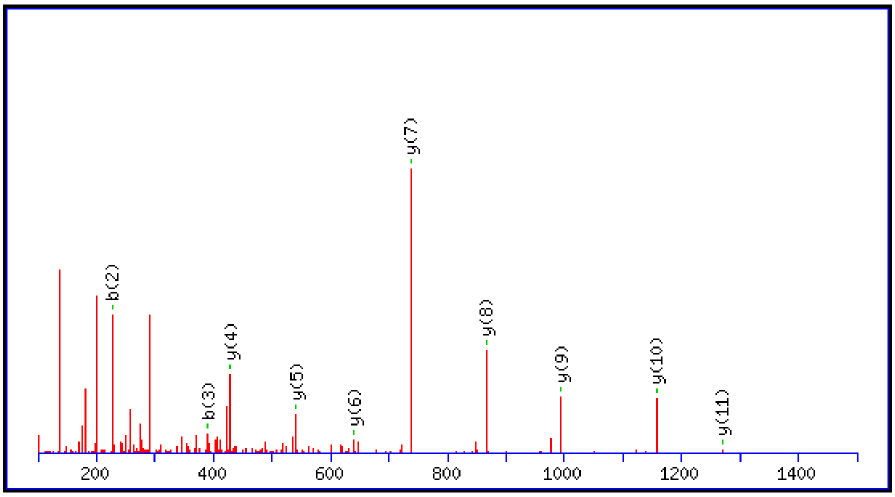
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLYQEPVLGPVR**
Found in **Solyc00g999999**, BetaCasein

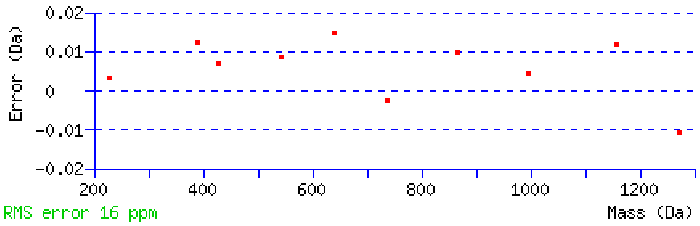
Match to Query 4790: 1382.732640 from(692.373596,2+)
Title: cyr_090306_meja_005_bi9_2_p.01809.01809.2_39.624mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

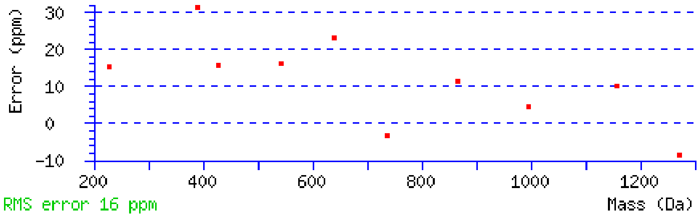
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1382.79
Ions Score: 74 **Expect:** 1.7e-005
Matches : 10/104 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					L							12
2	**227.18**	114.09					L	***1270.72***	635.86	1253.69	627.35	1252.70	626.86	11
3	**390.24**	195.62					Y	***1157.63***	579.32	1140.60	570.81	1139.62	570.31	10
4	518.30	259.65	501.27	251.14			Q	***994.57***	497.79	977.54	489.27	976.56	488.78	9
5	647.34	324.17	630.31	315.66	629.33	315.17	E	***866.51***	433.76	849.48	425.25	848.50	424.75	8
6	744.39	372.70	727.37	364.19	726.38	363.69	P	***737.47***	369.24	720.44	360.72			7
7	843.46	422.23	826.43	413.72	825.45	413.23	V	***640.41***	320.71	623.39	312.20			6
8	956.55	478.78	939.52	470.26	938.53	469.77	L	***541.35***	271.18	524.32	262.66			5
9	1013.57	507.29	996.54	498.77	995.56	498.28	G	***428.26***	214.63	411.24	206.12			4
10	1110.62	555.81	1093.59	547.30	1092.61	546.81	P	371.24	186.12	354.21	177.61			3
11	1209.69	605.35	1192.66	596.83	1191.68	596.34	V	274.19	137.60	257.16	129.08			2
12							R	175.12	88.06	158.09	79.55			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.1	1382.79	-0.06	LLYQEPVLGPVR
15.8	1382.72	0.01	IIYQALFWTASA
15.8	1382.68	0.05	LLSEDNPPKYHA
12.5	1382.76	-0.02	ALFADEPVVVARP
10.9	1382.77	-0.03	IFEQLLARHEK
10.8	1382.78	-0.05	ILYPLSIHLSLD
9.8	1382.72	0.02	ELPRLQEKDQQ
9.3	1382.69	0.04	WSGPLVEPASAGGR
7.0	1382.78	-0.04	LLKKNTPASPDTV
7.0	1382.74	-0.01	LTREIDDLPSPK

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

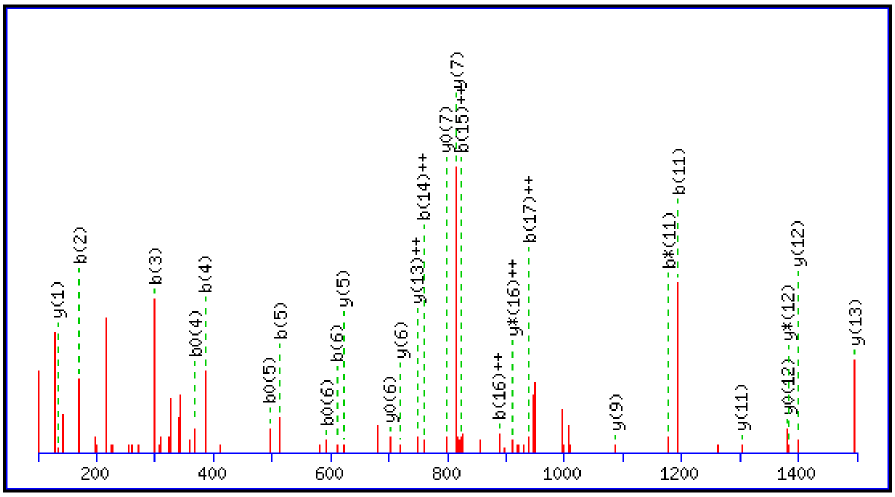
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVQSKPPSKRDPPKMQTD**
Found in **Solyc05g051750.2.1**, genomic_reference:SL2.40ch05 gene_region:61277162-61281598 transcript_region:SL2.40ch05:61277162..61281598- functional_description:""Prosystemin (AHRD V1 ***-Q5MBK9_BETVU); contains Interpro domain(s) IPR009966 Prosystemin ""

Match to Query 11574: 2009.072240 from(1005.543396,2+)
Title: cyr_090307_meja_05_2_bi3_p.00991.00991.2_21.524mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

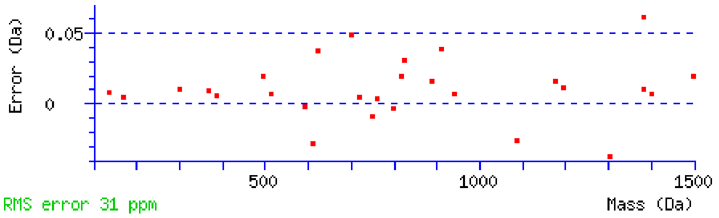
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

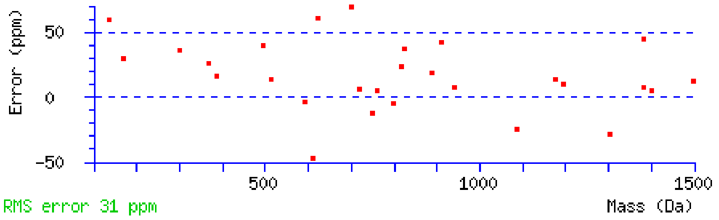


Monoisotopic mass of neutral peptide Mr(calc): 2009.04
Ions Score: 38 **Expect:** 0.05
Matches : 28/190 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.04	36.53					A							18
2	***171.11***	86.06					V	1939.01	970.01	1921.98	961.49	1921.00	961.00	17
3	***299.17***	150.09	282.14	141.58			Q	1839.94	920.47	1822.91	911.96	1821.93	911.47	16
4	***386.20***	193.61	369.18	185.09	368.19	184.60	S	1711.88	856.44	1694.85	847.93	1693.87	847.44	15
5	***514.30***	257.65	497.27	249.14	496.29	248.65	K	1624.85	812.93	1607.82	804.41	1606.84	803.92	14
6	***611.35***	306.18	594.32	297.67	593.34	297.17	P	***1496.75***	748.88	1479.73	740.37	1478.74	739.87	13
7	708.40	354.71	691.38	346.19	690.39	345.70	P	***1399.70***	700.35	1382.67	691.84	1381.69	691.35	12
8	795.44	398.22	778.41	389.71	777.43	389.22	S	***1302.65***	651.83	1285.62	643.31	1284.64	642.82	11
9	923.53	462.27	906.50	453.76	905.52	453.26	K	1215.62	608.31	1198.59	599.80	1197.60	599.31	10
10	1079.63	540.32	1062.61	531.81	1061.62	531.31	R	***1087.52***	544.26	1070.49	535.75	1069.51	535.26	9
11	***1194.66***	597.83	1177.63	589.32	1176.65	588.83	D	931.42	466.21	914.39	457.70	913.41	457.21	8
12	1291.71	646.36	1274.69	637.85	1273.70	637.35	P	***816.39***	408.70	799.37	400.19	798.38	399.69	7
13	1388.76	694.89	1371.74	686.37	1370.75	685.88	P	***719.34***	360.17	702.31	351.66	701.33	351.17	6

14	1516.86	***758.93***	1499.83	750.42	1498.85	749.93	**K**	***622.29***	311.65	605.26	303.13	604.28	302.64	**5**
15	1647.90	***824.45***	1630.87	815.94	1629.89	815.45	**M**	494.19	247.60	477.16	239.09	476.18	238.59	**4**
16	1775.96	***888.48***	1758.93	879.97	1757.95	879.48	**Q**	363.15	182.08	346.12	173.57	345.14	173.07	**3**
17	1877.01	***939.01***	1859.98	930.49	1859.00	930.00	**T**	235.09	118.05			217.08	109.04	**2**
18							**D**	***134.04***	67.53			116.03	58.52	**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.2	2009.04	0.04	AVQSKPPSKRDPPKMQTD
16.8	2009.15	-0.08	QGISKLQPQISAKVVALTE
6.3	2009.03	0.04	XMRELQRSRSSAPQNPR
5.2	2009.10	-0.03	KGVTAGDLHKALLLSIPSSC
4.4	2009.11	-0.04	RNSRRSPSRSKSPKPRN
2.4	2009.07	0.01	NLTVIVICFSPDPPPRIE
1.1	2008.99	0.08	VKASQARNSFQKVMNNGM
1.1	2009.07	0.00	GIDLPPFAKSAPASPTRER
1.1	2008.99	0.08	PYKIGAADMDGFLNELQK
0.9	2009.05	0.02	EEVRPKDHAECKRLATK

