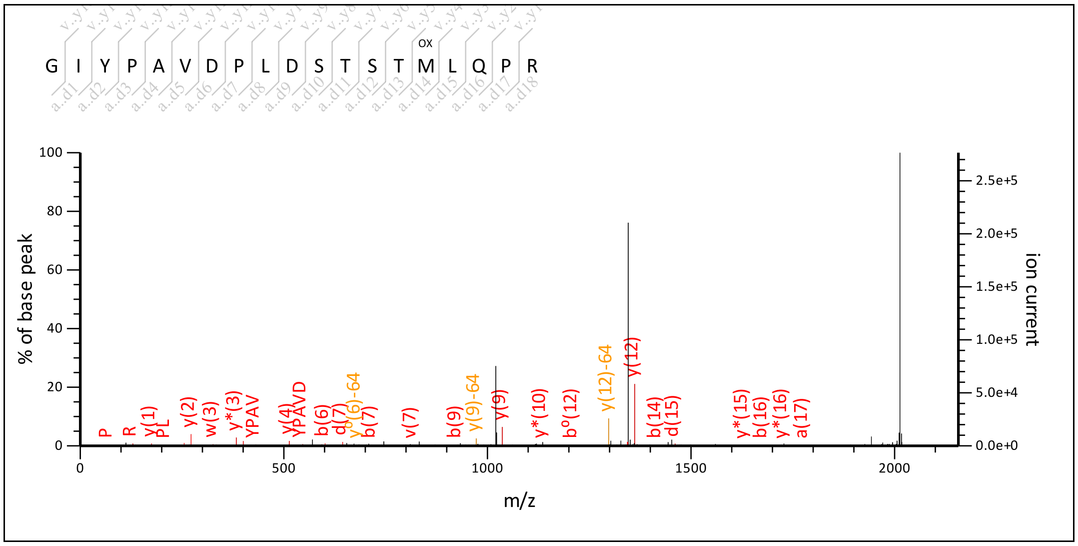
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **GIYPAVDPLDSTSTMLQPR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 29: 2076.112824 from(2077.120100,1+) intensity(0.0000) index(15)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221241, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



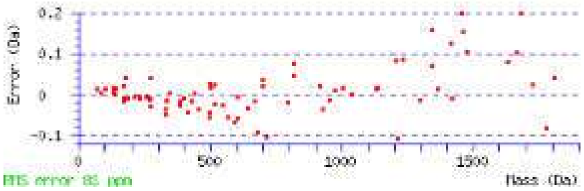
0 to 2156.66

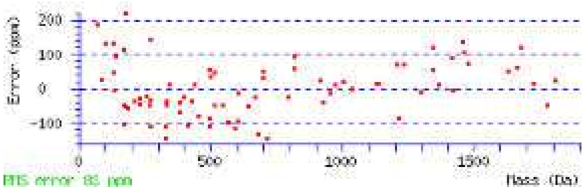
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2076.0198
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 36 **Expect:** 0.88
Matches : 90/459 fragment ions using 199 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			***171.1128***			115.0866	129.1022	I	1961.9273	1974.9477	1988.9634	2020.0056	2002.9790
3	136.0757	306.1812			***334.1761***					Y	1798.8640			1906.9215	1889.8950
4	70.0651	403.2340			***431.2289***			377.2183		P	1701.8112	1700.8160		1743.8582	1726.8316
5	44.0495	474.2711			***502.2660***					A	1630.7741			1646.8054	1629.7789
6	72.0808	573.3395			***601.3344***			559.3239		V	1531.7057	1544.7261		1575.7683	1558.7418
7	88.0393	688.3665		670.3559	***716.3614***		698.3508	644.3766		D	1416.6788	1415.6835		**1476.6999**	1459.6733
8	70.0651	785.4192		767.4087	***813.4141***		795.4036	759.4036		P	1319.6260	1318.6307		**1361.6729**	1344.6464
9	86.0964	898.5033		880.4927	***926.4982***		908.4876	856.4563		L	1206.5419	1205.5467		1264.6202	1247.5936
10	88.0393	1013.5302		995.5197	1041.5251		1023.5146	969.5404		D	1091.5150	1090.5197		1151.5361	1134.5096
11	60.0444	1100.5623		1082.5517	***1128.5572***		1110.5466	1084.5673		S	1004.4830	1003.4877		**1036.5092**	1019.4826
12	74.0600	1201.6099		1183.5994	***1229.6048***		1211.5943	1185.6150	1187.5943	T	903.4353	916.4557	918.4349	949.4771	932.4506
13	60.0444	1288.6420		1270.6314	1316.6369		1298.6263	1272.6470		S	816.4033	815.4080		848.4295	831.4029
14	74.0600	1389.6896		1371.6791	***1417.6846***		1399.6740	1373.6947	1375.6740	T	715.3556	728.3760	730.3552	761.3974	744.3709
15	120.0478	1536.7250		1518.7145	1564.7200		1546.7094	1460.7268		M	568.3202	567.3249		660.3498	643.3232
16	86.0964	1649.8091		1631.7985	***1677.8040***		1659.7935	1607.7622		L	455.2361	454.2409		**513.3144**	496.2878
17	101.0709	1777.8677	1760.8411	1759.8571	***1805.8626***	1788.8360	1787.8520	1720.8462		Q	327.1775	326.1823		**400.2303**	383.2037
18	70.0651	1874.9204	1857.8939	1856.9099	1902.9154	1885.8888	1884.9048	1848.9048		P	230.1248	229.1295		**272.1717**	255.1452
19	129.1135									R	74.0237	73.0284		**175.1190**	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IY	249.1598	277.1547	IYP	346.2125	374.2074	IYPA	417.2496	445.2445
IYPAV	516.3180	544.3130	IYPAVD	631.3450	659.3399	YP	233.1285	261.1234
YPA	304.1656	332.1605	YPAV	403.2340	431.2289	YPAVD	518.2609	546.2558
YPAVDP	615.3137	643.3086	PA	141.1022	169.0972	PAV	240.1707	268.1656
PAVD	355.1976	383.1925	PAVDP	452.2504	480.2453	PAVDPL	565.3344	593.3293
PAVDPLD	680.3614	708.3563	AV	143.1179	171.1128	AVD	258.1448	286.1397
AVDP	355.1976	383.1925	AVDPL	468.2817	496.2766	AVDPLD	583.3086	611.3035
AVDPLDS	670.3406	698.3355	VD	187.1077	215.1026	VDP	284.1605	312.1554
VDPL	397.2445	425.2395	VDPLD	512.2715	540.2664	VDPLDS	599.3035	627.2984
DP	185.0921	213.0870	DPL	298.1761	326.1710	DPLD	413.2031	441.1980
DPLDS	500.2351	528.2300	DPLDST	601.2828	629.2777	DPLDSTS	688.3148	716.3097
PL	183.1492	211.1441	PLD	298.1761	326.1710	PLDS	385.2082	413.2031
PLDST	486.2558	514.2508	PLDSTS	573.2879	601.2828	PLDSTST	674.3355	702.3305
LD	201.1234	229.1183	LDS	288.1554	316.1503	LDST	389.2031	417.1980
LDSTS	476.2351	504.2300	LDSTST	577.2828	605.2777	DS	175.0713	203.0662
DST	276.1190	304.1139	DSTS	363.1510	391.1460	DSTST	464.1987	492.1936
DSTSTM	611.2341	639.2290	ST	161.0921	189.0870	STS	248.1241	276.1190
STST	349.1718	377.1667	STSTM	496.2072	524.2021	STSTML	609.2912	637.2862
TS	161.0921	189.0870	TST	262.1397	290.1347	TSTM	409.1751	437.1701
TSTML	522.2592	550.2541	TSTMLQ	650.3178	678.3127	ST	161.0921	189.0870
STM	308.1275	336.1224	STML	421.2115	449.2064	STMLQ	549.2701	577.2650
STMLQP	646.3229	674.3178	TM	221.0954	249.0904	TML	334.1795	362.1744
TMLQ	462.2381	490.2330	TMLQP	559.2908	587.2858	ML	233.1318	261.1267
MLQ	361.1904	389.1853	MLQP	458.2432	486.2381	LQ	214.1550	242.1499
LQP	311.2078	339.2027	QP	198.1237	226.1186			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.3	2075.9834	0.1295	GEYPAVDPLDSTSTMLQPR
79.3	2075.0357	1.0771	GKYPAVDPLDSTSTMLQPR
79.3	2074.9994	1.1135	GQYPAVDPLDSTSTMLQPR
64.6	2076.0198	0.0931	GIYPSVDPLDSTSTMLQPR
53.3	2074.9993	1.1135	GIYPANDPLDSTSTMLQPR
53.3	2075.9834	0.1295	GIYPADDPLDSTSTMLQPR
51.2	2076.0384	0.0744	GIYPAVMPLDSTSTMLQPR
40.2	2076.0384	0.0744	GIYPAVDPLMSTSTMLQPR
36.3	2076.0561	0.0567	GIYPAVDPLDSTSTMLKPR
36.3	2076.0198	0.0931	GIYPAVDPLDSTSTMLQPR

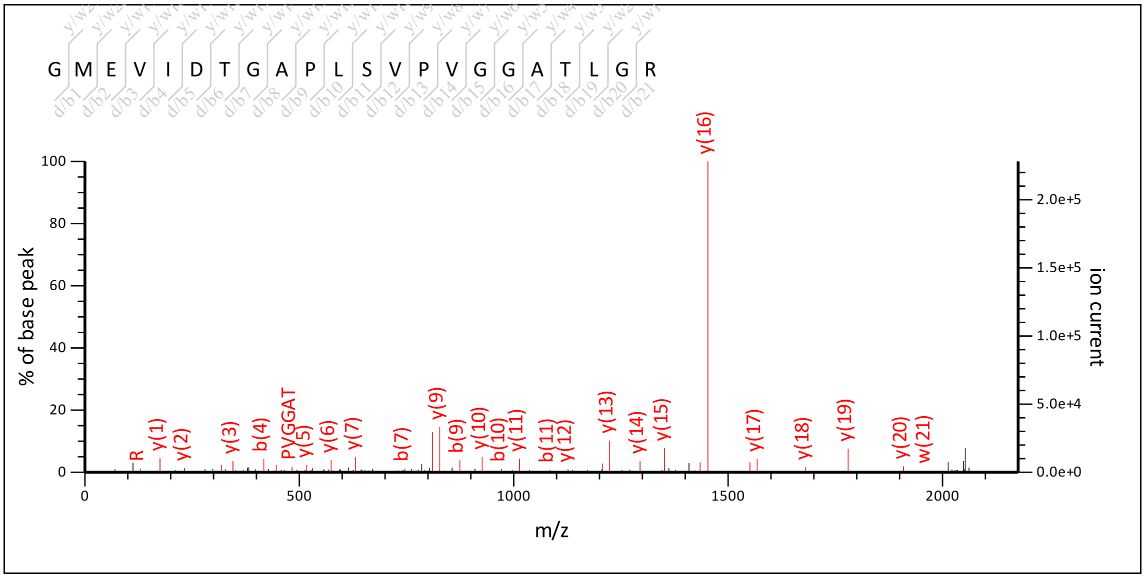
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **GMEVIDTGAPLSVPVGGATLGR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 31: 2096.196324 from(2097.203600,1+) intensity(0.0000) index(16)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221226, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 2176.41

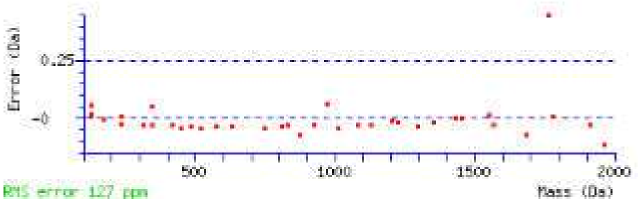
Label all possible matches ○ Label matches used for scoring ●

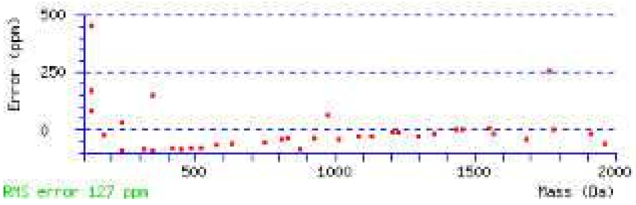
```
Monoisotopic mass of neutral peptide Mr(calc): 2096.0936
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 185  Expect: 1.5e-15
Matches : 38/423 fragment ions using 42 most intense peaks   (help)
```

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	30.0338	30.0338		58.0287		44.0495		G							22
2	104.0528	161.0743		189.0692		101.0709		M	1964.0447	1963.0495		2040.0794	2023.0529	2022.0688	21
3	102.0550	290.1169	272.1063	**318.1118**	300.1013	232.1114		E	1835.0021	1834.0069		***1909.0389***	1892.0124	1891.0284	20
4	72.0808	389.1853	371.1748	**417.1802**	399.1697	375.1697		V	1735.9337	1748.9541		***1779.9963***	1762.9698	1761.9858	19
5	86.0964	502.2694	484.2588	530.2643	512.2537	474.2381	488.2537	I	1622.8497	1635.8701	1649.8857	***1680.9279***	1663.9014	1662.9173	18
6	88.0393	617.2963	599.2858	645.2912	627.2807	573.3065		D	1507.8227	1506.8275		***1567.8438***	1550.8173	1549.8333	17
7	74.0600	718.3440	700.3334	**746.3389**	728.3284	702.3491	704.3284	T	1406.7750	1419.7954	1421.7747	***1452.8169***	1435.7904	1434.8063	16
8	30.0338	775.3655	757.3549	803.3604	785.3498			G				***1351.7692***	1334.7427	1333.7587	15
9	44.0495	846.4026	828.3920	**874.3975**	856.3869			A	1278.7165			***1294.7478***	1277.7212	1276.7372	14
10	70.0651	943.4553	925.4448	**971.4503**	953.4397	917.4397		P	1181.6637	1180.6685		***1223.7106***	1206.6841	1205.7001	13
11	86.0964	1056.5394	1038.5288	**1084.5343**	1066.5238	1014.4925		L	1068.5796	1067.5844		***1126.6579***	1109.6313	1108.6473	12
12	60.0444	1143.5714	1125.5609	1171.5664	1153.5558	1127.5765		S	981.5476	980.5524		***1013.5738***	996.5473	995.5633	11
13	72.0808	1242.6399	1224.6293	1270.6348	1252.6242	1228.6242		V	882.4792	895.4996		***926.5418***	909.5152	908.5312	10
14	70.0651	1339.6926	1321.6821	1367.6875	1349.6770	1313.6770		P	785.4264	784.4312		***827.4734***	810.4468	809.4628	9
15	72.0808	1438.7610	1420.7505	1466.7559	1448.7454	1424.7454		V	686.3580	699.3784		730.4206	713.3941	712.4100	8
16	30.0338	1495.7825	1477.7719	1523.7774	1505.7668			G				***631.3522***	614.3257	613.3416	7
17	30.0338	1552.8040	1534.7934	1580.7989	1562.7883			G				***574.3307***	557.3042	556.3202	6
18	44.0495	1623.8411	1605.8305	1651.8360	1633.8254			A	501.2780			***517.3093***	500.2827	499.2987	5
19	74.0600	1724.8888	1706.8782	1752.8837	1734.8731	1708.8938	1710.8731	T	400.2303	413.2507	415.2300	***446.2722***	429.2456	428.2616	4

20	86.0964	1837.9728	1819.9622	1865.9677	1847.9572	1795.9259		L	287.1462	286.1510		***345.2245***	328.1979		3
21	30.0338	1894.9943	1876.9837	1922.9892	1904.9786			G				***232.1404***	215.1139		2
22	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ME	233.0954	261.0904	**MEV**	332.1639	360.1588	**MEVI**	445.2479	473.2428
MEVID	560.2749	588.2698	**MEVIDT**	661.3225	689.3175	**EV**	201.1234	229.1183
EVI	314.2074	342.2023	**EVID**	429.2344	457.2293	**EVIDT**	530.2821	558.2770
EVIDTG	587.3035	615.2984	**EVIDTGA**	658.3406	686.3355	**VI**	185.1648	213.1598
VID	300.1918	328.1867	**VIDT**	401.2395	429.2344	**VIDTG**	458.2609	486.2558
VIDTGA	529.2980	557.2930	**VIDTGAP**	626.3508	654.3457	**ID**	201.1234	229.1183
IDT	302.1710	330.1660	**IDTG**	359.1925	387.1874	**IDTGA**	430.2296	458.2245
IDTGAP	527.2824	555.2773	**IDTGAPL**	640.3665	668.3614	**DT**	189.0870	217.0819
DTG	246.1084	274.1034	**DTGA**	317.1456	345.1405	**DTGAP**	414.1983	442.1932
DTGAPL	527.2824	555.2773	**DTGAPLS**	614.3144	642.3093	**TG**	131.0815	159.0764
TGA	202.1186	230.1135	**TGAP**	299.1714	327.1663	**TGAPL**	412.2554	440.2504
TGAPLS	499.2875	527.2824	**TGAPLSV**	598.3559	626.3508	**TGAPLSVP**	695.4087	723.4036
GA	101.0709	129.0659	**GAP**	198.1237	226.1186	**GAPL**	311.2078	339.2027
GAPLS	398.2398	426.2347	**GAPLSV**	497.3082	525.3031	**GAPLSVP**	594.3610	622.3559
GAPLSVPV	693.4294	721.4243	**AP**	141.1022	169.0972	**APL**	254.1863	282.1812
APLS	341.2183	369.2132	**APLSV**	440.2867	468.2817	**APLSVP**	537.3395	565.3344
APLSVPV	636.4079	664.4028	**APLSVPVG**	693.4294	721.4243	**PL**	183.1492	211.1441
PLS	270.1812	298.1761	**PLSV**	369.2496	397.2445	**PLSVP**	466.3024	494.2973
PLSVPV	565.3708	593.3657	**PLSVPVG**	622.3923	650.3872	**PLSVPVGG**	679.4137	707.4087
LS	173.1285	201.1234	**LSV**	272.1969	300.1918	**LSVP**	369.2496	397.2445
LSVPV	468.3180	496.3130	**LSVPVG**	525.3395	553.3344	**LSVPVGG**	582.3610	610.3559
LSVPVGGA	653.3981	681.3930	**SV**	159.1128	187.1077	**SVP**	256.1656	284.1605
SVPV	355.2340	383.2289	**SVPVG**	412.2554	440.2504	**SVPVGG**	469.2769	497.2718
SVPVGGA	540.3140	568.3089	**SVPVGGAT**	641.3617	669.3566	**VP**	169.1335	197.1285
VPV	268.2020	296.1969	**VPVG**	325.2234	353.2183	**VPVGG**	382.2449	410.2398
VPVGGA	453.2820	481.2769	**VPVGGAT**	554.3297	582.3246	**VPVGGATL**	667.4137	695.4087
PV	169.1335	197.1285	**PVG**	226.1550	254.1499	**PVGG**	283.1765	311.1714
PVGGA	354.2136	382.2085	**PVGGAT**	455.2613	483.2562	**PVGGATL**	568.3453	596.3402
PVGGATLG	625.3668	653.3617	**VG**	129.1022	157.0972	**VGG**	186.1237	214.1186
VGGA	257.1608	285.1557	**VGGAT**	358.2085	386.2034	**VGGATL**	471.2926	499.2875
VGGATLG	528.3140	556.3089	**GG**	87.0553	115.0502	**GGA**	158.0924	186.0873
GGAT	259.1401	287.1350	**GGATL**	372.2241	400.2191	**GGATLG**	429.2456	457.2405
GA	101.0709	129.0659	**GAT**	202.1186	230.1135	**GATL**	315.2027	343.1976
GATLG	372.2241	400.2191	**AT**	145.0972	173.0921	**ATL**	258.1812	286.1761
ATLG	315.2027	343.1976	**TL**	187.1441	215.1390	**TLG**	244.1656	272.1605
LG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
185.0	2096.0936	0.1027	GMEVIDTGAPISVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPISVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPISVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPISVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPLSVPVGGATIGR
185.0	2096.0936	0.1027	GMEVIDTGAPLSVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPLSVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPLSVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPLSVPVGGATLGR
185.0	2096.0936	0.1027	GMEVIDTGAPLSVPVGGATLGR

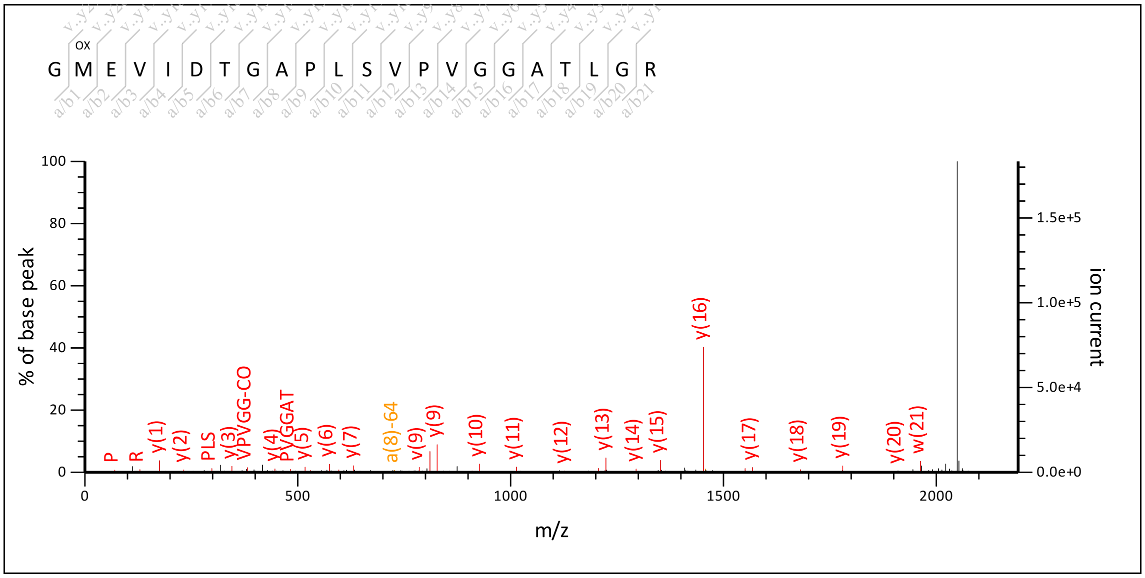
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **GMEVIDTGAPLSVPVGGATLGR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 33: 2112.183924 from(2113.191200,1+) intensity(0.0000) index(17)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221239, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 2192.25

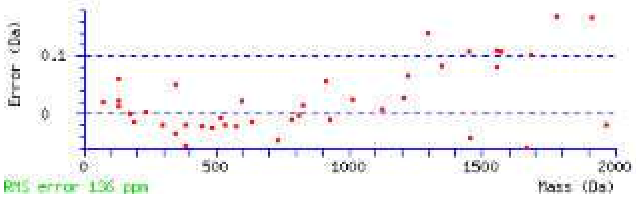
Label all possible matches ○ Label matches used for scoring ●

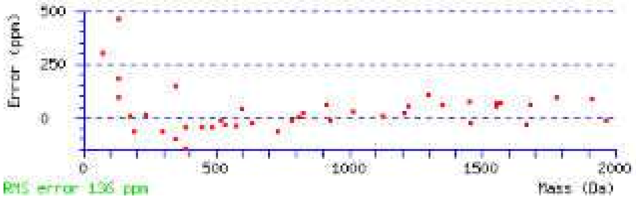
Monoisotopic mass of neutral peptide Mr(calc): 2112.0885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 141 **Expect:** 2.7e-11
Matches : 43/529 fragment ions using 63 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	30.0338	30.0338		58.0287		44.0495		G							22
2	120.0478	177.0692		205.0641		101.0709		M	1964.0447	1963.0495		2056.0743	2039.0478	2038.0638	21
3	102.0550	306.1118	288.1013	334.1067	316.0962	248.1063		E	1835.0021	1834.0069		***1909.0389***	1892.0124	1891.0284	20
4	72.0808	405.1802	387.1697	433.1751	415.1646	391.1646		V	1735.9337	1748.9541		***1779.9963***	1762.9698	1761.9858	19
5	86.0964	518.2643	500.2537	546.2592	528.2486	490.2330	504.2486	I	1622.8497	1635.8701	1649.8857	***1680.9279***	1663.9014	1662.9173	18
6	88.0393	633.2912	615.2807	661.2862	643.2756	589.3014		D	1507.8227	1506.8275		***1567.8438***	1550.8173	1549.8333	17
7	74.0600	734.3389	716.3284	762.3338	744.3233	718.3440	720.3233	T	1406.7750	1419.7954	1421.7747	***1452.8169***	1435.7904	1434.8063	16
8	30.0338	791.3604	773.3498	819.3553	801.3447			G				***1351.7692***	1334.7427	1333.7587	15
9	44.0495	862.3975	844.3869	890.3924	872.3818			A	1278.7165			***1294.7478***	1277.7212	1276.7372	14
10	70.0651	959.4503	941.4397	987.4452	969.4346	933.4346		P	1181.6637	1180.6684		***1223.7106***	1206.6841	1205.7001	13
11	86.0964	1072.5343	1054.5238	1100.5292	1082.5187	1030.4874		L	1068.5796	1067.5844		***1126.6579***	1109.6313	1108.6473	12
12	60.0444	1159.5664	1141.5558	1187.5613	1169.5507	1143.5714		S	981.5476	980.5524		***1013.5738***	996.5473	995.5633	11
13	72.0808	1258.6348	1240.6242	1286.6297	1268.6191	1244.6191		V	882.4792	895.4996		***926.5418***	909.5152	908.5312	10
14	70.0651	1355.6875	1337.6770	1383.6824	1365.6719	1329.6719		P	785.4264	784.4312		***827.4734***	810.4468	809.4628	9
15	72.0808	1454.7559	1436.7454	1482.7509	1464.7403	1440.7403		V	686.3580	699.3784		730.4206	713.3941	712.4100	8
16	30.0338	1511.7774	1493.7668	1539.7723	1521.7618			G				***631.3522***	614.3257	613.3416	7
17	30.0338	1568.7989	1550.7883	1596.7938	1578.7832			G				***574.3307***	557.3042	556.3202	6

18	44.0495	1639.8360	1621.8254	1667.8309	1649.8203			A	501.2780			***517.3093***	500.2827	499.2987	5
19	74.0600	1740.8837	1722.8731	1768.8786	1750.8680	1724.8888	1726.8680	T	400.2303	413.2507	415.2300	***446.2722***	429.2456	428.2616	4
20	86.0964	1853.9677	1835.9572	1881.9626	1863.9521	1811.9208		L	287.1462	286.1510		***345.2245***	328.1979		3
21	30.0338	1910.9892	1892.9786	1938.9841	1920.9735			G				***232.1404***	215.1139		2
22	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ME	249.0904	277.0853	MEV	348.1588	376.1537	MEVI	461.2428	489.2377
MEVID	576.2698	604.2647	MEVIDT	677.3175	705.3124	EV	201.1234	229.1183
EVI	314.2074	342.2023	EVID	429.2344	457.2293	EVIDT	530.2821	558.2770
EVIDTG	587.3035	615.2984	EVIDTGA	658.3406	686.3355	VI	185.1648	213.1598
VID	300.1918	328.1867	VIDT	401.2395	429.2344	VIDTG	458.2609	486.2558
VIDTGA	529.2980	557.2930	VIDTGAP	626.3508	654.3457	ID	201.1234	229.1183
IDT	302.1710	330.1660	IDTG	359.1925	387.1874	IDTGA	430.2296	458.2245
IDTGAP	527.2824	555.2773	IDTGAPL	640.3665	668.3614	DT	189.0870	217.0819
DTG	246.1084	274.1034	DTGA	317.1456	345.1405	DTGAP	414.1983	442.1932
DTGAPL	527.2824	555.2773	DTGAPLS	614.3144	642.3093	TG	131.0815	159.0764
TGA	202.1186	230.1135	TGAP	299.1714	327.1663	TGAPL	412.2554	440.2504
TGAPLS	499.2875	527.2824	TGAPLSV	598.3559	626.3508	TGAPLSVP	695.4087	723.4036
GA	101.0709	129.0659	GAP	198.1237	226.1186	GAPL	311.2078	339.2027
GAPLS	398.2398	426.2347	GAPLSV	497.3082	525.3031	GAPLSVP	594.3610	622.3559
GAPLSVPV	693.4294	721.4243	AP	141.1022	169.0972	APL	254.1863	282.1812
APLS	341.2183	369.2132	APLSV	440.2867	468.2817	APLSVP	537.3395	565.3344
APLSVPV	636.4079	664.4028	APLSVPVG	693.4294	721.4243	PL	183.1492	211.1441
PLS	270.1812	298.1761	PLSV	369.2496	397.2445	PLSVP	466.3024	494.2973
PLSVPV	565.3708	593.3657	PLSVPVG	622.3923	650.3872	PLSVPVGG	679.4137	707.4087
LS	173.1285	201.1234	LSV	272.1969	300.1918	LSVP	369.2496	397.2445
LSVPV	468.3180	496.3130	LSVPVG	525.3395	553.3344	LSVPVGG	582.3610	610.3559
LSVPVGGA	653.3981	681.3930	SV	159.1128	187.1077	SVP	256.1656	284.1605
SVPV	355.2340	383.2289	SVPVG	412.2554	440.2504	SVPVGG	469.2769	497.2718
SVPVGGA	540.3140	568.3089	SVPVGGAT	641.3617	669.3566	VP	169.1335	197.1285
VPV	268.2020	296.1969	VPVG	325.2234	353.2183	VPVGG	382.2449	410.2398
VPVGGA	453.2820	481.2769	VPVGGAT	554.3297	582.3246	VPVGGATL	667.4137	695.4087
PV	169.1335	197.1285	PVG	226.1550	254.1499	PVGG	283.1765	311.1714
PVGGA	354.2136	382.2085	PVGGAT	455.2613	483.2562	PVGGATL	568.3453	596.3402
PVGGATLG	625.3668	653.3617	VG	129.1022	157.0972	VGG	186.1237	214.1186
VGGA	257.1608	285.1557	VGGAT	358.2085	386.2034	VGGATL	471.2926	499.2875
VGGATLG	528.3140	556.3089	GG	87.0553	115.0502	GGA	158.0924	186.0873
GGAT	259.1401	287.1350	GGATL	372.2241	400.2191	GGATLG	429.2456	457.2405
GA	101.0709	129.0659	GAT	202.1186	230.1135	GATL	315.2027	343.1976
GATLG	372.2241	400.2191	AT	145.0972	173.0921	ATL	258.1812	286.1761
ATLG	315.2027	343.1976	TL	187.1441	215.1390	TLG	244.1656	272.1605
LG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
141.1	2112.0885	0.0954	GMEVIDTGAPISVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPISVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPISVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPISVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPLSVPVGGATIGR
141.1	2112.0885	0.0954	GMEVIDTGAPLSVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPLSVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPLSVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPLSVPVGGATLGR
141.1	2112.0885	0.0954	GMEVIDTGAPLSVPVGGATLGR

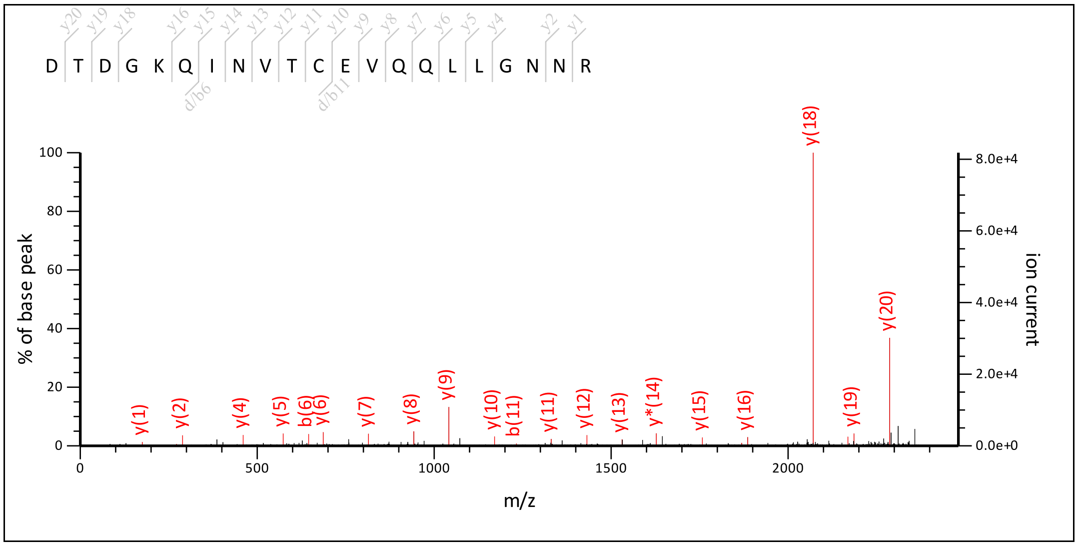
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **DTDGKQINVTCEVQQLLGNNR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 39: 2401.280124 from(2402.287400,1+) intensity(0.0000) index(19)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221235, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 2481.19

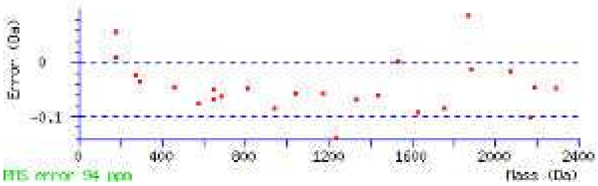
Label all possible matches ○ Label matches used for scoring ●

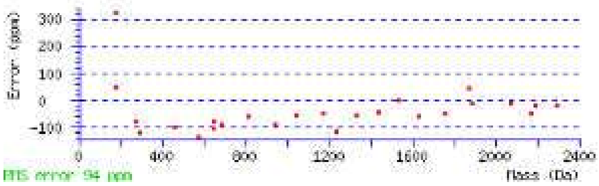
Monoisotopic mass of neutral peptide Mr(calc): 2401.1656
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 196 **Expect:** 8.1e-17
Matches : 25/395 fragment ions using 23 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D					
2	74.0600	189.0870		171.0764	217.0819		199.0713	173.0921	175.0713	T	2241.1041	2254.1245	2256.1037	***2287.1459***	2270.1194
3	88.0393	304.1139		286.1034	332.1088		314.0983	260.1241		D	2126.0771	2125.0819		***2186.0982***	2169.0717
4	30.0338	361.1354		343.1248	389.1303		371.1197			G				***2071.0713***	2054.0447
5	101.1073	489.2304	472.2038	471.2198	517.2253	500.1987	499.2147	432.1725		K	1940.9607	1939.9654		2014.0498	1997.0233
6	101.0709	617.2889	600.2624	599.2784	**645.2838**	628.2573	627.2733	560.2675		Q	1812.9021	1811.9069		***1885.9549***	1868.9283
7	86.0964	730.3730	713.3464	712.3624	758.3679	741.3414	740.3573	702.3417	716.3573	I	1699.8180	1712.8384	1726.8541	***1757.8963***	1740.8697
8	87.0553	844.4159	827.3894	826.4054	872.4108	855.3843	854.4003	801.4101		N	1585.7751	1584.7799		1644.8122	1627.7857
9	72.0808	943.4843	926.4578	925.4738	971.4793	954.4527	953.4687	929.4687		V	1486.7067	1499.7271		***1530.7693***	1513.7428
10	74.0600	1044.5320	1027.5055	1026.5214	1072.5269	1055.5004	1054.5164	1028.5371	1030.5164	T	1385.6590	1398.6794	1400.6587	***1431.7009***	1414.6743
11	133.0430	1204.5627	1187.5361	1186.5521	**1232.5576**	1215.5310	1214.5470	1115.5691		C	1225.6284	1224.6331		***1330.6532***	1313.6267
12	102.0550	1333.6053	1316.5787	1315.5947	1361.6002	1344.5736	1343.5896	1275.5998		E	1096.5858	1095.5905		***1170.6226***	1153.5960
13	72.0808	1432.6737	1415.6471	1414.6631	1460.6686	1443.6420	1442.6580	1418.6580		V	997.5174	1010.5378		***1041.5800***	1024.5534
14	101.0709	1560.7322	1543.7057	1542.7217	1588.7272	1571.7006	1570.7166	1503.7108		Q	869.4588	868.4635		***942.5116***	925.4850
15	101.0709	1688.7908	1671.7643	1670.7803	1716.7857	1699.7592	1698.7752	1631.7694		Q	741.4002	740.4050		***814.4530***	797.4264
16	86.0964	1801.8749	1784.8483	1783.8643	1829.8698	1812.8433	1811.8592	1759.8279		L	628.3161	627.3209		***686.3944***	669.3678
17	86.0964	1914.9590	1897.9324	1896.9484	1942.9539	1925.9273	1924.9433	1872.9120		L	515.2321	514.2368		***573.3103***	556.2838
18	30.0338	1971.9804	1954.9539	1953.9699	1999.9753	1982.9488	1981.9648			G				***460.2263***	443.1997
19	87.0553	2086.0233	2068.9968	2068.0128	2114.0183	2096.9917	2096.0077	2043.0175		N	344.1677	343.1724		403.2048	386.1783
20	87.0553	2200.0663	2183.0397	2182.0557	2228.0612	2211.0346	2210.0506	2157.0605		N	230.1248	229.1295		***289.1619***	272.1353
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

TD	189.0870	217.0819	**TDG**	246.1084	274.1034	**TDGK**	374.2034	402.1983
TDGKQ	502.2620	530.2569	**TDGKQI**	615.3461	643.3410	**DG**	145.0608	173.0557
DGK	273.1557	301.1506	**DGKQ**	401.2143	429.2092	**DGKQI**	514.2984	542.2933
DGKQIN	628.3413	656.3362	**GK**	158.1288	186.1237	**GKQ**	286.1874	314.1823
GKQI	399.2714	427.2663	**GKQIN**	513.3144	541.3093	**GKQINV**	612.3828	640.3777
KQ	229.1659	257.1608	**KQI**	342.2500	370.2449	**KQIN**	456.2929	484.2878
KQINV	555.3613	583.3562	**KQINVT**	656.4090	684.4039	**QI**	214.1550	242.1499
QIN	328.1979	356.1928	**QINV**	427.2663	455.2613	**QINVT**	528.3140	556.3089
QINVTC	688.3447	716.3396	**IN**	200.1394	228.1343	**INV**	299.2078	327.2027
INVT	400.2554	428.2504	**INVTC**	560.2861	588.2810	**INVTCE**	689.3287	717.3236
NV	186.1237	214.1186	**NVT**	287.1714	315.1663	**NVTC**	447.2020	475.1969
NVTCE	576.2446	604.2395	**NVTCEV**	675.3130	703.3080	**VT**	173.1285	201.1234
VTC	333.1591	361.1540	**VTCE**	462.2017	490.1966	**VTCEV**	561.2701	589.2650
VTCEVQ	689.3287	717.3236	**TC**	234.0907	262.0856	**TCE**	363.1333	391.1282
TCEV	462.2017	490.1966	**TCEVQ**	590.2603	618.2552	**CE**	262.0856	290.0805
CEV	361.1540	389.1489	**CEVQ**	489.2126	517.2075	**CEVQQ**	617.2712	645.2661
EV	201.1234	229.1183	**EVQ**	329.1819	357.1769	**EVQQ**	457.2405	485.2354
EVQQL	570.3246	598.3195	**EVQQLL**	683.4087	711.4036	**VQ**	200.1394	228.1343
VQQ	328.1979	356.1928	**VQQL**	441.2820	469.2769	**VQQLL**	554.3661	582.3610
VQQLLG	611.3875	639.3824	**QQ**	229.1295	257.1244	**QQL**	342.2136	370.2085
QQLL	455.2976	483.2926	**QQLLG**	512.3191	540.3140	**QQLLGN**	626.3620	654.3570
QL	214.1550	242.1499	**QLL**	327.2391	355.2340	**QLLG**	384.2605	412.2554
QLLGN	498.3035	526.2984	**QLLGNN**	612.3464	640.3413	**LL**	199.1805	227.1754
LLG	256.2020	284.1969	**LLGN**	370.2449	398.2398	**LLGNN**	484.2878	512.2827
LG	143.1179	171.1128	**LGN**	257.1608	285.1557	**LGNN**	371.2037	399.1987
GN	144.0768	172.0717	**GNN**	258.1197	286.1146	**NN**	201.0982	229.0931





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
195.6	2401.1656	0.1145	DTDGKQINVTCEVQQLLGNNR
195.6	2401.1292	0.1509	DTDGQQINVTCEVQQLLGNNR
195.6	2401.1292	0.1509	DTDGQQINVTCEVQQLLGNNR
149.7	2401.1543	0.1258	DTLGEEINVTCEVQQLLGNNR
149.7	2401.1292	0.1509	DTNGQEINVTCEVQQLLGNNR
146.3	2401.1842	0.0959	MTVGQQINVTCEVQQLLGNNR
141.4	2400.1452	1.1349	DTNGQQINVTCEVQQLLGNNR
126.0	2401.1292	0.1509	DNTGQEINVTCEVQQLLGNNR
124.4	2402.1132	-0.8331	DTDGEQINVTCEVQQLLGNNR
121.6	2401.1478	0.1323	DIAGQCINVTCEVQQLLGNNR

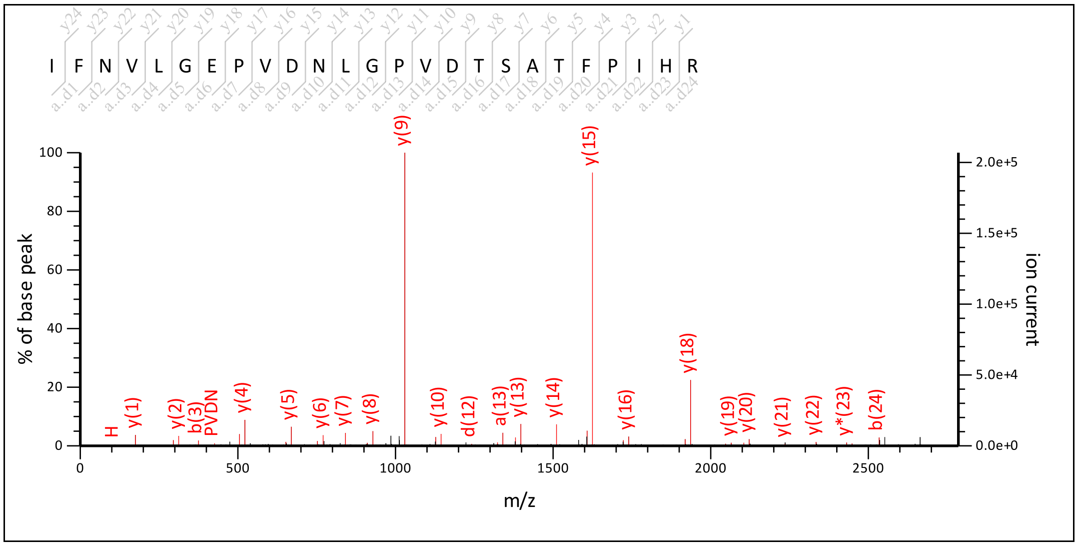
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 87

MS/MS Fragmentation of **IFNVLGEPVDNLGPVDTSATFPIHR**
Found in **gi|11466794** in **NCBInr**, ATP synthase CF1 beta subunit [Oryza sativa Japonica Group]

Match to Query 41: 2707.533024 from(2708.540300,1+) intensity(0.0000) index(20)
Title: Label: D11, Spot_Id: 216640, Peak_List_Id: 221225, MSMS Job_Run_Id: 21346, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_D11_135997699500.txt



0 to 2785.71

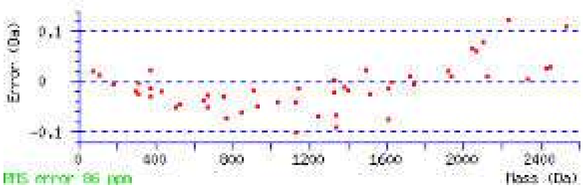
Label all possible matches ○ Label matches used for scoring ●

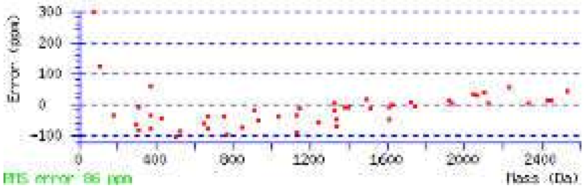
Monoisotopic mass of neutral peptide Mr(calc): 2707.3970
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 177 **Expect:** 4.4e-15
Matches : 52/505 fragment ions using 54 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		I					
2	120.0808	233.1648			261.1598					F	2503.2576			2595.3202	2578.2936
3	87.0553	347.2078	330.1812		375.2027	358.1761		304.2020		N	2389.2147	2388.2194		***2448.2518***	2431.2252
4	72.0808	446.2762	429.2496		474.2711	457.2445		432.2605		V	2290.1462	2303.1666		***2334.2088***	2317.1823
5	86.0964	559.3602	542.3337		587.3552	570.3286		517.3133		L	2177.0622	2176.0669		***2235.1404***	2218.1139
6	30.0338	616.3817	599.3552		644.3766	627.3501				G				***2122.0564***	2105.0298
7	102.0550	745.4243	728.3978	727.4137	773.4192	756.3927	755.4087	687.4188		E	1990.9981	1990.0029		***2065.0349***	2048.0083
8	70.0651	842.4771	825.4505	824.4665	870.4720	853.4454	852.4614	816.4614		P	1893.9454	1892.9501		***1935.9923***	1918.9658
9	72.0808	941.5455	924.5189	923.5349	969.5404	952.5138	951.5298	927.5298		V	1794.8769	1807.8973		1838.9395	1821.9130
10	88.0393	1056.5724	1039.5459	1038.5619	1084.5673	1067.5408	1066.5568	1012.5826		D	1679.8500	1678.8547		***1739.8711***	1722.8446
11	87.0553	1170.6153	1153.5888	1152.6048	1198.6103	1181.5837	1180.5997	1127.6095		N	1565.8071	1564.8118		***1624.8442***	1607.8176
12	86.0964	1283.6994	1266.6729	1265.6888	1311.6943	1294.6678	1293.6838	1241.6525		L	1452.7230	1451.7278		***1510.8013***	1493.7747
13	30.0338	1340.7209	1323.6943	1322.7103	1368.7158	1351.6892	1350.7052			G				***1397.7172***	1380.6906
14	70.0651	1437.7736	1420.7471	1419.7631	1465.7686	1448.7420	1447.7580	1411.7580		P	1298.6488	1297.6535		***1340.6957***	1323.6692
15	72.0808	1536.8421	1519.8155	1518.8315	1564.8370	1547.8104	1546.8264	1522.8264		V	1199.5804	1212.6008		1243.6430	1226.6164
16	88.0393	1651.8690	1634.8424	1633.8584	1679.8639	1662.8374	1661.8533	1607.8792		D	1084.5534	1083.5582		***1144.5745***	1127.5480
17	74.0600	1752.9167	1735.8901	1734.9061	1780.9116	1763.8850	1762.9010	1736.9218	1738.9010	T	983.5057	996.5261	998.5054	***1029.5476***	1012.5211
18	60.0444	1839.9487	1822.9222	1821.9381	1867.9436	1850.9171	1849.9331	1823.9538		S	896.4737	895.4785		***928.4999***	911.4734
19	44.0495	1910.9858	1893.9593	1892.9753	1938.9807	1921.9542	1920.9702			A	825.4366			***841.4679***	824.4413
20	74.0600	2012.0335	1995.0069	1994.0229	2040.0284	2023.0019	2022.0178	1996.0386	1998.0178	T	724.3889	737.4093	739.3886	***770.4308***	753.4042
21	120.0808	2159.1019	2142.0754	2141.0913	2187.0968	2170.0703	2169.0863			F	577.3205			***669.3831***	652.3566
22	70.0651	2256.1547	2239.1281	2238.1441	2284.1496	2267.1230	2266.1390	2230.1390		P	480.2677	479.2725		***522.3147***	505.2881
23	86.0964	2369.2387	2352.2122	2351.2282	2397.2337	2380.2071	2379.2231	2341.2074	2355.2231	I	367.1837	380.2041	394.2197	425.2619	408.2354

24	110.0713	2506.2977	2489.2711	2488.2871	2534.2926	2517.2660	2516.2820			**H**	230.1248			***312.1779***	295.1513	
25	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FN	234.1237	262.1186	**FNV**	333.1921	361.1870	**FNVL**	446.2762	474.2711
FNVLG	503.2976	531.2926	**FNVLGE**	632.3402	660.3352	**NV**	186.1237	214.1186
NVL	299.2078	327.2027	**NVLG**	356.2292	384.2241	**NVLGE**	485.2718	513.2667
NVLGEP	582.3246	610.3195	**NVLGEPV**	681.3930	709.3879	**VL**	185.1648	213.1598
VLG	242.1863	270.1812	**VLGE**	371.2289	399.2238	**VLGEP**	468.2817	496.2766
VLGEPV	567.3501	595.3450	**VLGEPVD**	682.3770	710.3719	**LG**	143.1179	171.1128
LGE	272.1605	300.1554	**LGEP**	369.2132	397.2082	**LGEPV**	468.2817	496.2766
LGEPVD	583.3086	611.3035	**LGEPVDN**	697.3515	725.3464	**GE**	159.0764	187.0713
GEP	256.1292	284.1241	**GEPV**	355.1976	383.1925	**GEPVD**	470.2245	498.2195
GEPVDN	584.2675	612.2624	**GEPVDNL**	697.3515	725.3464	**EP**	199.1077	227.1026
EPV	298.1761	326.1710	**EPVD**	413.2031	441.1980	**EPVDN**	527.2460	555.2409
EPVDNL	640.3301	668.3250	**EPVDNLG**	697.3515	725.3464	**PV**	169.1335	197.1285
PVD	284.1605	312.1554	**PVDN**	398.2034	426.1983	**PVDNL**	511.2875	539.2824
PVDNLG	568.3089	596.3039	**PVDNLGP**	665.3617	693.3566	**VD**	187.1077	215.1026
VDN	301.1506	329.1456	**VDNL**	414.2347	442.2296	**VDNLG**	471.2562	499.2511
VDNLGP	568.3089	596.3039	**VDNLGPV**	667.3774	695.3723	**DN**	202.0822	230.0771
DNL	315.1663	343.1612	**DNLG**	372.1878	400.1827	**DNLGP**	469.2405	497.2354
DNLGPV	568.3089	596.3039	**DNLGPVD**	683.3359	711.3308	**NL**	200.1394	228.1343
NLG	257.1608	285.1557	**NLGP**	354.2136	382.2085	**NLGPV**	453.2820	481.2769
NLGPVD	568.3089	596.3039	**NLGPVDT**	669.3566	697.3515	**LG**	143.1179	171.1128
LGP	240.1707	268.1656	**LGPV**	339.2391	367.2340	**LGPVD**	454.2660	482.2609
LGPVDT	555.3137	583.3086	**LGPVDTS**	642.3457	670.3406	**GP**	127.0866	155.0815
GPV	226.1550	254.1499	**GPVD**	341.1819	369.1769	**GPVDT**	442.2296	470.2245
GPVDTS	529.2617	557.2566	**GPVDTSA**	600.2988	628.2937	**PV**	169.1335	197.1285
PVD	284.1605	312.1554	**PVDT**	385.2082	413.2031	**PVDTS**	472.2402	500.2351
PVDTSA	543.2773	571.2722	**PVDTSAT**	644.3250	672.3199	**VD**	187.1077	215.1026
VDT	288.1554	316.1503	**VDTS**	375.1874	403.1823	**VDTSA**	446.2245	474.2195
VDTSAT	547.2722	575.2671	**VDTSATF**	694.3406	722.3355	**DT**	189.0870	217.0819
DTS	276.1190	304.1139	**DTSA**	347.1561	375.1510	**DTSAT**	448.2038	476.1987
DTSATF	595.2722	623.2671	**DTSATFP**	692.3250	720.3199	**TS**	161.0921	189.0870
TSA	232.1292	260.1241	**TSAT**	333.1769	361.1718	**TSATF**	480.2453	508.2402
TSATFP	577.2980	605.2930	**TSATFPI**	690.3821	718.3770	**SA**	131.0815	159.0764
SAT	232.1292	260.1241	**SATF**	379.1976	407.1925	**SATFP**	476.2504	504.2453
SATFPI	589.3344	617.3293	**AT**	145.0972	173.0921	**ATF**	292.1656	320.1605
ATFP	389.2183	417.2132	**ATFPI**	502.3024	530.2973	**ATFPIH**	639.3613	667.3562
TF	221.1285	249.1234	**TFP**	318.1812	346.1761	**TFPI**	431.2653	459.2602
TFPIH	568.3242	596.3191	**FP**	217.1335	245.1285	**FPI**	330.2176	358.2125
FPIH	467.2765	495.2714	**PI**	183.1492	211.1441	**PIH**	320.2081	348.2030
IH	223.1553	251.1503						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence

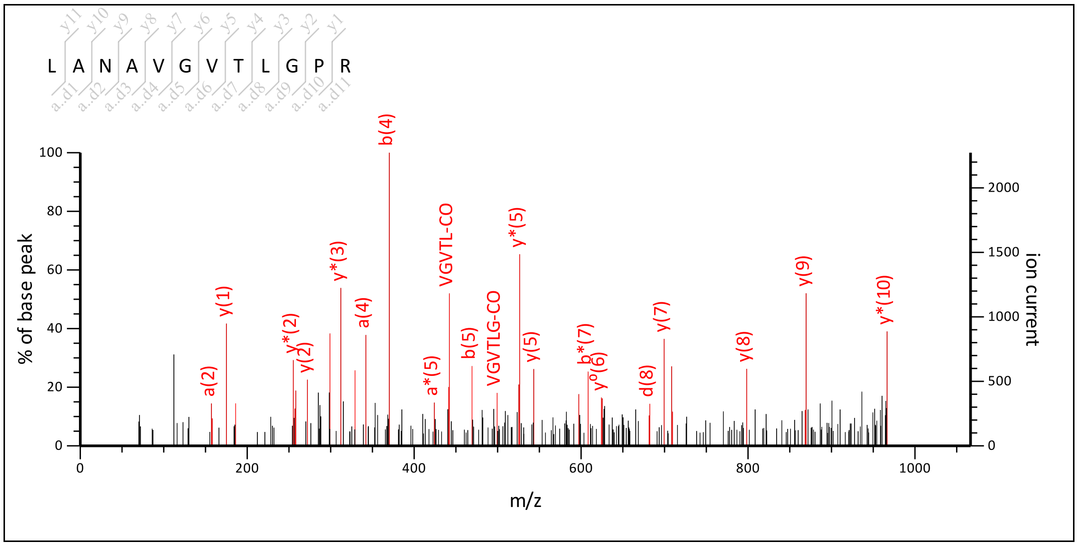
177.0	2707.3970	0.1360	IFNVLGEPVDNLGPVDTSATFPIHR
160.7	2707.3970	0.1360	IFNVLGEPVDNLGPVDTGTTFPIHR
159.1	2707.3970	0.1361	IFNVLGEPVDNLGPVESSATFPIHR
158.0	2708.3559	-0.8228	NFNVLGEPVDNLGPVDTGTTFPIHR
144.1	2707.3640	0.1691	IFNVLGEPVDNLGPVDTSTMSPIHR
143.6	2707.3970	0.1360	IFNVLGEPVDNLGPVESGTTFPIHR
142.7	2708.3558	-0.8228	NFNVLGEPVDNLGPVDASTTFPIHR
142.7	2707.3970	0.1360	IFNVIGEPVDNLGPVDASTTFPIHR
142.7	2707.3970	0.1360	IFNVLGEPVDNLGPVDASTTFPIHR
142.7	2707.3970	0.1360	IFNVLGEPVDNLGPVDASTTFPIHR

Mascot Search Results

Peptide View Spot no 90

MS/MS Fragmentation of **LANAVGVTLGPR**
Found in **gi|115488160** in **NCBInr**, Os12g0277500 [Oryza sativa Japonica Group]

Match to Query 41: 1166.729224 from(1167.736500,1+) intensity(0.0000) index(14)
Title: Label: D12, Spot_Id: 219853, Peak_List_Id: 227214, MSMS Job_Run_Id: 21955, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_D12_136868220000.txt



0 to 1066.56

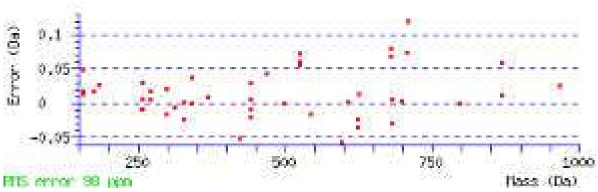
Label all possible matches ○ Label matches used for scoring ●

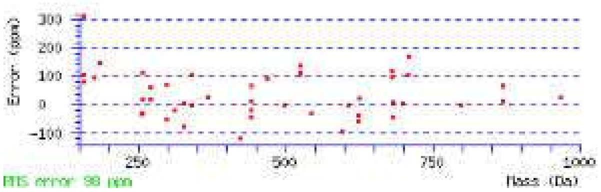
Monoisotopic mass of neutral peptide Mr(calc): 1166.6772
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 0.011
Matches : 52/196 fragment ions using 45 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964			114.0913			44.0495		L							12
2	44.0495	**157.1335**			185.1285					A	1038.5691			1054.6004	1037.5738	1036.5898	11
3	87.0553	271.1765	254.1499		**299.1714**	282.1448		228.1707		N	924.5261	923.5309		983.5633	966.5367	965.5527	10
4	44.0495	**342.2136**	325.1870		**370.2085**	353.1819				A	853.4890			***869.5203***	852.4938	851.5098	9
5	72.0808	**441.2820**	424.2554		**469.2769**	452.2504		427.2663		V	754.4206	767.4410		***798.4832***	781.4567	780.4727	8
6	30.0338	498.3035	481.2769		**526.2984**	509.2718				G				***699.4148***	682.3883	681.4042	7
7	72.0808	**597.3719**	580.3453		**625.3668**	608.3402		583.3562		V	598.3307	611.3511		642.3933	625.3668	624.3828	6
8	74.0600	698.4196	681.3930	680.4090	726.4145	709.3879	708.4039	682.4246	684.4039	T	497.2831	510.3035	512.2827	***543.3249***	526.2984	525.3144	5
9	86.0964	811.5036	794.4771	793.4931	839.4985	822.4720	821.4880	769.4567		L	384.1990	383.2037		***442.2772***	425.2507		4
10	30.0338	**868.5251**	851.4985	850.5145	896.5200	879.4934	878.5094			G				***329.1932***	312.1666		3
11	70.0651	965.5778	948.5513	947.5673	993.5728	976.5462	975.5622	939.5622		P	230.1248	229.1295		***272.1717***	255.1452		2
12	129.1135									R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AN	158.0924	186.0873	ANA	229.1295	257.1244	ANAV	328.1979	356.1928
ANAVG	385.2194	413.2143	ANAVGV	484.2878	512.2827	ANAVGVT	585.3355	613.3304
ANAVGVTL	698.4196	726.4145	NA	158.0924	186.0873	NAV	257.1608	285.1557
NAVG	314.1823	342.1772	NAVGV	413.2507	441.2456	NAVGVT	514.2984	542.2933
NAVGVTL	627.3824	655.3774	NAVGVTLG	684.4039	712.3988	AV	143.1179	171.1128
AVG	200.1394	228.1343	AVGV	299.2078	327.2027	AVGVT	400.2554	428.2504
AVGVTL	513.3395	541.3344	AVGVTLG	570.3610	598.3559	AVGVTLGP	667.4137	695.4087
VG	129.1022	157.0972	VGV	228.1707	256.1656	VGVT	329.2183	357.2132
VGVTL	442.3024	470.2973	VGVTLG	499.3239	527.3188	VGVTLGP	596.3766	624.3715

GV	129.1022	157.0972	**GVT**	230.1499	258.1448	**GVTL**	343.2340	371.2289
GVTLG	400.2554	428.2504	**GVTLGP**	497.3082	525.3031	**VT**	173.1285	201.1234
VTL	286.2125	314.2074	**VTLG**	343.2340	371.2289	**VTLGP**	440.2867	468.2817
TL	187.1441	215.1390	**TLG**	244.1656	272.1605	**TLGP**	341.2183	369.2132
LG	143.1179	171.1128	**LGP**	240.1707	268.1656	**GP**	127.0866	155.0815





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.9	1166.6772	0.0521	LANAVGVTLGPR
42.9	1166.6771	0.0521	AKVAVEQLGPR
42.8	1166.6519	0.0773	AAIAAAREAAPR
39.5	1166.6408	0.0884	VGGAGVIAVPDGR
38.2	1166.6884	0.0408	VRAAAGTVVAPR
37.1	1166.6884	0.0408	TRIAVQGIGPR
36.2	1166.6884	0.0409	VNAIAPVARTR
35.4	1166.6771	0.0521	GAQIVKELGPR
34.6	1166.6520	0.0772	AARVAAEAGVPR
33.5	1166.6520	0.0772	VGAAAEARGLPR

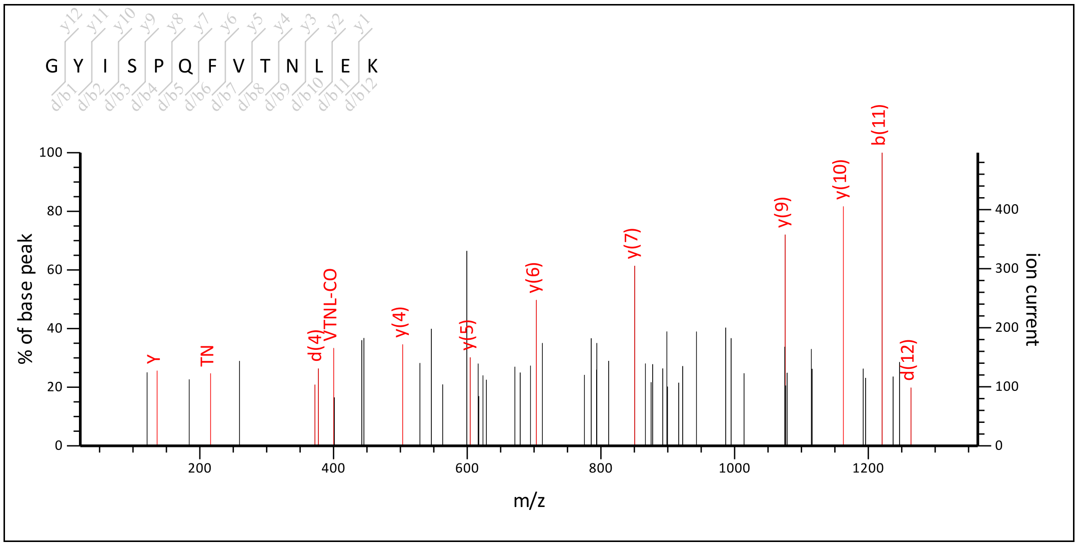
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 90

MS/MS Fragmentation of **GYISPQFVTNLEK**
Found in **gi|115488160** in **NCBInr**, Os12g0277500 [Oryza sativa Japonica Group]

Match to Query 56: 1494.815124 from(1495.822400,1+) intensity(0.0000) index(18)
Title: Label: D12, Spot_Id: 219853, Peak_List_Id: 227229, MSMS Job_Run_Id: 21955, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_D12_136868220000.txt



21.14 to 1363.82

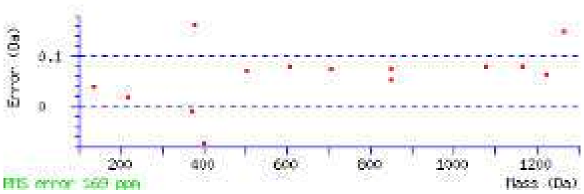
Label all possible matches ○ Label matches used for scoring ●

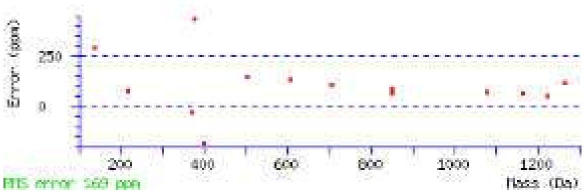
```
Monoisotopic mass of neutral peptide Mr(calc): 1494.7718
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19  Expect: 3.5e+02
Matches : 14/216 fragment ions using 34 most intense peaks   (help)
```

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	30.0338	30.0338			58.0287			44.0495		G						
2	136.0757	193.0972			221.0921					Y	1330.7001			1438.7577	1421.7311	142
3	86.0964	306.1812			334.1761			278.1499	292.1656	I	1217.6161	1230.6365	1244.6521	1275.6943	1258.6678	125
4	60.0444	393.2132		375.2027	421.2082		403.1976	377.2183		S	1130.5841	1129.5888		***1162.6103***	1145.5837	114
5	70.0651	490.2660		472.2554	518.2609		500.2504	464.2504		P	1033.5313	1032.5360		***1075.5782***	1058.5517	105
6	101.0709	618.3246	601.2980	600.3140	646.3195	629.2930	628.3089	561.3031		Q	905.4727	904.4775		978.5255	961.4989	96
7	120.0808	765.3930	748.3665	747.3824	793.3879	776.3614	775.3774			F	758.4043			***850.4669***	833.4403	83
8	72.0808	864.4614	847.4349	846.4509	892.4563	875.4298	874.4458	850.4458		V	659.3359	672.3563		***703.3985***	686.3719	68
9	74.0600	965.5091	948.4825	947.4985	993.5040	976.4775	975.4934	949.5142	951.4934	T	558.2882	571.3086	573.2879	***604.3301***	587.3035	58
10	87.0553	1079.5520	1062.5255	1061.5415	1107.5469	1090.5204	1089.5364	1036.5462		N	444.2453	443.2500		***503.2824***	486.2558	48
11	86.0964	1192.6361	1175.6095	1174.6255	1220.6310	1203.6045	1202.6204	1150.5891		L	331.1612	330.1660		389.2395	372.2129	37
12	102.0550	1321.6787	1304.6521	1303.6681	1349.6736	1332.6470	1331.6630	1263.6732		E	202.1186	201.1234		276.1554	259.1288	25
13	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YI	249.1598	277.1547	YIS	336.1918	364.1867	YISP	433.2445	461.2395
YISPQ	561.3031	589.2980	IS	173.1285	201.1234	ISP	270.1812	298.1761
ISPQ	398.2398	426.2347	ISPQF	545.3082	573.3031	ISPQFV	644.3766	672.3715
SP	157.0972	185.0921	SPQ	285.1557	313.1506	SPQF	432.2241	460.2191
SPQFV	531.2926	559.2875	SPQFVT	632.3402	660.3352	PQ	198.1237	226.1186
PQF	345.1921	373.1870	PQFV	444.2605	472.2554	PQFVT	545.3082	573.3031
PQFVTN	659.3511	687.3461	QF	248.1394	276.1343	QFV	347.2078	375.2027
QFVT	448.2554	476.2504	QFVTN	562.2984	590.2933	QFVTNL	675.3824	703.3774

FV	219.1492	247.1441	**FVT**	320.1969	348.1918	**FVTN**	434.2398	462.2347
FVTNL	547.3239	575.3188	**FVTNLE**	676.3665	704.3614	**VT**	173.1285	201.1234
VTN	287.1714	315.1663	**VTNL**	400.2554	428.2504	**VTNLE**	529.2980	557.2930
TN	188.1030	216.0979	**TNL**	301.1870	329.1819	**TNLE**	430.2296	458.2245
NL	200.1394	228.1343	**NLE**	329.1819	357.1769	**LE**	215.1390	243.1339





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.2	1494.7718	0.0433	GYISPQFVTNLEK
18.4	1494.7718	0.0433	FQPEKYVLNTEK
10.2	1494.8770	-0.0618	GGDVISRVIPLLEK
9.1	1494.7718	0.0433	YVAPENGGLLAYTK
8.4	1494.7235	0.0916	SKALESDEVMAATK
8.4	1494.7790	0.0361	TLASEPPPGQNKTR
8.3	1494.7712	0.0439	MTTSTLRTTQDLK
7.9	1494.7653	0.0498	SLGYPGAMKWLTR
7.6	1494.7565	0.0586	QSTEKEVLAYAEK
7.1	1494.7534	0.0617	TMRNAMAITLTEK

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

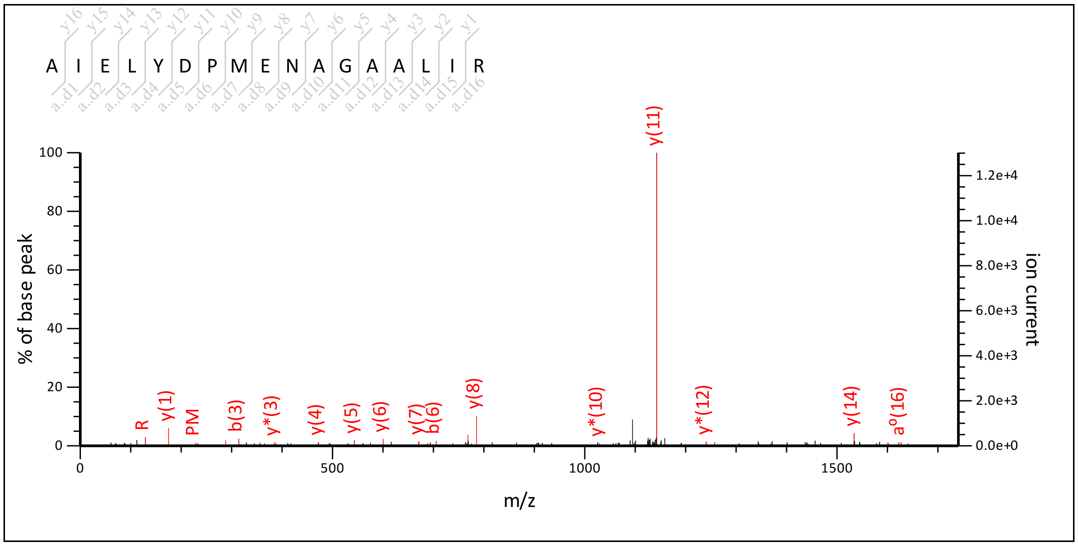
MATRIX SCIENCE

Mascot Search Results

Peptide View Spot no 90

MS/MS Fragmentation of **AIELYDPMENAGAALIR**
Found in **gi|115488160** in **NCBInr**, Os12g0277500 [Oryza sativa Japonica Group]

Match to Query 63: 1846.017124 from(1847.024400,1+) intensity(0.0000) index(21)
Title: Label: D12, Spot_Id: 219853, Peak_List_Id: 227218, MSMS Job_Run_Id: 21955, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_D12_136868220000.txt



0 to 1740.62

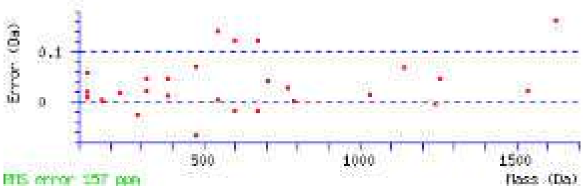
Label all possible matches ○ Label matches used for scoring ●

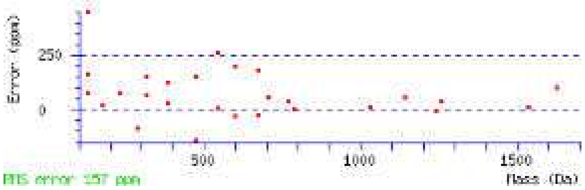
Monoisotopic mass of neutral peptide Mr(calc): 1845.9294
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 0.0073
Matches : 28/293 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	86.0964	157.1335			185.1285			129.1022	143.1179	I	1717.8214	1730.8418	1744.8574	1775.8996	1758.8731
3	102.0550	286.1761		268.1656	**314.1710**		296.1605	228.1707		E	1588.7788	1587.7836		1662.8156	1645.7890
4	86.0964	399.2602		381.2496	427.2551		409.2445	357.2132		L	1475.6947	1474.6995		***1533.7730***	1516.7464
5	136.0757	562.3235		544.3130	590.3184		572.3079			Y	1312.6314			1420.6889	1403.6624
6	88.0393	677.3505		659.3399	**705.3454**		687.3348	633.3606		D	1197.6045	1196.6092		***1257.6256***	1240.5990
7	70.0651	774.4032		756.3927	802.3981		784.3876	748.3876		P	1100.5517	1099.5565		***1142.5987***	1125.5721
8	104.0528	905.4437		887.4332	933.4386		915.4281	845.4403		M	969.5112	968.5160		1045.5459	1028.5193
9	102.0550	1034.4863		1016.4757	1062.4812		1044.4707	976.4808		E	840.4686	839.4734		914.5054	897.4789
10	87.0553	1148.5292	1131.5027	1130.5187	1176.5242	1159.4976	1158.5136	1105.5234		N	726.4257	725.4305		***785.4628***	768.4363
11	44.0495	1219.5664	1202.5398	1201.5558	1247.5613	1230.5347	1229.5507			A	655.3886			***671.4199***	654.3933
12	30.0338	1276.5878	1259.5613	1258.5772	1304.5827	1287.5562	1286.5722			G				***600.3828***	583.3562
13	44.0495	1347.6249	1330.5984	1329.6144	1375.6198	1358.5933	1357.6093			A	527.3300			***543.3613***	526.3348
14	44.0495	1418.6620	1401.6355	1400.6515	1446.6570	1429.6304	1428.6464			A	456.2929			***472.3242***	455.2976
15	86.0964	1531.7461	1514.7196	1513.7355	1559.7410	1542.7145	1541.7305	1489.6992		L	343.2088	342.2136		401.2871	384.2605
16	86.0964	1644.8302	1627.8036	1626.8196	1672.8251	1655.7985	1654.8145	1616.7989	1630.8145	I	230.1248	243.1452	257.1608	***288.2030***	271.1765
17	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IE	215.1390	243.1339	**IEL**	328.2231	356.2180	**IELY**	491.2864	519.2813
IELYD	606.3134	634.3083	**EL**	215.1390	243.1339	**ELY**	378.2023	406.1973
ELYD	493.2293	521.2242	**ELYDP**	590.2821	618.2770	**LY**	249.1598	277.1547
LYD	364.1867	392.1816	**LYDP**	461.2395	489.2344	**LYDPM**	592.2799	620.2749

YD	251.1026	279.0975	**YDP**	348.1554	376.1503	**YDPM**	479.1959	507.1908
YDPME	608.2385	636.2334	**DP**	185.0921	213.0870	**DPM**	316.1326	344.1275
DPME	445.1751	473.1701	**DPMEN**	559.2181	587.2130	**DPMENA**	630.2552	658.2501
DPMENAG	687.2767	715.2716	**PM**	201.1056	229.1005	**PME**	330.1482	358.1431
PMEN	444.1911	472.1860	**PMENA**	515.2282	543.2232	**PMENAG**	572.2497	600.2446
PMENAGA	643.2868	671.2817	**ME**	233.0954	261.0904	**MEN**	347.1384	375.1333
MENA	418.1755	446.1704	**MENAG**	475.1969	503.1919	**MENAGA**	546.2341	574.2290
MENAGAA	617.2712	645.2661	**EN**	216.0979	244.0928	**ENA**	287.1350	315.1299
ENAG	344.1565	372.1514	**ENAGA**	415.1936	443.1885	**ENAGAA**	486.2307	514.2256
ENAGAAL	599.3148	627.3097	**NA**	158.0924	186.0873	**NAG**	215.1139	243.1088
NAGA	286.1510	314.1459	**NAGAA**	357.1881	385.1830	**NAGAAL**	470.2722	498.2671
NAGAALI	583.3562	611.3511	**AG**	101.0709	129.0659	**AGA**	172.1081	200.1030
AGAA	243.1452	271.1401	**AGAAL**	356.2292	384.2241	**AGAALI**	469.3133	497.3082
GA	101.0709	129.0659	**GAA**	172.1081	200.1030	**GAAL**	285.1921	313.1870
GAALI	398.2762	426.2711	**AA**	115.0866	143.0815	**AAL**	228.1707	256.1656
AALI	341.2547	369.2496	**AL**	157.1335	185.1285	**ALI**	270.2176	298.2125
LI	199.1805	227.1754						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.4	1845.9294	0.0877	AIELYDPMENAGAALIR
28.4	1845.9155	0.1016	CIVINAPAFRDNTEAR
28.3	1845.8890	0.1281	RMEASLDNENAKPDLK
24.8	1845.9230	0.0942	LDAPEMCPVFAGRVIR
24.2	1846.0101	0.0071	QAIYTAAFAAAPAGAALLR
19.6	1845.9149	0.1023	AELLYDVIDKSDFYR
19.2	1845.8969	0.1202	RWISEIENNGTATEAR
17.7	1845.8527	0.1644	DVNMGGDTPVSAAALQER
17.4	1845.8817	0.1354	VTLGGDGAEDARATTAADR
17.2	1845.8832	0.1339	GFDCGPANALLDAWALR

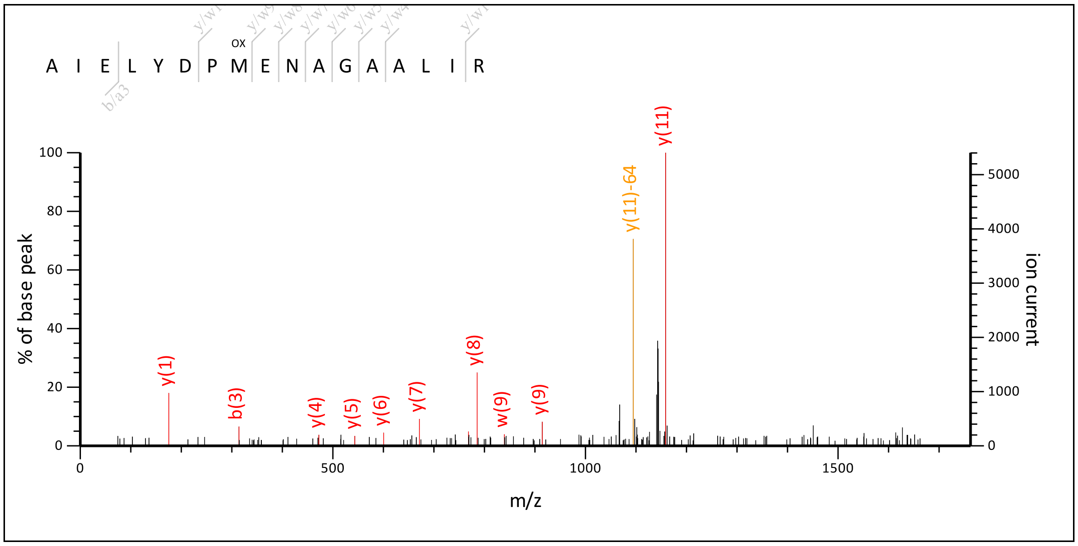
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 90**

MS/MS Fragmentation of **AIELYDPMENAGAALIR**
Found in **gi|115488160** in **NCBInr**, Os12g0277500 [Oryza sativa Japonica Group]

Match to Query 65: 1862.005224 from(1863.012500,1+) intensity(0.0000) index(22)
Title: Label: D12, Spot_Id: 219853, Peak_List_Id: 227217, MSMS Job_Run_Id: 21955, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_D12_136868220000.txt



0 to 1762.25

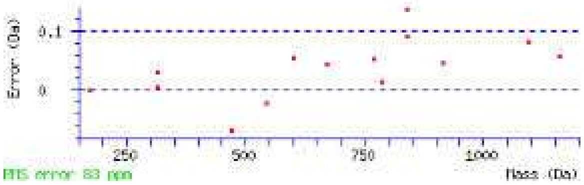
Label all possible matches ○ Label matches used for scoring ●

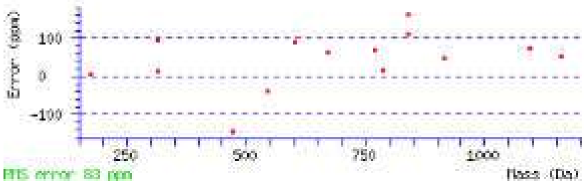
Monoisotopic mass of neutral peptide Mr(calc): 1861.9243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 33 **Expect:** 13
Matches : 14/419 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	86.0964	157.1335			185.1285			129.1022	143.1179	I	1733.8163	1746.8367	1760.8524	1791.8946	1774.8680
3	102.0550	286.1761		268.1656	314.1710		296.1605	228.1707		E	1604.7737	1603.7785		1678.8105	1661.7839
4	86.0964	399.2602		381.2496	427.2551		409.2445	357.2132		L	1491.6897	1490.6944		1549.7679	1532.7414
5	136.0757	562.3235		544.3130	590.3184		572.3079			Y	1328.6263			1436.6838	1419.6573
6	88.0393	677.3505		659.3399	705.3454		687.3348	633.3606		D	1213.5994	1212.6041		1273.6205	1256.5940
7	70.0651	774.4032		756.3927	802.3981		784.3876	748.3876		P	1116.5466	1115.5514		***1158.5936***	1141.5670
8	120.0478	921.4386		903.4281	949.4335		931.4230	845.4403		M	969.5112	968.5160		1061.5408	1044.5143
9	102.0550	1050.4812		1032.4707	1078.4761		1060.4656	992.4757		E	840.4686	839.4734		***914.5054***	897.4789
10	87.0553	1164.5242	1147.4976	1146.5136	1192.5191	1175.4925	1174.5085	1121.5183		N	726.4257	725.4305		***785.4628***	768.4363
11	44.0495	1235.5613	1218.5347	1217.5507	1263.5562	1246.5296	1245.5456			A	655.3886			***671.4199***	654.3933
12	30.0338	1292.5827	1275.5562	1274.5722	1320.5776	1303.5511	1302.5671			G				***600.3828***	583.3562
13	44.0495	1363.6198	1346.5933	1345.6093	1391.6148	1374.5882	1373.6042			A	527.3300			***543.3613***	526.3348
14	44.0495	1434.6570	1417.6304	1416.6464	1462.6519	1445.6253	1444.6413			A	456.2929			***472.3242***	455.2976
15	86.0964	1547.7410	1530.7145	1529.7305	1575.7359	1558.7094	1557.7254	1505.6941		L	343.2088	342.2136		401.2871	384.2605
16	86.0964	1660.8251	1643.7985	1642.8145	1688.8200	1671.7935	1670.8094	1632.7938	1646.8094	I	230.1248	243.1452	257.1608	288.2030	271.1765
17	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IE	215.1390	243.1339	IEL	328.2231	356.2180	IELY	491.2864	519.2813

IELYD	606.3134	634.3083	**EL**	215.1390	243.1339	**ELY**	378.2023	406.1973
ELYD	493.2293	521.2242	**ELYDP**	590.2821	618.2770	**LY**	249.1598	277.1547
LYD	364.1867	392.1816	**LYDP**	461.2395	489.2344	**LYDPM**	608.2749	636.2698
YD	251.1026	279.0975	**YDP**	348.1554	376.1503	**YDPM**	495.1908	523.1857
YDPME	624.2334	652.2283	**DP**	185.0921	213.0870	**DPM**	332.1275	360.1224
DPME	461.1701	489.1650	**DPMEN**	575.2130	603.2079	**DPMENA**	646.2501	674.2450
PM	217.1005	245.0954	**PME**	346.1431	374.1380	**PMEN**	460.1860	488.1810
PMENA	531.2232	559.2181	**PMENAG**	588.2446	616.2395	**PMENAGA**	659.2817	687.2767
ME	249.0904	277.0853	**MEN**	363.1333	391.1282	**MENA**	434.1704	462.1653
MENAG	491.1919	519.1868	**MENAGA**	562.2290	590.2239	**MENAGAA**	633.2661	661.2610
EN	216.0979	244.0928	**ENA**	287.1350	315.1299	**ENAG**	344.1565	372.1514
ENAGA	415.1936	443.1885	**ENAGAA**	486.2307	514.2256	**ENAGAAL**	599.3148	627.3097
NA	158.0924	186.0873	**NAG**	215.1139	243.1088	**NAGA**	286.1510	314.1459
NAGAA	357.1881	385.1830	**NAGAAL**	470.2722	498.2671	**NAGAALI**	583.3562	611.3511
AG	101.0709	129.0659	**AGA**	172.1081	200.1030	**AGAA**	243.1452	271.1401
AGAAL	356.2292	384.2241	**AGAALI**	469.3133	497.3082	**GA**	101.0709	129.0659
GAA	172.1081	200.1030	**GAAL**	285.1921	313.1870	**GAALI**	398.2762	426.2711
AA	115.0866	143.0815	**AAL**	228.1707	256.1656	**AALI**	341.2547	369.2496
AL	157.1335	185.1285	**ALI**	270.2176	298.2125	**LI**	199.1805	227.1754





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.0	1861.9243	0.0809	AIELYDPMENAGAALIR
15.5	1862.0737	-0.0685	GAGIIRVDIEPAGAALIAR
14.2	1862.0513	-0.0460	VLAEAPAPVTEALEALIR
13.7	1862.0196	-0.0144	SQMAAALLTHPAAGAVVVR
13.4	1861.9871	0.0181	SGGPAGGERPGTAPAGRVLR
11.8	1861.9356	0.0696	GAKTALENEMPNVGFLR
11.4	1862.0951	-0.0898	SSLLASIIFILAIVGMAK
10.2	1862.0486	-0.0434	LSGQNAGAAALPAVTLRPR
10.0	1861.8961	0.1091	MMKVSQNATSVTIHCR
9.9	1861.9641	0.0411	DSAILLTVIMLSACSPR

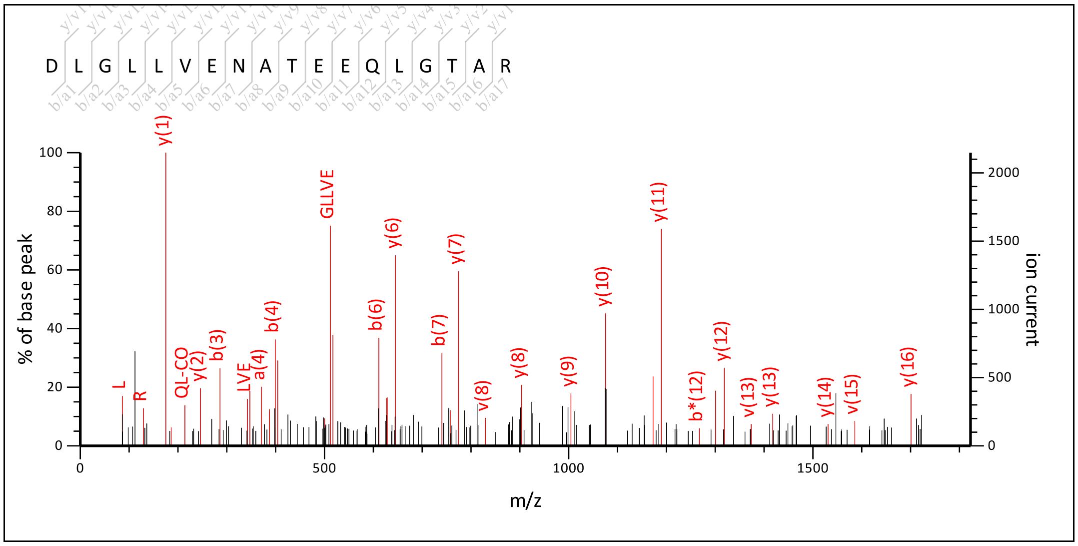
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 90

MS/MS Fragmentation of **DLGLLVENATEEQLGTAR**
Found in **gi|115488160** in **NCBInr**, Os12g0277500 [Oryza sativa Japonica Group]

Match to Query 67: 1928.089624 from(1929.096900,1+) intensity(0.0000) index(23)
Title: Label: D12, Spot_Id: 219853, Peak_List_Id: 227213, MSMS Job_Run_Id: 21955, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_D12_136868220000.txt



0 to 1822.72

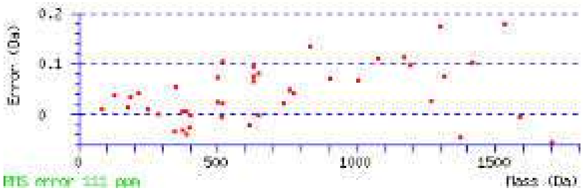
Label all possible matches ○ Label matches used for scoring ●

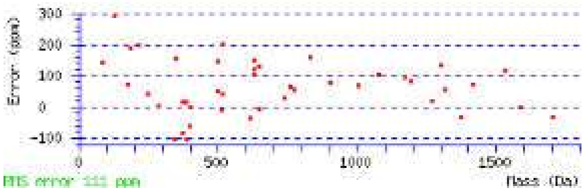
Monoisotopic mass of neutral peptide Mr(calc): 1927.9851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 1e-06
Matches : 48/332 fragment ions using 68 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D					
2	86.0964	201.1234		183.1128	229.1183		211.1077	159.0764		L	1755.8872	1754.8919		1813.9654	1796.9389
3	30.0338	258.1448		240.1343	**286.1397**		268.1292			G				***1700.8814***	1683.8548
4	86.0964	371.2289		353.2183	**399.2238**		381.2132	329.1819		L	1585.7816	1584.7864		1643.8599	1626.8333
5	86.0964	484.3130		466.3024	**512.3079**		494.2973	442.2660		L	1472.6976	1471.7023		***1530.7758***	1513.7493
6	72.0808	583.3814		565.3708	**611.3763**		593.3657	569.3657		V	1373.6292	1386.6496		***1417.6918***	1400.6652
7	102.0550	712.4240		694.4134	**740.4189**		722.4083	654.4185		E	1244.5866	1243.5913		***1318.6233***	1301.5968
8	87.0553	826.4669	809.4403	808.4563	854.4618	837.4353	836.4512	783.4611		N	1130.5436	1129.5484		***1189.5808***	1172.5542
9	44.0495	897.5040	880.4775	879.4934	925.4989	908.4724	907.4884			A	1059.5065			***1075.5378***	1058.5113
10	74.0600	998.5517	981.5251	980.5411	1026.5466	1009.5201	1008.5360	982.5568	984.5360	T	958.4589	971.4793	973.4585	***1004.5007***	987.4742
11	102.0550	1127.5943	1110.5677	1109.5837	1155.5892	1138.5626	1137.5786	1069.5888		E	829.4163	828.4210		***903.4530***	886.4265
12	102.0550	1256.6369	1239.6103	1238.6263	1284.6318	1267.6052	1266.6212	1198.6314		E	700.3737	699.3784		***774.4104***	757.3839
13	101.0709	1384.6955	1367.6689	1366.6849	1412.6904	1395.6638	1394.6798	1327.6740		Q	572.3151	571.3198		***645.3679***	628.3413
14	86.0964	1497.7795	1480.7530	1479.7689	1525.7744	1508.7479	1507.7639	1455.7326		L	459.2310	458.2358		***517.3093***	500.2827
15	30.0338	1554.8010	1537.7744	1536.7904	1582.7959	1565.7693	1564.7853			G				***404.2252***	387.1987
16	74.0600	1655.8487	1638.8221	1637.8381	1683.8436	1666.8170	1665.8330	1639.8537	1641.8330	T	301.1619	314.1823	316.1615	***347.2037***	330.1772
17	44.0495	1726.8858	1709.8592	1708.8752	1754.8807	1737.8541	1736.8701			A	230.1248			***246.1561***	229.1295
18	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LG	143.1179	171.1128	**LGL**	256.2020	284.1969	**LGLL**	369.2860	397.2809
LGLLV	468.3544	496.3493	**LGLLVE**	597.3970	625.3919	**GL**	143.1179	171.1128
GLL	256.2020	284.1969	**GLLV**	355.2704	383.2653	**GLLVE**	484.3130	512.3079

GLLVEN	598.3559	626.3508	**GLLVENA**	669.3930	697.3879	**LL**	199.1805	227.1754
LLV	298.2489	326.2438	**LLVE**	427.2915	455.2864	**LLVEN**	541.3344	569.3293
LLVENA	612.3715	640.3665	**LV**	185.1648	213.1598	**LVE**	314.2074	342.2023
LVEN	428.2504	456.2453	**LVENA**	499.2875	527.2824	**LVENAT**	600.3352	628.3301
VE	201.1234	229.1183	**VEN**	315.1663	343.1612	**VENA**	386.2034	414.1983
VENAT	487.2511	515.2460	**VENATE**	616.2937	644.2886	**EN**	216.0979	244.0928
ENA	287.1350	315.1299	**ENAT**	388.1827	416.1776	**ENATE**	517.2253	545.2202
ENATEE	646.2679	674.2628	**NA**	158.0924	186.0873	**NAT**	259.1401	287.1350
NATE	388.1827	416.1776	**NATEE**	517.2253	545.2202	**NATEEQ**	645.2838	673.2788
AT	145.0972	173.0921	**ATE**	274.1397	302.1347	**ATEE**	403.1823	431.1773
ATEEQ	531.2409	559.2358	**ATEEQL**	644.3250	672.3199	**TE**	203.1026	231.0975
TEE	332.1452	360.1401	**TEEQ**	460.2038	488.1987	**TEEQL**	573.2879	601.2828
TEEQLG	630.3093	658.3042	**EE**	231.0975	259.0925	**EEQ**	359.1561	387.1510
EEQL	472.2402	500.2351	**EEQLG**	529.2617	557.2566	**EEQLGT**	630.3093	658.3042
EQ	230.1135	258.1084	**EQL**	343.1976	371.1925	**EQLG**	400.2191	428.2140
EQLGT	501.2667	529.2617	**EQLGTA**	572.3039	600.2988	**QL**	214.1550	242.1499
QLG	271.1765	299.1714	**QLGT**	372.2241	400.2191	**QLGTA**	443.2613	471.2562
LG	143.1179	171.1128	**LGT**	244.1656	272.1605	**LGTA**	315.2027	343.1976
GT	131.0815	159.0764	**GTA**	202.1186	230.1135	**TA**	145.0972	173.0921





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
103.2	1927.9851	0.1046	DLGLLVENATEEQLGTAR
42.6	1927.9673	0.1223	DILAVVECVVGEEGANVR
29.5	1928.0367	0.0529	DIGIIIDYLRELQPDR
26.1	1928.0513	0.0383	QGIVLMKNQGSLPLSTAR
25.1	1927.9599	0.1297	ILGNNVNTLSEDEQAGVR
24.7	1927.9673	0.1223	AIVDLDTNTVLMDLSHR
24.2	1928.0149	0.0747	ATILIVEDNEANMRLAR
23.7	1927.9309	0.1587	LAVDLPADLSCDLGGDAAR
22.9	1927.9262	0.1634	DTEIETITATNEVTYTK
22.9	1927.9309	0.1587	AAMGYTGSASIEELQTKR

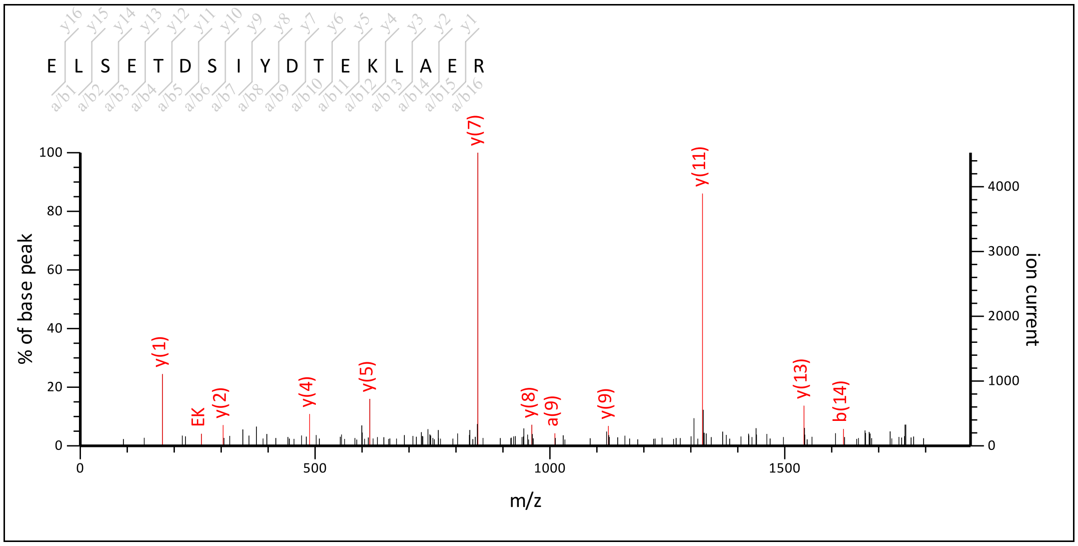
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 90**

MS/MS Fragmentation of **ELSETDSIYDTEKLAER**
Found in **gi|115488160** in **NCBInr**, Os12g0277500 [Oryza sativa Japonica Group]

Match to Query 69: 1998.051924 from(1999.059200,1+) intensity(0.0000) index(24)
Title: Label: D12, Spot_Id: 219853, Peak_List_Id: 227219, MSMS Job_Run_Id: 21955, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_D12_136868220000.txt



0 to 1895.61

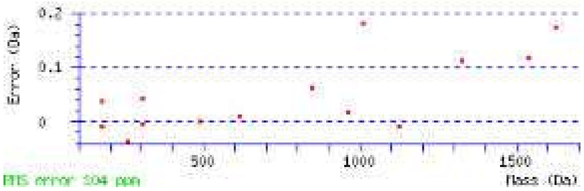
Label all possible matches ○ Label matches used for scoring ●

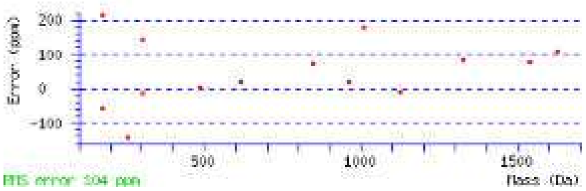
Monoisotopic mass of neutral peptide Mr(calc): 1997.9429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 0.042
Matches : 14/300 fragment ions using 18 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	86.0964	215.1390		197.1285	243.1339		225.1234	173.0921		L	1811.8294	1810.8341		1869.9076	1852.8811
3	60.0444	302.1710		284.1605	330.1660		312.1554	286.1761		S	1724.7974	1723.8021		1756.8236	1739.7970
4	102.0550	431.2136		413.2031	459.2086		441.1980	373.2082		E	1595.7548	1594.7595		1669.7915	1652.7650
5	74.0600	532.2613		514.2508	560.2562		542.2457	516.2664	518.2457	T	1494.7071	1507.7275	1509.7067	***1540.7489***	1523.7224
6	88.0393	647.2883		629.2777	675.2832		657.2726	603.2984		D	1379.6801	1378.6849		1439.7013	1422.6747
7	60.0444	734.3203		716.3097	762.3152		744.3046	718.3254		S	1292.6481	1291.6529		***1324.6743***	1307.6478
8	86.0964	847.4044		829.3938	875.3993		857.3887	819.3731	833.3887	I	1179.5640	1192.5844	1206.6001	1237.6423	1220.6157
9	136.0757	1010.4677		992.4571	1038.4626		1020.4520			Y	1016.5007			***1124.5582***	1107.5317
10	88.0393	1125.4946		1107.4841	1153.4895		1135.4790	1081.5048		D	901.4738	900.4785		***961.4949***	944.4684
11	74.0600	1226.5423		1208.5317	1254.5372		1236.5267	1210.5474	1212.5267	T	800.4261	813.4465	815.4258	***846.4680***	829.4414
12	102.0550	1355.5849		1337.5743	1383.5798		1365.5692	1297.5794		E	671.3835	670.3883		745.4203	728.3937
13	101.1073	1483.6799	1466.6533	1465.6693	1511.6748	1494.6482	1493.6642	1426.6220		K	543.2885	542.2933		***616.3777***	599.3511
14	86.0964	1596.7639	1579.7374	1578.7534	1624.7588	1607.7323	1606.7483	1554.7170		L	430.2045	429.2092		***488.2827***	471.2562
15	44.0495	1667.8010	1650.7745	1649.7905	1695.7960	1678.7694	1677.7854			A	359.1674			375.1987	358.1721
16	102.0550	1796.8436	1779.8171	1778.8331	1824.8385	1807.8120	1806.8280	1738.8382		E	230.1248	229.1295		***304.1615***	287.1350
17	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LS	173.1285	201.1234	LSE	302.1710	330.1660	LSET	403.2187	431.2136
LSETD	518.2457	546.2406	LSETDS	605.2777	633.2726	SE	189.0870	217.0819
SET	290.1347	318.1296	SETD	405.1616	433.1565	SETDS	492.1936	520.1885
SETDSI	605.2777	633.2726	ET	203.1026	231.0975	ETD	318.1296	346.1245

ETDS	405.1616	433.1565	**ETDSI**	518.2457	546.2406	**ETDSIY**	681.3090	709.3039
TD	189.0870	217.0819	**TDS**	276.1190	304.1139	**TDSI**	389.2031	417.1980
TDSIY	552.2664	580.2613	**TDSIYD**	667.2933	695.2883	**DS**	175.0713	203.0662
DSI	288.1554	316.1503	**DSIY**	451.2187	479.2136	**DSIYD**	566.2457	594.2406
DSIYDT	667.2933	695.2883	**SI**	173.1285	201.1234	**SIY**	336.1918	364.1867
SIYD	451.2187	479.2136	**SIYDT**	552.2664	580.2613	**SIYDTE**	681.3090	709.3039
IY	249.1598	277.1547	**IYD**	364.1867	392.1816	**IYDT**	465.2344	493.2293
IYDTE	594.2770	622.2719	**YD**	251.1026	279.0975	**YDT**	352.1503	380.1452
YDTE	481.1929	509.1878	**YDTEK**	609.2879	637.2828	**DT**	189.0870	217.0819
DTE	318.1296	346.1245	**DTEK**	446.2245	474.2195	**DTEKL**	559.3086	587.3035
DTEKLA	630.3457	658.3406	**TE**	203.1026	231.0975	**TEK**	331.1976	359.1925
TEKL	444.2817	472.2766	**TEKLA**	515.3188	543.3137	**TEKLAE**	644.3614	672.3563
EK	230.1499	258.1448	**EKL**	343.2340	371.2289	**EKLA**	414.2711	442.2660
EKLAE	543.3137	571.3086	**KL**	214.1914	242.1863	**KLA**	285.2285	313.2234
KLAE	414.2711	442.2660	**LA**	157.1335	185.1285	**LAE**	286.1761	314.1710
AE	173.0921	201.0870						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.7	1997.9429	0.1090	ELSETDSIYDTEKLAER
28.5	1998.0786	-0.0266	KLDIQLFPPTTEQIAER
22.1	1997.8744	0.1775	IEMILDCPTDDKMTER
21.1	1998.1837	-0.1318	IQSLTIRLLDLVTGTLSR
20.0	1998.0105	0.0414	SAHIWISSRDMVQLAER
18.7	1997.8836	0.1683	GLCQGQWHADLNTMPDR
17.1	1997.8791	0.1728	CVACVAKNADNMIETMR
17.0	1998.0323	0.0197	LQEQPWQGAIFAAAALER
16.9	1998.0647	-0.0127	AQATALRVAGVDWATIAER
16.9	1998.0316	0.0203	LAARAPACNLDLLSDAATR

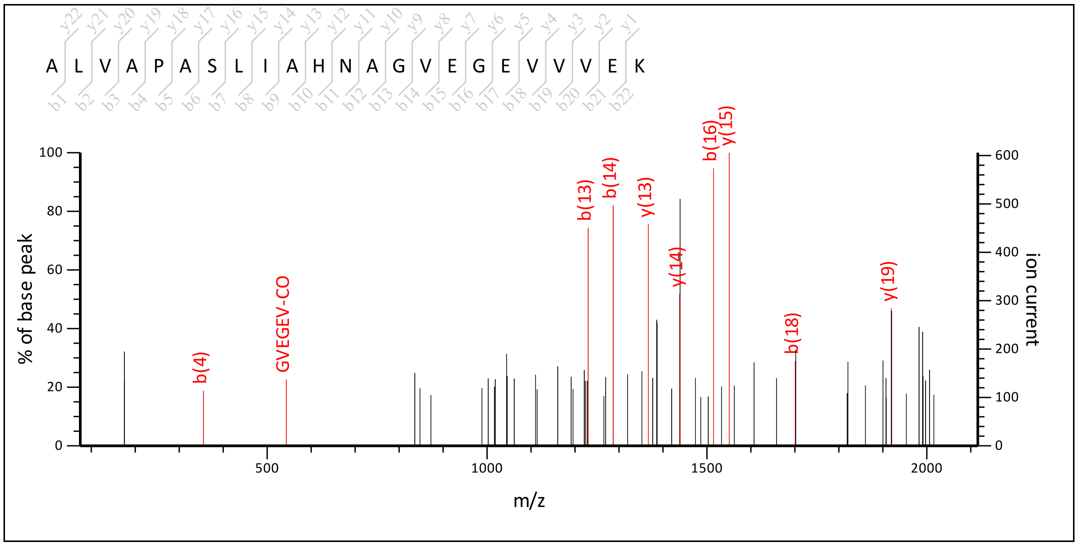
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 90

MS/MS Fragmentation of **ALVAPASLIAHNAGVEGEVVVEK**
Found in **gi|115488160** in **NCBInr**, Os12g0277500 [Oryza sativa Japonica Group]

Match to Query 72: 2272.367024 from(2273.374300,1+) intensity(0.0000) index(25)
Title: Label: D12, Spot_Id: 219853, Peak_List_Id: 227230, MSMS Job_Run_Id: 21955, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_D12_136868220000.txt



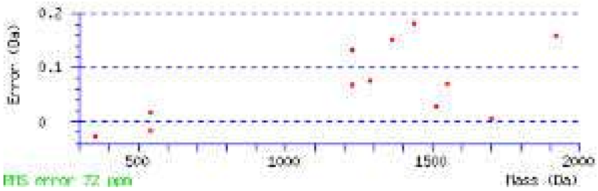
74.93 to 2115.99

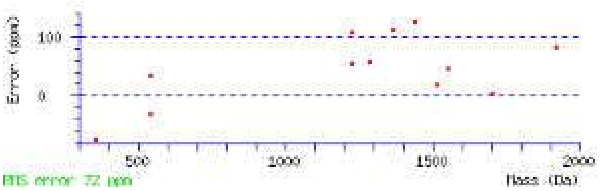
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2272.2427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18  Expect: 1.8e+02
Matches : 12/444 fragment ions using 28 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	86.0964	157.1335			185.1285			115.0866		L	2144.1346	2143.1394		2202.2129	2185.1863
3	72.0808	256.2020			284.1969			242.1863		V	2045.0662	2058.0866		2089.1288	2072.1022
4	44.0495	327.2391			***355.2340***					A	1974.0291			1990.0604	1973.0338
5	70.0651	424.2918			452.2867			398.2762		P	1876.9763	1875.9811		***1919.0233***	1901.9967
6	44.0495	495.3289			523.3239					A	1805.9392			1821.9705	1804.9440
7	60.0444	582.3610		564.3504	610.3559		592.3453	566.3661		S	1718.9072	1717.9119		1750.9334	1733.9068
8	86.0964	695.4450		677.4345	723.4400		705.4294	653.3981		L	1605.8231	1604.8279		1663.9014	1646.8748
9	86.0964	808.5291		790.5185	836.5240		818.5135	780.4978	794.5135	I	1492.7390	1505.7594	1519.7751	***1550.8173***	1533.7907
10	44.0495	879.5662		861.5557	907.5611		889.5506			A	1421.7019			***1437.7332***	1420.7067
11	110.0713	1016.6251		998.6146	1044.6200		1026.6095			H	1284.6430			***1366.6961***	1349.6696
12	87.0553	1130.6681	1113.6415	1112.6575	1158.6630	1141.6364	1140.6524	1087.6622		N	1170.6001	1169.6048		***1229.6372***	1212.6107
13	44.0495	1201.7052	1184.6786	1183.6946	***1229.7001***	1212.6735	1211.6895			A	1099.5630			1115.5943	1098.5677
14	30.0338	1258.7266	1241.7001	1240.7161	***1286.7215***	1269.6950	1268.7110			G				1044.5572	1027.5306
15	72.0808	1357.7950	1340.7685	1339.7845	1385.7900	1368.7634	1367.7794	1343.7794		V	943.4731	956.4935		987.5357	970.5092
16	102.0550	1486.8376	1469.8111	1468.8271	***1514.8326***	1497.8060	1496.8220	1428.8322		E	814.4305	813.4353		888.4673	871.4407
17	30.0338	1543.8591	1526.8326	1525.8485	1571.8540	1554.8275	1553.8435			G				759.4247	742.3981
18	102.0550	1672.9017	1655.8751	1654.8911	***1700.8966***	1683.8701	1682.8860	1614.8962		E	628.3665	627.3712		702.4032	685.3767
19	72.0808	1771.9701	1754.9436	1753.9595	1799.9650	1782.9385	1781.9545	1757.9545		V	529.2980	542.3184		573.3606	556.3341
20	72.0808	1871.0385	1854.0120	1853.0280	1899.0334	1882.0069	1881.0229	1857.0229		V	430.2296	443.2500		474.2922	457.2657
21	72.0808	1970.1069	1953.0804	1952.0964	1998.1019	1981.0753	1980.0913	1956.0913		V	331.1612	344.1816		375.2238	358.1973
22	102.0550	2099.1495	2082.1230	2081.1390	2127.1444	2110.1179	2109.1339	2041.1441		E	202.1186	201.1234		276.1554	259.1288
23	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LV	185.1648	213.1598	LVA	256.2020	284.1969	LVAP	353.2547	381.2496
LVAPA	424.2918	452.2867	LVAPAS	511.3239	539.3188	LVAPASL	624.4079	652.4028
VA	143.1179	171.1128	VAP	240.1707	268.1656	VAPA	311.2078	339.2027
VAPAS	398.2398	426.2347	VAPASL	511.3239	539.3188	VAPASLI	624.4079	652.4028
VAPASLIA	695.4450	723.4400	AP	141.1022	169.0972	APA	212.1394	240.1343
APAS	299.1714	327.1663	APASL	412.2554	440.2504	APASLI	525.3395	553.3344
APASLIA	596.3766	624.3715	PA	141.1022	169.0972	PAS	228.1343	256.1292
PASL	341.2183	369.2132	PASLI	454.3024	482.2973	PASLIA	525.3395	553.3344
PASLIAH	662.3984	690.3933	AS	131.0815	159.0764	ASL	244.1656	272.1605
ASLI	357.2496	385.2445	ASLIA	428.2867	456.2817	ASLIAH	565.3457	593.3406
ASLIAHN	679.3886	707.3835	SL	173.1285	201.1234	SLI	286.2125	314.2074
SLIA	357.2496	385.2445	SLIAH	494.3085	522.3035	SLIAHN	608.3515	636.3464
SLIAHNA	679.3886	707.3835	LI	199.1805	227.1754	LIA	270.2176	298.2125
LIAH	407.2765	435.2714	LIAHN	521.3194	549.3144	LIAHNA	592.3566	620.3515
LIAHNAG	649.3780	677.3729	IA	157.1335	185.1285	IAH	294.1925	322.1874
IAHN	408.2354	436.2303	IAHNA	479.2725	507.2674	IAHNAG	536.2940	564.2889
IAHNAGV	635.3624	663.3573	AH	181.1084	209.1033	AHN	295.1513	323.1462
AHNA	366.1884	394.1833	AHNAG	423.2099	451.2048	AHNAGV	522.2783	550.2732
AHNAGVE	651.3209	679.3158	HN	224.1142	252.1091	HNA	295.1513	323.1462
HNAG	352.1728	380.1677	HNAGV	451.2412	479.2361	HNAGVE	580.2838	608.2787
HNAGVEG	637.3052	665.3002	NA	158.0924	186.0873	NAG	215.1139	243.1088
NAGV	314.1823	342.1772	NAGVE	443.2249	471.2198	NAGVEG	500.2463	528.2413
NAGVEGE	629.2889	657.2838	AG	101.0709	129.0659	AGV	200.1394	228.1343
AGVE	329.1819	357.1769	AGVEG	386.2034	414.1983	AGVEGE	515.2460	543.2409
AGVEGEV	614.3144	642.3093	GV	129.1022	157.0972	GVE	258.1448	286.1397
GVEG	315.1663	343.1612	GVEGE	444.2089	472.2038	GVEGEV	543.2773	571.2722
GVEGEVV	642.3457	670.3406	VE	201.1234	229.1183	VEG	258.1448	286.1397
VEGE	387.1874	415.1823	VEGEV	486.2558	514.2508	VEGEVV	585.3243	613.3192
VEGEVVV	684.3927	712.3876	EG	159.0764	187.0713	EGE	288.1190	316.1139
EGEV	387.1874	415.1823	EGEVV	486.2558	514.2508	EGEVVV	585.3243	613.3192
GE	159.0764	187.0713	GEV	258.1448	286.1397	GEVV	357.2132	385.2082
GEVVV	456.2817	484.2766	GEVVVE	585.3243	613.3192	EV	201.1234	229.1183
EVV	300.1918	328.1867	EVVV	399.2602	427.2551	EVVVE	528.3028	556.2977
VV	171.1492	199.1441	VVV	270.2176	298.2125	VVVE	399.2602	427.2551
VV	171.1492	199.1441	VVE	300.1918	328.1867	VE	201.1234	229.1183





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.8	2272.2427	0.1243	ALVAPASLIAHNAGVEGEVVVEK
10.0	2272.2501	0.1169	LDLVMVILFKGIPLGSTDGER
9.6	2272.3810	-0.0140	LLQVGVLLAVLYVGLVLFGSSI
9.6	2272.1786	0.1884	GRWLLPTYLEAERPADMVR
9.3	2272.2215	0.1455	SYIANIPDAVLALPQKQEFR
7.8	2272.2290	0.1381	QAQFLALAVTYFLSVLMVSR

7.7	2272.3195	0.0476	ILQALDVAAAFLLVVVALDYR
7.7	2272.2144	0.1527	IVAASVFFYDFLVTVPSEIR
6.8	2272.1569	0.2102	GMPELHGLIPALGSLMDRGHR
6.4	2272.1825	0.1845	TASGGGGGFVPKPVDEHHLVRR

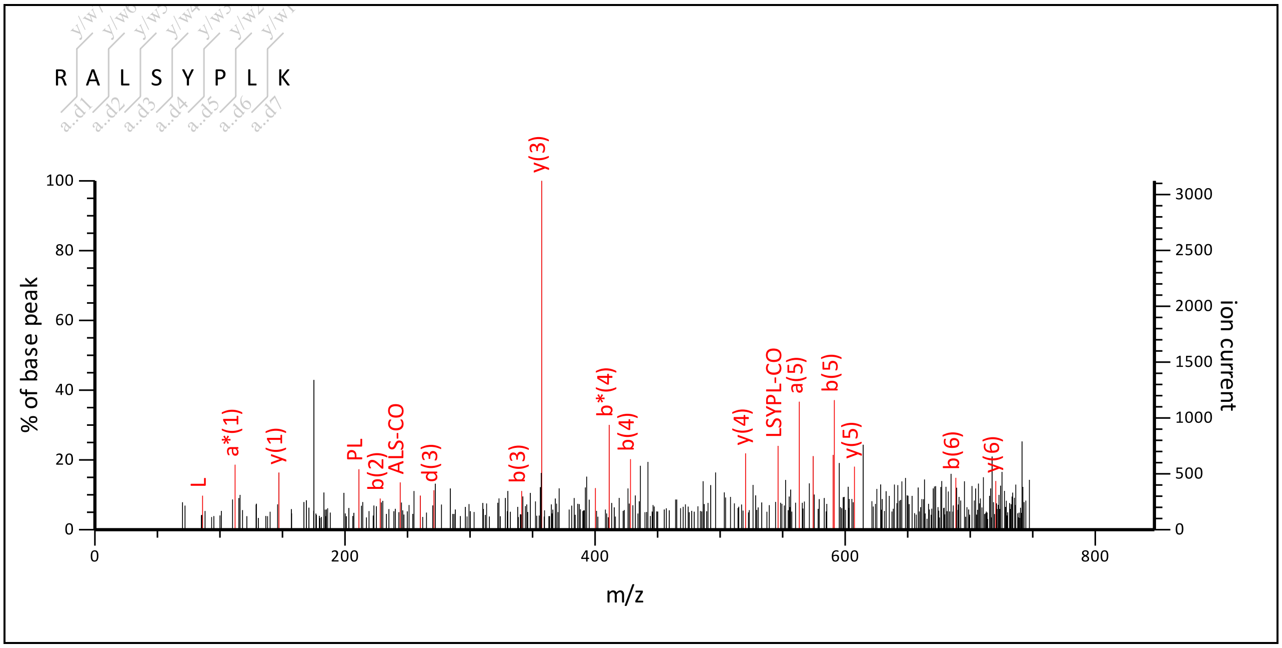
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 92

MS/MS Fragmentation of **RALSYPLK**
Found in **gi|15231255** in **NCBInr**, TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]

Match to Query 45: 946.585864 from(947.593140,1+) intensity(0.0000) index(5)
Title: Label: E15, Spot_Id: 219902, Peak_List_Id: 228294, MSMS Job_Run_Id: 21986, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E15_136868276000.txt



0 to 847.31

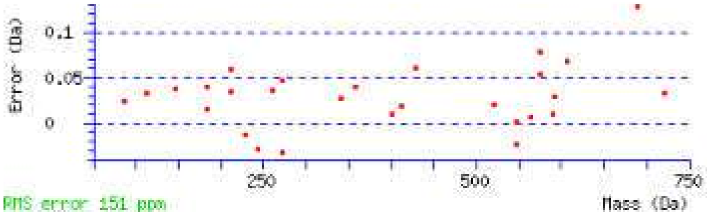
Label all possible matches ○ Label matches used for scoring ●

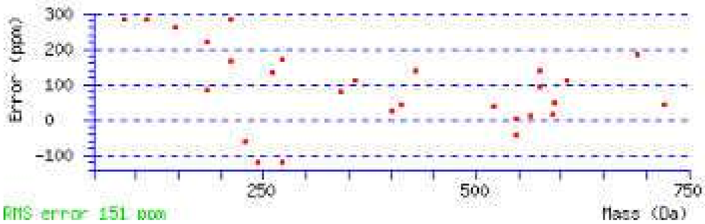
Monoisotopic mass of neutral peptide Mr(calc): 946.5600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 61
Matches : 30/108 fragment ions using 56 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	129.1135	129.1135	112.0869		157.1084	140.0818		44.0495	R						8
2	44.0495	200.1506	183.1240		**228.1455**	211.1190			A	775.4349		791.4662	774.4396	773.4556	7
3	86.0964	313.2346	296.2081		**341.2296**	324.2030		271.1877	L	662.3508	661.3556	***720.4291***	703.4025	702.4185	6
4	60.0444	**400.2667**	383.2401	382.2561	**428.2616**	411.2350	410.2510	384.2718	S	575.3188	574.3235	***607.3450***	590.3184	589.3344	5
5	136.0757	**563.3300**	546.3035	545.3194	**591.3249**	574.2984	573.3144		Y	412.2554		***520.3130***	503.2864		4
6	70.0651	660.3828	643.3562	642.3722	**688.3777**	671.3511	670.3671	634.3671	P	315.2027	314.2074	***357.2496***	340.2231		3
7	86.0964	773.4668	756.4403	755.4563	801.4618	784.4352	783.4512	731.4199	L	202.1186	201.1234	***260.1969***	243.1703		2
8	101.1073								K	74.0237	73.0284	***147.1128***	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AL	157.1335	185.1285	ALS	244.1656	272.1605	ALSY	407.2289	435.2238
ALSYP	504.2817	532.2766	ALSYPL	617.3657	645.3606	LS	173.1285	201.1234
LSY	336.1918	364.1867	LSYP	433.2445	461.2395	LSYPL	546.3286	574.3235
SY	223.1077	251.1026	SYP	320.1605	348.1554	SYPL	433.2445	461.2395

YP	233.1285	261.1234	**YPL**	346.2125	374.2074	**PL**	183.1492	211.1441





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.0	946.5487	0.0371	KLDAYLPK
27.0	946.5124	0.0735	QLDAYIPK
26.7	946.4946	0.0913	QMPAYIPK
26.4	946.5487	0.0371	DLKYALPK
26.0	946.5600	0.0259	RALSYPIK
26.0	946.5600	0.0259	RALSYPLK
25.5	946.5236	0.0623	REAAYLPK
25.3	946.5236	0.0623	NGGKAYLPK
25.1	946.5851	0.0007	KVLSYLPK
25.1	946.5487	0.0371	INISYIPK

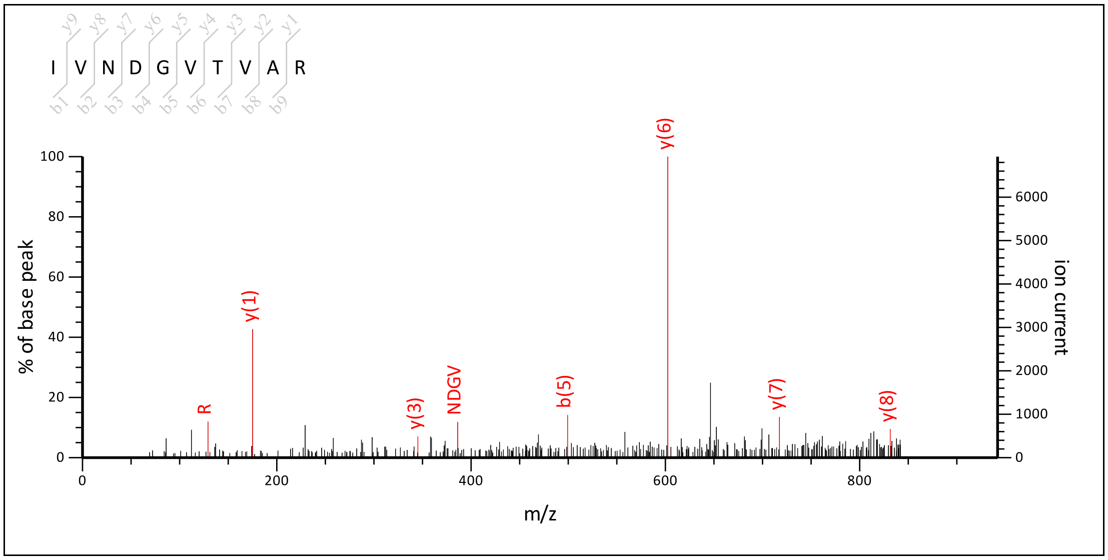
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 92

MS/MS Fragmentation of **IVNDGVTVAR**
Found in **gi|15231255** in **NCBInr**, TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]

Match to Query 97: 1042.616524 from(1043.623800,1+) intensity(0.0000) index(9)
Title: Label: E15, Spot_Id: 219902, Peak_List_Id: 228297, MSMS Job_Run_Id: 21986, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E15_136868276000.txt



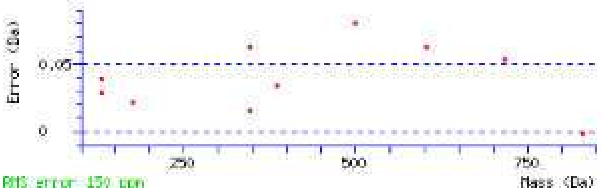
0 to 941.95

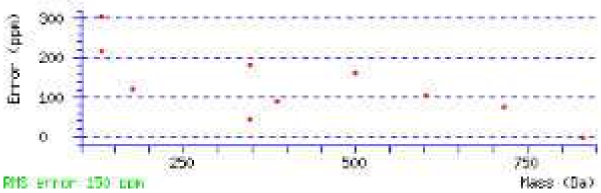
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1042.5771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.44
Matches : 11/156 fragment ions using 8 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964			114.0913			44.0495		**I**							10
2	72.0808	185.1648			213.1598			171.1492		**V**	886.4377	899.4581		930.5003	913.4738	912.4898	9
3	87.0553	299.2078	282.1812		327.2027	310.1761		256.2020		**N**	772.3948	771.3995		***831.4319***	814.4054	813.4213	8
4	88.0393	414.2347	397.2082	396.2241	442.2296	425.2031	424.2191	370.2449		**D**	657.3679	656.3726		***717.3890***	700.3624	699.3784	7
5	30.0338	471.2562	454.2296	453.2456	**499.2511**	482.2245	481.2405			**G**				***602.3620***	585.3355	584.3515	6
6	72.0808	570.3246	553.2980	552.3140	598.3195	581.2930	580.3089	556.3089		**V**	501.2780	514.2984		545.3406	528.3140	527.3300	5
7	74.0600	671.3723	654.3457	653.3617	699.3672	682.3406	681.3566	655.3774	657.3566	**T**	400.2303	413.2507	415.2300	446.2722	429.2456	428.2616	4
8	72.0808	770.4407	753.4141	752.4301	798.4356	781.4090	780.4250	756.4250		**V**	301.1619	314.1823		***345.2245***	328.1979		3
9	44.0495	841.4778	824.4512	823.4672	869.4727	852.4462	851.4621			**A**	230.1248			246.1561	229.1295		2
10	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VN	186.1237	214.1186	**VND**	301.1506	329.1456	**VNDG**	358.1721	386.1670
VNDGV	457.2405	485.2354	**VNDGVT**	558.2882	586.2831	**VNDGVTV**	657.3566	685.3515
ND	202.0822	230.0771	**NDG**	259.1037	287.0986	**NDGV**	358.1721	386.1670
NDGVT	459.2198	487.2147	**NDGVTV**	558.2882	586.2831	**NDGVTVA**	629.3253	657.3202
DG	145.0608	173.0557	**DGV**	244.1292	272.1241	**DGVT**	345.1769	373.1718
DGVTV	444.2453	472.2402	**DGVTVA**	515.2824	543.2773	**GV**	129.1022	157.0972
GVT	230.1499	258.1448	**GVTV**	329.2183	357.2132	**GVTVA**	400.2554	428.2504
VT	173.1285	201.1234	**VTV**	272.1969	300.1918	**VTVA**	343.2340	371.2289
TV	173.1285	201.1234	**TVA**	244.1656	272.1605	**VA**	143.1179	171.1128





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.9	1042.5771	0.0394	IVNDGVTVAR
32.2	1042.5407	0.0758	VLNADGELGR
31.8	1042.5883	0.0282	IVNDGTRLR
31.8	1042.5407	0.0758	LVNDGLEQR
31.8	1042.5407	0.0758	LVNDINAER
31.8	1042.5883	0.0282	VLNDAISRR
31.8	1042.5883	0.0282	VLNDALSRR
31.7	1042.5771	0.0394	LVASAQEGLR
31.7	1042.5771	0.0394	LVSAAEQGIR
31.7	1042.6135	0.0030	LVTKQEIGR

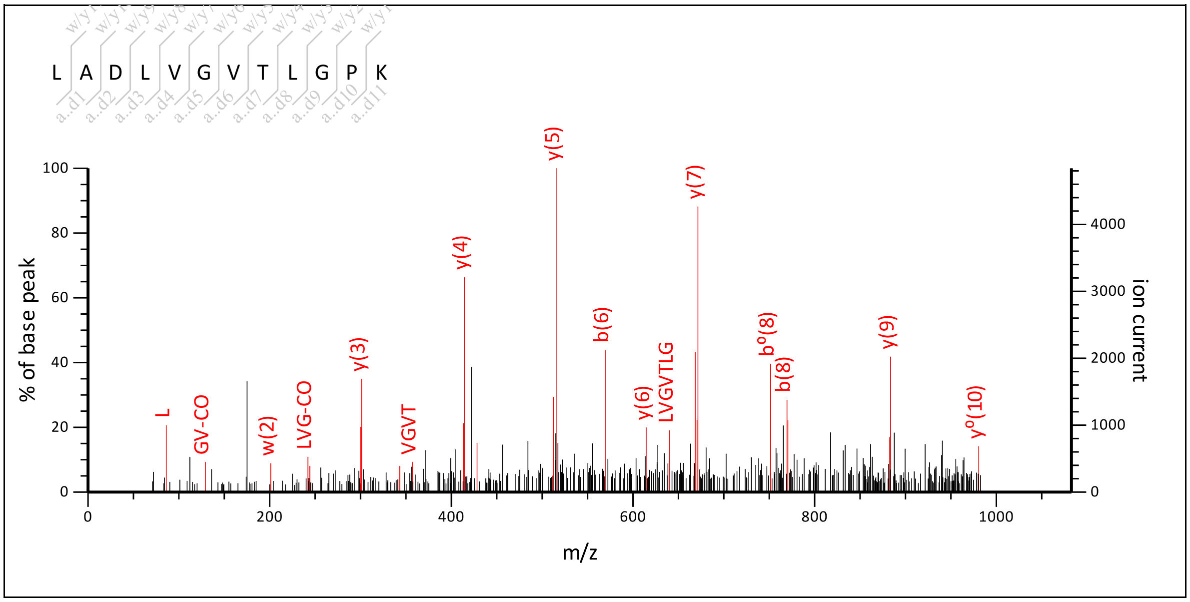
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 92

MS/MS Fragmentation of **LADLVGVTLGPK**
Found in **gi|15231255** in **NCBInr**, TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]

Match to Query 157: 1181.733724 from(1182.741000,1+) intensity(0.0000) index(13)
Title: Label: E15, Spot_Id: 219902, Peak_List_Id: 228292, MSMS Job_Run_Id: 21986, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E15_136868276000.txt



0 to 1082.71

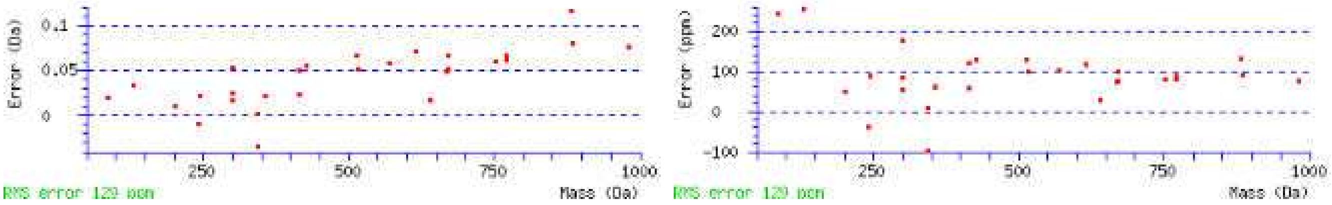
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1181.7020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 0.049
Matches : 40/186 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	**86.0964**		114.0913		44.0495		**L**							12
2	44.0495	157.1335		185.1285				**A**	1053.5939			1069.6252	1052.5986	1051.6146	11
3	88.0393	272.1605	254.1499	**300.1554**	282.1448	228.1707		**D**	938.5669	937.5717		998.5881	981.5615	980.5775	10
4	86.0964	385.2445	367.2340	**413.2395**	395.2289	343.1976		**L**	825.4829	824.4876		***883.5611***	866.5346	865.5506	9
5	72.0808	484.3130	466.3024	**512.3079**	494.2973	470.2973		**V**	726.4145	739.4349		***770.4771***	753.4505	752.4665	8
6	30.0338	541.3344	523.3239	**569.3293**	551.3188			**G**				***671.4087***	654.3821	653.3981	7
7	72.0808	**640.4028**	622.3923	**668.3978**	650.3872	626.3872		**V**	570.3246	583.3450		***614.3872***	597.3606	596.3766	6
8	74.0600	741.4505	723.4400	**769.4454**	751.4349	725.4556	727.4349	**T**	469.2769	482.2973	484.2766	***515.3188***	498.2922	497.3082	5
9	86.0964	854.5346	836.5240	**882.5295**	864.5189	812.4876		**L**	356.1928	355.1976		***414.2711***	397.2445		4
10	30.0338	911.5560	893.5455	939.5510	921.5404			**G**				***301.1870***	284.1605		3
11	70.0651	1008.6088	990.5982	1036.6037	1018.5932	982.5932		**P**	202.1186	201.1234		***244.1656***	227.1390		2
12	101.1073							**K**	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AD	159.0764	187.0713	**ADL**	272.1605	300.1554	**ADLV**	371.2289	399.2238
ADLVG	428.2504	456.2453	**ADLVGV**	527.3188	555.3137	**ADLVGVT**	628.3665	656.3614
DL	201.1234	229.1183	**DLV**	300.1918	328.1867	**DLVG**	357.2132	385.2082
DLVGV	456.2817	484.2766	**DLVGVT**	557.3293	585.3243	**DLVGVTL**	670.4134	698.4083

LV	185.1648	213.1598	**LVG**	242.1863	270.1812	**LVGV**	341.2547	369.2496
LVGVT	442.3024	470.2973	**LVGVTL**	555.3865	583.3814	**LVGVTLG**	612.4079	640.4028
VG	129.1022	157.0972	**VGV**	228.1707	256.1656	**VGVT**	329.2183	357.2132
VGVTL	442.3024	470.2973	**VGVTLG**	499.3239	527.3188	**VGVTLGP**	596.3766	624.3715
GV	129.1022	157.0972	**GVT**	230.1499	258.1448	**GVTL**	343.2340	371.2289
GVTLG	400.2554	428.2504	**GVTLGP**	497.3082	525.3031	**VT**	173.1285	201.1234
VTL	286.2125	314.2074	**VTLG**	343.2340	371.2289	**VTLGP**	440.2867	468.2817
TL	187.1441	215.1390	**TLG**	244.1656	272.1605	**TLGP**	341.2183	369.2132
LG	143.1179	171.1128	**LGP**	240.1707	268.1656	**GP**	127.0866	155.0815



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.7	1181.7020	0.0317	LADLVGVTLGPK
46.5	1181.7244	0.0093	LVATASRVLPR
45.2	1181.7244	0.0093	LSQLTRPVIR
45.1	1181.6768	0.0569	QITAEVGVLPR
44.1	1181.6768	0.0569	VGLDVLSINPR
43.9	1181.7132	0.0205	IASGLTGVVPIR
43.4	1181.6404	0.0933	LDVAGLVENPR
38.1	1181.6880	0.0457	DLVQSVRIPR
37.9	1181.6517	0.0821	AVISATRDPPR
37.9	1181.6516	0.0821	IANDERLVPR

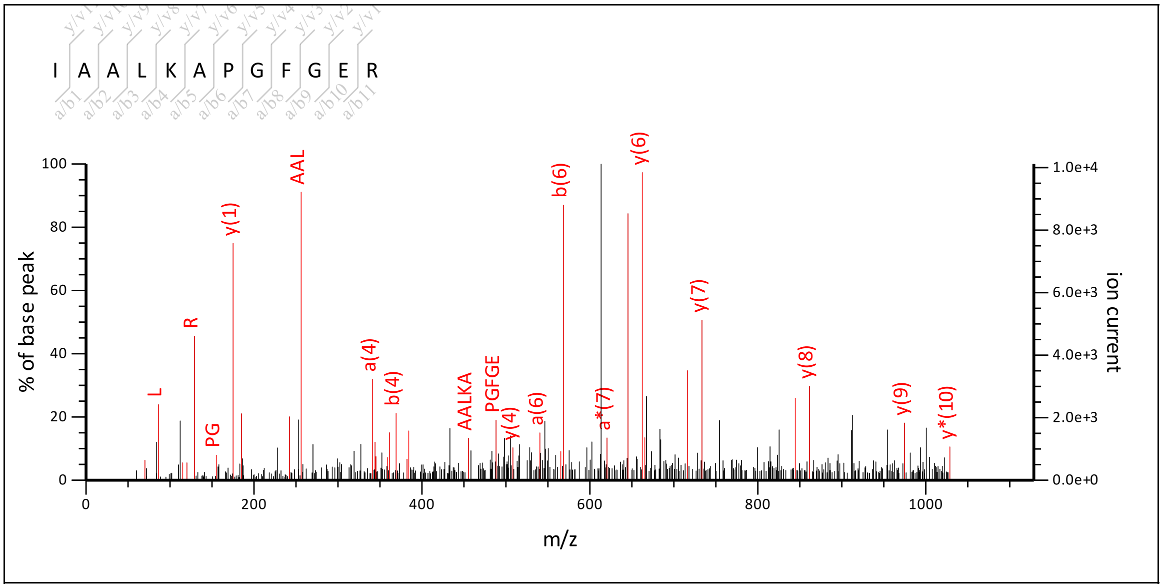
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 92

MS/MS Fragmentation of **IAALKAPGFGER**
Found in **gi|15231255** in **NCBInr**, TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]

Match to Query 179: 1228.734624 from(1229.741900,1+) intensity(0.0000) index(15)
Title: Label: E15, Spot_Id: 219902, Peak_List_Id: 228286, MSMS Job_Run_Id: 21986, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E15_136868276000.txt



0 to 1128.68

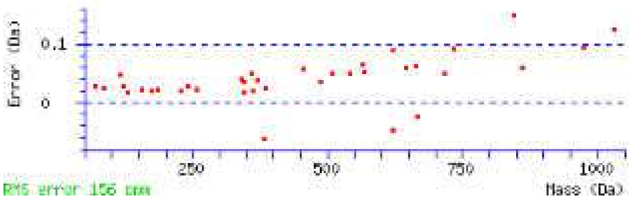
Label all possible matches ○ Label matches used for scoring ●

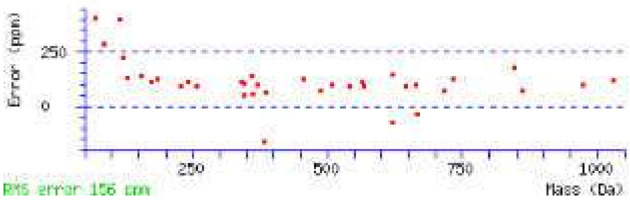
Monoisotopic mass of neutral peptide Mr(calc): 1228.6928
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 8.8
Matches : 42/179 fragment ions using 80 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	86.0964	**86.0964**			114.0913			44.0495	**I**						12
2	44.0495	157.1335			**185.1285**				**A**	1100.5847		1116.6160	1099.5895	1098.6055	11
3	44.0495	**228.1707**			**256.1656**				**A**	1029.5476		1045.5789	1028.5524	1027.5683	10
4	86.0964	**341.2547**			**369.2496**			299.2078	**L**	916.4635	915.4683	***974.5418***	957.5152	956.5312	9
5	101.1073	469.3497	452.3231		497.3446	480.3180		412.2918	**K**	788.3686	787.3733	***861.4577***	844.4312	843.4472	8
6	44.0495	**540.3868**	523.3602		**568.3817**	551.3552			**A**	717.3315		***733.3628***	716.3362	715.3522	7
7	70.0651	637.4396	620.4130		**665.4345**	648.4079		611.4239	**P**	620.2787	619.2835	***662.3257***	645.2991	644.3151	6
8	30.0338	694.4610	677.4345		722.4559	705.4294			**G**			***565.2729***	548.2463	547.2623	5
9	120.0808	841.5294	824.5029		869.5244	852.4978			**F**	416.1888		***508.2514***	491.2249	490.2409	4
10	30.0338	898.5509	881.5244		926.5458	909.5193			**G**			***361.1830***	344.1565	343.1724	3
11	102.0550	1027.5935	1010.5669	1009.5829	1055.5884	1038.5619	1037.5778	969.5880	**E**	230.1248	229.1295	304.1615	287.1350	286.1510	2
12	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AA	115.0866	143.0815	**AAL**	228.1707	256.1656	**AALK**	356.2656	384.2605
AALKA	427.3027	455.2976	**AALKAP**	524.3555	552.3504	**AALKAPG**	581.3770	609.3719
AL	157.1335	185.1285	**ALK**	285.2285	313.2234	**ALKA**	356.2656	384.2605
ALKAP	453.3184	481.3133	**ALKAPG**	510.3398	538.3348	**ALKAPGF**	657.4083	685.4032
LK	214.1914	242.1863	**LKA**	285.2285	313.2234	**LKAP**	382.2813	410.2762

LKAPG	439.3027	467.2976	**LKAPGF**	586.3711	614.3661	**LKAPGFG**	643.3926	671.3875
KA	172.1444	200.1394	**KAP**	269.1972	297.1921	**KAPG**	326.2187	354.2136
KAPGF	473.2871	501.2820	**KAPGFG**	530.3085	558.3035	**KAPGFGE**	659.3511	687.3461
AP	141.1022	169.0972	**APG**	198.1237	226.1186	**APGF**	345.1921	373.1870
APGFG	402.2136	430.2085	**APGFGE**	531.2562	559.2511	**PG**	127.0866	155.0815
PGF	274.1550	302.1499	**PGFG**	331.1765	359.1714	**PGFGE**	460.2191	488.2140
GF	177.1022	205.0972	**GFG**	234.1237	262.1186	**GFGE**	363.1663	391.1612
FG	177.1022	205.0972	**FGE**	306.1448	334.1397	**GE**	159.0764	187.0713





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.6	1228.6928	0.0418	GPTAKIPFAATR
35.8	1228.6928	0.0418	IAAIKAPGFGER
35.4	1228.6775	0.0571	AGIVNIVSATER
35.0	1228.6928	0.0418	IAALKAPGFGER
34.6	1228.6663	0.0683	VGLVNIGEEATK
32.1	1228.6775	0.0571	ALALAGASTLDAR
31.3	1228.7325	0.0021	IAAIKIGMLGSR
29.8	1228.6775	0.0571	LAAQLAESGITR
29.7	1228.6710	0.0636	TGPAGLIGRMTR
29.6	1228.6775	0.0571	ALAKALDADSVR

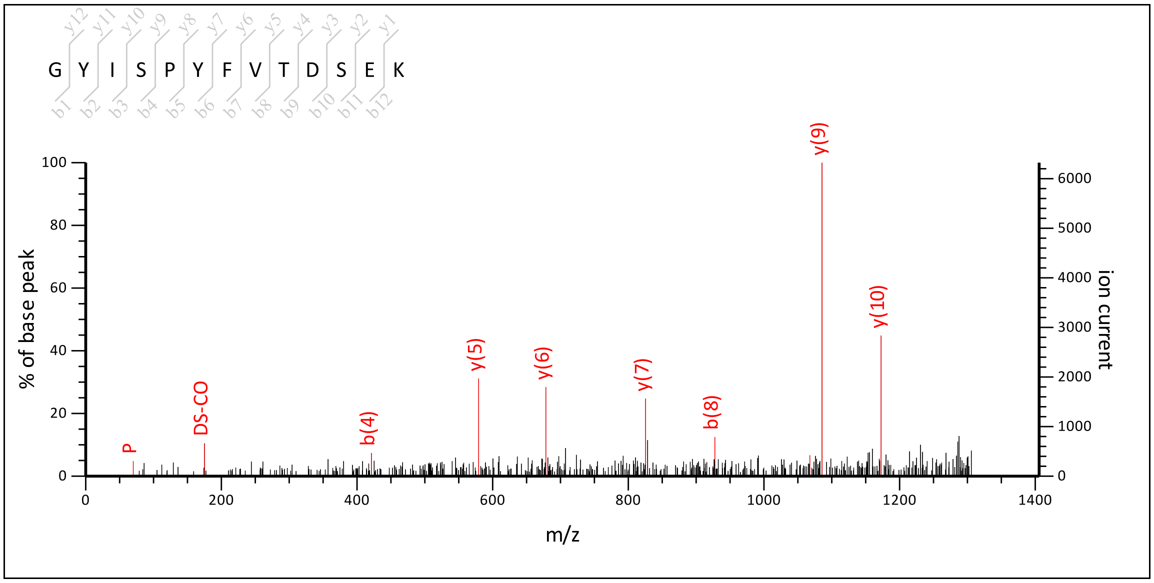
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 92

MS/MS Fragmentation of **GYISPYFVTDSEK**
Found in **gi|15231255** in **NCBInr**, TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]

Match to Query 256: 1504.756124 from(1505.763400,1+) intensity(0.0000) index(24)
Title: Label: E15, Spot_Id: 219902, Peak_List_Id: 228296, MSMS Job_Run_Id: 21986, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E15_136868276000.txt



0 to 1405.75

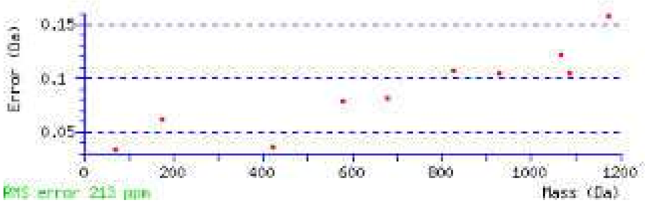
Label all possible matches ○ Label matches used for scoring ●

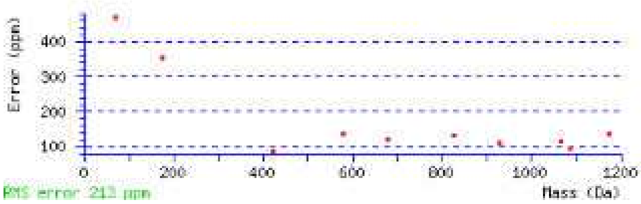
Monoisotopic mass of neutral peptide Mr(calc): 1504.7086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 15
Matches : 10/199 fragment ions using 13 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	30.0338	30.0338		58.0287		44.0495		G							13
2	136.0757	193.0972		221.0921				Y	1340.6369			1448.6944	1431.6678	1430.6838	12
3	86.0964	306.1812		334.1761		278.1499	292.1656	I	1227.5528	1240.5732	1254.5889	1285.6311	1268.6045	1267.6205	11
4	60.0444	393.2132	375.2027	**421.2082**	403.1976	377.2183		S	1140.5208	1139.5255		***1172.5470***	1155.5204	1154.5364	10
5	70.0651	490.2660	472.2554	518.2609	500.2504	464.2504		P	1043.4680	1042.4728		***1085.5150***	1068.4884	1067.5044	9
6	136.0757	653.3293	635.3188	681.3243	663.3137			Y	880.4047			988.4622	971.4357	970.4516	8
7	120.0808	800.3978	782.3872	828.3927	810.3821			F	733.3363			***825.3989***	808.3723	807.3883	7
8	72.0808	899.4662	881.4556	**927.4611**	909.4505	885.4505		V	634.2679	647.2883		***678.3305***	661.3039	660.3199	6
9	74.0600	1000.5138	982.5033	1028.5088	1010.4982	984.5189	986.4982	T	533.2202	546.2406	548.2198	***579.2620***	562.2355	561.2515	5
10	88.0393	1115.5408	1097.5302	1143.5357	1125.5251	1071.5510		D	418.1932	417.1980		478.2144	461.1878	460.2038	4
11	60.0444	1202.5728	1184.5623	1230.5677	1212.5572	1186.5779		S	331.1612	330.1660		363.1874	346.1609	345.1769	3
12	102.0550	1331.6154	1313.6048	1359.6103	1341.5998	1273.6099		E	202.1186	201.1234		276.1554	259.1288	258.1448	2
13	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YI	249.1598	277.1547	YIS	336.1918	364.1867	YISP	433.2445	461.2395
YISPY	596.3079	624.3028	IS	173.1285	201.1234	ISP	270.1812	298.1761
ISPY	433.2445	461.2395	ISPYF	580.3130	608.3079	ISPYFV	679.3814	707.3763
SP	157.0972	185.0921	SPY	320.1605	348.1554	SPYF	467.2289	495.2238

SPYFV	566.2973	594.2922	**SPYFVT**	667.3450	695.3399	**PY**	233.1285	261.1234
PYF	380.1969	408.1918	**PYFV**	479.2653	507.2602	**PYFVT**	580.3130	608.3079
PYFVTD	695.3399	723.3348	**YF**	283.1441	311.1390	**YFV**	382.2125	410.2074
YFVT	483.2602	511.2551	**YFVTD**	598.2871	626.2821	**YFVTDS**	685.3192	713.3141
FV	219.1492	247.1441	**FVT**	320.1969	348.1918	**FVTD**	435.2238	463.2187
FVTDS	522.2558	550.2508	**FVTDSE**	651.2984	679.2933	**VT**	173.1285	201.1234
VTD	288.1554	316.1503	**VTDS**	375.1874	403.1823	**VTDSE**	504.2300	532.2249
TD	189.0870	217.0819	**TDS**	276.1190	304.1139	**TDSE**	405.1616	433.1565
DS	175.0713	203.0662	**DSE**	304.1139	332.1088	**SE**	189.0870	217.0819





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.5	1504.7086	0.0475	GYISPYFVTDTDK
33.5	1504.6756	0.0806	GYISPYMVTDTDK
33.5	1504.7086	0.0475	GYLSPYFVTDTDK
33.5	1504.6756	0.0806	GYLSPYMVTDTDK
33.5	1504.7086	0.0476	GYISPYFVTDSEK
33.5	1504.6756	0.0806	GYISPYMVTDSEK
33.5	1504.7086	0.0476	GYLSPYFVTDSEK
33.5	1504.6756	0.0806	GYLSPYMVSDTEK
33.5	1504.6756	0.0806	GYLSPYMVTDSEK
32.9	1504.7191	0.0370	SMDSSADPLNVTLR

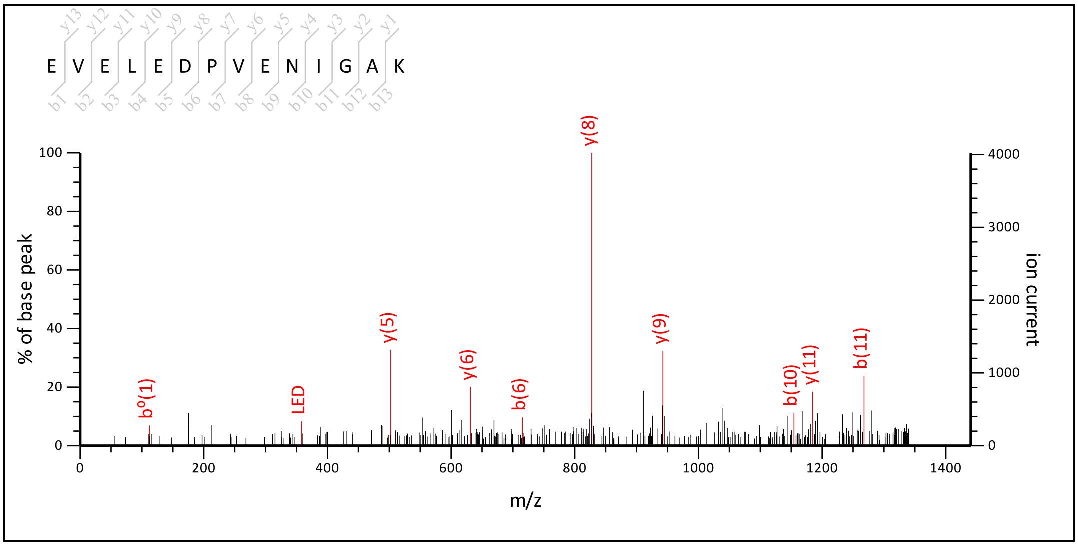
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 92

MS/MS Fragmentation of **EVELEDPVENIGAK**
Found in **gi|15231255** in **NCBInr**, TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]

Match to Query 262: 1540.817724 from(1541.825000,1+) intensity(0.0000) index(25)
Title: Label: E15, Spot_Id: 219902, Peak_List_Id: 228309, MSMS Job_Run_Id: 21986, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E15_136868276000.txt



0 to 1440.41

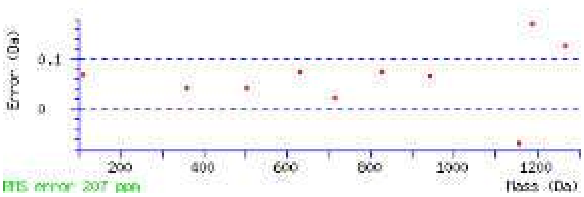
Label all possible matches ○ Label matches used for scoring ●

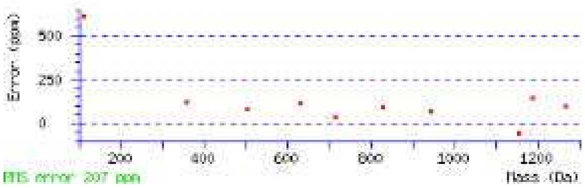
Monoisotopic mass of neutral peptide Mr(calc): 1540.7620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 3.6
Matches : 11/237 fragment ions using 13 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E						
2	72.0808	201.1234		183.1128	229.1183		211.1077	187.1077		V	1368.6642	1381.6846		1412.7268	1395.7002	13
3	102.0550	330.1660		312.1554	***358.1609***		340.1503	272.1605		E	1239.6216	1238.6263		1313.6583	1296.6318	12
4	86.0964	443.2500		425.2395	471.2449		453.2344	401.2031		L	1126.5375	1125.5422		***1184.6157***	1167.5892	11
5	102.0550	572.2926		554.2821	600.2875		582.2770	514.2871		E	997.4949	996.4997		1071.5317	1054.5051	10
6	88.0393	687.3196		669.3090	***715.3145***		697.3039	643.3297		D	882.4680	881.4727		***942.4891***	925.4625	92
7	70.0651	784.3723		766.3618	812.3672		794.3567	758.3567		P	785.4152	784.4199		***827.4621***	810.4356	8
8	72.0808	883.4407		865.4302	911.4357		893.4251	869.4251		V	686.3468	699.3672		730.4094	713.3828	7
9	102.0550	1012.4833		994.4728	1040.4782		1022.4677	954.4779		E	557.3042	556.3089		***631.3410***	614.3144	6
10	87.0553	1126.5263	1109.4997	1108.5157	***1154.5212***	1137.4946	1136.5106	1083.5204		N	443.2613	442.2660		***502.2984***	485.2718	
11	86.0964	1239.6103	1222.5838	1221.5998	***1267.6052***	1250.5787	1249.5947	1211.5790	1225.5947	I	330.1772	343.1976	357.2132	388.2554	371.2289	
12	30.0338	1296.6318	1279.6052	1278.6212	1324.6267	1307.6002	1306.6161			G				275.1714	258.1448	
13	44.0495	1367.6689	1350.6424	1349.6583	1395.6638	1378.6373	1377.6533			A	202.1186			218.1499	201.1234	
14	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VE	201.1234	229.1183	VEL	314.2074	342.2023	VELE	443.2500	471.2449
VELED	558.2770	586.2719	VELEDP	655.3297	683.3246	EL	215.1390	243.1339
ELE	344.1816	372.1765	ELED	459.2086	487.2035	ELEDP	556.2613	584.2562
ELEDPV	655.3297	683.3246	LE	215.1390	243.1339	LED	330.1660	358.1609
LEDP	427.2187	455.2136	LEDPV	526.2871	554.2821	LEDPVE	655.3297	683.3246
ED	217.0819	245.0768	EDP	314.1347	342.1296	EDPV	413.2031	441.1980
EDPVE	542.2457	570.2406	EDPVEN	656.2886	684.2835	DP	185.0921	213.0870

DPV	284.1605	312.1554	**DPVE**	413.2031	441.1980	**DPVEN**	527.2460	555.2409
DPVENI	640.3301	668.3250	**DPVENIG**	697.3515	725.3464	**PV**	169.1335	197.1285
PVE	298.1761	326.1710	**PVEN**	412.2191	440.2140	**PVENI**	525.3031	553.2980
PVENIG	582.3246	610.3195	**PVENIGA**	653.3617	681.3566	**VE**	201.1234	229.1183
VEN	315.1663	343.1612	**VENI**	428.2504	456.2453	**VENIG**	485.2718	513.2667
VENIGA	556.3089	584.3039	**EN**	216.0979	244.0928	**ENI**	329.1819	357.1769
ENIG	386.2034	414.1983	**ENIGA**	457.2405	485.2354	**NI**	200.1394	228.1343
NIG	257.1608	285.1557	**NIGA**	328.1979	356.1928	**IG**	143.1179	171.1128
IGA	214.1550	242.1499	**GA**	101.0709	129.0659			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.3	1540.7620	0.0557	EVELEDPVENIGAK
28.2	1540.8322	-0.0144	ETSGQAGTPIVLRGR
26.8	1540.8865	-0.0687	EPLYLVVPETLLR
22.4	1540.7621	0.0557	EDLLEDAGVDPAGLK
21.9	1540.8474	-0.0297	VSTSKPFPVPNRGR
21.8	1540.7409	0.0768	FSYSDDPINDLKK
20.1	1540.8322	-0.0144	SGIDAVGQVDLGVRR
20.0	1540.7845	0.0332	GTAGTDPDGILQAGLR
19.0	1540.7998	0.0179	WGEQVDPVKSQIR
17.9	1540.8685	-0.0508	GLGSDATLVLINGRR

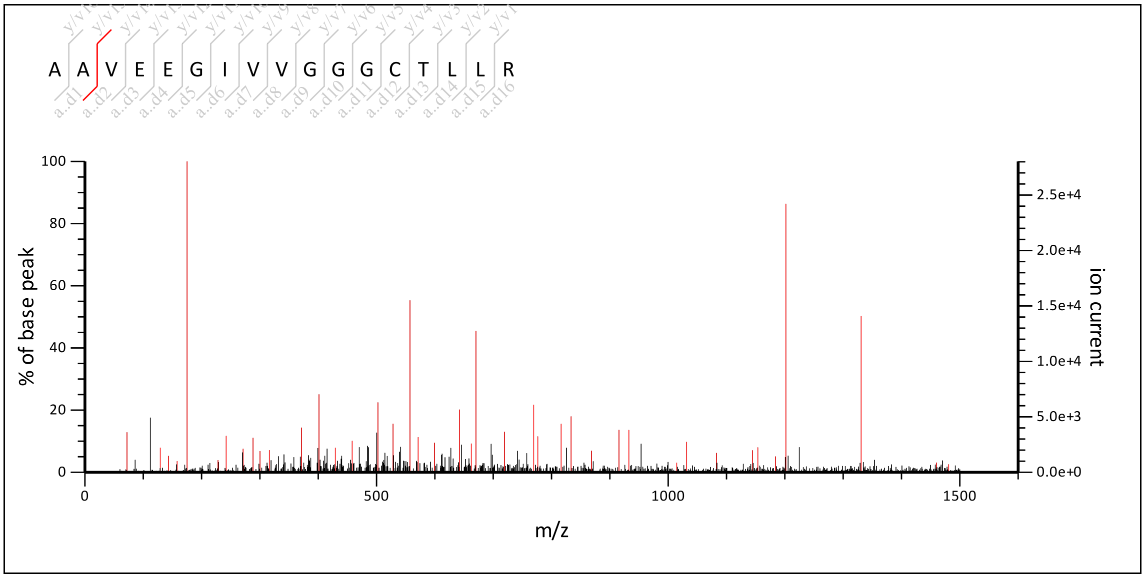
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 92

MS/MS Fragmentation of **AAVEEGIVVGGGCTLLR**
Found in **gi|15231255** in **NCBInr**, TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]

Match to Query 275: 1699.963424 from(1700.970700,1+) intensity(0.0000) index(27)
Title: Label: E15, Spot_Id: 219902, Peak_List_Id: 228285, MSMS Job_Run_Id: 21986, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_E15_136868276000.txt



0 to 1600.02

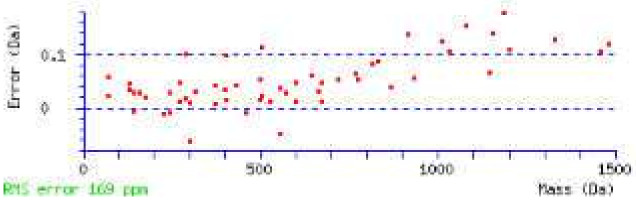
Label all possible matches ○ Label matches used for scoring ●

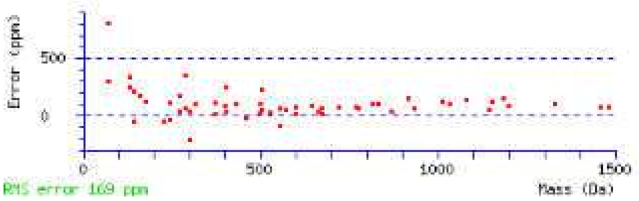
Monoisotopic mass of neutral peptide Mr(calc): 1699.8927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 111 **Expect:** 2.1e-07
Matches : 66/298 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	44.0495	44.0495		**72.0444**		44.0495		A							17
2	44.0495	115.0866		**143.0815**				A	1613.8316			1629.8629	1612.8363	1611.8523	16
3	72.0808	214.1550		**242.1499**		200.1394		V	1514.7632	1527.7836		1558.8258	1541.7992	1540.8152	15
4	102.0550	343.1976	325.1870	**371.1925**	353.1819	285.1921		E	1385.7206	1384.7253		***1459.7573***	1442.7308	1441.7468	14
5	102.0550	472.2402	454.2296	**500.2351**	482.2245	414.2347		E	1256.6780	1255.6827		***1330.7147***	1313.6882	1312.7042	13
6	30.0338	529.2617	511.2511	**557.2566**	539.2460			G				***1201.6722***	1184.6456	1183.6616	12
7	86.0964	642.3457	624.3352	**670.3406**	652.3301	614.3144	628.3301	I	1086.5724	1099.5928	1113.6085	***1144.6507***	1127.6241	1126.6401	11
8	72.0808	741.4141	723.4036	**769.4090**	751.3985	727.3985		V	987.5040	1000.5244		***1031.5666***	1014.5401	1013.5561	10
9	72.0808	840.4825	822.4720	**868.4775**	850.4669	826.4669		V	888.4356	901.4560		***932.4982***	915.4717	914.4876	9
10	30.0338	897.5040	879.4934	925.4989	907.4884			G				***833.4298***	816.4033	815.4192	8
11	30.0338	954.5255	936.5149	982.5204	964.5098			G				***776.4083***	759.3818	758.3978	7
12	30.0338	1011.5469	993.5364	1039.5419	1021.5313			G				***719.3869***	702.3603	701.3763	6
13	133.0430	1171.5776	1153.5670	1199.5725	1181.5619	1082.5841		C	557.3406	556.3453		***662.3654***	645.3389	644.3548	5
14	74.0600	1272.6253	1254.6147	1300.6202	1282.6096	1256.6304	1258.6096	T	456.2929	469.3133	471.2926	***502.3348***	485.3082	484.3242	4
15	86.0964	1385.7093	1367.6988	1413.7042	1395.6937	1343.6624		L	343.2088	342.2136		***401.2871***	384.2605		3
16	86.0964	1498.7934	1480.7828	1526.7883	1508.7777	1456.7464		L	230.1248	229.1295		***288.2030***	271.1765		2
17	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AV	143.1179	171.1128	AVE	272.1605	300.1554	AVEE	401.2031	429.1980

AVEEG	458.2245	486.2195	**AVEEGI**	571.3086	599.3035	**AVEEGIV**	670.3770	698.3719
VE	201.1234	229.1183	**VEE**	330.1660	358.1609	**VEEG**	387.1874	415.1823
VEEGI	500.2715	528.2664	**VEEGIV**	599.3399	627.3348	**VEEGIVV**	698.4083	726.4032
EE	231.0975	259.0925	**EEG**	288.1190	316.1139	**EEGI**	401.2031	429.1980
EEGIV	500.2715	528.2664	**EEGIVV**	599.3399	627.3348	**EEGIVVG**	656.3614	684.3563
EG	159.0764	187.0713	**EGI**	272.1605	300.1554	**EGIV**	371.2289	399.2238
EGIVV	470.2973	498.2922	**EGIVVG**	527.3188	555.3137	**EGIVVGG**	584.3402	612.3352
EGIVVGGG	641.3617	669.3566	**GI**	143.1179	171.1128	**GIV**	242.1863	270.1812
GIVV	341.2547	369.2496	**GIVVG**	398.2762	426.2711	**GIVVGG**	455.2976	483.2926
GIVVGGG	512.3191	540.3140	**GIVVGGGC**	672.3498	700.3447	**IV**	185.1648	213.1598
IVV	284.2333	312.2282	**IVVG**	341.2547	369.2496	**IVVGG**	398.2762	426.2711
IVVGGG	455.2976	483.2926	**IVVGGGC**	615.3283	643.3232	**VV**	171.1492	199.1441
VVG	228.1707	256.1656	**VVGG**	285.1921	313.1870	**VVGGG**	342.2136	370.2085
VVGGGC	502.2442	530.2391	**VVGGGCT**	603.2919	631.2868	**VG**	129.1022	157.0972
VGG	186.1237	214.1186	**VGGG**	243.1452	271.1401	**VGGGC**	403.1758	431.1707
VGGGCT	504.2235	532.2184	**VGGGCTL**	617.3076	645.3025	**GG**	87.0553	115.0502
GGG	144.0768	172.0717	**GGGC**	304.1074	332.1023	**GGGCT**	405.1551	433.1500
GGGCTL	518.2391	546.2341	**GGGCTLL**	631.3232	659.3181	**GG**	87.0553	115.0502
GGC	247.0859	275.0809	**GGCT**	348.1336	376.1285	**GGCTL**	461.2177	489.2126
GGCTLL	574.3017	602.2967	**GC**	190.0645	218.0594	**GCT**	291.1122	319.1071
GCTL	404.1962	432.1911	**GCTLL**	517.2803	545.2752	**CT**	234.0907	262.0856
CTL	347.1748	375.1697	**CTLL**	460.2588	488.2537	**TL**	187.1441	215.1390
TLL	300.2282	328.2231	**LL**	199.1805	227.1754			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
110.7	1699.8927	0.0707	AAVEEGIVVGGGCTLIR
110.7	1699.8927	0.0707	AAVEEGIVVGGGCTLLR
74.7	1699.8927	0.0707	AAVEEGVVIGGGCTLLR
57.2	1699.8927	0.0707	AAVEEGIVLGGGCSLLR
38.9	1699.9356	0.0278	GLLDTGIVDISTDLLR
36.3	1699.9046	0.0589	EAFEGPWDLVRLIR
33.8	1699.9178	0.0456	AAVEEVIGVLLGMQAGK
33.5	1699.9145	0.0490	SSLIRPDDFIPIAEK
33.2	1699.9551	0.0083	LLAMVVAAGMVMLPLR
32.4	1699.9356	0.0278	AGLSIDLTDSIDVLLR

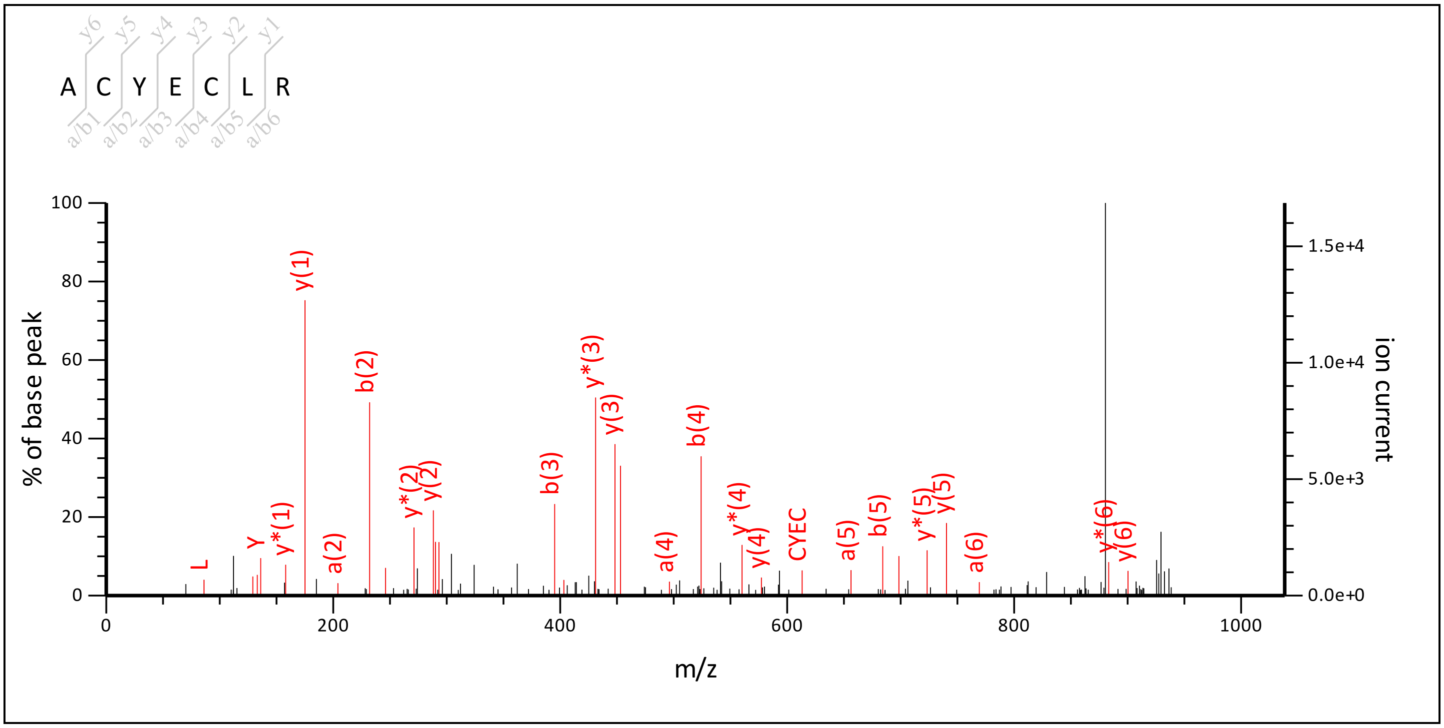
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **ACYECLR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 2: 970.467514 from(971.474790,1+) intensity(0.0000) index(0)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221252, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



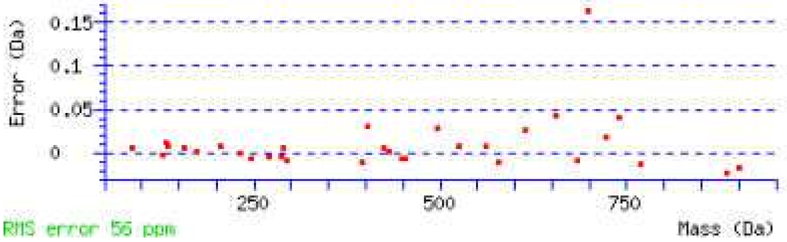
0 to 1038.4

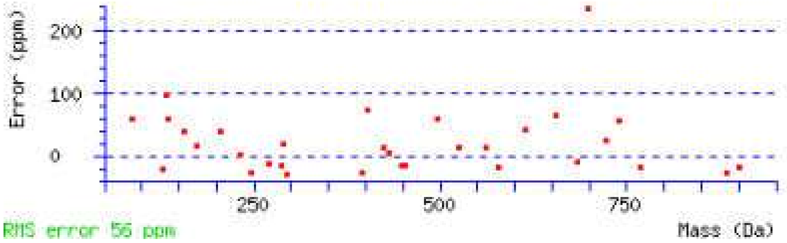
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 970.4001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 1.7
Matches : 35/75 fragment ions using 54 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		72.0444		44.0495	**A**						7
2	133.0430	**204.0801**		**232.0750**		115.0866	**C**	795.3454	794.3502	***900.3702***	883.3437	882.3597	6
3	136.0757	367.1435		**395.1384**			**Y**	632.2821		***740.3396***	723.3130	722.3290	5
4	102.0550	**496.1860**	478.1755	**524.1810**	506.1704	438.1806	**E**	503.2395	502.2442	***577.2763***	560.2497	559.2657	4
5	133.0430	**656.2167**	638.2061	**684.2116**	666.2010	567.2232	**C**	343.2088	342.2136	***448.2337***	431.2071		3
6	86.0964	**769.3008**	751.2902	797.2957	779.2851	727.2538	**L**	230.1248	229.1295	***288.2030***	271.1765		2
7	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
CY	296.1063	324.1013	**CYE**	425.1489	453.1438	**CYEC**	585.1796	613.1745
CYECL	698.2636	726.2586	**YE**	265.1183	293.1132	**YEC**	425.1489	453.1438
YECL	538.2330	566.2279	**EC**	262.0856	290.0805	**ECL**	375.1697	403.1646
CL	246.1271	274.1220						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.9	970.4001	0.0675	ACYECIR
35.9	970.4001	0.0675	ACYECLR
35.9	970.4001	0.0675	ACYECLR
35.9	970.4001	0.0675	ACYECLR
35.9	970.4001	0.0675	ACYECLR
29.5	970.4807	-0.0132	ACFAPHLR
22.4	970.4364	0.0311	CVYMNIR
22.4	969.4412	1.0263	MVYECLR
20.6	970.5382	-0.0707	LANPKCLR
19.2	969.5243	0.9432	AAATPAAELR

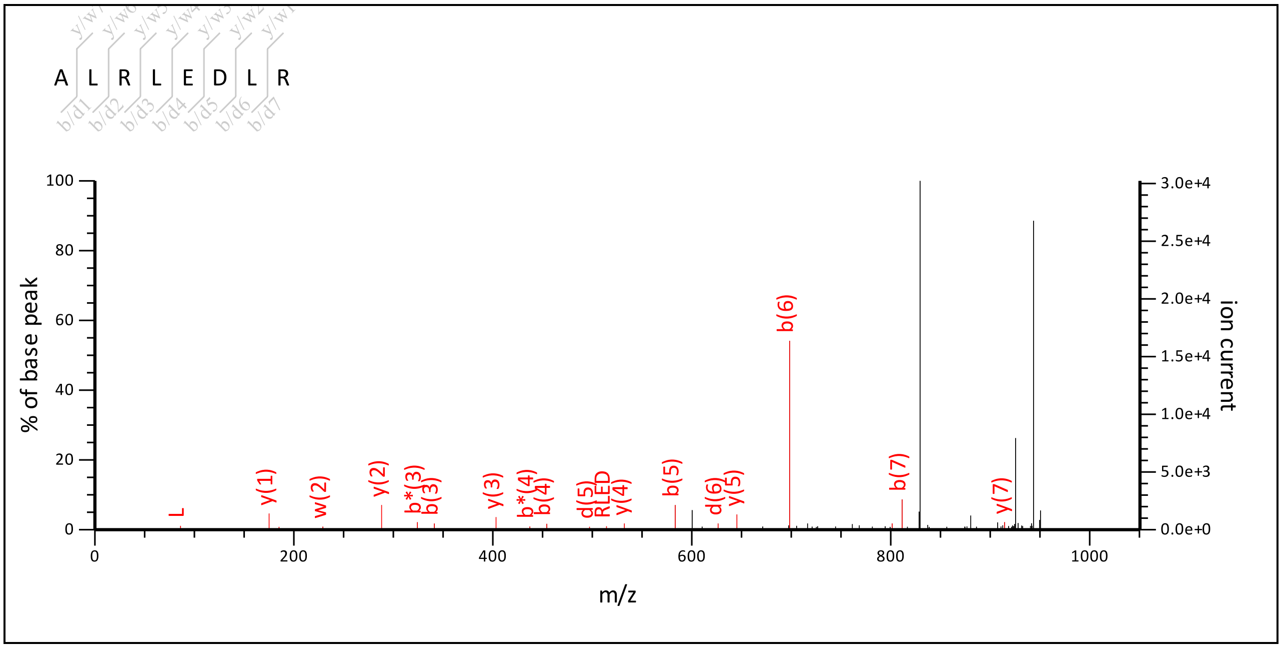
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **ALRLEDLR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 4: 984.639634 from(985.646910,1+) intensity(0.0000) index(1)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221259, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



0 to 1050.54

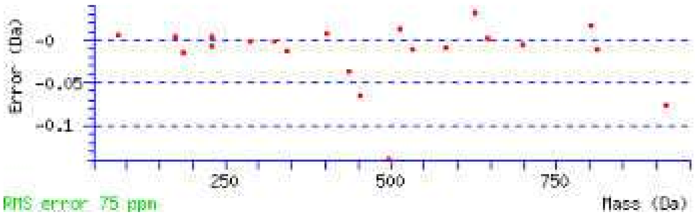
Label all possible matches ○ Label matches used for scoring ●

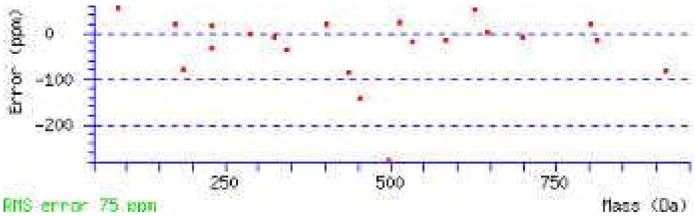
Monoisotopic mass of neutral peptide Mr(calc): 984.5716
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.092
Matches : 24/106 fragment ions using 34 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495			72.0444			44.0495	A						8
2	86.0964	157.1335			**185.1285**			115.0866	L	856.4635	855.4683	***914.5418***	897.5152	896.5312	7
3	129.1135	313.2346	296.2081		**341.2296**	324.2030		228.1707	R	700.3624	699.3672	***801.4577***	784.4312	783.4472	6
4	86.0964	426.3187	409.2922		**454.3136**	437.2871		384.2718	L	587.2784	586.2831	***645.3566***	628.3301	627.3461	5
5	102.0550	555.3613	538.3348	537.3507	**583.3562**	566.3297	565.3457	497.3558	E	458.2358	457.2405	***532.2726***	515.2460	514.2620	4
6	88.0393	670.3883	653.3617	652.3777	**698.3832**	681.3566	680.3726	626.3984	D	343.2088	342.2136	***403.2300***	386.2034	385.2194	3
7	86.0964	783.4723	766.4458	765.4617	**811.4672**	794.4407	793.4567	741.4254	L	230.1248	229.1295	***288.2030***	271.1765		2
8	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LR	242.1975	270.1925	LRL	355.2816	383.2765	LRLE	484.3242	512.3191
LRLED	599.3511	627.3461	RL	242.1975	270.1925	RLE	371.2401	399.2350
RLED	486.2671	514.2620	RLEDL	599.3511	627.3461	LE	215.1390	243.1339
LED	330.1660	358.1609	LEDL	443.2500	471.2449	ED	217.0819	245.0768

EDL	330.1660	358.1609	**DL**	201.1234	229.1183			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.9	984.5716	0.0680	ALRIEDLR
50.9	984.5716	0.0680	ALRIEDLR
50.7	984.0796	0.5600	ALRLEBLR
50.7	984.0796	0.5600	ALRLEBLR
49.1	984.5716	0.0680	AIRLEDLR
49.1	984.5716	0.0680	AIRLEDLR
49.1	984.5716	0.0680	ALRLEDIR
49.1	984.5716	0.0680	ALRLEDIR
49.1	984.5716	0.0680	ALRLEDLR
49.1	984.5716	0.0680	ALRLEDLR

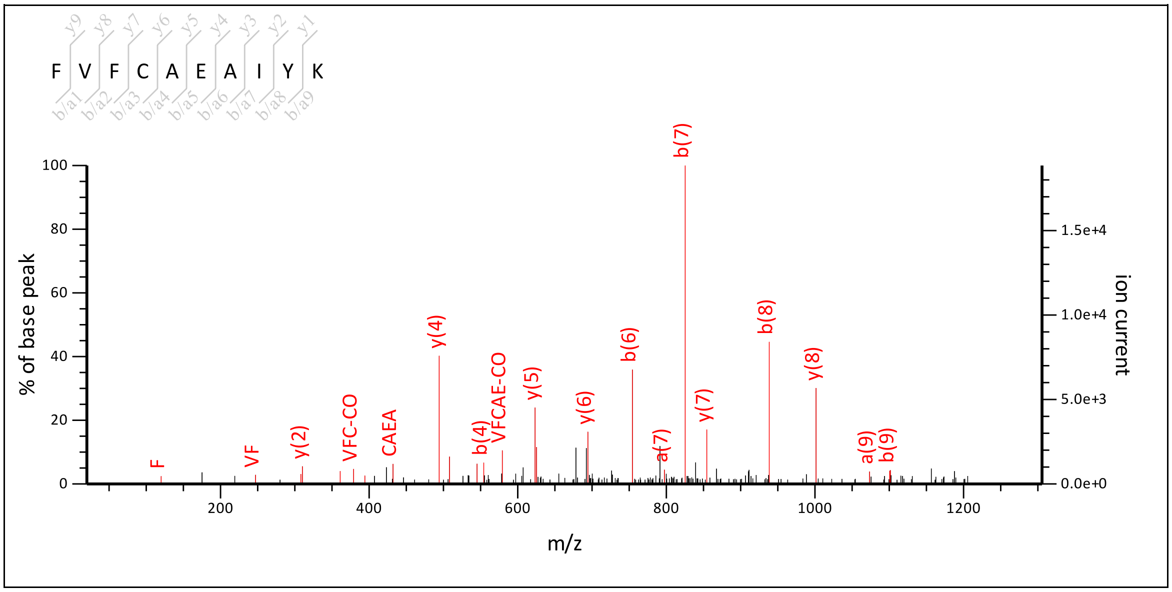
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **FVFCAEAIYK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 9: 1246.668124 from(1247.675400,1+) intensity(0.0000) index(4)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221255, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



20.1 to 1305.58

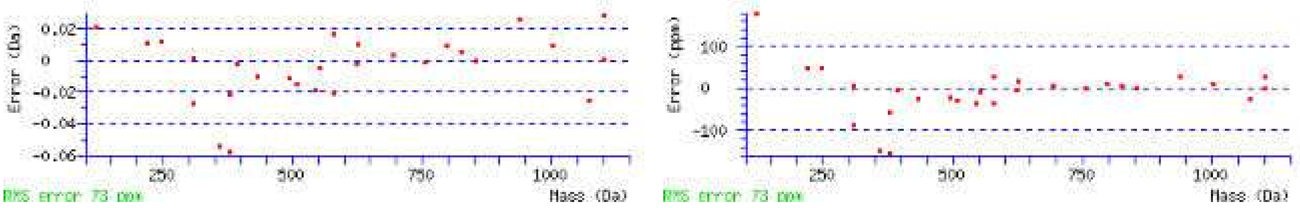
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1246.6056
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 0.0011
Matches : 32/129 fragment ions using 33 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	120.0808	**120.0808**		148.0757		44.0495		F							10
2	72.0808	**219.1492**		***247.1441***		205.1335		V	1056.4819	1069.5023		***1100.5445***	1083.5179	1082.5339	9
3	120.0808	366.2176		***394.2125***				F	909.4135			***1001.4761***	984.4495	983.4655	8
4	133.0430	526.2483		***554.2432***		437.2547		C	749.3828	748.3876		***854.4077***	837.3811	836.3971	7
5	44.0495	597.2854		***625.2803***				A	678.3457			***694.3770***	677.3505	676.3665	6
6	102.0550	726.3280	708.3174	***754.3229***	736.3123	668.3225		E	549.3031	548.3079		***623.3399***	606.3134	605.3293	5
7	44.0495	**797.3651**	779.3545	***825.3600***	807.3494			A	478.2660			***494.2973***	477.2708		4
8	86.0964	910.4491	892.4386	***938.4441***	920.4335	882.4178	896.4335	I	365.1819	378.2023	392.2180	423.2602	406.2336		3
9	136.0757	**1073.5125**	1055.5019	***1101.5074***	1083.4968			Y	202.1186			***310.1761***	293.1496		2
10	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VF	219.1492	247.1441	VFC	379.1798	407.1748	VFCA	450.2170	478.2119
VFCAE	579.2595	607.2545	VFCAEA	650.2967	678.2916	FC	280.1114	308.1063
FCA	351.1485	379.1435	FCAE	480.1911	508.1860	FCAEA	551.2282	579.2232
FCAEAI	664.3123	692.3072	CA	204.0801	232.0750	CAE	333.1227	361.1176
CAEA	404.1598	432.1547	CAEAI	517.2439	545.2388	CAEAIY	680.3072	708.3021
AE	173.0921	201.0870	AEA	244.1292	272.1241	AEAI	357.2132	385.2082

AEAIY	520.2766	548.2715	**EA**	173.0921	201.0870	**EAI**	286.1761	314.1710
EAIY	449.2395	477.2344	**AI**	157.1335	185.1285	**AIY**	320.1969	348.1918
IY	249.1598	277.1547						



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.5	1246.6056	0.0625	FVFCAEAIYK
67.5	1246.6056	0.0625	FVFCAEAIYK
67.5	1246.6056	0.0625	FVFCAEAIYK
67.5	1246.6056	0.0625	FVFCAEAIYK
67.5	1246.6056	0.0625	FVFCAEAIYK
67.5	1246.6056	0.0625	FVFCAEAIYK
67.5	1246.6056	0.0625	FVFCAEAIYK
67.5	1246.6056	0.0625	FVFCAEALYK
67.5	1246.6056	0.0625	FVFCAEALYK
67.5	1246.6056	0.0625	FVFCAEALYK

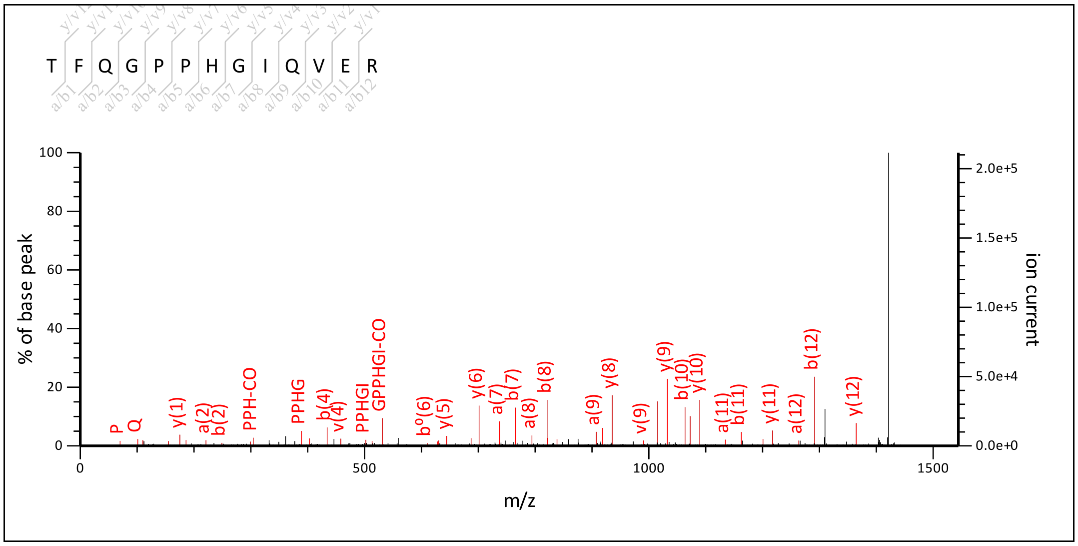
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **TFQGPPHGIQVER**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 11: 1464.832324 from(1465.839600,1+) intensity(0.0000) index(5)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221246, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



0 to 1544.37

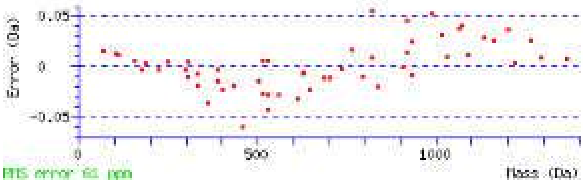
Label all possible matches ○ Label matches used for scoring ●

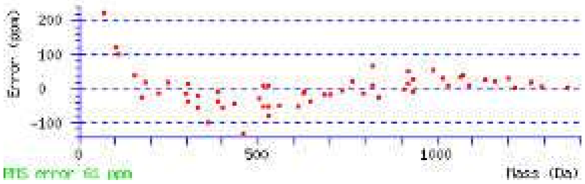
Monoisotopic mass of neutral peptide Mr(calc): 1464.7474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 117 **Expect:** 1.5e-08
Matches : 61/229 fragment ions using 56 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	120.0808	**221.1285**		203.1179	**249.1234**		231.1128			F	1272.6444			***1364.7070***	1347.6804	134
3	101.0709	349.1870	332.1605	331.1765	377.1819	360.1554	359.1714	292.1656		Q	1144.5858	1143.5905		***1217.6385***	1200.6120	119
4	30.0338	406.2085	389.1819	388.1979	**434.2034**	417.1769	416.1928			G				***1089.5800***	1072.5534	107
5	70.0651	503.2613	486.2347	485.2507	**531.2562**	514.2296	513.2456	477.2456		P	990.5116	989.5163		***1032.5585***	1015.5320	101
6	70.0651	600.3140	583.2875	582.3035	**628.3089**	611.2824	610.2984	574.2984		P	893.4588	892.4635		***935.5057***	918.4792	91
7	110.0713	**737.3729**	720.3464	719.3624	**765.3679**	748.3413	747.3573			H	756.3999			***838.4530***	821.4264	82
8	30.0338	**794.3944**	777.3679	776.3838	**822.3893**	805.3628	804.3787			G				***701.3941***	684.3675	68
9	86.0964	**907.4785**	890.4519	889.4679	**935.4734**	918.4468	917.4628	879.4472	893.4628	I	586.2944	599.3148	613.3304	***644.3726***	627.3461	62
10	101.0709	1035.5370	1018.5105	1017.5265	**1063.5320**	1046.5054	1045.5214	978.5156		Q	458.2358	457.2405		***531.2885***	514.2620	51
11	72.0808	**1134.6055**	1117.5789	1116.5949	**1162.6004**	1145.5738	1144.5898	1120.5898		V	359.1674	372.1878		***403.2300***	386.2034	38
12	102.0550	**1263.6480**	1246.6215	1245.6375	**1291.6430**	1274.6164	1273.6324	1205.6426		E	230.1248	229.1295		***304.1615***	287.1350	28
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQG	305.1608	333.1557	FQGP	402.2136	430.2085
FQGPP	499.2663	527.2613	FQGPPH	636.3253	664.3202	FQGPPHG	693.3467	721.3416
QG	158.0924	186.0873	QGP	255.1452	283.1401	QGPP	352.1979	380.1928
QGPPH	489.2568	517.2518	QGPPHG	546.2783	574.2732	QGPPHGI	659.3624	687.3573
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPH	361.1983	389.1932
GPPHG	418.2197	446.2146	GPPHGI	531.3038	559.2987	GPPHGIQ	659.3624	687.3573
PP	167.1179	195.1128	PPH	304.1768	332.1717	PPHG	361.1983	389.1932
PPHGI	474.2823	502.2772	PPHGIQ	602.3409	630.3358	PH	207.1240	235.1190

PHG	264.1455	292.1404	**PHGI**	377.2296	405.2245	**PHGIQ**	505.2881	533.2831
PHGIQV	604.3566	632.3515	**HG**	167.0927	195.0877	**HGI**	280.1768	308.1717
HGIQ	408.2354	436.2303	**HGIQV**	507.3038	535.2987	**HGIQVE**	636.3464	664.3413
GI	143.1179	171.1128	**GIQ**	271.1765	299.1714	**GIQV**	370.2449	398.2398
GIQVE	499.2875	527.2824	**IQ**	214.1550	242.1499	**IQV**	313.2234	341.2183
IQVE	442.2660	470.2609	**QV**	200.1394	228.1343	**QVE**	329.1819	357.1769
VE	201.1234	229.1183						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
116.9	1464.7838	0.0486	TFKGPPHGIQVER
116.9	1464.7838	0.0486	TFKGPPHGIQVER
116.9	1464.7838	0.0486	TFQGPPHGIKVER
116.9	1464.7838	0.0486	TFQGPPHGIKVER
116.9	1464.7474	0.0849	TFQGPPHGIQVER
116.9	1464.7474	0.0849	TFQGPPHGIQVER
116.9	1464.7474	0.0849	TFQGPPHGIQVER
116.9	1464.7474	0.0849	TFQGPPHGIQVER
116.9	1464.7474	0.0849	TFQGPPHGIQVER
116.9	1464.7474	0.0849	TFQGPPHGIQVER

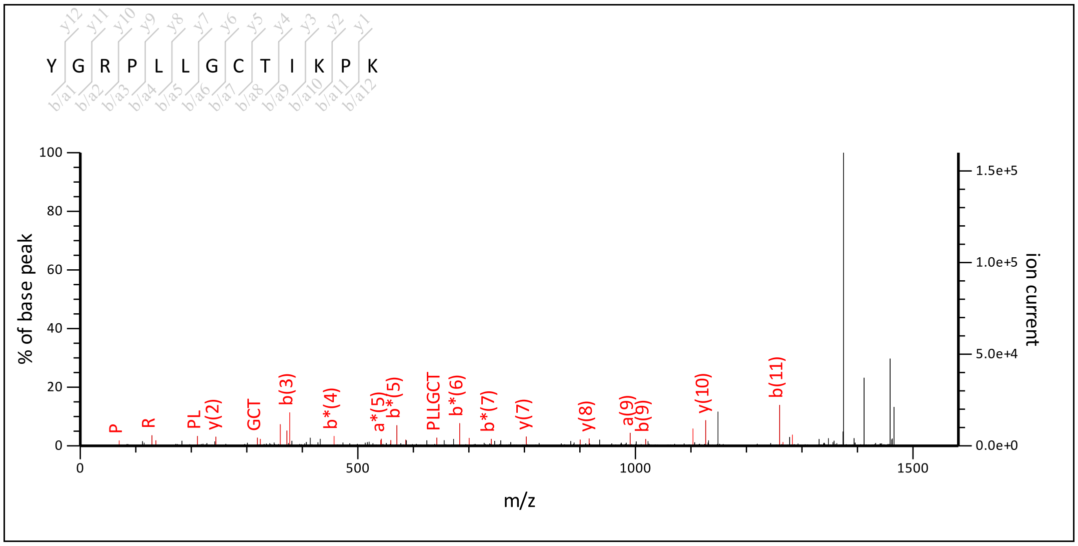
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 96**

MS/MS Fragmentation of **YGRPLLGCTIKPK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 13: 1501.927124 from(1502.934400,1+) intensity(0.0000) index(6)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221250, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_1359977701000.txt



0 to 1581.78

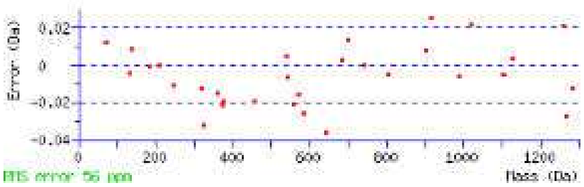
Label all possible matches ○ Label matches used for scoring ●

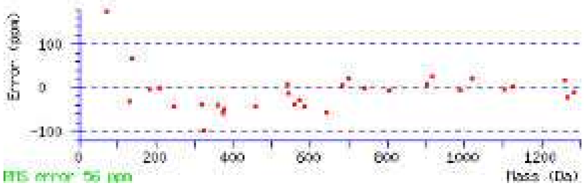
Monoisotopic mass of neutral peptide Mr(calc): 1501.8439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.61
Matches : 33/211 fragment ions using 44 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	136.0757	**136.0757**			164.0706			44.0495		**Y**					
2	30.0338	193.0972			221.0921					**G**				1339.7879	1322.7613
3	129.1135	349.1983	332.1717		**377.1932**	360.1666		264.1343		**R**	1181.6711	1180.6758		***1282.7664***	1265.7398
4	70.0651	446.2510	429.2245		474.2459	457.2194		420.2354		**P**	1084.6183	1083.6231		***1126.6653***	1109.6387
5	86.0964	**559.3351**	542.3085		587.3300	570.3035		517.2881		**L**	971.5343	970.5390		1029.6125	1012.5860
6	86.0964	672.4192	655.3926		**700.4141**	683.3875		630.3722		**L**	858.4502	857.4550		***916.5285***	899.5019
7	30.0338	729.4406	712.4141		757.4355	740.4090				**G**				***803.4444***	786.4178
8	133.0430	889.4713	872.4447		917.4662	900.4396		800.4777		**C**	641.3981	640.4028		746.4229	729.3964
9	74.0600	**990.5189**	973.4924	972.5084	**1018.5139**	1001.4873	1000.5033	974.5240	976.5033	**T**	540.3504	553.3708	555.3501	***586.3923***	569.3657
10	86.0964	**1103.6030**	1086.5765	1085.5924	1131.5979	1114.5714	1113.5874	1075.5717	1089.5874	**I**	427.2663	440.2867	454.3024	485.3446	468.3180
11	101.1073	1231.6980	1214.6714	1213.6874	**1259.6929**	1242.6663	1241.6823	1174.6401		**K**	299.1714	298.1761		***372.2605***	355.2340
12	70.0651	1328.7507	1311.7242	1310.7402	1356.7457	1339.7191	1338.7351	1302.7351		**P**	202.1186	201.1234		***244.1656***	227.1390
13	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GR	186.1349	214.1299	**GRP**	283.1877	311.1826	**GRPL**	396.2718	424.2667
GRPLL	509.3558	537.3507	**GRPLLG**	566.3773	594.3722	**RP**	226.1662	254.1612
RPL	339.2503	367.2452	**RPLL**	452.3344	480.3293	**RPLLG**	509.3558	537.3507
RPLLGC	669.3865	697.3814	**PL**	183.1492	211.1441	**PLL**	296.2333	324.2282
PLLG	353.2547	381.2496	**PLLGC**	513.2854	541.2803	**PLLGCT**	614.3330	642.3280
LL	199.1805	227.1754	**LLG**	256.2020	284.1969	**LLGC**	416.2326	444.2275
LLGCT	517.2803	545.2752	**LLGCTI**	630.3643	658.3593	**LG**	143.1179	171.1128
LGC	303.1485	331.1435	**LGCT**	404.1962	432.1911	**LGCTI**	517.2803	545.2752

LGCTIK	645.3752	673.3702	**GC**	190.0645	218.0594	**GCT**	291.1122	319.1071
GCTI	404.1962	432.1911	**GCTIK**	532.2912	560.2861	**GCTIKP**	629.3439	657.3389
CT	234.0907	262.0856	**CTI**	347.1748	375.1697	**CTIK**	475.2697	503.2646
CTIKP	572.3225	600.3174	**TI**	187.1441	215.1390	**TIK**	315.2391	343.2340
TIKP	412.2918	440.2867	**IK**	214.1914	242.1863	**IKP**	311.2442	339.2391
KP	198.1601	226.1550						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.4	1501.8439	0.0832	YGRPILGCTIKPK
40.4	1501.8439	0.0832	YGRPILGCTIKPK
40.4	1501.8439	0.0832	YGRPLIGCTIKPK
40.4	1501.8439	0.0832	YGRPLLGCTIKPK
40.4	1501.8439	0.0832	YGRPLLGCTIKPK
40.4	1501.8439	0.0832	YGRPLLGCTIKPK
40.4	1501.8439	0.0832	YGRPLLGCTIKPK
40.4	1501.8439	0.0832	YGRPLLGCTIKPK
40.4	1501.8439	0.0832	YGRPLLGCTIKPK
40.4	1501.8439	0.0832	YGRPLLGCTIKPK

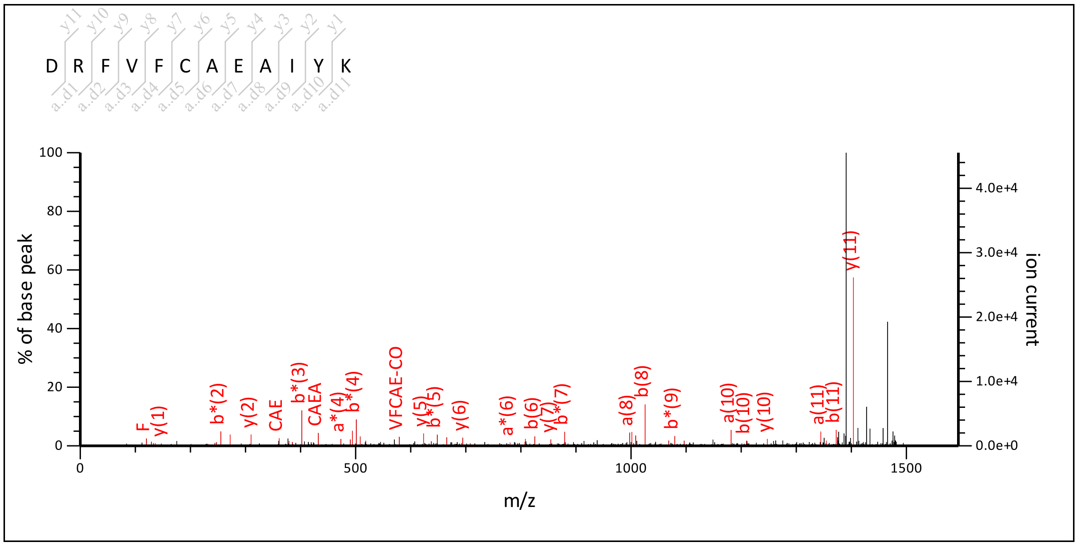
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **DRFVFCAEAIYK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 15: 1517.823824 from(1518.831100,1+) intensity(0.0000) index(7)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221258, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



0 to 1594.38

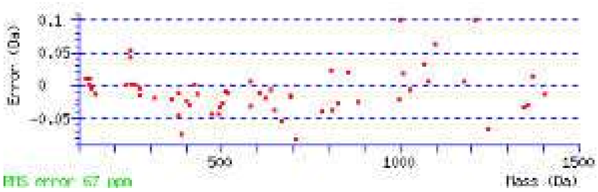
Label all possible matches ○ Label matches used for scoring ●

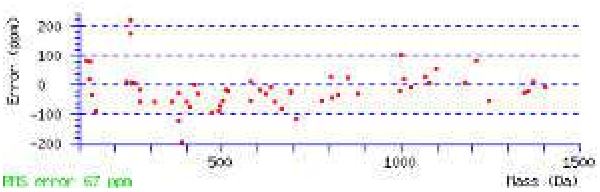
Monoisotopic mass of neutral peptide Mr(calc): 1517.7337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.042
Matches : 59/194 fragment ions using 99 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D					
2	129.1135	**244.1404**	227.1139	226.1299	**272.1353**	255.1088	254.1248	159.0764		R	1302.6187	1301.6235		***1403.7140***	1386.6875
3	120.0808	391.2088	374.1823	373.1983	419.2037	402.1772	401.1932			F	1155.5503			***1247.6129***	1230.5864
4	72.0808	**490.2772**	473.2507	472.2667	**518.2722**	501.2456	500.2616	476.2616		V	1056.4819	1069.5023		1100.5445	1083.5179
5	120.0808	**637.3457**	620.3191	619.3351	**665.3406**	648.3140	647.3300			F	909.4135			***1001.4761***	984.4495
6	133.0430	797.3763	780.3498	779.3657	**825.3712**	808.3447	807.3607	708.3828		C	749.3828	748.3876		***854.4077***	837.3811
7	44.0495	868.4134	851.3869	850.4029	896.4083	879.3818	878.3978			A	678.3457			***694.3770***	677.3505
8	102.0550	**997.4560**	980.4295	979.4454	**1025.4509**	1008.4244	1007.4404	939.4505		E	549.3031	548.3079		***623.3399***	606.3134
9	44.0495	**1068.4931**	1051.4666	1050.4826	**1096.4880**	1079.4615	1078.4775			A	478.2660			***494.2973***	477.2708
10	86.0964	**1181.5772**	1164.5506	1163.5666	**1209.5721**	1192.5456	1191.5615	1153.5459	1167.5615	I	365.1819	378.2023	392.2180	***423.2602***	406.2336
11	136.0757	**1344.6405**	1327.6140	1326.6300	**1372.6354**	1355.6089	1354.6249			Y	202.1186			***310.1761***	293.1496
12	101.1073									K	74.0237	73.0284		***147.1128***	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RF	276.1819	304.1768	RFV	375.2503	403.2452	RFVF	522.3187	550.3136
RFVFC	682.3494	710.3443	FV	219.1492	247.1441	FVF	366.2176	394.2125
FVFC	526.2483	554.2432	FVFCA	597.2854	625.2803	VF	219.1492	247.1441
VFC	379.1798	407.1748	VFCA	450.2170	478.2119	VFCAE	579.2595	607.2545
VFCAEA	650.2967	678.2916	FC	280.1114	308.1063	FCA	351.1485	379.1435
FCAE	480.1911	508.1860	FCAEA	551.2282	579.2232	FCAEAI	664.3123	692.3072
CA	204.0801	232.0750	CAE	333.1227	361.1176	CAEA	404.1598	432.1547
CAEAI	517.2439	545.2388	CAEAIY	680.3072	708.3021	AE	173.0921	201.0870
AEA	244.1292	272.1241	AEAI	357.2132	385.2082	AEAIY	520.2766	548.2715

EA	173.0921	201.0870	**EAI**	286.1761	314.1710	**EAIY**	449.2395	477.2344
AI	157.1335	185.1285	**AIY**	320.1969	348.1918	**IY**	249.1598	277.1547





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.6	1517.7007	0.1232	DRFVMCAEAIYK
52.6	1517.7007	0.1232	DRMVFCAEALYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK
51.1	1517.7337	0.0902	DRFVFCAEAIYK

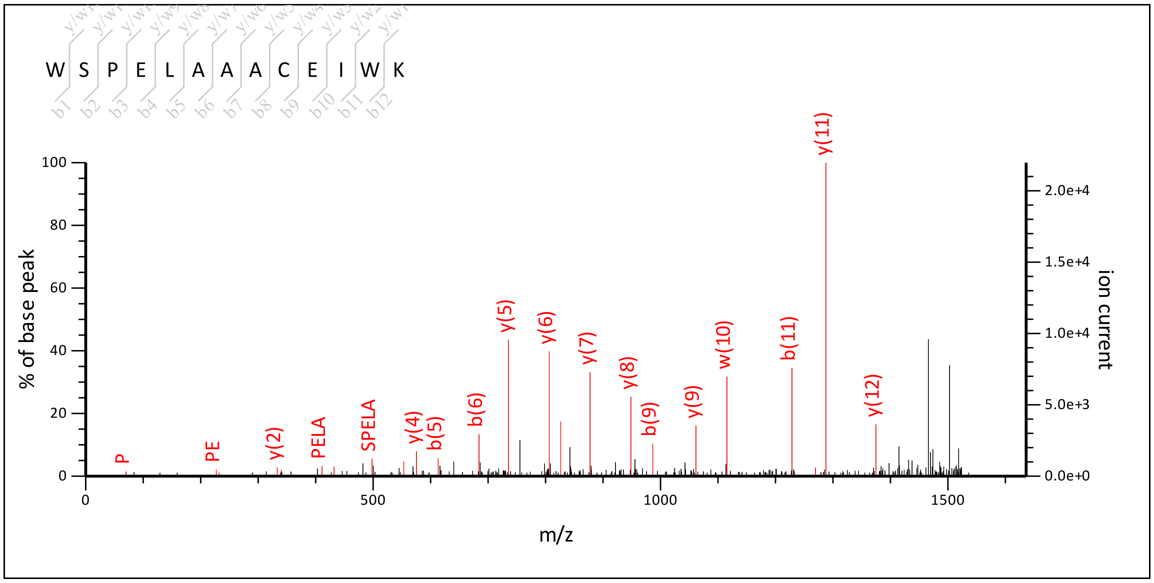
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **WSPELAAACEIWK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 17: 1559.808024 from(1560.815300,1+) intensity(0.0000) index(8)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221257, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



0 to 1636.08

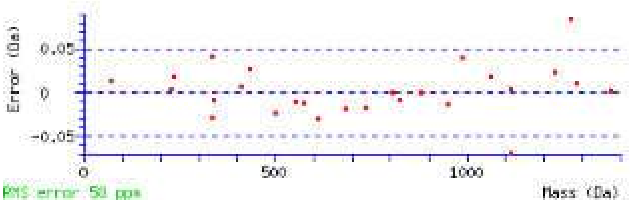
Label all possible matches ○ Label matches used for scoring ●

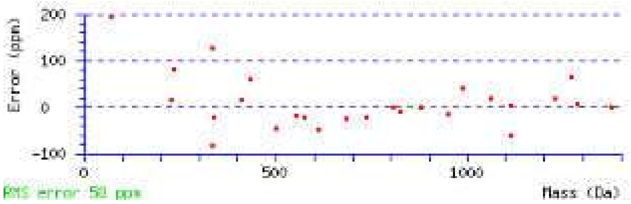
Monoisotopic mass of neutral peptide Mr(calc): 1559.7442
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 0.00022
Matches : 26/203 fragment ions using 30 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	159.0917	159.0917		187.0866		44.0495		W							13
2	60.0444	246.1237	228.1131	274.1186	256.1081	230.1288		S	1342.6460	1341.6508		***1374.6722***	1357.6457	1356.6616	12
3	70.0651	343.1765	325.1659	371.1714	353.1608	317.1608		P	1245.5932	1244.5980		***1287.6402***	1270.6136	1269.6296	11
4	102.0550	472.2191	454.2085	500.2140	482.2034	414.2136		E	1116.5506	1115.5554		1190.5874	1173.5609	1172.5769	10
5	86.0964	585.3031	567.2926	**613.2980**	595.2875	543.2562		L	1003.4666	1002.4713		***1061.5448***	1044.5183	1043.5343	9
6	44.0495	656.3402	638.3297	**684.3352**	666.3246			A	932.4295			***948.4608***	931.4342	930.4502	8
7	44.0495	727.3774	709.3668	755.3723	737.3617			A	861.3924			***877.4237***	860.3971	859.4131	7
8	44.0495	798.4145	780.4039	**826.4094**	808.3988			A	790.3552			***806.3865***	789.3600	788.3760	6
9	133.0430	958.4451	940.4345	**986.4400**	968.4295	869.4516		C	630.3246	629.3293		***735.3494***	718.3229	717.3389	5
10	102.0550	1087.4877	1069.4771	**1115.4826**	1097.4721	1029.4822		E	501.2820	500.2867		***575.3188***	558.2922	557.3082	4
11	86.0964	1200.5718	1182.5612	**1228.5667**	1210.5561	1172.5405	1186.5561	I	388.1979	401.2183	415.2340	446.2762	429.2496		3
12	159.0917	1386.6511	1368.6405	1414.6460	1396.6354			W	202.1186			***333.1921***	316.1656		2
13	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SP	157.0972	185.0921	SPE	286.1397	314.1347	SPEL	399.2238	427.2187
SPELA	470.2609	498.2558	SPELAA	541.2980	569.2930	SPELAAA	612.3352	640.3301
PE	199.1077	227.1026	PEL	312.1918	340.1867	PELA	383.2289	411.2238
PELAA	454.2660	482.2609	PELAAA	525.3031	553.2980	PELAAAC	685.3338	713.3287

EL	215.1390	243.1339	**ELA**	286.1761	314.1710	**ELAA**	357.2132	385.2082
ELAAA	428.2504	456.2453	**ELAAAC**	588.2810	616.2759	**LA**	157.1335	185.1285
LAA	228.1707	256.1656	**LAAA**	299.2078	327.2027	**LAAAC**	459.2384	487.2333
LAAACE	588.2810	616.2759	**AA**	115.0866	143.0815	**AAA**	186.1237	214.1186
AAAC	346.1544	374.1493	**AAACE**	475.1969	503.1919	**AAACEI**	588.2810	616.2759
AA	115.0866	143.0815	**AAC**	275.1172	303.1122	**AACE**	404.1598	432.1547
AACEI	517.2439	545.2388	**AC**	204.0801	232.0750	**ACE**	333.1227	361.1176
ACEI	446.2068	474.2017	**ACEIW**	632.2861	660.2810	**CE**	262.0856	290.0805
CEI	375.1697	403.1646	**CEIW**	561.2490	589.2439	**EI**	215.1390	243.1339
EIW	401.2183	429.2132	**IW**	272.1757	300.1707			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.7	1559.7442	0.0638	WSPEIAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK
73.7	1559.7442	0.0638	WSPELAAACEIWK

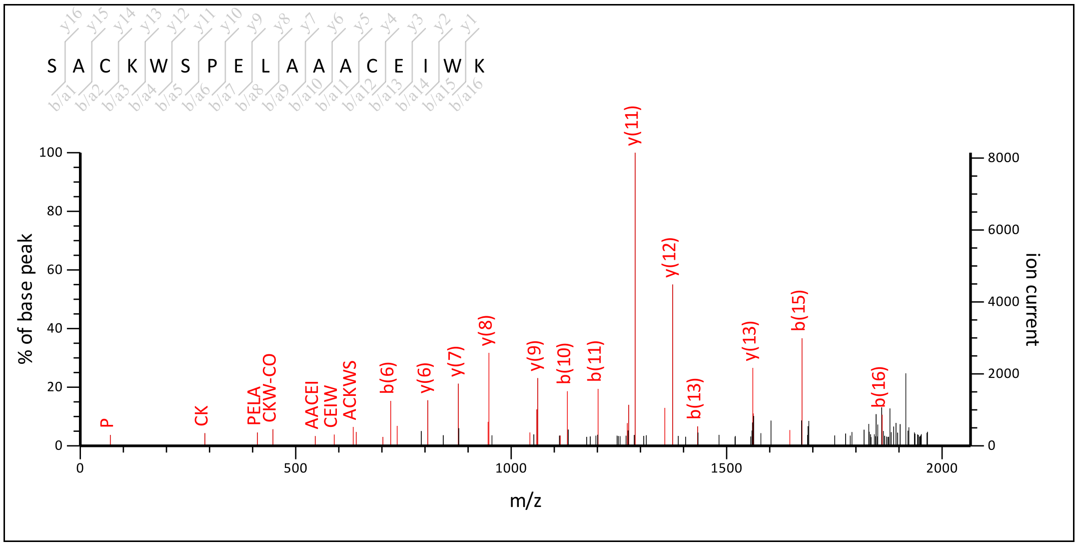
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **SACKWSPELAAACEIWK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 20: 2006.005524 from(2007.012800,1+) intensity(0.0000) index(10)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221262, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



0 to 2066.02

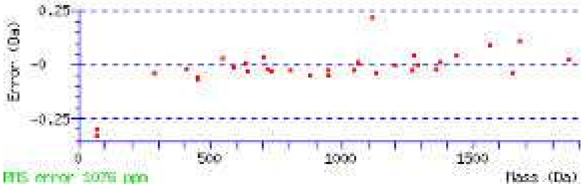
Label all possible matches ○ Label matches used for scoring ●

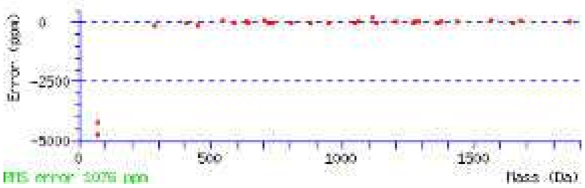
Monoisotopic mass of neutral peptide Mr(calc): 2005.9390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 84 **Expect:** 1.5e-05
Matches : 35/305 fragment ions using 47 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		**S**						
2	44.0495	131.0815		113.0709	159.0764		141.0659			**A**	1903.8830			1919.9143	1902.8877	19
3	133.0430	291.1122		273.1016	319.1071		301.0965	202.1186		**C**	1743.8523	1742.8571		1848.8771	1831.8506	18
4	101.1073	419.2071	402.1806	401.1966	***447.2020***	430.1755	429.1915	362.1493		**K**	1615.7573	1614.7621		1688.8465	1671.8199	16
5	159.0917	605.2864	588.2599	587.2759	***633.2813***	616.2548	615.2708			**W**	1429.6780			**1560.7515**	1543.7250	15
6	60.0444	692.3185	675.2919	674.3079	***720.3134***	703.2868	702.3028	676.3235		**S**	1342.6460	1341.6508		**1374.6722**	1357.6457	13
7	70.0651	789.3712	772.3447	771.3607	817.3661	800.3396	799.3556	763.3556		**P**	1245.5932	1244.5980		**1287.6402**	1270.6136	12
8	102.0550	918.4138	901.3873	900.4032	***946.4087***	929.3822	928.3982	860.4083		**E**	1116.5506	1115.5554		1190.5874	1173.5609	11
9	86.0964	1031.4979	1014.4713	1013.4873	***1059.4928***	1042.4662	1041.4822	989.4509		**L**	1003.4666	1002.4713		**1061.5448**	1044.5183	10
10	44.0495	1102.5350	1085.5084	1084.5244	***1130.5299***	1113.5034	1112.5193			**A**	932.4295			**948.4608**	931.4342	9
11	44.0495	1173.5721	1156.5456	1155.5615	***1201.5670***	1184.5405	1183.5565			**A**	861.3924			**877.4237**	860.3971	8
12	44.0495	1244.6092	1227.5827	1226.5987	***1272.6041***	1255.5776	1254.5936			**A**	790.3552			**806.3865**	789.3600	7
13	133.0430	1404.6399	1387.6133	1386.6293	***1432.6348***	1415.6082	1414.6242	1315.6463		**C**	630.3246	629.3293		**735.3494**	718.3229	7
14	102.0550	1533.6825	1516.6559	1515.6719	***1561.6774***	1544.6508	1543.6668	1475.6770		**E**	501.2820	500.2867		575.3188	558.2922	5
15	86.0964	1646.7665	1629.7400	1628.7560	***1674.7614***	1657.7349	1656.7509	1618.7352	1632.7509	**I**	388.1979	401.2183	415.2340	446.2762	429.2496	
16	159.0917	1832.8458	1815.8193	1814.8353	***1860.8408***	1843.8142	1842.8302			**W**	202.1186			333.1921	316.1656	
17	101.1073									**K**	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AC	204.0801	232.0750	**ACK**	332.1751	360.1700	**ACKW**	518.2544	546.2493
ACKWS	605.2864	633.2813	**CK**	261.1380	289.1329	**CKW**	447.2173	475.2122
CKWS	534.2493	562.2442	**CKWSP**	631.3021	659.2970	**KW**	287.1866	315.1816
KWS	374.2187	402.2136	**KWSP**	471.2714	499.2663	**KWSPE**	600.3140	628.3089

WS	246.1237	274.1186	**WSP**	343.1765	371.1714	**WSPE**	472.2191	500.2140
WSPEL	585.3031	613.2980	**WSPELA**	656.3402	684.3352	**SP**	157.0972	185.0921
SPE	286.1397	314.1347	**SPEL**	399.2238	427.2187	**SPELA**	470.2609	498.2558
SPELAA	541.2980	569.2930	**SPELAAA**	612.3352	640.3301	**PE**	199.1077	227.1026
PEL	312.1918	340.1867	**PELA**	383.2289	411.2238	**PELAA**	454.2660	482.2609
PELAAA	525.3031	553.2980	**PELAAAC**	685.3338	713.3287	**EL**	215.1390	243.1339
ELA	286.1761	314.1710	**ELAA**	357.2132	385.2082	**ELAAA**	428.2504	456.2453
ELAAAC	588.2810	616.2759	**LA**	157.1335	185.1285	**LAA**	228.1707	256.1656
LAAA	299.2078	327.2027	**LAAAC**	459.2384	487.2333	**LAAACE**	588.2810	616.2759
AA	115.0866	143.0815	**AAA**	186.1237	214.1186	**AAAC**	346.1544	374.1493
AAACE	475.1969	503.1919	**AAACEI**	588.2810	616.2759	**AA**	115.0866	143.0815
AAC	275.1172	303.1122	**AACE**	404.1598	432.1547	**AACEI**	517.2439	545.2388
AC	204.0801	232.0750	**ACE**	333.1227	361.1176	**ACEI**	446.2068	474.2017
ACEIW	632.2861	660.2810	**CE**	262.0856	290.0805	**CEI**	375.1697	403.1646
CEIW	561.2490	589.2439	**EI**	215.1390	243.1339	**EIW**	401.2183	429.2132
IW	272.1757	300.1707						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.1	2005.9390	0.0666	SACKWSPELAAACEIWK
62.1	2006.8866	-0.8811	SACKWSPELAAACEIWE
41.2	2006.8866	-0.8811	EACSWSPELAAACEIWK
36.8	2004.9615	1.0441	ETSKWSPELAAACEIWK
15.7	2006.0334	-0.0278	QKTGASFILPASAQHGHEK
14.8	2006.1452	-0.1397	TKIVFSSNALLSIPEFLK
14.4	2005.9487	0.0569	MAAAANSSASAAGAGGGSAAAAGLK
11.6	2005.9449	0.0607	SGVGCKMEIVPETEQGSAK
11.4	2004.9977	1.0079	NSSRSYHIIAASESQSLR
11.2	2005.9390	0.0665	MDLVGTSNVKAWMGYFR

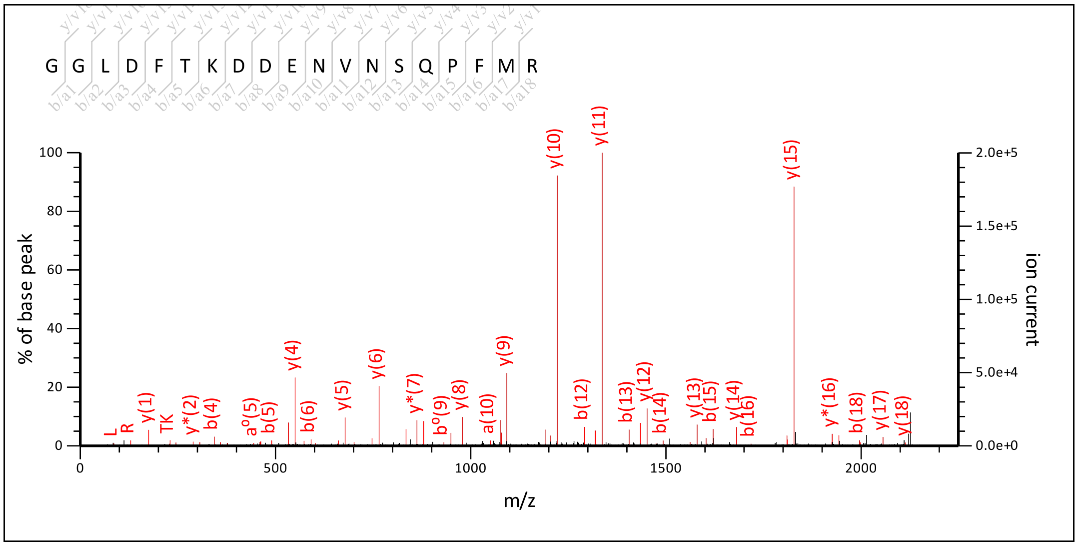
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **GGLDFTKDDENVNSQPFMR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 24: 2169.069124 from(2170.076400,1+) intensity(0.0000) index(12)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221248, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



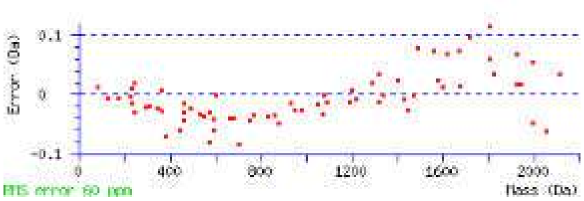
Label all possible matches ○ Label matches used for scoring ●

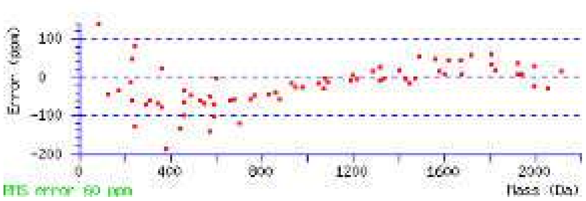
Monoisotopic mass of neutral peptide Mr(calc): 2168.9797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 138 **Expect:** 8e-11
Matches : 72/340 fragment ions using 84 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	30.0338	30.0338			58.0287			44.0495		G						
2	30.0338	87.0553			115.0502					G				***2112.9655***	2095.9389	209
3	86.0964	200.1394			**228.1343**			158.0924		L	1997.8658	1996.8705		***2055.9440***	2038.9175	203
4	88.0393	315.1663		297.1557	**343.1612**		325.1506	271.1765		D	1882.8388	1881.8436		***1942.8600***	1925.8334	192
5	120.0808	462.2347		444.2241	**490.2296**		472.2191			F	1735.7704			***1827.8330***	1810.8065	180
6	74.0600	563.2824		545.2718	**591.2773**		573.2667	547.2875	549.2667	T	1634.7227	1647.7431	1649.7224	***1680.7646***	1663.7381	166
7	101.1073	691.3774	674.3508	673.3668	719.3723	702.3457	701.3617	634.3195		K	1506.6278	1505.6325		***1579.7169***	1562.6904	156
8	88.0393	806.4043	789.3777	788.3937	**834.3992**	817.3727	816.3886	762.4145		D	1391.6008	1390.6056		***1451.6220***	1434.5954	143
9	88.0393	921.4312	904.4047	903.4207	**949.4262**	932.3996	931.4156	877.4414		D	1276.5739	1275.5786		***1336.5950***	1319.5685	131
10	102.0550	1050.4738	1033.4473	1032.4633	**1078.4687**	1061.4422	1060.4582	992.4684		E	1147.5313	1146.5361		***1221.5681***	1204.5415	120
11	87.0553	1164.5168	1147.4902	1146.5062	**1192.5117**	1175.4851	1174.5011	1121.5109		N	1033.4884	1032.4931		***1092.5255***	1075.4989	107
12	72.0808	1263.5852	1246.5586	1245.5746	**1291.5801**	1274.5535	1273.5695	1249.5695		V	934.4200	947.4404		***978.4826***	961.4560	96
13	87.0553	1377.6281	1360.6016	1359.6175	**1405.6230**	1388.5965	1387.6124	1334.6223		N	820.3770	819.3818		***879.4141***	862.3876	86
14	60.0444	1464.6601	1447.6336	1446.6496	**1492.6550**	1475.6285	1474.6445	1448.6652		S	733.3450	732.3498		***765.3712***	748.3447	74
15	101.0709	1592.7187	1575.6922	1574.7081	**1620.7136**	1603.6871	1602.7031	1535.6972		Q	605.2864	604.2912		***678.3392***	661.3126	
16	70.0651	1689.7715	1672.7449	1671.7609	**1717.7664**	1700.7398	1699.7558	1663.7558		P	508.2337	507.2384		***550.2806***	533.2541	
17	120.0808	1836.8399	1819.8133	1818.8293	1864.8348	1847.8082	1846.8242			F	361.1653			453.2279	436.2013	
18	104.0528	1967.8804	1950.8538	1949.8698	**1995.8753**	1978.8487	1977.8647	1907.8770		M	230.1248	229.1295		***306.1594***	289.1329	
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	GLD	258.1448	286.1397	GLDF	405.2132	433.2082
GLDFT	506.2609	534.2558	GLDFTK	634.3559	662.3508	LD	201.1234	229.1183

LDF	348.1918	376.1867	**LDFT**	449.2395	477.2344	**LDFTK**	577.3344	605.3293
LDFTKD	692.3614	720.3563	**DF**	235.1077	263.1026	**DFT**	336.1554	364.1503
DFTK	464.2504	492.2453	**DFTKD**	579.2773	607.2722	**DFTKDD**	694.3042	722.2992
FT	221.1285	249.1234	**FTK**	349.2234	377.2183	**FTKD**	464.2504	492.2453
FTKDD	579.2773	607.2722	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDD	432.2089	460.2038	**TKDDE**	561.2515	589.2464	**TKDDEN**	675.2944	703.2893
KD	216.1343	244.1292	**KDD**	331.1612	359.1561	**KDDE**	460.2038	488.1987
KDDEN	574.2467	602.2416	**KDDENV**	673.3151	701.3101	**DD**	203.0662	231.0612
DDE	332.1088	360.1038	**DDEN**	446.1518	474.1467	**DDENV**	545.2202	573.2151
DDENVN	659.2631	687.2580	**DE**	217.0819	245.0768	**DEN**	331.1248	359.1197
DENV	430.1932	458.1882	**DENVN**	544.2362	572.2311	**DENVNS**	631.2682	659.2631
EN	216.0979	244.0928	**ENV**	315.1663	343.1612	**ENVN**	429.2092	457.2041
ENVNS	516.2413	544.2362	**ENVNSQ**	644.2998	672.2947	**NV**	186.1237	214.1186
NVN	300.1666	328.1615	**NVNS**	387.1987	415.1936	**NVNSQ**	515.2572	543.2522
NVNSQP	612.3100	640.3049	**VN**	186.1237	214.1186	**VNS**	273.1557	301.1506
VNSQ	401.2143	429.2092	**VNSQP**	498.2671	526.2620	**VNSQPF**	645.3355	673.3304
NS	174.0873	202.0822	**NSQ**	302.1459	330.1408	**NSQP**	399.1987	427.1936
NSQPF	546.2671	574.2620	**NSQPFM**	677.3076	705.3025	**SQ**	188.1030	216.0979
SQP	285.1557	313.1506	**SQPF**	432.2241	460.2191	**SQPFM**	563.2646	591.2595
QP	198.1237	226.1186	**QPF**	345.1921	373.1870	**QPFM**	476.2326	504.2275
PF	217.1335	245.1285	**PFM**	348.1740	376.1689	**FM**	251.1213	279.1162





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
138.1	2168.9797	0.0894	GGIDFTKDDENVNSQPFMR
138.1	2168.9797	0.0894	GGIDFTKDDENVNSQPFMR
138.1	2169.0161	0.0531	GGLDFTKDDENVNSKPFMR
138.1	2168.9797	0.0894	GGLDFTKDDENVNSQPFMR
138.1	2168.9797	0.0894	GGLDFTKDDENVNSQPFMR
138.1	2168.9797	0.0894	GGLDFTKDDENVNSQPFMR
138.1	2168.9797	0.0894	GGLDFTKDDENVNSQPFMR
138.1	2168.9797	0.0894	GGLDFTKDDENVNSQPFMR
138.1	2168.9797	0.0894	GGLDFTKDDENVNSQPFMR
138.1	2168.9797	0.0894	GGLDFTKDDENVNSQPFMR

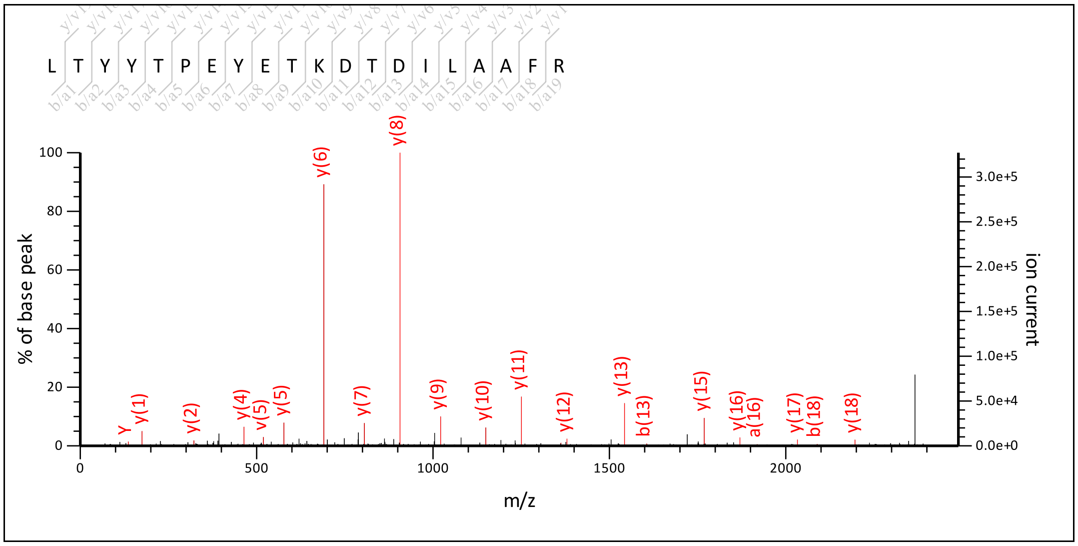
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTYYTPEYETKDTDILAAFR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 28: 2409.267424 from(2410.274700,1+) intensity(0.0000) index(14)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221247, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



0 to 2489.35

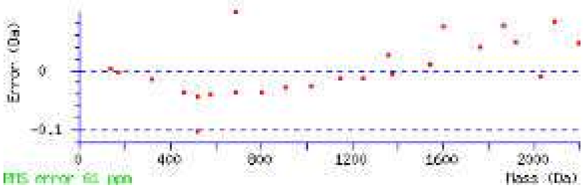
Label all possible matches ○ Label matches used for scoring ●

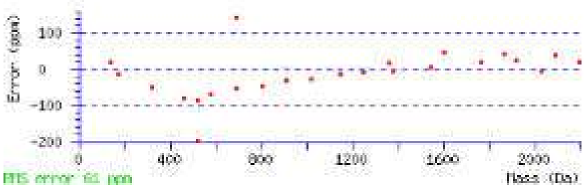
Monoisotopic mass of neutral peptide Mr(calc): 2409.1740
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 162 **Expect:** 2.5e-13
Matches : 26/356 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		L					
2	74.0600	187.1441		169.1335	215.1390		197.1285	171.1492	173.1285	T	2251.0554	2264.0758	2266.0550	2297.0972	2280.0707
3	136.0757	350.2074		332.1969	378.2023		360.1918			Y	2087.9920			***2196.0495***	2179.0230
4	136.0757	513.2708		495.2602	541.2657		523.2551			Y	1924.9287			***2032.9862***	2015.9597
5	74.0600	614.3184		596.3079	642.3134		624.3028	598.3235	600.3028	T	1823.8810	1836.9014	1838.8807	***1869.9229***	1852.8963
6	70.0651	711.3712		693.3606	739.3661		721.3556	685.3556		P	1726.8283	1725.8330		***1768.8752***	1751.8487
7	102.0550	840.4138		822.4032	868.4087		850.3981	782.4083		E	1597.7857	1596.7904		1671.8224	1654.7959
8	136.0757	1003.4771		985.4666	1031.4720		1013.4615			Y	1434.7223			***1542.7799***	1525.7533
9	102.0550	1132.5197		1114.5092	1160.5146		1142.5041	1074.5142		E	1305.6797	1304.6845		***1379.7165***	1362.6900
10	74.0600	1233.5674		1215.5568	1261.5623		1243.5517	1217.5725	1219.5517	T	1204.6321	1217.6525	1219.6317	***1250.6739***	1233.6474
11	101.1073	1361.6624	1344.6358	1343.6518	1389.6573	1372.6307	1371.6467	1304.6045		K	1076.5371	1075.5419		***1149.6262***	1132.5997
12	88.0393	1476.6893	1459.6628	1458.6787	1504.6842	1487.6577	1486.6737	1432.6995		D	961.5102	960.5149		***1021.5313***	1004.5047
13	74.0600	1577.7370	1560.7104	1559.7264	**1605.7319**	1588.7054	1587.7213	1561.7421	1563.7213	T	860.4625	873.4829	875.4621	***906.5043***	889.4778
14	88.0393	1692.7639	1675.7374	1674.7534	1720.7588	1703.7323	1702.7483	1648.7741		D	745.4355	744.4403		***805.4567***	788.4301
15	86.0964	1805.8480	1788.8214	1787.8374	1833.8429	1816.8164	1815.8323	1777.8167	1791.8323	I	632.3515	645.3719	659.3875	***690.4297***	673.4032
16	86.0964	1918.9321	1901.9055	1900.9215	1946.9270	1929.9004	1928.9164	1876.8851		L	519.2674	518.2722		***577.3457***	560.3191
17	44.0495	1989.9692	1972.9426	1971.9586	2017.9641	2000.9375	1999.9535			A	448.2303			***464.2616***	447.2350
18	44.0495	2061.0063	2043.9797	2042.9957	**2089.0012**	2071.9746	2070.9906			A	377.1932			393.2245	376.1979
19	120.0808	2208.0747	2191.0481	2190.0641	2236.0696	2219.0431	2218.0590			F	230.1248			***322.1874***	305.1608
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TY	237.1234	265.1183	TYY	400.1867	428.1816	TYYT	501.2344	529.2293

TYYTP	598.2871	626.2821	**YY**	299.1390	327.1339	**YYT**	400.1867	428.1816
YYTP	497.2395	525.2344	**YYTPE**	626.2821	654.2770	**YT**	237.1234	265.1183
YTP	334.1761	362.1710	**YTPE**	463.2187	491.2136	**YTPEY**	626.2821	654.2770
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPEY**	463.2187	491.2136
TPEYE	592.2613	620.2562	**TPEYET**	693.3090	721.3039	**PE**	199.1077	227.1026
PEY	362.1710	390.1660	**PEYE**	491.2136	519.2086	**PEYET**	592.2613	620.2562
EY	265.1183	293.1132	**EYE**	394.1609	422.1558	**EYET**	495.2086	523.2035
EYETK	623.3035	651.2984	**YE**	265.1183	293.1132	**YET**	366.1660	394.1609
YETK	494.2609	522.2558	**YETKD**	609.2879	637.2828	**ET**	203.1026	231.0975
ETK	331.1976	359.1925	**ETKD**	446.2245	474.2195	**ETKDT**	547.2722	575.2671
ETKDTD	662.2992	690.2941	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDT	418.2296	446.2245	**TKDTD**	533.2566	561.2515	**TKDTDI**	646.3406	674.3355
KD	216.1343	244.1292	**KDT**	317.1819	345.1769	**KDTD**	432.2089	460.2038
KDTDI	545.2930	573.2879	**KDTDIL**	658.3770	686.3719	**DT**	189.0870	217.0819
DTD	304.1139	332.1088	**DTDI**	417.1980	445.1929	**DTDIL**	530.2821	558.2770
DTDILA	601.3192	629.3141	**DTDILAA**	672.3563	700.3512	**TD**	189.0870	217.0819
TDI	302.1710	330.1660	**TDIL**	415.2551	443.2500	**TDILA**	486.2922	514.2871
TDILAA	557.3293	585.3243	**DI**	201.1234	229.1183	**DIL**	314.2074	342.2023
DILA	385.2445	413.2395	**DILAA**	456.2817	484.2766	**DILAAF**	603.3501	631.3450
IL	199.1805	227.1754	**ILA**	270.2176	298.2125	**ILAA**	341.2547	369.2496
ILAAF	488.3231	516.3180	**LA**	157.1335	185.1285	**LAA**	228.1707	256.1656
LAAF	375.2391	403.2340	**AA**	115.0866	143.0815	**AAF**	262.1550	290.1499
AF	191.1179	219.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
161.7	2408.6820	0.5854	ITYYTPEYETKDTBILAAFR
161.7	2409.1740	0.0934	ITYYTPEYETKDTDILAAFR
161.7	2409.1740	0.0934	ITYYTPEYETKDTDILAAFR
161.7	2408.6820	0.5854	LTYYTPEYETKDTBILAAFR
161.7	2409.1740	0.0934	LTYYTPEYETKDTDIIAAFR
161.7	2409.1740	0.0934	LTYYTPEYETKDTDILAAFR
161.7	2409.1740	0.0934	LTYYTPEYETKDTDILAAFR
161.7	2409.1740	0.0934	LTYYTPEYETKDTDILAAFR
161.7	2409.1740	0.0934	LTYYTPEYETKDTDILAAFR
161.7	2409.1740	0.0934	LTYYTPEYETKDTDILAAFR

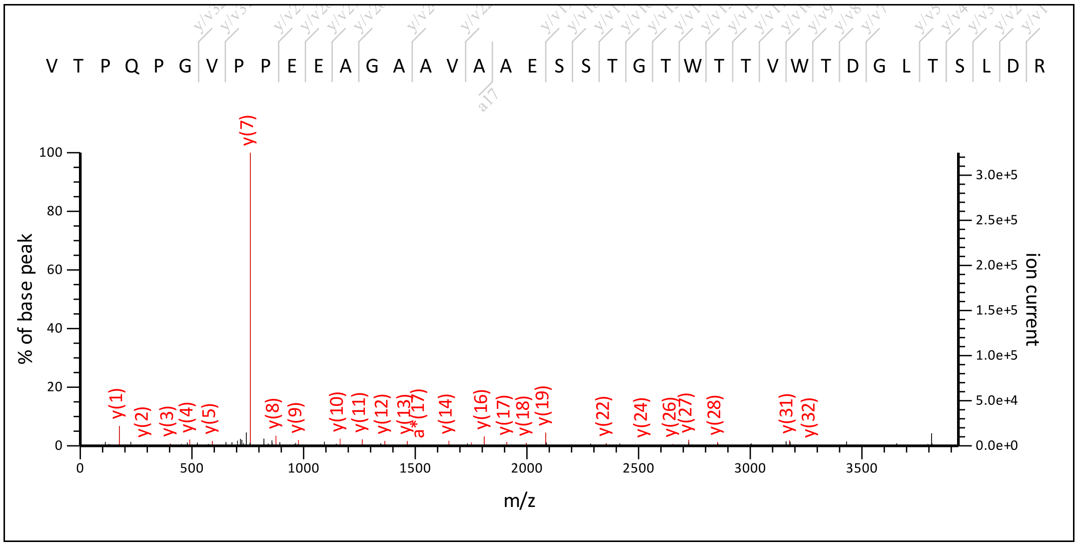
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 96

MS/MS Fragmentation of **VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 36: 3854.980224 from(3855.987500,1+) intensity(0.0000) index(17)
Title: Label: E11, Spot_Id: 216641, Peak_List_Id: 221253, MSMS Job_Run_Id: 21347, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\RAJESH\12-1-13 raj\ppw_E11_135997701000.txt



0 to 3931.96

Label all possible matches ○ Label matches used for scoring ●

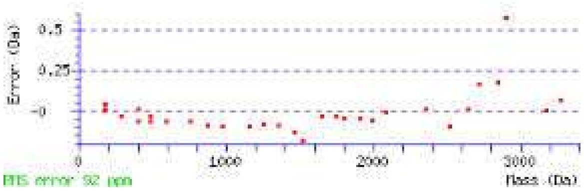
Monoisotopic mass of neutral peptide Mr(calc): 3853.8647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 208 **Expect:** 3.6e-18
Matches : 31/837 fragment ions using 38 most intense peaks (help)

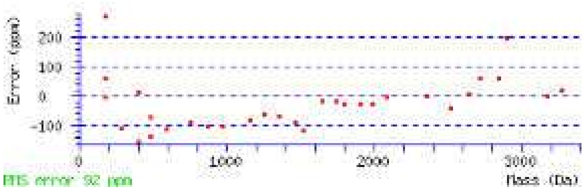
#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	74.0600	173.1285		155.1179	201.1234		183.1128	157.1335	159.1128	T	3709.7616	3722.7820	3724.7613	3755.8035	3738.7770
3	70.0651	270.1812		252.1707	298.1761		280.1656	244.1656		P	3612.7089	3611.7136		3654.7558	3637.7293
4	101.0709	398.2398	381.2132	380.2292	426.2347	409.2082	408.2241	341.2183		Q	3484.6503	3483.6551		3557.7031	3540.6765
5	70.0651	495.2926	478.2660	477.2820	523.2875	506.2609	505.2769	469.2769		P	3387.5975	3386.6023		3429.6445	3412.6179
6	30.0338	552.3140	535.2875	534.3035	580.3089	563.2824	562.2984			G				3332.5917	3315.5652
7	72.0808	651.3824	634.3559	633.3719	679.3774	662.3508	661.3668	637.3668		V	3231.5077	3244.5281		***3275.5703***	3258.5437
8	70.0651	748.4352	731.4087	730.4246	776.4301	759.4036	758.4196	722.4196		P	3134.4549	3133.4596		***3176.5018***	3159.4753
9	70.0651	845.4880	828.4614	827.4774	873.4829	856.4563	855.4723	819.4723		P	3037.4021	3036.4069		3079.4491	3062.4225
10	102.0550	974.5306	957.5040	956.5200	1002.5255	985.4989	984.5149	916.5251		E	2908.3595	2907.3643		2982.3963	2965.3698
11	102.0550	1103.5732	1086.5466	1085.5626	1131.5681	1114.5415	1113.5575	1045.5677		E	2779.3169	2778.3217		***2853.3537***	2836.3272
12	44.0495	1174.6103	1157.5837	1156.5997	1202.6052	1185.5786	1184.5946			A	2708.2798			***2724.3111***	2707.2846
13	30.0338	1231.6317	1214.6052	1213.6212	1259.6266	1242.6001	1241.6161			G				***2653.2740***	2636.2475
14	44.0495	1302.6688	1285.6423	1284.6583	1330.6638	1313.6372	1312.6532			A	2580.2213			2596.2526	2579.2260
15	44.0495	1373.7060	1356.6794	1355.6954	1401.7009	1384.6743	1383.6903			A	2509.1841			***2525.2154***	2508.1889
16	72.0808	1472.7744	1455.7478	1454.7638	1500.7693	1483.7427	1482.7587	1458.7587		V	2410.1157	2423.1361		2454.1783	2437.1518
17	44.0495	1543.8115	1526.7849	1525.8009	1571.8064	1554.7799	1553.7958			A	2339.0786			***2355.1099***	2338.0834
18	44.0495	1614.8486	1597.8221	1596.8380	1642.8435	1625.8170	1624.8329			A	2268.0415			2284.0728	2267.0462
19	102.0550	1743.8912	1726.8646	1725.8806	1771.8861	1754.8596	1753.8755	1685.8857		E	2138.9989	2138.0037		2213.0357	2196.0091
20	60.0444	1830.9232	1813.8967	1812.9127	1858.9181	1841.8916	1840.9076	1814.9283		S	2051.9669	2050.9716		***2083.9931***	2066.9665
21	60.0444	1917.9552	1900.9287	1899.9447	1945.9502	1928.9236	1927.9396	1901.9603		S	1964.9348	1963.9396		***1996.9611***	1979.9345
22	74.0600	2019.0029	2001.9764	2000.9924	2046.9978	2029.9713	2028.9873	2003.0080	2004.9873	T	1863.8872	1876.9076	1878.8868	***1909.9290***	1892.9025

23	30.0338	2076.0244	2058.9978	2058.0138	2104.0193	2086.9928	2086.0087			**G**				***1808.8814***	1791.8548
24	74.0600	2177.0721	2160.0455	2159.0615	2205.0670	2188.0404	2187.0564	2161.0772	2163.0564	**T**	1705.8180	1718.8384	1720.8177	***1751.8599***	1734.8333
25	159.0917	2363.1514	2346.1248	2345.1408	2391.1463	2374.1197	2373.1357			**W**	1519.7387			***1650.8122***	1633.7857
26	74.0600	2464.1991	2447.1725	2446.1885	2492.1940	2475.1674	2474.1834	2448.2041	2450.1834	**T**	1418.6910	1431.7114	1433.6907	***1464.7329***	1447.7064
27	74.0600	2565.2467	2548.2202	2547.2362	2593.2417	2576.2151	2575.2311	2549.2518	2551.2311	**T**	1317.6434	1330.6638	1332.6430	***1363.6852***	1346.6587
28	72.0808	2664.3152	2647.2886	2646.3046	2692.3101	2675.2835	2674.2995	2650.2995		**V**	1218.5749	1231.5953		***1262.6375***	1245.6110
29	159.0917	2850.3945	2833.3679	2832.3839	2878.3894	2861.3628	2860.3788			**W**	1032.4956			***1163.5691***	1146.5426
30	74.0600	2951.4421	2934.4156	2933.4316	2979.4371	2962.4105	2961.4265	2935.4472	2937.4265	**T**	931.4480	944.4684	946.4476	***977.4898***	960.4633
31	88.0393	3066.4691	3049.4425	3048.4585	3094.4640	3077.4375	3076.4534	3022.4793		**D**	816.4210	815.4258		***876.4421***	859.4156
32	30.0338	3123.4906	3106.4640	3105.4800	3151.4855	3134.4589	3133.4749			**G**				***761.4152***	744.3886
33	86.0964	3236.5746	3219.5481	3218.5641	3264.5695	3247.5430	3246.5590	3194.5277		**L**	646.3155	645.3202		704.3937	687.3672
34	74.0600	3337.6223	3320.5957	3319.6117	3365.6172	3348.5907	3347.6066	3321.6274	3323.6066	**T**	545.2678	558.2882	560.2675	***591.3097***	574.2831
35	60.0444	3424.6543	3407.6278	3406.6438	3452.6492	3435.6227	3434.6387	3408.6594		**S**	458.2358	457.2405		***490.2620***	473.2354
36	86.0964	3537.7384	3520.7118	3519.7278	3565.7333	3548.7068	3547.7227	3495.6914		**L**	345.1517	344.1565		***403.2300***	386.2034
37	88.0393	3652.7653	3635.7388	3634.7548	3680.7602	3663.7337	3662.7497	3608.7755		**D**	230.1248	229.1295		***290.1459***	273.1193
38	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TP	171.1128	199.1077	**TPQ**	299.1714	327.1663	**TPQP**	396.2241	424.2191
TPQPG	453.2456	481.2405	**TPQPGV**	552.3140	580.3089	**TPQPGVP**	649.3668	677.3617
PQ	198.1237	226.1186	**PQP**	295.1765	323.1714	**PQPG**	352.1979	380.1928
PQPGV	451.2663	479.2613	**PQPGVP**	548.3191	576.3140	**PQPGVPP**	645.3719	673.3668
QP	198.1237	226.1186	**QPG**	255.1452	283.1401	**QPGV**	354.2136	382.2085
QPGVP	451.2663	479.2613	**QPGVPP**	548.3191	576.3140	**QPGVPPE**	677.3617	705.3566
PG	127.0866	155.0815	**PGV**	226.1550	254.1499	**PGVP**	323.2078	351.2027
PGVPP	420.2605	448.2554	**PGVPPE**	549.3031	577.2980	**PGVPPEE**	678.3457	706.3406
GV	129.1022	157.0972	**GVP**	226.1550	254.1499	**GVPP**	323.2078	351.2027
GVPPE	452.2504	480.2453	**GVPPEE**	581.2930	609.2879	**GVPPEEA**	652.3301	680.3250
VP	169.1335	197.1285	**VPP**	266.1863	294.1812	**VPPE**	395.2289	423.2238
VPPEE	524.2715	552.2664	**VPPEEA**	595.3086	623.3035	**VPPEEAG**	652.3301	680.3250
PP	167.1179	195.1128	**PPE**	296.1605	324.1554	**PPEE**	425.2031	453.1980
PPEEA	496.2402	524.2351	**PPEEAG**	553.2617	581.2566	**PPEEAGA**	624.2988	652.2937
PPEEAGAA	695.3359	723.3308	**PE**	199.1077	227.1026	**PEE**	328.1503	356.1452
PEEA	399.1874	427.1823	**PEEAG**	456.2089	484.2038	**PEEAGA**	527.2460	555.2409
PEEAGAA	598.2831	626.2780	**PEEAGAAV**	697.3515	725.3464	**EE**	231.0975	259.0925
EEA	302.1347	330.1296	**EEAG**	359.1561	387.1510	**EEAGA**	430.1932	458.1882
EEAGAA	501.2304	529.2253	**EEAGAAV**	600.2988	628.2937	**EEAGAAVA**	671.3359	699.3308
EA	173.0921	201.0870	**EAG**	230.1135	258.1084	**EAGA**	301.1506	329.1456
EAGAA	372.1878	400.1827	**EAGAAV**	471.2562	499.2511	**EAGAAVA**	542.2933	570.2882
EAGAAVAA	613.3304	641.3253	**AG**	101.0709	129.0659	**AGA**	172.1081	200.1030
AGAA	243.1452	271.1401	**AGAAV**	342.2136	370.2085	**AGAAVA**	413.2507	441.2456
AGAAVAA	484.2878	512.2827	**AGAAVAAE**	613.3304	641.3253	**GA**	101.0709	129.0659
GAA	172.1081	200.1030	**GAAV**	271.1765	299.1714	**GAAVA**	342.2136	370.2085
GAAVAA	413.2507	441.2456	**GAAVAAE**	542.2933	570.2882	**GAAVAAES**	629.3253	657.3202
AA	115.0866	143.0815	**AAV**	214.1550	242.1499	**AAVA**	285.1921	313.1870
AAVAA	356.2292	384.2241	**AAVAAE**	485.2718	513.2667	**AAVAAES**	572.3039	600.2988
AAVAAESS	659.3359	687.3308	**AV**	143.1179	171.1128	**AVA**	214.1550	242.1499
AVAA	285.1921	313.1870	**AVAAE**	414.2347	442.2296	**AVAAES**	501.2667	529.2617
AVAAESS	588.2988	616.2937	**AVAAESST**	689.3464	717.3414	**VA**	143.1179	171.1128
VAA	214.1550	242.1499	**VAAE**	343.1976	371.1925	**VAAES**	430.2296	458.2245
VAAESS	517.2617	545.2566	**VAAESST**	618.3093	646.3042	**VAAESSTG**	675.3308	703.3257
AA	115.0866	143.0815	**AAE**	244.1292	272.1241	**AAES**	331.1612	359.1561
AAESS	418.1932	446.1882	**AAESST**	519.2409	547.2358	**AAESSTG**	576.2624	604.2573
AAESSTGT	677.3101	705.3050	**AE**	173.0921	201.0870	**AES**	260.1241	288.1190
AESS	347.1561	375.1510	**AESST**	448.2038	476.1987	**AESSTG**	505.2253	533.2202
AESSTGT	606.2729	634.2679	**ES**	189.0870	217.0819	**ESS**	276.1190	304.1139

ESST	377.1667	405.1616	**ESSTG**	434.1882	462.1831	**ESSTGT**	535.2358	563.2307
SS	147.0764	175.0713	**SST**	248.1241	276.1190	**SSTG**	305.1456	333.1405
SSTGT	406.1932	434.1882	**SSTGTW**	592.2726	620.2675	**SSTGTWT**	693.3202	721.3151
ST	161.0921	189.0870	**STG**	218.1135	246.1084	**STGT**	319.1612	347.1561
STGTW	505.2405	533.2354	**STGTWT**	606.2882	634.2831	**TG**	131.0815	159.0764
TGT	232.1292	260.1241	**TGTW**	418.2085	446.2034	**TGTWT**	519.2562	547.2511
TGTWTT	620.3039	648.2988	**GT**	131.0815	159.0764	**GTW**	317.1608	345.1557
GTWT	418.2085	446.2034	**GTWTT**	519.2562	547.2511	**GTWTTV**	618.3246	646.3195
TW	260.1394	288.1343	**TWT**	361.1870	389.1819	**TWTT**	462.2347	490.2296
TWTTV	561.3031	589.2980	**WT**	260.1394	288.1343	**WTT**	361.1870	389.1819
WTTV	460.2554	488.2504	**WTTVW**	646.3348	674.3297	**TT**	175.1077	203.1026
TTV	274.1761	302.1710	**TTVW**	460.2554	488.2504	**TTVWT**	561.3031	589.2980
TTVWTD	676.3301	704.3250	**TV**	173.1285	201.1234	**TVW**	359.2078	387.2027
TVWT	460.2554	488.2504	**TVWTD**	575.2824	603.2773	**TVWTDG**	632.3039	660.2988
VW	258.1601	286.1550	**VWT**	359.2078	387.2027	**VWTD**	474.2347	502.2296
VWTDG	531.2562	559.2511	**VWTDGL**	644.3402	672.3352	**WT**	260.1394	288.1343
WTD	375.1663	403.1612	**WTDG**	432.1878	460.1827	**WTDGL**	545.2718	573.2667
WTDGLT	646.3195	674.3144	**TD**	189.0870	217.0819	**TDG**	246.1084	274.1034
TDGL	359.1925	387.1874	**TDGLT**	460.2402	488.2351	**TDGLTS**	547.2722	575.2671
TDGLTSL	660.3563	688.3512	**DG**	145.0608	173.0557	**DGL**	258.1448	286.1397
DGLT	359.1925	387.1874	**DGLTS**	446.2245	474.2195	**DGLTSL**	559.3086	587.3035
DGLTSLD	674.3355	702.3305	**GL**	143.1179	171.1128	**GLT**	244.1656	272.1605
GLTS	331.1976	359.1925	**GLTSL**	444.2817	472.2766	**GLTSLD**	559.3086	587.3035
LT	187.1441	215.1390	**LTS**	274.1761	302.1710	**LTSL**	387.2602	415.2551
LTSLD	502.2871	530.2821	**TS**	161.0921	189.0870	**TSL**	274.1761	302.1710
TSLD	389.2031	417.1980	**SL**	173.1285	201.1234	**SLD**	288.1554	316.1503
LD	201.1234	229.1183						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
229.8	3854.8487	0.1315	VTPEPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
229.8	3854.8487	0.1315	VTPEPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
216.9	3854.9075	0.0727	VTPQPGVPAREAGAAVAAESSTGTWTTVWTDGLTSLDR
208.1	3854.8309	0.1493	MTPPPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
208.1	3855.8439	-0.8637	TTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
208.1	3853.9011	1.0792	VTPKPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
208.1	3853.8647	1.1155	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGITSLDR
208.1	3853.8647	1.1155	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGITSLDR
208.1	3853.8647	1.1155	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSIDR
208.1	3853.8647	1.1155	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR

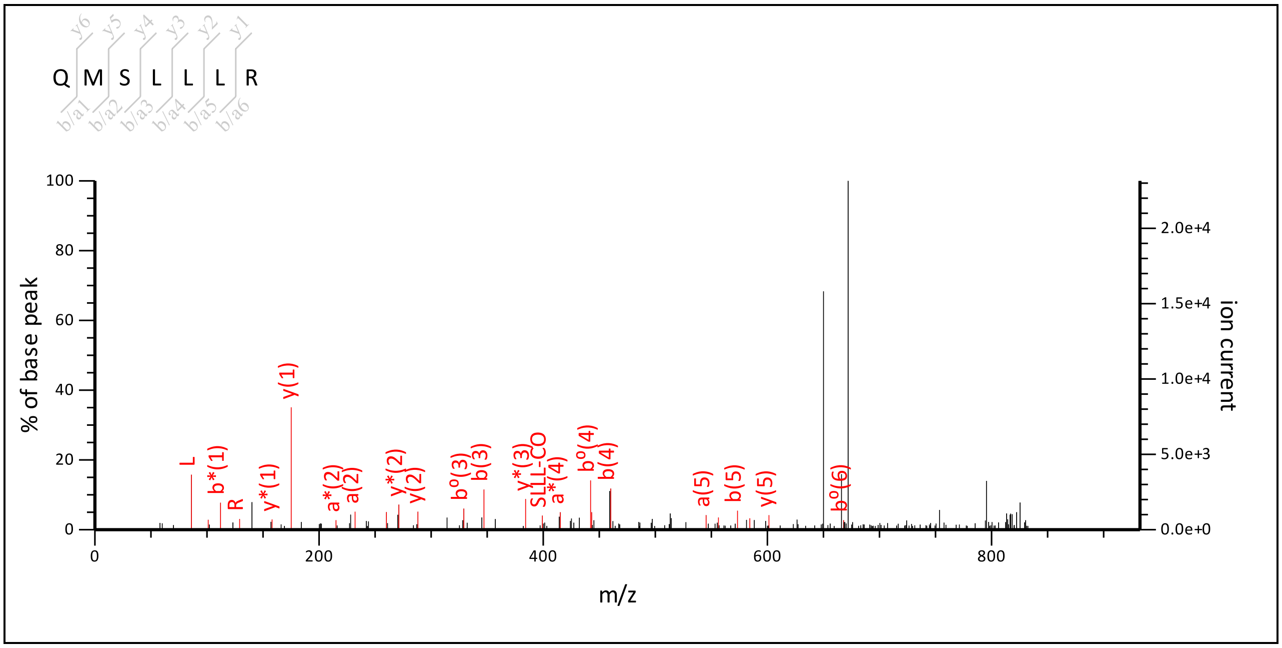
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **QMSLLLR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 5: 859.545454 from(860.552730,1+) intensity(0.0000) index(0)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221405, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



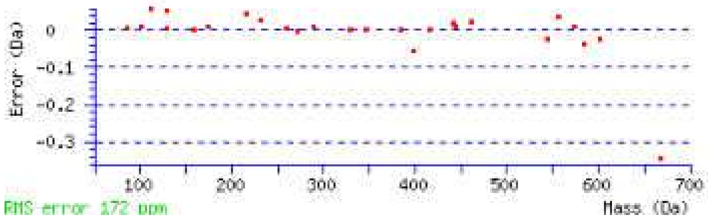
0 to 932.41

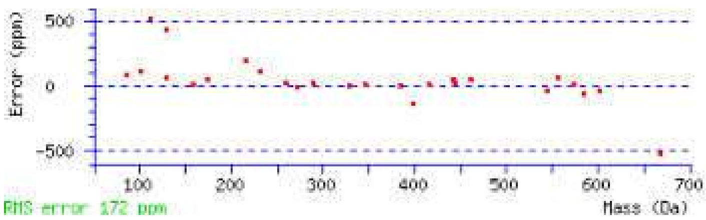
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 859.4949
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 12
Matches : 29/91 fragment ions using 40 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	101.0709	**101.0709**	84.0444		***129.0659***	112.0393		44.0495	**Q**						7
2	104.0528	**232.1114**	215.0849		***260.1063***	243.0798		172.1081	**M**	656.4090	655.4137	732.4437	715.4171	714.4331	6
3	60.0444	319.1435	302.1169	301.1329	***347.1384***	330.1118	329.1278	303.1485	**S**	569.3770	568.3817	**601.4032**	584.3766	583.3926	5
4	86.0964	432.2275	415.2010	414.2170	***460.2224***	443.1959	442.2119	390.1806	**L**	456.2929	455.2976	514.3711	497.3446		4
5	86.0964	**545.3116**	528.2850	527.3010	***573.3065***	556.2799	555.2959	503.2646	**L**	343.2088	342.2136	401.2871	384.2605		3
6	86.0964	658.3956	641.3691	640.3851	686.3906	669.3640	668.3800	616.3487	**L**	230.1248	229.1295	**288.2030**	271.1765		2
7	129.1135								**R**	74.0237	73.0284	**175.1190**	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
MS	191.0849	219.0798	**MSL**	304.1689	332.1639	**MSLL**	417.2530	445.2479
MSLLL	530.3371	558.3320	**SL**	173.1285	201.1234	**SLL**	286.2125	314.2074
SLLL	399.2966	427.2915	**LL**	199.1805	227.1754	**LLL**	312.2646	340.2595
LL	199.1805	227.1754						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.8	859.4586	0.0869	MGVLIDGR
30.2	859.4222	0.1233	GMPDLATR
28.4	859.4949	0.0505	QMSLILR
28.4	859.4949	0.0505	QMSLLLR
24.7	858.4923	1.0532	ASKLLDGR
22.6	858.4811	1.0644	LEGGLAATK
22.5	859.4586	0.0869	GIVMIDGR
22.3	859.4586	0.0869	AVVMLDGR
22.3	860.4352	-0.8897	GDKTIDGR
22.3	859.4399	0.1055	IGETLDGR

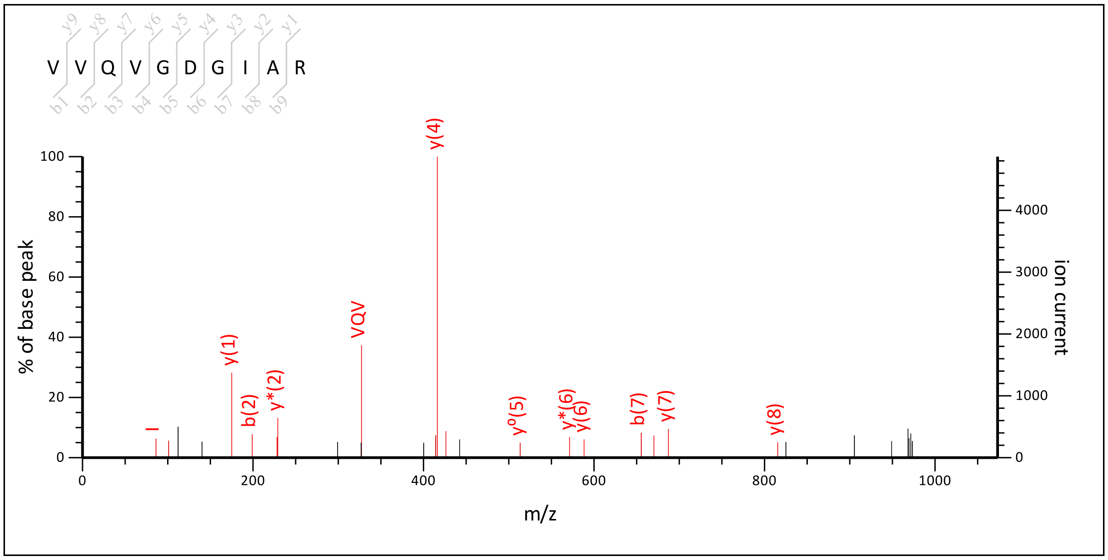
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **VVQVGDGIAR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 14: 1012.631024 from(1013.638300,1+) intensity(0.0000) index(3)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221421, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



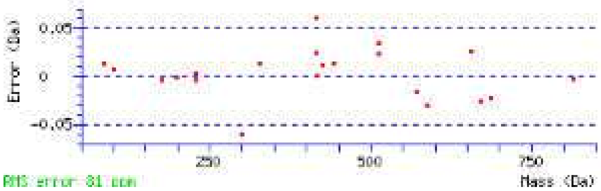
0 to 1073.36

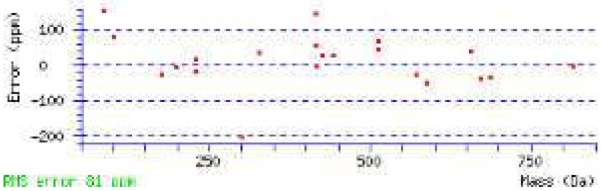
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1012.5666
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.54
Matches : 24/148 fragment ions using 26 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	72.0808			100.0757			44.0495		V							10
2	72.0808	171.1492			***199.1441***			157.1335		V	870.4428	883.4632		914.5054	897.4789	896.4948	9
3	101.0709	299.2078	282.1812		***327.2027***	310.1761		242.1863		Q	742.3842	741.3890		***815.4370***	798.4104	797.4264	8
4	72.0808	398.2762	381.2496		***426.2711***	409.2445		384.2605		V	643.3158	656.3362		***687.3784***	670.3519	669.3679	7
5	30.0338	455.2976	438.2711		483.2926	466.2660				G				***588.3100***	571.2835	570.2994	6
6	88.0393	570.3246	553.2980	552.3140	598.3195	581.2930	580.3089	526.3348		D	471.2674	470.2722		531.2885	514.2620	513.2780	5
7	30.0338	627.3461	610.3195	609.3355	***655.3410***	638.3144	637.3304			G				***416.2616***	399.2350		4
8	86.0964	740.4301	723.4036	722.4196	768.4250	751.3985	750.4145	712.3988	726.4145	I	301.1619	314.1823	328.1979	359.2401	342.2136		3
9	44.0495	811.4672	794.4407	793.4567	839.4621	822.4356	821.4516			A	230.1248			246.1561	229.1295		2
10	129.1135									R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VQ	200.1394	228.1343	VQV	299.2078	327.2027	VQVG	356.2292	384.2241
VQVGD	471.2562	499.2511	VQVGDG	528.2776	556.2726	VQVGDGI	641.3617	669.3566
QV	200.1394	228.1343	QVG	257.1608	285.1557	QVGD	372.1878	400.1827
QVGDG	429.2092	457.2041	QVGDGI	542.2933	570.2882	QVGDGIA	613.3304	641.3253
VG	129.1022	157.0972	VGD	244.1292	272.1241	VGDG	301.1506	329.1456
VGDGI	414.2347	442.2296	VGDGIA	485.2718	513.2667	GD	145.0608	173.0557
GDG	202.0822	230.0771	GDGI	315.1663	343.1612	GDGIA	386.2034	414.1983
DG	145.0608	173.0557	DGI	258.1448	286.1397	DGIA	329.1819	357.1769
GI	143.1179	171.1128	GIA	214.1550	242.1499	IA	157.1335	185.1285





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.3	1012.5666	0.0645	VVQVGDGIAR
32.8	1012.5666	0.0645	VQVVTAGSPR
25.6	1012.6393	-0.0083	LGGVVTKIAR
24.6	1012.5777	0.0533	RAVDAAAAIR
22.6	1012.5665	0.0645	NIVVSAPSAR
22.4	1012.5665	0.0645	LAAASVAAPSR
21.6	1013.5730	-0.9420	AAGQVRGLSR
21.4	1013.5869	-0.9559	LLVSGEVAAR
21.4	1013.6022	-0.9712	ILGAFPLQR
21.2	1012.5778	0.0532	VVQRDAVAR

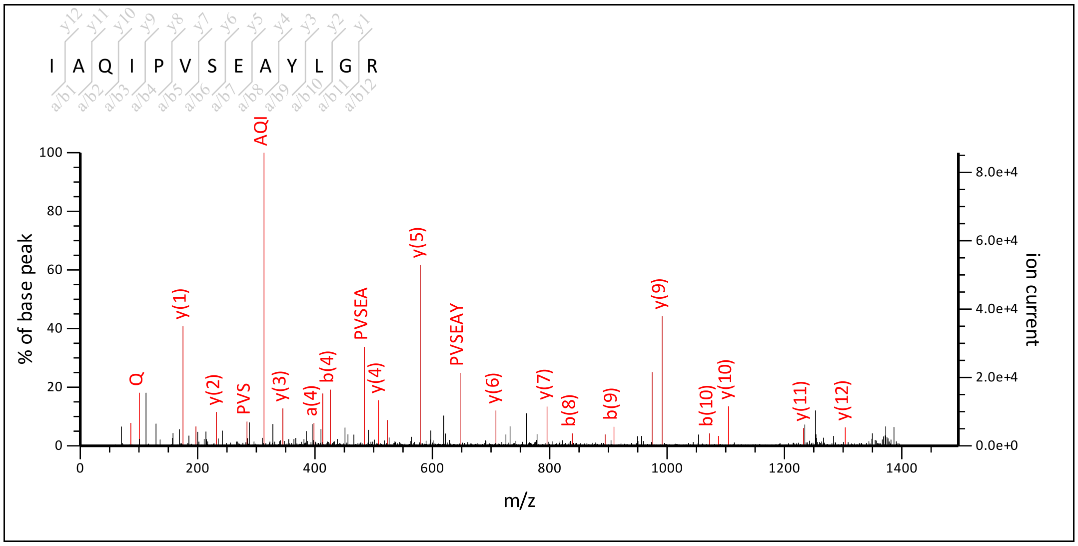
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **IAQIPVSEAYLGR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 40: 1415.861624 from(1416.868900,1+) intensity(0.0000) index(9)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221389, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 1496.46

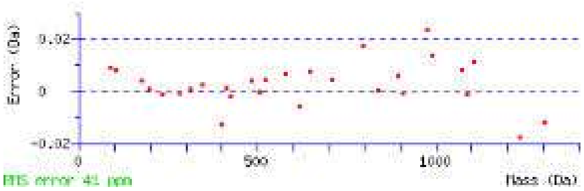
Label all possible matches ○ Label matches used for scoring ●

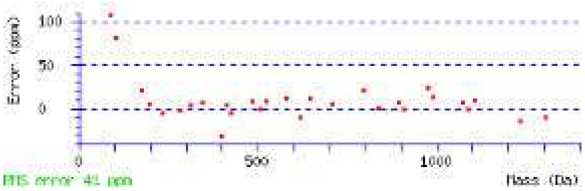
Monoisotopic mass of neutral peptide Mr(calc): 1415.7772
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 106 **Expect:** 1.4e-07
Matches : 33/212 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		I					
2	44.0495	157.1335			185.1285					A	1287.6692			***1303.7005***	1286.6739
3	101.0709	285.1921	268.1656		**313.1870**	296.1605		228.1707		Q	1159.6106	1158.6154		***1232.6634***	1215.6368
4	86.0964	398.2762	381.2496		**426.2711**	409.2445		370.2449	384.2605	I	1046.5265	1059.5469	1073.5626	***1104.6048***	1087.5782
5	70.0651	495.3289	478.3024		**523.3239**	506.2973		469.3133		P	949.4738	948.4785		***991.5207***	974.4942
6	72.0808	594.3974	577.3708		622.3923	605.3657		580.3817		V	850.4054	863.4258		***894.4680***	877.4414
7	60.0444	681.4294	664.4028	663.4188	709.4243	692.3978	691.4137	665.4345		S	763.3733	762.3781		***795.3995***	778.3730
8	102.0550	810.4720	793.4454	792.4614	**838.4669**	821.4403	820.4563	752.4665		E	634.3307	633.3355		***708.3675***	691.3410
9	44.0495	881.5091	864.4825	863.4985	**909.5040**	892.4775	891.4934			A	563.2936			***579.3249***	562.2984
10	136.0757	1044.5724	1027.5459	1026.5619	**1072.5673**	1055.5408	1054.5568			Y	400.2303			***508.2878***	491.2613
11	86.0964	1157.6565	1140.6299	1139.6459	1185.6514	1168.6249	1167.6408	1115.6095		L	287.1462	286.1510		***345.2245***	328.1979
12	30.0338	1214.6780	1197.6514	1196.6674	1242.6729	1225.6463	1224.6623			G				***232.1404***	215.1139
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AQ	172.1081	200.1030	**AQI**	285.1921	313.1870	**AQIP**	382.2449	410.2398
AQIPV	481.3133	509.3082	**AQIPVS**	568.3453	596.3402	**AQIPVSE**	697.3879	725.3828
QI	214.1550	242.1499	**QIP**	311.2078	339.2027	**QIPV**	410.2762	438.2711
QIPVS	497.3082	525.3031	**QIPVSE**	626.3508	654.3457	**QIPVSEA**	697.3879	725.3828
IP	183.1492	211.1441	**IPV**	282.2176	310.2125	**IPVS**	369.2496	397.2445
IPVSE	498.2922	526.2871	**IPVSEA**	569.3293	597.3243	**PV**	169.1335	197.1285
PVS	256.1656	284.1605	**PVSE**	385.2082	413.2031	**PVSEA**	456.2453	484.2402
PVSEAY	619.3086	647.3035	**VS**	159.1128	187.1077	**VSE**	288.1554	316.1503

VSEA	359.1925	387.1874	**VSEAY**	522.2558	550.2508	**VSEAYL**	635.3399	663.3348
VSEAYLG	692.3614	720.3563	**SE**	189.0870	217.0819	**SEA**	260.1241	288.1190
SEAY	423.1874	451.1823	**SEAYL**	536.2715	564.2664	**SEAYLG**	593.2930	621.2879
EA	173.0921	201.0870	**EAY**	336.1554	364.1503	**EAYL**	449.2395	477.2344
EAYLG	506.2609	534.2558	**AY**	207.1128	235.1077	**AYL**	320.1969	348.1918
AYLG	377.2183	405.2132	**YL**	249.1598	277.1547	**YLG**	306.1812	334.1761
LG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
105.8	1415.7772	0.0844	IAQIPVSEAYLGR
103.6	1415.7772	0.0844	LAQIPVSEAYLGR
85.2	1415.7773	0.0844	IAQIPVSESFLGR
56.4	1415.7772	0.0844	IAQIPIGESYIGR
22.9	1415.7368	0.1248	IAGALQADSEASRK
20.7	1415.8136	0.0480	LLAQELLQYGLR
20.2	1416.7473	-0.8857	NPTNHQIELVPR
20.1	1415.8500	0.0116	KIAVALAEILYGR
17.9	1415.7885	0.0731	RGADPVLSYIAVR
17.8	1415.7343	0.1273	IKALHLYDCQR

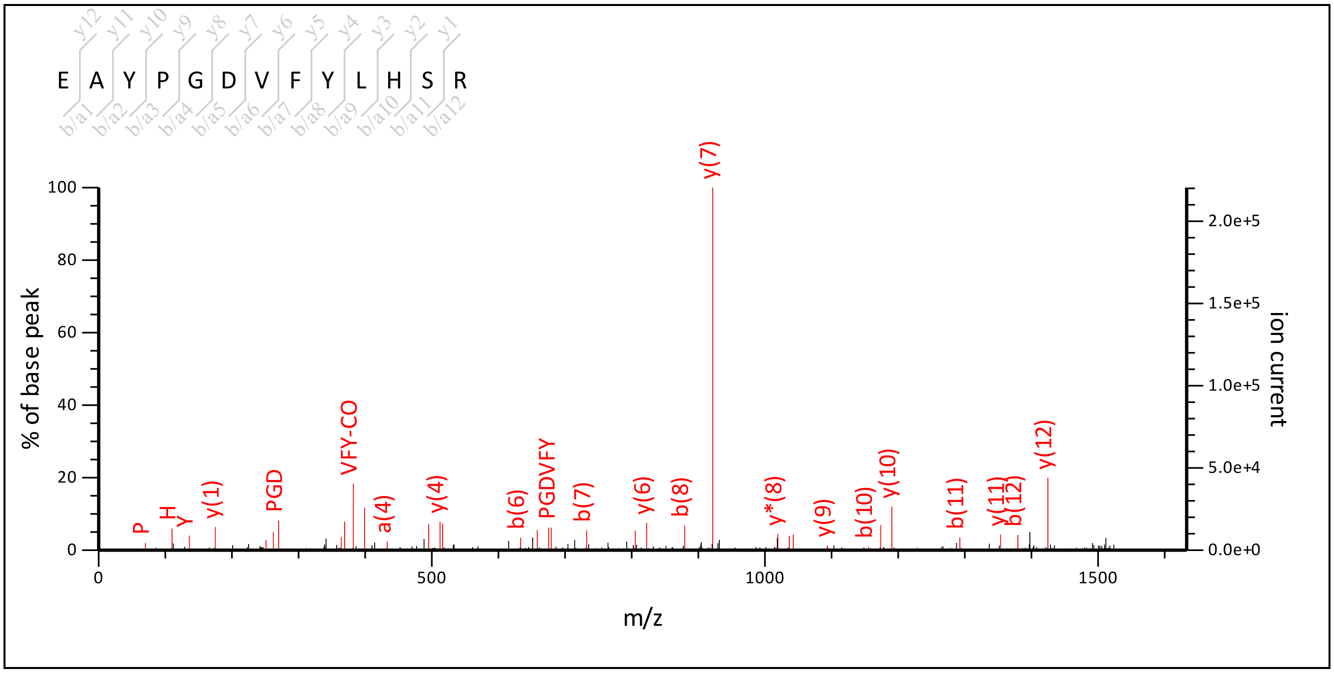
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **EAYPGDVFYLHSR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 52: 1552.821724 from(1553.829000,1+) intensity(0.0000) index(14)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221390, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 1632.96

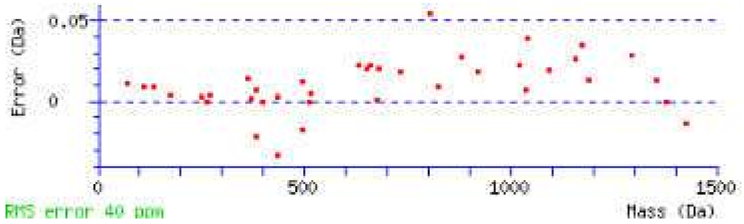
Label all possible matches ○ Label matches used for scoring ●

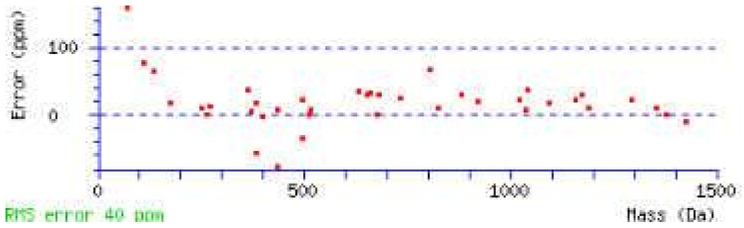
Monoisotopic mass of neutral peptide Mr(calc): 1552.7310
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 112 **Expect:** 3.4e-08
Matches : 42/195 fragment ions using 45 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	102.0550	102.0550	84.0444	130.0499	112.0393	44.0495	E						13
2	44.0495	173.0921	155.0815	201.0870	183.0764		A	1408.6644		***1424.6957***	1407.6692	1406.6852	12
3	136.0757	336.1554	318.1448	**364.1503**	346.1397		Y	1245.6011		***1353.6586***	1336.6321	1335.6480	11
4	70.0651	433.2082	415.1976	461.2031	443.1925	407.1925	P	1148.5483	1147.5531	***1190.5953***	1173.5687	1172.5847	10
5	30.0338	490.2296	472.2191	518.2245	500.2140		G			***1093.5425***	1076.5160	1075.5320	9
6	88.0393	605.2566	587.2460	**633.2515**	615.2409	561.2667	D	976.4999	975.5047	***1036.5211***	1019.4945	1018.5105	8
7	72.0808	704.3250	686.3144	**732.3199**	714.3093	690.3093	V	877.4315	890.4519	***921.4941***	904.4676	903.4835	7
8	120.0808	851.3934	833.3828	**879.3883**	861.3777		F	730.3631		***822.4257***	805.3991	804.4151	6
9	136.0757	1014.4567	996.4462	**1042.4516**	1024.4411		Y	567.2998		***675.3573***	658.3307	657.3467	5
10	86.0964	1127.5408	1109.5302	**1155.5357**	1137.5251	1085.4938	L	454.2157	453.2205	***512.2940***	495.2674	494.2834	4
11	110.0713	1264.5997	1246.5891	**1292.5946**	1274.5841		H	317.1568		***399.2099***	382.1833	381.1993	3
12	60.0444	1351.6317	1333.6212	**1379.6266**	1361.6161	1335.6368	S	230.1248	229.1295	***262.1510***	245.1244	244.1404	2

13	129.1135						R	74.0237	73.0284	*175.1190*	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AY	207.1128	235.1077	**AYP**	304.1656	332.1605	**AYPG**	361.1870	389.1819
AYPGD	476.2140	504.2089	**AYPGDV**	575.2824	603.2773	**YP**	233.1285	261.1234
YPG	290.1499	318.1448	**YPGD**	405.1769	433.1718	**YPGDV**	504.2453	532.2402
YPGDVF	651.3137	679.3086	**PG**	127.0866	155.0815	**PGD**	242.1135	270.1084
PGDV	341.1819	369.1769	**PGDVF**	488.2504	516.2453	**PGDVFY**	651.3137	679.3086
GD	145.0608	173.0557	**GDV**	244.1292	272.1241	**GDVF**	391.1976	419.1925
GDVFY	554.2609	582.2558	**GDVFYL**	667.3450	695.3399	**DV**	187.1077	215.1026
DVF	334.1761	362.1710	**DVFY**	497.2395	525.2344	**DVFYL**	610.3235	638.3184
VF	219.1492	247.1441	**VFY**	382.2125	410.2074	**VFYL**	495.2966	523.2915
VFYLH	632.3555	660.3504	**FY**	283.1441	311.1390	**FYL**	396.2282	424.2231
FYLH	533.2871	561.2820	**FYLHS**	620.3191	648.3140	**YL**	249.1598	277.1547
YLH	386.2187	414.2136	**YLHS**	473.2507	501.2456	**LH**	223.1553	251.1503
LHS	310.1874	338.1823	**HS**	197.1033	225.0982			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
111.8	1552.7310	0.0907	EAYPGDVFYIHSR
111.8	1552.7310	0.0907	EAYPGDVFYLHSR
19.7	1552.7998	0.0219	LRVYTVQDAAFDR
17.3	1552.7191	0.1026	LSYPEDLGMQASSR
17.1	1552.8725	-0.0508	LRPRYFSISSSLK
15.7	1552.7369	0.0848	EAYSDSQLIEKDR
15.3	1552.8249	-0.0032	EFSLVGRNIYIDK
15.2	1552.8144	0.0073	EGMDISVRHLLQR
15.1	1552.7555	0.0662	ISPLYSAEGTCLSR
14.5	1552.7609	0.0608	FLREWMLYHSR

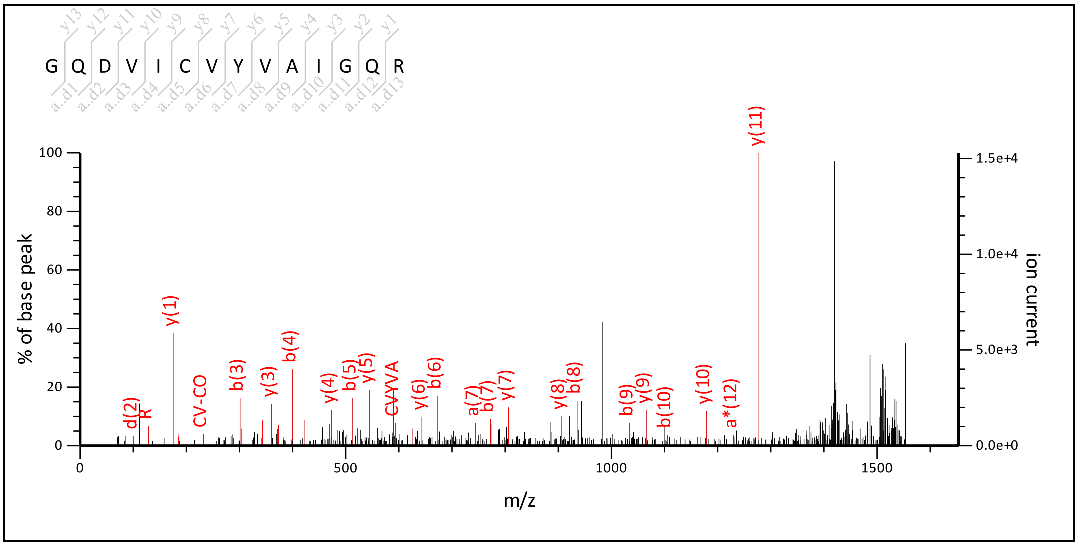
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **GQDVICVYVAIGQR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 55: 1576.897524 from(1577.904800,1+) intensity(0.0000) index(15)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221403, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 1653.47

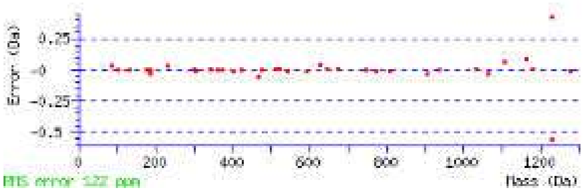
Label all possible matches ○ Label matches used for scoring ●

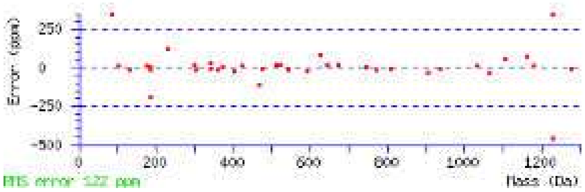
Monoisotopic mass of neutral peptide Mr(calc): 1576.8032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 0.0012
Matches : 43/233 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	101.0709	158.0924	141.0659		**186.0873**	169.0608		101.0709		Q	1447.7362	1446.7410		1520.7890	1503.7624
3	88.0393	273.1193	256.0928	255.1088	**301.1143**	284.0877	283.1037	229.1295		D	1332.7093	1331.7140		1392.7304	1375.7038
4	72.0808	372.1878	355.1612	354.1772	**400.1827**	383.1561	382.1721	358.1721		V	1233.6409	1246.6613		***1277.7035***	1260.6769
5	86.0964	485.2718	468.2453	467.2613	**513.2667**	496.2402	495.2562	457.2405	471.2562	I	1120.5568	1133.5772	1147.5928	***1178.6350***	1161.6085
6	133.0430	645.3025	628.2759	627.2919	**673.2974**	656.2708	655.2868	556.3089		C	960.5261	959.5309		***1065.5510***	1048.5244
7	72.0808	744.3709	727.3443	726.3603	**772.3658**	755.3393	754.3552	730.3552		V	861.4577	874.4781		***905.5203***	888.4938
8	136.0757	907.4342	890.4077	889.4237	**935.4291**	918.4026	917.4186			Y	698.3944			***806.4519***	789.4254
9	72.0808	1006.5026	989.4761	988.4921	**1034.4975**	1017.4710	1016.4870	992.4870		V	599.3260	612.3464		***643.3886***	626.3620
10	44.0495	1077.5397	1060.5132	1059.5292	**1105.5347**	1088.5081	1087.5241			A	528.2889			***544.3202***	527.2936
11	86.0964	1190.6238	1173.5973	1172.6132	1218.6187	1201.5922	1200.6082	1162.5925	1176.6082	I	415.2048	428.2252	442.2409	***473.2831***	456.2565
12	30.0338	1247.6453	1230.6187	1229.6347	1275.6402	1258.6136	1257.6296			G				***360.1990***	343.1724
13	101.0709	1375.7038	1358.6773	1357.6933	1403.6988	1386.6722	1385.6882	1318.6824		Q	230.1248	229.1295		***303.1775***	286.1510
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QD	216.0979	244.0928	QDV	315.1663	343.1612	QDVI	428.2504	456.2453
QDVIC	588.2810	616.2759	QDVICV	687.3494	715.3443	DV	187.1077	215.1026
DVI	300.1918	328.1867	DVIC	460.2224	488.2173	DVICV	559.2908	587.2858
VI	185.1648	213.1598	VIC	345.1955	373.1904	VICV	444.2639	472.2588
VICVY	607.3272	635.3221	IC	246.1271	274.1220	ICV	345.1955	373.1904
ICVY	508.2588	536.2537	ICVYV	607.3272	635.3221	ICVYVA	678.3643	706.3593
CV	232.1114	260.1063	CVY	395.1748	423.1697	CVYV	494.2432	522.2381

CVYVA	565.2803	593.2752	**CVYVAI**	678.3643	706.3593	**VY**	235.1441	263.1390
VYV	334.2125	362.2074	**VYVA**	405.2496	433.2445	**VYVAI**	518.3337	546.3286
VYVAIG	575.3552	603.3501	**YV**	235.1441	263.1390	**YVA**	306.1812	334.1761
YVAI	419.2653	447.2602	**YVAIG**	476.2867	504.2817	**YVAIGQ**	604.3453	632.3402
VA	143.1179	171.1128	**VAI**	256.2020	284.1969	**VAIG**	313.2234	341.2183
VAIGQ	441.2820	469.2769	**AI**	157.1335	185.1285	**AIG**	214.1550	242.1499
AIGQ	342.2136	370.2085	**IG**	143.1179	171.1128	**IGQ**	271.1765	299.1714
GQ	158.0924	186.0873						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.8	1576.8032	0.0943	GQDVICVYVAIGQR
65.8	1576.8032	0.0944	GENVICVYVAIGQR
53.8	1575.8192	1.0784	GQNVICVYVAIGQR
20.0	1577.7169	-0.8193	GAGDSLAEAAQSSESAK
17.6	1577.6926	-0.7951	VNDVICTMSGSHSR
17.0	1576.9413	-0.0438	QHLVLITATKLQGR
16.7	1575.8290	1.0685	DLMTTALAATTAKPR
16.0	1575.7059	1.1916	QMSDASGRAASDQPR
15.0	1576.7733	0.1243	ASAAVYPASEDELVR
14.2	1576.8243	0.0732	QTGLSGSSAIVIAAMR

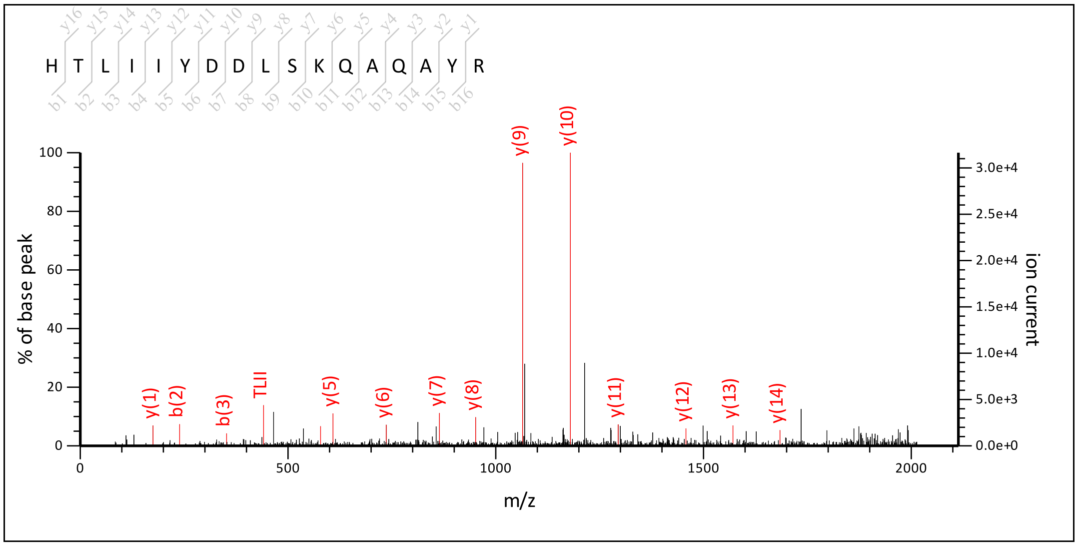
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **HTLIIYDDLSKQAQAYR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 69: 2034.170424 from(2035.177700,1+) intensity(0.0000) index(19)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221401, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 2113.44

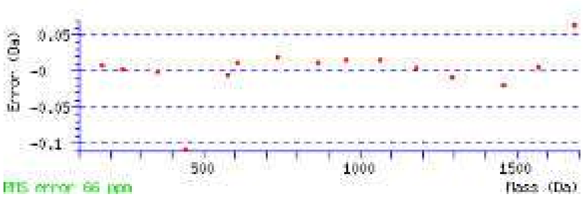
Label all possible matches ○ Label matches used for scoring ●

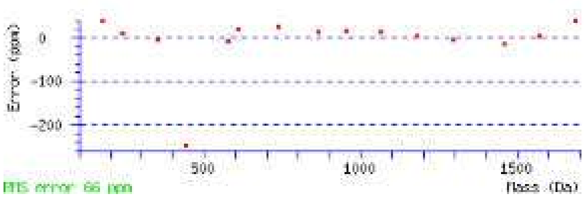
Monoisotopic mass of neutral peptide Mr(calc): 2034.0534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 90 **Expect:** 3.8e-06
Matches : 15/292 fragment ions using 20 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	110.0713	110.0713			138.0662			44.0495		H					
2	74.0600	211.1190		193.1084	**239.1139**		221.1033	195.1240	197.1033	T	1851.9599	1864.9803	1866.9596	1898.0018	1880.9753
3	86.0964	324.2030		306.1925	**352.1979**		334.1874	282.1561		L	1738.8759	1737.8806		1796.9541	1779.9276
4	86.0964	437.2871		419.2765	465.2820		447.2714	409.2558	423.2714	I	1625.7918	1638.8122	1652.8279	***1683.8701***	1666.8435
5	86.0964	550.3711		532.3606	**578.3661**		560.3555	522.3398	536.3555	I	1512.7077	1525.7281	1539.7438	***1570.7860***	1553.7594
6	136.0757	713.4345		695.4239	741.4294		723.4188			Y	1349.6444			***1457.7019***	1440.6754
7	88.0393	828.4614		810.4509	856.4563		838.4458	784.4716		D	1234.6175	1233.6222		***1294.6386***	1277.6121
8	88.0393	943.4884		925.4778	971.4833		953.4727	899.4985		D	1119.5905	1118.5953		***1179.6117***	1162.5851
9	86.0964	1056.5724		1038.5619	1084.5673		1066.5568	1014.5255		L	1006.5065	1005.5112		***1064.5847***	1047.5582
10	60.0444	1143.6045		1125.5939	1171.5994		1153.5888	1127.6095		S	919.4744	918.4792		***951.5007***	934.4741
11	101.1073	1271.6994	1254.6729	1253.6888	1299.6943	1282.6678	1281.6838	1214.6416		K	791.3795	790.3842		***864.4686***	847.4421
12	101.0709	1399.7580	1382.7314	1381.7474	1427.7529	1410.7264	1409.7423	1342.7365		Q	663.3209	662.3257		***736.3737***	719.3471
13	44.0495	1470.7951	1453.7686	1452.7845	1498.7900	1481.7635	1480.7795			A	592.2838			***608.3151***	591.2885
14	101.0709	1598.8537	1581.8271	1580.8431	1626.8486	1609.8220	1608.8380	1541.8322		Q	464.2252	463.2300		537.2780	520.2514
15	44.0495	1669.8908	1652.8642	1651.8802	1697.8857	1680.8592	1679.8751			A	393.1881			409.2194	392.1928
16	136.0757	1832.9541	1815.9276	1814.9436	1860.9490	1843.9225	1842.9385			Y	230.1248			338.1823	321.1557
17	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TL	187.1441	215.1390	TLI	300.2282	328.2231	TLII	413.3122	441.3071
TLIIY	576.3756	604.3705	TLIIYD	691.4025	719.3974	LI	199.1805	227.1754
LII	312.2646	340.2595	LIIY	475.3279	503.3228	LIIYD	590.3548	618.3497
II	199.1805	227.1754	IIY	362.2438	390.2387	IIYD	477.2708	505.2657

IIYDD	592.2977	620.2926	**IY**	249.1598	277.1547	**IYD**	364.1867	392.1816
IYDD	479.2136	507.2086	**IYDDL**	592.2977	620.2926	**IYDDLS**	679.3297	707.3246
YD	251.1026	279.0975	**YDD**	366.1296	394.1245	**YDDL**	479.2136	507.2086
YDDLS	566.2457	594.2406	**YDDLSK**	694.3406	722.3355	**DD**	203.0662	231.0612
DDL	316.1503	344.1452	**DDLS**	403.1823	431.1773	**DDLSK**	531.2773	559.2722
DDLSKQ	659.3359	687.3308	**DL**	201.1234	229.1183	**DLS**	288.1554	316.1503
DLSK	416.2504	444.2453	**DLSKQ**	544.3089	572.3039	**DLSKQA**	615.3461	643.3410
LS	173.1285	201.1234	**LSK**	301.2234	329.2183	**LSKQ**	429.2820	457.2769
LSKQA	500.3191	528.3140	**LSKQAQ**	628.3777	656.3726	**LSKQAQA**	699.4148	727.4097
SK	188.1394	216.1343	**SKQ**	316.1979	344.1928	**SKQA**	387.2350	415.2300
SKQAQ	515.2936	543.2885	**SKQAQA**	586.3307	614.3257	**KQ**	229.1659	257.1608
KQA	300.2030	328.1979	**KQAQ**	428.2616	456.2565	**KQAQA**	499.2987	527.2936
KQAQAY	662.3620	690.3570	**QA**	172.1081	200.1030	**QAQ**	300.1666	328.1615
QAQA	371.2037	399.1987	**QAQAY**	534.2671	562.2620	**AQ**	172.1081	200.1030
AQA	243.1452	271.1401	**AQAY**	406.2085	434.2034	**QA**	172.1081	200.1030
QAY	335.1714	363.1663	**AY**	207.1128	235.1077			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
89.9	2034.0534	0.1170	HTLIIYDDLSKQAQAYR
13.3	2034.0534	0.1170	HTLVIYDDLTKQAQAYR
9.9	2033.0694	1.1010	GSFYATDLDLVLHTRGIR
9.7	2033.9768	0.1936	LVFMGGGSYSFDLEDLLR
8.9	2033.9906	0.1799	TYSLPSSVNDQTPDLELR
7.8	2033.0518	1.1186	ASMKLAPFFFGPYLIMGK
7.2	2035.0051	-0.8346	EHFDLSQPAFLQIAEYK
6.6	2033.0438	1.1267	YMPTLATAGLPAGMLAAAAAR
6.6	2034.0357	0.1347	VGEFKPPTPSGRMDFTLR
6.4	2033.0188	1.1516	ASMKLAPMFFGPYLIMGK

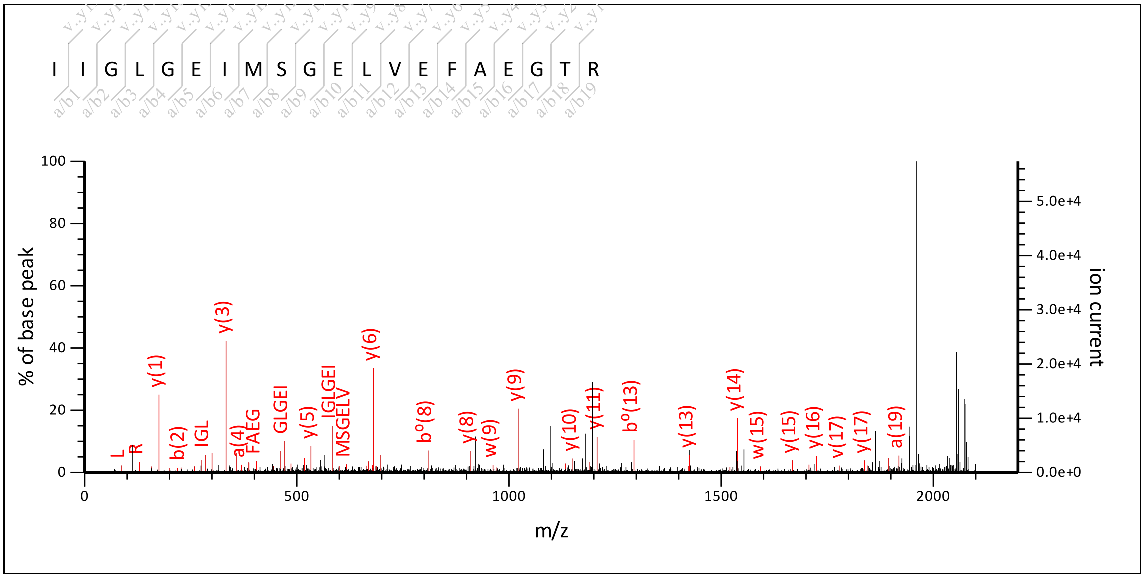
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **IIGLGEIMSGELVEFAEGTR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 78: 2120.200724 from(2121.208000,1+) intensity(0.0000) index(21)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221395, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 2199.42

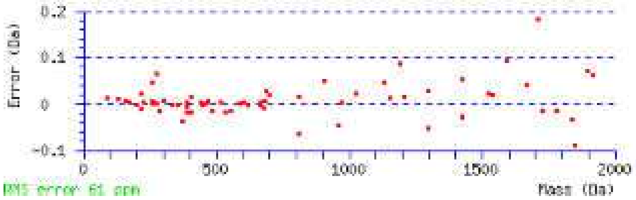
Label all possible matches ○ Label matches used for scoring ●

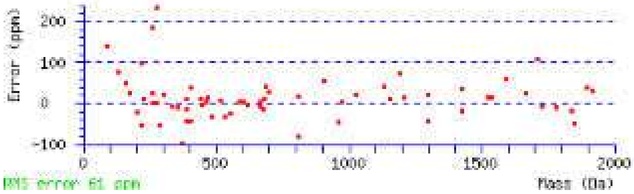
Monoisotopic mass of neutral peptide Mr(calc): 2120.0823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 107 **Expect:** 6.2e-08
Matches : 81/345 fragment ions using 126 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	**86.0964**		114.0913		44.0495		I							20
2	86.0964	**199.1805**		**227.1754**		171.1492	185.1648	I	1949.9273	1962.9477	1976.9634	2008.0056	1990.9790	1989.9950	19
3	30.0338	256.2020		**284.1969**				G				***1894.9215***	1877.8950	1876.9109	18
4	86.0964	**369.2860**		397.2809		327.2391		L	1779.8218	1778.8265		***1837.9000***	1820.8735	1819.8895	17
5	30.0338	426.3075		454.3024				G				***1724.8160***	1707.7894	1706.8054	16
6	102.0550	**555.3501**	537.3395	**583.3450**	565.3344	497.3446		E	1593.7577	1592.7625		***1667.7945***	1650.7680	1649.7839	15
7	86.0964	**668.4341**	650.4236	**696.4291**	678.4185	640.4028	654.4185	I	1480.6737	1493.6941	1507.7097	***1538.7519***	1521.7254	1520.7414	14
8	104.0528	799.4746	781.4641	827.4695	809.4590	739.4713		M	1349.6332	1348.6379		***1425.6679***	1408.6413	1407.6573	13
9	60.0444	886.5067	868.4961	914.5016	896.4910	870.5117		S	1262.6012	1261.6059		***1294.6274***	1277.6008	1276.6168	12
10	30.0338	943.5281	925.5176	**971.5230**	953.5125			G				***1207.5953***	1190.5688	1189.5848	11
11	102.0550	1072.5707	1054.5601	1100.5656	1082.5551	1014.5652		E	1076.5371	1075.5419		***1150.5739***	1133.5473	1132.5633	10
12	86.0964	1185.6548	1167.6442	1213.6497	1195.6391	1143.6078		L	963.4530	962.4578		***1021.5313***	1004.5047	1003.5207	9
13	72.0808	1284.7232	1266.7126	1312.7181	1294.7075	1270.7075		V	864.3846	877.4050		***908.4472***	891.4207	890.4367	8
14	102.0550	1413.7658	1395.7552	1441.7607	1423.7501	1355.7603		E	735.3420	734.3468		***809.3788***	792.3523	791.3682	7
15	120.0808	1560.8342	1542.8236	1588.8291	1570.8185			F	588.2736			***680.3362***	663.3097	662.3257	6
16	44.0495	1631.8713	1613.8607	1659.8662	1641.8557			A	517.2365			***533.2678***	516.2413	515.2572	5
17	102.0550	1760.9139	1742.9033	1788.9088	1770.8983	1702.9084		E	388.1939	387.1987		***462.2307***	445.2041	444.2201	4
18	30.0338	1817.9354	1799.9248	**1845.9303**	1827.9197			G				***333.1881***	316.1615	315.1775	3
19	74.0600	**1918.9830**	1900.9725	1946.9780	1928.9674	1902.9881	1904.9674	T	230.1248	243.1452	245.1244	***276.1666***	259.1401	258.1561	2

20	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IG	143.1179	171.1128	**IGL**	256.2020	284.1969	**IGLG**	313.2234	341.2183
IGLGE	442.2660	470.2609	**IGLGEI**	555.3501	583.3450	**IGLGEIM**	686.3906	714.3855
GL	143.1179	171.1128	**GLG**	200.1394	228.1343	**GLGE**	329.1819	357.1769
GLGEI	442.2660	470.2609	**GLGEIM**	573.3065	601.3014	**GLGEIMS**	660.3385	688.3334
LG	143.1179	171.1128	**LGE**	272.1605	300.1554	**LGEI**	385.2445	413.2395
LGEIM	516.2850	544.2799	**LGEIMS**	603.3171	631.3120	**LGEIMSG**	660.3385	688.3334
GE	159.0764	187.0713	**GEI**	272.1605	300.1554	**GEIM**	403.2010	431.1959
GEIMS	490.2330	518.2279	**GEIMSG**	547.2545	575.2494	**GEIMSGE**	676.2971	704.2920
EI	215.1390	243.1339	**EIM**	346.1795	374.1744	**EIMS**	433.2115	461.2064
EIMSG	490.2330	518.2279	**EIMSGE**	619.2756	647.2705	**IM**	217.1369	245.1318
IMS	304.1689	332.1639	**IMSG**	361.1904	389.1853	**IMSGE**	490.2330	518.2279
IMSGEL	603.3171	631.3120	**MS**	191.0849	219.0798	**MSG**	248.1063	276.1013
MSGE	377.1489	405.1438	**MSGEL**	490.2330	518.2279	**MSGELV**	589.3014	617.2963
SG	117.0659	145.0608	**SGE**	246.1084	274.1034	**SGEL**	359.1925	387.1874
SGELV	458.2609	486.2558	**SGELVE**	587.3035	615.2984	**GE**	159.0764	187.0713
GEL	272.1605	300.1554	**GELV**	371.2289	399.2238	**GELVE**	500.2715	528.2664
GELVEF	647.3399	675.3348	**EL**	215.1390	243.1339	**ELV**	314.2074	342.2023
ELVE	443.2500	471.2449	**ELVEF**	590.3184	618.3134	**ELVEFA**	661.3556	689.3505
LV	185.1648	213.1598	**LVE**	314.2074	342.2023	**LVEF**	461.2758	489.2708
LVEFA	532.3130	560.3079	**LVEFAE**	661.3556	689.3505	**VE**	201.1234	229.1183
VEF	348.1918	376.1867	**VEFA**	419.2289	447.2238	**VEFAE**	548.2715	576.2664
VEFAEG	605.2930	633.2879	**EF**	249.1234	277.1183	**EFA**	320.1605	348.1554
EFAE	449.2031	477.1980	**EFAEG**	506.2245	534.2195	**EFAEGT**	607.2722	635.2671
FA	191.1179	219.1128	**FAE**	320.1605	348.1554	**FAEG**	377.1819	405.1769
FAEGT	478.2296	506.2245	**AE**	173.0921	201.0870	**AEG**	230.1135	258.1084
AEGT	331.1612	359.1561	**EG**	159.0764	187.0713	**EGT**	260.1241	288.1190
GT	131.0815	159.0764						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
107.1	2120.0823	0.1184	IIGLGEIMSGELVEFAEGTR
57.8	2119.0983	1.1024	IIGLGQIMSGELVEFAEGTR
28.2	2119.1347	1.0660	IIGLGEIMSGELVKFAEGTR
28.2	2119.0983	1.1024	IIGLGEIMSGELVQFAEGTR
11.1	2119.1473	1.0534	SWHRAGVLLLGAQSCLPVR
10.9	2121.0717	-0.8710	WMHELNFKQVIFSLDSK
10.8	2121.0875	-0.8868	LLDSGMEKLVDDTSTLLSGK
10.7	2120.0969	0.1038	CLLTLLMSTAAIPGGSESRK
10.6	2121.2045	-1.0038	AGEVLIPTIDDSTLPIALRK

10.3	2120.0175	0.1833	TAPSGPWSATSGLDPISSFSR

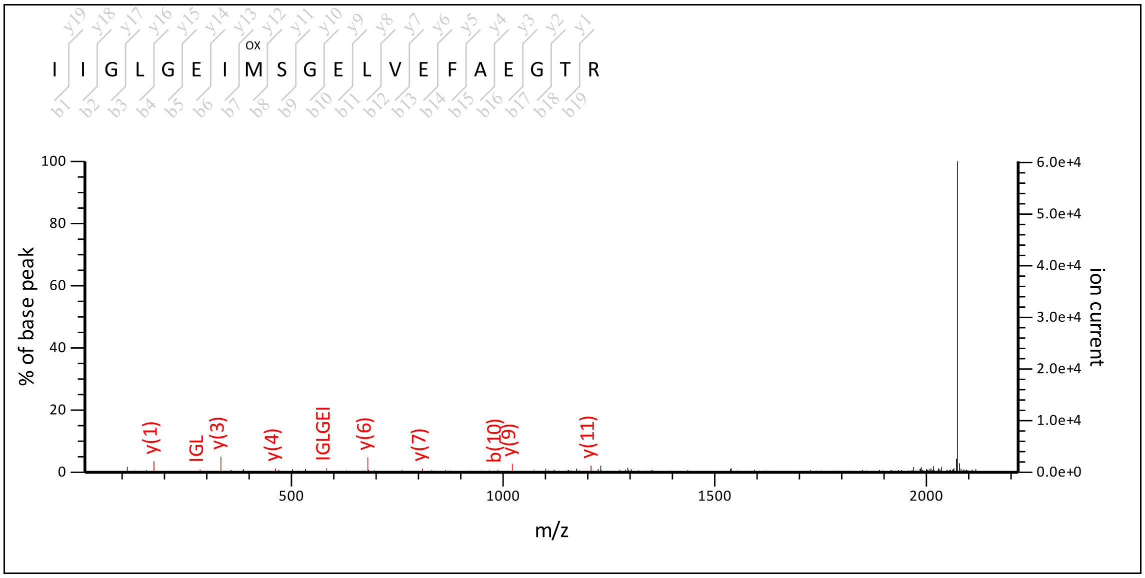
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **IIGLGEIMSGELVEFAEGTR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 80: 2136.190724 from(2137.198000,1+) intensity(0.0000) index(22)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221413, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



12.1 to 2216.75

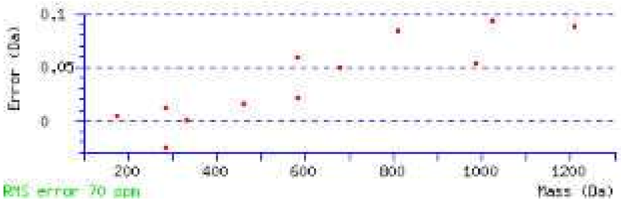
Label all possible matches ○ Label matches used for scoring ●

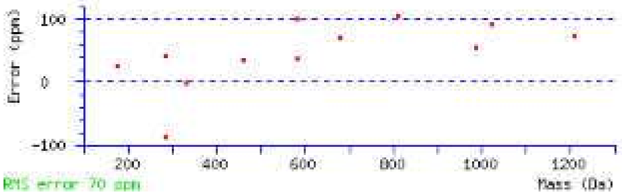
Monoisotopic mass of neutral peptide Mr(calc): 2136.0773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 37 **Expect:** 0.6
Matches : 15/473 fragment ions using 21 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		44.0495		I							20
2	86.0964	199.1805		227.1754		171.1492	185.1648	I	1965.9222	1978.9426	1992.9583	2024.0005	2006.9739	2005.9899	19
3	30.0338	256.2020		***284.1969***				G				1910.9164	1893.8899	1892.9059	18
4	86.0964	369.2860		397.2809		327.2391		L	1795.8167	1794.8215		1853.8950	1836.8684	1835.8844	17
5	30.0338	426.3075		454.3024				G				1740.8109	1723.7843	1722.8003	16
6	102.0550	555.3501	537.3395	***583.3450***	565.3344	497.3446		E	1609.7527	1608.7574		1683.7894	1666.7629	1665.7789	15
7	86.0964	668.4341	650.4236	696.4291	678.4185	640.4028	654.4185	I	1496.6686	1509.6890	1523.7046	1554.7468	1537.7203	1536.7363	14
8	120.0478	815.4695	797.4590	843.4645	825.4539	739.4713		M	1349.6332	1348.6379		1441.6628	1424.6362	1423.6522	13
9	60.0444	902.5016	884.4910	930.4965	912.4859	886.5067		S	1262.6012	1261.6059		1294.6274	1277.6008	1276.6168	12
10	30.0338	959.5230	941.5125	***987.5179***	969.5074			G				***1207.5953***	1190.5688	1189.5848	11
11	102.0550	1088.5656	1070.5551	1116.5605	1098.5500	1030.5601		E	1076.5371	1075.5419		1150.5739	1133.5473	1132.5633	10
12	86.0964	1201.6497	1183.6391	1229.6446	1211.6340	1159.6027		L	963.4530	962.4578		***1021.5313***	1004.5047	1003.5207	9
13	72.0808	1300.7181	1282.7075	1328.7130	1310.7025	1286.7025		V	864.3846	877.4050		908.4472	891.4207	890.4367	8
14	102.0550	1429.7607	1411.7501	1457.7556	1439.7450	1371.7552		E	735.3420	734.3468		***809.3788***	792.3523	791.3682	7
15	120.0808	1576.8291	1558.8185	1604.8240	1586.8135			F	588.2736			***680.3362***	663.3097	662.3257	6
16	44.0495	1647.8662	1629.8557	1675.8611	1657.8506			A	517.2365			533.2678	516.2413	515.2572	5
17	102.0550	1776.9088	1758.8983	1804.9037	1786.8932	1718.9033		E	388.1939	387.1987		***462.2307***	445.2041	444.2201	4

18	30.0338	1833.9303	1815.9197	1861.9252	1843.9146			G				***333.1881***	316.1615	315.1775	3
19	74.0600	1934.9780	1916.9674	1962.9729	1944.9623	1918.9830	1920.9623	T	230.1248	243.1452	245.1244	276.1666	259.1401	258.1561	2
20	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IG	143.1179	171.1128	IGL	256.2020	284.1969	IGLG	313.2234	341.2183
IGLGE	442.2660	470.2609	IGLGEI	555.3501	583.3450	GL	143.1179	171.1128
GLG	200.1394	228.1343	GLGE	329.1819	357.1769	GLGEI	442.2660	470.2609
GLGEIM	589.3014	617.2963	GLGEIMS	676.3334	704.3284	LG	143.1179	171.1128
LGE	272.1605	300.1554	LGEI	385.2445	413.2395	LGEIM	532.2799	560.2749
LGEIMS	619.3120	647.3069	LGEIMSG	676.3334	704.3284	GE	159.0764	187.0713
GEI	272.1605	300.1554	GEIM	419.1959	447.1908	GEIMS	506.2279	534.2228
GEIMSG	563.2494	591.2443	GEIMSGE	692.2920	720.2869	EI	215.1390	243.1339
EIM	362.1744	390.1693	EIMS	449.2064	477.2014	EIMSG	506.2279	534.2228
EIMSGE	635.2705	663.2654	IM	233.1318	261.1267	IMS	320.1639	348.1588
IMSG	377.1853	405.1802	IMSGE	506.2279	534.2228	IMSGEL	619.3120	647.3069
MS	207.0798	235.0747	MSG	264.1013	292.0962	MSGE	393.1438	421.1388
MSGEL	506.2279	534.2228	MSGELV	605.2963	633.2912	SG	117.0659	145.0608
SGE	246.1084	274.1034	SGEL	359.1925	387.1874	SGELV	458.2609	486.2558
SGELVE	587.3035	615.2984	GE	159.0764	187.0713	GEL	272.1605	300.1554
GELV	371.2289	399.2238	GELVE	500.2715	528.2664	GELVEF	647.3399	675.3348
EL	215.1390	243.1339	ELV	314.2074	342.2023	ELVE	443.2500	471.2449
ELVEF	590.3184	618.3134	ELVEFA	661.3556	689.3505	LV	185.1648	213.1598
LVE	314.2074	342.2023	LVEF	461.2758	489.2708	LVEFA	532.3130	560.3079
LVEFAE	661.3556	689.3505	VE	201.1234	229.1183	VEF	348.1918	376.1867
VEFA	419.2289	447.2238	VEFAE	548.2715	576.2664	VEFAEG	605.2930	633.2879
EF	249.1234	277.1183	EFA	320.1605	348.1554	EFAE	449.2031	477.1980
EFAEG	506.2245	534.2195	EFAEGT	607.2722	635.2671	FA	191.1179	219.1128
FAE	320.1605	348.1554	FAEG	377.1819	405.1769	FAEGT	478.2296	506.2245
AE	173.0921	201.0870	AEG	230.1135	258.1084	AEGT	331.1612	359.1561
EG	159.0764	187.0713	EGT	260.1241	288.1190	GT	131.0815	159.0764





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.3	2136.0773	0.1135	IIGLGEIMSGELVEFAEGTR
27.2	2135.0932	1.0975	IIGLGQIMSGELVEFAEGTR
11.4	2136.2307	-0.0399	LATLALILVLVSFSHSPEAR
9.5	2136.0898	0.1009	SHGRVVVNASVESWLPMPR
9.2	2136.0198	0.1709	KDLFTGTYMPSTELTGGFR
9.1	2135.9793	0.2114	SNYAFSMLTGRGSEASISDK
8.8	2137.1354	-0.9447	GPWKNPEVLEMIQVVNLR
8.0	2135.0854	1.1054	VIRGSFFANGWLWSWPGR
7.7	2136.0496	0.1411	QLIGPAMYFGLMGDGQPIGR

7.7	2136.0125	0.1782	SLMMPGSPSEAGLSRSLMNR

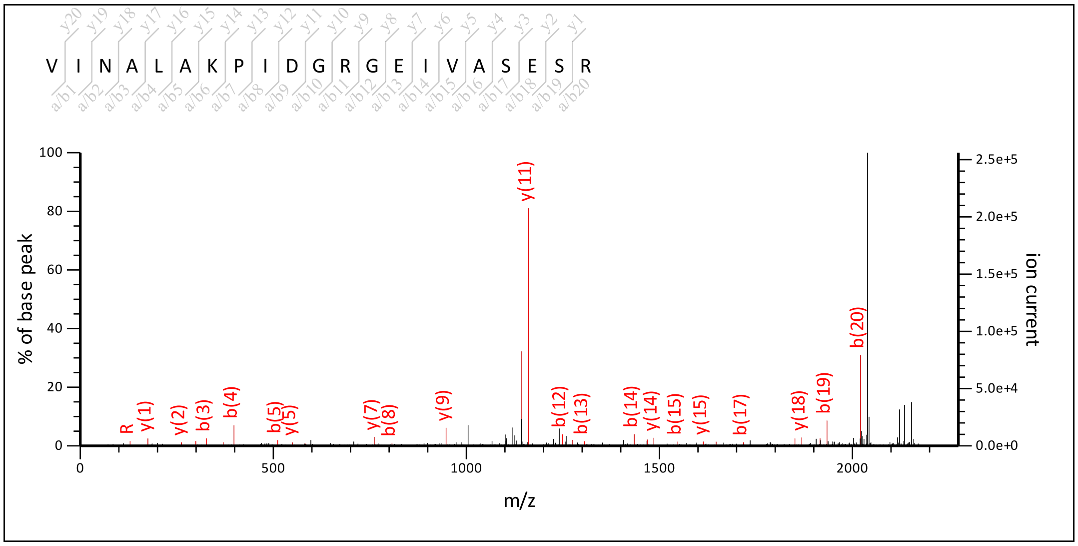
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **VINALAKPIDGRGEIVASESR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 88: 2194.327924 from(2195.335200,1+) intensity(0.0000) index(24)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221393, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 2274.56

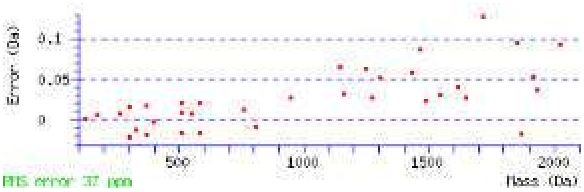
Label all possible matches ○ Label matches used for scoring ●

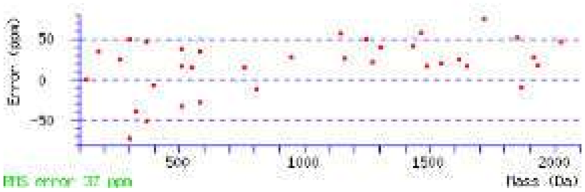
Monoisotopic mass of neutral peptide Mr(calc): 2194.2069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 98 **Expect:** 4.2e-07
Matches : 37/406 fragment ions using 44 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	86.0964	185.1648			213.1598			157.1335	171.1492	I	2038.0676	2051.0880	2065.1036	2096.1458	2079.1193
3	87.0553	299.2078	282.1812		***327.2027***	310.1761		256.2020		N	1924.0247	1923.0294		1983.0618	1966.0352
4	44.0495	370.2449	353.2183		***398.2398***	381.2132				A	1852.9876			***1869.0189***	1851.9923
5	86.0964	483.3289	466.3024		***511.3239***	494.2973		441.2820		L	1739.9035	1738.9082		1797.9817	1780.9552
6	44.0495	554.3661	537.3395		***582.3610***	565.3344				A	1668.8664			1684.8977	1667.8711
7	101.1073	682.4610	665.4345		710.4559	693.4294		625.4032		K	1540.7714	1539.7762		***1613.8606***	1596.8340
8	70.0651	779.5138	762.4872		***807.5087***	790.4822		753.4981		P	1443.7186	1442.7234		***1485.7656***	1468.7390
9	86.0964	892.5978	875.5713		920.5928	903.5662		864.5665	878.5822	I	1330.6346	1343.6550	1357.6706	1388.7128	1371.6863
10	88.0393	1007.6248	990.5982	989.6142	1035.6197	1018.5932	1017.6091	963.6350		D	1215.6076	1214.6124		***1275.6288***	1258.6022
11	30.0338	1064.6463	1047.6197	1046.6357	1092.6412	1075.6146	1074.6306			G				***1160.6018***	1143.5753
12	129.1135	1220.7474	1203.7208	1202.7368	***1248.7423***	1231.7157	1230.7317	1135.6834		R	1002.4851	1001.4898		1103.5804	1086.5538
13	30.0338	1277.7688	1260.7423	1259.7583	***1305.7637***	1288.7372	1287.7532			G				***947.4793***	930.4527
14	102.0550	1406.8114	1389.7849	1388.8009	***1434.8063***	1417.7798	1416.7958	1348.8059		E	816.4210	815.4258		890.4578	873.4312
15	86.0964	1519.8955	1502.8689	1501.8849	***1547.8904***	1530.8639	1529.8798	1491.8642	1505.8798	I	703.3369	716.3573	730.3730	***761.4152***	744.3886
16	72.0808	1618.9639	1601.9374	1600.9533	***1646.9588***	1629.9323	1628.9483	1604.9483		V	604.2685	617.2889		648.3311	631.3046
17	44.0495	1690.0010	1672.9745	1671.9905	***1717.9959***	1700.9694	1699.9854			A	533.2314			***549.2627***	532.2362
18	60.0444	1777.0330	1760.0065	1759.0225	1805.0280	1788.0014	1787.0174	1761.0381		S	446.1994	445.2041		478.2256	461.1991
19	102.0550	1906.0756	1889.0491	1888.0651	***1934.0706***	1917.0440	1916.0600	1848.0702		E	317.1568	316.1615		391.1936	374.1670
20	60.0444	1993.1077	1976.0811	1975.0971	***2021.1026***	2004.0760	2003.0920	1977.1128		S	230.1248	229.1295		***262.1510***	245.1244
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

IN	200.1394	228.1343	**INA**	271.1765	299.1714	**INAL**	384.2605	412.2554
INALA	455.2976	483.2926	**INALAK**	583.3926	611.3875	**INALAKP**	680.4454	708.4403
NA	158.0924	186.0873	**NAL**	271.1765	299.1714	**NALA**	342.2136	370.2085
NALAK	470.3085	498.3035	**NALAKP**	567.3613	595.3562	**NALAKPI**	680.4454	708.4403
AL	157.1335	185.1285	**ALA**	228.1707	256.1656	**ALAK**	356.2656	384.2605
ALAKP	453.3184	481.3133	**ALAKPI**	566.4024	594.3974	**ALAKPID**	681.4294	709.4243
LA	157.1335	185.1285	**LAK**	285.2285	313.2234	**LAKP**	382.2813	410.2762
LAKPI	495.3653	523.3602	**LAKPID**	610.3923	638.3872	**LAKPIDG**	667.4137	695.4087
AK	172.1444	200.1394	**AKP**	269.1972	297.1921	**AKPI**	382.2813	410.2762
AKPID	497.3082	525.3031	**AKPIDG**	554.3297	582.3246	**KP**	198.1601	226.1550
KPI	311.2442	339.2391	**KPID**	426.2711	454.2660	**KPIDG**	483.2926	511.2875
KPIDGR	639.3937	667.3886	**KPIDGRG**	696.4151	724.4100	**PI**	183.1492	211.1441
PID	298.1761	326.1710	**PIDG**	355.1976	383.1925	**PIDGR**	511.2987	539.2936
PIDGRG	568.3202	596.3151	**PIDGRGE**	697.3628	725.3577	**ID**	201.1234	229.1183
IDG	258.1448	286.1397	**IDGR**	414.2459	442.2409	**IDGRG**	471.2674	499.2623
IDGRGE	600.3100	628.3049	**DG**	145.0608	173.0557	**DGR**	301.1619	329.1568
DGRG	358.1833	386.1783	**DGRGE**	487.2259	515.2209	**DGRGEI**	600.3100	628.3049
DGRGEIV	699.3784	727.3733	**GR**	186.1349	214.1299	**GRG**	243.1564	271.1513
GRGE	372.1990	400.1939	**GRGEI**	485.2831	513.2780	**GRGEIV**	584.3515	612.3464
GRGEIVA	655.3886	683.3835	**RG**	186.1349	214.1299	**RGE**	315.1775	343.1724
RGEI	428.2616	456.2565	**RGEIV**	527.3300	555.3249	**RGEIVA**	598.3671	626.3620
RGEIVAS	685.3991	713.3941	**GE**	159.0764	187.0713	**GEI**	272.1605	300.1554
GEIV	371.2289	399.2238	**GEIVA**	442.2660	470.2609	**GEIVAS**	529.2980	557.2930
GEIVASE	658.3406	686.3355	**EI**	215.1390	243.1339	**EIV**	314.2074	342.2023
EIVA	385.2445	413.2395	**EIVAS**	472.2766	500.2715	**EIVASE**	601.3192	629.3141
EIVASES	688.3512	716.3461	**IV**	185.1648	213.1598	**IVA**	256.2020	284.1969
IVAS	343.2340	371.2289	**IVASE**	472.2766	500.2715	**IVASES**	559.3086	587.3035
VA	143.1179	171.1128	**VAS**	230.1499	258.1448	**VASE**	359.1925	387.1874
VASES	446.2245	474.2195	**AS**	131.0815	159.0764	**ASE**	260.1241	288.1190
ASES	347.1561	375.1510	**SE**	189.0870	217.0819	**SES**	276.1190	304.1139
ES	189.0870	217.0819						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
97.9	2194.2069	0.1210	VINALAKPIDGRGEIVASESR
16.6	2194.0807	0.2472	SFADRAVLSLQSNPGWGFDK
14.9	2194.0993	0.2286	TWMNWPNITPPALQLPGSR
12.7	2194.2223	0.1056	LSRGTVFVVPSGHPIVVTSSR
11.9	2194.1706	0.1574	VINALGKPIDGRGEIPSSESR
11.8	2194.0484	0.2796	LFHAIFFVQGDEHASSDFK
11.6	2194.2011	0.1269	LHIINGIAQGLLYLHNYSR
10.2	2194.0350	0.2930	VGAGLTNLGSDGDASNGTSSLSSK
10.2	2194.1899	0.1381	RYVYLLPVLALDPSAHPDR
9.0	2194.9491	-0.6211	AFDAMQAWDGVGGGHATYDAR

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

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **SVYEPLQTGLIAIDSMIPIGR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 90: 2272.342124 from(2273.349400,1+) intensity(0.0000) index(25)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221394, MSMS Job_Run_Id: 21364, Comment:
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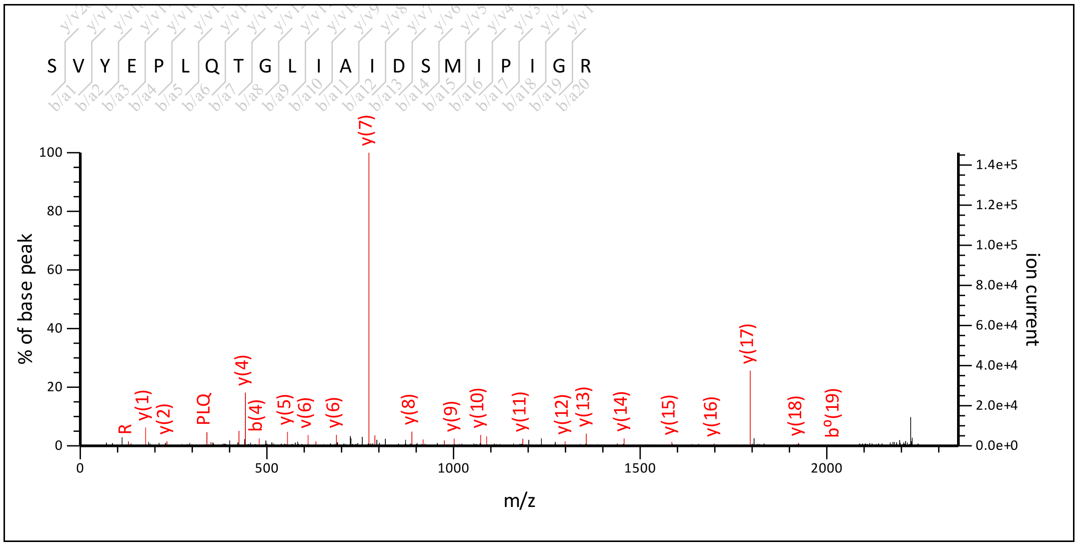


0 to 2352.6

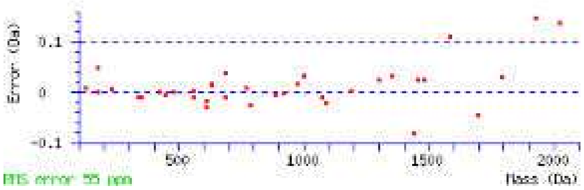
Label all possible matches ○ Label matches used for scoring ●

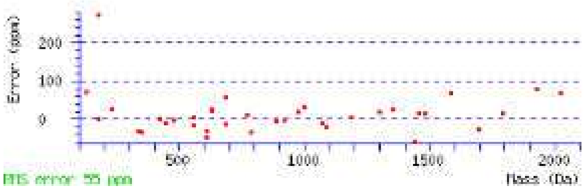
Monoisotopic mass of neutral peptide Mr(calc): 2272.2137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 144 **Expect:** 1e-11
Matches : 37/409 fragment ions using 44 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	72.0808	159.1128		141.1022	187.1077		169.0972	145.0972		V	2142.1264	2155.1468		2186.1890	2169.1624
3	136.0757	322.1761		304.1656	**350.1710**		332.1605			Y	1979.0630			2087.1205	2070.0940
4	102.0550	451.2187		433.2082	**479.2136**		461.2031	393.2132		E	1850.0204	1849.0252		***1924.0572***	1907.0307
5	70.0651	548.2715		530.2609	576.2664		558.2558	522.2558		P	1752.9677	1751.9724		***1795.0146***	1777.9881
6	86.0964	661.3556		643.3450	689.3505		671.3399	619.3086		L	1639.8836	1638.8884		***1697.9619***	1680.9353
7	101.0709	789.4141	772.3876	771.4036	817.4090	800.3825	799.3985	732.3927		Q	1511.8250	1510.8298		***1584.8778***	1567.8512
8	74.0600	890.4618	873.4353	872.4512	**918.4567**	901.4302	900.4462	874.4669	876.4462	T	1410.7773	1423.7977	1425.7770	***1456.8192***	1439.7927
9	30.0338	947.4833	930.4567	929.4727	**975.4782**	958.4516	957.4676			G				***1355.7715***	1338.7450
10	86.0964	1060.5673	1043.5408	1042.5568	**1088.5623**	1071.5357	1070.5517	1018.5204		L	1240.6718	1239.6766		***1298.7501***	1281.7235
11	86.0964	1173.6514	1156.6249	1155.6408	1201.6463	1184.6198	1183.6358	1145.6201	1159.6358	I	1127.5878	1140.6082	1154.6238	***1185.6660***	1168.6395
12	44.0495	1244.6885	1227.6620	1226.6780	1272.6834	1255.6569	1254.6729			A	1056.5506			***1072.5819***	1055.5554
13	86.0964	1357.7726	1340.7460	1339.7620	1385.7675	1368.7409	1367.7569	1329.7413	1343.7569	I	943.4666	956.4870	970.5026	***1001.5448***	984.5183
14	88.0393	1472.7995	1455.7730	1454.7890	1500.7944	1483.7679	1482.7839	1428.8097		D	828.4396	827.4444		***888.4608***	871.4342
15	60.0444	1559.8316	1542.8050	1541.8210	1587.8265	1570.7999	1569.8159	1543.8366		S	741.4076	740.4124		***773.4338***	756.4073
16	104.0528	1690.8720	1673.8455	1672.8615	1718.8670	1701.8404	1700.8564	1630.8687		M	610.3671	609.3719		***686.4018***	669.3752
17	86.0964	1803.9561	1786.9296	1785.9455	1831.9510	1814.9245	1813.9404	1775.9248	1789.9405	I	497.2831	510.3035	524.3191	***555.3613***	538.3348
18	70.0651	1901.0089	1883.9823	1882.9983	1929.0038	1911.9772	1910.9932	1874.9932		P	400.2303	399.2350		***442.2772***	425.2507
19	86.0964	2014.0929	1997.0664	1996.0824	2042.0878	2025.0613	2024.0773	1986.0616	2000.0773	I	287.1462	300.1666	314.1823	345.2245	328.1979
20	30.0338	2071.1144	2054.0878	2053.1038	2099.1093	2082.0828	2081.0987			G				***232.1404***	215.1139
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

VY	235.1441	263.1390	**VYE**	364.1867	392.1816	**VYEP**	461.2395	489.2344
VYEPL	574.3235	602.3184	**YE**	265.1183	293.1132	**YEP**	362.1710	390.1660
YEPL	475.2551	503.2500	**YEPLQ**	603.3137	631.3086	**EP**	199.1077	227.1026
EPL	312.1918	340.1867	**EPLQ**	440.2504	468.2453	**EPLQT**	541.2980	569.2930
EPLQTG	598.3195	626.3144	**PL**	183.1492	211.1441	**PLQ**	311.2078	339.2027
PLQT	412.2554	440.2504	**PLQTG**	469.2769	497.2718	**PLQTGL**	582.3610	610.3559
PLQTGLI	695.4450	723.4400	**LQ**	214.1550	242.1499	**LQT**	315.2027	343.1976
LQTG	372.2241	400.2191	**LQTGL**	485.3082	513.3031	**LQTGLI**	598.3923	626.3872
LQTGLIA	669.4294	697.4243	**QT**	202.1186	230.1135	**QTG**	259.1401	287.1350
QTGL	372.2241	400.2191	**QTGLI**	485.3082	513.3031	**QTGLIA**	556.3453	584.3402
QTGLIAI	669.4294	697.4243	**TG**	131.0815	159.0764	**TGL**	244.1656	272.1605
TGLI	357.2496	385.2445	**TGLIA**	428.2867	456.2817	**TGLIAI**	541.3708	569.3657
TGLIAID	656.3978	684.3927	**GL**	143.1179	171.1128	**GLI**	256.2020	284.1969
GLIA	327.2391	355.2340	**GLIAI**	440.3231	468.3180	**GLIAID**	555.3501	583.3450
GLIAIDS	642.3821	670.3770	**LI**	199.1805	227.1754	**LIA**	270.2176	298.2125
LIAI	383.3017	411.2966	**LIAID**	498.3286	526.3235	**LIAIDS**	585.3606	613.3556
IA	157.1335	185.1285	**IAI**	270.2176	298.2125	**IAID**	385.2445	413.2395
IAIDS	472.2766	500.2715	**IAIDSM**	603.3171	631.3120	**AI**	157.1335	185.1285
AID	272.1605	300.1554	**AIDS**	359.1925	387.1874	**AIDSM**	490.2330	518.2279
AIDSMI	603.3171	631.3120	**ID**	201.1234	229.1183	**IDS**	288.1554	316.1503
IDSM	419.1959	447.1908	**IDSMI**	532.2799	560.2749	**IDSMIP**	629.3327	657.3276
DS	175.0713	203.0662	**DSM**	306.1118	334.1067	**DSMI**	419.1959	447.1908
DSMIP	516.2486	544.2436	**DSMIPI**	629.3327	657.3276	**DSMIPIG**	686.3542	714.3491
SM	191.0849	219.0798	**SMI**	304.1689	332.1639	**SMIP**	401.2217	429.2166
SMIPI	514.3058	542.3007	**SMIPIG**	571.3272	599.3221	**MI**	217.1369	245.1318
MIP	314.1897	342.1846	**MIPI**	427.2737	455.2687	**MIPIG**	484.2952	512.2901
IP	183.1492	211.1441	**IPI**	296.2333	324.2282	**IPIG**	353.2547	381.2496
PI	183.1492	211.1441	**PIG**	240.1707	268.1656	**IG**	143.1179	171.1128





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
144.3	2272.2137	0.1284	SVYEPIQTGLIAIDSMIPIGR
144.3	2272.2137	0.1284	SVYEPLQTGIIAIDSMIPIGR
144.3	2272.2137	0.1284	SVYEPLQTGLIAIDSMIPIGR
144.3	2272.2137	0.1284	SVYEPLQTGLIAIDSMIPIGR
131.1	2272.2137	0.1284	SVYEPLQTGIIAIDAMIPIGR
131.1	2272.2137	0.1284	SVYEPLQTGLIAIDAMIPIGR
94.2	2272.2137	0.1284	SVYEPLQTGILSIDAMIPIGR
18.1	2272.1919	0.1502	LMAKDLILSAIMSLAETHSGR
17.7	2272.2137	0.1284	SVFEPLQTGLIAIDSMIPIGR
17.7	2272.1807	0.1614	SVMEPLQTGLIAIDSMIPIGR

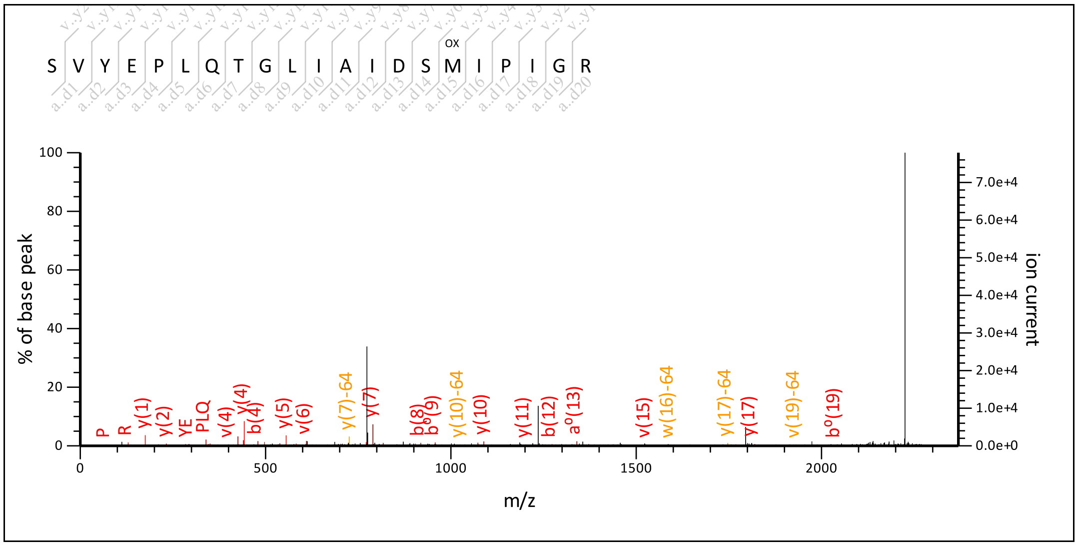
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 97**

MS/MS Fragmentation of **SVYEPLQTGLIAIDSMIPIGR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 92: 2288.339424 from(2289.346700,1+) intensity(0.0000) index(26)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221407, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 2369.31

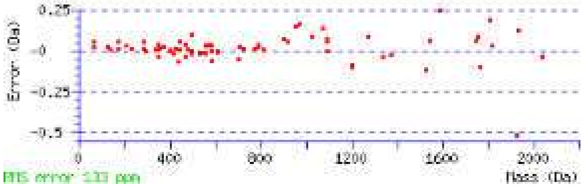
Label all possible matches ○ Label matches used for scoring ●

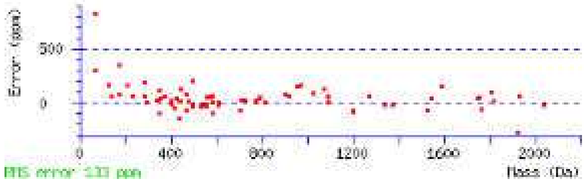
Monoisotopic mass of neutral peptide Mr(calc): 2288.2086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 41 **Expect:** 0.19
Matches : 86/553 fragment ions using 143 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	72.0808	159.1128		141.1022	187.1077		169.0972	145.0972		V	2158.1213	2171.1417		2202.1839	2185.1573
3	136.0757	322.1761		304.1656	***350.1710***		332.1605			Y	1995.0579			2103.1155	2086.0889
4	102.0550	451.2187		433.2082	***479.2136***		461.2031	393.2132		E	1866.0153	1865.0201		1940.0521	1923.0256
5	70.0651	548.2715		530.2609	***576.2664***		558.2558	522.2558		P	1768.9626	1767.9673		***1811.0095***	1793.9830
6	86.0964	661.3556		643.3450	689.3505		671.3399	619.3086		L	1655.8785	1654.8833		1713.9568	1696.9302
7	101.0709	789.4141	772.3876	771.4036	***817.4090***	800.3825	799.3985	732.3927		Q	1527.8199	1526.8247		1600.8727	1583.8462
8	74.0600	890.4618	873.4353	872.4512	***918.4567***	901.4302	900.4462	874.4669	876.4462	T	1426.7723	1439.7927	1441.7719	1472.8141	1455.7876
9	30.0338	947.4833	930.4567	929.4727	***975.4782***	958.4516	957.4676			G				***1371.7664***	1354.7399
10	86.0964	1060.5673	1043.5408	1042.5568	***1088.5623***	1071.5357	1070.5517	1018.5204		L	1256.6667	1255.6715		1314.7450	1297.7184
11	86.0964	1173.6514	1156.6249	1155.6408	***1201.6463***	1184.6198	1183.6358	1145.6201	1159.6358	I	1143.5827	1156.6031	1170.6187	***1201.6609***	1184.6344
12	44.0495	1244.6885	1227.6620	1226.6780	***1272.6834***	1255.6569	1254.6729			A	1072.5456			***1088.5769***	1071.5503
13	86.0964	1357.7726	1340.7460	1339.7620	1385.7675	1368.7409	1367.7569	1329.7413	1343.7569	I	959.4615	972.4819	986.4975	1017.5397	1000.5132
14	88.0393	1472.7995	1455.7730	1454.7890	1500.7944	1483.7679	1482.7839	1428.8097		D	844.4345	843.4393		***904.4557***	887.4291
15	60.0444	1559.8316	1542.8050	1541.8210	1587.8265	1570.7999	1569.8159	1543.8366		S	757.4025	756.4073		***789.4287***	772.4022
16	120.0478	1706.8670	1689.8404	1688.8564	1734.8619	1717.8353	1716.8513	1630.8687		M	610.3671	609.3719		***702.3967***	685.3702
17	86.0964	1819.9510	1802.9245	1801.9404	1847.9459	1830.9194	1829.9354	1791.9197	1805.9354	I	497.2831	510.3035	524.3191	***555.3613***	538.3348
18	70.0651	1917.0038	1899.9772	1898.9932	1944.9987	1927.9721	1926.9881	1890.9881		P	400.2303	399.2350		***442.2772***	425.2507
19	86.0964	2030.0878	2013.0613	2012.0773	2058.0828	2041.0562	2040.0722	2002.0565	2016.0722	I	287.1462	300.1666	314.1823	***345.2245***	328.1979
20	30.0338	2087.1093	2070.0828	2069.0987	2115.1042	2098.0777	2097.0937			G				***232.1404***	215.1139

21	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VY	235.1441	263.1390	**VYE**	364.1867	392.1816	**VYEP**	461.2395	489.2344
VYEPL	574.3235	602.3184	**YE**	265.1183	293.1132	**YEP**	362.1710	390.1660
YEPL	475.2551	503.2500	**YEPLQ**	603.3137	631.3086	**EP**	199.1077	227.1026
EPL	312.1918	340.1867	**EPLQ**	440.2504	468.2453	**EPLQT**	541.2980	569.2930
EPLQTG	598.3195	626.3144	**PL**	183.1492	211.1441	**PLQ**	311.2078	339.2027
PLQT	412.2554	440.2504	**PLQTG**	469.2769	497.2718	**PLQTGL**	582.3610	610.3559
PLQTGLI	695.4450	723.4400	**LQ**	214.1550	242.1499	**LQT**	315.2027	343.1976
LQTG	372.2241	400.2191	**LQTGL**	485.3082	513.3031	**LQTGLI**	598.3923	626.3872
LQTGLIA	669.4294	697.4243	**QT**	202.1186	230.1135	**QTG**	259.1401	287.1350
QTGL	372.2241	400.2191	**QTGLI**	485.3082	513.3031	**QTGLIA**	556.3453	584.3402
QTGLIAI	669.4294	697.4243	**TG**	131.0815	159.0764	**TGL**	244.1656	272.1605
TGLI	357.2496	385.2445	**TGLIA**	428.2867	456.2817	**TGLIAI**	541.3708	569.3657
TGLIAID	656.3978	684.3927	**GL**	143.1179	171.1128	**GLI**	256.2020	284.1969
GLIA	327.2391	355.2340	**GLIAI**	440.3231	468.3180	**GLIAID**	555.3501	583.3450
GLIAIDS	642.3821	670.3770	**LI**	199.1805	227.1754	**LIA**	270.2176	298.2125
LIAI	383.3017	411.2966	**LIAID**	498.3286	526.3235	**LIAIDS**	585.3606	613.3556
IA	157.1335	185.1285	**IAI**	270.2176	298.2125	**IAID**	385.2445	413.2395
IAIDS	472.2766	500.2715	**IAIDSM**	619.3120	647.3069	**AI**	157.1335	185.1285
AID	272.1605	300.1554	**AIDS**	359.1925	387.1874	**AIDSM**	506.2279	534.2228
AIDSMI	619.3120	647.3069	**ID**	201.1234	229.1183	**IDS**	288.1554	316.1503
IDSM	435.1908	463.1857	**IDSMI**	548.2749	576.2698	**IDSMIP**	645.3276	673.3225
DS	175.0713	203.0662	**DSM**	322.1067	350.1016	**DSMI**	435.1908	463.1857
DSMIP	532.2436	560.2385	**DSMIPI**	645.3276	673.3225	**SM**	207.0798	235.0747
SMI	320.1639	348.1588	**SMIP**	417.2166	445.2115	**SMIPI**	530.3007	558.2956
SMIPIG	587.3221	615.3171	**MI**	233.1318	261.1267	**MIP**	330.1846	358.1795
MIPI	443.2687	471.2636	**MIPIG**	500.2901	528.2850	**IP**	183.1492	211.1441
IPI	296.2333	324.2282	**IPIG**	353.2547	381.2496	**PI**	183.1492	211.1441
PIG	240.1707	268.1656	**IG**	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.5	2288.2086	0.1308	SVYEPIQTGLIAIDSMIPIGR
41.5	2288.2086	0.1308	SVYEPLQTGIIAIDSMIPIGR
41.5	2288.2086	0.1308	SVYEPLQTGLIAIDSMIPIGR
41.5	2288.2086	0.1308	SVYEPLQTGLIAIDSMIPIGR
39.1	2288.2086	0.1308	SVYEPLQTGILSIDAMIPIGR
13.6	2288.1206	0.2189	ENDIELSTTPLSPSEKQCIK
10.8	2287.3007	1.0387	TMILSVLSSPALVSGLMVVRAK
8.7	2288.1042	0.2352	RGVEPDVVTYTALMDGHCLR
7.7	2288.1273	0.2121	SADAVLVFMHQHPIATHWGR
7.7	2288.1518	0.1876	LGFGLDTHVCTSLVLANCRR

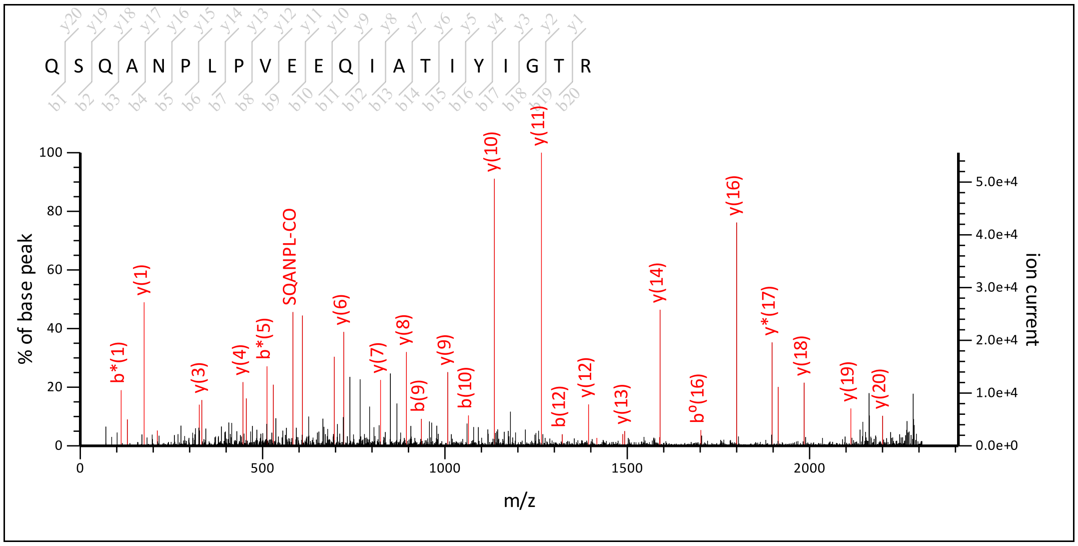
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **QSQANPLPVEEQIATIYIGTR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 97: 2327.341824 from(2328.349100,1+) intensity(0.0000) index(28)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221391, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 2408.04

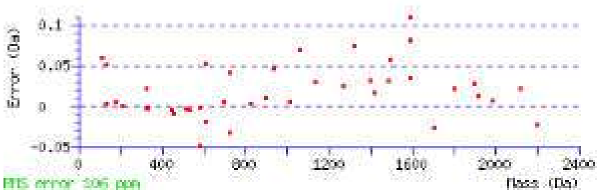
Label all possible matches ○ Label matches used for scoring ●