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

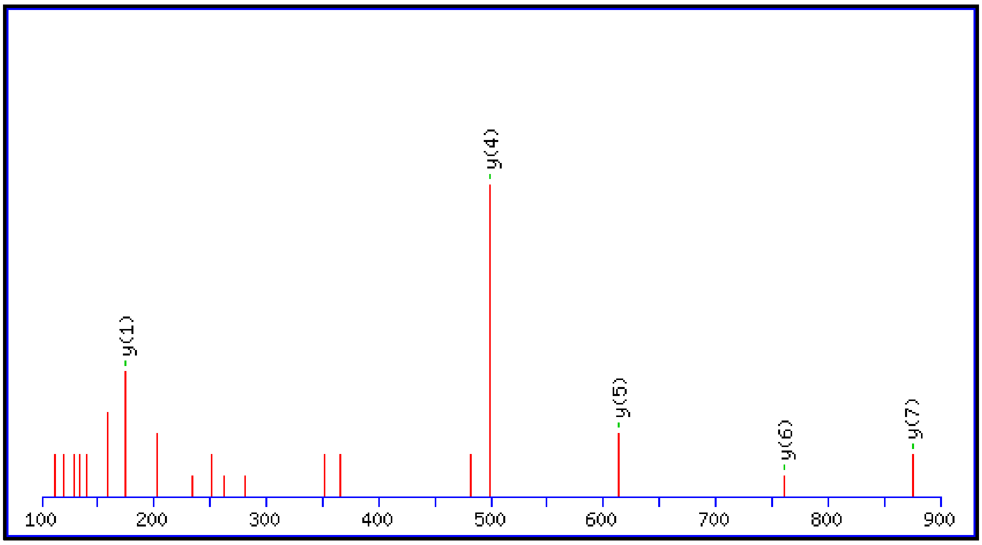
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSNFDPVKR**
Found in **Solyc05g025600.1.1**, evidence_code:10F1H0E1IEG genomic_reference:SL2.40ch05 gene_region:34412777-34413112 transcript_region:SL2.40ch05:34412777..34413112- go_terms:GO:0016020 functional_description:""Chloroplast photosystem II subunit X (Fragment) (AHRD V1 ***- B1PPX5_9M

Match to Query 1777: 1060.554052 from(531.284302,2+)
Title: cyr_090307_meja_05_2_bi4_p.01162.01162.2_26.161mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

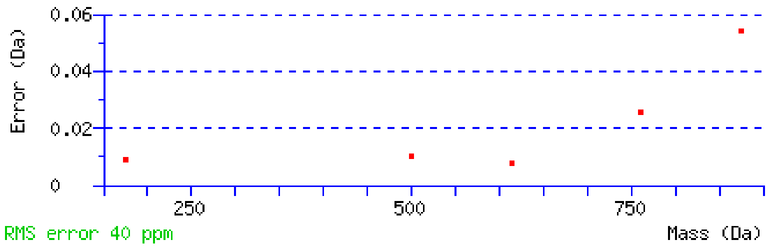
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

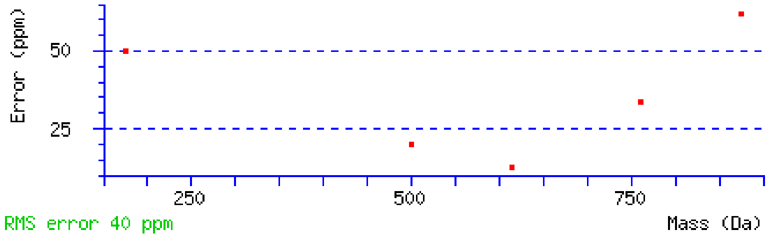


Monoisotopic mass of neutral peptide Mr(calc): 1060.57
Ions Score: 41 **Expect:** 0.055
Matches : 5/82 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.08	50.54					**V**							9
2	187.11	94.06			169.10	85.05	**S**	962.51	481.76	945.48	473.24	944.49	472.75	8
3	301.15	151.08	284.12	142.57	283.14	142.07	**N**	***875.47***	438.24	858.45	429.73	857.46	429.24	7
4	448.22	224.61	431.19	216.10	430.21	215.61	**F**	***761.43***	381.22	744.40	372.71	743.42	372.21	6
5	563.25	282.13	546.22	273.61	545.24	273.12	**D**	***614.36***	307.68	597.34	299.17	596.35	298.68	5
6	660.30	330.65	643.27	322.14	642.29	321.65	**P**	***499.34***	250.17	482.31	241.66			4
7	759.37	380.19	742.34	371.67	741.36	371.18	**V**	402.28	201.64	385.26	193.13			3
8	887.46	444.23	870.44	435.72	869.45	435.23	**K**	303.21	152.11	286.19	143.60			2

9							**R**	*175.12*	88.06	158.09	79.55			**1**





NCBI **BLAST** search of [VSNFDPVKR]
(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	1060.57	-0.01	VSNFDPVKR
19.0	1060.58	-0.03	WNFPRKTL
11.8	1060.53	0.02	WNFLLPNSA
10.3	1060.52	0.04	AGGDFAAPTVVG
9.9	1060.52	0.03	WNDVCLRR
9.9	1060.51	0.05	WNNPLDFR
9.0	1060.49	0.06	AAQVEDSWR
9.0	1060.59	-0.03	VLSAKDSVSR
8.8	1060.50	0.05	DARRGESDR
8.1	1060.58	-0.03	WNFGLRVLG

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

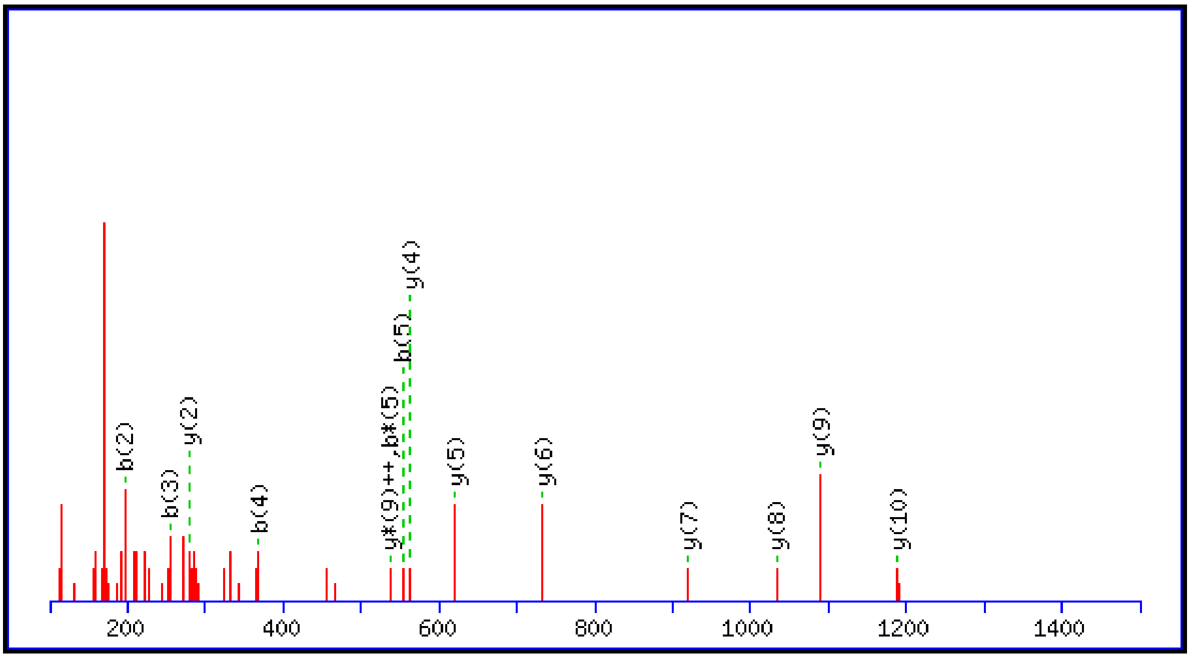
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PVGNWIGQRPY**
Found in **Solyc00g174340.1.1**, evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch00 gene_region:18121213-18121692 transcript_region:SL2.40ch00:18121213..18121692- go_terms:GO:0005515 functional_description:""Pathogenesis-related protein 1b (AHRD V1 ***- Q941G6_SOLTU); contains I

Match to Query 3794: 1285.702244 from(643.858398,2+)
Title: cyr_090307_meja_05_2_bi10_p.01776.01776.2_36.844mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

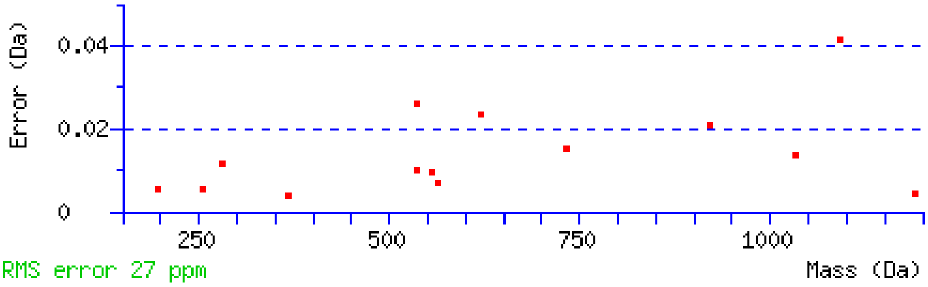
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

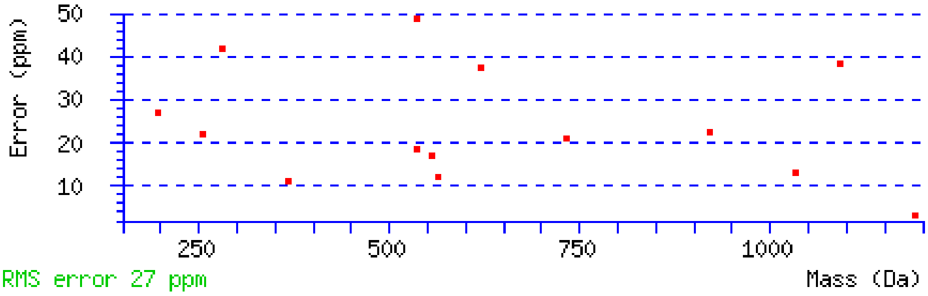


Monoisotopic mass of neutral peptide Mr(calc): 1285.66
Ions Score: 53 **Expect:** 0.0024
Matches : 14/70 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	98.06	49.53			**P**					**11**