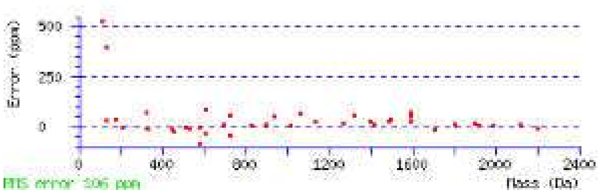
```
Monoisotopic mass of neutral peptide Mr(calc): 2327.2121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 167  Expect: 5.1e-14
Matches : 43/423 fragment ions using 46 most intense peaks    (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.0709	101.0709	84.0444		**129.0659**	112.0393		44.0495		Q					
2	60.0444	188.1030	171.0764	170.0924	216.0979	199.0713	198.0873	172.1081		S	2168.1346	2167.1394		***2200.1608***	2183.1343
3	101.0709	316.1615	299.1350	298.1510	344.1565	327.1299	326.1459	259.1401		Q	2040.0760	2039.0808		***2113.1288***	2096.1022
4	44.0495	387.1987	370.1721	369.1881	415.1936	398.1670	397.1830			A	1969.0389			***1985.0702***	1968.0437
5	87.0553	501.2416	484.2150	483.2310	**529.2365**	512.2100	511.2259	458.2358		N	1854.9960	1854.0007		***1914.0331***	1897.0066
6	70.0651	598.2944	581.2678	580.2838	626.2893	609.2627	608.2787	572.2787		P	1757.9432	1756.9480		***1799.9902***	1782.9636
7	86.0964	711.3784	694.3519	693.3678	739.3733	722.3468	721.3628	669.3315		L	1644.8592	1643.8639		1702.9374	1685.9109
8	70.0651	808.4312	791.4046	790.4206	836.4261	819.3995	818.4155	782.4155		P	1547.8064	1546.8112		***1589.8534***	1572.8268
9	72.0808	907.4996	890.4730	889.4890	**935.4945**	918.4680	917.4839	893.4839		V	1448.7380	1461.7584		***1492.8006***	1475.7740
10	102.0550	1036.5422	1019.5156	1018.5316	**1064.5371**	1047.5106	1046.5265	978.5367		E	1319.6954	1318.7001		***1393.7322***	1376.7056
11	102.0550	1165.5848	1148.5582	1147.5742	1193.5797	1176.5531	1175.5691	1107.5793		E	1190.6528	1189.6576		***1264.6896***	1247.6630
12	101.0709	1293.6434	1276.6168	1275.6328	**1321.6383**	1304.6117	1303.6277	1236.6219		Q	1062.5942	1061.5990		***1135.6470***	1118.6204
13	86.0964	1406.7274	1389.7009	1388.7169	1434.7223	1417.6958	1416.7118	1378.6961	1392.7118	I	949.5102	962.5306	976.5462	***1007.5884***	990.5619
14	44.0495	1477.7645	1460.7380	1459.7540	1505.7594	1488.7329	1487.7489			A	878.4730			***894.5043***	877.4778
15	74.0600	1578.8122	1561.7857	1560.8016	1606.8071	1589.7806	1588.7966	1562.8173	1564.7966	T	777.4254	790.4458	792.4250	***823.4672***	806.4407
16	86.0964	1691.8963	1674.8697	1673.8857	1719.8912	1702.8646	1701.8806	1663.8650	1677.8806	I	664.3413	677.3617	691.3774	***722.4196***	705.3930
17	136.0757	1854.9596	1837.9331	1836.9490	1882.9545	1865.9280	1864.9440			Y	501.2780			***609.3355***	592.3089
18	86.0964	1968.0437	1951.0171	1950.0331	1996.0386	1979.0120	1978.0280	1940.0124	1954.0280	I	388.1939	401.2143	415.2300	***446.2722***	429.2456
19	30.0338	2025.0651	2008.0386	2007.0546	2053.0600	2036.0335	2035.0495			G				***333.1881***	316.1615
20	74.0600	2126.1128	2109.0863	2108.1022	2154.1077	2137.0812	2136.0972	2110.1179	2112.0972	T	230.1248	243.1452	245.1244	276.1666	259.1401
21	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

SQ	188.1030	216.0979	**SQA**	259.1401	287.1350	**SQAN**	373.1830	401.1779
SQANP	470.2358	498.2307	**SQANPL**	583.3198	611.3148	**SQANPLP**	680.3726	708.3675
QA	172.1081	200.1030	**QAN**	286.1510	314.1459	**QANP**	383.2037	411.1987
QANPL	496.2878	524.2827	**QANPLP**	593.3406	621.3355	**QANPLPV**	692.4090	720.4039
AN	158.0924	186.0873	**ANP**	255.1452	283.1401	**ANPL**	368.2292	396.2241
ANPLP	465.2820	493.2769	**ANPLPV**	564.3504	592.3453	**ANPLPVE**	693.3930	721.3879
NP	184.1081	212.1030	**NPL**	297.1921	325.1870	**NPLP**	394.2449	422.2398
NPLPV	493.3133	521.3082	**NPLPVE**	622.3559	650.3508	**PL**	183.1492	211.1441
PLP	280.2020	308.1969	**PLPV**	379.2704	407.2653	**PLPVE**	508.3130	536.3079
PLPVEE	637.3556	665.3505	**LP**	183.1492	211.1441	**LPV**	282.2176	310.2125
LPVE	411.2602	439.2551	**LPVEE**	540.3028	568.2977	**LPVEEQ**	668.3614	696.3563
PV	169.1335	197.1285	**PVE**	298.1761	326.1710	**PVEE**	427.2187	455.2136
PVEEQ	555.2773	583.2722	**PVEEQI**	668.3614	696.3563	**VE**	201.1234	229.1183
VEE	330.1660	358.1609	**VEEQ**	458.2245	486.2195	**VEEQI**	571.3086	599.3035
VEEQIA	642.3457	670.3406	**EE**	231.0975	259.0925	**EEQ**	359.1561	387.1510
EEQI	472.2402	500.2351	**EEQIA**	543.2773	571.2722	**EEQIAT**	644.3250	672.3199
EQ	230.1135	258.1084	**EQI**	343.1976	371.1925	**EQIA**	414.2347	442.2296
EQIAT	515.2824	543.2773	**EQIATI**	628.3665	656.3614	**QI**	214.1550	242.1499
QIA	285.1921	313.1870	**QIAT**	386.2398	414.2347	**QIATI**	499.3239	527.3188
QIATIY	662.3872	690.3821	**IA**	157.1335	185.1285	**IAT**	258.1812	286.1761
IATI	371.2653	399.2602	**IATIY**	534.3286	562.3235	**IATIYI**	647.4127	675.4076
AT	145.0972	173.0921	**ATI**	258.1812	286.1761	**ATIY**	421.2445	449.2395
ATIYI	534.3286	562.3235	**ATIYIG**	591.3501	619.3450	**ATIYIGT**	692.3978	720.3927
TI	187.1441	215.1390	**TIY**	350.2074	378.2023	**TIYI**	463.2915	491.2864
TIYIG	520.3130	548.3079	**TIYIGT**	621.3606	649.3556	**IY**	249.1598	277.1547
IYI	362.2438	390.2387	**IYIG**	419.2653	447.2602	**IYIGT**	520.3130	548.3079
YI	249.1598	277.1547	**YIG**	306.1812	334.1761	**YIGT**	407.2289	435.2238
IG	143.1179	171.1128	**IGT**	244.1656	272.1605	**GT**	131.0815	159.0764





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
167.3	2327.2121	0.1297	QSQANPLPVEEQIATIYIGTR
17.5	2326.2218	1.1201	TGTMSLFPLLMAGIVSIAYWR
17.2	2327.2155	0.1263	MTTVSTLTALAGETALRSSFVR
16.4	2327.1427	0.1991	TLENSHPDLKELDVSTNMLR
13.7	2327.2824	0.0594	QFMFGVKPTTLALHSITIPAR
13.6	2326.1448	1.1970	RQLNAALDVMNAATTGDGTHVR
12.8	2328.2226	-0.8808	AGNRIPGLSIVIDEATWDFVR
11.1	2327.0899	0.2519	MYAQEGGMRLVSHPIAAHDGR
10.8	2326.1917	1.1501	QEDLIVYGQSVGSGPTLHLASR
9.4	2326.1917	1.1501	QEDVILYGQSVGSGPTLHLASR

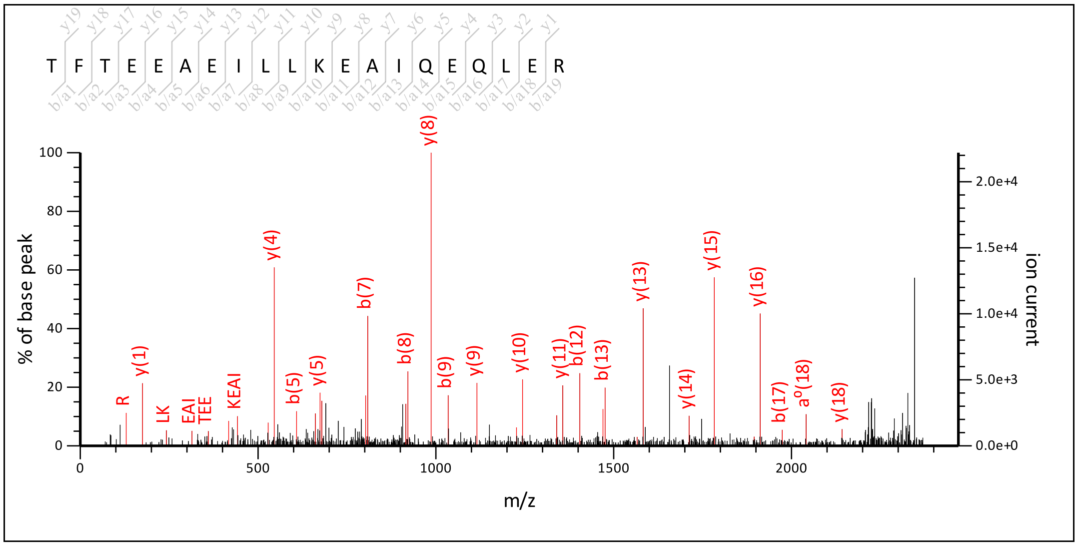
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 97

MS/MS Fragmentation of **TFTEEAEILLKEAIQEQLER**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 99: 2389.375824 from(2390.383100,1+) intensity(0.0000) index(29)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221397, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



0 to 2469.35

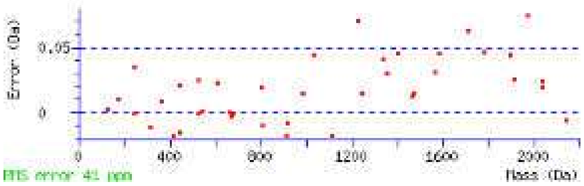
Label all possible matches ○ Label matches used for scoring ●

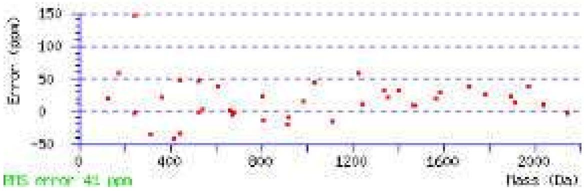
Monoisotopic mass of neutral peptide Mr(calc): 2389.2376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 152 **Expect:** 1.5e-12
Matches : 45/373 fragment ions using 46 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	120.0808	221.1285		203.1179	249.1234		231.1128			F	2197.1347			2289.1973	2272.1707
3	74.0600	322.1761		304.1656	350.1710		332.1605	306.1812	308.1605	T	2096.0870	2109.1074	2111.0867	***2142.1289***	2125.1023
4	102.0550	451.2187		433.2082	479.2136		461.2031	393.2132		E	1967.0444	1966.0491		***2041.0812***	2024.0546
5	102.0550	580.2613		562.2508	**608.2562**		590.2457	522.2558		E	1838.0018	1837.0066		***1912.0386***	1895.0120
6	44.0495	651.2984		633.2879	**679.2933**		661.2828			A	1766.9647			***1782.9960***	1765.9694
7	102.0550	780.3410		762.3305	**808.3359**		790.3254	722.3355		E	1637.9221	1636.9268		***1711.9589***	1694.9323
8	86.0964	893.4251		875.4145	**921.4200**		903.4094	865.3938	879.4094	I	1524.8380	1537.8584	1551.8741	***1582.9163***	1565.8897
9	86.0964	1006.5092		988.4986	**1034.5041**		1016.4935	964.4622		L	1411.7540	1410.7587		***1469.8322***	1452.8057
10	86.0964	1119.5932		1101.5827	1147.5881		1129.5776	1077.5463		L	1298.6699	1297.6747		***1356.7482***	1339.7216
11	101.1073	1247.6882	1230.6616	1229.6776	1275.6831	1258.6565	1257.6725	1190.6303		K	1170.5749	1169.5797		***1243.6641***	1226.6375
12	102.0550	1376.7308	1359.7042	1358.7202	**1404.7257**	1387.6991	1386.7151	1318.7253		E	1041.5324	1040.5371		***1115.5691***	1098.5426
13	44.0495	1447.7679	1430.7413	1429.7573	**1475.7628**	1458.7363	1457.7522			A	970.4952			***986.5265***	969.5000
14	86.0964	1560.8520	1543.8254	1542.8414	1588.8469	1571.8203	1570.8363	1532.8207	1546.8363	I	857.4112	870.4316	884.4472	***915.4894***	898.4629
15	101.0709	1688.9105	1671.8840	1670.9000	1716.9054	1699.8789	1698.8949	1631.8891		Q	729.3526	728.3573		***802.4054***	785.3788
16	102.0550	1817.9531	1800.9266	1799.9426	1845.9480	1828.9215	1827.9375	1759.9476		E	600.3100	599.3148		***674.3468***	657.3202
17	101.0709	1946.0117	1928.9852	1928.0011	**1974.0066**	1956.9801	1955.9961	1888.9902		Q	472.2514	471.2562		***545.3042***	528.2776
18	86.0964	2059.0958	2042.0692	2041.0852	2087.0907	2070.0641	2069.0801	2017.0488		L	359.1674	358.1721		***417.2456***	400.2191
19	102.0550	2188.1384	2171.1118	2170.1278	2216.1333	2199.1067	2198.1227	2130.1329		E	230.1248	229.1295		304.1615	287.1350
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FT	221.1285	249.1234	FTE	350.1710	378.1660	FTEE	479.2136	507.2086

FTEEA	550.2508	578.2457	**FTEEAE**	679.2933	707.2883	**TE**	203.1026	231.0975
TEE	332.1452	360.1401	**TEEA**	403.1823	431.1773	**TEEAE**	532.2249	560.2198
TEEAEI	645.3090	673.3039	**EE**	231.0975	259.0925	**EEA**	302.1347	330.1296
EEAE	431.1773	459.1722	**EEAEI**	544.2613	572.2562	**EEAEIL**	657.3454	685.3403
EA	173.0921	201.0870	**EAE**	302.1347	330.1296	**EAEI**	415.2187	443.2136
EAEIL	528.3028	556.2977	**EAEILL**	641.3869	669.3818	**AE**	173.0921	201.0870
AEI	286.1761	314.1710	**AEIL**	399.2602	427.2551	**AEILL**	512.3443	540.3392
AEILLK	640.4392	668.4341	**EI**	215.1390	243.1339	**EIL**	328.2231	356.2180
EILL	441.3071	469.3021	**EILLK**	569.4021	597.3970	**EILLKE**	698.4447	726.4396
IL	199.1805	227.1754	**ILL**	312.2646	340.2595	**ILLK**	440.3595	468.3544
ILLKE	569.4021	597.3970	**ILLKEA**	640.4392	668.4341	**LL**	199.1805	227.1754
LLK	327.2755	355.2704	**LLKE**	456.3180	484.3130	**LLKEA**	527.3552	555.3501
LLKEAI	640.4392	668.4341	**LK**	214.1914	242.1863	**LKE**	343.2340	371.2289
LKEA	414.2711	442.2660	**LKEAI**	527.3552	555.3501	**LKEAIQ**	655.4137	683.4087
KE	230.1499	258.1448	**KEA**	301.1870	329.1819	**KEAI**	414.2711	442.2660
KEAIQ	542.3297	570.3246	**KEAIQE**	671.3723	699.3672	**EA**	173.0921	201.0870
EAI	286.1761	314.1710	**EAIQ**	414.2347	442.2296	**EAIQE**	543.2773	571.2722
EAIQEQ	671.3359	699.3308	**AI**	157.1335	185.1285	**AIQ**	285.1921	313.1870
AIQE	414.2347	442.2296	**AIQEQ**	542.2933	570.2882	**AIQEQL**	655.3774	683.3723
IQ	214.1550	242.1499	**IQE**	343.1976	371.1925	**IQEQ**	471.2562	499.2511
IQEQL	584.3402	612.3352	**QE**	230.1135	258.1084	**QEQ**	358.1721	386.1670
QEQL	471.2562	499.2511	**QEQLE**	600.2988	628.2937	**EQ**	230.1135	258.1084
EQL	343.1976	371.1925	**EQLE**	472.2402	500.2351	**QL**	214.1550	242.1499
QLE	343.1976	371.1925	**LE**	215.1390	243.1339			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
152.3	2389.2376	0.1382	TFTEEAEILLKEAIQEQIER
152.3	2389.2376	0.1382	TFTEEAEILLKEAIQEQLER
93.3	2388.2536	1.1222	TFTEQAEILLKEAIQEQLER
59.0	2390.1965	-0.8206	TFTEEAENLLKEAIQEQIER
22.2	2390.1675	-0.7917	ALCEKDSLPEAVALLDEFENK
17.3	2389.1597	0.2161	NLNHESIIRYCTSWIDVNR
14.4	2390.0696	-0.6938	DNGTAEMVTDEGAIYFTKDAAR
13.7	2388.9621	0.4138	GDDMYMETSDDLIRHMQER
13.6	2390.2515	-0.8757	GFNPESGLLVLVDKSLITMDSR
11.8	2390.2151	-0.8393	IVVSQAELLLMEGNANPSTFNK

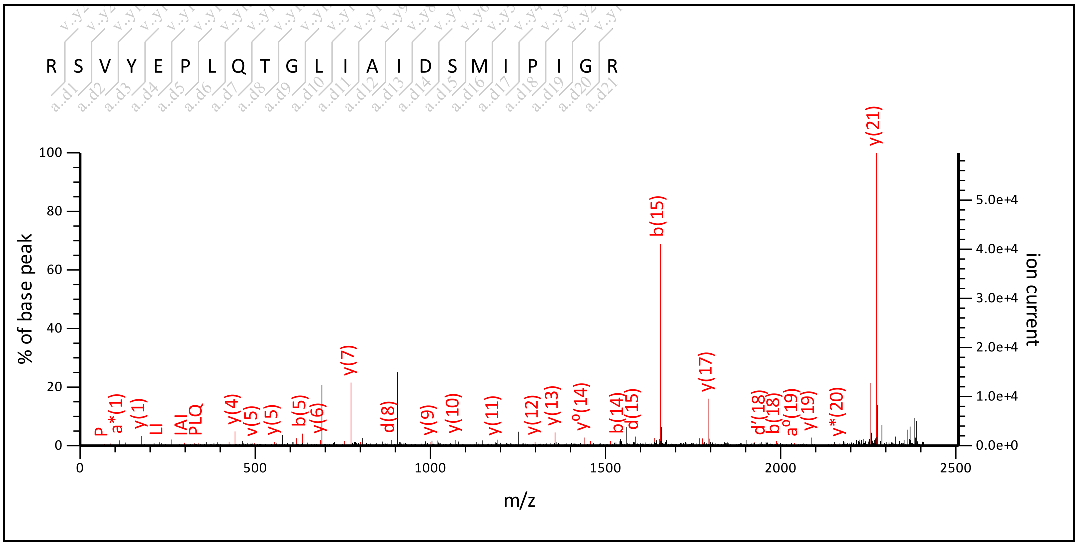
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 97**

MS/MS Fragmentation of **RSVYEPLQTGLIAIDSMIPIGR**
Found in **gi|11466784** in **NCBInr**, ATP synthase CF1 alpha subunit [Oryza sativa Japonica Group]

Match to Query 103: 2428.453424 from(2429.460700,1+) intensity(0.0000) index(31)
Title: Label: I11, Spot_Id: 216645, Peak_List_Id: 221402, MSMS Job_Run_Id: 21364, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Akansha BHU\RAJESH\12-1-13 raj\ppw_I11_136074508400.txt



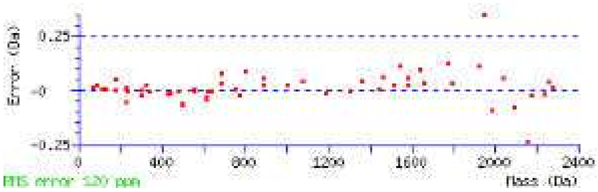
0 to 2507.8

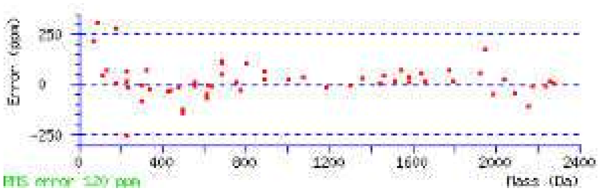
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2428.3148
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 2.4e-07
Matches : 69/442 fragment ions using 96 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	129.1135	129.1135	112.0869		157.1084	140.0818		44.0495		R					
2	60.0444	216.1455	199.1190	198.1349	244.1404	227.1139	226.1298	200.1506		S	2241.1948	2240.1995		***2273.2210***	2256.1944
3	72.0808	315.2139	298.1874	297.2033	343.2088	326.1823	325.1983	301.1983		V	2142.1264	2155.1468		2186.1890	2169.1624
4	136.0757	478.2772	461.2507	460.2667	506.2722	489.2456	488.2616			Y	1979.0630			***2087.1205***	2070.0940
5	102.0550	607.3198	590.2933	589.3093	**635.3148**	618.2882	617.3042	549.3144		E	1850.0204	1849.0252		***1924.0572***	1907.0307
6	70.0651	704.3726	687.3461	686.3620	732.3675	715.3410	714.3570	678.3570		P	1752.9677	1751.9724		***1795.0146***	1777.9881
7	86.0964	817.4567	800.4301	799.4461	845.4516	828.4250	827.4410	775.4097		L	1639.8836	1638.8884		1697.9619	1680.9353
8	101.0709	945.5152	928.4887	927.5047	973.5102	956.4836	955.4996	888.4938		Q	1511.8250	1510.8298		***1584.8778***	1567.8512
9	74.0600	1046.5629	1029.5364	1028.5524	1074.5578	1057.5313	1056.5473	1030.5680	1032.5473	T	1410.7773	1423.7977	1425.7770	***1456.8192***	1439.7927
10	30.0338	1103.5844	1086.5578	1085.5738	1131.5793	1114.5528	1113.5687			G				***1355.7715***	1338.7450
11	86.0964	1216.6684	1199.6419	1198.6579	1244.6634	1227.6368	1226.6528	1174.6215		L	1240.6718	1239.6766		***1298.7501***	1281.7235
12	86.0964	1329.7525	1312.7260	1311.7419	1357.7474	1340.7209	1339.7369	1301.7212	1315.7369	I	1127.5878	1140.6082	1154.6238	***1185.6660***	1168.6395
13	44.0495	1400.7896	1383.7631	1382.7791	1428.7845	1411.7580	1410.7740			A	1056.5506			***1072.5819***	1055.5554
14	86.0964	1513.8737	1496.8471	1495.8631	**1541.8686**	1524.8421	1523.8580	1485.8424	1499.8580	I	943.4666	956.4870	970.5026	***1001.5448***	984.5183
15	88.0393	1628.9006	1611.8741	1610.8901	**1656.8955**	1639.8690	1638.8850	1584.9108		D	828.4396	827.4444		***888.4608***	871.4342
16	60.0444	1715.9327	1698.9061	1697.9221	1743.9276	1726.9010	1725.9170	1699.9377		S	741.4076	740.4124		***773.4338***	756.4073
17	104.0528	1846.9731	1829.9466	1828.9626	1874.9681	1857.9415	1856.9575	1786.9698		M	610.3671	609.3719		***686.4018***	669.3752
18	86.0964	1960.0572	1943.0307	1942.0466	**1988.0521**	1971.0256	1970.0416	1932.0259	1946.0416	I	497.2831	510.3035	524.3191	***555.3613***	538.3348
19	70.0651	2057.1100	2040.0834	2039.0994	2085.1049	2068.0783	2067.0943	2031.0943		P	400.2303	399.2350		***442.2772***	425.2507
20	86.0964	2170.1940	2153.1675	2152.1835	2198.1890	2181.1624	2180.1784	2142.1627	2156.1784	I	287.1462	300.1666	314.1823	345.2245	328.1979
21	30.0338	2227.2155	2210.1890	2209.2049	**2255.2104**	2238.1839	2237.1999			G				***232.1404***	215.1139
22	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SV	159.1128	187.1077	SVY	322.1761	350.1710	SVYE	451.2187	479.2136
SVYEP	548.2715	576.2664	SVYEPL	661.3556	689.3505	VY	235.1441	263.1390
VYE	364.1867	392.1816	VYEP	461.2395	489.2344	VYEPL	574.3235	602.3184
YE	265.1183	293.1132	YEP	362.1710	390.1660	YEPL	475.2551	503.2500
YEPLQ	603.3137	631.3086	EP	199.1077	227.1026	EPL	312.1918	340.1867
EPLQ	440.2504	468.2453	EPLQT	541.2980	569.2930	EPLQTG	598.3195	626.3144
PL	183.1492	211.1441	PLQ	311.2078	339.2027	PLQT	412.2554	440.2504
PLQTG	469.2769	497.2718	PLQTGL	582.3610	610.3559	PLQTGLI	695.4450	723.4400
LQ	214.1550	242.1499	LQT	315.2027	343.1976	LQTG	372.2241	400.2191
LQTGL	485.3082	513.3031	LQTGLI	598.3923	626.3872	LQTGLIA	669.4294	697.4243
QT	202.1186	230.1135	QTG	259.1401	287.1350	QTGL	372.2241	400.2191
QTGLI	485.3082	513.3031	QTGLIA	556.3453	584.3402	QTGLIAI	669.4294	697.4243
TG	131.0815	159.0764	TGL	244.1656	272.1605	TGLI	357.2496	385.2445
TGLIA	428.2867	456.2817	TGLIAI	541.3708	569.3657	TGLIAID	656.3978	684.3927
GL	143.1179	171.1128	GLI	256.2020	284.1969	GLIA	327.2391	355.2340
GLIAI	440.3231	468.3180	GLIAID	555.3501	583.3450	GLIAIDS	642.3821	670.3770
LI	199.1805	227.1754	LIA	270.2176	298.2125	LIAI	383.3017	411.2966
LIAID	498.3286	526.3235	LIAIDS	585.3606	613.3556	IA	157.1335	185.1285
IAI	270.2176	298.2125	IAID	385.2445	413.2395	IAIDS	472.2766	500.2715
IAIDSM	603.3171	631.3120	AI	157.1335	185.1285	AID	272.1605	300.1554
AIDS	359.1925	387.1874	AIDSM	490.2330	518.2279	AIDSMI	603.3171	631.3120
ID	201.1234	229.1183	IDS	288.1554	316.1503	IDSM	419.1959	447.1908
IDSMI	532.2799	560.2749	IDSMIP	629.3327	657.3276	DS	175.0713	203.0662
DSM	306.1118	334.1067	DSMI	419.1959	447.1908	DSMIP	516.2486	544.2436
DSMIPI	629.3327	657.3276	DSMIPIG	686.3542	714.3491	SM	191.0849	219.0798
SMI	304.1689	332.1639	SMIP	401.2217	429.2166	SMIPI	514.3058	542.3007
SMIPIG	571.3272	599.3221	MI	217.1369	245.1318	MIP	314.1897	342.1846
MIPI	427.2737	455.2687	MIPIG	484.2952	512.2901	IP	183.1492	211.1441
IPI	296.2333	324.2282	IPIG	353.2547	381.2496	PI	183.1492	211.1441
PIG	240.1707	268.1656	IG	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.4	2428.3148	0.1386	RSVYEPIQTGLIAIDSMIPIGR
100.4	2428.3148	0.1386	RSVYEPLQTGIIAIDSMIPIGR
100.4	2428.3148	0.1386	RSVYEPLQTGLIAIDSMIPIGR
100.4	2428.3148	0.1386	RSVYEPLQTGLIAIDSMIPIGR
88.6	2428.3148	0.1386	RSVYEPLQTGIIAIDAMIPIGR
88.6	2428.3148	0.1386	RSVYEPLQTGLIAIDAMIPIGR
65.3	2428.3148	0.1386	RSVYEPLQTGILSIDAMIPIGR
44.8	2428.1257	0.3278	MTYYTPNYETKDTDILAAFR
34.5	2429.1097	-0.6563	MTYYTPDYETKDTDILAAFR
34.5	2429.1097	-0.6563	MTYYTPDYETKDTDILAAFR

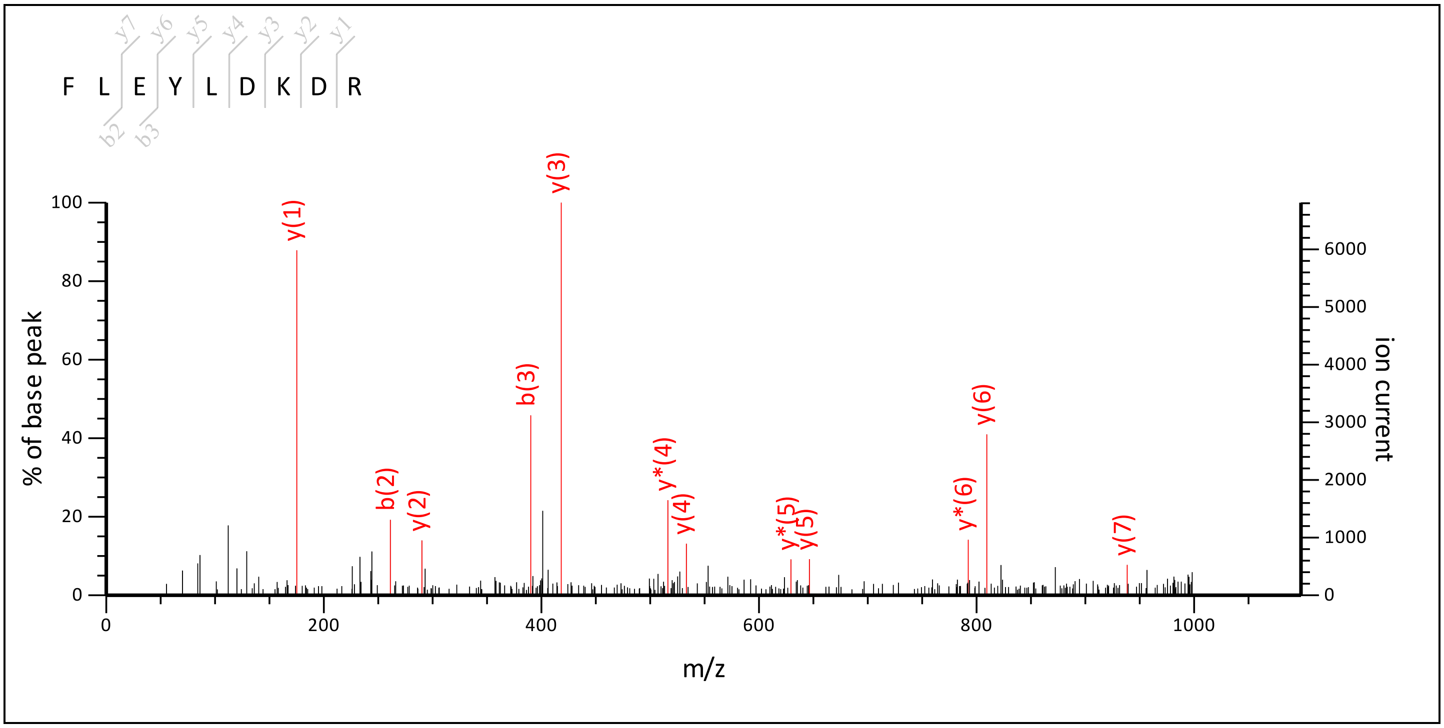
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 101

MS/MS Fragmentation of **FLEYLDKDR**
Found in **gi|75114857** in **NCBInr**, RecName: Full=ATP-dependent zinc metalloprotease FTSH 2, chloroplastic; Short=OsFTSH2; Flags: Precursor

Match to Query 16: 1197.624024 from(1198.631300,1+) intensity(0.0000) index(6)
Title: Label: H1, Spot_Id: 219681, Peak_List_Id: 224997, MSMS Job_Run_Id: 21760, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_H1_136842035700.txt



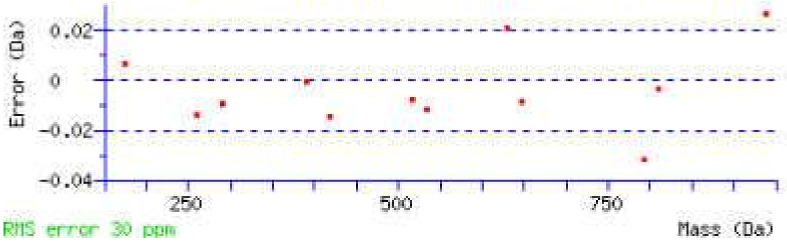
0 to 1098.23

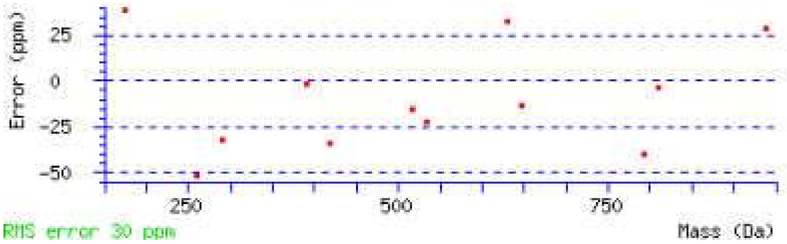
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1197.6030
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.022
Matches : 12/36 fragment ions using 20 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	120.0808		148.0757		F			9
2	233.1648		**261.1598**		L	1051.5419	1034.5153	8
3	362.2074		**390.2023**		E	***938.4578***	921.4312	7
4	525.2708		553.2657		Y	***809.4152***	792.3886	6
5	638.3548		666.3497		L	***646.3519***	629.3253	5
6	753.3818		781.3767		D	***533.2678***	516.2413	4
7	881.4767	864.4502	909.4716	892.4451	K	***418.2409***	401.2143	3

8	996.5037	979.4771	1024.4986	1007.4720	**D**	***290.1459***	273.1193	**2**
9					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.1	1197.6030	0.0211	FLEYLDKDR
22.8	1197.6030	0.0211	LFELYKDDR
22.0	1197.5302	0.0938	IFEDFEAGDR
22.0	1197.5302	0.0938	LFEDFEAGDR
20.2	1197.6030	0.0211	LEFIYDAATR
18.2	1197.5818	0.0422	LFEYGGYPPR
18.2	1197.5448	0.0792	MEEYSRDLR
17.6	1197.5812	0.0428	MLASNLYTNR
13.6	1197.5886	0.0354	MLEIYVCVR
13.5	1197.6104	0.0137	MIEYLVTWK

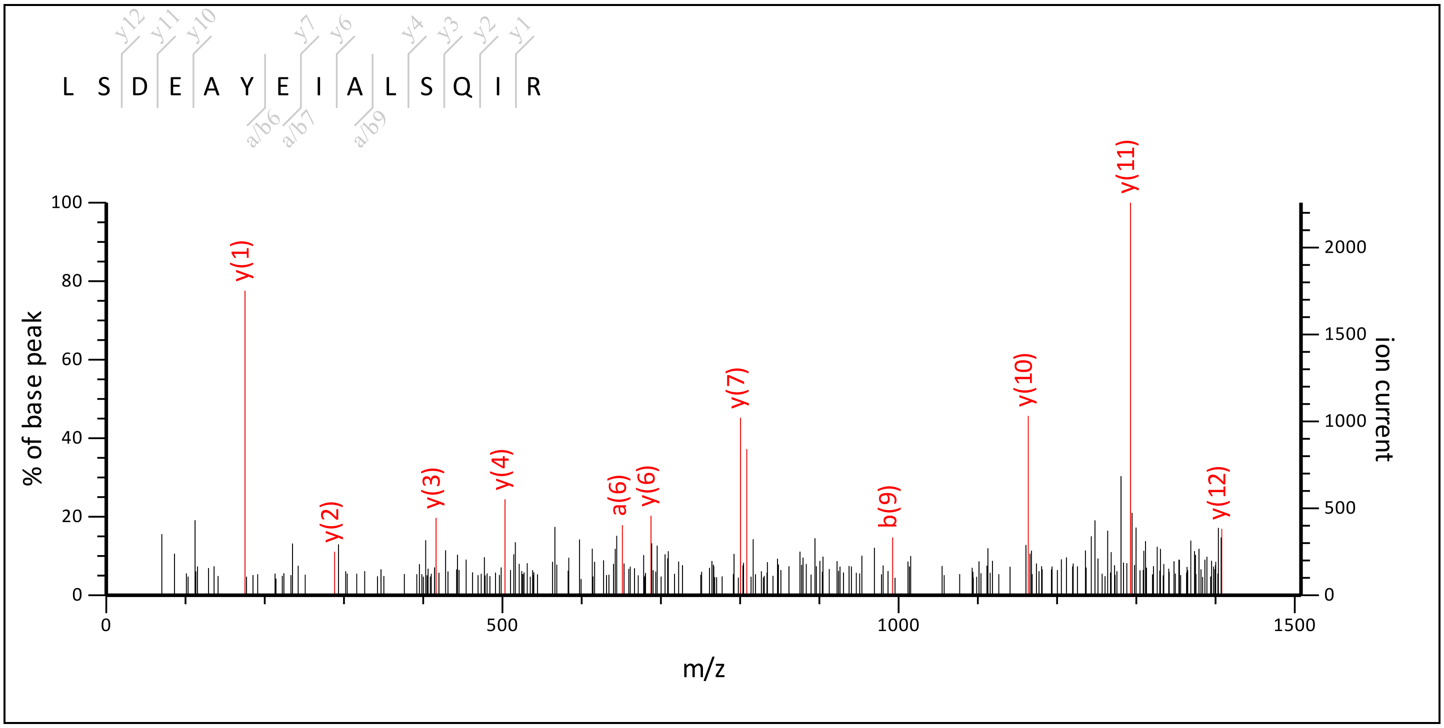
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 101

MS/MS Fragmentation of **LSDEAYEIALSQIR**
Found in **gi|75114857** in **NCBInr**, RecName: Full=ATP-dependent zinc metalloprotease FTSH 2, chloroplastic; Short=OsFTSH2; Flags: Precursor

Match to Query 20: 1606.863224 from(1607.870500,1+) intensity(0.0000) index(8)
Title: Label: H1, Spot_Id: 219681, Peak_List_Id: 225000, MSMS Job_Run_Id: 21760, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_H1_136842035700.txt



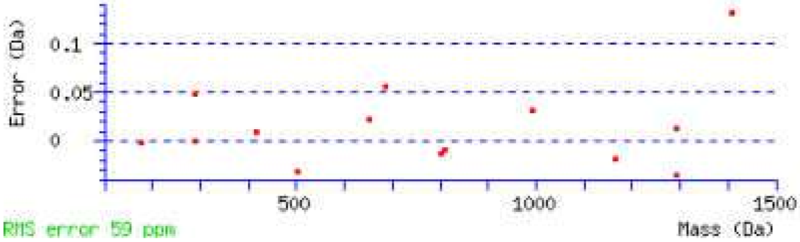
0 to 1507.84

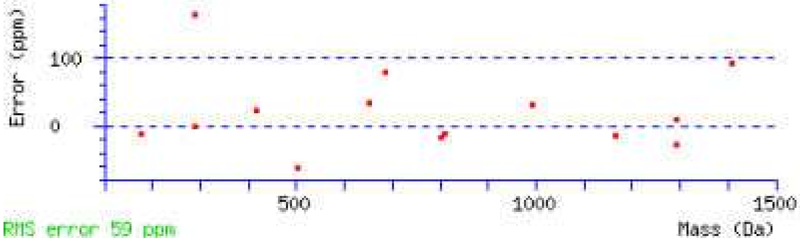
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1606.8202
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.028
Matches : 14/56 fragment ions using 28 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		L			14
2	173.1285		201.1234		S	1494.7435	1477.7169	13
3	**288.1554**		316.1503		D	***1407.7114***	1390.6849	12
4	417.1980		445.1929		E	***1292.6845***	1275.6579	11
5	488.2351		516.2300		A	***1163.6419***	1146.6154	10
6	**651.2984**		679.2933		Y	1092.6048	1075.5782	9
7	780.3410		**808.3359**		E	929.5415	912.5149	8

8	893.4251		921.4200		**I**	***800.4989***	783.4723	**7**
9	964.4622		**992.4571**		**A**	***687.4148***	670.3883	**6**
10	1077.5463		1105.5412		**L**	616.3777	599.3511	**5**
11	1164.5783		1192.5732		**S**	***503.2936***	486.2671	**4**
12	**1292.6369**	1275.6103	1320.6318	1303.6052	**Q**	***416.2616***	399.2350	**3**
13	1405.7209	1388.6944	1433.7159	1416.6893	**I**	***288.2030***	271.1765	**2**
14					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.9	1606.8202	0.0430	LSDEAYEIALSQIR
20.5	1606.8177	0.0455	SMAYYVINYSKLR
11.2	1606.8865	-0.0232	MAFLLNNTALSKLR
9.3	1606.8539	0.0093	QAVADHANNLASKIR
8.2	1606.9671	-0.1039	LVDIVVFLHRQIR
8.0	1606.8250	0.0383	LSDRGYVMVNGQIR
7.9	1606.8791	-0.0158	EAGDASAILPPRAIAR
7.8	1606.7813	0.0819	ISDYMYRFLDLR
7.2	1606.7621	0.1012	LSDDGAVETRMELR
6.7	1606.9195	-0.0563	LLEFPSLIAQHALR

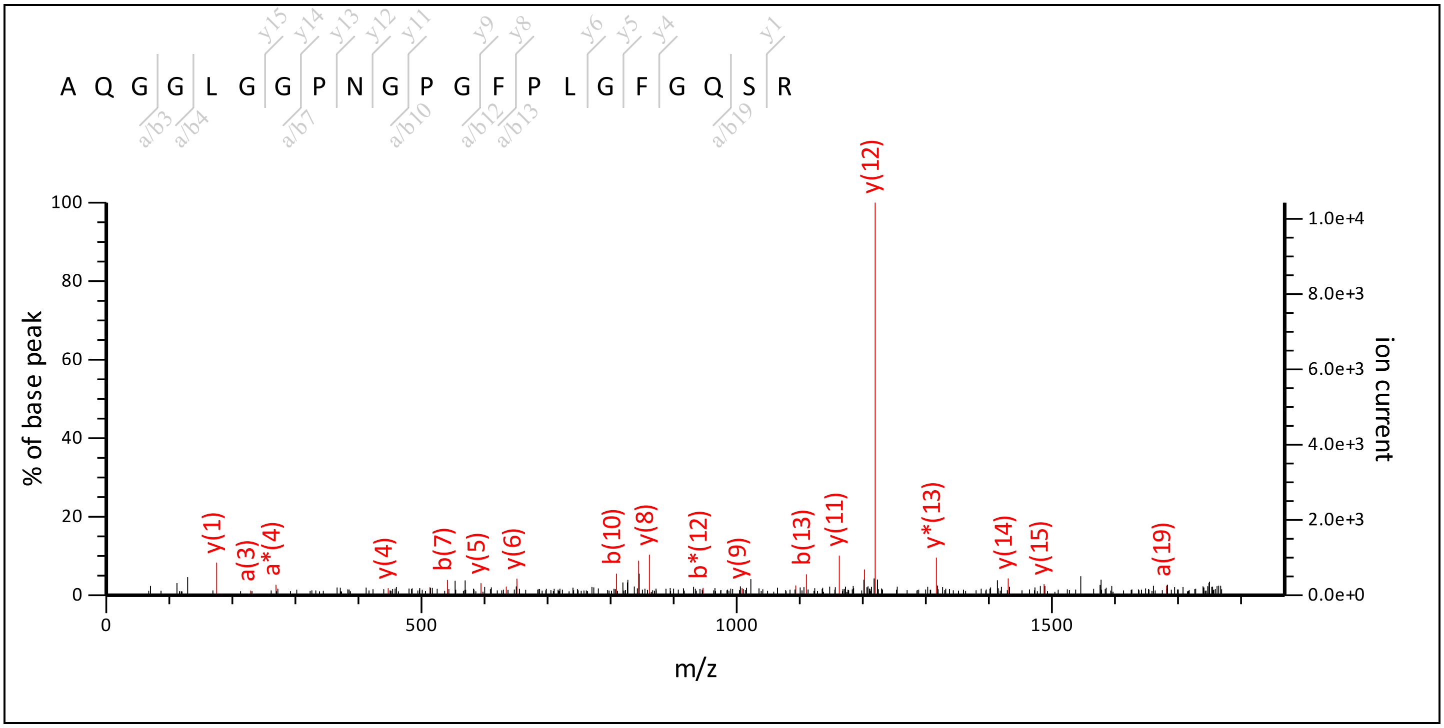
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 101**

MS/MS Fragmentation of **AQGGLGGPNGPGFPLGFGQSR**
Found in **gi|75114857** in **NCBInr**, RecName: Full=ATP-dependent zinc metalloprotease FTSH 2, chloroplastic; Short=OsFTSH2; Flags: Precursor

Match to Query 22: 1970.016724 from(1971.024000,1+) intensity(0.0000) index(9)
Title: Label: H1, Spot_Id: 219681, Peak_List_Id: 224998, MSMS Job_Run_Id: 21760, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_H1_136842035700.txt



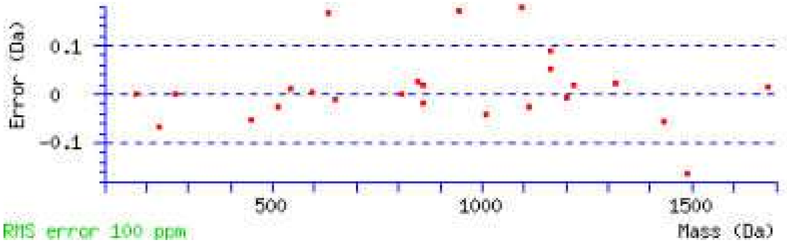
0 to 1869.23

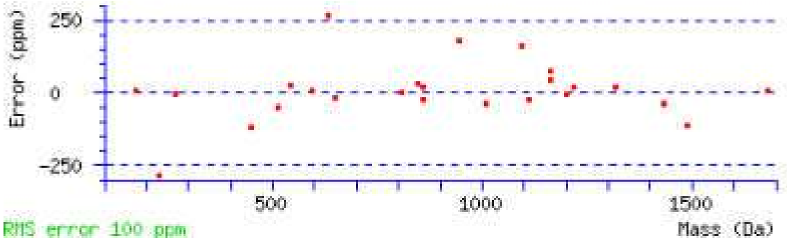
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1969.9759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 22 **Expect:** 9.4
Matches : 25/118 fragment ions using 87 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			21
2	172.1081	155.0815	200.1030	183.0764	Q	1899.9460	1882.9195	20
3	**229.1295**	212.1030	257.1244	240.0979	G	1771.8874	1754.8609	19
4	286.1510	269.1244	314.1459	297.1193	G	1714.8660	1697.8394	18
5	399.2350	382.2085	427.2300	410.2034	L	1657.8445	1640.8180	17
6	456.2565	439.2300	484.2514	467.2249	G	1544.7605	1527.7339	16
7	**513.2780**	496.2514	**541.2729**	524.2463	G	***1487.7390***	1470.7124	15

8	610.3307	593.3042	638.3257	621.2991	**P**	***1430.7175***	1413.6910	**14**
9	724.3737	707.3471	752.3686	735.3420	**N**	1333.6648	1316.6382	**13**
10	781.3951	764.3686	**809.3900**	792.3635	**G**	***1219.6218***	1202.5953	**12**
11	878.4479	861.4213	906.4428	889.4163	**P**	***1162.6004***	1145.5738	**11**
12	935.4694	918.4428	963.4643	946.4377	**G**	1065.5476	1048.5211	**10**
13	1082.5378	1065.5112	**1110.5327**	1093.5061	**F**	***1008.5261***	991.4996	**9**
14	1179.5905	1162.5640	1207.5854	1190.5589	**P**	***861.4577***	844.4312	**8**
15	1292.6746	1275.6480	1320.6695	1303.6430	**L**	764.4050	747.3784	**7**
16	1349.6961	1332.6695	1377.6910	1360.6644	**G**	***651.3209***	634.2944	**6**
17	1496.7645	1479.7379	1524.7594	1507.7328	**F**	***594.2994***	577.2729	**5**
18	1553.7859	1536.7594	1581.7809	1564.7543	**G**	***447.2310***	430.2045	**4**
19	**1681.8445**	1664.8180	1709.8394	1692.8129	**Q**	390.2096	373.1830	**3**
20	1768.8765	1751.8500	1796.8715	1779.8449	**S**	262.1510	245.1244	**2**
21					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
22.4	1969.9759	0.0408	AQGGLGGPNGPGFPLGFGQSR
4.7	1970.1676	-0.1509	KILALPTTRPQTLSLYR
4.7	1970.0044	0.0123	LSYLGPGGLTARTASFGMR
4.5	1969.9350	0.0818	RLGMGTNMYPSSSLLGDR
4.5	1969.9350	0.0818	RLGMGTNMYPSSSLLGDR
4.5	1970.0334	-0.0167	GANPNVVIGAIVGGPDHLDR
4.3	1969.9455	0.0712	MIGTDAFQETPIVEFTR
4.1	1969.9970	0.0197	QIGGQTHQVAAKVDEYAR
1.2	1969.8622	0.1545	EVMVYGGGGGAMEREGAER

0.9	1969.9567	0.0600	IELPADLGNEWPSMDKR

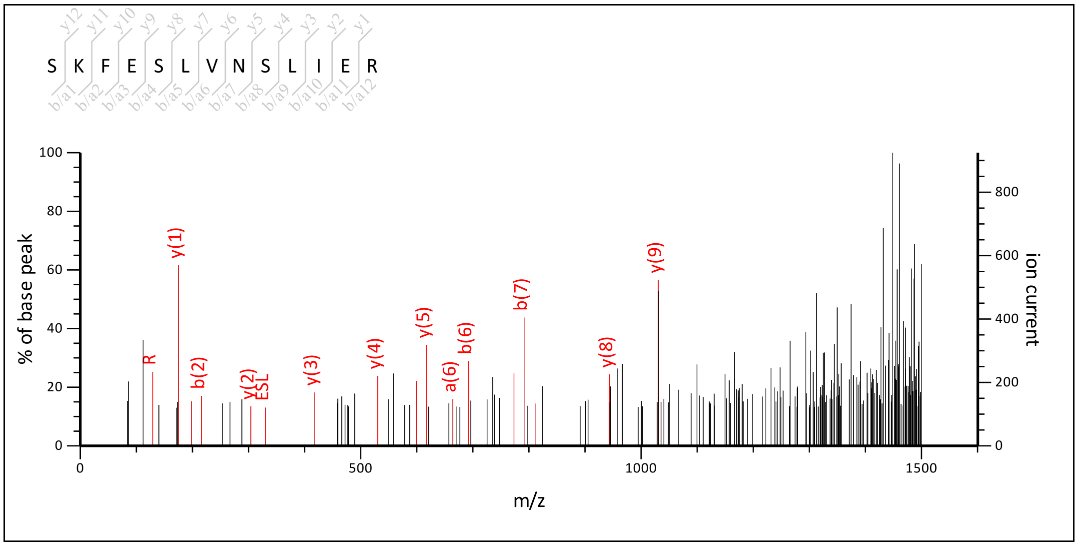
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 102

MS/MS Fragmentation of **SKFESLVNSLIER**
Found in **gi|115448989** in **NCBInr**, Os02g0774300 [Oryza sativa Japonica Group]

Match to Query 7: 1520.957424 from(1521.964700,1+) intensity(0.0000) index(2)
Title: Label: J5, Spot_Id: 228915, Peak_List_Id: 257482, MSMS Job_Run_Id: 24918, Comment:
Data file ppw_J5_138985127800.txt



0 to 1600.43

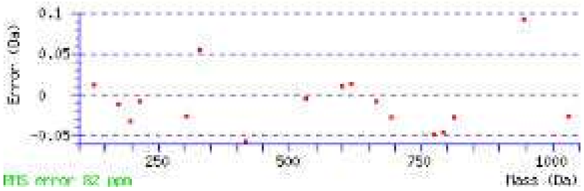
Label all possible matches ○ Label matches used for scoring ●

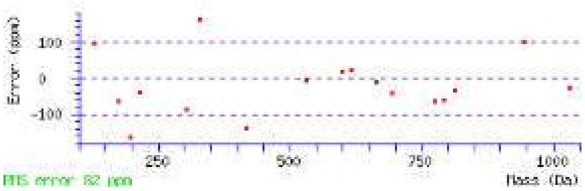
Monoisotopic mass of neutral peptide Mr(calc): 1520.8198
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 23 **Expect:** 3
Matches : 17/234 fragment ions using 45 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	101.1073	188.1394	171.1128	170.1288	***216.1343***	199.1077	198.1237	131.0815		K	1361.7060	1360.7107		1434.7951	1417.7686
3	120.0808	335.2078	318.1812	317.1972	363.2027	346.1761	345.1921			F	1214.6375			1306.7001	1289.6736
4	102.0550	464.2504	447.2238	446.2398	492.2453	475.2187	474.2347	406.2449		E	1085.5949	1084.5997		1159.6317	1142.6052
5	60.0444	551.2824	534.2558	533.2718	579.2773	562.2508	561.2667	535.2875		S	998.5629	997.5677		***1030.5891***	1013.5626
6	86.0964	664.3665	647.3399	646.3559	***692.3614***	675.3348	674.3508	622.3195		L	885.4789	884.4836		***943.5571***	926.5306
7	72.0808	763.4349	746.4083	745.4243	***791.4298***	774.4032	773.4192	749.4192		V	786.4104	799.4308		830.4730	813.4465
8	87.0553	877.4778	860.4512	859.4672	905.4727	888.4462	887.4621	834.4720		N	672.3675	671.3723		731.4046	714.3781
9	60.0444	964.5098	947.4833	946.4993	992.5047	975.4782	974.4942	948.5149		S	585.3355	584.3402		***617.3617***	600.3352
10	86.0964	1077.5939	1060.5673	1059.5833	1105.5888	1088.5622	1087.5782	1035.5469		L	472.2514	471.2562		***530.3297***	513.3031
11	86.0964	1190.6779	1173.6514	1172.6674	1218.6729	1201.6463	1200.6623	1162.6466	1176.6623	I	359.1674	372.1878	386.2034	***417.2456***	400.2191
12	102.0550	1319.7205	1302.6940	1301.7100	1347.7155	1330.6889	1329.7049	1261.7151		E	230.1248	229.1295		***304.1615***	287.1350
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KF	248.1757	276.1707	**KFE**	377.2183	405.2132	**KFES**	464.2504	492.2453
KFESL	577.3344	605.3293	**KFESLV**	676.4028	704.3978	**FE**	249.1234	277.1183
FES	336.1554	364.1503	**FESL**	449.2395	477.2344	**FESLV**	548.3079	576.3028
FESLVN	662.3508	690.3457	**ES**	189.0870	217.0819	**ESL**	302.1710	330.1660
ESLV	401.2395	429.2344	**ESLVN**	515.2824	543.2773	**ESLVNS**	602.3144	630.3093
SL	173.1285	201.1234	**SLV**	272.1969	300.1918	**SLVN**	386.2398	414.2347
SLVNS	473.2718	501.2667	**SLVNSL**	586.3559	614.3508	**SLVNSLI**	699.4399	727.4349

LV	185.1648	213.1598	**LVN**	299.2078	327.2027	**LVNS**	386.2398	414.2347
LVNSL	499.3239	527.3188	**LVNSLI**	612.4079	640.4028	**VN**	186.1237	214.1186
VNS	273.1557	301.1506	**VNSL**	386.2398	414.2347	**VNSLI**	499.3239	527.3188
VNSLIE	628.3665	656.3614	**NS**	174.0873	202.0822	**NSL**	287.1714	315.1663
NSLI	400.2554	428.2504	**NSLIE**	529.2980	557.2930	**SL**	173.1285	201.1234
SLI	286.2125	314.2074	**SLIE**	415.2551	443.2500	**LI**	199.1805	227.1754
LIE	328.2231	356.2180	**IE**	215.1390	243.1339			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.2	1520.8198	0.1376	SKFESLVNSLIER
17.6	1520.8674	0.0900	KQVSLEDAIIHIR
15.0	1520.8198	0.1376	SKFESLVSNLIER
13.4	1520.8463	0.1111	AGQVAKAFGAYGILR
9.2	1520.8311	0.1264	QRTLATAYSLIER
7.7	1520.8423	0.1151	QLNLARSAGPPELR
6.5	1520.8133	0.1441	LAMELSRLSQAFR
5.0	1520.8059	0.1515	NIQISHDPSKVQR
4.9	1520.8385	0.1190	SPCSSLVVKIYLR
3.9	1520.9039	0.0536	GLQGVVPKVLNEIR

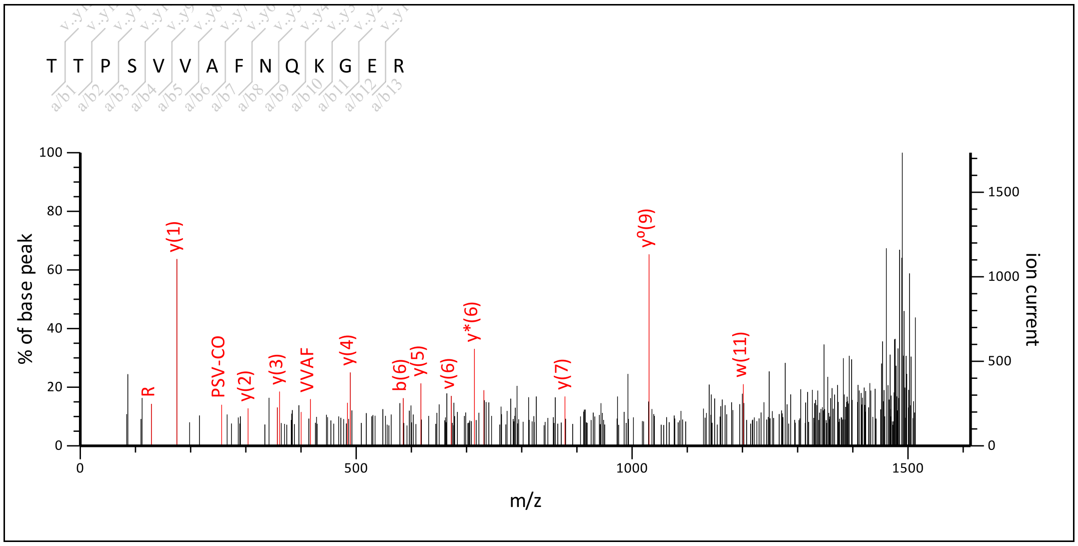
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 102

MS/MS Fragmentation of **TTPSVVAFNQKGER**
Found in **gi|115448989** in **NCBInr**, Os02g0774300 [Oryza sativa Japonica Group]

Match to Query 9: 1532.939124 from(1533.946400,1+) intensity(0.0000) index(3)
Title: Label: J5, Spot_Id: 228915, Peak_List_Id: 257483, MSMS Job_Run_Id: 24918, Comment:
Data file ppw_J5_138985127800.txt



0 to 1613.33

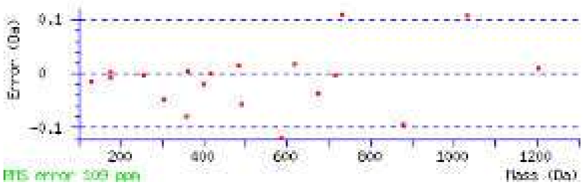
Label all possible matches ○ Label matches used for scoring ●

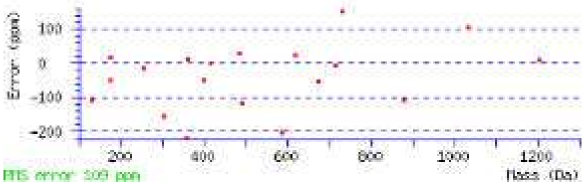
Monoisotopic mass of neutral peptide Mr(calc): 1532.7947
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 30
Matches : 20/239 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T					
2	74.0600	175.1077		157.0972	203.1026		185.0921	159.1128	161.0921	T	1386.7124	1399.7328	1401.7121	1432.7543	1415.7278
3	70.0651	272.1605		254.1499	300.1554		282.1448	246.1448		P	1289.6597	1288.6644		1331.7066	1314.6801
4	60.0444	359.1925		341.1819	387.1874		369.1769	343.1976		S	1202.6276	1201.6324		1234.6539	1217.6273
5	72.0808	458.2609		440.2504	486.2558		468.2453	444.2453		V	1103.5592	1116.5796		1147.6218	1130.5953
6	72.0808	557.3293		539.3188	585.3243		567.3137	543.3137		V	1004.4908	1017.5112		1048.5534	1031.5269
7	44.0495	628.3665		610.3559	656.3614		638.3508			A	933.4537			949.4850	932.4585
8	120.0808	775.4349		757.4243	803.4298		785.4192			F	786.3853			***878.4479***	861.4213
9	87.0553	889.4778	872.4512	871.4672	917.4727	900.4462	899.4621	846.4720		N	672.3424	671.3471		***731.3795***	714.3529
10	101.0709	1017.5364	1000.5098	999.5258	1045.5313	1028.5047	1027.5207	960.5149		Q	544.2838	543.2885		***617.3366***	600.3100
11	101.1073	1145.6313	1128.6048	1127.6208	1173.6263	1156.5997	1155.6157	1088.5735		K	416.1888	415.1936		***489.2780***	472.2514
12	30.0338	1202.6528	1185.6263	1184.6422	1230.6477	1213.6212	1212.6371			G				***361.1830***	344.1565
13	102.0550	1331.6954	1314.6688	1313.6848	1359.6903	1342.6638	1341.6797	1273.6899		E	230.1248	229.1295		***304.1615***	287.1350
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TP	171.1128	199.1077	**TPS**	258.1448	286.1397	**TPSV**	357.2132	385.2082
TPSVV	456.2817	484.2766	**TPSVVA**	527.3188	555.3137	**TPSVVAF**	674.3872	702.3821
PS	157.0972	185.0921	**PSV**	256.1656	284.1605	**PSVV**	355.2340	383.2289
PSVVA	426.2711	454.2660	**PSVVAF**	573.3395	601.3344	**PSVVAFN**	687.3824	715.3774
SV	159.1128	187.1077	**SVV**	258.1812	286.1761	**SVVA**	329.2183	357.2132
SVVAF	476.2867	504.2817	**SVVAFN**	590.3297	618.3246	**VV**	171.1492	199.1441

VVA	242.1863	270.1812	**VVAF**	389.2547	417.2496	**VVAFN**	503.2976	531.2926
VVAFNQ	631.3562	659.3511	**VA**	143.1179	171.1128	**VAF**	290.1863	318.1812
VAFN	404.2292	432.2241	**VAFNQ**	532.2878	560.2827	**VAFNQK**	660.3828	688.3777
AF	191.1179	219.1128	**AFN**	305.1608	333.1557	**AFNQ**	433.2194	461.2143
AFNQK	561.3144	589.3093	**AFNQKG**	618.3358	646.3307	**FN**	234.1237	262.1186
FNQ	362.1823	390.1772	**FNQK**	490.2772	518.2722	**FNQKG**	547.2987	575.2936
FNQKGE	676.3413	704.3362	**NQ**	215.1139	243.1088	**NQK**	343.2088	371.2037
NQKG	400.2303	428.2252	**NQKGE**	529.2729	557.2678	**QK**	229.1659	257.1608
QKG	286.1874	314.1823	**QKGE**	415.2300	443.2249	**KG**	158.1288	186.1237
KGE	287.1714	315.1663	**GE**	159.0764	187.0713			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.5	1532.8423	0.0968	VSINFSRLQNLSR
15.2	1532.7947	0.1444	TTPSVVAFNQKGER
8.4	1532.7947	0.1444	VSFGLSVEQAAAAQR
8.3	1532.7868	0.1523	KAGVELLDMGSLER
7.0	1532.8602	0.0789	SVIFPIIFEALER
6.3	1532.8351	0.1040	VSLFQDILGLSWR
6.2	1532.8306	0.1085	KSMVVADVIPVMTK
5.9	1532.8055	0.1337	VSEAVLLMGLCVSR
5.0	1532.7981	0.1410	GMSSVLLVNSVGQAR
4.8	1532.8133	0.1258	AGGFLRLGVMDLER

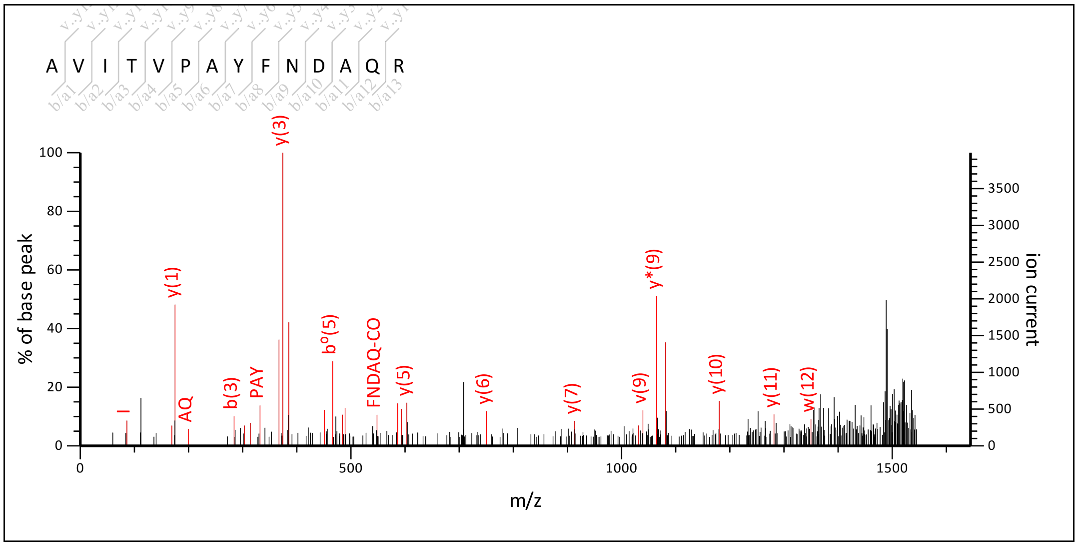
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 102

MS/MS Fragmentation of **AVITVPAYFNDAQR**
Found in **gi|115448989** in **NCBInr**, Os02g0774300 [Oryza sativa Japonica Group]

Match to Query 11: 1563.948424 from(1564.955700,1+) intensity(0.0000) index(4)
Title: Label: J5, Spot_Id: 228915, Peak_List_Id: 257481, MSMS Job_Run_Id: 24918, Comment:
Data file ppw_J5_138985127800.txt



0 to 1644.68

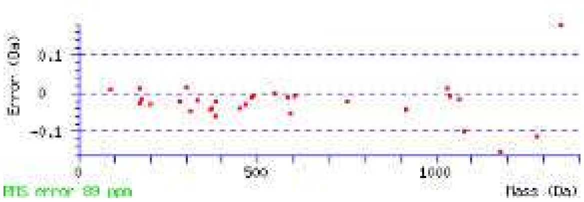
Label all possible matches ○ Label matches used for scoring ●

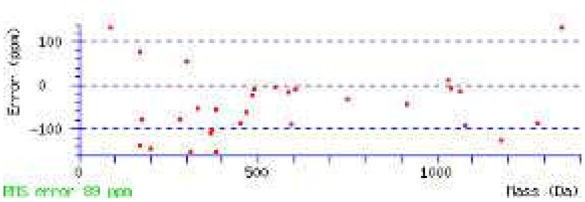
Monoisotopic mass of neutral peptide Mr(calc): 1563.8045
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.013
Matches : 31/226 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	44.0495	44.0495			72.0444			44.0495		A						
2	72.0808	143.1179			171.1128			129.1022		V	1449.7121	1462.7325		1493.7747	1476.7482	14
3	86.0964	256.2020			**284.1969**			228.1707	242.1863	I	1336.6280	1349.6484	1363.6641	1394.7063	1377.6797	13
4	74.0600	357.2496		339.2391	**385.2445**		367.2340	341.2547	343.2340	T	1235.5804	1248.6008	1250.5800	***1281.6222***	1264.5957	12
5	72.0808	456.3180		438.3075	**484.3130**		466.3024	442.3024		V	1136.5119	1149.5324		***1180.5745***	1163.5480	11
6	70.0651	553.3708		535.3602	581.3657		563.3552	527.3552		P	1039.4592	1038.4639		***1081.5061***	1064.4796	10
7	44.0495	624.4079		606.3974	652.4028		634.3923			A	968.4221			984.4534	967.4268	9
8	136.0757	787.4713		769.4607	815.4662		797.4556			Y	805.3587			***913.4163***	896.3897	8
9	120.0808	934.5397		916.5291	962.5346		944.5240			F	658.2903			***750.3529***	733.3264	7
10	87.0553	1048.5826	1031.5560	1030.5720	1076.5775	1059.5510	1058.5669	1005.5768		N	544.2474	543.2522		***603.2845***	586.2580	5
11	88.0393	1163.6095	1146.5830	1145.5990	1191.6045	1174.5779	1173.5939	1119.6197		D	429.2205	428.2252		***489.2416***	472.2150	4
12	44.0495	1234.6467	1217.6201	1216.6361	1262.6416	1245.6150	1244.6310			A	358.1833			***374.2146***	357.1881	
13	101.0709	1362.7052	1345.6787	1344.6947	1390.7001	1373.6736	1372.6896	1305.6838		Q	230.1248	229.1295		***303.1775***	286.1510	
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VI	185.1648	213.1598	VIT	286.2125	314.2074	VITV	385.2809	413.2758
VITVP	482.3337	510.3286	VITVPA	553.3708	581.3657	IT	187.1441	215.1390
ITV	286.2125	314.2074	ITVP	383.2653	411.2602	ITVPA	454.3024	482.2973
ITVPAY	617.3657	645.3606	TV	173.1285	201.1234	TVP	270.1812	298.1761
TVPA	341.2183	369.2132	TVPAY	504.2817	532.2766	TVPAYF	651.3501	679.3450
VP	169.1335	197.1285	VPA	240.1707	268.1656	VPAY	403.2340	431.2289

VPAYF	550.3024	578.2973	**VPAYFN**	664.3453	692.3402	**PA**	141.1022	169.0972
PAY	304.1656	332.1605	**PAYF**	451.2340	479.2289	**PAYFN**	565.2769	593.2718
PAYFND	680.3039	708.2988	**AY**	207.1128	235.1077	**AYF**	354.1812	382.1761
AYFN	468.2241	496.2191	**AYFND**	583.2511	611.2460	**AYFNDA**	654.2882	682.2831
YF	283.1441	311.1390	**YFN**	397.1870	425.1819	**YFND**	512.2140	540.2089
YFNDA	583.2511	611.2460	**FN**	234.1237	262.1186	**FND**	349.1506	377.1456
FNDA	420.1878	448.1827	**FNDAQ**	548.2463	576.2413	**ND**	202.0822	230.0771
NDA	273.1193	301.1143	**NDAQ**	401.1779	429.1728	**DA**	159.0764	187.0713
DAQ	287.1350	315.1299	**AQ**	172.1081	200.1030			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.5	1563.8045	0.1439	AVITVPAYFNDAQR
8.0	1563.7926	0.1558	MLSTTSSASGGISLPR
6.2	1563.8117	0.1367	KSVPASSSAPHNVQR
4.9	1563.8005	0.1479	IDIAASSDRFVTNR
4.5	1563.8521	0.0963	IEAAVHVWNLKER
4.0	1563.8113	0.1372	SIMAEALVTTMGKGR
3.7	1563.8153	0.1332	LAEAMLLFEKMPR
3.2	1563.7927	0.1558	ATAASGDIVVSSTMVR
3.2	1563.8620	0.0864	ATGSIKSLVYSPSVR
3.1	1563.8555	0.0929	VTALVNTSVAFMRR

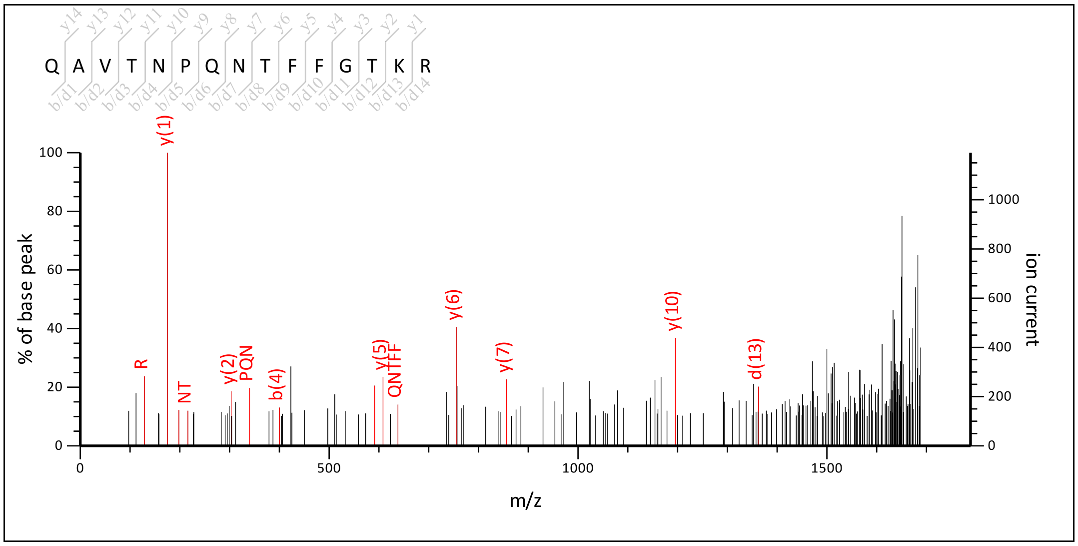
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 102**

MS/MS Fragmentation of **QAVTNPQNTFFGTKR**
Found in **gi|115448989** in **NCBInr**, Os02g0774300 [Oryza sativa Japonica Group]

Match to Query 15: 1708.022024 from(1709.029300,1+) intensity(0.0000) index(6)
Title: Label: J5, Spot_Id: 228915, Peak_List_Id: 257485, MSMS Job_Run_Id: 24918, Comment:
Data file ppw_J5_138985127800.txt



0 to 1788.57

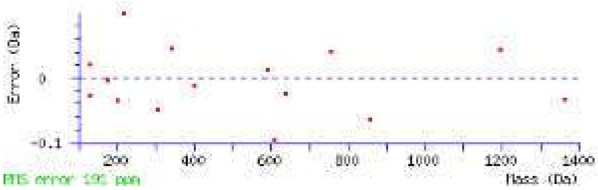
Label all possible matches ○ Label matches used for scoring ●

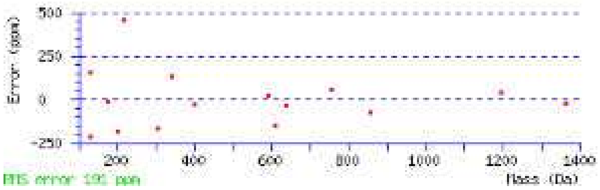
Monoisotopic mass of neutral peptide Mr(calc): 1707.8693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 37
Matches : 17/270 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.0709	101.0709	84.0444		**129.0659**	112.0393		44.0495		Q					
2	44.0495	172.1081	155.0815		200.1030	183.0764				A	1564.7867			1580.8180	1563.7914
3	72.0808	271.1765	254.1499		299.1714	282.1448		257.1608		V	1465.7183	1478.7387		1509.7809	1492.7543
4	74.0600	372.2241	355.1976	354.2136	**400.2191**	383.1925	382.2085	356.2292	358.2085	T	1364.6706	1377.6910	1379.6702	1410.7124	1393.6859
5	87.0553	486.2671	469.2405	468.2565	514.2620	497.2354	496.2514	443.2613		N	1250.6276	1249.6324		1309.6648	1292.6382
6	70.0651	583.3198	566.2933	565.3093	611.3148	594.2882	593.3042	557.3042		P	1153.5749	1152.5796		***1195.6218***	1178.5953
7	101.0709	711.3784	694.3519	693.3679	739.3733	722.3468	721.3628	654.3570		Q	1025.5163	1024.5211		1098.5691	1081.5425
8	87.0553	825.4213	808.3948	807.4108	853.4163	836.3897	835.4057	782.4155		N	911.4734	910.4781		970.5105	953.4839
9	74.0600	926.4690	909.4425	908.4585	954.4639	937.4374	936.4534	910.4741	912.4534	T	810.4257	823.4461	825.4254	***856.4676***	839.4410
10	120.0808	1073.5374	1056.5109	1055.5269	1101.5324	1084.5058	1083.5218			F	663.3573			***755.4199***	738.3933
11	120.0808	1220.6058	1203.5793	1202.5953	1248.6008	1231.5742	1230.5902			F	516.2889			***608.3515***	591.3249
12	30.0338	1277.6273	1260.6008	1259.6167	1305.6222	1288.5957	1287.6117			G				461.2831	444.2565
13	74.0600	1378.6750	1361.6484	1360.6644	1406.6699	1389.6434	1388.6593	1362.6801	1364.6593	T	358.2197	371.2401	373.2194	404.2616	387.2350
14	101.1073	1506.7700	1489.7434	1488.7594	1534.7649	1517.7383	1516.7543	1449.7121		K	230.1248	229.1295		***303.2139***	286.1874
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AV	143.1179	171.1128	AVT	244.1656	272.1605	AVTN	358.2085	386.2034
AVTNP	455.2613	483.2562	AVTNPQ	583.3198	611.3148	AVTNPQN	697.3628	725.3577
VT	173.1285	201.1234	VTN	287.1714	315.1663	VTNP	384.2241	412.2191
VTNPQ	512.2827	540.2776	VTNPQN	626.3257	654.3206	TN	188.1030	216.0979
TNP	285.1557	313.1506	TNPQ	413.2143	441.2092	TNPQN	527.2572	555.2522

TNPQNT	628.3049	656.2998	**NP**	184.1081	212.1030	**NPQ**	312.1666	340.1615
NPQN	426.2096	454.2045	**NPQNT**	527.2572	555.2522	**NPQNTF**	674.3257	702.3206
PQ	198.1237	226.1186	**PQN**	312.1666	340.1615	**PQNT**	413.2143	441.2092
PQNTF	560.2827	588.2776	**QN**	215.1139	243.1088	**QNT**	316.1615	344.1565
QNTF	463.2300	491.2249	**QNTFF**	610.2984	638.2933	**QNTFFG**	667.3198	695.3148
NT	188.1030	216.0979	**NTF**	335.1714	363.1663	**NTFF**	482.2398	510.2347
NTFFG	539.2613	567.2562	**NTFFGT**	640.3089	668.3039	**TF**	221.1285	249.1234
TFF	368.1969	396.1918	**TFFG**	425.2183	453.2132	**TFFGT**	526.2660	554.2609
TFFGTK	654.3610	682.3559	**FF**	267.1492	295.1441	**FFG**	324.1707	352.1656
FFGT	425.2183	453.2132	**FFGTK**	553.3133	581.3082	**FG**	177.1022	205.0972
FGT	278.1499	306.1448	**FGTK**	406.2449	434.2398	**GT**	131.0815	159.0764
GTK	259.1765	287.1714	**TK**	202.1550	230.1499			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.9	1707.8693	0.1527	QAVTNPQNTFFGTKR
11.5	1707.9189	0.1031	QSSLAISMASSLTLKR
5.7	1707.9090	0.1130	TVKSLLNSMPGATPHR
5.7	1707.8904	0.1316	GSQVVPGAKAVEEGPAGR
5.5	1707.9229	0.0991	ILIMQGEEITKVYR
5.1	1707.8726	0.1494	LCGPTGTIQAAAGAPAPR
4.5	1707.8540	0.1681	EEQRDSKPIPEPQR
4.4	1707.9056	0.1164	SRIWLGSYSTAVAAAR
4.1	1707.9169	0.1052	ISRPGLRVYSNYQR
3.6	1707.8766	0.1454	GWLFSMLNTNLLQR

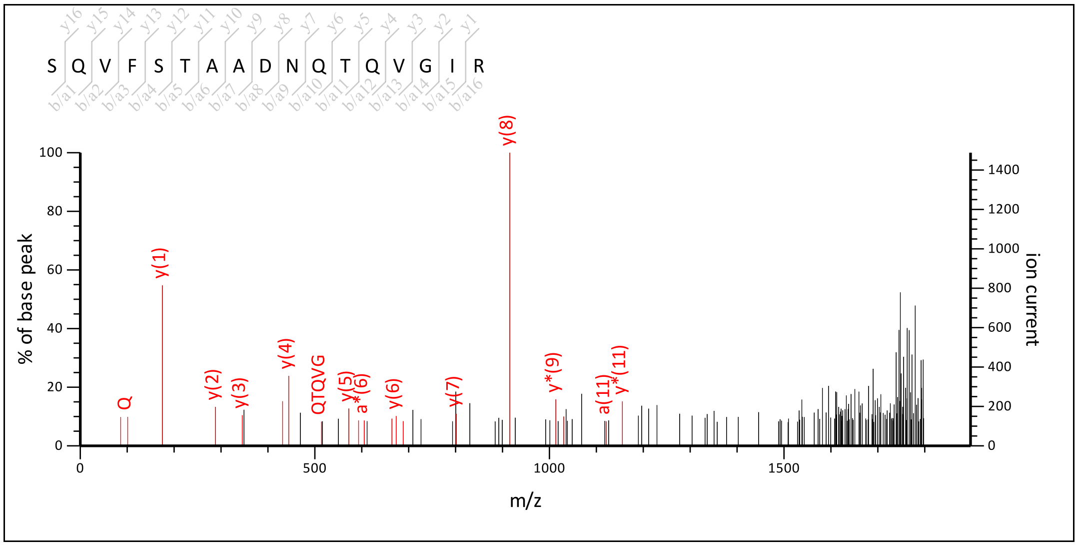
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 102

MS/MS Fragmentation of **SQVFSTAADNQTQVGIR**
Found in **gi|115448989** in **NCBInr**, Os02g0774300 [Oryza sativa Japonica Group]

Match to Query 17: 1821.065524 from(1822.072800,1+) intensity(0.0000) index(7)
Title: Label: J5, Spot_Id: 228915, Peak_List_Id: 257484, MSMS Job_Run_Id: 24918, Comment:
Data file ppw_J5_138985127800.txt



0 to 1897.59

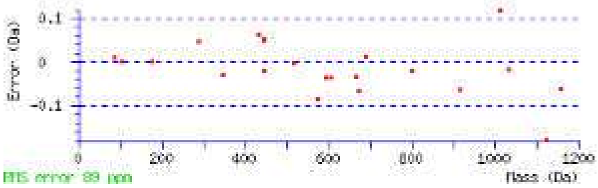
Label all possible matches ○ Label matches used for scoring ●

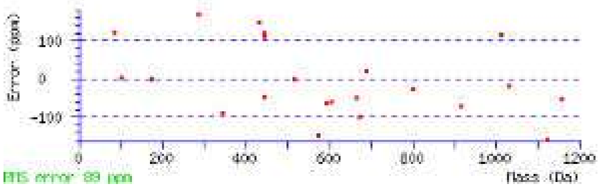
Monoisotopic mass of neutral peptide Mr(calc): `1820.9017`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `25` **Expect:** `7.8`
Matches : `24/326 fragment ions using 62 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	101.0709	188.1030	171.0764	170.0924	216.0979	199.0713	198.0873	131.0815		Q	1661.8242	1660.8289		1734.8769	1717.8504
3	72.0808	287.1714	270.1448	269.1608	315.1663	298.1397	297.1557	273.1557		V	1562.7558	1575.7762		1606.8184	1589.7918
4	120.0808	434.2398	417.2132	416.2292	462.2347	445.2082	444.2241			F	1415.6873			1507.7499	1490.7234
5	60.0444	521.2718	504.2453	503.2613	549.2667	532.2402	531.2562	505.2769		S	1328.6553	1327.6601		1360.6815	1343.6550
6	74.0600	622.3195	605.2930	604.3089	650.3144	633.2879	632.3039	606.3246	608.3039	T	1227.6076	1240.6280	1242.6073	1273.6495	1256.6230
7	44.0495	693.3566	676.3301	675.3461	721.3515	704.3250	703.3410			A	1156.5705			1172.6018	1155.5753
8	44.0495	764.3937	747.3672	746.3832	792.3886	775.3621	774.3781			A	1085.5334			1101.5647	1084.5382
9	88.0393	879.4207	862.3941	861.4101	907.4156	890.3890	889.4050	835.4308		D	970.5065	969.5112		***1030.5276***	1013.5010
10	87.0553	993.4636	976.4371	975.4530	1021.4585	1004.4320	1003.4479	950.4578		N	856.4635	855.4683		***915.5007***	898.4741
11	101.0709	1121.5222	1104.4956	1103.5116	1149.5171	1132.4905	1131.5065	1064.5007		Q	728.4050	727.4097		***801.4577***	784.4312
12	74.0600	1222.5699	1205.5433	1204.5593	1250.5648	1233.5382	1232.5542	1206.5749	1208.5542	T	627.3573	640.3777	642.3570	***673.3992***	656.3726
13	101.0709	1350.6284	1333.6019	1332.6179	1378.6234	1361.5968	1360.6128	1293.6070		Q	499.2987	498.3035		***572.3515***	555.3249
14	72.0808	1449.6968	1432.6703	1431.6863	1477.6918	1460.6652	1459.6812	1435.6812		V	400.2303	413.2507		***444.2929***	427.2663
15	30.0338	1506.7183	1489.6918	1488.7077	1534.7132	1517.6867	1516.7027			G				***345.2245***	328.1979
16	86.0964	1619.8024	1602.7758	1601.7918	1647.7973	1630.7707	1629.7867	1591.7711	1605.7867	I	230.1248	243.1452	257.1608	***288.2030***	271.1765
17	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QV	200.1394	228.1343	**QVF**	347.2078	375.2027	**QVFS**	434.2398	462.2347
QVFST	535.2875	563.2824	**QVFSTA**	606.3246	634.3195	**QVFSTAA**	677.3617	705.3566
VF	219.1492	247.1441	**VFS**	306.1812	334.1761	**VFST**	407.2289	435.2238

VFSTA	478.2660	506.2609	**VFSTAA**	549.3031	577.2980	**VFSTAAD**	664.3301	692.3250
FS	207.1128	235.1077	**FST**	308.1605	336.1554	**FSTA**	379.1976	407.1925
FSTAA	450.2347	478.2296	**FSTAAD**	565.2617	593.2566	**FSTAADN**	679.3046	707.2995
ST	161.0921	189.0870	**STA**	232.1292	260.1241	**STAA**	303.1663	331.1612
STAAD	418.1932	446.1882	**STAADN**	532.2362	560.2311	**STAADNQ**	660.2947	688.2897
TA	145.0972	173.0921	**TAA**	216.1343	244.1292	**TAAD**	331.1612	359.1561
TAADN	445.2041	473.1991	**TAADNQ**	573.2627	601.2576	**TAADNQT**	674.3104	702.3053
AA	115.0866	143.0815	**AAD**	230.1135	258.1084	**AADN**	344.1565	372.1514
AADNQ	472.2150	500.2100	**AADNQT**	573.2627	601.2576	**AD**	159.0764	187.0713
ADN	273.1193	301.1143	**ADNQ**	401.1779	429.1728	**ADNQT**	502.2256	530.2205
ADNQTQ	630.2842	658.2791	**DN**	202.0822	230.0771	**DNQ**	330.1408	358.1357
DNQT	431.1885	459.1834	**DNQTQ**	559.2471	587.2420	**DNQTQV**	658.3155	686.3104
NQ	215.1139	243.1088	**NQT**	316.1615	344.1565	**NQTQ**	444.2201	472.2150
NQTQV	543.2885	571.2835	**NQTQVG**	600.3100	628.3049	**QT**	202.1186	230.1135
QTQ	330.1772	358.1721	**QTQV**	429.2456	457.2405	**QTQVG**	486.2671	514.2620
QTQVGI	599.3511	627.3461	**TQ**	202.1186	230.1135	**TQV**	301.1870	329.1819
TQVG	358.2085	386.2034	**TQVGI**	471.2926	499.2875	**QV**	200.1394	228.1343
QVG	257.1608	285.1557	**QVGI**	370.2449	398.2398	**VG**	129.1022	157.0972
VGI	242.1863	270.1812	**GI**	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
24.5	1820.9017	0.1638	SQVFSTAADNQTQVGIR
11.6	1820.9322	0.1333	AWWSQTFDIAATRLR
9.6	1820.8945	0.1710	GLGFPAEDLEVSGFDLR
8.8	1820.9930	0.0725	MIRAYTQSAATLNLLR
8.0	1820.9454	0.1201	EGLAPINLVIETEMHR
7.1	1820.9421	0.1235	WEDYSLINKGSIQLR
6.6	1820.9376	0.1279	KVLMDDSMVLLGDTIR
6.1	1820.8913	0.1742	ALRLMEEMPYKPDGR
6.0	1820.9706	0.0949	ITMYPALTELQEKIR
5.9	1821.0182	0.0473	VKGTMLNYSTVLVQLR

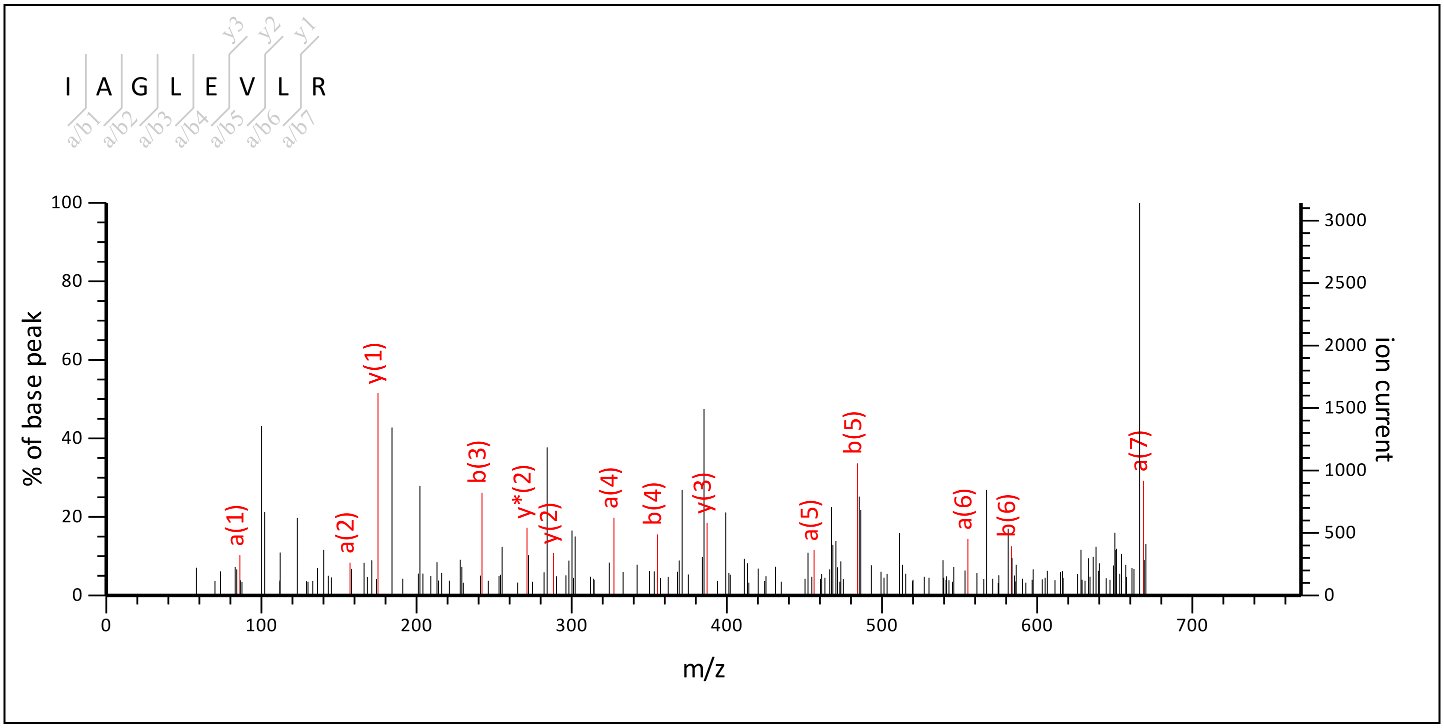
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 104**

MS/MS Fragmentation of **IAGLEVLR**
Found in **gi|6746592** in **NCBInr**, heat shock protein 70 [Arabidopsis thaliana]

Match to Query 2: 869.582934 from(870.590210,1+) intensity(0.0000) index(0)
Title: Label: F1, Spot_Id: 219679, Peak_List_Id: 224947, MSMS Job_Run_Id: 21758, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_F1_136842030500.txt

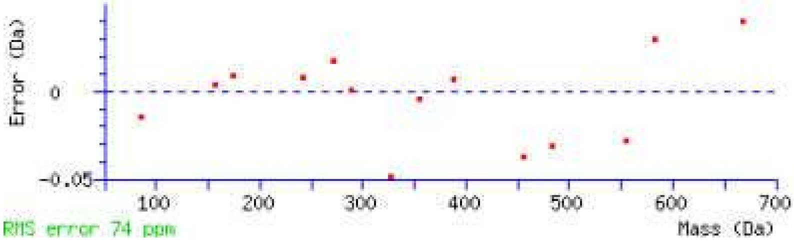


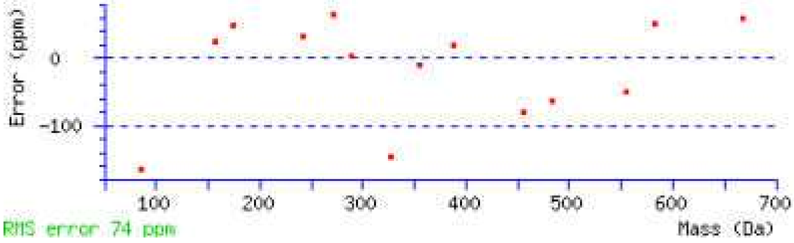
0 to 770.05

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 869.5334
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 7.1
Matches : 14/28 fragment ions using 48 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	*86.0964*	114.0913	I			8
2	*157.1335*	185.1285	A	757.4567	740.4301	7
3	214.1550	**242.1499**	G	686.4196	669.3930	6
4	*327.2391*	**355.2340**	L	629.3981	612.3715	5
5	*456.2817*	**484.2766**	E	516.3140	499.2875	4
6	*555.3501*	**583.3450**	V	**387.2714**	370.2449	3
7	*668.4341*	696.4291	L	**288.2030**	271.1765	2
8			R	**175.1190**	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
25.1	869.5083	0.0747	EIRLPSR
25.1	869.5083	0.0747	ELRLPSR
25.1	869.5083	0.0747	ERILPSR
25.1	869.5083	0.0747	ERLIPSR
22.6	869.5083	0.0746	IQGNAVLR
20.2	869.5334	0.0495	IAGLEVLR
19.3	869.5334	0.0495	VALDALLR
19.1	869.5195	0.0634	RGGGGVVLR
19.0	869.5335	0.0495	TVVVSPIR
18.2	869.5157	0.0673	LAMAVPLR

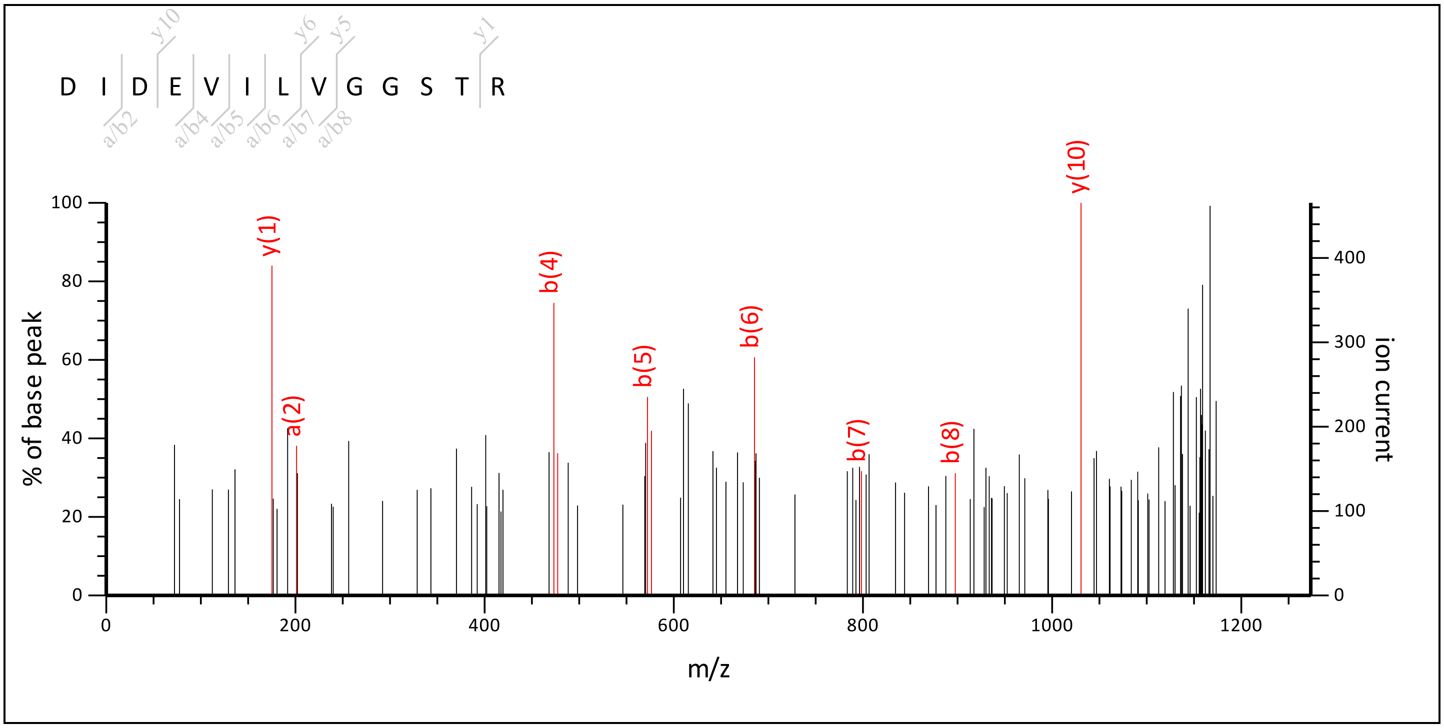
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 104

MS/MS Fragmentation of **DIDEVILVGGSTR**
Found in **gi|6746592** in **NCBInr**, heat shock protein 70 [Arabidopsis thaliana]

Match to Query 82: 1372.761024 from(1373.768300,1+) intensity(0.0000) index(16)
Title: Label: F1, Spot_Id: 219679, Peak_List_Id: 224942, MSMS Job_Run_Id: 21758, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_F1_136842030500.txt



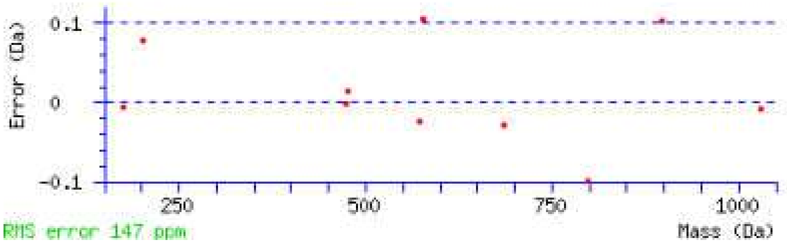
0 to 1273.42

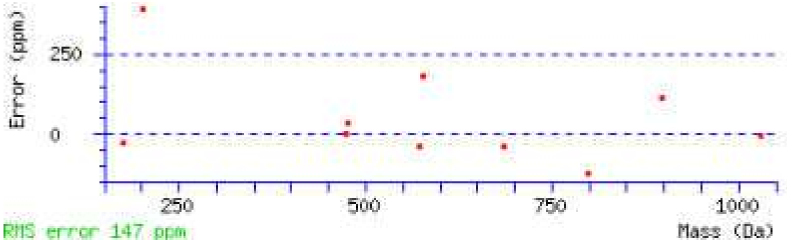
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1372.7198
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 6 **Expect:** 4.5e+02
Matches : 10/48 fragment ions using 45 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	88.0393	116.0342	**D**			**13**
2	201.1234	229.1183	**I**	1258.7001	1241.6736	**12**
3	316.1503	344.1452	**D**	1145.6161	1128.5895	**11**
4	445.1929	***473.1878***	**E**	***1030.5891***	1013.5626	**10**
5	544.2613	***572.2562***	**V**	901.5465	884.5200	**9**
6	657.3454	***685.3403***	**I**	802.4781	785.4516	**8**
7	770.4294	***798.4244***	**L**	689.3941	672.3675	**7**
8	869.4979	***897.4928***	**V**	***576.3100***	559.2835	**6**

9	926.5193	954.5142	**G**	*477.2416*	460.2150	**5**
10	983.5408	1011.5357	**G**	420.2201	403.1936	**4**
11	1070.5728	1098.5677	**S**	363.1987	346.1721	**3**
12	1171.6205	1199.6154	**T**	276.1666	259.1401	**2**
13			**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
9.7	1372.7133	0.0478	VLNASEVGMALNR
6.5	1372.6834	0.0776	AESIEELEAQVR
6.3	1372.7198	0.0412	DIDEVILVGGSTR
6.3	1372.7198	0.0412	DIDEVILVGGSTR
6.3	1372.7198	0.0412	DLDEVILVGGSTR
5.9	1372.7463	0.0147	QYANVLDKPLGR
3.6	1372.7350	0.0260	ETLEIFAPLANR
2.8	1372.6371	0.1239	QSKESFGGYTNR
2.5	1372.7939	-0.0329	AGYLRQLVGGIAR
2.5	1372.7939	-0.0329	LGRQLVFSNLAR

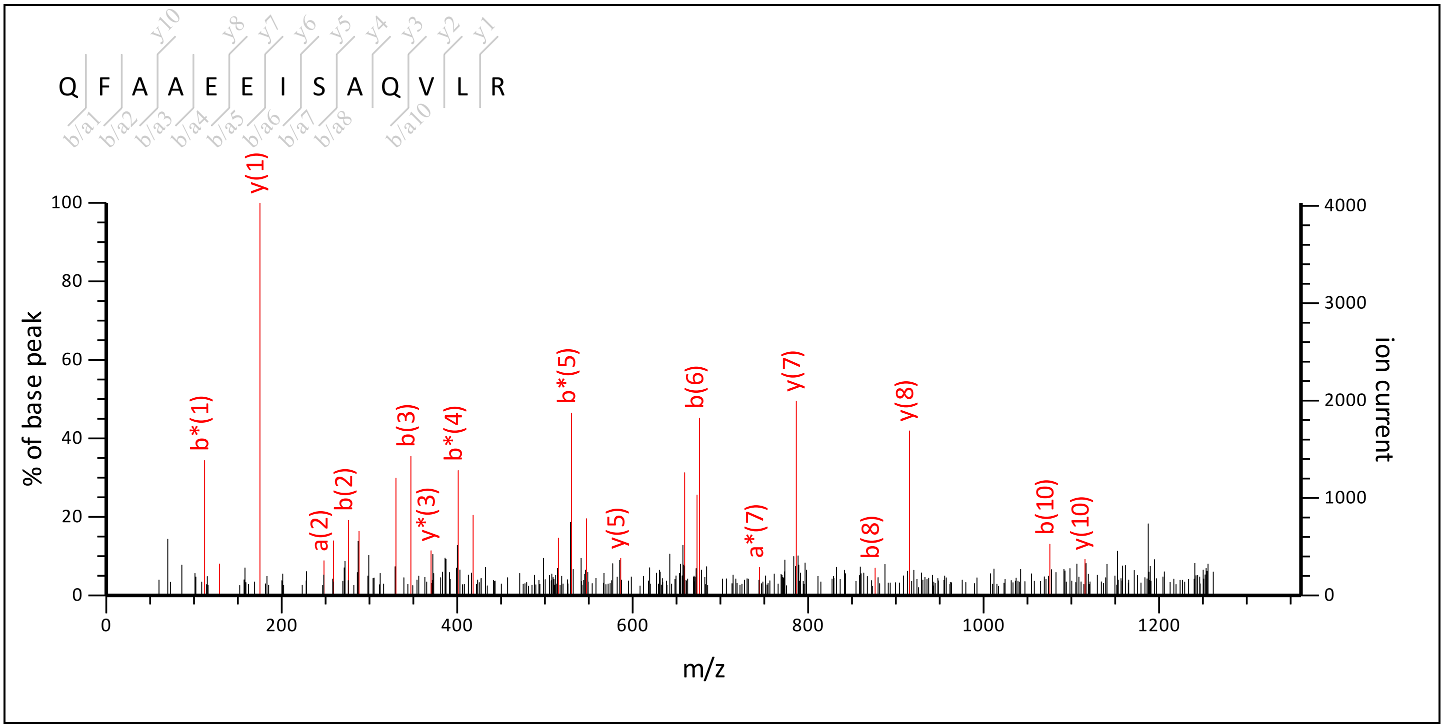
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 104**

MS/MS Fragmentation of **QFAAEEISAQVLR**
Found in **gi|6746592** in **NCBInr**, heat shock protein 70 [Arabidopsis thaliana]

Match to Query 90: 1460.814724 from(1461.822000,1+) intensity(0.0000) index(19)
Title: Label: F1, Spot_Id: 219679, Peak_List_Id: 224932, MSMS Job_Run_Id: 21758, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_F1_136842030500.txt



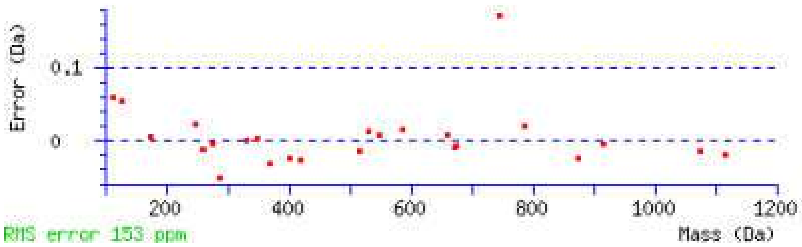
0 to 1361.77

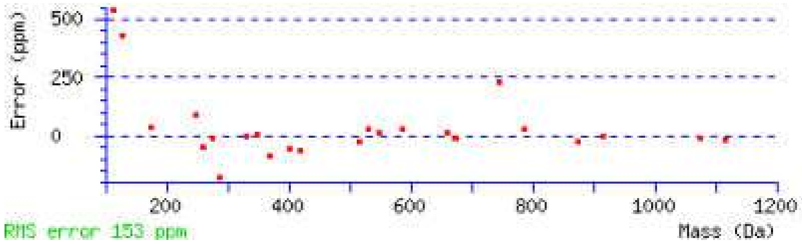
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1460.7623
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 0.0072
Matches : 25/72 fragment ions using 49 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	101.0709	84.0444	***129.0659***	112.0393	**Q**			**13**
2	248.1394	231.1128	***276.1343***	259.1077	**F**	1333.7110	1316.6845	**12**
3	319.1765	302.1499	***347.1714***	330.1448	**A**	1186.6426	1169.6161	**11**
4	390.2136	373.1870	***418.2085***	401.1819	**A**	***1115.6055***	1098.5790	**10**
5	519.2562	502.2296	***547.2511***	530.2245	**E**	1044.5684	1027.5419	**9**
6	648.2988	631.2722	***676.2937***	659.2671	**E**	***915.5258***	898.4993	**8**
7	761.3828	744.3563	789.3777	772.3512	**I**	***786.4832***	769.4567	**7**
8	848.4149	831.3883	***876.4098***	859.3832	**S**	***673.3991***	656.3726	**6**

9	919.4520	902.4254	947.4469	930.4203	**A**	***586.3671***	569.3406	**5**
10	1047.5106	1030.4840	***1075.5055***	1058.4789	**Q**	***515.3300***	498.3035	**4**
11	1146.5790	1129.5524	1174.5739	1157.5473	**V**	387.2714	370.2449	**3**
12	1259.6630	1242.6365	1287.6579	1270.6314	**L**	***288.2030***	271.1765	**2**
13					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	**Mr(calc)**	**Delta**	**Sequence**
54.3	1460.7623	0.0524	QFAAEEISAQVLR
36.8	1460.7194	0.0953	EAWCEVLRATAR
29.7	1460.8351	-0.0204	KFAAEQISSLVLR
23.7	1460.7405	0.0742	MQSEEALVRAATR
15.2	1460.7848	0.0299	QVIPHTGGSKANPR
13.0	1460.7293	0.0854	IDGDMKEAGQLLR
11.9	1460.8095	0.0053	LSLDLIMMAVLAR
11.6	1460.7293	0.0854	MSAINGVIEEKDR
10.5	1460.7657	0.0490	SLGEPISMTKQVR
10.3	1460.6929	0.1218	ESCIGQQEILER

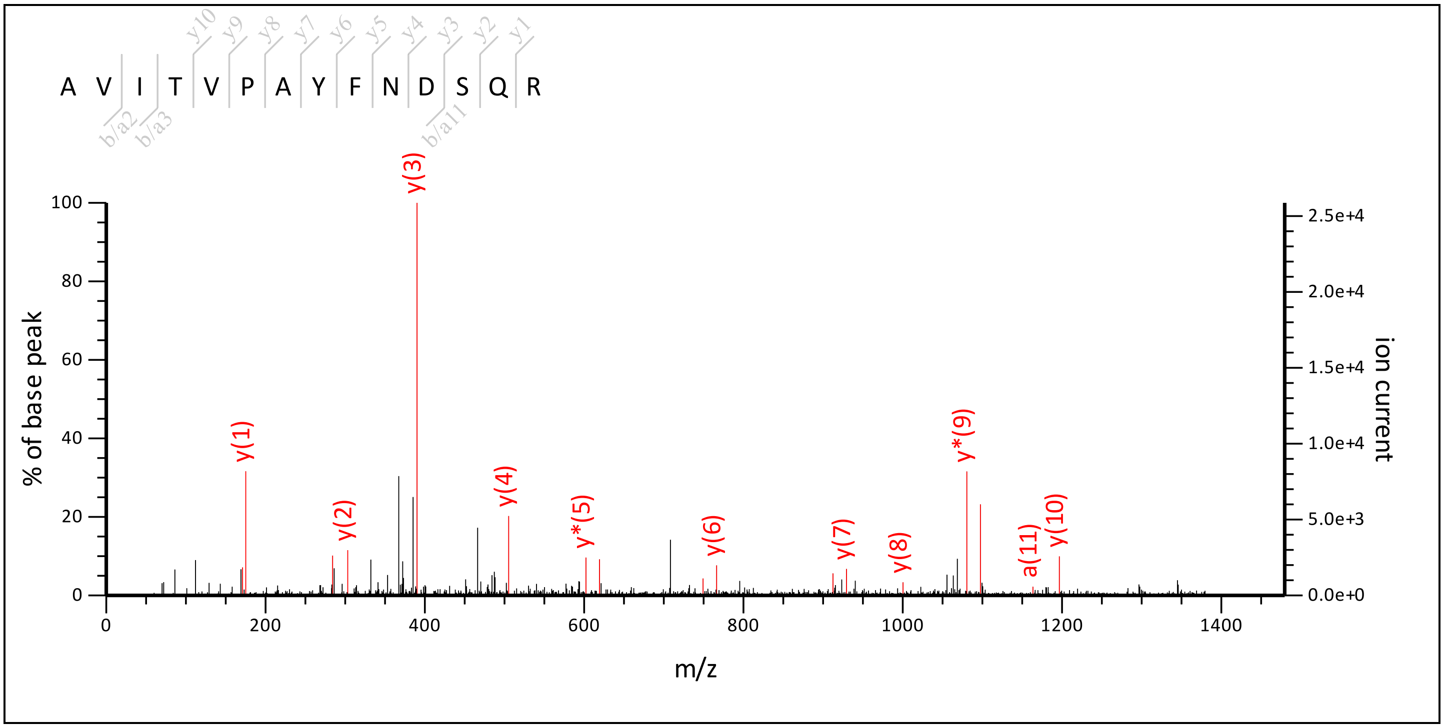
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 104

MS/MS Fragmentation of **AVITVPAYFNDSQR**
Found in **gi|6746592** in **NCBInr**, heat shock protein 70 [Arabidopsis thaliana]

Match to Query 99: 1579.854624 from(1580.861900,1+) intensity(0.0000) index(21)
Title: Label: F1, Spot_Id: 219679, Peak_List_Id: 224931, MSMS Job_Run_Id: 21758, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_F1_136842030500.txt



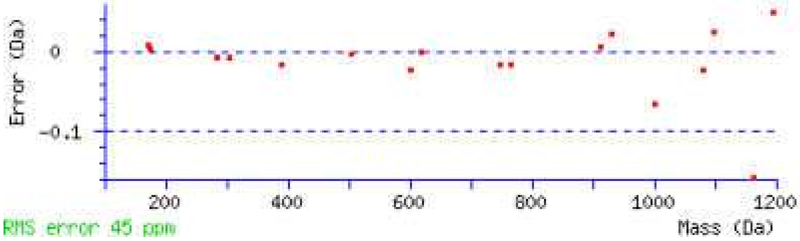
0 to 1479.56

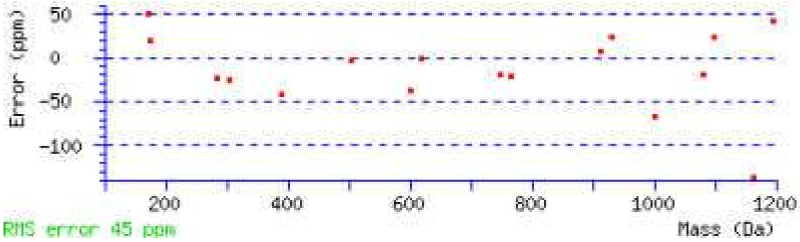
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1579.7995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 0.00018
Matches : 17/60 fragment ions using 28 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			14
2	143.1179		**171.1128**		V	1509.7696	1492.7431	13
3	256.2020		**284.1969**		I	1410.7012	1393.6747	12
4	357.2496		385.2445		T	1297.6171	1280.5906	11
5	456.3180		484.3130		V	***1196.5695***	1179.5429	10
6	553.3708		581.3657		P	***1097.5010***	1080.4745	9
7	624.4079		652.4028		A	***1000.4483***	983.4217	8
8	787.4713		815.4662		Y	***929.4112***	912.3846	7

9	934.5397		962.5346		**F**	***766.3478***	749.3213	**6**
10	1048.5826	1031.5560	1076.5775	1059.5510	**N**	***619.2794***	602.2529	**5**
11	1163.6095	1146.5830	1191.6045	1174.5779	**D**	***505.2365***	488.2100	**4**
12	1250.6416	1233.6150	1278.6365	1261.6099	**S**	***390.2096***	373.1830	**3**
13	1378.7001	1361.6736	1406.6951	1389.6685	**Q**	***303.1775***	286.1510	**2**
14					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
70.1	1579.7995	0.0552	AVITVPAYFNDSQR
11.7	1579.8392	0.0154	GITMTVGVAVFDSKR
11.7	1579.7413	0.1133	MGVLDGAERFDSQR
11.3	1579.7671	0.0876	IIYFDYYNDAKR
11.1	1579.9297	-0.0751	AVLTVPAGLGELTALR
9.9	1579.7399	0.1147	SSKSDEIENSLPMK
9.9	1579.8028	0.0518	KVLDMFDNLVSQR
9.7	1579.8206	0.0340	VTPSSSSLGVFESKR
9.5	1579.8318	0.0228	VNHSDVVEVVLQSR
9.3	1579.7876	0.0671	MAKSGGVSSSASSSLPK

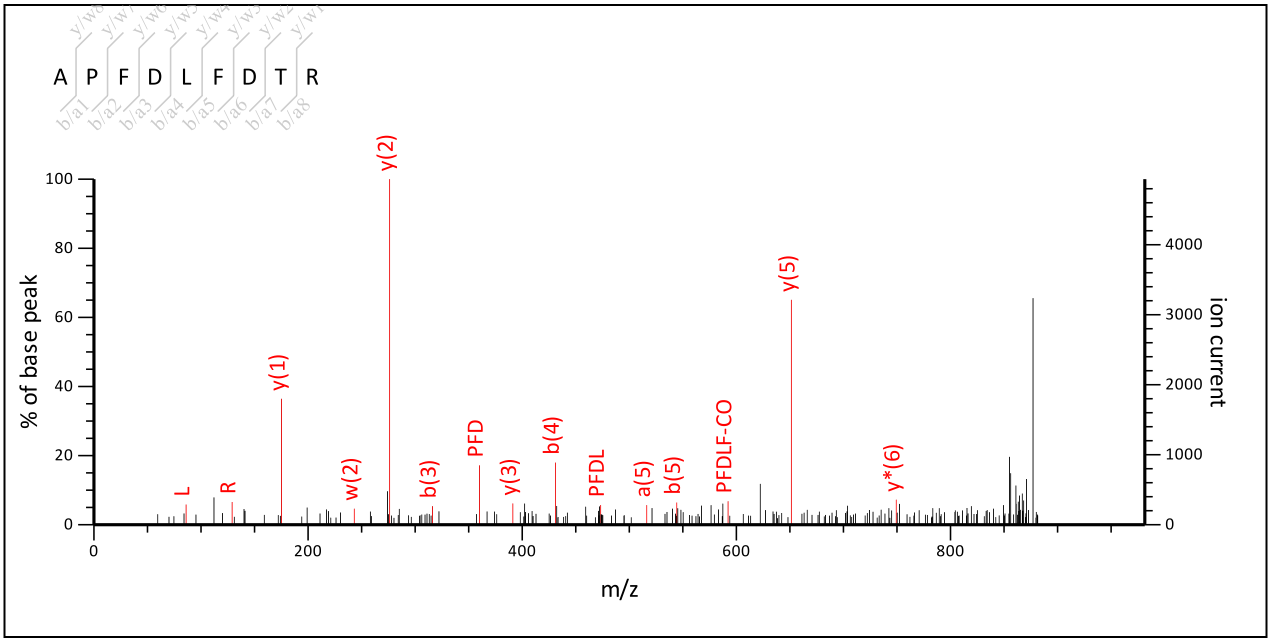
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 108

MS/MS Fragmentation of **APFDLFDTR**
Found in **gi|39104468** in **NCBInr**, heat shock protein 90 [Oryza sativa Japonica Group]

Match to Query 39: 1080.553724 from(1081.561000,1+) intensity(0.0000) index(13)
Title: Label: C2, Spot_Id: 219692, Peak_List_Id: 224833, MSMS Job_Run_Id: 21755, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C2_136842094000.txt



0 to 981.47

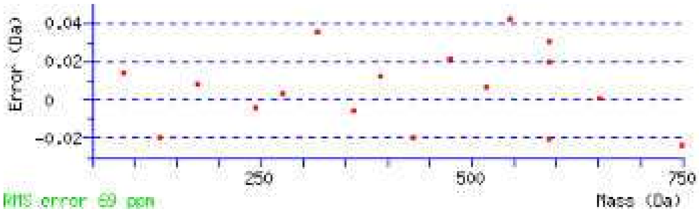
Label all possible matches ○ Label matches used for scoring ●

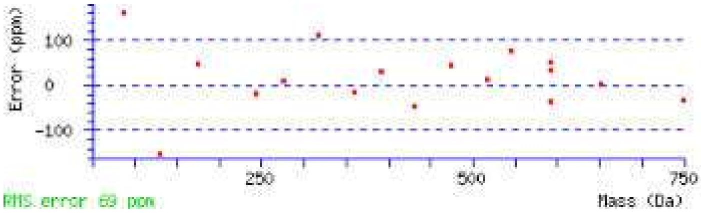
Monoisotopic mass of neutral peptide Mr(calc): 1080.5240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 16
Matches : 17/116 fragment ions using 27 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	44.0495	44.0495		72.0444		44.0495		A							9
2	70.0651	141.1022		169.0972		115.0866		P	968.4472	967.4520		1010.4942	993.4676	992.4836	8
3	120.0808	288.1707		***316.1656***				F	821.3788			913.4414	896.4149	895.4308	7
4	88.0393	403.1976	385.1870	***431.1925***	413.1819	359.2078		D	706.3519	705.3566		766.3730	749.3464	748.3624	6
5	86.0964	516.2817	498.2711	***544.2766***	526.2660	474.2347		L	593.2678	592.2726		***651.3461***	634.3195	633.3355	5
6	120.0808	663.3501	645.3395	691.3450	673.3344			F	446.1994			538.2620	521.2354	520.2514	4
7	88.0393	778.3770	760.3665	806.3719	788.3614	734.3872		D	331.1724	330.1772		***391.1936***	374.1670	373.1830	3
8	74.0600	879.4247	861.4141	907.4196	889.4090	863.4298	865.4090	T	230.1248	243.1452	245.1244	***276.1666***	259.1401	258.1561	2
9	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PF	217.1335	245.1285	PFD	332.1605	360.1554	PFDL	445.2445	473.2395
PFDLF	592.3130	620.3079	FD	235.1077	263.1026	FDL	348.1918	376.1867
FDLF	495.2602	523.2551	FDLFD	610.2871	638.2821	DL	201.1234	229.1183

DLF	348.1918	376.1867	**DLFD**	463.2187	491.2136	**DLFDT**	564.2664	592.2613
LF	233.1648	261.1598	**LFD**	348.1918	376.1867	**LFDT**	449.2395	477.2344
FD	235.1077	263.1026	**FDT**	336.1554	364.1503	**DT**	189.0870	217.0819





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.0	1080.5240	0.0297	APFDLFDTR
15.0	1080.5386	0.0151	LLGFCTGGTR
15.0	1080.5096	0.0441	LMWIDMTR
15.0	1080.5386	0.0151	MATYALQQR
14.7	1080.5234	0.0304	MAVAATGSTTR
13.8	1080.4870	0.0668	ETSINMNTR
13.7	1080.5056	0.0481	DMKMIQQR
13.7	1080.5200	0.0337	FDTSSLQQR
12.6	1080.6403	-0.0866	QALKPAIQGR
12.0	1080.5274	0.0263	GLMLYPDTR

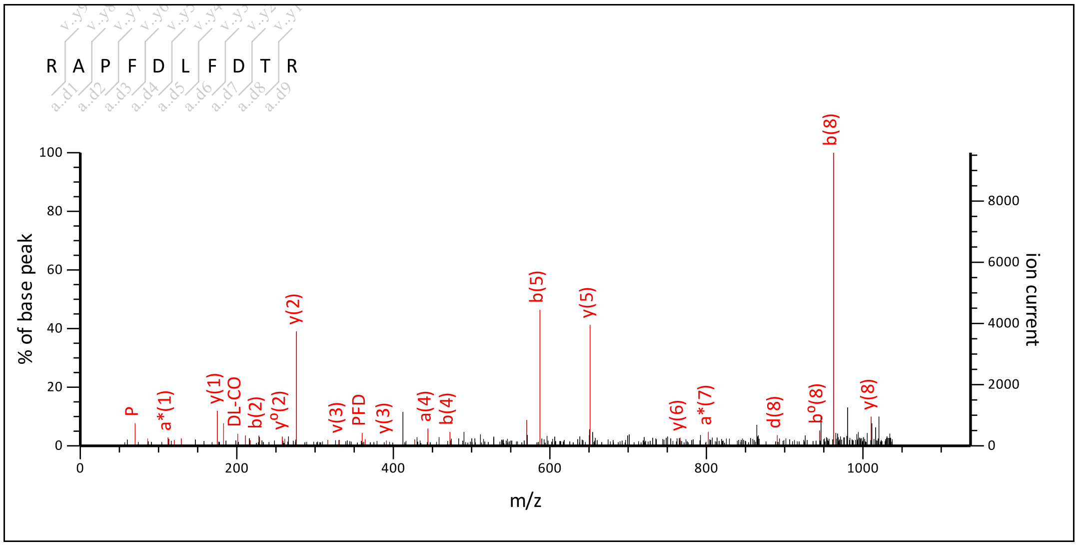
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 108

MS/MS Fragmentation of **RAPFDLFDTR**
Found in **gi|39104468** in **NCBInr**, heat shock protein 90 [Oryza sativa Japonica Group]

Match to Query 55: 1236.646424 from(1237.653700,1+) intensity(0.0000) index(17)
Title: Label: C2, Spot_Id: 219692, Peak_List_Id: 224827, MSMS Job_Run_Id: 21755, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C2_136842094000.txt



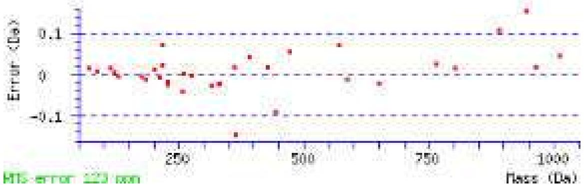
0 to 1137.47

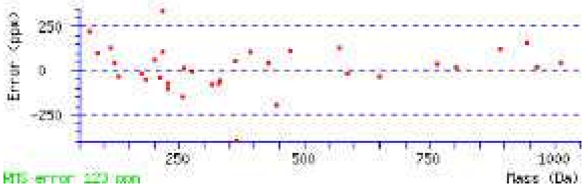
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1236.6251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 27
Matches : 37/151 fragment ions using 80 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	129.1135	**129.1135**	112.0869		157.1084	140.0818		44.0495		R						
2	44.0495	200.1506	183.1240		**228.1455**	211.1190				A	1065.5000			1081.5313	1064.5047	106
3	70.0651	297.2034	280.1768		325.1983	308.1717		271.1877		P	968.4472	967.4520		***1010.4942***	993.4676	99
4	120.0808	**444.2718**	427.2452		**472.2667**	455.2401				F	821.3788			913.4414	896.4149	89
5	88.0393	559.2987	542.2722	541.2881	**587.2936**	570.2671	569.2831	515.3089		D	706.3519	705.3566		***766.3730***	749.3464	74
6	86.0964	672.3828	655.3562	654.3722	700.3777	683.3511	682.3671	630.3358		L	593.2678	592.2726		***651.3461***	634.3195	63
7	120.0808	819.4512	802.4246	801.4406	847.4461	830.4196	829.4355			F	446.1994			538.2620	521.2354	52
8	88.0393	934.4781	917.4516	916.4676	**962.4730**	945.4465	944.4625	890.4883		D	331.1724	330.1772		***391.1936***	374.1670	37
9	74.0600	1035.5258	1018.4993	1017.5152	1063.5207	1046.4942	1045.5102	1019.5309	1021.5102	T	230.1248	243.1452	245.1244	***276.1666***	259.1401	25
10	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AP	141.1022	169.0972	**APF**	288.1707	316.1656	**APFD**	403.1976	431.1925
APFDL	516.2817	544.2766	**APFDLF**	663.3501	691.3450	**PF**	217.1335	245.1285
PFD	332.1605	360.1554	**PFDL**	445.2445	473.2395	**PFDLF**	592.3130	620.3079
FD	235.1077	263.1026	**FDL**	348.1918	376.1867	**FDLF**	495.2602	523.2551
FDLFD	610.2871	638.2821	**DL**	201.1234	229.1183	**DLF**	348.1918	376.1867
DLFD	463.2187	491.2136	**DLFDT**	564.2664	592.2613	**LF**	233.1648	261.1598
LFD	348.1918	376.1867	**LFDT**	449.2395	477.2344	**FD**	235.1077	263.1026
FDT	336.1554	364.1503	**DT**	189.0870	217.0819			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.9	1236.6132	0.0332	SMGSGVGEKITR
19.5	1236.6251	0.0213	RAPFDLFDTR
17.2	1236.6067	0.0397	MSTRKPTCTR
16.2	1236.5907	0.0557	KVTEEDMLEK
16.0	1236.7190	-0.0726	KVLVPPSGPSTR
16.0	1236.6132	0.0332	SMGSVGGEKITR
16.0	1236.5470	0.0995	SSTATADAEQEK
15.7	1236.5366	0.1098	NLPMDLMDEK
15.4	1236.5622	0.0842	NNTGLDEFAEK
15.2	1236.7303	-0.0838	VGVRAPATPLTR

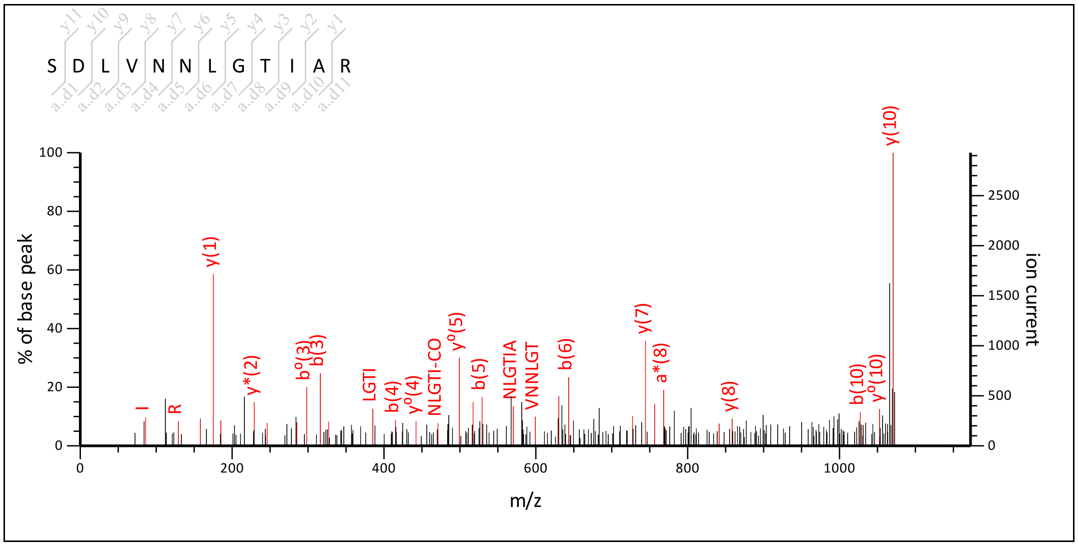
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 108

MS/MS Fragmentation of **SDLVNNLGTIAR**
Found in **gi|39104468** in **NCBInr**, heat shock protein 90 [Oryza sativa Japonica Group]

Match to Query 60: 1271.722724 from(1272.730000,1+) intensity(0.0000) index(18)
Title: Label: C2, Spot_Id: 219692, Peak_List_Id: 224835, MSMS Job_Run_Id: 21755, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C2_136842094000.txt



0 to 1172.54

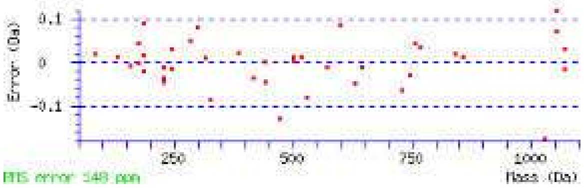
Label all possible matches ○ Label matches used for scoring ●

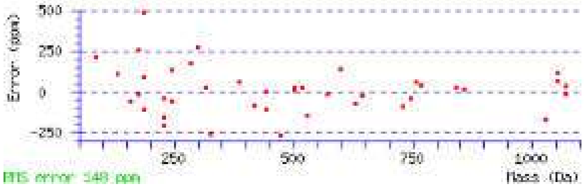
```
Monoisotopic mass of neutral peptide Mr(calc): 1271.6834
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.22
Matches : 43/207 fragment ions using 51 most intense peaks   (help)
```

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	y
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S						
2	88.0393	**175.0713**		157.0608	203.0662		185.0557	131.0815		D	1125.6375	1124.6422		1185.6586	1168.6321	1167.
3	86.0964	288.1554		270.1448	**316.1503**		298.1397	246.1084		L	1012.5534	1011.5582		***1070.6317***	1053.6051	1052.
4	72.0808	387.2238		369.2132	**415.2187**		397.2082	373.2082		V	913.4850	926.5054		957.5476	940.5211	939.
5	87.0553	501.2667	484.2402	483.2562	**529.2617**	512.2351	511.2511	458.2609		N	799.4421	798.4468		***858.4792***	841.4526	840.
6	87.0553	615.3097	598.2831	597.2991	**643.3046**	626.2780	625.2940	572.3039		N	685.3992	684.4039		***744.4363***	727.4097	726.
7	86.0964	728.3937	711.3672	710.3832	**756.3886**	739.3621	738.3781	686.3468		L	572.3151	571.3198		***630.3933***	613.3668	612.
8	30.0338	785.4152	768.3886	767.4046	813.4101	796.3836	795.3995			G				***517.3093***	500.2827	499.
9	74.0600	886.4629	869.4363	868.4523	914.4578	897.4312	896.4472	870.4680	872.4472	T	414.2459	427.2663	429.2456	460.2878	443.2613	442.
10	86.0964	999.5469	982.5204	981.5364	**1027.5419**	1010.5153	1009.5313	971.5156	985.5313	I	301.1619	314.1823	328.1979	359.2401	342.2136	
11	44.0495	**1070.5840**	1053.5575	1052.5735	1098.5790	1081.5524	1080.5684			A	230.1248			***246.1561***	229.1295	
12	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DL	201.1234	229.1183	DLV	300.1918	328.1867	DLVN	414.2347	442.2296
DLVNN	528.2776	556.2726	DLVNNL	641.3617	669.3566	DLVNNLG	698.3832	726.3781
LV	185.1648	213.1598	LVN	299.2078	327.2027	LVNN	413.2507	441.2456
LVNNL	526.3348	554.3297	LVNNLG	583.3562	611.3511	LVNNLGT	684.4039	712.3988
VN	186.1237	214.1186	VNN	300.1666	328.1615	VNNL	413.2507	441.2456
VNNLG	470.2722	498.2671	VNNLGT	571.3198	599.3148	VNNLGTI	684.4039	712.3988
NN	201.0982	229.0931	NNL	314.1823	342.1772	NNLG	371.2037	399.1987
NNLGT	472.2514	500.2463	NNLGTI	585.3355	613.3304	NNLGTIA	656.3726	684.3675
NL	200.1394	228.1343	NLG	257.1608	285.1557	NLGT	358.2085	386.2034

NLGTI	471.2926	499.2875	**NLGTIA**	542.3297	570.3246	**LG**	143.1179	171.1128
LGT	244.1656	272.1605	**LGTI**	357.2496	385.2445	**LGTIA**	428.2867	456.2817
GT	131.0815	159.0764	**GTI**	244.1656	272.1605	**GTIA**	315.2027	343.1976
TI	187.1441	215.1390	**TIA**	258.1812	286.1761	**IA**	157.1335	185.1285





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.1	1271.6834	0.0394	SDLVNNLGTIAR
30.3	1271.6834	0.0394	SDLVNNLATIGR
28.2	1271.6470	0.0758	QLIDSNTPAASR
26.2	1271.7020	0.0207	VSIAVGMPKGSAR
24.5	1271.7085	0.0142	TTLPETLIGTAR
21.7	1271.6833	0.0394	TTPLAEANTKAR
21.5	1271.6292	0.0935	MADPGASVNIAAR
20.4	1271.6833	0.0394	IAAATAAEEAKAR
19.9	1271.7197	0.0030	LAAEVSSQIKAR
18.4	1271.6833	0.0394	IVAEELERSAR

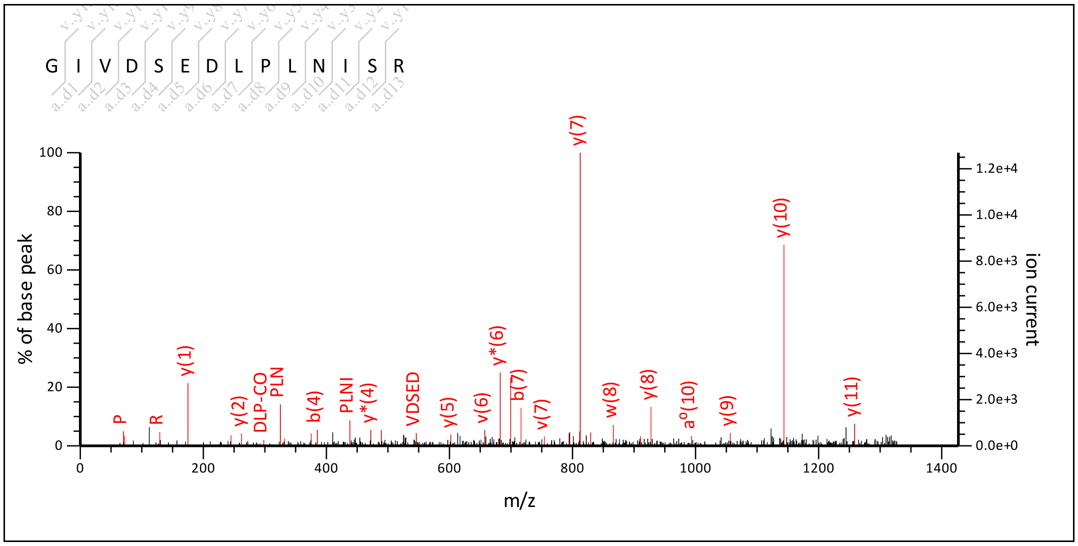
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 108**

MS/MS Fragmentation of **GIVDSEDLPLNISR**
Found in **gi|39104468** in **NCBInr**, heat shock protein 90 [Oryza sativa Japonica Group]

Match to Query 80: 1526.843524 from(1527.850800,1+) intensity(0.0000) index(25)
Title: Label: C2, Spot_Id: 219692, Peak_List_Id: 224828, MSMS Job_Run_Id: 21755, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C2_136842094000.txt



0 to 1427.16

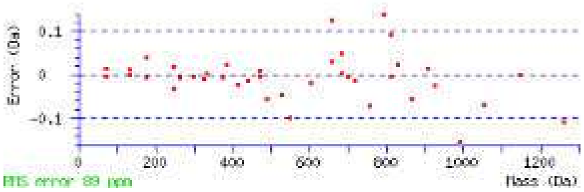
Label all possible matches ○ Label matches used for scoring ●

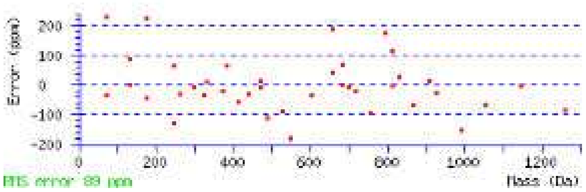
Monoisotopic mass of neutral peptide Mr(calc): 1526.7940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 81 **Expect:** 1.3e-05
Matches : 44/237 fragment ions using 52 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			115.0866	129.1022	I	1412.7016	1425.7220	1439.7376	1470.7798	1453.7533
3	72.0808	242.1863			270.1812			228.1707		V	1313.6332	1326.6536		1357.6958	1340.6692
4	88.0393	357.2132		339.2027	**385.2082**		367.1976	313.2234		D	1198.6062	1197.6110		***1258.6274***	1241.6008
5	60.0444	444.2453		426.2347	**472.2402**		454.2296	428.2504		S	1111.5742	1110.5790		***1143.6004***	1126.5739
6	102.0550	573.2879		555.2773	601.2828		583.2722	515.2824		E	982.5316	981.5364		***1056.5684***	1039.5419
7	88.0393	688.3148		670.3042	**716.3097**		698.2992	644.3250		D	867.5047	866.5094		***927.5258***	910.4993
8	86.0964	801.3989		783.3883	**829.3938**		811.3832	759.3519		L	754.4206	753.4254		***812.4989***	795.4723
9	70.0651	898.4516		880.4411	926.4466		908.4360	872.4360		P	657.3678	656.3726		***699.4148***	682.3882
10	86.0964	1011.5357		993.5251	1039.5306		1021.5201	969.4888		L	544.2838	543.2885		***602.3620***	585.3355
11	87.0553	1125.5786	1108.5521	1107.5681	1153.5735	1136.5470	1135.5630	1082.5728		N	430.2409	429.2456		***489.2780***	472.2514
12	86.0964	1238.6627	1221.6361	1220.6521	1266.6576	1249.6311	1248.6470	1210.6314	1224.6470	I	317.1568	330.1772	344.1928	***375.2350***	358.2085
13	60.0444	1325.6947	1308.6682	1307.6842	1353.6896	1336.6631	1335.6791	1309.6998		S	230.1248	229.1295		***262.1510***	245.1244
14	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IV	185.1648	213.1598	IVD	300.1918	328.1867	IVDS	387.2238	415.2187
IVDSE	516.2664	544.2613	IVDSED	631.2933	659.2883	VD	187.1077	215.1026
VDS	274.1397	302.1347	VDSE	403.1823	431.1773	VDSED	518.2093	546.2042
VDSEDL	631.2933	659.2883	DS	175.0713	203.0662	DSE	304.1139	332.1088
DSED	419.1409	447.1358	DSEDL	532.2249	560.2198	DSEDLP	629.2777	657.2726
SE	189.0870	217.0819	SED	304.1139	332.1088	SEDL	417.1980	445.1929
SEDLP	514.2508	542.2457	SEDLPL	627.3348	655.3297	ED	217.0819	245.0768

EDL	330.1660	358.1609	**EDLP**	427.2187	455.2136	**EDLPL**	540.3028	568.2977
EDLPLN	654.3457	682.3406	**DL**	201.1234	229.1183	**DLP**	298.1761	326.1710
DLPL	411.2602	439.2551	**DLPLN**	525.3031	553.2980	**DLPLNI**	638.3872	666.3821
LP	183.1492	211.1441	**LPL**	296.2333	324.2282	**LPLN**	410.2762	438.2711
LPLNI	523.3602	551.3552	**LPLNIS**	610.3923	638.3872	**PL**	183.1492	211.1441
PLN	297.1921	325.1870	**PLNI**	410.2762	438.2711	**PLNIS**	497.3082	525.3031
LN	200.1394	228.1343	**LNI**	313.2234	341.2183	**LNIS**	400.2554	428.2504
NI	200.1394	228.1343	**NIS**	287.1714	315.1663	**IS**	173.1285	201.1234





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
81.2	1526.7940	0.0495	GIVDSEDLPLNISR
25.5	1526.8052	0.0383	DRISNLPDELISR
22.8	1526.8973	-0.0538	FVPKVQLPFSPLR
21.3	1526.8239	0.0196	QMALQQLVAGSPLR
19.8	1526.8205	0.0230	NPFNENLPVKISR
15.6	1526.8165	0.0270	RNSAGETLSVQIPR
15.3	1526.8165	0.0271	IRAAESALNLEQGR
15.0	1526.7664	0.0772	AVVDSNMVHHYKK
14.1	1526.7073	0.1362	NRNDTSTYSNISR
13.7	1526.7913	0.0522	TVSSPRNSSSPRPR

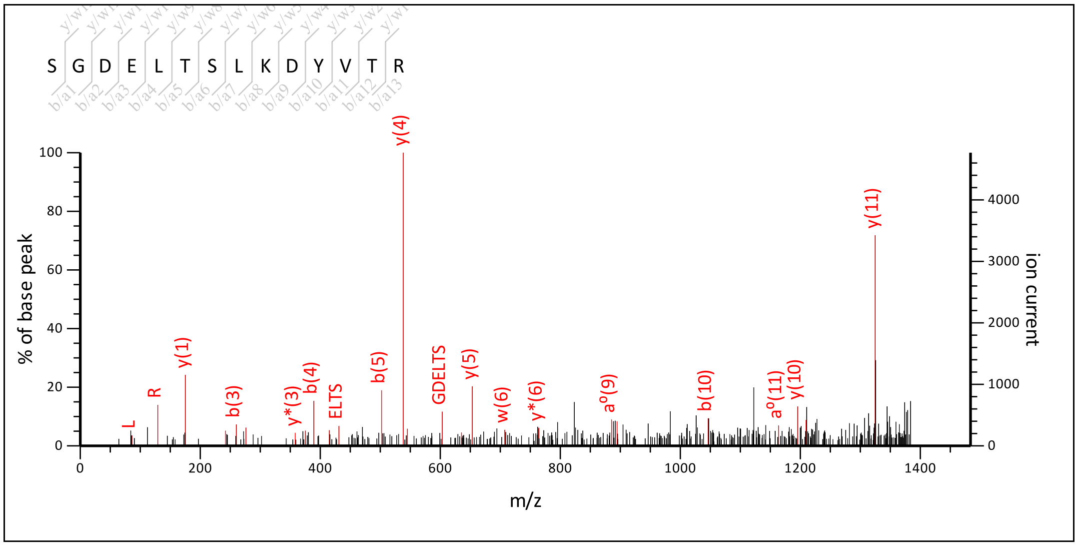
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 108

MS/MS Fragmentation of **SGDELTSLKDYVTR**
Found in **gi|39104468** in **NCBInr**, heat shock protein 90 [Oryza sativa Japonica Group]

Match to Query 88: 1582.835724 from(1583.843000,1+) intensity(0.0000) index(28)
Title: Label: C2, Spot_Id: 219692, Peak_List_Id: 224832, MSMS Job_Run_Id: 21755, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C2_136842094000.txt



0 to 1483.7

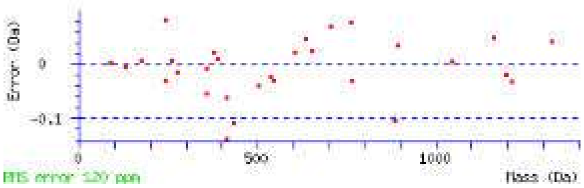
Label all possible matches ○ Label matches used for scoring ●

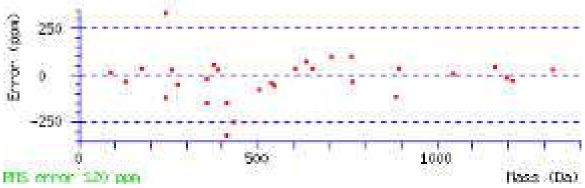
```
Monoisotopic mass of neutral peptide Mr(calc): 1582.7839
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.6
Matches : 33/240 fragment ions using 56 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		**S**					
2	30.0338	117.0659		99.0553	145.0608		127.0502			**G**				1496.7591	1479.7326
3	88.0393	232.0928		214.0822	***260.0877***		242.0771	188.1030		**D**	1379.7165	1378.7213		1439.7377	1422.7111
4	102.0550	361.1354		343.1248	***389.1303***		371.1197	303.1299		**E**	1250.6739	1249.6787		***1324.7107***	1307.6842
5	86.0964	474.2195		456.2089	***502.2144***		484.2038	432.1725		**L**	1137.5899	1136.5946		***1195.6681***	1178.6416
6	74.0600	575.2671		557.2566	***603.2620***		585.2515	559.2722	561.2515	**T**	1036.5422	1049.5626	1051.5419	1082.5841	1065.5575
7	60.0444	662.2992		644.2886	690.2941		672.2835	646.3042		**S**	949.5102	948.5149		981.5364	964.5098
8	86.0964	775.3832		757.3727	803.3781		785.3676	733.3363		**L**	836.4261	835.4308		***894.5043***	877.4778
9	101.1073	903.4782	886.4516	885.4676	931.4731	914.4466	913.4625	846.4203		**K**	708.3311	707.3359		781.4203	764.3937
10	88.0393	1018.5051	1001.4786	1000.4946	***1046.5000***	1029.4735	1028.4895	974.5153		**D**	593.3042	592.3089		***653.3253***	636.2988
11	136.0757	1181.5685	1164.5419	1163.5579	***1209.5634***	1192.5368	1191.5528			**Y**	430.2409			***538.2984***	521.2718
12	72.0808	1280.6369	1263.6103	1262.6263	1308.6318	1291.6052	1290.6212	1266.6212		**V**	331.1724	344.1928		***375.2350***	358.2085
13	74.0600	1381.6846	1364.6580	1363.6740	1409.6795	1392.6529	1391.6689	1365.6896	1367.6689	**T**	230.1248	243.1452	245.1244	***276.1666***	259.1401
14	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GD	145.0608	173.0557	**GDE**	274.1034	302.0983	**GDEL**	387.1874	415.1823
GDELT	488.2351	516.2300	**GDELTS**	575.2671	603.2620	**GDELTSL**	688.3512	716.3461
DE	217.0819	245.0768	**DEL**	330.1660	358.1609	**DELT**	431.2136	459.2086
DELTS	518.2457	546.2406	**DELTSL**	631.3297	659.3246	**EL**	215.1390	243.1339
ELT	316.1867	344.1816	**ELTS**	403.2187	431.2136	**ELTSL**	516.3028	544.2977
ELTSLK	644.3978	672.3927	**LT**	187.1441	215.1390	**LTS**	274.1761	302.1710
LTSL	387.2602	415.2551	**LTSLK**	515.3552	543.3501	**LTSLKD**	630.3821	658.3770

TS	161.0921	189.0870	**TSL**	274.1761	302.1710	**TSLK**	402.2711	430.2660
TSLKD	517.2980	545.2930	**TSLKDY**	680.3614	708.3563	**SL**	173.1285	201.1234
SLK	301.2234	329.2183	**SLKD**	416.2504	444.2453	**SLKDY**	579.3137	607.3086
SLKDYV	678.3821	706.3770	**LK**	214.1914	242.1863	**LKD**	329.2183	357.2132
LKDY	492.2817	520.2766	**LKDYV**	591.3501	619.3450	**LKDYVT**	692.3978	720.3927
KD	216.1343	244.1292	**KDY**	379.1976	407.1925	**KDYV**	478.2660	506.2609
KDYVT	579.3137	607.3086	**DY**	251.1026	279.0975	**DYV**	350.1710	378.1660
DYVT	451.2187	479.2136	**YV**	235.1441	263.1390	**YVT**	336.1918	364.1867
VT	173.1285	201.1234						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.5	1582.7839	0.0519	SGDELTSLKDYVTR
24.6	1582.7839	0.0519	SGEDLTSLKDYVTR
23.6	1582.9658	-0.1300	SITSILKPLEILTR
18.5	1582.7773	0.0584	KLHMPATTSPDDVR
15.4	1582.8468	-0.0110	SLTAHFSPPVTGITR
14.7	1582.7369	0.0988	TSSLSSSGGGCTAQRK
14.2	1582.6900	0.1458	DGSESWVEVQYER
13.2	1582.8243	0.0114	DTSLLQPGTFYLTK
12.8	1582.8905	-0.0548	KLQFGMVYVLTLR
12.7	1582.6901	0.1456	MEVLMNERMNER

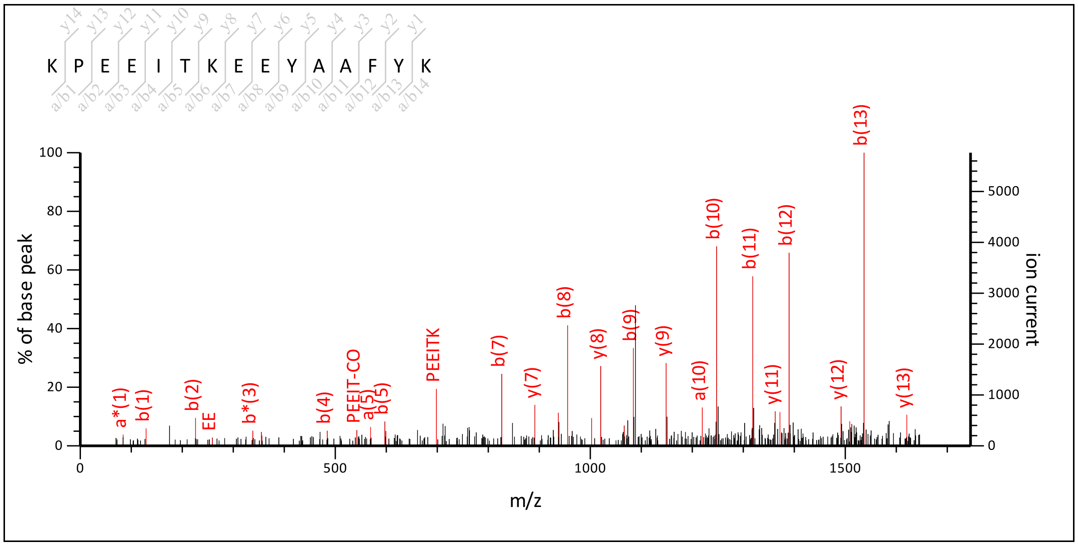
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 108**

MS/MS Fragmentation of **KPEEITKEEYAAFYK**
Found in **gi|39104468** in **NCBInr**, heat shock protein 90 [Oryza sativa Japonica Group]

Match to Query 94: 1844.956424 from(1845.963700,1+) intensity(0.0000) index(31)
Title: Label: C2, Spot_Id: 219692, Peak_List_Id: 224829, MSMS Job_Run_Id: 21755, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C2_136842094000.txt



0 to 1745.61

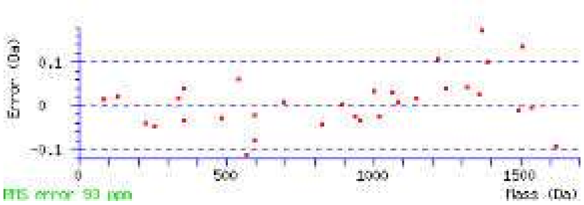
Label all possible matches ○ Label matches used for scoring ●

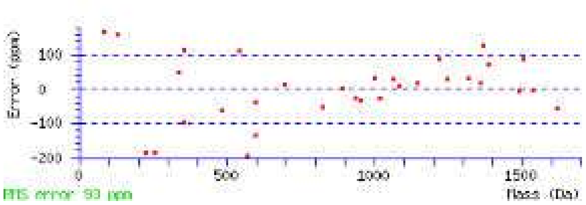
Monoisotopic mass of neutral peptide Mr(calc): 1844.9196
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 1.1e-07
Matches : 35/257 fragment ions using 48 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	101.1073	101.1073	84.0808		***129.1022***	112.0757		44.0495		K						
2	70.0651	198.1601	181.1335		***226.1550***	209.1285		172.1444		P	1675.7850	1674.7897		1717.8319	1700.8054	169
3	102.0550	327.2027	310.1761	309.1921	***355.1976***	338.1710	337.1870	269.1972		E	1546.7424	1545.7472		**1620.7792**	1603.7526	160
4	102.0550	456.2453	439.2187	438.2347	***484.2402***	467.2136	466.2296	398.2398		E	1417.6998	1416.7046		**1491.7366**	1474.7100	147
5	86.0964	**569.3293**	552.3028	551.3188	***597.3243***	580.2977	579.3137	541.2980	555.3137	I	1304.6157	1317.6361	1331.6518	**1362.6940**	1345.6674	134
6	74.0600	670.3770	653.3505	652.3665	***698.3719***	681.3454	680.3614	654.3821	656.3614	T	1203.5681	1216.5885	1218.5677	1249.6099	1232.5834	123
7	101.1073	798.4720	781.4454	780.4614	***826.4669***	809.4403	808.4563	741.4141		K	1075.4731	1074.4779		**1148.5623**	1131.5357	113
8	102.0550	927.5146	910.4880	909.5040	***955.5095***	938.4829	937.4989	869.5091		E	946.4305	945.4353		**1020.4673**	1003.4407	100
9	102.0550	1056.5572	1039.5306	1038.5466	***1084.5521***	1067.5255	1066.5415	998.5517		E	817.3879	816.3927		**891.4247**	874.3981	87
10	136.0757	**1219.6205**	1202.5939	1201.6099	***1247.6154***	1230.5889	1229.6048			Y	654.3246			762.3821	745.3556	
11	44.0495	1290.6576	1273.6311	1272.6470	***1318.6525***	1301.6260	1300.6420			A	583.2875			**599.3188**	582.2922	
12	44.0495	1361.6947	1344.6682	1343.6842	***1389.6896***	1372.6631	1371.6791			A	512.2504			528.2817	511.2551	
13	120.0808	**1508.7631**	1491.7366	1490.7526	***1536.7581***	1519.7315	1518.7475			F	365.1819			457.2445	440.2180	
14	136.0757	1671.8265	1654.7999	1653.8159	1699.8214	1682.7948	1681.8108			Y	202.1186			310.1761	293.1496	
15	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PE	199.1077	227.1026	PEE	328.1503	356.1452	PEEI	441.2344	469.2293
PEEIT	542.2821	570.2770	PEEITK	670.3770	698.3719	EE	231.0975	259.0925
EEI	344.1816	372.1765	EEIT	445.2293	473.2242	EEITK	573.3243	601.3192
EI	215.1390	243.1339	EIT	316.1867	344.1816	EITK	444.2817	472.2766
EITKE	573.3243	601.3192	IT	187.1441	215.1390	ITK	315.2391	343.2340
ITKE	444.2817	472.2766	ITKEE	573.3243	601.3192	TK	202.1550	230.1499

TKE	331.1976	359.1925	**TKEE**	460.2402	488.2351	**TKEEY**	623.3035	651.2984
TKEEYA	694.3406	722.3355	**KE**	230.1499	258.1448	**KEE**	359.1925	387.1874
KEEY	522.2558	550.2508	**KEEYA**	593.2930	621.2879	**KEEYAA**	664.3301	692.3250
EE	231.0975	259.0925	**EEY**	394.1609	422.1558	**EEYA**	465.1980	493.1929
EEYAA	536.2351	564.2300	**EEYAAF**	683.3035	711.2984	**EY**	265.1183	293.1132
EYA	336.1554	364.1503	**EYAA**	407.1925	435.1874	**EYAAF**	554.2609	582.2558
YA	207.1128	235.1077	**YAA**	278.1499	306.1448	**YAAF**	425.2183	453.2132
YAAFY	588.2817	616.2766	**AA**	115.0866	143.0815	**AAF**	262.1550	290.1499
AAFY	425.2183	453.2132	**AF**	191.1179	219.1128	**AFY**	354.1812	382.1761
FY	283.1441	311.1390						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
103.1	1844.9196	0.0369	KPEEITKEEYAAFYK
19.3	1844.8580	0.0984	NPEEITRDEYAAFYK
11.9	1844.9818	-0.0254	VMLPAVAKAGQIEEAFR
11.5	1844.8913	0.0651	MFLEKPQPPSMPNSAR
9.8	1844.9025	0.0539	KPSSAASLFGRMAMGFR
8.6	1845.0546	-0.0982	KPIMFVGGAGVGKTQLVK
8.5	1844.8767	0.0797	QYVEAGDWKAAVAMYK
8.5	1844.9917	-0.0353	RLILTQEEMEEVVLK
8.2	1844.9169	0.0395	LVPFASTWAQQANEGAR
8.1	1845.0294	-0.0730	KLLELMVLDNHLHVR

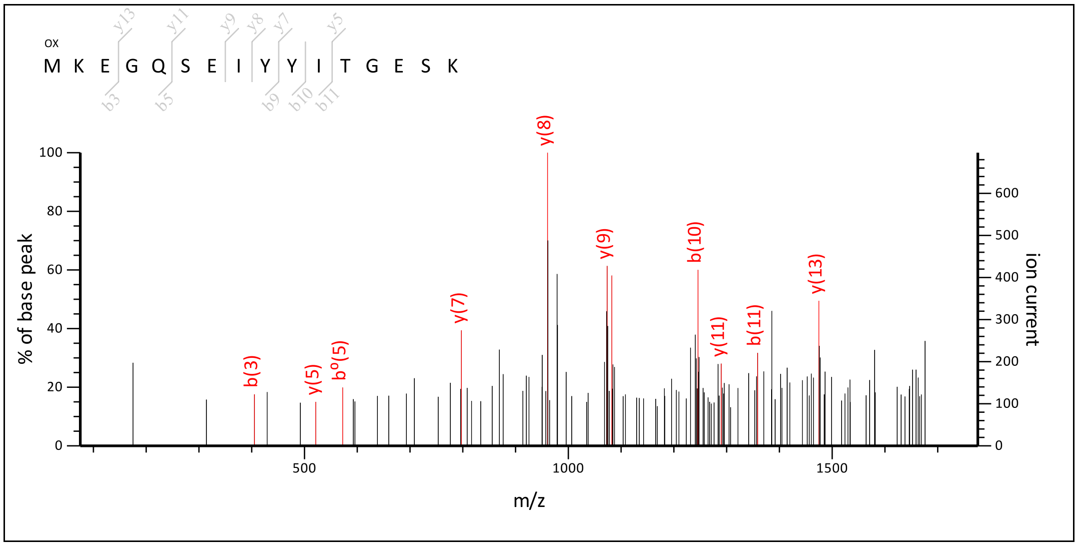
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 108

MS/MS Fragmentation of **MKEGQSEIYYITGESK**
Found in **gi|39104468** in **NCBInr**, heat shock protein 90 [Oryza sativa Japonica Group]

Match to Query 96: 1877.903324 from(1878.910600,1+) intensity(0.0000) index(32)
Title: Label: C2, Spot_Id: 219692, Peak_List_Id: 224847, MSMS Job_Run_Id: 21755, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_C2_136842094000.txt



75.12 to 1775.99

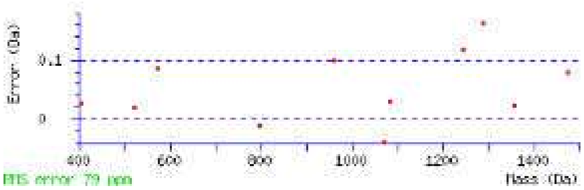
Label all possible matches ○ Label matches used for scoring ●

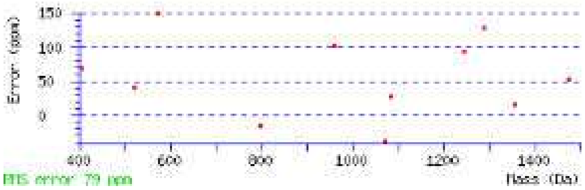
Monoisotopic mass of neutral peptide Mr(calc): 1877.8717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 17 **Expect:** 32
Matches : 11/385 fragment ions using 29 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	120.0478	120.0478			148.0427			44.0495		M					
2	101.1073	248.1427	231.1162		276.1376	259.1111		191.0849		K	1658.7544	1657.7592		1731.8436	1714.8170
3	102.0550	377.1853	360.1588	359.1748	**405.1802**	388.1537	387.1697	319.1798		E	1529.7118	1528.7166		1603.7486	1586.7221
4	30.0338	434.2068	417.1802	416.1962	462.2017	445.1751	444.1911			G				***1474.7060***	1457.6795
5	101.0709	562.2654	545.2388	544.2548	590.2603	573.2337	572.2497	505.2439		Q	1344.6318	1343.6365		1417.6846	1400.6580
6	60.0444	649.2974	632.2708	631.2868	677.2923	660.2658	659.2817	633.3025		S	1257.5998	1256.6045		***1289.6260***	1272.5994
7	102.0550	778.3400	761.3134	760.3294	806.3349	789.3083	788.3243	720.3345		E	1128.5572	1127.5619		1202.5939	1185.5674
8	86.0964	891.4240	874.3975	873.4135	919.4190	902.3924	901.4084	863.3927	877.4084	I	1015.4731	1028.4935	1042.5092	***1073.5514***	1056.5248
9	136.0757	1054.4874	1037.4608	1036.4768	**1082.4823**	1065.4557	1064.4717			Y	852.4098			***960.4673***	943.4407
10	136.0757	1217.5507	1200.5242	1199.5401	**1245.5456**	1228.5191	1227.5351			Y	689.3464			***797.4040***	780.3774
11	86.0964	1330.6348	1313.6082	1312.6242	**1358.6297**	1341.6031	1340.6191	1302.6035	1316.6191	I	576.2624	589.2828	603.2984	634.3406	617.3141
12	74.0600	1431.6824	1414.6559	1413.6719	1459.6774	1442.6508	1441.6668	1415.6875	1417.6668	T	475.2147	488.2351	490.2144	***521.2566***	504.2300
13	30.0338	1488.7039	1471.6774	1470.6933	1516.6988	1499.6723	1498.6883			G				420.2089	403.1823
14	102.0550	1617.7465	1600.7200	1599.7359	1645.7414	1628.7149	1627.7309	1559.7410		E	289.1506	288.1554		363.1874	346.1609
15	60.0444	1704.7785	1687.7520	1686.7680	1732.7734	1715.7469	1714.7629	1688.7836		S	202.1186	201.1234		234.1448	217.1183
16	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KE	230.1499	258.1448	KEG	287.1714	315.1663	KEGQ	415.2300	443.2249
KEGQS	502.2620	530.2569	KEGQSE	631.3046	659.2995	EG	159.0764	187.0713

EGQ	287.1350	315.1299	**EGQS**	374.1670	402.1619	**EGQSE**	503.2096	531.2045
EGQSEI	616.2937	644.2886	**GQ**	158.0924	186.0873	**GQS**	245.1244	273.1193
GQSE	374.1670	402.1619	**GQSEI**	487.2511	515.2460	**GQSEIY**	650.3144	678.3093
QS	188.1030	216.0979	**QSE**	317.1456	345.1405	**QSEI**	430.2296	458.2245
QSEIY	593.2930	621.2879	**SE**	189.0870	217.0819	**SEI**	302.1710	330.1660
SEIY	465.2344	493.2293	**SEIYY**	628.2977	656.2926	**EI**	215.1390	243.1339
EIY	378.2023	406.1973	**EIYY**	541.2657	569.2606	**EIYYI**	654.3497	682.3447
IY	249.1598	277.1547	**IYY**	412.2231	440.2180	**IYYI**	525.3071	553.3021
IYYIT	626.3548	654.3497	**IYYITG**	683.3763	711.3712	**YY**	299.1390	327.1339
YYI	412.2231	440.2180	**YYIT**	513.2708	541.2657	**YYITG**	570.2922	598.2871
YYITGE	699.3348	727.3297	**YI**	249.1598	277.1547	**YIT**	350.2074	378.2023
YITG	407.2289	435.2238	**YITGE**	536.2715	564.2664	**YITGES**	623.3035	651.2984
IT	187.1441	215.1390	**ITG**	244.1656	272.1605	**ITGE**	373.2082	401.2031
ITGES	460.2402	488.2351	**TG**	131.0815	159.0764	**TGE**	260.1241	288.1190
TGES	347.1561	375.1510	**GE**	159.0764	187.0713	**GES**	246.1084	274.1034
ES	189.0870	217.0819						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.2	1877.8717	0.0317	MKEGQSEIYYITGESK
17.2	1877.8717	0.0317	MKEGQSEIYYITGESK
17.2	1877.8353	0.0680	MQEGQSEIYYITGESK
15.4	1878.0251	-0.1217	ILFFIGDLEVASAEAKR
7.3	1878.0615	-0.1581	SSVLALILRFYDPISGK
6.4	1877.8764	0.0269	HGFEEAEMVKVMVSNR
6.4	1877.8248	0.0786	DCAGDDDAVAAGIICSLR
6.4	1877.8877	0.0157	GKVHVATCPHGTTCEPK
5.2	1877.9339	-0.0306	SSMAKVCDELAQVIGVR
4.9	1877.9345	-0.0312	VYEELNALMPFSPNVR

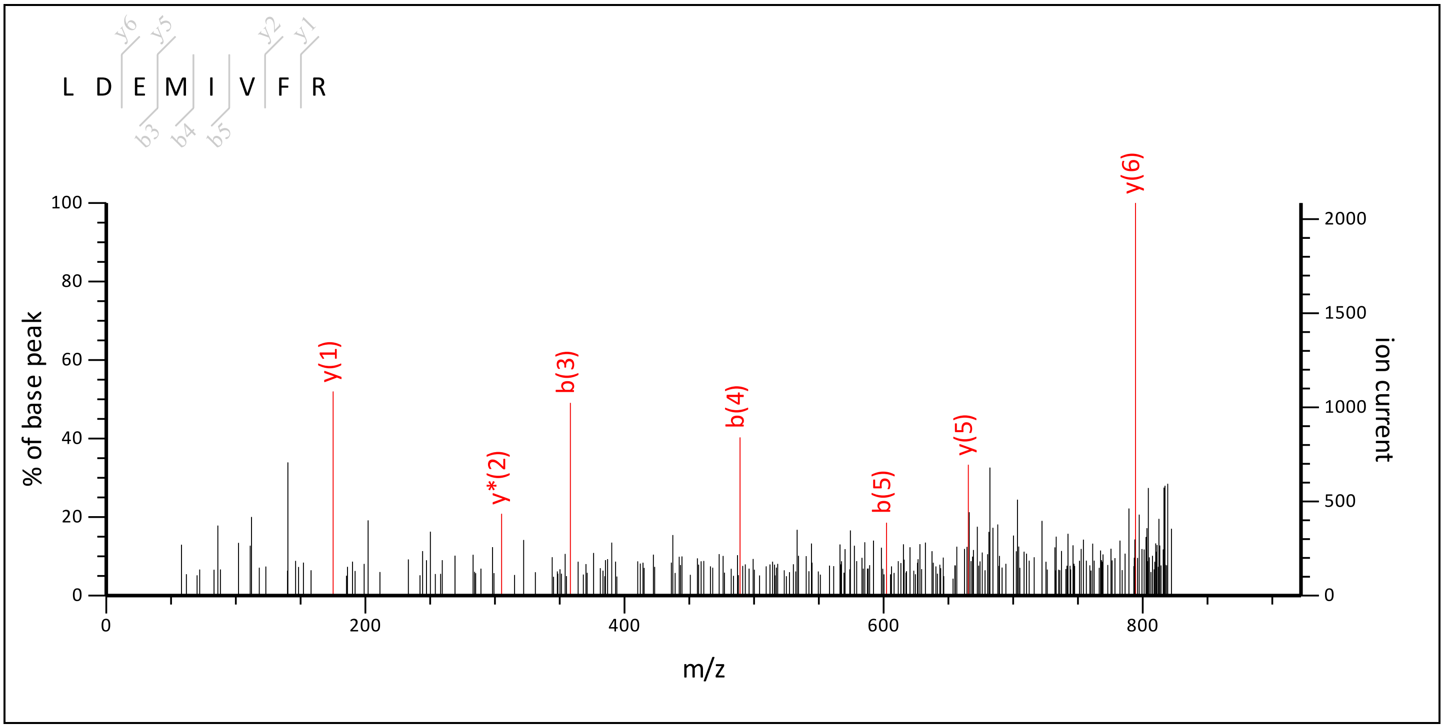
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 110

MS/MS Fragmentation of **LDEMIVFR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 88: 1021.553424 from(1022.560700,1+) intensity(0.0000) index(3)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226663, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt

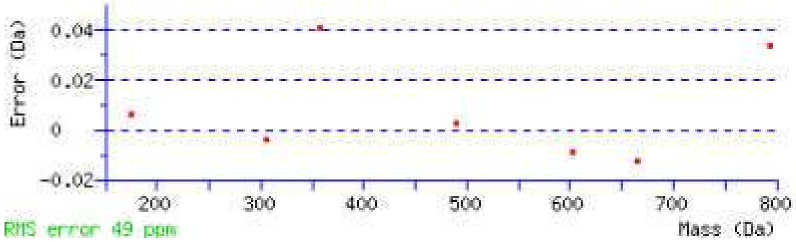


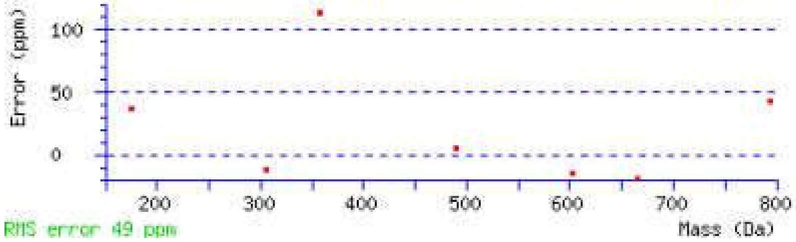
0 to 922.15

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1021.5266
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 48
Matches : 7/28 fragment ions using 8 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	86.0964	114.0913	L			8
2	201.1234	229.1183	D	909.4499	892.4233	7
3	330.1660	***358.1609***	E	***794.4229***	777.3964	6
4	461.2064	***489.2014***	M	***665.3803***	648.3538	5
5	574.2905	***602.2854***	I	534.3398	517.3133	4
6	673.3589	701.3538	V	421.2558	404.2292	3
7	820.4273	848.4223	F	322.1874	305.1608	2
8			R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.9	1021.5266	0.0268	IDEMLVFR
28.9	1021.5266	0.0268	LDEMIVFR
25.8	1021.4539	0.0996	DLEMPDFR
23.3	1021.4716	0.0818	EVEDIDFR
17.6	1021.4936	0.0598	DLELMVMR
17.6	1021.4716	0.0818	EVEDEVFR
17.6	1021.4903	0.0632	EVEMPVFR
17.6	1021.5055	0.0479	MPEPFVFR
17.6	1021.4685	0.0850	NNELMVMR
17.6	1021.4903	0.0632	VEEMPVFR

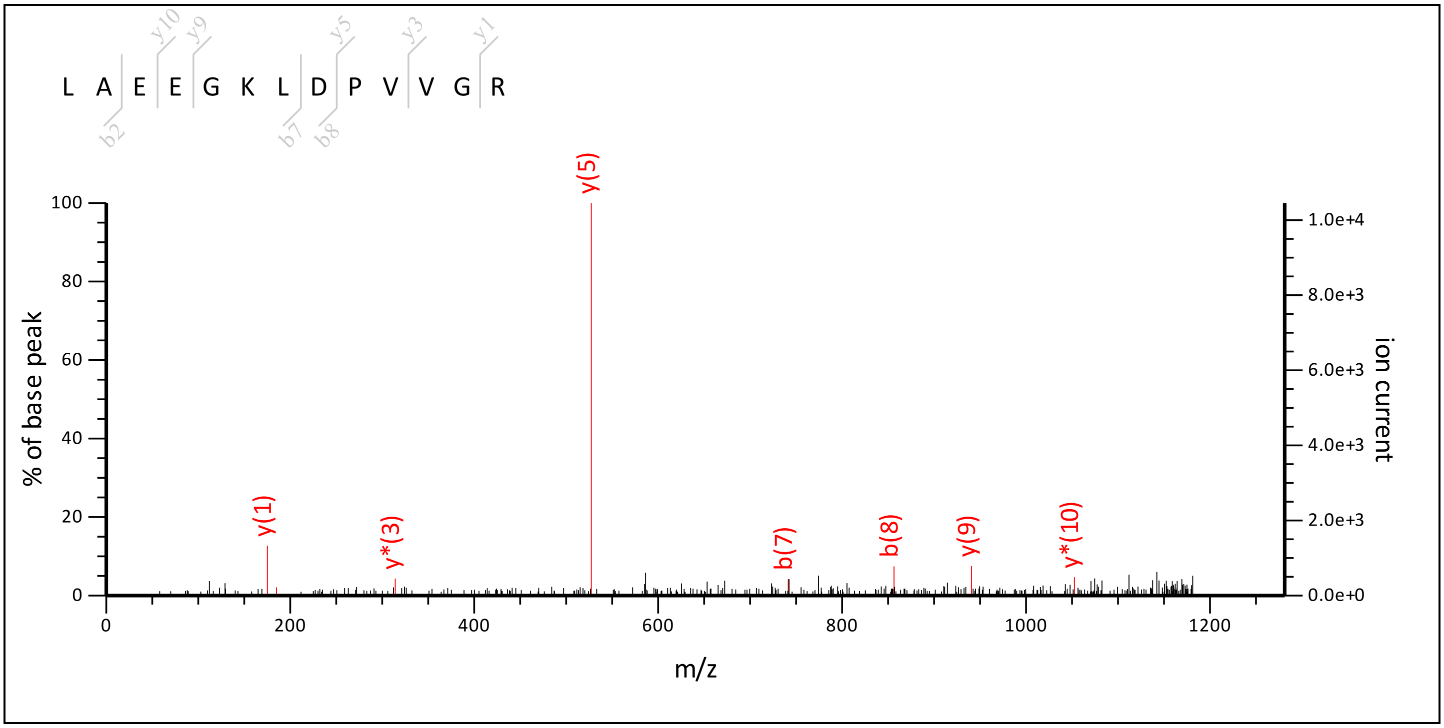
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 110

MS/MS Fragmentation of **LAEEGKLDPVVGR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 197: 1381.789724 from(1382.797000,1+) intensity(0.0000) index(15)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226664, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



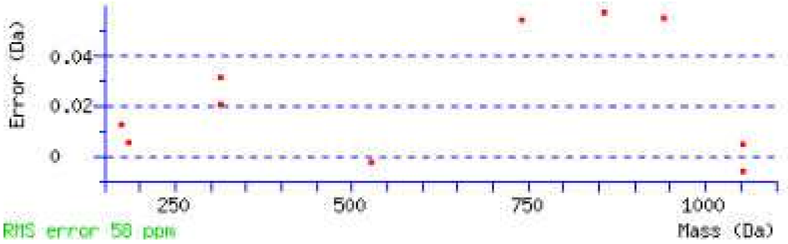
0 to 1281.23

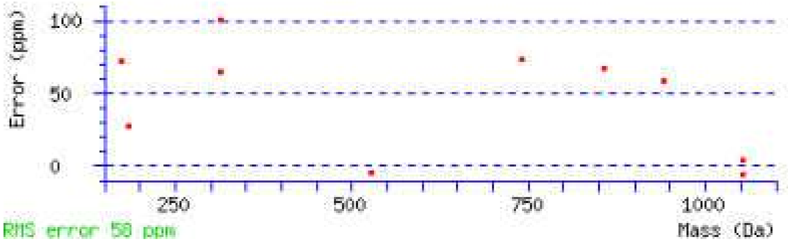
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1381.7565
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 4.3e+02
Matches : 10/62 fragment ions using 24 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		**L**			**13**
2	157.1335		***185.1285***		**A**	1269.6797	1252.6532	**12**
3	286.1761		***314.1710***		**E**	1198.6426	1181.6161	**11**
4	415.2187		443.2136		**E**	1069.6000	1052.5735	**10**
5	472.2402		500.2351		**G**	***940.5574***	923.5309	**9**
6	600.3352	583.3086	628.3301	611.3035	**K**	883.5360	866.5094	**8**
7	713.4192	696.3927	***741.4141***	724.3876	**L**	755.4410	738.4145	**7**
8	828.4462	811.4196	***856.4411***	839.4145	**D**	642.3570	625.3304	**6**

9	925.4989	908.4724	953.4938	936.4673	**P**	***527.3300***	510.3035	**5**
10	1024.5673	1007.5408	***1052.5623***	1035.5357	**V**	430.2772	413.2507	**4**
11	1123.6358	1106.6092	1151.6307	1134.6041	**V**	331.2088	314.1823	**3**
12	1180.6572	1163.6307	1208.6521	1191.6256	**G**	232.1404	215.1139	**2**
13					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.0	1381.7354	0.0543	ISPKTNGVTYFR
17.9	1381.7565	0.0332	LAEEGKLDPVVGR
17.9	1381.7215	0.0683	LAPSASNRQPWR
17.4	1381.7426	0.0471	IGTALANRGPEAGR
15.8	1381.7426	0.0471	NEAVLNRPQVSR
15.8	1381.7466	0.0431	SIAAALNRTFYR
15.3	1381.7062	0.0835	AGSITPNRPAADGR
14.9	1381.7790	0.0107	AVIDAGGGRVLGAAR
13.9	1381.8154	-0.0256	SVKIVSRPVNQR
13.9	1381.7677	0.0220	QKGEQTAIAIAPR

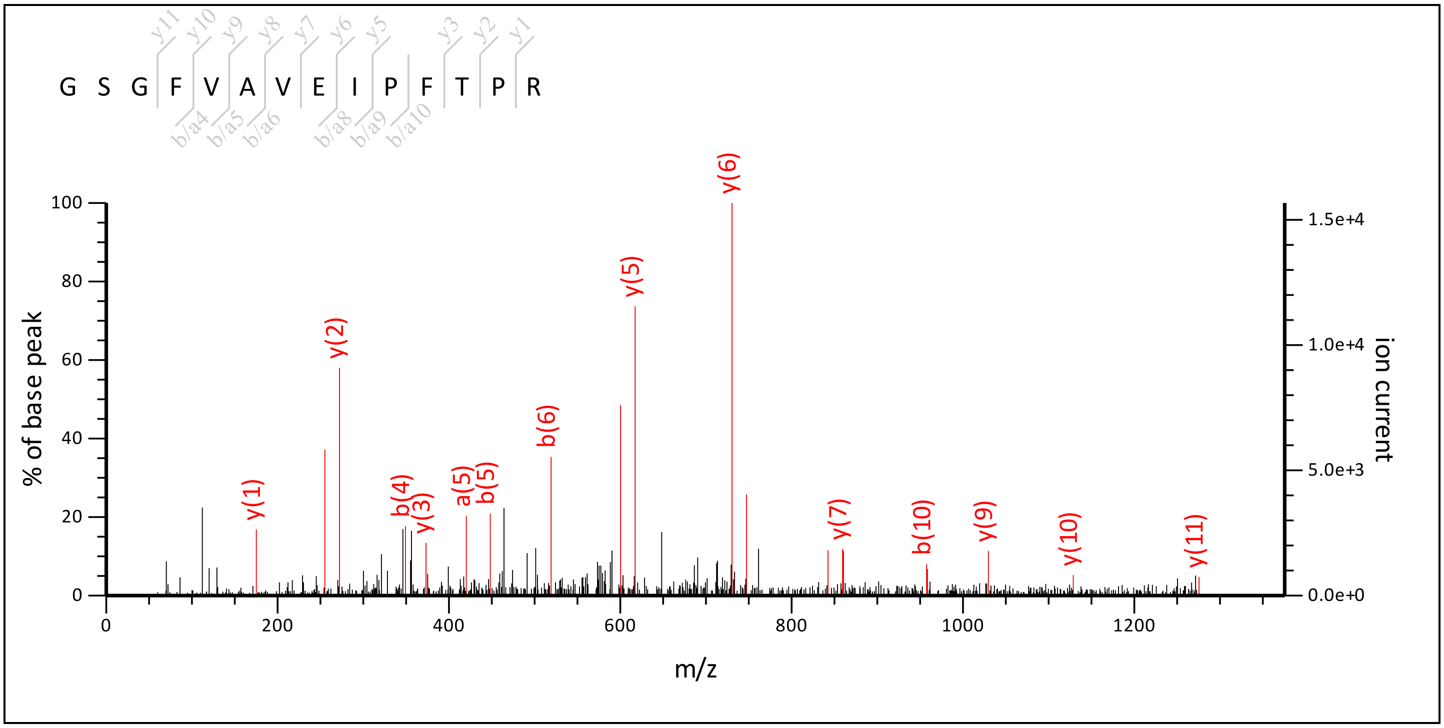
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 110

MS/MS Fragmentation of **GSGFVAVEIPFTPR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 213: 1475.807424 from(1476.814700,1+) intensity(0.0000) index(18)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226647, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



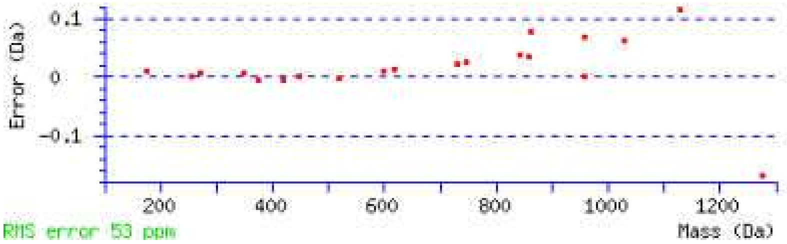
0 to 1375.54

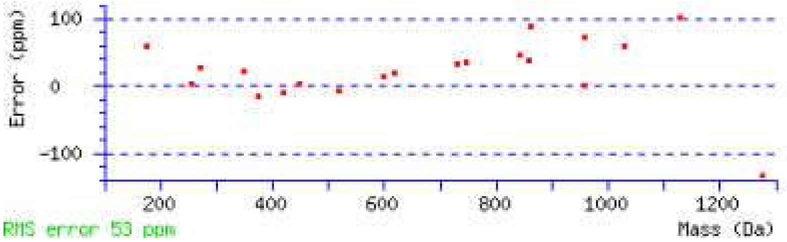
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1475.7773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62 **Expect:** 0.02
Matches : 20/52 fragment ions using 39 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	30.0338	58.0287	**G**			**14**
2	117.0659	145.0608	**S**	1419.7631	1402.7365	**13**
3	174.0873	202.0822	**G**	1332.7311	1315.7045	**12**
4	321.1557	**349.1506**	**F**	***1275.7096***	1258.6830	**11**
5	420.2241	**448.2191**	**V**	***1128.6412***	1111.6146	**10**
6	491.2613	**519.2562**	**A**	***1029.5728***	1012.5462	**9**
7	590.3297	618.3246	**V**	***958.5356***	941.5091	**8**
8	719.3723	**747.3672**	**E**	***859.4672***	842.4407	**7**

9	832.4563	**860.4512**	**I**	***730.4246***	713.3981	**6**
10	929.5091	**957.5040**	**P**	***617.3406***	600.3140	**5**
11	1076.5775	1104.5724	**F**	520.2878	503.2613	**4**
12	1177.6252	1205.6201	**T**	***373.2194***	356.1928	**3**
13	1274.6780	1302.6729	**P**	***272.1717***	255.1452	**2**
14			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.1	1475.7773	0.0301	GSGFVAVEIPFTPR
41.0	1475.7409	0.0665	GSGFTPAEIPFTPR
17.2	1475.7766	0.0308	RAGVSMELLSEIR
16.8	1475.7224	0.0850	RVMETLEQMAPR
16.7	1475.7845	0.0230	QNSSVTLRTFAPR
16.2	1475.7256	0.0818	FLEEVELEQGQR
15.2	1475.7265	0.0810	MKFPPLPETMNR
15.2	1475.6926	0.1148	EMLQDLIDTENR
15.1	1475.7038	0.1036	NSMVQPKTSSEPR
14.9	1475.7620	0.0454	VEYQPLVSLSEGR

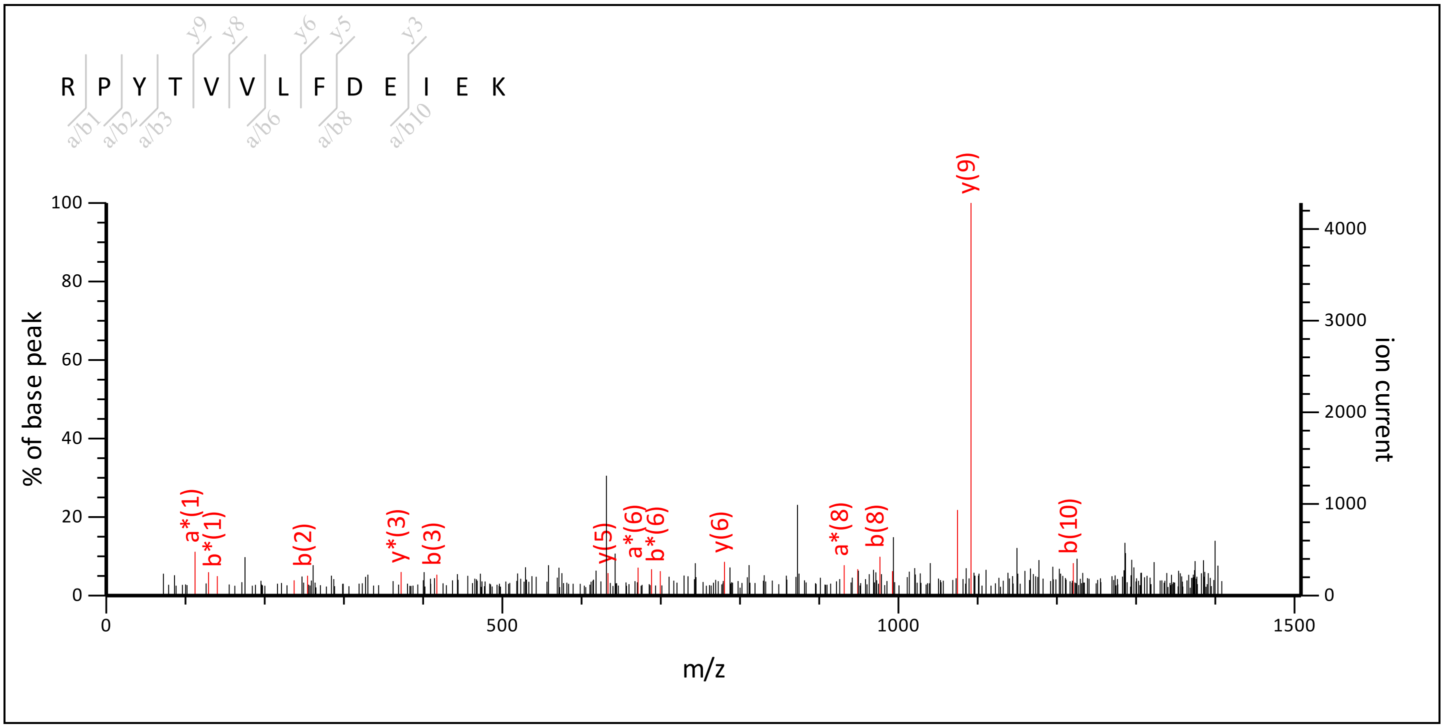
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 110

MS/MS Fragmentation of **RPYTVVLFDEIEK**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 236: 1607.891724 from(1608.899000,1+) intensity(0.0000) index(22)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226658, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



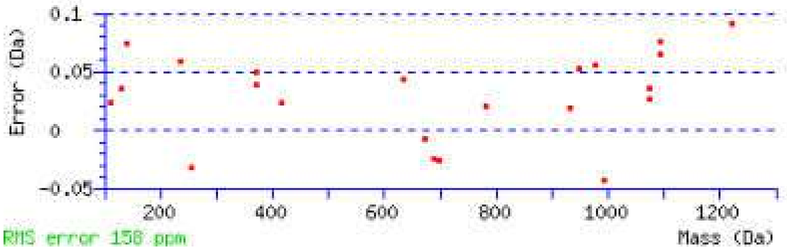
0 to 1508.17

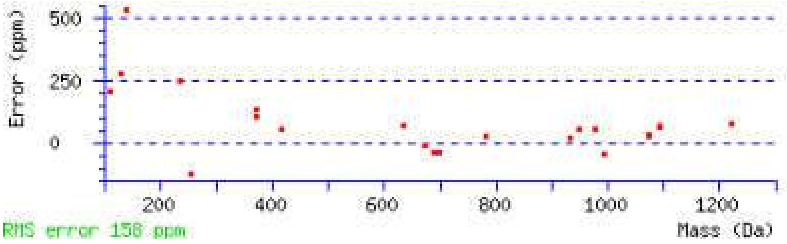
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1607.8559
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 7 **Expect:** 5.9e+03
Matches : 22/72 fragment ions using 70 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**129.1135**	112.0869	157.1084	140.0818	R			13
2	226.1662	209.1397	***254.1612***	237.1346	P	1452.7621	1435.7355	12
3	389.2296	372.2030	***417.2245***	400.1979	Y	1355.7093	1338.6828	11
4	490.2772	473.2507	518.2722	501.2456	T	1192.6460	1175.6194	10
5	589.3457	572.3191	617.3406	600.3140	V	***1091.5983***	1074.5718	9
6	**688.4141**	671.3875	716.4090	699.3824	V	***992.5299***	975.5033	8
7	801.4981	784.4716	829.4931	812.4665	L	893.4615	876.4349	7
8	**948.5666**	931.5400	***976.5615***	959.5349	F	***780.3774***	763.3509	6

9	1063.5935	1046.5669	***1091.5884***	1074.5619	**D**	***633.3090***	616.2824	**5**
10	1192.6361	1175.6095	***1220.6310***	1203.6045	**E**	518.2821	501.2555	**4**
11	1305.7201	1288.6936	1333.7151	1316.6885	**I**	389.2395	372.2129	**3**
12	1434.7627	1417.7362	1462.7577	1445.7311	**E**	276.1554	259.1288	**2**
13					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.6	1607.8090	0.0828	ARGSADLSAFMPLTR
11.1	1607.7348	0.1569	IDTLKEEMDEAGNK
11.1	1607.7348	0.1569	IESLKEEMDEAGNK
9.8	1607.7804	0.1113	AGRWAEAHPDETLR
7.8	1607.8341	0.0576	SELPMRTYIETLR
7.3	1607.8090	0.0827	ATIMTGQYGQINGVR
6.9	1607.8559	0.0358	RPYSVILFDEIEK
6.9	1607.8229	0.0689	RPYSVILMDEIEK
6.9	1607.8559	0.0358	RPYSVLLFDEIEK
6.9	1607.8559	0.0358	RPYTVVLFDEIEK

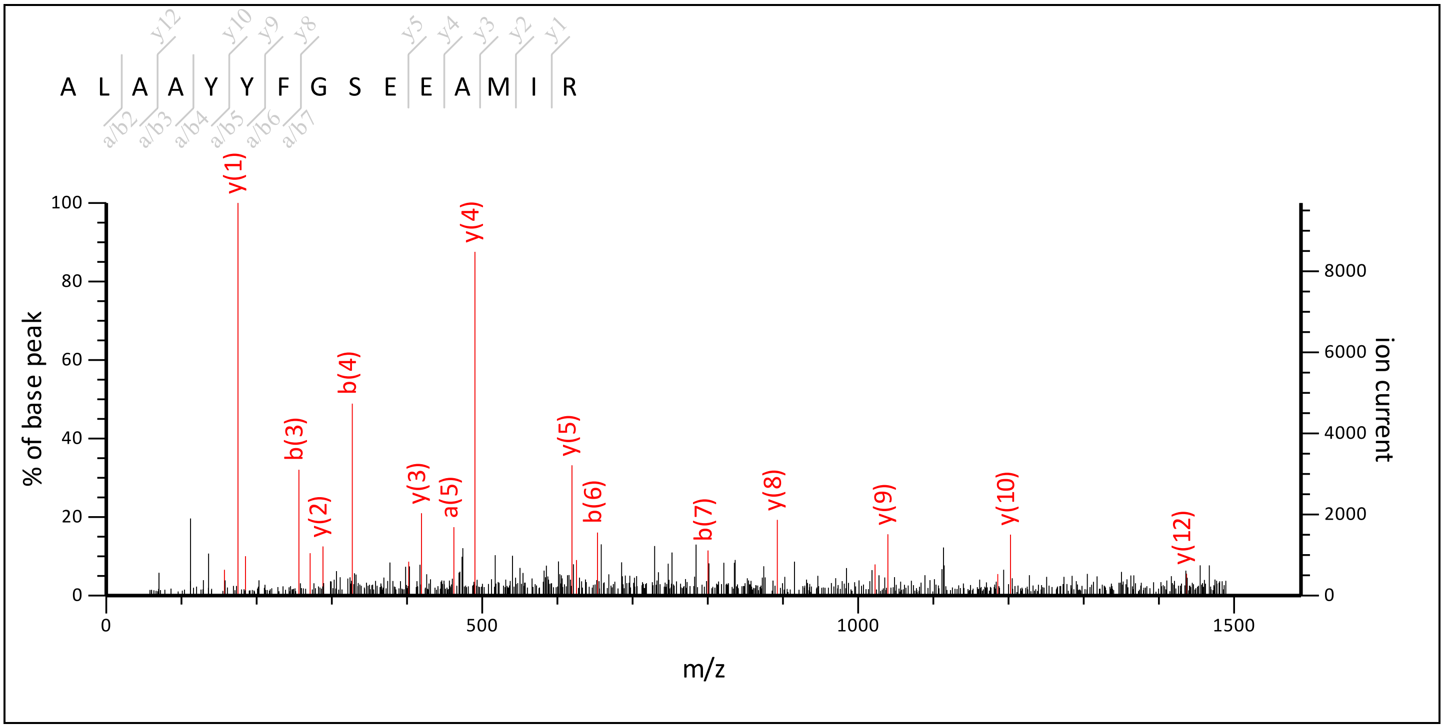
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 110**

MS/MS Fragmentation of **ALAAYYFGSEEAMIR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 242: 1690.842624 from(1691.849900,1+) intensity(0.0000) index(23)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226649, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



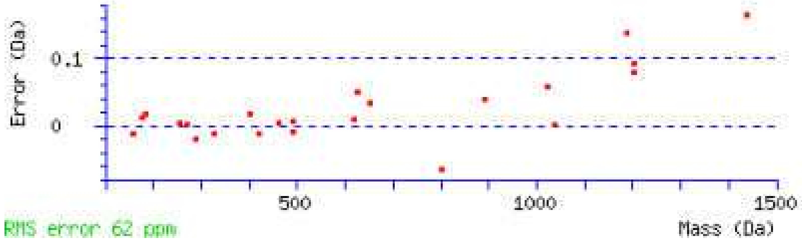
0 to 1588.97

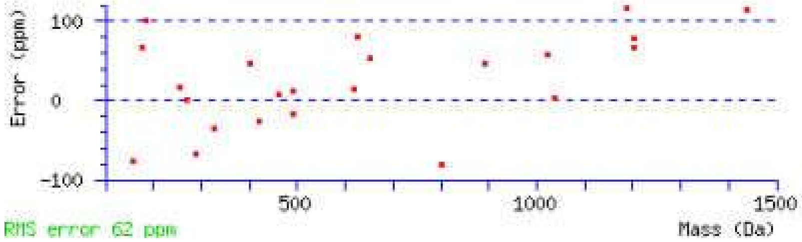
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1690.8024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.71
Matches : 23/56 fragment ions using 45 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	44.0495	72.0444	A			15
2	**157.1335**	***185.1285***	L	1620.7727	1603.7461	14
3	228.1707	***256.1656***	A	1507.6886	1490.6620	13
4	299.2078	***327.2027***	A	***1436.6515***	1419.6249	12
5	**462.2711**	***490.2660***	Y	1365.6144	1348.5878	11
6	**625.3344**	***653.3293***	Y	***1202.5510***	1185.5245	10
7	772.4028	***800.3978***	F	***1039.4877***	1022.4612	9
8	829.4243	857.4192	G	***892.4193***	875.3927	8

9	916.4563	944.4512	**S**	835.3978	818.3713	**7**
10	1045.4989	1073.4938	**E**	748.3658	731.3393	**6**
11	1174.5415	***1202.5364***	**E**	***619.3232***	602.2967	**5**
12	1245.5786	1273.5735	**A**	***490.2806***	473.2541	**4**
13	1376.6191	1404.6140	**M**	***419.2435***	402.2170	**3**
14	1489.7032	1517.6981	**I**	***288.2030***	271.1765	**2**
15			**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.5	1690.8024	0.0402	ALAAYYFGSEEAMIR
31.4	1690.8025	0.0402	ALASYFFGSEEAMIR
29.2	1690.8025	0.0402	SLAAYFFGSEEAMIR
16.0	1690.7001	0.1426	MNYLDMLCESIDR
14.4	1690.9770	-0.1344	SPAVLGKFYLAGSLLR
13.6	1690.7984	0.0442	RVAYTSETMYEGIR
12.9	1690.8092	0.0334	KLLMSFMSTMDSLR
12.9	1690.8092	0.0334	KLLMSFMSTMDSLR
12.8	1690.9406	-0.0980	VGYVAAPAALTVEFRK
12.5	1690.8613	-0.0187	YNLVYNHPKGSMIR

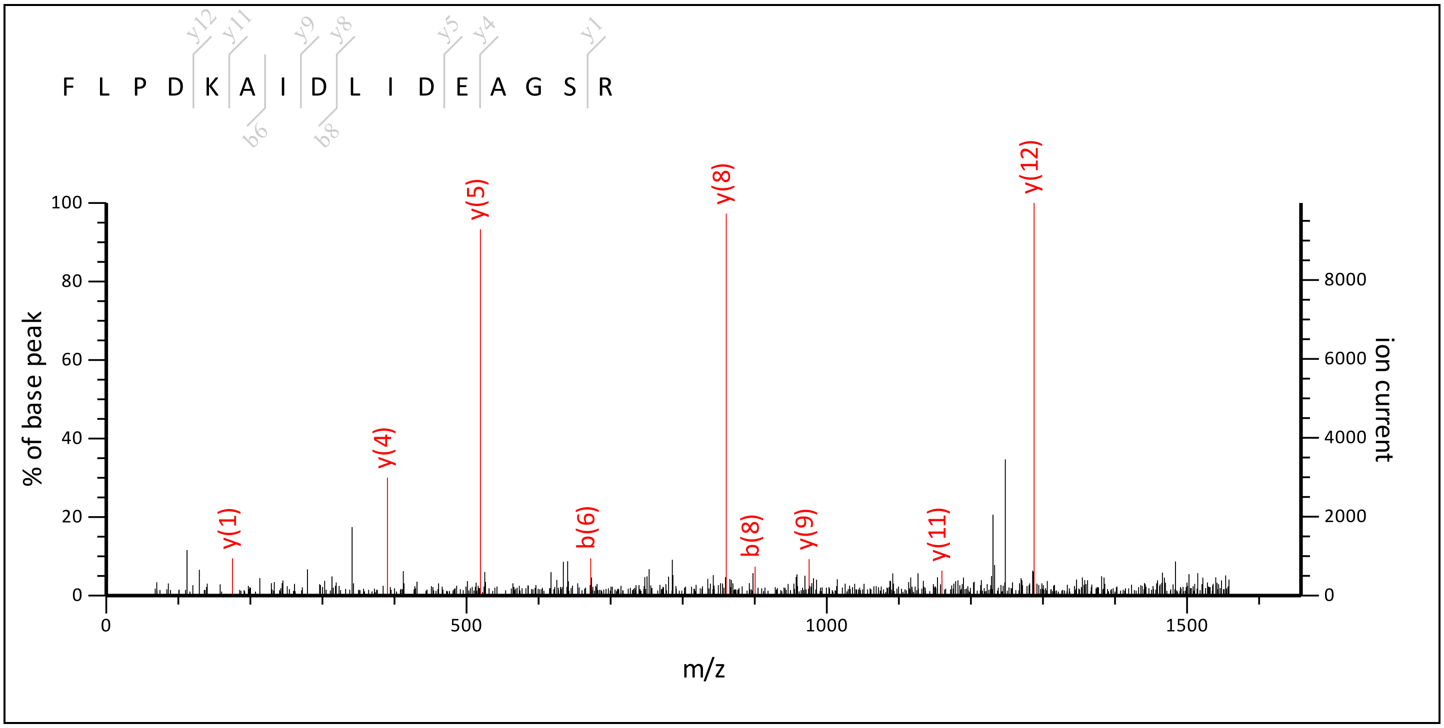
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 110**

MS/MS Fragmentation of **FLPDKAIDLIDEAGSR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 250: 1758.953624 from(1759.960900,1+) intensity(0.0000) index(24)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226653, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



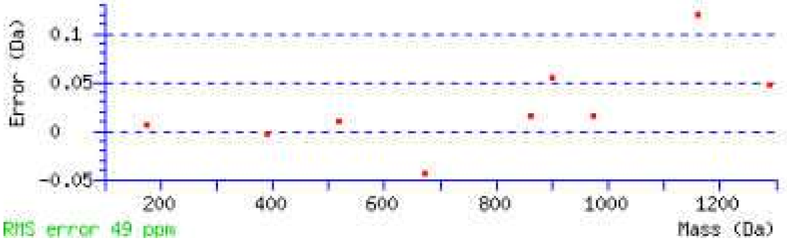
0 to 1658.11

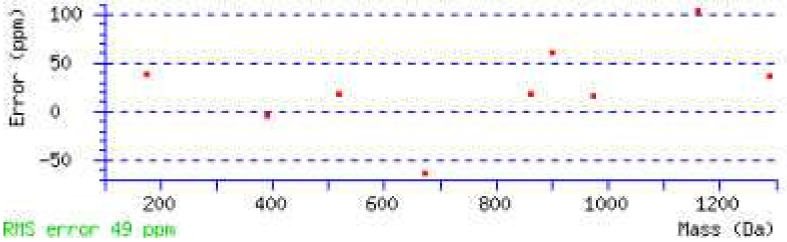
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1758.9152
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.91
Matches : 9/82 fragment ions using 15 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	120.0808		148.0757		F			16
2	233.1648		261.1598		L	1612.8541	1595.8275	15
3	330.2176		358.2125		P	1499.7700	1482.7435	14
4	445.2445		473.2395		D	1402.7172	1385.6907	13
5	573.3395	556.3130	601.3344	584.3079	K	*1287.6903*	1270.6638	12
6	644.3766	627.3501	**672.3715**	655.3450	A	*1159.5953*	1142.5688	11
7	757.4607	740.4341	785.4556	768.4291	I	1088.5582	1071.5317	10
8	872.4876	855.4611	**900.4825**	883.4560	D	*975.4742*	958.4476	9

9	985.5717	968.5451	1013.5666	996.5401	**L**	***860.4472***	843.4207	**8**
10	1098.6558	1081.6292	1126.6507	1109.6241	**I**	747.3632	730.3366	**7**
11	1213.6827	1196.6562	1241.6776	1224.6511	**D**	634.2791	617.2525	**6**
12	1342.7253	1325.6987	1370.7202	1353.6937	**E**	***519.2522***	502.2256	**5**
13	1413.7624	1396.7359	1441.7573	1424.7308	**A**	***390.2096***	373.1830	**4**
14	1470.7839	1453.7573	1498.7788	1481.7522	**G**	319.1724	302.1459	**3**
15	1557.8159	1540.7894	1585.8108	1568.7843	**S**	262.1510	245.1244	**2**
16					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.8	1758.9152	0.0384	FLPDKAIDIIDEAGSR
44.8	1758.9152	0.0384	FLPDKAIDLIDEAGSR
44.8	1758.9152	0.0384	FLPDKAIDLIDEGSAR
44.8	1758.9152	0.0384	FLPDKAIDLLDEAGSR
20.4	1758.9152	0.0384	FLPDKAIDLVDEAASR
20.4	1758.9152	0.0384	FLPDKAIDLVDEASAR
20.4	1758.9152	0.0384	FLPDKAIDLVDESAAR
20.4	1758.9152	0.0384	FLPDKAIDVIDEASAR
20.4	1758.8822	0.0715	MLPDKAIDLVDEAASR
17.3	1758.8114	0.1422	FELEHFGDYQRYR

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

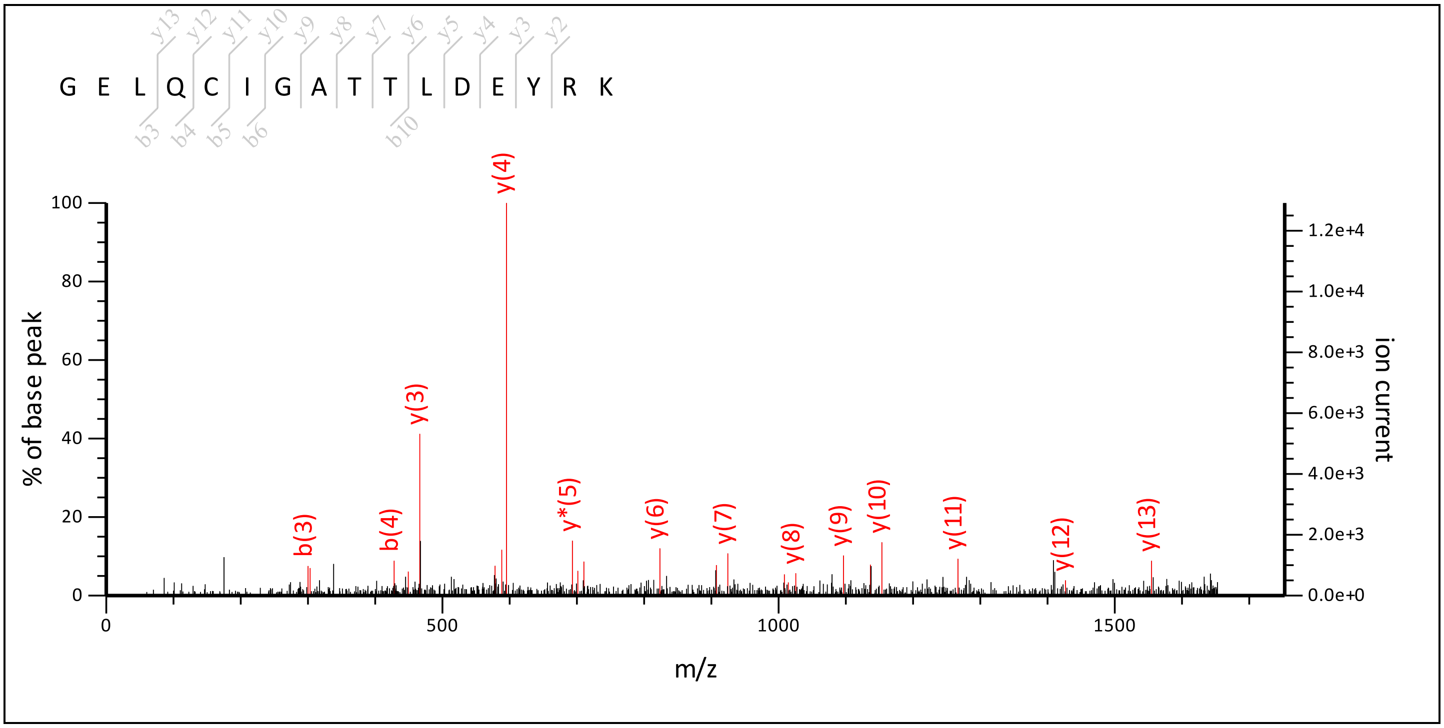
Mascot Search Results

Peptide View

Spot no 110

MS/MS Fragmentation of **GELQCIGATTLDEYRK**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 263: 1852.939724 from(1853.947000,1+) intensity(0.0000) index(25)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226651, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



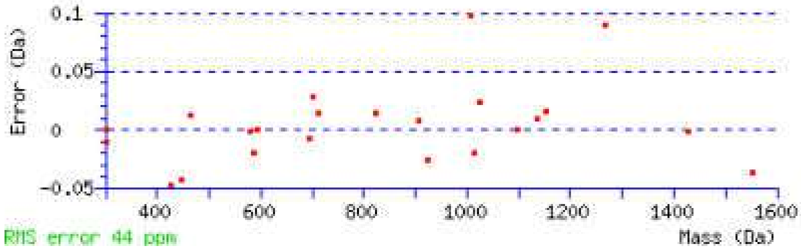
0 to 1752.74

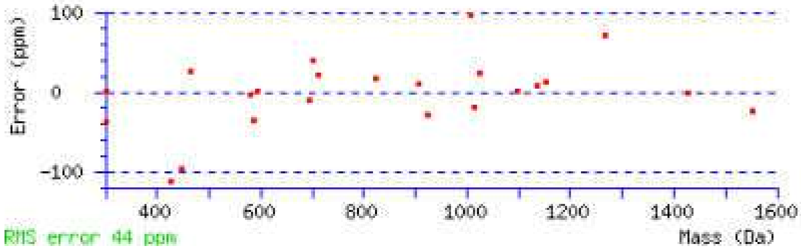
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1852.8989
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 0.0019
Matches : 23/84 fragment ions using 48 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			16
2	159.0764		187.0713		E	1796.8847	1779.8582	15
3	272.1605		**300.1554**		L	1667.8421	1650.8156	14
4	400.2191	383.1925	**428.2140**	411.1874	Q	***1554.7581***	1537.7315	13
5	560.2497	543.2232	**588.2446**	571.2181	C	***1426.6995***	1409.6729	12
6	673.3338	656.3072	**701.3287**	684.3021	I	***1266.6688***	1249.6423	11
7	730.3552	713.3287	758.3502	741.3236	G	***1153.5848***	1136.5582	10
8	801.3924	784.3658	829.3873	812.3607	A	***1096.5633***	1079.5368	9

9	902.4400	885.4135	930.4349	913.4084	**T**	***1025.5262***	1008.4997	**8**
10	1003.4877	986.4612	1031.4826	1014.4561	**T**	***924.4785***	907.4520	**7**
11	1116.5718	1099.5452	1144.5667	1127.5401	**L**	***823.4308***	806.4043	**6**
12	1231.5987	1214.5722	1259.5936	1242.5671	**D**	***710.3468***	693.3202	**5**
13	1360.6413	1343.6148	1388.6362	1371.6097	**E**	***595.3198***	578.2933	**4**
14	1523.7046	1506.6781	1551.6996	1534.6730	**Y**	***466.2772***	449.2507	**3**
15	1679.8057	1662.7792	1707.8007	1690.7741	**R**	***303.2139***	286.1874	**2**
16					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.7	1852.8989	0.0408	GELQCLGATTLDEYKR
71.7	1852.8989	0.0408	GEIQCIGATTIDEYRK
71.7	1852.8989	0.0408	GEIQCIGATTLDEYRK
71.7	1852.8989	0.0408	GELQCIGATTIDEYRK
71.7	1852.8989	0.0408	GELQCIGATTLDEYRK
71.7	1852.8989	0.0408	GELQCLGATTIDEYRK
71.7	1852.8989	0.0408	GELQCLGATTLDEYRK
66.5	1852.8737	0.0660	GELQCIGATTNNEYRK
57.8	1852.8989	0.0408	GELQCLGATTVEEYRK
23.4	1852.8228	0.1169	GVGGIDSWGSDVEEQYR

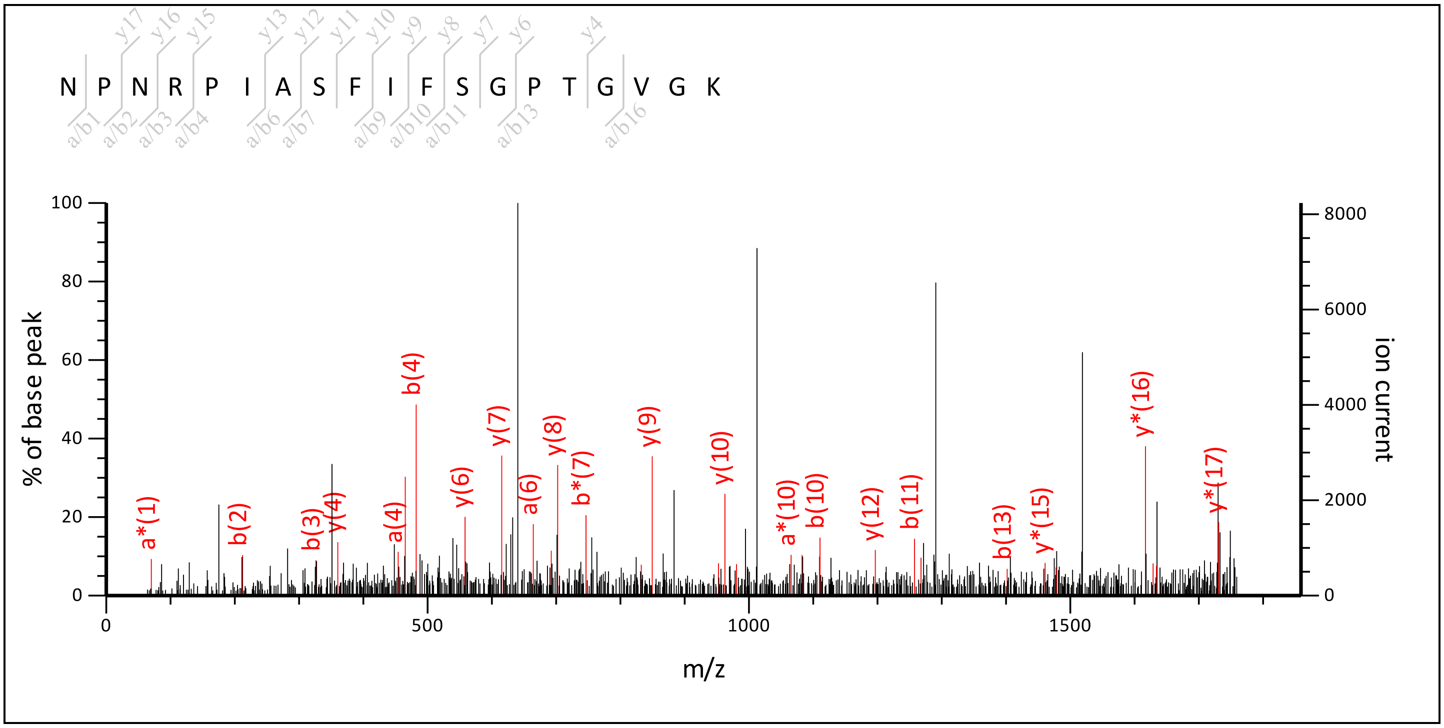
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 110**

MS/MS Fragmentation of **NPNRPIASFIFSGPTGVGK**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 274: 1958.077924 from(1959.085200,1+) intensity(0.0000) index(27)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226648, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



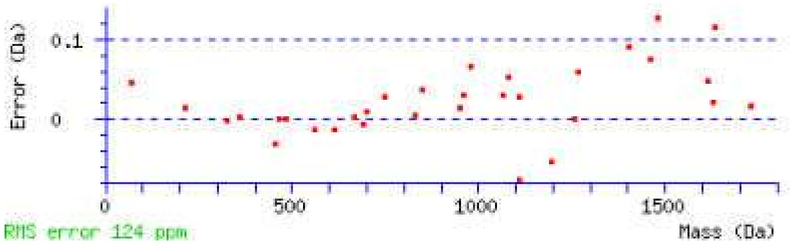
0 to 1858.94

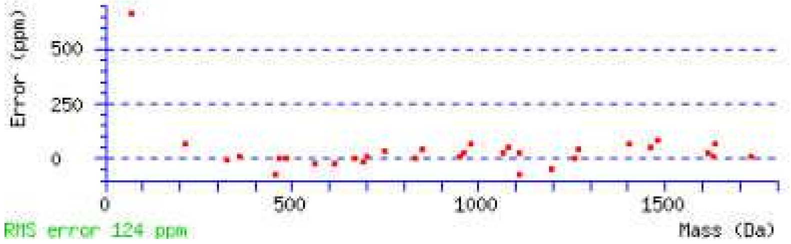
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1958.0374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 21
Matches : 32/108 fragment ions using 102 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	87.0553	70.0287	115.0502	98.0237	**N**			**19**
2	184.1081	167.0815	**212.1030**	195.0764	**P**	1845.0017	1827.9752	**18**
3	298.1510	281.1244	**326.1459**	309.1193	**N**	1747.9490	1730.9224	**17**
4	**454.2521**	437.2255	**482.2470**	465.2205	**R**	***1633.9061***	1616.8795	**16**
5	551.3049	534.2783	579.2998	562.2732	**P**	***1477.8049***	1460.7784	**15**
6	**664.3889**	647.3624	**692.3838**	675.3573	**I**	1380.7522	1363.7256	**14**
7	735.4260	718.3995	763.4209	746.3944	**A**	***1267.6681***	1250.6416	**13**
8	822.4581	805.4315	850.4530	833.4264	**S**	***1196.6310***	1179.6045	**12**

9	969.5265	952.4999	997.5214	980.4948	F	***1109.5990***	1092.5724	11
10	**1082.6105**	1065.5840	**1110.6055**	1093.5789	I	***962.5306***	945.5040	10
11	1229.6790	1212.6524	**1257.6739**	1240.6473	F	***849.4465***	832.4199	9
12	1316.7110	1299.6844	1344.7059	1327.6793	S	***702.3781***	685.3515	8
13	1373.7324	1356.7059	**1401.7274**	1384.7008	G	***615.3461***	598.3195	7
14	1470.7852	1453.7587	1498.7801	1481.7536	P	***558.3246***	541.2980	6
15	1571.8329	1554.8063	1599.8278	1582.8013	T	461.2718	444.2453	5
16	**1628.8544**	1611.8278	1656.8493	1639.8227	G	***360.2241***	343.1976	4
17	1727.9228	1710.8962	1755.9177	1738.8911	V	303.2027	286.1761	3
18	1784.9442	1767.9177	1812.9391	1795.9126	G	204.1343	187.1077	2
19					K	147.1128	130.0863	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.5	1958.0374	0.0405	NPNRPIASFIFSGPTGVGK
30.5	1958.0374	0.0405	NPNRPIASFLFSGPTGVGK
14.2	1957.9001	0.1778	FHYKICFNMPDIAMR
12.8	1957.9646	0.1133	TQIENYDFVFGQSRVR
10.6	1958.0594	0.0186	AGTLRVAAMPAMAIGFLPR
10.6	1958.0594	0.0186	AGTLRVAAMPAMAIGFLPR
9.8	1957.9785	0.0994	TQLDVVYQEFLVYADR
9.5	1957.9381	0.1398	GATIYAELAGEGNSLSSYR
8.6	1957.8873	0.1906	TISANMAPDEFTQKSMR
8.4	1957.9857	0.0922	DNLTEEEQRVLALWSR

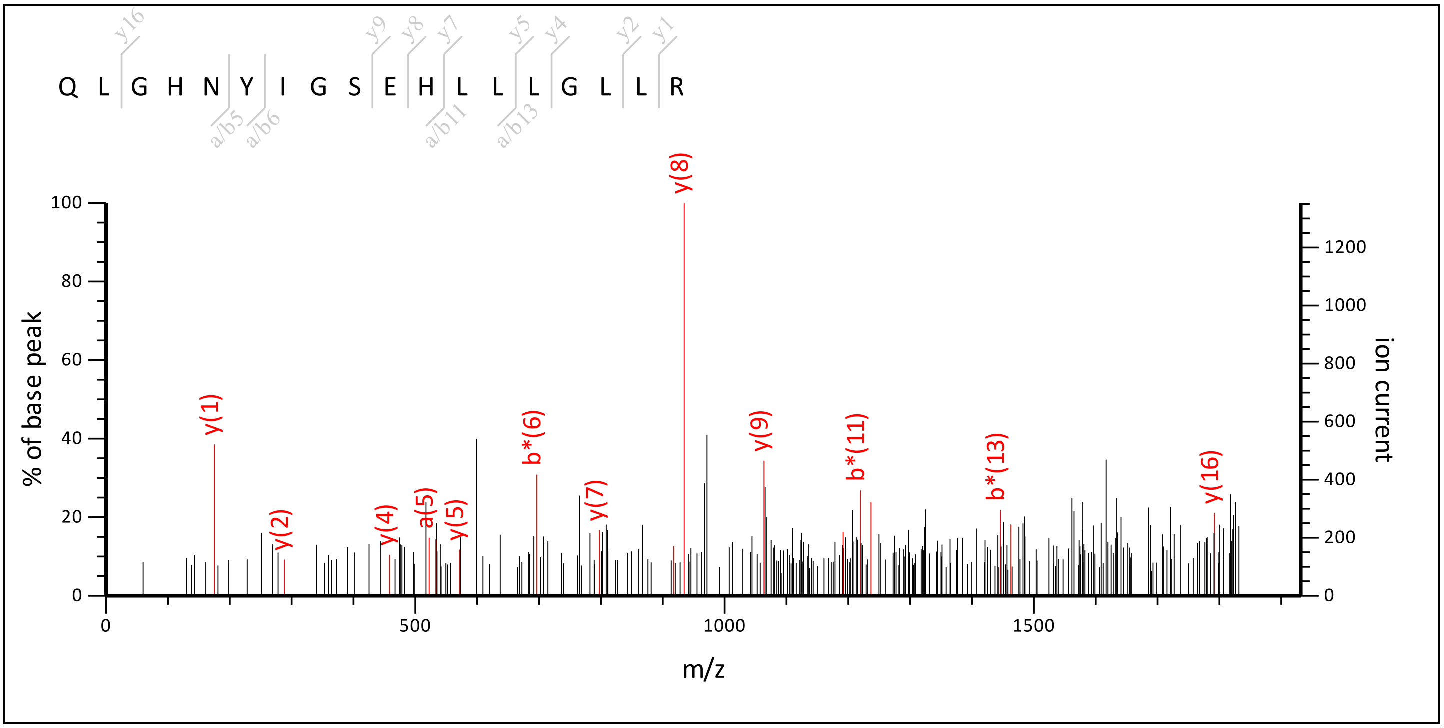
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 110

MS/MS Fragmentation of **QLGHNYIGSEHLLLGLLR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 280: 2032.161224 from(2033.168500,1+) intensity(0.0000) index(29)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226666, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



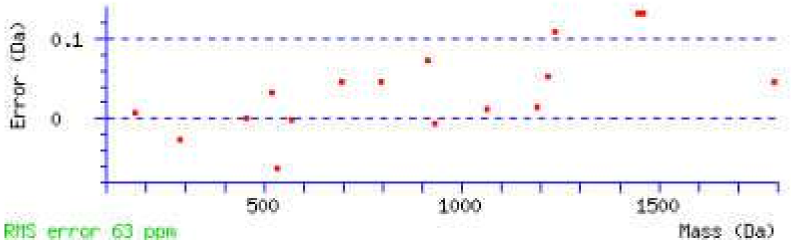
0 to 1931.57

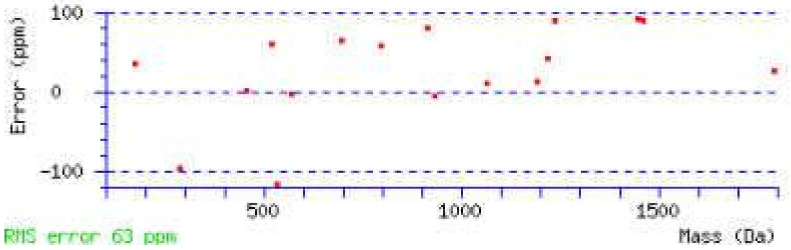
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2032.1218
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 5 **Expect:** 6.8e+03
Matches : 17/102 fragment ions using 89 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	101.0709	84.0444	129.0659	112.0393	Q			18
2	214.1550	197.1285	242.1499	225.1234	L	1905.0705	1888.0439	17
3	271.1765	254.1499	299.1714	282.1448	G	***1791.9864***	1774.9599	16
4	408.2354	391.2088	436.2303	419.2037	H	1734.9650	1717.9384	15
5	522.2783	505.2518	550.2732	533.2467	N	1597.9061	1580.8795	14
6	685.3416	668.3151	713.3365	696.3100	Y	1483.8631	1466.8366	13
7	798.4257	781.3991	826.4206	809.3941	I	1320.7998	1303.7732	12
8	855.4472	838.4206	883.4421	866.4155	G	1207.7157	1190.6892	11

9	942.4792	925.4526	970.4741	953.4476	**S**	1150.6943	1133.6677	**10**
10	1071.5218	1054.4952	1099.5167	1082.4902	**E**	***1063.6622***	1046.6357	**9**
11	1208.5807	1191.5541	**1236.5756**	1219.5491	**H**	***934.6196***	917.5931	**8**
12	1321.6648	1304.6382	1349.6597	1332.6331	**L**	***797.5607***	780.5342	**7**
13	1434.7488	1417.7223	**1462.7437**	1445.7172	**L**	684.4767	667.4501	**6**
14	1547.8329	1530.8063	1575.8278	1558.8013	**L**	***571.3926***	554.3661	**5**
15	1604.8544	1587.8278	1632.8493	1615.8227	**G**	***458.3085***	441.2820	**4**
16	1717.9384	1700.9119	1745.9333	1728.9068	**L**	401.2871	384.2605	**3**
17	1831.0225	1813.9959	1859.0174	1841.9908	**L**	***288.2030***	271.1765	**2**
18					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
4.6	2032.1582	0.0031	KLGHNYVGTEHILLGLIR
4.6	2032.1218	0.0395	QLGHNYIGSEHLLLGLLR
4.6	2032.1218	0.0394	QLGHNYVGTEHLLLGLIR
4.0	2032.0313	0.1300	FYMSATPRNHVPTAAVVR
2.0	2032.1470	0.0143	GIFVLQRIGDLVGYIDVR
0.7	2032.0888	0.0724	VMGLPLPRISDLAHGADVR
0.6	2032.0663	0.0949	AVFVSMPDSLSPLLTAVNR
0.4	2031.9644	0.1969	AAQNTLSSPTQMLNSSPGGR
0.3	2031.9585	0.2027	NTPMHIYAGNGNFVGDGIR
0.1	2032.0272	0.1340	LAQCPGPHTSATAPERALR

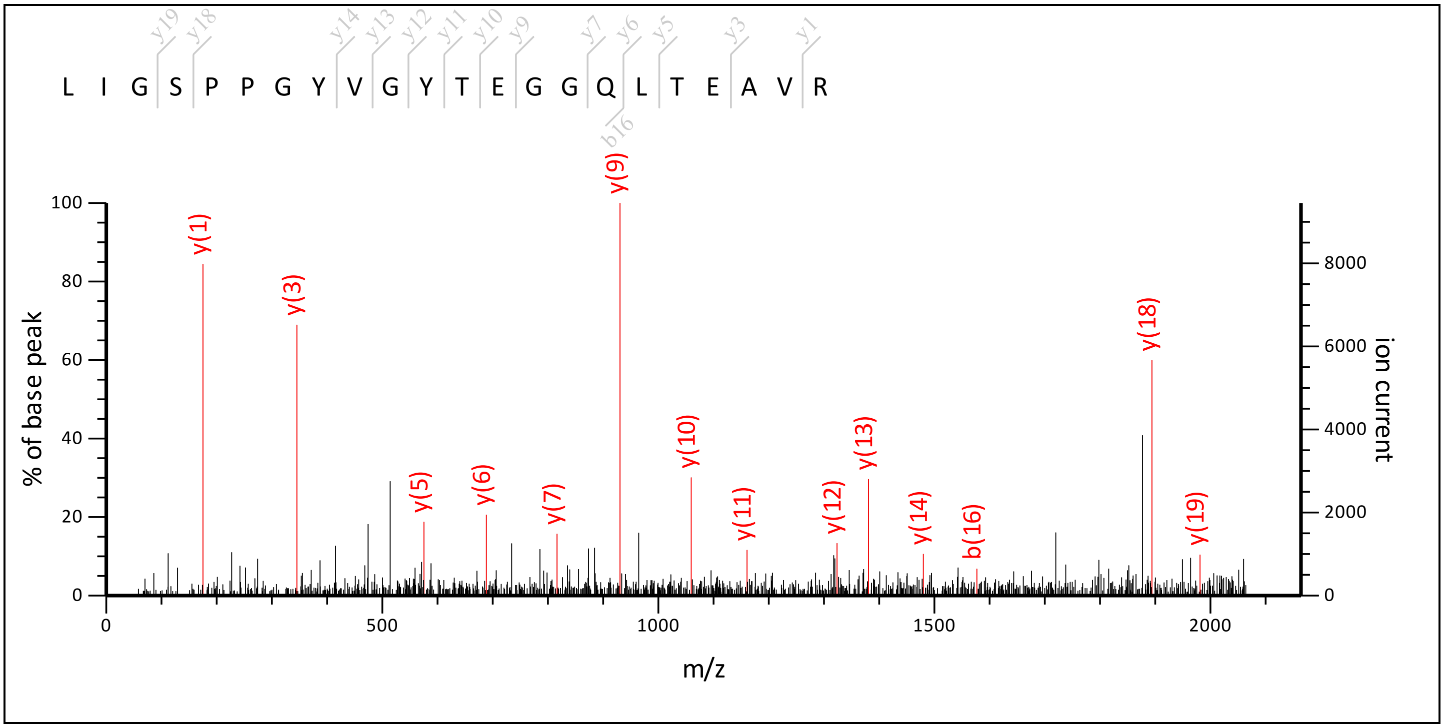
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 110

MS/MS Fragmentation of **LIGSPPGYVGYTEGGQLTEAVR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 295: 2263.184624 from(2264.191900,1+) intensity(0.0000) index(32)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226650, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



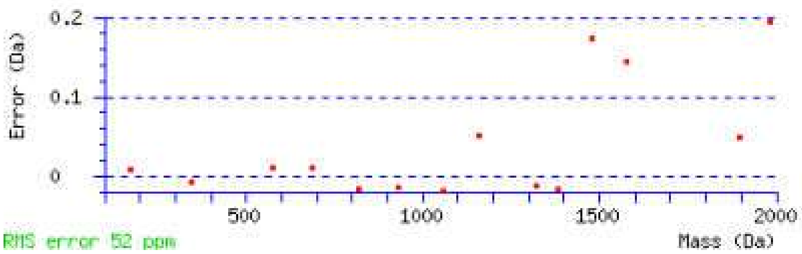
0 to 2164.02

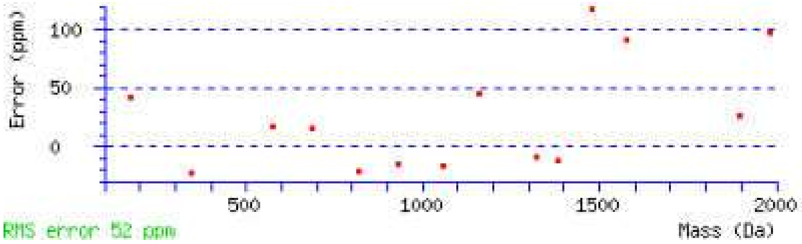
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2263.1485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 98 **Expect:** 3.7e-06
Matches : 14/96 fragment ions using 21 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		L			22
2	199.1805		227.1754		I	2151.0717	2134.0451	21
3	256.2020		284.1969		G	2037.9876	2020.9611	20
4	343.2340		371.2289		S	***1980.9662***	1963.9396	19
5	440.2867		468.2817		P	***1893.9341***	1876.9076	18
6	537.3395		565.3344		P	1796.8814	1779.8548	17
7	594.3610		622.3559		G	1699.8286	1682.8020	16
8	757.4243		785.4192		Y	1642.8071	1625.7806	15

9	856.4927		884.4876		**V**	***1479.7438***	1462.7173	**14**
10	913.5142		941.5091		**G**	***1380.6754***	1363.6488	**13**
11	1076.5775		1104.5724		**Y**	***1323.6539***	1306.6274	**12**
12	1177.6252		1205.6201		**T**	***1160.5906***	1143.5640	**11**
13	1306.6678		1334.6627		**E**	***1059.5429***	1042.5164	**10**
14	1363.6892		1391.6842		**G**	***930.5003***	913.4738	**9**
15	1420.7107		1448.7056		**G**	873.4789	856.4523	**8**
16	1548.7693	1531.7427	1576.7642	1559.7377	**Q**	***816.4574***	799.4308	**7**
17	1661.8534	1644.8268	1689.8483	1672.8217	**L**	***688.3988***	671.3723	**6**
18	1762.9010	1745.8745	1790.8959	1773.8694	**T**	***575.3148***	558.2882	**5**
19	1891.9436	1874.9171	1919.9385	1902.9120	**E**	474.2671	457.2405	**4**
20	1962.9807	1945.9542	1990.9757	1973.9491	**A**	***345.2245***	328.1979	**3**
21	2062.0492	2045.0226	2090.0441	2073.0175	**V**	274.1874	257.1608	**2**
22					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
97.9	2263.1485	0.0362	LIGSPPGYVGYTEGGQLTEAVR
58.0	2263.1121	0.0725	LIGSPPGYVGYDDGGQLTEAVR
58.0	2263.1485	0.0362	LIGSPPGYIGYSEGGQLTEAVR
33.5	2263.1484	0.0362	LIGAAPGYIGYEEGGQLTEAVR
33.5	2263.1597	0.0249	LIGAPPGYIGHEEGGQLTEAVR
33.5	2263.1485	0.0362	LIGTAPGFVGYEEGGQLTEAVR
23.1	2263.1121	0.0725	LVGSPPGYVGYDEGGQLTEAVR
16.6	2263.1484	0.0362	LIGAPAGYIGYDEAGQLTEAVR
16.6	2263.1484	0.0362	LIGAPAGYVGYEEAGQLTEAVR

16.6	2263.1597	0.0249	LIGAPPGYVGHEEAGQLTEAVR

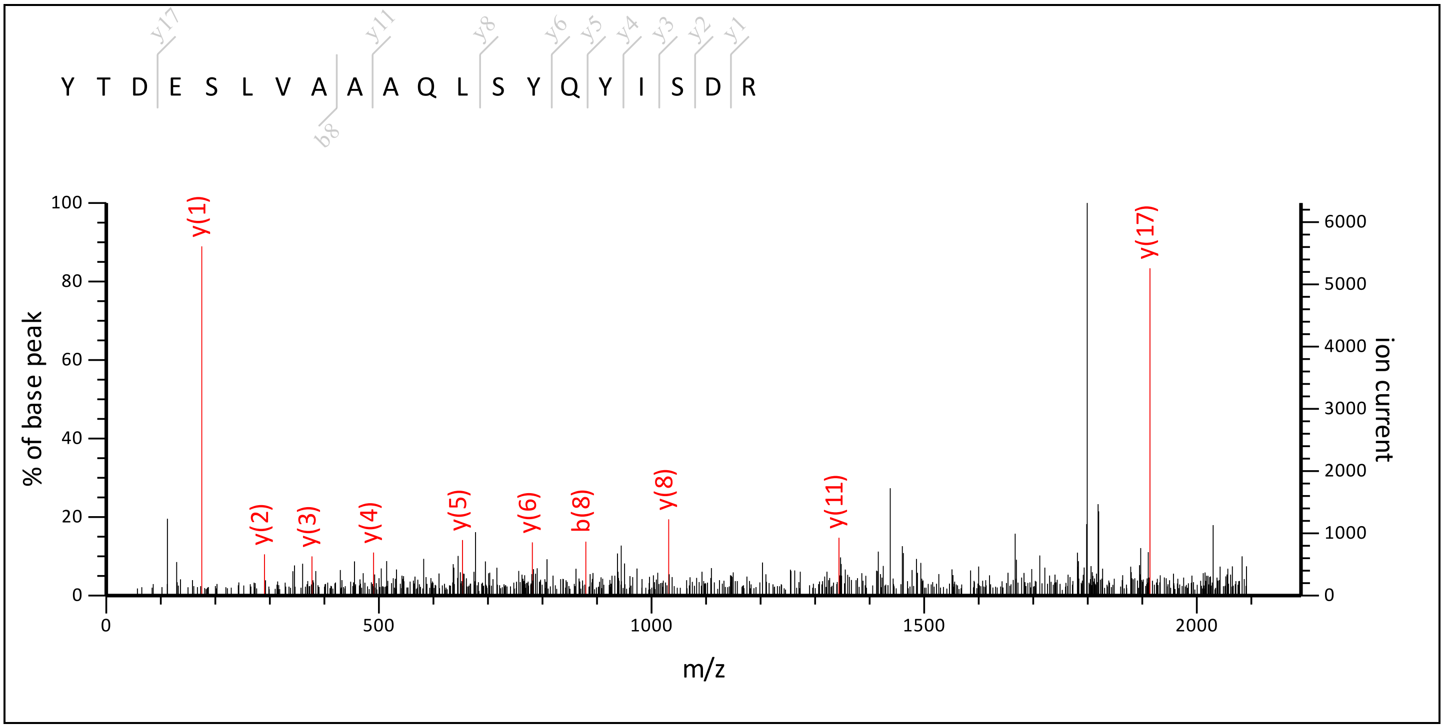
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 110**

MS/MS Fragmentation of **YTDESLVAAAQLSYQYISDR**
Found in **gi|18423214** in **NCBInr**, ATP-dependent Clp protease ATP-binding subunit ClpC [Arabidopsis thaliana]

Match to Query 300: 2292.128924 from(2293.136200,1+) intensity(0.0000) index(33)
Title: Label: C9, Spot_Id: 219804, Peak_List_Id: 226656, MSMS Job_Run_Id: 21852, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_C9_136859938300.txt



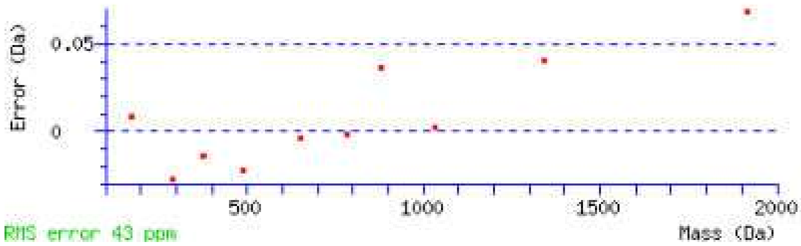
0 to 2191.06

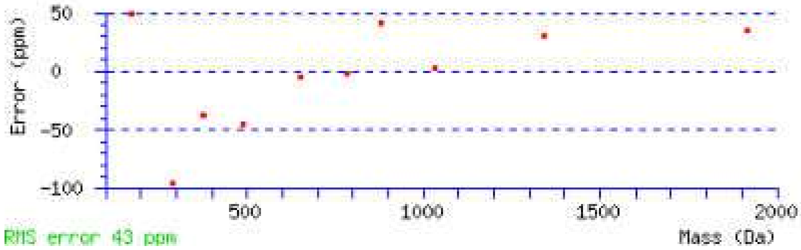
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2292.0910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 1.2
Matches : 10/94 fragment ions using 21 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	136.0757		164.0706		Y			20
2	237.1234		265.1183		T	2130.0350	2113.0084	19
3	352.1503		380.1452		D	2028.9873	2011.9607	18
4	481.1929		509.1878		E	*1913.9603*	1896.9338	17
5	568.2249		596.2198		S	1784.9177	1767.8912	16
6	681.3090		709.3039		L	1697.8857	1680.8592	15
7	780.3774		808.3723		V	1584.8016	1567.7751	14
8	851.4145		879.4094		A	1485.7332	1468.7067	13

9	922.4516		950.4466		A	1414.6961	1397.6696	12
10	993.4888		1021.4837		A	***1343.6590***	1326.6325	11
11	1121.5473	1104.5208	1149.5422	1132.5157	Q	1272.6219	1255.5953	10
12	1234.6314	1217.6048	1262.6263	1245.5998	L	1144.5633	1127.5368	9
13	1321.6634	1304.6369	1349.6583	1332.6318	S	***1031.4793***	1014.4527	8
14	1484.7268	1467.7002	1512.7217	1495.6951	Y	944.4472	927.4207	7
15	1612.7853	1595.7588	1640.7802	1623.7537	Q	***781.3839***	764.3573	6
16	1775.8487	1758.8221	1803.8436	1786.8170	Y	***653.3253***	636.2988	5
17	1888.9327	1871.9062	1916.9276	1899.9011	I	***490.2620***	473.2354	4
18	1975.9648	1958.9382	2003.9597	1986.9331	S	***377.1779***	360.1514	3
19	2090.9917	2073.9651	2118.9866	2101.9601	D	***290.1459***	273.1193	2
20					R	***175.1190***	158.0924	1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.5	2292.1274	0.0016	YTDDSLIAAAKLSYQYISDR
58.5	2292.0910	0.0380	YTDDSLIAAAQLSYQYISDR
56.0	2292.1274	0.0016	YTDDALISAAKLSYQYISDR
42.7	2292.0910	0.0380	YTDEALVSAAQLSYQYISDR
42.7	2292.0910	0.0380	YTDESLVAAAQLSYQYISDR
12.1	2292.0830	0.0460	VDRTISAIENVDTDSGATASDR
11.9	2292.1249	0.0041	FYDPIQALNTMFAKYISDR
10.3	2292.0991	0.0299	QNVINIDHTYSVEAMMKAGR
9.0	2292.2161	-0.0872	VHPPVPPPPTAAPRTTNMQIR
8.6	2292.1168	0.0121	EVSIVPRQAQGLSMQEYADR

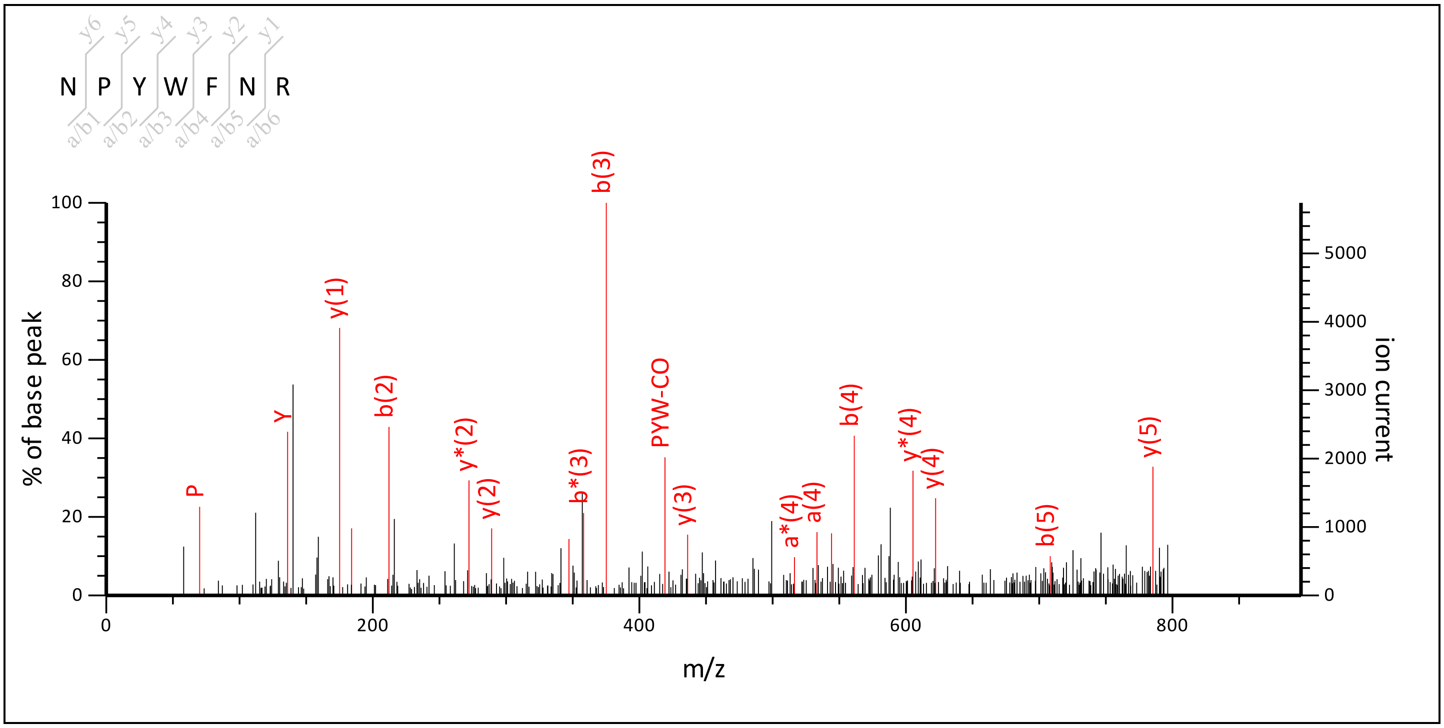
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 112**

MS/MS Fragmentation of **NPYWFNR**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 41: 995.498884 from(996.506160,1+) intensity(0.0000) index(4)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224896, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



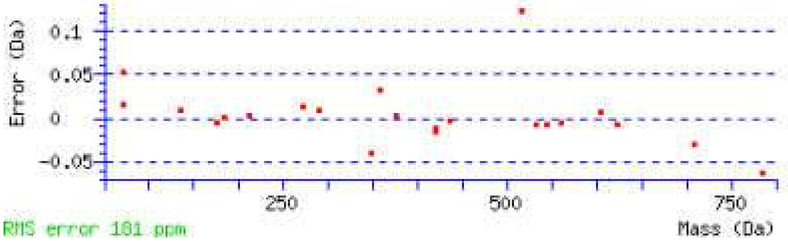
0 to 896.43

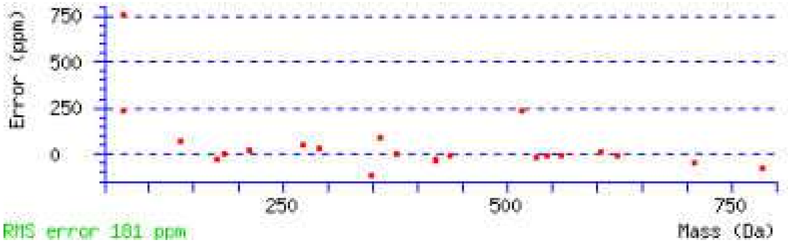
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 995.4613
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 2.2
Matches : 22/74 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	87.0553	87.0553	70.0287	115.0502	98.0237	44.0495	N					7
2	70.0651	**184.1081**	167.0815	**212.1030**	195.0764	158.0924	P	840.3787	839.3835	882.4257	865.3992	6
3	136.0757	**347.1714**	330.1448	**375.1663**	358.1397		Y	677.3154		***785.3729***	768.3464	5
4	159.0917	**533.2507**	516.2241	**561.2456**	544.2191		W	491.2361		***622.3096***	605.2831	4
5	120.0808	680.3191	663.2926	**708.3140**	691.2875		F	344.1677		***436.2303***	419.2037	3
6	87.0553	794.3620	777.3355	822.3569	805.3304	751.3562	N	230.1248	229.1295	***289.1619***	272.1353	2
7	129.1135						R	74.0237	73.0284	***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PY	233.1285	261.1234	**PYW**	419.2078	447.2027	**PYWF**	566.2762	594.2711
PYWFN	680.3191	708.3140	**YW**	322.1550	350.1499	**YWF**	469.2234	497.2183
YWFN	583.2663	611.2613	**WF**	306.1601	334.1550	**WFN**	420.2030	448.1979
FN	234.1237	262.1186						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.4	995.4613	0.0376	NPYWFNR
16.4	995.4825	0.0164	VGSGYPFNR
16.0	995.5036	-0.0047	GVPSGTEPPR
15.3	995.5261	-0.0272	SLSSGRHPR
14.9	995.4494	0.0494	ISAECFNR
14.9	995.4436	0.0553	WGWMFNR
14.7	995.5876	-0.0887	HGLKVSLSR
14.5	995.4573	0.0416	RGYSDWGR
14.3	995.4494	0.0495	FNAMAAAER
14.0	995.4421	0.0568	DRDSSFGGR

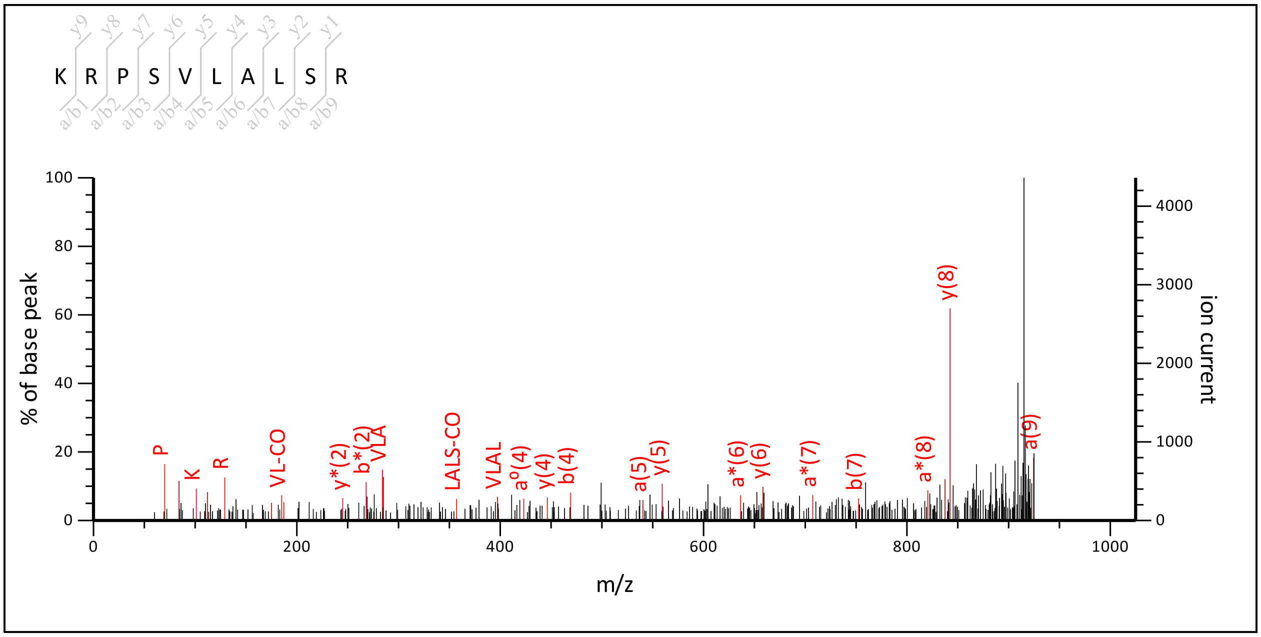
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KRPSVLALSR**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 75: 1125.736224 from(1126.743500,1+) intensity(0.0000) index(6)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224900, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1024.94

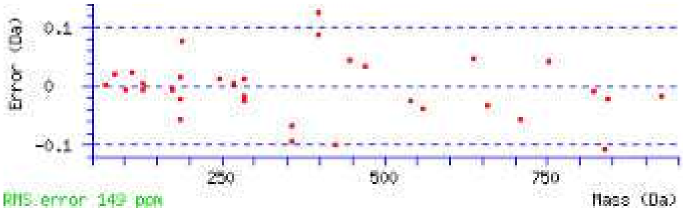
Label all possible matches ○ Label matches used for scoring ●

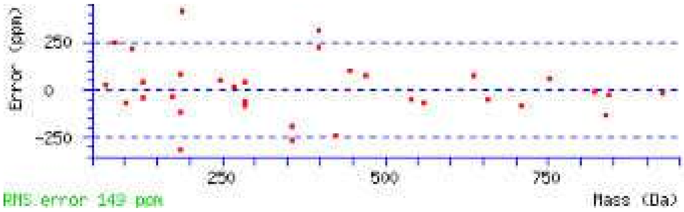
Monoisotopic mass of neutral peptide Mr(calc): 1125.6982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 4.2
Matches : 36/161 fragment ions using 54 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	101.1073	***101.1073***	84.0808		**129.1022**	112.0757		44.0495	**K**						**10**
2	129.1135	257.2084	240.1819		**285.2034**	268.1768		172.1444	**R**	897.5152	896.5200	998.6105	981.5840	980.6000	**9**
3	70.0651	354.2612	337.2346		382.2561	365.2296		328.2455	**P**	800.4625	799.4672	***842.5094***	825.4829	824.4989	**8**
4	60.0444	441.2932	424.2667	423.2827	**469.2881**	452.2616	451.2776	425.2983	**S**	713.4305	712.4352	745.4567	728.4301	727.4461	**7**
5	72.0808	***540.3616***	523.3351	522.3511	568.3566	551.3300	550.3460	526.3460	**V**	614.3620	627.3824	***658.4246***	641.3981	640.4141	**6**
6	86.0964	653.4457	636.4192	635.4351	681.4406	664.4141	663.4301	611.3988	**L**	501.2780	500.2827	***559.3562***	542.3297	541.3457	**5**
7	44.0495	724.4828	707.4563	706.4723	**752.4777**	735.4512	734.4672		**A**	430.2409		***446.2722***	429.2456	428.2616	**4**
8	86.0964	***837.5669***	820.5403	819.5563	865.5618	848.5352	847.5512	795.5199	**L**	317.1568	316.1615	375.2350	358.2085	357.2245	**3**
9	60.0444	***924.5989***	907.5724	906.5883	952.5938	935.5673	934.5833	908.6040	**S**	230.1248	229.1295	262.1510	245.1244	244.1404	**2**
10	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RP	226.1662	254.1612	**RPS**	313.1983	341.1932	**RPSV**	412.2667	440.2616
RPSVL	525.3507	553.3457	**RPSVLA**	596.3879	624.3828	**PS**	157.0972	185.0921
PSV	256.1656	284.1605	**PSVL**	369.2496	397.2445	**PSVLA**	440.2867	468.2817

PSVLAL	553.3708	581.3657	**PSVLALS**	640.4028	668.3978	**SV**	159.1128	187.1077
SVL	272.1969	300.1918	**SVLA**	343.2340	371.2289	**SVLAL**	456.3180	484.3130
SVLALS	543.3501	571.3450	**VL**	185.1648	213.1598	**VLA**	256.2020	284.1969
VLAL	369.2860	397.2809	**VLALS**	456.3180	484.3130	**LA**	157.1335	185.1285
LAL	270.2176	298.2125	**LALS**	357.2496	385.2445	**AL**	157.1335	185.1285
ALS	244.1656	272.1605	**LS**	173.1285	201.1234			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.1	1125.6982	0.0380	KRPSVIALSR
21.1	1125.6982	0.0380	KRPSVLALSR
21.1	1125.6618	0.0744	QRPSVLALSR
13.7	1125.6618	0.0744	RQVIASPISR
11.2	1125.6982	0.0380	QRAIVLSALR
8.6	1125.6328	0.1034	VGKAMHGVLAK
7.8	1125.6254	0.1108	RQLPDAALSR
7.4	1125.7121	0.0241	GGGLLAVLVSLK
7.0	1125.6506	0.0856	AGRILGPSLDK
7.0	1125.6506	0.0856	AGRLLGPSLDK

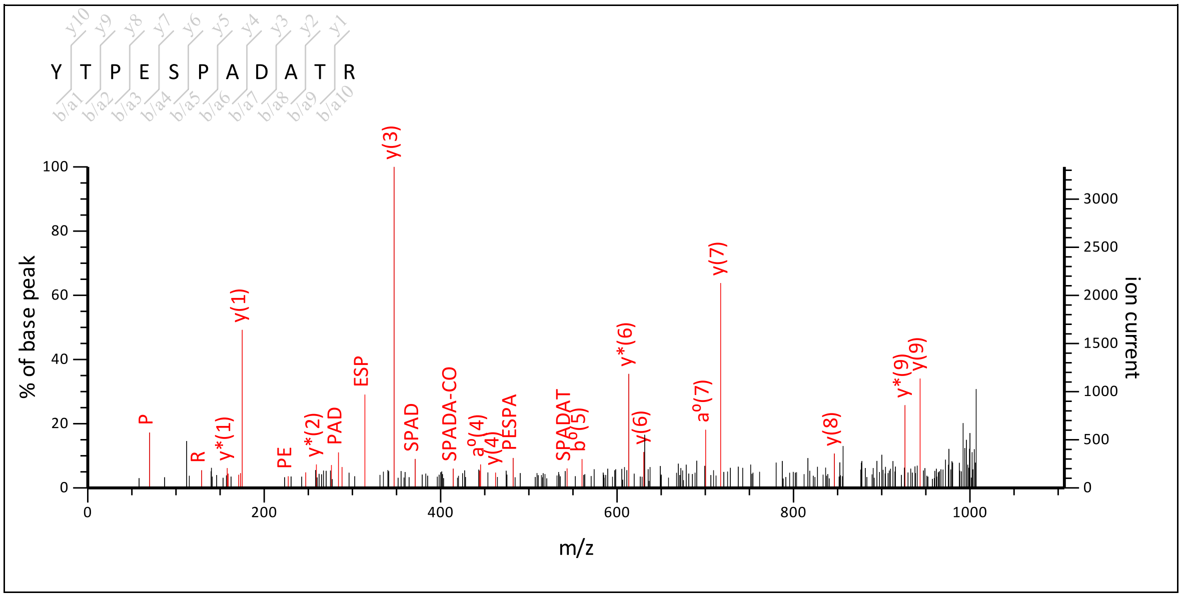
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 112**

MS/MS Fragmentation of **YTPESPADATR**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 84: 1206.597824 from(1207.605100,1+) intensity(0.0000) index(8)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224904, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1107.04

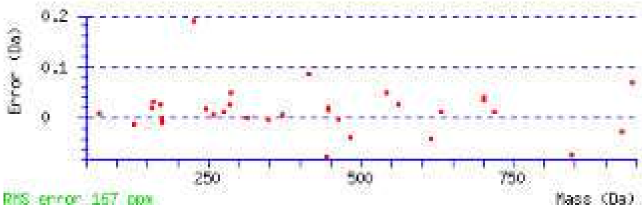
Label all possible matches ○ Label matches used for scoring ●

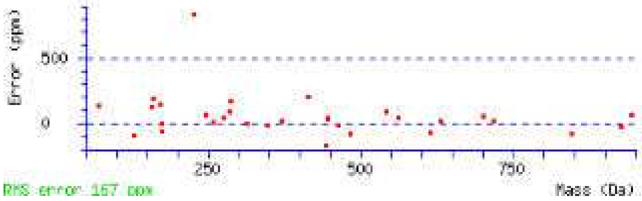
Monoisotopic mass of neutral peptide Mr(calc): 1206.5517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.16
Matches : 36/174 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	136.0757	136.0757		164.0706		44.0495		Y							11
2	74.0600	237.1234	219.1128	265.1183	247.1077	221.1285	223.1077	T	998.4538	1011.4742	1013.4534	1044.4956	1027.4691	1026.4851	10
3	70.0651	334.1761	316.1656	362.1710	344.1605	308.1605		P	901.4010	900.4058		***943.4480***	926.4214	925.4374	9
4	102.0550	463.2187	445.2082	491.2136	473.2031	405.2132		E	772.3584	771.3632		***846.3952***	829.3686	828.3846	8
5	60.0444	550.2508	532.2402	578.2457	560.2351	534.2558		S	685.3264	684.3311		***717.3526***	700.3260	699.3420	7
6	70.0651	647.3035	629.2930	675.2984	657.2879	621.2879		P	588.2736	587.2784		***630.3206***	613.2940	612.3100	6
7	44.0495	718.3406	700.3301	746.3355	728.3250			A	517.2365			533.2678	516.2413	515.2572	5
8	88.0393	833.3676	815.3570	861.3625	843.3519	789.3777		D	402.2096	401.2143		***462.2307***	445.2041	444.2201	4
9	44.0495	904.4047	886.3941	932.3996	914.3890			A	331.1724			***347.2037***	330.1772	329.1932	3
10	74.0600	1005.4524	987.4418	1033.4473	1015.4367	989.4575	991.4367	T	230.1248	243.1452	245.1244	***276.1666***	259.1401	258.1561	2
11	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TP	171.1128	199.1077	TPE	300.1554	328.1503	TPES	387.1874	415.1823
TPESP	484.2402	512.2351	TPESPA	555.2773	583.2722	TPESPAD	670.3042	698.2992
PE	199.1077	227.1026	PES	286.1397	314.1347	PESP	383.1925	411.1874
PESPA	454.2296	482.2245	PESPAD	569.2566	597.2515	PESPADA	640.2937	668.2886
ES	189.0870	217.0819	ESP	286.1397	314.1347	ESPA	357.1769	385.1718

ESPAD	472.2038	500.1987	**ESPADA**	543.2409	571.2358	**ESPADAT**	644.2886	672.2835
SP	157.0972	185.0921	**SPA**	228.1343	256.1292	**SPAD**	343.1612	371.1561
SPADA	414.1983	442.1932	**SPADAT**	515.2460	543.2409	**PA**	141.1022	169.0972
PAD	256.1292	284.1241	**PADA**	327.1663	355.1612	**PADAT**	428.2140	456.2089
AD	159.0764	187.0713	**ADA**	230.1135	258.1084	**ADAT**	331.1612	359.1561
DA	159.0764	187.0713	**DAT**	260.1241	288.1190	**AT**	145.0972	173.0921





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.3	1206.5517	0.0462	YTPESPADATR
16.6	1206.6721	-0.0743	TTTARGAVFVGK
15.1	1206.5373	0.0606	ISPEMQEAMR
14.1	1206.6720	-0.0742	YTRSILEGIR
13.8	1206.5373	0.0606	ISPEMQEAMR
13.6	1206.5914	0.0064	SIPEALTSMSR
13.6	1206.6026	-0.0048	AESLLSEMRR
12.2	1206.5914	0.0064	IISEGMVDATR
11.2	1206.5881	0.0097	FEDVSTPGVTR
11.2	1206.5411	0.0567	TMEEGQSGGRR

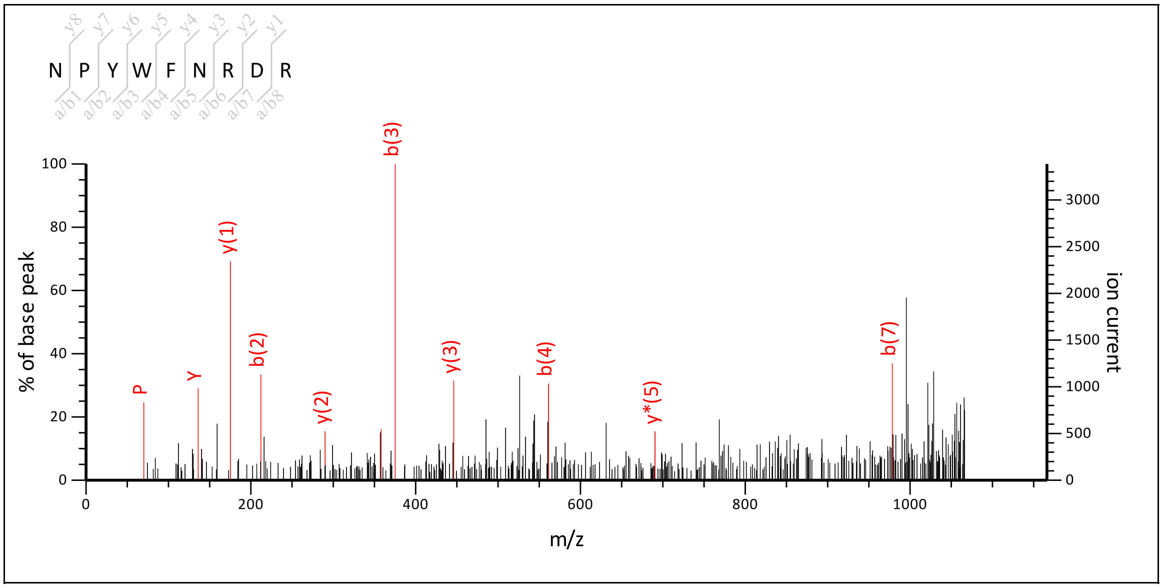
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **NPYWFNRDR**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 93: 1266.632824 from(1267.640100,1+) intensity(0.0000) index(10)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224897, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



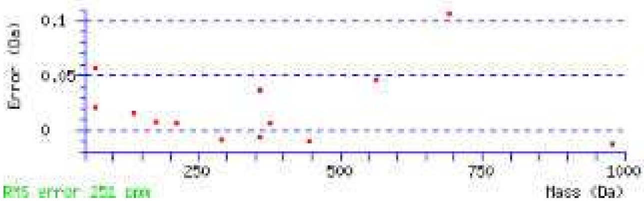
0 to 1166.12

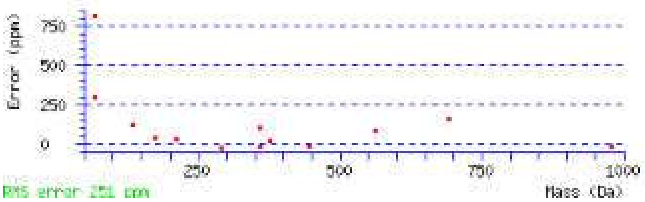
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1266.5894
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 19
Matches : 13/116 fragment ions using 20 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495	**N**						9
2	70.0651	184.1081	167.0815		***212.1030***	195.0764		158.0924	**P**	1111.5068	1110.5116	1153.5538	1136.5272	1135.5432	8
3	136.0757	347.1714	330.1448		***375.1663***	358.1397			**Y**	948.4435		1056.5010	1039.4744	1038.4904	7
4	159.0917	533.2507	516.2241		***561.2456***	544.2191			**W**	762.3642		893.4377	876.4111	875.4271	6
5	120.0808	680.3191	663.2926		708.3140	691.2875			**F**	615.2957		707.3583	690.3318	689.3478	5
6	87.0553	794.3620	777.3355		822.3569	805.3304		751.3562	**N**	501.2528	500.2576	560.2899	543.2634	542.2794	4
7	129.1135	950.4631	933.4366		***978.4581***	961.4315		865.3991	**R**	345.1517	344.1565	***446.2470***	429.2205	428.2364	3
8	88.0393	1065.4901	1048.4635	1047.4795	1093.4850	1076.4585	1075.4744	1021.5003	**D**	230.1248	229.1295	***290.1459***	273.1193	272.1353	2
9	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PY	233.1285	261.1234	**PYW**	419.2078	447.2027	**PYWF**	566.2762	594.2711
PYWFN	680.3191	708.3140	**YW**	322.1550	350.1499	**YWF**	469.2234	497.2183
YWFN	583.2663	611.2613	**WF**	306.1601	334.1550	**WFN**	420.2030	448.1979
WFNR	576.3041	604.2990	**WFNRD**	691.3311	719.3260	**FN**	234.1237	262.1186
FNR	390.2248	418.2197	**FNRD**	505.2518	533.2467	**NR**	243.1564	271.1513
NRD	358.1833	386.1783	**RD**	244.1404	272.1353			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	1266.5894	0.0434	NPYWFNRDR
16.6	1266.6292	0.0037	RLGFPCFNTR
15.8	1266.6932	-0.0604	NEALAVGIIPDR
15.4	1266.7197	-0.0869	VRFAPPLPTNR
13.8	1266.5762	0.0567	TLMESEDASLR
12.5	1266.6391	-0.0062	CVGEVPPPGLSR
12.5	1266.6568	-0.0239	EKVAAAPEPAER
12.0	1266.7157	-0.0828	TNIVAVGQGRPR
12.0	1266.6164	0.0164	ETRSSTSSVASR
11.9	1266.6092	0.0236	DSSLPYTELSR

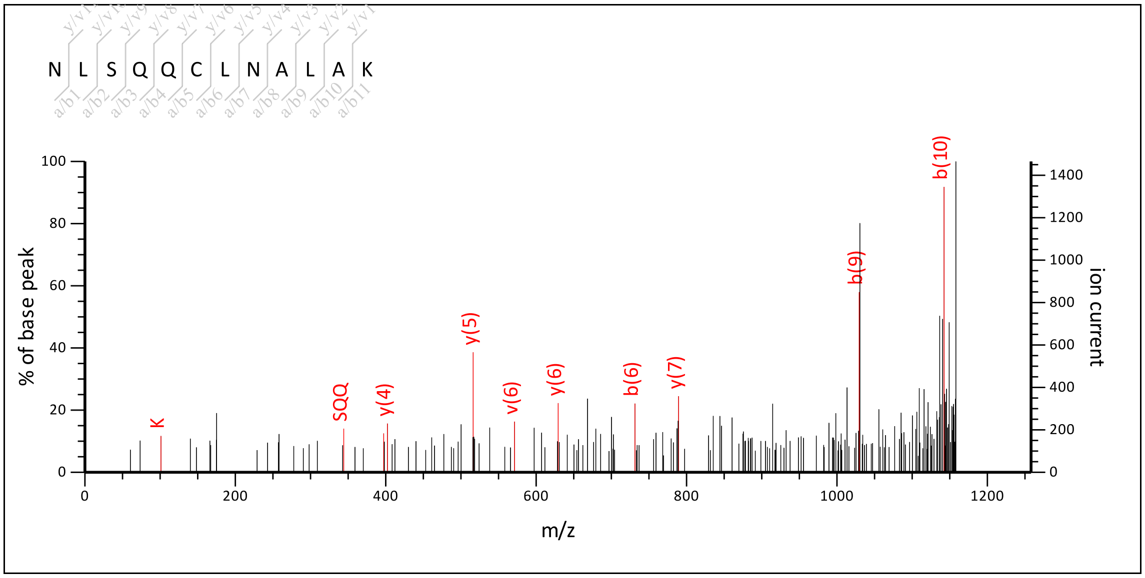
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **NLSQQCLNALAK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 100: 1358.729324 from(1359.736600,1+) intensity(0.0000) index(12)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224912, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1258.09

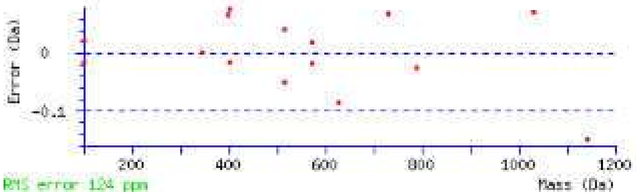
Label all possible matches ○ Label matches used for scoring ●

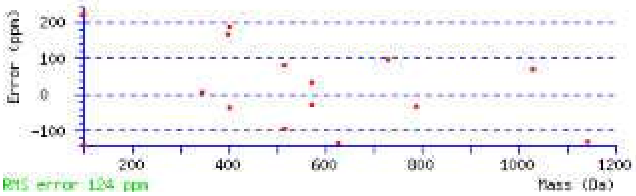
Monoisotopic mass of neutral peptide Mr(calc): 1358.6976
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 17 **Expect:** 41
Matches : 16/191 fragment ions using 22 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	87.0553	87.0553	70.0287		115.0502	98.0237		44.0495	N						12
2	86.0964	200.1394	183.1128		228.1343	211.1077		158.0924	L	1187.5837	1186.5885	1245.6620	1228.6354	1227.6514	11
3	60.0444	287.1714	270.1448	269.1608	315.1663	298.1397	297.1557	271.1765	S	1100.5517	1099.5565	1132.5779	1115.5514	1114.5674	10
4	101.0709	415.2300	398.2034	397.2194	443.2249	426.1983	425.2143	358.2085	Q	972.4931	971.4979	1045.5459	1028.5193		9
5	101.0709	543.2885	526.2620	525.2780	***571.2835***	554.2569	553.2729	486.2671	Q	844.4346	843.4393	917.4873	900.4608		8
6	133.0430	703.3192	686.2926	685.3086	***731.3141***	714.2876	713.3035	614.3256	C	684.4039	683.4087	***789.4287***	772.4022		7
7	86.0964	816.4032	799.3767	798.3927	844.3982	827.3716	826.3876	774.3563	L	571.3198	570.3246	***629.3981***	612.3715		6
8	87.0553	930.4462	913.4196	912.4356	958.4411	941.4145	940.4305	887.4404	N	457.2769	456.2817	***516.3140***	499.2875		5
9	44.0495	1001.4833	984.4567	983.4727	***1029.4782***	1012.4517	1011.4676		A	386.2398		***402.2711***	385.2445		4
10	86.0964	1114.5674	1097.5408	1096.5568	***1142.5623***	1125.5357	1124.5517	1072.5204	L	273.1557	272.1605	331.2340	314.2074		3
11	44.0495	1185.6045	1168.5779	1167.5939	1213.5994	1196.5728	1195.5888		A	202.1186		218.1499	201.1234		2
12	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LS	173.1285	201.1234	LSQ	301.1870	329.1819	LSQQ	429.2456	457.2405
LSQQC	589.2763	617.2712	SQ	188.1030	216.0979	SQQ	316.1615	344.1565
SQQC	476.1922	504.1871	SQQCL	589.2763	617.2712	QQ	229.1295	257.1244
QQC	389.1602	417.1551	QQCL	502.2442	530.2391	QQCLN	616.2872	644.2821
QQCLNA	687.3243	715.3192	QC	261.1016	289.0965	QCL	374.1857	402.1806
QCLN	488.2286	516.2235	QCLNA	559.2657	587.2606	QCLNAL	672.3498	700.3447

CL	246.1271	274.1220	**CLN**	360.1700	388.1649	**CLNA**	431.2071	459.2020
CLNAL	544.2912	572.2861	**CLNALA**	615.3283	643.3232	**LN**	200.1394	228.1343
LNA	271.1765	299.1714	**LNAL**	384.2605	412.2554	**LNALA**	455.2976	483.2926
NA	158.0924	186.0873	**NAL**	271.1765	299.1714	**NALA**	342.2136	370.2085
AL	157.1335	185.1285	**ALA**	228.1707	256.1656	**LA**	157.1335	185.1285





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.9	1358.6677	0.0616	QELAETQNDLAK
18.8	1358.7405	-0.0112	ELSVAESKVLER
16.9	1358.6976	0.0317	NISQQCLNALAK
16.9	1358.6976	0.0317	NLSQQCLNAIAK
16.9	1358.6976	0.0317	NLSQQCLNALAK
15.8	1358.7154	0.0140	SGKENLVADALSR
15.2	1358.6691	0.0603	DAAELASHYARR
14.5	1358.6976	0.0317	AGAMNALLESLNR
13.0	1358.7129	0.0164	ERVWCLDIIR
12.0	1358.6691	0.0602	KGGSVGGGGEVGGWR

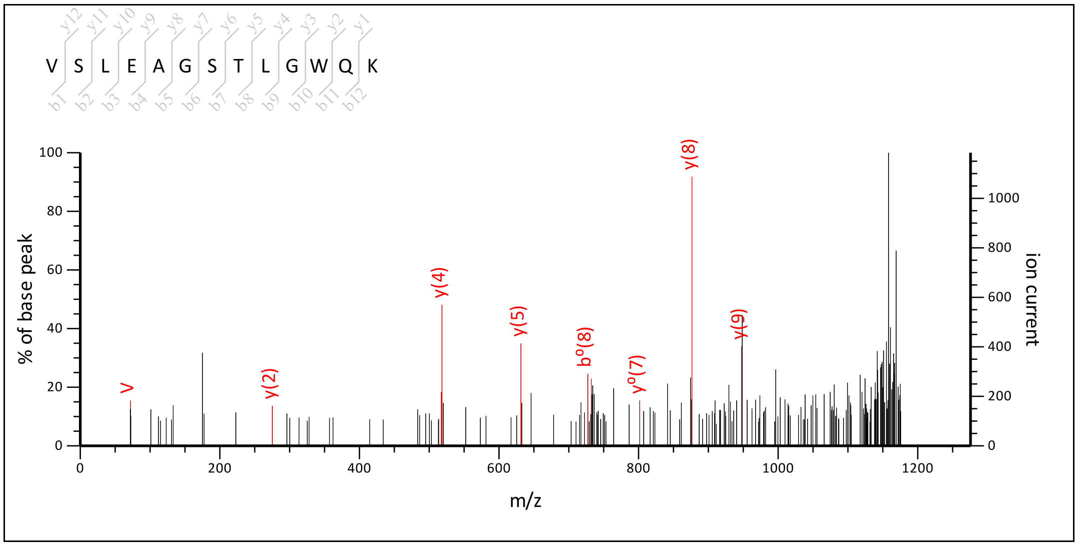
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **VSLEAGSTLGWQK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 102: 1374.747524 from(1375.754800,1+) intensity(0.0000) index(13)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224914, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1275.67

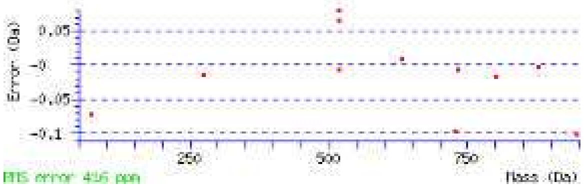
Label all possible matches ○ Label matches used for scoring ●

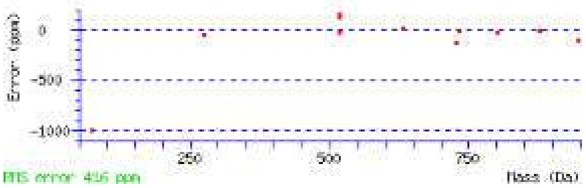
Monoisotopic mass of neutral peptide Mr(calc): 1374.7143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 13 **Expect:** 98
Matches : 12/208 fragment ions using 35 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	60.0444	159.1128		141.1022	187.1077		169.0972	143.1179		S	1244.6270	1243.6317		1276.6532	1259.6266
3	86.0964	272.1969		254.1863	300.1918		282.1812	230.1499		L	1131.5429	1130.5477		1189.6212	1172.5946
4	102.0550	401.2395		383.2289	429.2344		411.2238	343.2340		E	1002.5003	1001.5051		1076.5371	1059.5106
5	44.0495	472.2766		454.2660	500.2715		482.2609			A	931.4632			***947.4945***	930.4680
6	30.0338	529.2980		511.2875	557.2930		539.2824			G				***876.4574***	859.4308
7	60.0444	616.3301		598.3195	644.3250		626.3144	600.3352		S	787.4097	786.4145		819.4359	802.4094
8	74.0600	717.3777		699.3672	745.3727		727.3621	701.3828	703.3621	T	686.3620	699.3824	701.3617	***732.4039***	715.3774
9	86.0964	830.4618		812.4512	858.4567		840.4462	788.4149		L	573.2780	572.2827		***631.3562***	614.3297
10	30.0338	887.4833		869.4727	915.4782		897.4676			G				***518.2722***	501.2456
11	159.0917	1073.5626		1055.5520	1101.5575		1083.5469			W	330.1772			461.2507	444.2241
12	101.0709	1201.6212	1184.5946	1183.6106	1229.6161	1212.5895	1211.6055	1144.5997		Q	202.1186	201.1234		***275.1714***	258.1448
13	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SL	173.1285	201.1234	**SLE**	302.1710	330.1660	**SLEA**	373.2082	401.2031
SLEAG	430.2296	458.2245	**SLEAGS**	517.2617	545.2566	**SLEAGST**	618.3093	646.3042
LE	215.1390	243.1339	**LEA**	286.1761	314.1710	**LEAG**	343.1976	371.1925
LEAGS	430.2296	458.2245	**LEAGST**	531.2773	559.2722	**LEAGSTL**	644.3614	672.3563
EA	173.0921	201.0870	**EAG**	230.1135	258.1084	**EAGS**	317.1456	345.1405
EAGST	418.1932	446.1882	**EAGSTL**	531.2773	559.2722	**EAGSTLG**	588.2988	616.2937
AG	101.0709	129.0659	**AGS**	188.1030	216.0979	**AGST**	289.1506	317.1456
AGSTL	402.2347	430.2296	**AGSTLG**	459.2562	487.2511	**AGSTLGW**	645.3355	673.3304

GS	117.0659	145.0608	**GST**	218.1135	246.1084	**GSTL**	331.1976	359.1925
GSTLG	388.2191	416.2140	**GSTLGW**	574.2984	602.2933	**ST**	161.0921	189.0870
STL	274.1761	302.1710	**STLG**	331.1976	359.1925	**STLGW**	517.2769	545.2718
STLGWQ	645.3355	673.3304	**TL**	187.1441	215.1390	**TLG**	244.1656	272.1605
TLGW	430.2449	458.2398	**TLGWQ**	558.3035	586.2984	**LG**	143.1179	171.1128
LGW	329.1972	357.1921	**LGWQ**	457.2558	485.2507	**GW**	216.1131	244.1081
GWQ	344.1717	372.1666	**WQ**	287.1503	315.1452			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
13.0	1374.7143	0.0332	VSLEAGSTLGWQK
11.3	1374.6991	0.0485	VALSESTGLDQKQ
8.7	1374.6925	0.0550	GEELARAMETLR
8.7	1374.7177	0.0298	VAITDMKVDVER
6.8	1374.7363	0.0112	AKALVPMMETIR
6.4	1374.6813	0.0662	VQIMQELDDIR
6.1	1374.7004	0.0471	GAKAATGSQSVWGR
5.4	1374.7103	0.0373	ASNASSLEQLSLR
5.1	1374.6561	0.0914	AVEEAMDELGRR
5.1	1374.6991	0.0485	LSDTELASSSPLR

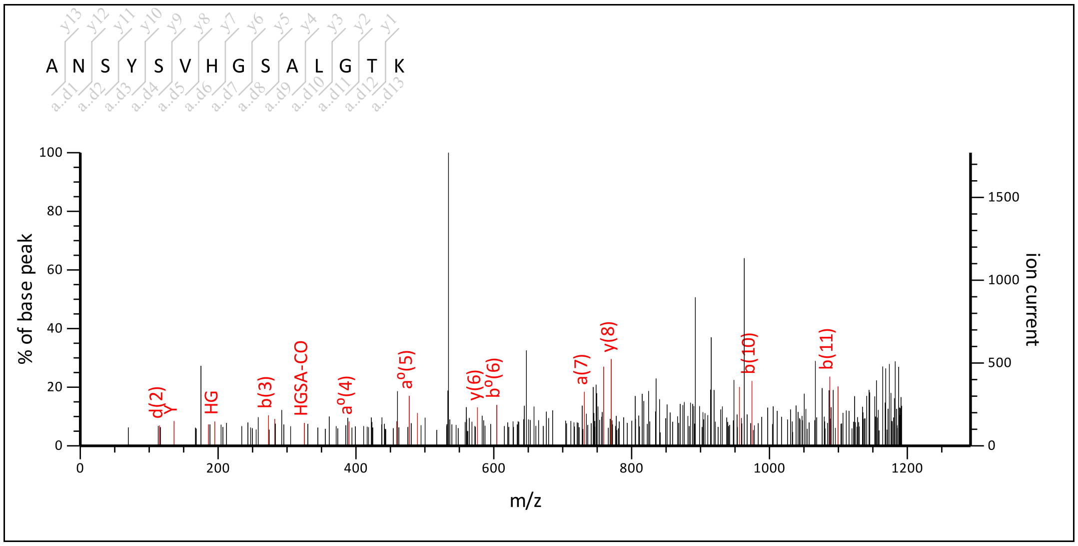
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **ANSYSVHGSALGTK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 105: 1390.736224 from(1391.743500,1+) intensity(0.0000) index(14)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224906, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1291.73

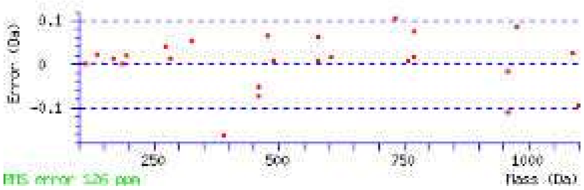
Label all possible matches ○ Label matches used for scoring ●

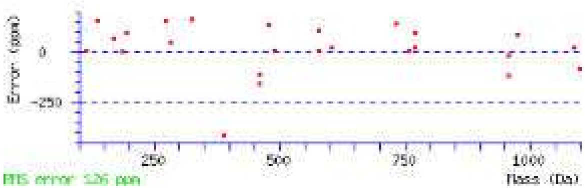
```
Monoisotopic mass of neutral peptide Mr(calc): 1390.6841
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 8  Expect: 3.2e+02
Matches : 25/253 fragment ions using 72 most intense peaks    (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	87.0553	158.0924	141.0659		***186.0873***	169.0608		115.0866		N	1261.6171	1260.6219		1320.6543	1303.6277
3	60.0444	245.1244	228.0979	227.1139	***273.1193***	256.0928	255.1088	229.1295		S	1174.5851	1173.5899		1206.6113	1189.5848
4	136.0757	408.1878	391.1612	390.1772	436.1827	419.1561	418.1721			Y	1011.5218			1119.5793	1102.5528
5	60.0444	495.2198	478.1932	477.2092	523.2147	506.1882	505.2041	479.2249		S	924.4898	923.4945		***956.5160***	939.4894
6	72.0808	594.2882	577.2617	576.2776	622.2831	605.2566	604.2726	580.2726		V	825.4213	838.4417		869.4839	852.4574
7	110.0713	731.3471	714.3206	713.3365	***759.3420***	742.3155	741.3315			H	688.3624			***770.4155***	753.3890
8	30.0338	788.3686	771.3420	770.3580	816.3635	799.3369	798.3529			G				633.3566	616.3301
9	60.0444	875.4006	858.3741	857.3900	903.3955	886.3690	885.3850	859.4057		S	544.3089	543.3137		***576.3352***	559.3086
10	44.0495	946.4377	929.4112	928.4272	***974.4326***	957.4061	956.4221			A	473.2718			***489.3031***	472.2766
11	86.0964	1059.5218	1042.4952	1041.5112	***1087.5167***	1070.4901	1069.5061	1017.4748		L	360.1878	359.1925		418.2660	401.2395
12	30.0338	1116.5432	1099.5167	1098.5327	1144.5382	1127.5116	1126.5276			G				305.1819	288.1554
13	74.0600	1217.5909	1200.5644	1199.5804	1245.5858	1228.5593	1227.5753	1201.5960	1203.5753	T	202.1186	215.1390	217.1183	248.1605	231.1339
14	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NS	174.0873	202.0822	NSY	337.1506	365.1456	NSYS	424.1827	452.1776
NSYSV	523.2511	551.2460	NSYSVH	660.3100	688.3049	SY	223.1077	251.1026
SYS	310.1397	338.1347	SYSV	409.2082	437.2031	SYSVH	546.2671	574.2620
SYSVHG	603.2885	631.2835	SYSVHGS	690.3206	718.3155	YS	223.1077	251.1026
YSV	322.1761	350.1710	YSVH	459.2350	487.2300	YSVHG	516.2565	544.2514
YSVHGS	603.2885	631.2835	YSVHGSA	674.3256	702.3206	SV	159.1128	187.1077
SVH	296.1717	324.1666	SVHG	353.1932	381.1881	SVHGS	440.2252	468.2201

SVHGSA	511.2623	539.2572	**SVHGSAL**	624.3464	652.3413	**SVHGSALG**	681.3678	709.3628
VH	209.1397	237.1346	**VHG**	266.1612	294.1561	**VHGS**	353.1932	381.1881
VHGSA	424.2303	452.2252	**VHGSAL**	537.3144	565.3093	**VHGSALG**	594.3358	622.3307
VHGSALGT	695.3835	723.3784	**HG**	167.0927	195.0877	**HGS**	254.1248	282.1197
HGSA	325.1619	353.1568	**HGSAL**	438.2459	466.2409	**HGSALG**	495.2674	523.2623
HGSALGT	596.3151	624.3100	**GS**	117.0659	145.0608	**GSA**	188.1030	216.0979
GSAL	301.1870	329.1819	**GSALG**	358.2085	386.2034	**GSALGT**	459.2562	487.2511
SA	131.0815	159.0764	**SAL**	244.1656	272.1605	**SALG**	301.1870	329.1819
SALGT	402.2347	430.2296	**AL**	157.1335	185.1285	**ALG**	214.1550	242.1499
ALGT	315.2027	343.1976	**LG**	143.1179	171.1128	**LGT**	244.1656	272.1605
GT	131.0815	159.0764						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
11.5	1390.7126	0.0236	VKATESELMDLR
11.3	1390.6298	0.1064	GRGGTQSSGGGSGGGGR
10.6	1390.6407	0.0955	RYMIMTTNMSK
8.8	1390.6407	0.0955	RYMIMTTNMSK
8.6	1390.6510	0.0852	NEGQAEMGSAILR
8.2	1390.6841	0.0521	ANSYSVHGSALGTK
7.6	1390.6623	0.0739	RASASSTSPSGMPR
7.3	1390.6576	0.0786	IAKEDSTDDIER
7.2	1390.6623	0.0739	GTLLDGSDMNGRR
6.8	1390.7431	-0.0069	HPISVFLYMLR

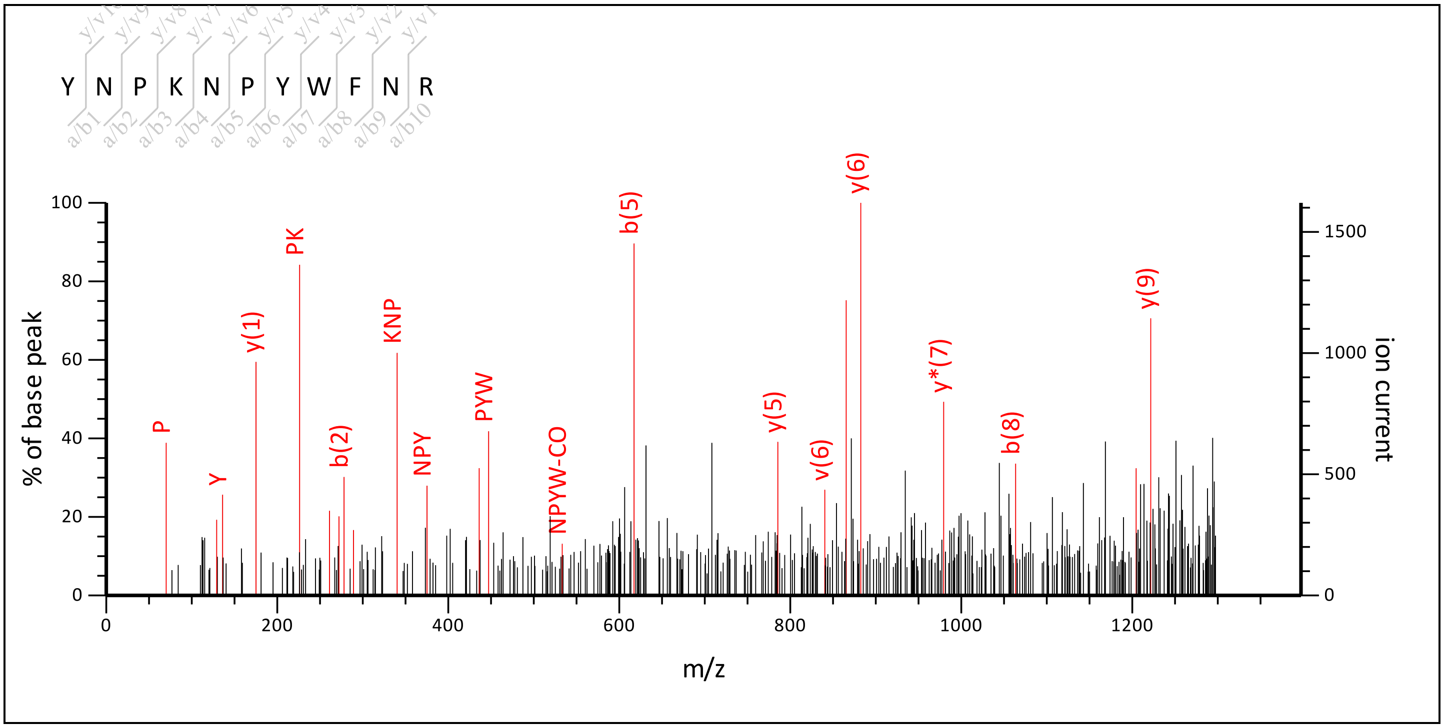
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **YNPKNPYWFNR**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 115: 1497.774024 from(1498.781300,1+) intensity(0.0000) index(17)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224902, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1397.32

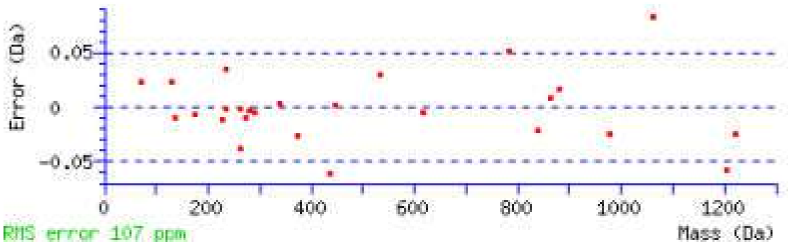
Label all possible matches ○ Label matches used for scoring ●

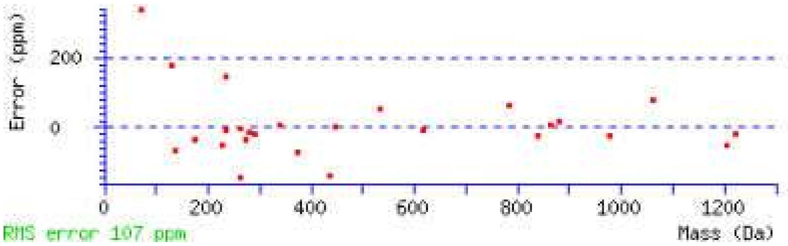
Monoisotopic mass of neutral peptide Mr(calc): 1497.7153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 20 **Expect:** 18
Matches : 32/144 fragment ions using 52 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	136.0757	136.0757		164.0706		44.0495	Y					11
2	87.0553	250.1186	233.0921	**278.1135**	261.0870	207.1128	N	1276.6222	1275.6269	1335.6593	1318.6327	10
3	70.0651	347.1714	330.1448	**375.1663**	358.1397	321.1557	P	1179.5694	1178.5742	***1221.6164***	1204.5898	9
4	101.1073	475.2663	458.2398	503.2613	486.2347	418.2085	K	1051.4744	1050.4792	1124.5636	1107.5370	8
5	87.0553	589.3093	572.2827	**617.3042**	600.2776	546.3035	N	937.4315	936.4363	996.4686	979.4421	7
6	70.0651	686.3620	669.3355	714.3570	697.3304	660.3464	P	840.3787	839.3835	***882.4257***	865.3992	6
7	136.0757	849.4254	832.3988	877.4203	860.3937		Y	677.3154		***785.3729***	768.3464	5
8	159.0917	1035.5047	1018.4781	**1063.4996**	1046.4730		W	491.2361		622.3096	605.2831	4

9	120.0808	1182.5731	1165.5465	1210.5680	1193.5415		**F**	344.1677		***436.2303***	419.2037	**3**
10	87.0553	1296.6160	1279.5895	1324.6109	1307.5844	1253.6102	**N**	230.1248	229.1295	***289.1619***	272.1353	**2**
11	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NP	184.1081	212.1030	**NPK**	312.2030	340.1979	**NPKN**	426.2459	454.2409
NPKNP	523.2987	551.2936	**NPKNPY**	686.3620	714.3570	**PK**	198.1601	226.1550
PKN	312.2030	340.1979	**PKNP**	409.2558	437.2507	**PKNPY**	572.3191	600.3140
KN	215.1503	243.1452	**KNP**	312.2030	340.1979	**KNPY**	475.2663	503.2613
KNPYW	661.3457	689.3406	**NP**	184.1081	212.1030	**NPY**	347.1714	375.1663
NPYW	533.2507	561.2456	**NPYWF**	680.3191	708.3140	**PY**	233.1285	261.1234
PYW	419.2078	447.2027	**PYWF**	566.2762	594.2711	**PYWFN**	680.3191	708.3140
YW	322.1550	350.1499	**YWF**	469.2234	497.2183	**YWFN**	583.2663	611.2613
WF	306.1601	334.1550	**WFN**	420.2030	448.1979	**FN**	234.1237	262.1186





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
20.3	1497.7153	0.0587	YNPKNPYWFNR
13.2	1497.8416	-0.0676	RPLPDYVQKVQR
10.7	1497.7834	-0.0094	MAVGGRGPAVGGGLQR
9.0	1497.7762	-0.0022	KLIAQCWEPTPR
9.0	1497.6751	0.0989	MLRCHAPPQCGR
8.2	1497.6332	0.1409	NYEDAVGSGSGSAER
7.9	1497.7333	0.0407	MGGLPPPVHGHMPR
7.5	1497.7113	0.0627	NTWRQVYDFNR
7.5	1497.8629	-0.0889	QPVILFSPMIPLK

7.4	1497.7609	0.0131	MEEGLGPLQQQIR

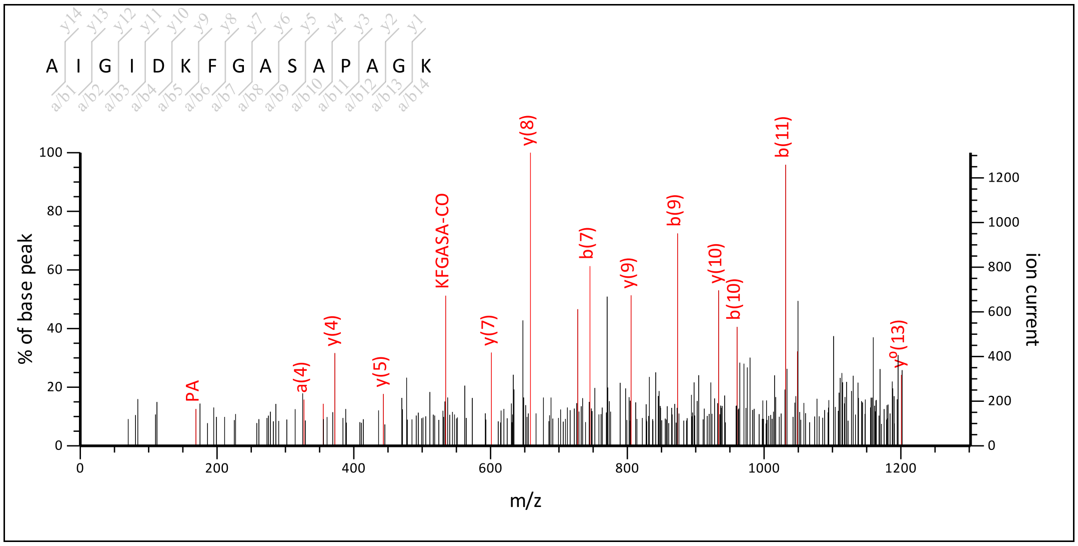
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **AIGIDKFGASAPAGK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 108: 1401.796924 from(1402.804200,1+) intensity(0.0000) index(15)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224911, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1301.89

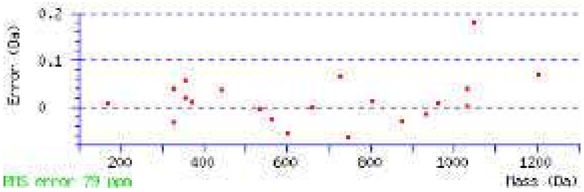
Label all possible matches ○ Label matches used for scoring ●

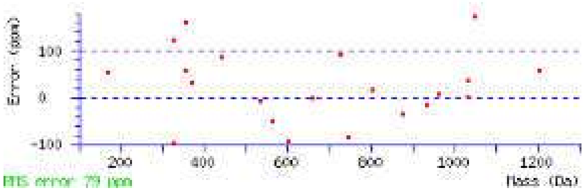
```
Monoisotopic mass of neutral peptide Mr(calc): 1401.7616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 1.2
Matches : 23/260 fragment ions using 36 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	44.0495	44.0495			72.0444			44.0495		A						
2	86.0964	157.1335			185.1285			129.1022	143.1179	I	1273.6535	1286.6739	1300.6896	1331.7318	1314.7052	13
3	30.0338	214.1550			242.1499					G				1218.6477	1201.6212	12
4	86.0964	327.2391			**355.2340**			299.2078	313.2234	I	1103.5480	1116.5684	1130.5841	1161.6263	1144.5997	11
5	88.0393	442.2660		424.2554	470.2609		452.2504	398.2762		D	988.5211	987.5258		***1048.5422***	1031.5156	10
6	101.1073	570.3610	553.3344	552.3504	598.3559	581.3293	580.3453	513.3031		K	860.4261	859.4308		***933.5152***	916.4887	9
7	120.0808	717.4294	700.4028	699.4188	**745.4243**	728.3978	727.4137			F	713.3577			***805.4203***	788.3937	7
8	30.0338	774.4509	757.4243	756.4403	802.4458	785.4192	784.4352			G				***658.3519***	641.3253	6
9	44.0495	845.4880	828.4614	827.4774	**873.4829**	856.4563	855.4723			A	585.2991			***601.3304***	584.3039	5
10	60.0444	932.5200	915.4934	914.5094	**960.5149**	943.4884	942.5043	916.5251		S	498.2671	497.2718		530.2933	513.2667	5
11	44.0495	1003.5571	986.5306	985.5465	**1031.5520**	1014.5255	1013.5415			A	427.2300			***443.2613***	426.2347	
12	70.0651	1100.6099	1083.5833	1082.5993	1128.6048	1111.5782	1110.5942	1074.5942		P	330.1772	329.1819		***372.2241***	355.1976	
13	44.0495	1171.6470	1154.6204	1153.6364	1199.6419	1182.6154	1181.6313			A	259.1401			275.1714	258.1448	
14	30.0338	1228.6684	1211.6419	1210.6579	1256.6634	1239.6368	1238.6528			G				204.1343	187.1077	
15	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IG	143.1179	171.1128	**IGI**	256.2020	284.1969	**IGID**	371.2289	399.2238
IGIDK	499.3239	527.3188	**IGIDKF**	646.3923	674.3872	**GI**	143.1179	171.1128
GID	258.1448	286.1397	**GIDK**	386.2398	414.2347	**GIDKF**	533.3082	561.3031
GIDKFG	590.3297	618.3246	**GIDKFGA**	661.3668	689.3617	**ID**	201.1234	229.1183
IDK	329.2183	357.2132	**IDKF**	476.2867	504.2817	**IDKFG**	533.3082	561.3031
IDKFGA	604.3453	632.3402	**IDKFGAS**	691.3774	719.3723	**DK**	216.1343	244.1292

DKF	363.2027	391.1976	**DKFG**	420.2241	448.2191	**DKFGA**	491.2613	519.2562
DKFGAS	578.2933	606.2882	**DKFGASA**	649.3304	677.3253	**KF**	248.1757	276.1707
KFG	305.1972	333.1921	**KFGA**	376.2343	404.2292	**KFGAS**	463.2663	491.2613
KFGASA	534.3035	562.2984	**KFGASAP**	631.3562	659.3511	**FG**	177.1022	205.0972
FGA	248.1394	276.1343	**FGAS**	335.1714	363.1663	**FGASA**	406.2085	434.2034
FGASAP	503.2613	531.2562	**FGASAPA**	574.2984	602.2933	**FGASAPAG**	631.3198	659.3148
GA	101.0709	129.0659	**GAS**	188.1030	216.0979	**GASA**	259.1401	287.1350
GASAP	356.1928	384.1878	**GASAPA**	427.2300	455.2249	**GASAPAG**	484.2514	512.2463
AS	131.0815	159.0764	**ASA**	202.1186	230.1135	**ASAP**	299.1714	327.1663
ASAPA	370.2085	398.2034	**ASAPAG**	427.2300	455.2249	**SA**	131.0815	159.0764
SAP	228.1343	256.1292	**SAPA**	299.1714	327.1663	**SAPAG**	356.1928	384.1878
AP	141.1022	169.0972	**APA**	212.1394	240.1343	**APAG**	269.1608	297.1557
PA	141.1022	169.0972	**PAG**	198.1237	226.1186	**AG**	101.0709	129.0659





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.7	1401.7616	0.0353	AIGIDKFGASAPAGK
22.3	1401.7073	0.0897	NTRAQANAVSQSR
17.0	1401.7517	0.0452	HAYGTKWSLIAR
13.8	1401.6888	0.1081	WDDIAGLEEAKR
12.6	1401.6597	0.1373	KDQAGQGQDSNVR
12.5	1401.7324	0.0645	QSREGQSQLITR
11.8	1401.6960	0.1009	DSIGVEGSNRVNR
11.3	1401.7728	0.0241	VGPLYQSRLVDR
9.3	1401.8344	-0.0375	RQSLLFTVTIPK
8.6	1401.6848	0.1121	DADAKQGSNELVR

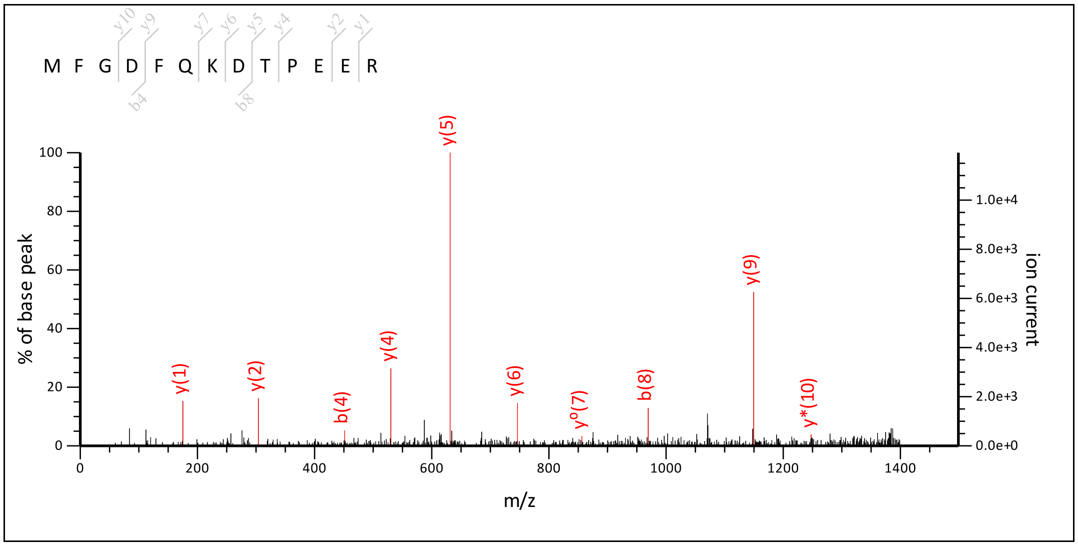
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **MFGDFQKDTPEER**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 132: 1598.764824 from(1599.772100,1+) intensity(0.0000) index(21)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224901, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1498.97

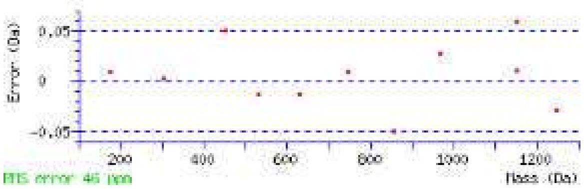
Label all possible matches ○ Label matches used for scoring ●

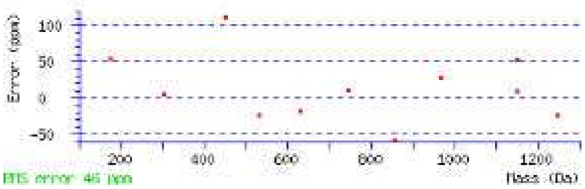
```
Monoisotopic mass of neutral peptide Mr(calc): 1598.7035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.14
Matches : 11/210 fragment ions using 14 most intense peaks    (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	104.0528	104.0528			132.0478			44.0495		**M**					
2	120.0808	251.1213			279.1162					**F**	1376.6077			1468.6703	1451.6438
3	30.0338	308.1427			336.1376					**G**				1321.6019	1304.5753
4	88.0393	423.1697		405.1591	**451.1646**		433.1540	379.1798		**D**	1204.5593	1203.5640		1264.5804	1247.5539
5	120.0808	570.2381		552.2275	598.2330		580.2224			**F**	1057.4909			***1149.5535***	1132.5269
6	101.0709	698.2967	681.2701	680.2861	726.2916	709.2650	708.2810	641.2752		**Q**	929.4323	928.4371		1002.4851	985.4585
7	101.1073	826.3916	809.3651	808.3811	854.3865	837.3600	836.3760	769.3338		**K**	801.3373	800.3421		874.4265	857.3999
8	88.0393	941.4186	924.3920	923.4080	**969.4135**	952.3869	951.4029	897.4287		**D**	686.3104	685.3151		***746.3315***	729.3050
9	74.0600	1042.4662	1025.4397	1024.4557	1070.4612	1053.4346	1052.4506	1026.4713	1028.4506	**T**	585.2627	598.2831	600.2624	***631.3046***	614.2780
10	70.0651	1139.5190	1122.4925	1121.5084	1167.5139	1150.4874	1149.5034	1113.5034		**P**	488.2100	487.2147		***530.2569***	513.2304
11	102.0550	1268.5616	1251.5351	1250.5510	1296.5565	1279.5300	1278.5460	1210.5561		**E**	359.1674	358.1721		433.2041	416.1776
12	102.0550	1397.6042	1380.5776	1379.5936	1425.5991	1408.5726	1407.5885	1339.5987		**E**	230.1248	229.1295		***304.1615***	287.1350
13	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FG	177.1022	205.0972	**FGD**	292.1292	320.1241	**FGDF**	439.1976	467.1925
FGDFQ	567.2562	595.2511	**FGDFQK**	695.3511	723.3461	**GD**	145.0608	173.0557
GDF	292.1292	320.1241	**GDFQ**	420.1878	448.1827	**GDFQK**	548.2827	576.2776
GDFQKD	663.3097	691.3046	**DF**	235.1077	263.1026	**DFQ**	363.1663	391.1612
DFQK	491.2613	519.2562	**DFQKD**	606.2882	634.2831	**FQ**	248.1394	276.1343
FQK	376.2343	404.2292	**FQKD**	491.2613	519.2562	**FQKDT**	592.3089	620.3039
FQKDTP	689.3617	717.3566	**QK**	229.1659	257.1608	**QKD**	344.1928	372.1878
QKDT	445.2405	473.2354	**QKDTP**	542.2933	570.2882	**QKDTPE**	671.3359	699.3308

KD	216.1343	244.1292	**KDT**	317.1819	345.1769	**KDTP**	414.2347	442.2296
KDTPE	543.2773	571.2722	**KDTPEE**	672.3199	700.3148	**DT**	189.0870	217.0819
DTP	286.1397	314.1347	**DTPE**	415.1823	443.1773	**DTPEE**	544.2249	572.2198
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPEE**	429.1980	457.1929
PE	199.1077	227.1026	**PEE**	328.1503	356.1452	**EE**	231.0975	259.0925





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.3	1598.7035	0.0613	MFGDFQKDTPEER
15.8	1598.7134	0.0514	LYSMEDVDEVVER
15.3	1598.8053	-0.0404	LSGSLLFHNTEPER
14.5	1598.8991	-0.1343	KAATSATDLKPIVER
14.4	1598.9032	-0.1384	LLALDGSALPVVFER
14.1	1598.8569	-0.0920	LQNFKLNYQYLR
13.8	1598.7974	-0.0326	MSIDSPQDPVLLER
13.5	1598.8879	-0.1231	EGKTLVILDDVLER
13.1	1598.8127	-0.0478	TTLAFFAGGMLGEIR
12.8	1598.8165	-0.0517	SQDKAQHAFGLLER

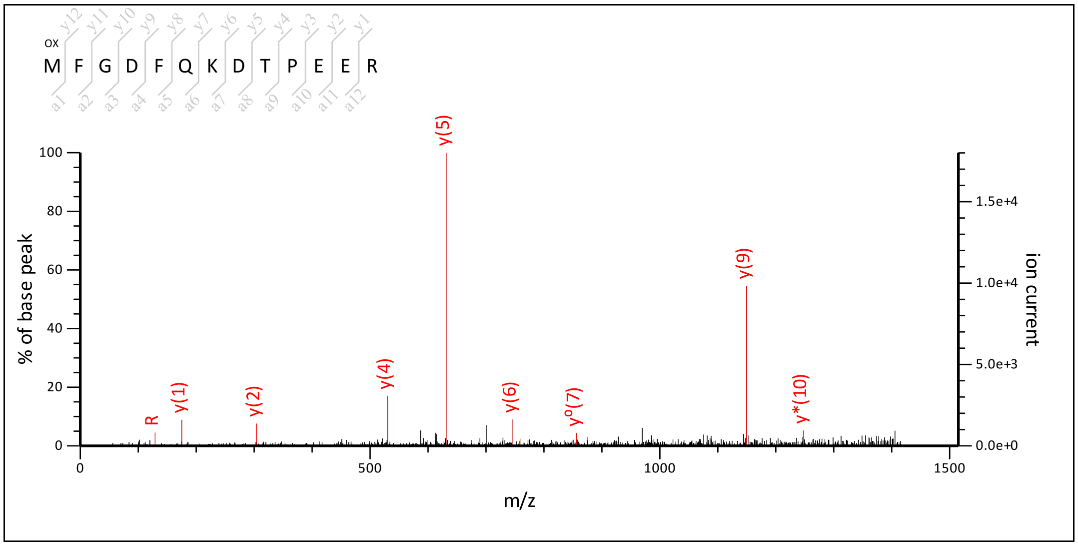
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **MFGDFQKDTPEER**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 134: 1614.742524 from(1615.749800,1+) intensity(0.0000) index(22)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224898, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1515.04

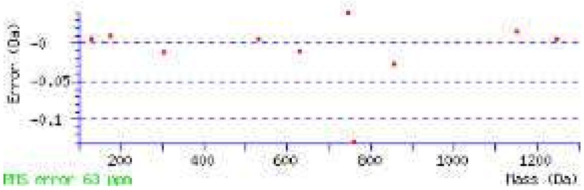
Label all possible matches ○ Label matches used for scoring ●

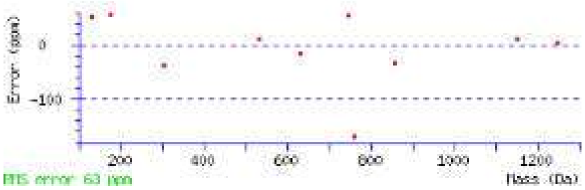
Monoisotopic mass of neutral peptide Mr(calc): 1614.6984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 **Expect:** 0.22
Matches : 10/276 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	120.0478	120.0478			148.0427			44.0495		M						
2	120.0808	267.1162			295.1111					F	1376.6077			1468.6703	1451.6438	14
3	30.0338	324.1376			352.1326					G				1321.6019	1304.5753	13
4	88.0393	439.1646		421.1540	467.1595		449.1489	395.1748		D	1204.5593	1203.5640		1264.5804	1247.5539	12
5	120.0808	586.2330		568.2224	614.2279		596.2173			F	1057.4909			***1149.5535***	1132.5269	11
6	101.0709	714.2916	697.2650	696.2810	742.2865	725.2599	724.2759	657.2701		Q	929.4323	928.4371		1002.4851	985.4585	9
7	101.1073	842.3865	825.3600	824.3760	870.3815	853.3549	852.3709	785.3287		K	801.3373	800.3421		874.4265	857.3999	8
8	88.0393	957.4135	940.3869	939.4029	985.4084	968.3818	967.3978	913.4237		D	686.3104	685.3151		***746.3315***	729.3050	7
9	74.0600	1058.4612	1041.4346	1040.4506	1086.4561	1069.4295	1068.4455	1042.4662	1044.4455	T	585.2627	598.2831	600.2624	***631.3046***	614.2780	6
10	70.0651	1155.5139	1138.4874	1137.5034	1183.5088	1166.4823	1165.4983	1129.4983		P	488.2100	487.2147		***530.2569***	513.2304	5
11	102.0550	1284.5565	1267.5300	1266.5460	1312.5514	1295.5249	1294.5409	1226.5510		E	359.1674	358.1721		433.2041	416.1776	4
12	102.0550	1413.5991	1396.5726	1395.5885	1441.5940	1424.5675	1423.5835	1355.5936		E	230.1248	229.1295		***304.1615***	287.1350	2
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FG	177.1022	205.0972	FGD	292.1292	320.1241	FGDF	439.1976	467.1925
FGDFQ	567.2562	595.2511	FGDFQK	695.3511	723.3461	GD	145.0608	173.0557
GDF	292.1292	320.1241	GDFQ	420.1878	448.1827	GDFQK	548.2827	576.2776
GDFQKD	663.3097	691.3046	DF	235.1077	263.1026	DFQ	363.1663	391.1612
DFQK	491.2613	519.2562	DFQKD	606.2882	634.2831	FQ	248.1394	276.1343

FQK	376.2343	404.2292	**FQKD**	491.2613	519.2562	**FQKDT**	592.3089	620.3039
FQKDTP	689.3617	717.3566	**QK**	229.1659	257.1608	**QKD**	344.1928	372.1878
QKDT	445.2405	473.2354	**QKDTP**	542.2933	570.2882	**QKDTPE**	671.3359	699.3308
KD	216.1343	244.1292	**KDT**	317.1819	345.1769	**KDTP**	414.2347	442.2296
KDTPE	543.2773	571.2722	**KDTPEE**	672.3199	700.3148	**DT**	189.0870	217.0819
DTP	286.1397	314.1347	**DTPE**	415.1823	443.1773	**DTPEE**	544.2249	572.2198
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPEE**	429.1980	457.1929
PE	199.1077	227.1026	**PEE**	328.1503	356.1452	**EE**	231.0975	259.0925





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.9	1614.6984	0.0441	MFGDFQKDTPEER
38.9	1614.6984	0.0441	MYGDFQKDTPEER
23.4	1614.7599	-0.0174	SFFVEMDETIIER
21.1	1614.8049	-0.0624	RVIQAGCATHAFER
15.9	1614.7083	0.0342	ESSEPESMTFTNLK
15.9	1614.6885	0.0540	QVLAYALDXTXDER
15.8	1614.6791	0.0634	TTSGNMDSSNKESNK
15.6	1614.8213	-0.0788	ALAISNDNGEIEITR
15.6	1614.7485	-0.0060	LEDNGVLDEDANGVR
14.3	1614.7494	-0.0069	SIDGDVTAPMMLHGR

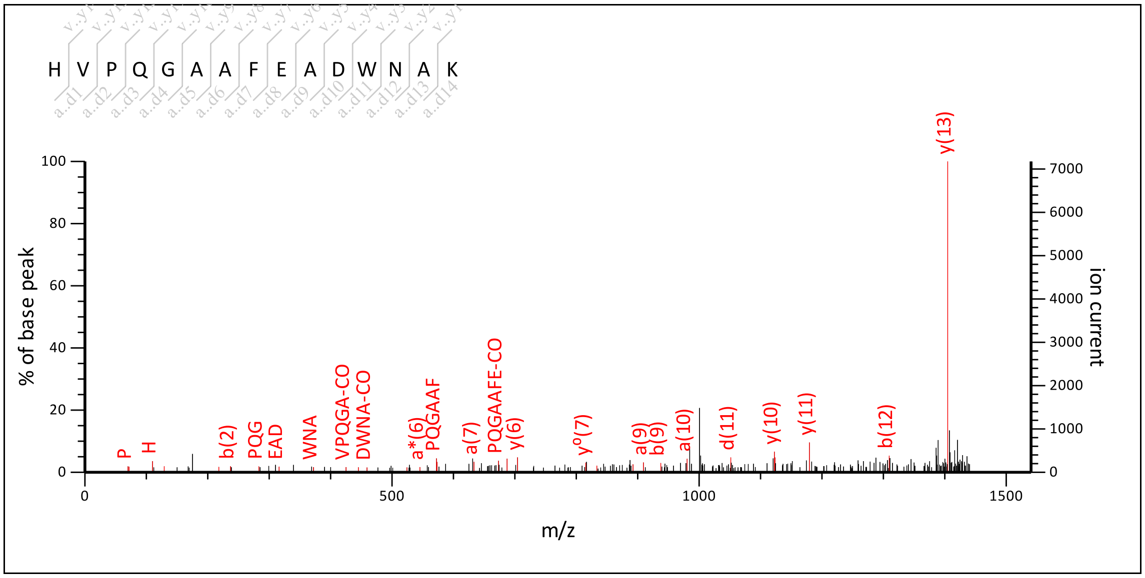
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **HVPQGAAFEADWNAK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 138: 1639.816324 from(1640.823600,1+) intensity(0.0000) index(23)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224908, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1540.43

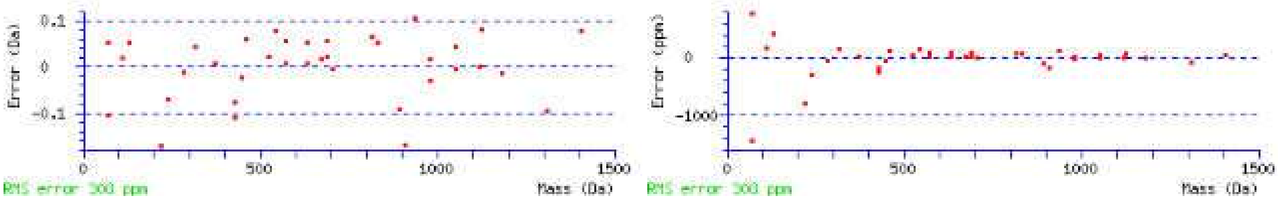
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1639.7743
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 2.8
Matches : 41/246 fragment ions using 94 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	110.0713	**110.0713**			138.0662			44.0495	H						15
2	72.0808	209.1397			**237.1346**			195.1240	V	1459.6601	1472.6805	1503.7227	1486.6961	1485.7121	14
3	70.0651	306.1925			334.1874			280.1768	P	1362.6073	1361.6121	***1404.6543***	1387.6277	1386.6437	13
4	101.0709	434.2510	417.2245		462.2459	445.2194		377.2296	Q	1234.5487	1233.5535	1307.6015	1290.5749	1289.5909	12
5	30.0338	491.2725	474.2459		519.2674	502.2409			G			***1179.5429***	1162.5164	1161.5323	11
6	44.0495	562.3096	545.2831		590.3045	573.2780			A	1106.4901		***1122.5214***	1105.4949	1104.5109	10
7	44.0495	**633.3467**	616.3202		661.3416	644.3151			A	1035.4530		***1051.4843***	1034.4578	1033.4738	9
8	120.0808	780.4151	763.3886		808.4100	791.3835			F	888.3846		***980.4472***	963.4207	962.4367	8
9	102.0550	**909.4577**	892.4312	891.4472	**937.4526**	920.4261	919.4421	851.4522	E	759.3420	758.3468	***833.3788***	816.3523	815.3682	7
10	44.0495	**980.4948**	963.4683	962.4843	1008.4898	991.4632	990.4792		A	688.3049		***704.3362***	687.3097	686.3256	6
11	88.0393	1095.5218	1078.4952	1077.5112	**1123.5167**	1106.4902	1105.5061	1051.5320	D	573.2780	572.2827	***633.2991***	616.2726	615.2885	5
12	159.0917	1281.6011	1264.5745	1263.5905	**1309.5960**	1292.5695	1291.5854		W	387.1987		518.2722	501.2456		4
13	87.0553	1395.6440	1378.6175	1377.6335	1423.6389	1406.6124	1405.6284	1352.6382	N	273.1557	272.1605	332.1928	315.1663		3
14	44.0495	1466.6811	1449.6546	1448.6706	1494.6761	1477.6495	1476.6655		A	202.1186		***218.1499***	201.1234		2
15	101.1073								K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VP	169.1335	197.1285	VPQ	297.1921	325.1870	VPQG	354.2136	382.2085
VPQGA	425.2507	453.2456	VPQGAA	496.2878	524.2827	VPQGAAF	643.3562	671.3511
PQ	198.1237	226.1186	PQG	255.1452	283.1401	PQGA	326.1823	354.1772

PQGAA	397.2194	425.2143	**PQGAAF**	544.2878	572.2827	**PQGAAFE**	673.3304	701.3253
QG	158.0924	186.0873	**QGA**	229.1295	257.1244	**QGAA**	300.1666	328.1615
QGAAF	447.2350	475.2300	**QGAAFE**	576.2776	604.2726	**QGAAFEA**	647.3148	675.3097
GA	101.0709	129.0659	**GAA**	172.1081	200.1030	**GAAF**	319.1765	347.1714
GAAFE	448.2191	476.2140	**GAAFEA**	519.2562	547.2511	**GAAFEAD**	634.2831	662.2780
AA	115.0866	143.0815	**AAF**	262.1550	290.1499	**AAFE**	391.1976	419.1925
AAFEA	462.2347	490.2296	**AAFEAD**	577.2617	605.2566	**AF**	191.1179	219.1128
AFE	320.1605	348.1554	**AFEA**	391.1976	419.1925	**AFEAD**	506.2245	534.2195
AFEADW	692.3039	720.2988	**FE**	249.1234	277.1183	**FEA**	320.1605	348.1554
FEAD	435.1874	463.1823	**FEADW**	621.2667	649.2617	**EA**	173.0921	201.0870
EAD	288.1190	316.1139	**EADW**	474.1983	502.1932	**EADWN**	588.2413	616.2362
EADWNA	659.2784	687.2733	**AD**	159.0764	187.0713	**ADW**	345.1557	373.1506
ADWN	459.1987	487.1936	**ADWNA**	530.2358	558.2307	**DW**	274.1186	302.1135
DWN	388.1615	416.1565	**DWNA**	459.1987	487.1936	**WN**	273.1346	301.1295
WNA	344.1717	372.1666	**NA**	158.0924	186.0873			



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.9	1639.7743	0.0420	HVPQGAAFEADWNAK
19.0	1639.8174	-0.0011	MSIHTALLCASPSPR
10.9	1639.7348	0.0815	VHVHVTGNCMEWR
10.3	1639.8716	-0.0552	HVALMSELSAVISQR
9.4	1639.7069	0.1094	AQVEMEMEAQIDSK
8.6	1639.8781	-0.0617	AAAASSLSAPAAPISLDK
8.4	1639.8907	-0.0743	HARPGSPVPTLAPGGAR
8.1	1639.7698	0.0465	MAIPTSDFLQMNTR
7.5	1639.8682	-0.0519	HVFSLGEGSPLTVAAR
7.4	1639.7916	0.0247	AFLHGDLTETVYMK

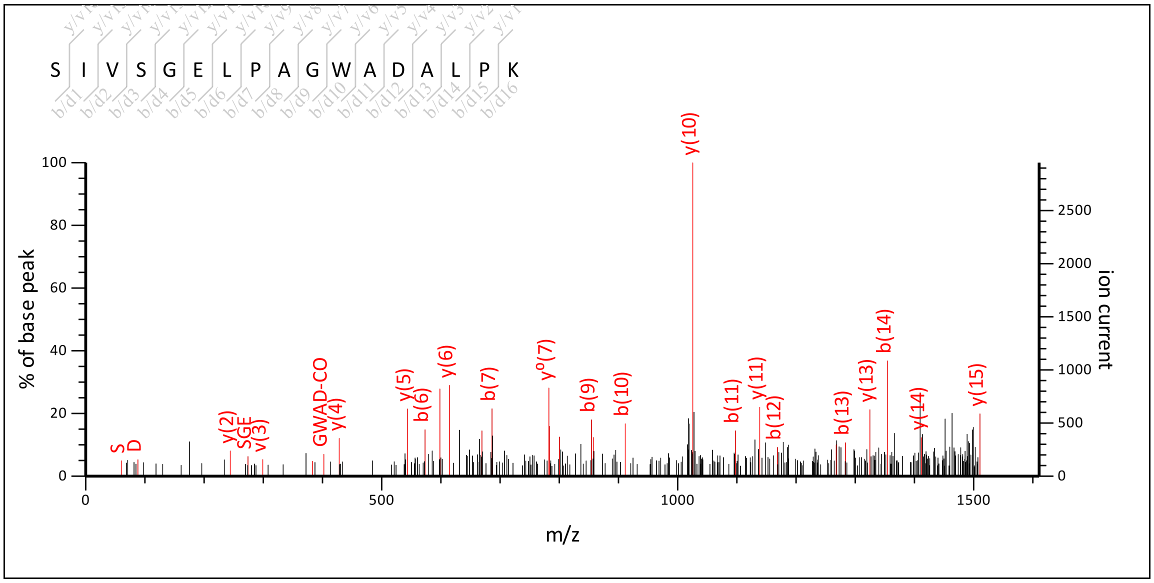
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **SIVSGELPAGWADALPK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 145: 1709.934824 from(1710.942100,1+) intensity(0.0000) index(25)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224909, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



0 to 1610.65

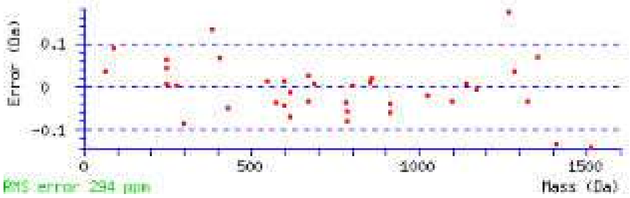
Label all possible matches ○ Label matches used for scoring ●

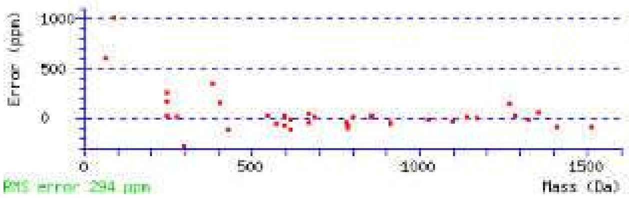
```
Monoisotopic mass of neutral peptide Mr(calc): 1709.8988
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 0.0011
Matches : 41/296 fragment ions using 75 most intense peaks   (help)
```

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444	42.0338	***88.0393***	70.0287	44.0495		**S**							**17**
2	86.0964	173.1285	155.1179	201.1234	183.1128	145.0972	159.1128	**I**	1565.7958	1578.8162	1592.8319	1623.8741	1606.8475	1605.8635	**16**
3	72.0808	272.1969	254.1863	300.1918	282.1812	258.1812		**V**	1466.7274	1479.7478		***1510.7900***	1493.7635	1492.7795	**15**
4	60.0444	359.2289	341.2183	387.2238	369.2132	343.2340		**S**	1379.6954	1378.7001		***1411.7216***	1394.6951	1393.7110	**14**
5	30.0338	416.2504	398.2398	444.2453	426.2347			**G**				***1324.6896***	1307.6630	1306.6790	**13**
6	102.0550	545.2930	527.2824	***573.2879***	555.2773	487.2875		**E**	1193.6313	1192.6361		***1267.6681***	1250.6416	1249.6575	**12**
7	86.0964	658.3770	640.3665	***686.3719***	668.3614	616.3301		**L**	1080.5473	1079.5520		***1138.6255***	1121.5990	1120.6150	**11**
8	70.0651	755.4298	737.4192	***783.4247***	765.4141	729.4141		**P**	983.4945	982.4993		***1025.5415***	1008.5149	1007.5309	**10**
9	44.0495	826.4669	808.4563	***854.4618***	836.4512			**A**	912.4574			928.4887	911.4621	910.4781	**9**
10	30.0338	883.4884	865.4778	***911.4833***	893.4727			**G**				***857.4516***	840.4250	839.4410	**8**
11	159.0917	1069.5677	1051.5571	***1097.5626***	1079.5520			**W**	669.3566			***800.4301***	783.4036	782.4196	**7**
12	44.0495	1140.6048	1122.5942	***1168.5997***	1150.5891			**A**	598.3195			***614.3508***	597.3243	596.3402	**6**
13	88.0393	1255.6317	1237.6212	***1283.6266***	1265.6161	1211.6419		**D**	483.2926	482.2973		***543.3137***	526.2871	525.3031	**5**
14	44.0495	1326.6688	1308.6583	***1354.6638***	1336.6532			**A**	412.2554			***428.2867***	411.2602		**4**
15	86.0964	1439.7529	1421.7423	1467.7478	1449.7373	1397.7060		**L**	299.1714	298.1761		357.2496	340.2231		**3**
16	70.0651	1536.8057	1518.7951	1564.8006	1546.7900	1510.7900		**P**	202.1186	201.1234		***244.1656***	227.1390		**2**
17	101.1073							**K**	74.0237	73.0284		147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb

IV	185.1648	213.1598	**IVS**	272.1969	300.1918	**IVSG**	329.2183	357.2132
IVSGE	458.2609	486.2558	**IVSGEL**	571.3450	599.3399	**IVSGELP**	668.3978	696.3927
VS	159.1128	187.1077	**VSG**	216.1343	244.1292	**VSGE**	345.1769	373.1718
VSGEL	458.2609	486.2558	**VSGELP**	555.3137	583.3086	**VSGELPA**	626.3508	654.3457
VSGELPAG	683.3723	711.3672	**SG**	117.0659	145.0608	**SGE**	246.1084	274.1034
SGEL	359.1925	387.1874	**SGELP**	456.2453	484.2402	**SGELPA**	527.2824	555.2773
SGELPAG	584.3039	612.2988	**GE**	159.0764	187.0713	**GEL**	272.1605	300.1554
GELP	369.2132	397.2082	**GELPA**	440.2504	468.2453	**GELPAG**	497.2718	525.2667
GELPAGW	683.3511	711.3461	**EL**	215.1390	243.1339	**ELP**	312.1918	340.1867
ELPA	383.2289	411.2238	**ELPAG**	440.2504	468.2453	**ELPAGW**	626.3297	654.3246
ELPAGWA	697.3668	725.3617	**LP**	183.1492	211.1441	**LPA**	254.1863	282.1812
LPAG	311.2078	339.2027	**LPAGW**	497.2871	525.2820	**LPAGWA**	568.3242	596.3191
LPAGWAD	683.3511	711.3461	**PA**	141.1022	169.0972	**PAG**	198.1237	226.1186
PAGW	384.2030	412.1979	**PAGWA**	455.2401	483.2350	**PAGWAD**	570.2671	598.2620
PAGWADA	641.3042	669.2991	**AG**	101.0709	129.0659	**AGW**	287.1503	315.1452
AGWA	358.1874	386.1823	**AGWAD**	473.2143	501.2092	**AGWADA**	544.2514	572.2463
AGWADAL	657.3355	685.3304	**GW**	216.1131	244.1081	**GWA**	287.1503	315.1452
GWAD	402.1772	430.1721	**GWADA**	473.2143	501.2092	**GWADAL**	586.2984	614.2933
GWADALP	683.3511	711.3461	**WA**	230.1288	258.1237	**WAD**	345.1557	373.1506
WADA	416.1928	444.1878	**WADAL**	529.2769	557.2718	**WADALP**	626.3297	654.3246
AD	159.0764	187.0713	**ADA**	230.1135	258.1084	**ADAL**	343.1976	371.1925
ADALP	440.2504	468.2453	**DA**	159.0764	187.0713	**DAL**	272.1605	300.1554
DALP	369.2132	397.2082	**AL**	157.1335	185.1285	**ALP**	254.1863	282.1812
LP	183.1492	211.1441						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.8	1709.8988	0.0360	SIVSGELPAGWADALPK
38.2	1709.8697	0.0652	VSDLSSPDQPASPRVR
27.2	1709.9213	0.0135	GLDADAATPVARWLVR
21.2	1709.8696	0.0652	SLEAEAGITGPAADPRR
19.0	1709.9617	-0.0269	GWLSLALVIGSPWGVR
19.0	1709.7721	0.1627	MPMSMSTMLPGSPRR
19.0	1709.7721	0.1627	MPMSMSTMLPGSPRR
17.2	1709.7721	0.1627	MPMSMSTMLPGSPRR
16.1	1709.9213	0.0135	DAGALLGAIPPHPAAPSR
16.1	1709.9788	-0.0440	ANVTGIILDQGKAVGVR

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

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **IYQEYGITAENVIATAK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 155: 1883.010524 from(1884.017800,1+) intensity(0.0000) index(28)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224905, MSMS Job_Run_Id: 21757, Comment:
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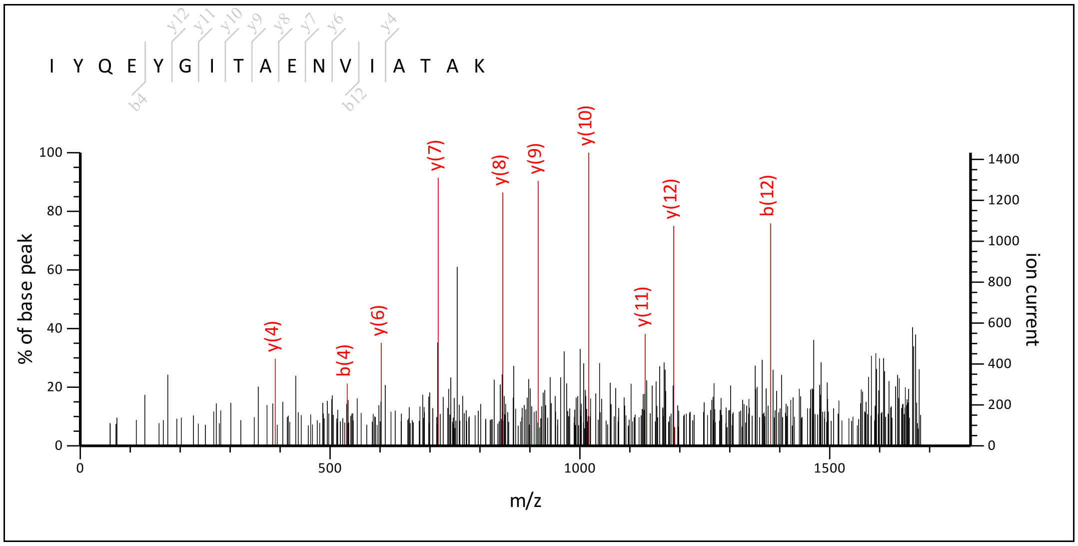


0 to 1781.86

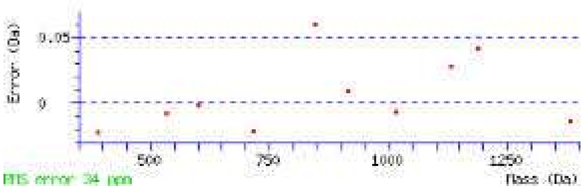
Label all possible matches ○ Label matches used for scoring ●

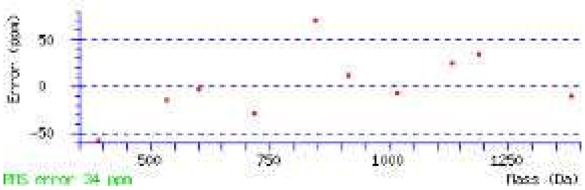
```
Monoisotopic mass of neutral peptide Mr(calc): 1882.9676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52  Expect: 0.0095
Matches : 10/318 fragment ions using 17 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		I					
2	136.0757	249.1598			277.1547					Y	1662.8333			1770.8909	1753.8643
3	101.0709	377.2183	360.1918		405.2132	388.1867		320.1969		Q	1534.7748	1533.7795		1607.8275	1590.8010
4	102.0550	506.2609	489.2344	488.2504	**534.2558**	517.2293	516.2453	448.2554		E	1405.7322	1404.7369		1479.7690	1462.7424
5	136.0757	669.3243	652.2977	651.3137	697.3192	680.2926	679.3086			Y	1242.6688			1350.7264	1333.6998
6	30.0338	726.3457	709.3192	708.3352	754.3406	737.3141	736.3301			G				***1187.6630***	1170.6365
7	86.0964	839.4298	822.4032	821.4192	867.4247	850.3981	849.4141	811.3985	825.4141	I	1072.5633	1085.5837	1099.5994	***1130.6416***	1113.6150
8	74.0600	940.4775	923.4509	922.4669	968.4724	951.4458	950.4618	924.4825	926.4618	T	971.5156	984.5360	986.5153	***1017.5575***	1000.5310
9	44.0495	1011.5146	994.4880	993.5040	1039.5095	1022.4829	1021.4989			A	900.4785			***916.5098***	899.4833
10	102.0550	1140.5572	1123.5306	1122.5466	1168.5521	1151.5255	1150.5415	1082.5517		E	771.4359	770.4407		***845.4727***	828.4462
11	87.0553	1254.6001	1237.5735	1236.5895	1282.5950	1265.5685	1264.5844	1211.5943		N	657.3930	656.3978		***716.4301***	699.4036
12	72.0808	1353.6685	1336.6420	1335.6579	**1381.6634**	1364.6369	1363.6529	1339.6529		V	558.3246	571.3450		***602.3872***	585.3606
13	86.0964	1466.7526	1449.7260	1448.7420	1494.7475	1477.7209	1476.7369	1438.7213	1452.7369	I	445.2405	458.2609	472.2766	503.3188	486.2922
14	44.0495	1537.7897	1520.7631	1519.7791	1565.7846	1548.7581	1547.7740			A	374.2034			***390.2347***	373.2082
15	74.0600	1638.8374	1621.8108	1620.8268	1666.8323	1649.8057	1648.8217	1622.8425	1624.8217	T	273.1557	286.1761	288.1554	319.1976	302.1710
16	44.0495	1709.8745	1692.8479	1691.8639	1737.8694	1720.8428	1719.8588			A	202.1186			218.1499	201.1234
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YQ	264.1343	292.1292	YQE	393.1769	421.1718	YQEY	556.2402	584.2351
YQEYG	613.2617	641.2566	QE	230.1135	258.1084	QEY	393.1769	421.1718
QEYG	450.1983	478.1932	QEYGI	563.2824	591.2773	QEYGIT	664.3301	692.3250
EY	265.1183	293.1132	EYG	322.1397	350.1347	EYGI	435.2238	463.2187

EYGIT	536.2715	564.2664	**EYGITA**	607.3086	635.3035	**YG**	193.0972	221.0921
YGI	306.1812	334.1761	**YGIT**	407.2289	435.2238	**YGITA**	478.2660	506.2609
YGITAE	607.3086	635.3035	**GI**	143.1179	171.1128	**GIT**	244.1656	272.1605
GITA	315.2027	343.1976	**GITAE**	444.2453	472.2402	**GITAEN**	558.2882	586.2831
GITAENV	657.3566	685.3515	**IT**	187.1441	215.1390	**ITA**	258.1812	286.1761
ITAE	387.2238	415.2187	**ITAEN**	501.2667	529.2617	**ITAENV**	600.3352	628.3301
TA	145.0972	173.0921	**TAE**	274.1397	302.1347	**TAEN**	388.1827	416.1776
TAENV	487.2511	515.2460	**TAENVI**	600.3352	628.3301	**TAENVIA**	671.3723	699.3672
AE	173.0921	201.0870	**AEN**	287.1350	315.1299	**AENV**	386.2034	414.1983
AENVI	499.2875	527.2824	**AENVIA**	570.3246	598.3195	**AENVIAT**	671.3723	699.3672
EN	216.0979	244.0928	**ENV**	315.1663	343.1612	**ENVI**	428.2504	456.2453
ENVIA	499.2875	527.2824	**ENVIAT**	600.3352	628.3301	**ENVIATA**	671.3723	699.3672
NV	186.1237	214.1186	**NVI**	299.2078	327.2027	**NVIA**	370.2449	398.2398
NVIAT	471.2926	499.2875	**NVIATA**	542.3297	570.3246	**VI**	185.1648	213.1598
VIA	256.2020	284.1969	**VIAT**	357.2496	385.2445	**VIATA**	428.2867	456.2817
IA	157.1335	185.1285	**IAT**	258.1812	286.1761	**IATA**	329.2183	357.2132
AT	145.0972	173.0921	**ATA**	216.1343	244.1292	**TA**	145.0972	173.0921





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.2	1882.9676	0.0429	IYQEYGITAENVIATAK
15.5	1883.0815	-0.0710	LPLPLYGLAQIMVRQR
12.6	1882.8657	0.1448	TTAENGDPSATSTNKFSR
9.3	1882.8843	0.1262	RMDSSTNEPLFTNVTR
8.1	1882.9206	0.0899	KEAPAAPAMTAAEAAAAEGR
7.6	1882.8666	0.1440	NGECGDGLRYLVEMVR
7.6	1882.9312	0.0793	NVYGPVTAAKTIYEDDK
6.5	1883.0000	0.0105	QGTLDPALATAEAGQTVIK
6.3	1882.9975	0.0130	ALTFSFSLAAVVVMGTNR
6.1	1882.9458	0.0647	MFVKEAQSATIASSIER

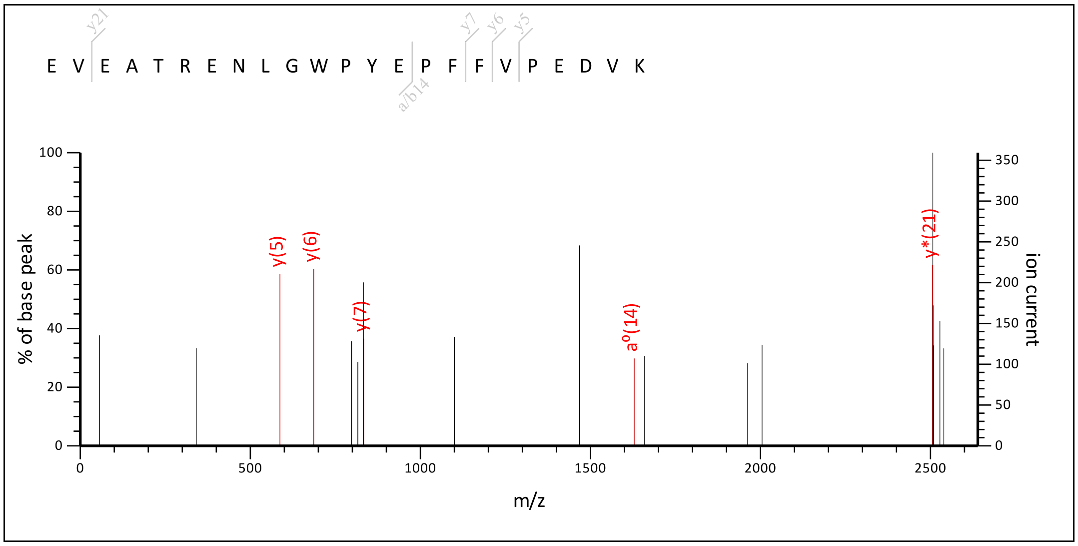
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 112

MS/MS Fragmentation of **EVEATRENLGWPYEPFFVPEDVK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 174: 2750.426324 from(2751.433600,1+) intensity(0.0000) index(34)
Title: Label: E1, Spot_Id: 219678, Peak_List_Id: 224930, MSMS Job_Run_Id: 21757, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E1_136842029000.txt



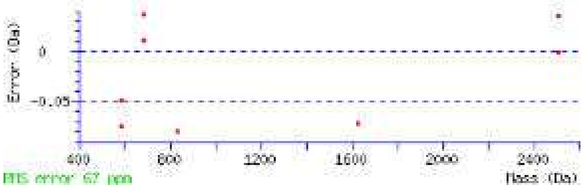
0 to 2639.17

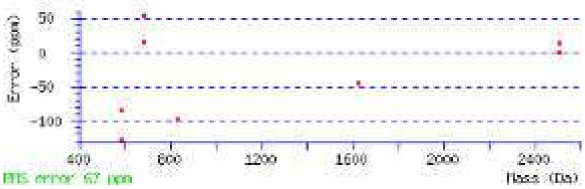
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2750.3228
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 3  Expect: 5.4e+02
Matches : 9/425 fragment ions using 14 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E					
2	72.0808	201.1234		183.1128	229.1183		211.1077	187.1077		V	2578.2249	2591.2453		2622.2875	2605.2609
3	102.0550	330.1660		312.1554	358.1609		340.1503	272.1605		E	2449.1823	2448.1870		2523.2191	2506.1925
4	44.0495	401.2031		383.1925	429.1980		411.1874			A	2378.1452			2394.1765	2377.1499
5	74.0600	502.2508		484.2402	530.2457		512.2351	486.2558	488.2351	T	2277.0975	2290.1179	2292.0972	2323.1394	2306.1128
6	129.1135	658.3519	641.3253	640.3413	***686.3468***	669.3202	668.3362	573.2879		R	2120.9964	2120.0011		2222.0917	2205.0651
7	102.0550	787.3945	770.3679	769.3839	815.3894	798.3628	797.3788	729.3890		E	1991.9538	1990.9585		2065.9906	2048.9640
8	87.0553	901.4374	884.4108	883.4268	929.4323	912.4058	911.4217	858.4316		N	1877.9109	1876.9156		1936.9480	1919.9214
9	86.0964	1014.5214	997.4949	996.5109	1042.5164	1025.4898	1024.5058	972.4745		L	1764.8268	1763.8316		1822.9051	1805.8785
10	30.0338	1071.5429	1054.5164	1053.5323	1099.5378	1082.5113	1081.5273			G				1709.8210	1692.7944
11	159.0917	1257.6222	1240.5957	1239.6117	1285.6171	1268.5906	1267.6066			W	1521.7260			1652.7995	1635.7730
12	70.0651	1354.6750	1337.6484	1336.6644	1382.6699	1365.6434	1364.6593	1328.6593		P	1424.6733	1423.6780		1466.7202	1449.6937
13	136.0757	1517.7383	1500.7118	1499.7278	1545.7332	1528.7067	1527.7227			Y	1261.6099			1369.6674	1352.6409
14	102.0550	1646.7809	1629.7544	1628.7703	1674.7758	1657.7493	1656.7653	1588.7754		E	1132.5673	1131.5721		1206.6041	1189.5776
15	70.0651	1743.8337	1726.8071	1725.8231	1771.8286	1754.8020	1753.8180	1717.8180		P	1035.5146	1034.5193		1077.5615	1060.5350
16	120.0808	1890.9021	1873.8755	1872.8915	1918.8970	1901.8705	1900.8864			F	888.4462			980.5088	963.4822
17	120.0808	2037.9705	2020.9440	2019.9599	2065.9654	2048.9389	2047.9549			F	741.3777			***833.4403***	816.4138
18	72.0808	2137.0389	2120.0124	2119.0284	2165.0338	2148.0073	2147.0233	2123.0233		V	642.3093	655.3297		***686.3719***	669.3454
19	70.0651	2234.0917	2217.0651	2216.0811	2262.0866	2245.0600	2244.0760	2208.0760		P	545.2566	544.2613		***587.3035***	570.2770
20	102.0550	2363.1343	2346.1077	2345.1237	2391.1292	2374.1026	2373.1186	2305.1288		E	416.2140	415.2187		490.2508	473.2242
21	88.0393	2478.1612	2461.1347	2460.1507	***2506.1561***	2489.1296	2488.1456	2434.1714		D	301.1870	300.1918		361.2082	344.1816
22	72.0808	2577.2296	2560.2031	2559.2191	2605.2245	2588.1980	2587.2140	2563.2140		V	202.1186	215.1390		246.1812	229.1547
23	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VE	201.1234	229.1183	**VEA**	272.1605	300.1554	**VEAT**	373.2082	401.2031
VEATR	529.3093	557.3042	**VEATRE**	658.3519	686.3468	**EA**	173.0921	201.0870
EAT	274.1397	302.1347	**EATR**	430.2409	458.2358	**EATRE**	559.2835	587.2784
EATREN	673.3264	701.3213	**AT**	145.0972	173.0921	**ATR**	301.1983	329.1932
ATRE	430.2409	458.2358	**ATREN**	544.2838	572.2787	**ATRENL**	657.3678	685.3628
TR	230.1612	258.1561	**TRE**	359.2037	387.1987	**TREN**	473.2467	501.2416
TRENL	586.3307	614.3256	**TRENLG**	643.3522	671.3471	**RE**	258.1561	286.1510
REN	372.1990	400.1939	**RENL**	485.2831	513.2780	**RENLG**	542.3045	570.2994
EN	216.0979	244.0928	**ENL**	329.1819	357.1769	**ENLG**	386.2034	414.1983
ENLGW	572.2827	600.2776	**ENLGWP**	669.3355	697.3304	**NL**	200.1394	228.1343
NLG	257.1608	285.1557	**NLGW**	443.2401	471.2350	**NLGWP**	540.2929	568.2878
LG	143.1179	171.1128	**LGW**	329.1972	357.1921	**LGWP**	426.2500	454.2449
LGWPY	589.3133	617.3082	**GW**	216.1131	244.1081	**GWP**	313.1659	341.1608
GWPY	476.2292	504.2241	**GWPYE**	605.2718	633.2667	**WP**	256.1444	284.1394
WPY	419.2078	447.2027	**WPYE**	548.2504	576.2453	**WPYEP**	645.3031	673.2980
PY	233.1285	261.1234	**PYE**	362.1710	390.1660	**PYEP**	459.2238	487.2187
PYEPF	606.2922	634.2871	**YE**	265.1183	293.1132	**YEP**	362.1710	390.1660
YEPF	509.2395	537.2344	**YEPFF**	656.3079	684.3028	**EP**	199.1077	227.1026
EPF	346.1761	374.1710	**EPFF**	493.2445	521.2395	**EPFFV**	592.3130	620.3079
EPFFVP	689.3657	717.3606	**PF**	217.1335	245.1285	**PFF**	364.2020	392.1969
PFFV	463.2704	491.2653	**PFFVP**	560.3231	588.3180	**PFFVPE**	689.3657	717.3606
FF	267.1492	295.1441	**FFV**	366.2176	394.2125	**FFVP**	463.2704	491.2653
FFVPE	592.3130	620.3079	**FV**	219.1492	247.1441	**FVP**	316.2020	344.1969
FVPE	445.2445	473.2395	**FVPED**	560.2715	588.2664	**FVPEDV**	659.3399	687.3348
VP	169.1335	197.1285	**VPE**	298.1761	326.1710	**VPED**	413.2031	441.1980
VPEDV	512.2715	540.2664	**PE**	199.1077	227.1026	**PED**	314.1347	342.1296
PEDV	413.2031	441.1980	**ED**	217.0819	245.0768	**EDV**	316.1503	344.1452
DV	187.1077	215.1026						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
2.8	2750.3228	0.1035	EVEATRENLGWPYEPFFVPEDVK
2.2	2750.3421	0.0842	FSGTFAGRRPCYFNTGVMVLDLAR
0.8	2750.3746	0.0517	MAAWWCFALLLVLCAPAGADVSKGK
0.8	2750.4136	0.0128	TDIVASSTGFGPPVMPIFAKMLVNSR
0.8	2750.2543	0.1721	VECILMGGTFMSLPADYHDYFIR
0.3	2750.3320	0.0943	DGDGIEVFLALDESSMLTLQQNLDK
0.3	2750.4643	-0.0380	ELEKVLGGKPYLGNDTFGFVDIALR
0.3	2750.4778	-0.0515	GVIGLFVFFFFVGVAFDKLWTWR
0.3	2750.5862	-0.1599	LIFAAVVFMGLAFLAFWLIVRPTR
0.3	2750.6114	-0.1851	LIFAAVVFMGLAFLVFWLIVRPTK

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

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 113**

MS/MS Fragmentation of **NPYWFNR**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 13: 995.495594 from(996.502870,1+) intensity(0.0000) index(4)
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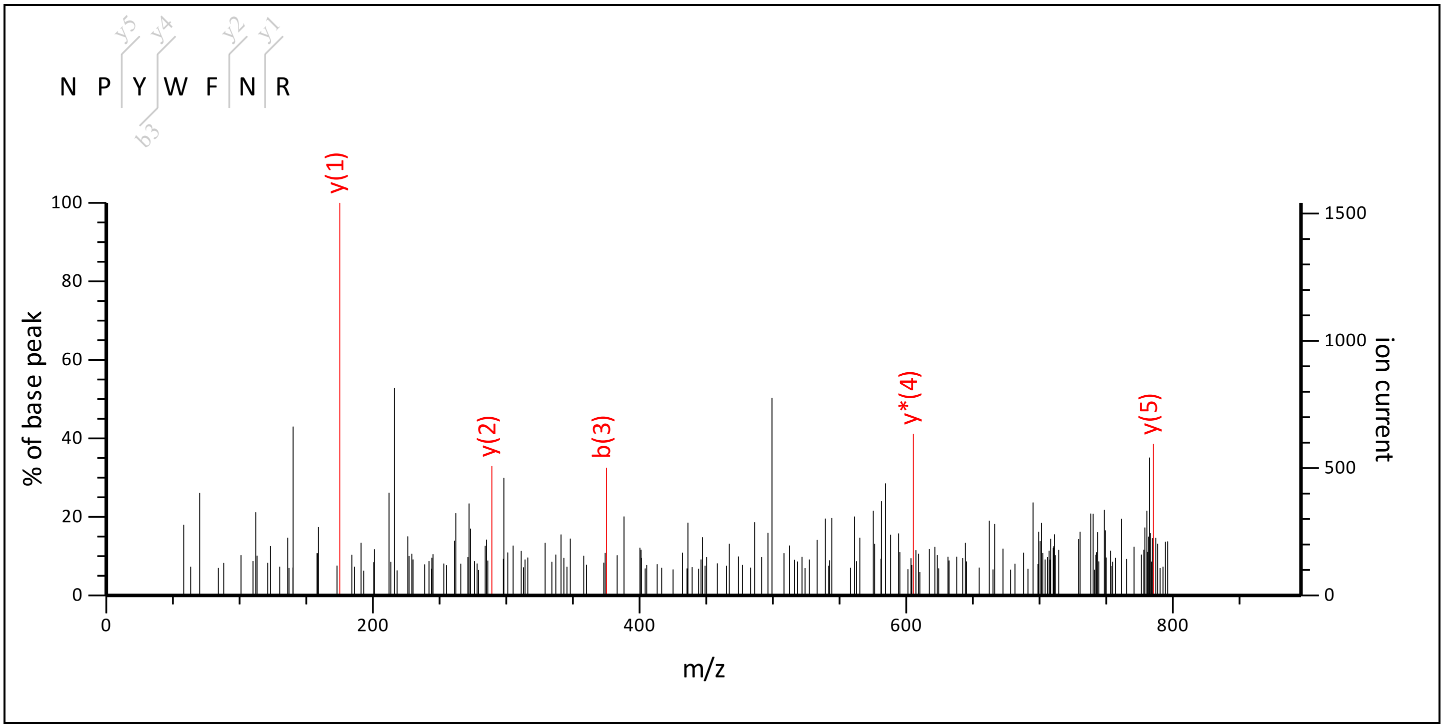


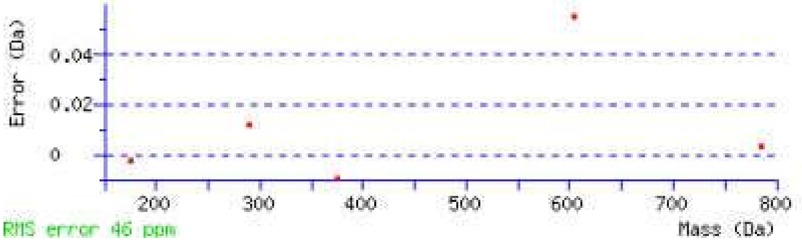
0 to 896.09

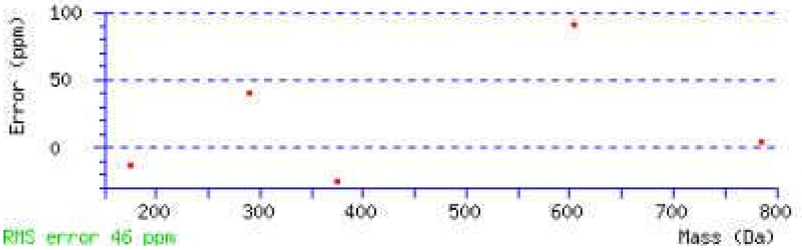
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 995.4613
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 13 **Expect:** 94
Matches : 5/74 fragment ions using 8 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	87.0553	87.0553	70.0287	115.0502	98.0237	44.0495	N					7
2	70.0651	184.1081	167.0815	212.1030	195.0764	158.0924	P	840.3787	839.3835	882.4257	865.3992	6
3	136.0757	347.1714	330.1448	**375.1663**	358.1397		Y	677.3154		***785.3729***	768.3464	5
4	159.0917	533.2507	516.2241	561.2456	544.2191		W	491.2361		622.3096	605.2831	4
5	120.0808	680.3191	663.2926	708.3140	691.2875		F	344.1677		436.2303	419.2037	3
6	87.0553	794.3620	777.3355	822.3569	805.3304	751.3562	N	230.1248	229.1295	***289.1619***	272.1353	2
7	129.1135						R	74.0237	73.0284	***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PY	233.1285	261.1234	**PYW**	419.2078	447.2027	**PYWF**	566.2762	594.2711
PYWFN	680.3191	708.3140	**YW**	322.1550	350.1499	**YWF**	469.2234	497.2183
YWFN	583.2663	611.2613	**WF**	306.1601	334.1550	**WFN**	420.2030	448.1979
FN	234.1237	262.1186						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.6	995.5625	-0.0669	TITHRVNR
15.2	995.5148	-0.0192	TLSRSYNR
13.1	995.4613	0.0343	NPYWFNR
12.0	995.5036	-0.0080	QSTFSATVR
11.9	995.4131	0.0825	CSSEPFNR
11.3	995.4825	0.0131	VGSGYPFNR
11.1	995.4971	-0.0015	MNLGGVHPR
11.0	995.4091	0.0865	GTGGSGTGSCR
10.9	995.4495	0.0461	GEIFNTCR
10.7	995.5036	-0.0080	TISSAFTNR

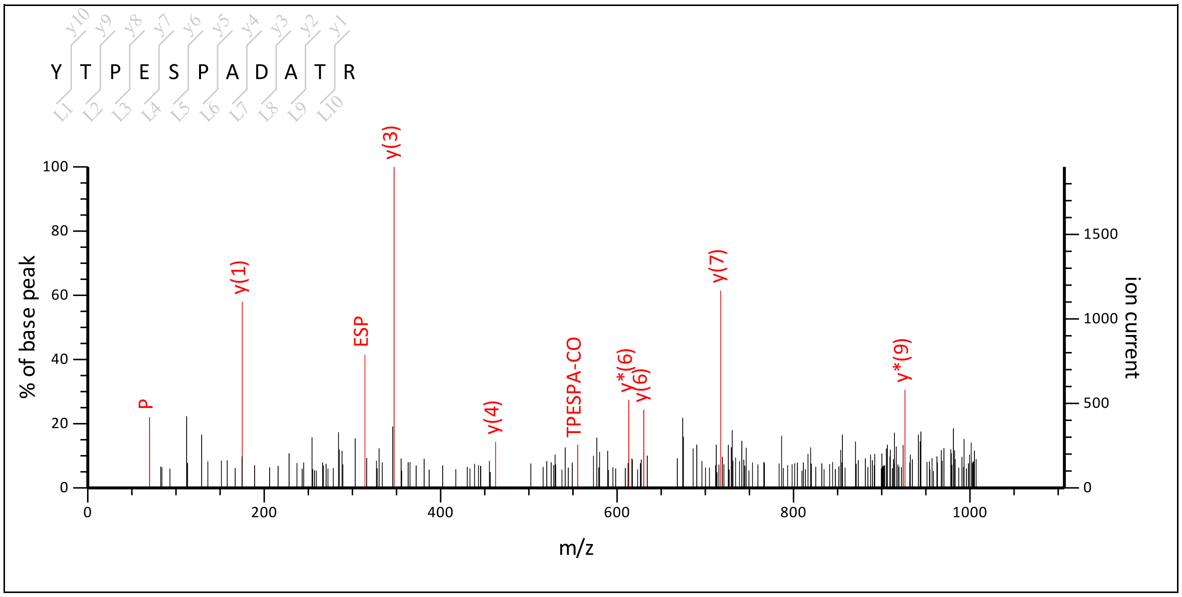
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 113

MS/MS Fragmentation of **YTPESPADATR**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 45: 1206.583424 from(1207.590700,1+) intensity(0.0000) index(13)
Title: Label: D1, Spot_Id: 219677, Peak_List_Id: 224868, MSMS Job_Run_Id: 21756, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D1_136842020900.txt



0 to 1107.02

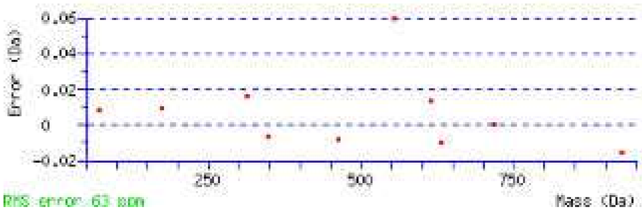
Label all possible matches ○ Label matches used for scoring ●

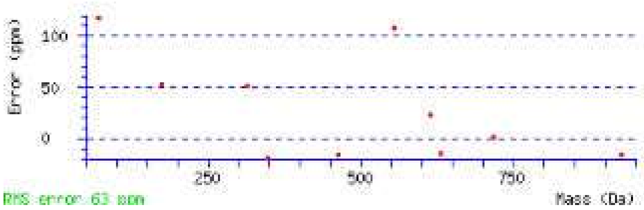
```
Monoisotopic mass of neutral peptide Mr(calc): 1206.5517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24  Expect: 9
Matches : 12/174 fragment ions using 20 most intense peaks   (help)
```

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	136.0757	136.0757		164.0706		44.0495		Y							11
2	74.0600	237.1234	219.1128	265.1183	247.1077	221.1285	223.1077	T	998.4538	1011.4742	1013.4534	1044.4956	1027.4691	1026.4851	10
3	70.0651	334.1761	316.1656	362.1710	344.1605	308.1605		P	901.4010	900.4058		943.4480	926.4214	925.4374	9
4	102.0550	463.2187	445.2082	491.2136	473.2031	405.2132		E	772.3584	771.3632		846.3952	829.3686	828.3846	8
5	60.0444	550.2508	532.2402	578.2457	560.2351	534.2558		S	685.3264	684.3311		***717.3526***	700.3260	699.3420	7
6	70.0651	647.3035	629.2930	675.2984	657.2879	621.2879		P	588.2736	587.2784		***630.3206***	613.2940	612.3100	6
7	44.0495	718.3406	700.3301	746.3355	728.3250			A	517.2365			533.2678	516.2413	515.2572	5
8	88.0393	833.3676	815.3570	861.3625	843.3519	789.3777		D	402.2096	401.2143		***462.2307***	445.2041	444.2201	4
9	44.0495	904.4047	886.3941	932.3996	914.3890			A	331.1724			***347.2037***	330.1772	329.1932	3
10	74.0600	1005.4524	987.4418	1033.4473	1015.4367	989.4575	991.4367	T	230.1248	243.1452	245.1244	276.1666	259.1401	258.1561	2
11	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPES**	387.1874	415.1823
TPESP	484.2402	512.2351	**TPESPA**	555.2773	583.2722	**TPESPAD**	670.3042	698.2992
PE	199.1077	227.1026	**PES**	286.1397	314.1347	**PESP**	383.1925	411.1874
PESPA	454.2296	482.2245	**PESPAD**	569.2566	597.2515	**PESPADA**	640.2937	668.2886
ES	189.0870	217.0819	**ESP**	286.1397	314.1347	**ESPA**	357.1769	385.1718

ESPAD	472.2038	500.1987	**ESPADA**	543.2409	571.2358	**ESPADAT**	644.2886	672.2835
SP	157.0972	185.0921	**SPA**	228.1343	256.1292	**SPAD**	343.1612	371.1561
SPADA	414.1983	442.1932	**SPADAT**	515.2460	543.2409	**PA**	141.1022	169.0972
PAD	256.1292	284.1241	**PADA**	327.1663	355.1612	**PADAT**	428.2140	456.2089
AD	159.0764	187.0713	**ADA**	230.1135	258.1084	**ADAT**	331.1612	359.1561
DA	159.0764	187.0713	**DAT**	260.1241	288.1190	**AT**	145.0972	173.0921





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.7	1206.5517	0.0318	YTPESPADATR
13.9	1206.5881	-0.0046	LLDAVFSDDGR
8.9	1206.6218	-0.0383	TNHHSVGKTAR
8.0	1206.6721	-0.0886	QVRASTSLAFK
7.9	1206.5153	0.0681	EWDDSIDATR
7.8	1206.6357	-0.0523	TFEIRTIGDR
7.8	1206.6357	-0.0523	TFELRTIGDR
7.5	1206.6244	-0.0410	EFLTQLEATR
7.5	1206.5014	0.0820	GHVHDEADGDR
7.5	1206.5485	0.0349	GMIQMIGGGGDR

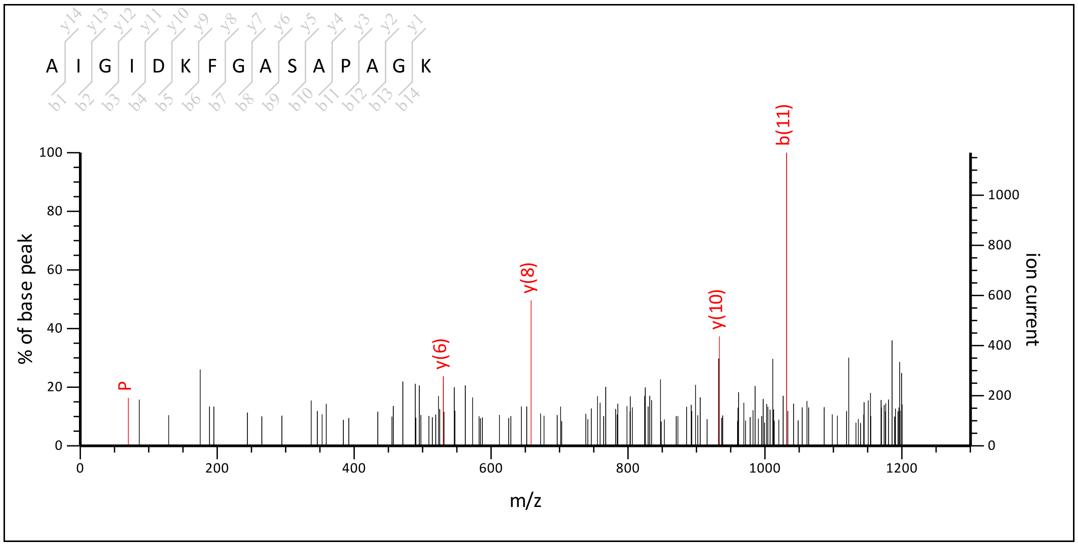
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 113

MS/MS Fragmentation of **AIGIDKFGASAPAGK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 68: 1401.770324 from(1402.777600,1+) intensity(0.0000) index(23)
Title: Label: D1, Spot_Id: 219677, Peak_List_Id: 224877, MSMS Job_Run_Id: 21756, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D1_136842020900.txt



0 to 1300.29

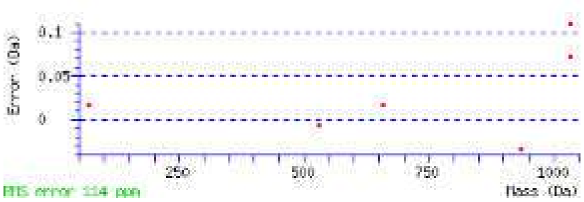
Label all possible matches ○ Label matches used for scoring ●

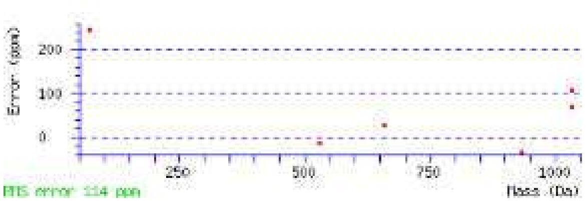
Monoisotopic mass of neutral peptide Mr(calc): 1401.7616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 5 **Expect:** 6e+02
Matches : 6/260 fragment ions using 12 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	86.0964	157.1335			185.1285			129.1022	143.1179	I	1273.6535	1286.6739	1300.6896	1331.7318	1314.7052
3	30.0338	214.1550			242.1499					G				1218.6477	1201.6212
4	86.0964	327.2391			355.2340			299.2078	313.2234	I	1103.5480	1116.5684	1130.5841	1161.6263	1144.5997
5	88.0393	442.2660		424.2554	470.2609		452.2504	398.2762		D	988.5211	987.5258		1048.5422	1031.5156
6	101.1073	570.3610	553.3344	552.3504	598.3559	581.3293	580.3453	513.3031		K	860.4261	859.4308		***933.5152***	916.4887
7	120.0808	717.4294	700.4028	699.4188	745.4243	728.3978	727.4137			F	713.3577			805.4203	788.3937
8	30.0338	774.4509	757.4243	756.4403	802.4458	785.4192	784.4352			G				***658.3519***	641.3253
9	44.0495	845.4880	828.4614	827.4774	873.4829	856.4563	855.4723			A	585.2991			601.3304	584.3039
10	60.0444	932.5200	915.4934	914.5094	960.5149	943.4884	942.5043	916.5251		S	498.2671	497.2718		***530.2933***	513.2667
11	44.0495	1003.5571	986.5306	985.5465	**1031.5520**	1014.5255	1013.5415			A	427.2300			443.2613	426.2347
12	70.0651	1100.6099	1083.5833	1082.5993	1128.6048	1111.5782	1110.5942	1074.5942		P	330.1772	329.1819		372.2241	355.1976
13	44.0495	1171.6470	1154.6204	1153.6364	1199.6419	1182.6154	1181.6313			A	259.1401			275.1714	258.1448
14	30.0338	1228.6684	1211.6419	1210.6579	1256.6634	1239.6368	1238.6528			G				204.1343	187.1077
15	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IG	143.1179	171.1128	IGI	256.2020	284.1969	IGID	371.2289	399.2238
IGIDK	499.3239	527.3188	IGIDKF	646.3923	674.3872	GI	143.1179	171.1128
GID	258.1448	286.1397	GIDK	386.2398	414.2347	GIDKF	533.3082	561.3031
GIDKFG	590.3297	618.3246	GIDKFGA	661.3668	689.3617	ID	201.1234	229.1183
IDK	329.2183	357.2132	IDKF	476.2867	504.2817	IDKFG	533.3082	561.3031
IDKFGA	604.3453	632.3402	IDKFGAS	691.3774	719.3723	DK	216.1343	244.1292

DKF	363.2027	391.1976	**DKFG**	420.2241	448.2191	**DKFGA**	491.2613	519.2562
DKFGAS	578.2933	606.2882	**DKFGASA**	649.3304	677.3253	**KF**	248.1757	276.1707
KFG	305.1972	333.1921	**KFGA**	376.2343	404.2292	**KFGAS**	463.2663	491.2613
KFGASA	534.3035	562.2984	**KFGASAP**	631.3562	659.3511	**FG**	177.1022	205.0972
FGA	248.1394	276.1343	**FGAS**	335.1714	363.1663	**FGASA**	406.2085	434.2034
FGASAP	503.2613	531.2562	**FGASAPA**	574.2984	602.2933	**FGASAPAG**	631.3198	659.3148
GA	101.0709	129.0659	**GAS**	188.1030	216.0979	**GASA**	259.1401	287.1350
GASAP	356.1928	384.1878	**GASAPA**	427.2300	455.2249	**GASAPAG**	484.2514	512.2463
AS	131.0815	159.0764	**ASA**	202.1186	230.1135	**ASAP**	299.1714	327.1663
ASAPA	370.2085	398.2034	**ASAPAG**	427.2300	455.2249	**SA**	131.0815	159.0764
SAP	228.1343	256.1292	**SAPA**	299.1714	327.1663	**SAPAG**	356.1928	384.1878
AP	141.1022	169.0972	**APA**	212.1394	240.1343	**APAG**	269.1608	297.1557
PA	141.1022	169.0972	**PAG**	198.1237	226.1186	**AG**	101.0709	129.0659





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
11.3	1401.7252	0.0451	KGWSASIDSVGPAK
7.2	1401.7326	0.0377	MEIPGVTFGVPAGK
6.9	1401.7034	0.0669	ILDRAMEVENGR
6.9	1401.6671	0.1033	GCGPGANTISIAER
6.2	1401.6848	0.0855	AQGDPSSTAAATVAR
5.9	1401.6671	0.1033	GCGPASASSVGLSPR
5.8	1401.6484	0.1219	GEANVGSGDSSPAVR
5.2	1401.7616	0.0087	TPQASAFAVELIR
5.2	1401.6381	0.1322	LHGALCDDMGLGK
5.1	1401.7616	0.0087	AIGIDKFGASAPAGK

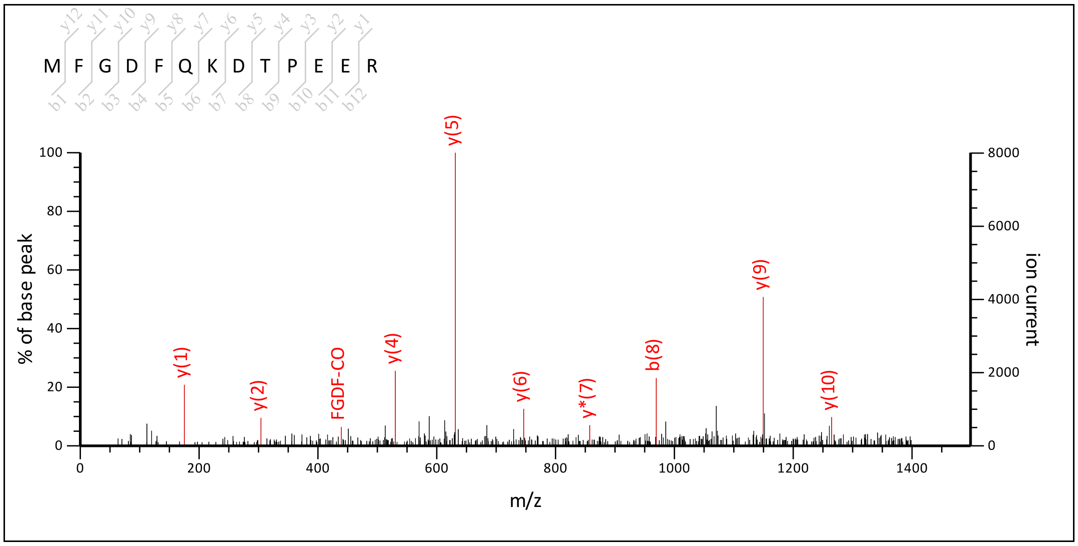
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 113

MS/MS Fragmentation of **MFGDFQKDTPEER**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 77: 1598.731824 from(1599.739100,1+) intensity(0.0000) index(26)
Title: Label: D1, Spot_Id: 219677, Peak_List_Id: 224863, MSMS Job_Run_Id: 21756, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D1_136842020900.txt



0 to 1498.45

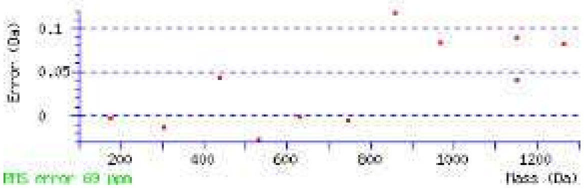
Label all possible matches ○ Label matches used for scoring ●

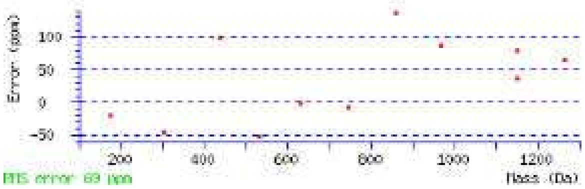
Monoisotopic mass of neutral peptide Mr(calc): `1598.7035`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `51` **Expect:** `0.012`
Matches : `11/210 fragment ions using 14 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	104.0528	104.0528			132.0478			44.0495		M						
2	120.0808	251.1213			279.1162					F	1376.6077			1468.6703	1451.6438	14
3	30.0338	308.1427			336.1376					G				1321.6019	1304.5753	13
4	88.0393	423.1697		405.1591	451.1646		433.1540	379.1798		D	1204.5593	1203.5640		***1264.5804***	1247.5539	12
5	120.0808	570.2381		552.2275	598.2330		580.2224			F	1057.4909			***1149.5535***	1132.5269	11
6	101.0709	698.2967	681.2701	680.2861	726.2916	709.2650	708.2810	641.2752		Q	929.4323	928.4371		1002.4851	985.4585	9
7	101.1073	826.3916	809.3651	808.3811	854.3865	837.3600	836.3760	769.3338		K	801.3373	800.3421		874.4265	857.3999	8
8	88.0393	941.4186	924.3920	923.4080	**969.4135**	952.3869	951.4029	897.4287		D	686.3104	685.3151		***746.3315***	729.3050	7
9	74.0600	1042.4662	1025.4397	1024.4557	1070.4612	1053.4346	1052.4506	1026.4713	1028.4506	T	585.2627	598.2831	600.2624	***631.3046***	614.2780	6
10	70.0651	1139.5190	1122.4925	1121.5084	1167.5139	1150.4874	1149.5034	1113.5034		P	488.2100	487.2147		***530.2569***	513.2304	5
11	102.0550	1268.5616	1251.5351	1250.5510	1296.5565	1279.5300	1278.5460	1210.5561		E	359.1674	358.1721		433.2041	416.1776	4
12	102.0550	1397.6042	1380.5776	1379.5936	1425.5991	1408.5726	1407.5885	1339.5987		E	230.1248	229.1295		***304.1615***	287.1350	2
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FG	177.1022	205.0972	FGD	292.1292	320.1241	FGDF	439.1976	467.1925
FGDFQ	567.2562	595.2511	FGDFQK	695.3511	723.3461	GD	145.0608	173.0557
GDF	292.1292	320.1241	GDFQ	420.1878	448.1827	GDFQK	548.2827	576.2776
GDFQKD	663.3097	691.3046	DF	235.1077	263.1026	DFQ	363.1663	391.1612
DFQK	491.2613	519.2562	DFQKD	606.2882	634.2831	FQ	248.1394	276.1343
FQK	376.2343	404.2292	FQKD	491.2613	519.2562	FQKDT	592.3089	620.3039
FQKDTP	689.3617	717.3566	QK	229.1659	257.1608	QKD	344.1928	372.1878
QKDT	445.2405	473.2354	QKDTP	542.2933	570.2882	QKDTPE	671.3359	699.3308