2	**197.13**	99.07			**V**	***1189.61***	595.31	1172.58	586.80	**10**
3	**254.15**	127.58			**G**	***1090.54***	545.78	1073.52	537.26	**9**
4	**368.19**	184.60	351.17	176.09	**N**	***1033.52***	517.26	1016.49	508.75	**8**
5	**554.27**	277.64	537.25	269.13	**W**	***919.48***	460.24	902.45	451.73	**7**
6	667.36	334.18	650.33	325.67	**I**	***733.40***	367.20	716.37	358.69	**6**
7	724.38	362.69	707.35	354.18	**G**	***620.32***	310.66	603.29	302.15	**5**
8	852.44	426.72	835.41	418.21	**Q**	***563.29***	282.15	546.27	273.64	**4**
9	1008.54	504.77	991.51	496.26	**R**	435.24	218.12	418.21	209.61	**3**
10	1105.59	553.30	1088.56	544.79	**P**	***279.13***	140.07			**2**
11					**Y**	182.08	91.54			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.4	1285.66	0.05	PVGNWIGQRPY
11.5	1285.69	0.01	ETHSVILLDLF
4.4	1285.63	0.07	PGVVDAQVNLATX
4.2	1285.64	0.06	LTGEKFRSPDH
3.8	1285.77	-0.07	KGRIVKTGDISI

3.4	1285.72	-0.02	RNPSLLKNMTL
2.8	1285.71	-0.01	LPLRVSGPVDHP
2.0	1285.64	0.06	VPGTRKQEWDA
1.3	1285.67	0.03	NGLAVVIICAQAD
1.1	1285.64	0.06	NADRPLLCNLAS

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

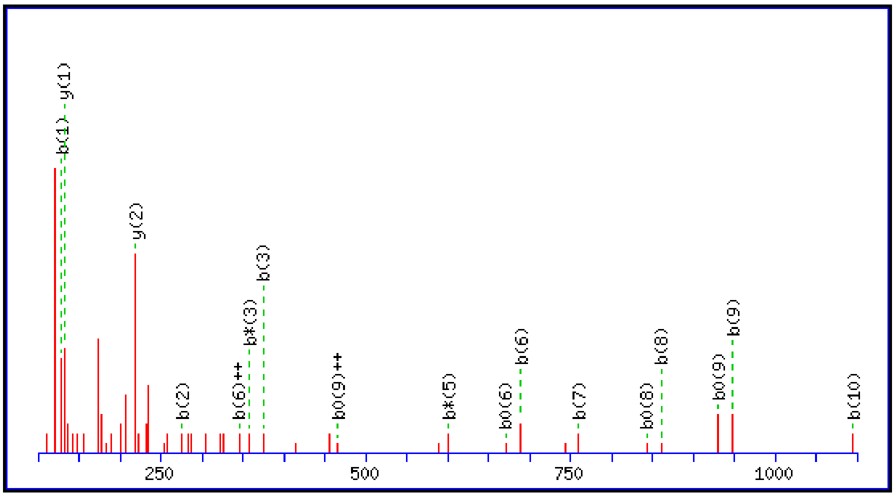
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFVENAATSFSI**
Found in **Solyc07g044860.2.1**, genomic_reference:SL2.40ch07 gene_region:55244985-55247025 transcript_region:SL2.40ch07:55244985..55247025- go_terms:GO:0008266 functional_description:""Oxygen-evolving enhancer protein 2, chloroplastic (AHRD V1 ***- PSBP_SOLLC); contains Interpro do

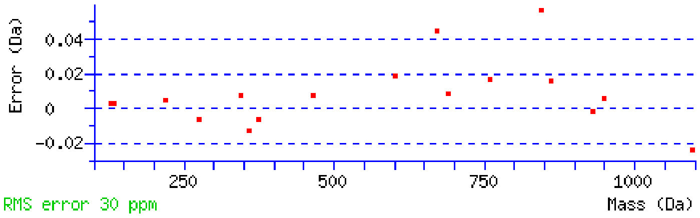
Match to Query 4138: 1312.692358 from(657.353455,2+)
Title: cyr_090307_meja_05_2_bi5_p.01704.01704.2_40.196mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

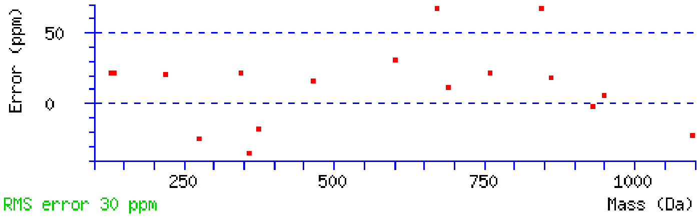
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1312.67
Ions Score: 49 **Expect:** 0.006
Matches : 17/110 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.10***	65.05	112.08	56.54			K							12
2	***276.17***	138.59	259.14	130.08			F	1185.58	593.29	1168.55	584.78	1167.57	584.29	11
3	***375.24***	188.12	358.21	179.61			V	1038.51	519.76	1021.48	511.25	1020.50	510.75	10
4	504.28	252.64	487.26	244.13	486.27	243.64	E	939.44	470.22	922.42	461.71	921.43	461.22	9
5	618.32	309.67	601.30	301.15	600.31	300.66	N	810.40	405.70	793.37	397.19	792.39	396.70	8
6	***689.36***	345.18	672.34	336.67	671.35	336.18	A	696.36	348.68			678.35	339.68	7
7	***760.40***	380.70	743.37	372.19	742.39	371.70	A	625.32	313.16			607.31	304.16	6
8	***861.45***	431.23	844.42	422.71	843.44	422.22	T	554.28	277.64			536.27	268.64	5
9	***948.48***	474.74	931.45	466.23	930.47	465.74	S	453.23	227.12			435.22	218.12	4
10	***1095.55***	548.28	1078.52	539.76	1077.54	539.27	F	366.20	183.60			348.19	174.60	3
11	1182.58	591.79	1165.55	583.28	1164.57	582.79	S	**219.13**	110.07			201.12	101.07	2
12							I	**132.10**	66.55					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	1312.67	0.03	KFVENAATSFSI
10.2	1312.63	0.06	SNFYINLNEVT
10.1	1312.63	0.06	TLCTNLGGTSFIS
9.2	1312.66	0.03	GDKINPNATPSSL
8.5	1312.65	0.05	FSFASVWNGVVT
8.2	1312.73	-0.04	IDHVKSKMRSI
8.2	1312.71	-0.02	ATRYSKQLFSI
7.5	1312.75	-0.06	PRLPKPASTFSL
7.1	1312.67	0.03	KLDGDYQKFLS
6.9	1312.70	-0.01	FVHADTGEVLII

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

MATRIX SCIENCE

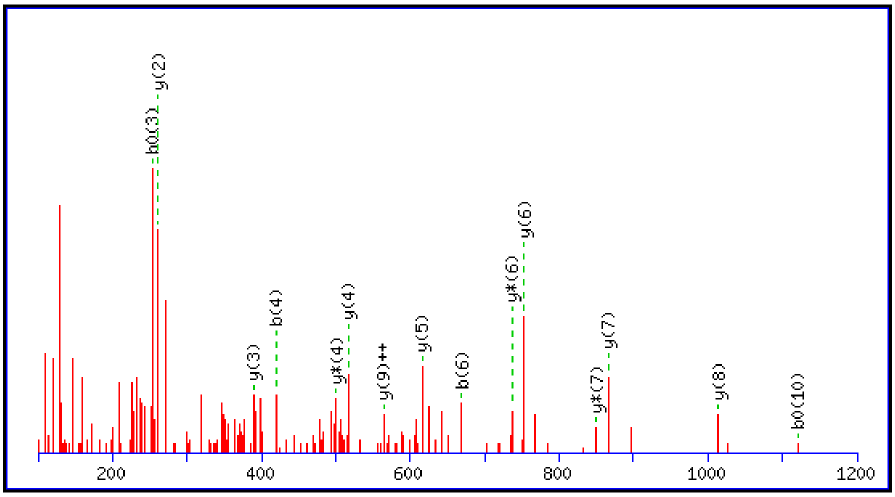
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASLFLHVQKNK**
Found in **Solyc01g007350.2.1**, genomic_reference:SL2.40ch01 gene_region:1856314-1857063 transcript_region:SL2.40ch01:1856314..1857063+ go_terms:GO:0009522 functional_description:""Photosystem I reaction center subunit VIII (AHRD V1 *-*- Q3V525_ACOCL); contains Interpro domain(s)

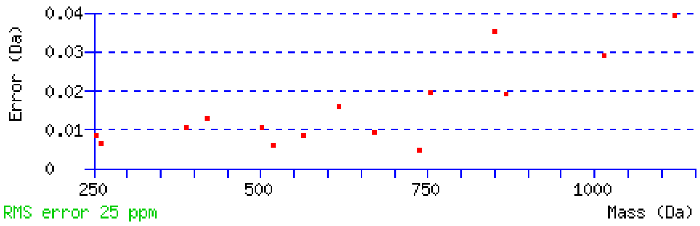
Match to Query 3731: 1283.748388 from(642.881470,2+)
Title: cyr_090307_meja_05_2_bi4_p.01271.01271.2_29.038mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

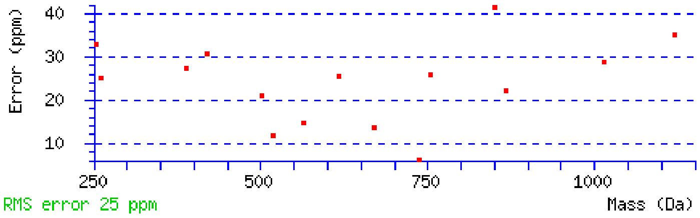
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1283.73
Ions Score: 57 **Expect:** 0.00068
Matches : 15/86 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					**A**							**11**
2	159.08	80.04			141.07	71.04	**S**	1213.71	607.36	1196.68	598.84	1195.69	598.35	**10**
3	272.16	136.58			254.15	127.58	**L**	1126.67	563.84	1109.65	555.33			**9**
4	**419.23**	210.12			401.22	201.11	**F**	***1013.59***	507.30	996.56	498.78			**8**
5	532.31	266.66			514.30	257.65	**L**	***866.52***	433.76	849.49	425.25			**7**
6	**669.37**	335.19			651.36	326.18	**H**	***753.44***	377.22	736.41	368.71			**6**
7	768.44	384.72			750.43	375.72	**V**	***616.38***	308.69	599.35	300.18			**5**
8	896.50	448.75	879.47	440.24	878.49	439.75	**Q**	***517.31***	259.16	500.28	250.64			**4**
9	1024.59	512.80	1007.57	504.29	1006.58	503.80	**K**	***389.25***	195.13	372.22	186.62			**3**
10	1138.64	569.82	1121.61	561.31	1120.63	560.82	**N**	***261.16***	131.08	244.13	122.57			**2**
11							**K**	147.11	74.06	130.09	65.55			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.9	1283.73	0.01	ASLFLHVQKNK
18.3	1283.66	0.09	LFFTGCVKAGLE
13.7	1283.66	0.09	KQLFVHVNADN
12.0	1283.72	0.03	SPSRLNIQKEL
9.8	1283.80	-0.06	DRLKRKVKEL
9.4	1283.76	-0.01	EAAQVKIREIK
8.8	1283.70	0.05	XMVAKVSHKLQG
8.1	1283.75	-0.00	TVALTPIVATWI
7.8	1283.79	-0.04	LFQKVIVEVLP
7.4	1283.69	0.06	LFQLHEQKIE