KD	216.1343	244.1292	**KDT**	317.1819	345.1769	**KDTP**	414.2347	442.2296
KDTPE	543.2773	571.2722	**KDTPEE**	672.3199	700.3148	**DT**	189.0870	217.0819
DTP	286.1397	314.1347	**DTPE**	415.1823	443.1773	**DTPEE**	544.2249	572.2198
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPEE**	429.1980	457.1929
PE	199.1077	227.1026	**PEE**	328.1503	356.1452	**EE**	231.0975	259.0925





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.5	1598.7035	0.0283	MFGDFQKDTPEER
14.8	1598.8879	-0.1561	EGKTLVILDDVLER
13.4	1598.7134	0.0184	LYSMEDVDEVVER
13.3	1598.7974	-0.0656	MSIDSPQDPVLLER
12.8	1598.7722	-0.0404	GAMVAHVSEDGEILR
12.3	1598.8165	-0.0847	SQDKAQHAFGLLER
11.6	1598.7909	-0.0591	MKPQGGSVAPICNPK
11.5	1598.8053	-0.0734	LSGSLLFHNTEPER
10.5	1598.7954	-0.0636	VFPWNNAPSGGGAIGR
9.5	1598.6990	0.0328	AMELIDEMEVTMR

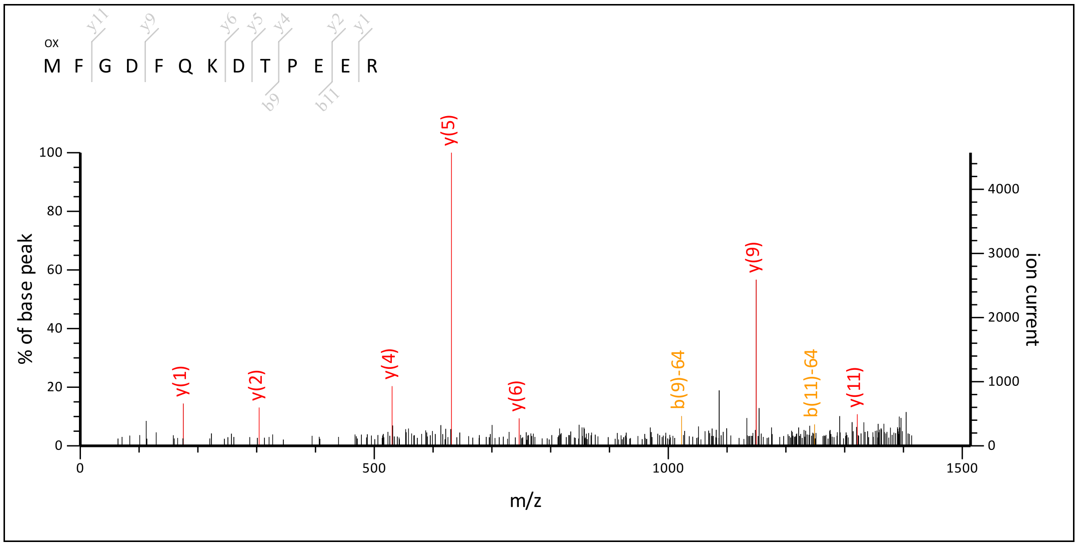
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 113

MS/MS Fragmentation of **MFGDFQKDTPEER**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 79: 1614.710724 from(1615.718000,1+) intensity(0.0000) index(27)
Title: Label: D1, Spot_Id: 219677, Peak_List_Id: 224862, MSMS Job_Run_Id: 21756, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D1_136842020900.txt



0 to 1514.04

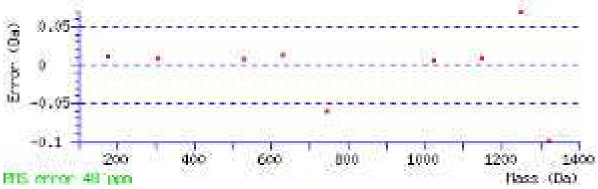
Label all possible matches ○ Label matches used for scoring ●

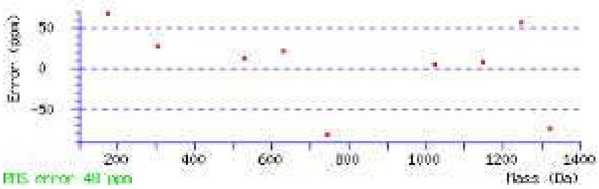
Monoisotopic mass of neutral peptide Mr(calc): 1614.6984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 47 **Expect:** 0.028
Matches : 9/276 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	56.0495	56.0495			84.0444			44.0495		M						
2	120.0808	203.1179			231.1128					F	1376.6077			1468.6703	1451.6438	145
3	30.0338	260.1394			288.1343					G				***1321.6019***	1304.5753	130
4	88.0393	375.1663		357.1557	403.1612		385.1506	331.1765		D	1204.5593	1203.5640		1264.5804	1247.5539	124
5	120.0808	522.2347		504.2241	550.2296		532.2191			F	1057.4909			***1149.5535***	1132.5269	113
6	101.0709	650.2933	633.2667	632.2827	678.2882	661.2617	660.2776	593.2718		Q	929.4323	928.4371		1002.4851	985.4585	98
7	101.1073	778.3883	761.3617	760.3777	806.3832	789.3566	788.3726	721.3304		K	801.3373	800.3421		874.4265	857.3999	85
8	88.0393	893.4152	876.3886	875.4046	921.4101	904.3836	903.3995	849.4254		D	686.3104	685.3151		***746.3315***	729.3050	72
9	74.0600	994.4629	977.4363	976.4523	**1022.4578**	1005.4312	1004.4472	978.4680	980.4472	T	585.2627	598.2831	600.2624	***631.3046***	614.2780	61
10	70.0651	1091.5156	1074.4891	1073.5051	1119.5106	1102.4840	1101.5000	1065.5000		P	488.2100	487.2147		***530.2569***	513.2304	51
11	102.0550	1220.5582	1203.5317	1202.5477	**1248.5531**	1231.5266	1230.5426	1162.5528		E	359.1674	358.1721		433.2041	416.1776	41
12	102.0550	1349.6008	1332.5743	1331.5903	1377.5957	1360.5692	1359.5852	1291.5953		E	230.1248	229.1295		***304.1615***	287.1350	28
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FG	177.1022	205.0972	FGD	292.1292	320.1241	FGDF	439.1976	467.1925
FGDFQ	567.2562	595.2511	FGDFQK	695.3511	723.3461	GD	145.0608	173.0557
GDF	292.1292	320.1241	GDFQ	420.1878	448.1827	GDFQK	548.2827	576.2776
GDFQKD	663.3097	691.3046	DF	235.1077	263.1026	DFQ	363.1663	391.1612
DFQK	491.2613	519.2562	DFQKD	606.2882	634.2831	FQ	248.1394	276.1343

FQK	376.2343	404.2292	**FQKD**	491.2613	519.2562	**FQKDT**	592.3089	620.3039
FQKDTP	689.3617	717.3566	**QK**	229.1659	257.1608	**QKD**	344.1928	372.1878
QKDT	445.2405	473.2354	**QKDTP**	542.2933	570.2882	**QKDTPE**	671.3359	699.3308
KD	216.1343	244.1292	**KDT**	317.1819	345.1769	**KDTP**	414.2347	442.2296
KDTPE	543.2773	571.2722	**KDTPEE**	672.3199	700.3148	**DT**	189.0870	217.0819
DTP	286.1397	314.1347	**DTPE**	415.1823	443.1773	**DTPEE**	544.2249	572.2198
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPEE**	429.1980	457.1929
PE	199.1077	227.1026	**PEE**	328.1503	356.1452	**EE**	231.0975	259.0925





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.2	1614.6984	0.0123	MFGDFQKDTPEER
40.6	1614.6984	0.0123	MYGDFQKDTPEER
25.2	1614.7242	-0.0135	MMRANTFTAQGAER
12.0	1614.8076	-0.0968	FGSEGSKIFMVLER
10.7	1614.7204	-0.0097	MFQKMEELCVER
10.4	1614.6885	0.0222	QVLAYALDXTXDER
10.3	1614.7083	0.0024	ESSEPESMTFTNLK
10.3	1614.7712	-0.0605	CFQEGLSYTIIER
10.2	1614.7599	-0.0492	SFFVEMDETIIER
10.2	1614.6879	0.0229	MMAQEHAHSSAVER

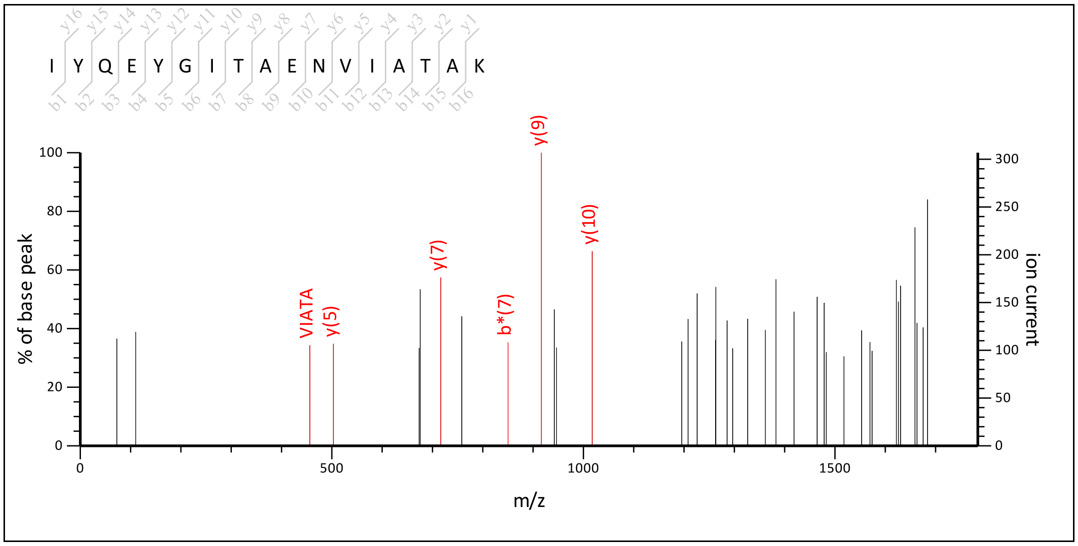
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 113**

MS/MS Fragmentation of **IYQEYGITAENVIATAK**
Found in **gi|28190676** in **NCBInr**, putative transketolase [Oryza sativa Japonica Group]

Match to Query 88: 1882.988524 from(1883.995800,1+) intensity(0.0000) index(30)
Title: Label: D1, Spot_Id: 219677, Peak_List_Id: 224891, MSMS Job_Run_Id: 21756, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_D1_136842020900.txt



0 to 1783.92

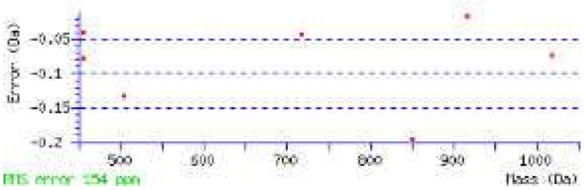
Label all possible matches ○ Label matches used for scoring ●

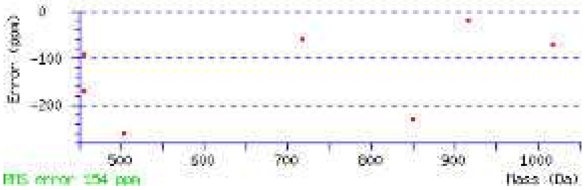
```
Monoisotopic mass of neutral peptide Mr(calc): 1882.9676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 10  Expect: 1.5e+02
Matches : 7/318 fragment ions using 13 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		I					
2	136.0757	249.1598			277.1547					Y	1662.8333			1770.8909	1753.8643
3	101.0709	377.2183	360.1918		405.2132	388.1867		320.1969		Q	1534.7748	1533.7795		1607.8275	1590.8010
4	102.0550	506.2609	489.2344	488.2504	534.2558	517.2293	516.2453	448.2554		E	1405.7322	1404.7369		1479.7690	1462.7424
5	136.0757	669.3243	652.2977	651.3137	697.3192	680.2926	679.3086			Y	1242.6688			1350.7264	1333.6998
6	30.0338	726.3457	709.3192	708.3352	754.3406	737.3141	736.3301			G				1187.6630	1170.6365
7	86.0964	839.4298	822.4032	821.4192	867.4247	850.3981	849.4141	811.3985	825.4141	I	1072.5633	1085.5837	1099.5994	1130.6416	1113.6150
8	74.0600	940.4775	923.4509	922.4669	968.4724	951.4458	950.4618	924.4825	926.4618	T	971.5156	984.5360	986.5153	***1017.5575***	1000.5310
9	44.0495	1011.5146	994.4880	993.5040	1039.5095	1022.4829	1021.4989			A	900.4785			***916.5098***	899.4833
10	102.0550	1140.5572	1123.5306	1122.5466	1168.5521	1151.5255	1150.5415	1082.5517		E	771.4359	770.4407		845.4727	828.4462
11	87.0553	1254.6001	1237.5735	1236.5895	1282.5950	1265.5685	1264.5844	1211.5943		N	657.3930	656.3978		***716.4301***	699.4036
12	72.0808	1353.6685	1336.6420	1335.6579	1381.6634	1364.6369	1363.6529	1339.6529		V	558.3246	571.3450		602.3872	585.3606
13	86.0964	1466.7526	1449.7260	1448.7420	1494.7475	1477.7209	1476.7369	1438.7213	1452.7369	I	445.2405	458.2609	472.2766	***503.3188***	486.2922
14	44.0495	1537.7897	1520.7631	1519.7791	1565.7846	1548.7581	1547.7740			A	374.2034			390.2347	373.2082
15	74.0600	1638.8374	1621.8108	1620.8268	1666.8323	1649.8057	1648.8217	1622.8425	1624.8217	T	273.1557	286.1761	288.1554	319.1976	302.1710
16	44.0495	1709.8745	1692.8479	1691.8639	1737.8694	1720.8428	1719.8588			A	202.1186			218.1499	201.1234
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YQ	264.1343	292.1292	YQE	393.1769	421.1718	YQEY	556.2402	584.2351
YQEYG	613.2617	641.2566	QE	230.1135	258.1084	QEY	393.1769	421.1718
QEYG	450.1983	478.1932	QEYGI	563.2824	591.2773	QEYGIT	664.3301	692.3250
EY	265.1183	293.1132	EYG	322.1397	350.1347	EYGI	435.2238	463.2187

EYGIT	536.2715	564.2664	**EYGITA**	607.3086	635.3035	**YG**	193.0972	221.0921
YGI	306.1812	334.1761	**YGIT**	407.2289	435.2238	**YGITA**	478.2660	506.2609
YGITAE	607.3086	635.3035	**GI**	143.1179	171.1128	**GIT**	244.1656	272.1605
GITA	315.2027	343.1976	**GITAE**	444.2453	472.2402	**GITAEN**	558.2882	586.2831
GITAENV	657.3566	685.3515	**IT**	187.1441	215.1390	**ITA**	258.1812	286.1761
ITAE	387.2238	415.2187	**ITAEN**	501.2667	529.2617	**ITAENV**	600.3352	628.3301
TA	145.0972	173.0921	**TAE**	274.1397	302.1347	**TAEN**	388.1827	416.1776
TAENV	487.2511	515.2460	**TAENVI**	600.3352	628.3301	**TAENVIA**	671.3723	699.3672
AE	173.0921	201.0870	**AEN**	287.1350	315.1299	**AENV**	386.2034	414.1983
AENVI	499.2875	527.2824	**AENVIA**	570.3246	598.3195	**AENVIAT**	671.3723	699.3672
EN	216.0979	244.0928	**ENV**	315.1663	343.1612	**ENVI**	428.2504	456.2453
ENVIA	499.2875	527.2824	**ENVIAT**	600.3352	628.3301	**ENVIATA**	671.3723	699.3672
NV	186.1237	214.1186	**NVI**	299.2078	327.2027	**NVIA**	370.2449	398.2398
NVIAT	471.2926	499.2875	**NVIATA**	542.3297	570.3246	**VI**	185.1648	213.1598
VIA	256.2020	284.1969	**VIAT**	357.2496	385.2445	**VIATA**	428.2867	456.2817
IA	157.1335	185.1285	**IAT**	258.1812	286.1761	**IATA**	329.2183	357.2132
AT	145.0972	173.0921	**ATA**	216.1343	244.1292	**TA**	145.0972	173.0921





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
10.4	1882.9676	0.0209	IYQEYGITAENVIATAK
10.4	1882.8730	0.1155	QIKNMIAETEQDYER
6.8	1883.0265	-0.0379	ISPTASGAALVSLKFEHR
2.2	1882.9135	0.0750	TVSVPMSLETYSWDLR
1.7	1882.8731	0.1154	NMAHGTSNSTTYTELLK
1.6	1883.0000	-0.0115	QGTLDPALATAEAGQTVIK
1.1	1883.0364	-0.0479	SLDSVVPVNGAALSEKLGK
0.7	1882.9346	0.0539	SILYQTMDISLVENNK
0.1	1882.9724	0.0162	LSAVCGGASFFERLLTR

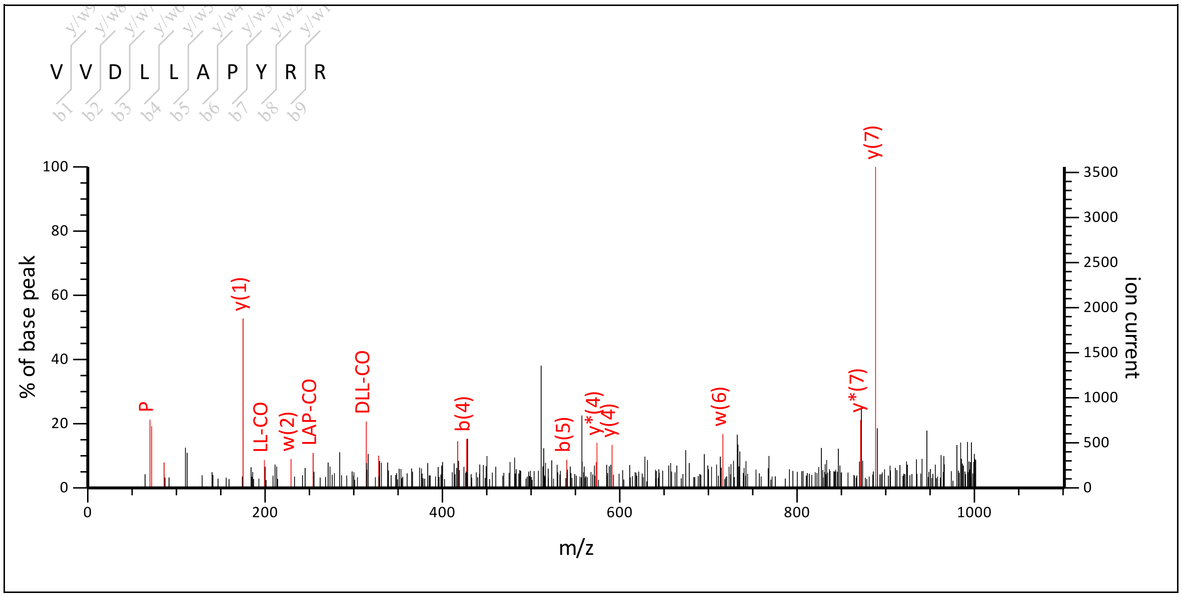
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **VVDLLAPYRR**
Found in **gi|11583** in **NCBInr**, ATPase, beta subunit [Hordeum vulgare]

Match to Query 127: 1200.726724 from(1201.734000,1+) intensity(0.0000) index(14)
Title: Label: I1, Spot_Id: 219682, Peak_List_Id: 225014, MSMS Job_Run_Id: 21761, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I1_136842037600.txt



0 to 1101.48

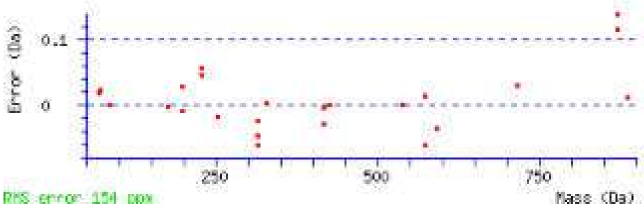
Label all possible matches ○ Label matches used for scoring ●

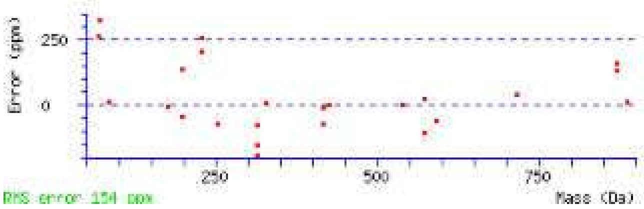
```
Monoisotopic mass of neutral peptide Mr(calc): 1200.6979
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15  Expect: 50
Matches : 27/136 fragment ions using 50 most intense peaks   (help)
```

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	Seq.	v	w	y	y*	y⁰	#
1	72.0808	72.0808			100.0757			44.0495	V						10
2	72.0808	171.1492			***199.1441***			157.1335	V	1058.5742	1071.5946	1102.6368	1085.6102	1084.6262	9
3	88.0393	286.1761		268.1656	***314.1710***		296.1605	242.1863	D	943.5472	942.5520	1003.5683	986.5418	985.5578	8
4	86.0964	399.2602		381.2496	***427.2551***		409.2445	357.2132	L	830.4631	829.4679	***888.5414***	871.5148		7
5	86.0964	512.3443		494.3337	***540.3392***		522.3286	470.2973	L	717.3791	716.3838	775.4573	758.4308		6
6	44.0495	583.3814		565.3708	611.3763		593.3657		A	646.3420		662.3733	645.3467		5
7	70.0651	680.4341		662.4236	708.4291		690.4185	654.4185	P	549.2892	548.2940	***591.3362***	574.3096		4
8	136.0757	843.4975		825.4869	***871.4924***		853.4818		Y	386.2259		494.2834	477.2568		3
9	129.1135	999.5986	982.5720	981.5880	1027.5935	1010.5669	1009.5829	914.5346	R	230.1248	229.1295	331.2201	314.1935		2
10	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VD	187.1077	215.1026	VDL	300.1918	328.1867	VDLL	413.2758	441.2708
VDLLA	484.3130	512.3079	VDLLAP	581.3657	609.3606	DL	201.1234	229.1183
DLL	314.2074	342.2023	DLLA	385.2445	413.2395	DLLAP	482.2973	510.2922
DLLAPY	645.3606	673.3556	LL	199.1805	227.1754	LLA	270.2176	298.2125
LLAP	367.2704	395.2653	LLAPY	530.3337	558.3286	LLAPYR	686.4348	714.4297
LA	157.1335	185.1285	LAP	254.1863	282.1812	LAPY	417.2496	445.2445

LAPYR	573.3507	601.3457	**AP**	141.1022	169.0972	**APY**	304.1656	332.1605
APYR	460.2667	488.2616	**PY**	233.1285	261.1234	**PYR**	389.2296	417.2245
YR	292.1768	320.1717						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.4	1200.6979	0.0288	VVDILAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.4	1200.6979	0.0288	VVDLLAPYRR
15.3	1200.6211	0.1056	QAVTNAQNTVR

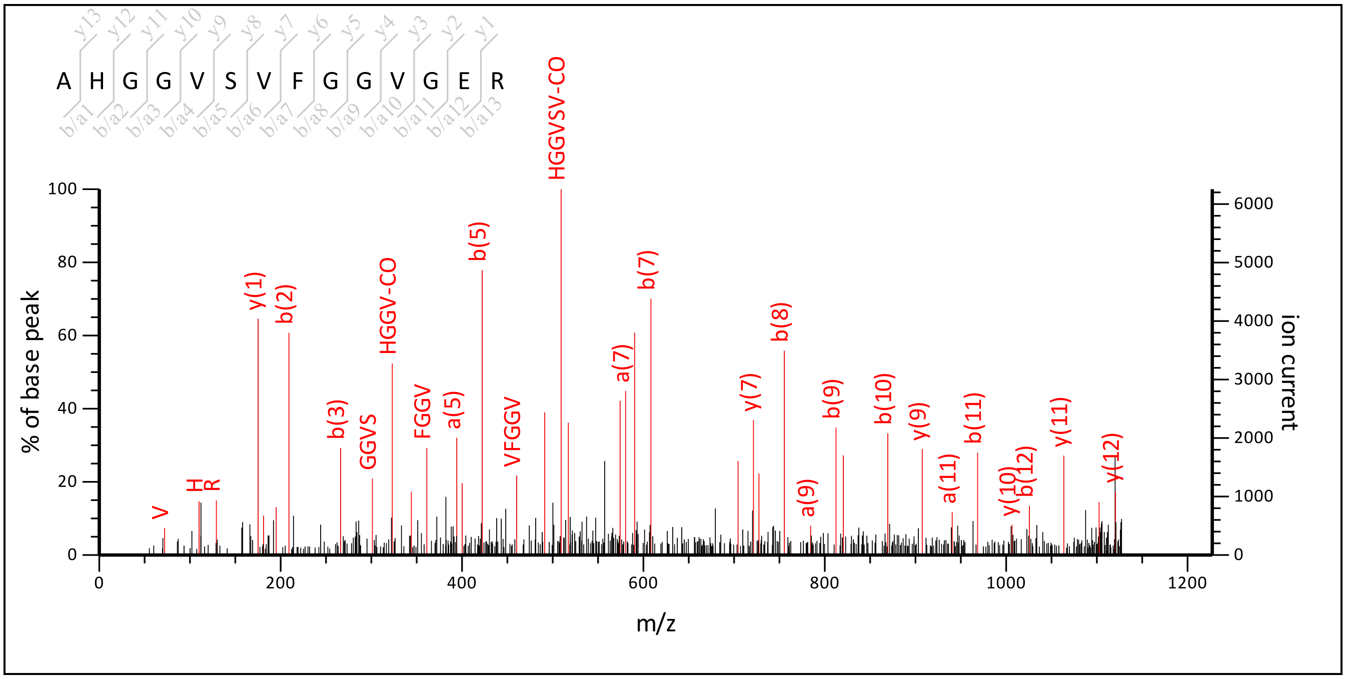
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 114**

MS/MS Fragmentation of **AHGGVSVFGGVGER**
Found in **gi|11583** in **NCBInr**, ATPase, beta subunit [Hordeum vulgare]

Match to Query 156: 1327.698024 from(1328.705300,1+) intensity(0.0000) index(16)
Title: Label: I1, Spot_Id: 219682, Peak_List_Id: 225009, MSMS Job_Run_Id: 21761, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I1_136842037600.txt



0 to 1227.25

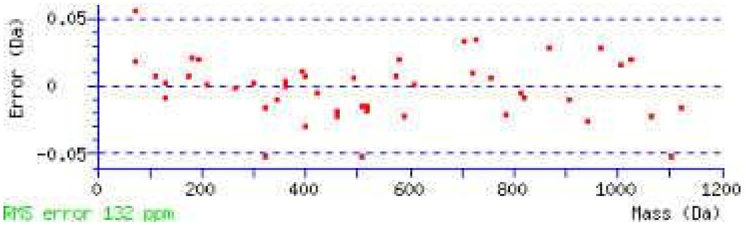
Label all possible matches ○ Label matches used for scoring ●

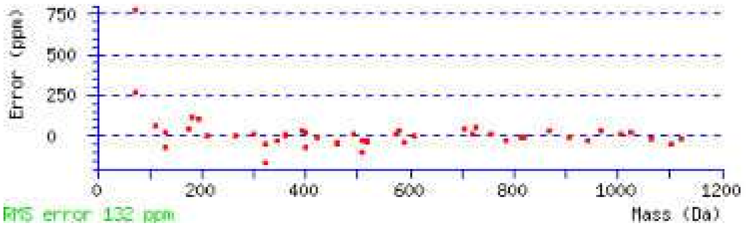
Monoisotopic mass of neutral peptide Mr(calc): 1327.6633
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 124 **Expect:** 8.7e-10
Matches : 52/220 fragment ions using 44 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		***72.0444***		44.0495	A						14
2	110.0713	**181.1084**		***209.1033***			H	1175.5804		1257.6335	1240.6069	1239.6229	13
3	30.0338	238.1299		***266.1248***			G			***1120.5745***	1103.5480	1102.5640	12
4	30.0338	295.1513		***323.1462***			G			***1063.5531***	1046.5265	1045.5425	11
5	72.0808	**394.2197**		***422.2146***		380.2041	V	962.4690	975.4894	***1006.5316***	989.5051	988.5211	10
6	60.0444	481.2518	463.2412	***509.2467***	491.2361	465.2568	S	875.4370	874.4417	***907.4632***	890.4367	889.4526	9
7	72.0808	**580.3202**	562.3096	***608.3151***	590.3045	566.3045	V	776.3686	789.3890	***820.4312***	803.4046	802.4206	8
8	120.0808	**727.3886**	709.3780	***755.3835***	737.3729		F	629.3002		***721.3628***	704.3362	703.3522	7
9	30.0338	**784.4100**	766.3995	***812.4050***	794.3944		G			***574.2944***	557.2678	556.2838	6
10	30.0338	841.4315	823.4209	***869.4264***	851.4159		G			***517.2729***	500.2463	499.2623	5
11	72.0808	**940.4999**	922.4894	***968.4948***	950.4843	926.4843	V	416.1888	429.2092	***460.2514***	443.2249	442.2409	4

12	30.0338	997.5214	979.5108	***1025.5163***	1007.5057		G			***361.1830***	344.1565	343.1724	3
13	102.0550	1126.5640	1108.5534	1154.5589	1136.5483	1068.5585	E	230.1248	229.1295	304.1615	287.1350	286.1510	2
14	129.1135						R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HG	167.0927	195.0877	HGG	224.1142	252.1091	HGGV	323.1826	351.1775
HGGVS	410.2146	438.2096	HGGVSV	509.2831	537.2780	HGGVSVF	656.3515	684.3464
GG	87.0553	115.0502	GGV	186.1237	214.1186	GGVS	273.1557	301.1506
GGVSV	372.2241	400.2191	GGVSVF	519.2926	547.2875	GGVSVFG	576.3140	604.3089
GGVSVFGG	633.3355	661.3304	GV	129.1022	157.0972	GVS	216.1343	244.1292
GVSV	315.2027	343.1976	GVSVF	462.2711	490.2660	GVSVFG	519.2926	547.2875
GVSVFGG	576.3140	604.3089	GVSVFGGV	675.3824	703.3774	VS	159.1128	187.1077
VSV	258.1812	286.1761	VSVF	405.2496	433.2445	VSVFG	462.2711	490.2660
VSVFGG	519.2926	547.2875	VSVFGGV	618.3610	646.3559	VSVFGGVG	675.3824	703.3774
SV	159.1128	187.1077	SVF	306.1812	334.1761	SVFG	363.2027	391.1976
SVFGG	420.2241	448.2191	SVFGGV	519.2926	547.2875	SVFGGVG	576.3140	604.3089
VF	219.1492	247.1441	VFG	276.1707	304.1656	VFGG	333.1921	361.1870
VFGGV	432.2605	460.2554	VFGGVG	489.2820	517.2769	VFGGVGE	618.3246	646.3195
FG	177.1022	205.0972	FGG	234.1237	262.1186	FGGV	333.1921	361.1870
FGGVG	390.2136	418.2085	FGGVGE	519.2562	547.2511	GG	87.0553	115.0502
GGV	186.1237	214.1186	GGVG	243.1452	271.1401	GGVGE	372.1878	400.1827
GV	129.1022	157.0972	GVG	186.1237	214.1186	GVGE	315.1663	343.1612
VG	129.1022	157.0972	VGE	258.1448	286.1397	GE	159.0764	187.0713





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER

124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER
124.2	1327.6633	0.0347	AHGGVSVFGGVGER

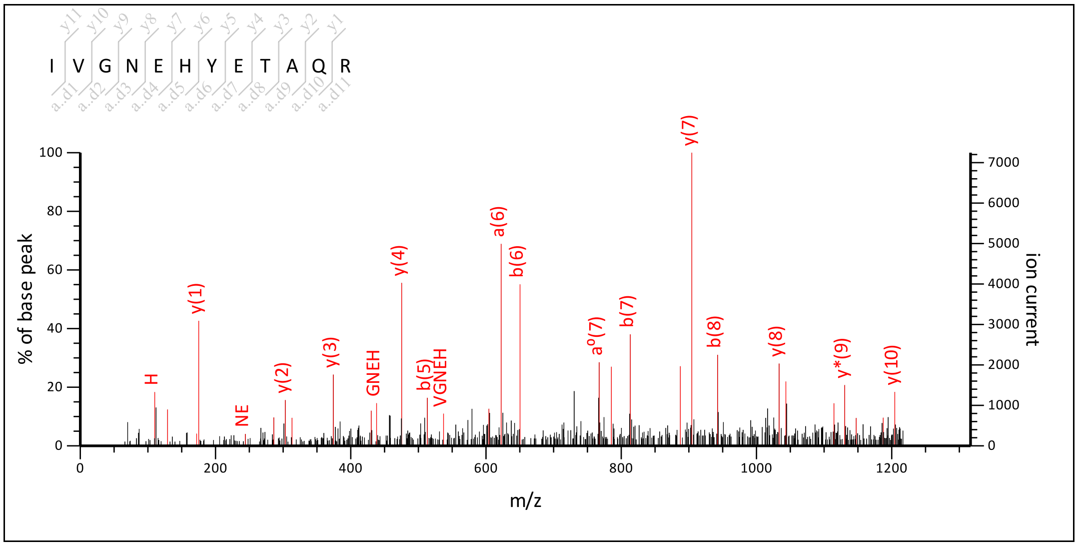
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **IVGNEHYETAQR**
Found in **gi|11583** in **NCBInr**, ATPase, beta subunit [Hordeum vulgare]

Match to Query 175: 1415.721924 from(1416.729200,1+) intensity(0.0000) index(18)
Title: Label: I1, Spot_Id: 219682, Peak_List_Id: 225010, MSMS Job_Run_Id: 21761, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I1_136842037600.txt



0 to 1316.55

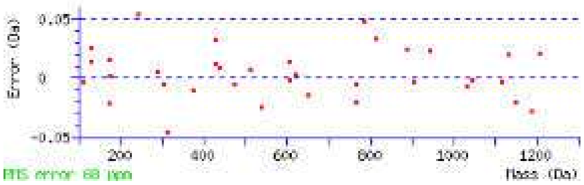
Label all possible matches ○ Label matches used for scoring ●

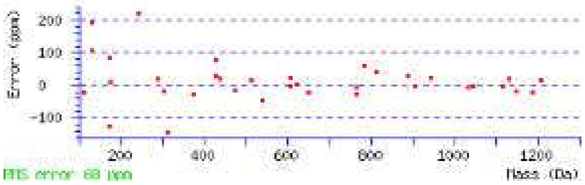
Monoisotopic mass of neutral peptide Mr(calc): 1415.6793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 93 **Expect:** 1.1e-06
Matches : 36/181 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		**I**					
2	72.0808	185.1648			213.1598			171.1492		**V**	1259.5400	1272.5604		1303.6026	1286.5760
3	30.0338	242.1863			270.1812					**G**				***1204.5341***	1187.5076
4	87.0553	356.2292	339.2027		384.2241	367.1976		313.2234		**N**	1088.4756	1087.4803		***1147.5127***	1130.4861
5	102.0550	485.2718	468.2453	467.2613	**513.2667**	496.2402	495.2562	427.2663		**E**	959.4330	958.4377		***1033.4697***	1016.4432
6	110.0713	**622.3307**	605.3042	604.3202	**650.3256**	633.2991	632.3151			**H**	822.3741			***904.4272***	887.4006
7	136.0757	**785.3941**	768.3675	767.3835	**813.3890**	796.3624	795.3784			**Y**	659.3107			***767.3682***	750.3417
8	102.0550	914.4367	897.4101	896.4261	**942.4316**	925.4050	924.4210	856.4312		**E**	530.2681	529.2729		***604.3049***	587.2784
9	74.0600	1015.4843	998.4578	997.4738	**1043.4793**	1026.4527	1025.4687	999.4894	1001.4687	**T**	429.2205	442.2409	444.2201	***475.2623***	458.2358
10	44.0495	1086.5214	1069.4949	1068.5109	**1114.5164**	1097.4898	1096.5058			**A**	358.1833			***374.2146***	357.1881
11	101.0709	1214.5800	1197.5535	1196.5695	1242.5749	1225.5484	1224.5644	1157.5586		**Q**	230.1248	229.1295		***303.1775***	286.1510
12	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VG	129.1022	157.0972	**VGN**	243.1452	271.1401	**VGNE**	372.1878	400.1827
VGNEH	509.2467	537.2416	**VGNEHY**	672.3100	700.3049	**GN**	144.0768	172.0717
GNE	273.1193	301.1143	**GNEH**	410.1783	438.1732	**GNEHY**	573.2416	601.2365
NE	216.0979	244.0928	**NEH**	353.1568	381.1517	**NEHY**	516.2201	544.2150
NEHYE	645.2627	673.2576	**EH**	239.1139	267.1088	**EHY**	402.1772	430.1721
EHYE	531.2198	559.2147	**EHYET**	632.2675	660.2624	**HY**	273.1346	301.1295
HYE	402.1772	430.1721	**HYET**	503.2249	531.2198	**HYETA**	574.2620	602.2569
YE	265.1183	293.1132	**YET**	366.1660	394.1609	**YETA**	437.2031	465.1980
YETAQ	565.2617	593.2566	**ET**	203.1026	231.0975	**ETA**	274.1397	302.1347

ETAQ	402.1983	430.1932	**TA**	145.0972	173.0921	**TAQ**	273.1557	301.1506
AQ	172.1081	200.1030						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
92.6	1415.6793	0.0426	IVGNEHYETAQR
92.6	1415.6793	0.0426	IVGNEHYETAQR
76.7	1415.7157	0.0062	IVGDKHYETAQR
76.7	1415.7157	0.0062	IVGDKHYETAQR
76.7	1415.6793	0.0426	IVGDQHYETAQR
76.7	1415.6793	0.0426	IVGENHYETAQR
76.7	1415.6793	0.0426	IVGENHYETAQR
76.7	1415.7157	0.0062	IVGKDHYETAQR
76.7	1415.7157	0.0062	IVGKDHYETAQR
27.4	1415.7157	0.0062	IVGDEHYKTAQR

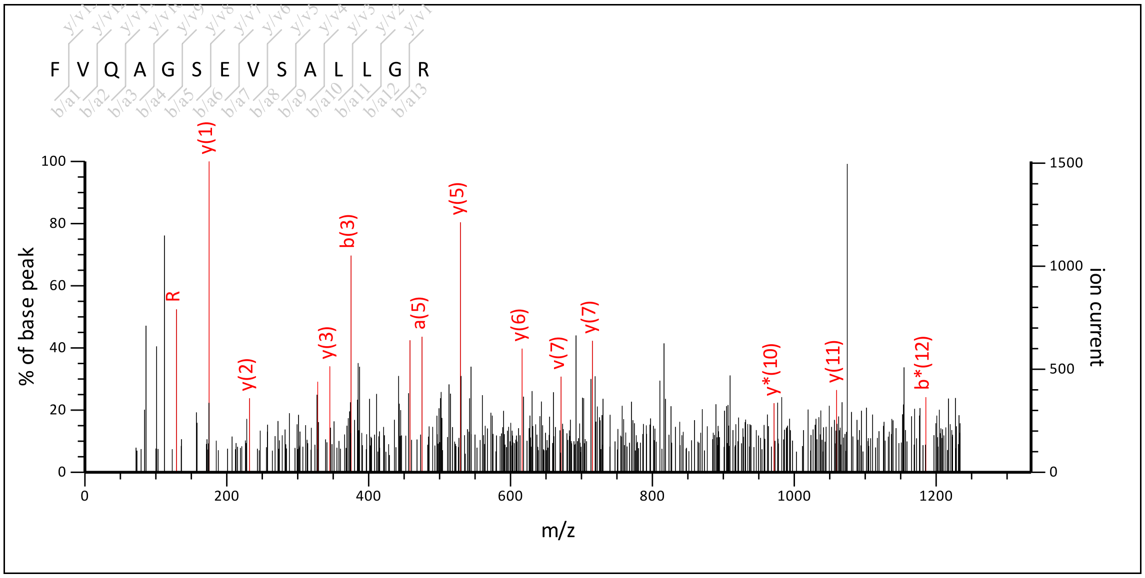
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **FVQAGSEVSALLGR**
Found in **gi|11583** in **NCBInr**, ATPase, beta subunit [Hordeum vulgare]

Match to Query 181: 1432.815824 from(1433.823100,1+) intensity(0.0000) index(19)
Title: Label: I1, Spot_Id: 219682, Peak_List_Id: 225016, MSMS Job_Run_Id: 21761, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I1_136842037600.txt



0 to 1333.81

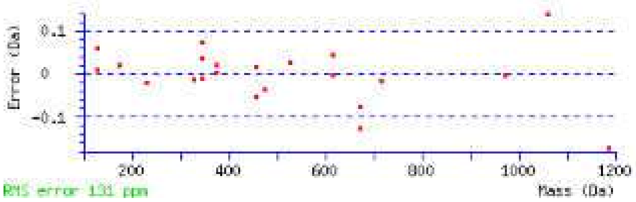
Label all possible matches ○ Label matches used for scoring ●

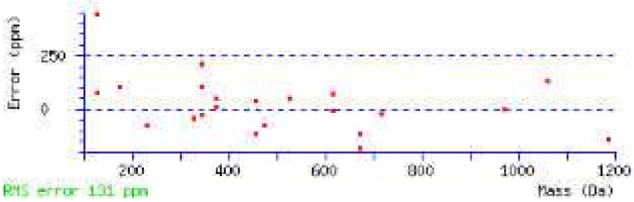
Monoisotopic mass of neutral peptide Mr(calc): 1432.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.037
Matches : 23/243 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	120.0808	120.0808			148.0757			44.0495	**F**						**14**
2	72.0808	219.1492			247.1441			205.1335	**V**	1242.6437	1255.6641	1286.7063	1269.6797	1268.6957	**13**
3	101.0709	347.2078	330.1812		375.2027	358.1761		290.1863	**Q**	1114.5851	1113.5899	1187.6379	1170.6113	1169.6273	**12**
4	44.0495	418.2449	401.2183		446.2398	429.2132			**A**	1043.5480		***1059.5793***	1042.5527	1041.5687	**11**
5	30.0338	475.2663	458.2398		503.2613	486.2347			**G**			988.5422	971.5156	970.5316	**10**
6	60.0444	562.2984	545.2718	544.2878	590.2933	573.2667	572.2827	546.3035	**S**	899.4945	898.4993	931.5207	914.4942	913.5102	**9**
7	102.0550	691.3410	674.3144	673.3304	719.3359	702.3093	701.3253	633.3355	**E**	770.4519	769.4567	844.4887	827.4621	826.4781	**8**
8	72.0808	790.4094	773.3828	772.3988	818.4043	801.3777	800.3937	776.3937	**V**	671.3835	684.4039	***715.4461***	698.4196	697.4355	**7**
9	60.0444	877.4414	860.4149	859.4308	905.4363	888.4098	887.4258	861.4465	**S**	584.3515	583.3562	***616.3777***	599.3511	598.3671	**6**
10	44.0495	948.4785	931.4520	930.4680	976.4734	959.4469	958.4629		**A**	513.3144		***529.3457***	512.3191		**5**
11	86.0964	1061.5626	1044.5360	1043.5520	1089.5575	1072.5310	1071.5469	1019.5156	**L**	400.2303	399.2350	***458.3085***	441.2820		**4**
12	86.0964	1174.6466	1157.6201	1156.6361	1202.6416	1185.6150	1184.6310	1132.5997	**L**	287.1462	286.1510	***345.2245***	328.1979		**3**
13	30.0338	1231.6681	1214.6416	1213.6575	1259.6630	1242.6365	1241.6525		**G**			***232.1404***	215.1139		**2**
14	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VQ	200.1394	228.1343	**VQA**	271.1765	299.1714	**VQAG**	328.1979	356.1928
VQAGS	415.2300	443.2249	**VQAGSE**	544.2726	572.2675	**VQAGSEV**	643.3410	671.3359
QA	172.1081	200.1030	**QAG**	229.1295	257.1244	**QAGS**	316.1615	344.1565
QAGSE	445.2041	473.1991	**QAGSEV**	544.2726	572.2675	**QAGSEVS**	631.3046	659.2995

AG	101.0709	129.0659	**AGS**	188.1030	216.0979	**AGSE**	317.1456	345.1405
AGSEV	416.2140	444.2089	**AGSEVS**	503.2460	531.2409	**AGSEVSA**	574.2831	602.2780
AGSEVSAL	687.3672	715.3621	**GS**	117.0659	145.0608	**GSE**	246.1084	274.1034
GSEV	345.1769	373.1718	**GSEVS**	432.2089	460.2038	**GSEVSA**	503.2460	531.2409
GSEVSAL	616.3301	644.3250	**SE**	189.0870	217.0819	**SEV**	288.1554	316.1503
SEVS	375.1874	403.1823	**SEVSA**	446.2245	474.2195	**SEVSAL**	559.3086	587.3035
SEVSALL	672.3927	700.3876	**EV**	201.1234	229.1183	**EVS**	288.1554	316.1503
EVSA	359.1925	387.1874	**EVSAL**	472.2766	500.2715	**EVSALL**	585.3606	613.3556
EVSALLG	642.3821	670.3770	**VS**	159.1128	187.1077	**VSA**	230.1499	258.1448
VSAL	343.2340	371.2289	**VSALL**	456.3180	484.3130	**VSALLG**	513.3395	541.3344
SA	131.0815	159.0764	**SAL**	244.1656	272.1605	**SALL**	357.2496	385.2445
SALLG	414.2711	442.2660	**AL**	157.1335	185.1285	**ALL**	270.2176	298.2125
ALLG	327.2391	355.2340	**LL**	199.1805	227.1754	**LLG**	256.2020	284.1969
LG	143.1179	171.1128						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.4	1432.7674	0.0484	FVQAGSEVSAILGR
47.4	1432.7674	0.0484	FVQAGSEVSALIGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR
47.4	1432.7674	0.0484	FVQAGSEVSALLGR

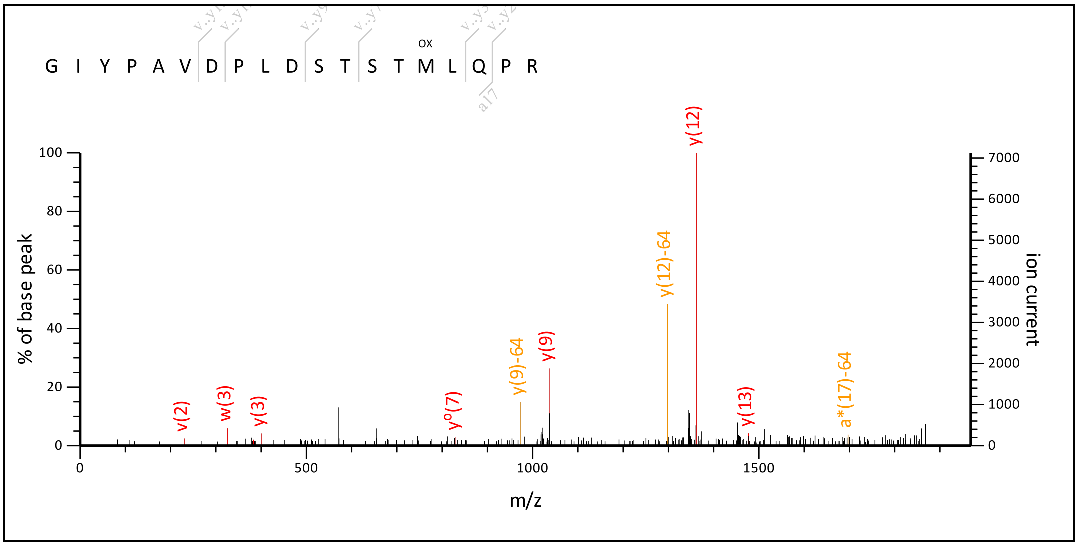
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **GIYPAVDPLDSTSTMLQPR**
Found in **gi|11583** in **NCBInr**, ATPase, beta subunit [Hordeum vulgare]

Match to Query 232: 2076.058624 from(2077.065900,1+) intensity(0.0000) index(31)
Title: Label: I1, Spot_Id: 219682, Peak_List_Id: 225028, MSMS Job_Run_Id: 21761, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I1_136842037600.txt



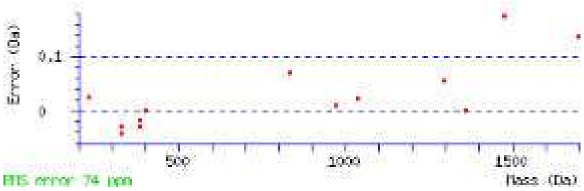
0 to 1968.07

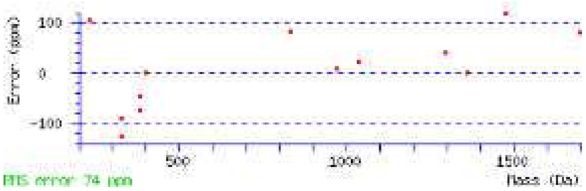
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2076.0198
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M15     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 2  Expect: 9.9e+02
Matches : 15/459 fragment ions using 36 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			115.0866	129.1022	I	1961.9273	1974.9477	1988.9634	2020.0056	2002.9790
3	136.0757	306.1812			334.1761					Y	1798.8640			1906.9215	1889.8950
4	70.0651	403.2340			431.2289			377.2183		P	1701.8112	1700.8160		1743.8582	1726.8316
5	44.0495	474.2711			502.2660					A	1630.7741			1646.8054	1629.7789
6	72.0808	573.3395			601.3344			559.3239		V	1531.7057	1544.7261		1575.7683	1558.7418
7	88.0393	688.3665		670.3559	716.3614		698.3508	644.3766		D	1416.6788	1415.6835		***1476.6999***	1459.6733
8	70.0651	785.4192		767.4087	813.4141		795.4036	759.4036		P	1319.6260	1318.6307		***1361.6729***	1344.6464
9	86.0964	898.5033		880.4927	926.4982		908.4876	856.4563		L	1206.5419	1205.5467		1264.6202	1247.5936
10	88.0393	1013.5302		995.5197	1041.5251		1023.5146	969.5404		D	1091.5150	1090.5197		1151.5361	1134.5096
11	60.0444	1100.5623		1082.5517	1128.5572		1110.5466	1084.5673		S	1004.4830	1003.4877		***1036.5092***	1019.4826
12	74.0600	1201.6099		1183.5994	1229.6048		1211.5943	1185.6150	1187.5943	T	903.4353	916.4557	918.4349	949.4771	932.4506
13	60.0444	1288.6420		1270.6314	1316.6369		1298.6263	1272.6470		S	816.4033	815.4080		848.4295	831.4029
14	74.0600	1389.6896		1371.6791	1417.6846		1399.6740	1373.6947	1375.6740	T	715.3556	728.3760	730.3552	761.3974	744.3709
15	120.0478	1536.7250		1518.7145	1564.7200		1546.7094	1460.7268		M	568.3202	567.3249		660.3498	643.3232
16	86.0964	1649.8091		1631.7985	1677.8040		1659.7935	1607.7622		L	455.2361	454.2409		513.3144	496.2878
17	101.0709	1777.8677	1760.8411	1759.8571	1805.8626	1788.8360	1787.8520	1720.8462		Q	327.1775	326.1823		***400.2303***	383.2037
18	70.0651	1874.9204	1857.8939	1856.9099	1902.9154	1885.8888	1884.9048	1848.9048		P	230.1248	229.1295		272.1717	255.1452
19	129.1135									R	74.0237	73.0284		175.1190	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IY	249.1598	277.1547	**IYP**	346.2125	374.2074	**IYPA**	417.2496	445.2445
IYPAV	516.3180	544.3130	**IYPAVD**	631.3450	659.3399	**YP**	233.1285	261.1234
YPA	304.1656	332.1605	**YPAV**	403.2340	431.2289	**YPAVD**	518.2609	546.2558
YPAVDP	615.3137	643.3086	**PA**	141.1022	169.0972	**PAV**	240.1707	268.1656
PAVD	355.1976	383.1925	**PAVDP**	452.2504	480.2453	**PAVDPL**	565.3344	593.3293
PAVDPLD	680.3614	708.3563	**AV**	143.1179	171.1128	**AVD**	258.1448	286.1397
AVDP	355.1976	383.1925	**AVDPL**	468.2817	496.2766	**AVDPLD**	583.3086	611.3035
AVDPLDS	670.3406	698.3355	**VD**	187.1077	215.1026	**VDP**	284.1605	312.1554
VDPL	397.2445	425.2395	**VDPLD**	512.2715	540.2664	**VDPLDS**	599.3035	627.2984
DP	185.0921	213.0870	**DPL**	298.1761	326.1710	**DPLD**	413.2031	441.1980
DPLDS	500.2351	528.2300	**DPLDST**	601.2828	629.2777	**DPLDSTS**	688.3148	716.3097
PL	183.1492	211.1441	**PLD**	298.1761	326.1710	**PLDS**	385.2082	413.2031
PLDST	486.2558	514.2508	**PLDSTS**	573.2879	601.2828	**PLDSTST**	674.3355	702.3305
LD	201.1234	229.1183	**LDS**	288.1554	316.1503	**LDST**	389.2031	417.1980
LDSTS	476.2351	504.2300	**LDSTST**	577.2828	605.2777	**DS**	175.0713	203.0662
DST	276.1190	304.1139	**DSTS**	363.1510	391.1460	**DSTST**	464.1987	492.1936
DSTSTM	611.2341	639.2290	**ST**	161.0921	189.0870	**STS**	248.1241	276.1190
STST	349.1718	377.1667	**STSTM**	496.2072	524.2021	**STSTML**	609.2912	637.2862
TS	161.0921	189.0870	**TST**	262.1397	290.1347	**TSTM**	409.1751	437.1701
TSTML	522.2592	550.2541	**TSTMLQ**	650.3178	678.3127	**ST**	161.0921	189.0870
STM	308.1275	336.1224	**STML**	421.2115	449.2064	**STMLQ**	549.2701	577.2650
STMLQP	646.3229	674.3178	**TM**	221.0954	249.0904	**TML**	334.1795	362.1744
TMLQ	462.2381	490.2330	**TMLQP**	559.2908	587.2858	**ML**	233.1318	261.1267
MLQ	361.1904	389.1853	**MLQP**	458.2432	486.2381	**LQ**	214.1550	242.1499
LQP	311.2078	339.2027	**QP**	198.1237	226.1186			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
3.9	2076.0595	-0.0009	TQRMILTQEEMEEVVLK
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMIQPR
2.0	2076.0561	0.0025	GIYPAVDPLDSTSTMLKPR
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMLQPR
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMLQPR
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMLQPR
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMLQPR
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMLQPR
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMLQPR
2.0	2076.0198	0.0389	GIYPAVDPLDSTSTMLQPR

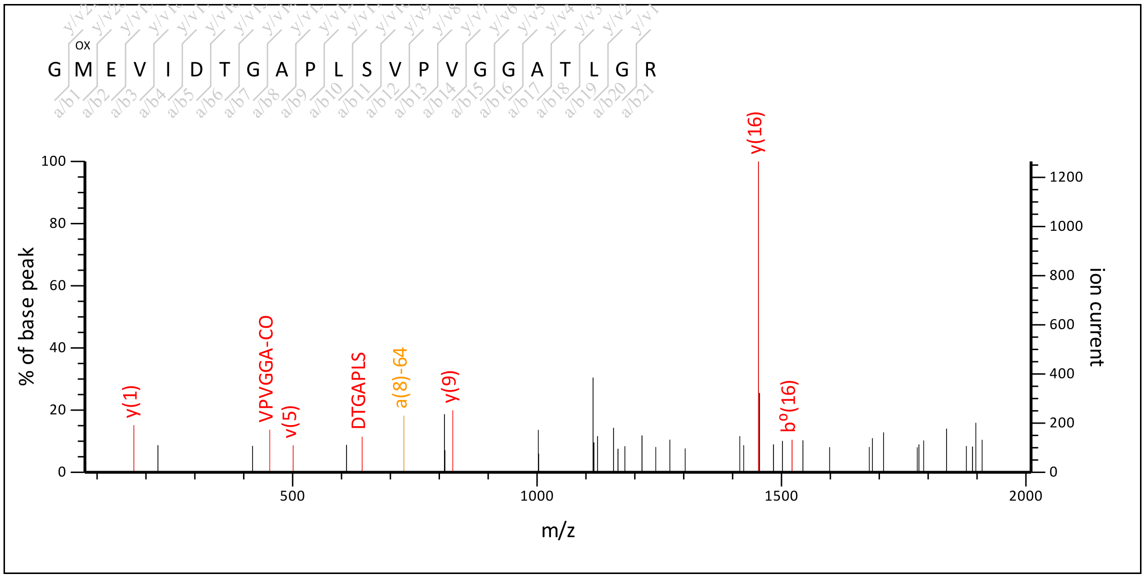
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **GMEVIDTGAPLSVPVGGATLGR**
Found in **gi|11583** in **NCBInr**, ATPase, beta subunit [Hordeum vulgare]

Match to Query 234: 2112.123324 from(2113.130600,1+) intensity(0.0000) index(32)
Title: Label: I1, Spot_Id: 219682, Peak_List_Id: 225041, MSMS Job_Run_Id: 21761, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_I1_136842037600.txt



75.13 to 2010.5

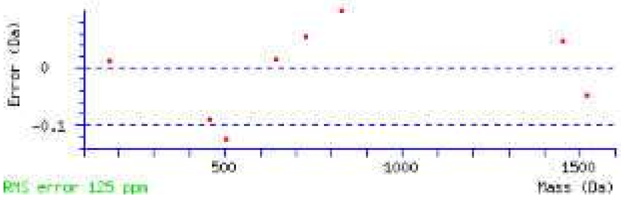
Label all possible matches ○ Label matches used for scoring ●

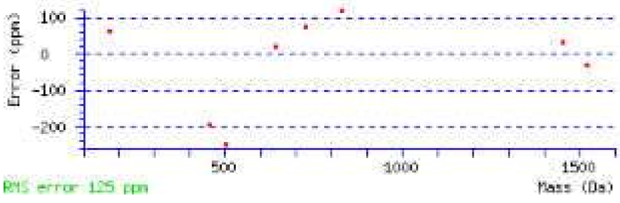
Monoisotopic mass of neutral peptide Mr(calc): 2112.0885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 3 **Expect:** 6.6e+02
Matches : 8/535 fragment ions using 16 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	30.0338	30.0338		58.0287		44.0495		G							22
2	56.0495	113.0709		141.0659		101.0709		M	1964.0447	1963.0495		1992.0760	1975.0495	1974.0655	21
3	102.0550	242.1135	224.1030	270.1084	252.0979	184.1081		E	1835.0021	1834.0069		1909.0389	1892.0124	1891.0284	20
4	72.0808	341.1819	323.1714	369.1769	351.1663	327.1663		V	1735.9337	1748.9541		1779.9963	1762.9698	1761.9858	19
5	86.0964	454.2660	436.2554	482.2609	464.2504	426.2347	440.2504	I	1622.8497	1635.8701	1649.8857	1680.9279	1663.9014	1662.9173	18
6	88.0393	569.2930	551.2824	597.2879	579.2773	525.3031		D	1507.8227	1506.8275		1567.8438	1550.8173	1549.8333	17
7	74.0600	670.3406	652.3301	698.3355	680.3250	654.3457	656.3250	T	1406.7750	1419.7954	1421.7747	***1452.8169***	1435.7904	1434.8063	16
8	30.0338	727.3621	709.3515	755.3570	737.3464			G				1351.7692	1334.7427	1333.7587	15
9	44.0495	798.3992	780.3886	826.3941	808.3836			A	1278.7165			1294.7478	1277.7212	1276.7372	14
10	70.0651	895.4520	877.4414	923.4469	905.4363	869.4363		P	1181.6637	1180.6684		1223.7106	1206.6841	1205.7001	13
11	86.0964	1008.5360	990.5255	1036.5310	1018.5204	966.4891		L	1068.5796	1067.5844		1126.6579	1109.6313	1108.6473	12
12	60.0444	1095.5681	1077.5575	1123.5630	1105.5524	1079.5732		S	981.5476	980.5524		1013.5738	996.5473	995.5633	11
13	72.0808	1194.6365	1176.6259	1222.6314	1204.6208	1180.6208		V	882.4792	895.4996		926.5418	909.5152	908.5312	10
14	70.0651	1291.6892	1273.6787	1319.6842	1301.6736	1265.6736		P	785.4264	784.4312		*827.4734*	810.4468	809.4628	9
15	72.0808	1390.7577	1372.7471	1418.7526	1400.7420	1376.7420		V	686.3580	699.3784		730.4206	713.3941	712.4100	8
16	30.0338	1447.7791	1429.7686	1475.7740	1457.7635			G				631.3522	614.3257	613.3416	7
17	30.0338	1504.8006	1486.7900	1532.7955	1514.7849			G				574.3307	557.3042	556.3202	6

18	44.0495	1575.8377	1557.8271	1603.8326	1585.8221			A	501.2780			517.3093	500.2827	499.2987	5
19	74.0600	1676.8854	1658.8748	1704.8803	1686.8697	1660.8905	1662.8697	T	400.2303	413.2507	415.2300	446.2722	429.2456	428.2616	4
20	86.0964	1789.9694	1771.9589	1817.9644	1799.9538	1747.9225		L	287.1462	286.1510		345.2245	328.1979		3
21	30.0338	1846.9909	1828.9803	1874.9858	1856.9753			G				232.1404	215.1139		2
22	129.1135							R	74.0237	73.0284		*175.1190*	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ME	185.0921	213.0870	MEV	284.1605	312.1554	MEVI	397.2445	425.2395
MEVID	512.2715	540.2664	MEVIDT	613.3192	641.3141	MEVIDTG	670.3406	698.3355
EV	201.1234	229.1183	EVI	314.2074	342.2023	EVID	429.2344	457.2293
EVIDT	530.2821	558.2770	EVIDTG	587.3035	615.2984	EVIDTGA	658.3406	686.3355
VI	185.1648	213.1598	VID	300.1918	328.1867	VIDT	401.2395	429.2344
VIDTG	458.2609	486.2558	VIDTGA	529.2980	557.2930	VIDTGAP	626.3508	654.3457
ID	201.1234	229.1183	IDT	302.1710	330.1660	IDTG	359.1925	387.1874
IDTGA	430.2296	458.2245	IDTGAP	527.2824	555.2773	IDTGAPL	640.3665	668.3614
DT	189.0870	217.0819	DTG	246.1084	274.1034	DTGA	317.1456	345.1405
DTGAP	414.1983	442.1932	DTGAPL	527.2824	555.2773	DTGAPLS	614.3144	642.3093
TG	131.0815	159.0764	TGA	202.1186	230.1135	TGAP	299.1714	327.1663
TGAPL	412.2554	440.2504	TGAPLS	499.2875	527.2824	TGAPLSV	598.3559	626.3508
TGAPLSVP	695.4087	723.4036	GA	101.0709	129.0659	GAP	198.1237	226.1186
GAPL	311.2078	339.2027	GAPLS	398.2398	426.2347	GAPLSV	497.3082	525.3031
GAPLSVP	594.3610	622.3559	GAPLSVPV	693.4294	721.4243	AP	141.1022	169.0972
APL	254.1863	282.1812	APLS	341.2183	369.2132	APLSV	440.2867	468.2817
APLSVP	537.3395	565.3344	APLSVPV	636.4079	664.4028	APLSVPVG	693.4294	721.4243
PL	183.1492	211.1441	PLS	270.1812	298.1761	PLSV	369.2496	397.2445
PLSVP	466.3024	494.2973	PLSVPV	565.3708	593.3657	PLSVPVG	622.3923	650.3872
PLSVPVGG	679.4137	707.4087	LS	173.1285	201.1234	LSV	272.1969	300.1918
LSVP	369.2496	397.2445	LSVPV	468.3180	496.3130	LSVPVG	525.3395	553.3344
LSVPVGG	582.3610	610.3559	LSVPVGGA	653.3981	681.3930	SV	159.1128	187.1077
SVP	256.1656	284.1605	SVPV	355.2340	383.2289	SVPVG	412.2554	440.2504
SVPVGG	469.2769	497.2718	SVPVGGA	540.3140	568.3089	SVPVGGAT	641.3617	669.3566
VP	169.1335	197.1285	VPV	268.2020	296.1969	VPVG	325.2234	353.2183
VPVGG	382.2449	410.2398	VPVGGA	453.2820	481.2769	VPVGGAT	554.3297	582.3246
VPVGGATL	667.4137	695.4087	PV	169.1335	197.1285	PVG	226.1550	254.1499
PVGG	283.1765	311.1714	PVGGA	354.2136	382.2085	PVGGAT	455.2613	483.2562
PVGGATL	568.3453	596.3402	PVGGATLG	625.3668	653.3617	VG	129.1022	157.0972
VGG	186.1237	214.1186	VGGA	257.1608	285.1557	VGGAT	358.2085	386.2034
VGGATL	471.2926	499.2875	VGGATLG	528.3140	556.3089	GG	87.0553	115.0502
GGA	158.0924	186.0873	GGAT	259.1401	287.1350	GGATL	372.2241	400.2191
GGATLG	429.2456	457.2405	GA	101.0709	129.0659	GAT	202.1186	230.1135
GATL	315.2027	343.1976	GATLG	372.2241	400.2191	AT	145.0972	173.0921
ATL	258.1812	286.1761	ATLG	315.2027	343.1976	TL	187.1441	215.1390
TLG	244.1656	272.1605	LG	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
6.2	2112.0819	0.0414	EMGAQKPQIQNPTAIMIAR
5.2	2111.9793	0.1440	SSTSNDMFQLIQQLTEDR
3.4	2112.0885	0.0348	GMEVIDTGAPISVPVGGATLGR
3.4	2112.0885	0.0348	GMEVIDTGAPISVPVGGATLGR
3.4	2112.0885	0.0348	GMEVIDTGAPISVPVGGATLGR
3.4	2112.0885	0.0348	GMEVIDTGAPISVPVGGATLGR
3.4	2112.0885	0.0348	GMEVIDTGAPLSVPVGGATIGR
3.4	2112.0885	0.0348	GMEVIDTGAPLSVPVGGATLGR
3.4	2112.0885	0.0348	GMEVIDTGAPLSVPVGGATLGR
3.4	2112.0885	0.0348	GMEVIDTGAPLSVPVGGATLGR

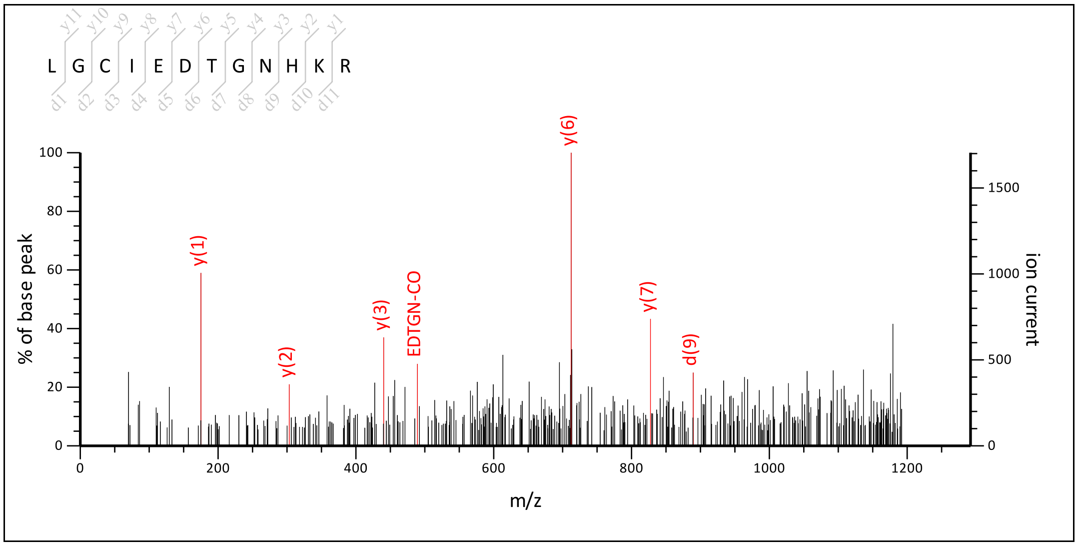
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 116

MS/MS Fragmentation of **LGCIEDTGNHKR**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 38: 1398.791424 from(1399.798700,1+) intensity(0.0000) index(13)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226016, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



0 to 1291.96

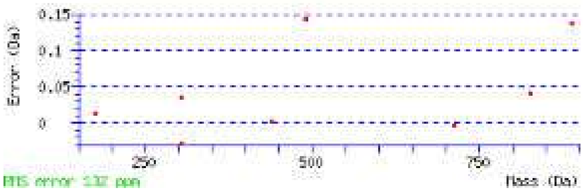
Label all possible matches ○ Label matches used for scoring ●

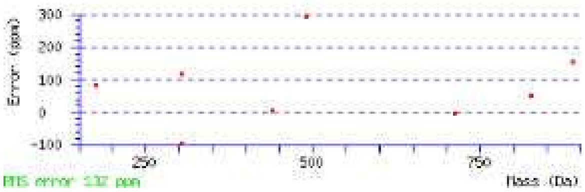
Monoisotopic mass of neutral peptide Mr(calc): 1398.6674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 1e+02
Matches : 9/181 fragment ions using 12 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	86.0964	86.0964			114.0913			44.0495		L						
2	30.0338	143.1179			171.1128					G				1286.5906	1269.5641	12
3	133.0430	**303.1485**			331.1435			214.1550		C	1124.5443	1123.5491		1229.5691	1212.5426	12
4	86.0964	416.2326			444.2275			388.2013	402.2170	I	1011.4602	1024.4806	1038.4963	1069.5385	1052.5119	10
5	102.0550	545.2752		527.2646	573.2701		555.2595	487.2697		E	882.4177	881.4224		956.4544	939.4279	9
6	88.0393	660.3021		642.2916	688.2971		670.2865	616.3123		D	767.3907	766.3955		***827.4118***	810.3853	8
7	74.0600	761.3498		743.3393	789.3447		771.3342	745.3549	747.3342	T	666.3430	679.3634	681.3427	***712.3849***	695.3583	6
8	30.0338	818.3713		800.3607	846.3662		828.3556			G				611.3372	594.3107	
9	87.0553	932.4142	915.3877	914.4036	960.4091	943.3826	942.3986	889.4084		N	495.2786	494.2834		554.3158	537.2892	
10	110.0713	1069.4731	1052.4466	1051.4626	1097.4680	1080.4415	1079.4575			H	358.2197			***440.2728***	423.2463	
11	101.1073	1197.5681	1180.5415	1179.5575	1225.5630	1208.5364	1207.5524	1140.5102		K	230.1248	229.1295		***303.2139***	286.1874	
12	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GC	190.0645	218.0594	GCI	303.1485	331.1435	GCIE	432.1911	460.1860
GCIED	547.2181	575.2130	GCIEDT	648.2658	676.2607	CI	246.1271	274.1220
CIE	375.1697	403.1646	CIED	490.1966	518.1915	CIEDT	591.2443	619.2392
CIEDTG	648.2658	676.2607	IE	215.1390	243.1339	IED	330.1660	358.1609
IEDT	431.2136	459.2086	IEDTG	488.2351	516.2300	IEDTGN	602.2780	630.2729
ED	217.0819	245.0768	EDT	318.1296	346.1245	EDTG	375.1510	403.1460
EDTGN	489.1940	517.1889	EDTGNH	626.2529	654.2478	DT	189.0870	217.0819
DTG	246.1084	274.1034	DTGN	360.1514	388.1463	DTGNH	497.2103	525.2052
DTGNHK	625.3052	653.3002	TG	131.0815	159.0764	TGN	245.1244	273.1193

TGNH	382.1833	410.1783	**TGNHK**	510.2783	538.2732	**GN**	144.0768	172.0717
GNH	281.1357	309.1306	**GNHK**	409.2306	437.2255	**NH**	224.1142	252.1091
NHK	352.2092	380.2041	**HK**	238.1662	266.1612			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.1	1398.7078	0.0836	MDVQVPSGPWKR
25.3	1398.6674	0.1240	LGCIEDTGNHKR
22.3	1398.6640	0.1274	LWSDADSGAGHKR
22.2	1398.6537	0.1378	GRPMMDVYFQR
16.3	1398.8194	-0.0280	KASALAAVDTLIAR
15.8	1398.7467	0.0447	GITEATDPVAAAKR
14.8	1398.6852	0.1063	DETQVGVDPRAGR
14.8	1398.8380	-0.0466	ITMINNAILLKR
14.4	1398.6852	0.1063	AGTTSAGQLGEHVR
14.2	1398.7467	0.0447	SLERSDVDLPLR

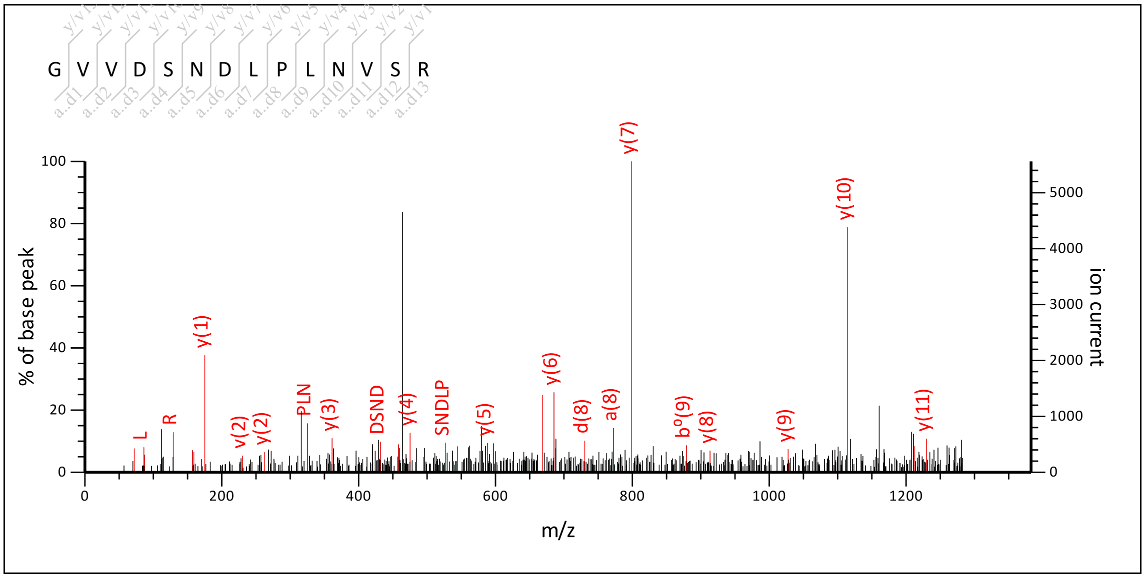
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 116

MS/MS Fragmentation of **GVVDSNDLPLNVSR**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 46: 1483.886124 from(1484.893400,1+) intensity(0.0000) index(16)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226005, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



0 to 1382.65

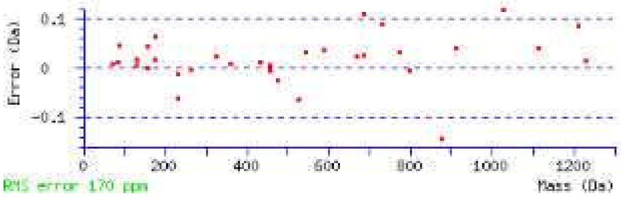
Label all possible matches ○ Label matches used for scoring ●

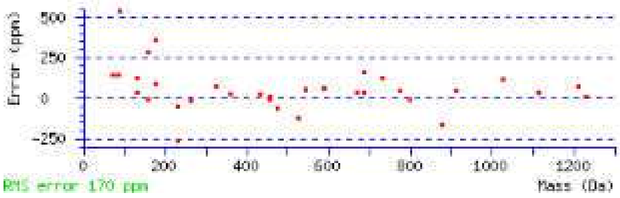
Monoisotopic mass of neutral peptide Mr(calc): 1483.7631
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 0.022
Matches : 39/243 fragment ions using 65 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	30.0338	30.0338			58.0287			44.0495	G						14
2	72.0808	**129.1022**			**157.0972**			115.0866	V	1383.6863	1396.7067	1427.7489	1410.7223	1409.7383	13
3	72.0808	228.1707			256.1656			214.1550	V	1284.6179	1297.6383	1328.6805	1311.6539	1310.6699	12
4	88.0393	343.1976		325.1870	371.1925		353.1819	299.2078	D	1169.5909	1168.5957	***1229.6121***	1212.5855	1211.6015	11
5	60.0444	430.2296		412.2191	**458.2245**		440.2140	414.2347	S	1082.5589	1081.5636	***1114.5851***	1097.5586	1096.5745	10
6	87.0553	**544.2726**	527.2460	526.2620	572.2675	555.2409	554.2569	501.2667	N	968.5160	967.5207	***1027.5531***	1010.5265	1009.5425	9
7	88.0393	659.2995	642.2729	641.2889	**687.2944**	670.2679	669.2838	615.3097	D	853.4890	852.4938	***913.5102***	896.4836	895.4996	8
8	86.0964	**772.3836**	755.3570	754.3730	800.3785	783.3519	782.3679	730.3366	L	740.4050	739.4097	***798.4832***	781.4567	780.4726	7
9	70.0651	869.4363	852.4098	851.4258	897.4312	880.4047	879.4207	843.4207	P	643.3522	642.3570	***685.3991***	668.3726	667.3886	6
10	86.0964	982.5204	965.4938	964.5098	1010.5153	993.4888	992.5047	940.4734	L	530.2681	529.2729	***588.3464***	571.3198	570.3358	5
11	87.0553	1096.5633	1079.5368	1078.5527	1124.5582	1107.5317	1106.5477	1053.5575	N	416.2252	415.2300	***475.2623***	458.2358	457.2518	4
12	72.0808	1195.6317	1178.6052	1177.6212	1223.6266	1206.6001	1205.6161	1181.6161	V	317.1568	330.1772	***361.2194***	344.1928	343.2088	3
13	60.0444	1282.6638	1265.6372	1264.6532	1310.6587	1293.6321	1292.6481	1266.6688	S	230.1248	229.1295	***262.1510***	245.1244	244.1404	2
14	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VV	171.1492	199.1441	VVD	286.1761	314.1710	VVDS	373.2082	401.2031
VVDSN	487.2511	515.2460	VVDSND	602.2780	630.2729	VD	187.1077	215.1026
VDS	274.1397	302.1347	VDSN	388.1827	416.1776	VDSND	503.2096	531.2045
VDSNDL	616.2937	644.2886	DS	175.0713	203.0662	DSN	289.1143	317.1092

DSND	404.1412	432.1361	**DSNDL**	517.2253	545.2202	**DSNDLP**	614.2780	642.2729
SN	174.0873	202.0822	**SND**	289.1143	317.1092	**SNDL**	402.1983	430.1932
SNDLP	499.2511	527.2460	**SNDLPL**	612.3352	640.3301	**ND**	202.0822	230.0771
NDL	315.1663	343.1612	**NDLP**	412.2191	440.2140	**NDLPL**	525.3031	553.2980
NDLPLN	639.3461	667.3410	**DL**	201.1234	229.1183	**DLP**	298.1761	326.1710
DLPL	411.2602	439.2551	**DLPLN**	525.3031	553.2980	**DLPLNV**	624.3715	652.3665
LP	183.1492	211.1441	**LPL**	296.2333	324.2282	**LPLN**	410.2762	438.2711
LPLNV	509.3446	537.3395	**LPLNVS**	596.3766	624.3715	**PL**	183.1492	211.1441
PLN	297.1921	325.1870	**PLNV**	396.2605	424.2554	**PLNVS**	483.2926	511.2875
LN	200.1394	228.1343	**LNV**	299.2078	327.2027	**LNVS**	386.2398	414.2347
NV	186.1237	214.1186	**NVS**	273.1557	301.1506	**VS**	159.1128	187.1077





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.3	1483.7631	0.1230	GVVDSNDLPLNVSR
30.3	1483.7783	0.1078	VLSAVDQLPHSFR
27.6	1483.7743	0.1118	IADADAAAVRAVADR
26.4	1483.7995	0.0867	GLVDTNSLPLNVSR
23.1	1483.7631	0.1231	IADDLGLQPSNVSR
21.3	1483.8107	0.0754	GVISIDQSPIRGSR
20.0	1483.7994	0.0867	DISKENIPINSVR
19.8	1483.8107	0.0754	VDRNEIAVGLGVSR
19.4	1483.8511	0.0351	IAENALTLAKVWR
19.1	1483.8470	0.0391	LAAELNVSLVGRSR

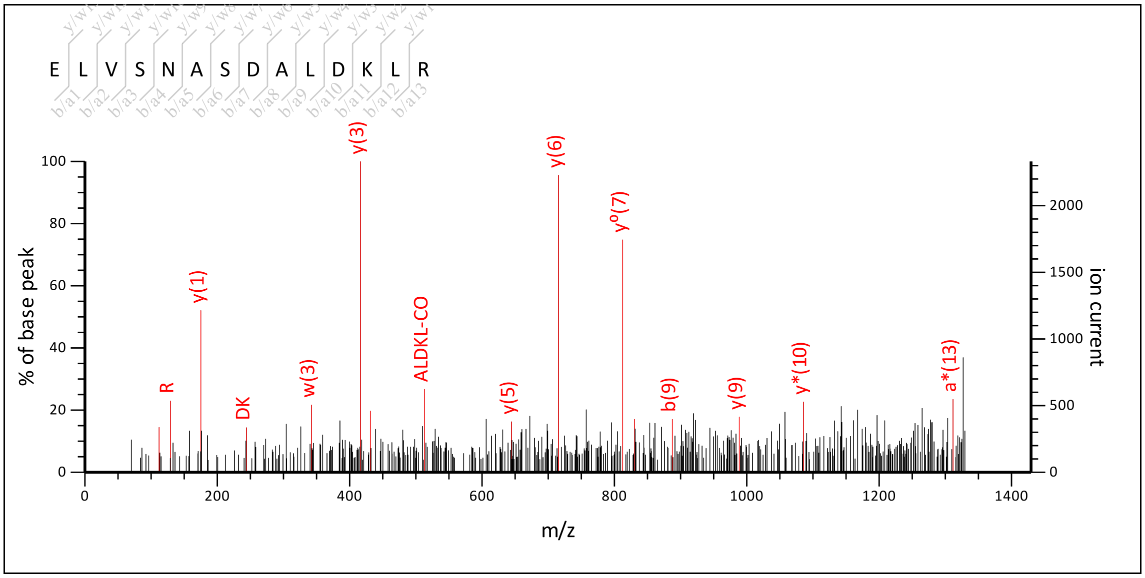
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **ELVSNASDALDKLR**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 50: 1529.926724 from(1530.934000,1+) intensity(0.0000) index(18)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226013, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



0 to 1429.53

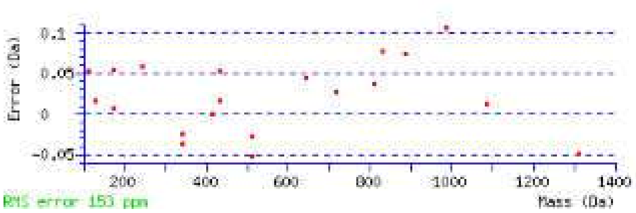
Label all possible matches ○ Label matches used for scoring ●

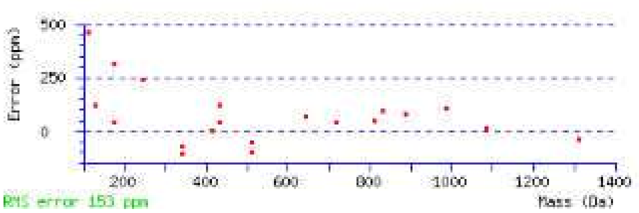
```
Monoisotopic mass of neutral peptide Mr(calc): 1529.8049
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 21
Matches : 20/254 fragment ions using 26 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495	E						14
2	86.0964	215.1390		197.1285	243.1339		225.1234	173.0921	L	1343.6914	1342.6961	1401.7696	1384.7431	1383.7591	13
3	72.0808	314.2074		296.1969	**342.2023**		324.1918	300.1918	V	1244.6230	1257.6434	1288.6856	1271.6590	1270.6750	12
4	60.0444	401.2395		383.2289	429.2344		411.2238	385.2445	S	1157.5909	1156.5957	1189.6171	1172.5906	1171.6066	11
5	87.0553	515.2824	498.2558	497.2718	543.2773	526.2508	525.2667	472.2766	N	1043.5480	1042.5527	1102.5851	1085.5586	1084.5745	10
6	44.0495	586.3195	569.2930	568.3089	614.3144	597.2879	596.3039		A	972.5109		***988.5422***	971.5156	970.5316	9
7	60.0444	673.3515	656.3250	655.3410	701.3464	684.3199	683.3359	657.3566	S	885.4789	884.4836	917.5051	900.4785	899.4945	8
8	88.0393	788.3785	771.3519	770.3679	816.3734	799.3468	798.3628	744.3886	D	770.4519	769.4567	***830.4730***	813.4465	812.4625	7
9	44.0495	859.4156	842.3890	841.4050	**887.4105**	870.3840	869.3999		A	699.4148		***715.4461***	698.4196	697.4355	6
10	86.0964	972.4996	955.4731	954.4891	1000.4946	983.4680	982.4840	930.4527	L	586.3307	585.3355	***644.4090***	627.3824	626.3984	5
11	88.0393	1087.5266	1070.5000	1069.5160	1115.5215	1098.4950	1097.5109	1043.5368	D	471.3038	470.3085	531.3249	514.2984	513.3144	4
12	101.1073	1215.6216	1198.5950	1197.6110	1243.6165	1226.5899	1225.6059	1158.5637	K	343.2088	342.2136	***416.2980***	399.2714		3
13	86.0964	1328.7056	1311.6791	1310.6951	1356.7005	1339.6740	1338.6900	1286.6587	L	230.1248	229.1295	288.2030	271.1765		2
14	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LV	185.1648	213.1598	LVS	272.1969	300.1918	LVSN	386.2398	414.2347
LVSNA	457.2769	485.2718	LVSNAS	544.3089	572.3039	LVSNASD	659.3359	687.3308
VS	159.1128	187.1077	VSN	273.1557	301.1506	VSNA	344.1928	372.1878
VSNAS	431.2249	459.2198	VSNASD	546.2518	574.2467	VSNASDA	617.2889	645.2838

SN	174.0873	202.0822	**SNA**	245.1244	273.1193	**SNAS**	332.1565	360.1514
SNASD	447.1834	475.1783	**SNASDA**	518.2205	546.2154	**SNASDAL**	631.3046	659.2995
NA	158.0924	186.0873	**NAS**	245.1244	273.1193	**NASD**	360.1514	388.1463
NASDA	431.1885	459.1834	**NASDAL**	544.2726	572.2675	**NASDALD**	659.2995	687.2944
AS	131.0815	159.0764	**ASD**	246.1084	274.1034	**ASDA**	317.1456	345.1405
ASDAL	430.2296	458.2245	**ASDALD**	545.2566	573.2515	**ASDALDK**	673.3515	701.3464
SD	175.0713	203.0662	**SDA**	246.1084	274.1034	**SDAL**	359.1925	387.1874
SDALD	474.2195	502.2144	**SDALDK**	602.3144	630.3093	**DA**	159.0764	187.0713
DAL	272.1605	300.1554	**DALD**	387.1874	415.1823	**DALDK**	515.2824	543.2773
DALDKL	628.3665	656.3614	**AL**	157.1335	185.1285	**ALD**	272.1605	300.1554
ALDK	400.2554	428.2504	**ALDKL**	513.3395	541.3344	**LD**	201.1234	229.1183
LDK	329.2183	357.2132	**LDKL**	442.3024	470.2973	**DK**	216.1343	244.1292
DKL	329.2183	357.2132	**KL**	214.1914	242.1863			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.2	1529.8413	0.0854	TTLQDIADRVGITK
29.9	1529.8049	0.1218	EIVSNASDALDKIR
29.9	1529.8049	0.1218	ELVSNASDAIDKLR
29.9	1529.8049	0.1218	ELVSNASDALDKIR
29.9	1529.8049	0.1218	ELVSNASDALDKLR
29.9	1529.8049	0.1218	EVISNASDALDKIR
29.9	1529.8049	0.1218	EVISNSADALDKIR
26.4	1529.7872	0.1396	QDRLMAPGESLSVK
25.8	1529.8202	0.1065	FLQGPGTDKDALLR
25.7	1529.8348	0.0919	MLSAARLDGTVQIR

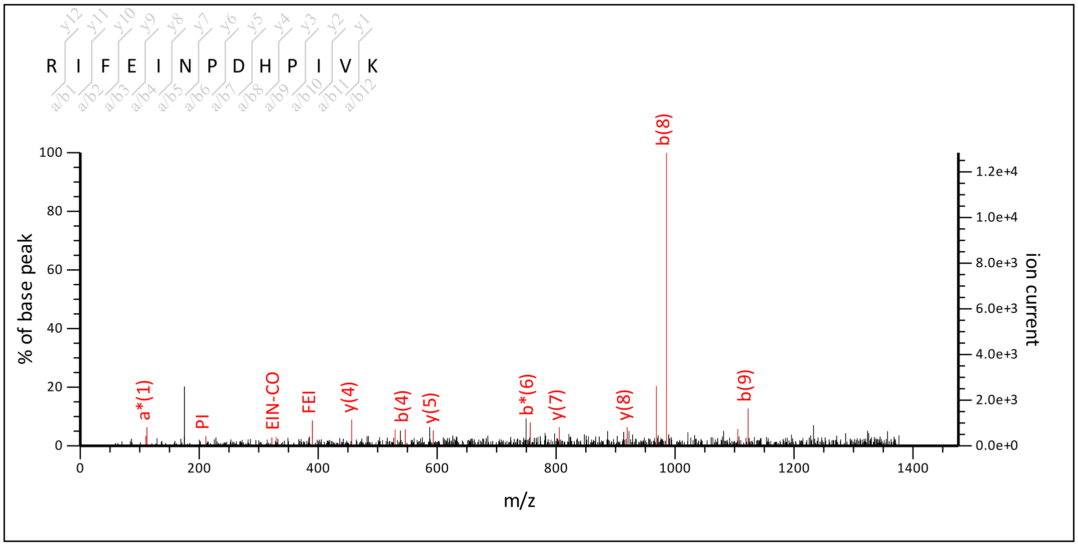
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **RIFEINPDHPIVK**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 58: 1577.003924 from(1578.011200,1+) intensity(0.0000) index(21)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226006, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



0 to 1476.33

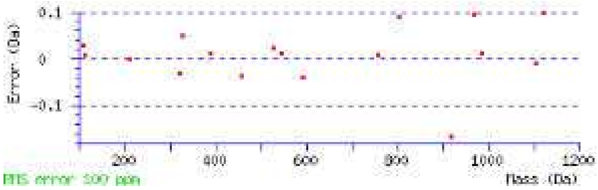
Label all possible matches ○ Label matches used for scoring ●

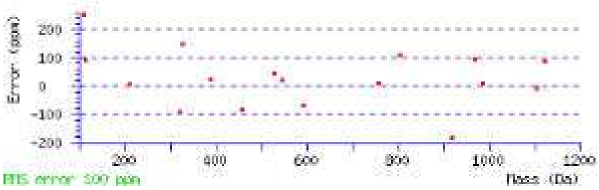
Monoisotopic mass of neutral peptide Mr(calc): 1576.8725
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 15 **Expect:** 2.2e+02
Matches : 19/225 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	129.1135	129.1135	112.0869		157.1084	140.0818		44.0495		R					
2	86.0964	242.1975	225.1710		270.1925	253.1659		214.1662	228.1819	I	1363.7005	1376.7209	1390.7365	1421.7787	1404.7522
3	120.0808	389.2660	372.2394		417.2609	400.2343				F	1216.6321			1308.6947	1291.6681
4	102.0550	518.3085	501.2820	500.2980	***546.3035***	529.2769	528.2929	460.3031		E	1087.5895	1086.5942		1161.6262	1144.5997
5	86.0964	631.3926	614.3661	613.3820	659.3875	642.3610	641.3770	603.3613	617.3770	I	974.5054	987.5258	1001.5415	1032.5837	1015.5571
6	87.0553	745.4355	728.4090	727.4250	773.4304	756.4039	755.4199	702.4297		N	860.4625	859.4672		***919.4996***	902.4730
7	70.0651	842.4883	825.4617	824.4777	870.4832	853.4567	852.4726	816.4726		P	763.4097	762.4145		***805.4567***	788.4301
8	88.0393	957.5152	940.4887	939.5047	***985.5102***	968.4836	967.4996	913.5254		D	648.3828	647.3875		708.4039	691.3774
9	110.0713	1094.5742	1077.5476	1076.5636	***1122.5691***	1105.5425	1104.5585			H	511.3239			***593.3770***	576.3504
10	70.0651	1191.6269	1174.6004	1173.6164	1219.6218	1202.5953	1201.6113	1165.6113		P	414.2711	413.2758		***456.3180***	439.2915
11	86.0964	1304.7110	1287.6844	1286.7004	1332.7059	1315.6793	1314.6953	1276.6797	1290.6953	I	301.1870	314.2074	328.2231	359.2653	342.2387
12	72.0808	1403.7794	1386.7528	1385.7688	1431.7743	1414.7478	1413.7637	1389.7637		V	202.1186	215.1390		246.1812	229.1547
13	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IF	233.1648	261.1598	**IFE**	362.2074	390.2023	**IFEI**	475.2915	503.2864
IFEIN	589.3344	617.3293	**IFEINP**	686.3872	714.3821	**FE**	249.1234	277.1183
FEI	362.2074	390.2023	**FEIN**	476.2504	504.2453	**FEINP**	573.3031	601.2980
FEINPD	688.3301	716.3250	**EI**	215.1390	243.1339	**EIN**	329.1819	357.1769
EINP	426.2347	454.2296	**EINPD**	541.2617	569.2566	**EINPDH**	678.3206	706.3155
IN	200.1394	228.1343	**INP**	297.1921	325.1870	**INPD**	412.2191	440.2140
INPDH	549.2780	577.2729	**INPDHP**	646.3307	674.3256	**NP**	184.1081	212.1030
NPD	299.1350	327.1299	**NPDH**	436.1939	464.1888	**NPDHP**	533.2467	561.2416

NPDHPI	646.3307	674.3256	**PD**	185.0921	213.0870	**PDH**	322.1510	350.1459
PDHP	419.2037	447.1987	**PDHPI**	532.2878	560.2827	**PDHPIV**	631.3562	659.3511
DH	225.0982	253.0931	**DHP**	322.1510	350.1459	**DHPI**	435.2350	463.2300
DHPIV	534.3035	562.2984	**HP**	207.1240	235.1190	**HPI**	320.2081	348.2030
HPIV	419.2765	447.2714	**PI**	183.1492	211.1441	**PIV**	282.2176	310.2125
IV	185.1648	213.1598						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.1	1576.8838	0.1202	KNVNHIVWADLIR
15.3	1576.9049	0.0990	VERAHALLTLDLAR
15.3	1576.8725	0.1314	RIFEINPDHPIVK
14.8	1576.9566	0.0474	LPIIRVLFGIQHR
13.5	1576.8508	0.1532	MRPAHAVIDLDALR
12.0	1576.8725	0.1314	LPTALAALAYRDFR
11.7	1576.8759	0.1280	MAKILVVDDHPAIR
11.5	1576.8685	0.1354	REPPIVEVERPTR
11.5	1576.8573	0.1466	QPLHTVIADVAELR
11.4	1576.9300	0.0739	IKSSIEITIHIAPR

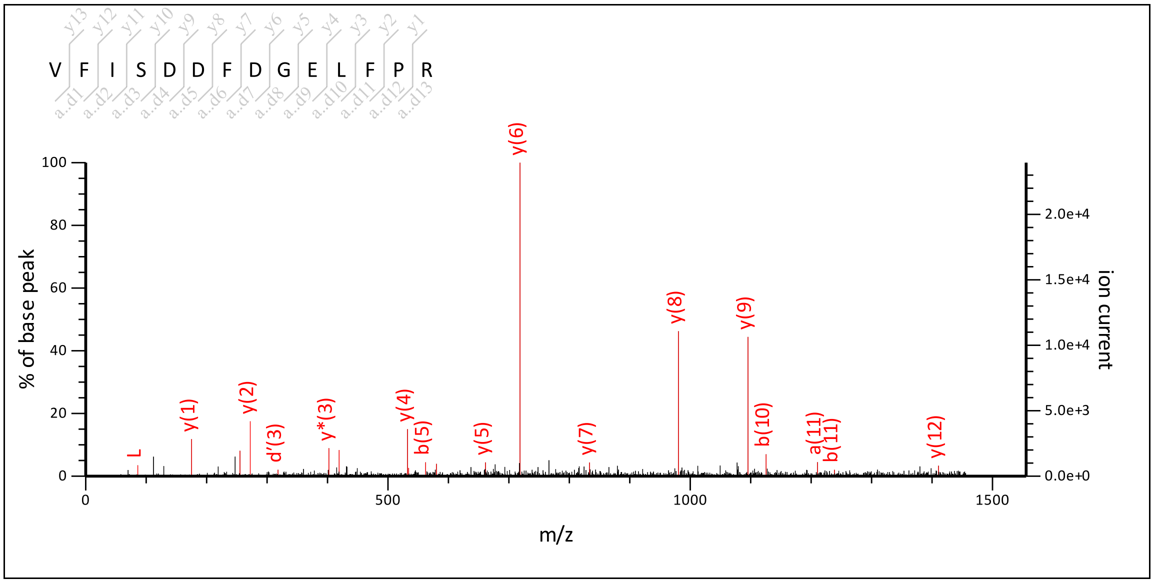
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 114

MS/MS Fragmentation of **VFISDDFDGELFPR**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 62: 1655.925424 from(1656.932700,1+) intensity(0.0000) index(22)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226001, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



0 to 1555.67

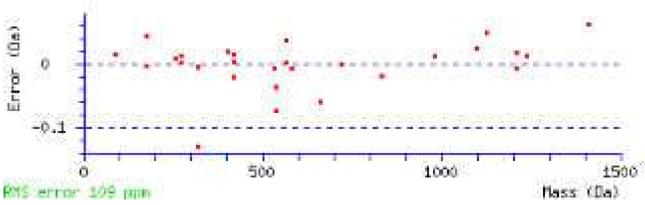
Label all possible matches ○ Label matches used for scoring ●

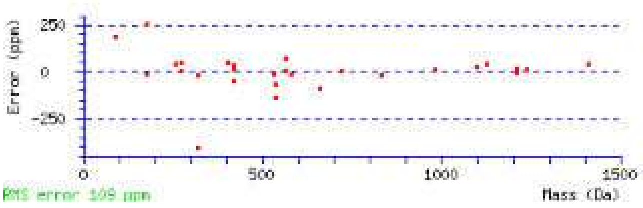
Monoisotopic mass of neutral peptide Mr(calc): 1655.7832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 1.3e-05
Matches : 31/215 fragment ions using 28 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	72.0808		100.0757		44.0495		V							14
2	120.0808	219.1492		247.1441				F	1465.6594			1557.7220	1540.6955	1539.7114	13
3	86.0964	332.2333		360.2282		304.2020	318.2176	I	1352.5753	1365.5957	1379.6114	***1410.6536***	1393.6270	1392.6430	12
4	60.0444	**419.2653**	401.2547	447.2602	429.2496	403.2704		S	1265.5433	1264.5481		1297.5695	1280.5430	1279.5590	11
5	88.0393	**534.2922**	516.2817	**562.2871**	544.2766	490.3024		D	1150.5164	1149.5211		***1210.5375***	1193.5109	1192.5269	10
6	88.0393	649.3192	631.3086	677.3141	659.3035	605.3293		D	1035.4894	1034.4942		***1095.5106***	1078.4840	1077.5000	9
7	120.0808	796.3876	778.3770	824.3825	806.3719			F	888.4210			***980.4836***	963.4571	962.4730	8
8	88.0393	911.4145	893.4040	939.4094	921.3989	867.4247		D	773.3941	772.3988		***833.4152***	816.3886	815.4046	7
9	30.0338	968.4360	950.4254	996.4309	978.4203			G				***718.3883***	701.3617	700.3777	6
10	102.0550	1097.4786	1079.4680	**1125.4735**	1107.4629	1039.4731		E	587.3300	586.3348		***661.3668***	644.3402	643.3562	5
11	86.0964	**1210.5626**	1192.5521	**1238.5576**	1220.5470	1168.5157		L	474.2459	473.2507		***532.3242***	515.2976		4
12	120.0808	1357.6311	1339.6205	1385.6260	1367.6154			F	327.1775			***419.2401***	402.2136		3
13	70.0651	1454.6838	1436.6733	1482.6787	1464.6682	1428.6682		P	230.1248	229.1295		***272.1717***	255.1452		2
14	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FI	233.1648	261.1598	**FIS**	320.1969	348.1918	**FISD**	435.2238	463.2187
FISDD	550.2508	578.2457	**FISDDF**	697.3192	725.3141	**IS**	173.1285	201.1234
ISD	288.1554	316.1503	**ISDD**	403.1823	431.1773	**ISDDF**	550.2508	578.2457

ISDDFD	665.2777	693.2726	**SD**	175.0713	203.0662	**SDD**	290.0983	318.0932
SDDF	437.1667	465.1616	**SDDFD**	552.1936	580.1885	**SDDFDG**	609.2151	637.2100
DD	203.0662	231.0612	**DDF**	350.1347	378.1296	**DDFD**	465.1616	493.1565
DDFDG	522.1831	550.1780	**DDFDGE**	651.2257	679.2206	**DF**	235.1077	263.1026
DFD	350.1347	378.1296	**DFDG**	407.1561	435.1510	**DFDGE**	536.1987	564.1936
DFDGEL	649.2828	677.2777	**FD**	235.1077	263.1026	**FDG**	292.1292	320.1241
FDGE	421.1718	449.1667	**FDGEL**	534.2558	562.2508	**FDGELF**	681.3243	709.3192
DG	145.0608	173.0557	**DGE**	274.1034	302.0983	**DGEL**	387.1874	415.1823
DGELF	534.2558	562.2508	**DGELFP**	631.3086	659.3035	**GE**	159.0764	187.0713
GEL	272.1605	300.1554	**GELF**	419.2289	447.2238	**GELFP**	516.2817	544.2766
EL	215.1390	243.1339	**ELF**	362.2074	390.2023	**ELFP**	459.2602	487.2551
LF	233.1648	261.1598	**LFP**	330.2176	358.2125	**FP**	217.1335	245.1285





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.9	1655.7832	0.1423	VFISDDFDGELFPR
33.9	1655.8757	0.0497	QALHARTLGFHHPR
33.9	1655.8757	0.0497	QALHARTLGFHHPR
27.6	1655.7791	0.1463	FDIREYDSVLDER
27.6	1655.8076	0.1178	EVPPEIEITDDMIR
26.4	1655.8606	0.0648	NCALFVFRDLFVR
23.9	1655.8155	0.1099	VFTVDNSSSTLFPSR
22.5	1655.8883	0.0371	IPIHTFGITDSNTLK
22.5	1655.8406	0.0848	LDAILGYFTEDKSGK
21.4	1655.8065	0.1190	DRFLFWMQNIMR

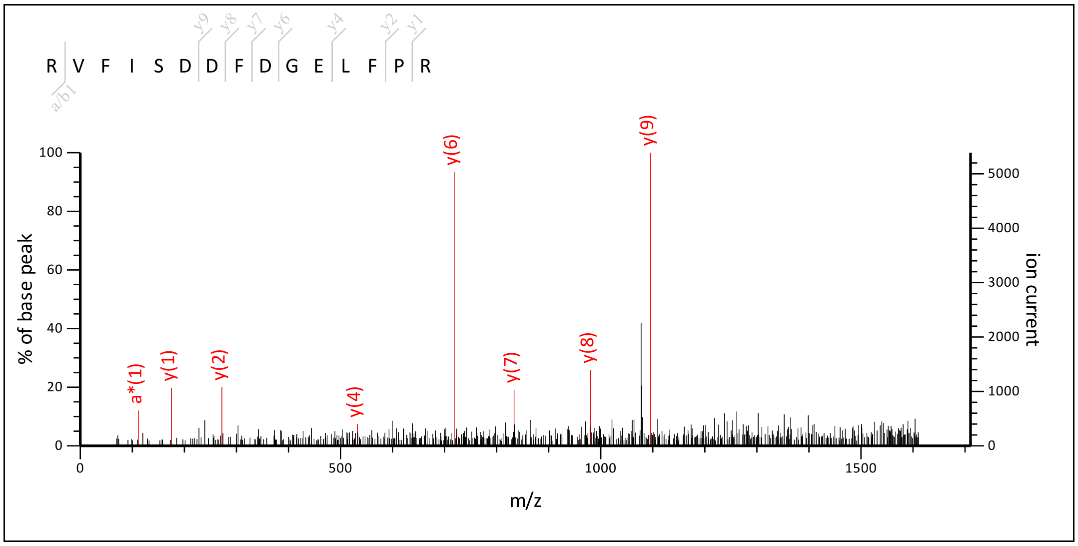
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 114**

MS/MS Fragmentation of **RVFISDDFDGELFPR**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 71: 1812.035424 from(1813.042700,1+) intensity(0.0000) index(26)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226011, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



0 to 1710.5

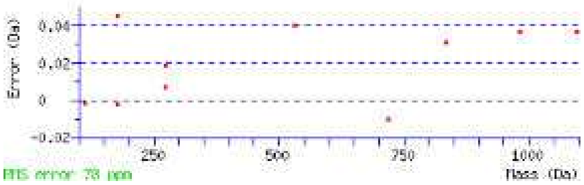
Label all possible matches ○ Label matches used for scoring ●

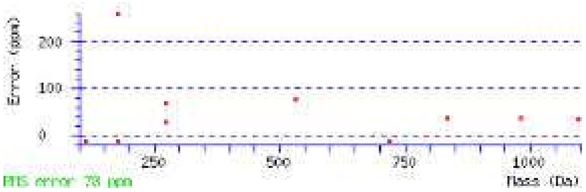
Monoisotopic mass of neutral peptide Mr(calc): 1811.8843
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 10
Matches : 14/262 fragment ions using 16 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	129.1135	129.1135	112.0869		157.1084	140.0818		44.0495		R					
2	72.0808	228.1819	211.1553		256.1768	239.1503		214.1662		V	1612.7278	1625.7482		1656.7904	1639.7639
3	120.0808	375.2503	358.2238		403.2452	386.2187				F	1465.6594			1557.7220	1540.6955
4	86.0964	488.3344	471.3078		516.3293	499.3027		460.3031	474.3187	I	1352.5753	1365.5957	1379.6114	1410.6536	1393.6270
5	60.0444	575.3664	558.3398	557.3558	603.3613	586.3348	585.3507	559.3715		S	1265.5433	1264.5481		1297.5695	1280.5430
6	88.0393	690.3933	673.3668	672.3828	**718.3882**	701.3617	700.3777	646.4035		D	1150.5164	1149.5211		1210.5375	1193.5109
7	88.0393	805.4203	788.3937	787.4097	**833.4152**	816.3886	815.4046	761.4304		D	1035.4894	1034.4942		***1095.5106***	1078.4840
8	120.0808	952.4887	935.4621	934.4781	**980.4836**	963.4571	962.4730			F	888.4210			***980.4836***	963.4571
9	88.0393	1067.5156	1050.4891	1049.5051	**1095.5105**	1078.4840	1077.5000	1023.5258		D	773.3941	772.3988		***833.4152***	816.3886
10	30.0338	1124.5371	1107.5105	1106.5265	1152.5320	1135.5055	1134.5214			G				***718.3883***	701.3617
11	102.0550	1253.5797	1236.5531	1235.5691	1281.5746	1264.5481	1263.5640	1195.5742		E	587.3300	586.3348		661.3668	644.3402
12	86.0964	1366.6638	1349.6372	1348.6532	1394.6587	1377.6321	1376.6481	1324.6168		L	474.2459	473.2507		***532.3242***	515.2976
13	120.0808	1513.7322	1496.7056	1495.7216	1541.7271	1524.7005	1523.7165			F	327.1775			419.2401	402.2136
14	70.0651	1610.7849	1593.7584	1592.7744	1638.7798	1621.7533	1620.7693	1584.7693		P	230.1248	229.1295		***272.1717***	255.1452
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VF	219.1492	247.1441	VFI	332.2333	360.2282	VFIS	419.2653	447.2602
VFISD	534.2922	562.2871	VFISDD	649.3192	677.3141	FI	233.1648	261.1598
FIS	320.1969	348.1918	FISD	435.2238	463.2187	FISDD	550.2508	578.2457
FISDDF	697.3192	725.3141	IS	173.1285	201.1234	ISD	288.1554	316.1503
ISDD	403.1823	431.1773	ISDDF	550.2508	578.2457	ISDDFD	665.2777	693.2726
SD	175.0713	203.0662	SDD	290.0983	318.0932	SDDF	437.1667	465.1616

SDDFD	552.1936	580.1885	**SDDFDG**	609.2151	637.2100	**DD**	203.0662	231.0612
DDF	350.1347	378.1296	**DDFD**	465.1616	493.1565	**DDFDG**	522.1831	550.1780
DDFDGE	651.2257	679.2206	**DF**	235.1077	263.1026	**DFD**	350.1347	378.1296
DFDG	407.1561	435.1510	**DFDGE**	536.1987	564.1936	**DFDGEL**	649.2828	677.2777
FD	235.1077	263.1026	**FDG**	292.1292	320.1241	**FDGE**	421.1718	449.1667
FDGEL	534.2558	562.2508	**FDGELF**	681.3243	709.3192	**DG**	145.0608	173.0557
DGE	274.1034	302.0983	**DGEL**	387.1874	415.1823	**DGELF**	534.2558	562.2508
DGELFP	631.3086	659.3035	**GE**	159.0764	187.0713	**GEL**	272.1605	300.1554
GELF	419.2289	447.2238	**GELFP**	516.2817	544.2766	**EL**	215.1390	243.1339
ELF	362.2074	390.2023	**ELFP**	459.2602	487.2551	**LF**	233.1648	261.1598
LFP	330.2176	358.2125	**FP**	217.1335	245.1285			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.1	1811.8843	0.1512	RVFISDDFDGELFPR
20.3	1811.9755	0.0599	ILHGTPVDPGQVRNGPR
19.9	1811.8836	0.1518	VGPVKADELADASGCAPR
18.2	1811.9741	0.0613	KNILGILLDDVSENNR
16.7	1811.8802	0.1552	AGDLGPGDLLAPHPDDPR
16.2	1811.9027	0.1327	HHAAVDADVHQLAEKR
16.2	1811.9027	0.1327	HHAAVDADVHQLAEKR
15.7	1811.8955	0.1399	IGFTPWDGHPLAQSVR
15.3	1811.9027	0.1327	ALANIGGRAPSSWDGGAGR
14.8	1811.9265	0.1089	IVTTHADIEDKDQTVK

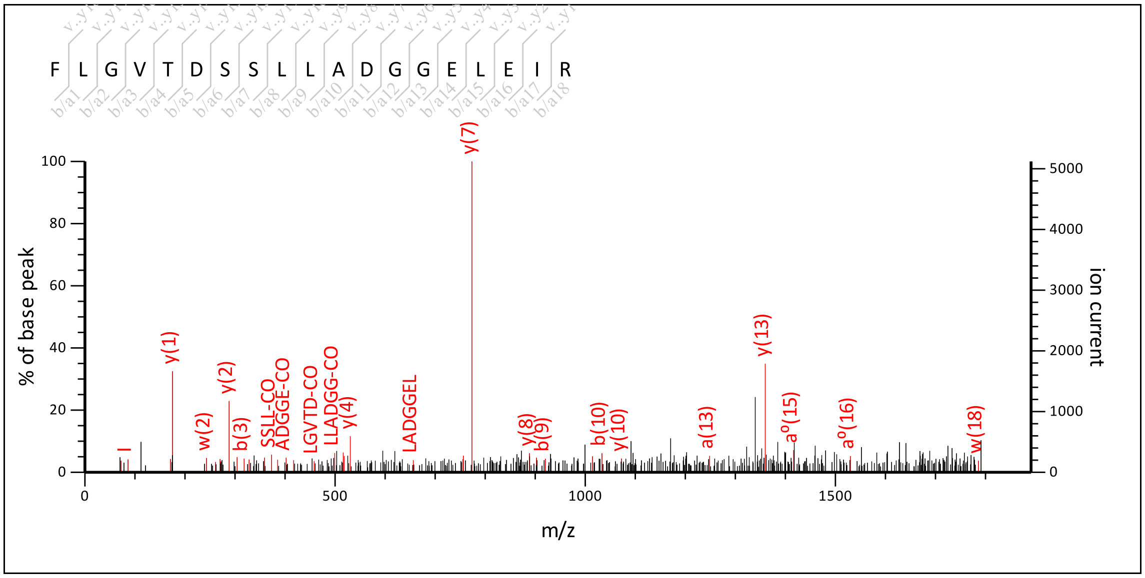
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 116**

MS/MS Fragmentation of **FLGVTDSSLLADGGELEIR**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 74: 1991.202924 from(1992.210200,1+) intensity(0.0000) index(27)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226014, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



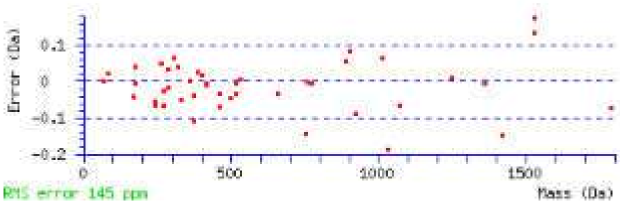
0 to 1891.03

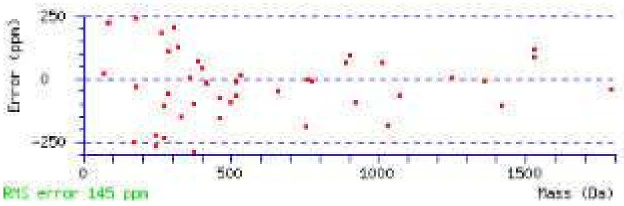
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1991.0211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 2.4e+02
Matches : 54/342 fragment ions using 125 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	120.0808	120.0808		148.0757		44.0495		F							19
2	86.0964	233.1648		***261.1598***		191.1179		L	1786.8817	1785.8865		1844.9600	1827.9334	1826.9494	18
3	30.0338	290.1863		***318.1812***				G				1731.8759	1714.8494	1713.8654	17
4	72.0808	389.2547		***417.2496***		375.2391		V	1630.7919	1643.8123		1674.8545	1657.8279	1656.8439	16
5	74.0600	490.3024	472.2918	***518.2973***	500.2867	474.3075	476.2867	T	1529.7442	1542.7646	1544.7439	1575.7861	1558.7595	1557.7755	15
6	88.0393	605.3293	587.3188	633.3243	615.3137	561.3395		D	1414.7172	1413.7220		1474.7384	1457.7118	1456.7278	14
7	60.0444	692.3614	674.3508	720.3563	702.3457	676.3665		S	1327.6852	1326.6900		***1359.7114***	1342.6849	1341.7009	13
8	60.0444	779.3934	761.3828	807.3883	789.3777	763.3985		S	1240.6532	1239.6579		1272.6794	1255.6529	1254.6688	12
9	86.0964	892.4775	874.4669	***920.4724***	902.4618	850.4305		L	1127.5691	1126.5739		1185.6474	1168.6208	1167.6368	11
10	86.0964	1005.5615	987.5510	***1033.5564***	1015.5459	963.5146		L	1014.4851	1013.4898		***1072.5633***	1055.5368	1054.5527	10
11	44.0495	1076.5986	1058.5881	1104.5936	1086.5830			A	943.4480			959.4793	942.4527	941.4687	9
12	88.0393	1191.6256	1173.6150	1219.6205	1201.6099	1147.6358		D	828.4210	827.4258		***888.4421***	871.4156	870.4316	8
13	30.0338	1248.6470	1230.6365	1276.6420	1258.6314			G				***773.4152***	756.3886	755.4046	7
14	30.0338	1305.6685	1287.6579	1333.6634	1315.6529			G				716.3937	699.3672	698.3832	6
15	102.0550	1434.7111	1416.7005	1462.7060	1444.6955	1376.7056		E	585.3355	584.3402		659.3723	642.3457	641.3617	5
16	86.0964	1547.7952	1529.7846	1575.7901	1557.7795	1505.7482		L	472.2514	471.2562		***530.3297***	513.3031	512.3191	4
17	102.0550	1676.8378	1658.8272	1704.8327	1686.8221	1618.8323		E	343.2088	342.2136		***417.2456***	400.2191	399.2350	3
18	86.0964	1789.9218	1771.9113	1817.9167	1799.9062	1761.8905	1775.9062	I	230.1248	243.1452	257.1608	***288.2030***	271.1765		2
19	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LG	143.1179	171.1128	**LGV**	242.1863	270.1812	**LGVT**	343.2340	371.2289
LGVTD	458.2609	486.2558	**LGVTDS**	545.2930	573.2879	**LGVTDSS**	632.3250	660.3199
GV	129.1022	157.0972	**GVT**	230.1499	258.1448	**GVTD**	345.1769	373.1718
GVTDS	432.2089	460.2038	**GVTDSS**	519.2409	547.2358	**GVTDSSL**	632.3250	660.3199
VT	173.1285	201.1234	**VTD**	288.1554	316.1503	**VTDS**	375.1874	403.1823
VTDSS	462.2195	490.2144	**VTDSSL**	575.3035	603.2984	**VTDSSLL**	688.3876	716.3825
TD	189.0870	217.0819	**TDS**	276.1190	304.1139	**TDSS**	363.1510	391.1460
TDSSL	476.2351	504.2300	**TDSSLL**	589.3192	617.3141	**TDSSLLA**	660.3563	688.3512
DS	175.0713	203.0662	**DSS**	262.1034	290.0983	**DSSL**	375.1874	403.1823
DSSLL	488.2715	516.2664	**DSSLLA**	559.3086	587.3035	**DSSLLAD**	674.3355	702.3305
SS	147.0764	175.0713	**SSL**	260.1605	288.1554	**SSLL**	373.2445	401.2395
SSLLA	444.2817	472.2766	**SSLLAD**	559.3086	587.3035	**SSLLADG**	616.3301	644.3250
SSLLADGG	673.3515	701.3464	**SL**	173.1285	201.1234	**SLL**	286.2125	314.2074
SLLA	357.2496	385.2445	**SLLAD**	472.2766	500.2715	**SLLADG**	529.2980	557.2930
SLLADGG	586.3195	614.3144	**LL**	199.1805	227.1754	**LLA**	270.2176	298.2125
LLAD	385.2445	413.2395	**LLADG**	442.2660	470.2609	**LLADGG**	499.2875	527.2824
LLADGGE	628.3301	656.3250	**LA**	157.1335	185.1285	**LAD**	272.1605	300.1554
LADG	329.1819	357.1769	**LADGG**	386.2034	414.1983	**LADGGE**	515.2460	543.2409
LADGGEL	628.3301	656.3250	**AD**	159.0764	187.0713	**ADG**	216.0979	244.0928
ADGG	273.1193	301.1143	**ADGGE**	402.1619	430.1569	**ADGGEL**	515.2460	543.2409
ADGGELE	644.2886	672.2835	**DG**	145.0608	173.0557	**DGG**	202.0822	230.0771
DGGE	331.1248	359.1197	**DGGEL**	444.2089	472.2038	**DGGELE**	573.2515	601.2464
DGGELEI	686.3355	714.3305	**GG**	87.0553	115.0502	**GGE**	216.0979	244.0928
GGEL	329.1819	357.1769	**GGELE**	458.2245	486.2195	**GGELEI**	571.3086	599.3035
GE	159.0764	187.0713	**GEL**	272.1605	300.1554	**GELE**	401.2031	429.1980
GELEI	514.2871	542.2821	**EL**	215.1390	243.1339	**ELE**	344.1816	372.1765
ELEI	457.2657	485.2606	**LE**	215.1390	243.1339	**LEI**	328.2231	356.2180
EI	215.1390	243.1339						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
17.6	1991.0211	0.1818	FLGVTDSSLLADGGELEIR
14.4	1991.0701	0.1328	HRAEQIVAASGVPWTTLR
12.9	1991.0265	0.1764	SNFNVAAPILFWGDTAIR
12.0	1991.0800	0.1230	VAPPGRSLADLAADAALDLR
11.0	1991.0490	0.1540	ALHKFQPNALVHFGEQR
10.7	1991.0258	0.1771	IMYSLHNGTSSISAKNLR
9.9	1991.0225	0.1804	GASQKGVYIDTVYGHQIR
9.5	1991.0476	0.1553	YSIPPENIIGHSDIAPLR
9.3	1991.0258	0.1771	IDLVLSTHNDQSMHLLR
8.9	1991.0106	0.1923	TGSNLCDVTVTAGKQTALR

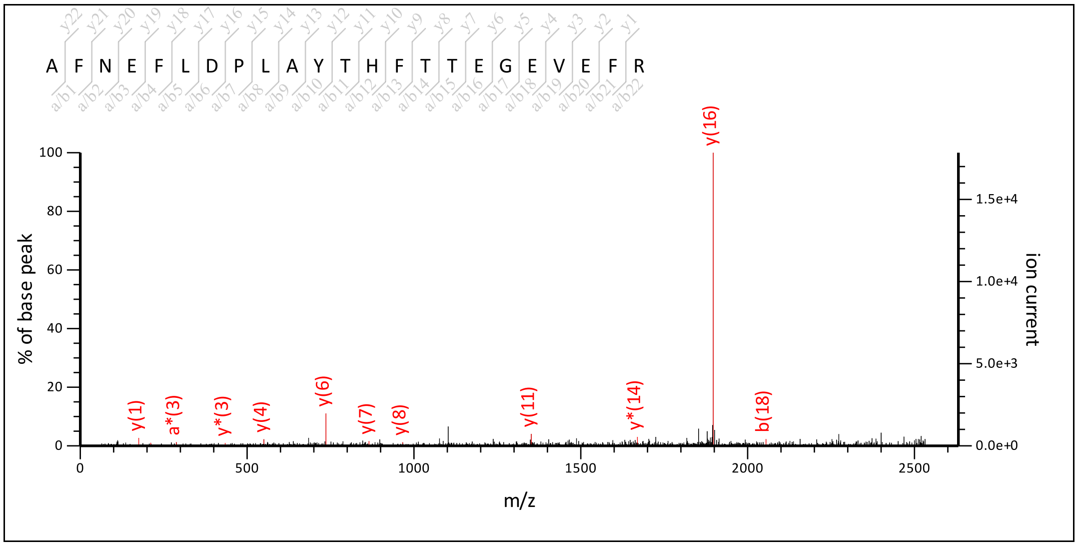
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 116

MS/MS Fragmentation of **AFNEFLDPLAYTHFTTEGEVEFR**
Found in **gi|115477014** in **NCBInr**, Os08g0487800 [Oryza sativa Japonica Group]

Match to Query 87: 2732.527924 from(2733.535200,1+) intensity(0.0000) index(33)
Title: Label: M6, Spot_Id: 219766, Peak_List_Id: 226009, MSMS Job_Run_Id: 21831, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M6_136859901000.txt



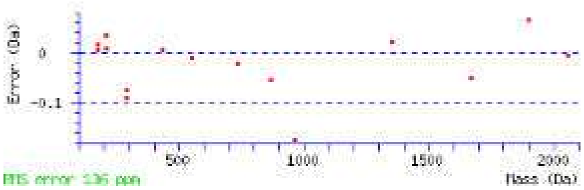
0 to 2631.64

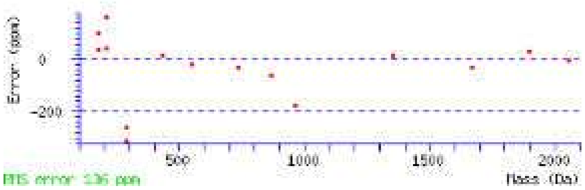
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2732.2758
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 10 **Expect:** 1.9e+03
Matches : 17/434 fragment ions using 50 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			72.0444			44.0495		A					
2	120.0808	191.1179			219.1128					F	2570.1834			2662.2460	2645.2195
3	87.0553	305.1608	288.1343		333.1557	316.1292		262.1550		N	2456.1405	2455.1452		2515.1776	2498.1510
4	102.0550	434.2034	417.1769	416.1928	462.1983	445.1718	444.1878	376.1979		E	2327.0979	2326.1026		2401.1347	2384.1081
5	120.0808	581.2718	564.2453	563.2613	609.2667	592.2402	591.2562			F	2180.0295			2272.0921	2255.0655
6	86.0964	694.3559	677.3293	676.3453	722.3508	705.3243	704.3402	652.3089		L	2066.9454	2065.9502		2125.0237	2107.9971
7	88.0393	809.3828	792.3563	791.3723	837.3777	820.3512	819.3672	765.3930		D	1951.9185	1950.9232		2011.9396	1994.9131
8	70.0651	906.4356	889.4090	888.4250	934.4305	917.4040	916.4199	880.4199		P	1854.8657	1853.8705		***1896.9127***	1879.8861
9	86.0964	1019.5197	1002.4931	1001.5091	1047.5146	1030.4880	1029.5040	977.4727		L	1741.7816	1740.7864		1799.8599	1782.8333
10	44.0495	1090.5568	1073.5302	1072.5462	1118.5517	1101.5251	1100.5411			A	1670.7445			1686.7758	1669.7493
11	136.0757	1253.6201	1236.5936	1235.6095	1281.6150	1264.5885	1263.6045			Y	1507.6812			1615.7387	1598.7122
12	74.0600	1354.6678	1337.6412	1336.6572	1382.6627	1365.6361	1364.6521	1338.6729	1340.6521	T	1406.6335	1419.6539	1421.6332	1452.6754	1435.6488
13	110.0713	1491.7267	1474.7001	1473.7161	1519.7216	1502.6951	1501.7110			H	1269.5746			***1351.6277***	1334.6012
14	120.0808	1638.7951	1621.7686	1620.7845	1666.7900	1649.7635	1648.7795			F	1122.5062			1214.5688	1197.5422
15	74.0600	1739.8428	1722.8162	1721.8322	1767.8377	1750.8112	1749.8271	1723.8479	1725.8271	T	1021.4585	1034.4789	1036.4582	1067.5004	1050.4738
16	74.0600	1840.8905	1823.8639	1822.8799	1868.8854	1851.8588	1850.8748	1824.8955	1826.8748	T	920.4108	933.4312	935.4105	***966.4527***	949.4262
17	102.0550	1969.9331	1952.9065	1951.9225	1997.9280	1980.9014	1979.9174	1911.9276		E	791.3682	790.3730		***865.4050***	848.3785
18	30.0338	2026.9545	2009.9280	2008.9440	2054.9494	2037.9229	2036.9389			G				***736.3624***	719.3359
19	102.0550	2155.9971	2138.9706	2137.9865	2183.9920	2166.9655	2165.9815	2097.9916		E	605.3042	604.3089		679.3410	662.3144
20	72.0808	2255.0655	2238.0390	2237.0550	2283.0604	2266.0339	2265.0499	2241.0499		V	506.2358	519.2562		***550.2984***	533.2718
21	102.0550	2384.1081	2367.0816	2366.0976	2412.1030	2395.0765	2394.0925	2326.1026		E	377.1932	376.1979		451.2300	434.2034
22	120.0808	2531.1765	2514.1500	2513.1660	2559.1714	2542.1449	2541.1609			F	230.1248			322.1874	305.1608
23	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FN	234.1237	262.1186	**FNE**	363.1663	391.1612	**FNEF**	510.2347	538.2296
FNEFL	623.3188	651.3137	**NE**	216.0979	244.0928	**NEF**	363.1663	391.1612
NEFL	476.2504	504.2453	**NEFLD**	591.2773	619.2722	**NEFLDP**	688.3301	716.3250
EF	249.1234	277.1183	**EFL**	362.2074	390.2023	**EFLD**	477.2344	505.2293
EFLDP	574.2871	602.2821	**EFLDPL**	687.3712	715.3661	**FL**	233.1648	261.1598
FLD	348.1918	376.1867	**FLDP**	445.2445	473.2395	**FLDPL**	558.3286	586.3235
FLDPLA	629.3657	657.3606	**LD**	201.1234	229.1183	**LDP**	298.1761	326.1710
LDPL	411.2602	439.2551	**LDPLA**	482.2973	510.2922	**LDPLAY**	645.3606	673.3556
DP	185.0921	213.0870	**DPL**	298.1761	326.1710	**DPLA**	369.2132	397.2082
DPLAY	532.2766	560.2715	**DPLAYT**	633.3243	661.3192	**PL**	183.1492	211.1441
PLA	254.1863	282.1812	**PLAY**	417.2496	445.2445	**PLAYT**	518.2973	546.2922
PLAYTH	655.3562	683.3511	**LA**	157.1335	185.1285	**LAY**	320.1969	348.1918
LAYT	421.2445	449.2395	**LAYTH**	558.3035	586.2984	**AY**	207.1128	235.1077
AYT	308.1605	336.1554	**AYTH**	445.2194	473.2143	**AYTHF**	592.2878	620.2827
AYTHFT	693.3355	721.3304	**YT**	237.1234	265.1183	**YTH**	374.1823	402.1772
YTHF	521.2507	549.2456	**YTHFT**	622.2984	650.2933	**TH**	211.1190	239.1139
THF	358.1874	386.1823	**THFT**	459.2350	487.2300	**THFTT**	560.2827	588.2776
THFTTE	689.3253	717.3202	**HF**	257.1397	285.1346	**HFT**	358.1874	386.1823
HFTT	459.2350	487.2300	**HFTTE**	588.2776	616.2726	**HFTTEG**	645.2991	673.2940
FT	221.1285	249.1234	**FTT**	322.1761	350.1710	**FTTE**	451.2187	479.2136
FTTEG	508.2402	536.2351	**FTTEGE**	637.2828	665.2777	**TT**	175.1077	203.1026
TTE	304.1503	332.1452	**TTEG**	361.1718	389.1667	**TTEGE**	490.2144	518.2093
TTEGEV	589.2828	617.2777	**TE**	203.1026	231.0975	**TEG**	260.1241	288.1190
TEGE	389.1667	417.1616	**TEGEV**	488.2351	516.2300	**TEGEVE**	617.2777	645.2726
EG	159.0764	187.0713	**EGE**	288.1190	316.1139	**EGEV**	387.1874	415.1823
EGEVE	516.2300	544.2249	**EGEVEF**	663.2984	691.2933	**GE**	159.0764	187.0713
GEV	258.1448	286.1397	**GEVE**	387.1874	415.1823	**GEVEF**	534.2558	562.2508
EV	201.1234	229.1183	**EVE**	330.1660	358.1609	**EVEF**	477.2344	505.2293
VE	201.1234	229.1183	**VEF**	348.1918	376.1867	**EF**	249.1234	277.1183





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
9.8	2732.2758	0.2521	AFNEFLDPLAYTHFTTEGEVEFR
7.4	2732.3446	0.1833	LQYGDLEHVLDTGLHDYLTDFLR
6.5	2732.4650	0.0629	HTITNLDPPLVAPFDGYSLHKILR
6.1	2732.3592	0.1687	MGYGTAGQALAVLLGTDGHQLEVFER
6.0	2732.3895	0.1384	QEGFDAVVNAANAWLRPGGGVAGAIHR
5.7	2732.3446	0.1833	LEAFFAGTDDGTKLPHVDEWLALR
5.4	2732.3379	0.1900	GHEQSQIGAHGATPFSDAEVARQALR
5.0	2732.3340	0.1939	DKLIEGVQFHPESIASEHGHAMLR
4.9	2732.4650	0.0629	KTHPPVLTDLNEGFLYVTGHLPIR
4.0	2732.3055	0.2224	SLDFDSARLPNPHIRPEHEEWR

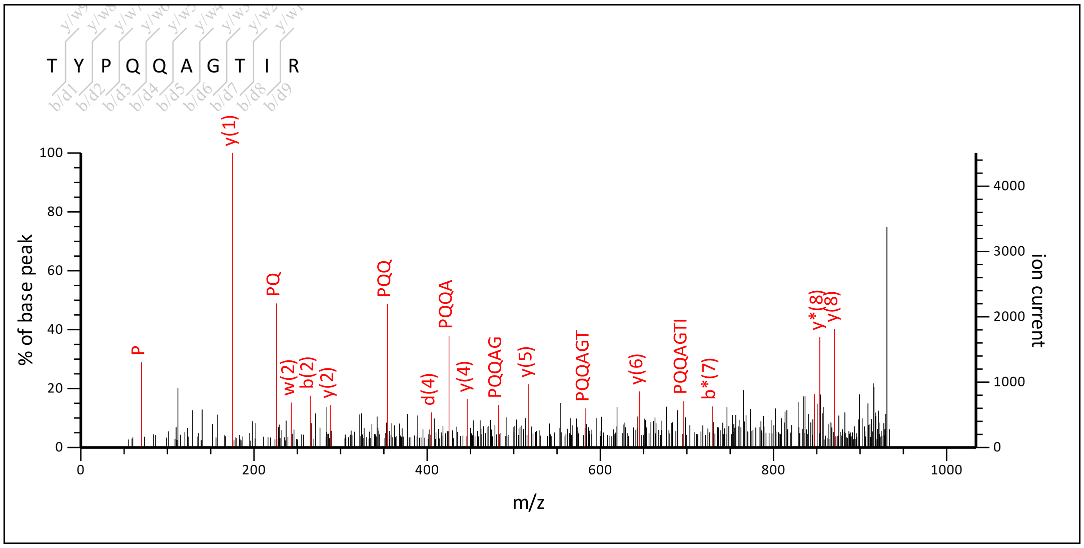
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 118

MS/MS Fragmentation of **TYPQQAGTIR**
Found in **gi|108711192** in **NCBInr**, Eukaryotic translation initiation factor 5A-2, putative, expressed [Oryza sativa Japonica Group]

Match to Query 30: 1133.637124 from(1134.644400,1+) intensity(0.0000) index(8)
Title: Label: N8, Spot_Id: 219799, Peak_List_Id: 226504, MSMS Job_Run_Id: 21847, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N8_136859933900.txt



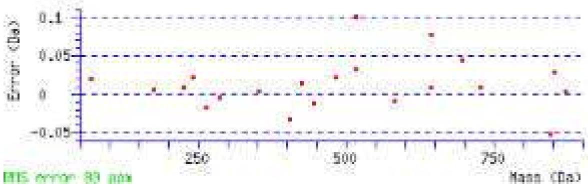
0 to 1033.86

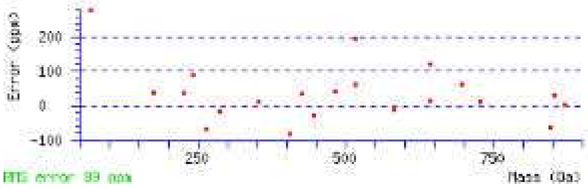
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1133.5829
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 3.5
Matches : 21/159 fragment ions using 27 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		**T**							10
2	136.0757	237.1234		219.1128	**265.1183**		247.1077			**Y**	925.4850			1033.5425	1016.5160	1015.5320	9
3	70.0651	334.1761		316.1656	362.1710		344.1605	308.1605		**P**	828.4322	827.4370		***870.4792***	853.4526	852.4686	8
4	101.0709	462.2347	445.2082	444.2241	490.2296	473.2031	472.2191	405.2132		**Q**	700.3737	699.3784		773.4264	756.3999	755.4159	7
5	101.0709	590.2933	573.2667	572.2827	618.2882	601.2617	600.2776	533.2718		**Q**	572.3151	571.3198		***645.3679***	628.3413	627.3573	6
6	44.0495	661.3304	644.3039	643.3198	689.3253	672.2988	671.3148			**A**	501.2780			***517.3093***	500.2827	499.2987	5
7	30.0338	718.3519	701.3253	700.3413	746.3468	729.3202	728.3362			**G**				***446.2722***	429.2456	428.2616	4
8	74.0600	819.3995	802.3730	801.3890	**847.3945**	830.3679	829.3839	803.4046	805.3839	**T**	343.2088	356.2292	358.2085	389.2507	372.2241	371.2401	3
9	86.0964	932.4836	915.4571	914.4730	960.4785	943.4520	942.4680	904.4523	918.4680	**I**	230.1248	243.1452	257.1608	***288.2030***	271.1765		2
10	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YP	233.1285	261.1234	**YPQ**	361.1870	389.1819	**YPQQ**	489.2456	517.2405
YPQQA	560.2827	588.2776	**YPQQAG**	617.3042	645.2991	**PQ**	198.1237	226.1186
PQQ	326.1823	354.1772	**PQQA**	397.2194	425.2143	**PQQAG**	454.2409	482.2358
PQQAGT	555.2885	583.2835	**PQQAGTI**	668.3726	696.3675	**QQ**	229.1295	257.1244
QQA	300.1666	328.1615	**QQAG**	357.1881	385.1830	**QQAGT**	458.2358	486.2307
QQAGTI	571.3198	599.3148	**QA**	172.1081	200.1030	**QAG**	229.1295	257.1244
QAGT	330.1772	358.1721	**QAGTI**	443.2613	471.2562	**AG**	101.0709	129.0659
AGT	202.1186	230.1135	**AGTI**	315.2027	343.1976	**GT**	131.0815	159.0764
GTI	244.1656	272.1605	**TI**	187.1441	215.1390			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.2	1133.5829	0.0542	TYPQQAGTIR
24.8	1133.5499	0.0873	GAAAMAEAASIR
22.5	1133.6669	-0.0298	QAVAGLLGHLR
20.3	1133.5802	0.0569	APGAGAGHGAGRR
20.2	1133.6379	-0.0008	KPKAMAGFLR
19.8	1133.6557	-0.0186	ILDPIHGTIR
19.3	1133.5651	0.0720	MKETYGHIR
19.1	1133.6193	0.0178	AAGKPGYTTLR
18.8	1133.6040	0.0331	GETTTQTKIR
18.2	1133.6227	0.0145	NALAMTKTLR

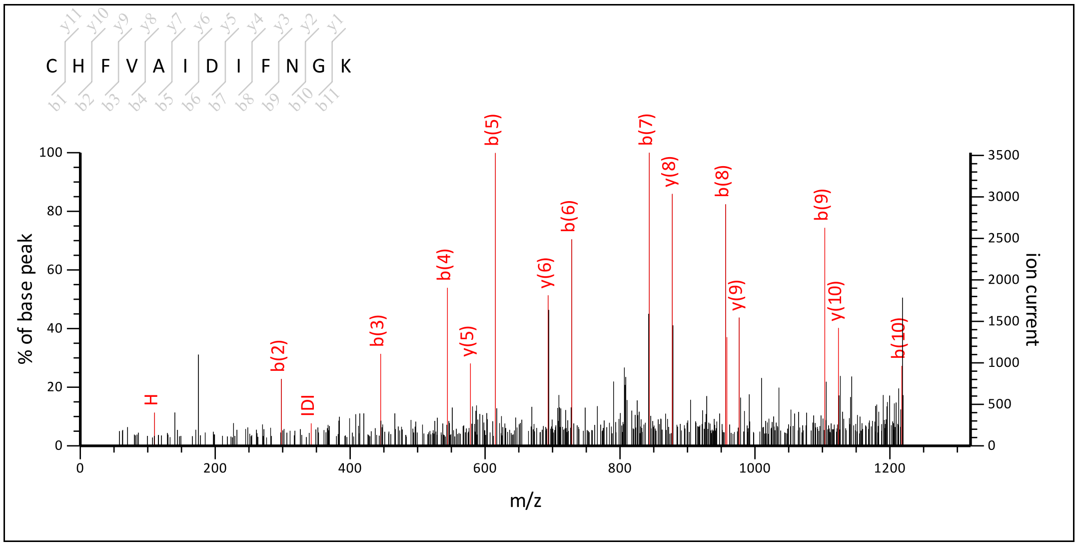
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 118

MS/MS Fragmentation of **CHFVAIDIFNGK**
Found in **gi|108711192** in **NCBInr**, Eukaryotic translation initiation factor 5A-2, putative, expressed [Oryza sativa Japonica Group]

Match to Query 61: 1419.753224 from(1420.760500,1+) intensity(0.0000) index(17)
Title: Label: N8, Spot_Id: 219799, Peak_List_Id: 226513, MSMS Job_Run_Id: 21847, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N8_136859933900.txt



0 to 1319.53

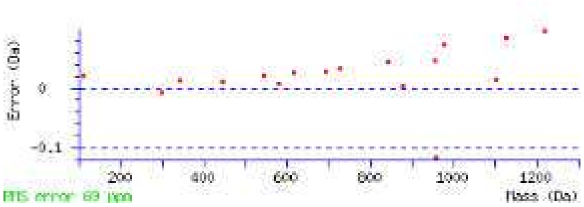
Label all possible matches ○ Label matches used for scoring ●

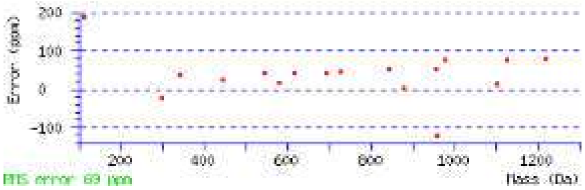
Monoisotopic mass of neutral peptide Mr(calc): 1419.6969
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 0.0017
Matches : 17/172 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	y
1	133.0430	133.0430			161.0379			44.0495		C						
2	110.0713	270.1019			***298.0968***					H	1178.6204			1260.6735	1243.6470	1242.
3	120.0808	417.1703			***445.1653***					F	1031.5520			**1123.6146**	1106.5881	1105.
4	72.0808	516.2387			***544.2337***			502.2231		V	932.4836	945.5040		**976.5462**	959.5197	958.
5	44.0495	587.2759			***615.2708***					A	861.4465			**877.4778**	860.4512	859.
6	86.0964	700.3599			***728.3548***			672.3286	686.3443	I	748.3624	761.3828	775.3985	806.4407	789.4141	788.
7	88.0393	815.3869		797.3763	***843.3818***		825.3712	771.3970		D	633.3355	632.3402		**693.3566**	676.3301	675.
8	86.0964	928.4709		910.4604	***956.4658***		938.4553	900.4396	914.4553	I	520.2514	533.2718	547.2875	**578.3297**	561.3031	
9	120.0808	1075.5393		1057.5288	***1103.5343***		1085.5237			F	373.1830			465.2456	448.2191	
10	87.0553	1189.5823	1172.5557	1171.5717	***1217.5772***	1200.5506	1199.5666	1146.5765		N	259.1401	258.1448		318.1772	301.1506	
11	30.0338	1246.6037	1229.5772	1228.5932	1274.5987	1257.5721	1256.5881			G				204.1343	187.1077	
12	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HF	257.1397	285.1346	HFV	356.2081	384.2030	HFVA	427.2452	455.2401
HFVAI	540.3293	568.3242	HFVAID	655.3562	683.3511	FV	219.1492	247.1441
FVA	290.1863	318.1812	FVAI	403.2704	431.2653	FVAID	518.2973	546.2922
FVAIDI	631.3814	659.3763	VA	143.1179	171.1128	VAI	256.2020	284.1969
VAID	371.2289	399.2238	VAIDI	484.3130	512.3079	VAIDIF	631.3814	659.3763
AI	157.1335	185.1285	AID	272.1605	300.1554	AIDI	385.2445	413.2395
AIDIF	532.3130	560.3079	AIDIFN	646.3559	674.3508	ID	201.1234	229.1183
IDI	314.2074	342.2023	IDIF	461.2758	489.2708	IDIFN	575.3188	603.3137
IDIFNG	632.3402	660.3352	DI	201.1234	229.1183	DIF	348.1918	376.1867

DIFN	462.2347	490.2296	**DIFNG**	519.2562	547.2511	**IF**	233.1648	261.1598
IFN	347.2078	375.2027	**IFNG**	404.2292	432.2241	**FN**	234.1237	262.1186
FNG	291.1452	319.1401	**NG**	144.0768	172.0717			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.0	1419.6969	0.0563	CHFVAIDIFNGK
73.0	1419.6969	0.0563	CHFVALDIFNGK
44.2	1419.6664	0.0868	VGSDNAVLDMIDR
43.3	1419.7511	0.0022	DPLFAVITFNQR
40.2	1419.6969	0.0563	CHFVAIDVFNAK
39.9	1419.6552	0.0981	DDLEGLIDLMDR
36.6	1419.6882	0.0651	LEDDLGIDIFDR
33.6	1419.7106	0.0426	HADAALAALAPEDR
33.1	1419.7246	0.0287	DSDLFDILDLVR
32.6	1419.7544	-0.0012	LSPFVALGCITSR

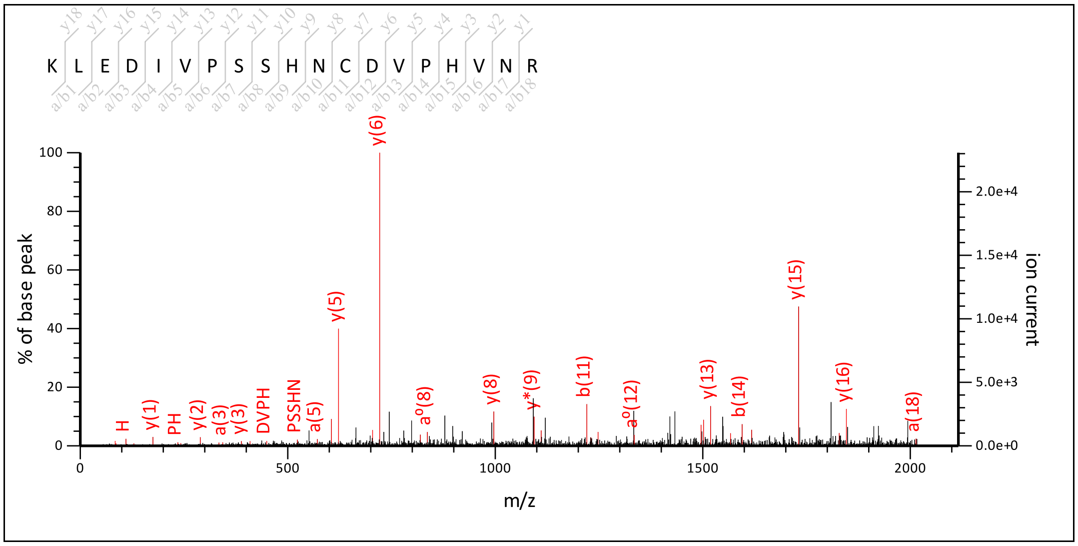
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 118

MS/MS Fragmentation of **KLEDIVPSSHNCDVPHVNR**
Found in **gi|108711192** in **NCBInr**, Eukaryotic translation initiation factor 5A-2, putative, expressed [Oryza sativa Japonica Group]

Match to Query 106: 2215.193424 from(2216.200700,1+) intensity(0.0000) index(32)
Title: Label: N8, Spot_Id: 219799, Peak_List_Id: 226503, MSMS Job_Run_Id: 21847, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N8_136859933900.txt



0 to 2115.94

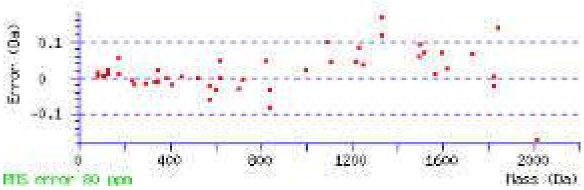
Label all possible matches ○ Label matches used for scoring ●

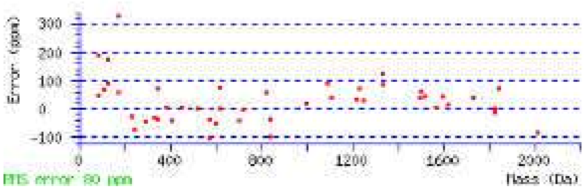
Monoisotopic mass of neutral peptide Mr(calc): 2215.0804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 75 **Expect:** 0.00073
Matches : 49/358 fragment ions using 80 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	101.1073	101.1073	84.0808		**129.1022**	112.0757		44.0495		K					
2	86.0964	214.1914	197.1648		**242.1863**	225.1598		172.1444		L	2029.9145	2028.9192		2087.9927	2070.9662
3	102.0550	**343.2340**	326.2074	325.2234	371.2289	354.2023	353.2183	285.2285		E	1900.8719	1899.8766		1974.9086	1957.8821
4	88.0393	458.2609	441.2344	440.2504	486.2558	469.2293	468.2453	414.2711		D	1785.8449	1784.8497		***1845.8661***	1828.8395
5	86.0964	**571.3450**	554.3184	553.3344	599.3399	582.3134	581.3293	543.3137	557.3293	I	1672.7609	1685.7813	1699.7969	***1730.8391***	1713.8126
6	72.0808	670.4134	653.3869	652.4028	698.4083	681.3818	680.3978	656.3978		V	1573.6924	1586.7128		***1617.7550***	1600.7285
7	70.0651	767.4662	750.4396	749.4556	795.4611	778.4345	777.4505	741.4505		P	1476.6397	1475.6444		***1518.6866***	1501.6601
8	60.0444	854.4982	837.4716	836.4876	882.4931	865.4666	864.4825	838.5033		S	1389.6077	1388.6124		1421.6339	1404.6073
9	60.0444	941.5302	924.5037	923.5197	969.5251	952.4986	951.5146	925.5353		S	1302.5756	1301.5804		***1334.6018***	1317.5753
10	110.0713	1078.5891	1061.5626	1060.5786	1106.5840	1089.5575	1088.5735			H	1165.5167			***1247.5698***	1230.5433
11	87.0553	1192.6321	1175.6055	1174.6215	**1220.6270**	1203.6004	1202.6164	1149.6262		N	1051.4738	1050.4785		***1110.5109***	1093.4844
12	133.0430	1352.6627	1335.6362	1334.6521	1380.6576	1363.6311	1362.6471	1263.6692		C	891.4431	890.4479		***996.4680***	979.4414
13	88.0393	1467.6897	1450.6631	1449.6791	**1495.6846**	1478.6580	1477.6740	1423.6998		D	776.4162	775.4209		***836.4373***	819.4108
14	72.0808	**1566.7581**	1549.7315	1548.7475	**1594.7530**	1577.7264	1576.7424	1552.7424		V	677.3478	690.3682		***721.4104***	704.3838
15	70.0651	1663.8108	1646.7843	1645.8003	1691.8057	1674.7792	1673.7952	1637.7952		P	580.2950	579.2998		***622.3420***	605.3154
16	110.0713	1800.8697	1783.8432	1782.8592	**1828.8647**	1811.8381	1810.8541			H	443.2361			525.2892	508.2627
17	72.0808	1899.9382	1882.9116	1881.9276	1927.9331	1910.9065	1909.9225	1885.9225		V	344.1677	357.1881		***388.2303***	371.2037
18	87.0553	**2013.9811**	1996.9545	1995.9705	2041.9760	2024.9495	2023.9654	1970.9753		N	230.1248	229.1295		***289.1619***	272.1353
19	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LE	215.1390	243.1339	LED	330.1660	358.1609	LEDI	443.2500	471.2449
LEDIV	542.3184	570.3134	LEDIVP	639.3712	667.3661	ED	217.0819	245.0768

EDI	330.1660	358.1609	**EDIV**	429.2344	457.2293	**EDIVP**	526.2871	554.2821
EDIVPS	613.3192	641.3141	**DI**	201.1234	229.1183	**DIV**	300.1918	328.1867
DIVP	397.2445	425.2395	**DIVPS**	484.2766	512.2715	**DIVPSS**	571.3086	599.3035
IV	185.1648	213.1598	**IVP**	282.2176	310.2125	**IVPS**	369.2496	397.2445
IVPSS	456.2817	484.2766	**IVPSSH**	593.3406	621.3355	**VP**	169.1335	197.1285
VPS	256.1656	284.1605	**VPSS**	343.1976	371.1925	**VPSSH**	480.2565	508.2514
VPSSHN	594.2994	622.2943	**PS**	157.0972	185.0921	**PSS**	244.1292	272.1241
PSSH	381.1881	409.1830	**PSSHN**	495.2310	523.2259	**PSSHNC**	655.2617	683.2566
SS	147.0764	175.0713	**SSH**	284.1353	312.1302	**SSHN**	398.1783	426.1732
SSHNC	558.2089	586.2038	**SSHNCD**	673.2358	701.2308	**SH**	197.1033	225.0982
SHN	311.1462	339.1411	**SHNC**	471.1769	499.1718	**SHNCD**	586.2038	614.1987
SHNCDV	685.2722	713.2671	**HN**	224.1142	252.1091	**HNC**	384.1448	412.1398
HNCD	499.1718	527.1667	**HNCDV**	598.2402	626.2351	**HNCDVP**	695.2930	723.2879
NC	247.0859	275.0809	**NCD**	362.1129	390.1078	**NCDV**	461.1813	489.1762
NCDVP	558.2341	586.2290	**NCDVPH**	695.2930	723.2879	**CD**	248.0700	276.0649
CDV	347.1384	375.1333	**CDVP**	444.1911	472.1860	**CDVPH**	581.2500	609.2450
CDVPHV	680.3185	708.3134	**DV**	187.1077	215.1026	**DVP**	284.1605	312.1554
DVPH	421.2194	449.2143	**DVPHV**	520.2878	548.2827	**DVPHVN**	634.3307	662.3257
VP	169.1335	197.1285	**VPH**	306.1925	334.1874	**VPHV**	405.2609	433.2558
VPHVN	519.3038	547.2987	**PH**	207.1240	235.1190	**PHV**	306.1925	334.1874
PHVN	420.2354	448.2303	**HV**	209.1397	237.1346	**HVN**	323.1826	351.1775
VN	186.1237	214.1186						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
74.9	2215.0804	0.1130	KLEDIVPSSHNCDVPHVNR
23.0	2215.1848	0.0086	NDQVVDIVLEDLAAVHQIPK
17.4	2215.1233	0.0701	HVGNDVVVLIFKEQSSSSDR
17.2	2215.0918	0.1016	MEMTLFLNESYIFHRLR
15.2	2215.1518	0.0416	DLAAKGEVDTVLVALVDMQGR
14.8	2215.0914	0.1021	MIMVGTMAITLWVIGWAMK
14.3	2215.0651	0.1283	QTIAHMSTLNQRLESAEDR
13.8	2215.1056	0.0879	VHRMEDTTWIPLVASTTSR
13.8	2215.0918	0.1016	MEMTLFLNESYIFHRLR
13.2	2215.1129	0.0805	DIPHEKVMILECIFSVNR

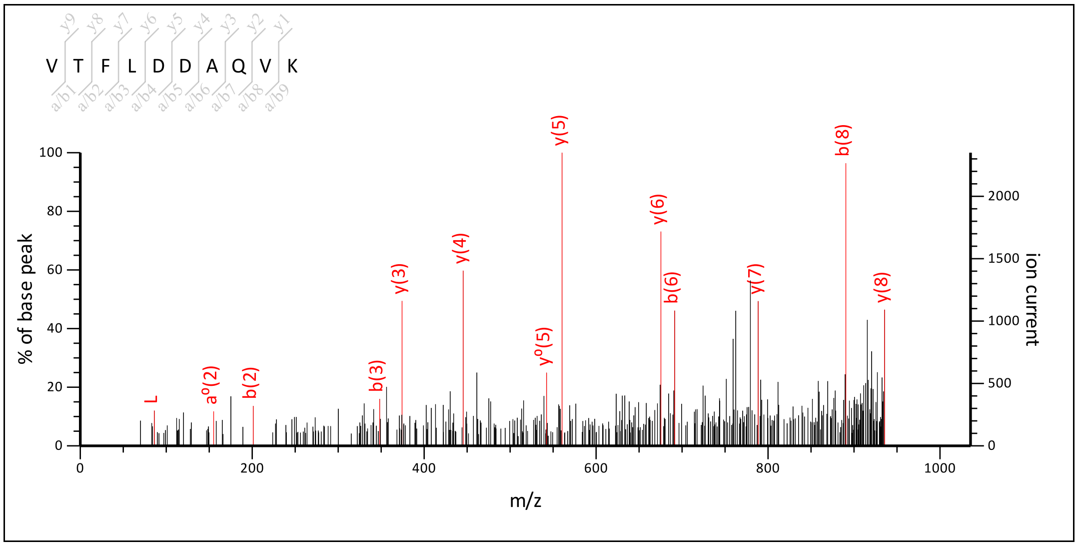
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 120

MS/MS Fragmentation of **VTFLDDAQVK**
Found in **gi|4239821** in **NCBInr**, germin-like protein 1 [Oryza sativa]

Match to Query 115: 1134.630224 from(1135.637500,1+) intensity(0.0000) index(13)
Title: Label: G18, Spot_Id: 219952, Peak_List_Id: 228894, MSMS Job_Run_Id: 22004, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_G18_136868326500.txt



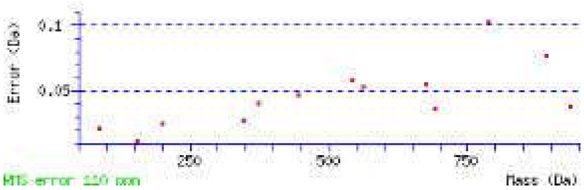
0 to 1035.52

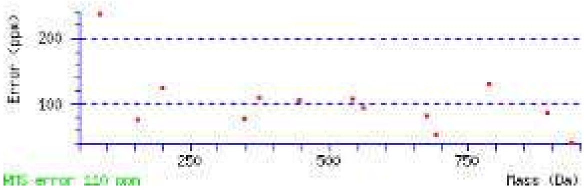
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1134.5921
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 3.1
Matches : 15/146 fragment ions using 18 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	y⁰
1	72.0808	72.0808			100.0757			44.0495		V						
2	74.0600	173.1285		155.1179	**201.1234**		183.1128	157.1335	159.1128	T	990.4891	1003.5095	1005.4888	1036.5310	1019.5044	1018.5204
3	120.0808	320.1969		302.1863	**348.1918**		330.1812			F	843.4207			***935.4833***	918.4567	917.4727
4	86.0964	433.2809		415.2704	461.2758		443.2653	391.2340		L	730.3366	729.3414		***788.4149***	771.3883	770.4043
5	88.0393	548.3079		530.2973	576.3028		558.2922	504.3180		D	615.3097	614.3144		***675.3308***	658.3042	657.3202
6	88.0393	663.3348		645.3243	**691.3297**		673.3192	619.3450		D	500.2827	499.2875		***560.3039***	543.2773	542.2933
7	44.0495	734.3719		716.3614	762.3668		744.3563			A	429.2456			***445.2769***	428.2504	
8	101.0709	862.4305	845.4040	844.4199	**890.4254**	873.3989	872.4149	805.4090		Q	301.1870	300.1918		***374.2398***	357.2132	
9	72.0808	961.4989	944.4724	943.4884	989.4938	972.4673	971.4833	947.4833		V	202.1186	215.1390		246.1812	229.1547	
10	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TF	221.1285	249.1234	TFL	334.2125	362.2074	TFLD	449.2395	477.2344
TFLDD	564.2664	592.2613	TFLDDA	635.3035	663.2984	FL	233.1648	261.1598
FLD	348.1918	376.1867	FLDD	463.2187	491.2136	FLDDA	534.2558	562.2508
FLDDAQ	662.3144	690.3093	LD	201.1234	229.1183	LDD	316.1503	344.1452
LDDA	387.1874	415.1823	LDDAQ	515.2460	543.2409	LDDAQV	614.3144	642.3093
DD	203.0662	231.0612	DDA	274.1034	302.0983	DDAQ	402.1619	430.1569
DDAQV	501.2304	529.2253	DA	159.0764	187.0713	DAQ	287.1350	315.1299
DAQV	386.2034	414.1983	AQ	172.1081	200.1030	AQV	271.1765	299.1714
QV	200.1394	228.1343						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.0	1134.5921	0.0381	VTFLDDAQVK
37.7	1134.5418	0.0884	AEFIDDGGRR
34.8	1134.5591	0.0711	TVMPDSDKVK
33.9	1134.5855	0.0447	YLPSVMAGAAR
32.1	1134.5306	0.0996	TVFPDTGDGAR
32.0	1134.6219	0.0083	IDFIAMAKAR
30.4	1134.6761	-0.0458	LSLALYTKAR
29.4	1134.5669	0.0633	EAFTELAAQR
29.1	1134.6067	0.0236	SLLMDTTKAR
29.1	1134.5404	0.0898	LETEDDKSAK

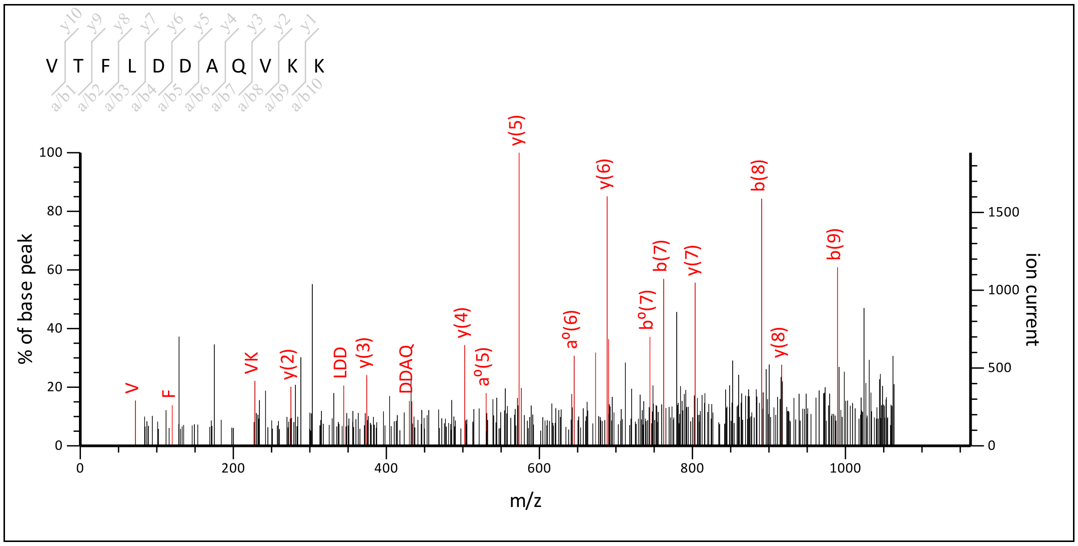
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 120

MS/MS Fragmentation of **VTFLDDAQVKK**
Found in **gi|4239821** in **NCBInr**, germin-like protein 1 [Oryza sativa]

Match to Query 127: 1262.729324 from(1263.736600,1+) intensity(0.0000) index(16)
Title: Label: G18, Spot_Id: 219952, Peak_List_Id: 228895, MSMS Job_Run_Id: 22004, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_G18_136868326500.txt



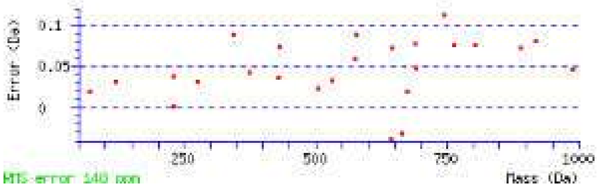
0 to 1163.44

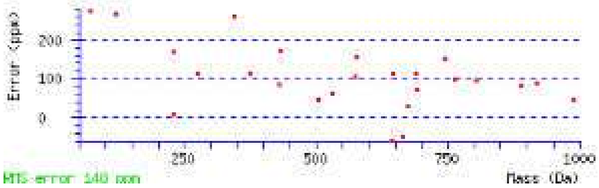
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1262.6871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 16
Matches : 27/168 fragment ions using 50 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	72.0808	**72.0808**			100.0757			44.0495		V						
2	74.0600	173.1285		155.1179	201.1234		183.1128	157.1335	159.1128	T	1118.5841	1131.6045	1133.5837	1164.6259	1147.5994	11
3	120.0808	320.1969		302.1863	348.1918		330.1812			F	971.5156			1063.5782	1046.5517	10
4	86.0964	**433.2809**		415.2704	461.2758		443.2653	391.2340		L	858.4316	857.4363		***916.5098***	899.4833	8
5	88.0393	548.3079		530.2973	**576.3028**		558.2922	504.3180		D	743.4046	742.4094		***803.4258***	786.3992	7
6	88.0393	663.3348		645.3243	691.3297		673.3192	619.3450		D	628.3777	627.3824		***688.3988***	671.3723	6
7	44.0495	734.3719		716.3614	**762.3668**		744.3563			A	557.3406			***573.3719***	556.3453	
8	101.0709	862.4305	845.4040	844.4199	**890.4254**	873.3989	872.4149	805.4090		Q	429.2820	428.2867		***502.3348***	485.3082	
9	72.0808	961.4989	944.4724	943.4884	**989.4938**	972.4673	971.4833	947.4833		V	330.2136	343.2340		***374.2762***	357.2496	
10	101.1073	1089.5939	1072.5673	1071.5833	1117.5888	1100.5623	1099.5782	1032.5360		K	202.1186	201.1234		***275.2078***	258.1812	
11	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TF	221.1285	249.1234	TFL	334.2125	362.2074	TFLD	449.2395	477.2344
TFLDD	564.2664	592.2613	TFLDDA	635.3035	663.2984	FL	233.1648	261.1598
FLD	348.1918	376.1867	FLDD	463.2187	491.2136	FLDDA	534.2558	562.2508
FLDDAQ	662.3144	690.3093	LD	201.1234	229.1183	LDD	316.1503	344.1452
LDDA	387.1874	415.1823	LDDAQ	515.2460	543.2409	LDDAQV	614.3144	642.3093
DD	203.0662	231.0612	DDA	274.1034	302.0983	DDAQ	402.1619	430.1569
DDAQV	501.2304	529.2253	DDAQVK	629.3253	657.3202	DA	159.0764	187.0713
DAQ	287.1350	315.1299	DAQV	386.2034	414.1983	DAQVK	514.2984	542.2933
AQ	172.1081	200.1030	AQV	271.1765	299.1714	AQVK	399.2714	427.2663
QV	200.1394	228.1343	QVK	328.2343	356.2292	VK	200.1757	228.1707





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
45.6	1262.6289	0.1004	MTDVIDAKAQR
35.7	1262.7234	0.0059	IIFTTDAAKGVK
33.2	1262.6871	0.0423	VTFLDDAQVKK
33.0	1262.6255	0.1038	VFEEADAKAQR
32.1	1262.6077	0.1216	ELMDSWKAAGR
31.9	1262.6329	0.0964	LPEGFMAEVVR
31.8	1262.6448	0.0845	QFILWDWQK
31.6	1262.6077	0.1216	ELMADWKAAGR
28.8	1262.6363	0.0931	MEKLMGPSVQK
28.7	1262.6983	0.0311	LFLSVSGEQKR

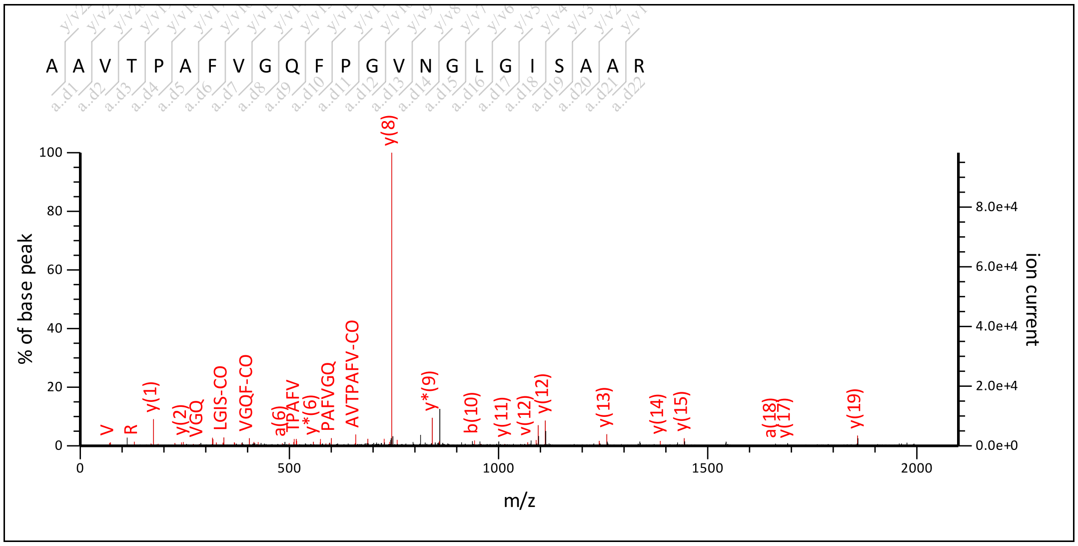
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 120

MS/MS Fragmentation of **AAVTPAFVGQFPGVNGLGISAAR**
Found in **gi|4239821** in **NCBInr**, germin-like protein 1 [Oryza sativa]

Match to Query 150: 2199.290324 from(2200.297600,1+) intensity(0.0000) index(23)
Title: Label: G18, Spot_Id: 219952, Peak_List_Id: 228893, MSMS Job_Run_Id: 22004, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_G18_136868326500.txt



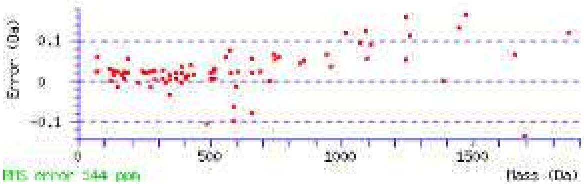
0 to 2099.29

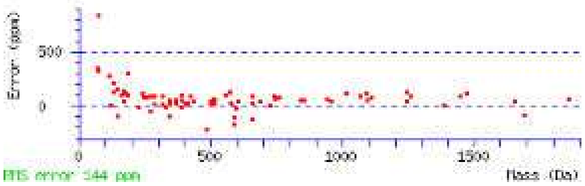
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2199.1801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77  Expect: 0.00032
Matches : 105/447 fragment ions using 160 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	44.0495	44.0495			**72.0444**			44.0495		**A**					
2	44.0495	**115.0866**			**143.0815**					**A**	2113.1189			2129.1502	2112.1237
3	72.0808	214.1550			**242.1499**			200.1394		**V**	2014.0505	2027.0709		2058.1131	2041.0865
4	74.0600	315.2027		297.1921	**343.1976**		325.1870	299.2078	301.1870	**T**	1913.0028	1926.0232	1928.0025	1959.0447	1942.0181
5	70.0651	412.2554		394.2449	440.2504		422.2398	386.2398		**P**	1815.9500	1814.9548		***1857.9970***	1840.9704
6	44.0495	**483.2926**		465.2820	**511.2875**		493.2769			**A**	1744.9129			1760.9442	1743.9177
7	120.0808	630.3610		612.3504	**658.3559**		640.3453			**F**	1597.8445			***1689.9071***	1672.8806
8	72.0808	729.4294		711.4188	**757.4243**		739.4137	715.4137		**V**	1498.7761	1511.7965		1542.8387	1525.8122
9	30.0338	786.4509		768.4403	814.4458		796.4352			**G**				***1443.7703***	1426.7437
10	101.0709	914.5094	897.4829	896.4989	**942.5043**	925.4778	924.4938	857.4880		**Q**	1313.6961	1312.7008		***1386.7488***	1369.7223
11	120.0808	1061.5778	1044.5513	1043.5673	**1089.5728**	1072.5462	1071.5622			**F**	1166.6276			***1258.6902***	1241.6637
12	70.0651	1158.6306	1141.6041	1140.6200	1186.6255	1169.5990	1168.6150	1132.6150		**P**	1069.5749	1068.5796		***1111.6218***	1094.5953
13	30.0338	1215.6521	1198.6255	1197.6415	1243.6470	1226.6204	1225.6364			**G**				***1014.5691***	997.5425
14	72.0808	1314.7205	1297.6939	1296.7099	1342.7154	1325.6889	1324.7048	1300.7048		**V**	913.4850	926.5054		***957.5476***	940.5211
15	87.0553	1428.7634	1411.7369	1410.7528	1456.7583	1439.7318	1438.7478	1385.7576		**N**	799.4421	798.4468		***858.4792***	841.4526
16	30.0338	1485.7849	1468.7583	1467.7743	1513.7798	1496.7532	1495.7692			**G**				***744.4363***	727.4097
17	86.0964	1598.8689	1581.8424	1580.8584	1626.8639	1609.8373	1608.8533	1556.8220		**L**	629.3365	628.3413		***687.4148***	670.3883
18	30.0338	**1655.8904**	1638.8639	1637.8798	1683.8853	1666.8588	1665.8748			**G**				***574.3307***	557.3042
19	86.0964	1768.9745	1751.9479	1750.9639	1796.9694	1779.9428	1778.9588	1740.9432	1754.9588	**I**	459.2310	472.2514	486.2671	***517.3093***	500.2827
20	60.0444	1856.0065	1838.9799	1837.9959	1884.0014	1866.9749	1865.9908	1840.0116		**S**	372.1990	371.2037		***404.2252***	387.1987
21	44.0495	1927.0436	1910.0171	1909.0330	1955.0385	1938.0120	1937.0280			**A**	301.1619			***317.1932***	300.1666
22	44.0495	1998.0807	1981.0542	1980.0702	2026.0756	2009.0491	2008.0651			**A**	230.1248			***246.1561***	229.1295
23	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AV	143.1179	171.1128	**AVT**	244.1656	272.1605	**AVTP**	341.2183	369.2132
AVTPA	412.2554	440.2504	**AVTPAF**	559.3239	587.3188	**AVTPAFV**	658.3923	686.3872
VT	173.1285	201.1234	**VTP**	270.1812	298.1761	**VTPA**	341.2183	369.2132
VTPAF	488.2867	516.2817	**VTPAFV**	587.3552	615.3501	**VTPAFVG**	644.3766	672.3715
TP	171.1128	199.1077	**TPA**	242.1499	270.1448	**TPAF**	389.2183	417.2132
TPAFV	488.2867	516.2817	**TPAFVG**	545.3082	573.3031	**TPAFVGQ**	673.3668	701.3617
PA	141.1022	169.0972	**PAF**	288.1707	316.1656	**PAFV**	387.2391	415.2340
PAFVG	444.2605	472.2554	**PAFVGQ**	572.3191	600.3140	**AF**	191.1179	219.1128
AFV	290.1863	318.1812	**AFVG**	347.2078	375.2027	**AFVGQ**	475.2663	503.2613
AFVGQF	622.3348	650.3297	**FV**	219.1492	247.1441	**FVG**	276.1707	304.1656
FVGQ	404.2292	432.2241	**FVGQF**	551.2976	579.2926	**FVGQFP**	648.3504	676.3453
VG	129.1022	157.0972	**VGQ**	257.1608	285.1557	**VGQF**	404.2292	432.2241
VGQFP	501.2820	529.2769	**VGQFPG**	558.3035	586.2984	**VGQFPGV**	657.3719	685.3668
GQ	158.0924	186.0873	**GQF**	305.1608	333.1557	**GQFP**	402.2136	430.2085
GQFPG	459.2350	487.2300	**GQFPGV**	558.3035	586.2984	**GQFPGVN**	672.3464	700.3413
QF	248.1394	276.1343	**QFP**	345.1921	373.1870	**QFPG**	402.2136	430.2085
QFPGV	501.2820	529.2769	**QFPGVN**	615.3249	643.3198	**QFPGVNG**	672.3464	700.3413
FP	217.1335	245.1285	**FPG**	274.1550	302.1499	**FPGV**	373.2234	401.2183
FPGVN	487.2663	515.2613	**FPGVNG**	544.2878	572.2827	**FPGVNGL**	657.3719	685.3668
PG	127.0866	155.0815	**PGV**	226.1550	254.1499	**PGVN**	340.1979	368.1928
PGVNG	397.2194	425.2143	**PGVNGL**	510.3035	538.2984	**PGVNGLG**	567.3249	595.3198
PGVNGLGI	680.4090	708.4039	**GV**	129.1022	157.0972	**GVN**	243.1452	271.1401
GVNG	300.1666	328.1615	**GVNGL**	413.2507	441.2456	**GVNGLG**	470.2722	498.2671
GVNGLGI	583.3562	611.3511	**GVNGLGIS**	670.3882	698.3832	**VN**	186.1237	214.1186
VNG	243.1452	271.1401	**VNGL**	356.2292	384.2241	**VNGLG**	413.2507	441.2456
VNGLGI	526.3348	554.3297	**VNGLGIS**	613.3668	641.3617	**VNGLGISA**	684.4039	712.3988
NG	144.0768	172.0717	**NGL**	257.1608	285.1557	**NGLG**	314.1823	342.1772
NGLGI	427.2663	455.2613	**NGLGIS**	514.2984	542.2933	**NGLGISA**	585.3355	613.3304
NGLGISAA	656.3726	684.3675	**GL**	143.1179	171.1128	**GLG**	200.1394	228.1343
GLGI	313.2234	341.2183	**GLGIS**	400.2554	428.2504	**GLGISA**	471.2926	499.2875
GLGISAA	542.3297	570.3246	**LG**	143.1179	171.1128	**LGI**	256.2020	284.1969
LGIS	343.2340	371.2289	**LGISA**	414.2711	442.2660	**LGISAA**	485.3082	513.3031
GI	143.1179	171.1128	**GIS**	230.1499	258.1448	**GISA**	301.1870	329.1819
GISAA	372.2241	400.2191	**IS**	173.1285	201.1234	**ISA**	244.1656	272.1605
ISAA	315.2027	343.1976	**SA**	131.0815	159.0764	**SAA**	202.1186	230.1135
AA	115.0866	143.0815						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.9	2199.1801	0.1103	AAVTPAFVGQFPGVNGLGISAAR
27.2	2199.1800	0.1103	AAVTPAFAAQFPGLNGLGLSAAR
18.2	2199.1746	0.1157	SNLSAAIDDVDKIIDLLSAAR
18.2	2199.2164	0.0739	IQTWQATIWLASGLKTAVGR
15.8	2199.0920	0.1984	LISDIDERNATLSNEWAPR

15.0	2199.1106	0.1797	INDAMGHAVGDDFLKIVTQR
14.3	2199.1430	0.1473	GMVEAGLITRDDVSVGTRPAR
14.2	2199.1800	0.1103	ELAFVPDAVVHYQLRSTVR
14.1	2199.1131	0.1772	NQAETISEQKAQETPVTGIR
13.2	2199.1933	0.0970	IEPLGMTGAGGLTEILAKVTGR

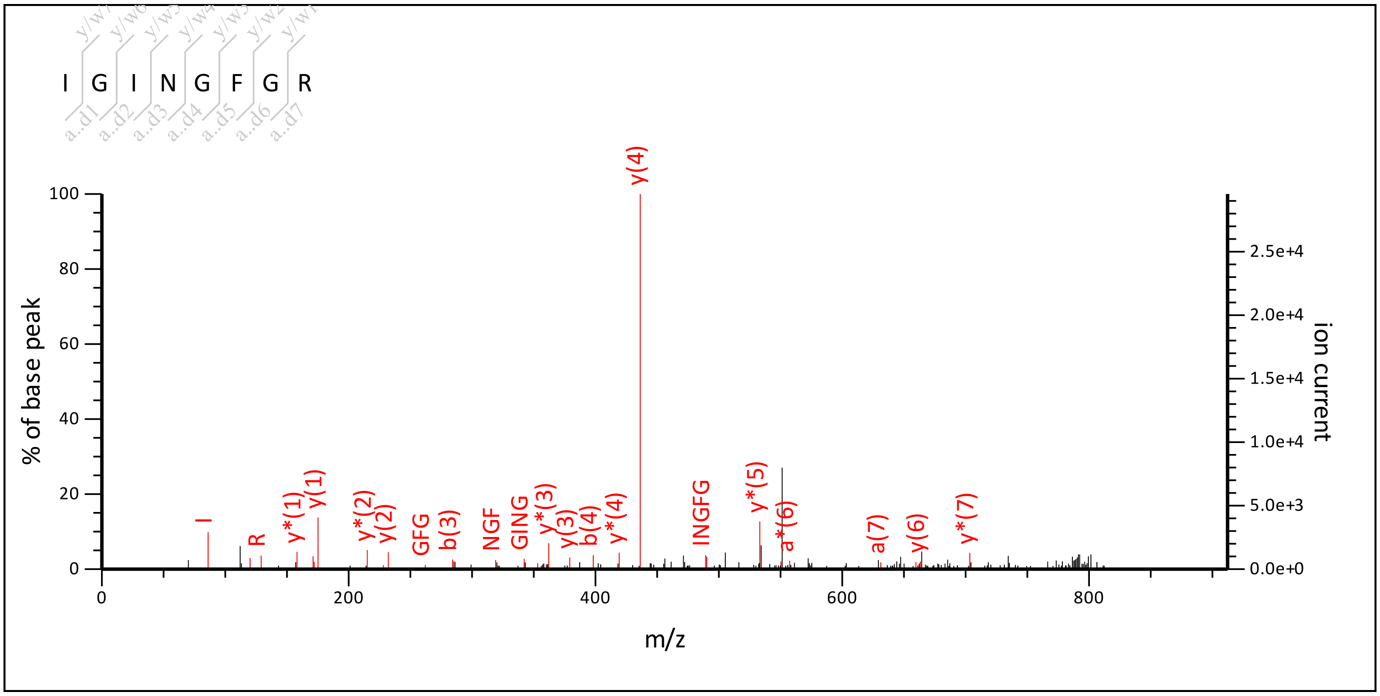
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 125

MS/MS Fragmentation of **IGINGFGR**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 5: 833.447684 from(834.454960,1+) intensity(0.0000) index(1)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221672, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



0 to 912.28

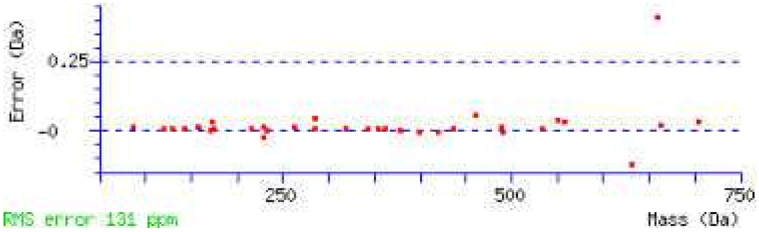
Label all possible matches ○ Label matches used for scoring ●

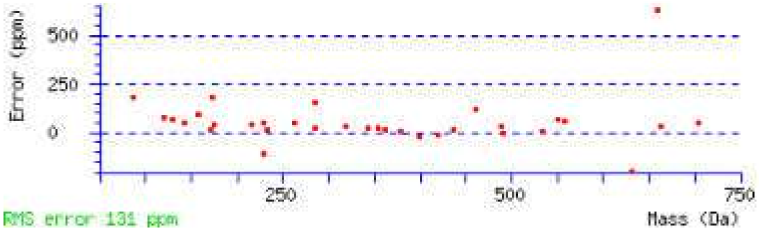
Monoisotopic mass of neutral peptide Mr(calc): 832.4555
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 11
Matches : 40/86 fragment ions using 72 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	d'	Seq.	v	w	w'	y	y*	#
1	86.0964	**86.0964**		114.0913		44.0495		**I**						**8**
2	30.0338	**143.1179**		**171.1128**				**G**				720.3787	703.3522	**7**
3	86.0964	256.2020		**284.1969**		228.1707	242.1863	**I**	605.2790	618.2994	632.3151	***663.3573***	646.3307	**6**
4	87.0553	370.2449	353.2183	**398.2398**	381.2132	327.2391		**N**	491.2361	490.2409		***550.2732***	533.2467	**5**
5	30.0338	427.2663	410.2398	455.2613	438.2347			**G**				***436.2303***	419.2037	**4**
6	120.0808	574.3348	557.3082	602.3297	585.3031			**F**	287.1462			***379.2088***	362.1823	**3**
7	30.0338	**631.3562**	614.3297	**659.3511**	642.3246			**G**				***232.1404***	215.1139	**2**
8	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GI	143.1179	171.1128	**GIN**	257.1608	285.1557	**GING**	314.1823	342.1772