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

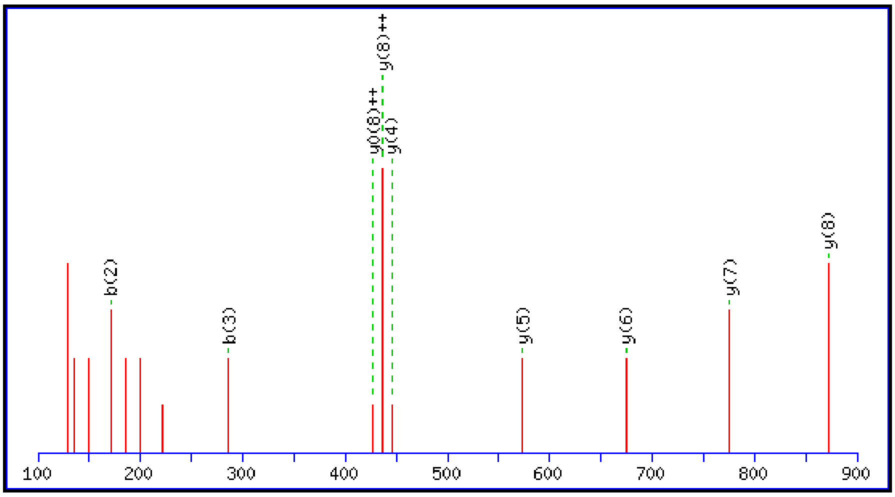
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGDPTTKRQAA**
Found in **Solyc12g035280.1.1**, evidence_code:10F0H1E0IEG genomic_reference:SL2.40ch12 gene_region:24188931-24194609 transcript_region:SL2.40ch12:24188931..24194609- go_terms:GO:0003676,GO:0016020,GO:0000166 functional_description:""Photosystem II CP47 chlorophyll apoprotein (AHRD

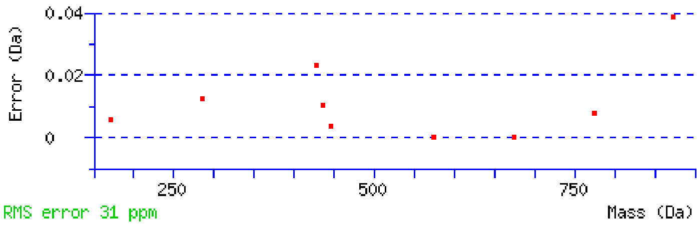
Match to Query 2439: 1156.646580 from(579.330566,2+)
Title: cyr_090307_meja_05_2_bi4_p.00982.00982.2_21.468mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

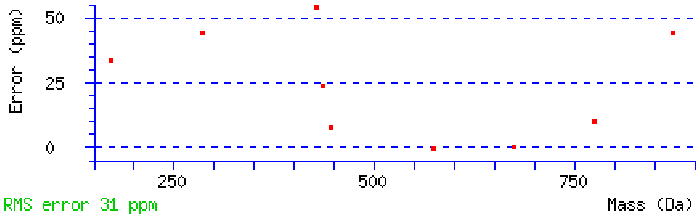
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1156.62
Ions Score: 46 **Expect:** 0.017
Matches : 9/90 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					L							11
2	**171.11**	86.06					G	1044.54	522.78	1027.52	514.26	1026.53	513.77	10
3	**286.14**	143.57			268.13	134.57	D	987.52	494.26	970.50	485.75	969.51	485.26	9
4	383.19	192.10			365.18	183.09	P	***872.49***	436.75	855.47	428.24	854.48	427.75	8
5	484.24	242.62			466.23	233.62	T	***775.44***	388.22	758.42	379.71	757.43	379.22	7
6	585.29	293.15			567.28	284.14	T	***674.39***	337.70	657.37	329.19	656.38	328.70	6
7	713.38	357.20	696.36	348.68	695.37	348.19	K	***573.35***	287.18	556.32	278.66			5
8	869.48	435.25	852.46	426.73	851.47	426.24	R	***445.25***	223.13	428.23	214.62			4
9	997.54	499.27	980.52	490.76	979.53	490.27	Q	289.15	145.08	272.12	136.57			3
10	1068.58	534.79	1051.55	526.28	1050.57	525.79	A	161.09	81.05					2
11							A	90.05	45.53					1





NCBI **BLAST** search of LGDPTTKRQAA
(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	1156.62	0.03	LGDPTTKRQAA
19.4	1156.60	0.05	GEVPTSEKPTL
17.3	1156.68	-0.03	XMVRIFPPIG
17.3	1156.64	0.00	XMVRIFPPIG
15.2	1156.65	0.00	REAIDKLVDV
12.8	1156.73	-0.09	AGKVKFIKLPG
11.9	1156.63	0.01	VADLTSQLLPT
11.8	1156.69	-0.05	KKARSLGLGDL
11.6	1156.58	0.06	ERTKSLATHD
9.8	1156.66	-0.01	RETSISVLRP

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

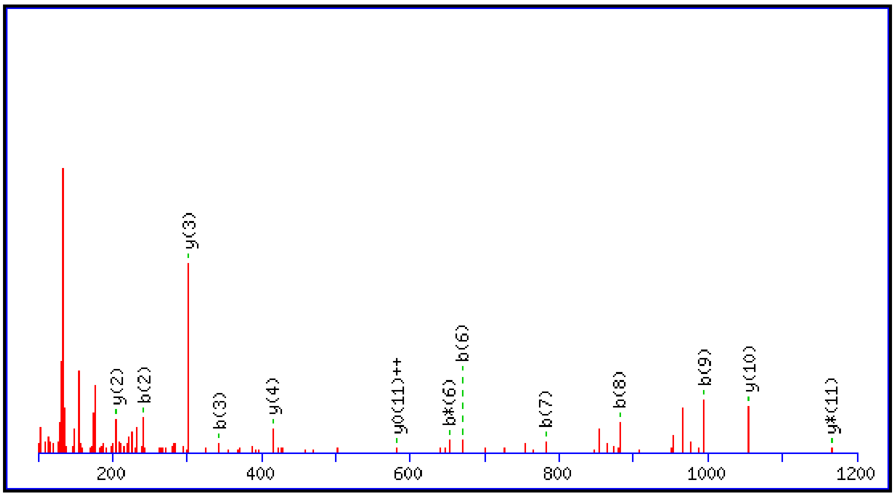
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQTAVRLVLPGE**
Found in **Solyc02g038690.1.1**, evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch02 gene_region:22029221-22029625 transcript_region:SL2.40ch02:22029221..22029625- go_terms:GO:0005515,GO:0003677 functional_description:""Histone H2B (AHRD V1 ***- A2IBL2_NICBE); contains Interpro d

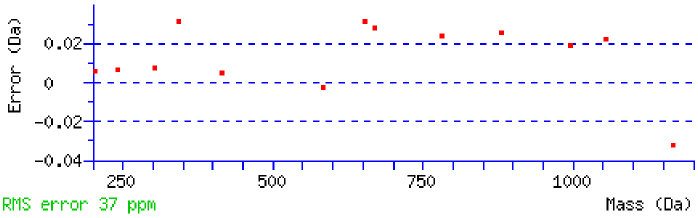
Match to Query 3916: 1294.796484 from(648.405518,2+)
Title: cyr_090307_meja_05_2_bi3_p.01769.01769.2_41.813mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

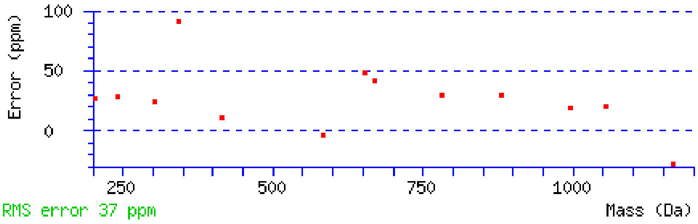
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1294.76
Ions Score: 38 **Expect:** 0.024
Matches : 13/114 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					I							12
2	***242.15***	121.58	225.12	113.07			Q	1182.68	591.85	1165.66	583.33	1164.67	582.84	11
3	***343.20***	172.10	326.17	163.59	325.19	163.10	T	**1054.63**	527.82	1037.60	519.30	1036.61	518.81	10
4	414.23	207.62	397.21	199.11	396.22	198.62	A	953.58	477.29	936.55	468.78	935.57	468.29	9
5	513.30	257.16	496.28	248.64	495.29	248.15	V	882.54	441.77	865.51	433.26	864.53	432.77	8
6	***669.40***	335.21	652.38	326.69	651.39	326.20	R	783.47	392.24	766.45	383.73	765.46	383.23	7
7	***782.49***	391.75	765.46	383.23	764.48	382.74	L	627.37	314.19			609.36	305.18	6
8	***881.56***	441.28	864.53	432.77	863.55	432.28	V	514.29	257.65			496.28	248.64	5
9	***994.64***	497.82	977.61	489.31	976.63	488.82	L	**415.22**	208.11			397.21	199.11	4
10	1091.69	546.35	1074.67	537.84	1073.68	537.35	P	**302.13**	151.57			284.12	142.57	3
11	1148.72	574.86	1131.69	566.35	1130.70	565.86	G	**205.08**	103.04			187.07	94.04	2
12							E	148.06	74.53			130.05	65.53	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.2	1294.76	0.04	IQTAVRLVLPGE
9.0	1294.86	-0.06	LKTLALNLVLVV
6.0	1294.70	0.10	LQQRLDAQLPN
3.4	1294.75	0.05	AGLTPSLLQVLPS
3.2	1294.76	0.04	KCIPRILGIPW
3.1	1294.75	0.04	LQTIILAFITY
2.2	1294.70	0.10	LQELANRQQPV
1.8	1294.79	0.01	KVLPSTTPGIGLI
1.8	1294.73	0.07	PGFIKEAGLPPVA
1.5	1294.71	0.08	VEVSESHILAVL

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

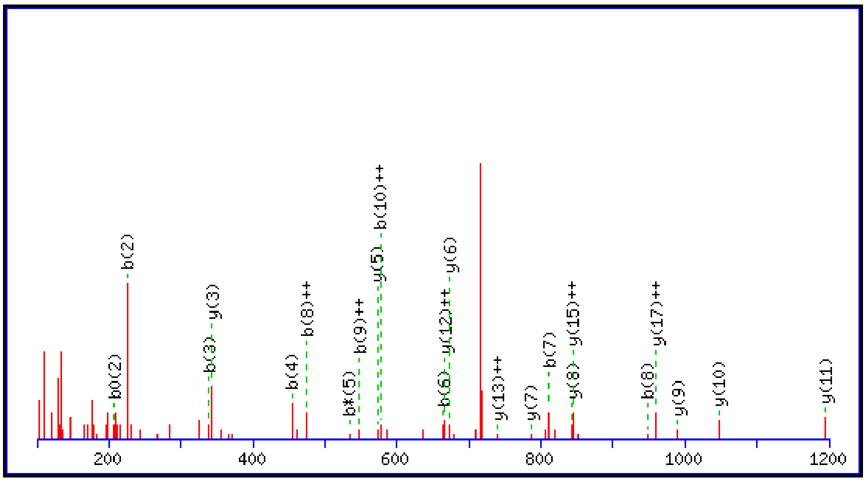
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHNDPLFHFGFGLTTKPVK**
Found in **Solyc11g071640.1.1**, evidence_code:10F0H1E1IEG genomic_reference:SL2.40ch11 gene_region:52141513-52144602 transcript_region:SL2.40ch11:52141513..52144602+ go_terms:GO:0008810 functional_description:""Beta-D-glucosidase (AHRD V1 ***- O82074_TROMA); contains Interpro domai

Match to Query 12989: 2141.157126 from(714.726318,3+)
Title: cyr_090307_meja_05_2_bi3_p.01767.01767.3_41.750mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

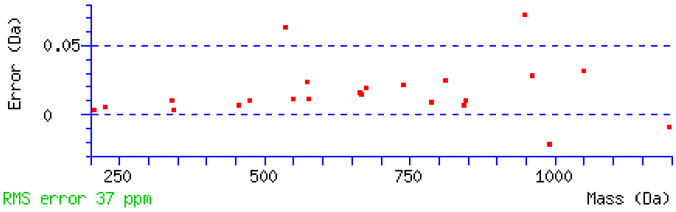
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

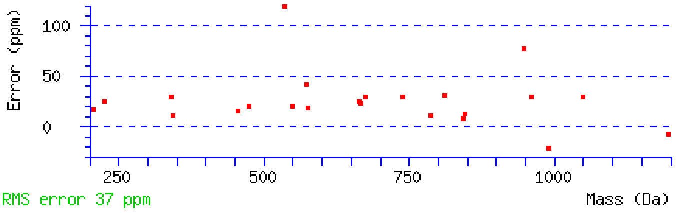


Monoisotopic mass of neutral peptide Mr(calc): 2141.11
Ions Score: 47 **Expect:** 0.0065
Matches : 23/204 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.04	44.52			70.03	35.52	**S**							**19**
2	***225.10***	113.05			207.09	104.05	**H**	2055.08	1028.04	2038.05	1019.53	2037.07	1019.04	**18**
3	***339.14***	170.07	322.11	161.56	321.13	161.07	**N**	1918.02	959.51	1901.00	951.00	1900.01	950.51	**17**
4	***454.17***	227.59	437.14	219.07	436.16	218.58	**D**	1803.98	902.49	1786.95	893.98	1785.97	893.49	**16**
5	551.22	276.11	534.19	267.60	533.21	267.11	**P**	1688.95	844.98	1671.93	836.47	1670.94	835.97	**15**
6	***664.30***	332.66	647.28	324.14	646.29	323.65	**L**	1591.90	796.45	1574.87	787.94	1573.89	787.45	**14**
7	***811.37***	406.19	794.35	397.68	793.36	397.19	**F**	1478.82	739.91	1461.79	731.40	1460.80	730.91	**13**
8	***948.43***	**474.72**	931.41	466.21	930.42	465.71	**H**	1331.75	666.38	1314.72	657.86	1313.74	657.37	**12**
9	1095.50	**548.25**	1078.47	539.74	1077.49	539.25	**F**	***1194.69***	597.85	1177.66	589.33	1176.68	588.84	**11**
10	1152.52	**576.76**	1135.50	568.25	1134.51	567.76	**G**	***1047.62***	524.31	1030.59	515.80	1029.61	515.31	**10**
11	1299.59	650.30	1282.56	641.79	1281.58	641.29	**F**	***990.60***	495.80	973.57	487.29	972.59	486.80	**9**
12	1356.61	678.81	1339.59	670.30	1338.60	669.80	**G**	***843.53***	422.27	826.50	413.76	825.52	413.26	**8**
13	1469.70	735.35	1452.67	726.84	1451.69	726.35	**L**	***786.51***	393.76	769.48	385.24	768.50	384.75	**7**
14	1570.74	785.88	1553.72	777.36	1552.73	776.87	**T**	***673.42***	337.22	656.40	328.70	655.41	328.21	**6**
15	1671.79	836.40	1654.76	827.89	1653.78	827.39	**T**	***572.38***	286.69	555.35	278.18	554.37	277.69	**5**

16	1799.89	900.45	1782.86	891.93	1781.88	891.44	**K**	471.33	236.17	454.30	227.65			**4**
17	1896.94	948.97	1879.91	940.46	1878.93	939.97	**P**	*343.23*	172.12	326.21	163.61			**3**
18	1996.01	998.51	1978.98	989.99	1978.00	989.50	**V**	246.18	123.59	229.15	115.08			**2**
19							**K**	147.11	74.06	130.09	65.55			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	2141.11	0.05	SHNDPLFHFGFGLTTKPVK
0.8	2141.20	-0.05	KKPSYLEIMFIVMILIFG
0.3	2141.09	0.06	TYPSYVWLTLQLPMVLMS
0.3	2141.11	0.04	QKYKEGKSMLERFKICGP
0.2	2141.23	-0.07	RSVPLYDKKGHKMKSVRL

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

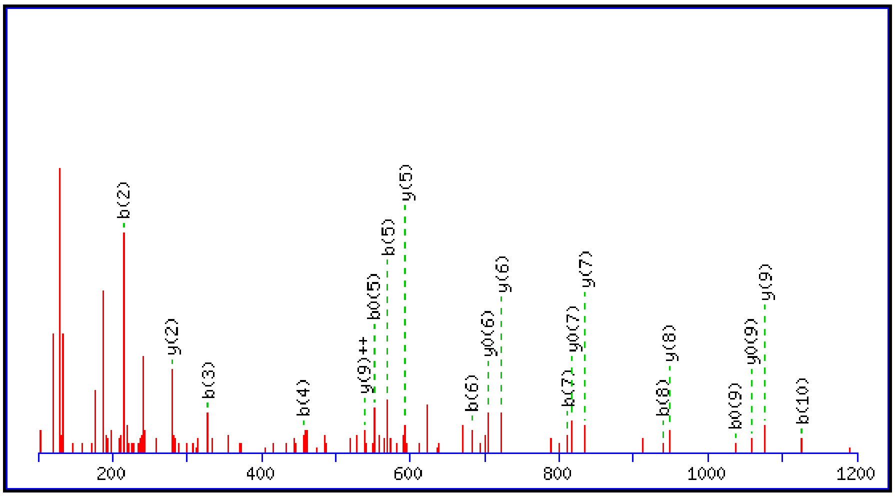
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVLKLLEKDAFL**
Found in **Solyc01g104170.2.1**, genomic_reference:SL2.40ch01 gene_region:84393496-84398307 transcript_region:SL2.40ch01:84393496..84398307- go_terms:GO:0008381 functional_description:""Ankyrin repeat domain-containing protein 2 (AHRD V1 ***- B6TNC0_MAIZE); contains Interpro domain(

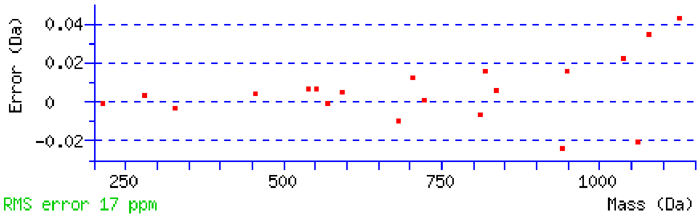
Match to Query 4438: 1402.818334 from(702.416443,2+)
Title: cyr_090307_un_05_2_bi3_p.02067.02067.2_50.469mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\un_merge\merged 0307_un.mgf

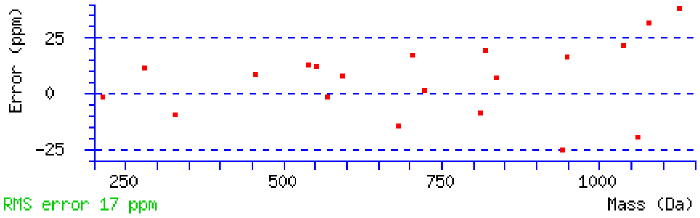
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1402.81
Ions Score: 42 **Expect:** 0.018
Matches : 20/112 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.03	58.52			98.02	49.52	D							12
2	***215.10***	108.05			197.09	99.05	V	1288.79	644.90	1271.76	636.38	1270.78	635.89	11
3	***328.19***	164.60			310.18	155.59	L	1189.72	595.36	1172.69	586.85	1171.71	586.36	10
4	***456.28***	228.64	439.26	220.13	438.27	219.64	K	**1076.64**	538.82	1059.61	530.31	1058.62	529.82	9
5	***569.37***	285.19	552.34	276.67	551.36	276.18	L	**948.54**	474.77	931.51	466.26	930.53	465.77	8
6	***682.45***	341.73	665.42	333.22	664.44	332.72	L	**835.46**	418.23	818.43	409.72	817.45	409.23	7
7	***811.49***	406.25	794.47	397.74	793.48	397.24	E	**722.37**	361.69	705.35	353.18	704.36	352.68	6
8	***939.59***	470.30	922.56	461.78	921.58	461.29	K	**593.33**	297.17	576.30	288.66	575.32	288.16	5
9	1054.61	527.81	1037.59	519.30	1036.60	518.81	D	465.23	233.12			447.22	224.12	4
10	***1125.65***	563.33	1108.62	554.82	1107.64	554.32	A	350.21	175.61					3
11	1272.72	636.86	1255.69	628.35	1254.71	627.86	F	**279.17**	140.09					2
12							L	132.10	66.55					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	1402.81	0.01	DVLKLLEKDAFL
10.2	1402.80	0.02	KYLPLFWQLVP
9.8	1402.78	0.04	CSHKIIHLDIKP
9.6	1402.86	-0.04	LKGYFLLLNIPL
8.6	1402.77	0.05	KIVLDDELQALF
7.9	1402.76	0.06	KQALQQLSQMKT
7.8	1402.86	-0.04	LTLKPFPVITKF
7.7	1402.83	-0.01	LTLEKDLRRIF
7.1	1402.83	-0.01	KLLVMCEKRRK
5.9	1402.81	0.01	SVGIVMALSTVLIT