GINGF	461.2507	489.2456	**GINGFG**	518.2722	546.2671	**IN**	200.1394	228.1343
ING	257.1608	285.1557	**INGF**	404.2292	432.2241	**INGFG**	461.2507	489.2456
NG	144.0768	172.0717	**NGF**	291.1452	319.1401	**NGFG**	348.1666	376.1615
GF	177.1022	205.0972	**GFG**	234.1237	262.1186	**FG**	177.1022	205.0972





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.8	832.4555	0.9921	VAINGFGR
31.4	833.4065	0.0411	GILDTCR
31.4	833.4395	0.0081	IGLDFNR
29.6	833.4396	0.0081	VADLGFGR
28.4	832.4555	0.9921	IGINGFGR
28.1	834.3984	-0.9507	GNIDFNR
27.7	832.4555	0.9921	LGINGFGR
27.2	833.4256	0.0220	QRGGGFGR
26.6	834.4195	-0.9719	TSNTLSGR
25.9	833.4144	0.0333	IGGGGFGGGR

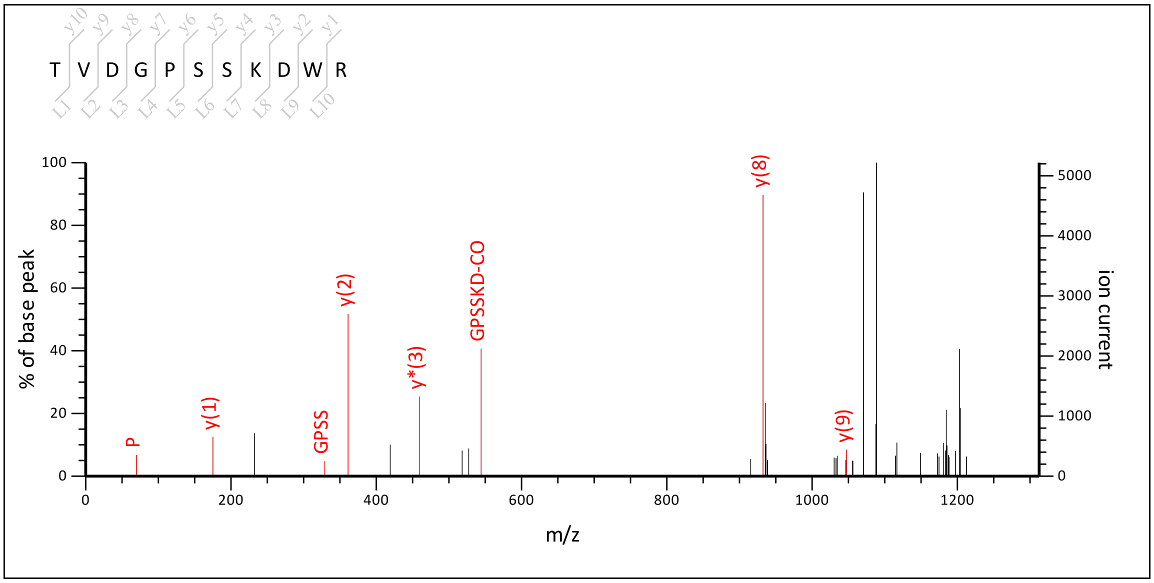
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 125

MS/MS Fragmentation of **TVDGPSSKDWR**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 25: 1246.611824 from(1247.619100,1+) intensity(0.0000) index(7)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221687, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



0 to 1312.55

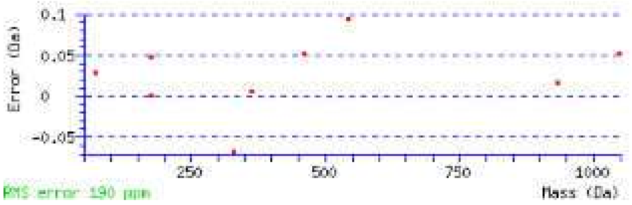
Label all possible matches ○ Label matches used for scoring ●

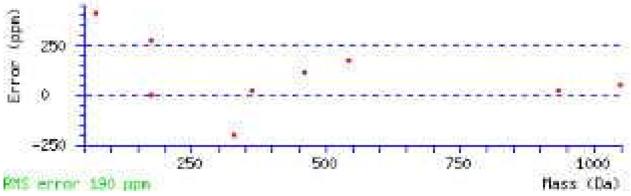
Monoisotopic mass of neutral peptide Mr(calc): 1246.5942
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 16 **Expect:** 1.7e+02
Matches : 11/173 fragment ions using 17 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	Seq.	v	w	y	y*	y⁰	#
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495	**T**						**11**
2	72.0808	173.1285		155.1179	201.1234		183.1128	159.1128	**V**	1102.4912	1115.5116	1146.5538	1129.5273	1128.5432	**10**
3	88.0393	288.1554		270.1448	316.1503		298.1397	244.1656	**D**	987.4643	986.4690	***1047.4854***	1030.4588	1029.4748	**9**
4	30.0338	345.1769		327.1663	373.1718		355.1612		**G**			***932.4585***	915.4319	914.4479	**8**
5	70.0651	442.2296		424.2191	470.2245		452.2140	416.2140	**P**	833.3900	832.3948	875.4370	858.4104	857.4264	**7**
6	60.0444	529.2617		511.2511	557.2566		539.2460	513.2667	**S**	746.3580	745.3628	778.3842	761.3577	760.3737	**6**
7	60.0444	616.2937		598.2831	644.2886		626.2780	600.2988	**S**	659.3260	658.3307	691.3522	674.3256	673.3416	**5**
8	101.1073	744.3886	727.3621	726.3781	772.3836	755.3570	754.3730	687.3308	**K**	531.2310	530.2358	604.3202	587.2936	586.3096	**4**
9	88.0393	859.4156	842.3890	841.4050	887.4105	870.3840	869.3999	815.4258	**D**	416.2041	415.2088	476.2252	459.1987	458.2146	**3**
10	159.0917	1045.4949	1028.4684	1027.4843	1073.4898	1056.4633	1055.4792		**W**	230.1248		***361.1983***	344.1717		**2**
11	129.1135								**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VD	187.1077	215.1026	**VDG**	244.1292	272.1241	**VDGP**	341.1819	369.1769
VDGPS	428.2140	456.2089	**VDGPSS**	515.2460	543.2409	**VDGPSSK**	643.3410	671.3359
DG	145.0608	173.0557	**DGP**	242.1135	270.1084	**DGPS**	329.1456	357.1405
DGPSS	416.1776	444.1725	**DGPSSK**	544.2726	572.2675	**DGPSSKD**	659.2995	687.2944
GP	127.0866	155.0815	**GPS**	214.1186	242.1135	**GPSS**	301.1506	329.1456
GPSSK	429.2456	457.2405	**GPSSKD**	544.2726	572.2675	**PS**	157.0972	185.0921

PSS	244.1292	272.1241	**PSSK**	372.2241	400.2191	**PSSKD**	487.2511	515.2460
PSSKDW	673.3304	701.3253	**SS**	147.0764	175.0713	**SSK**	275.1714	303.1663
SSKD	390.1983	418.1932	**SSKDW**	576.2776	604.2726	**SK**	188.1394	216.1343
SKD	303.1663	331.1612	**SKDW**	489.2456	517.2405	**KD**	216.1343	244.1292
KDW	402.2136	430.2085	**DW**	274.1186	302.1135			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
19.6	1246.6895	-0.0776	RGVLHPEAVGGR
16.8	1247.6445	-1.0326	VDVMISRAWR
16.2	1245.5884	1.0234	TGRMGSPQADAR
15.6	1247.5378	-0.9260	VDADTDAASNGGR
15.6	1246.5942	0.0176	TVDGPSSKDWR
15.6	1246.5942	0.0176	TVDGPSSKDWR
15.6	1246.5578	0.0540	TVDGPSSQDWR
15.5	1247.5201	-0.9083	CGVAEGGDGDVGR
15.3	1247.5717	-0.9599	MQEFSSHLNR
14.9	1245.5997	1.0122	TGRGGGCGGALQR

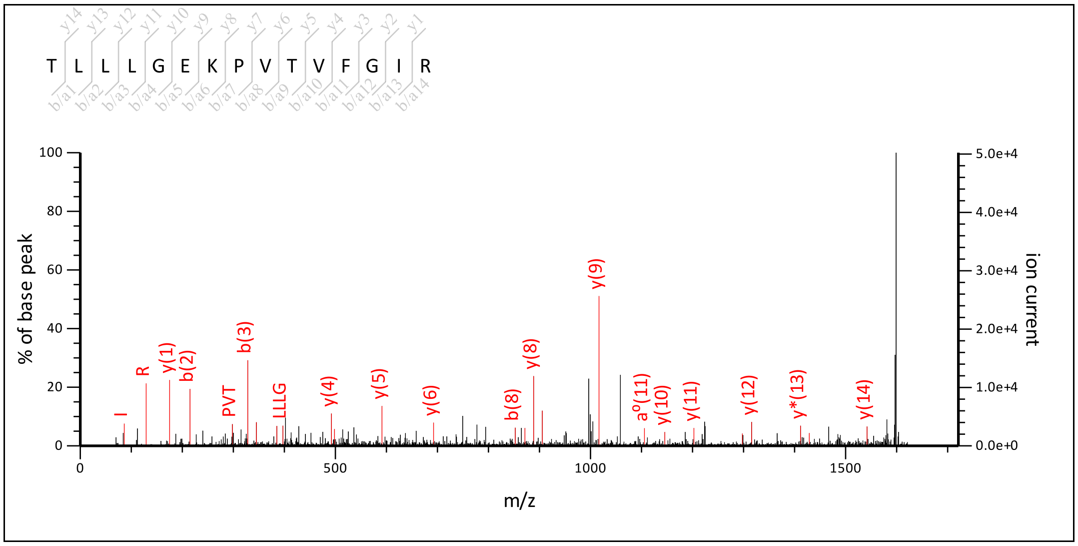
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 125**

MS/MS Fragmentation of **TLLLGEKPVTVFGIR**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 43: 1641.998624 from(1643.005900,1+) intensity(0.0000) index(13)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221664, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



0 to 1721.05

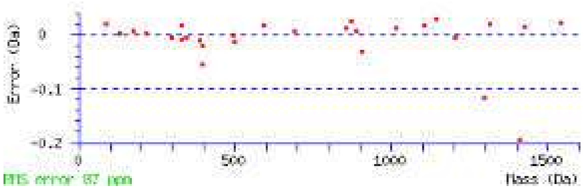
Label all possible matches ○ Label matches used for scoring ●

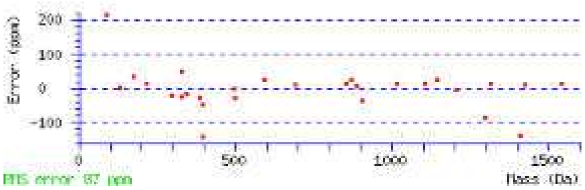
```
Monoisotopic mass of neutral peptide Mr(calc): 1641.9818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 79  Expect: 5.1e-05
Matches : 32/265 fragment ions using 48 most intense peaks   (help)
```

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	86.0964	187.1441		169.1335	**215.1390**		197.1285	145.0972		L	1483.8631	1482.8679		***1541.9414***	1524.9148	15
3	86.0964	300.2282		282.2176	**328.2231**		310.2125	258.1812		L	1370.7791	1369.7838		***1428.8573***	1411.8308	14
4	86.0964	413.3122		395.3017	441.3071		423.2966	371.2653		L	1257.6950	1256.6997		***1315.7732***	1298.7467	12
5	30.0338	470.3337		452.3231	**498.3286**		480.3180			G				***1202.6892***	1185.6626	11
6	102.0550	599.3763		581.3657	627.3712		609.3606	541.3708		E	1071.6309	1070.6357		***1145.6677***	1128.6412	11
7	101.1073	727.4713	710.4447	709.4607	755.4662	738.4396	737.4556	670.4134		K	943.5360	942.5407		***1016.6251***	999.5986	9
8	70.0651	824.5240	807.4975	806.5135	**852.5189**	835.4924	834.5084	798.5084		P	846.4832	845.4880		***888.5302***	871.5036	8
9	72.0808	923.5924	906.5659	905.5819	951.5873	934.5608	933.5768	909.5768		V	747.4148	760.4352		791.4774	774.4509	7
10	74.0600	1024.6401	1007.6136	1006.6295	1052.6350	1035.6085	1034.6245	1008.6452	1010.6245	T	646.3671	659.3875	661.3668	***692.4090***	675.3824	6
11	72.0808	1123.7085	1106.6820	1105.6980	1151.7034	1134.6769	1133.6929	1109.6929		V	547.2987	560.3191		***591.3613***	574.3348	
12	120.0808	1270.7769	1253.7504	1252.7664	1298.7719	1281.7453	1280.7613			F	400.2303			***492.2929***	475.2663	
13	30.0338	1327.7984	1310.7719	1309.7878	1355.7933	1338.7668	1337.7828			G				***345.2245***	328.1979	
14	86.0964	1440.8825	1423.8559	1422.8719	1468.8774	1451.8508	1450.8668	1412.8512	1426.8668	I	230.1248	243.1452	257.1608	288.2030	271.1765	
15	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LL	199.1805	227.1754	**LLL**	312.2646	340.2595	**LLLG**	369.2860	397.2809
LLLGE	498.3286	526.3235	**LLLGEK**	626.4236	654.4185	**LL**	199.1805	227.1754
LLG	256.2020	284.1969	**LLGE**	385.2445	413.2395	**LLGEK**	513.3395	541.3344
LLGEKP	610.3923	638.3872	**LG**	143.1179	171.1128	**LGE**	272.1605	300.1554
LGEK	400.2554	428.2504	**LGEKP**	497.3082	525.3031	**LGEKPV**	596.3766	624.3715
LGEKPVT	697.4243	725.4192	**GE**	159.0764	187.0713	**GEK**	287.1714	315.1663

GEKP	384.2241	412.2191	**GEKPV**	483.2926	511.2875	**GEKPVT**	584.3402	612.3352
GEKPVTV	683.4087	711.4036	**EK**	230.1499	258.1448	**EKP**	327.2027	355.1976
EKPV	426.2711	454.2660	**EKPVT**	527.3188	555.3137	**EKPVTV**	626.3872	654.3821
KP	198.1601	226.1550	**KPV**	297.2285	325.2234	**KPVT**	398.2762	426.2711
KPVTV	497.3446	525.3395	**KPVTVF**	644.4130	672.4079	**PV**	169.1335	197.1285
PVT	270.1812	298.1761	**PVTV**	369.2496	397.2445	**PVTVF**	516.3180	544.3130
PVTVFG	573.3395	601.3344	**PVTVFGI**	686.4236	714.4185	**VT**	173.1285	201.1234
VTV	272.1969	300.1918	**VTVF**	419.2653	447.2602	**VTVFG**	476.2867	504.2817
VTVFGI	589.3708	617.3657	**TV**	173.1285	201.1234	**TVF**	320.1969	348.1918
TVFG	377.2183	405.2132	**TVFGI**	490.3024	518.2973	**VF**	219.1492	247.1441
VFG	276.1707	304.1656	**VFGI**	389.2547	417.2496	**FG**	177.1022	205.0972
FGI	290.1863	318.1812	**GI**	143.1179	171.1128			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.0	1641.9818	0.0168	TLLLGEKPVTVFGIR
19.1	1642.7991	-0.8005	LTSASPYGWLPDSHL
15.7	1641.8508	0.1478	VDLVALSGSHTIGMAR
13.0	1642.9076	-0.9090	TISIVDVPAGKAMLGR
13.0	1642.9076	-0.9090	TLSIVDVPAGKAMLGR
12.1	1642.9406	-0.9420	ITLLTRSAWLAEAAK
11.6	1641.9202	0.0784	SAKNPVIIAGAGLFER
11.4	1641.7417	0.2570	TGDAGASDLYTMERR
11.3	1641.9202	0.0784	LLTPSLNLLHQHEK
11.1	1641.8151	0.1835	KPYFEEDKGGFLGR

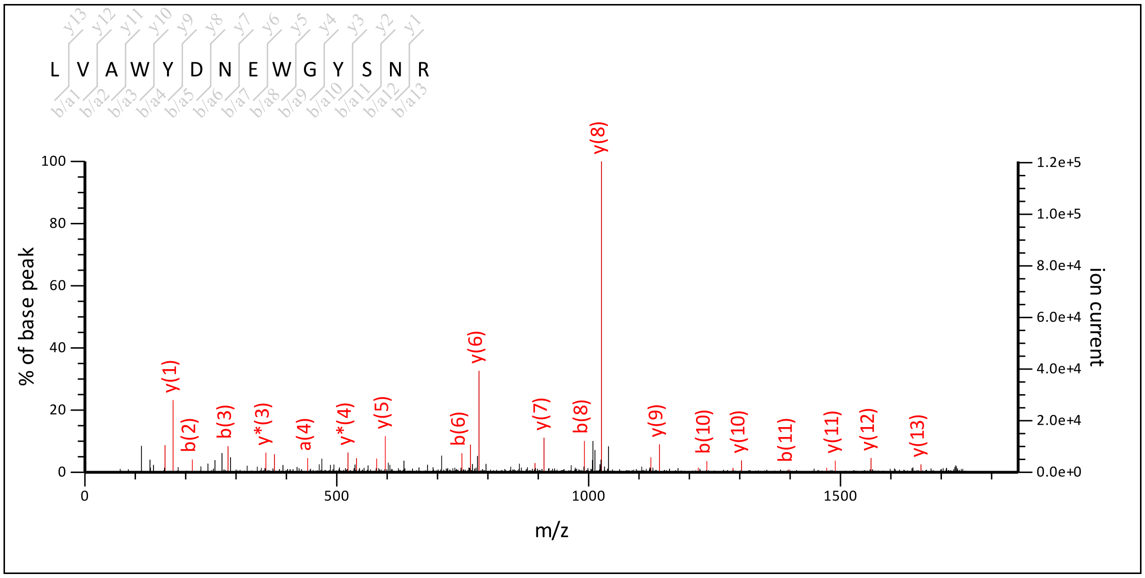
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 125

MS/MS Fragmentation of **LVAWYDNEWGYSNR**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 52: 1771.824924 from(1772.832200,1+) intensity(0.0000) index(17)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221661, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



0 to 1852.71

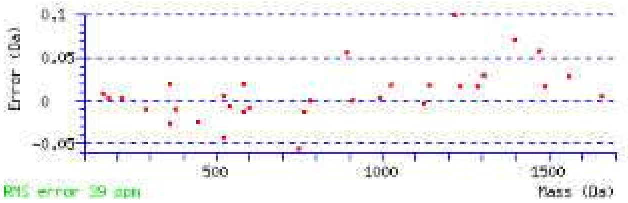
Label all possible matches ○ Label matches used for scoring ●