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

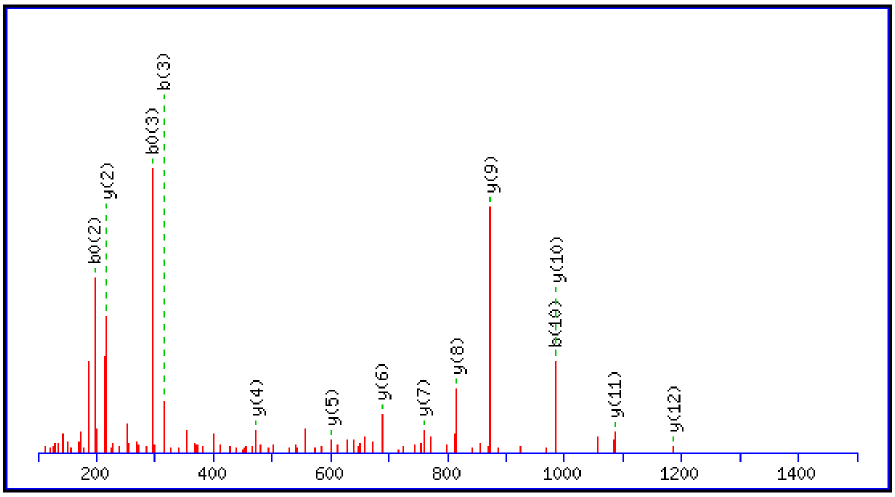
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTVIGGASERVPT**
Found in **Solyc06g063370.2.1**, genomic_reference:SL2.40ch06 gene_region:36437291-36439451 transcript_region:SL2.40ch06:36437291..36439451- go_terms:GO:0016020 functional_description:""Chlorophyll a-b binding protein 1A, chloroplastic (AHRD V1 ***- CB2A_PYRPY); contains Interpro do

Match to Query 3961: 1298.752294 from(650.383423,2+)
Title: cyr_090307_meja_05_2_bi5_p.01493.01493.2_34.706mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

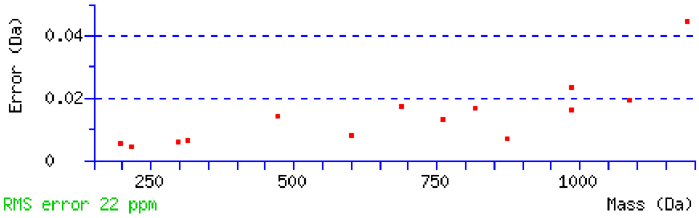
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

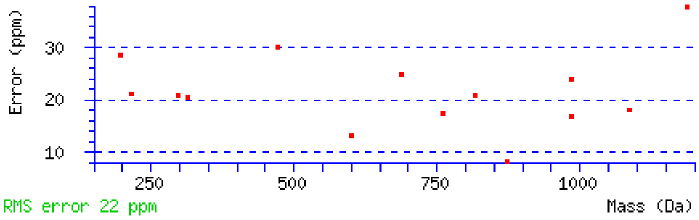


Monoisotopic mass of neutral peptide Mr(calc): 1298.72
Ions Score: 87 **Expect:** 7.7e-007
Matches : 14/118 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.09	57.55					L							13
2	215.14	108.07			197.13	99.07	T	***1186.64***	593.82	1169.62	585.31	1168.63	584.82	12
3	**314.21**	157.61			296.20	148.60	V	***1085.59***	543.30	1068.57	534.79	1067.58	534.30	11
4	427.29	214.15			409.28	205.14	I	***986.53***	493.77	969.50	485.25	968.52	484.76	10
5	484.31	242.66			466.30	233.65	G	***873.44***	437.22	856.42	428.71	855.43	428.22	9
6	541.33	271.17			523.32	262.17	G	***816.42***	408.71	799.39	400.20	798.41	399.71	8
7	612.37	306.69			594.36	297.68	A	***759.40***	380.20	742.37	371.69	741.39	371.20	7
8	699.40	350.21			681.39	341.20	S	***688.36***	344.68	671.34	336.17	670.35	335.68	6
9	828.45	414.73			810.44	405.72	E	***601.33***	301.17	584.30	292.66	583.32	292.16	5
10	**984.55**	492.78	967.52	484.26	966.54	483.77	R	***472.29***	236.65	455.26	228.13	454.28	227.64	4
11	1083.62	542.31	1066.59	533.80	1065.61	533.31	V	316.19	158.60			298.18	149.59	3
12	1180.67	590.84	1163.64	582.32	1162.66	581.83	P	***217.12***	109.06			199.11	100.06	2

13							T	120.07	60.54			102.05	51.53	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.5	1298.72	0.03	LTVIGGASERVPT
23.6	1298.75	0.00	LTVLRGRGMPSL
23.0	1298.77	-0.01	TVLINALRKTGN
20.5	1298.68	0.07	LISLQGQEIANN
16.6	1298.73	0.03	LSICIPTKGATVP
13.4	1298.66	0.09	TLVLPESPDTVE
13.4	1298.69	0.07	TLVLYSRIGYD
12.5	1298.80	-0.04	ISILPSFPGIKK
12.1	1298.65	0.10	CIPTKGATVPPDT
12.1	1298.69	0.06	ISLLPPSMVSQAG

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

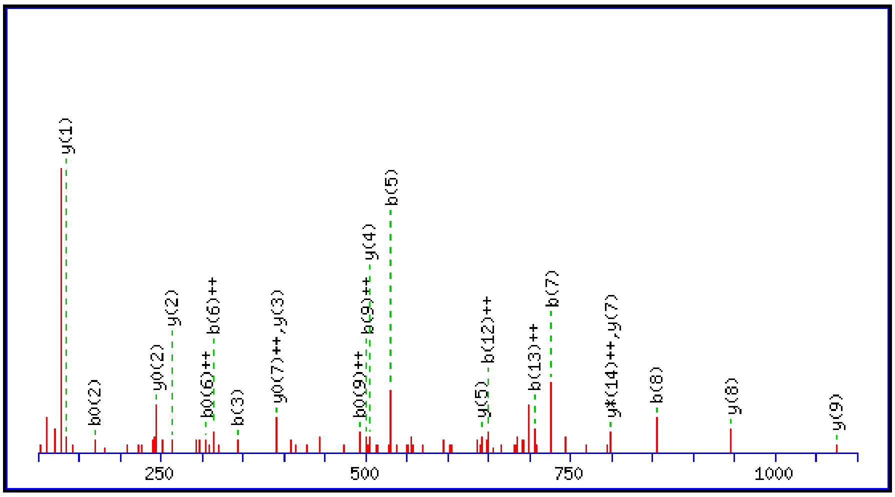
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGRSTPVKFSAHLKED**
Found in **Solyc01g087520.2.1**, genomic_reference:SL2.40ch01 gene_region:74221192-74222066 transcript_region:SL2.40ch01:74221192..74222066+ go_terms:GO:0009536 functional_description:""Ferredoxin-thioredoxin reductase variable chain (AHRD V1 *-*- B6UCW8_MAIZE); contains Interpro do

Match to Query 9316: 1799.897421 from(600.973083,3+)
Title: cyr_090307_meja_05_2_bi4_p.01178.01178.3_26.584mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

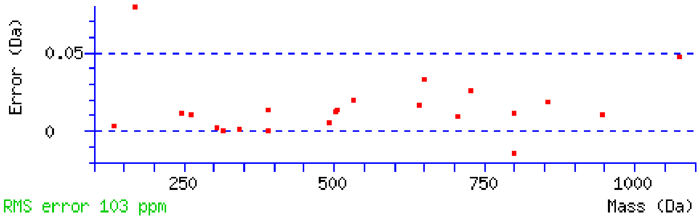
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

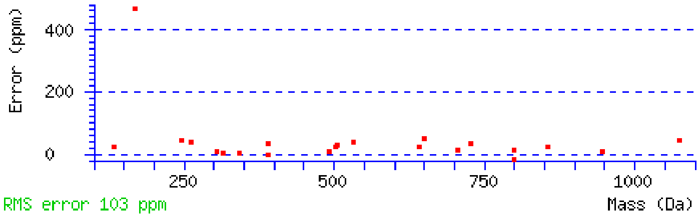


Monoisotopic mass of neutral peptide Mr(calc): 1799.92
Ions Score: 40 **Expect:** 0.043
Matches : 22/172 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.05	65.53			112.04	56.52	E							16
2	187.07	94.04			169.06	85.03	G	1671.88	836.44	1654.85	827.93	1653.87	827.44	15
3	**343.17**	172.09	326.15	163.58	325.16	163.08	R	1614.86	807.93	1597.83	799.42	1596.85	798.93	14
4	430.20	215.61	413.18	207.09	412.19	206.60	S	1458.76	729.88	1441.73	721.37	1440.75	720.88	13
5	**531.25**	266.13	514.23	257.62	513.24	257.12	T	1371.73	686.37	1354.70	677.85	1353.72	677.36	12
6	628.30	**314.66**	611.28	306.14	610.29	305.65	P	1270.68	635.84	1253.65	627.33	1252.67	626.84	11
7	**727.37**	364.19	710.35	355.68	709.36	355.19	V	1173.63	587.32	1156.60	578.80	1155.62	578.31	10
8	**855.47**	428.24	838.44	419.72	837.46	419.23	K	***1074.56***	537.78	1057.53	529.27	1056.55	528.78	9
9	1002.54	**501.77**	985.51	493.26	984.53	492.77	F	***946.46***	473.74	929.44	465.22	928.45	464.73	8
10	1089.57	545.29	1072.54	536.77	1071.56	536.28	S	***799.39***	400.20	782.37	391.69	781.38	391.20	7
11	1160.61	580.81	1143.58	572.29	1142.60	571.80	A	712.36	356.68	695.34	348.17	694.35	347.68	6
12	1297.66	**649.34**	1280.64	640.82	1279.65	640.33	H	***641.33***	321.17	624.30	312.65	623.31	312.16	5

13	1410.75	**705.88**	1393.72	697.36	1392.74	696.87	**L**	***504.27***	252.64	487.24	244.12	486.26	243.63	**4**
14	1538.84	769.93	1521.82	761.41	1520.83	760.92	**K**	***391.18***	196.09	374.16	187.58	373.17	187.09	**3**
15	1667.89	834.45	1650.86	825.93	1649.88	825.44	**E**	***263.09***	132.05			245.08	123.04	**2**
16							**D**	***134.04***	67.53			116.03	58.52	**1**





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

All matches to this query

Score	**Mr(calc):**	**Delta**	**Sequence**
39.7	1799.92	-0.02	EGRSTPVKFSAHLKED
12.5	1799.91	-0.02	KVLEQEKMVEYYKN
12.2	1799.90	0.00	QFKICTPKKVMSFED
11.3	1799.82	0.08	QLDADLAAGMGMPDNGPK
9.7	1799.92	-0.03	IVEFHTKAVMNGNLDL
8.8	1799.97	-0.07	QLLLVSSNFRWSLHT
8.5	1799.86	0.04	FDQLENQKARTNHAE
7.4	1799.96	-0.07	KVARTIADLEESENIL
6.7	1799.94	-0.04	KKLEEYVPSHEGVASK
6.0	1799.86	0.04	CDLNAPIQDVVEVSTPT

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

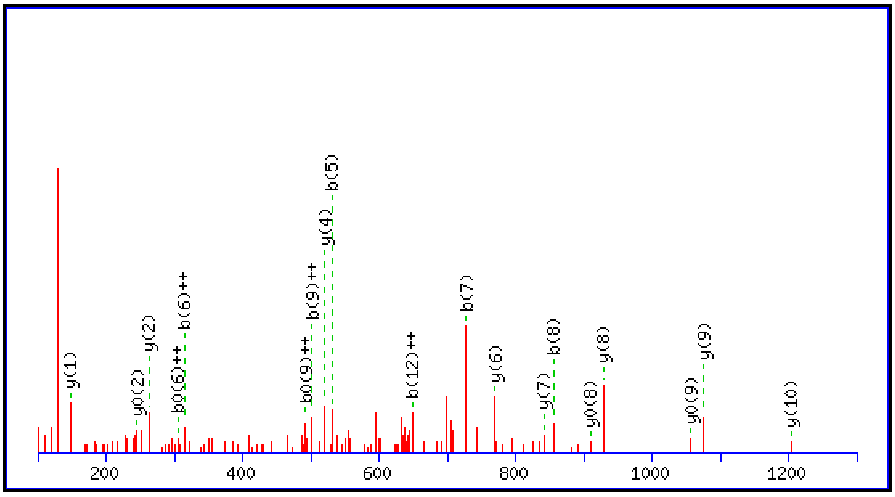
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGRSTPVKFSAHLKEDE**
Found in **Solyc01g087520.2.1**, genomic_reference:SL2.40ch01 gene_region:74221192-74222066 transcript_region:SL2.40ch01:74221192..74222066+ go_terms:GO:0009536 functional_description:""Ferredoxin-thioredoxin reductase variable chain (AHRD V1 *-*- B6UCW8_MAIZE); contains Interpro do

Match to Query 10727: 1929.009849 from(644.010559,3+)
Title: cyr_090307_meja_05_2_bi4_p.01182.01182.3_26.690mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

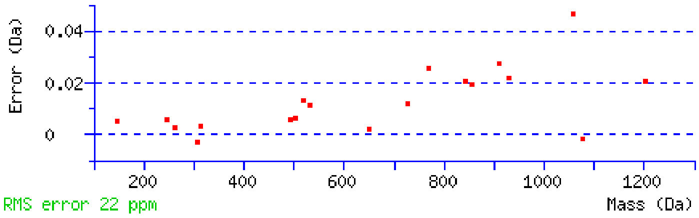
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

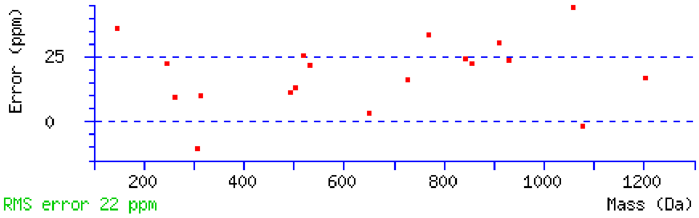


Monoisotopic mass of neutral peptide Mr(calc): 1928.96
Ions Score: 68 **Expect:** 6.3e-005
Matches : 19/182 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.05	65.53			112.04	56.52	E							17
2	187.07	94.04			169.06	85.03	G	1800.92	900.97	1783.90	892.45	1782.91	891.96	16
3	343.17	172.09	326.15	163.58	325.16	163.08	R	1743.90	872.45	1726.88	863.94	1725.89	863.45	15
4	430.20	215.61	413.18	207.09	412.19	206.60	S	1587.80	794.40	1570.77	785.89	1569.79	785.40	14
5	**531.25**	266.13	514.23	257.62	513.24	257.12	T	1500.77	750.89	1483.74	742.38	1482.76	741.88	13
6	628.30	**314.66**	611.28	306.14	610.29	305.65	P	1399.72	700.36	1382.70	691.85	1381.71	691.36	12
7	**727.37**	364.19	710.35	355.68	709.36	355.19	V	1302.67	651.84	1285.64	643.32	1284.66	642.83	11
8	**855.47**	428.24	838.44	419.72	837.46	419.23	K	***1203.60***	602.30	1186.57	593.79	1185.59	593.30	10
9	1002.54	**501.77**	985.51	493.26	984.53	492.77	F	***1075.51***	538.26	1058.48	529.74	1057.49	529.25	9
10	1089.57	545.29	1072.54	536.77	1071.56	536.28	S	***928.44***	464.72	911.41	456.21	910.43	455.72	8
11	1160.61	580.81	1143.58	572.29	1142.60	571.80	A	***841.41***	421.21	824.38	412.69	823.39	412.20	7
12	1297.66	**649.34**	1280.64	640.82	1279.65	640.33	H	***770.37***	385.69	753.34	377.17	752.36	376.68	6

13	1410.75	705.88	1393.72	697.36	1392.74	696.87	**L**	633.31	317.16	616.28	308.64	615.30	308.15	**5**
14	1538.84	769.93	1521.82	761.41	1520.83	760.92	**K**	***520.22***	260.62	503.20	252.10	502.21	251.61	**4**
15	1667.89	834.45	1650.86	825.93	1649.88	825.44	**E**	392.13	196.57			374.12	187.56	**3**
16	1782.91	891.96	1765.89	883.45	1764.90	882.96	**D**	***263.09***	132.05			245.08	123.04	**2**
17							**E**	***148.06***	74.53			130.05	65.53	**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.7	1928.96	0.05	EGRSTPVKFSAHLKEDE
8.0	1928.97	0.04	KLNEIEQAAVIHYDGVM
6.7	1929.10	-0.09	KYDLLESILVRQRLSP
6.3	1928.97	0.04	EGKTLVVGAEEPAPKKACC
5.2	1929.01	0.00	QKIEEVEKEYPGAPLSI
4.6	1929.02	-0.01	LQDLSGKLFKTISDLDH
4.2	1928.93	0.08	QQVANSKVPVVENGETQC
3.4	1929.09	-0.08	QRLISEKIWSVHHIIA
2.9	1928.98	0.03	KHVYNGVGHAFHILHNS
2.7	1929.01	0.00	GMVLIRGNSMVTIEALEP

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

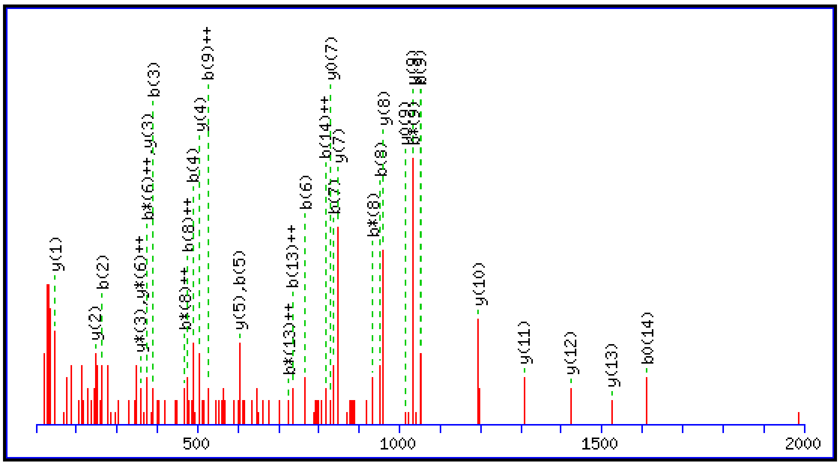
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNKVNYANVSTNNYALDEVEEVK**
Found in **Solyc09g063130.2.1**, genomic_reference:SL2.40ch09 gene_region:56787134-56789056 transcript_region:SL2.40ch09:56787134..56789056+ go_terms:GO:0009536,GO:0009538 functional_description:""Photosystem I reaction center subunit IV A (AHRD V1 *-*- B6TH55_MAIZE); contains Inter

Match to Query 17240: 2659.363548 from(887.461792,3+)
Title: cyr_090307_meja_05_2_bi3_p.01650.01650.3_38.703mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

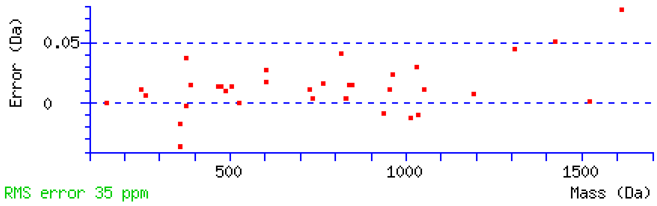
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

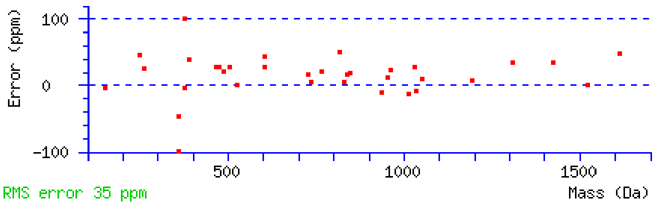


Monoisotopic mass of neutral peptide Mr(calc): 2659.28
Ions Score: 91 **Expect:** 2.2e-007
Matches : 34/240 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.08	74.54					**F**							**23**
2	***262.12***	131.56	245.09	123.05			**N**	2513.22	1257.11	2496.19	1248.60	2495.20	1248.11	**22**
3	***390.21***	195.61	373.19	187.10			**K**	2399.17	1200.09	2382.15	1191.58	2381.16	1191.08	**21**
4	***489.28***	245.14	472.26	236.63			**V**	2271.08	1136.04	2254.05	1127.53	2253.07	1127.04	**20**
5	***603.32***	302.17	586.30	293.65			**N**	2172.01	1086.51	2154.98	1077.99	2154.00	1077.50	**19**
6	***766.39***	383.70	749.36	375.18			**Y**	2057.97	1029.49	2040.94	1020.97	2039.96	1020.48	**18**
7	***837.43***	419.22	820.40	410.70			**A**	1894.90	947.96	1877.88	939.44	1876.89	938.95	**17**
8	***951.47***	**476.24**	934.44	467.72			**N**	1823.87	912.44	1806.84	903.92	1805.86	903.43	**16**
9	***1050.54***	**525.77**	1033.51	517.26			**V**	1709.82	855.42	1692.80	846.90	1691.81	846.41	**15**
10	1137.57	569.29	1120.54	560.77	1119.56	560.28	**S**	1610.75	805.88	1593.73	797.37	1592.74	796.88	**14**
11	1238.62	619.81	1221.59	611.30	1220.61	610.81	**T**	***1523.72***	762.36	1506.70	753.85	1505.71	753.36	**13**
12	1352.66	676.83	1335.63	668.32	1334.65	667.83	**N**	***1422.67***	711.84	1405.65	703.33	1404.66	702.84	**12**
13	1466.70	**733.85**	1449.68	725.34	1448.69	724.85	**N**	***1308.63***	654.82	1291.61	646.31	1290.62	645.81	**11**
14	1629.77	**815.39**	1612.74	806.87	1611.76	806.38	**Y**	***1194.59***	597.80	1177.56	589.28	1176.58	588.79	**10**
15	1700.80	850.90	1683.78	842.39	1682.79	841.90	**A**	***1031.53***	516.27	1014.50	507.75	1013.51	507.26	**9**
16	1813.89	907.45	1796.86	898.93	1795.88	898.44	**L**	***960.49***	480.75	943.46	472.23	942.48	471.74	**8**