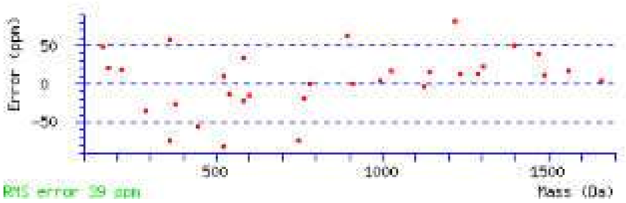
```
Monoisotopic mass of neutral peptide Mr(calc): 1771.7954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 111  Expect: 3.7e-08
Matches : 33/207 fragment ions using 34 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	86.0964	86.0964			114.0913			44.0495	L						14
2	72.0808	185.1648			**213.1598**			171.1492	V	1615.6560	1628.6764	***1659.7186***	1642.6921	1641.7081	13
3	44.0495	256.2020			**284.1969**				A	1544.6189		***1560.6502***	1543.6237	1542.6397	12
4	159.0917	442.2813			470.2762				W	1358.5396		***1489.6131***	1472.5866	1471.6026	11
5	136.0757	605.3446			633.3395				Y	1195.4763		***1303.5338***	1286.5073	1285.5232	10
6	88.0393	720.3715		702.3610	**748.3665**		730.3559	676.3817	D	1080.4493	1079.4541	***1140.4705***	1123.4439	1122.4599	9
7	87.0553	834.4145	817.3879	816.4039	862.4094	845.3828	844.3988	791.4087	N	966.4064	965.4112	***1025.4435***	1008.4170	1007.4330	8
8	102.0550	963.4571	946.4305	945.4465	**991.4520**	974.4254	973.4414	905.4516	E	837.3638	836.3686	***911.4006***	894.3741	893.3900	7
9	159.0917	1149.5364	1132.5098	1131.5258	1177.5313	1160.5047	1159.5207		W	651.2845		***782.3580***	765.3315	764.3474	6
10	30.0338	1206.5578	1189.5313	1188.5473	**1234.5527**	1217.5262	1216.5422		G			***596.2787***	579.2522	578.2681	5
11	136.0757	1369.6212	1352.5946	1351.6106	**1397.6161**	1380.5895	1379.6055		Y	431.1997		***539.2572***	522.2307	521.2467	4
12	60.0444	1456.6532	1439.6266	1438.6426	1484.6481	1467.6216	1466.6375	1440.6583	S	344.1677	343.1724	***376.1939***	359.1674	358.1833	3
13	87.0553	1570.6961	1553.6696	1552.6856	1598.6910	1581.6645	1580.6805	1527.6903	N	230.1248	229.1295	289.1619	272.1353		2
14	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VA	143.1179	171.1128	VAW	329.1972	357.1921	VAWY	492.2605	520.2554
VAWYD	607.2875	635.2824	AW	230.1288	258.1237	AWY	393.1921	421.1870
AWYD	508.2191	536.2140	AWYDN	622.2620	650.2569	WY	322.1550	350.1499
WYD	437.1819	465.1769	WYDN	551.2249	579.2198	WYDNE	680.2675	708.2624

YD	251.1026	279.0975	**YDN**	365.1456	393.1405	**YDNE**	494.1882	522.1831
YDNEW	680.2675	708.2624	**DN**	202.0822	230.0771	**DNE**	331.1248	359.1197
DNEW	517.2041	545.1991	**DNEWG**	574.2256	602.2205	**NE**	216.0979	244.0928
NEW	402.1772	430.1721	**NEWG**	459.1987	487.1936	**NEWGY**	622.2620	650.2569
EW	288.1343	316.1292	**EWG**	345.1557	373.1506	**EWGY**	508.2191	536.2140
EWGYS	595.2511	623.2460	**WG**	216.1131	244.1081	**WGY**	379.1765	407.1714
WGYS	466.2085	494.2034	**WGYSN**	580.2514	608.2463	**GY**	193.0972	221.0921
GYS	280.1292	308.1241	**GYSN**	394.1721	422.1670	**YS**	223.1077	251.1026
YSN	337.1506	365.1456	**SN**	174.0873	202.0822			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
110.9	1771.7954	0.0295	LVAWYDNEWGYSNR
26.7	1771.8476	-0.0226	IADIGLAKEPGEDDSDK
23.4	1771.8927	-0.0678	LVCDKDYPDKPPAVR
20.1	1770.9450	0.8799	KEALPHADMALLPPPR
16.6	1771.7683	0.0567	KTDYAADGAEEATGAMR
16.5	1771.8529	-0.0280	EKDPYLFSSNNFVGR
15.8	1771.7811	0.0439	LVDHMWPDFACEPR
15.5	1772.8152	-0.9902	MYGTSDPTAAERTAFR
15.4	1771.8410	-0.0161	IINEPTAAAIACEEDR
15.3	1771.9944	-0.1695	LVLPLPEKSLQGAHDR

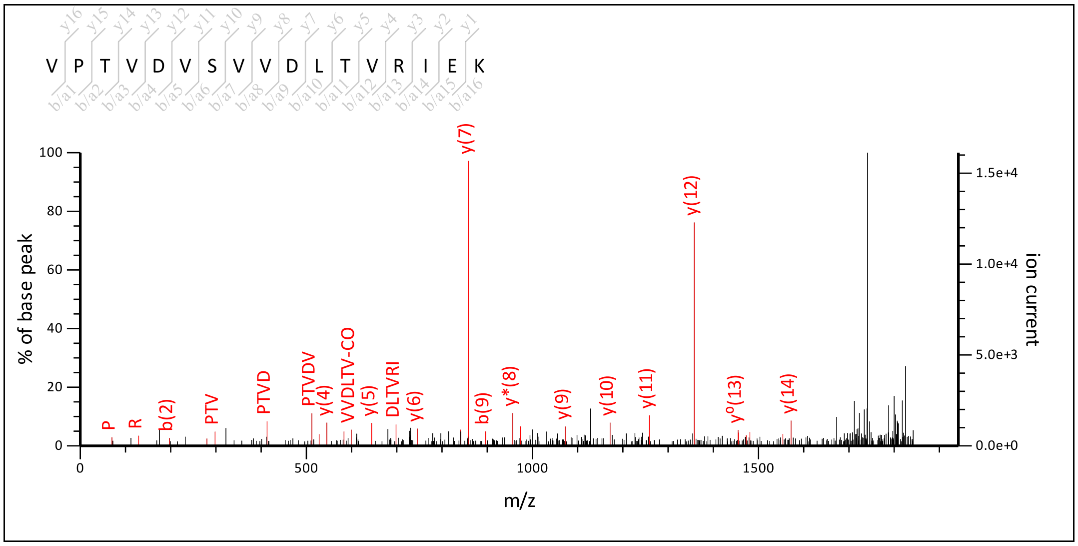
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 125

MS/MS Fragmentation of **VPTVDVSVVDLTVRIEK**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 67: 1868.081724 from(1869.089000,1+) intensity(0.0000) index(22)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221677, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



0 to 1942.06

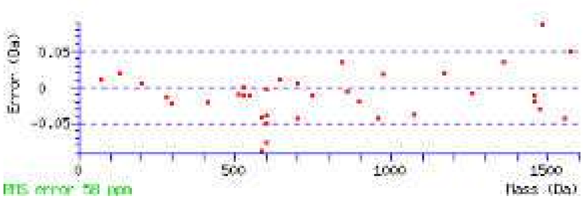
Label all possible matches ○ Label matches used for scoring ●

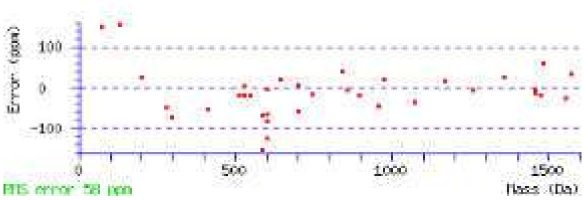
Monoisotopic mass of neutral peptide Mr(calc): 1868.0619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 0.0016
Matches : 39/309 fragment ions using 54 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	70.0651	169.1335			**197.1285**			143.1179		P	1727.9538	1726.9585		1770.0007	1752.9742
3	74.0600	270.1812		252.1707	**298.1761**		280.1656	254.1863	256.1656	T	1626.9061	1639.9265	1641.9058	1672.9480	1655.9214
4	72.0808	369.2496		351.2391	397.2445		379.2340	355.2340		V	1527.8377	1540.8581		***1571.9003***	1554.8737
5	88.0393	484.2766		466.2660	**512.2715**		494.2609	440.2867		D	1412.8108	1411.8155		***1472.8319***	1455.8053
6	72.0808	583.3450		565.3344	611.3399		593.3293	569.3293		V	1313.7423	1326.7627		***1357.8049***	1340.7784
7	60.0444	670.3770		652.3665	**698.3719**		680.3614	654.3821		S	1226.7103	1225.7151		***1258.7365***	1241.7100
8	72.0808	769.4454		751.4349	797.4403		779.4298	755.4298		V	1127.6419	1140.6623		***1171.7045***	1154.6780
9	72.0808	868.5138		850.5033	**896.5088**		878.4982	854.4982		V	1028.5735	1041.5939		***1072.6361***	1055.6095
10	88.0393	983.5408		965.5302	1011.5357		993.5251	939.5510		D	913.5465	912.5513		***973.5677***	956.5411
11	86.0964	1096.6249		1078.6143	1124.6198		1106.6092	1054.5779		L	800.4625	799.4672		***858.5407***	841.5142
12	74.0600	1197.6725		1179.6620	1225.6674		1207.6569	1181.6776	1183.6569	T	699.4148	712.4352	714.4145	***745.4567***	728.4301
13	72.0808	1296.7409		1278.7304	1324.7359		1306.7253	1282.7253		V	600.3464	613.3668		***644.4090***	627.3824
14	129.1135	1452.8421	1435.8155	1434.8315	**1480.8370**	1463.8104	1462.8264	1367.7781		R	444.2453	443.2500		***545.3406***	528.3140
15	86.0964	1565.9261	1548.8996	1547.9156	1593.9210	1576.8945	1575.9105	1537.8948	1551.9105	I	331.1612	344.1816	358.1973	389.2395	372.2129
16	102.0550	1694.9687	1677.9422	1676.9581	1722.9636	1705.9371	1704.9531	1636.9632		E	202.1186	201.1234		276.1554	259.1288
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PT	171.1128	199.1077	PTV	270.1812	298.1761	PTVD	385.2082	413.2031
PTVDV	484.2766	512.2715	PTVDVS	571.3086	599.3035	PTVDVSV	670.3770	698.3719
TV	173.1285	201.1234	TVD	288.1554	316.1503	TVDV	387.2238	415.2187
TVDVS	474.2558	502.2508	TVDVSV	573.3243	601.3192	TVDVSVV	672.3927	700.3876

VD	187.1077	215.1026	**VDV**	286.1761	314.1710	**VDVS**	373.2082	401.2031
VDVSV	472.2766	500.2715	**VDVSVV**	571.3450	599.3399	**VDVSVVD**	686.3719	714.3668
DV	187.1077	215.1026	**DVS**	274.1397	302.1347	**DVSV**	373.2082	401.2031
DVSVV	472.2766	500.2715	**DVSVVD**	587.3035	615.2984	**VS**	159.1128	187.1077
VSV	258.1812	286.1761	**VSVV**	357.2496	385.2445	**VSVVD**	472.2766	500.2715
VSVVDL	585.3606	613.3556	**VSVVDLT**	686.4083	714.4032	**SV**	159.1128	187.1077
SVV	258.1812	286.1761	**SVVD**	373.2082	401.2031	**SVVDL**	486.2922	514.2871
SVVDLT	587.3399	615.3348	**SVVDLTV**	686.4083	714.4032	**VV**	171.1492	199.1441
VVD	286.1761	314.1710	**VVDL**	399.2602	427.2551	**VVDLT**	500.3079	528.3028
VVDLTV	599.3763	627.3712	**VD**	187.1077	215.1026	**VDL**	300.1918	328.1867
VDLT	401.2395	429.2344	**VDLTV**	500.3079	528.3028	**VDLTVR**	656.4090	684.4039
DL	201.1234	229.1183	**DLT**	302.1710	330.1660	**DLTV**	401.2395	429.2344
DLTVR	557.3406	585.3355	**DLTVRI**	670.4246	698.4196	**LT**	187.1441	215.1390
LTV	286.2125	314.2074	**LTVR**	442.3136	470.3085	**LTVRI**	555.3977	583.3926
LTVRIE	684.4403	712.4352	**TV**	173.1285	201.1234	**TVR**	329.2296	357.2245
TVRI	442.3136	470.3085	**TVRIE**	571.3562	599.3511	**VR**	228.1819	256.1768
VRI	341.2659	369.2609	**VRIE**	470.3085	498.3035	**RI**	242.1975	270.1925
RIE	371.2401	399.2350	**IE**	215.1390	243.1339			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRIEK
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRLEK
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRLEK
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRLEK
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRLEK
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRLEK
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRLEK
64.1	1868.0619	0.0198	VPTVDVSVVDLTVRLEK
50.1	1868.0255	0.0562	VPEADVSVVDLTVRLEK
41.3	1867.0415	1.0402	VPQADVSVVDLTVRLEK

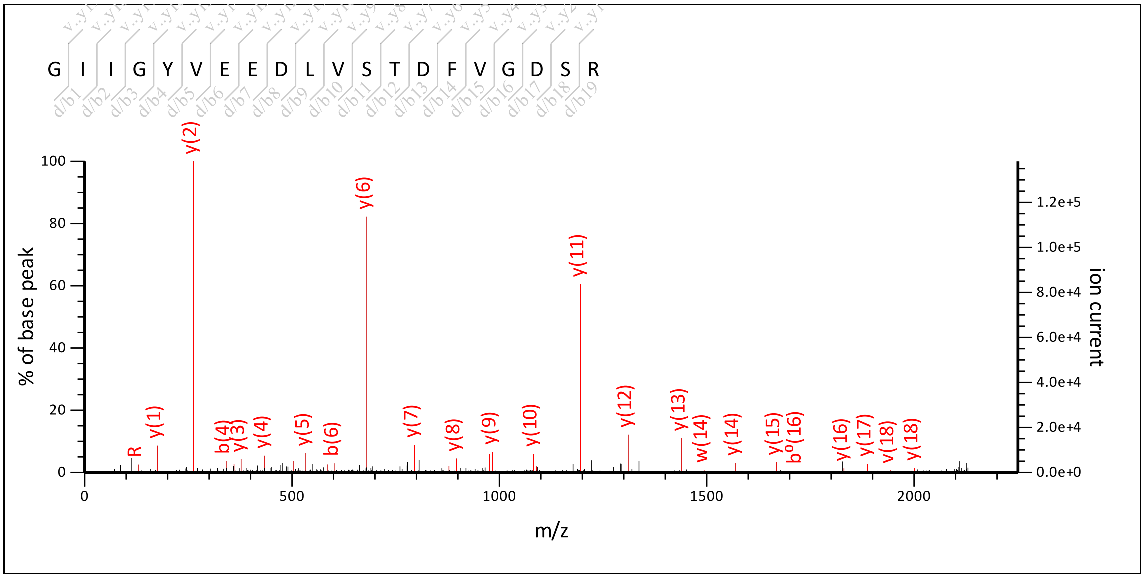
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 125

MS/MS Fragmentation of **GIIGYVEEDLVSTDFVGDSR**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 82: 2170.072324 from(2171.079600,1+) intensity(0.0000) index(26)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221665, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



0 to 2250.34

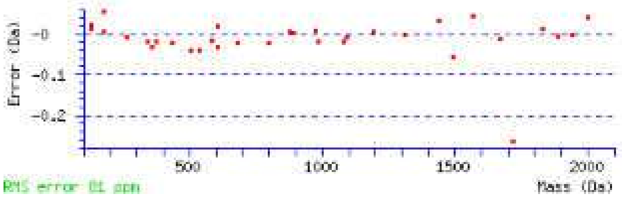
Label all possible matches ○ Label matches used for scoring ●

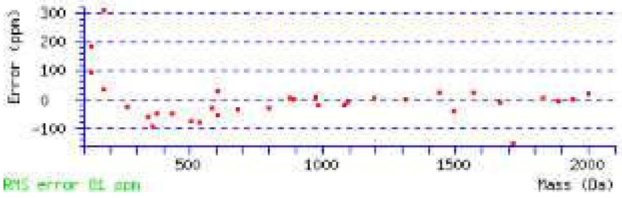
Monoisotopic mass of neutral peptide Mr(calc): 2170.0430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 168 **Expect:** 8.2e-14
Matches : 35/344 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	30.0338	30.0338		58.0287		44.0495		G							20
2	86.0964	143.1179		171.1128		115.0866	129.1022	I	2055.9506	2068.9710	2082.9866	2114.0288	2097.0023	2096.0182	19
3	86.0964	256.2020		284.1969		228.1707	242.1863	I	1942.8665	1955.8869	1969.9025	***2000.9447***	1983.9182	1982.9342	18
4	30.0338	313.2234		**341.2183**				G				***1887.8607***	1870.8341	1869.8501	17
5	136.0757	476.2867		**504.2817**				Y	1722.7817			***1830.8392***	1813.8127	1812.8287	16
6	72.0808	575.3552		**603.3501**		561.3395		V	1623.7133	1636.7337		***1667.7759***	1650.7493	1649.7653	15
7	102.0550	704.3978	686.3872	732.3927	714.3821	646.3923		E	1494.6707	1493.6754		***1568.7075***	1551.6809	1550.6969	14
8	102.0550	833.4403	815.4298	861.4353	843.4247	775.4349		E	1365.6281	1364.6329		***1439.6649***	1422.6383	1421.6543	13
9	88.0393	948.4673	930.4567	**976.4622**	958.4516	904.4775		D	1250.6012	1249.6059		***1310.6223***	1293.5957	1292.6117	12
10	86.0964	1061.5514	1043.5408	**1089.5463**	1071.5357	1019.5044		L	1137.5171	1136.5218		***1195.5953***	1178.5688	1177.5848	11
11	72.0808	1160.6198	1142.6092	1188.6147	1170.6041	1146.6041		V	1038.4487	1051.4691		***1082.5113***	1065.4847	1064.5007	10
12	60.0444	1247.6518	1229.6412	1275.6467	1257.6361	1231.6569		S	951.4167	950.4214		***983.4429***	966.4163	965.4323	9
13	74.0600	1348.6995	1330.6889	1376.6944	1358.6838	1332.7046	1334.6838	T	850.3690	863.3894	865.3686	***896.4108***	879.3843	878.4003	8
14	88.0393	1463.7264	1445.7159	1491.7213	1473.7108	1419.7366		D	735.3420	734.3468		***795.3632***	778.3366	777.3526	7
15	120.0808	1610.7948	1592.7843	1638.7897	1620.7792			F	588.2736			***680.3362***	663.3097	662.3257	6
16	72.0808	1709.8632	1691.8527	1737.8582	1719.8476	1695.8476		V	489.2052	502.2256		***533.2678***	516.2413	515.2572	5
17	30.0338	1766.8847	1748.8741	1794.8796	1776.8691			G				***434.1994***	417.1728	416.1888	4
18	88.0393	1881.9117	1863.9011	1909.9066	1891.8960	1837.9218		D	317.1568	316.1615		***377.1779***	360.1514	359.1674	3
19	60.0444	1968.9437	1950.9331	1996.9386	1978.9280	1952.9488		S	230.1248	229.1295		***262.1510***	245.1244	244.1404	2

20	129.1135						**R**	74.0237	73.0284		*175.1190*	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
II	199.1805	227.1754	**IIG**	256.2020	284.1969	**IIGY**	419.2653	447.2602
IIGYV	518.3337	546.3286	**IIGYVE**	647.3763	675.3712	**IG**	143.1179	171.1128
IGY	306.1812	334.1761	**IGYV**	405.2496	433.2445	**IGYVE**	534.2922	562.2871
IGYVEE	663.3348	691.3297	**GY**	193.0972	221.0921	**GYV**	292.1656	320.1605
GYVE	421.2082	449.2031	**GYVEE**	550.2508	578.2457	**GYVEED**	665.2777	693.2726
YV	235.1441	263.1390	**YVE**	364.1867	392.1816	**YVEE**	493.2293	521.2242
YVEED	608.2562	636.2511	**VE**	201.1234	229.1183	**VEE**	330.1660	358.1609
VEED	445.1929	473.1878	**VEEDL**	558.2770	586.2719	**VEEDLV**	657.3454	685.3403
EE	231.0975	259.0925	**EED**	346.1245	374.1194	**EEDL**	459.2086	487.2035
EEDLV	558.2770	586.2719	**EEDLVS**	645.3090	673.3039	**ED**	217.0819	245.0768
EDL	330.1660	358.1609	**EDLV**	429.2344	457.2293	**EDLVS**	516.2664	544.2613
EDLVST	617.3141	645.3090	**DL**	201.1234	229.1183	**DLV**	300.1918	328.1867
DLVS	387.2238	415.2187	**DLVST**	488.2715	516.2664	**DLVSTD**	603.2984	631.2933
LV	185.1648	213.1598	**LVS**	272.1969	300.1918	**LVST**	373.2445	401.2395
LVSTD	488.2715	516.2664	**LVSTDF**	635.3399	663.3348	**VS**	159.1128	187.1077
VST	260.1605	288.1554	**VSTD**	375.1874	403.1823	**VSTDF**	522.2558	550.2508
VSTDFV	621.3243	649.3192	**VSTDFVG**	678.3457	706.3406	**ST**	161.0921	189.0870
STD	276.1190	304.1139	**STDF**	423.1874	451.1823	**STDFV**	522.2558	550.2508
STDFVG	579.2773	607.2722	**STDFVGD**	694.3042	722.2992	**TD**	189.0870	217.0819
TDF	336.1554	364.1503	**TDFV**	435.2238	463.2187	**TDFVG**	492.2453	520.2402
TDFVGD	607.2722	635.2671	**TDFVGDS**	694.3042	722.2992	**DF**	235.1077	263.1026
DFV	334.1761	362.1710	**DFVG**	391.1976	419.1925	**DFVGD**	506.2245	534.2195
DFVGDS	593.2566	621.2515	**FV**	219.1492	247.1441	**FVG**	276.1707	304.1656
FVGD	391.1976	419.1925	**FVGDS**	478.2296	506.2245	**VG**	129.1022	157.0972
VGD	244.1292	272.1241	**VGDS**	331.1612	359.1561	**GD**	145.0608	173.0557
GDS	232.0928	260.0877	**DS**	175.0713	203.0662			





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
168.1	2170.0430	0.0293	GIIGYVEEDLVSTDFVGDSR
168.1	2170.0430	0.0293	GILGYVEEDLVSTDFVGDSR
150.3	2170.0430	0.0293	GILGYIDEDLVSTDFVGDSR
97.6	2170.0430	0.0293	GILGYIEEDVVSTDFVGDSR
69.3	2170.0430	0.0293	GILGYVEEDVVSTDFIGDSR
43.7	2170.0430	0.0293	GILGYIEDDVVSTDFIGDSR
43.7	2170.0430	0.0293	GILGYIEDDVVSTDFIGDSR
32.7	2170.0430	0.0293	GIIGYVDEDLVSTDFLGDSR
32.7	2170.0430	0.0293	GILGYVDEDLVSTDFLGDSR
18.6	2171.0019	-0.9296	GILGYTEEDVVSNDFVGDSR

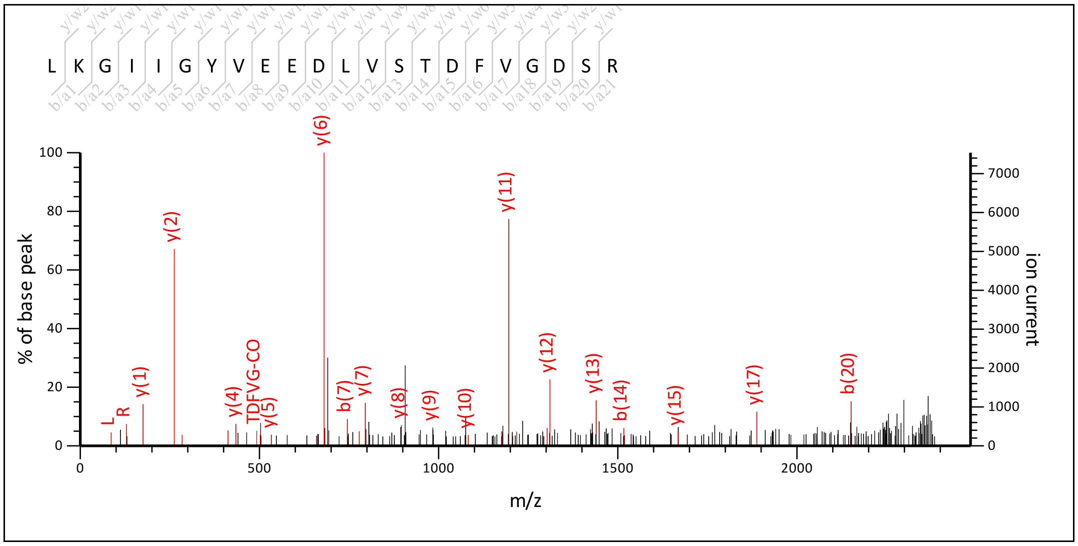
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 125

MS/MS Fragmentation of **LKGIIGYVEEDLVSTDFVGDSR**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 91: 2411.252524 from(2412.259800,1+) intensity(0.0000) index(30)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221679, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



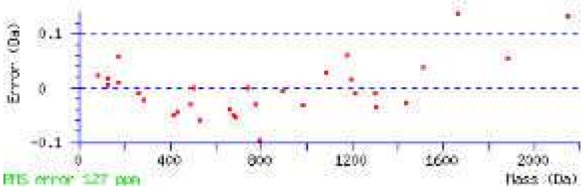
0 to 2484.37

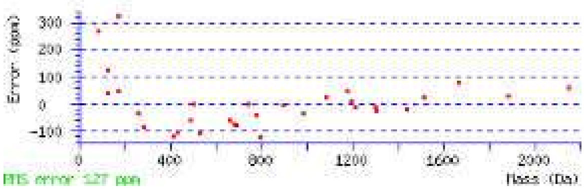
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2411.2220
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 0.02
Matches : 37/419 fragment ions using 86 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		L					
2	101.1073	214.1914	197.1648		242.1863	225.1598		157.1335		K	2226.0561	2225.0608		2299.1452	2282.1187
3	30.0338	271.2129	254.1863		299.2078	282.1812				G				2171.0503	2154.0237
4	86.0964	384.2969	367.2704		**412.2918**	395.2653		356.2656	370.2813	I	2055.9506	2068.9710	2082.9866	2114.0288	2097.0023
5	86.0964	497.3810	480.3544		525.3759	508.3493		469.3497	483.3653	I	1942.8665	1955.8869	1969.9025	2000.9447	1983.9182
6	30.0338	554.4024	537.3759		582.3974	565.3708				G				***1887.8607***	1870.8341
7	136.0757	717.4658	700.4392		**745.4607**	728.4341				Y	1722.7817			1830.8392	1813.8127
8	72.0808	816.5342	799.5076		844.5291	827.5026		802.5185		V	1623.7133	1636.7337		***1667.7759***	1650.7493
9	102.0550	945.5768	928.5502	927.5662	973.5717	956.5451	955.5611	887.5713		E	1494.6707	1493.6754		1568.7075	1551.6809
10	102.0550	1074.6194	1057.5928	1056.6088	1102.6143	1085.5877	1084.6037	1016.6139		E	1365.6281	1364.6329		***1439.6649***	1422.6383
11	88.0393	1189.6463	1172.6198	1171.6358	**1217.6412**	1200.6147	1199.6307	1145.6565		D	1250.6012	1249.6059		***1310.6223***	1293.5957
12	86.0964	1302.7304	1285.7038	1284.7198	1330.7253	1313.6987	1312.7147	1260.6834		L	1137.5171	1136.5218		***1195.5953***	1178.5688
13	72.0808	1401.7988	1384.7722	1383.7882	1429.7937	1412.7672	1411.7831	1387.7831		V	1038.4487	1051.4691		***1082.5113***	1065.4847
14	60.0444	1488.8308	1471.8043	1470.8203	**1516.8257**	1499.7992	1498.8152	1472.8359		S	951.4167	950.4214		***983.4429***	966.4163
15	74.0600	1589.8785	1572.8520	1571.8679	1617.8734	1600.8469	1599.8629	1573.8836	1575.8629	T	850.3690	863.3894	865.3686	***896.4108***	879.3843
16	88.0393	1704.9054	1687.8789	1686.8949	1732.9004	1715.8738	1714.8898	1660.9156		D	735.3420	734.3468		***795.3632***	778.3366
17	120.0808	1851.9739	1834.9473	1833.9633	1879.9688	1862.9422	1861.9582			F	588.2736			***680.3362***	663.3097
18	72.0808	1951.0423	1934.0157	1933.0317	1979.0372	1962.0106	1961.0266	1937.0266		V	489.2052	502.2256		***533.2678***	516.2413
19	30.0338	2008.0637	1991.0372	1990.0532	2036.0587	2019.0321	2018.0481			G				***434.1994***	417.1728
20	88.0393	2123.0907	2106.0641	2105.0801	**2151.0856**	2134.0590	2133.0750	2079.1009		D	317.1568	316.1615		377.1779	360.1514
21	60.0444	2210.1227	2193.0962	2192.1121	2238.1176	2221.0911	2220.1071	2194.1278		S	230.1248	229.1295		***262.1510***	245.1244
22	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KG	158.1288	186.1237	**KGI**	271.2129	299.2078	**KGII**	384.2969	412.2918
KGIIG	441.3184	469.3133	**KGIIGY**	604.3817	632.3766	**GI**	143.1179	171.1128
GII	256.2020	284.1969	**GIIG**	313.2234	341.2183	**GIIGY**	476.2867	504.2817
GIIGYV	575.3552	603.3501	**II**	199.1805	227.1754	**IIG**	256.2020	284.1969
IIGY	419.2653	447.2602	**IIGYV**	518.3337	546.3286	**IIGYVE**	647.3763	675.3712
IG	143.1179	171.1128	**IGY**	306.1812	334.1761	**IGYV**	405.2496	433.2445
IGYVE	534.2922	562.2871	**IGYVEE**	663.3348	691.3297	**GY**	193.0972	221.0921
GYV	292.1656	320.1605	**GYVE**	421.2082	449.2031	**GYVEE**	550.2508	578.2457
GYVEED	665.2777	693.2726	**YV**	235.1441	263.1390	**YVE**	364.1867	392.1816
YVEE	493.2293	521.2242	**YVEED**	608.2562	636.2511	**VE**	201.1234	229.1183
VEE	330.1660	358.1609	**VEED**	445.1929	473.1878	**VEEDL**	558.2770	586.2719
VEEDLV	657.3454	685.3403	**EE**	231.0975	259.0925	**EED**	346.1245	374.1194
EEDL	459.2086	487.2035	**EEDLV**	558.2770	586.2719	**EEDLVS**	645.3090	673.3039
ED	217.0819	245.0768	**EDL**	330.1660	358.1609	**EDLV**	429.2344	457.2293
EDLVS	516.2664	544.2613	**EDLVST**	617.3141	645.3090	**DL**	201.1234	229.1183
DLV	300.1918	328.1867	**DLVS**	387.2238	415.2187	**DLVST**	488.2715	516.2664
DLVSTD	603.2984	631.2933	**LV**	185.1648	213.1598	**LVS**	272.1969	300.1918
LVST	373.2445	401.2395	**LVSTD**	488.2715	516.2664	**LVSTDF**	635.3399	663.3348
VS	159.1128	187.1077	**VST**	260.1605	288.1554	**VSTD**	375.1874	403.1823
VSTDF	522.2558	550.2508	**VSTDFV**	621.3243	649.3192	**VSTDFVG**	678.3457	706.3406
ST	161.0921	189.0870	**STD**	276.1190	304.1139	**STDF**	423.1874	451.1823
STDFV	522.2558	550.2508	**STDFVG**	579.2773	607.2722	**STDFVGD**	694.3042	722.2992
TD	189.0870	217.0819	**TDF**	336.1554	364.1503	**TDFV**	435.2238	463.2187
TDFVG	492.2453	520.2402	**TDFVGD**	607.2722	635.2671	**TDFVGDS**	694.3042	722.2992
DF	235.1077	263.1026	**DFV**	334.1761	362.1710	**DFVG**	391.1976	419.1925
DFVGD	506.2245	534.2195	**DFVGDS**	593.2566	621.2515	**FV**	219.1492	247.1441
FVG	276.1707	304.1656	**FVGD**	391.1976	419.1925	**FVGDS**	478.2296	506.2245
VG	129.1022	157.0972	**VGD**	244.1292	272.1241	**VGDS**	331.1612	359.1561
GD	145.0608	173.0557	**GDS**	232.0928	260.0877	**DS**	175.0713	203.0662





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.9	2411.2220	0.0305	LKGIIGYVEEDLVSTDFVGDSR
51.9	2411.2220	0.0305	LKGILGYVEEDLVSTDFVGDSR
24.6	2411.2220	0.0305	LKGILGYIEEDVVSTDFVGDSR
12.9	2411.2162	0.0364	ELGLPDYWKDPVGFLTGYVSR
10.1	2410.6799	0.5727	LTYYTPMYZTKDTDILAAFR
9.8	2411.1896	0.0629	LTYYTVEYETKDTDILAAFR
9.7	2410.1773	1.0752	FLPSQLEVFNGLAISMQNCSR
9.4	2411.1719	0.0806	LTYYTPIYQTMDTDILAAFR
9.4	2411.1719	0.0806	LTYYTPLYQTMDTDILAAFR
9.4	2410.9087	0.3439	ADCSYMDVEALTDEMEEESR

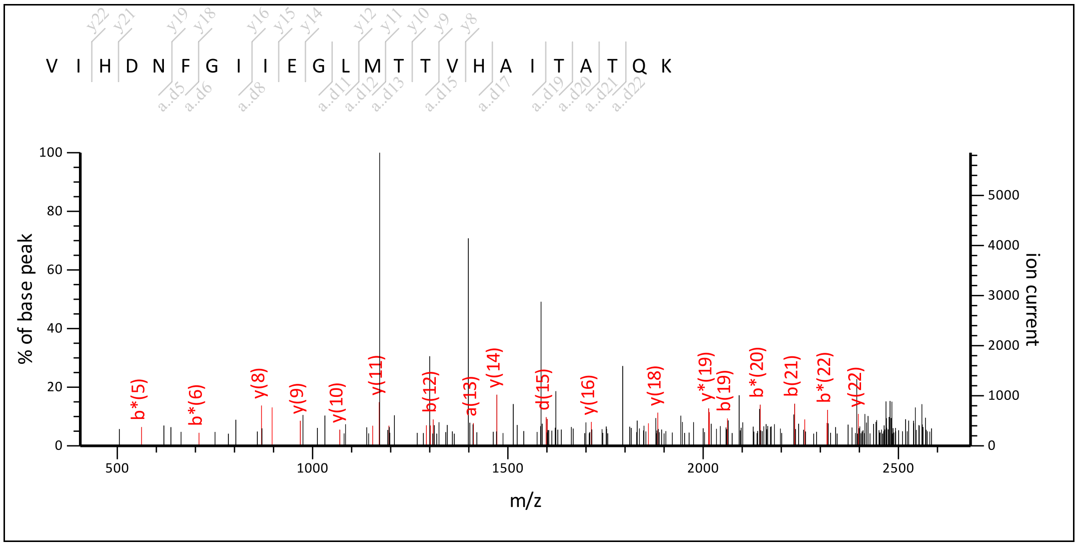
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 125**

MS/MS Fragmentation of **VIHDNFGIIEGLMTTVHAITATQK**
Found in **gi|968996** in **NCBInr**, glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Match to Query 99: 2608.415124 from(2609.422400,1+) intensity(0.0000) index(32)
Title: Label: P10, Spot_Id: 216636, Peak_List_Id: 221684, MSMS Job_Run_Id: 21387, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_P10_136117687500.txt



405.19 to 2684.61

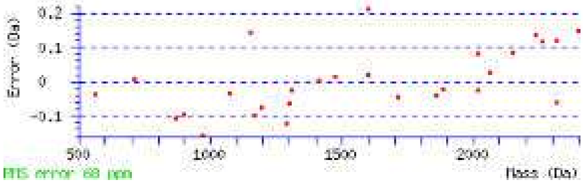
Label all possible matches ○ Label matches used for scoring ●

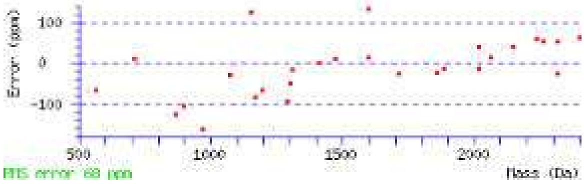
Monoisotopic mass of neutral peptide Mr(calc): 2608.3683
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 4.5
Matches : 28/481 fragment ions using 79 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	86.0964	185.1648			213.1598			157.1335	171.1492	I	2452.2289	2465.2493	2479.2650	2510.3072	2493.2806
3	110.0713	322.2238			350.2187					H	2315.1700			***2397.2231***	2380.1966
4	88.0393	437.2507		419.2401	465.2456		447.2350	393.2609		D	2200.1431	2199.1478		***2260.1642***	2243.1376
5	87.0553	551.2936	534.2671	533.2831	579.2885	562.2620	561.2780	508.2878		N	2086.1001	2085.1049		2145.1373	2128.1107
6	120.0808	698.3620	681.3355	680.3515	726.3569	709.3304	708.3464			F	1939.0317			2031.0943	2014.0678
7	30.0338	755.3835	738.3569	737.3729	783.3784	766.3519	765.3678			G				***1884.0259***	1866.9994
8	86.0964	868.4676	851.4410	850.4570	**896.4625**	879.4359	878.4519	840.4363	854.4519	I	1768.9262	1781.9466	1795.9623	1827.0044	1809.9779
9	86.0964	981.5516	964.5251	963.5411	1009.5465	992.5200	991.5360	953.5203	967.5360	I	1655.8421	1668.8625	1682.8782	***1713.9204***	1696.8938
10	102.0550	1110.5942	1093.5677	1092.5837	1138.5891	1121.5626	1120.5786	1052.5887		E	1526.7995	1525.8043		***1600.8363***	1583.8098
11	30.0338	1167.6157	1150.5891	1149.6051	**1195.6106**	1178.5840	1177.6000			G				***1471.7937***	1454.7672
12	86.0964	1280.6997	1263.6732	1262.6892	**1308.6947**	1291.6681	1290.6841	1238.6528		L	1356.6940	1355.6988		1414.7723	1397.7457
13	104.0528	1411.7402	1394.7137	1393.7297	1439.7351	1422.7086	1421.7246	1351.7369		M	1225.6535	1224.6583		***1301.6882***	1284.6617
14	74.0600	1512.7879	1495.7614	1494.7773	1540.7828	1523.7563	1522.7723	1496.7930	1498.7723	T	1124.6059	1137.6263	1139.6055	***1170.6477***	1153.6212
15	74.0600	1613.8356	1596.8090	1595.8250	1641.8305	1624.8040	1623.8199	1597.8407	1599.8199	T	1023.5582	1036.5786	1038.5578	***1069.6000***	1052.5735
16	72.0808	1712.9040	1695.8775	1694.8934	1740.8989	1723.8724	1722.8884	1698.8884		V	924.4898	937.5102		***968.5524***	951.5258
17	110.0713	1849.9629	1832.9364	1831.9524	1877.9578	1860.9313	1859.9473			H	787.4308			***869.4839***	852.4574
18	44.0495	1921.0000	1903.9735	1902.9895	1948.9949	1931.9684	1930.9844			A	716.3937			732.4250	715.3985
19	86.0964	2034.0841	2017.0575	2016.0735	**2062.0790**	2045.0525	2044.0684	2006.0528	2020.0684	I	603.3097	616.3301	630.3457	661.3879	644.3614
20	74.0600	2135.1318	2118.1052	2117.1212	2163.1267	2146.1001	2145.1161	2119.1369	2121.1161	T	502.2620	515.2824	517.2617	548.3039	531.2773
21	44.0495	2206.1689	2189.1423	2188.1583	**2234.1638**	2217.1373	2216.1532			A	431.2249			447.2562	430.2296
22	74.0600	2307.2166	2290.1900	2289.2060	2335.2115	2318.1849	2317.2009	2291.2217	2293.2009	T	330.1772	343.1976	345.1769	376.2191	359.1925
23	101.0709	2435.2751	2418.2486	2417.2646	2463.2701	2446.2435	2445.2595	2378.2537		Q	202.1186	201.1234		275.1714	258.1448

24	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IH	223.1553	251.1503	IHD	338.1823	366.1772	IHDN	452.2252	480.2201
IHDNF	599.2936	627.2885	IHDNFG	656.3151	684.3100	HD	225.0982	253.0931
HDN	339.1411	367.1361	HDNF	486.2096	514.2045	HDNFG	543.2310	571.2259
HDNFGI	656.3151	684.3100	DN	202.0822	230.0771	DNF	349.1506	377.1456
DNFG	406.1721	434.1670	DNFGI	519.2562	547.2511	DNFGII	632.3402	660.3352
NF	234.1237	262.1186	NFG	291.1452	319.1401	NFGI	404.2292	432.2241
NFGII	517.3133	545.3082	NFGIIE	646.3559	674.3508	FG	177.1022	205.0972
FGI	290.1863	318.1812	FGII	403.2704	431.2653	FGIIE	532.3130	560.3079
FGIIEG	589.3344	617.3293	GI	143.1179	171.1128	GII	256.2020	284.1969
GIIE	385.2445	413.2395	GIIEG	442.2660	470.2609	GIIEGL	555.3501	583.3450
GIIEGLM	686.3906	714.3855	II	199.1805	227.1754	IIE	328.2231	356.2180
IIEG	385.2445	413.2395	IIEGL	498.3286	526.3235	IIEGLM	629.3691	657.3640
IE	215.1390	243.1339	IEG	272.1605	300.1554	IEGL	385.2445	413.2395
IEGLM	516.2850	544.2799	IEGLMT	617.3327	645.3276	EG	159.0764	187.0713
EGL	272.1605	300.1554	EGLM	403.2010	431.1959	EGLMT	504.2486	532.2436
EGLMTT	605.2963	633.2912	GL	143.1179	171.1128	GLM	274.1584	302.1533
GLMT	375.2061	403.2010	GLMTT	476.2537	504.2486	GLMTTV	575.3221	603.3171
LM	217.1369	245.1318	LMT	318.1846	346.1795	LMTT	419.2323	447.2272
LMTTV	518.3007	546.2956	LMTTVH	655.3596	683.3545	MT	205.1005	233.0954
MTT	306.1482	334.1431	MTTV	405.2166	433.2115	MTTVH	542.2755	570.2704
MTTVHA	613.3126	641.3076	TT	175.1077	203.1026	TTV	274.1761	302.1710
TTVH	411.2350	439.2300	TTVHA	482.2722	510.2671	TTVHAI	595.3562	623.3511
TTVHAIT	696.4039	724.3988	TV	173.1285	201.1234	TVH	310.1874	338.1823
TVHA	381.2245	409.2194	TVHAI	494.3085	522.3035	TVHAIT	595.3562	623.3511
TVHAITA	666.3933	694.3883	VH	209.1397	237.1346	VHA	280.1768	308.1717
VHAI	393.2609	421.2558	VHAIT	494.3085	522.3035	VHAITA	565.3457	593.3406
VHAITAT	666.3933	694.3883	HA	181.1084	209.1033	HAI	294.1925	322.1874
HAIT	395.2401	423.2350	HAITA	466.2772	494.2722	HAITAT	567.3249	595.3198
HAITATQ	695.3835	723.3784	AI	157.1335	185.1285	AIT	258.1812	286.1761
AITA	329.2183	357.2132	AITAT	430.2660	458.2609	AITATQ	558.3246	586.3195
IT	187.1441	215.1390	ITA	258.1812	286.1761	ITAT	359.2289	387.2238
ITATQ	487.2875	515.2824	TA	145.0972	173.0921	TAT	246.1448	274.1397
TATQ	374.2034	402.1983	AT	145.0972	173.0921	ATQ	273.1557	301.1506
TQ	202.1186	230.1135						





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.5	2608.3683	0.0468	VIHDNFGIIEGLMTTVHAITATQK
17.4	2608.4047	0.0104	VIHDKFGIVEGLMTTVHAITATQK
1.9	2609.2908	-0.8756	MSAAAAFLPPAPAVPTRPDQDDSLR
0.9	2608.4145	0.0006	VEMAELTPINGKVEIAELKPINGK
0.7	2607.2938	1.1214	SYDVPGIAGTIPCPLCRSAIASFR
0.6	2608.1395	0.2756	WGEMVMGSQIDATRATSHGGGDGTR

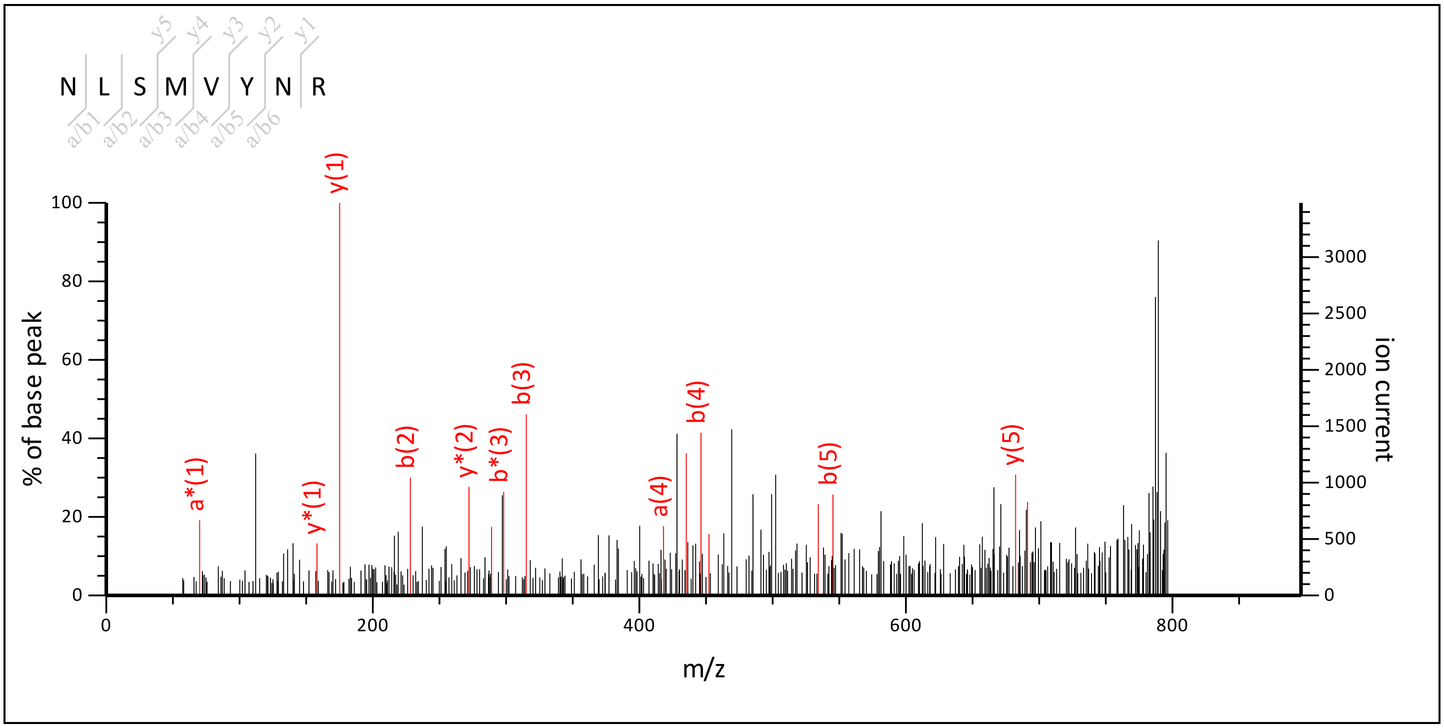
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 127**

MS/MS Fragmentation of **NLSMVYNR**
Found in **gi|285014508** in **NCBInr**, ATP synthase subunit [Triticum aestivum]

Match to Query 72: 995.500534 from(996.507810,1+) intensity(0.0000) index(5)
Title: Label: K3, Spot_Id: 219716, Peak_List_Id: 225409, MSMS Job_Run_Id: 21777, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K3_136842144100.txt

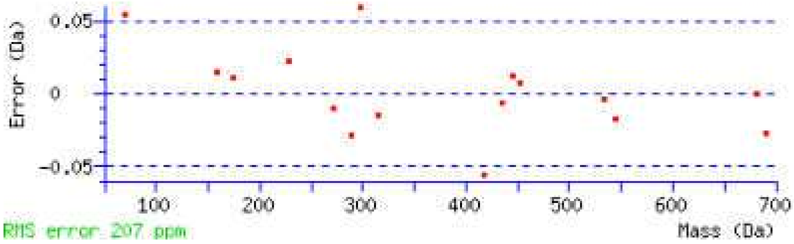


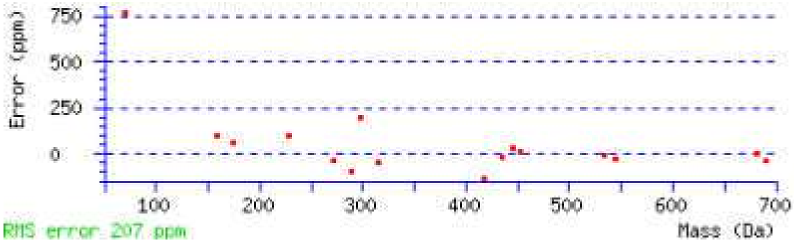
0 to 896.44

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 995.4858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 12 **Expect:** 1.4e+02
Matches : 16/42 fragment ions using 48 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	87.0553	70.0287	115.0502	98.0237	**N**			**8**
2	200.1394	183.1128	***228.1343***	211.1077	**L**	882.4502	865.4237	**7**
3	287.1714	270.1448	***315.1663***	298.1397	**S**	769.3661	752.3396	**6**
4	418.2119	401.1853	***446.2068***	429.1802	**M**	***682.3341***	665.3076	**5**
5	517.2803	500.2537	***545.2752***	528.2486	**V**	551.2936	534.2671	**4**
6	680.3436	663.3171	708.3385	691.3120	**Y**	***452.2252***	435.1987	**3**
7	794.3865	777.3600	822.3815	805.3549	**N**	***289.1619***	272.1353	**2**
8					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
12.9	995.4825	0.0180	QEGVGGFFR
12.5	995.4825	0.0181	KWTDQYR
12.5	995.4977	0.0028	KWTYWGR
12.5	995.5261	-0.0255	QGETIHRR
12.5	995.4165	0.0841	QGETMVCR
12.5	995.4165	0.0841	QSVTMDCR
11.5	995.4858	0.0147	NLSMVYNR
9.9	995.5261	-0.0255	INSHVRDR
9.5	995.4825	0.0181	DAKTGYWR
9.5	995.5876	-0.0871	GTRTPPLVR

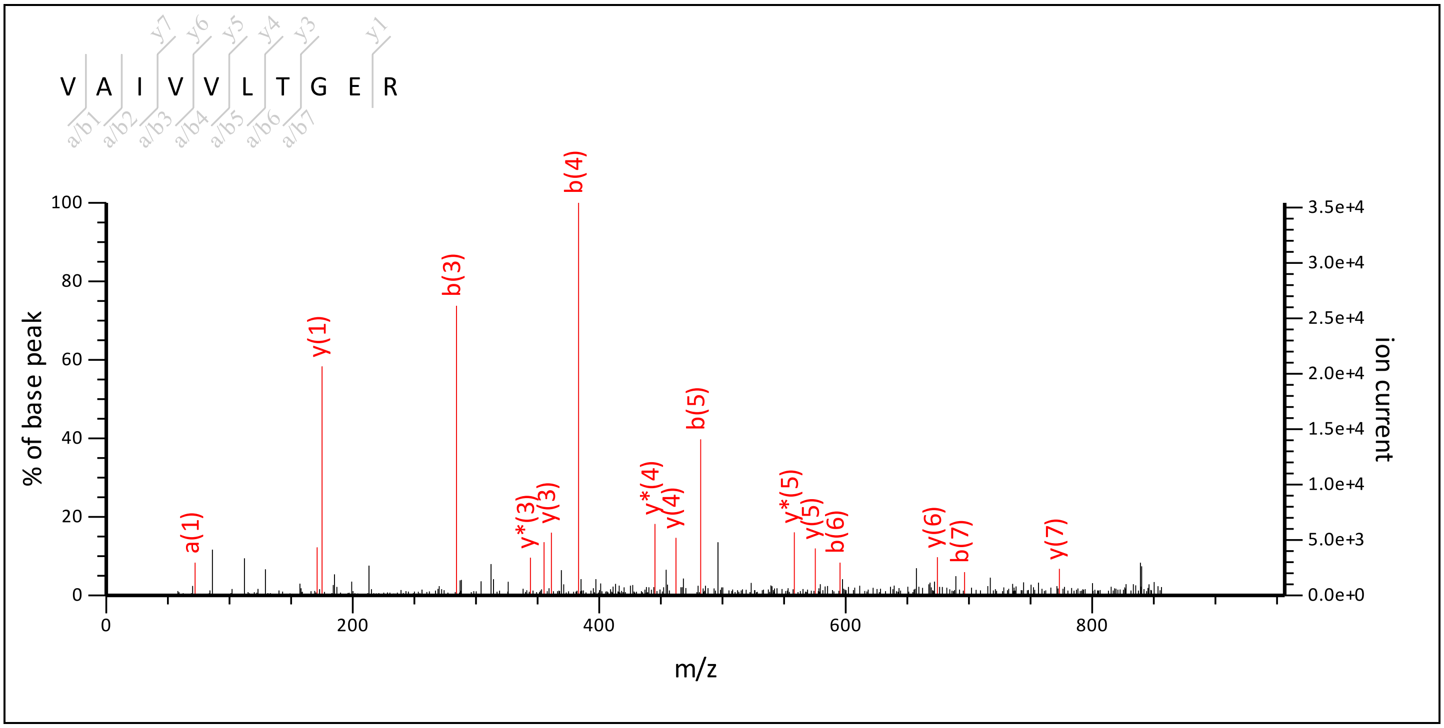
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 127

MS/MS Fragmentation of **VAIVVLTGER**
Found in **gi|285014508** in **NCBInr**, ATP synthase subunit [Triticum aestivum]

Match to Query 102: 1055.641924 from(1056.649200,1+) intensity(0.0000) index(8)
Title: Label: K3, Spot_Id: 219716, Peak_List_Id: 225400, MSMS Job_Run_Id: 21777, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K3_136842144100.txt



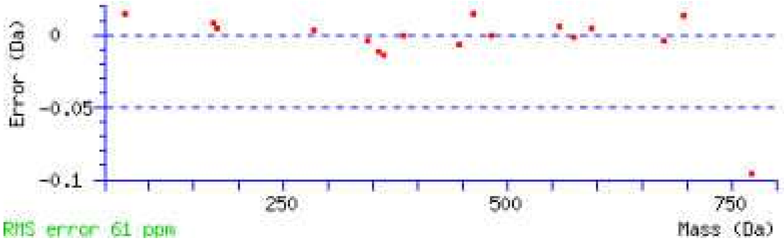
0 to 956.21

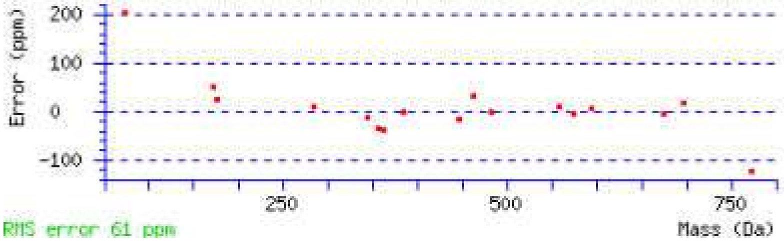
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1055.6339
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.015
Matches : 17/36 fragment ions using 24 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	**72.0808**	100.0757	**V**			**10**
2	143.1179	***171.1128***	**A**	957.5728	940.5462	**9**
3	256.2020	***284.1969***	**I**	886.5356	869.5091	**8**
4	**355.2704**	***383.2653***	**V**	***773.4516***	756.4250	**7**
5	454.3388	***482.3337***	**V**	***674.3832***	657.3566	**6**
6	567.4228	***595.4178***	**L**	***575.3148***	558.2882	**5**
7	668.4705	***696.4654***	**T**	***462.2307***	445.2041	**4**
8	725.4920	753.4869	**G**	***361.1830***	344.1565	**3**

9	854.5346	882.5295	**E**	304.1615	287.1350	**2**
10			**R**	*175.1190*	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.7	1055.6339	0.0080	VAIVVLTGER
49.7	1055.6339	0.0080	VALVVLTGER
36.5	1055.6227	0.0192	AIVVVDVVDK
30.2	1055.6451	-0.0032	LLRVLETGR
22.9	1055.6637	-0.0218	IRLVLGVMR
22.9	1055.6815	-0.0396	LLRVLVTSR
20.8	1055.5368	0.1051	VVLMCAAHR
20.2	1055.6703	-0.0283	VLVAVVKSNK
19.7	1055.6339	0.0080	LGLVVGGLGSGK
19.6	1055.5876	0.0543	VIAVQQGWR

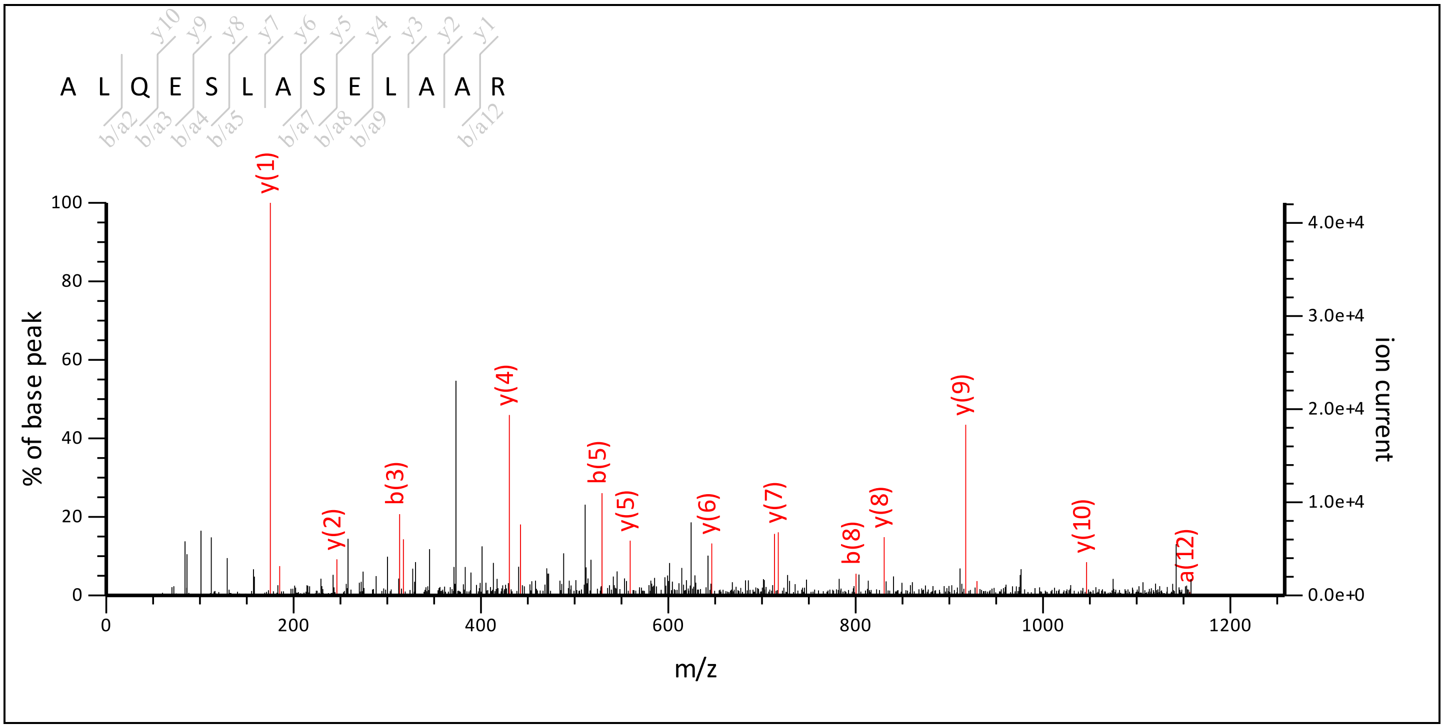
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 127

MS/MS Fragmentation of **ALQESLASELAAR**
Found in **gi|285014508** in **NCBInr**, ATP synthase subunit [Triticum aestivum]

Match to Query 196: 1357.730924 from(1358.738200,1+) intensity(0.0000) index(20)
Title: Label: K3, Spot_Id: 219716, Peak_List_Id: 225399, MSMS Job_Run_Id: 21777, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K3_136842144100.txt



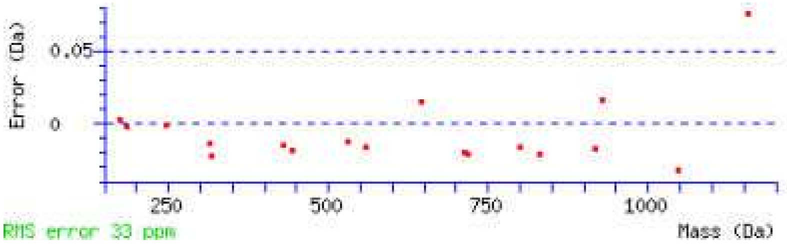
0 to 1257.99

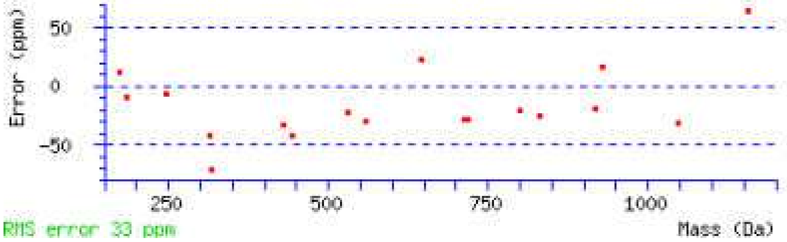
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1357.7201
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 0.00092
Matches : 18/68 fragment ions using 36 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			13
2	157.1335		**185.1285**		L	1287.6903	1270.6638	12
3	285.1921	268.1656	**313.1870**	296.1605	Q	1174.6062	1157.5797	11
4	414.2347	397.2082	**442.2296**	425.2031	E	***1046.5477***	1029.5211	10
5	501.2667	484.2402	**529.2617**	512.2351	S	***917.5051***	900.4785	9
6	614.3508	597.3243	642.3457	625.3192	L	***830.4730***	813.4465	8
7	685.3879	668.3614	**713.3828**	696.3563	A	***717.3890***	700.3624	7
8	772.4199	755.3934	**800.4149**	783.3883	S	***646.3519***	629.3253	6

9	901.4625	884.4360	**929.4575**	912.4309	**E**	***559.3198***	542.2933	**5**
10	1014.5466	997.5201	1042.5415	1025.5150	**L**	***430.2772***	413.2507	**4**
11	1085.5837	1068.5572	1113.5786	1096.5521	**A**	***317.1932***	300.1666	**3**
12	1156.6208	1139.5943	1184.6157	1167.5892	**A**	***246.1561***	229.1295	**2**
13					**R**	***175.1190***	158.0924	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
63.7	1357.7201	0.0108	ALQESIASELAAR
63.7	1357.7201	0.0108	ALQESLASELAAR
35.1	1357.7201	0.0108	SLQEALASELAAR
31.4	1357.7201	0.0108	KALEESAAELAAR
22.9	1357.7201	0.0108	IATTASPVSGAEVR
19.5	1357.7751	-0.0442	KALITCLEIAAR
18.9	1357.6950	0.0359	QALADDTDRVVR
18.1	1357.7354	-0.0044	KAISELDGWLAR
18.1	1357.6837	0.0472	QALTDLAAPSSER
16.9	1357.7929	-0.0620	KITDATLSVIAAR

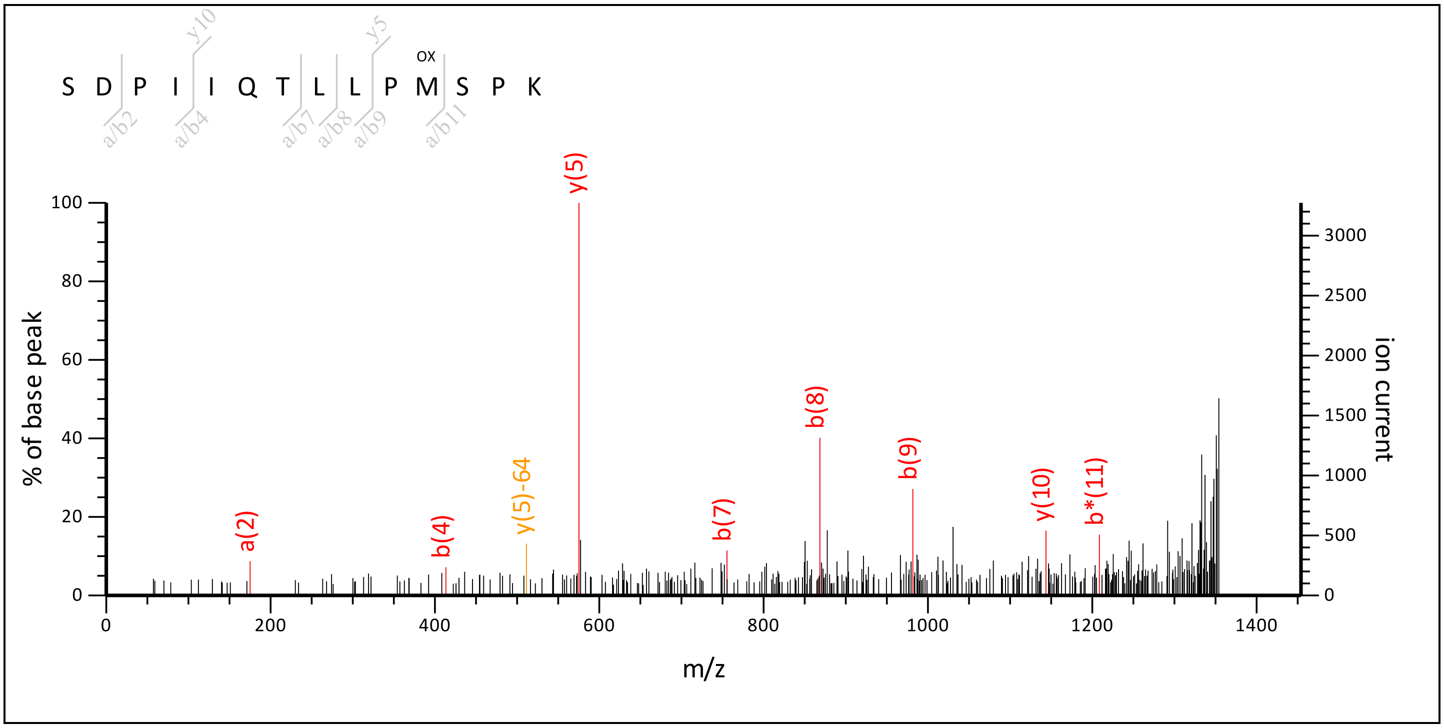
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 127

MS/MS Fragmentation of **SDPIIQTLLPMSPK**
Found in **gi|285014508** in **NCBInr**, ATP synthase subunit [Triticum aestivum]

Match to Query 232: 1554.818724 from(1555.826000,1+) intensity(0.0000) index(22)
Title: Label: K3, Spot_Id: 219716, Peak_List_Id: 225421, MSMS Job_Run_Id: 21777, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_K3_136842144100.txt



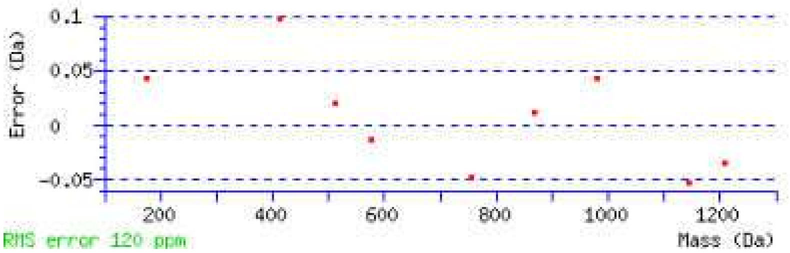
0 to 1454.01

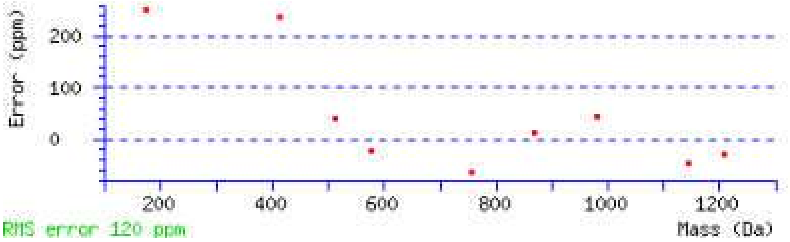
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1554.8327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 19 **Expect:** 25
Matches : 9/100 fragment ions using 13 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	60.0444		88.0393		S			14
2	175.0713		203.0662		D	1468.8080	1451.7814	13
3	272.1241		300.1190		P	1353.7810	1336.7545	12
4	385.2082		*413.2031*		I	1256.7283	1239.7017	11
5	498.2922		526.2871		I	1143.6442	1126.6177	10
6	626.3508	609.3243	654.3457	637.3192	Q	1030.5601	1013.5336	9

7	727.3985	710.3719	***755.3934***	738.3668	**T**	902.5016	885.4750	**8**
8	840.4825	823.4560	***868.4775***	851.4509	**L**	801.4539	784.4273	**7**
9	953.5666	936.5401	***981.5615***	964.5350	**L**	688.3698	671.3433	**6**
10	1050.6194	1033.5928	1078.6143	1061.5877	**P**	**575.2858**	558.2592	**5**
11	1197.6548	1180.6282	1225.6497	1208.6231	**M**	478.2330	461.2064	**4**
12	1284.6868	1267.6603	1312.6817	1295.6552	**S**	331.1976	314.1710	**3**
13	1381.7396	1364.7130	1409.7345	1392.7079	**P**	244.1656	227.1390	**2**
14					**K**	147.1128	130.0863	**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.9	1554.8327	-0.0140	SDPIIQTLLPMSPK
12.6	1554.9286	-0.1099	SIVLWRILLLSGW
10.6	1554.8630	-0.0443	AFEIARVHGLISSR
10.5	1554.8163	0.0024	FIPCGLIQLHAMR
10.5	1554.8163	0.0024	FLPCGLIQLHAMR
10.5	1554.8374	-0.0187	SLEMNILMAKLHR
9.9	1554.8089	0.0098	LMSLGGSRYFRPR
9.9	1554.7402	0.0786	WPINMEHGWTIR
9.1	1554.9344	-0.1157	ALKDELLLLSTLAR
8.3	1554.8729	-0.0542	AIIDLQELIESRR

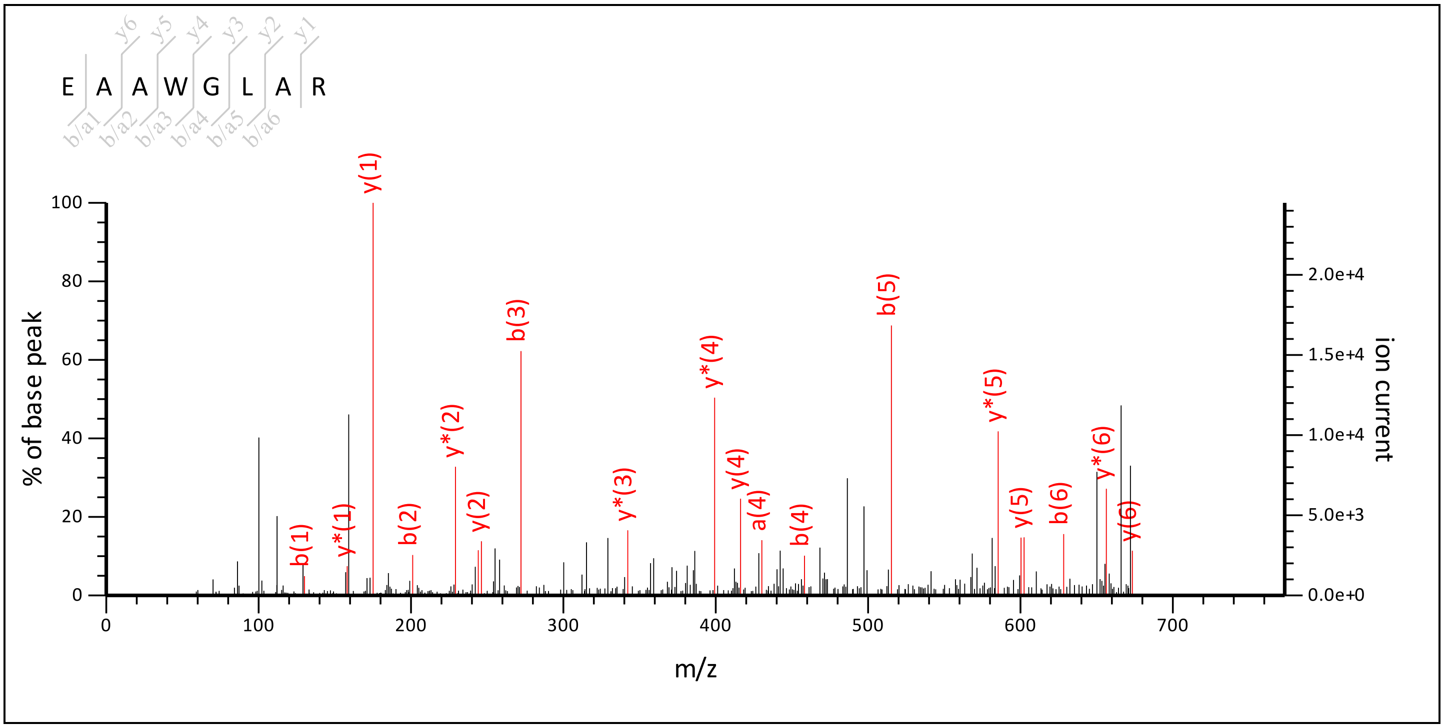
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **EAAWGLAR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 2: 872.510124 from(873.517400,1+) intensity(0.0000) index(0)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228510, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



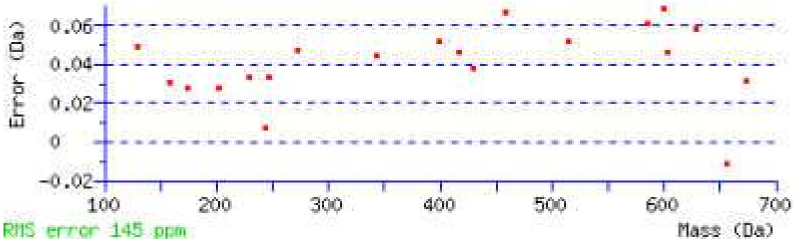
0 to 773.41

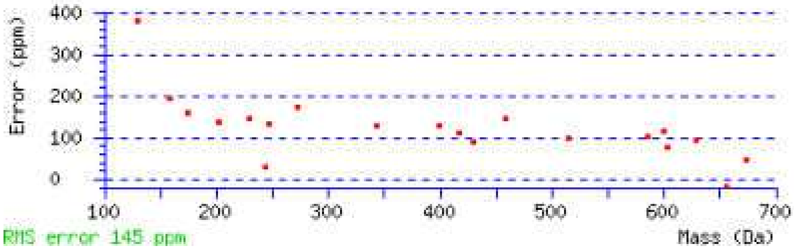
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 872.4504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 29 **Expect:** 3.7
Matches : 20/28 fragment ions using 49 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	102.0550	***130.0499***	E			8
2	173.0921	***201.0870***	A	744.4151	727.3886	7
3	**244.1292**	***272.1241***	A	**673.3780**	656.3515	6
4	**430.2085**	***458.2034***	W	**602.3409**	585.3144	5
5	487.2300	***515.2249***	G	**416.2616**	399.2350	4
6	**600.3140**	***628.3089***	L	359.2401	342.2136	3
7	671.3511	699.3461	A	**246.1561**	229.1295	2

8			**R**	**175.1190**	158.0924	**1**





NCBI **BLAST** search of EAAWGLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.8	872.4504	0.0597	EAAWGLAR
25.0	872.5080	0.0022	GTIGVSLAR
24.2	872.4352	0.0749	VDNDAIAR
23.3	872.4604	0.0498	VGDATPSVK
22.2	872.4352	0.0750	KEAEGSPR
22.2	872.4716	0.0386	VGTAVAEAR
22.2	872.5080	0.0022	ISAVSVAAR
22.0	872.4352	0.0750	EAATAPSAR
21.9	872.4716	0.0386	LASDAVAAR
21.5	872.5192	-0.0091	TVASRIAR

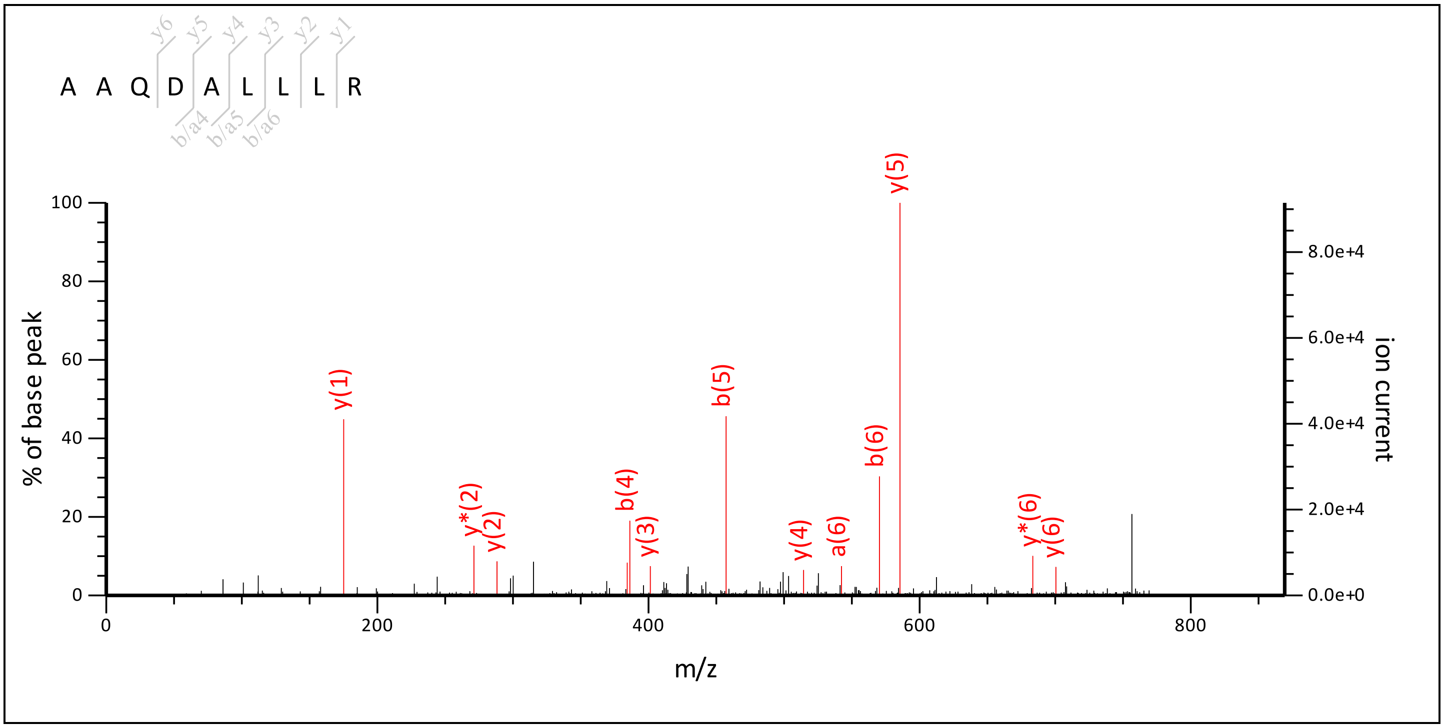
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **AAQDALLLR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 23: 969.593984 from(970.601260,1+) intensity(0.0000) index(5)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228496, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



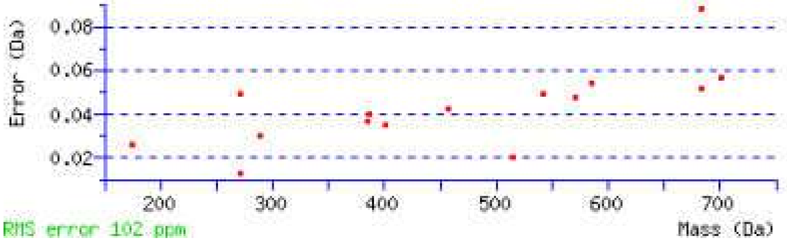
0 to 869.29

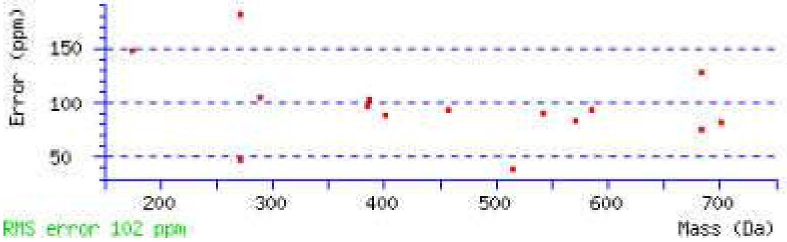
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 969.5607
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.2
Matches : 15/44 fragment ions using 24 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		**A**			**9**
2	115.0866		143.0815		**A**	899.5309	882.5043	**8**
3	243.1452	226.1186	**271.1401**	254.1135	**Q**	828.4938	811.4672	**7**
4	358.1721	341.1456	**386.1670**	369.1405	**D**	***700.4352***	683.4087	**6**
5	429.2092	412.1827	**457.2041**	440.1776	**A**	***585.4083***	568.3817	**5**
6	542.2933	525.2667	**570.2882**	553.2617	**L**	***514.3711***	497.3446	**4**
7	655.3774	638.3508	**683.3723**	666.3457	**L**	***401.2871***	384.2605	**3**

8	768.4614	751.4349	796.4563	779.4298	**L**	***288.2030***	271.1765	**2**
9					**R**	***175.1190***	158.0924	**1**





NCBI **BLAST** search of AAQDALLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.0	969.5607	0.0333	AAQDALLIR
38.0	969.5607	0.0333	AAQDALLLR
31.3	969.6335	-0.0395	ITKNLLIR
31.2	969.6335	-0.0395	ITGKGLIIR
27.3	969.6409	-0.0469	LVLMLLIR
26.3	969.5355	0.0584	NNAQAALLR
26.2	969.6335	-0.0395	KLSGLAIIR
26.2	969.5760	0.0180	QAWLAILR
25.5	969.5681	0.0259	LPDMLLIR
24.3	969.5971	-0.0031	QTINILLR

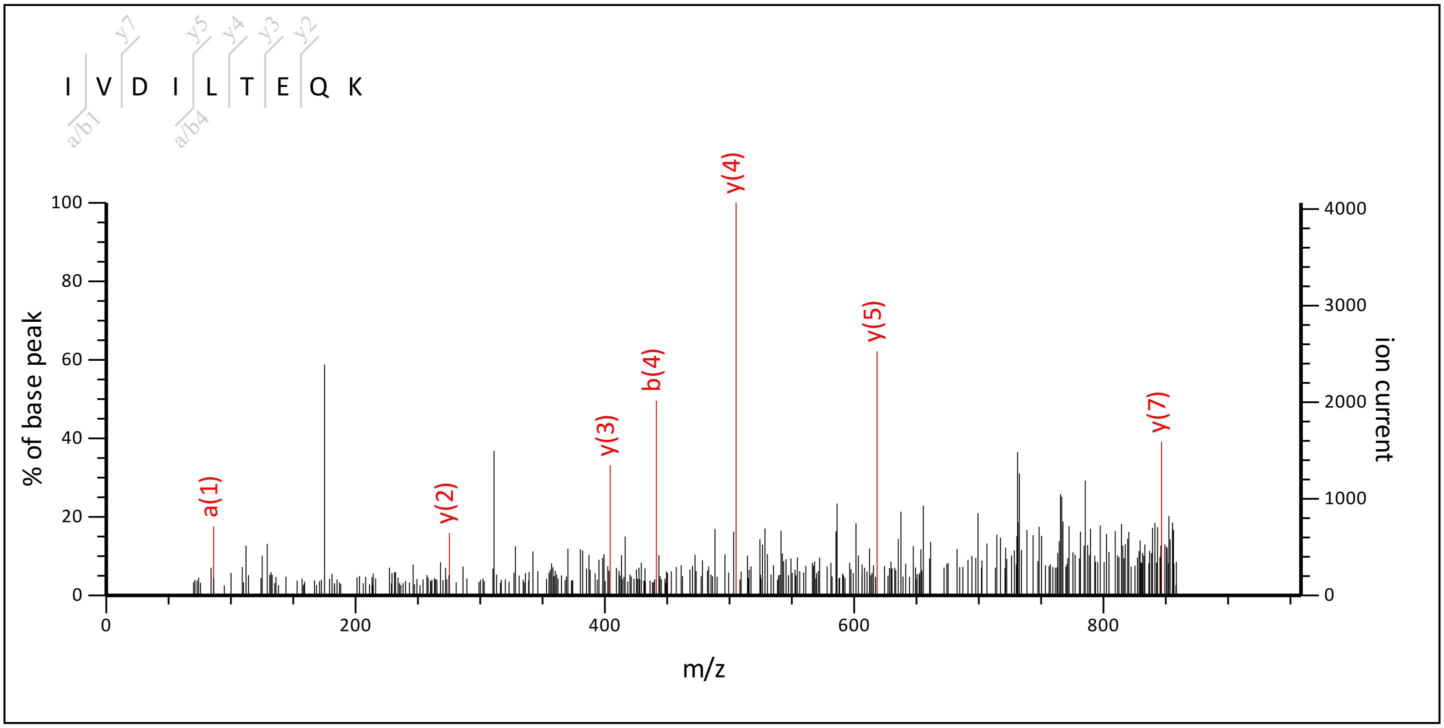
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **IVDILTEQK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 43: 1057.631124 from(1058.638400,1+) intensity(0.0000) index(9)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228509, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



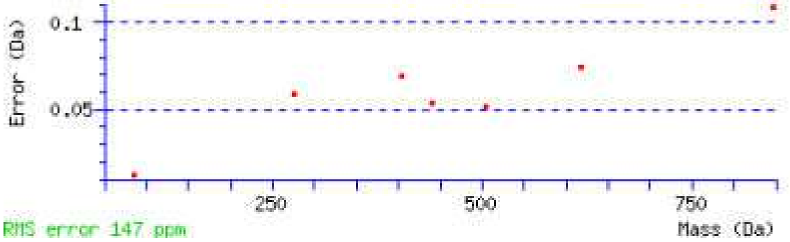
0 to 958.47

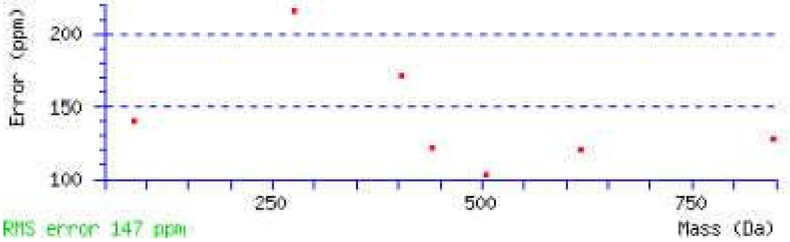
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1057.6019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 23
Matches : 7/34 fragment ions using 16 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		**I**			**9**
2	185.1648		213.1598		**V**	945.5251	928.4986	**8**
3	300.1918		328.1867		**D**	***846.4567***	829.4302	**7**
4	413.2758		441.2708		**I**	731.4298	714.4032	**6**
5	526.3599		554.3548		**L**	***618.3457***	601.3192	**5**
6	627.4076		655.4025		**T**	***505.2617***	488.2351	**4**
7	756.4502		784.4451		**E**	***404.2140***	387.1874	**3**

8	884.5088	867.4822	912.5037	895.4771	**Q**	*275.1714*	258.1448	**2**
9					**K**	147.1128	130.0863	**1**





NCBI **BLAST** search of IVDILTEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.5	1057.5768	0.0544	VIEVLSQDR
23.5	1057.5768	0.0544	VLDLLQSDR
23.5	1057.6318	-0.0006	VLVELAMKR
19.0	1057.5603	0.0708	RHFLVCAR
18.9	1057.6019	0.0292	IVDILTEQK
18.9	1057.6318	-0.0006	IVNNIVMKK
18.5	1057.5597	0.0714	QFQTIFFK
13.8	1057.6495	-0.0184	LLLTLGSSVR
13.5	1057.5768	0.0544	IVNNIGDVSK
12.9	1057.5628	0.0683	RAVAAGESAAR

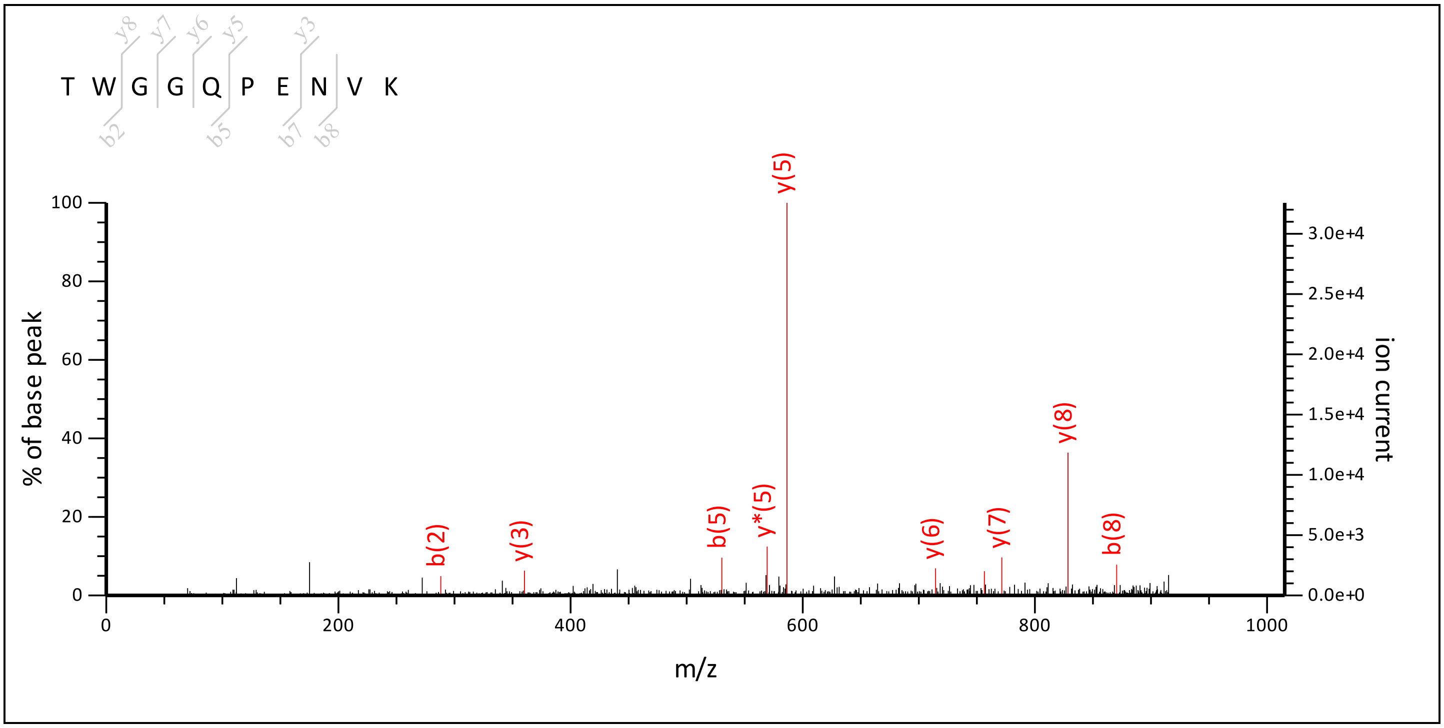
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **TWGGQPENVK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 59: 1114.579024 from(1115.586300,1+) intensity(0.0000) index(13)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228501, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



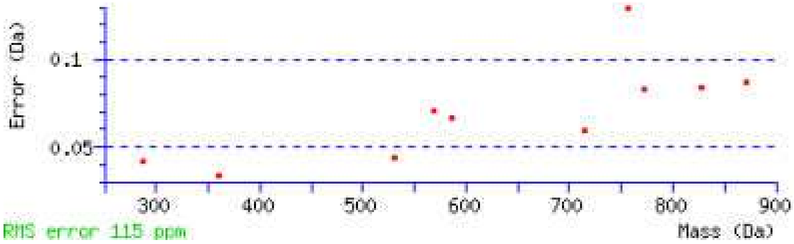
0 to 1015.18

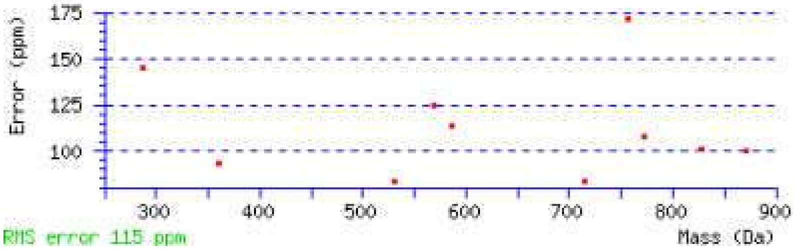
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1114.5407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 2.1
Matches : 10/46 fragment ions using 18 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	74.0600		102.0550		T			10
2	260.1394		*288.1343*		W	1014.5003	997.4738	9
3	317.1608		345.1557		G	*828.4210*	811.3945	8
4	374.1823		402.1772		G	*771.3995*	754.3730	7
5	502.2409	485.2143	*530.2358*	513.2092	Q	*714.3781*	697.3515	6
6	599.2936	582.2671	627.2885	610.2620	P	*586.3195*	569.2930	5
7	728.3362	711.3097	*756.3311*	739.3046	E	489.2667	472.2402	4

8	842.3791	825.3526	*870.3741*	853.3475	**N**	*360.2241*	343.1976	**3**
9	941.4476	924.4210	969.4425	952.4159	**V**	246.1812	229.1547	**2**
10					**K**	147.1128	130.0863	**1**





NCBI **BLAST** search of [TWGGQPENVK]
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways]

All matches to this query

Score	Mr(calc)	Delta	Sequence
30.6	1114.5407	0.0383	TWGGQPENVK
25.9	1114.5804	-0.0014	MNKPDIEIR
25.9	1114.6532	-0.0742	AKAMALELLR
25.9	1114.6094	-0.0304	ISSNKPLSNR
24.2	1114.5991	-0.0201	MPLMLQNIR
24.1	1114.6095	-0.0304	QTLDKAGGGLR
23.3	1114.5731	0.0060	AISGSNPSGVAR
23.0	1114.6346	-0.0556	DATELVAKLR
22.6	1114.5618	0.0172	DEDGLGALGLR
22.2	1114.6207	-0.0417	SSARAGNVVVR

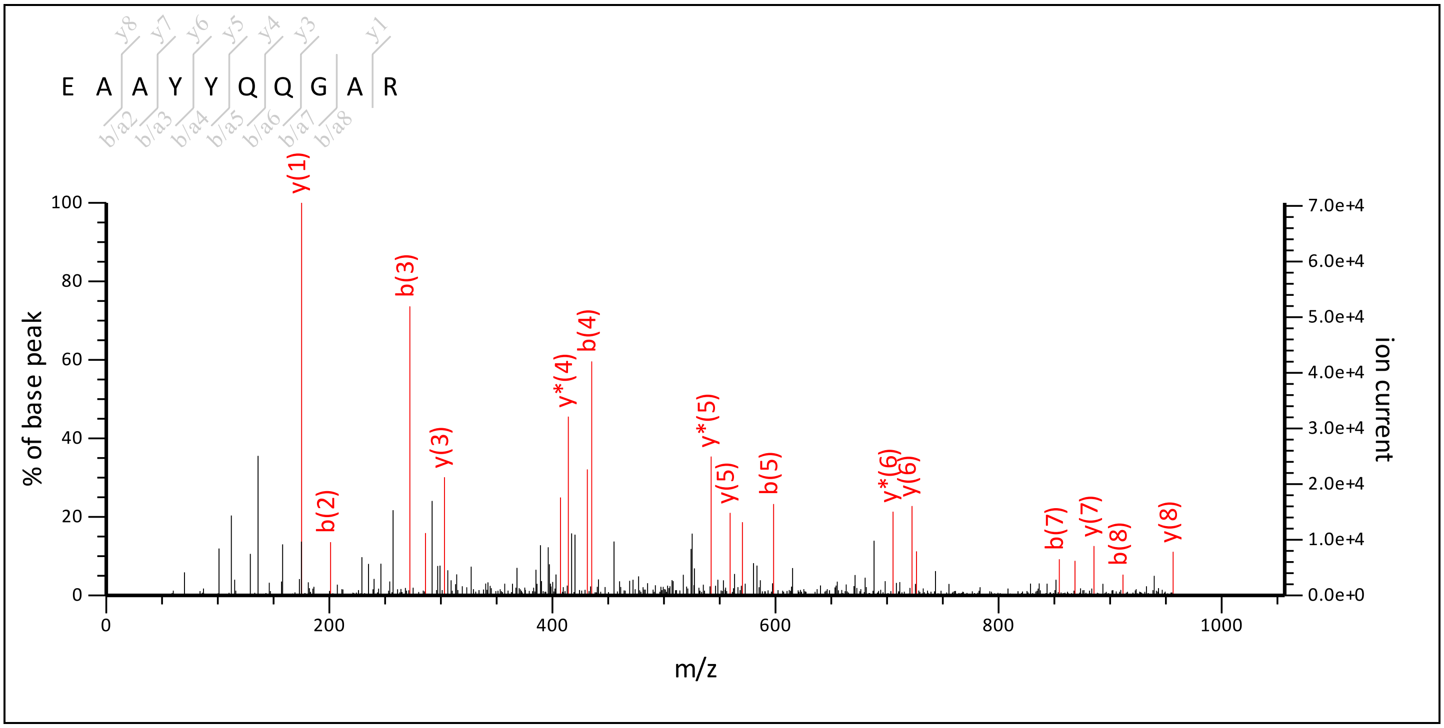
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **EAAYYQQGAR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 73: 1155.574624 from(1156.581900,1+) intensity(0.0000) index(15)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228495, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



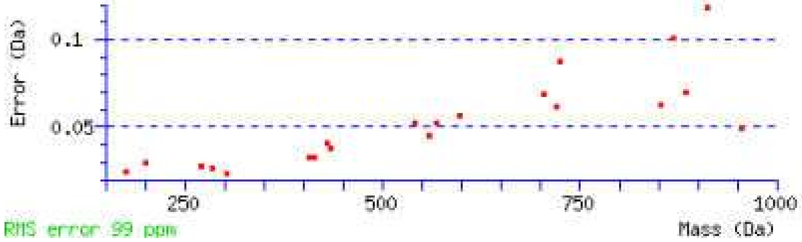
0 to 1056.51

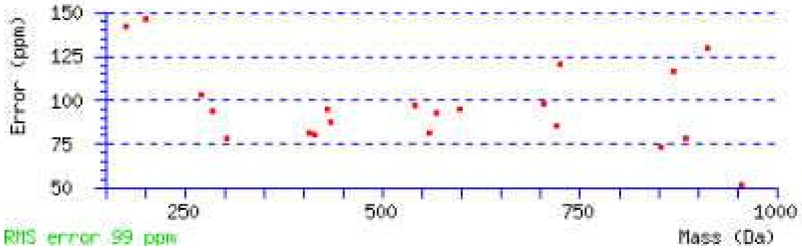
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1155.5309
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.034
Matches : 21/44 fragment ions using 36 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	102.0550		130.0499		E			10
2	173.0921		***201.0870***		A	1027.4956	1010.4690	9
3	244.1292		***272.1241***		A	***956.4585***	939.4319	8
4	**407.1925**		***435.1874***		Y	***885.4213***	868.3948	7
5	**570.2558**		***598.2508***		Y	***722.3580***	705.3315	6
6	698.3144	681.2879	***726.3093***	709.2828	Q	***559.2947***	542.2681	5
7	826.3730	809.3464	***854.3679***	837.3414	Q	***431.2361***	414.2096	4

8	883.3945	866.3679	***911.3894***	894.3628	**G**	***303.1775***	286.1510	**3**
9	954.4316	937.4050	982.4265	965.3999	**A**	246.1561	229.1295	**2**
10					**R**	***175.1190***	158.0924	**1**





NCBI **BLAST** search of EAAYYQQGAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
48.4	1155.5309	0.0438	EAAYYQQGAR
35.7	1155.5672	0.0074	AAEYYKQGAR
26.4	1155.6472	-0.0726	LSAGQIRQQR
23.9	1155.6288	-0.0542	TLGSISYFLR
21.9	1155.5745	0.0002	RQPSEQQQR
21.8	1155.5931	-0.0185	RGCPAIAGAGAR
21.8	1155.5996	-0.0250	QVLQEQQQR
20.9	1155.5924	-0.0178	ISAYTEGFLR
20.5	1155.5455	0.0292	SSPRMDPNPR
19.4	1155.6108	-0.0362	QAQAQAQKAGR

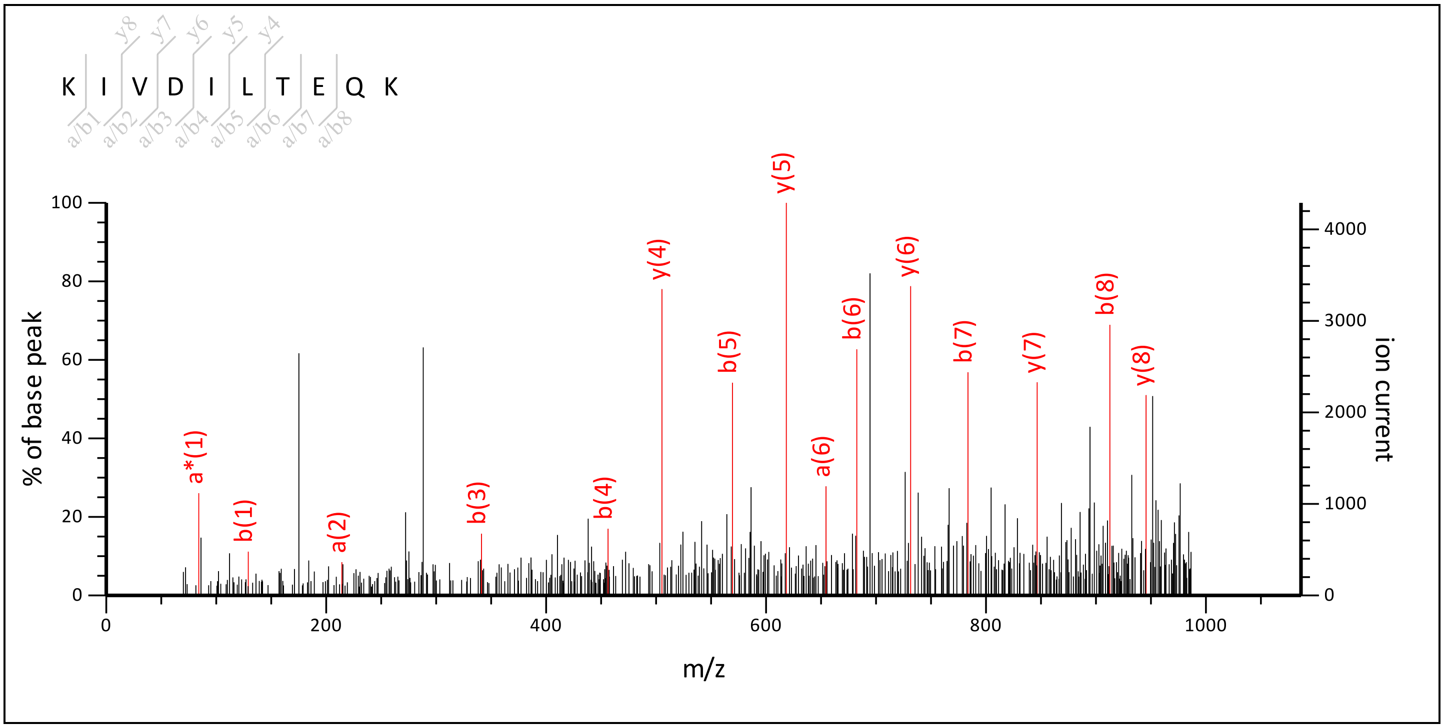
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 128**

MS/MS Fragmentation of **KIVDILTEQK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 81: 1185.734224 from(1186.741500,1+) intensity(0.0000) index(17)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228507, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



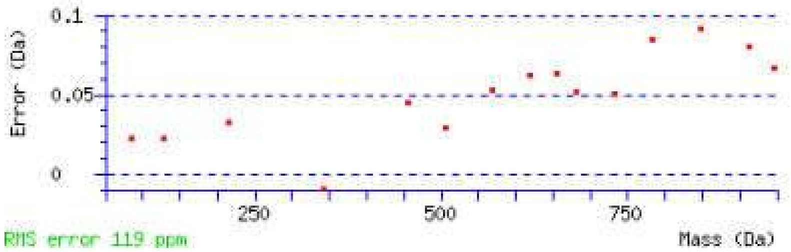
0 to 1086.44

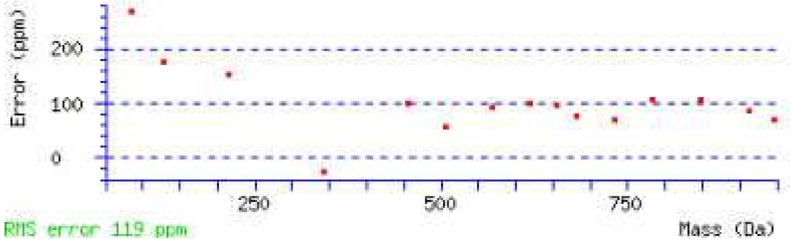
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1185.6969
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.14
Matches : 15/54 fragment ions using 30 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	101.1073	84.0808	***129.1022***	112.0757	K			10
2	**214.1914**	197.1648	242.1863	225.1598	I	1058.6092	1041.5827	9
3	313.2598	296.2333	***341.2547***	324.2282	V	**945.5251**	928.4986	8
4	428.2867	411.2602	***456.2817***	439.2551	D	**846.4567**	829.4302	7
5	541.3708	524.3443	***569.3657***	552.3392	I	**731.4298**	714.4032	6
6	**654.4549**	637.4283	***682.4498***	665.4232	L	**618.3457**	601.3192	5
7	755.5026	738.4760	***783.4975***	766.4709	T	**505.2617**	488.2351	4

8	884.5451	867.5186	*912.5401*	895.5135	**E**	404.2140	387.1874	**3**
9	1012.6037	995.5772	1040.5986	1023.5721	**Q**	275.1714	258.1448	**2**
10					**K**	147.1128	130.0863	**1**





NCBI **BLAST** search of KIVDILTEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
39.5	1185.6969	0.0374	KIVDILTEQK
17.8	1185.6362	0.0980	VIPQMIGCIR
16.3	1185.6692	0.0650	NPLMLFAKPR
16.2	1185.6466	0.0876	QLVDGTRELR
14.3	1185.6367	0.0976	HHEELIPRR
13.5	1185.6328	0.1014	QLVPMWSIGR
13.3	1185.6539	0.0803	IMASNTLLAPR
12.7	1185.6466	0.0876	IQLTLGGQGGSR
11.7	1185.7737	-0.0394	KLTILLYLLP
11.7	1185.7332	0.0010	QIITLLSSIAK

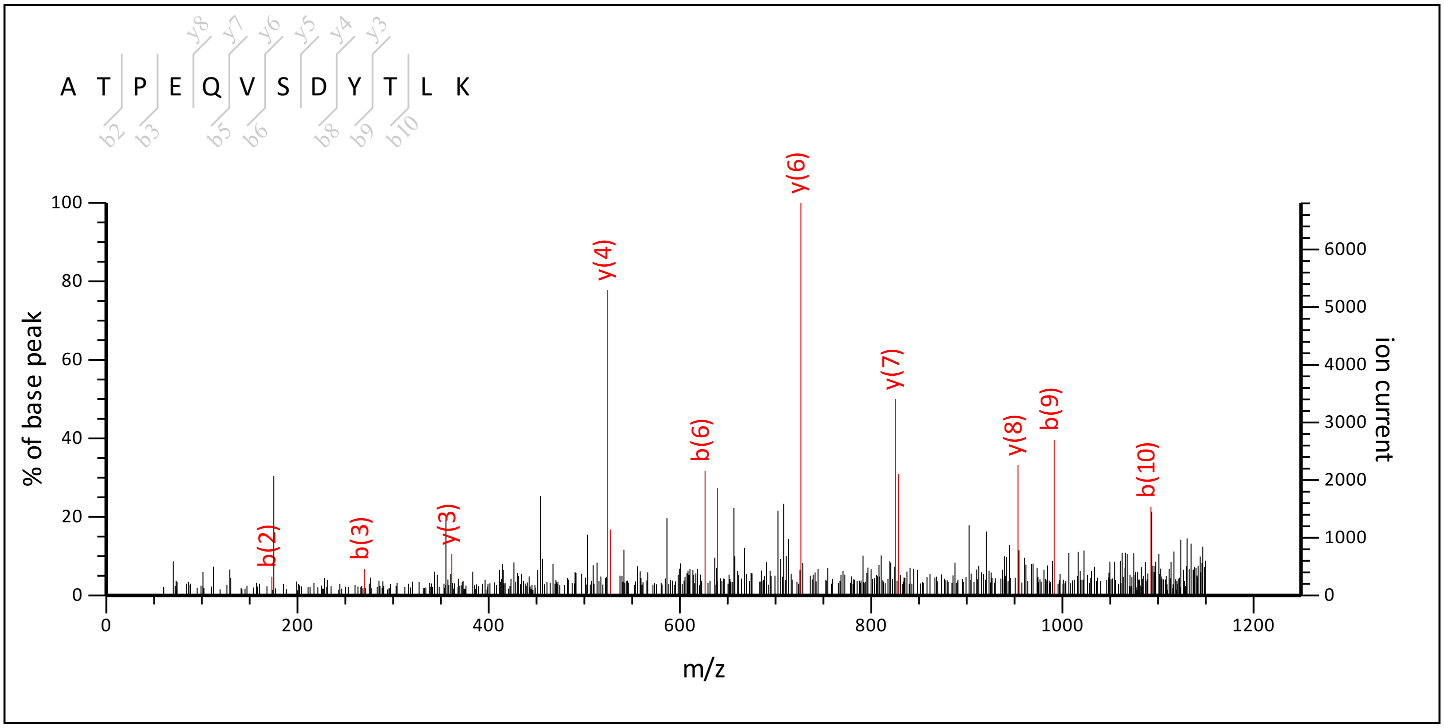
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 128**

MS/MS Fragmentation of **ATPEQVSDYTLK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 97: 1350.713224 from(1351.720500,1+) intensity(0.0000) index(20)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228506, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



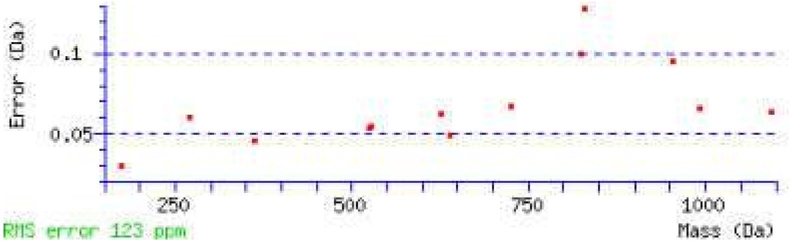
0 to 1249.53

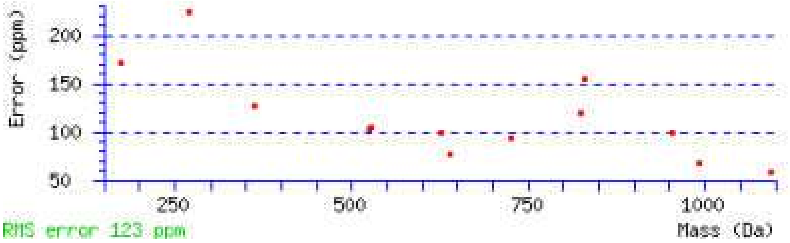
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1350.6667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.019
Matches : 13/58 fragment ions using 22 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			12
2	145.0972		***173.0921***		T	1280.6369	1263.6103	11
3	242.1499		***270.1448***		P	1179.5892	1162.5626	10
4	371.1925		399.1874		E	1082.5364	1065.5099	9
5	499.2511	482.2245	***527.2460***	510.2195	Q	***953.4938***	936.4673	8
6	598.3195	581.2930	***626.3144***	609.2879	V	***825.4353***	808.4087	7
7	685.3515	668.3250	713.3464	696.3199	S	***726.3668***	709.3403	6

8	800.3785	783.3519	***828.3734***	811.3468	**D**	***639.3348***	622.3083	**5**
9	963.4418	946.4153	***991.4367***	974.4102	**Y**	***524.3079***	507.2813	**4**
10	1064.4895	1047.4629	***1092.4844***	1075.4578	**T**	***361.2445***	344.2180	**3**
11	1177.5735	1160.5470	1205.5685	1188.5419	**L**	260.1969	243.1703	**2**
12					**K**	147.1128	130.0863	**1**





NCBI **BLAST** search of ATPEQVSDYTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.2	1350.6667	0.0465	ATPEQVSDYTLK
11.6	1350.5883	0.1249	MTVMMDWIHR
11.1	1350.7329	-0.0197	RVSLAVYMLGDK
10.8	1350.6384	0.0749	QMTAAMELRER
8.8	1350.7118	0.0014	EKVGIVFMSWR
8.1	1350.6891	0.0241	LKNAAAGTTEYGR
8.0	1350.7296	-0.0163	LRAQFPDYTIK
7.6	1350.7296	-0.0163	ALKWLTDYSVR
7.6	1350.7116	0.0016	LRQEQAISHGGR
7.3	1350.7368	-0.0236	ELVGGNGVPPRTR

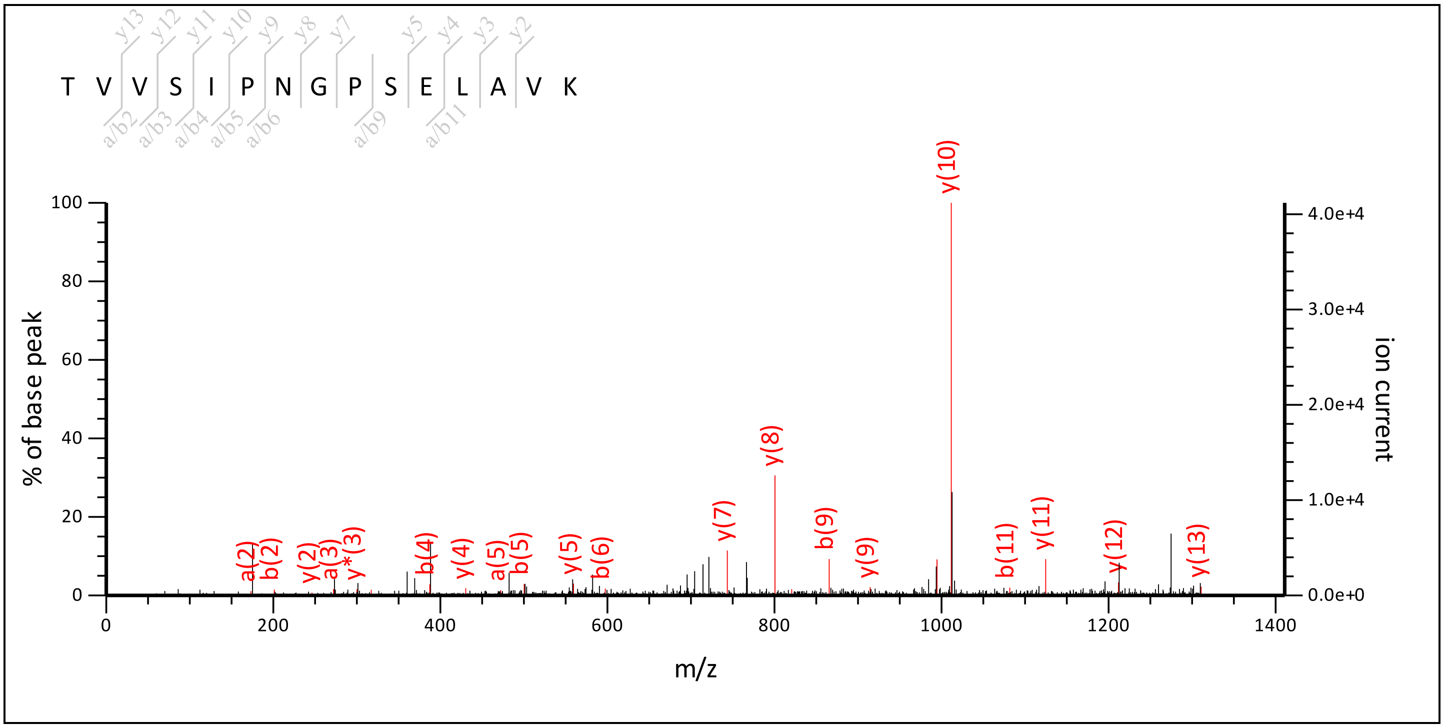
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **TVVSIPNGPSELAVK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 109: 1509.888924 from(1510.896200,1+) intensity(0.0000) index(23)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228500, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



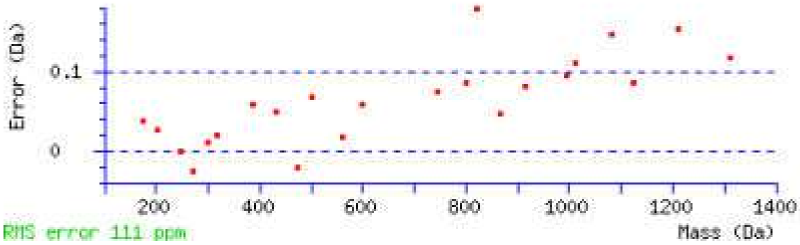
0 to 1410.85

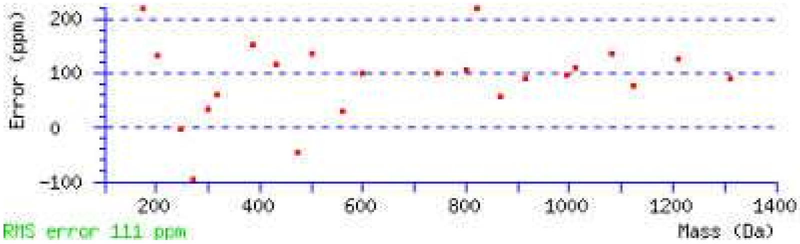
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1509.8403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 1.3
Matches : 24/72 fragment ions using 104 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	74.0600		102.0550		T			15
2	**173.1285**		**201.1234**		V	1409.7999	1392.7733	14
3	**272.1969**		**300.1918**		V	***1310.7314***	1293.7049	13
4	359.2289		**387.2238**		S	***1211.6630***	1194.6365	12
5	**472.3130**		**500.3079**		I	***1124.6310***	1107.6045	11
6	569.3657		**597.3606**		P	***1011.5469***	994.5204	10
7	683.4087	666.3821	711.4036	694.3770	N	***914.4942***	897.4676	9

8	740.4301	723.4036	768.4250	751.3985	**G**	***800.4512***	783.4247	**8**
9	837.4829	820.4563	**865.4778**	848.4512	**P**	***743.4298***	726.4032	**7**
10	924.5149	907.4884	952.5098	935.4833	**S**	646.3770	629.3505	**6**
11	1053.5575	1036.5310	**1081.5524**	1064.5259	**E**	***559.3450***	542.3184	**5**
12	1166.6416	1149.6150	1194.6365	1177.6099	**L**	***430.3024***	413.2758	**4**
13	1237.6787	1220.6521	1265.6736	1248.6470	**A**	***317.2183***	300.1918	**3**
14	1336.7471	1319.7205	1364.7420	1347.7155	**V**	***246.1812***	229.1547	**2**
15					**K**	147.1128	130.0863	**1**





NCBI **BLAST** search of TVVSIPNGPSELAVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.9	1509.8403	0.0487	TVVSIPNGPSELAVK
17.0	1509.8164	0.0725	AQVAEFLHNIRGR
12.4	1509.8450	0.0440	QCLPSVTRPLALR
11.6	1509.8263	0.0626	SIQGISHTSIQLAR
9.2	1509.8337	0.0552	MNLAVAAALPSVTPR
9.1	1509.7787	0.1102	DLSSPTPPTKQSPR
8.8	1509.8450	0.0440	IVEQCRGVPLAIR
8.8	1509.7827	0.1062	IDKEEFYNLALR
8.3	1509.7787	0.1102	EQELPINQGDIVR
8.0	1509.8151	0.0738	LENDNLTPNLVLR

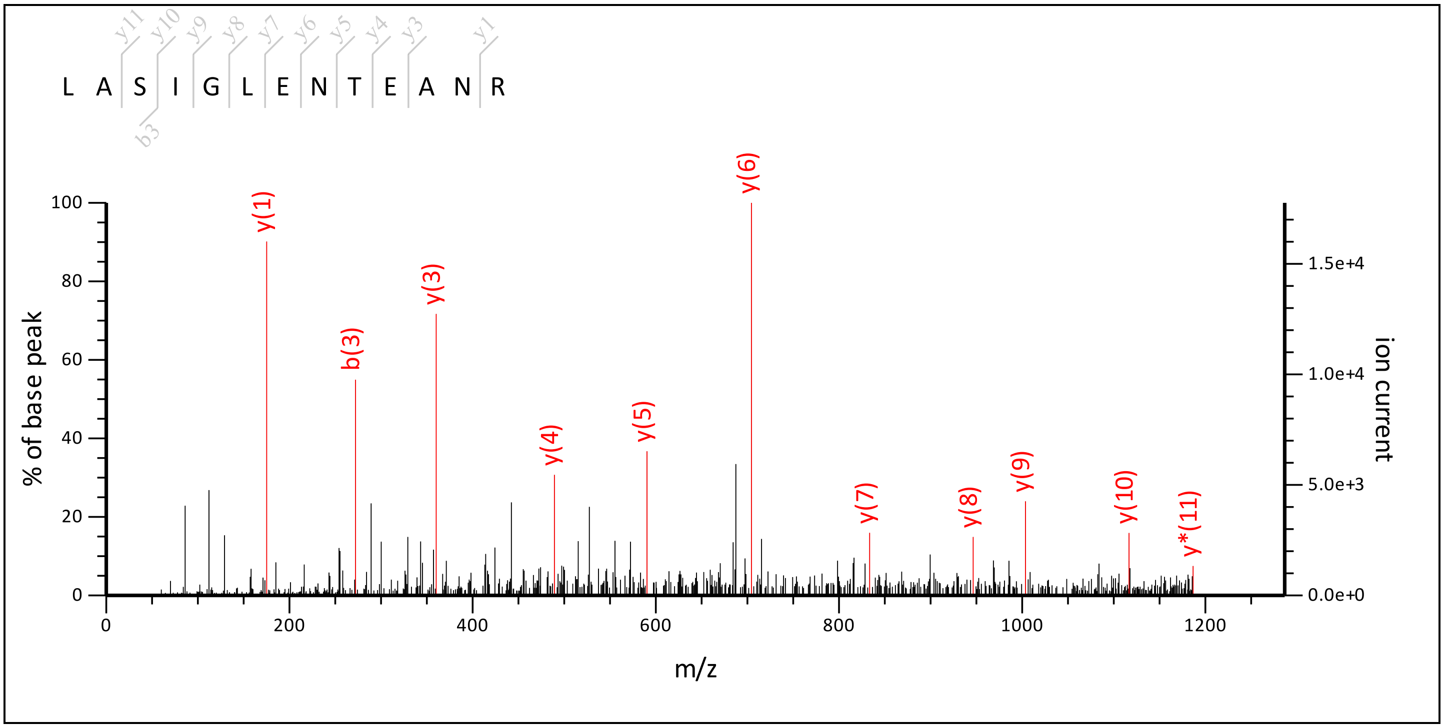
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 128**

MS/MS Fragmentation of **LASIGLENTEANR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 102: 1386.768724 from(1387.776000,1+) intensity(0.0000) index(22)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228497, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



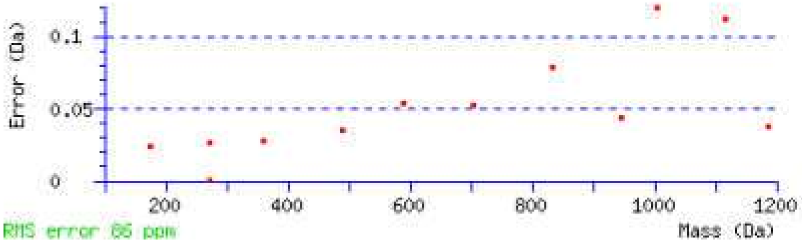
0 to 1286.61

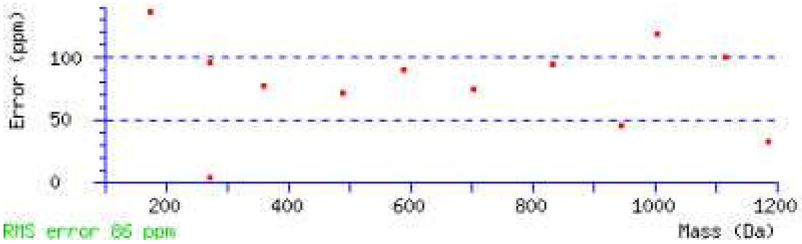
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1386.7103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 1.2e-06
Matches : 12/58 fragment ions using 12 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	86.0964		114.0913		**L**			**13**
2	157.1335		185.1285		**A**	1274.6335	1257.6070	**12**
3	244.1656		**272.1605**		**S**	1203.5964	1186.5699	**11**
4	357.2496		385.2445		**I**	***1116.5644***	1099.5378	**10**
5	414.2711		442.2660		**G**	***1003.4803***	986.4538	**9**
6	527.3552		555.3501		**L**	***946.4588***	929.4323	**8**
7	656.3978		684.3927		**E**	***833.3748***	816.3482	**7**

8	770.4407	753.4141	798.4356	781.4090	**N**	***704.3322***	687.3056	**6**
9	871.4884	854.4618	899.4833	882.4567	**T**	***590.2893***	573.2627	**5**
10	1000.5310	983.5044	1028.5259	1011.4993	**E**	***489.2416***	472.2150	**4**
11	1071.5681	1054.5415	1099.5630	1082.5364	**A**	***360.1990***	343.1724	**3**
12	1185.6110	1168.5844	1213.6059	1196.5794	**N**	289.1619	272.1353	**2**
13					**R**	***175.1190***	158.0924	**1**





NCBI **BLAST** search of LASIGLENTEANR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
92.1	1386.7103	0.0585	LASIGLENTEANR
22.8	1386.7255	0.0432	LADAVIAGANPGYR
20.3	1386.6851	0.0836	RDAATGVLDANER
16.4	1386.7653	0.0034	LASGLLLEMRER
16.0	1386.7289	0.0398	TLGLGDQKPTAMR
15.0	1386.8711	-0.1024	IIDIHKIIGLPR
15.0	1386.7871	-0.0184	ILGYLSEGLGLPR
14.8	1386.7103	0.0584	LASIGVENVESNR
14.2	1386.8169	-0.0482	ISALPAMLIFRR
14.2	1386.7103	0.0584	DQIVQTLTEAGGR

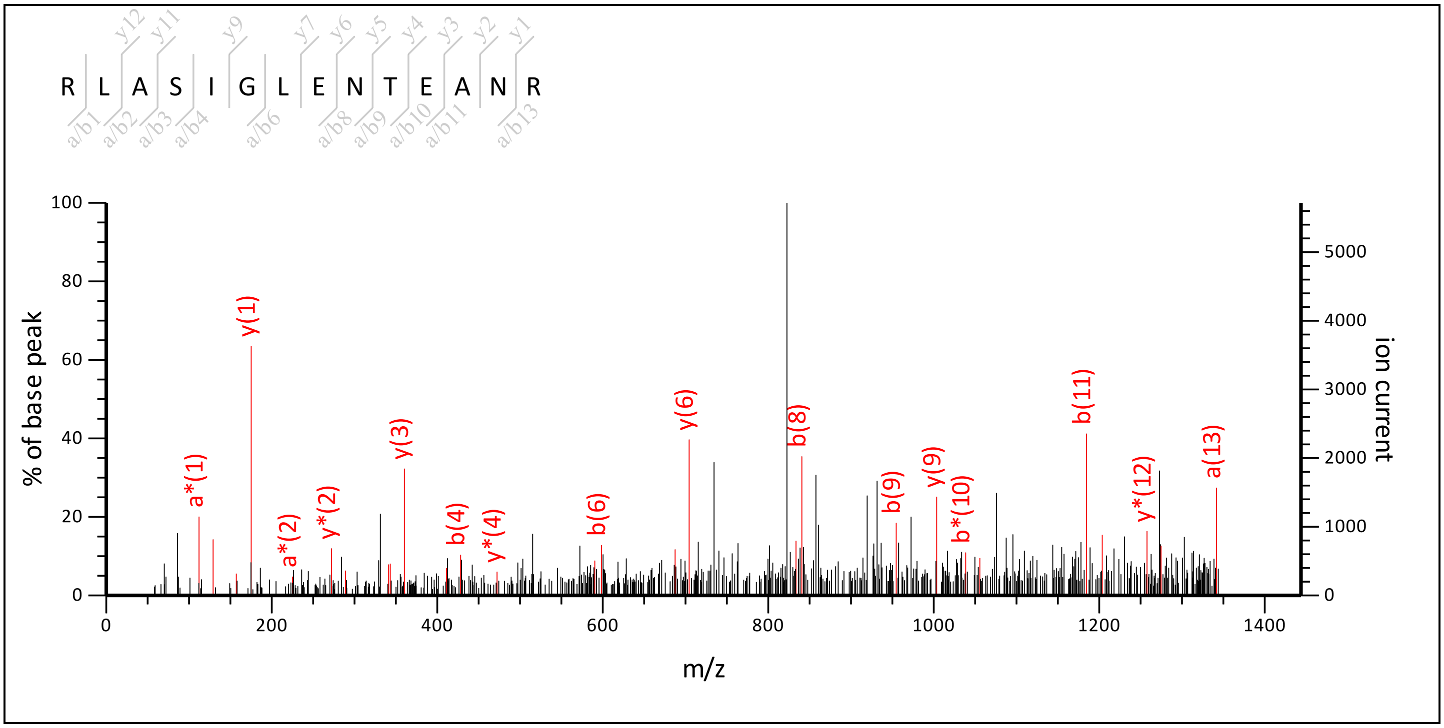
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **RLASIGLENTEANR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 113: 1542.876224 from(1543.883500,1+) intensity(0.0000) index(24)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228508, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



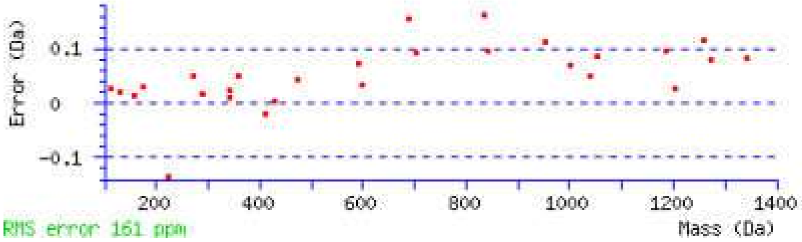
0 to 1443.81

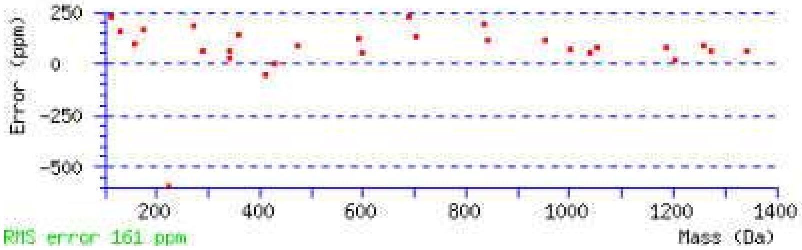
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1542.8114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.22
Matches : 28/78 fragment ions using 91 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**129.1135**	112.0869	***157.1084***	140.0818	R			14
2	242.1975	225.1710	270.1925	253.1659	L	1387.7176	1370.6910	13
3	313.2347	296.2081	***341.2296***	324.2030	A	***1274.6335***	1257.6070	12
4	400.2667	383.2401	***428.2616***	411.2350	S	***1203.5964***	1186.5699	11
5	513.3507	496.3242	541.3457	524.3191	I	1116.5644	1099.5378	10
6	570.3722	553.3457	***598.3671***	581.3406	G	***1003.4803***	986.4538	9
7	683.4563	666.4297	711.4512	694.4246	L	946.4588	929.4323	8

8	812.4989	795.4723	840.4938	823.4672	E	833.3748	816.3482	7
9	926.5418	909.5152	954.5367	937.5102	N	704.3322	687.3056	6
10	1027.5895	1010.5629	1055.5844	1038.5578	T	590.2893	573.2627	5
11	1156.6321	1139.6055	1184.6270	1167.6004	E	489.2416	472.2150	4
12	1227.6692	1210.6426	1255.6641	1238.6375	A	360.1990	343.1724	3
13	1341.7121	1324.6856	1369.7070	1352.6805	N	289.1619	272.1353	2
14					R	175.1190	158.0924	1





NCBI **BLAST** search of RLASIGLENTEANR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.5	1542.8114	0.0649	RLASIGLENTEANR
15.0	1542.7539	0.1223	RDGSEAAWVATQPR
14.5	1542.7247	0.1515	AGARGGADDSNGSRPR
11.5	1542.8114	0.0648	ANSSLVLTTDNRPR
10.6	1542.8226	0.0536	DRLSAAVTASSGRPR
9.2	1542.8478	0.0284	ASLATAGVTDAALARR
8.8	1542.8114	0.0648	LASIGVENVESNRR
8.8	1542.7725	0.1037	RWLLGCVPGSENR
8.2	1542.8300	0.0462	VLSMSRLGGAGSVGPR
7.4	1542.7685	0.1077	RLDGGGGGSMDLRPR

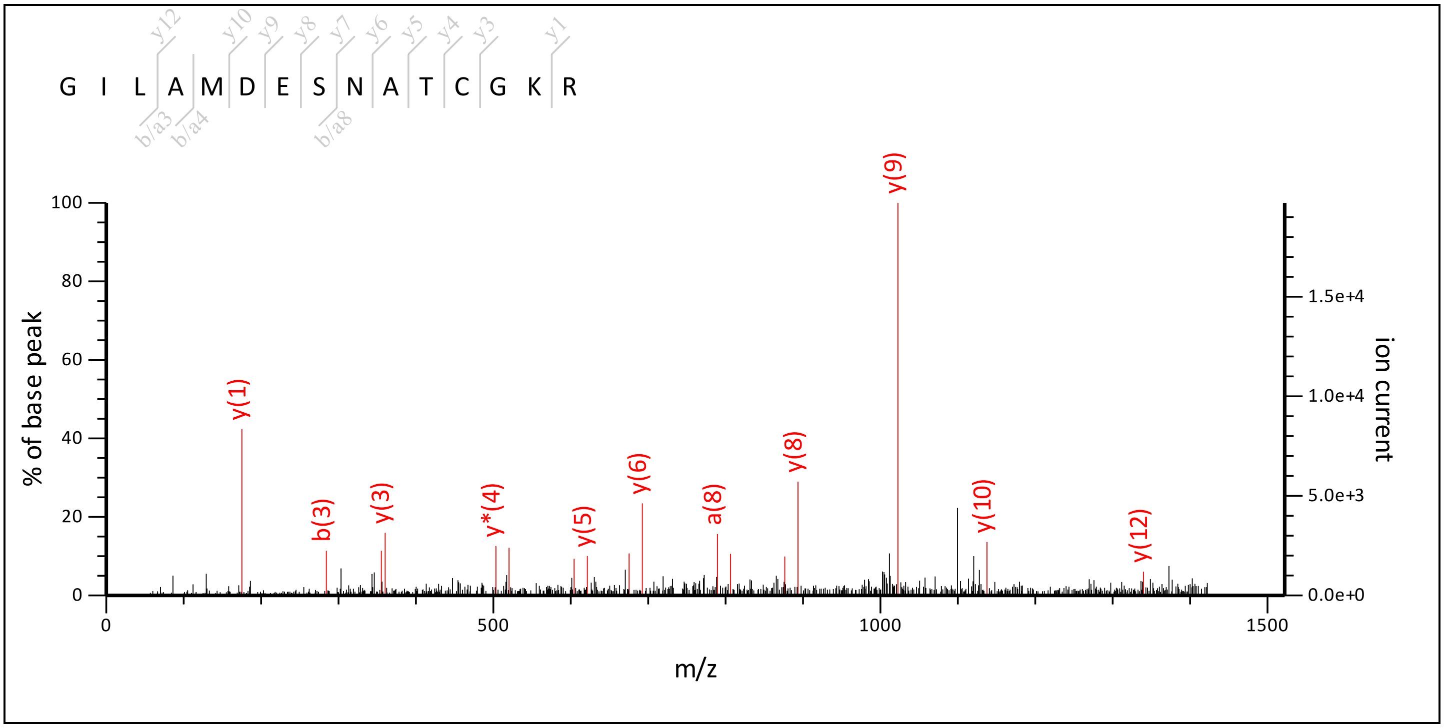
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **GILAMDESNATCGKR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 118: 1621.832324 from(1622.839600,1+) intensity(0.0000) index(26)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228499, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



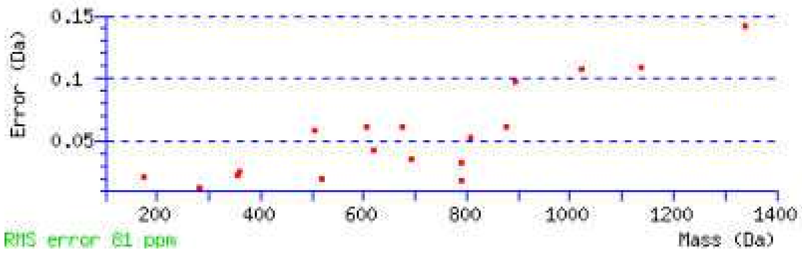
0 to 1522.21

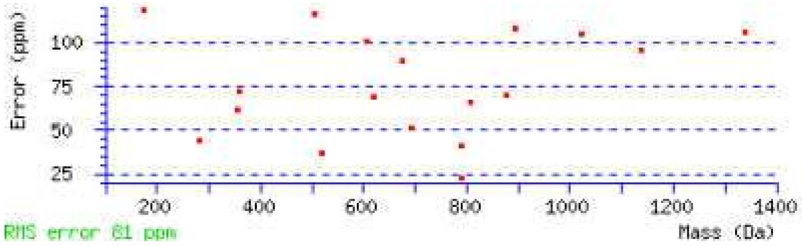
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1621.7552
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 9.8e-05
Matches : 18/68 fragment ions using 28 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			15
2	143.1179		171.1128		I	1565.7410	1548.7145	14
3	256.2020		**284.1969**		L	1452.6570	1435.6304	13
4	327.2391		**355.2340**		A	***1339.5729***	1322.5464	12
5	458.2796		486.2745		M	1268.5358	1251.5092	11
6	573.3065		601.3014		D	***1137.4953***	1120.4688	10
7	702.3491		730.3440		E	***1022.4684***	1005.4418	9

8	789.3811		817.3760		S	***893.4258***	876.3992	8
9	903.4240	886.3975	931.4190	914.3924	N	***806.3937***	789.3672	7
10	974.4612	957.4346	1002.4561	985.4295	A	***692.3508***	675.3243	6
11	1075.5088	1058.4823	1103.5038	1086.4772	T	***621.3137***	604.2872	5
12	1235.5395	1218.5129	1263.5344	1246.5079	C	***520.2660***	503.2395	4
13	1292.5609	1275.5344	1320.5559	1303.5293	G	***360.2354***	343.2088	3
14	1420.6559	1403.6294	1448.6508	1431.6243	K	303.2139	286.1874	2
15					R	***175.1190***	158.0924	1





NCBI **BLAST** search of GILAMDESNATCGKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.6	1621.7552	0.0771	GILAMDESNATCGKR
15.2	1621.8246	0.0077	GEMLPGSQSVPVHIR
11.1	1621.7292	0.1031	SGDGASASSNSAAGASAVR
10.1	1621.7849	0.0475	TRPFVEAFAADQDR
8.6	1621.7267	0.1056	GAGERDFTPAQGNMR
7.8	1621.8345	-0.0022	SISIESISLDMSKGR
6.8	1621.8763	-0.0439	LFLIQQGMAFNGKR
6.8	1621.8246	0.0077	HLPLGPDKDMLGSAR
6.7	1621.6800	0.1524	RDVCVYMCGGAR
6.4	1621.7696	0.0627	GSTGSAASTNPAADLFR

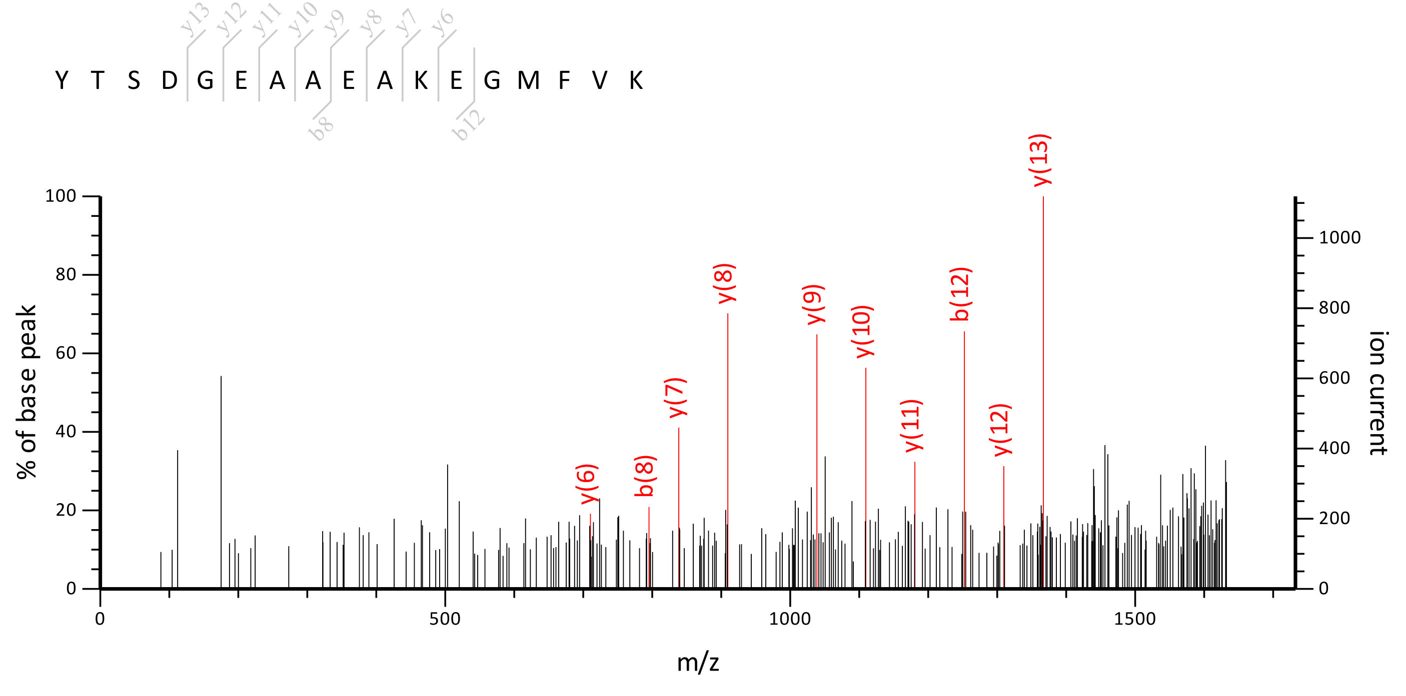
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 128**

MS/MS Fragmentation of **YTSDGEAAEAKEGMFVK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 124: 1831.899124 from(1832.906400,1+) intensity(0.0000) index(27)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228529, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



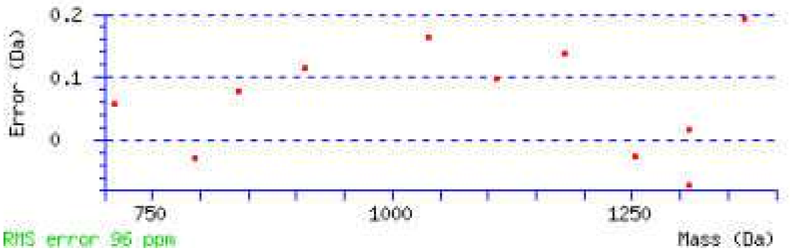
0 to 1732.3

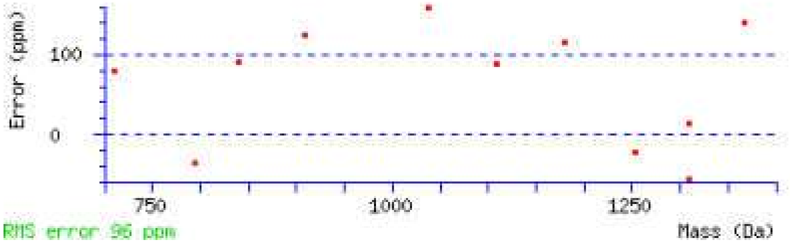
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1831.8298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 26 **Expect:** 4.1
Matches : 11/76 fragment ions using 32 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	136.0757		164.0706		Y			17
2	237.1234		265.1183		T	1669.7738	1652.7472	16
3	324.1554		352.1503		S	1568.7261	1551.6996	15
4	439.1823		467.1773		D	1481.6941	1464.6675	14
5	496.2038		524.1987		G	*1366.6671*	1349.6406	13
6	625.2464		653.2413		E	*1309.6457*	1292.6191	12
7	696.2835		724.2784		A	*1180.6031*	1163.5765	11

8	767.3206		**795.3155**		A	***1109.5660***	1092.5394	10
9	896.3632		924.3581		E	***1038.5288***	1021.5023	9
10	967.4003		995.3952		A	***909.4863***	892.4597	8
11	1095.4953	1078.4687	1123.4902	1106.4637	K	***838.4491***	821.4226	7
12	1224.5379	1207.5113	**1252.5328**	1235.5063	E	***710.3542***	693.3276	6
13	1281.5594	1264.5328	**1309.5543**	1292.5277	G	581.3116	564.2850	5
14	1412.5998	1395.5733	1440.5948	1423.5682	M	524.2901	507.2636	4
15	1559.6683	1542.6417	1587.6632	1570.6366	F	393.2496	376.2231	3
16	1658.7367	1641.7101	1686.7316	1669.7050	V	246.1812	229.1547	2
17					K	147.1128	130.0863	1





NCBI **BLAST** search of YTSDGEAAEAKEGMFVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.1	1831.8298	0.0693	YTSDGEAAEAKEGMFVK
8.9	1831.8748	0.0244	ACGHQVAHGDLALADAAR
5.4	1831.8201	0.0790	MDMGPCPKMHSLQLR
2.3	1831.9540	-0.0549	AAVKPNSVVAKDGSGNYR
0.9	1831.7643	0.1349	DDGDAQEEVMTNLHSR
0.4	1831.9462	-0.0471	TSTIKNTGQLLEQMPR
0.3	1831.9904	-0.0913	AGGIAPEQALHIGDSLRK
0.2	1831.9866	-0.0874	TQIYGPAEMIQILAIR

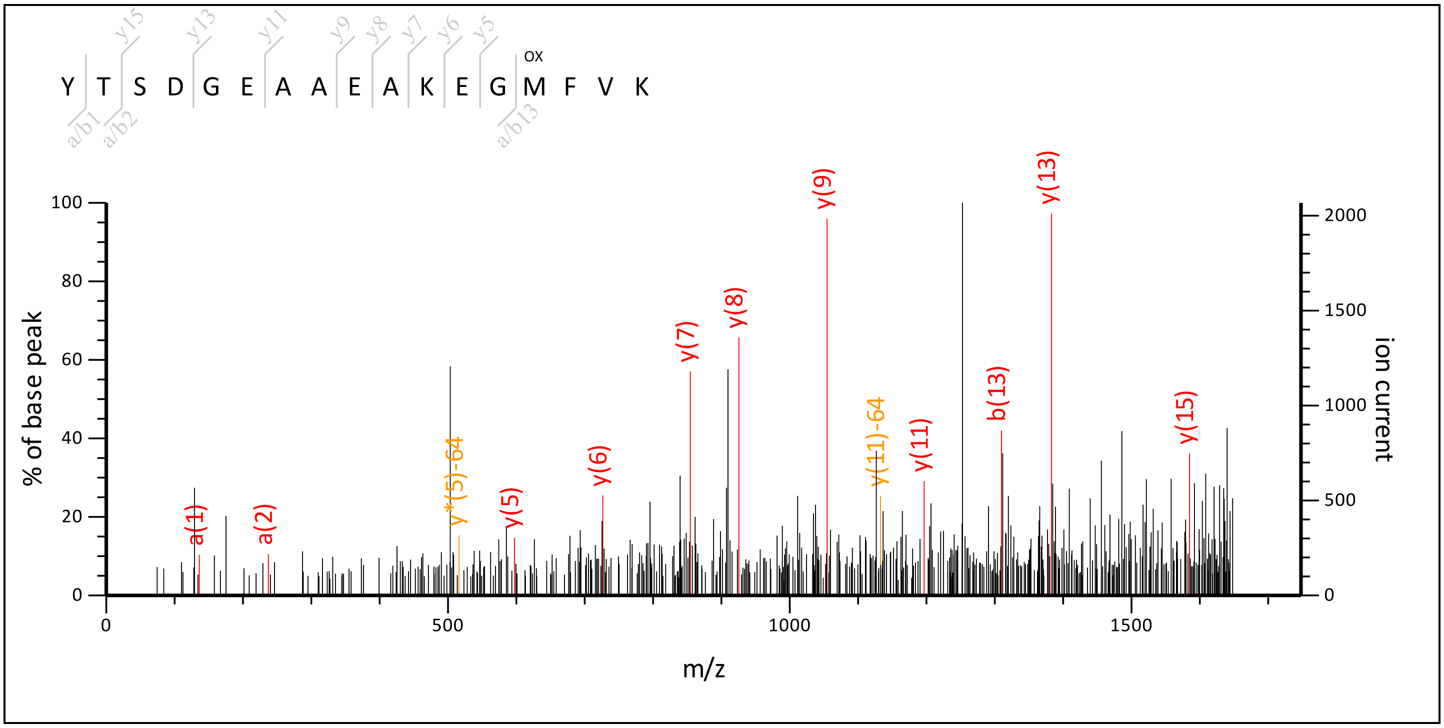
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **YTSDGEAAEAKEGMFVK**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 126: 1847.893824 from(1848.901100,1+) intensity(0.0000) index(28)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228512, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



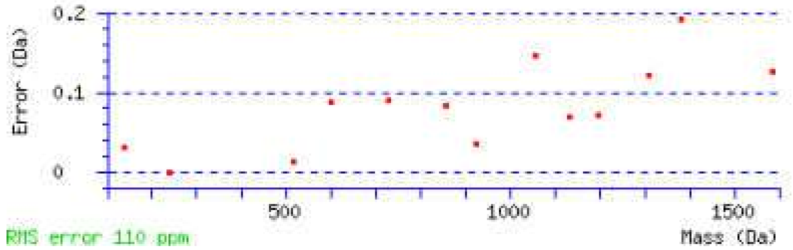
0 to 1747.99

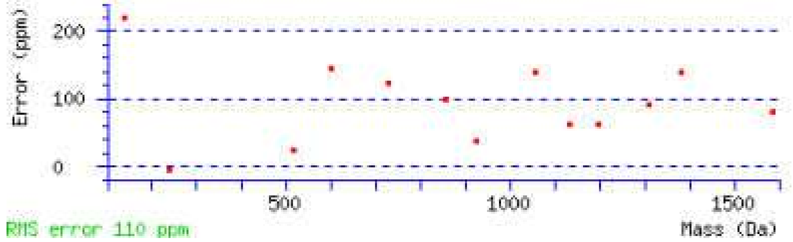
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1847.8247
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 **Expect:** 2.6
Matches : 13/114 fragment ions using 32 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	**136.0757**		164.0706		**Y**			**17**
2	**237.1234**		265.1183		**T**	1685.7687	1668.7421	**16**
3	324.1554		352.1503		**S**	***1584.7210***	1567.6945	**15**
4	439.1823		467.1773		**D**	1497.6890	1480.6624	**14**
5	496.2038		524.1987		**G**	***1382.6620***	1365.6355	**13**
6	625.2464		653.2413		**E**	1325.6406	1308.6140	**12**

7	696.2835		724.2784		A	***1196.5980***	1179.5714	11
8	767.3206		795.3155		A	1125.5609	1108.5343	10
9	896.3632		924.3581		E	***1054.5238***	1037.4972	9
10	967.4003		995.3952		A	***925.4812***	908.4546	8
11	1095.4953	1078.4687	1123.4902	1106.4637	K	***854.4441***	837.4175	7
12	1224.5379	1207.5113	1252.5328	1235.5063	E	***726.3491***	709.3225	6
13	1281.5594	1264.5328	1309.5543	1292.5277	G	***597.3065***	580.2799	5
14	1428.5948	1411.5682	1456.5897	1439.5631	M	540.2850	523.2585	4
15	1575.6632	1558.6366	1603.6581	1586.6315	F	393.2496	376.2231	3
16	1674.7316	1657.7050	1702.7265	1685.6999	V	246.1812	229.1547	2
17					K	147.1128	130.0863	1





NCBI **BLAST** search of [YTSDGEAAEAKEGMFVK]
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways]

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.1	1847.8247	0.0691	YTSDGEAAEAKEGMFVK
10.0	1847.8148	0.0790	LSYGDQMTQVWDYSR
6.1	1847.9278	-0.0340	RHQALLYAESQNYQK
3.4	1847.7883	0.1055	YTSDGEAAEASENMFVK
2.4	1847.8795	0.0143	QSGKPVEKNMQTNSER
1.9	1847.8618	0.0320	MAVATADGGQVTNGCKPR
1.6	1847.8988	-0.0050	RFTHALQVSEWMTDK
1.5	1847.8207	0.0731	GDSHDTIQVEMVSTDAK
1.2	1847.9741	-0.0803	TLVDLAVDPASSHPVTAR
0.8	1847.9853	-0.0915	NAASPSPVALSAAVSTHLR

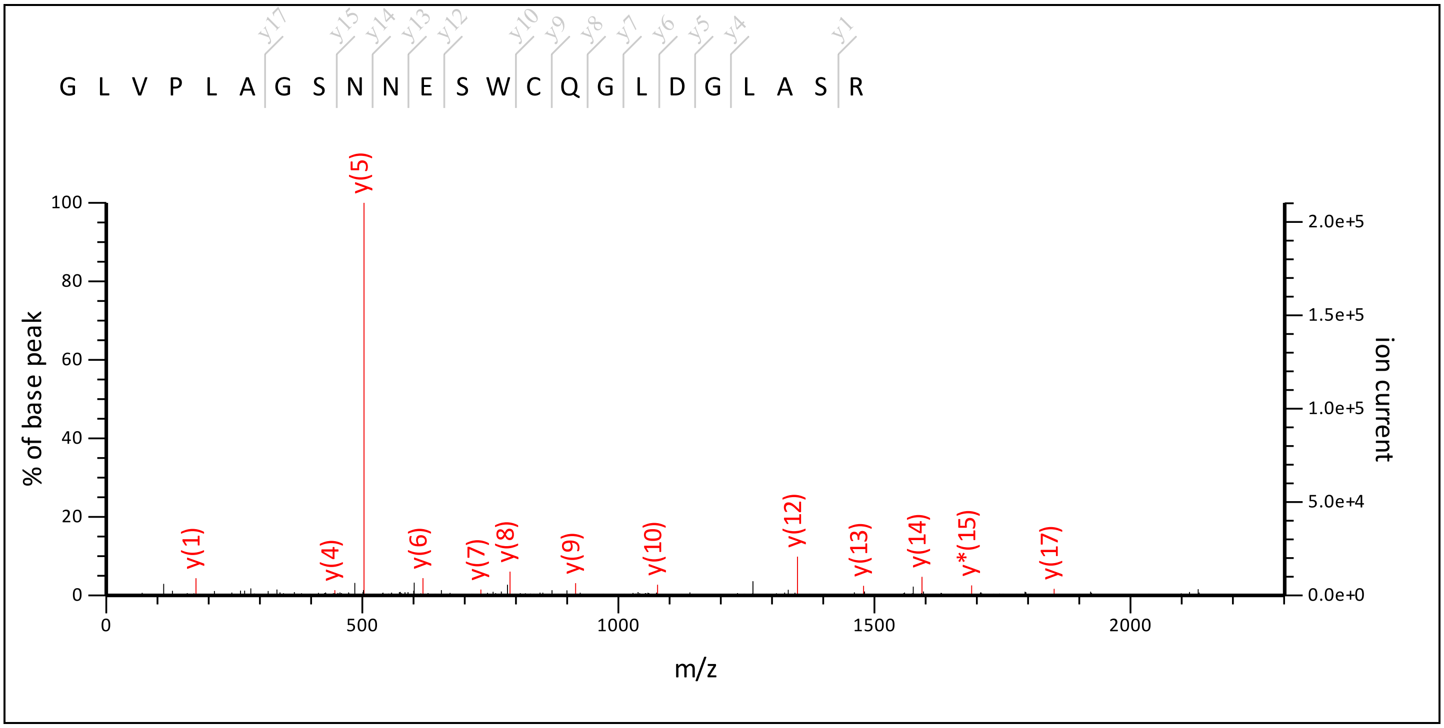
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 128**

MS/MS Fragmentation of **GLVPLAGSNNESWCQGLDGLASR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 136: 2400.242224 from(2401.249500,1+) intensity(0.0000) index(31)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228498, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



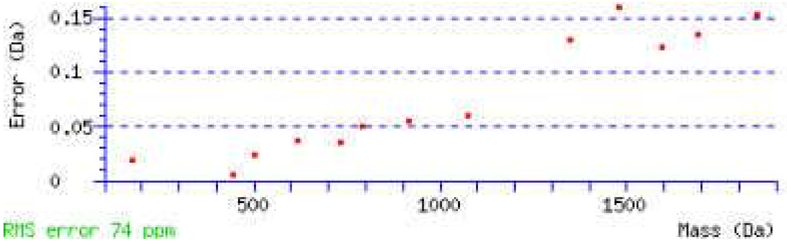
0 to 2301.13

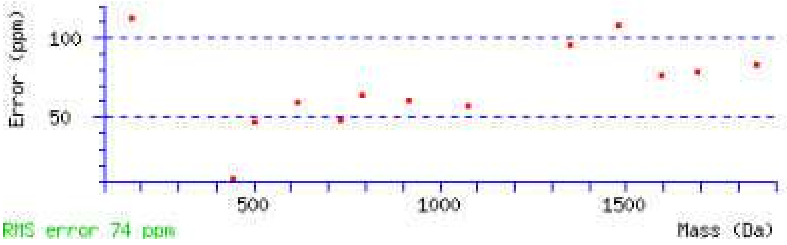
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2400.1492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 85 **Expect:** 3.9e-06
Matches : 13/116 fragment ions using 22 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	30.0338		58.0287		G			23
2	143.1179		171.1128		L	2344.1350	2327.1085	22
3	242.1863		270.1812		V	2231.0510	2214.0244	21
4	339.2391		367.2340		P	2131.9825	2114.9560	20
5	452.3231		480.3180		L	2034.9298	2017.9032	19
6	523.3602		551.3552		A	1921.8457	1904.8192	18
7	580.3817		608.3766		G	***1850.8086***	1833.7821	17

8	667.4137		695.4087		**S**	1793.7871	1776.7606	**16**
9	781.4567	764.4301	809.4516	792.4250	**N**	1706.7551	1689.7286	**15**
10	895.4996	878.4730	923.4945	906.4680	**N**	***1592.7122***	1575.6856	**14**
11	1024.5422	1007.5156	1052.5371	1035.5105	**E**	***1478.6693***	1461.6427	**13**
12	1111.5742	1094.5477	1139.5691	1122.5426	**S**	***1349.6267***	1332.6001	**12**
13	1297.6535	1280.6270	1325.6484	1308.6219	**W**	1262.5946	1245.5681	**11**
14	1457.6842	1440.6576	1485.6791	1468.6525	**C**	***1076.5153***	1059.4888	**10**
15	1585.7428	1568.7162	1613.7377	1596.7111	**Q**	***916.4847***	899.4581	**9**
16	1642.7642	1625.7377	1670.7591	1653.7326	**G**	***788.4261***	771.3995	**8**
17	1755.8483	1738.8217	1783.8432	1766.8166	**L**	***731.4046***	714.3781	**7**
18	1870.8752	1853.8487	1898.8701	1881.8436	**D**	***618.3206***	601.2940	**6**
19	1927.8967	1910.8701	1955.8916	1938.8651	**G**	***503.2936***	486.2671	**5**
20	2040.9808	2023.9542	2068.9757	2051.9491	**L**	***446.2722***	429.2456	**4**
21	2112.0179	2094.9913	2140.0128	2122.9862	**A**	333.1881	316.1615	**3**
22	2199.0499	2182.0233	2227.0448	2210.0183	**S**	262.1510	245.1244	**2**
23					**R**	***175.1190***	158.0924	**1**





NCBI **BLAST** search of GLVPLAGSNNESWCQGLDGLASR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.7	2400.1492	0.0930	GLVPLAGSNNESWCQGLDGLASR
8.7	2400.1267	0.1155	GSYADELVTFEVACAGLDVAASR
8.7	2400.1193	0.1229	WASSAPATAVAEAEAEALGDGDGVR
8.5	2400.0573	0.1849	AAADDCPAMVPDLDLDLDGEAAR
6.2	2400.1487	0.0935	STLNSTMTMKTLCLINNEWK
5.9	2400.1591	0.0831	SSASVAQTMGTVSYVGALVGEQSR
5.1	2400.0872	0.1551	LNGEMCLMDREFSAEVGALSR

5.1	2400.0872	0.1551	LNGEMCLMDREFSAEVGALSR
5.0	2400.0625	0.1797	MGSEGRAWNGAAGSSGHGGGGGGVEAK
4.9	2400.0565	0.1858	ATDDAGDEEEAATTFGSTTATALR

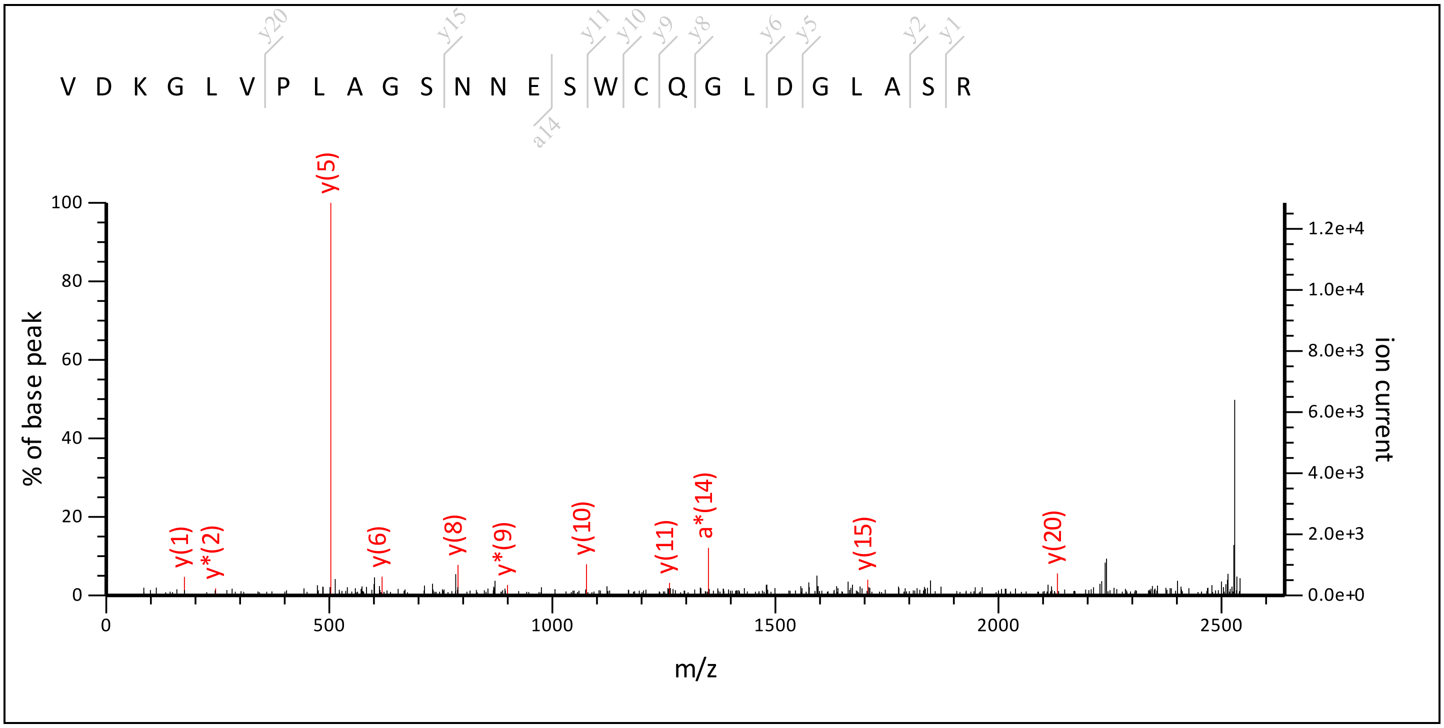
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 128**

MS/MS Fragmentation of **VDKGLVPLAGSNNESWCQGLDGLASR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 141: 2742.443424 from(2743.450700,1+) intensity(0.0000) index(33)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228518, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



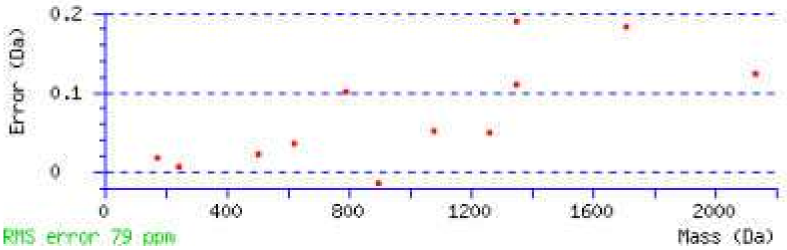
0 to 2641.64

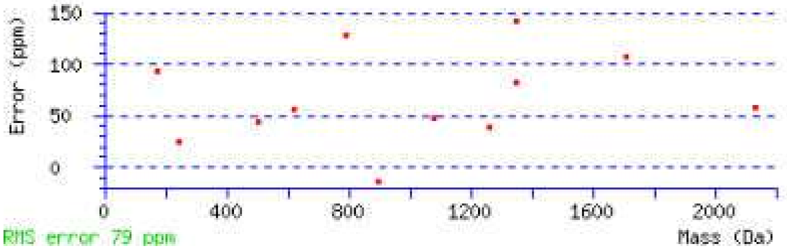
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2742.3395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.13
Matches : 12/146 fragment ions using 25 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	72.0808		100.0757		**V**			**26**
2	187.1077		215.1026		**D**	2644.2784	2627.2518	**25**
3	315.2027	298.1761	343.1976	326.1710	**K**	2529.2514	2512.2249	**24**
4	372.2241	355.1976	400.2191	383.1925	**G**	2401.1565	2384.1299	**23**
5	485.3082	468.2817	513.3031	496.2766	**L**	2344.1350	2327.1085	**22**
6	584.3766	567.3501	612.3715	595.3450	**V**	2231.0510	2214.0244	**21**
7	681.4294	664.4028	709.4243	692.3978	**P**	***2131.9825***	2114.9560	**20**

8	794.5135	777.4869	822.5084	805.4818	L	2034.9298	2017.9032	19
9	865.5506	848.5240	893.5455	876.5189	A	1921.8457	1904.8192	18
10	922.5720	905.5455	950.5669	933.5404	G	1850.8086	1833.7821	17
11	1009.6041	992.5775	1037.5990	1020.5724	S	1793.7871	1776.7606	16
12	1123.6470	1106.6204	1151.6419	1134.6154	N	***1706.7551***	1689.7286	15
13	1237.6899	1220.6634	1265.6848	1248.6583	N	1592.7122	1575.6856	14
14	1366.7325	1349.7060	1394.7274	1377.7009	E	1478.6693	1461.6427	13
15	1453.7645	1436.7380	1481.7594	1464.7329	S	***1349.6267***	1332.6001	12
16	1639.8438	1622.8173	1667.8388	1650.8122	W	***1262.5946***	1245.5681	11
17	1799.8745	1782.8479	1827.8694	1810.8429	C	***1076.5153***	1059.4888	10
18	1927.9331	1910.9065	1955.9280	1938.9014	Q	916.4847	899.4581	9
19	1984.9545	1967.9280	2012.9495	1995.9229	G	***788.4261***	771.3995	8
20	2098.0386	2081.0121	2126.0335	2109.0070	L	731.4046	714.3781	7
21	2213.0655	2196.0390	2241.0605	2224.0339	D	***618.3206***	601.2940	6
22	2270.0870	2253.0605	2298.0819	2281.0554	G	***503.2936***	486.2671	5
23	2383.1711	2366.1445	2411.1660	2394.1394	L	446.2722	429.2456	4
24	2454.2082	2437.1816	2482.2031	2465.1766	A	333.1881	316.1615	3
25	2541.2402	2524.2137	2569.2351	2552.2086	S	262.1510	245.1244	2
26					R	***175.1190***	158.0924	1





NCBI **BLAST** search of VDKGLVPLAGSNNESWCQGLDGLASR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
38.9	2742.3395	0.1039	VDKGLVPLAGSNNESWCQGLDGLASR
0.8	2742.3687	0.0747	MLEERVLLPGGPGEVELDVADWYR
0.7	2742.2840	0.1594	TTSKLDQDAALSLFEDMVQLGCER
0.7	2742.2079	0.2355	DVTDFDFSSNNQYIASSSMDKTVR

0.6	2742.3887	0.0547	CLDILHIHKGFFIQQSVFGACPR
0.6	2742.3523	0.0911	CLDILHIHQGFFIQQSVFGACPR
0.4	2742.2694	0.1740	EELAAGEMTEDSLGAFFDIVDQSLR

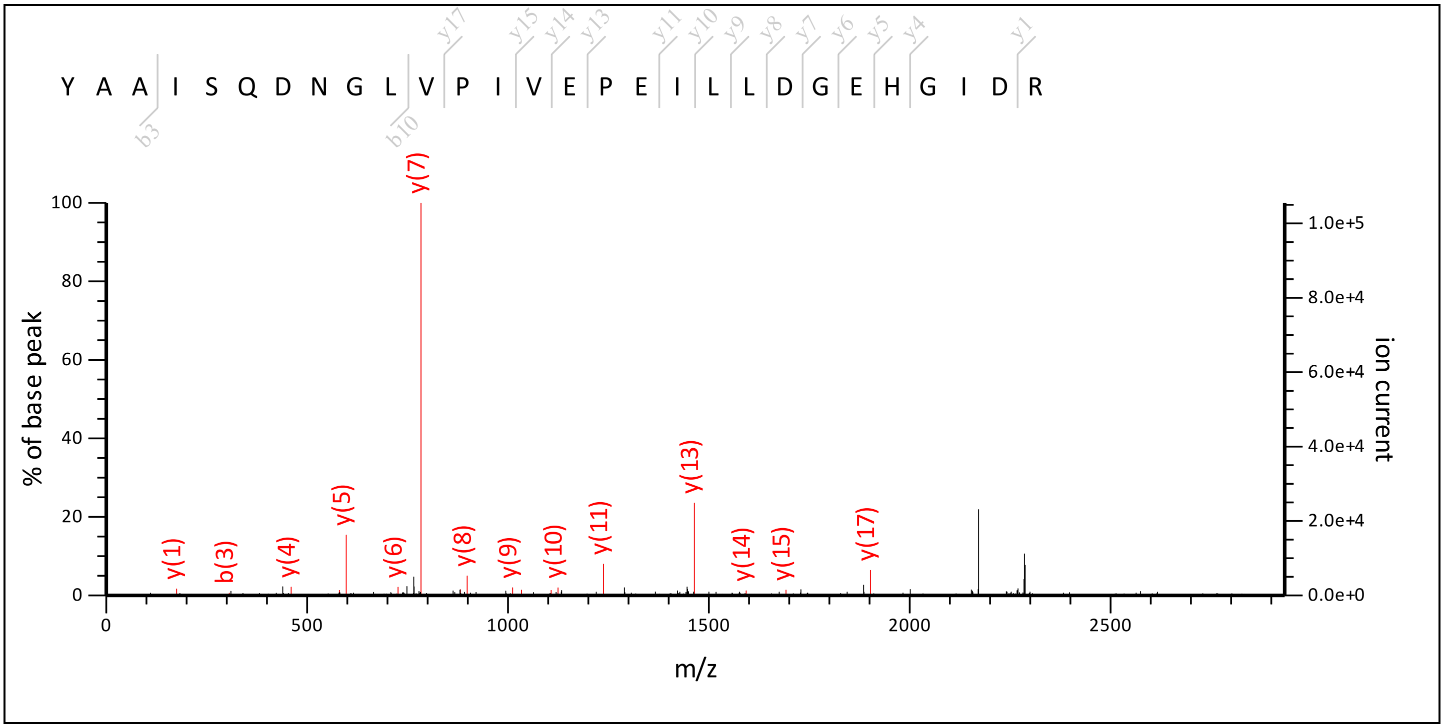
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 128

MS/MS Fragmentation of **YAAISQDNGLVPIVEPEILLDGEHGIDR**
Found in **gi|108864048** in **NCBInr**, Fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed [Oryza sativa Japonica Group]

Match to Query 143: 3032.659724 from(3033.667000,1+) intensity(0.0000) index(34)
Title: Label: K15, Spot_Id: 219908, Peak_List_Id: 228505, MSMS Job_Run_Id: 21992, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_K15_136868296900.txt



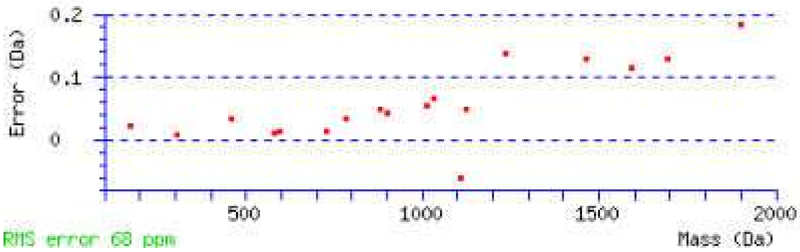
0 to 2933.39

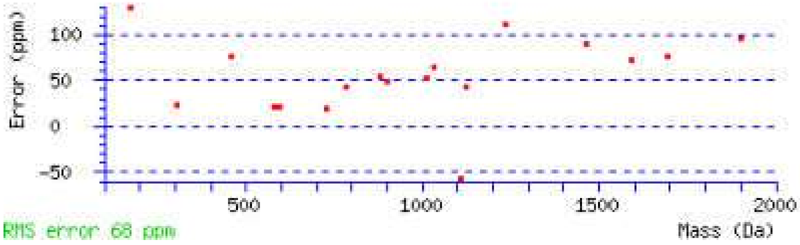
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 3032.5455
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.015
Matches : 18/152 fragment ions using 56 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	136.0757		164.0706		Y			28
2	207.1128		235.1077		A	2870.4894	2853.4629	27
3	278.1499		306.1448		A	2799.4523	2782.4258	26
4	391.2340		419.2289		I	2728.4152	2711.3887	25
5	478.2660		506.2609		S	2615.3311	2598.3046	24
6	606.3246	589.2980	634.3195	617.2930	Q	2528.2991	2511.2726	23
7	721.3515	704.3250	749.3464	732.3199	D	2400.2405	2383.2140	22

8	835.3945	818.3679	863.3894	846.3628	**N**	2285.2136	2268.1870	**21**
9	892.4159	875.3894	920.4108	903.3843	**G**	2171.1707	2154.1441	**20**
10	1005.5000	988.4734	**1033.4949**	1016.4684	**L**	2114.1492	2097.1226	**19**
11	1104.5684	1087.5419	1132.5633	1115.5368	**V**	2001.0651	1984.0386	**18**
12	1201.6212	1184.5946	1229.6161	1212.5895	**P**	***1901.9967***	1884.9702	**17**
13	1314.7052	1297.6787	1342.7001	1325.6736	**I**	1804.9440	1787.9174	**16**
14	1413.7736	1396.7471	1441.7686	1424.7420	**V**	***1691.8599***	1674.8333	**15**
15	1542.8162	1525.7897	1570.8112	1553.7846	**E**	***1592.7915***	1575.7649	**14**
16	1639.8690	1622.8425	1667.8639	1650.8374	**P**	***1463.7489***	1446.7223	**13**
17	1768.9116	1751.8850	1796.9065	1779.8800	**E**	1366.6961	1349.6696	**12**
18	1881.9957	1864.9691	1909.9906	1892.9640	**I**	***1237.6535***	1220.6270	**11**
19	1995.0797	1978.0532	2023.0746	2006.0481	**L**	***1124.5695***	1107.5429	**10**
20	2108.1638	2091.1372	2136.1587	2119.1321	**L**	***1011.4854***	994.4588	**9**
21	2223.1907	2206.1642	2251.1856	2234.1591	**D**	***898.4013***	881.3748	**8**
22	2280.2122	2263.1856	2308.2071	2291.1806	**G**	***783.3744***	766.3478	**7**
23	2409.2548	2392.2282	2437.2497	2420.2231	**E**	***726.3529***	709.3264	**6**
24	2546.3137	2529.2871	2574.3086	2557.2821	**H**	***597.3103***	580.2838	**5**
25	2603.3352	2586.3086	2631.3301	2614.3035	**G**	***460.2514***	443.2249	**4**
26	2716.4192	2699.3927	2744.4141	2727.3876	**I**	403.2300	386.2034	**3**
27	2831.4462	2814.4196	2859.4411	2842.4145	**D**	290.1459	273.1193	**2**
28					**R**	***175.1190***	158.0924	**1**





NCBI **BLAST** search of YAAISQDNGLVPIVEPEILLDGEHGIDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
47.2	3032.5455	0.1143	YAAISQDNGLVPIVEPEILLDGEHGIDR
31.6	3032.5455	0.1143	YAAISQDNGLVPIVEPEILLDGDHGIER

5.0	3032.7539	-0.0942	LSHLNFVLDILLPHSIHLEILVQTLR
3.6	3032.5957	0.0640	LGIEPYSVEVLPSGELLILDSANSNLYK
1.9	3032.7539	-0.0941	LAHLNYVLDLLIPHSIHLEILVQTLR
1.7	3032.5165	0.1432	TPADVTALFTVLVSNYTAAVTDLYGMGAR
1.7	3032.5224	0.1374	VIGILADEHHVRAAGQCHGNDRPVGAGAR
0.6	3032.5140	0.1457	MLLGFGIGCAIQSVPIYVSEVAPYNYR
0.4	3032.4696	0.1902	TTMDSHEGADITGAFRPGVLAALMGVSGAGK
0.1	3032.8552	-0.1955	FSRPIIPDIKIMLVVVAVSVIIGLVIGR

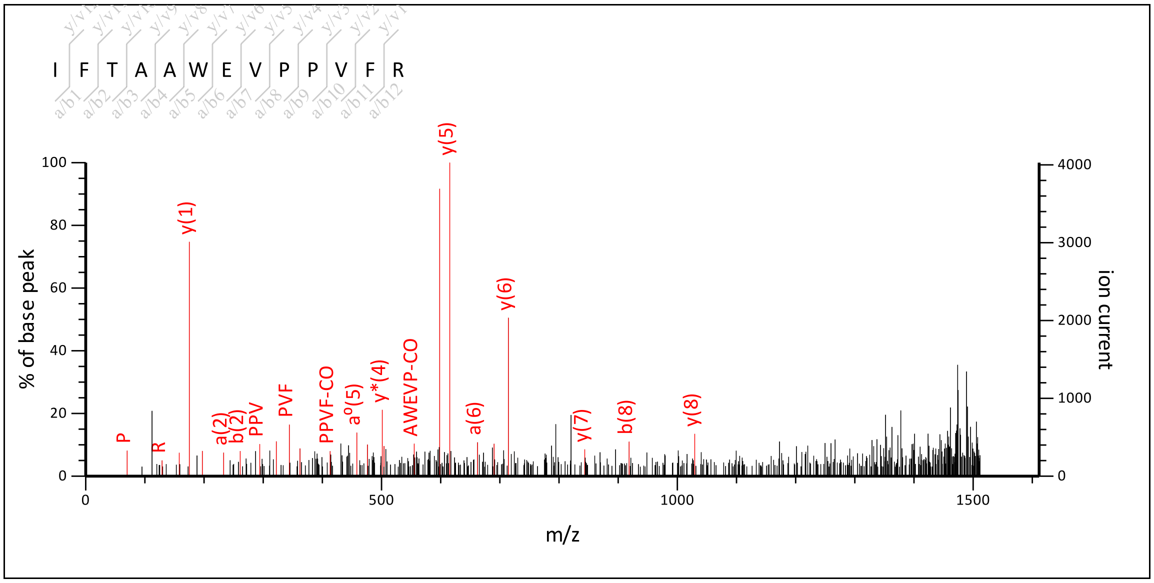
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 129

MS/MS Fragmentation of **IFTAAWEVPPVFR**
Found in **gi|115456389** in **NCBInr**, Os03g0831500 [Oryza sativa Japonica Group]

Match to Query 6: 1531.939524 from(1532.946800,1+) intensity(0.0000) index(2)
Title: Label: C7, Spot_Id: 228940, Peak_List_Id: 257494, MSMS Job_Run_Id: 24921, Comment:
Data file ppw_C7_138985139300.txt



0 to 1611.56

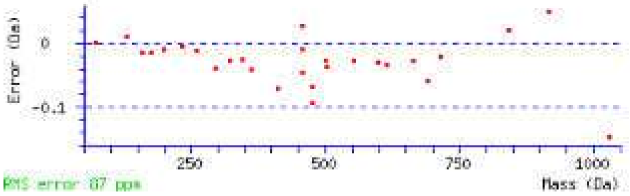
Label all possible matches ○ Label matches used for scoring ●

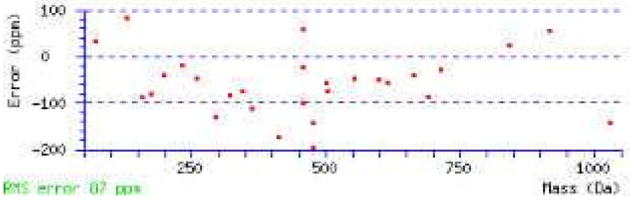
Monoisotopic mass of neutral peptide Mr(calc): 1531.8187
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 7.4
Matches : 32/193 fragment ions using 60 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		44.0495		**I**							**13**
2	120.0808	**233.1648**		***261.1598***				**F**	1327.6793			1419.7419	1402.7154	1401.7314	**12**
3	74.0600	334.2125	316.2020	***362.2074***	344.1969	318.2176	320.1969	**T**	1226.6317	1239.6521	1241.6313	1272.6735	1255.6470	1254.6630	**11**
4	44.0495	405.2496	387.2391	433.2445	415.2340			**A**	1155.5946			1171.6259	1154.5993	1153.6153	**10**
5	44.0495	**476.2867**	458.2762	***504.2817***	486.2711			**A**	1084.5574			1100.5887	1083.5622	1082.5782	**9**
6	159.0917	**662.3661**	644.3555	***690.3610***	672.3504			**W**	898.4781			***1029.5516***	1012.5251	1011.5411	**8**
7	102.0550	791.4087	773.3981	819.4036	801.3930	733.4032		**E**	769.4355	768.4403		***843.4723***	826.4458	825.4618	**7**
8	72.0808	890.4771	872.4665	***918.4720***	900.4614	876.4614		**V**	670.3671	683.3875		***714.4297***	697.4032		**6**
9	70.0651	987.5298	969.5193	1015.5247	997.5142	961.5142		**P**	573.3144	572.3191		***615.3613***	598.3348		**5**
10	70.0651	1084.5826	1066.5720	1112.5775	1094.5669	1058.5669		**P**	476.2616	475.2663		518.3085	501.2820		**4**
11	72.0808	1183.6510	1165.6404	1211.6459	1193.6354	1169.6354		**V**	377.1932	390.2136		421.2558	404.2292		**3**
12	120.0808	1330.7194	1312.7089	1358.7143	1340.7038			**F**	230.1248			***322.1874***	305.1608		**2**
13	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FT	221.1285	249.1234	**FTA**	292.1656	320.1605	**FTAA**	363.2027	391.1976
FTAAW	549.2820	577.2769	**FTAAWE**	678.3246	706.3195	**TA**	145.0972	173.0921
TAA	216.1343	244.1292	**TAAW**	402.2136	430.2085	**TAAWE**	531.2562	559.2511

TAAWEV	630.3246	658.3195	**AA**	115.0866	143.0815	**AAW**	301.1659	329.1608
AAWE	430.2085	458.2034	**AAWEV**	529.2769	557.2718	**AAWEVP**	626.3297	654.3246
AW	230.1288	258.1237	**AWE**	359.1714	387.1663	**AWEV**	458.2398	486.2347
AWEVP	555.2926	583.2875	**AWEVPP**	652.3453	680.3402	**WE**	288.1343	316.1292
WEV	387.2027	415.1976	**WEVP**	484.2554	512.2504	**WEVPP**	581.3082	609.3031
WEVPPV	680.3766	708.3715	**EV**	201.1234	229.1183	**EVP**	298.1761	326.1710
EVPP	395.2289	423.2238	**EVPPV**	494.2973	522.2922	**EVPPVF**	641.3657	669.3606
VP	169.1335	197.1285	**VPP**	266.1863	294.1812	**VPPV**	365.2547	393.2496
VPPVF	512.3231	540.3180	**PP**	167.1179	195.1128	**PPV**	266.1863	294.1812
PPVF	413.2547	441.2496	**PV**	169.1335	197.1285	**PVF**	316.2020	344.1969
VF	219.1492	247.1441						





NCBI **BLAST** search of IFTAAWEVPPVFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.3	1531.8187	0.1208	IFTAAWEVPPVFR
17.9	1531.8181	0.1215	AYQAQKEVMVIPR
15.2	1531.8028	0.1367	TMIAASVPINSASVR
13.6	1531.8107	0.1289	KGTQAFGSASPALAAR
8.1	1531.7969	0.1426	AMHFKDLPSLAFR
8.1	1531.8293	0.1103	ARFLMALLADANAR
7.3	1531.7882	0.1513	EIFNADDLVEVLR
7.0	1531.7889	0.1506	LRSMRPGGSATDLR
6.4	1531.8107	0.1288	VSNSVQGGNGIVVFR
6.4	1531.8246	0.1149	ALPAATSTTFLTNPK

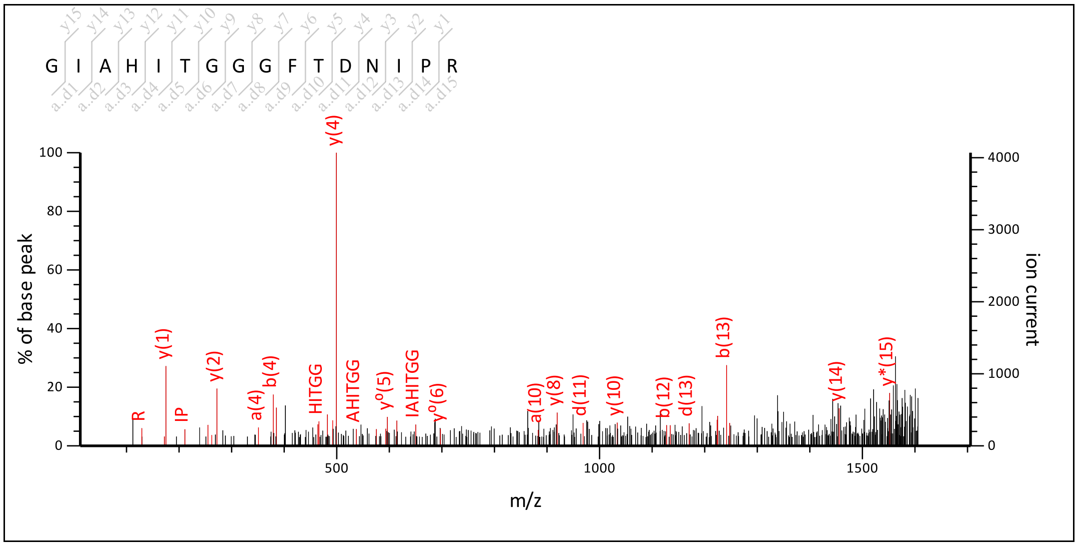
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 129

MS/MS Fragmentation of **GIAHITGGGFTDNIPR**
Found in **gi|115456389** in **NCBInr**, Os03g0831500 [Oryza sativa Japonica Group]

Match to Query 8: 1624.974324 from(1625.981600,1+) intensity(0.0000) index(3)
Title: Label: C7, Spot_Id: 228940, Peak_List_Id: 257495, MSMS Job_Run_Id: 24921, Comment:
Data file ppw_C7_138985139300.txt



12.09 to 1705.72

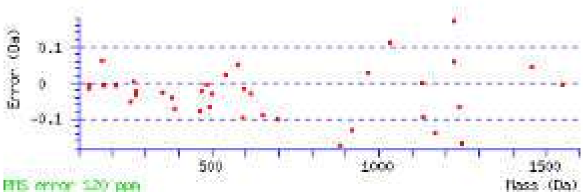
Label all possible matches ○ Label matches used for scoring ●

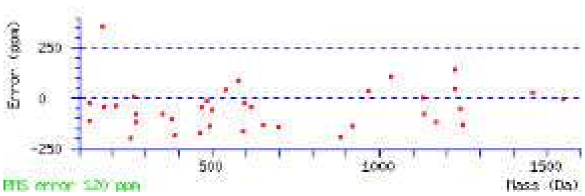
Monoisotopic mass of neutral peptide Mr(calc): 1624.8322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.79
Matches : 39/277 fragment ions using 105 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	86.0964	143.1179			171.1128			115.0866	129.1022	I	1510.7397	1523.7601	1537.7758	1568.8180	1551.7914
3	44.0495	214.1550			242.1499					A	1439.7026			***1455.7339***	1438.7074
4	110.0713	**351.2139**			**379.2088**					H	1302.6437			1384.6968	1367.6702
5	86.0964	**464.2980**			**492.2929**			436.2667	450.2823	I	1189.5596	1202.5800	1216.5957	***1247.6379***	1230.6113
6	74.0600	565.3457		547.3351	**593.3406**		575.3300	549.3507	551.3300	T	1088.5119	1101.5324	1103.5116	***1134.5538***	1117.5273
7	30.0338	622.3671		604.3566	**650.3620**		632.3515			G				***1033.5061***	1016.4796
8	30.0338	679.3886		661.3780	707.3835		689.3729			G				976.4847	959.4581
9	30.0338	736.4101		718.3995	764.4050		746.3944			G				***919.4632***	902.4367
10	120.0808	**883.4785**		865.4679	911.4734		893.4628			F	770.3791			862.4417	845.4152
11	74.0600	984.5261		966.5156	1012.5211		994.5105	968.5312	970.5105	T	669.3315	682.3519	684.3311	715.3733	698.3468
12	88.0393	1099.5531		1081.5425	**1127.5480**		1109.5374	1055.5633		D	554.3045	553.3093		***614.3256***	597.2991
13	87.0553	1213.5960	1196.5695	1195.5854	**1241.5909**	1224.5644	1223.5804	1170.5902		N	440.2616	439.2663		***499.2987***	482.2722
14	86.0964	1326.6801	1309.6535	1308.6695	1354.6750	1337.6484	1336.6644	1298.6488	1312.6644	I	327.1775	340.1979	354.2136	***385.2558***	368.2292
15	70.0651	1423.7328	1406.7063	1405.7223	1451.7278	1434.7012	1433.7172	1397.7172		P	230.1248	229.1295		***272.1717***	255.1452
16	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IA	157.1335	185.1285	IAH	294.1925	322.1874	IAHI	407.2765	435.2714
IAHIT	508.3242	536.3191	IAHITG	565.3457	593.3406	IAHITGG	622.3671	650.3620
IAHITGGG	679.3886	707.3835	AH	181.1084	209.1033	AHI	294.1925	322.1874
AHIT	395.2401	423.2350	AHITG	452.2616	480.2565	AHITGG	509.2831	537.2780

AHITGGG	566.3045	594.2994	**HI**	223.1553	251.1503	**HIT**	324.2030	352.1979
HITG	381.2245	409.2194	**HITGG**	438.2459	466.2409	**HITGGG**	495.2674	523.2623
HITGGGF	642.3358	670.3307	**IT**	187.1441	215.1390	**ITG**	244.1656	272.1605
ITGG	301.1870	329.1819	**ITGGG**	358.2085	386.2034	**ITGGGF**	505.2769	533.2718
ITGGGFT	606.3246	634.3195	**TG**	131.0815	159.0764	**TGG**	188.1030	216.0979
TGGG	245.1244	273.1193	**TGGGF**	392.1928	420.1878	**TGGGFT**	493.2405	521.2354
TGGGFTD	608.2675	636.2624	**GG**	87.0553	115.0502	**GGG**	144.0768	172.0717
GGGF	291.1452	319.1401	**GGGFT**	392.1928	420.1878	**GGGFTD**	507.2198	535.2147
GGGFTDN	621.2627	649.2576	**GG**	87.0553	115.0502	**GGF**	234.1237	262.1186
GGFT	335.1714	363.1663	**GGFTD**	450.1983	478.1932	**GGFTDN**	564.2413	592.2362
GGFTDNI	677.3253	705.3202	**GF**	177.1022	205.0972	**GFT**	278.1499	306.1448
GFTD	393.1769	421.1718	**GFTDN**	507.2198	535.2147	**GFTDNI**	620.3039	648.2988
FT	221.1285	249.1234	**FTD**	336.1554	364.1503	**FTDN**	450.1983	478.1932
FTDNI	563.2824	591.2773	**FTDNIP**	660.3352	688.3301	**TD**	189.0870	217.0819
TDN	303.1299	331.1248	**TDNI**	416.2140	444.2089	**TDNIP**	513.2667	541.2617
DN	202.0822	230.0771	**DNI**	315.1663	343.1612	**DNIP**	412.2191	440.2140
NI	200.1394	228.1343	**NIP**	297.1921	325.1870	**IP**	183.1492	211.1441





NCBI **BLAST** search of GIAHITGGGFTDNIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
31.5	1624.8322	0.1422	GIAHITGGGFTDNIPR
31.5	1624.8322	0.1422	GLAHITGGGFTDNIPR
10.1	1624.9260	0.0483	SAILNDAIRVVGELR
9.8	1624.9161	0.0582	EALAIARFPASARPR
7.5	1624.8429	0.1314	ACGLPVIMPGDKVPR
7.5	1624.8321	0.1422	NLGFNGNQLEGPLPR
6.3	1624.9162	0.0582	KLVDAVHHVAGLNPR
6.0	1624.8249	0.1494	LYAYYGNLEGPIPR
6.0	1624.9664	0.0079	AKLAADYLIAPVKPR
5.6	1624.8533	0.1211	ETTTPPSRSVALNPR

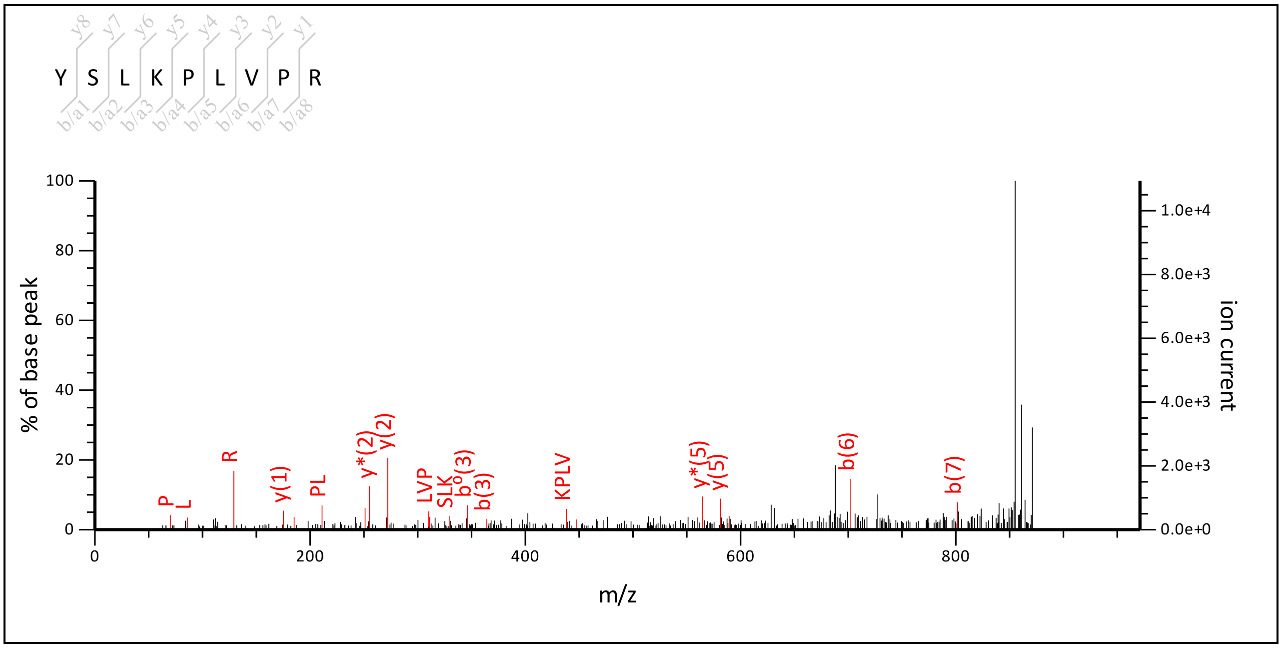
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 131

MS/MS Fragmentation of **YSLKPLVPR**
Found in **gi|114386664** in **NCBInr**, phosphoglycerate kinase [Oryza sativa Indica Group]

Match to Query 129: 1071.698424 from(1072.705700,1+) intensity(0.0000) index(19)
Title: Label: I12, Spot_Id: 219858, Peak_List_Id: 227380, MSMS Job_Run_Id: 21960, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I12_136868236700.txt



0 to 971.15

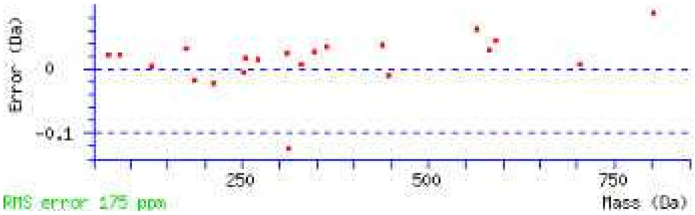
Label all possible matches ○ Label matches used for scoring ●

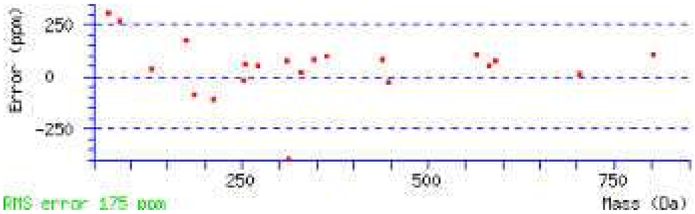
Monoisotopic mass of neutral peptide Mr(calc): 1071.6440
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 19 **Expect:** 1.8e+02
Matches : 25/130 fragment ions using 45 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	136.0757	136.0757			164.0706			44.0495	Y						9
2	60.0444	223.1077		205.0972	***251.1026***		233.0921	207.1128	S	877.5618	876.5666	909.5880	892.5615	891.5774	8
3	86.0964	336.1918		318.1812	***364.1867***		346.1761	294.1448	L	764.4777	763.4825	822.5560	805.5294		7
4	101.1073	464.2867	447.2602	446.2762	492.2817	475.2551	474.2711	407.2289	K	636.3828	635.3875	709.4719	692.4454		6
5	70.0651	561.3395	544.3130	543.3289	***589.3344***	572.3079	571.3239	535.3239	P	539.3300	538.3348	***581.3770***	564.3504		5
6	86.0964	674.4236	657.3970	656.4130	***702.4185***	685.3919	684.4079	632.3766	L	426.2459	425.2507	484.3242	467.2976		4
7	72.0808	773.4920	756.4654	755.4814	***801.4869***	784.4604	783.4763	759.4763	V	327.1775	340.1979	371.2401	354.2136		3
8	70.0651	870.5448	853.5182	852.5342	898.5397	881.5131	880.5291	844.5291	P	230.1248	229.1295	***272.1717***	255.1452		2
9	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SL	173.1285	201.1234	**SLK**	301.2234	329.2183	**SLKP**	398.2762	426.2711
SLKPL	511.3602	539.3552	**SLKPLV**	610.4287	638.4236	**LK**	214.1914	242.1863
LKP	311.2442	339.2391	**LKPL**	424.3282	452.3231	**LKPLV**	523.3966	551.3915

LKPLVP	620.4494	648.4443	**KP**	198.1601	226.1550	**KPL**	311.2442	339.2391
KPLV	410.3126	438.3075	**KPLVP**	507.3653	535.3602	**PL**	183.1492	211.1441
PLV	282.2176	310.2125	**PLVP**	379.2704	407.2653	**LV**	185.1648	213.1598
LVP	282.2176	310.2125	**VP**	169.1335	197.1285			





NCBI **BLAST** search of YSLKPLVPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
23.3	1071.6553	0.0431	HLLPVAAVPR
19.4	1071.6440	0.0544	YSLKPLVPR
17.5	1071.6110	0.0874	KLSEMLVPR
16.8	1071.6189	0.0795	DRLVLFGPR
16.5	1071.6077	0.0908	YSLIPGAVPR
15.9	1071.6077	0.0908	LASGPYVIPR
15.7	1071.6077	0.0908	SYLQLPVPR
15.3	1071.6077	0.0908	LAGELIGFPR
14.8	1071.6077	0.0908	QSIPYLVPR
14.7	1071.6077	0.0908	NTLYPIVPR

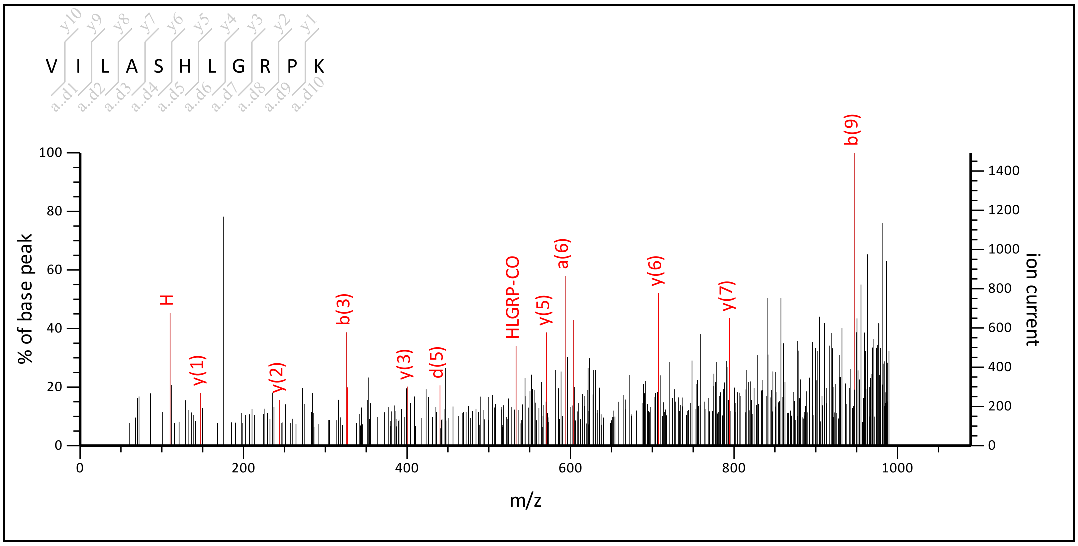
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 131

MS/MS Fragmentation of **VILASHLGRPK**
Found in **gi|114386664** in **NCBInr**, phosphoglycerate kinase [Oryza sativa Indica Group]

Match to Query 176: 1189.783624 from(1190.790900,1+) intensity(0.0000) index(23)
Title: Label: I12, Spot_Id: 219858, Peak_List_Id: 227381, MSMS Job_Run_Id: 21960, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I12_136868236700.txt



0 to 1089.53

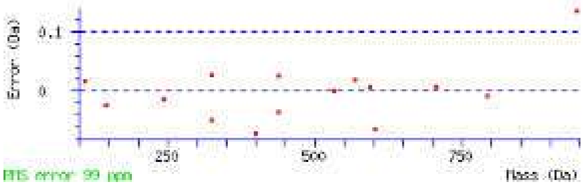
Label all possible matches ○ Label matches used for scoring ●

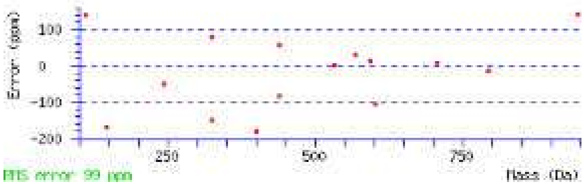
Monoisotopic mass of neutral peptide Mr(calc): 1189.7295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 21
Matches : 16/159 fragment ions using 30 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0
1	72.0808	72.0808			100.0757			44.0495		V						
2	86.0964	185.1648			213.1598			157.1335	171.1492	I	1033.5901	1046.6105	1060.6262	1091.6684	1074.6418	1073.6
3	86.0964	298.2489			**326.2438**			256.2020		L	920.5061	919.5108		978.5843	961.5578	960.5
4	44.0495	369.2860			397.2809					A	849.4690			865.5003	848.4737	847.4
5	60.0444	456.3180		438.3075	484.3130		466.3024	440.3231		S	762.4369	761.4417		***794.4631***	777.4366	776.4
6	110.0713	593.3770		575.3664	621.3719		603.3613			H	625.3780			***707.4311***	690.4046	
7	86.0964	706.4610		688.4505	734.4559		716.4454	664.4141		L	512.2940	511.2987		***570.3722***	553.3457	
8	30.0338	763.4825		745.4719	791.4774		773.4668			G				457.2881	440.2616	
9	129.1135	919.5836	902.5570	901.5730	**947.5785**	930.5520	929.5679	834.5196		R	299.1714	298.1761		***400.2667***	383.2401	
10	70.0651	1016.6364	999.6098	998.6258	1044.6313	1027.6047	1026.6207	990.6207		P	202.1186	201.1234		***244.1656***	227.1390	
11	101.1073									K	74.0237	73.0284		***147.1128***	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IL	199.1805	227.1754	ILA	270.2176	298.2125	ILAS	357.2496	385.2445
ILASH	494.3085	522.3035	ILASHL	607.3926	635.3875	ILASHLG	664.4141	692.4090
LA	157.1335	185.1285	LAS	244.1656	272.1605	LASH	381.2245	409.2194
LASHL	494.3085	522.3035	LASHLG	551.3300	579.3249	AS	131.0815	159.0764
ASH	268.1404	296.1353	ASHL	381.2245	409.2194	ASHLG	438.2459	466.2409
ASHLGR	594.3471	622.3420	ASHLGRP	691.3998	719.3947	SH	197.1033	225.0982
SHL	310.1874	338.1823	SHLG	367.2088	395.2037	SHLGR	523.3099	551.3049
SHLGRP	620.3627	648.3576	HL	223.1553	251.1503	HLG	280.1768	308.1717
HLGR	436.2779	464.2728	HLGRP	533.3307	561.3256	LG	143.1179	171.1128
LGR	299.2190	327.2139	LGRP	396.2718	424.2667	GR	186.1349	214.1299

GRP	283.1877	311.1826	**RP**	226.1662	254.1612			





NCBI **BLAST** search of VILASHLGRPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.2	1189.7295	0.0541	IVIASHLGRPK
26.2	1189.7295	0.0541	IVLASHLGRPK
26.2	1189.7295	0.0541	LIVASHLGRPK
26.2	1189.7295	0.0541	LVLASHLGRPK
24.8	1189.7295	0.0541	VIIASHLGRPK
24.8	1189.7295	0.0541	VILASHLGRPK
24.8	1189.7295	0.0541	VLLASHLGRPK
23.4	1189.7295	0.0541	AILVSHLGRPK
23.1	1189.7295	0.0541	IIIGSHLGRPK
23.1	1189.7295	0.0541	IILGSHLGRPK

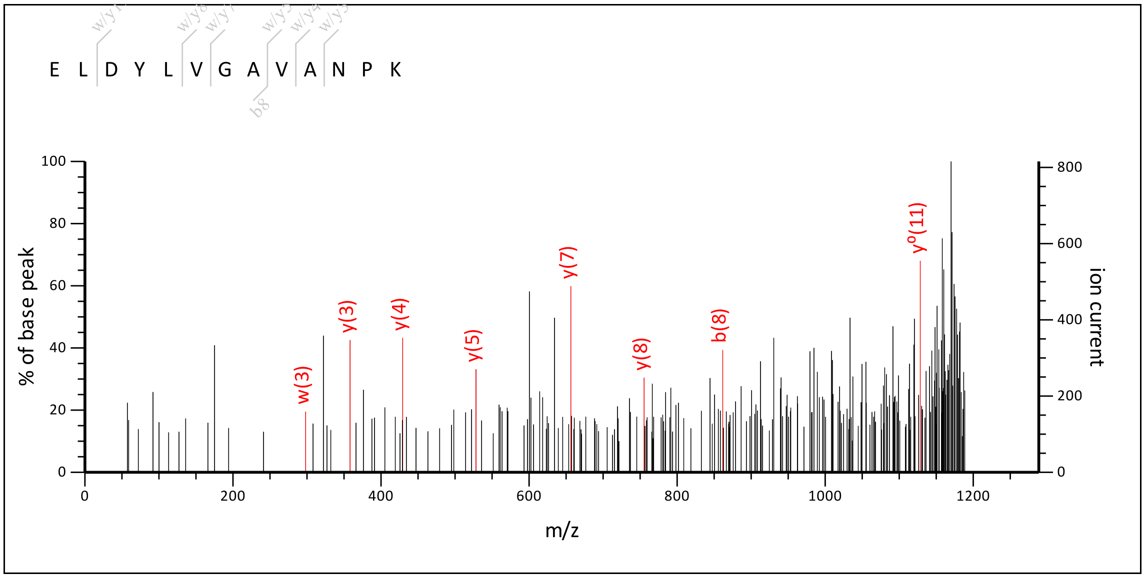
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 131

MS/MS Fragmentation of **ELDYLVGAVANPK**
Found in **gi|114386664** in **NCBInr**, phosphoglycerate kinase [Oryza sativa Indica Group]

Match to Query 207: 1387.781324 from(1388.788600,1+) intensity(0.0000) index(27)
Title: Label: I12, Spot_Id: 219858, Peak_List_Id: 227394, MSMS Job_Run_Id: 21960, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I12_136868236700.txt



0 to 1288.56

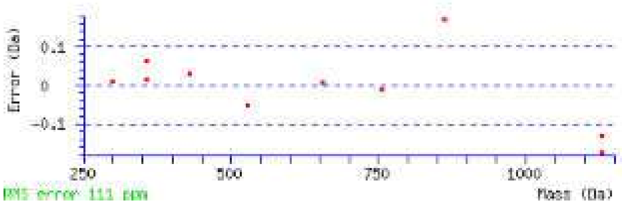
Label all possible matches ○ Label matches used for scoring ●

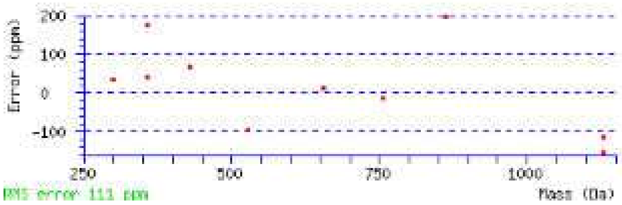
Monoisotopic mass of neutral peptide Mr(calc): 1387.7347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 11 **Expect:** 2.7e+03
Matches : 10/206 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495	**E**						13
2	86.0964	215.1390		197.1285	243.1339		225.1234	173.0921	**L**	1201.6212	1200.6259	1259.6994	1242.6729	1241.6889	12
3	88.0393	330.1660		312.1554	**358.1609**		340.1503	286.1761	**D**	1086.5942	1085.5990	1146.6154	1129.5888	1128.6048	11
4	136.0757	493.2293		475.2187	521.2242		503.2136		**Y**	923.5309		1031.5884	1014.5619		10
5	86.0964	606.3134		588.3028	634.3083		616.2977	564.2664	**L**	810.4468	809.4516	868.5251	851.4985		9
6	72.0808	705.3818		687.3712	733.3767		715.3661	691.3661	**V**	711.3784	724.3988	***755.4410***	738.4145		8
7	30.0338	762.4032		744.3927	790.3981		772.3876		**G**			***656.3726***	639.3461		7
8	44.0495	833.4403		815.4298	**861.4353**		843.4247		**A**	583.3198		599.3511	582.3246		6
9	72.0808	932.5088		914.4982	960.5037		942.4931	918.4931	**V**	484.2514	497.2718	***528.3140***	511.2875		5
10	44.0495	1003.5459		985.5353	1031.5408		1013.5302		**A**	413.2143		***429.2456***	412.2191		4
11	87.0553	1117.5888	1100.5623	1099.5782	1145.5837	1128.5572	1127.5732	1074.5830	**N**	299.1714	298.1761	***358.2085***	341.1819		3
12	70.0651	1214.6416	1197.6150	1196.6310	1242.6365	1225.6099	1224.6259	1188.6259	**P**	202.1186	201.1234	244.1656	227.1390		2
13	101.1073								**K**	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LD	201.1234	229.1183	**LDY**	364.1867	392.1816	**LDYL**	477.2708	505.2657
LDYLV	576.3392	604.3341	**LDYLVG**	633.3606	661.3556	**DY**	251.1026	279.0975
DYL	364.1867	392.1816	**DYLV**	463.2551	491.2500	**DYLVG**	520.2766	548.2715
DYLVGA	591.3137	619.3086	**DYLVGAV**	690.3821	718.3770	**YL**	249.1598	277.1547
YLV	348.2282	376.2231	**YLVG**	405.2496	433.2445	**YLVGA**	476.2867	504.2817

YLVGAV	575.3552	603.3501	**YLVGAVA**	646.3923	674.3872	**LV**	185.1648	213.1598
LVG	242.1863	270.1812	**LVGA**	313.2234	341.2183	**LVGAV**	412.2918	440.2867
LVGAVA	483.3289	511.3239	**LVGAVAN**	597.3719	625.3668	**LVGAVANP**	694.4246	722.4196
VG	129.1022	157.0972	**VGA**	200.1394	228.1343	**VGAV**	299.2078	327.2027
VGAVA	370.2449	398.2398	**VGAVAN**	484.2878	512.2827	**VGAVANP**	581.3406	609.3355
GA	101.0709	129.0659	**GAV**	200.1394	228.1343	**GAVA**	271.1765	299.1714
GAVAN	385.2194	413.2143	**GAVANP**	482.2722	510.2671	**AV**	143.1179	171.1128
AVA	214.1550	242.1499	**AVAN**	328.1979	356.1928	**AVANP**	425.2507	453.2456
VA	143.1179	171.1128	**VAN**	257.1608	285.1557	**VANP**	354.2136	382.2085
AN	158.0924	186.0873	**ANP**	255.1452	283.1401	**NP**	184.1081	212.1030





NCBI **BLAST** search of ELDYLVGAVANPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
12.5	1387.6918	0.0895	IMVVDDHQLFR
12.3	1387.6554	0.1259	FLNVASGNTYMR
11.9	1387.7534	0.0280	LFPAVQVGLEGMK
10.7	1387.7347	0.0466	ELDYLVGAVANPK
10.7	1387.6918	0.0895	EIVDNLVFHMR
10.6	1387.6554	0.1259	IEIGDQPWQMR
10.3	1387.7857	-0.0044	LELTINALKAMR
10.1	1387.7394	0.0419	QVGATAKVCWLR
9.8	1387.7307	0.0506	NVQSVITTSTPNK
9.5	1387.7208	0.0605	KAIASYVQDHTR

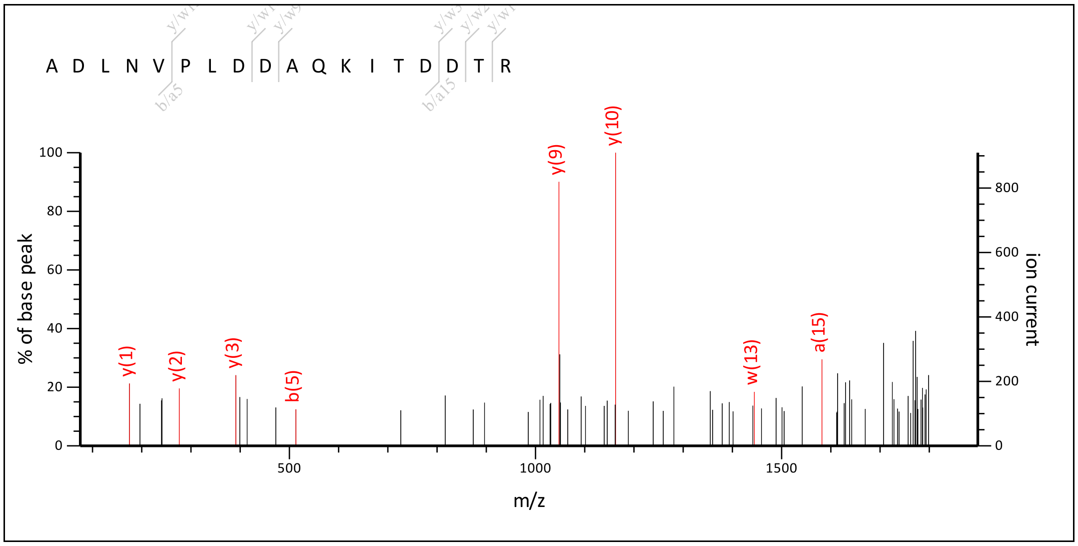
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 131

MS/MS Fragmentation of **ADLNVPLDDAQKITDDTR**
Found in **gi|114386664** in **NCBInr**, phosphoglycerate kinase [Oryza sativa Indica Group]

Match to Query 219: 1999.097724 from(2000.105000,1+) intensity(0.0000) index(30)
Title: Label: I12, Spot_Id: 219858, Peak_List_Id: 227401, MSMS Job_Run_Id: 21960, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I12_136868236700.txt



75.14 to 1898.59

Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1998.9858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 16  Expect: 6.2e+02
Matches : 8/347 fragment ions using 16 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	44.0495	44.0495			72.0444			44.0495		A						
2	88.0393	159.0764		141.0659	187.0713		169.0608	115.0866		D	1868.9348	1867.9396		1928.9560	1911.9294	19
3	86.0964	272.1605		254.1499	300.1554		282.1448	230.1135		L	1755.8508	1754.8555		1813.9290	1796.9025	17
4	87.0553	386.2034	369.1769	368.1928	414.1983	397.1718	396.1878	343.1976		N	1641.8079	1640.8126		1700.8450	1683.8184	16
5	72.0808	485.2718	468.2453	467.2613	513.2667	496.2402	495.2562	471.2562		V	1542.7394	1555.7598		1586.8020	1569.7755	15
6	70.0651	582.3246	565.2980	564.3140	610.3195	593.2930	592.3089	556.3089		P	1445.6867	1444.6914		1487.7336	1470.7071	14
7	86.0964	695.4087	678.3821	677.3981	723.4036	706.3770	705.3930	653.3617		L	1332.6026	1331.6074		1390.6809	1373.6543	13
8	88.0393	810.4356	793.4090	792.4250	838.4305	821.4040	820.4199	766.4458		D	1217.5757	1216.5804		1277.5968	1260.5703	12
9	88.0393	925.4625	908.4360	907.4520	953.4575	936.4309	935.4469	881.4727		D	1102.5487	1101.5535		***1162.5699***	1145.5433	11
10	44.0495	996.4997	979.4731	978.4891	1024.4946	1007.4680	1006.4840			A	1031.5116			***1047.5429***	1030.5164	10
11	101.0709	1124.5582	1107.5317	1106.5477	1152.5531	1135.5266	1134.5426	1067.5368		Q	903.4530	902.4578		976.5058	959.4793	9
12	101.1073	1252.6532	1235.6266	1234.6426	1280.6481	1263.6216	1262.6375	1195.5953		K	775.3581	774.3628		848.4472	831.4207	8
13	86.0964	1365.7373	1348.7107	1347.7267	1393.7322	1376.7056	1375.7216	1337.7060	1351.7216	I	662.2740	675.2944	689.3101	720.3523	703.3257	7
14	74.0600	1466.7849	1449.7584	1448.7744	1494.7798	1477.7533	1476.7693	1450.7900	1452.7693	T	561.2263	574.2467	576.2260	607.2682	590.2416	5
15	88.0393	1581.8119	1564.7853	1563.8013	1609.8068	1592.7802	1591.7962	1537.8220		D	446.1994	445.2041		506.2205	489.1940	4
16	88.0393	1696.8388	1679.8123	1678.8283	1724.8337	1707.8072	1706.8232	1652.8490		D	331.1724	330.1772		***391.1936***	374.1670	3
17	74.0600	1797.8865	1780.8600	1779.8759	1825.8814	1808.8549	1807.8709	1781.8916	1783.8709	T	230.1248	243.1452	245.1244	***276.1666***	259.1401	2
18	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DL	201.1234	229.1183	DLN	315.1663	343.1612	DLNV	414.2347	442.2296
DLNVP	511.2875	539.2824	DLNVPL	624.3715	652.3665	LN	200.1394	228.1343
LNV	299.2078	327.2027	LNVP	396.2605	424.2554	LNVPL	509.3446	537.3395

LNVPLD	624.3715	652.3665	**NV**	186.1237	214.1186	**NVP**	283.1765	311.1714
NVPL	396.2605	424.2554	**NVPLD**	511.2875	539.2824	**NVPLDD**	626.3144	654.3093
NVPLDDA	697.3515	725.3464	**VP**	169.1335	197.1285	**VPL**	282.2176	310.2125
VPLD	397.2445	425.2395	**VPLDD**	512.2715	540.2664	**VPLDDA**	583.3086	611.3035
PL	183.1492	211.1441	**PLD**	298.1761	326.1710	**PLDD**	413.2031	441.1980
PLDDA	484.2402	512.2351	**PLDDAQ**	612.2988	640.2937	**LD**	201.1234	229.1183
LDD	316.1503	344.1452	**LDDA**	387.1874	415.1823	**LDDAQ**	515.2460	543.2409
LDDAQK	643.3410	671.3359	**DD**	203.0662	231.0612	**DDA**	274.1034	302.0983
DDAQ	402.1619	430.1569	**DDAQK**	530.2569	558.2518	**DDAQKI**	643.3410	671.3359
DA	159.0764	187.0713	**DAQ**	287.1350	315.1299	**DAQK**	415.2300	443.2249
DAQKI	528.3140	556.3089	**DAQKIT**	629.3617	657.3566	**AQ**	172.1081	200.1030
AQK	300.2030	328.1979	**AQKI**	413.2871	441.2820	**AQKIT**	514.3348	542.3297
AQKITD	629.3617	657.3566	**QK**	229.1659	257.1608	**QKI**	342.2500	370.2449
QKIT	443.2976	471.2926	**QKITD**	558.3246	586.3195	**QKITDD**	673.3515	701.3464
KI	214.1914	242.1863	**KIT**	315.2391	343.2340	**KITD**	430.2660	458.2609
KITDD	545.2930	573.2879	**KITDDT**	646.3406	674.3355	**IT**	187.1441	215.1390
ITD	302.1710	330.1660	**ITDD**	417.1980	445.1929	**ITDDT**	518.2457	546.2406
TD	189.0870	217.0819	**TDD**	304.1139	332.1088	**TDDT**	405.1616	433.1565
DD	203.0662	231.0612	**DDT**	304.1139	332.1088	**DT**	189.0870	217.0819

NCBI **BLAST** search of ADLNVPLDDAQKITDDTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
15.7	1998.9858	0.1119	ADLNVPLDDAQKITDDTR
11.6	1998.9568	0.1409	AEEEPVTAPEMPVDKTTR
10.2	1999.0698	0.0279	QLLSNGLLGGSVTSGKPESR
9.7	1998.9833	0.1144	MTLFIPTGNLSPSPHDTR
9.5	1998.9905	0.1072	MSTVHGTNRPSTLINDTR
9.5	1999.0335	0.0642	TVPVDRVAPSTAGGTTVDTR
9.1	1999.1354	-0.0376	LALLEAAGVDAVLVLEFTR
9.0	1999.0999	-0.0021	FKSMTLIILGIGFVGMTR
7.9	1999.0738	0.0239	DETLPKYVTNILQPVNR
7.8	1999.0024	0.0953	FSSHRGLGLVGDVFHDTR

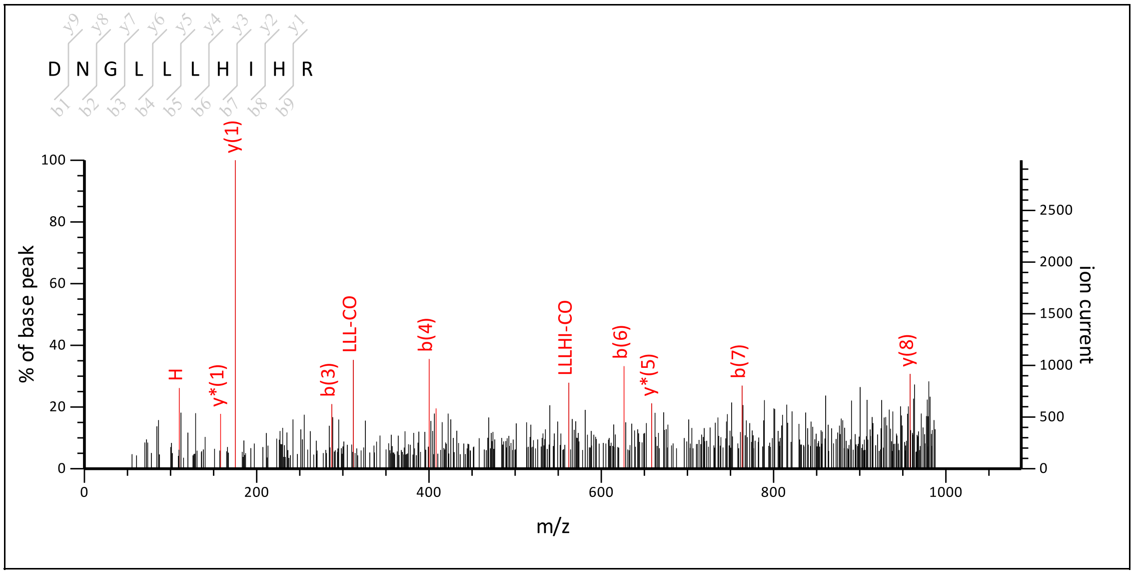
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 132

MS/MS Fragmentation of **DNGLLLHIHR**
Found in **gi|328682245** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Pseudocephalozia lepidozioides]

Match to Query 190: 1186.671924 from(1187.679200,1+) intensity(0.0000) index(19)
Title: Label: J4, Spot_Id: 219731, Peak_List_Id: 225365, MSMS Job_Run_Id: 21776, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J4_136842177300.txt



0 to 1087.49

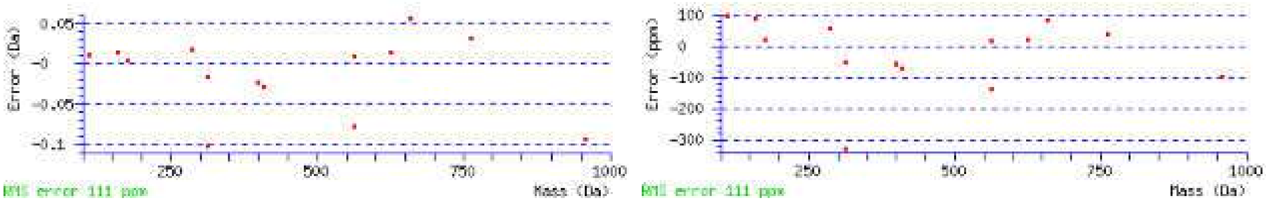
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1186.6571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 28 **Expect:** 4.9
Matches : 15/151 fragment ions using 20 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	#
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D						10
2	87.0553	202.0822	185.0557	184.0717	230.0771	213.0506	212.0666	159.0764		N	1013.6003	1012.6051		1072.6374	1055.6109	9
3	30.0338	259.1037	242.0771	241.0931	***287.0986***	270.0721	269.0880			G				***958.5945***	941.5679	8
4	86.0964	372.1878	355.1612	354.1772	***400.1827***	383.1561	382.1721	330.1408		L	843.4948	842.4995		901.5730	884.5465	7
5	86.0964	485.2718	468.2453	467.2613	513.2667	496.2402	495.2562	443.2249		L	730.4107	729.4155		788.4890	771.4624	6
6	86.0964	598.3559	581.3293	580.3453	***626.3508***	609.3243	608.3402	556.3089		L	617.3267	616.3314		675.4049	658.3784	5
7	110.0713	735.4148	718.3882	717.4042	***763.4097***	746.3832	745.3991			H	480.2677			***562.3208***	545.2943	4
8	86.0964	848.4989	831.4723	830.4883	876.4938	859.4672	858.4832	820.4676	834.4832	I	367.1837	380.2041	394.2197	425.2619	408.2354	3
9	110.0713	985.5578	968.5312	967.5472	1013.5527	996.5261	995.5421			H	230.1248			***312.1779***	295.1513	2
10	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NG	144.0768	172.0717	NGL	257.1608	285.1557	NGLL	370.2449	398.2398
NGLLL	483.3289	511.3239	NGLLLH	620.3879	648.3828	GL	143.1179	171.1128
GLL	256.2020	284.1969	GLLL	369.2860	397.2809	GLLLH	506.3449	534.3398
GLLLHI	619.4290	647.4239	LL	199.1805	227.1754	LLL	312.2646	340.2595
LLLH	449.3235	477.3184	LLLHI	562.4075	590.4024	LLLHIH	699.4664	727.4614
LL	199.1805	227.1754	LLH	336.2394	364.2343	LLHI	449.3235	477.3184
LLHIH	586.3824	614.3773	LH	223.1553	251.1503	LHI	336.2394	364.2343
LHIH	473.2983	501.2932	HI	223.1553	251.1503	HIH	360.2142	388.2092

IH	223.1553	251.1503						



NCBI **BLAST** search of DNGLLLHIHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
28.5	1186.6571	0.0149	DNGILIHIHR
28.5	1186.6571	0.0149	DNGILLHIHR
28.5	1186.6571	0.0149	DNGILLHIHR
28.5	1186.6571	0.0149	DNGILLHIHR
28.5	1186.6571	0.0149	DNGLILHIHR
28.5	1186.6571	0.0149	DNGLILHIHR
28.5	1186.6571	0.0149	DNGLLIHIHR
28.5	1186.6571	0.0149	DNGLLIHIHR
28.5	1186.6571	0.0149	DNGLLLHIHR
28.5	1186.6571	0.0149	DNGLLLHIHR

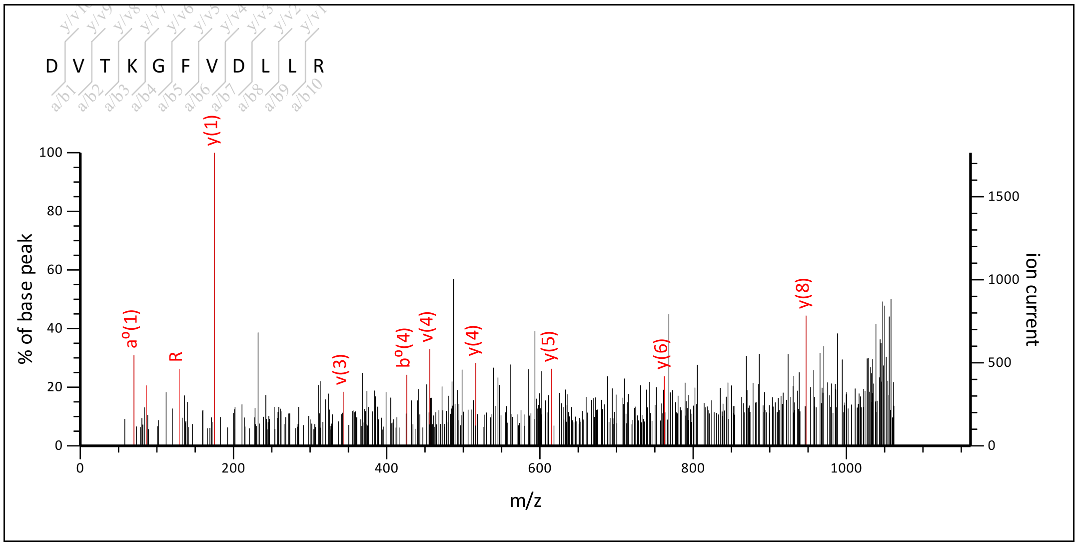
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 132

MS/MS Fragmentation of **DVTKGFVDLLR**
Found in **gi|328682245** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Pseudocephalozia lepidozioides]

Match to Query 226: 1261.707424 from(1262.714700,1+) intensity(0.0000) index(22)
Title: Label: J4, Spot_Id: 219731, Peak_List_Id: 225380, MSMS Job_Run_Id: 21776, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J4_136842177300.txt



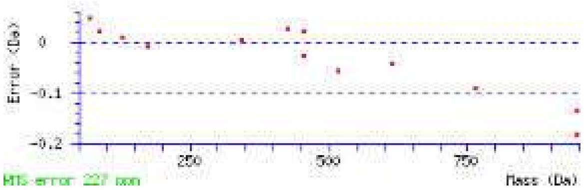
0 to 1162.1

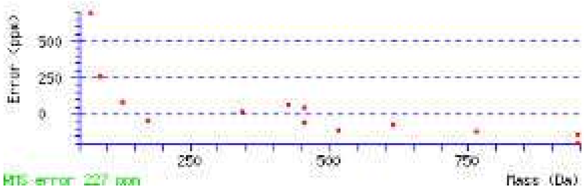
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1261.7030
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 8 **Expect:** 3e+02
Matches : 14/179 fragment ions using 33 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		**D**					
2	72.0808	187.1077		169.0972	215.1026		197.0921	173.0921		**V**	1103.6208	1116.6412		1147.6834	1130.6568
3	74.0600	288.1554		270.1448	316.1503		298.1397	272.1605	274.1397	**T**	1002.5731	1015.5935	1017.5728	1048.6150	1031.5884
4	101.1073	416.2504	399.2238	398.2398	444.2453	427.2187	426.2347	359.1925		**K**	874.4781	873.4829		***947.5673***	930.5407
5	30.0338	473.2718	456.2453	455.2613	501.2667	484.2402	483.2562			**G**				819.4723	802.4458
6	120.0808	620.3402	603.3137	602.3297	648.3352	631.3086	630.3246			**F**	670.3883			***762.4509***	745.4243
7	72.0808	719.4087	702.3821	701.3981	747.4036	730.3770	729.3930	705.3930		**V**	571.3198	584.3402		***615.3824***	598.3559
8	88.0393	834.4356	817.4090	816.4250	862.4305	845.4040	844.4199	790.4458		**D**	456.2929	455.2976		***516.3140***	499.2875
9	86.0964	947.5197	930.4931	929.5091	975.5146	958.4880	957.5040	905.4727		**L**	343.2088	342.2136		401.2871	384.2605
10	86.0964	1060.6037	1043.5772	1042.5932	1088.5986	1071.5721	1070.5881	1018.5568		**L**	230.1248	229.1295		288.2030	271.1765
11	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VT	173.1285	201.1234	**VTK**	301.2234	329.2183	**VTKG**	358.2449	386.2398
VTKGF	505.3133	533.3082	**VTKGFV**	604.3817	632.3766	**TK**	202.1550	230.1499
TKG	259.1765	287.1714	**TKGF**	406.2449	434.2398	**TKGFV**	505.3133	533.3082
TKGFVD	620.3402	648.3352	**KG**	158.1288	186.1237	**KGF**	305.1972	333.1921
KGFV	404.2656	432.2605	**KGFVD**	519.2926	547.2875	**KGFVDL**	632.3766	660.3715
GF	177.1022	205.0972	**GFV**	276.1707	304.1656	**GFVD**	391.1976	419.1925
GFVDL	504.2817	532.2766	**GFVDLL**	617.3657	645.3606	**FV**	219.1492	247.1441
FVD	334.1761	362.1710	**FVDL**	447.2602	475.2551	**FVDLL**	560.3443	588.3392
VD	187.1077	215.1026	**VDL**	300.1918	328.1867	**VDLL**	413.2758	441.2708
DL	201.1234	229.1183	**DLL**	314.2074	342.2023	**LL**	199.1805	227.1754





NCBI **BLAST** search of DVTKGFVDLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
11.8	1261.6779	0.0296	RIYDIEGQLR
11.3	1261.6779	0.0296	RLYDIEGQLR
10.1	1261.6085	0.0989	SQELECKVGGR
9.5	1261.6449	0.0626	RSPSSMTDLLR
9.3	1261.6779	0.0295	LRYVGVDDGLR
8.8	1261.7030	0.0044	IVQLYAESALR
8.5	1261.6336	0.0738	MLSSEPGVLTGR
8.3	1261.7030	0.0044	DVTKGFVDLLR
8.3	1261.6667	0.0408	DVTQGFVDLLR
8.3	1261.6084	0.0990	MSEARLAAEER

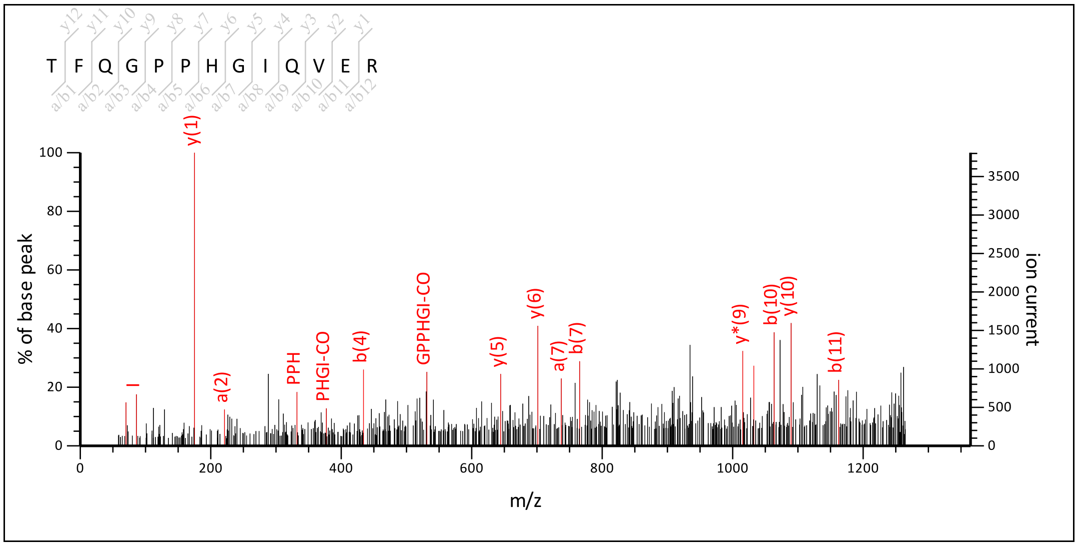
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 132

MS/MS Fragmentation of **TFQGPPHGIQVER**
Found in **gi|328682245** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Pseudocephalozia lepidozioides]

Match to Query 340: 1464.765024 from(1465.772300,1+) intensity(0.0000) index(29)
Title: Label: J4, Spot_Id: 219731, Peak_List_Id: 225364, MSMS Job_Run_Id: 21776, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_J4_136842177300.txt



0 to 1364.6

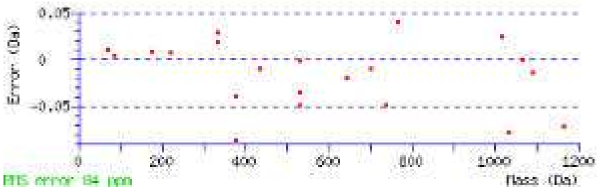
Label all possible matches ○ Label matches used for scoring ●

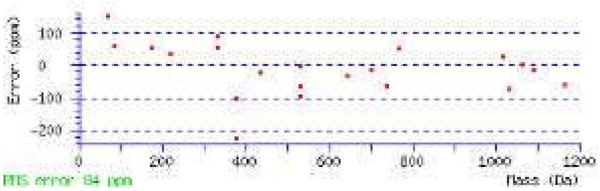
Monoisotopic mass of neutral peptide Mr(calc): 1464.7474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.29
Matches : 22/229 fragment ions using 26 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	120.0808	**221.1285**		203.1179	249.1234		231.1128			F	1272.6444			1364.7070	1347.6804	134
3	101.0709	349.1870	332.1605	331.1765	***377.1819***	360.1554	359.1714	292.1656		Q	1144.5858	1143.5905		1217.6385	1200.6120	119
4	30.0338	406.2085	389.1819	388.1979	***434.2034***	417.1769	416.1928			G				***1089.5800***	1072.5534	107
5	70.0651	503.2613	486.2347	485.2507	***531.2562***	514.2296	513.2456	477.2456		P	990.5116	989.5163		***1032.5585***	1015.5320	101
6	70.0651	600.3140	583.2875	582.3035	628.3089	611.2824	610.2984	574.2984		P	893.4588	892.4635		935.5057	918.4792	91
7	110.0713	**737.3729**	720.3464	719.3624	***765.3679***	748.3413	747.3573			H	756.3999			838.4530	821.4264	82
8	30.0338	794.3944	777.3679	776.3838	822.3893	805.3628	804.3787			G				***701.3941***	684.3675	68
9	86.0964	907.4785	890.4519	889.4679	935.4734	918.4468	917.4628	879.4472	893.4628	I	586.2944	599.3148	613.3304	***644.3726***	627.3461	62
10	101.0709	1035.5370	1018.5105	1017.5265	***1063.5320***	1046.5054	1045.5214	978.5156		Q	458.2358	457.2405		***531.2885***	514.2620	51
11	72.0808	1134.6055	1117.5789	1116.5949	***1162.6004***	1145.5738	1144.5898	1120.5898		V	359.1674	372.1878		403.2300	386.2034	38
12	102.0550	1263.6480	1246.6215	1245.6375	1291.6430	1274.6164	1273.6324	1205.6426		E	230.1248	229.1295		304.1615	287.1350	28
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQG	305.1608	333.1557	FQGP	402.2136	430.2085
FQGPP	499.2663	527.2613	FQGPPH	636.3253	664.3202	FQGPPHG	693.3467	721.3416
QG	158.0924	186.0873	QGP	255.1452	283.1401	QGPP	352.1979	380.1928
QGPPH	489.2568	517.2518	QGPPHG	546.2783	574.2732	QGPPHGI	659.3624	687.3573
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPH	361.1983	389.1932
GPPHG	418.2197	446.2146	GPPHGI	531.3038	559.2987	GPPHGIQ	659.3624	687.3573
PP	167.1179	195.1128	PPH	304.1768	332.1717	PPHG	361.1983	389.1932
PPHGI	474.2823	502.2772	PPHGIQ	602.3409	630.3358	PH	207.1240	235.1190

PHG	264.1455	292.1404	**PHGI**	377.2296	405.2245	**PHGIQ**	505.2881	533.2831
PHGIQV	604.3566	632.3515	**HG**	167.0927	195.0877	**HGI**	280.1768	308.1717
HGIQ	408.2354	436.2303	**HGIQV**	507.3038	535.2987	**HGIQVE**	636.3464	664.3413
GI	143.1179	171.1128	**GIQ**	271.1765	299.1714	**GIQV**	370.2449	398.2398
GIQVE	499.2875	527.2824	**IQ**	214.1550	242.1499	**IQV**	313.2234	341.2183
IQVE	442.2660	470.2609	**QV**	200.1394	228.1343	**QVE**	329.1819	357.1769
VE	201.1234	229.1183						





NCBI **BLAST** search of TFQGPPHGIQVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.5	1464.7838	-0.0187	TFKGPPHGIQVER
41.5	1464.7838	-0.0187	TFKGPPHGIQVER
41.5	1464.7838	-0.0187	TFQGPPHGIKVER
41.5	1464.7838	-0.0187	TFQGPPHGIKVER
41.5	1464.7474	0.0176	TFQGPPHGIQVER
41.5	1464.7474	0.0176	TFQGPPHGIQVER
41.5	1464.7474	0.0176	TFQGPPHGIQVER
41.5	1464.7474	0.0176	TFQGPPHGIQVER
41.5	1464.7474	0.0176	TFQGPPHGIQVER
41.5	1464.7474	0.0176	TFQGPPHGIQVER

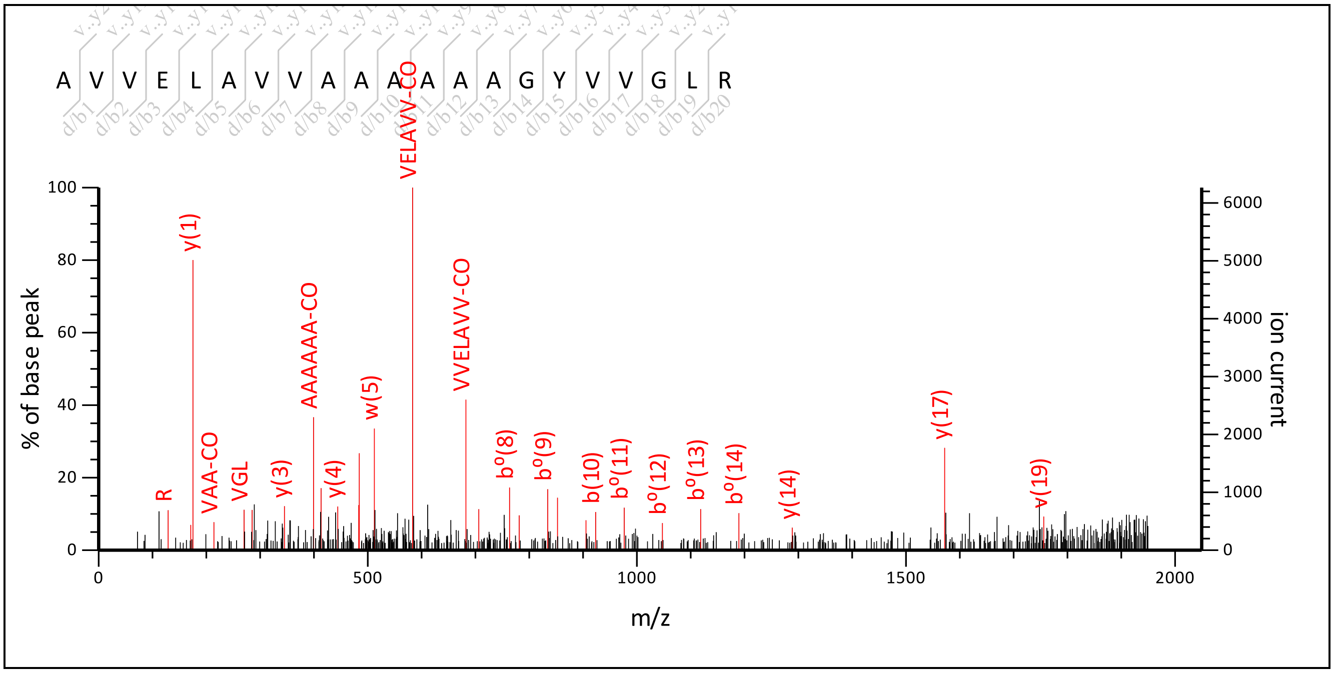
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View **Spot no 134**

MS/MS Fragmentation of **AVVELAVVAAAAAAGYVVGLR**
Found in **gi|78708842** in **NCBInr**, IAP100, putative, expressed [Oryza sativa Japonica Group]

Match to Query 31: 1969.329924 from(1970.337200,1+) intensity(0.0000) index(11)
Title: Label: D6, Spot_Id: 228925, Peak_List_Id: 257500, MSMS Job_Run_Id: 24922, Comment:
Data file ppw_D6_138985129300.txt



0 to 2049.43

Label all possible matches ○ Label matches used for scoring ●

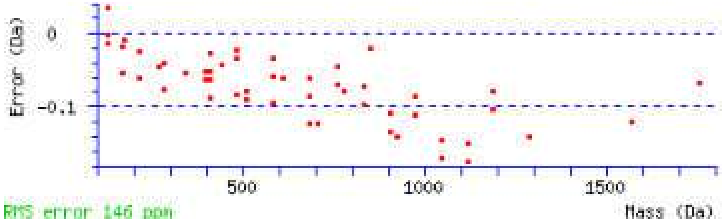
Monoisotopic mass of neutral peptide Mr(calc): 1969.1360
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 81 **Expect:** 4.1e-07
Matches : 78/381 fragment ions using 57 most intense peaks (help)

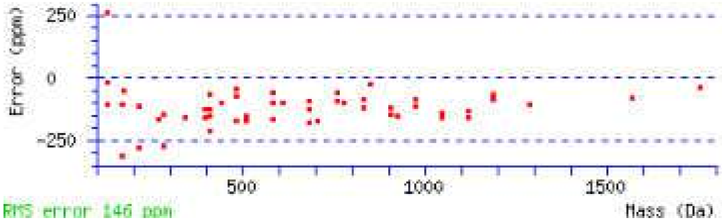
#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		72.0444		44.0495	A						21
2	72.0808	143.1179		***171.1128***		129.1022	V	1855.0436	1868.0640	1899.1062	1882.0797	1881.0956	20
3	72.0808	242.1863		***270.1812***		228.1707	V	1755.9752	1768.9956	1800.0378	1783.0112	1782.0272	19
4	102.0550	371.2289	353.2183	***399.2238***	381.2132	313.2234	E	1626.9326	1625.9374	1700.9694	1683.9428	1682.9588	18
5	86.0964	484.3130	466.3024	***512.3079***	494.2973	442.2660	L	1513.8485	1512.8533	***1571.9268***	1554.9002		17
6	44.0495	555.3501	537.3395	***583.3450***	565.3344		A	1442.8114		1458.8427	1441.8162		16
7	72.0808	654.4185	636.4079	***682.4134***	664.4028	640.4028	V	1343.7430	1356.7634	1387.8056	1370.7791		15
8	72.0808	753.4869	735.4763	***781.4818***	763.4713	739.4713	V	1244.6746	1257.6950	***1288.7372***	1271.7106		14
9	44.0495	824.5240	806.5135	***852.5189***	834.5084		A	1173.6375		***1189.6688***	1172.6422		13
10	44.0495	895.5611	877.5506	***923.5560***	905.5455		A	1102.6004		***1118.6317***	1101.6051		12
11	44.0495	966.5982	948.5877	994.5932	976.5826		A	1031.5633		***1047.5946***	1030.5680		11

12	44.0495	1037.6354	1019.6248	1065.6303	1047.6197		**A**	960.5261		***976.5574***	959.5309		**10**
13	44.0495	1108.6725	1090.6619	1136.6674	1118.6568		**A**	889.4890		***905.5203***	888.4938		**9**
14	44.0495	1179.7096	1161.6990	1207.7045	1189.6939		**A**	818.4519		***834.4832***	817.4567		**8**
15	30.0338	1236.7310	1218.7205	1264.7260	1246.7154		**G**			***763.4461***	746.4196		**7**
16	136.0757	1399.7944	1381.7838	1427.7893	1409.7787		**Y**	598.3671		***706.4246***	689.3981		**6**
17	72.0808	1498.8628	1480.8522	1526.8577	1508.8471	1484.8471	**V**	499.2987	512.3191	543.3613	526.3348		**5**
18	72.0808	1597.9312	1579.9206	1625.9261	1607.9156	1583.9156	**V**	400.2303	413.2507	***444.2929***	427.2663		**4**
19	30.0338	1654.9527	1636.9421	1682.9476	1664.9370		**G**			***345.2245***	328.1979		**3**
20	86.0964	1768.0367	1750.0262	1796.0316	1778.0211	1725.9898	**L**	230.1248	229.1295	288.2030	271.1765		**2**
21	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VV	171.1492	199.1441	**VVE**	300.1918	328.1867	**VVEL**	413.2758	441.2708
VVELA	484.3130	512.3079	**VVELAV**	583.3814	611.3763	**VVELAVV**	682.4498	710.4447
VE	201.1234	229.1183	**VEL**	314.2074	342.2023	**VELA**	385.2445	413.2395
VELAV	484.3130	512.3079	**VELAVV**	583.3814	611.3763	**VELAVVA**	654.4185	682.4134
EL	215.1390	243.1339	**ELA**	286.1761	314.1710	**ELAV**	385.2445	413.2395
ELAVV	484.3130	512.3079	**ELAVVA**	555.3501	583.3450	**ELAVVAA**	626.3872	654.3821
ELAVVAAA	697.4243	725.4192	**LA**	157.1335	185.1285	**LAV**	256.2020	284.1969
LAVV	355.2704	383.2653	**LAVVA**	426.3075	454.3024	**LAVVAA**	497.3446	525.3395
LAVVAAA	568.3817	596.3766	**LAVVAAAA**	639.4188	667.4137	**AV**	143.1179	171.1128
AVV	242.1863	270.1812	**AVVA**	313.2234	341.2183	**AVVAA**	384.2605	412.2554
AVVAAA	455.2976	483.2926	**AVVAAAA**	526.3348	554.3297	**AVVAAAAA**	597.3719	625.3668
AVVAAAAAA	668.4090	696.4039	**VV**	171.1492	199.1441	**VVA**	242.1863	270.1812
VVAA	313.2234	341.2183	**VVAAA**	384.2605	412.2554	**VVAAAA**	455.2976	483.2926
VVAAAAA	526.3348	554.3297	**VVAAAAAA**	597.3719	625.3668	**VVAAAAAAG**	654.3933	682.3883
VA	143.1179	171.1128	**VAA**	214.1550	242.1499	**VAAA**	285.1921	313.1870
VAAAA	356.2292	384.2241	**VAAAAA**	427.2663	455.2613	**VAAAAAA**	498.3035	526.2984
VAAAAAAG	555.3249	583.3198	**AA**	115.0866	143.0815	**AAA**	186.1237	214.1186
AAAA	257.1608	285.1557	**AAAAA**	328.1979	356.1928	**AAAAAA**	399.2350	427.2300
AAAAAAG	456.2565	484.2514	**AAAAAAGY**	619.3198	647.3148	**AA**	115.0866	143.0815
AAA	186.1237	214.1186	**AAAA**	257.1608	285.1557	**AAAAA**	328.1979	356.1928
AAAAAG	385.2194	413.2143	**AAAAAGY**	548.2827	576.2776	**AAAAAGYV**	647.3511	675.3461
AA	115.0866	143.0815	**AAA**	186.1237	214.1186	**AAAA**	257.1608	285.1557
AAAAG	314.1823	342.1772	**AAAAGY**	477.2456	505.2405	**AAAAGYV**	576.3140	604.3089
AAAAGYVV	675.3824	703.3774	**AA**	115.0866	143.0815	**AAA**	186.1237	214.1186
AAAG	243.1452	271.1401	**AAAGY**	406.2085	434.2034	**AAAGYV**	505.2769	533.2718
AAAGYVV	604.3453	632.3402	**AAAGYVVG**	661.3668	689.3617	**AA**	115.0866	143.0815
AAG	172.1081	200.1030	**AAGY**	335.1714	363.1663	**AAGYV**	434.2398	462.2347
AAGYVV	533.3082	561.3031	**AAGYVVG**	590.3297	618.3246	**AG**	101.0709	129.0659
AGY	264.1343	292.1292	**AGYV**	363.2027	391.1976	**AGYVV**	462.2711	490.2660
AGYVVG	519.2926	547.2875	**AGYVVGL**	632.3766	660.3715	**GY**	193.0972	221.0921
GYV	292.1656	320.1605	**GYVV**	391.2340	419.2289	**GYVVG**	448.2554	476.2504
GYVVGL	561.3395	589.3344	**YV**	235.1441	263.1390	**YVV**	334.2125	362.2074
YVVG	391.2340	419.2289	**YVVGL**	504.3180	532.3130	**VV**	171.1492	199.1441

VVG	228.1707	256.1656	**VVGL**	341.2547	369.2496	**VG**	129.1022	157.0972
VGL	242.1863	270.1812	**GL**	143.1179	171.1128			





NCBI **BLAST** search of AVVELAVVAAAAAAGYVVGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
81.2	1969.1360	0.1939	AVVELAVVAAAAAAGYVVGLR
10.8	1969.1724	0.1575	QLLILSLAINKFSGSIPR
8.4	1969.1645	0.1654	LLAELLQMQQTIILAKK
8.2	1969.1585	0.1714	VGLIAVNDGILLRNHIPR
7.8	1969.2088	0.1211	LPSERIIPLVPSLVAPLR
5.4	1969.2339	0.0960	LLLLSAAAASAFLLLLTLR
4.2	1969.1724	0.1575	VLIVERVIEFLGLQSVR
4.2	1969.1472	0.1827	VLSERVPAEVLAAHPLLR
4.0	1969.1459	0.1840	DLVALTNEALLISITQKK
2.5	1969.1612	0.1687	LDFDIVIIGAGIIGLTIAR

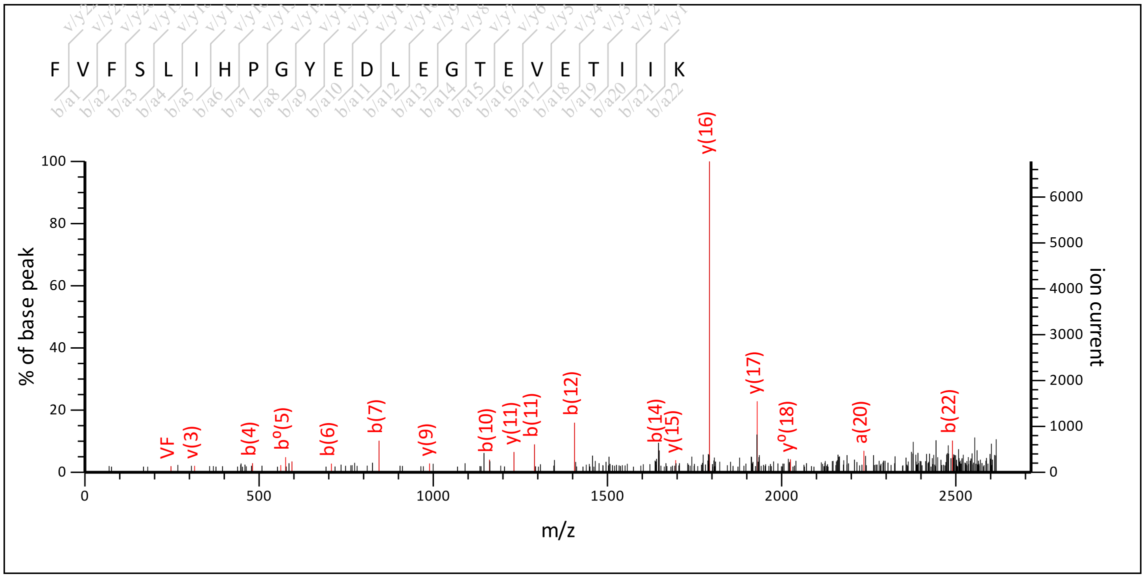
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 134

MS/MS Fragmentation of **FVFSLIHPGYEDLEGTEVETIIK**
Found in **gi|78708842** in **NCBInr**, IAP100, putative, expressed [Oryza sativa Japonica Group]

Match to Query 37: 2635.513724 from(2636.521000,1+) intensity(0.0000) index(14)
Title: Label: D6, Spot_Id: 228925, Peak_List_Id: 257508, MSMS Job_Run_Id: 24922, Comment:
Data file ppw_D6_138985129300.txt



0 to 2715.99

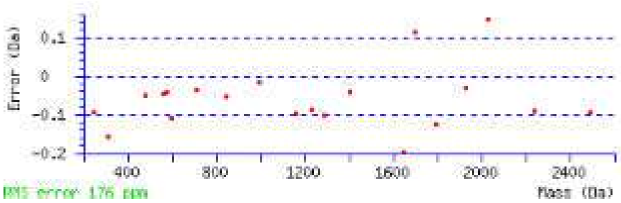
Label all possible matches ○ Label matches used for scoring ●

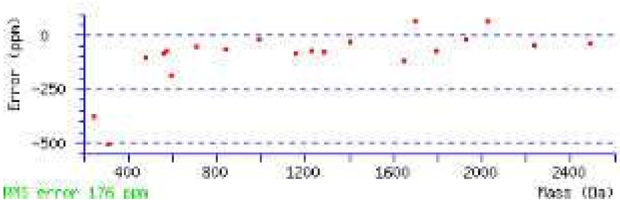
Monoisotopic mass of neutral peptide Mr(calc): 2635.3421
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.38
Matches : 21/410 fragment ions using 52 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	120.0808	120.0808		148.0757		44.0495		F							23
2	72.0808	219.1492		***247.1441***		205.1335		V	2445.2184	2458.2388		2489.2810	2472.2545	2471.2704	22
3	120.0808	366.2176		394.2125				F	2298.1500			2390.2126	2373.1860	2372.2020	21
4	60.0444	453.2496	435.2391	***481.2445***	463.2340	437.2547		S	2211.1180	2210.1227		2243.1442	2226.1176	2225.1336	20
5	86.0964	566.3337	548.3231	***594.3286***	576.3180	524.2867		L	2098.0339	2097.0386		2156.1121	2139.0856	2138.1016	19
6	86.0964	679.4178	661.4072	***707.4127***	689.4021	651.3865	665.4021	I	1984.9498	1997.9702	2011.9859	2043.0281	2026.0015	2025.0175	18
7	110.0713	816.4767	798.4661	***844.4716***	826.4610			H	1847.8909			**1929.9440**	1912.9175	1911.9335	17
8	70.0651	913.5294	895.5189	941.5244	923.5138	887.5138		P	1750.8382	1749.8429		**1792.8851**	1775.8586	1774.8745	16
9	30.0338	970.5509	952.5403	998.5458	980.5352			G				**1695.8323**	1678.8058	1677.8218	15
10	136.0757	1133.6142	1115.6037	***1161.6091***	1143.5986			Y	1530.7534			1638.8109	1621.7843	1620.8003	14
11	102.0550	1262.6568	1244.6463	***1290.6517***	1272.6412	1204.6513		E	1401.7108	1400.7155		1475.7475	1458.7210	1457.7370	13
12	88.0393	1377.6838	1359.6732	***1405.6787***	1387.6681	1333.6939		D	1286.6838	1285.6886		1346.7050	1329.6784	1328.6944	12
13	86.0964	1490.7678	1472.7573	1518.7627	1500.7522	1448.7209		L	1173.5998	1172.6045		**1231.6780**	1214.6515	1213.6674	11
14	102.0550	1619.8104	1601.7999	***1647.8053***	1629.7948	1561.8049		E	1044.5572	1043.5619		1118.5939	1101.5674	1100.5834	10
15	30.0338	1676.8319	1658.8213	1704.8268	1686.8162			G				**989.5514**	972.5248	971.5408	9
16	74.0600	1777.8796	1759.8690	1805.8745	1787.8639	1761.8846	1763.8639	T	886.4880	899.5084	901.4877	932.5299	915.5033	914.5193	8
17	102.0550	1906.9222	1888.9116	1934.9171	1916.9065	1848.9167		E	757.4454	756.4502		831.4822	814.4557	813.4716	7
18	72.0808	2005.9906	1987.9800	2033.9855	2015.9749	1991.9749		V	658.3770	671.3974		702.4396	685.4131	684.4291	6
19	102.0550	2135.0332	2117.0226	2163.0281	2145.0175	2077.0277		E	529.3344	528.3392		603.3712	586.3447	585.3606	5

20	74.0600	2236.0808	2218.0703	2264.0758	2246.0652	2220.0859	2222.0652	**T**	428.2867	441.3071	443.2864	474.3286	457.3021	456.3180	**4**
21	86.0964	2349.1649	2331.1543	2377.1598	2359.1493	2321.1336	2335.1493	**I**	315.2027	328.2231	342.2387	373.2809	356.2544		**3**
22	86.0964	2462.2490	2444.2384	***2490.2439***	2472.2333	2434.2177	2448.2333	**I**	202.1186	215.1390	229.1547	260.1969	243.1703		**2**
23	101.1073							**K**	74.0237	73.0284		147.1128	130.0863		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VF	219.1492	247.1441	**VFS**	306.1812	334.1761	**VFSL**	419.2653	447.2602
VFSLI	532.3493	560.3443	**VFSLIH**	669.4083	697.4032	**FS**	207.1128	235.1077
FSL	320.1969	348.1918	**FSLI**	433.2809	461.2758	**FSLIH**	570.3398	598.3348
FSLIHP	667.3926	695.3875	**SL**	173.1285	201.1234	**SLI**	286.2125	314.2074
SLIH	423.2714	451.2663	**SLIHP**	520.3242	548.3191	**SLIHPG**	577.3457	605.3406
LI	199.1805	227.1754	**LIH**	336.2394	364.2343	**LIHP**	433.2922	461.2871
LIHPG	490.3136	518.3085	**LIHPGY**	653.3770	681.3719	**IH**	223.1553	251.1503
IHP	320.2081	348.2030	**IHPG**	377.2296	405.2245	**IHPGY**	540.2929	568.2878
IHPGYE	669.3355	697.3304	**HP**	207.1240	235.1190	**HPG**	264.1455	292.1404
HPGY	427.2088	455.2037	**HPGYE**	556.2514	584.2463	**HPGYED**	671.2784	699.2733
PG	127.0866	155.0815	**PGY**	290.1499	318.1448	**PGYE**	419.1925	447.1874
PGYED	534.2195	562.2144	**PGYEDL**	647.3035	675.2984	**GY**	193.0972	221.0921
GYE	322.1397	350.1347	**GYED**	437.1667	465.1616	**GYEDL**	550.2508	578.2457
GYEDLE	679.2933	707.2883	**YE**	265.1183	293.1132	**YED**	380.1452	408.1401
YEDL	493.2293	521.2242	**YEDLE**	622.2719	650.2668	**YEDLEG**	679.2933	707.2883
ED	217.0819	245.0768	**EDL**	330.1660	358.1609	**EDLE**	459.2086	487.2035
EDLEG	516.2300	544.2249	**EDLEGT**	617.2777	645.2726	**DL**	201.1234	229.1183
DLE	330.1660	358.1609	**DLEG**	387.1874	415.1823	**DLEGT**	488.2351	516.2300
DLEGTE	617.2777	645.2726	**LE**	215.1390	243.1339	**LEG**	272.1605	300.1554
LEGT	373.2082	401.2031	**LEGTE**	502.2508	530.2457	**LEGTEV**	601.3192	629.3141
EG	159.0764	187.0713	**EGT**	260.1241	288.1190	**EGTE**	389.1667	417.1616
EGTEV	488.2351	516.2300	**EGTEVE**	617.2777	645.2726	**GT**	131.0815	159.0764
GTE	260.1241	288.1190	**GTEV**	359.1925	387.1874	**GTEVE**	488.2351	516.2300
GTEVET	589.2828	617.2777	**TE**	203.1026	231.0975	**TEV**	302.1710	330.1660
TEVE	431.2136	459.2086	**TEVET**	532.2613	560.2562	**TEVETI**	645.3454	673.3403
EV	201.1234	229.1183	**EVE**	330.1660	358.1609	**EVET**	431.2136	459.2086
EVETI	544.2977	572.2926	**EVETII**	657.3818	685.3767	**VE**	201.1234	229.1183
VET	302.1710	330.1660	**VETI**	415.2551	443.2500	**VETII**	528.3392	556.3341
ET	203.1026	231.0975	**ETI**	316.1867	344.1816	**ETII**	429.2708	457.2657
TI	187.1441	215.1390	**TII**	300.2282	328.2231	**II**	199.1805	227.1754





NCBI **BLAST** search of FVFSLIHPGYEDLEGTEVETIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
33.9	2635.3421	0.1716	FVFSLIHPGYEDLEGTEVETIIK
1.5	2635.2878	0.2259	ENSKITVTGTVTGGSEGSSHVQWFK
0.9	2635.2828	0.2309	KGFIMNHHLPLTYDFHSYMIR
0.9	2635.2700	0.2437	KYGLAADNVIDAYLVDANGMVHDR

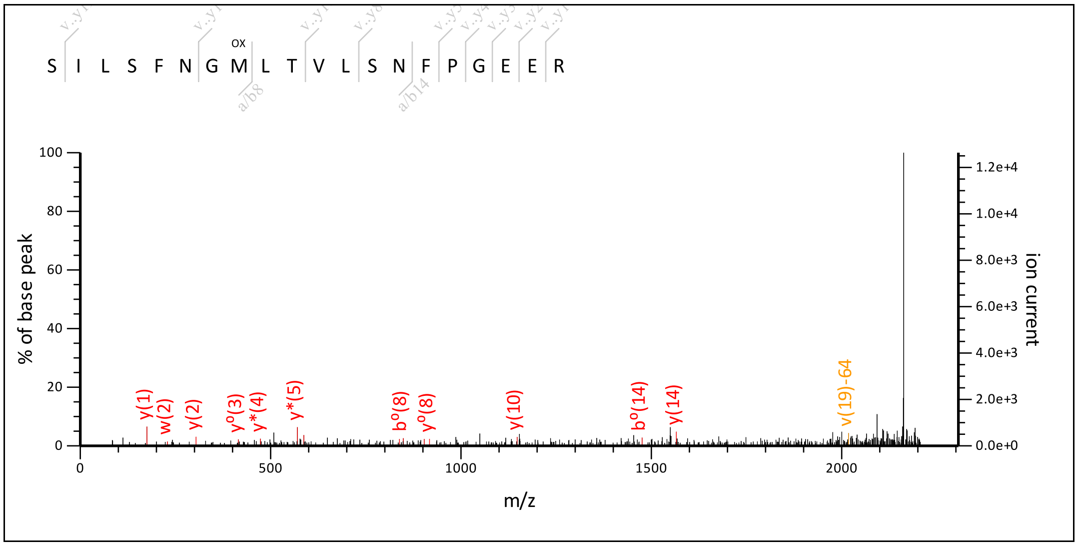
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 134**

MS/MS Fragmentation of **SILSFNGMLTVLSNFPGEER**
Found in **gi|78708842** in **NCBInr**, IAP100, putative, expressed [Oryza sativa Japonica Group]

Match to Query 33: 2226.272224 from(2227.279500,1+) intensity(0.0000) index(12)
Title: Label: D6, Spot_Id: 228925, Peak_List_Id: 257512, MSMS Job_Run_Id: 24922, Comment:
Data file ppw_D6_138985129300.txt



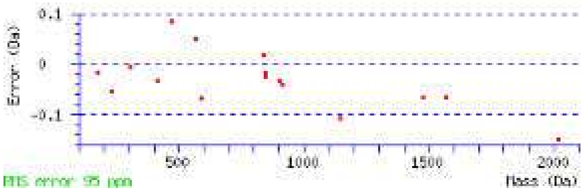
0 to 2306.52

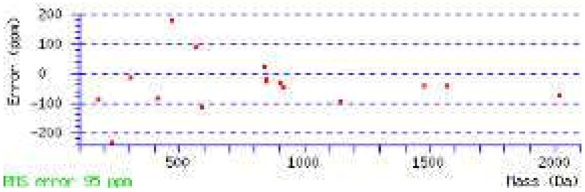
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2226.0991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 10 **Expect:** 1.2e+02
Matches : 16/538 fragment ions using 44 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	86.0964	173.1285		155.1179	201.1234		183.1128	145.0972	159.1128	I	2081.9961	2095.0165	2109.0321	2140.0743	2123.0478
3	86.0964	286.2125		268.2020	314.2074		296.1969	244.1656		L	1968.9120	1967.9168		2026.9903	2009.9637
4	60.0444	373.2445		355.2340	401.2395		383.2289	357.2496		S	1881.8800	1880.8847		1913.9062	1896.8796
5	120.0808	520.3130		502.3024	548.3079		530.2973			F	1734.8116			1826.8742	1809.8476
6	87.0553	634.3559	617.3293	616.3453	662.3508	645.3243	644.3402	591.3501		N	1620.7686	1619.7734		1679.8057	1662.7792
7	30.0338	691.3773	674.3508	673.3668	719.3723	702.3457	701.3617			G				***1565.7628***	1548.7363
8	120.0478	838.4127	821.3862	820.4022	866.4077	849.3811	848.3971	762.4145		M	1416.7118	1415.7165		1508.7414	1491.7148
9	86.0964	951.4968	934.4703	933.4862	979.4917	962.4652	961.4812	909.4499		L	1303.6277	1302.6325		1361.7060	1344.6794
10	74.0600	1052.5445	1035.5179	1034.5339	1080.5394	1063.5129	1062.5288	1036.5496	1038.5288	T	1202.5800	1215.6004	1217.5797	1248.6219	1231.5953
11	72.0808	1151.6129	1134.5864	1133.6023	1179.6078	1162.5813	1161.5973	1137.5973		V	1103.5116	1116.5320		***1147.5742***	1130.5477
12	86.0964	1264.6970	1247.6704	1246.6864	1292.6919	1275.6653	1274.6813	1222.6500		L	990.4275	989.4323		1048.5058	1031.4793
13	60.0444	1351.7290	1334.7024	1333.7184	1379.7239	1362.6974	1361.7133	1335.7341		S	903.3955	902.4003		935.4217	918.3952
14	87.0553	1465.7719	1448.7454	1447.7614	1493.7668	1476.7403	1475.7563	1422.7661		N	789.3526	788.3573		***848.3897***	831.3632
15	120.0808	1612.8403	1595.8138	1594.8298	1640.8353	1623.8087	1622.8247			F	642.2842			734.3468	717.3202
16	70.0651	1709.8931	1692.8666	1691.8825	1737.8880	1720.8615	1719.8775	1683.8775		P	545.2314	544.2362		***587.2784***	570.2518
17	30.0338	1766.9146	1749.8880	1748.9040	1794.9095	1777.8829	1776.8989			G				490.2256	473.1991
18	102.0550	1895.9572	1878.9306	1877.9466	1923.9521	1906.9255	1905.9415	1837.9517		E	359.1674	358.1721		433.2041	416.1776
19	102.0550	2024.9998	2007.9732	2006.9892	2052.9947	2035.9681	2034.9841	1966.9943		E	230.1248	229.1295		***304.1615***	287.1350
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IL	199.1805	227.1754	**ILS**	286.2125	314.2074	**ILSF**	433.2809	461.2758
ILSFN	547.3239	575.3188	**ILSFNG**	604.3453	632.3402	**LS**	173.1285	201.1234
LSF	320.1969	348.1918	**LSFN**	434.2398	462.2347	**LSFNG**	491.2613	519.2562
LSFNGM	638.2967	666.2916	**SF**	207.1128	235.1077	**SFN**	321.1557	349.1506
SFNG	378.1772	406.1721	**SFNGM**	525.2126	553.2075	**SFNGML**	638.2967	666.2916
FN	234.1237	262.1186	**FNG**	291.1452	319.1401	**FNGM**	438.1806	466.1755
FNGML	551.2646	579.2595	**FNGMLT**	652.3123	680.3072	**NG**	144.0768	172.0717
NGM	291.1122	319.1071	**NGML**	404.1962	432.1911	**NGMLT**	505.2439	533.2388
NGMLTV	604.3123	632.3072	**GM**	177.0692	205.0641	**GML**	290.1533	318.1482
GMLT	391.2010	419.1959	**GMLTV**	490.2694	518.2643	**GMLTVL**	603.3534	631.3484
GMLTVLS	690.3855	718.3804	**ML**	233.1318	261.1267	**MLT**	334.1795	362.1744
MLTV	433.2479	461.2428	**MLTVL**	546.3320	574.3269	**MLTVLS**	633.3640	661.3589
LT	187.1441	215.1390	**LTV**	286.2125	314.2074	**LTVL**	399.2966	427.2915
LTVLS	486.3286	514.3235	**LTVLSN**	600.3715	628.3665	**TV**	173.1285	201.1234
TVL	286.2125	314.2074	**TVLS**	373.2445	401.2395	**TVLSN**	487.2875	515.2824
TVLSNF	634.3559	662.3508	**VL**	185.1648	213.1598	**VLS**	272.1969	300.1918
VLSN	386.2398	414.2347	**VLSNF**	533.3082	561.3031	**VLSNFP**	630.3610	658.3559
VLSNFPG	687.3824	715.3774	**LS**	173.1285	201.1234	**LSN**	287.1714	315.1663
LSNF	434.2398	462.2347	**LSNFP**	531.2926	559.2875	**LSNFPG**	588.3140	616.3089
SN	174.0873	202.0822	**SNF**	321.1557	349.1506	**SNFP**	418.2085	446.2034
SNFPG	475.2300	503.2249	**SNFPGE**	604.2726	632.2675	**NF**	234.1237	262.1186
NFP	331.1765	359.1714	**NFPG**	388.1979	416.1928	**NFPGE**	517.2405	545.2354
NFPGEE	646.2831	674.2780	**FP**	217.1335	245.1285	**FPG**	274.1550	302.1499
FPGE	403.1976	431.1925	**FPGEE**	532.2402	560.2351	**PG**	127.0866	155.0815
PGE	256.1292	284.1241	**PGEE**	385.1718	413.1667	**GE**	159.0764	187.0713
GEE	288.1190	316.1139	**EE**	231.0975	259.0925			





NCBI **BLAST** search of SILSFNGMLTVLSNFPGEER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
9.9	2226.0991	0.1732	SILSFNGMLTVLSNFPGEER
4.1	2226.0521	0.2201	FRQLVVENAGTICGGMSSER
2.8	2226.0661	0.2061	GTGITANVVAPGSTGTPMMYTGK
2.8	2226.0661	0.2061	GTGITANVVAPGSTGTPMMYTGK
0.9	2226.1644	0.1078	GAEGWNLLKVLETVAAEAAER
0.2	2226.0600	0.2122	GVGGGGLQPQFVDHRAAMEER

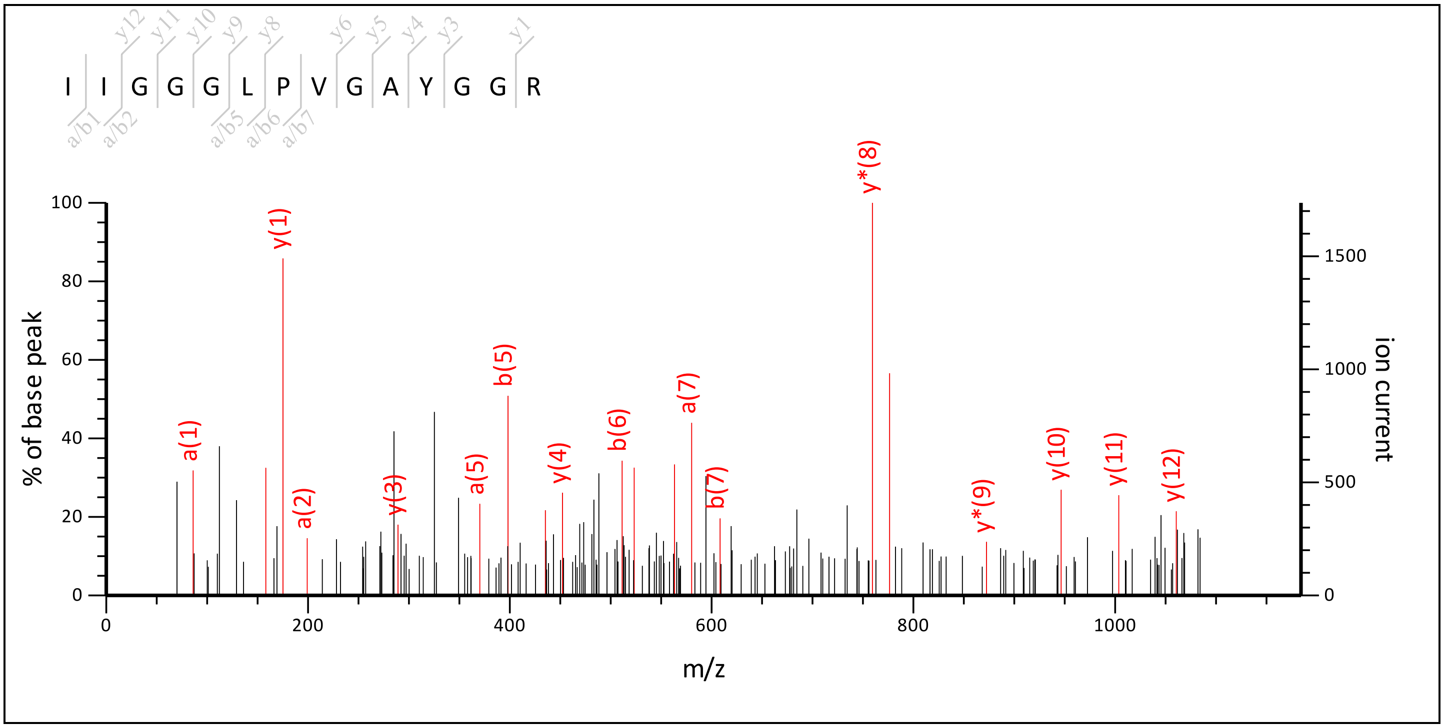
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 136

MS/MS Fragmentation of **IIGGGLPVGAYGGR**
Found in **gi|255571784** in **NCBInr**, glutamate-1-semialdehyde 2,1-aminomutase, putative [Ricinus communis]

Match to Query 129: 1285.712124 from(1286.719400,1+) intensity(0.0000) index(14)
Title: Label: E3, Spot_Id: 219710, Peak_List_Id: 225248, MSMS Job_Run_Id: 21771, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E3_136842129700.txt



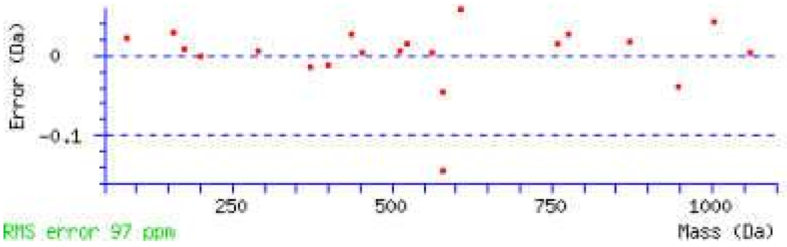
0 to 1184.19

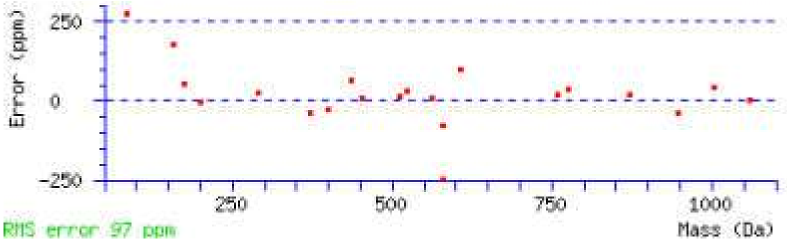
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1285.7143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.027
Matches : 21/52 fragment ions using 42 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	**86.0964**	114.0913	**I**			**14**
2	**199.1805**	227.1754	**I**	1173.6375	1156.6109	**13**
3	256.2020	284.1969	**G**	***1060.5534***	1043.5269	**12**
4	313.2234	341.2183	**G**	***1003.5320***	986.5054	**11**
5	**370.2449**	**398.2398**	**G**	***946.5105***	929.4839	**10**
6	483.3289	**511.3239**	**L**	889.4890	872.4625	**9**
7	**580.3817**	**608.3766**	**P**	***776.4050***	759.3784	**8**
8	679.4501	707.4450	**V**	679.3522	662.3257	**7**

9	736.4716	764.4665	**G**	***580.2838***	563.2572	**6**
10	807.5087	835.5036	**A**	***523.2623***	506.2358	**5**
11	970.5720	998.5669	**Y**	***452.2252***	435.1987	**4**
12	1027.5935	1055.5884	**G**	***289.1619***	272.1353	**3**
13	1084.6150	1112.6099	**G**	232.1404	215.1139	**2**
14			**R**	***175.1190***	158.0924	**1**





NCBI **BLAST** search of IIGGGLPVGAYGGR
(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	1285.7143	-0.0022	IIGGGLPVGAYGGR
12.5	1285.6680	0.0441	RAGFFGAPPPNR
12.3	1285.7619	-0.0497	LLGHRLPLDPR
11.2	1285.6561	0.0560	RAIGLGEASPCR
10.8	1285.7870	-0.0749	ARLGIFILDLR
10.8	1285.6925	0.0197	ARLGLVECVNR
10.8	1285.7142	-0.0021	VIKGLEAWASGR
10.8	1285.6779	0.0343	VLQGLEAWASGR
10.8	1285.6237	0.0884	DPANIVWMANR
10.1	1285.7255	-0.0134	NVALIGHLQHGK

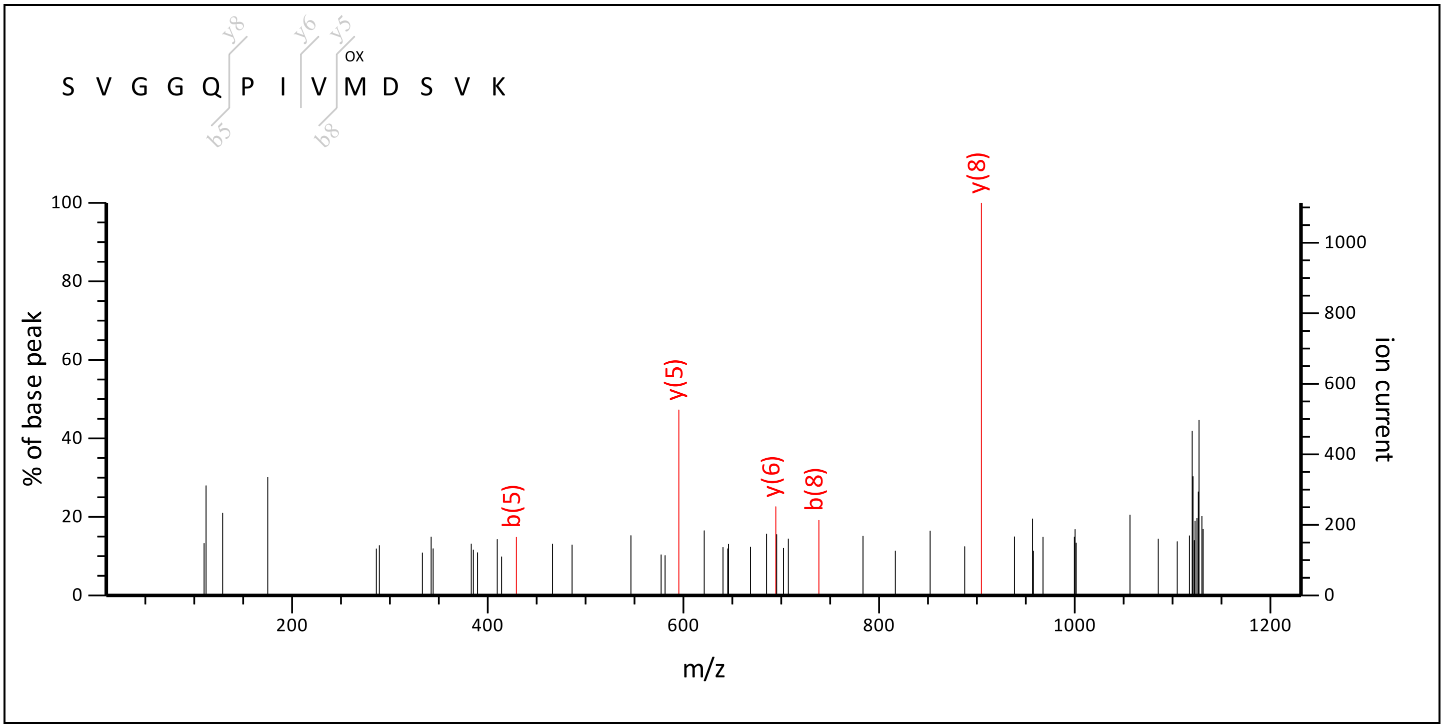
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 136

MS/MS Fragmentation of **SVGGQPIVMDSVK**
Found in **gi|255571784** in **NCBInr**, glutamate-1-semialdehyde 2,1-aminomutase, putative [Ricinus communis]

Match to Query 144: 1331.678724 from(1332.686000,1+) intensity(0.0000) index(16)
Title: Label: E3, Spot_Id: 219710, Peak_List_Id: 225269, MSMS Job_Run_Id: 21771, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_E3_136842129700.txt



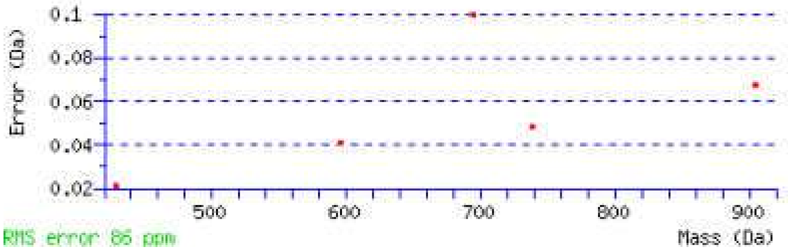
10.08 to 1231.27

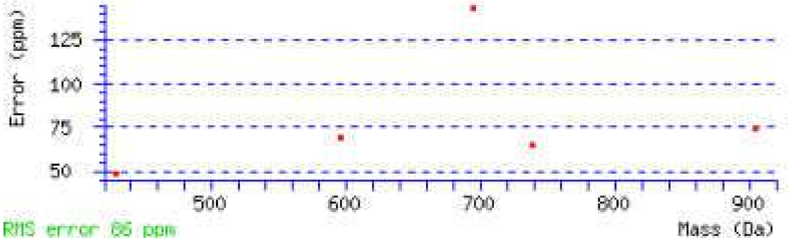
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1331.6755
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 8 **Expect:** 3.4e+02
Matches : 5/96 fragment ions using 11 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	60.0444		88.0393		S			13
2	159.1128		187.1077		V	1245.6508	1228.6242	12
3	216.1343		244.1292		G	1146.5823	1129.5558	11
4	273.1557		301.1506		G	1089.5609	1072.5343	10
5	401.2143	384.1878	**429.2092**	412.1827	Q	1032.5394	1015.5129	9
6	498.2671	481.2405	526.2620	509.2354	P	***904.4808***	887.4543	8

7	611.3511	594.3246	639.3461	622.3195	I	807.4281	790.4015	7
8	710.4196	693.3930	**738.4145**	721.3879	V	***694.3440***	677.3175	6
9	857.4550	840.4284	885.4499	868.4233	M	***595.2756***	578.2490	5
10	972.4819	955.4553	1000.4768	983.4503	D	448.2402	431.2136	4
11	1059.5139	1042.4874	1087.5088	1070.4823	S	333.2132	316.1867	3
12	1158.5823	1141.5558	1186.5773	1169.5507	V	246.1812	229.1547	2
13					K	147.1128	130.0863	1





NCBI **BLAST** search of SVGGQPIVMDSVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
8.5	1331.7272	-0.0484	MVVVVLPSFGER
8.3	1331.6755	0.0032	LTDVPLVCSSNK
8.0	1331.7085	-0.0298	SVGGQPIVFDSVK
8.0	1331.6755	0.0032	SVGGQPIVMDSVK
7.0	1331.6881	-0.0094	CGAGGHVVGLHLR
6.0	1331.6721	0.0066	DISILPPYGDSR
6.0	1331.6833	-0.0046	DKANLPNYIER
6.0	1331.7310	-0.0522	VDITIPHRPER
6.0	1331.6980	-0.0192	KMGIAAGGLGAGTGR
5.7	1331.6469	0.0318	EALDPFNEKNR

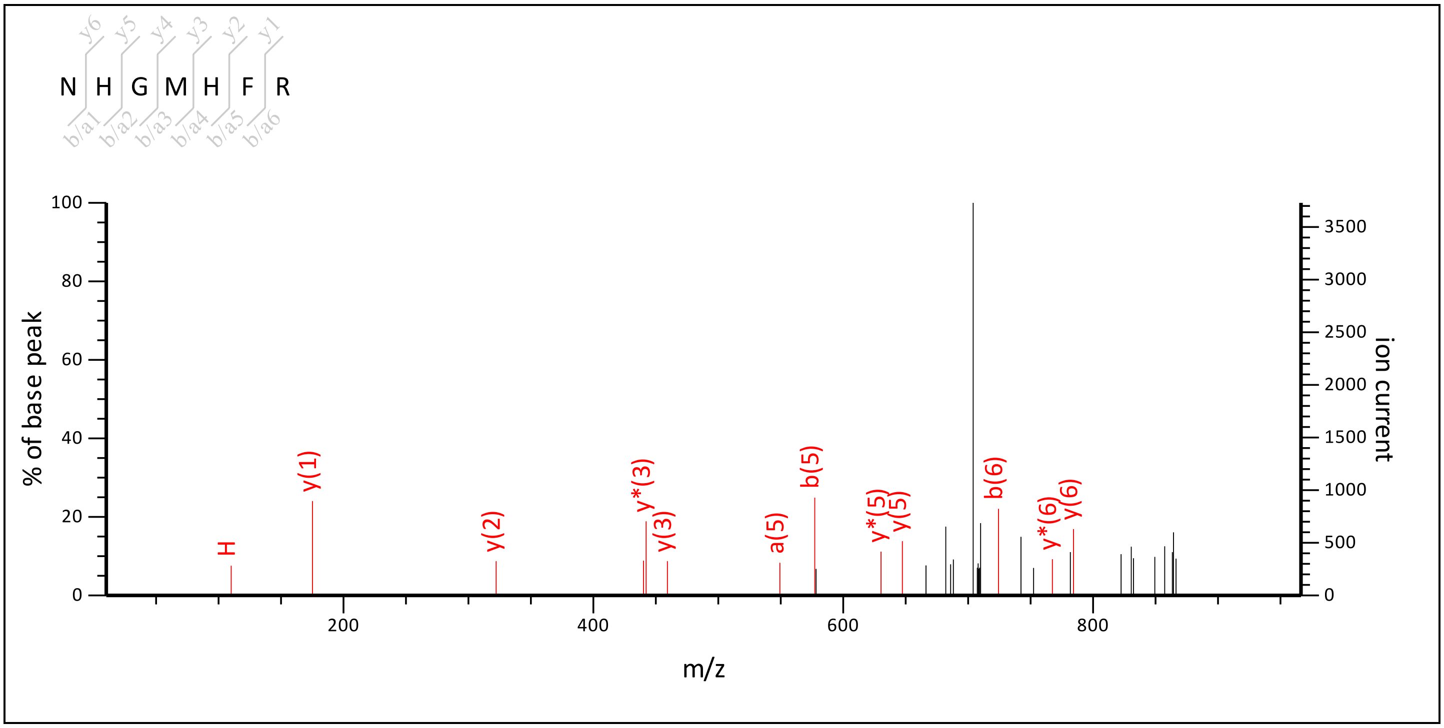
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **NHGMHFR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 5: 897.483694 from(898.490970,1+) intensity(0.0000) index(0)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221801, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



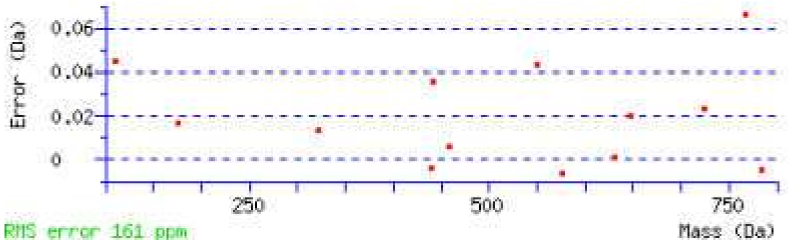
10.12 to 966.42

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 897.4028
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 27 **Expect:** 12
Matches : 14/72 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	b	b*	d	Seq.	v	w	y	y*	#
1	87.0553	87.0553	70.0287	115.0502	98.0237	44.0495	**N**					7
2	110.0713	224.1142	207.0877	252.1091	235.0826		**H**	702.3140		***784.3671***	767.3406	6
3	30.0338	281.1357	264.1091	309.1306	292.1040		**G**			***647.3082***	630.2817	5
4	104.0528	412.1761	395.1496	**440.1711**	423.1445	352.1728	**M**	514.2521	513.2568	590.2868	573.2602	4
5	110.0713	549.2351	532.2085	**577.2300**	560.2034		**H**	377.1932		***459.2463***	442.2197	3
6	120.0808	696.3035	679.2769	**724.2984**	707.2718		**F**	230.1248		***322.1874***	305.1608	2
7	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HG	167.0927	195.0877	**HGM**	298.1332	326.1281	**HGMH**	435.1921	463.1870
HGMHF	582.2605	610.2555	**GM**	161.0743	189.0692	**GMH**	298.1332	326.1281
GMHF	445.2016	473.1966	**MH**	241.1118	269.1067	**MHF**	388.1802	416.1751
HF	257.1397	285.1346						



NCBI **BLAST** search of NHGMHFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.3	897.4028	0.0809	NHGMHFR
27.3	897.4028	0.0809	NHGMHFR
27.3	897.4028	0.0809	NHGMHFR
27.3	897.4028	0.0809	NHGMHFR
27.3	897.4028	0.0809	NHGMHFR
27.3	897.4028	0.0809	NHGMHFR
27.3	897.4028	0.0809	NHGMHFR
27.3	897.3698	0.1139	NHGMHMR
19.5	898.3868	-0.9031	DHGMHFR
19.5	898.3868	-0.9031	DHGMHFR

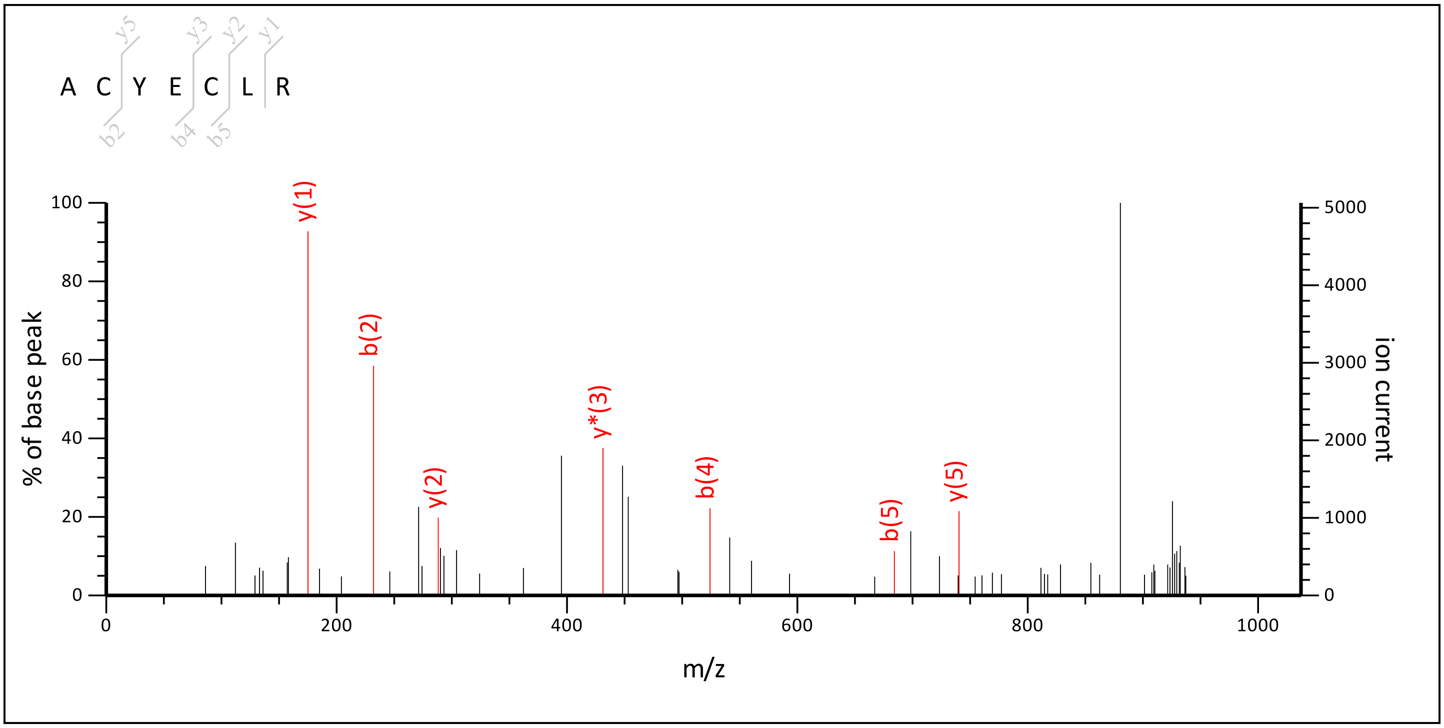
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 138**

MS/MS Fragmentation of **ACYECLR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 9: 970.493154 from(971.500430,1+) intensity(0.0000) index(2)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221791, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



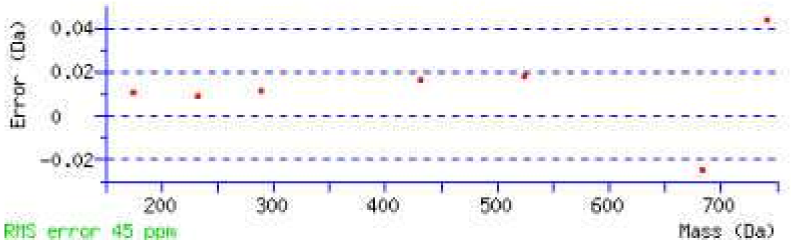
0 to 1037.24

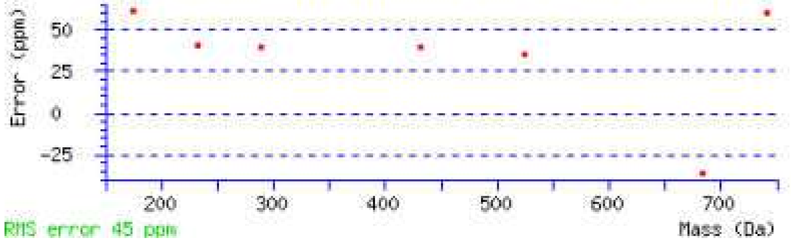
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 970.4001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24 **Expect:** 26
Matches : 7/75 fragment ions using 9 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	44.0495	44.0495		72.0444		44.0495	**A**						7
2	133.0430	204.0801		***232.0750***		115.0866	**C**	795.3454	794.3502	900.3702	883.3437	882.3597	6
3	136.0757	367.1435		395.1384			**Y**	632.2821		***740.3396***	723.3130	722.3290	5
4	102.0550	496.1860	478.1755	***524.1810***	506.1704	438.1806	**E**	503.2395	502.2442	577.2763	560.2497	559.2657	4
5	133.0430	656.2167	638.2061	***684.2116***	666.2010	567.2232	**C**	343.2088	342.2136	448.2337	431.2071		3
6	86.0964	769.3008	751.2902	797.2957	779.2851	727.2538	**L**	230.1248	229.1295	***288.2030***	271.1765		2
7	129.1135						**R**	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
CY	296.1063	324.1013	**CYE**	425.1489	453.1438	**CYEC**	585.1796	613.1745
CYECL	698.2636	726.2586	**YE**	265.1183	293.1132	**YEC**	425.1489	453.1438
YECL	538.2330	566.2279	**EC**	262.0856	290.0805	**ECL**	375.1697	403.1646
CL	246.1271	274.1220						





NCBI **BLAST** search of ACYECLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
29.3	970.5243	-0.0311	MRPRAQGR
24.0	970.4001	0.0931	ACYECIR
24.0	970.4001	0.0931	ACYECLR
24.0	970.4001	0.0931	ACYECLR
24.0	970.4001	0.0931	ACYECLR
24.0	970.4001	0.0931	ACYECLR
22.2	970.4953	-0.0021	RMCHVLR
17.8	971.4607	-0.9675	SSNCHVIR
17.5	970.4953	-0.0021	MRVHCLR
16.6	970.4807	0.0125	ACFAPHLR

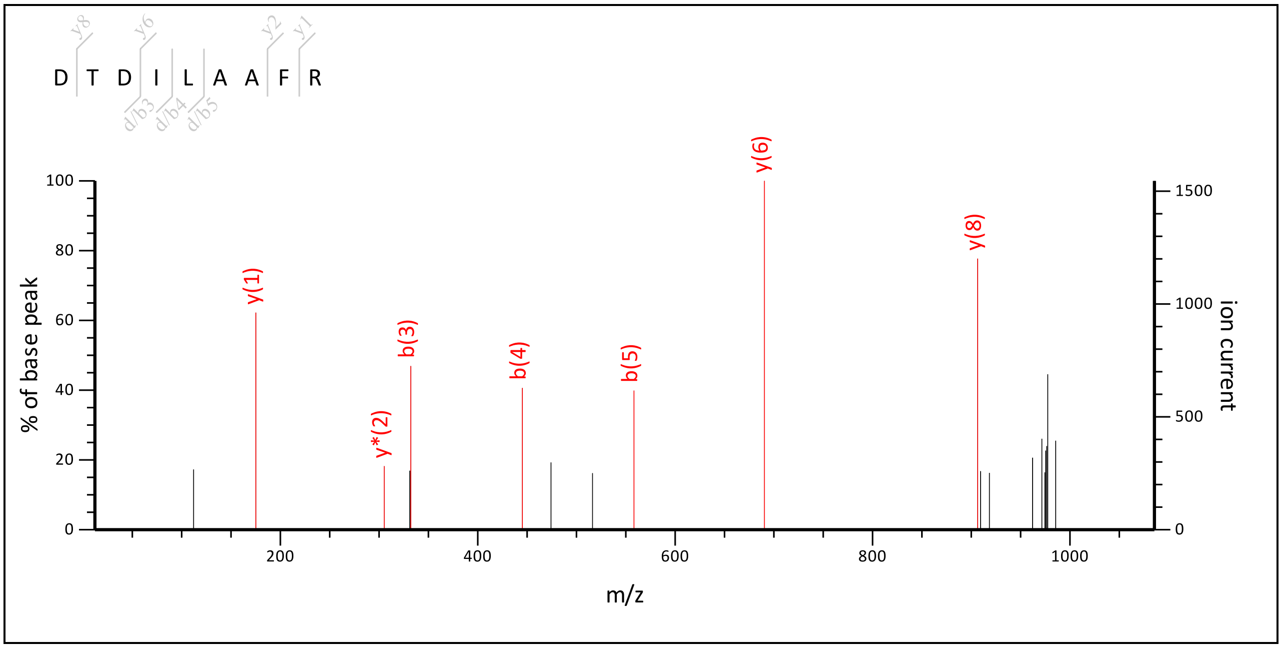
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **DTDILAAFR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 13: 1020.621424 from(1021.628700,1+) intensity(0.0000) index(4)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221802, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



12.1 to 1085.58

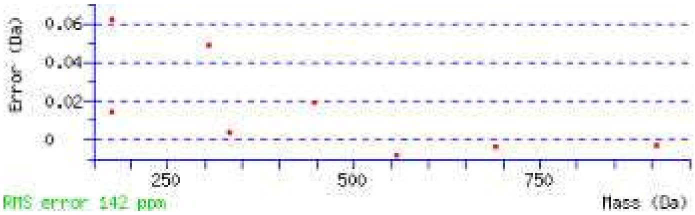
Label all possible matches ○ Label matches used for scoring ●

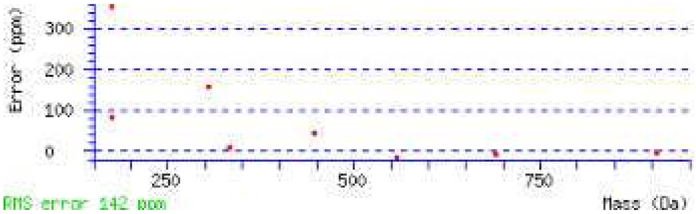
Monoisotopic mass of neutral peptide Mr(calc): 1020.5240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 4.6
Matches : 8/121 fragment ions using 8 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	88.0393	88.0393	70.0287	116.0342	98.0237	44.0495		**D**							9
2	74.0600	189.0870	171.0764	217.0819	199.0713	173.0921	175.0713	**T**	860.4625	873.4829	875.4621	***906.5043***	889.4778	888.4938	8
3	88.0393	304.1139	286.1034	***332.1088***	314.0983	260.1241		**D**	745.4355	744.4403		805.4567	788.4301	787.4461	7
4	86.0964	417.1980	399.1874	***445.1929***	427.1823	389.1667	403.1823	**I**	632.3515	645.3719	659.3875	***690.4297***	673.4032		6
5	86.0964	530.2821	512.2715	***558.2770***	540.2664	488.2351		**L**	519.2674	518.2722		577.3457	560.3191		5
6	44.0495	601.3192	583.3086	629.3141	611.3035			**A**	448.2303			464.2616	447.2350		4
7	44.0495	672.3563	654.3457	700.3512	682.3406			**A**	377.1932			393.2245	376.1979		3
8	120.0808	819.4247	801.4141	847.4196	829.4090			**F**	230.1248			322.1874	305.1608		2
9	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TD	189.0870	217.0819	**TDI**	302.1710	330.1660	**TDIL**	415.2551	443.2500
TDILA	486.2922	514.2871	**TDILAA**	557.3293	585.3243	**DI**	201.1234	229.1183
DIL	314.2074	342.2023	**DILA**	385.2445	413.2395	**DILAA**	456.2817	484.2766

DILAAF	603.3501	631.3450	**IL**	199.1805	227.1754	**ILA**	270.2176	298.2125
ILAA	341.2547	369.2496	**ILAAF**	488.3231	516.3180	**LA**	157.1335	185.1285
LAA	228.1707	256.1656	**LAAF**	375.2391	403.2340	**AA**	115.0866	143.0815
AAF	262.1550	290.1499	**AF**	191.1179	219.1128			





NCBI **BLAST** search of DTDILAAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.6	1020.5240	0.0974	DTDIIAAFR
32.6	1020.5240	0.0974	DTDIIAAFR
32.6	1020.5240	0.0974	DTDILAAFR
32.6	1020.5240	0.0974	DTDILAAFR
32.6	1020.5240	0.0974	DTDILAAFR
32.6	1020.5240	0.0974	DTDILAAFR
32.6	1020.5240	0.0974	DTDILAAFR
32.6	1020.5240	0.0974	DTDILAAFR
32.6	1020.5240	0.0974	DTDILAAFR
32.6	1020.5240	0.0974	DTDILAAFR

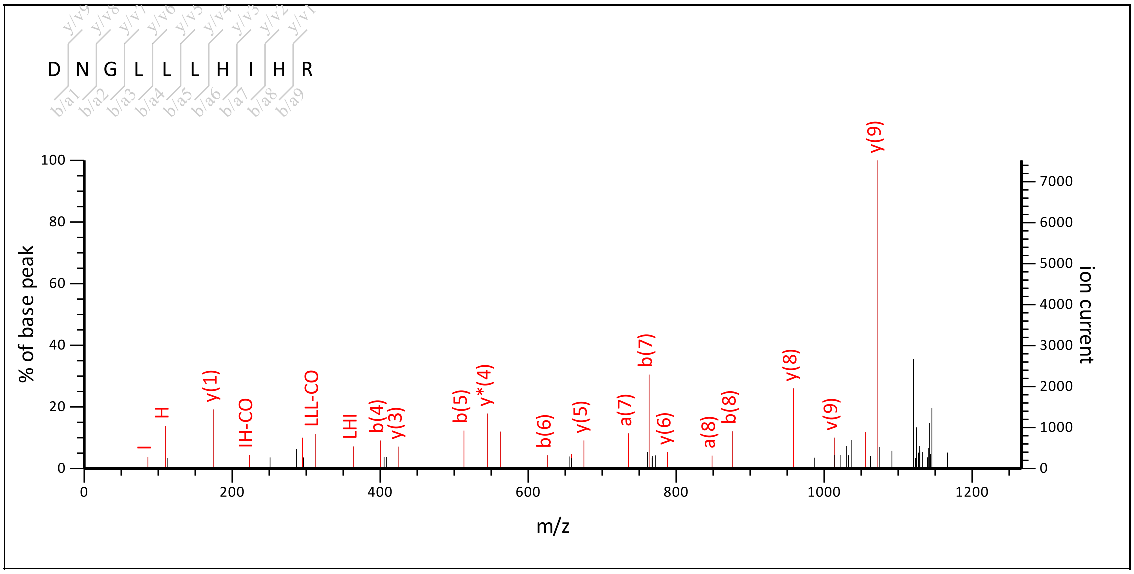
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **DNGLLLHIHR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 23: 1186.770824 from(1187.778100,1+) intensity(0.0000) index(8)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221795, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



0 to 1266.66

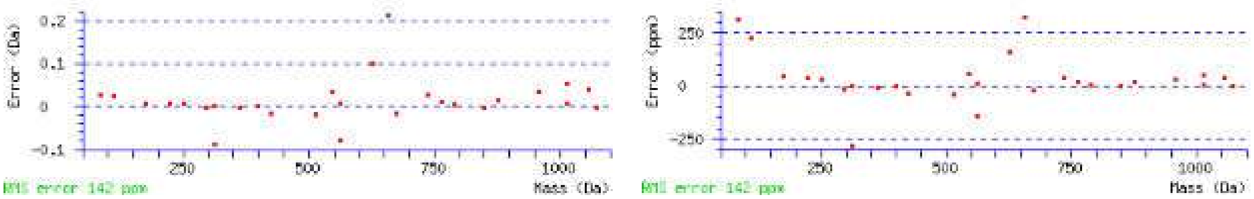
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1186.6571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 0.00039
Matches : 37/151 fragment ions using 30 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	#
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D						10
2	87.0553	202.0822	185.0557	184.0717	230.0771	213.0506	212.0666	159.0764		N	1013.6003	1012.6051		***1072.6374***	1055.6109	9
3	30.0338	259.1037	242.0771	241.0931	287.0986	270.0721	269.0880			G				***958.5945***	941.5679	8
4	86.0964	372.1878	355.1612	354.1772	**400.1827**	383.1561	382.1721	330.1408		L	843.4948	842.4995		901.5730	884.5465	7
5	86.0964	485.2718	468.2453	467.2613	**513.2667**	496.2402	495.2562	443.2249		L	730.4107	729.4155		***788.4890***	771.4624	6
6	86.0964	598.3559	581.3293	580.3453	**626.3508**	609.3243	608.3402	556.3089		L	617.3267	616.3314		***675.4049***	658.3784	5
7	110.0713	**735.4148**	718.3882	717.4042	**763.4097**	746.3832	745.3991			H	480.2677			***562.3208***	545.2943	4
8	86.0964	**848.4989**	831.4723	830.4883	**876.4938**	859.4672	858.4832	820.4676	834.4832	I	367.1837	380.2041	394.2197	***425.2619***	408.2354	3
9	110.0713	985.5578	968.5312	967.5472	**1013.5527**	996.5261	995.5421			H	230.1248			***312.1779***	295.1513	2
10	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
NG	144.0768	172.0717	**NGL**	257.1608	285.1557	**NGLL**	370.2449	398.2398
NGLLL	483.3289	511.3239	**NGLLLH**	620.3879	648.3828	**GL**	143.1179	171.1128
GLL	256.2020	284.1969	**GLLL**	369.2860	397.2809	**GLLLH**	506.3449	534.3398
GLLLHI	619.4290	647.4239	**LL**	199.1805	227.1754	**LLL**	312.2646	340.2595
LLLH	449.3235	477.3184	**LLLHI**	562.4075	590.4024	**LLLHIH**	699.4664	727.4614
LL	199.1805	227.1754	**LLH**	336.2394	364.2343	**LLHI**	449.3235	477.3184
LLHIH	586.3824	614.3773	**LH**	223.1553	251.1503	**LHI**	336.2394	364.2343
LHIH	473.2983	501.2932	**HI**	223.1553	251.1503	**HIH**	360.2142	388.2092

IH	223.1553	251.1503						



NCBI **BLAST** search of DNGLLLHIHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.5	1186.6571	0.1138	DNGILIHIHR
72.5	1186.6571	0.1138	DNGILLHIHR
72.5	1186.6571	0.1138	DNGILLHIHR
72.5	1186.6571	0.1138	DNGILLHIHR
72.5	1186.6571	0.1138	DNGLILHIHR
72.5	1186.6571	0.1138	DNGLILHIHR
72.5	1186.6571	0.1138	DNGLLIHIHR
72.5	1186.6571	0.1138	DNGLLIHIHR
72.5	1186.6571	0.1138	DNGLLLHIHR
72.5	1186.6571	0.1138	DNGLLLHIHR

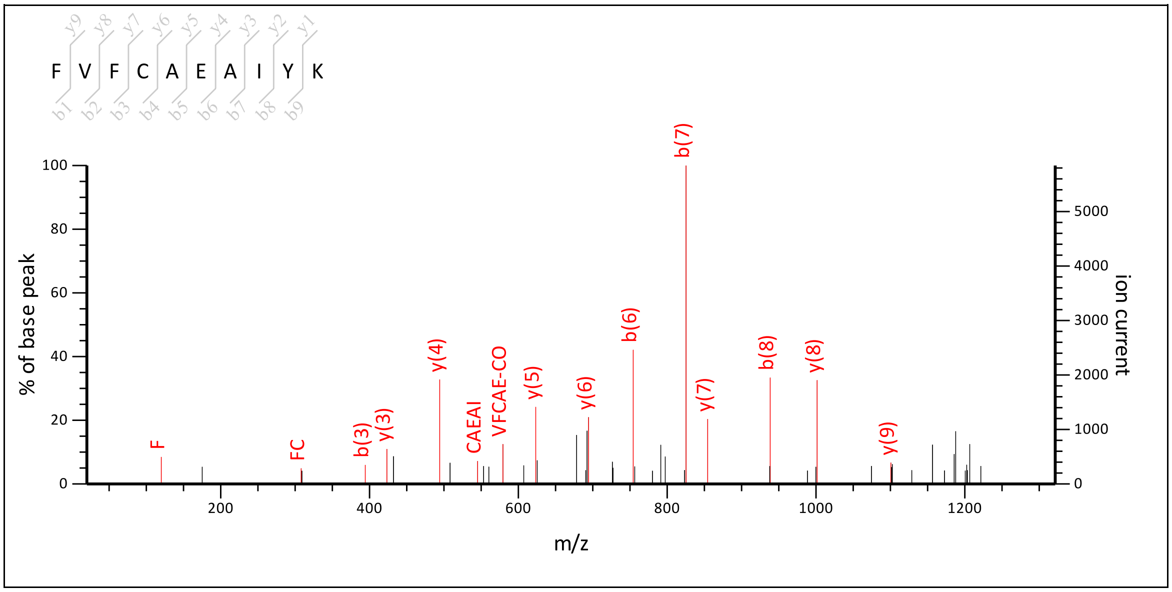
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **FVFCAEAIYK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 25: 1246.718424 from(1247.725700,1+) intensity(0.0000) index(9)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221789, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



20.1 to 1321.49

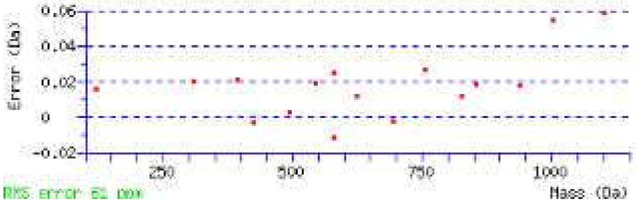
Label all possible matches ○ Label matches used for scoring ●

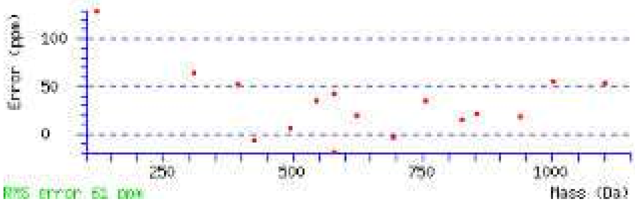
Monoisotopic mass of neutral peptide Mr(calc): 1246.6056
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 0.041
Matches : 18/129 fragment ions using 22 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	120.0808	120.0808		148.0757		44.0495		F							10
2	72.0808	219.1492		247.1441		205.1335		V	1056.4819	1069.5023		***1100.5445***	1083.5179	1082.5339	9
3	120.0808	366.2176		**394.2125**				F	909.4135			***1001.4761***	984.4495	983.4655	8
4	133.0430	526.2483		554.2432		437.2547		C	749.3828	748.3876		***854.4077***	837.3811	836.3971	7
5	44.0495	597.2854		625.2803				A	678.3457			***694.3770***	677.3505	676.3665	6
6	102.0550	726.3280	708.3174	**754.3229**	736.3123	668.3225		E	549.3031	548.3079		***623.3399***	606.3134	605.3293	5
7	44.0495	797.3651	779.3545	**825.3600**	807.3494			A	478.2660			***494.2973***	477.2708		4
8	86.0964	910.4491	892.4386	**938.4441**	920.4335	882.4178	896.4335	I	365.1819	378.2023	392.2180	***423.2602***	406.2336		3
9	136.0757	1073.5125	1055.5019	1101.5074	1083.4968			Y	202.1186			310.1761	293.1496		2
10	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
VF	219.1492	247.1441	VFC	379.1798	407.1748	VFCA	450.2170	478.2119
VFCAE	579.2595	607.2545	VFCAEA	650.2967	678.2916	FC	280.1114	308.1063
FCA	351.1485	379.1435	FCAE	480.1911	508.1860	FCAEA	551.2282	579.2232
FCAEAI	664.3123	692.3072	CA	204.0801	232.0750	CAE	333.1227	361.1176
CAEA	404.1598	432.1547	CAEAI	517.2439	545.2388	CAEAIY	680.3072	708.3021
AE	173.0921	201.0870	AEA	244.1292	272.1241	AEAI	357.2132	385.2082

AEAIY	520.2766	548.2715	**EA**	173.0921	201.0870	**EAI**	286.1761	314.1710
EAIY	449.2395	477.2344	**AI**	157.1335	185.1285	**AIY**	320.1969	348.1918
IY	249.1598	277.1547						





NCBI **BLAST** search of FVFCAEAIYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.8	1246.6056	0.1128	FVFCAEAIYK
51.8	1246.6056	0.1128	FVFCAEAIYK
51.8	1246.6056	0.1128	FVFCAEAIYK
51.8	1246.6056	0.1128	FVFCAEAIYK
51.8	1246.6056	0.1128	FVFCAEAIYK
51.8	1246.6056	0.1128	FVFCAEAIYK
51.8	1246.6056	0.1128	FVFCAEAIYK
51.8	1246.6056	0.1128	FVFCAEALYK
51.8	1246.6056	0.1128	FVFCAEALYK
51.8	1246.6056	0.1128	FVFCAEALYK

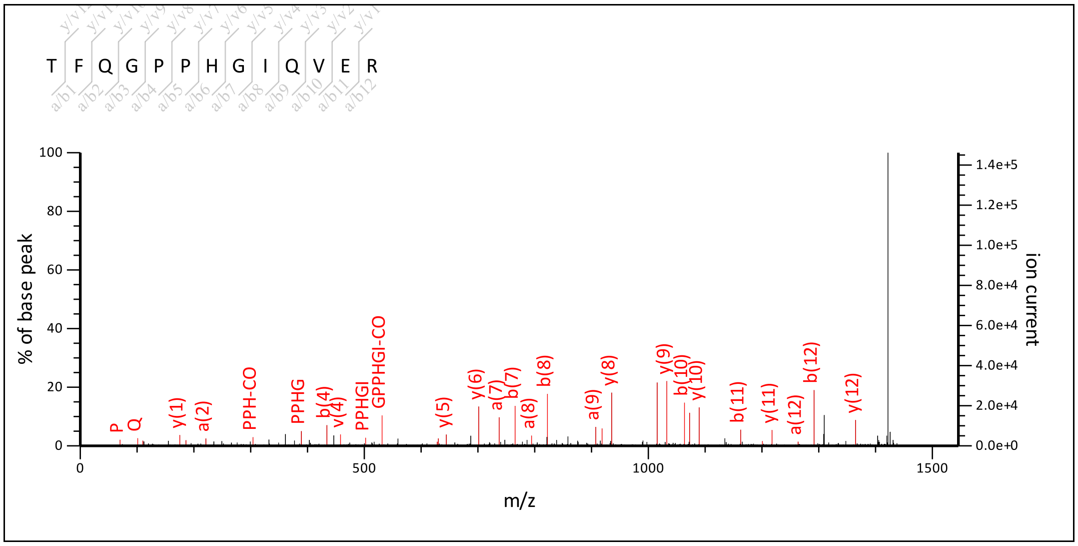
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **TFQGPPHGIQVER**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 39: 1464.881124 from(1465.888400,1+) intensity(0.0000) index(12)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221779, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



0 to 1545.82

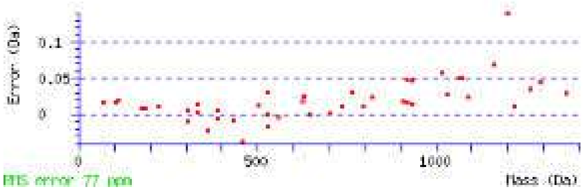
Label all possible matches ○ Label matches used for scoring ●

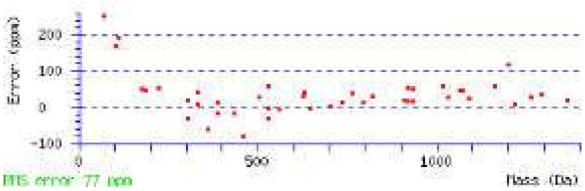
Monoisotopic mass of neutral peptide Mr(calc): 1464.7474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 100 **Expect:** 6.5e-07
Matches : 48/229 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	120.0808	**221.1285**		203.1179	249.1234		231.1128			F	1272.6444			***1364.7070***	1347.6804	134
3	101.0709	349.1870	332.1605	331.1765	377.1819	360.1554	359.1714	292.1656		Q	1144.5858	1143.5905		***1217.6385***	1200.6120	119
4	30.0338	406.2085	389.1819	388.1979	***434.2034***	417.1769	416.1928			G				***1089.5800***	1072.5534	107
5	70.0651	503.2613	486.2347	485.2507	***531.2562***	514.2296	513.2456	477.2456		P	990.5116	989.5163		***1032.5585***	1015.5320	101
6	70.0651	600.3140	583.2875	582.3035	***628.3089***	611.2824	610.2984	574.2984		P	893.4588	892.4635		***935.5057***	918.4792	91
7	110.0713	**737.3729**	720.3464	719.3624	***765.3679***	748.3413	747.3573			H	756.3999			838.4530	821.4264	82
8	30.0338	**794.3944**	777.3679	776.3838	***822.3893***	805.3628	804.3787			G				***701.3941***	684.3675	68
9	86.0964	**907.4785**	890.4519	889.4679	***935.4734***	918.4468	917.4628	879.4472	893.4628	I	586.2944	599.3148	613.3304	***644.3726***	627.3461	62
10	101.0709	1035.5370	1018.5105	1017.5265	***1063.5320***	1046.5054	1045.5214	978.5156		Q	458.2358	457.2405		***531.2885***	514.2620	51
11	72.0808	1134.6055	1117.5789	1116.5949	***1162.6004***	1145.5738	1144.5898	1120.5898		V	359.1674	372.1878		403.2300	386.2034	38
12	102.0550	**1263.6480**	1246.6215	1245.6375	***1291.6430***	1274.6164	1273.6324	1205.6426		E	230.1248	229.1295		***304.1615***	287.1350	28
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQG	305.1608	333.1557	FQGP	402.2136	430.2085
FQGPP	499.2663	527.2613	FQGPPH	636.3253	664.3202	FQGPPHG	693.3467	721.3416
QG	158.0924	186.0873	QGP	255.1452	283.1401	QGPP	352.1979	380.1928
QGPPH	489.2568	517.2518	QGPPHG	546.2783	574.2732	QGPPHGI	659.3624	687.3573
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPH	361.1983	389.1932
GPPHG	418.2197	446.2146	GPPHGI	531.3038	559.2987	GPPHGIQ	659.3624	687.3573
PP	167.1179	195.1128	PPH	304.1768	332.1717	PPHG	361.1983	389.1932
PPHGI	474.2823	502.2772	PPHGIQ	602.3409	630.3358	PH	207.1240	235.1190

PHG	264.1455	292.1404	**PHGI**	377.2296	405.2245	**PHGIQ**	505.2881	533.2831
PHGIQV	604.3566	632.3515	**HG**	167.0927	195.0877	**HGI**	280.1768	308.1717
HGIQ	408.2354	436.2303	**HGIQV**	507.3038	535.2987	**HGIQVE**	636.3464	664.3413
GI	143.1179	171.1128	**GIQ**	271.1765	299.1714	**GIQV**	370.2449	398.2398
GIQVE	499.2875	527.2824	**IQ**	214.1550	242.1499	**IQV**	313.2234	341.2183
IQVE	442.2660	470.2609	**QV**	200.1394	228.1343	**QVE**	329.1819	357.1769
VE	201.1234	229.1183						





NCBI **BLAST** search of TFQGPPHGIQVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.3	1464.7838	0.0974	TFKGPPHGIQVER
100.3	1464.7838	0.0974	TFKGPPHGIQVER
100.3	1464.7838	0.0974	TFQGPPHGIKVER
100.3	1464.7838	0.0974	TFQGPPHGIKVER
100.3	1464.7474	0.1337	TFQGPPHGIQVER
100.3	1464.7474	0.1337	TFQGPPHGIQVER
100.3	1464.7474	0.1337	TFQGPPHGIQVER
100.3	1464.7474	0.1337	TFQGPPHGIQVER
100.3	1464.7474	0.1337	TFQGPPHGIQVER
100.3	1464.7474	0.1337	TFQGPPHGIQVER

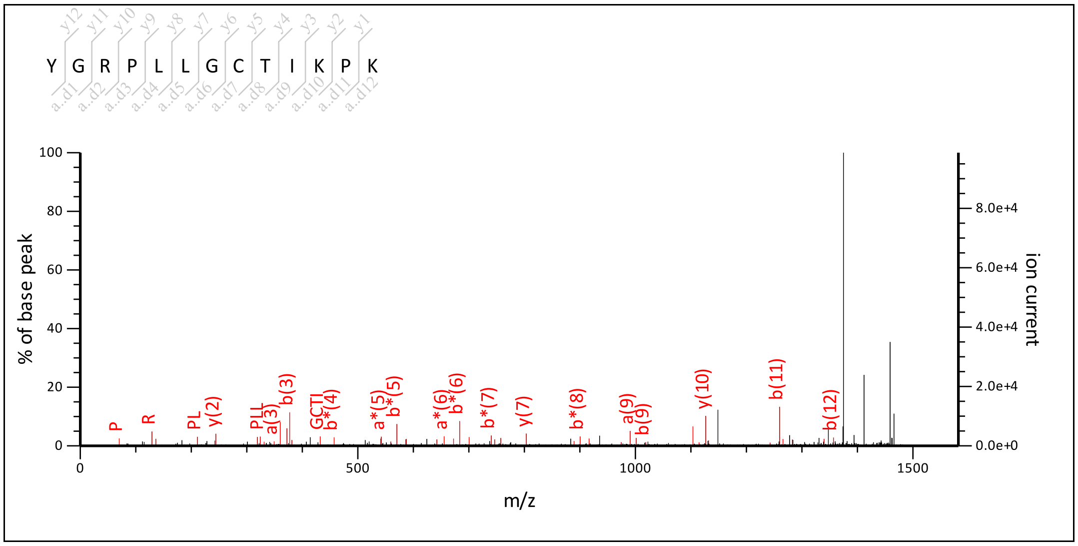
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 138**

MS/MS Fragmentation of **YGRPLLGCTIKPK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 42: 1501.975524 from(1502.982800,1+) intensity(0.0000) index(13)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221782, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



0 to 1581.87

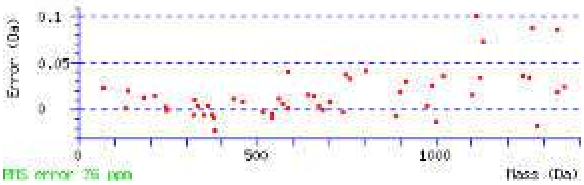
Label all possible matches ○ Label matches used for scoring ●

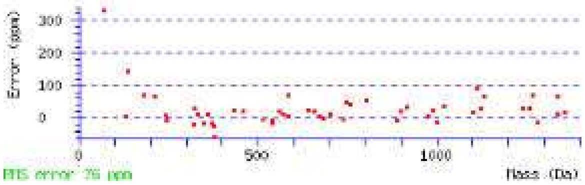
Monoisotopic mass of neutral peptide Mr(calc): `1501.8439`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `46` **Expect:** `0.14`
Matches : `54/211 fragment ions using 88 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	136.0757	**136.0757**			164.0706			44.0495		**Y**					
2	30.0338	193.0972			221.0921					**G**				***1339.7879***	1322.7613
3	129.1135	**349.1983**	332.1717		***377.1932***	360.1666		264.1343		**R**	1181.6711	1180.6758		***1282.7664***	1265.7398
4	70.0651	446.2510	429.2245		474.2459	457.2194		420.2354		**P**	1084.6183	1083.6231		***1126.6653***	1109.6387
5	86.0964	**559.3351**	542.3085		***587.3300***	570.3035		517.2881		**L**	971.5343	970.5390		1029.6125	1012.5860
6	86.0964	**672.4192**	655.3926		***700.4141***	683.3875		630.3722		**L**	858.4502	857.4550		***916.5285***	899.5019
7	30.0338	729.4406	712.4141		***757.4355***	740.4090				**G**				***803.4444***	786.4178
8	133.0430	**889.4713**	872.4447		917.4662	900.4396		800.4777		**C**	641.3981	640.4028		***746.4229***	729.3964
9	74.0600	**990.5189**	973.4924	972.5084	***1018.5139***	1001.4873	1000.5033	974.5240	976.5033	**T**	540.3504	553.3708	555.3501	***586.3923***	569.3657
10	86.0964	**1103.6030**	1086.5765	1085.5924	***1131.5979***	1114.5714	1113.5874	1075.5717	1089.5874	**I**	427.2663	440.2867	454.3024	485.3446	468.3180
11	101.1073	1231.6980	1214.6714	1213.6874	***1259.6929***	1242.6663	1241.6823	1174.6401		**K**	299.1714	298.1761		***372.2605***	355.2340
12	70.0651	1328.7507	1311.7242	1310.7402	***1356.7457***	1339.7191	1338.7351	1302.7351		**P**	202.1186	201.1234		***244.1656***	227.1390
13	101.1073									**K**	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GR	186.1349	214.1299	**GRP**	283.1877	311.1826	**GRPL**	396.2718	424.2667
GRPLL	509.3558	537.3507	**GRPLLG**	566.3773	594.3722	**RP**	226.1662	254.1612
RPL	339.2503	367.2452	**RPLL**	452.3344	480.3293	**RPLLG**	509.3558	537.3507
RPLLGC	669.3865	697.3814	**PL**	183.1492	211.1441	**PLL**	296.2333	324.2282
PLLG	353.2547	381.2496	**PLLGC**	513.2854	541.2803	**PLLGCT**	614.3330	642.3280
LL	199.1805	227.1754	**LLG**	256.2020	284.1969	**LLGC**	416.2326	444.2275
LLGCT	517.2803	545.2752	**LLGCTI**	630.3643	658.3593	**LG**	143.1179	171.1128
LGC	303.1485	331.1435	**LGCT**	404.1962	432.1911	**LGCTI**	517.2803	545.2752

LGCTIK	645.3752	673.3702	**GC**	190.0645	218.0594	**GCT**	291.1122	319.1071
GCTI	404.1962	432.1911	**GCTIK**	532.2912	560.2861	**GCTIKP**	629.3439	657.3389
CT	234.0907	262.0856	**CTI**	347.1748	375.1697	**CTIK**	475.2697	503.2646
CTIKP	572.3225	600.3174	**TI**	187.1441	215.1390	**TIK**	315.2391	343.2340
TIKP	412.2918	440.2867	**IK**	214.1914	242.1863	**IKP**	311.2442	339.2391
KP	198.1601	226.1550						





NCBI **BLAST** search of YGRPLLGCTIKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
46.4	1501.8439	0.1316	YGRPILGCTIKPK
46.4	1501.8439	0.1316	YGRPILGCTIKPK
46.4	1501.8439	0.1316	YGRPLIGCTIKPK
46.4	1501.8439	0.1316	YGRPLLGCTIKPK
46.4	1501.8439	0.1316	YGRPLLGCTIKPK
46.4	1501.8439	0.1316	YGRPLLGCTIKPK
46.4	1501.8439	0.1316	YGRPLLGCTIKPK
46.4	1501.8439	0.1316	YGRPLLGCTIKPK
46.4	1501.8439	0.1316	YGRPLLGCTIKPK
46.4	1501.8439	0.1316	YGRPLLGCTIKPK

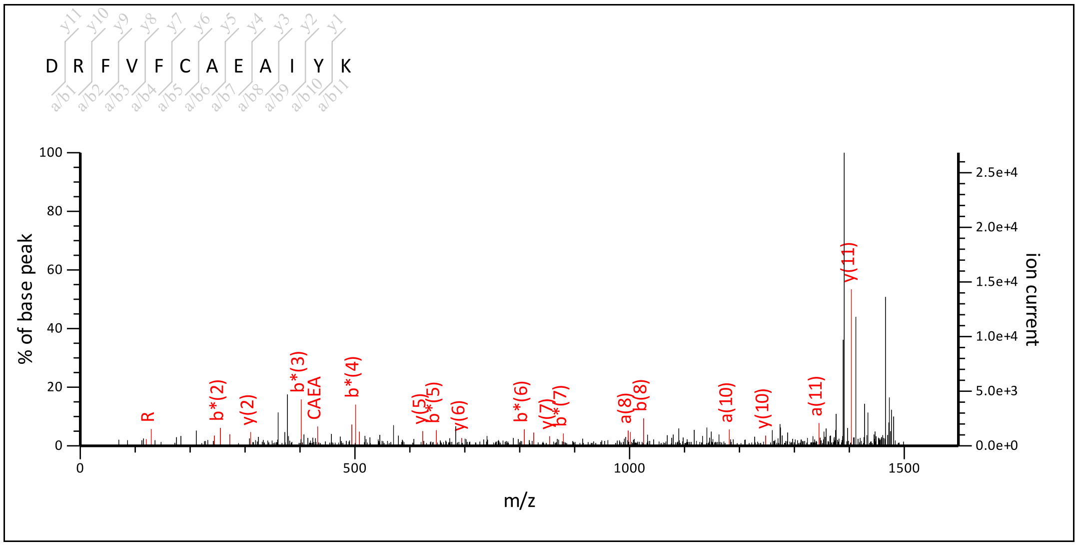
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **DRFVFCAEAIYK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 45: 1517.880924 from(1518.888200,1+) intensity(0.0000) index(14)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221787, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



0 to 1598.56

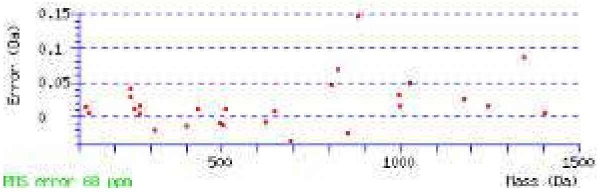
Label all possible matches ○ Label matches used for scoring ●

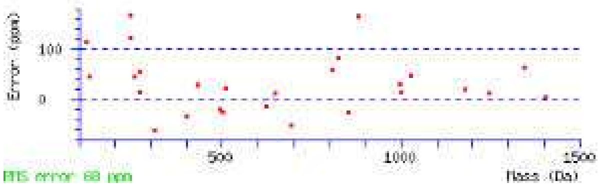
Monoisotopic mass of neutral peptide Mr(calc): 1517.7337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.34
Matches : 28/194 fragment ions using 45 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	88.0393	88.0393		70.0287	116.0342		98.0237	44.0495		D						
2	129.1135	**244.1404**	227.1139	226.1299	**272.1353**	255.1088	254.1248	159.0764		R	1302.6187	1301.6235		***1403.7140***	1386.6875	138
3	120.0808	391.2088	374.1823	373.1983	419.2037	402.1772	401.1932			F	1155.5503			***1247.6129***	1230.5864	122
4	72.0808	490.2772	473.2507	472.2667	518.2722	501.2456	500.2616	476.2616		V	1056.4819	1069.5023		1100.5445	1083.5179	108
5	120.0808	637.3457	620.3191	619.3351	665.3406	648.3140	647.3300			F	909.4135			***1001.4761***	984.4495	98
6	133.0430	797.3763	780.3498	779.3657	**825.3712**	808.3447	807.3607	708.3828		C	749.3828	748.3876		***854.4077***	837.3811	83
7	44.0495	868.4134	851.3869	850.4029	896.4083	879.3818	878.3978			A	678.3457			***694.3770***	677.3505	67
8	102.0550	**997.4560**	980.4295	979.4454	**1025.4509**	1008.4244	1007.4404	939.4505		E	549.3031	548.3079		***623.3399***	606.3134	60
9	44.0495	1068.4931	1051.4666	1050.4826	1096.4880	1079.4615	1078.4775			A	478.2660			***494.2973***	477.2708	
10	86.0964	**1181.5772**	1164.5506	1163.5666	1209.5721	1192.5456	1191.5615	1153.5459	1167.5615	I	365.1819	378.2023	392.2180	423.2602	406.2336	
11	136.0757	**1344.6405**	1327.6140	1326.6300	1372.6354	1355.6089	1354.6249			Y	202.1186			***310.1761***	293.1496	
12	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RF	276.1819	304.1768	RFV	375.2503	403.2452	RFVF	522.3187	550.3136
RFVFC	682.3494	710.3443	FV	219.1492	247.1441	FVF	366.2176	394.2125
FVFC	526.2483	554.2432	FVFCA	597.2854	625.2803	VF	219.1492	247.1441
VFC	379.1798	407.1748	VFCA	450.2170	478.2119	VFCAE	579.2595	607.2545
VFCAEA	650.2967	678.2916	FC	280.1114	308.1063	FCA	351.1485	379.1435
FCAE	480.1911	508.1860	FCAEA	551.2282	579.2232	FCAEAI	664.3123	692.3072
CA	204.0801	232.0750	CAE	333.1227	361.1176	CAEA	404.1598	432.1547
CAEAI	517.2439	545.2388	CAEAIY	680.3072	708.3021	AE	173.0921	201.0870
AEA	244.1292	272.1241	AEAI	357.2132	385.2082	AEAIY	520.2766	548.2715

EA	173.0921	201.0870	**EAI**	286.1761	314.1710	**EAIY**	449.2395	477.2344
AI	157.1335	185.1285	**AIY**	320.1969	348.1918	**IY**	249.1598	277.1547





NCBI **BLAST** search of DRFVFCAEAIYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
43.3	1517.7007	0.1803	DRFVMCAEAIYK
43.3	1517.7007	0.1803	DRMVFCAEALYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK
42.0	1517.7337	0.1473	DRFVFCAEAIYK

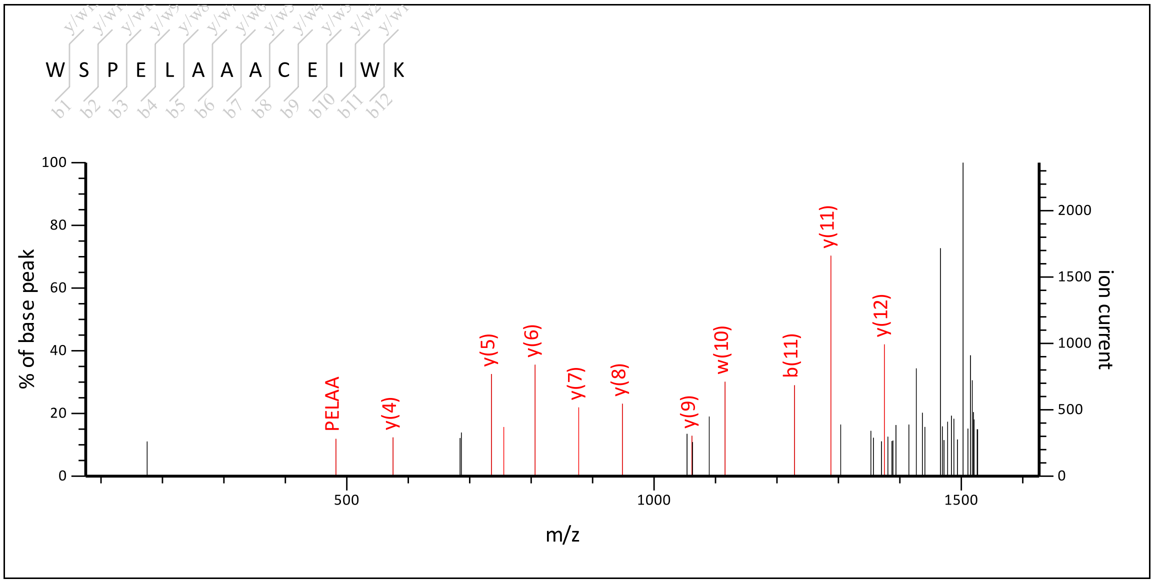
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **WSPELAAACEIWK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 48: 1559.877824 from(1560.885100,1+) intensity(0.0000) index(15)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221798, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



75.13 to 1626.66

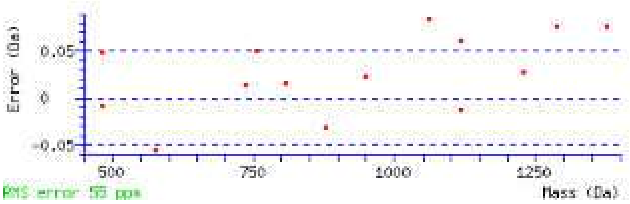
Label all possible matches ○ Label matches used for scoring ●

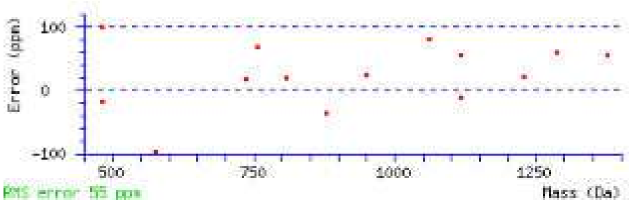
Monoisotopic mass of neutral peptide Mr(calc): 1559.7442
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 0.016
Matches : 14/203 fragment ions using 19 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	159.0917	159.0917		187.0866		44.0495		W							13
2	60.0444	246.1237	228.1131	274.1186	256.1081	230.1288		S	1342.6460	1341.6508		***1374.6722***	1357.6457	1356.6616	12
3	70.0651	343.1765	325.1659	371.1714	353.1608	317.1608		P	1245.5932	1244.5980		***1287.6402***	1270.6136	1269.6296	11
4	102.0550	472.2191	454.2085	500.2140	482.2034	414.2136		E	1116.5506	1115.5554		1190.5874	1173.5609	1172.5769	10
5	86.0964	585.3031	567.2926	613.2980	595.2875	543.2562		L	1003.4666	1002.4713		***1061.5448***	1044.5183	1043.5343	9
6	44.0495	656.3402	638.3297	684.3352	666.3246			A	932.4295			***948.4608***	931.4342	930.4502	8
7	44.0495	727.3774	709.3668	**755.3723**	737.3617			A	861.3924			***877.4237***	860.3971	859.4131	7
8	44.0495	798.4145	780.4039	826.4094	808.3988			A	790.3552			***806.3865***	789.3600	788.3760	6
9	133.0430	958.4451	940.4345	986.4400	968.4295	869.4516		C	630.3246	629.3293		***735.3494***	718.3229	717.3389	5
10	102.0550	1087.4877	1069.4771	**1115.4826**	1097.4721	1029.4822		E	501.2820	500.2867		***575.3188***	558.2922	557.3082	4
11	86.0964	1200.5718	1182.5612	**1228.5667**	1210.5561	1172.5405	1186.5561	I	388.1979	401.2183	415.2340	446.2762	429.2496		3
12	159.0917	1386.6511	1368.6405	1414.6460	1396.6354			W	202.1186			333.1921	316.1656		2
13	101.1073							K	74.0237	73.0284		147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SP	157.0972	185.0921	SPE	286.1397	314.1347	SPEL	399.2238	427.2187
SPELA	470.2609	498.2558	SPELAA	541.2980	569.2930	SPELAAA	612.3352	640.3301
PE	199.1077	227.1026	PEL	312.1918	340.1867	PELA	383.2289	411.2238
PELAA	454.2660	482.2609	PELAAA	525.3031	553.2980	PELAAAC	685.3338	713.3287

EL	215.1390	243.1339	**ELA**	286.1761	314.1710	**ELAA**	357.2132	385.2082
ELAAA	428.2504	456.2453	**ELAAAC**	588.2810	616.2759	**LA**	157.1335	185.1285
LAA	228.1707	256.1656	**LAAA**	299.2078	327.2027	**LAAAC**	459.2384	487.2333
LAAACE	588.2810	616.2759	**AA**	115.0866	143.0815	**AAA**	186.1237	214.1186
AAAC	346.1544	374.1493	**AAACE**	475.1969	503.1919	**AAACEI**	588.2810	616.2759
AA	115.0866	143.0815	**AAC**	275.1172	303.1122	**AACE**	404.1598	432.1547
AACEI	517.2439	545.2388	**AC**	204.0801	232.0750	**ACE**	333.1227	361.1176
ACEI	446.2068	474.2017	**ACEIW**	632.2861	660.2810	**CE**	262.0856	290.0805
CEI	375.1697	403.1646	**CEIW**	561.2490	589.2439	**EI**	215.1390	243.1339
EIW	401.2183	429.2132	**IW**	272.1757	300.1707			





NCBI **BLAST** search of WSPELAAACEIWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
55.1	1559.7442	0.1336	WSPEIAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK
55.1	1559.7442	0.1336	WSPELAAACEIWK

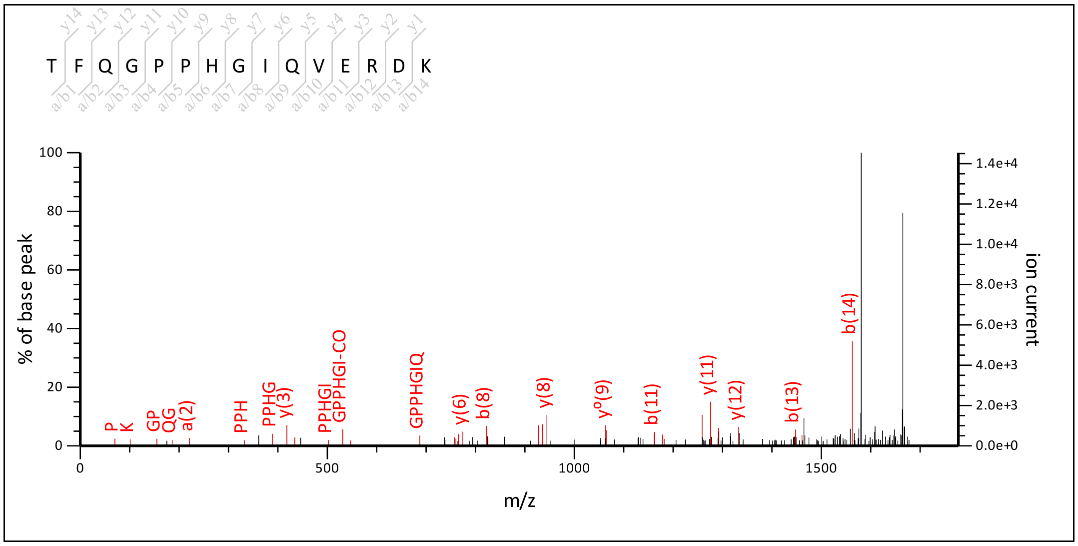
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **TFQGPPHGIQVERDK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 52: 1708.021624 from(1709.028900,1+) intensity(0.0000) index(17)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221792, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



0 to 1777.44

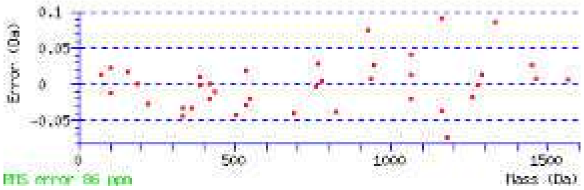
Label all possible matches ○ Label matches used for scoring ●

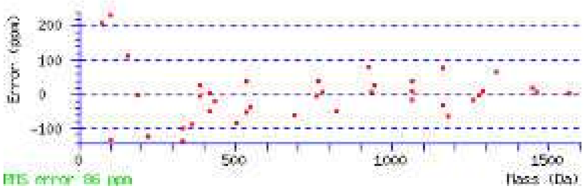
```
Monoisotopic mass of neutral peptide Mr(calc): 1707.8693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72  Expect: 0.00033
Matches : 44/273 fragment ions using 46 most intense peaks   (help)
```

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*	
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495		T						
2	120.0808	221.1285		203.1179	249.1234		231.1128			F	1515.7663			1607.8289	1590.8023	158
3	101.0709	349.1870	332.1605	331.1765	377.1819	360.1554	359.1714	292.1656		Q	1387.7077	1386.7124		***1460.7605***	1443.7339	144
4	30.0338	406.2085	389.1819	388.1979	***434.2034***	417.1769	416.1928			G				***1332.7019***	1315.6753	131
5	70.0651	503.2613	486.2347	485.2507	***531.2562***	514.2296	513.2456	477.2456		P	1233.6335	1232.6382		***1275.6804***	1258.6539	125
6	70.0651	600.3140	583.2875	582.3035	628.3089	611.2824	610.2984	574.2984		P	1136.5807	1135.5854		***1178.6276***	1161.6011	116
7	110.0713	737.3729	720.3464	719.3624	***765.3679***	748.3413	747.3573			H	999.5218			1081.5749	1064.5483	106
8	30.0338	794.3944	777.3679	776.3838	***822.3893***	805.3628	804.3787			G				***944.5160***	927.4894	92
9	86.0964	907.4785	890.4519	889.4679	***935.4734***	918.4468	917.4628	879.4472	893.4628	I	829.4163	842.4367	856.4523	887.4945	870.4680	86
10	101.0709	1035.5370	1018.5105	1017.5265	***1063.5320***	1046.5054	1045.5214	978.5156		Q	701.3577	700.3624		***774.4104***	757.3839	75
11	72.0808	1134.6055	1117.5789	1116.5949	***1162.6004***	1145.5738	1144.5898	1120.5898		V	602.2893	615.3097		646.3519	629.3253	62
12	102.0550	1263.6480	1246.6215	1245.6375	***1291.6430***	1274.6164	1273.6324	1205.6426		E	473.2467	472.2514		***547.2835***	530.2569	52
13	129.1135	1419.7492	1402.7226	1401.7386	***1447.7441***	1430.7175	1429.7335	1334.6852		R	317.1456	316.1503		***418.2409***	401.2143	40
14	88.0393	1534.7761	1517.7496	1516.7655	***1562.7710***	1545.7445	1544.7605	1490.7863		D	202.1186	201.1234		262.1397	245.1132	24
15	101.1073									K	74.0237	73.0284		147.1128	130.0863	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FQ	248.1394	276.1343	FQG	305.1608	333.1557	FQGP	402.2136	430.2085
FQGPP	499.2663	527.2613	FQGPPH	636.3253	664.3202	FQGPPHG	693.3467	721.3416
QG	158.0924	186.0873	QGP	255.1452	283.1401	QGPP	352.1979	380.1928
QGPPH	489.2568	517.2518	QGPPHG	546.2783	574.2732	QGPPHGI	659.3624	687.3573
GP	127.0866	155.0815	GPP	224.1394	252.1343	GPPH	361.1983	389.1932
GPPHG	418.2197	446.2146	GPPHGI	531.3038	559.2987	GPPHGIQ	659.3624	687.3573

PP	167.1179	195.1128	**PPH**	304.1768	332.1717	**PPHG**	361.1983	389.1932
PPHGI	474.2823	502.2772	**PPHGIQ**	602.3409	630.3358	**PH**	207.1240	235.1190
PHG	264.1455	292.1404	**PHGI**	377.2296	405.2245	**PHGIQ**	505.2881	533.2831
PHGIQV	604.3566	632.3515	**HG**	167.0927	195.0877	**HGI**	280.1768	308.1717
HGIQ	408.2354	436.2303	**HGIQV**	507.3038	535.2987	**HGIQVE**	636.3464	664.3413
GI	143.1179	171.1128	**GIQ**	271.1765	299.1714	**GIQV**	370.2449	398.2398
GIQVE	499.2875	527.2824	**GIQVER**	655.3886	683.3835	**IQ**	214.1550	242.1499
IQV	313.2234	341.2183	**IQVE**	442.2660	470.2609	**IQVER**	598.3671	626.3620
QV	200.1394	228.1343	**QVE**	329.1819	357.1769	**QVER**	485.2831	513.2780
QVERD	600.3100	628.3049	**VE**	201.1234	229.1183	**VER**	357.2245	385.2194
VERD	472.2514	500.2463	**ER**	258.1561	286.1510	**ERD**	373.1830	401.1779
RD	244.1404	272.1353						





NCBI **BLAST** search of TFQGPPHGIQVERDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
73.2	1707.8805	0.1411	TFQGPPHGIQVERSR
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK
72.2	1707.8693	0.1523	TFQGPPHGIQVERDK

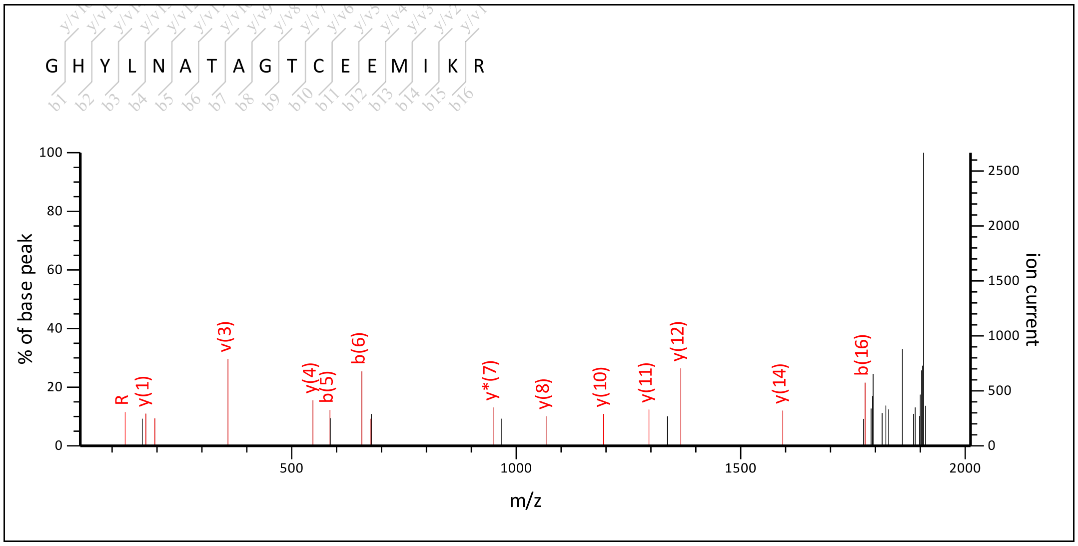
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **GHYLNATAGTCEEMIKR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 56: 1950.081824 from(1951.089100,1+) intensity(0.0000) index(19)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221800, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



29.1 to 2011.82

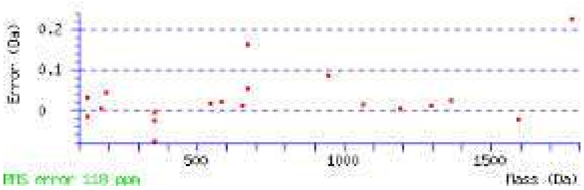
Label all possible matches ○ Label matches used for scoring ●

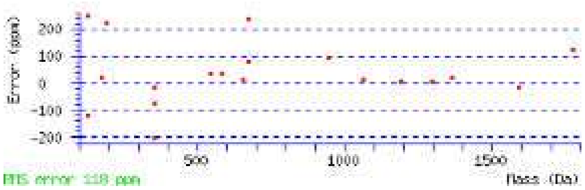
Monoisotopic mass of neutral peptide Mr(calc): 1949.9087
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.034
Matches : 19/302 fragment ions using 24 most intense peaks (help)

#	Immon.	a	a*	a0	b	b*	b0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	110.0713	167.0927			**195.0877**					H	1811.8415			1893.8946	1876.8680
3	136.0757	330.1561			**358.1510**					Y	1648.7782			1756.8357	1739.8091
4	86.0964	443.2401			471.2350			401.1932		L	1535.6941	1534.6988		***1593.7723***	1576.7458
5	87.0553	557.2831	540.2565		**585.2780**	568.2514		514.2772		N	1421.6512	1420.6559		1480.6883	1463.6617
6	44.0495	628.3202	611.2936		**656.3151**	639.2885				A	1350.6140			***1366.6453***	1349.6188
7	74.0600	729.3679	712.3413	711.3573	757.3628	740.3362	739.3522	713.3729	715.3522	T	1249.5664	1262.5868	1264.5660	***1295.6082***	1278.5817
8	44.0495	800.4050	783.3784	782.3944	828.3999	811.3733	810.3893			A	1178.5293			***1194.5606***	1177.5340
9	30.0338	857.4264	840.3999	839.4159	885.4213	868.3948	867.4108			G				1123.5234	1106.4969
10	74.0600	958.4741	941.4476	940.4635	986.4690	969.4425	968.4585	942.4792	944.4585	T	1020.4601	1033.4805	1035.4598	***1066.5020***	1049.4754
11	133.0430	1118.5048	1101.4782	1100.4942	1146.4997	1129.4731	1128.4891	1029.5112		C	860.4295	859.4342		965.4543	948.4277
12	102.0550	1247.5473	1230.5208	1229.5368	1275.5423	1258.5157	1257.5317	1189.5419		E	731.3869	730.3916		805.4236	788.3971
13	102.0550	1376.5899	1359.5634	1358.5794	1404.5849	1387.5583	1386.5743	1318.5845		E	602.3443	601.3490		***676.3811***	659.3545
14	104.0528	1507.6304	1490.6039	1489.6199	1535.6253	1518.5988	1517.6148	1447.6271		M	471.3038	470.3085		***547.3385***	530.3119
15	86.0964	1620.7145	1603.6879	1602.7039	1648.7094	1631.6829	1630.6988	1592.6832	1606.6988	I	358.2197	371.2401	385.2558	416.2980	399.2714
16	101.1073	1748.8095	1731.7829	1730.7989	**1776.8044**	1759.7778	1758.7938	1691.7516		K	230.1248	229.1295		303.2139	286.1874
17	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HY	273.1346	301.1295	HYL	386.2187	414.2136	HYLN	500.2616	528.2565
HYLNA	571.2987	599.2936	HYLNAT	672.3464	700.3413	YL	249.1598	277.1547
YLN	363.2027	391.1976	YLNA	434.2398	462.2347	YLNAT	535.2875	563.2824
YLNATA	606.3246	634.3195	YLNATAG	663.3461	691.3410	LN	200.1394	228.1343

LNA	271.1765	299.1714	**LNAT**	372.2241	400.2191	**LNATA**	443.2613	471.2562
LNATAG	500.2827	528.2776	**LNATAGT**	601.3304	629.3253	**NA**	158.0924	186.0873
NAT	259.1401	287.1350	**NATA**	330.1772	358.1721	**NATAG**	387.1987	415.1936
NATAGT	488.2463	516.2413	**NATAGTC**	648.2770	676.2719	**AT**	145.0972	173.0921
ATA	216.1343	244.1292	**ATAG**	273.1557	301.1506	**ATAGT**	374.2034	402.1983
ATAGTC	534.2341	562.2290	**ATAGTCE**	663.2767	691.2716	**TA**	145.0972	173.0921
TAG	202.1186	230.1135	**TAGT**	303.1663	331.1612	**TAGTC**	463.1969	491.1919
TAGTCE	592.2395	620.2345	**AG**	101.0709	129.0659	**AGT**	202.1186	230.1135
AGTC	362.1493	390.1442	**AGTCE**	491.1919	519.1868	**AGTCEE**	620.2345	648.2294
GT	131.0815	159.0764	**GTC**	291.1122	319.1071	**GTCE**	420.1547	448.1497
GTCEE	549.1973	577.1923	**GTCEEM**	680.2378	708.2327	**TC**	234.0907	262.0856
TCE	363.1333	391.1282	**TCEE**	492.1759	520.1708	**TCEEM**	623.2164	651.2113
CE	262.0856	290.0805	**CEE**	391.1282	419.1231	**CEEM**	522.1687	550.1636
CEEMI	635.2527	663.2477	**EE**	231.0975	259.0925	**EEM**	362.1380	390.1329
EEMI	475.2221	503.2170	**EEMIK**	603.3171	631.3120	**EM**	233.0954	261.0904
EMI	346.1795	374.1744	**EMIK**	474.2745	502.2694	**MI**	217.1369	245.1318
MIK	345.2319	373.2268	**IK**	214.1914	242.1863			





NCBI **BLAST** search of GHYLNATAGTCEEMIKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
51.4	1949.9087	0.1731	GHYINATAGTCEEMIKR
51.4	1949.9087	0.1731	GHYINATAGTCEEMLKR
51.4	1949.9087	0.1731	GHYLNATAGTCEEIMKR
51.4	1949.9087	0.1731	GHYLNATAGTCEEIMKR
51.4	1949.9087	0.1731	GHYLNATAGTCEELMKR
51.4	1949.9087	0.1731	GHYLNATAGTCEELMKR
51.4	1949.9087	0.1731	GHYLNATAGTCEEMIKR
51.4	1949.9087	0.1731	GHYLNATAGTCEEMIKR
51.4	1949.9087	0.1731	GHYLNATAGTCEEMIKR
51.4	1949.9087	0.1731	GHYLNATAGTCEEMIKR

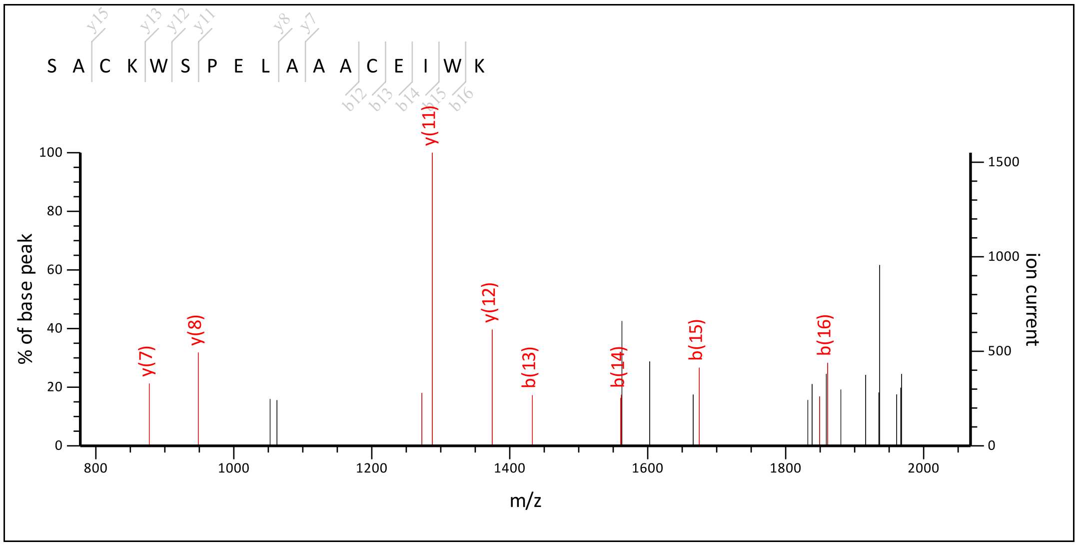
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **SACKWSPELAAACEIWK**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 58: 2006.113724 from(2007.121000,1+) intensity(0.0000) index(20)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221803, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



777.43 to 2067.97

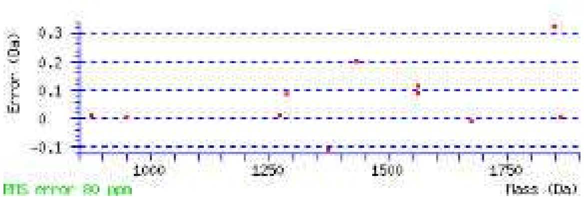
Label all possible matches ○ Label matches used for scoring ●

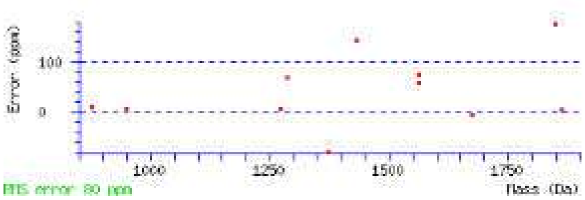
Monoisotopic mass of neutral peptide Mr(calc): 2005.9390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.27
Matches : 11/305 fragment ions using 22 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	60.0444	60.0444		42.0338	88.0393		70.0287	44.0495		S					
2	44.0495	131.0815		113.0709	159.0764		141.0659			A	1903.8830			1919.9143	1902.8877
3	133.0430	291.1122		273.1016	319.1071		301.0965	202.1186		C	1743.8523	1742.8571		***1848.8771***	1831.8506
4	101.1073	419.2071	402.1806	401.1966	447.2020	430.1755	429.1915	362.1493		K	1615.7573	1614.7621		1688.8465	1671.8199
5	159.0917	605.2864	588.2599	587.2759	633.2813	616.2548	615.2708			W	1429.6780			***1560.7515***	1543.7250
6	60.0444	692.3185	675.2919	674.3079	720.3134	703.2868	702.3028	676.3235		S	1342.6460	1341.6508		***1374.6722***	1357.6457
7	70.0651	789.3712	772.3447	771.3607	817.3661	800.3396	799.3556	763.3556		P	1245.5932	1244.5980		***1287.6402***	1270.6136
8	102.0550	918.4138	901.3873	900.4032	946.4087	929.3822	928.3982	860.4083		E	1116.5506	1115.5554		1190.5874	1173.5609
9	86.0964	1031.4979	1014.4713	1013.4873	1059.4928	1042.4662	1041.4822	989.4509		L	1003.4666	1002.4713		1061.5448	1044.5183
10	44.0495	1102.5350	1085.5084	1084.5244	1130.5299	1113.5034	1112.5193			A	932.4295			***948.4608***	931.4342
11	44.0495	1173.5721	1156.5456	1155.5615	1201.5670	1184.5405	1183.5565			A	861.3924			***877.4237***	860.3971
12	44.0495	1244.6092	1227.5827	1226.5987	***1272.6041***	1255.5776	1254.5936			A	790.3552			806.3865	789.3600
13	133.0430	1404.6399	1387.6133	1386.6293	***1432.6348***	1415.6082	1414.6242	1315.6463		C	630.3246	629.3293		735.3494	718.3229
14	102.0550	1533.6825	1516.6559	1515.6719	***1561.6774***	1544.6508	1543.6668	1475.6770		E	501.2820	500.2867		575.3188	558.2922
15	86.0964	1646.7665	1629.7400	1628.7560	***1674.7614***	1657.7349	1656.7509	1618.7352	1632.7509	I	388.1979	401.2183	415.2340	446.2762	429.2496
16	159.0917	1832.8458	1815.8193	1814.8353	***1860.8408***	1843.8142	1842.8302			W	202.1186			333.1921	316.1656
17	101.1073									K	74.0237	73.0284		147.1128	130.0863

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AC	204.0801	232.0750	ACK	332.1751	360.1700	ACKW	518.2544	546.2493
ACKWS	605.2864	633.2813	CK	261.1380	289.1329	CKW	447.2173	475.2122
CKWS	534.2493	562.2442	CKWSP	631.3021	659.2970	KW	287.1866	315.1816
KWS	374.2187	402.2136	KWSP	471.2714	499.2663	KWSPE	600.3140	628.3089

WS	246.1237	274.1186	**WSP**	343.1765	371.1714	**WSPE**	472.2191	500.2140
WSPEL	585.3031	613.2980	**WSPELA**	656.3402	684.3352	**SP**	157.0972	185.0921
SPE	286.1397	314.1347	**SPEL**	399.2238	427.2187	**SPELA**	470.2609	498.2558
SPELAA	541.2980	569.2930	**SPELAAA**	612.3352	640.3301	**PE**	199.1077	227.1026
PEL	312.1918	340.1867	**PELA**	383.2289	411.2238	**PELAA**	454.2660	482.2609
PELAAA	525.3031	553.2980	**PELAAAC**	685.3338	713.3287	**EL**	215.1390	243.1339
ELA	286.1761	314.1710	**ELAA**	357.2132	385.2082	**ELAAA**	428.2504	456.2453
ELAAAC	588.2810	616.2759	**LA**	157.1335	185.1285	**LAA**	228.1707	256.1656
LAAA	299.2078	327.2027	**LAAAC**	459.2384	487.2333	**LAAACE**	588.2810	616.2759
AA	115.0866	143.0815	**AAA**	186.1237	214.1186	**AAAC**	346.1544	374.1493
AAACE	475.1969	503.1919	**AAACEI**	588.2810	616.2759	**AA**	115.0866	143.0815
AAC	275.1172	303.1122	**AACE**	404.1598	432.1547	**AACEI**	517.2439	545.2388
AC	204.0801	232.0750	**ACE**	333.1227	361.1176	**ACEI**	446.2068	474.2017
ACEIW	632.2861	660.2810	**CE**	262.0856	290.0805	**CEI**	375.1697	403.1646
CEIW	561.2490	589.2439	**EI**	215.1390	243.1339	**EIW**	401.2183	429.2132
IW	272.1757	300.1707						





NCBI **BLAST** search of SACKWSPELAAACEIWK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.3	2005.9390	0.1748	SACKWSPELAAACEIWK
14.5	2006.1023	0.0114	ALFLPIYQLVEMGNVRK
14.2	2006.8866	-0.7729	SACKWSPELAAACEIWE
14.1	2006.8866	-0.7729	EACSWSPELAAACEIWK
13.3	2004.9615	1.1523	ETSKWSPELAAACEIWK
11.3	2005.9217	0.1920	GAGGNAFPWSNAMLQWQR
7.5	2006.0506	0.0631	AILMIINAANTYQQVAEK
7.3	2005.9311	0.1826	AGTGTAMFSMGIFMALQEK
6.7	2006.0196	0.0941	HFCFQIRVSPLNYTPK
6.4	2005.8254	0.2884	CLDADCGVGAFSMMLAEK

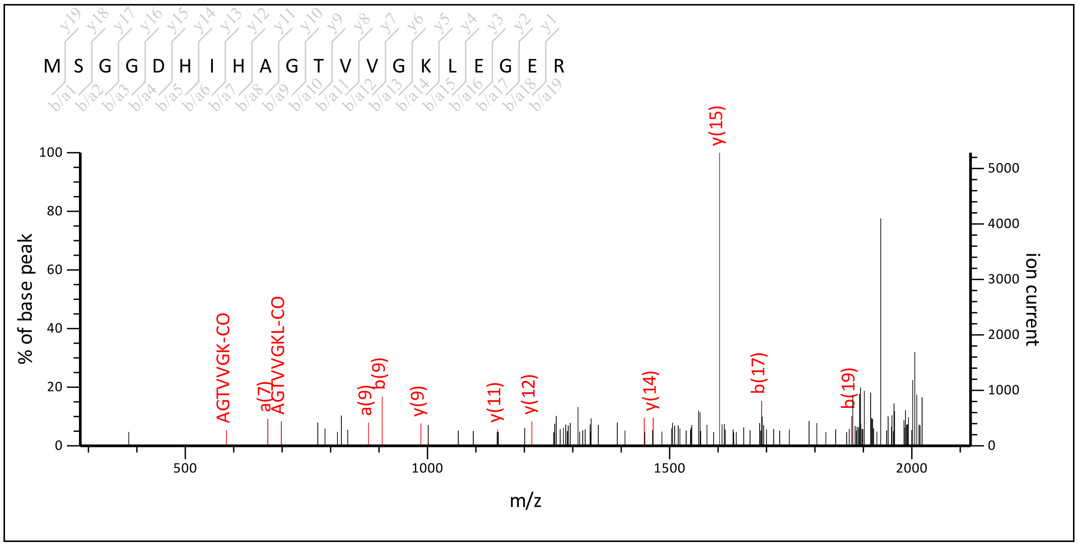
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 138**

MS/MS Fragmentation of **MSGGDHIHAGTVVGKLEGER**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 60: 2049.192924 from(2050.200200,1+) intensity(0.0000) index(21)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221797, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



283.17 to 2121.21

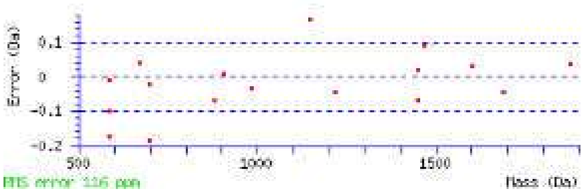
Label all possible matches ○ Label matches used for scoring ●

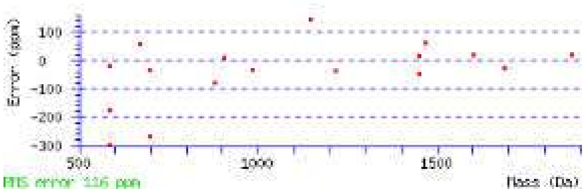
```
Monoisotopic mass of neutral peptide Mr(calc): 2049.0062
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 24  Expect: 14
Matches : 17/369 fragment ions using 30 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	104.0528	104.0528			132.0478			44.0495		M					
2	60.0444	191.0849		173.0743	219.0798		201.0692	175.0900		S	1886.9468	1885.9515		1918.9730	1901.9464
3	30.0338	248.1063		230.0958	276.1013		258.0907			G				1831.9409	1814.9144
4	30.0338	305.1278		287.1172	333.1227		315.1122			G				1774.9195	1757.8929
5	88.0393	420.1547		402.1442	448.1497		430.1391	376.1649		D	1657.8769	1656.8816		1717.8980	1700.8715
6	110.0713	557.2137		539.2031	***585.2086***		567.1980			H	1520.8180			***1602.8711***	1585.8445
7	86.0964	**670.2977**		652.2872	***698.2926***		680.2821	642.2664	656.2821	I	1407.7339	1420.7543	1434.7700	***1465.8122***	1448.7856
8	110.0713	807.3566		789.3461	835.3515		817.3410			H	1270.6750			1352.7281	1335.7015
9	44.0495	**878.3937**		860.3832	***906.3887***		888.3781			A	1199.6379			***1215.6692***	1198.6426
10	30.0338	935.4152		917.4046	963.4101		945.3996			G				***1144.6321***	1127.6055
11	74.0600	1036.4629		1018.4523	1064.4578		1046.4472	1020.4680	1022.4472	T	1041.5687	1054.5891	1056.5684	1087.6106	1070.5841
12	72.0808	1135.5313		1117.5207	1163.5262		1145.5157	1121.5157		V	942.5003	955.5207		***986.5629***	969.5364
13	72.0808	1234.5997		1216.5892	1262.5946		1244.5841	1220.5841		V	843.4319	856.4523		887.4945	870.4680
14	30.0338	1291.6212		1273.6106	1319.6161		1301.6055			G				788.4261	771.3995
15	101.1073	1419.7161	1402.6896	1401.7056	***1447.7111***	1430.6845	1429.7005	1362.6583		K	658.3155	657.3202		731.4046	714.3781
16	86.0964	1532.8002	1515.7737	1514.7896	1560.7951	1543.7686	1542.7846	1490.7533		L	545.2314	544.2362		603.3097	586.2831
17	102.0550	1661.8428	1644.8163	1643.8322	***1689.8377***	1672.8112	1671.8272	1603.8373		E	416.1888	415.1936		490.2256	473.1991
18	30.0338	1718.8643	1701.8377	1700.8537	1746.8592	1729.8326	1728.8486			G				361.1830	344.1565
19	102.0550	1847.9069	1830.8803	1829.8963	***1875.9018***	1858.8752	1857.8912	1789.9014		E	230.1248	229.1295		304.1615	287.1350
20	129.1135									R	74.0237	73.0284		175.1190	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SG	117.0659	145.0608	SGG	174.0873	202.0822	SGGD	289.1143	317.1092

SGGDH	426.1732	454.1681	**SGGDHI**	539.2572	567.2522	**SGGDHIH**	676.3161	704.3111
GG	87.0553	115.0502	**GGD**	202.0822	230.0771	**GGDH**	339.1411	367.1361
GGDHI	452.2252	480.2201	**GGDHIH**	589.2841	617.2790	**GGDHIHA**	660.3212	688.3161
GD	145.0608	173.0557	**GDH**	282.1197	310.1146	**GDHI**	395.2037	423.1987
GDHIH	532.2627	560.2576	**GDHIHA**	603.2998	631.2947	**GDHIHAG**	660.3212	688.3161
DH	225.0982	253.0931	**DHI**	338.1823	366.1772	**DHIH**	475.2412	503.2361
DHIHA	546.2783	574.2732	**DHIHAG**	603.2998	631.2947	**HI**	223.1553	251.1503
HIH	360.2142	388.2092	**HIHA**	431.2514	459.2463	**HIHAG**	488.2728	516.2677
HIHAGT	589.3205	617.3154	**HIHAGTV**	688.3889	716.3838	**IH**	223.1553	251.1503
IHA	294.1925	322.1874	**IHAG**	351.2139	379.2088	**IHAGT**	452.2616	480.2565
IHAGTV	551.3300	579.3249	**IHAGTVV**	650.3984	678.3933	**HA**	181.1084	209.1033
HAG	238.1299	266.1248	**HAGT**	339.1775	367.1724	**HAGTV**	438.2459	466.2409
HAGTVV	537.3144	565.3093	**HAGTVVG**	594.3358	622.3307	**AG**	101.0709	129.0659
AGT	202.1186	230.1135	**AGTV**	301.1870	329.1819	**AGTVV**	400.2554	428.2504
AGTVVG	457.2769	485.2718	**AGTVVGK**	585.3719	613.3668	**AGTVVGKL**	698.4559	726.4509
GT	131.0815	159.0764	**GTV**	230.1499	258.1448	**GTVV**	329.2183	357.2132
GTVVG	386.2398	414.2347	**GTVVGK**	514.3348	542.3297	**GTVVGKL**	627.4188	655.4137
TV	173.1285	201.1234	**TVV**	272.1969	300.1918	**TVVG**	329.2183	357.2132
TVVGK	457.3133	485.3082	**TVVGKL**	570.3974	598.3923	**TVVGKLE**	699.4400	727.4349
VV	171.1492	199.1441	**VVG**	228.1707	256.1656	**VVGK**	356.2656	384.2605
VVGKL	469.3497	497.3446	**VVGKLE**	598.3923	626.3872	**VVGKLEG**	655.4137	683.4087
VG	129.1022	157.0972	**VGK**	257.1972	285.1921	**VGKL**	370.2813	398.2762
VGKLE	499.3239	527.3188	**VGKLEG**	556.3453	584.3402	**VGKLEGE**	685.3879	713.3828
GK	158.1288	186.1237	**GKL**	271.2129	299.2078	**GKLE**	400.2554	428.2504
GKLEG	457.2769	485.2718	**GKLEGE**	586.3195	614.3144	**KL**	214.1914	242.1863
KLE	343.2340	371.2289	**KLEG**	400.2554	428.2504	**KLEGE**	529.2980	557.2930
LE	215.1390	243.1339	**LEG**	272.1605	300.1554	**LEGE**	401.2031	429.1980
EG	159.0764	187.0713	**EGE**	288.1190	316.1139	**GE**	159.0764	187.0713





NCBI **BLAST** search of MSGGDHIHAGTVVGKLEGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
27.4	2048.5142	0.6787	MAGGDHIHAGTVVGKLZGER
24.2	2049.0062	0.1867	MAGGDHIHAGTVVGKLEGER
24.2	2049.0062	0.1867	MAGGDHIHAGTVVGKLEGER
24.2	2049.0062	0.1867	MSGGDHIHAGTVVGKIEGER
24.2	2049.0062	0.1867	MSGGDHIHAGTVVGKLEGER
24.2	2049.0062	0.1867	MSGGDHIHAGTVVGKLEGER
24.2	2049.0062	0.1867	MSGGDHIHAGTVVGKLEGER
24.2	2049.0062	0.1867	MSGGDHIHAGTVVGKLEGER
24.2	2049.0062	0.1867	MSGGDHIHAGTVVGKLEGER
24.2	2049.0062	0.1867	MSGGDHIHAGTVVGKLEGER

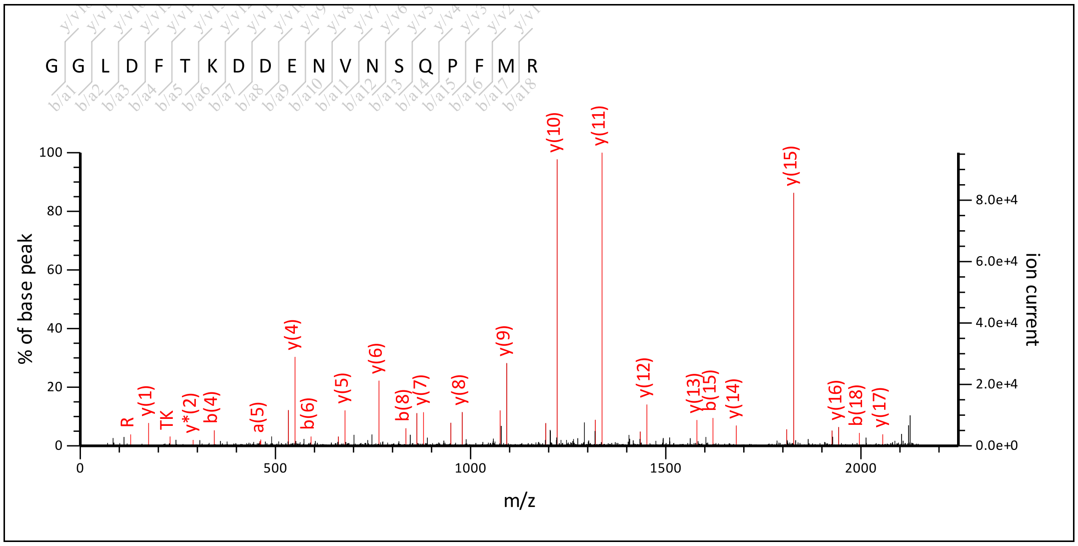
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **GGLDFTKDDENVNSQPFMR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 70: 2169.171224 from(2170.178500,1+) intensity(0.0000) index(23)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221781, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



0 to 2249.66

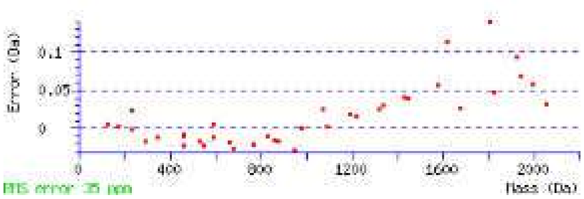
Label all possible matches ○ Label matches used for scoring ●

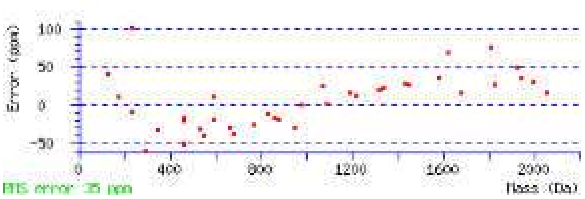
Monoisotopic mass of neutral peptide Mr(calc): 2168.9797
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 137 **Expect:** 9.5e-11
Matches : 40/340 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	30.0338	30.0338			58.0287			44.0495		**G**						
2	30.0338	87.0553			115.0502					**G**				2112.9655	2095.9389	209
3	86.0964	200.1394			228.1343			158.0924		**L**	1997.8658	1996.8705		***2055.9440***	2038.9175	203
4	88.0393	315.1663		297.1557	**343.1612**		325.1506	271.1765		**D**	1882.8388	1881.8436		***1942.8600***	1925.8334	192
5	120.0808	462.2347		444.2241	490.2296		472.2191			**F**	1735.7704			***1827.8330***	1810.8065	180
6	74.0600	563.2824		545.2718	**591.2773**		573.2667	547.2875	549.2667	**T**	1634.7227	1647.7431	1649.7224	***1680.7646***	1663.7381	166
7	101.1073	691.3774	674.3508	673.3668	719.3723	702.3457	701.3617	634.3195		**K**	1506.6278	1505.6325		***1579.7169***	1562.6904	156
8	88.0393	806.4043	789.3777	788.3937	**834.3992**	817.3727	816.3886	762.4145		**D**	1391.6008	1390.6056		***1451.6220***	1434.5954	143
9	88.0393	921.4312	904.4047	903.4207	**949.4262**	932.3996	931.4156	877.4414		**D**	1276.5739	1275.5786		***1336.5950***	1319.5685	131
10	102.0550	1050.4738	1033.4473	1032.4633	1078.4687	1061.4422	1060.4582	992.4684		**E**	1147.5313	1146.5361		***1221.5681***	1204.5415	120
11	87.0553	1164.5168	1147.4902	1146.5062	**1192.5117**	1175.4851	1174.5011	1121.5109		**N**	1033.4884	1032.4931		***1092.5255***	1075.4989	107
12	72.0808	1263.5852	1246.5586	1245.5746	1291.5801	1274.5535	1273.5695	1249.5695		**V**	934.4200	947.4404		***978.4826***	961.4560	96
13	87.0553	1377.6281	1360.6016	1359.6175	1405.6230	1388.5965	1387.6124	1334.6223		**N**	820.3770	819.3818		***879.4141***	862.3876	86
14	60.0444	1464.6601	1447.6336	1446.6496	1492.6550	1475.6285	1474.6445	1448.6652		**S**	733.3450	732.3498		***765.3712***	748.3447	74
15	101.0709	1592.7187	1575.6922	1574.7081	**1620.7136**	1603.6871	1602.7031	1535.6972		**Q**	605.2864	604.2912		***678.3392***	661.3126	
16	70.0651	1689.7715	1672.7449	1671.7609	1717.7664	1700.7398	1699.7558	1663.7558		**P**	508.2337	507.2384		***550.2806***	533.2541	
17	120.0808	1836.8399	1819.8133	1818.8293	1864.8348	1847.8082	1846.8242			**F**	361.1653			453.2279	436.2013	
18	104.0528	1967.8804	1950.8538	1949.8698	**1995.8753**	1978.8487	1977.8647	1907.8770		**M**	230.1248	229.1295		306.1594	289.1329	
19	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GL	143.1179	171.1128	**GLD**	258.1448	286.1397	**GLDF**	405.2132	433.2082
GLDFT	506.2609	534.2558	**GLDFTK**	634.3559	662.3508	**LD**	201.1234	229.1183

LDF	348.1918	376.1867	**LDFT**	449.2395	477.2344	**LDFTK**	577.3344	605.3293
LDFTKD	692.3614	720.3563	**DF**	235.1077	263.1026	**DFT**	336.1554	364.1503
DFTK	464.2504	492.2453	**DFTKD**	579.2773	607.2722	**DFTKDD**	694.3042	722.2992
FT	221.1285	249.1234	**FTK**	349.2234	377.2183	**FTKD**	464.2504	492.2453
FTKDD	579.2773	607.2722	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDD	432.2089	460.2038	**TKDDE**	561.2515	589.2464	**TKDDEN**	675.2944	703.2893
KD	216.1343	244.1292	**KDD**	331.1612	359.1561	**KDDE**	460.2038	488.1987
KDDEN	574.2467	602.2416	**KDDENV**	673.3151	701.3101	**DD**	203.0662	231.0612
DDE	332.1088	360.1038	**DDEN**	446.1518	474.1467	**DDENV**	545.2202	573.2151
DDENVN	659.2631	687.2580	**DE**	217.0819	245.0768	**DEN**	331.1248	359.1197
DENV	430.1932	458.1882	**DENVN**	544.2362	572.2311	**DENVNS**	631.2682	659.2631
EN	216.0979	244.0928	**ENV**	315.1663	343.1612	**ENVN**	429.2092	457.2041
ENVNS	516.2413	544.2362	**ENVNSQ**	644.2998	672.2947	**NV**	186.1237	214.1186
NVN	300.1666	328.1615	**NVNS**	387.1987	415.1936	**NVNSQ**	515.2572	543.2522
NVNSQP	612.3100	640.3049	**VN**	186.1237	214.1186	**VNS**	273.1557	301.1506
VNSQ	401.2143	429.2092	**VNSQP**	498.2671	526.2620	**VNSQPF**	645.3355	673.3304
NS	174.0873	202.0822	**NSQ**	302.1459	330.1408	**NSQP**	399.1987	427.1936
NSQPF	546.2671	574.2620	**NSQPFM**	677.3076	705.3025	**SQ**	188.1030	216.0979
SQP	285.1557	313.1506	**SQPF**	432.2241	460.2191	**SQPFM**	563.2646	591.2595
QP	198.1237	226.1186	**QPF**	345.1921	373.1870	**QPFM**	476.2326	504.2275
PF	217.1335	245.1285	**PFM**	348.1740	376.1689	**FM**	251.1213	279.1162





NCBI **BLAST** search of GGLDFTKDDENVNSQPFMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
137.3	2168.9797	0.1915	GGIDFTKDDENVNSQPFMR
137.3	2168.9797	0.1915	GGIDFTKDDENVNSQPFMR
137.3	2169.0161	0.1552	GGLDFTKDDENVNSKPFMR
137.3	2168.9797	0.1915	GGLDFTKDDENVNSQPFMR
137.3	2168.9797	0.1915	GGLDFTKDDENVNSQPFMR
137.3	2168.9797	0.1915	GGLDFTKDDENVNSQPFMR
137.3	2168.9797	0.1915	GGLDFTKDDENVNSQPFMR
137.3	2168.9797	0.1915	GGLDFTKDDENVNSQPFMR
137.3	2168.9797	0.1915	GGLDFTKDDENVNSQPFMR
137.3	2168.9797	0.1915	GGLDFTKDDENVNSQPFMR

Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **LTYYTPEYETKDTDILAAFR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 81: 2409.381124 from(2410.388400,1+) intensity(0.0000) index(27)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221780, MSMS Job_Run_Id: 21391, Comment:
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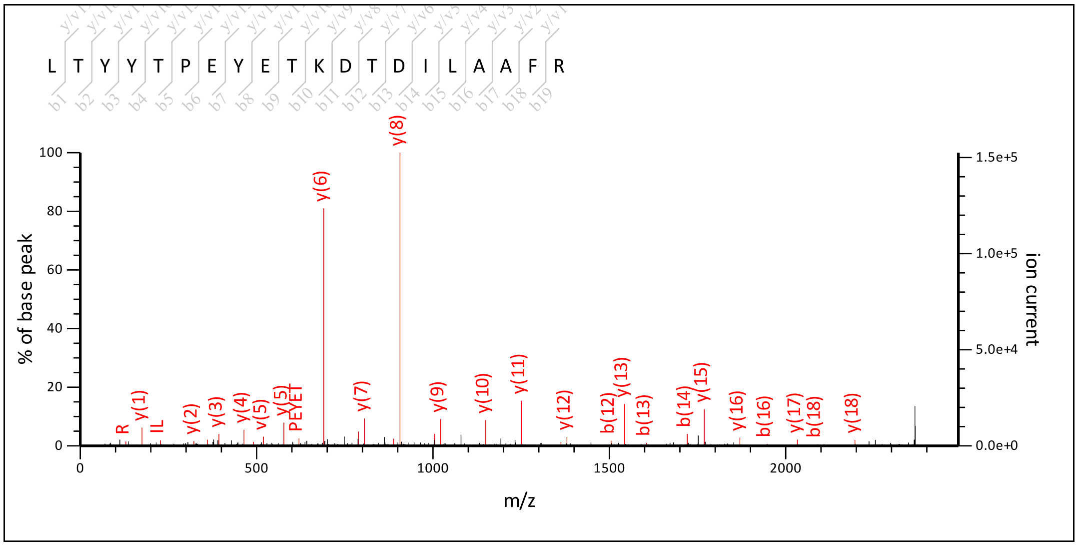


0 to 2489.53

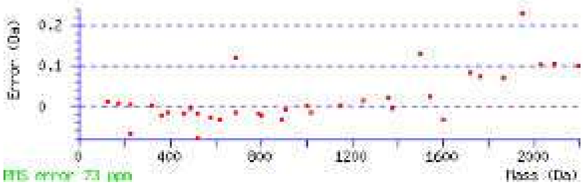
Label all possible matches ○ Label matches used for scoring ●

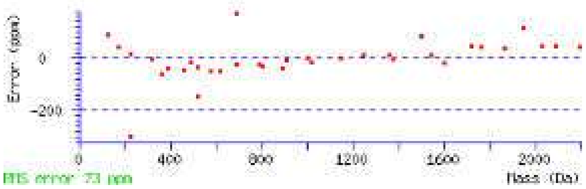
```
Monoisotopic mass of neutral peptide Mr(calc): 2409.1740
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 138  Expect: 5.2e-11
Matches : 38/356 fragment ions using 48 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		L					
2	74.0600	187.1441		169.1335	215.1390		197.1285	171.1492	173.1285	T	2251.0554	2264.0758	2266.0550	2297.0972	2280.0707
3	136.0757	350.2074		332.1969	378.2023		360.1918			Y	2087.9920			***2196.0495***	2179.0230
4	136.0757	513.2708		495.2602	541.2657		523.2551			Y	1924.9287			***2032.9862***	2015.9597
5	74.0600	614.3184		596.3079	642.3134		624.3028	598.3235	600.3028	T	1823.8810	1836.9014	1838.8807	***1869.9229***	1852.8963
6	70.0651	711.3712		693.3606	739.3661		721.3556	685.3556		P	1726.8283	1725.8330		***1768.8752***	1751.8487
7	102.0550	840.4138		822.4032	868.4087		850.3981	782.4083		E	1597.7857	1596.7904		1671.8224	1654.7959
8	136.0757	1003.4771		985.4666	1031.4720		1013.4615			Y	1434.7223			***1542.7799***	1525.7533
9	102.0550	1132.5197		1114.5092	1160.5146		1142.5041	1074.5142		E	1305.6797	1304.6845		***1379.7165***	1362.6900
10	74.0600	1233.5674		1215.5568	1261.5623		1243.5517	1217.5725	1219.5517	T	1204.6321	1217.6525	1219.6317	***1250.6739***	1233.6474
11	101.1073	1361.6624	1344.6358	1343.6518	1389.6573	1372.6307	1371.6467	1304.6045		K	1076.5371	1075.5419		***1149.6262***	1132.5997
12	88.0393	1476.6893	1459.6628	1458.6787	**1504.6842**	1487.6577	1486.6737	1432.6995		D	961.5102	960.5149		***1021.5313***	1004.5047
13	74.0600	1577.7370	1560.7104	1559.7264	**1605.7319**	1588.7054	1587.7213	1561.7421	1563.7213	T	860.4625	873.4829	875.4621	***906.5043***	889.4778
14	88.0393	1692.7639	1675.7374	1674.7534	**1720.7588**	1703.7323	1702.7483	1648.7741		D	745.4355	744.4403		***805.4567***	788.4301
15	86.0964	1805.8480	1788.8214	1787.8374	1833.8429	1816.8164	1815.8323	1777.8167	1791.8323	I	632.3515	645.3719	659.3875	***690.4297***	673.4032
16	86.0964	1918.9321	1901.9055	1900.9215	**1946.9270**	1929.9004	1928.9164	1876.8851		L	519.2674	518.2722		***577.3457***	560.3191
17	44.0495	1989.9692	1972.9426	1971.9586	2017.9641	2000.9375	1999.9535			A	448.2303			***464.2616***	447.2350
18	44.0495	2061.0063	2043.9797	2042.9957	**2089.0012**	2071.9746	2070.9906			A	377.1932			***393.2245***	376.1979
19	120.0808	2208.0747	2191.0481	2190.0641	2236.0696	2219.0431	2218.0590			F	230.1248			***322.1874***	305.1608
20	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TY	237.1234	265.1183	TYY	400.1867	428.1816	TYYT	501.2344	529.2293

TYYTP	598.2871	626.2821	**YY**	299.1390	327.1339	**YYT**	400.1867	428.1816
YYTP	497.2395	525.2344	**YYTPE**	626.2821	654.2770	**YT**	237.1234	265.1183
YTP	334.1761	362.1710	**YTPE**	463.2187	491.2136	**YTPEY**	626.2821	654.2770
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPEY**	463.2187	491.2136
TPEYE	592.2613	620.2562	**TPEYET**	693.3090	721.3039	**PE**	199.1077	227.1026
PEY	362.1710	390.1660	**PEYE**	491.2136	519.2086	**PEYET**	592.2613	620.2562
EY	265.1183	293.1132	**EYE**	394.1609	422.1558	**EYET**	495.2086	523.2035
EYETK	623.3035	651.2984	**YE**	265.1183	293.1132	**YET**	366.1660	394.1609
YETK	494.2609	522.2558	**YETKD**	609.2879	637.2828	**ET**	203.1026	231.0975
ETK	331.1976	359.1925	**ETKD**	446.2245	474.2195	**ETKDT**	547.2722	575.2671
ETKDTD	662.2992	690.2941	**TK**	202.1550	230.1499	**TKD**	317.1819	345.1769
TKDT	418.2296	446.2245	**TKDTD**	533.2566	561.2515	**TKDTDI**	646.3406	674.3355
KD	216.1343	244.1292	**KDT**	317.1819	345.1769	**KDTD**	432.2089	460.2038
KDTDI	545.2930	573.2879	**KDTDIL**	658.3770	686.3719	**DT**	189.0870	217.0819
DTD	304.1139	332.1088	**DTDI**	417.1980	445.1929	**DTDIL**	530.2821	558.2770
DTDILA	601.3192	629.3141	**DTDILAA**	672.3563	700.3512	**TD**	189.0870	217.0819
TDI	302.1710	330.1660	**TDIL**	415.2551	443.2500	**TDILA**	486.2922	514.2871
TDILAA	557.3293	585.3243	**DI**	201.1234	229.1183	**DIL**	314.2074	342.2023
DILA	385.2445	413.2395	**DILAA**	456.2817	484.2766	**DILAAF**	603.3501	631.3450
IL	199.1805	227.1754	**ILA**	270.2176	298.2125	**ILAA**	341.2547	369.2496
ILAAF	488.3231	516.3180	**LA**	157.1335	185.1285	**LAA**	228.1707	256.1656
LAAF	375.2391	403.2340	**AA**	115.0866	143.0815	**AAF**	262.1550	290.1499
AF	191.1179	219.1128						





NCBI **BLAST** search of LTYYTPEYETKDTDILAAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
137.9	2409.1740	0.2071	ITYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	ITYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDIIAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDILAAFR
137.9	2409.1740	0.2071	LTYYTPEYETKDTDILAAFR

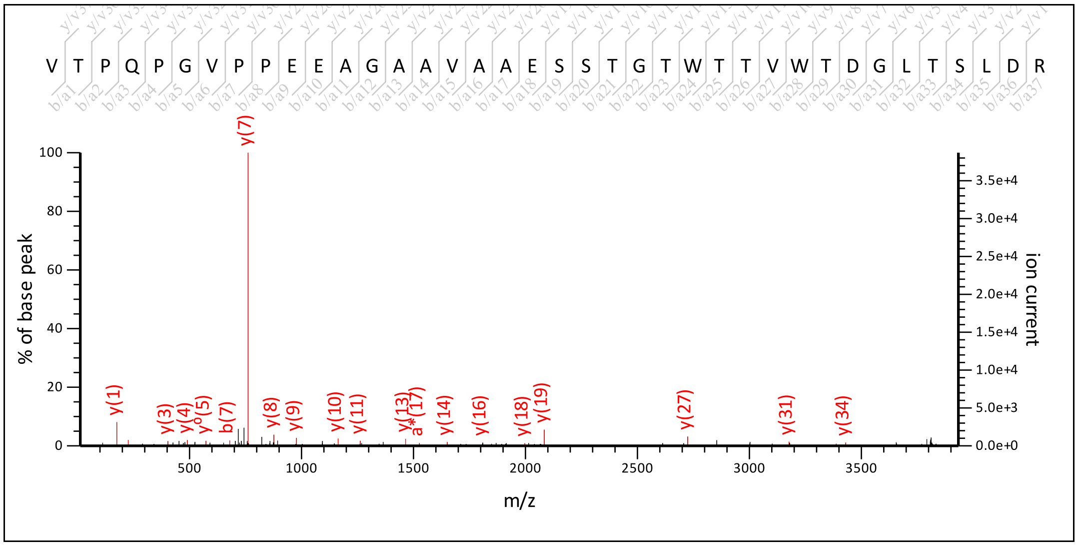
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 138

MS/MS Fragmentation of **VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR**
Found in **gi|11466795** in **NCBInr**, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Oryza sativa Japonica Group]

Match to Query 98: 3854.228524 from(3855.235800,1+) intensity(0.0000) index(34)
Title: Label: F12, Spot_Id: 216658, Peak_List_Id: 221796, MSMS Job_Run_Id: 21391, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\Cotton leaves\RAJESH\12-1-13 raj\ppw_F12_136117698300.txt



12.11 to 3933.21

Label all possible matches ○ Label matches used for scoring ●

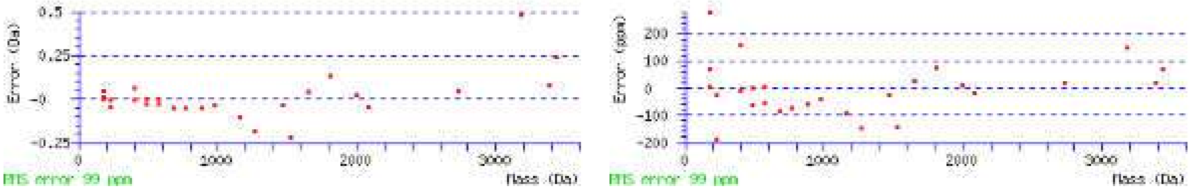
```
Monoisotopic mass of neutral peptide Mr(calc): 3853.8647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 104  Expect: 8.1e-08
Matches : 29/837 fragment ions using 31 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	72.0808	72.0808			100.0757			44.0495		V					
2	74.0600	173.1285		155.1179	201.1234		183.1128	157.1335	159.1128	T	3709.7616	3722.7820	3724.7613	3755.8035	3738.7770
3	70.0651	270.1812		252.1707	298.1761		280.1656	244.1656		P	3612.7089	3611.7136		3654.7558	3637.7293
4	101.0709	398.2398	381.2132	380.2292	426.2347	409.2082	408.2241	341.2183		Q	3484.6503	3483.6551		3557.7031	3540.6765
5	70.0651	495.2926	478.2660	477.2820	523.2875	506.2609	505.2769	469.2769		P	3387.5975	3386.6023		***3429.6445***	3412.6179
6	30.0338	552.3140	535.2875	534.3035	580.3089	563.2824	562.2984			G				3332.5917	3315.5652
7	72.0808	651.3824	634.3559	633.3719	679.3774	662.3508	661.3668	637.3668		V	3231.5077	3244.5281		3275.5703	3258.5437
8	70.0651	748.4352	731.4087	730.4246	776.4301	759.4036	758.4196	722.4196		P	3134.4549	3133.4596		***3176.5018***	3159.4753
9	70.0651	845.4880	828.4614	827.4774	873.4829	856.4563	855.4723	819.4723		P	3037.4021	3036.4069		3079.4491	3062.4225
10	102.0550	974.5306	957.5040	956.5200	1002.5255	985.4989	984.5149	916.5251		E	2908.3595	2907.3643		2982.3963	2965.3698
11	102.0550	1103.5732	1086.5466	1085.5626	1131.5681	1114.5415	1113.5575	1045.5677		E	2779.3169	2778.3217		2853.3537	2836.3272
12	44.0495	1174.6103	1157.5837	1156.5997	1202.6052	1185.5786	1184.5946			A	2708.2798			***2724.3111***	2707.2846
13	30.0338	1231.6317	1214.6052	1213.6212	1259.6266	1242.6001	1241.6161			G				2653.2740	2636.2475
14	44.0495	1302.6688	1285.6423	1284.6583	1330.6638	1313.6372	1312.6532			A	2580.2213			2596.2526	2579.2260
15	44.0495	1373.7060	1356.6794	1355.6954	1401.7009	1384.6743	1383.6903			A	2509.1841			2525.2154	2508.1889
16	72.0808	1472.7744	1455.7478	1454.7638	1500.7693	1483.7427	1482.7587	1458.7587		V	2410.1157	2423.1361		2454.1783	2437.1518
17	44.0495	1543.8115	1526.7849	1525.8009	1571.8064	1554.7799	1553.7958			A	2339.0786			2355.1099	2338.0834
18	44.0495	1614.8486	1597.8221	1596.8380	1642.8435	1625.8170	1624.8329			A	2268.0415			2284.0728	2267.0462
19	102.0550	1743.8912	1726.8646	1725.8806	1771.8861	1754.8596	1753.8755	1685.8857		E	2138.9989	2138.0037		2213.0357	2196.0091
20	60.0444	1830.9232	1813.8967	1812.9127	1858.9181	1841.8916	1840.9076	1814.9283		S	2051.9669	2050.9716		***2083.9931***	2066.9665
21	60.0444	1917.9552	1900.9287	1899.9447	1945.9502	1928.9236	1927.9396	1901.9603		S	1964.9348	1963.9396		***1996.9611***	1979.9345
22	74.0600	2019.0029	2001.9764	2000.9924	2046.9978	2029.9713	2028.9873	2003.0080	2004.9873	T	1863.8872	1876.9076	1878.8868	1909.9290	1892.9025

23	30.0338	2076.0244	2058.9978	2058.0138	2104.0193	2086.9928	2086.0087			**G**				***1808.8814***	1791.8548
24	74.0600	2177.0721	2160.0455	2159.0615	2205.0670	2188.0404	2187.0564	2161.0772	2163.0564	**T**	1705.8180	1718.8384	1720.8177	1751.8599	1734.8333
25	159.0917	2363.1514	2346.1248	2345.1408	2391.1463	2374.1197	2373.1357			**W**	1519.7387			***1650.8122***	1633.7857
26	74.0600	2464.1991	2447.1725	2446.1885	2492.1940	2475.1674	2474.1834	2448.2041	2450.1834	**T**	1418.6910	1431.7114	1433.6907	***1464.7329***	1447.7064
27	74.0600	2565.2467	2548.2202	2547.2362	2593.2417	2576.2151	2575.2311	2549.2518	2551.2311	**T**	1317.6434	1330.6638	1332.6430	1363.6852	1346.6587
28	72.0808	2664.3152	2647.2886	2646.3046	2692.3101	2675.2835	2674.2995	2650.2995		**V**	1218.5749	1231.5953		***1262.6375***	1245.6110
29	159.0917	2850.3945	2833.3679	2832.3839	2878.3894	2861.3628	2860.3788			**W**	1032.4956			***1163.5691***	1146.5426
30	74.0600	2951.4421	2934.4156	2933.4316	2979.4371	2962.4105	2961.4265	2935.4472	2937.4265	**T**	931.4480	944.4684	946.4476	***977.4898***	960.4633
31	88.0393	3066.4691	3049.4425	3048.4585	3094.4640	3077.4375	3076.4534	3022.4793		**D**	816.4210	815.4258		***876.4421***	859.4156
32	30.0338	3123.4906	3106.4640	3105.4800	3151.4855	3134.4589	3133.4749			**G**				***761.4152***	744.3886
33	86.0964	3236.5746	3219.5481	3218.5641	3264.5695	3247.5430	3246.5590	3194.5277		**L**	646.3155	645.3202		704.3937	687.3672
34	74.0600	3337.6223	3320.5957	3319.6117	3365.6172	3348.5907	3347.6066	3321.6274	3323.6066	**T**	545.2678	558.2882	560.2675	591.3097	574.2831
35	60.0444	3424.6543	3407.6278	3406.6438	3452.6492	3435.6227	3434.6387	3408.6594		**S**	458.2358	457.2405		***490.2620***	473.2354
36	86.0964	3537.7384	3520.7118	3519.7278	3565.7333	3548.7068	3547.7227	3495.6914		**L**	345.1517	344.1565		***403.2300***	386.2034
37	88.0393	3652.7653	3635.7388	3634.7548	3680.7602	3663.7337	3662.7497	3608.7755		**D**	230.1248	229.1295		290.1459	273.1193
38	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TP	171.1128	199.1077	**TPQ**	299.1714	327.1663	**TPQP**	396.2241	424.2191
TPQPG	453.2456	481.2405	**TPQPGV**	552.3140	580.3089	**TPQPGVP**	649.3668	677.3617
PQ	198.1237	226.1186	**PQP**	295.1765	323.1714	**PQPG**	352.1979	380.1928
PQPGV	451.2663	479.2613	**PQPGVP**	548.3191	576.3140	**PQPGVPP**	645.3719	673.3668
QP	198.1237	226.1186	**QPG**	255.1452	283.1401	**QPGV**	354.2136	382.2085
QPGVP	451.2663	479.2613	**QPGVPP**	548.3191	576.3140	**QPGVPPE**	677.3617	705.3566
PG	127.0866	155.0815	**PGV**	226.1550	254.1499	**PGVP**	323.2078	351.2027
PGVPP	420.2605	448.2554	**PGVPPE**	549.3031	577.2980	**PGVPPEE**	678.3457	706.3406
GV	129.1022	157.0972	**GVP**	226.1550	254.1499	**GVPP**	323.2078	351.2027
GVPPE	452.2504	480.2453	**GVPPEE**	581.2930	609.2879	**GVPPEEA**	652.3301	680.3250
VP	169.1335	197.1285	**VPP**	266.1863	294.1812	**VPPE**	395.2289	423.2238
VPPEE	524.2715	552.2664	**VPPEEA**	595.3086	623.3035	**VPPEEAG**	652.3301	680.3250
PP	167.1179	195.1128	**PPE**	296.1605	324.1554	**PPEE**	425.2031	453.1980
PPEEA	496.2402	524.2351	**PPEEAG**	553.2617	581.2566	**PPEEAGA**	624.2988	652.2937
PPEEAGAA	695.3359	723.3308	**PE**	199.1077	227.1026	**PEE**	328.1503	356.1452
PEEA	399.1874	427.1823	**PEEAG**	456.2089	484.2038	**PEEAGA**	527.2460	555.2409
PEEAGAA	598.2831	626.2780	**PEEAGAAV**	697.3515	725.3464	**EE**	231.0975	259.0925
EEA	302.1347	330.1296	**EEAG**	359.1561	387.1510	**EEAGA**	430.1932	458.1882
EEAGAA	501.2304	529.2253	**EEAGAAV**	600.2988	628.2937	**EEAGAAVA**	671.3359	699.3308
EA	173.0921	201.0870	**EAG**	230.1135	258.1084	**EAGA**	301.1506	329.1456
EAGAA	372.1878	400.1827	**EAGAAV**	471.2562	499.2511	**EAGAAVA**	542.2933	570.2882
EAGAAVAA	613.3304	641.3253	**AG**	101.0709	129.0659	**AGA**	172.1081	200.1030
AGAA	243.1452	271.1401	**AGAAV**	342.2136	370.2085	**AGAAVA**	413.2507	441.2456
AGAAVAA	484.2878	512.2827	**AGAAVAAE**	613.3304	641.3253	**GA**	101.0709	129.0659
GAA	172.1081	200.1030	**GAAV**	271.1765	299.1714	**GAAVA**	342.2136	370.2085
GAAVAA	413.2507	441.2456	**GAAVAAE**	542.2933	570.2882	**GAAVAAES**	629.3253	657.3202
AA	115.0866	143.0815	**AAV**	214.1550	242.1499	**AAVA**	285.1921	313.1870
AAVAA	356.2292	384.2241	**AAVAAE**	485.2718	513.2667	**AAVAAES**	572.3039	600.2988
AAVAAESS	659.3359	687.3308	**AV**	143.1179	171.1128	**AVA**	214.1550	242.1499
AVAA	285.1921	313.1870	**AVAAE**	414.2347	442.2296	**AVAAES**	501.2667	529.2617
AVAAESS	588.2988	616.2937	**AVAAESST**	689.3464	717.3414	**VA**	143.1179	171.1128
VAA	214.1550	242.1499	**VAAE**	343.1976	371.1925	**VAAES**	430.2296	458.2245
VAAESS	517.2617	545.2566	**VAAESST**	618.3093	646.3042	**VAAESSTG**	675.3308	703.3257
AA	115.0866	143.0815	**AAE**	244.1292	272.1241	**AAES**	331.1612	359.1561
AAESS	418.1932	446.1882	**AAESST**	519.2409	547.2358	**AAESSTG**	576.2624	604.2573
AAESSTGT	677.3101	705.3050	**AE**	173.0921	201.0870	**AES**	260.1241	288.1190
AESS	347.1561	375.1510	**AESST**	448.2038	476.1987	**AESSTG**	505.2253	533.2202

AESSTGT	606.2729	634.2679	**ES**	189.0870	217.0819	**ESS**	276.1190	304.1139
ESST	377.1667	405.1616	**ESSTG**	434.1882	462.1831	**ESSTGT**	535.2358	563.2307
SS	147.0764	175.0713	**SST**	248.1241	276.1190	**SSTG**	305.1456	333.1405
SSTGT	406.1932	434.1882	**SSTGTW**	592.2726	620.2675	**SSTGTWT**	693.3202	721.3151
ST	161.0921	189.0870	**STG**	218.1135	246.1084	**STGT**	319.1612	347.1561
STGTW	505.2405	533.2354	**STGTWT**	606.2882	634.2831	**TG**	131.0815	159.0764
TGT	232.1292	260.1241	**TGTW**	418.2085	446.2034	**TGTWT**	519.2562	547.2511
TGTWTT	620.3039	648.2988	**GT**	131.0815	159.0764	**GTW**	317.1608	345.1557
GTWT	418.2085	446.2034	**GTWTT**	519.2562	547.2511	**GTWTTV**	618.3246	646.3195
TW	260.1394	288.1343	**TWT**	361.1870	389.1819	**TWTT**	462.2347	490.2296
TWTTV	561.3031	589.2980	**WT**	260.1394	288.1343	**WTT**	361.1870	389.1819
WTTV	460.2554	488.2504	**WTTVW**	646.3348	674.3297	**TT**	175.1077	203.1026
TTV	274.1761	302.1710	**TTVW**	460.2554	488.2504	**TTVWT**	561.3031	589.2980
TTVWTD	676.3301	704.3250	**TV**	173.1285	201.1234	**TVW**	359.2078	387.2027
TVWT	460.2554	488.2504	**TVWTD**	575.2824	603.2773	**TVWTDG**	632.3039	660.2988
VW	258.1601	286.1550	**VWT**	359.2078	387.2027	**VWTD**	474.2347	502.2296
VWTDG	531.2562	559.2511	**VWTDGL**	644.3402	672.3352	**WT**	260.1394	288.1343
WTD	375.1663	403.1612	**WTDG**	432.1878	460.1827	**WTDGL**	545.2718	573.2667
WTDGLT	646.3195	674.3144	**TD**	189.0870	217.0819	**TDG**	246.1084	274.1034
TDGL	359.1925	387.1874	**TDGLT**	460.2402	488.2351	**TDGLTS**	547.2722	575.2671
TDGLTSL	660.3563	688.3512	**DG**	145.0608	173.0557	**DGL**	258.1448	286.1397
DGLT	359.1925	387.1874	**DGLTS**	446.2245	474.2195	**DGLTSL**	559.3086	587.3035
DGLTSLD	674.3355	702.3305	**GL**	143.1179	171.1128	**GLT**	244.1656	272.1605
GLTS	331.1976	359.1925	**GLTSL**	444.2817	472.2766	**GLTSLD**	559.3086	587.3035
LT	187.1441	215.1390	**LTS**	274.1761	302.1710	**LTSL**	387.2602	415.2551
LTSLD	502.2871	530.2821	**TS**	161.0921	189.0870	**TSL**	274.1761	302.1710
TSLD	389.2031	417.1980	**SL**	173.1285	201.1234	**SLD**	288.1554	316.1503
LD	201.1234	229.1183						



NCBI **BLAST** search of VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
121.0	3854.8487	-0.6202	VTPEPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
121.0	3854.8487	-0.6202	VTPEPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
110.7	3854.9075	-0.6790	VTPQPGVPAERAGAAVAAESSTGTWTTVWTDGLTSLDR
110.7	3854.9075	-0.6790	VTPQPGVPAREAGAAVAAESSTGTWTTVWTDGLTSLDR
104.0	3853.9011	0.3275	VTPKPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
104.0	3853.8647	0.3638	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGITSLDR
104.0	3853.8647	0.3638	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGITSLDR
104.0	3853.8647	0.3638	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSIDR
104.0	3853.8647	0.3638	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
104.0	3853.8647	0.3638	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR

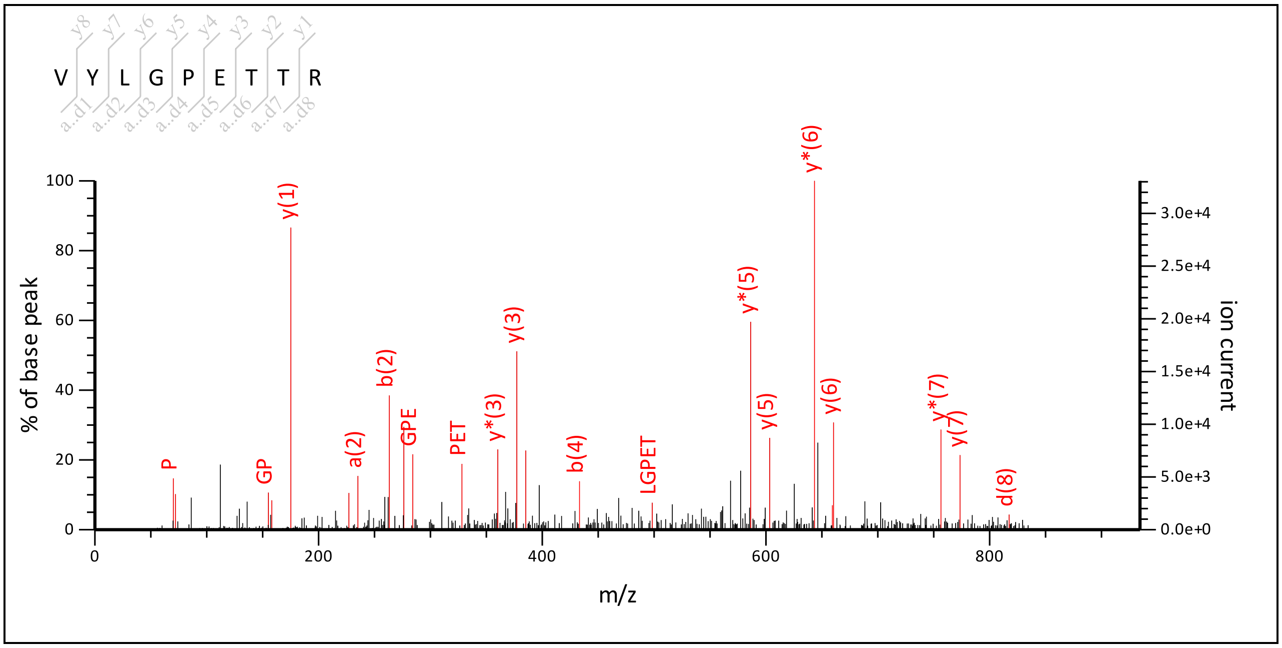
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 144

MS/MS Fragmentation of **VYLGPETTR**
Found in **gi|11466848** in **NCBInr**, photosystem I subunit VII [Oryza sativa Japonica Group]

Match to Query 92: 1034.576824 from(1035.584100,1+) intensity(0.0000) index(7)
Title: Label: N13, Spot_Id: 219879, Peak_List_Id: 228110, MSMS Job_Run_Id: 21981, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N13_136868255600.txt



0 to 934.41

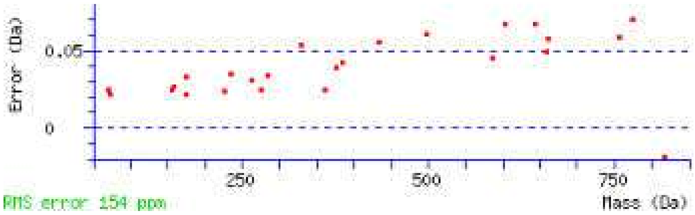
Label all possible matches ○ Label matches used for scoring ●

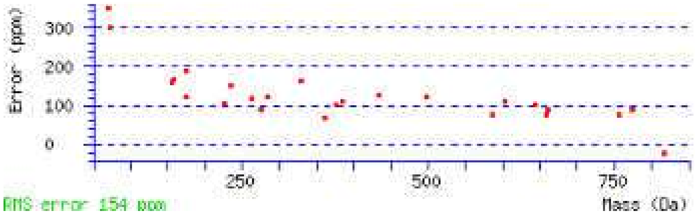
Monoisotopic mass of neutral peptide Mr(calc): 1034.5397
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 1.2
Matches : 26/117 fragment ions using 32 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	72.0808	**72.0808**		100.0757		44.0495		**V**							9
2	136.0757	**235.1441**		**263.1390**				**Y**	828.4210			936.4785	919.4520	918.4680	8
3	86.0964	348.2282		376.2231		306.1812		**L**	715.3369	714.3417		***773.4152***	756.3886	755.4046	7
4	30.0338	405.2496		**433.2445**				**G**				***660.3311***	643.3046	642.3206	6
5	70.0651	502.3024		530.2973		476.2867		**P**	561.2627	560.2675		***603.3097***	586.2831	585.2991	5
6	102.0550	631.3450	613.3344	**659.3399**	641.3293	573.3395		**E**	432.2201	431.2249		506.2569	489.2304	488.2463	4
7	74.0600	732.3927	714.3821	760.3876	742.3770	716.3978	718.3770	**T**	331.1724	344.1928	346.1721	***377.2143***	360.1878	359.2037	3
8	74.0600	833.4403	815.4298	861.4353	843.4247	817.4454	819.4247	**T**	230.1248	243.1452	245.1244	***276.1666***	259.1401	258.1561	2
9	129.1135							**R**	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YL	249.1598	277.1547	**YLG**	306.1812	334.1761	**YLGP**	403.2340	431.2289
YLGPE	532.2766	560.2715	**YLGPET**	633.3243	661.3192	**LG**	143.1179	171.1128
LGP	240.1707	268.1656	**LGPE**	369.2132	397.2082	**LGPET**	470.2609	498.2558

LGPETT	571.3086	599.3035	**GP**	127.0866	155.0815	**GPE**	256.1292	284.1241
GPET	357.1769	385.1718	**GPETT**	458.2245	486.2195	**PE**	199.1077	227.1026
PET	300.1554	328.1503	**PETT**	401.2031	429.1980	**ET**	203.1026	231.0975
ETT	304.1503	332.1452	**TT**	175.1077	203.1026			





NCBI **BLAST** search of VYLGPETTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
44.8	1034.5397	0.0372	VYLGPETTR
41.0	1034.5430	0.0338	MDIGIITTR
35.4	1034.4889	0.0879	DMLGSMLPR
32.5	1034.4855	0.0913	MDLPWTTR
31.6	1034.5760	0.0008	YVLGLLDSR
27.3	1034.5067	0.0702	MDLGLVDTR
24.7	1034.4855	0.0913	AMDVSFPPR
24.4	1034.5509	0.0259	VHPVPETTR
24.2	1034.4815	0.0953	MDLGQAQTR
24.2	1034.5509	0.0259	YVLGAQGATR

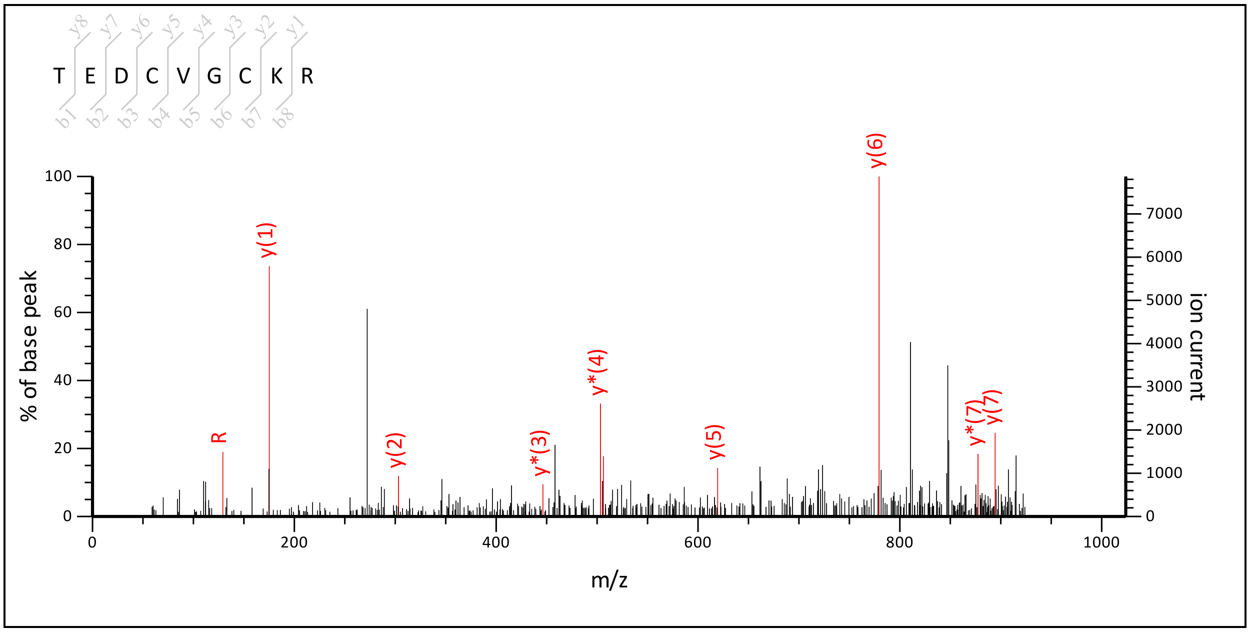
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 144

MS/MS Fragmentation of **TEDCVGCKR**
Found in **gi|11466848** in **NCBInr**, photosystem I subunit VII [Oryza sativa Japonica Group]

Match to Query 146: 1123.525024 from(1124.532300,1+) intensity(0.0000) index(14)
Title: Label: N13, Spot_Id: 219879, Peak_List_Id: 228117, MSMS Job_Run_Id: 21981, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N13_136868255600.txt



0 to 1023.86

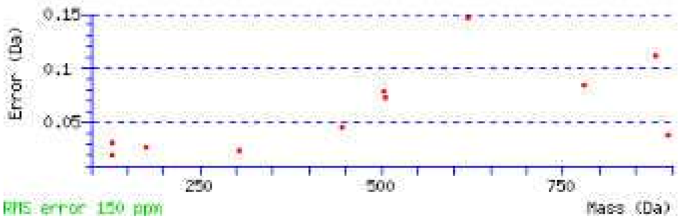
Label all possible matches ○ Label matches used for scoring ●

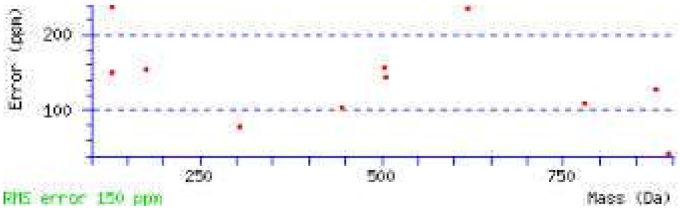
Monoisotopic mass of neutral peptide Mr(calc): 1123.4750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 25 **Expect:** 1.1e+02
Matches : 11/120 fragment ions using 18 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	74.0600	74.0600		56.0495	102.0550		84.0444	44.0495	T						9
2	102.0550	203.1026		185.0921	231.0975		213.0870	145.0972	E	949.3978	948.4026	1023.4346	1006.4081	1005.4241	8
3	88.0393	318.1296		300.1190	346.1245		328.1139	274.1397	D	834.3709	833.3757	***894.3920***	877.3655	876.3815	7
4	133.0430	478.1602		460.1497	506.1551		488.1446	389.1667	C	674.3403	673.3450	***779.3651***	762.3385		6
5	72.0808	577.2286		559.2181	605.2236		587.2130	563.2130	V	575.2718	588.2922	***619.3344***	602.3079		5
6	30.0338	634.2501		616.2395	662.2450		644.2345		G			520.2660	503.2395		4
7	133.0430	794.2808		776.2702	822.2757		804.2651	705.2872	C	358.2197	357.2245	463.2446	446.2180		3
8	101.1073	922.3757	905.3492	904.3652	950.3706	933.3441	932.3601	865.3179	K	230.1248	229.1295	***303.2139***	286.1874		2
9	129.1135								R	74.0237	73.0284	***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ED	217.0819	245.0768	EDC	377.1125	405.1075	EDCV	476.1810	504.1759
EDCVG	533.2024	561.1973	EDCVGC	693.2331	721.2280	DC	248.0700	276.0649
DCV	347.1384	375.1333	DCVG	404.1598	432.1547	DCVGC	564.1905	592.1854
DCVGCK	692.2854	720.2804	CV	232.1114	260.1063	CVG	289.1329	317.1278

CVGC	449.1635	477.1585	**CVGCK**	577.2585	605.2534	**VG**	129.1022	157.0972
VGC	289.1329	317.1278	**VGCK**	417.2279	445.2228	**GC**	190.0645	218.0594
GCK	318.1594	346.1544	**CK**	261.1380	289.1329			





NCBI **BLAST** search of TEDCVGCKR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
26.7	1123.4928	0.0323	ETDMETARR
24.7	1123.4750	0.0500	TEDCVGCKR
24.7	1123.4750	0.0500	TEDCVGCKR
24.7	1123.4750	0.0500	TEDCVGCKR
24.7	1123.4387	0.0864	TEDCVGCQR
24.0	1123.4240	0.1010	DDDFNMDPR
24.0	1123.5873	-0.0623	ETPPLEVSPR
24.0	1123.4894	0.0356	ETPSHDADPR
23.6	1123.5873	-0.0623	ETDYLIKSR
23.6	1123.5332	-0.0082	VMDFEAGLSR

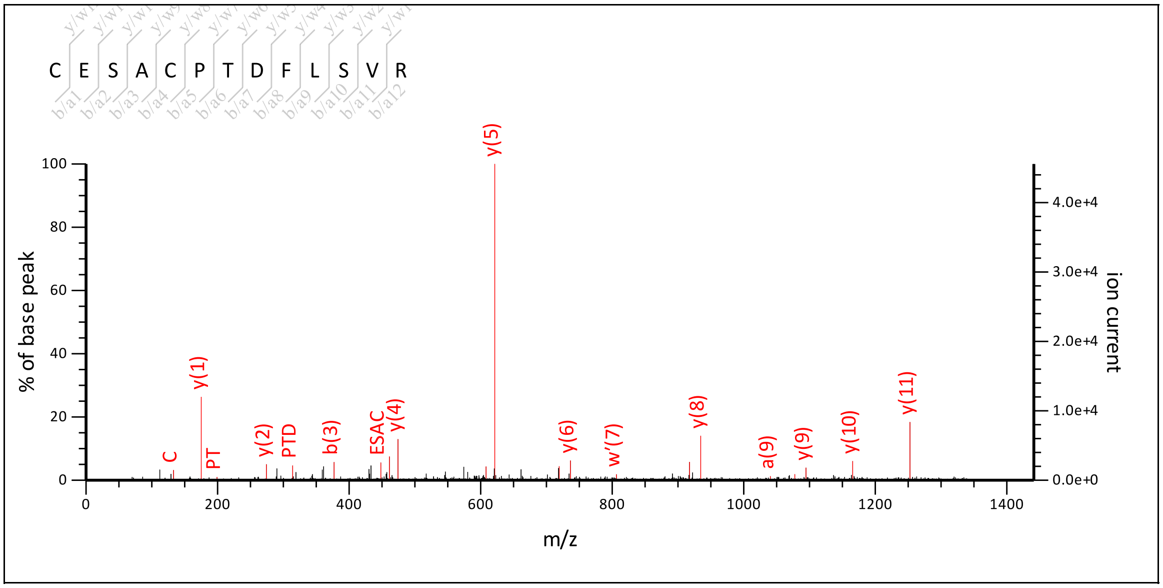
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 144**

MS/MS Fragmentation of **CESACPTDFLSVR**
Found in **gi|11466848** in **NCBInr**, photosystem I subunit VII [Oryza sativa Japonica Group]

Match to Query 266: 1540.737724 from(1541.745000,1+) intensity(0.0000) index(31)
Title: Label: N13, Spot_Id: 219879, Peak_List_Id: 228112, MSMS Job_Run_Id: 21981, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N13_136868255600.txt



0 to 1441.07

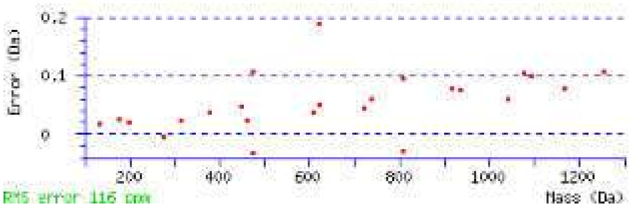
Label all possible matches ○ Label matches used for scoring ●

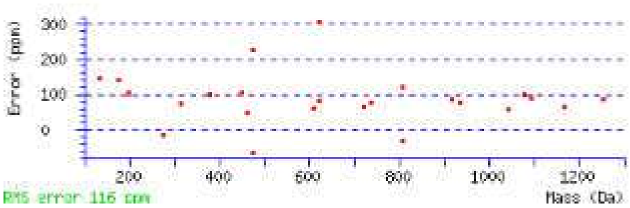
Monoisotopic mass of neutral peptide Mr(calc): 1540.6650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 79 **Expect:** 0.0004
Matches : 27/205 fragment ions using 26 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	133.0430	**133.0430**		161.0379		44.0495		C							13
2	102.0550	262.0856	244.0750	290.0805	272.0700	204.0801		E	1307.6049	1306.6096		1381.6416	1364.6151	1363.6311	12
3	60.0444	349.1176	331.1071	**377.1125**	359.1020	333.1227		S	1220.5728	1219.5776		***1252.5990***	1235.5725	1234.5885	11
4	44.0495	420.1547	402.1442	**448.1497**	430.1391			A	1149.5357			***1165.5670***	1148.5405	1147.5565	10
5	133.0430	580.1854	562.1748	**608.1803**	590.1697	491.1919		C	989.5051	988.5098		***1094.5299***	1077.5034	1076.5193	9
6	70.0651	677.2382	659.2276	705.2331	687.2225	651.2225		P	892.4523	891.4571		***934.4993***	917.4727	916.4887	8
7	74.0600	778.2858	760.2753	**806.2808**	788.2702	762.2909	764.2702	T	791.4046	804.4250	806.4043	837.4465	820.4199	819.4359	7
8	88.0393	893.3128	875.3022	921.3077	903.2971	849.3230		D	676.3777	675.3824		***736.3988***	719.3723	718.3882	6
9	120.0808	**1040.3812**	1022.3706	1068.3761	1050.3655			F	529.3093			***621.3719***	604.3453	603.3613	5
10	86.0964	1153.4653	1135.4547	1181.4602	1163.4496	1111.4183		L	416.2252	415.2300		***474.3035***	457.2769	456.2929	4
11	60.0444	1240.4973	1222.4867	1268.4922	1250.4816	1224.5024		S	329.1932	328.1979		361.2194	344.1928	343.2088	3
12	72.0808	1339.5657	1321.5551	1367.5606	1349.5501	1325.5501		V	230.1248	243.1452		***274.1874***	257.1608		2
13	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ES	189.0870	217.0819	ESA	260.1241	288.1190	ESAC	420.1547	448.1497
ESACP	517.2075	545.2024	ESACPT	618.2552	646.2501	SA	131.0815	159.0764
SAC	291.1122	319.1071	SACP	388.1649	416.1598	SACPT	489.2126	517.2075
SACPTD	604.2395	632.2345	AC	204.0801	232.0750	ACP	301.1329	329.1278

ACPT	402.1806	430.1755	**ACPTD**	517.2075	545.2024	**ACPTDF**	664.2759	692.2708
CP	230.0958	258.0907	**CPT**	331.1435	359.1384	**CPTD**	446.1704	474.1653
CPTDF	593.2388	621.2337	**PT**	171.1128	199.1077	**PTD**	286.1397	314.1347
PTDF	433.2082	461.2031	**PTDFL**	546.2922	574.2871	**PTDFLS**	633.3243	661.3192
TD	189.0870	217.0819	**TDF**	336.1554	364.1503	**TDFL**	449.2395	477.2344
TDFLS	536.2715	564.2664	**TDFLSV**	635.3399	663.3348	**DF**	235.1077	263.1026
DFL	348.1918	376.1867	**DFLS**	435.2238	463.2187	**DFLSV**	534.2922	562.2871
FL	233.1648	261.1598	**FLS**	320.1969	348.1918	**FLSV**	419.2653	447.2602
LS	173.1285	201.1234	**LSV**	272.1969	300.1918	**SV**	159.1128	187.1077





NCBI **BLAST** search of CESACPTDFLSVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
78.9	1540.6650	0.0727	CESACPTDFLSVR
31.3	1540.7522	-0.0144	LFGGNETDYALSVR
29.4	1540.7960	-0.0582	GMELFIVDFLSVR
29.4	1540.7047	0.0330	LRMMEIDMAEVR
27.3	1540.7634	-0.0257	KSGTQFSGPTGYGVR
27.3	1540.6902	0.0476	AMVAEMFGQEVADK
26.9	1540.7331	0.0046	IIDFSDEMTLVDK
26.8	1540.8144	-0.0767	HRPGVSISSMLSVR
25.8	1540.7456	-0.0079	VNYACKQAGIFDR
23.8	1540.7490	-0.0113	MAANNKYQMVISR

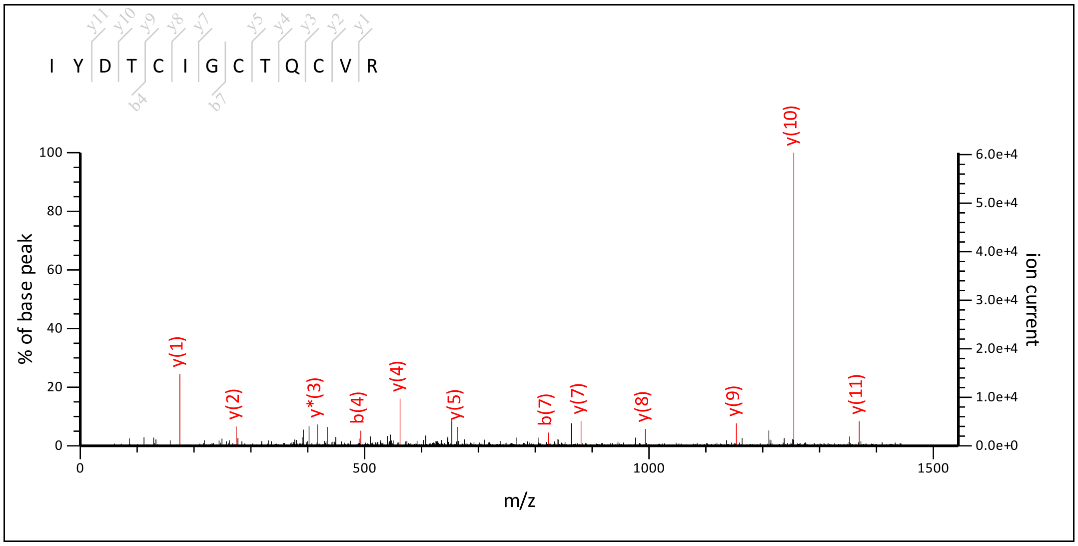
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 144

MS/MS Fragmentation of **IYDTCIGCTQCVR**
Found in **gi|11466848** in **NCBInr**, photosystem I subunit VII [Oryza sativa Japonica Group]

Match to Query 278: 1644.784724 from(1645.792000,1+) intensity(0.0000) index(32)
Title: Label: N13, Spot_Id: 219879, Peak_List_Id: 228111, MSMS Job_Run_Id: 21981, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_N13_136868255600.txt



0 to 1544.04

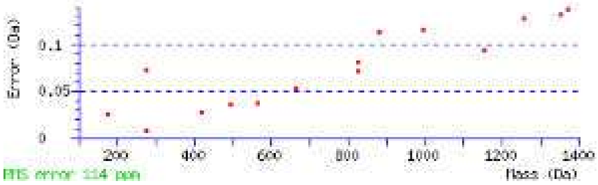
Label all possible matches ○ Label matches used for scoring ●

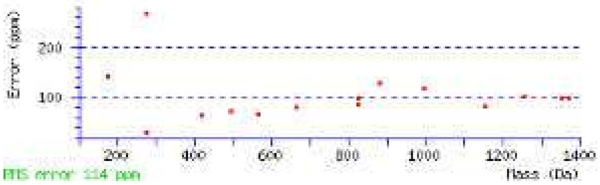
Monoisotopic mass of neutral peptide Mr(calc): 1644.7059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 1.5e-06
Matches : 15/207 fragment ions using 14 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	86.0964	86.0964			114.0913			44.0495		I					
2	136.0757	249.1598			277.1547					Y	1424.5715			1532.6290	1515.6025
3	88.0393	364.1867		346.1761	392.1816		374.1710	320.1969		D	1309.5446	1308.5493		***1369.5657***	1352.5392
4	74.0600	465.2344		447.2238	**493.2293**		475.2187	449.2395	451.2187	T	1208.4969	1221.5173	1223.4966	***1254.5388***	1237.5122
5	133.0430	625.2650		607.2545	653.2599		635.2494	536.2715		C	1048.4663	1047.4710		***1153.4911***	1136.4645
6	86.0964	738.3491		720.3385	766.3440		748.3334	710.3178	724.3334	I	935.3822	948.4026	962.4183	***993.4604***	976.4339
7	30.0338	795.3706		777.3600	**823.3655**		805.3549			G				***880.3764***	863.3498
8	133.0430	955.4012		937.3906	983.3961		965.3856	866.4077		C	718.3301	717.3348		***823.3549***	806.3284
9	74.0600	1056.4489		1038.4383	1084.4438		1066.4332	1040.4540	1042.4332	T	617.2824	630.3028	632.2821	***663.3243***	646.2977
10	101.0709	1184.5075	1167.4809	1166.4969	1212.5024	1195.4758	1194.4918	1127.4860		Q	489.2238	488.2286		***562.2766***	545.2500
11	133.0430	1344.5381	1327.5116	1326.5275	1372.5330	1355.5065	1354.5225	1255.5446		C	329.1932	328.1979		434.2180	417.1915
12	72.0808	1443.6065	1426.5800	1425.5960	1471.6014	1454.5749	1453.5909	1429.5909		V	230.1248	243.1452		***274.1874***	257.1608
13	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YD	251.1026	279.0975	YDT	352.1503	380.1452	YDTC	512.1810	540.1759
YDTCI	625.2650	653.2599	YDTCIG	682.2865	710.2814	DT	189.0870	217.0819
DTC	349.1176	377.1125	DTCI	462.2017	490.1966	DTCIG	519.2232	547.2181
DTCIGC	679.2538	707.2487	TC	234.0907	262.0856	TCI	347.1748	375.1697
TCIG	404.1962	432.1911	TCIGC	564.2269	592.2218	TCIGCT	665.2745	693.2695
CI	246.1271	274.1220	CIG	303.1485	331.1435	CIGC	463.1792	491.1741
CIGCT	564.2269	592.2218	CIGCTQ	692.2854	720.2804	IG	143.1179	171.1128
IGC	303.1485	331.1435	IGCT	404.1962	432.1911	IGCTQ	532.2548	560.2497

IGCTQC	692.2854	720.2804	**GC**	190.0645	218.0594	**GCT**	291.1122	319.1071
GCTQ	419.1707	447.1656	**GCTQC**	579.2014	607.1963	**GCTQCV**	678.2698	706.2647
CT	234.0907	262.0856	**CTQ**	362.1493	390.1442	**CTQC**	522.1799	550.1748
CTQCV	621.2483	649.2432	**TQ**	202.1186	230.1135	**TQC**	362.1493	390.1442
TQCV	461.2177	489.2126	**QC**	261.1016	289.0965	**QCV**	360.1700	388.1649
CV	232.1114	260.1063						





NCBI **BLAST** search of IYDTCIGCTQCVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
103.3	1644.7059	0.0789	IYDTCIGCTQCVR
32.1	1644.7532	0.0315	FEDNFINNAFTTGR
26.5	1644.6834	0.1013	DEFTCIASCSMLPV
26.3	1644.9199	-0.1352	KLKPEGNLLYDTVR
25.1	1644.8584	-0.0736	VPPSERFGLTTAQSR
24.5	1644.7995	-0.0148	YEVTKTTQDYEIR
24.4	1644.8181	-0.0334	DTGMTFLEYVSKVR
24.4	1644.7025	0.0822	DDWFVCGMRSSGTK
24.3	1644.7236	0.0611	LYDCTLDATDMRR
22.0	1644.7453	0.0394	MEDFNIYKDIADR

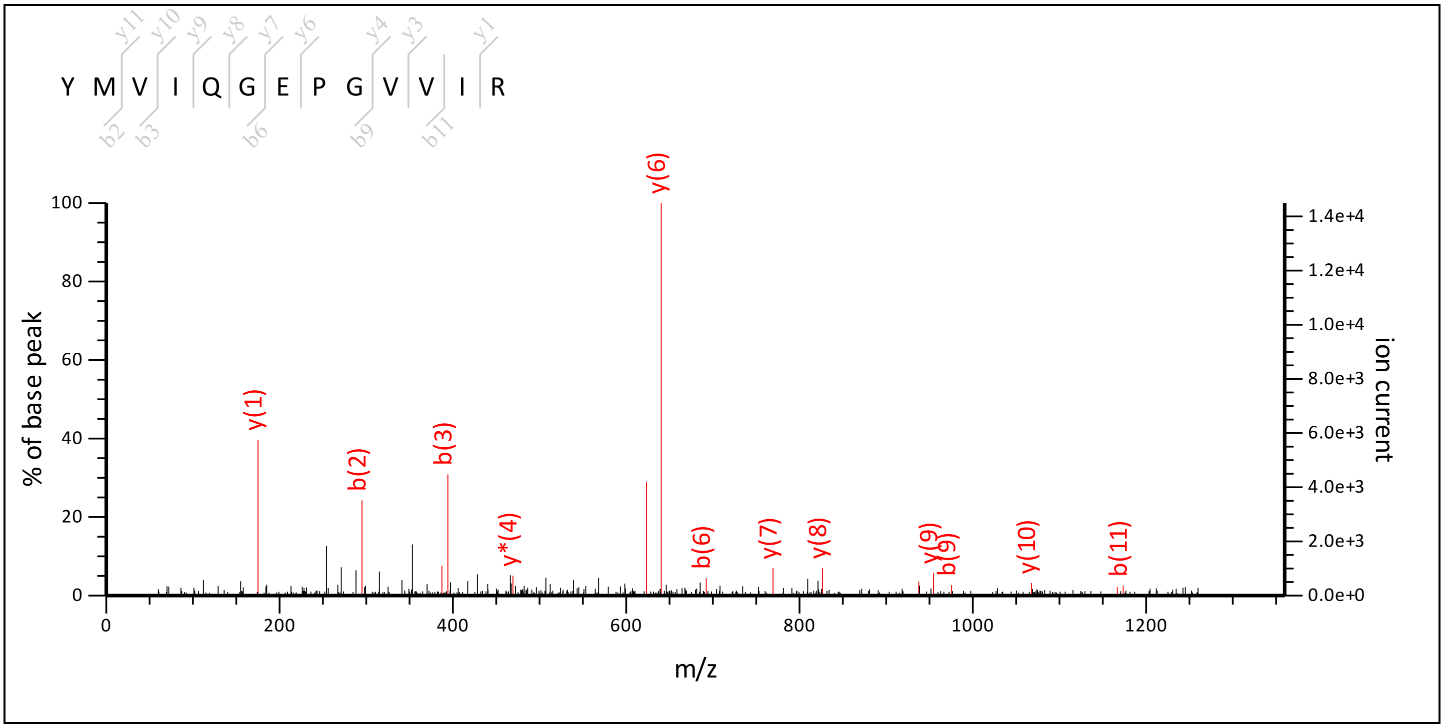
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 147

MS/MS Fragmentation of **YMVIQGEPGVVIR**
Found in **gi|115466468** in **NCBInr**, Os06g0152100 [Oryza sativa Japonica Group]

Match to Query 10: 1459.820824 from(1460.828100,1+) intensity(0.0000) index(9)
Title: Label: B9, Spot_Id: 219803, Peak_List_Id: 226603, MSMS Job_Run_Id: 21850, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B9_136859937100.txt



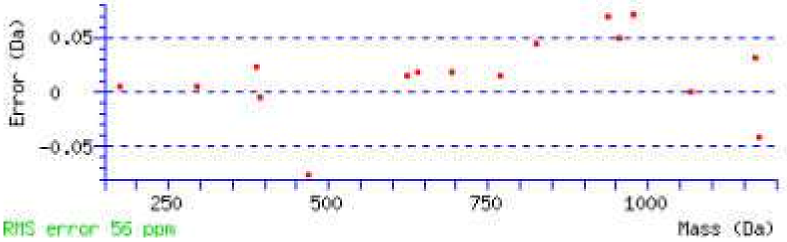
0 to 1359.91

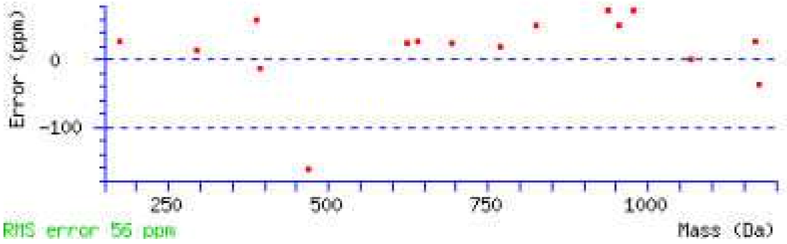
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1459.7857
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 0.0026
Matches : 16/64 fragment ions using 24 most intense peaks (help)

#	a	a*	b	b*	Seq.	y	y*	#
1	136.0757		164.0706		**Y**			**13**
2	267.1162		***295.1111***		**M**	1297.7297	1280.7031	**12**
3	366.1846		***394.1795***		**V**	***1166.6892***	1149.6626	**11**
4	479.2687		507.2636		**I**	***1067.6208***	1050.5942	**10**
5	607.3272	590.3007	635.3221	618.2956	**Q**	***954.5367***	937.5102	**9**
6	664.3487	647.3221	***692.3436***	675.3171	**G**	***826.4781***	809.4516	**8**
7	793.3913	776.3647	821.3862	804.3597	**E**	***769.4567***	752.4301	**7**
8	890.4441	873.4175	918.4390	901.4124	**P**	***640.4141***	623.3875	**6**

9	947.4655	930.4390	***975.4604***	958.4339	G	543.3613	526.3348	5
10	1046.5339	1029.5074	1074.5288	1057.5023	V	486.3398	469.3133	4
11	1145.6023	1128.5758	***1173.5973***	1156.5707	V	***387.2714***	370.2449	3
12	1258.6864	1241.6599	1286.6813	1269.6548	I	288.2030	271.1765	2
13					R	***175.1190***	158.0924	1





NCBI **BLAST** search of YMVIQGEPGVVIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
58.5	1459.7857	0.0351	YMVIQGEPGVVIR
36.3	1459.7857	0.0351	YMVLQGDPGIVIR
20.7	1459.7969	0.0239	YMVIRGEPGAVIR
12.8	1459.7307	0.0901	LSSFVSISSSSFGR
11.2	1459.6991	0.1218	TSVPRVWAGGDCR
9.0	1459.7341	0.0868	VVEAAVAEQGLCSK
8.8	1459.7130	0.1079	DVDVGWPGIMSIR
7.2	1459.7055	0.1153	SPSPPPEEQISHR
6.6	1459.8618	-0.0410	MVMKLKPSILIR
6.6	1459.7897	0.0311	VMYLFVEYKLR

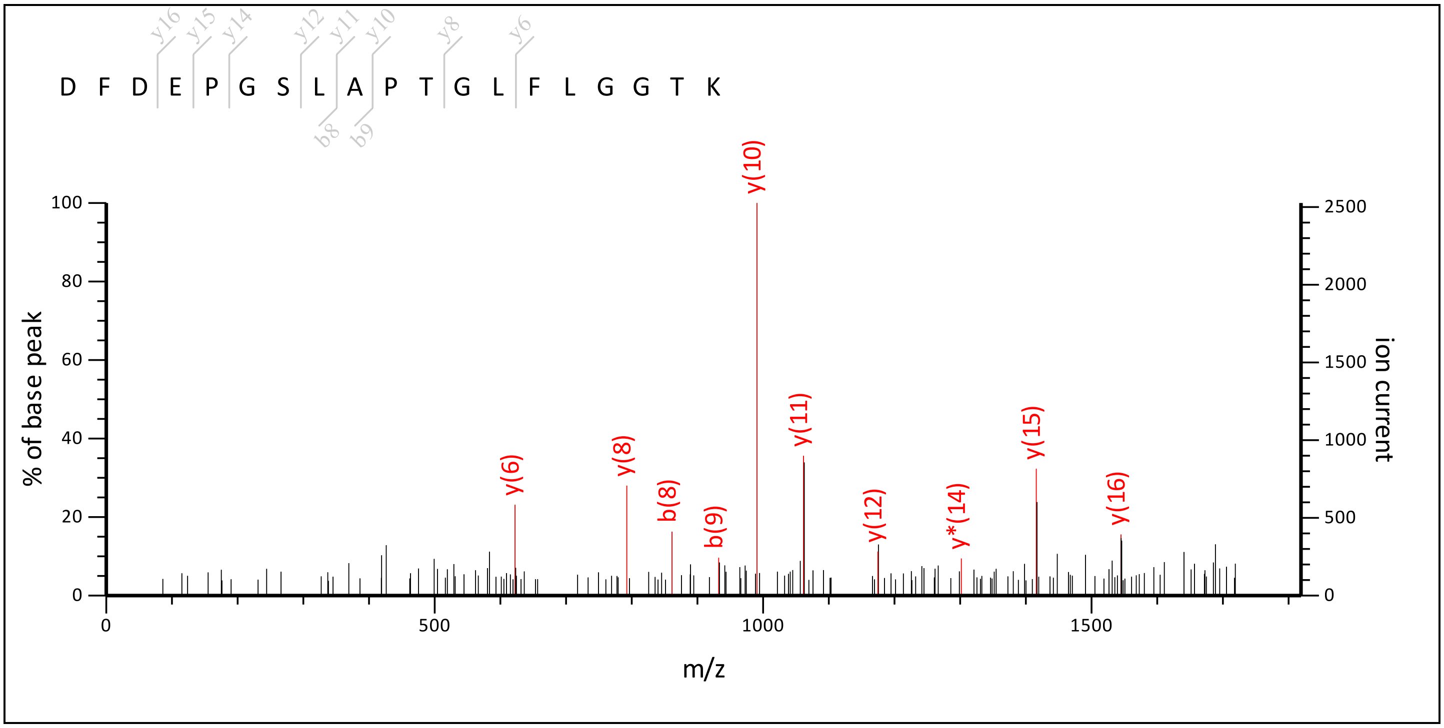
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 147

MS/MS Fragmentation of **DFDEPGSLAPTGLFLGGTK**
Found in **gi|115466468** in **NCBInr**, Os06g0152100 [Oryza sativa Japonica Group]

Match to Query 17: 1920.978924 from(1921.986200,1+) intensity(0.0000) index(12)
Title: Label: B9, Spot_Id: 219803, Peak_List_Id: 226607, MSMS Job_Run_Id: 21850, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_B9_136859937100.txt



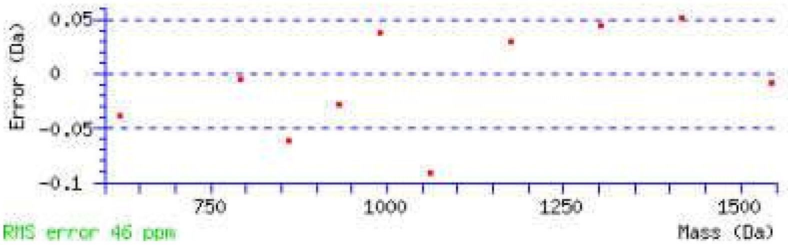
0 to 1818.87

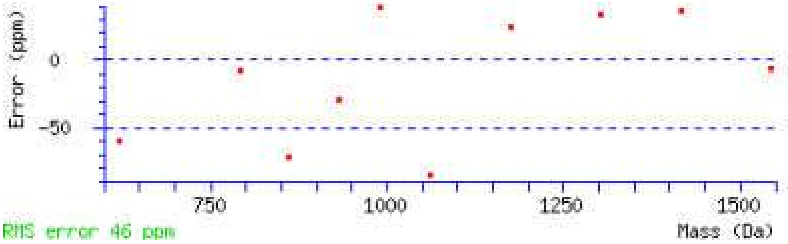
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1920.9469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 18 **Expect:** 24
Matches : 10/72 fragment ions using 34 most intense peaks (help)

#	a	b	Seq.	y	y*	#
1	88.0393	116.0342	D			19
2	235.1077	263.1026	F	1806.9272	1789.9007	18
3	350.1347	378.1296	D	1659.8588	1642.8323	17
4	479.1773	507.1722	E	*1544.8319*	1527.8053	16
5	576.2300	604.2249	P	*1415.7893*	1398.7627	15
6	633.2515	661.2464	G	1318.7365	1301.7100	14
7	720.2835	748.2784	S	1261.7151	1244.6885	13
8	833.3676	**861.3625**	L	*1174.6830*	1157.6565	12

9	904.4047	**932.3996**	A	***1061.5990***	1044.5724	11
10	1001.4575	1029.4524	P	***990.5619***	973.5353	10
11	1102.5051	1130.5000	T	893.5091	876.4825	9
12	1159.5266	1187.5215	G	***792.4614***	775.4349	8
13	1272.6107	1300.6056	L	735.4400	718.4134	7
14	1419.6791	1447.6740	F	***622.3559***	605.3293	6
15	1532.7631	1560.7581	L	475.2875	458.2609	5
16	1589.7846	1617.7795	G	362.2034	345.1769	4
17	1646.8061	1674.8010	G	305.1819	288.1554	3
18	1747.8537	1775.8487	T	248.1605	231.1339	2
19			K	147.1128	130.0863	1





NCBI **BLAST** search of DFDEPGSLAPTGLFLGGTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
18.2	1920.9469	0.0320	DFDEPGSLAPTGLFLGGTK
7.4	1920.9792	-0.0003	ETFEELKIGSDGSLLQR
5.8	1920.8822	0.0967	MGPNGQFIAGTAMTAPADR
3.9	1920.8861	0.0928	MNGGGGQRGTYGSGPPSGLR
1.5	1921.0673	-0.0883	SSIFDAKAGIALNLNFIK
1.3	1920.9945	-0.0156	YLTVAEAIEWNKTIDR
1.1	1920.8735	0.1055	GSVEENTSEGALANMGDLK
1.0	1920.8935	0.0855	CLTGSGMPGAGNPAGAGPPPR
0.8	1920.8822	0.0967	WICGLCAEAIKDENSR
0.7	1920.9945	-0.0156	TIDANQAFAEIGNFLIGK

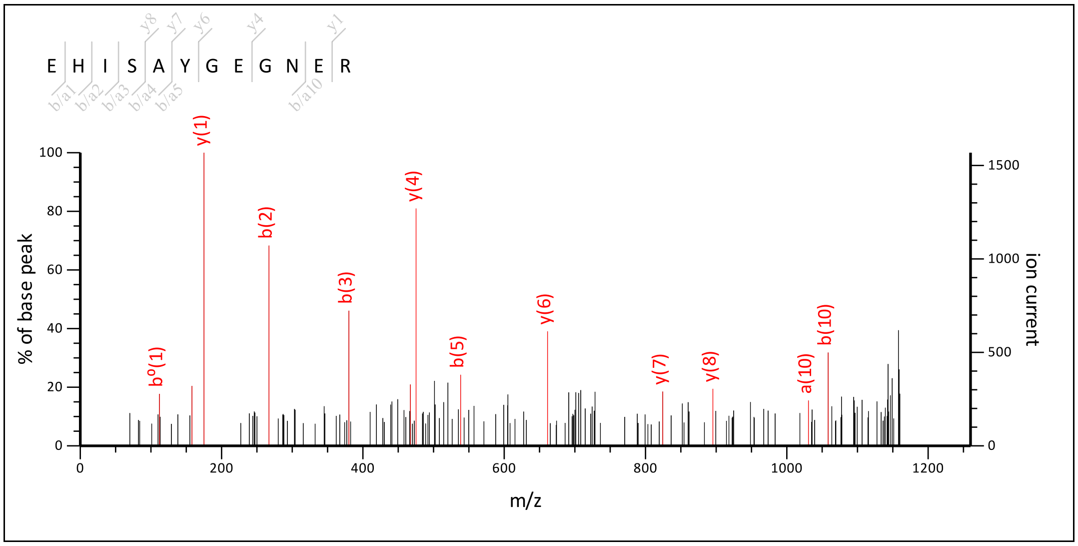
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 148

MS/MS Fragmentation of **EHISAYGEGNER**
Found in **gi|146741370** in **NCBInr**, glutamine synthetase [Avicennia marina]

Match to Query 42: 1360.585724 from(1361.593000,1+) intensity(0.0000) index(14)
Title: Label: F3, Spot_Id: 219711, Peak_List_Id: 225288, MSMS Job_Run_Id: 21772, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_F3_136842142900.txt



0 to 1260.01

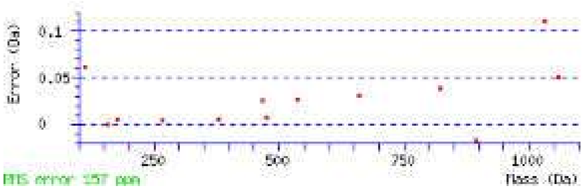
Label all possible matches ○ Label matches used for scoring ●

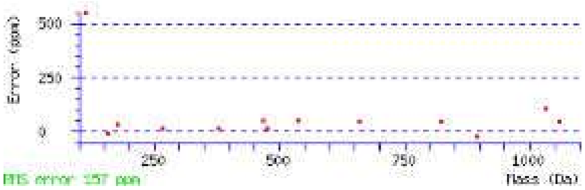
Monoisotopic mass of neutral peptide Mr(calc): 1360.6007
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.61
Matches : 13/190 fragment ions using 22 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	102.0550	102.0550		84.0444	130.0499		112.0393	44.0495		E						
2	110.0713	239.1139		221.1033	***267.1088***		249.0982			H	1150.5123			1232.5654	1215.5389	12
3	86.0964	352.1979		334.1874	***380.1928***		362.1823	324.1666	338.1823	I	1037.4283	1050.4487	1064.4643	1095.5065	1078.4800	10
4	60.0444	439.2300		421.2194	***467.2249***		449.2143	423.2350		S	950.3963	949.4010		982.4225	965.3959	96
5	44.0495	510.2671		492.2565	***538.2620***		520.2514			A	879.3591			***895.3904***	878.3639	87
6	136.0757	673.3304		655.3198	701.3253		683.3148			Y	716.2958			***824.3533***	807.3268	80
7	30.0338	730.3519		712.3413	758.3468		740.3362			G				***661.2900***	644.2634	64
8	102.0550	859.3945		841.3839	887.3894		869.3788	801.3890		E	530.2318	529.2365		604.2685	587.2420	58
9	30.0338	916.4159		898.4054	944.4108		926.4003			G				***475.2259***	458.1994	45
10	87.0553	1030.4588	1013.4323	1012.4483	***1058.4538***	1041.4272	1040.4432	987.4530		N	359.1674	358.1721		418.2045	401.1779	40
11	102.0550	1159.5014	1142.4749	1141.4909	1187.4964	1170.4698	1169.4858	1101.4960		E	230.1248	229.1295		304.1615	287.1350	28
12	129.1135									R	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HI	223.1553	251.1503	HIS	310.1874	338.1823	HISA	381.2245	409.2194
HISAY	544.2878	572.2827	HISAYG	601.3093	629.3042	IS	173.1285	201.1234
ISA	244.1656	272.1605	ISAY	407.2289	435.2238	ISAYG	464.2504	492.2453
ISAYGE	593.2930	621.2879	ISAYGEG	650.3144	678.3093	SA	131.0815	159.0764
SAY	294.1448	322.1397	SAYG	351.1663	379.1612	SAYGE	480.2089	508.2038
SAYGEG	537.2304	565.2253	SAYGEGN	651.2733	679.2682	AY	207.1128	235.1077
AYG	264.1343	292.1292	AYGE	393.1769	421.1718	AYGEG	450.1983	478.1932
AYGEGN	564.2413	592.2362	AYGEGNE	693.2838	721.2788	YG	193.0972	221.0921
YGE	322.1397	350.1347	YGEG	379.1612	407.1561	YGEGN	493.2041	521.1991

YGEGNE	622.2467	650.2416	**GE**	159.0764	187.0713	**GEG**	216.0979	244.0928
GEGN	330.1408	358.1357	**GEGNE**	459.1834	487.1783	**EG**	159.0764	187.0713
EGN	273.1193	301.1143	**EGNE**	402.1619	430.1569	**GN**	144.0768	172.0717
GNE	273.1193	301.1143	**NE**	216.0979	244.0928			





NCBI **BLAST** search of EHISAYGEGNER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
34.2	1360.6007	-0.0150	EHISAYGEGNER
21.5	1360.6007	-0.0150	EHIASYGEGNER
13.1	1360.6524	-0.0667	RFYFSTNSSPR
12.8	1360.5969	-0.0112	AYMLDVDAYER
12.5	1360.6405	-0.0548	TTTSMHGDIGVAR
9.4	1360.6775	-0.0918	EHEAAIEFFLR
8.8	1360.6582	-0.0725	EKSTSQAPQTER
8.8	1360.5686	0.0171	SMTMARECGFR
8.8	1360.5686	0.0171	SMTMARECGFR
8.0	1360.5870	-0.0013	NMFEYSNWVR

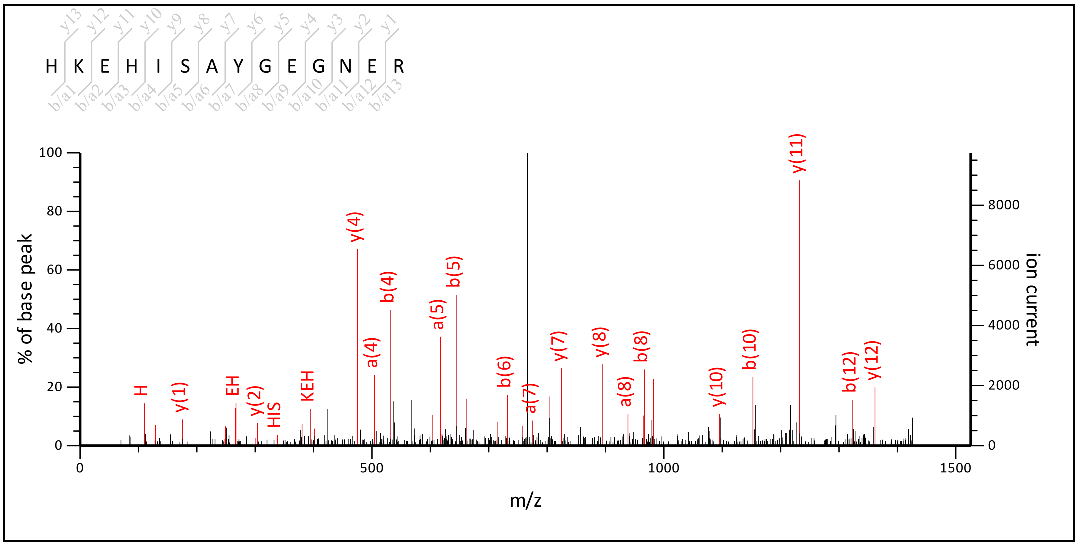
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 148

MS/MS Fragmentation of **HKEHISAYGEGNER**
Found in **gi|146741370** in **NCBInr**, glutamine synthetase [Avicennia marina]

Match to Query 68: 1625.733124 from(1626.740400,1+) intensity(0.0000) index(25)
Title: Label: F3, Spot_Id: 219711, Peak_List_Id: 225282, MSMS Job_Run_Id: 21772, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_F3_136842142900.txt



0 to 1525.63

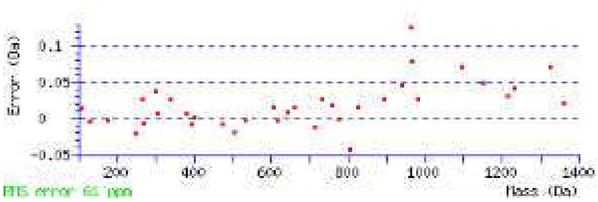
Label all possible matches ○ Label matches used for scoring ●

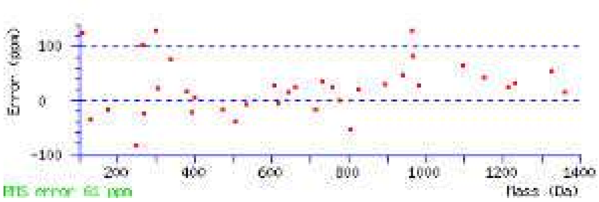
```
Monoisotopic mass of neutral peptide Mr(calc): 1625.7546
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 77  Expect: 2.8e-05
Matches : 40/247 fragment ions using 56 most intense peaks   (help)
```

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	
1	110.0713	**110.0713**			138.0662			44.0495		**H**						
2	101.1073	238.1662	221.1397		**266.1612**	249.1346		181.1084		**K**	1416.6138	1415.6186		1489.7030	1472.6764	14
3	102.0550	367.2088	350.1823	349.1983	**395.2037**	378.1772	377.1932	309.2034		**E**	1287.5713	1286.5760		***1361.6080***	1344.5815	13
4	110.0713	**504.2677**	487.2412	486.2572	**532.2627**	515.2361	514.2521			**H**	1150.5123			***1232.5654***	1215.5389	12
5	86.0964	**617.3518**	600.3253	599.3412	**645.3467**	628.3202	627.3362	589.3205	603.3362	**I**	1037.4283	1050.4487	1064.4643	***1095.5065***	1078.4800	10
6	60.0444	704.3838	687.3573	686.3733	**732.3787**	715.3522	714.3682	688.3889		**S**	950.3962	949.4010		***982.4225***	965.3959	9
7	44.0495	**775.4209**	758.3944	757.4104	**803.4159**	786.3893	785.4053			**A**	879.3591			***895.3904***	878.3639	8
8	136.0757	**938.4843**	921.4577	920.4737	**966.4792**	949.4526	948.4686			**Y**	716.2958			***824.3533***	807.3268	8
9	30.0338	995.5057	978.4792	977.4952	1023.5007	1006.4741	1005.4901			**G**				***661.2900***	644.2634	6
10	102.0550	1124.5483	1107.5218	1106.5378	**1152.5432**	1135.5167	1134.5327	1066.5429		**E**	530.2317	529.2365		***604.2685***	587.2420	5
11	30.0338	1181.5698	1164.5432	1163.5592	1209.5647	1192.5382	1191.5541			**G**				***475.2259***	458.1994	4
12	87.0553	1295.6127	1278.5862	1277.6022	**1323.6076**	1306.5811	1305.5971	1252.6069		**N**	359.1674	358.1721		418.2045	401.1779	4
13	102.0550	1424.6553	1407.6288	1406.6448	1452.6502	1435.6237	1434.6397	1366.6498		**E**	230.1248	229.1295		***304.1615***	287.1350	2
14	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924	

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KE	230.1499	258.1448	**KEH**	367.2088	395.2037	**KEHI**	480.2929	508.2878
KEHIS	567.3249	595.3198	**KEHISA**	638.3620	666.3569	**EH**	239.1139	267.1088
EHI	352.1979	380.1928	**EHIS**	439.2300	467.2249	**EHISA**	510.2671	538.2620
EHISAY	673.3304	701.3253	**HI**	223.1553	251.1503	**HIS**	310.1874	338.1823
HISA	381.2245	409.2194	**HISAY**	544.2878	572.2827	**HISAYG**	601.3093	629.3042
IS	173.1285	201.1234	**ISA**	244.1656	272.1605	**ISAY**	407.2289	435.2238
ISAYG	464.2504	492.2453	**ISAYGE**	593.2930	621.2879	**ISAYGEG**	650.3144	678.3093

SA	131.0815	159.0764	**SAY**	294.1448	322.1397	**SAYG**	351.1663	379.1612
SAYGE	480.2089	508.2038	**SAYGEG**	537.2304	565.2253	**SAYGEGN**	651.2733	679.2682
AY	207.1128	235.1077	**AYG**	264.1343	292.1292	**AYGE**	393.1769	421.1718
AYGEG	450.1983	478.1932	**AYGEGN**	564.2413	592.2362	**AYGEGNE**	693.2838	721.2788
YG	193.0972	221.0921	**YGE**	322.1397	350.1347	**YGEG**	379.1612	407.1561
YGEGN	493.2041	521.1991	**YGEGNE**	622.2467	650.2416	**GE**	159.0764	187.0713
GEG	216.0979	244.0928	**GEGN**	330.1408	358.1357	**GEGNE**	459.1834	487.1783
EG	159.0764	187.0713	**EGN**	273.1193	301.1143	**EGNE**	402.1619	430.1569
GN	144.0768	172.0717	**GNE**	273.1193	301.1143	**NE**	216.0979	244.0928





NCBI **BLAST** search of HKEHISAYGEGNER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
77.4	1625.7546	-0.0215	HKEHISAYGEGNER
61.9	1625.7546	-0.0215	HKEHIASYGEGNER
22.3	1625.7937	-0.0606	FDIVIGSELAYDER
19.0	1625.7579	-0.0248	RHEAMQAAAAAGADEK
16.3	1625.8162	-0.0830	QGHGVWTEAESVAKK
14.4	1625.8460	-0.1129	HASVATWAAAKMQVR
13.0	1625.7250	0.0081	SGGRSTVSAMAVDGCR
11.9	1625.7005	0.0327	GRAEADNFMSHGYR
10.0	1625.7579	-0.0248	MSPEALEHAARNER
9.3	1625.7607	-0.0276	SDFTDMLLSIQNDK

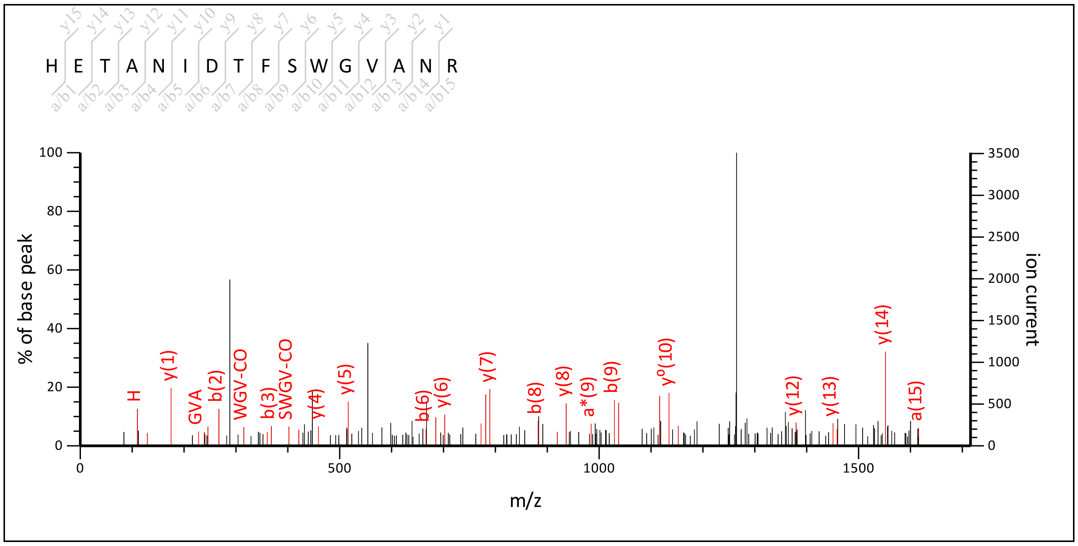
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View **Spot no 148**

MS/MS Fragmentation of **HETANIDTFSWGVANR**
Found in **gi|146741370** in **NCBInr**, glutamine synthetase [Avicennia marina]

Match to Query 81: 1816.824524 from(1817.831800,1+) intensity(0.0000) index(30)
Title: Label: F3, Spot_Id: 219711, Peak_List_Id: 225286, MSMS Job_Run_Id: 21772, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\farah BHU\spot set plate\Farah-Garima 11May 2013\ppw_F3_136842142900.txt



0 to 1715.77

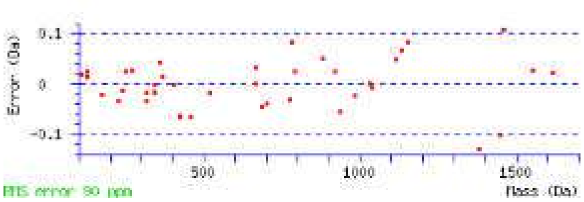
Label all possible matches ○ Label matches used for scoring ●

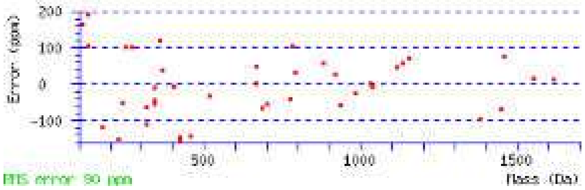
Monoisotopic mass of neutral peptide Mr(calc): `1816.8493`
Fixed modifications: `Carbamidomethyl (C) (apply to specified residues or termini only)`
Ions Score: `57` **Expect:** `0.0029`
Matches : `43/283 fragment ions using 80 most intense peaks` (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	110.0713	**110.0713**			138.0662			44.0495		**H**					
2	102.0550	**239.1139**		221.1033	**267.1088**		249.0982	181.1084		**E**	1606.7608	1605.7656		1680.7976	1663.7711
3	74.0600	340.1615		322.1510	**368.1565**		350.1459	324.1666	326.1459	**T**	1505.7132	1518.7336	1520.7128	***1551.7550***	1534.7285
4	44.0495	411.1987		393.1881	439.1936		421.1830			**A**	1434.6761			***1450.7074***	1433.6808
5	87.0553	525.2416	508.2150	507.2310	553.2365	536.2100	535.2259	482.2358		**N**	1320.6331	1319.6379		***1379.6702***	1362.6437
6	86.0964	638.3256	621.2991	620.3151	**666.3206**	649.2940	648.3100	610.2943	624.3100	**I**	1207.5491	1220.5695	1234.5851	1265.6273	1248.6008
7	88.0393	753.3526	736.3260	735.3420	**781.3475**	764.3210	763.3369	709.3628		**D**	1092.5221	1091.5269		***1152.5432***	1135.5167
8	74.0600	854.4003	837.3737	836.3897	**882.3952**	865.3686	864.3846	838.4054	840.3846	**T**	991.4744	1004.4948	1006.4741	***1037.5163***	1020.4898
9	120.0808	1001.4687	984.4421	983.4581	**1029.4636**	1012.4371	1011.4530			**F**	844.4060			***936.4686***	919.4421
10	60.0444	1088.5007	1071.4742	1070.4901	**1116.4956**	1099.4691	1098.4851	1072.5058		**S**	757.3740	756.3787		***789.4002***	772.3737
11	159.0917	1274.5800	1257.5535	1256.5695	1302.5749	1285.5484	1284.5644			**W**	571.2947			***702.3682***	685.3416
12	30.0338	1331.6015	1314.5749	1313.5909	1359.5964	1342.5699	1341.5858			**G**				***516.2889***	499.2623
13	72.0808	1430.6699	1413.6434	1412.6593	**1458.6648**	1441.6383	1440.6543	1416.6543		**V**	415.2048	428.2252		***459.2674***	442.2409
14	44.0495	1501.7070	1484.6805	1483.6965	1529.7019	1512.6754	1511.6914			**A**	344.1677			***360.1990***	343.1724
15	87.0553	**1615.7499**	1598.7234	1597.7394	1643.7449	1626.7183	1625.7343	1572.7441		**N**	230.1248	229.1295		289.1619	272.1353
16	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ET	203.1026	231.0975	**ETA**	274.1397	302.1347	**ETAN**	388.1827	416.1776
ETANI	501.2667	529.2617	**ETANID**	616.2937	644.2886	**TA**	145.0972	173.0921
TAN	259.1401	287.1350	**TANI**	372.2241	400.2191	**TANID**	487.2511	515.2460
TANIDT	588.2988	616.2937	**AN**	158.0924	186.0873	**ANI**	271.1765	299.1714
ANID	386.2034	414.1983	**ANIDT**	487.2511	515.2460	**ANIDTF**	634.3195	662.3144

NI	200.1394	228.1343	**NID**	315.1663	343.1612	**NIDT**	416.2140	444.2089
NIDTF	563.2824	591.2773	**NIDTFS**	650.3144	678.3093	**ID**	201.1234	229.1183
IDT	302.1710	330.1660	**IDTF**	449.2395	477.2344	**IDTFS**	536.2715	564.2664
DT	189.0870	217.0819	**DTF**	336.1554	364.1503	**DTFS**	423.1874	451.1823
DTFSW	609.2667	637.2617	**DTFSWG**	666.2882	694.2831	**TF**	221.1285	249.1234
TFS	308.1605	336.1554	**TFSW**	494.2398	522.2347	**TFSWG**	551.2613	579.2562
TFSWGV	650.3297	678.3246	**FS**	207.1128	235.1077	**FSW**	393.1921	421.1870
FSWG	450.2136	478.2085	**FSWGV**	549.2820	577.2769	**FSWGVA**	620.3191	648.3140
SW	246.1237	274.1186	**SWG**	303.1452	331.1401	**SWGV**	402.2136	430.2085
SWGVA	473.2507	501.2456	**SWGVAN**	587.2936	615.2885	**WG**	216.1131	244.1081
WGV	315.1816	343.1765	**WGVA**	386.2187	414.2136	**WGVAN**	500.2616	528.2565
GV	129.1022	157.0972	**GVA**	200.1394	228.1343	**GVAN**	314.1823	342.1772
VA	143.1179	171.1128	**VAN**	257.1608	285.1557	**AN**	158.0924	186.0873





NCBI **BLAST** search of HETANIDTFSWGVANR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
62.6	1816.8493	-0.0247	HETADINTFSWGVANR
57.4	1816.8493	-0.0247	HETANIDTFSWGVANR
38.3	1816.8856	-0.0611	HETASIDKFSWGVANR
38.3	1816.8493	-0.0247	HETASIDQFSWGVANR
15.4	1816.9254	-0.1009	VTSATLCASKPFHTAAR
11.5	1816.8335	-0.0090	DSMFECLESIKVTSR
10.2	1816.9795	-0.1550	SLKKPLSSTSVGNWSAR
10.1	1816.8964	-0.0719	YTMVSAPQSIMAPHLR
9.9	1816.9908	-0.1662	GLNLRPHQISDEGLLR
9.8	1816.8858	-0.0613	MASSTAAPPMRPCRLR

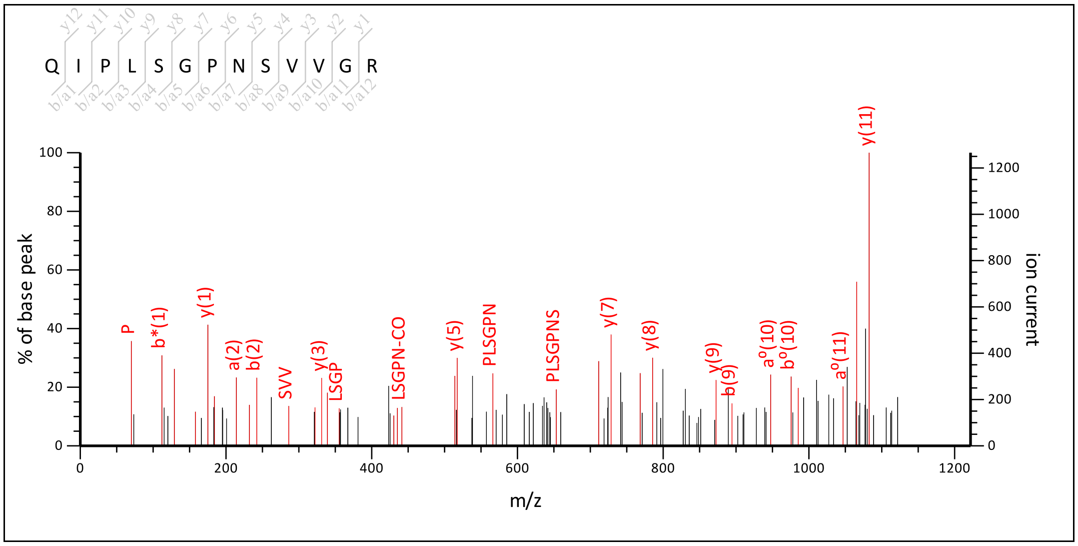
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 151

MS/MS Fragmentation of **QIPLSGPNSVVGR**
Found in **gi|42408425** in **NCBInr**, putative superoxide dismutase [Cu-Zn], chloroplast precursor [Oryza sativa Japonica Group]

Match to Query 26: 1322.758124 from(1323.765400,1+) intensity(0.0000) index(8)
Title: Label: M10, Spot_Id: 219830, Peak_List_Id: 226964, MSMS Job_Run_Id: 21862, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M10_136859956100.txt



0 to 1221.84

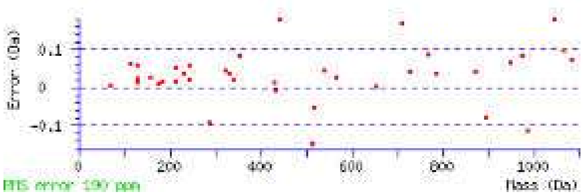
Label all possible matches ○ Label matches used for scoring ●

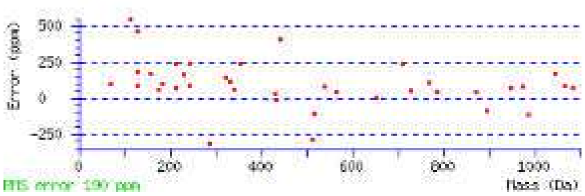
Monoisotopic mass of neutral peptide Mr(calc): 1322.7307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 0.05
Matches : 40/233 fragment ions using 66 most intense peaks (help)

#	Immon.	a	a*	a⁰	b	b*	b⁰	d	d'	Seq.	v	w	w'	y	y*
1	101.0709	101.0709	84.0444		**129.0659**	112.0393		44.0495		**Q**					
2	86.0964	214.1550	197.1285		**242.1499**	225.1234		186.1237	200.1394	**I**	1137.6011	1150.6215	1164.6371	1195.6793	1178.6528
3	70.0651	311.2078	294.1812		**339.2027**	322.1761		285.1921		**P**	1040.5483	1039.5531		***1082.5953***	1065.5687
4	86.0964	424.2918	407.2653		452.2867	435.2602		382.2449		**L**	927.4643	926.4690		***985.5425***	968.5160
5	60.0444	511.3239	494.2973	493.3133	539.3188	522.2922	521.3082	495.3289		**S**	840.4322	839.4370		***872.4585***	855.4319
6	30.0338	568.3453	551.3188	550.3348	596.3402	579.3137	578.3297			**G**				***785.4264***	768.3999
7	70.0651	665.3981	648.3715	647.3875	693.3930	676.3665	675.3824	639.3824		**P**	686.3580	685.3628		***728.4050***	711.3784
8	87.0553	779.4410	762.4145	761.4304	807.4359	790.4094	789.4254	736.4352		**N**	572.3151	571.3198		631.3522	614.3256
9	60.0444	866.4730	849.4465	848.4625	**894.4680**	877.4414	876.4574	850.4781		**S**	485.2831	484.2878		***517.3093***	500.2827
10	72.0808	965.5415	948.5149	947.5309	993.5364	976.5098	975.5258	951.5258		**V**	386.2146	399.2350		***430.2772***	413.2507
11	72.0808	1064.6099	1047.5833	1046.5993	1092.6048	1075.5782	1074.5942	1050.5942		**V**	287.1462	300.1666		***331.2088***	314.1823
12	30.0338	1121.6313	1104.6048	1103.6208	1149.6262	1132.5997	1131.6157			**G**				***232.1404***	215.1139
13	129.1135									**R**	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IP	183.1492	211.1441	**IPL**	296.2333	324.2282	**IPLS**	383.2653	411.2602
IPLSG	440.2867	468.2817	**IPLSGP**	537.3395	565.3344	**IPLSGPN**	651.3824	679.3774
PL	183.1492	211.1441	**PLS**	270.1812	298.1761	**PLSG**	327.2027	355.1976
PLSGP	424.2554	452.2504	**PLSGPN**	538.2984	566.2933	**PLSGPNS**	625.3304	653.3253
LS	173.1285	201.1234	**LSG**	230.1499	258.1448	**LSGP**	327.2027	355.1976
LSGPN	441.2456	469.2405	**LSGPNS**	528.2776	556.2726	**LSGPNSV**	627.3460	655.3410
SG	117.0659	145.0608	**SGP**	214.1186	242.1135	**SGPN**	328.1615	356.1565
SGPNS	415.1936	443.1885	**SGPNSV**	514.2620	542.2569	**SGPNSVV**	613.3304	641.3253

SGPNSVVG	670.3519	698.3468	**GP**	127.0866	155.0815	**GPN**	241.1295	269.1244
GPNS	328.1615	356.1565	**GPNSV**	427.2300	455.2249	**GPNSVV**	526.2984	554.2933
GPNSVVG	583.3198	611.3148	**PN**	184.1081	212.1030	**PNS**	271.1401	299.1350
PNSV	370.2085	398.2034	**PNSVV**	469.2769	497.2718	**PNSVVG**	526.2984	554.2933
NS	174.0873	202.0822	**NSV**	273.1557	301.1506	**NSVV**	372.2241	400.2191
NSVVG	429.2456	457.2405	**SV**	159.1128	187.1077	**SVV**	258.1812	286.1761
SVVG	315.2027	343.1976	**VV**	171.1492	199.1441	**VVG**	228.1707	256.1656
VG	129.1022	157.0972						





NCBI **BLAST** search of QIPLSGPNSVVGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
57.4	1322.7307	0.0275	QIPLSGPNSVVGR
29.4	1322.6983	0.0598	IQTVPGFASTFR
24.2	1322.7670	-0.0089	LQPQEKLGVVGR
23.1	1322.8034	-0.0453	KIPINLQTQIR
20.0	1322.6731	0.0850	AVAYFSPADARR
19.4	1322.7055	0.0526	QIEGAPATPGARR
19.1	1322.7207	0.0374	GALGVWSGAPPRR
19.0	1322.6691	0.0890	GLAADENAPPGRR
18.8	1322.7306	0.0275	VAAAALNPVDAGVR
18.7	1322.7307	0.0275	AAVVTPGGVNSPVR

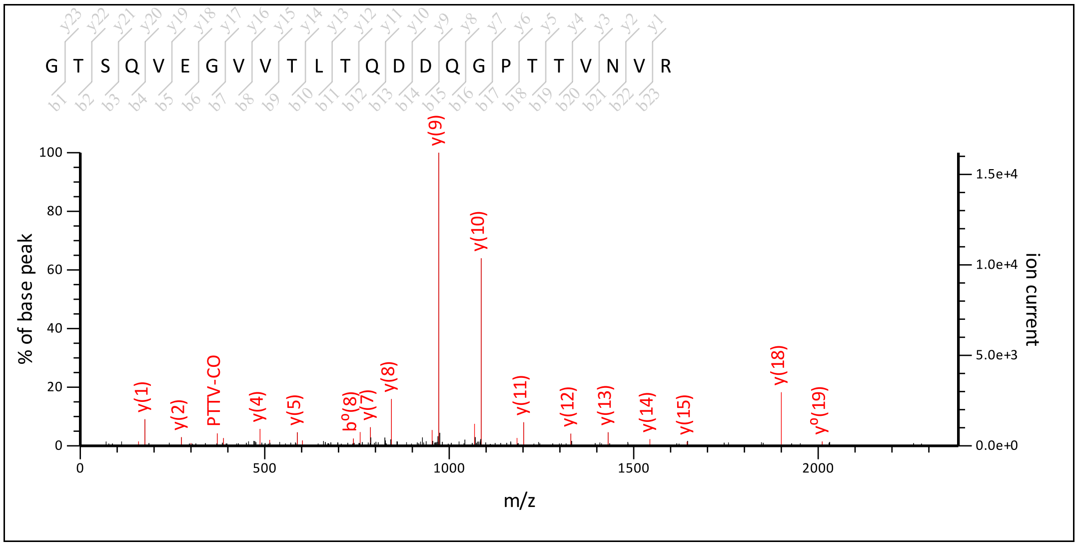
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 151

MS/MS Fragmentation of **GTSQVEGVVTLTQDDQGPTTVNVR**
Found in **gi|42408425** in **NCBInr**, putative superoxide dismutase [Cu-Zn], chloroplast precursor [Oryza sativa Japonica Group]

Match to Query 60: 2500.314024 from(2501.321300,1+) intensity(0.0000) index(19)
Title: Label: M10, Spot_Id: 219830, Peak_List_Id: 226965, MSMS Job_Run_Id: 21862, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_M10_136859956100.txt



0 to 2380.01

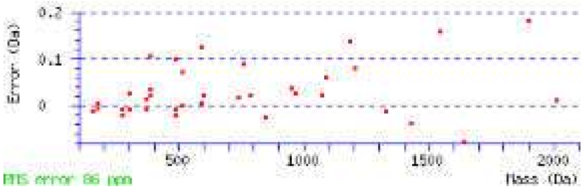
Label all possible matches ○ Label matches used for scoring ●

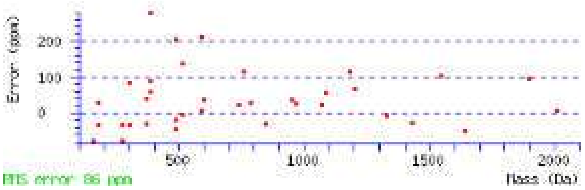
Monoisotopic mass of neutral peptide Mr(calc): 2500.2406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 3.1e-07
Matches : 40/497 fragment ions using 42 most intense peaks (help)

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*
1	30.0338	30.0338			58.0287			44.0495		G					
2	74.0600	131.0815		113.0709	159.0764		141.0659	115.0866	117.0659	T	2398.1845	2411.2049	2413.1841	2444.2263	2427.1998
3	60.0444	218.1135		200.1030	246.1084		228.0979	202.1186		S	2311.1524	2310.1572		2343.1787	2326.1521
4	101.0709	346.1721	329.1456	328.1615	374.1670	357.1405	356.1565	289.1506		Q	2183.0939	2182.0986		2256.1466	2239.1201
5	72.0808	445.2405	428.2140	427.2300	473.2354	456.2089	455.2249	431.2249		V	2084.0255	2097.0459		2128.0881	2111.0615
6	102.0550	574.2831	557.2566	556.2726	**602.2780**	585.2515	584.2675	516.2776		E	1954.9829	1953.9876		2029.0196	2011.9931
7	30.0338	631.3046	614.2780	613.2940	659.2995	642.2729	641.2889			G				***1899.9770***	1882.9505
8	72.0808	730.3730	713.3464	712.3624	**758.3679**	741.3414	740.3573	716.3573		V	1798.8930	1811.9134		1842.9556	1825.9290
9	72.0808	829.4414	812.4149	811.4308	857.4363	840.4098	839.4258	815.4258		V	1699.8246	1712.8450		1743.8872	1726.8606
10	74.0600	930.4891	913.4625	912.4785	958.4840	941.4575	940.4734	914.4942	916.4734	T	1598.7769	1611.7973	1613.7766	***1644.8188***	1627.7922
11	86.0964	1043.5732	1026.5466	1025.5626	1071.5681	1054.5415	1053.5575	1001.5262		L	1485.6928	1484.6976		***1543.7711***	1526.7445
12	74.0600	1144.6208	1127.5943	1126.6103	1172.6157	1155.5892	1154.6052	1128.6259	1130.6052	T	1384.6451	1397.6656	1399.6448	***1430.6870***	1413.6605
13	101.0709	1272.6794	1255.6529	1254.6688	1300.6743	1283.6478	1282.6638	1215.6579		Q	1256.5866	1255.5913		***1329.6393***	1312.6128
14	88.0393	1387.7064	1370.6798	1369.6958	1415.7013	1398.6747	1397.6907	1343.7165		D	1141.5596	1140.5644		***1201.5808***	1184.5542
15	88.0393	1502.7333	1485.7067	1484.7227	1530.7282	1513.7017	1512.7176	1458.7435		D	1026.5327	1025.5374		***1086.5538***	1069.5273
16	101.0709	1630.7919	1613.7653	1612.7813	1658.7868	1641.7602	1640.7762	1573.7704		Q	898.4741	897.4789		***971.5269***	954.5003
17	30.0338	1687.8133	1670.7868	1669.8028	1715.8083	1698.7817	1697.7977			G				***843.4683***	826.4417
18	70.0651	1784.8661	1767.8396	1766.8555	1812.8610	1795.8345	1794.8505	1758.8505		P	744.3999	743.4046		***786.4468***	769.4203
19	74.0600	1885.9138	1868.8872	1867.9032	1913.9087	1896.8821	1895.8981	1869.9189	1871.8981	T	643.3522	656.3726	658.3519	689.3941	672.3675
20	74.0600	1986.9615	1969.9349	1968.9509	2014.9564	1997.9298	1996.9458	1970.9665	1972.9458	T	542.3045	555.3249	557.3042	***588.3464***	571.3198
21	72.0808	2086.0299	2069.0033	2068.0193	2114.0248	2096.9982	2096.0142	2072.0142		V	443.2361	456.2565		***487.2987***	470.2722
22	87.0553	2200.0728	2183.0463	2182.0622	2228.0677	2211.0412	2210.0572	2157.0670		N	329.1932	328.1979		***388.2303***	371.2037

23	72.0808	2299.1412	2282.1147	2281.1306	2327.1361	2310.1096	2309.1256	2285.1256		V	230.1248	243.1452		***274.1874***	257.1608
24	129.1135									R	74.0237	73.0284		***175.1190***	158.0924

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
TS	161.0921	189.0870	**TSQ**	289.1506	317.1456	**TSQV**	388.2191	416.2140
TSQVE	517.2617	545.2566	**TSQVEG**	574.2831	602.2780	**TSQVEGV**	673.3515	701.3464
SQ	188.1030	216.0979	**SQV**	287.1714	315.1663	**SQVE**	416.2140	444.2089
SQVEG	473.2354	501.2304	**SQVEGV**	572.3039	600.2988	**SQVEGVV**	671.3723	699.3672
QV	200.1394	228.1343	**QVE**	329.1819	357.1769	**QVEG**	386.2034	414.1983
QVEGV	485.2718	513.2667	**QVEGVV**	584.3402	612.3352	**QVEGVVT**	685.3879	713.3828
VE	201.1234	229.1183	**VEG**	258.1448	286.1397	**VEGV**	357.2132	385.2082
VEGVV	456.2817	484.2766	**VEGVVT**	557.3293	585.3243	**VEGVVTL**	670.4134	698.4083
EG	159.0764	187.0713	**EGV**	258.1448	286.1397	**EGVV**	357.2132	385.2082
EGVVT	458.2609	486.2558	**EGVVTL**	571.3450	599.3399	**EGVVTLT**	672.3927	700.3876
GV	129.1022	157.0972	**GVV**	228.1707	256.1656	**GVVT**	329.2183	357.2132
GVVTL	442.3024	470.2973	**GVVTLT**	543.3501	571.3450	**GVVTLTQ**	671.4087	699.4036
VV	171.1492	199.1441	**VVT**	272.1969	300.1918	**VVTL**	385.2809	413.2758
VVTLT	486.3286	514.3235	**VVTLTQ**	614.3872	642.3821	**VT**	173.1285	201.1234
VTL	286.2125	314.2074	**VTLT**	387.2602	415.2551	**VTLTQ**	515.3188	543.3137
VTLTQD	630.3457	658.3406	**TL**	187.1441	215.1390	**TLT**	288.1918	316.1867
TLTQ	416.2504	444.2453	**TLTQD**	531.2773	559.2722	**TLTQDD**	646.3042	674.2992
LT	187.1441	215.1390	**LTQ**	315.2027	343.1976	**LTQD**	430.2296	458.2245
LTQDD	545.2566	573.2515	**LTQDDQ**	673.3151	701.3101	**TQ**	202.1186	230.1135
TQD	317.1456	345.1405	**TQDD**	432.1725	460.1674	**TQDDQ**	560.2311	588.2260
TQDDQG	617.2525	645.2475	**QD**	216.0979	244.0928	**QDD**	331.1248	359.1197
QDDQ	459.1834	487.1783	**QDDQG**	516.2049	544.1998	**QDDQGP**	613.2576	641.2525
DD	203.0662	231.0612	**DDQ**	331.1248	359.1197	**DDQG**	388.1463	416.1412
DDQGP	485.1991	513.1940	**DDQGPT**	586.2467	614.2416	**DDQGPTT**	687.2944	715.2893
DQ	216.0979	244.0928	**DQG**	273.1193	301.1143	**DQGP**	370.1721	398.1670
DQGPT	471.2198	499.2147	**DQGPTT**	572.2675	600.2624	**DQGPTTV**	671.3359	699.3308
QG	158.0924	186.0873	**QGP**	255.1452	283.1401	**QGPT**	356.1928	384.1878
QGPTT	457.2405	485.2354	**QGPTTV**	556.3089	584.3039	**QGPTTVN**	670.3519	698.3468
GP	127.0866	155.0815	**GPT**	228.1343	256.1292	**GPTT**	329.1819	357.1769
GPTTV	428.2504	456.2453	**GPTTVN**	542.2933	570.2882	**GPTTVNV**	641.3617	669.3566
PT	171.1128	199.1077	**PTT**	272.1605	300.1554	**PTTV**	371.2289	399.2238
PTTVN	485.2718	513.2667	**PTTVNV**	584.3402	612.3352	**TT**	175.1077	203.1026
TTV	274.1761	302.1710	**TTVN**	388.2191	416.2140	**TTVNV**	487.2875	515.2824
TV	173.1285	201.1234	**TVN**	287.1714	315.1663	**TVNV**	386.2398	414.2347
VN	186.1237	214.1186	**VNV**	285.1921	313.1870	**NV**	186.1237	214.1186





NCBI **BLAST** search of GTSQVEGVVTLTQDDQGPTTVNVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
108.2	2500.2406	0.0734	GTSQVEGVVTLTQDDQGPTTVNVR
26.0	2500.2406	0.0735	GNSTVEGVVTLTQENEGPTTVNVR
21.9	2500.2347	0.0793	EFHADGSVKDGSVTSNPVWLTVR
21.0	2500.4087	-0.0947	LISGVLMLAINLEFKSPATNVVR

20.5	2500.3002	0.0138	YNAVGYTSSFVLLDYPAGVIPVR
17.7	2500.1515	0.1625	FTLWVYMNTAGDGAEKLMHER
16.9	2500.1475	0.1665	LLGGCLGDGRVQMGDDSFHPLEQ
16.6	2500.1507	0.1633	ATHFPTVTTAWSDDGADPIDDLR
16.4	2500.0668	0.2472	LCNMEYMIESKDGGEHSDLTR
16.4	2500.0668	0.2472	LCNMEYMIESKDGGEHSDLTR

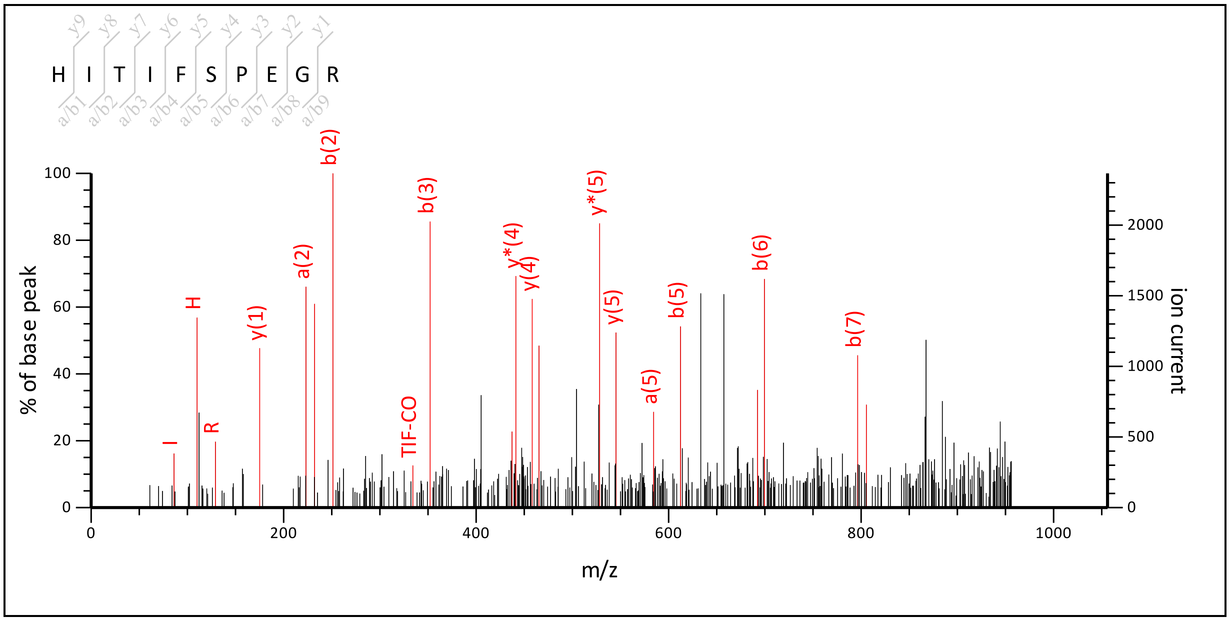
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 154

MS/MS Fragmentation of **HITIFSPEGR**
Found in **gi|449447912** in **NCBInr**, PREDICTED: proteasome subunit alpha type-6-like [Cucumis sativus]

Match to Query 89: 1155.663124 from(1156.670400,1+) intensity(0.0000) index(18)
Title: Label: I20, Spot_Id: 219986, Peak_List_Id: 229408, MSMS Job_Run_Id: 22020, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I20_136868358300.txt



0 to 1056.01

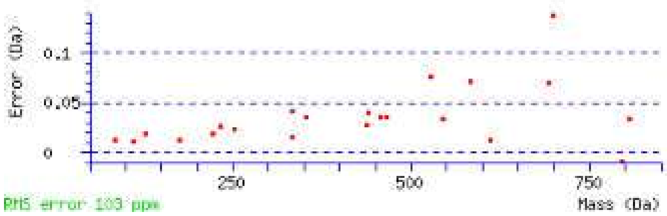
Label all possible matches ○ Label matches used for scoring ●

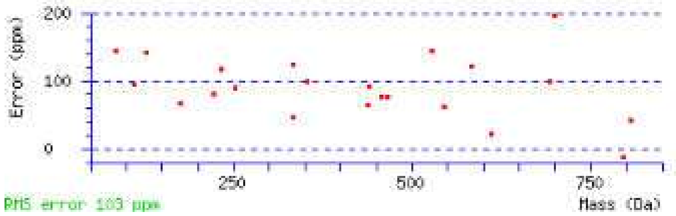
Monoisotopic mass of neutral peptide Mr(calc): 1155.6037
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 2.7
Matches : 24/145 fragment ions using 36 most intense peaks (help)

#	Immon.	a	a⁰	b	b⁰	d	d'	Seq.	v	w	w'	y	y*	y⁰	#
1	110.0713	**110.0713**		138.0662		44.0495		H							10
2	86.0964	**223.1553**		***251.1503***		195.1240	209.1397	I	961.4738	974.4942	988.5098	1019.5520	1002.5255	1001.5415	9
3	74.0600	324.2030	306.1925	***352.1979***	334.1874	308.2081	310.1874	T	860.4261	873.4465	875.4258	906.4680	889.4414	888.4574	8
4	86.0964	**437.2871**	419.2765	***465.2820***	447.2714	409.2558	423.2714	I	747.3420	760.3624	774.3781	***805.4203***	788.3937	787.4097	7
5	120.0808	**584.3555**	566.3449	***612.3504***	594.3398			F	600.2736			***692.3362***	675.3097	674.3256	6
6	60.0444	671.3875	653.3770	***699.3824***	681.3719	655.3926		S	513.2416	512.2463		***545.2678***	528.2413	527.2572	5
7	70.0651	768.4403	750.4297	***796.4352***	778.4246	742.4246		P	416.1888	415.1936		***458.2358***	441.2092	440.2252	4
8	102.0550	897.4829	879.4723	925.4778	907.4672	839.4774		E	287.1462	286.1510		361.1830	344.1565	343.1724	3
9	30.0338	954.5043	936.4938	982.4993	964.4887			G				***232.1404***	215.1139		2
10	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
IT	187.1441	215.1390	ITI	300.2282	328.2231	ITIF	447.2966	475.2915
ITIFS	534.3286	562.3235	ITIFSP	631.3814	659.3763	TI	187.1441	215.1390
TIF	334.2125	362.2074	TIFS	421.2445	449.2395	TIFSP	518.2973	546.2922
TIFSPE	647.3399	675.3348	IF	233.1648	261.1598	IFS	320.1969	348.1918

IFSP	417.2496	445.2445	**IFSPE**	546.2922	574.2871	**IFSPEG**	603.3137	631.3086
FS	207.1128	235.1077	**FSP**	304.1656	332.1605	**FSPE**	433.2082	461.2031
FSPEG	490.2296	518.2245	**SP**	157.0972	185.0921	**SPE**	286.1397	314.1347
SPEG	343.1612	371.1561	**PE**	199.1077	227.1026	**PEG**	256.1292	284.1241
EG	159.0764	187.0713						





NCBI **BLAST** search of HITIFSPEGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
40.8	1155.6037	0.0595	HITIFSPEGR
40.8	1155.6037	0.0595	HLTIFSPEGR
24.4	1155.6149	0.0483	HLYGGKAPSAR
23.7	1155.6036	0.0595	IHEIFSSPAR
22.9	1155.5785	0.0846	DVHPHLPADR
22.4	1155.5958	0.0673	SYTIMSVALR
22.3	1155.6288	0.0343	HLELFVVGDK
22.1	1155.6036	0.0595	HLNQFLAADK
22.0	1155.6360	0.0271	RAGITLPADSR
21.9	1155.5996	0.0635	LVGGREPSEGR

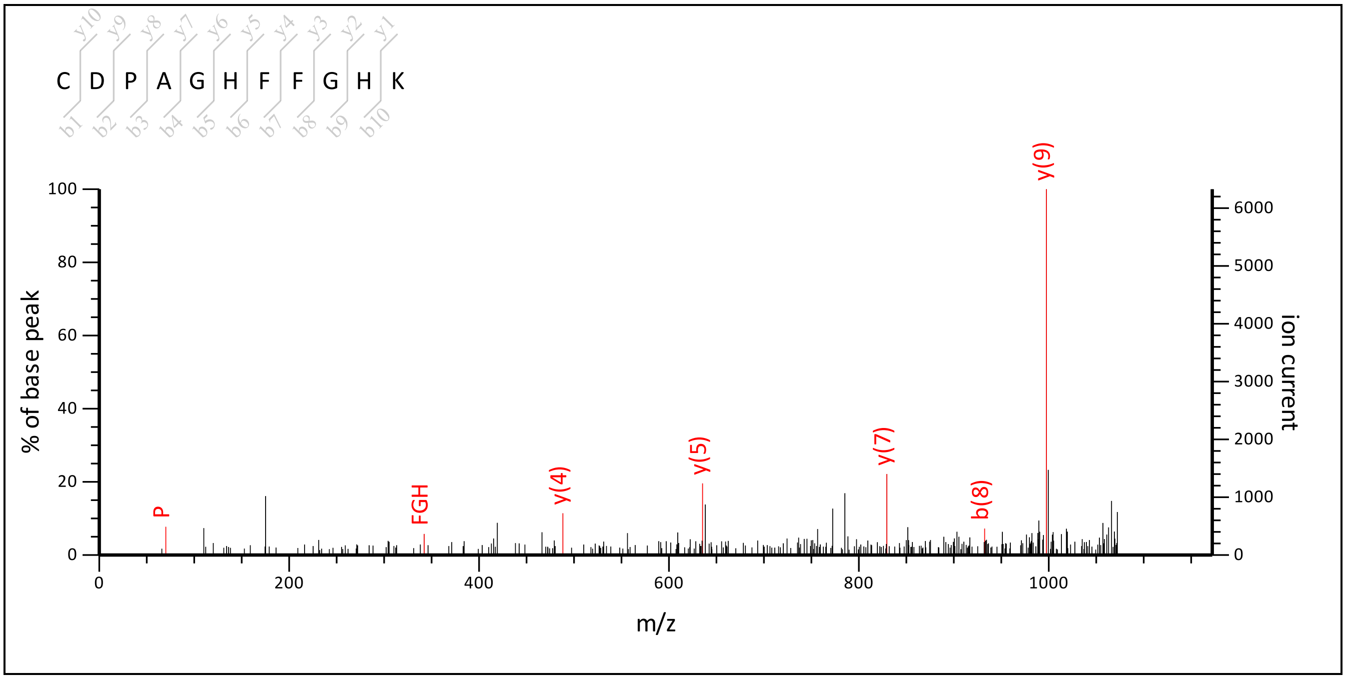
Mascot: http://www.matrixscience.com/

Mascot Search Results

Peptide View Spot no 154

MS/MS Fragmentation of CDPAGHFFGHK
Found in gi|449447912 in NCBInr, PREDICTED: proteasome subunit alpha type-6-like [Cucumis sativus]

Match to Query 116: 1271.602924 from(1272.610200,1+) intensity(0.0000) index(25)
Title: Label: I20, Spot_Id: 219986, Peak_List_Id: 229420, MSMS Job_Run_Id: 22020, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I20_136868358300.txt



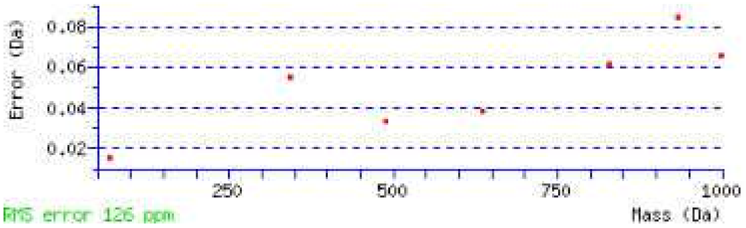
0 to 1172.2

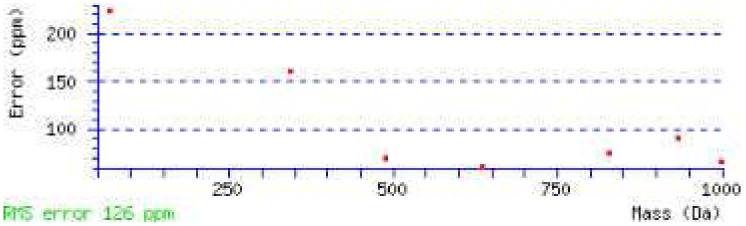
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1271.5506
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 21 **Expect:** 2.5e+02
Matches : 8/145 fragment ions using 11 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	Seq.	v	w	y	y*	y^0	#
1	133.0430	133.0430		161.0379		44.0495	C						11
2	88.0393	248.0700	230.0594	276.0649	258.0543	204.0801	D	1052.5061	1051.5108	1112.5272	1095.5007	1094.5166	10
3	70.0651	345.1227	327.1122	373.1176	355.1071	319.1071	P	955.4533	954.4581	***997.5003***	980.4737		9
4	44.0495	416.1598	398.1493	444.1547	426.1442		A	884.4162		900.4475	883.4209		8
5	30.0338	473.1813	455.1707	501.1762	483.1656		G			***829.4104***	812.3838		7
6	110.0713	610.2402	592.2296	638.2351	620.2246		H	690.3358		772.3889	755.3624		6
7	120.0808	757.3086	739.2981	785.3035	767.2930		F	543.2674		***635.3300***	618.3035		5
8	120.0808	904.3770	886.3665	**932.3719**	914.3614		F	396.1990		***488.2616***	471.2350		4
9	30.0338	961.3985	943.3879	989.3934	971.3828		G			341.1932	324.1666		3
10	110.0713	1098.4574	1080.4468	1126.4523	1108.4418		H	202.1186		284.1717	267.1452		2
11	101.1073						K	74.0237	73.0284	147.1128	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DP	185.0921	213.0870	**DPA**	256.1292	284.1241	**DPAG**	313.1506	341.1456
DPAGH	450.2096	478.2045	**DPAGHF**	597.2780	625.2729	**PA**	141.1022	169.0972
PAG	198.1237	226.1186	**PAGH**	335.1826	363.1775	**PAGHF**	482.2510	510.2459
PAGHFF	629.3194	657.3144	**PAGHFFG**	686.3409	714.3358	**AG**	101.0709	129.0659
AGH	238.1299	266.1248	**AGHF**	385.1983	413.1932	**AGHFF**	532.2667	560.2616
AGHFFG	589.2881	617.2831	**GH**	167.0927	195.0877	**GHF**	314.1612	342.1561
GHFF	461.2296	489.2245	**GHFFG**	518.2510	546.2459	**GHFFGH**	655.3099	683.3049
HF	257.1397	285.1346	**HFF**	404.2081	432.2030	**HFFG**	461.2296	489.2245
HFFGH	598.2885	626.2834	**FF**	267.1492	295.1441	**FFG**	324.1707	352.1656
FFGH	461.2296	489.2245	**FG**	177.1022	205.0972	**FGH**	314.1612	342.1561
GH	167.0927	195.0877						





NCBI **BLAST** search of CDPAGHFFGHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
21.7	1271.6808	-0.0779	VVMNPPFNKAR
21.4	1271.5506	0.0523	CDPAGHFFGHK
21.3	1271.6445	-0.0415	KFGHAPSEMLR
19.6	1271.6002	0.0027	KMGGMTFVDVR
19.3	1271.5968	0.0061	MKAGFSFPSER
18.9	1271.6656	-0.0627	SMGPANQVTLVR
18.9	1271.7085	-0.1056	TSSPADLLLLSR
18.9	1271.5969	0.0061	MGATGFGFELAR
18.6	1271.6907	-0.0878	HEKVTAMIVTK
17.5	1271.6411	-0.0382	KFNFTFQANR

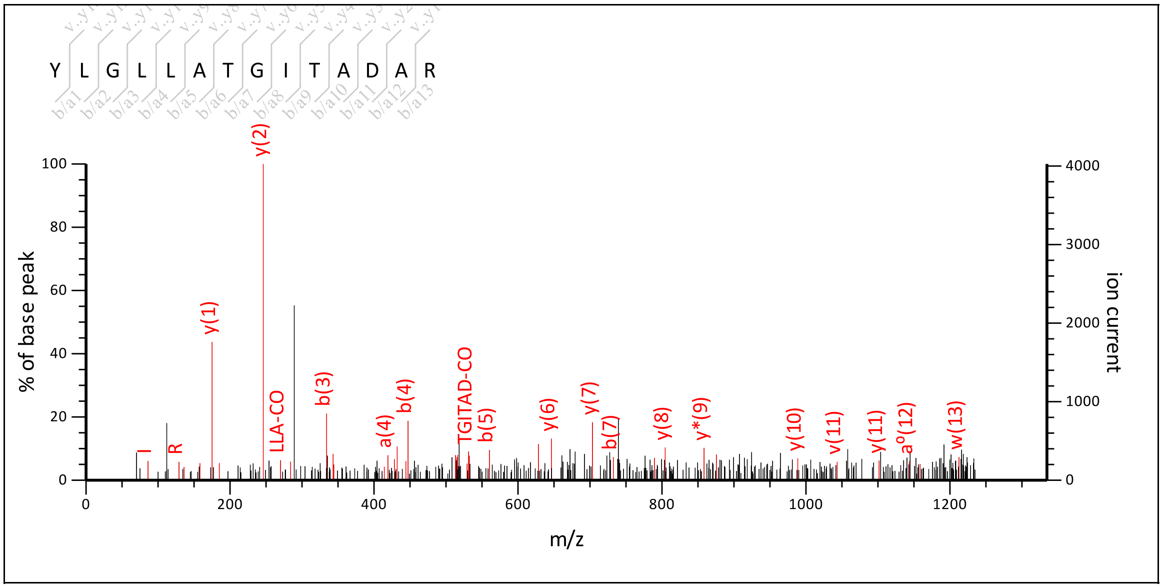
Mascot: http://www.matrixscience.com/

MATRIX SCIENCE Mascot Search Results

Peptide View Spot no 154

MS/MS Fragmentation of **YLGLLATGITADAR**
Found in **gi|449447912** in **NCBInr**, PREDICTED: proteasome subunit alpha type-6-like [Cucumis sativus]

Match to Query 137: 1433.869924 from(1434.877200,1+) intensity(0.0000) index(30)
Title: Label: I20, Spot_Id: 219986, Peak_List_Id: 229413, MSMS Job_Run_Id: 22020, Comment:
Data file C:\Documents and Settings\Administrator\Desktop\Farah-Garima 11May 2013\ppw_I20_136868358300.txt



0 to 1334.74

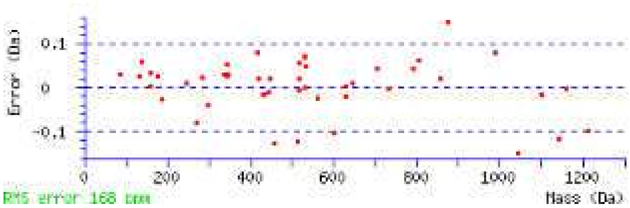
Label all possible matches ○ Label matches used for scoring ●

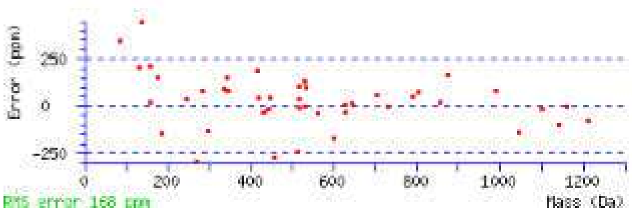
Monoisotopic mass of neutral peptide Mr(calc): 1433.7878
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 3.6
Matches : 60/228 fragment ions using 120 most intense peaks (help)

#	Immon.	a	a^0	b	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	136.0757	**136.0757**		164.0706		44.0495		Y							14
2	86.0964	249.1598		277.1547		207.1128		L	1213.6535	1212.6583		1271.7318	1254.7052	1253.7212	13
3	30.0338	306.1812		**334.1761**				G				***1158.6477***	1141.6212	1140.6372	12
4	86.0964	**419.2653**		**447.2602**		377.2183		L	1043.5480	1042.5528		***1101.6263***	1084.5997	1083.6157	11
5	86.0964	**532.3493**		**560.3443**		490.3024		L	930.4639	929.4687		***988.5422***	971.5156	970.5316	10
6	44.0495	603.3865		631.3814				A	859.4268			***875.4581***	858.4316	857.4476	9
7	74.0600	704.4341	686.4236	**732.4291**	714.4185	688.4392	690.4185	T	758.3791	771.3995	773.3788	***804.4210***	787.3945	786.4104	8
8	30.0338	761.4556	743.4450	**789.4505**	771.4400			G				***703.3733***	686.3468	685.3628	7
9	86.0964	874.5397	856.5291	902.5346	884.5240	846.5084	860.5240	I	588.2736	601.2940	615.3097	***646.3519***	629.3253	628.3413	6
10	74.0600	975.5873	957.5768	1003.5823	985.5717	959.5924	961.5717	T	487.2259	500.2463	502.2256	533.2678	516.2413	515.2572	5
11	44.0495	1046.6245	1028.6139	1074.6194	1056.6088			A	416.1888			***432.2201***	415.1936	414.2096	4
12	88.0393	1161.6514	1143.6408	1189.6463	1171.6358	1117.6616		D	301.1619	300.1666		361.1830	344.1565	343.1724	3
13	44.0495	1232.6885	1214.6780	1260.6834	1242.6729			A	230.1248			***246.1561***	229.1295		2
14	129.1135							R	74.0237	73.0284		***175.1190***	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LG	143.1179	171.1128	LGL	256.2020	284.1969	LGLL	369.2860	397.2809
LGLLA	440.3231	468.3180	LGLLAT	541.3708	569.3657	LGLLATG	598.3923	626.3872
GL	143.1179	171.1128	GLL	256.2020	284.1969	GLLA	327.2391	355.2340

GLLAT	428.2867	456.2817	**GLLATG**	485.3082	513.3031	**GLLATGI**	598.3923	626.3872
GLLATGIT	699.4400	727.4349	**LL**	199.1805	227.1754	**LLA**	270.2176	298.2125
LLAT	371.2653	399.2602	**LLATG**	428.2867	456.2817	**LLATGI**	541.3708	569.3657
LLATGIT	642.4185	670.4134	**LA**	157.1335	185.1285	**LAT**	258.1812	286.1761
LATG	315.2027	343.1976	**LATGI**	428.2867	456.2817	**LATGIT**	529.3344	557.3293
LATGITA	600.3715	628.3665	**AT**	145.0972	173.0921	**ATG**	202.1186	230.1135
ATGI	315.2027	343.1976	**ATGIT**	416.2504	444.2453	**ATGITA**	487.2875	515.2824
ATGITAD	602.3144	630.3093	**ATGITADA**	673.3515	701.3464	**TG**	131.0815	159.0764
TGI	244.1656	272.1605	**TGIT**	345.2132	373.2082	**TGITA**	416.2504	444.2453
TGITAD	531.2773	559.2722	**TGITADA**	602.3144	630.3093	**GI**	143.1179	171.1128
GIT	244.1656	272.1605	**GITA**	315.2027	343.1976	**GITAD**	430.2296	458.2245
GITADA	501.2667	529.2617	**IT**	187.1441	215.1390	**ITA**	258.1812	286.1761
ITAD	373.2082	401.2031	**ITADA**	444.2453	472.2402	**TA**	145.0972	173.0921
TAD	260.1241	288.1190	**TADA**	331.1612	359.1561	**AD**	159.0764	187.0713
ADA	230.1135	258.1084	**DA**	159.0764	187.0713			





NCBI **BLAST** search of YLGLLATGITADAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
36.7	1433.7878	0.0821	YLGLLATGITADAR
36.3	1433.7878	0.0821	YIGLLATGLTADAR
23.4	1433.7449	0.1250	MSPDLVLFRNAR
20.5	1433.7337	0.1363	IYGEPAAAMAVVAR
20.5	1433.7337	0.1362	TVVMLVNDPGFAR
20.3	1433.7878	0.0821	IVAYLVGTVSQER
19.8	1433.7514	0.1185	KDINGIYLVDER
19.6	1433.7370	0.1329	MSVIIMNDLLGGR
19.1	1433.8242	0.0457	LYGLLATTAKQQK
17.2	1433.7627	0.1073	LSVFNAAKDTVNR

Mascot: http://www.matrixscience.com/