17	1928.91	964.96	1911.89	956.45	1910.90	955.96	**D**	***847.40***	424.21	830.38	415.69	829.39	415.20	**7**
18	2057.96	1029.48	2040.93	1020.97	2039.95	1020.48	**E**	732.38	366.69	715.35	358.18	714.37	357.69	**6**
19	2157.02	1079.02	2140.00	1070.50	2139.01	1070.01	**V**	***603.33***	302.17	586.31	293.66	585.32	293.17	**5**
20	2286.07	1143.54	2269.04	1135.02	2268.06	1134.53	**E**	***504.27***	252.64	487.24	244.12	486.26	243.63	**4**
21	2415.11	1208.06	2398.08	1199.55	2397.10	1199.05	**E**	***375.22***	188.12	358.20	179.60	357.21	179.11	**3**
22	2514.18	1257.59	2497.15	1249.08	2496.17	1248.59	**V**	***246.18***	123.59	229.15	115.08			**2**
23							**K**	***147.11***	74.06	130.09	65.55			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.0	2659.28	0.09	FNKVNYANVSTNNYALDEVEEVK
5.2	2659.28	0.08	SYQQPSRIAYIEFFVKPEVDED
0.3	2659.40	-0.03	GNFANTNYIFQVIFALPLIVFCR
0.3	2659.28	0.09	KPDDERDQLDNTPSSDVQMLKTK

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

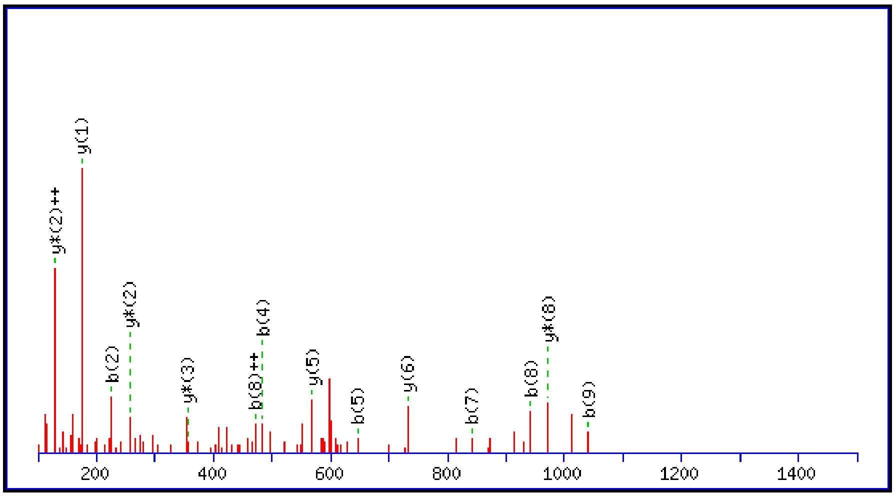
Mascot Search Results

Peptide View

MS/MS Fragmentation of **PKTRYPVVVR**
Found in **Solyc09g063130.2.1**, genomic_reference:SL2.40ch09 gene_region:56787134-56789056 transcript_region:SL2.40ch09:56787134..56789056+ go_terms:GO:0009536,GO:0009538 functional_description:""Photosystem I reaction center subunit IV A (AHRD V1 *-*- B6TH55_MAIZE); contains Inter

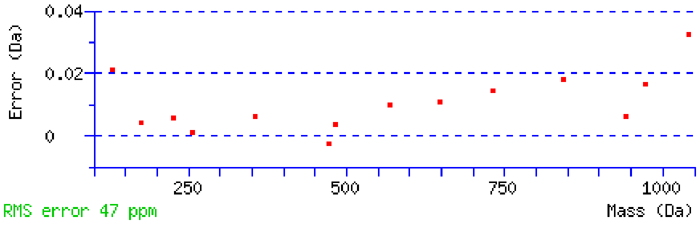
Match to Query 2869: 1213.713964 from(607.864258,2+)
Title: cyr_090307_meja_05_2_bi3_p.01139.01139.2_25.378mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

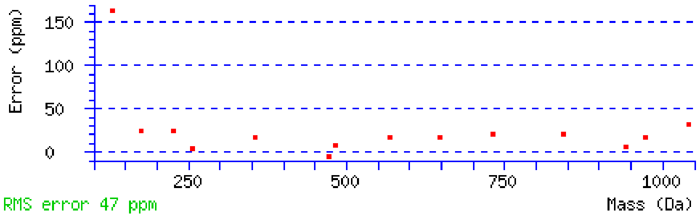
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1213.73
Ions Score: 46 **Expect:** 0.0086
Matches : 14/88 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	98.06	49.53					P							10
2	***226.16***	113.58	209.13	105.07			K	1117.68	559.35	1100.66	550.83	1099.67	550.34	9
3	327.20	164.10	310.18	155.59	309.19	155.10	T	989.59	495.30	972.56	486.78	971.58	486.29	8
4	***483.30***	242.16	466.28	233.64	465.29	233.15	R	888.54	444.77	871.51	436.26			7
5	***646.37***	323.69	629.34	315.17	628.36	314.68	Y	**732.44**	366.72	715.41	358.21			6
6	743.42	372.21	726.39	363.70	725.41	363.21	P	**569.38**	285.19	552.35	276.68			5
7	***842.49***	421.75	825.46	413.23	824.48	412.74	V	472.32	236.67	455.30	228.15			4
8	***941.56***	**471.28**	924.53	462.77	923.55	462.28	V	373.26	187.13	356.23	178.62			3
9	***1040.63***	520.82	1023.60	512.30	1022.61	511.81	V	274.19	137.60	257.16	129.08			2
10							R	**175.12**	88.06	158.09	79.55			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	1213.73	-0.02	PKTRYPVVVR
25.3	1213.67	0.04	QLCVQRNVVR
20.0	1213.77	-0.06	KKLTKRERR
18.8	1213.69	0.02	ELLRESGRVR
15.9	1213.71	0.01	QVQVCVRKVR
15.0	1213.64	0.07	QLNDKERVAAA
13.5	1213.70	0.02	MKVQGIGQVVR
13.2	1213.64	0.07	QQDVKIDVNR
12.2	1213.71	-0.00	KGAQTAASLVLR
11.4	1213.64	0.07	KPLVMYSLTY

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

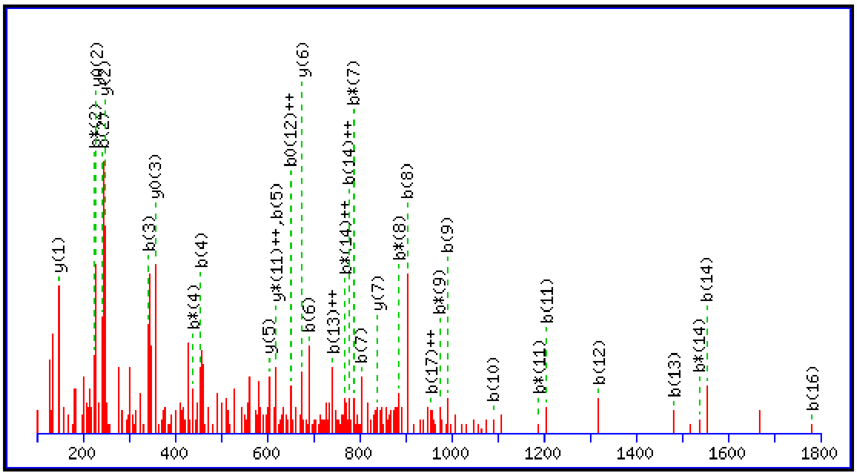
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NKVNYANVSTNNYALDEVE**
Found in **Solyc09g063130.2.1**, genomic_reference:SL2.40ch09 gene_region:56787134-56789056 transcript_region:SL2.40ch09:56787134..56789056+ go_terms:GO:0009536,GO:0009538 functional_description:""Photosystem I reaction center subunit IV A (AHRD V1 *-*- B6TH55_MAIZE); contains Inter

Match to Query 13107: 2156.001806 from(1079.008179,2+)
Title: cyr_090307_meja_05_2_bi3_p.01559.01559.2_36.335mins
Data file G:\Processed DATA\mgf\090307_uniqua_mgf\MGF\for Merge\merged meja0307 (2).mgf

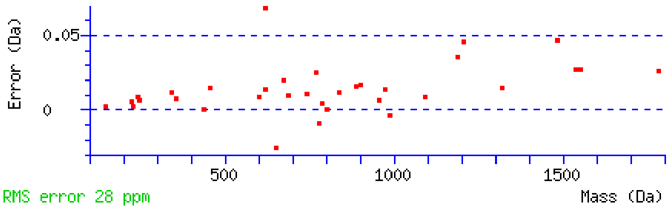
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

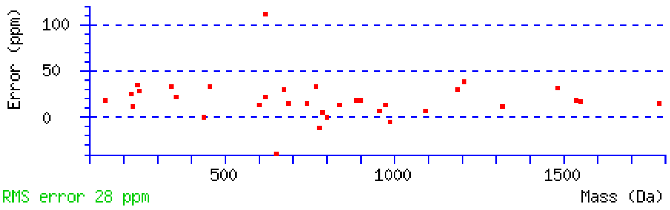


Monoisotopic mass of neutral peptide Mr(calc): 2156.00
Ions Score: 86 **Expect:** 5.7e-007
Matches : 34/186 fragment ions using 62 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.05	58.03	98.02	49.52			N							19
2	***243.15***	122.08	226.12	113.56			K	2042.97	1021.99	2025.94	1013.47	2024.96	1012.98	18
3	***342.21***	171.61	325.19	163.10			V	1914.87	957.94	1897.85	949.43	1896.86	948.93	17
4	***456.26***	228.63	439.23	220.12			N	1815.80	908.41	1798.78	899.89	1797.79	899.40	16
5	***619.32***	310.16	602.29	301.65			Y	1701.76	851.38	1684.73	842.87	1683.75	842.38	15
6	***690.36***	345.68	673.33	337.17			A	1538.70	769.85	1521.67	761.34	1520.69	760.85	14
7	***804.40***	402.70	787.37	394.19			N	1467.66	734.33	1450.63	725.82	1449.65	725.33	13
8	***903.47***	452.24	886.44	443.72			V	1353.62	677.31	1336.59	668.80	1335.61	668.31	12
9	***990.50***	495.75	973.47	487.24	972.49	486.75	S	1254.55	627.78	1237.52	619.26	1236.54	618.77	11
10	***1091.55***	546.28	1074.52	537.76	1073.54	537.27	T	1167.52	584.26	1150.49	575.75	1149.51	575.26	10
11	***1205.59***	603.30	1188.56	594.79	1187.58	594.29	N	1066.47	533.74	1049.44	525.22	1048.46	524.73	9
12	***1319.63***	660.32	1302.61	651.81	1301.62	651.32	N	952.43	476.72	935.40	468.20	934.42	467.71	8
13	***1482.70***	**741.85**	1465.67	733.34	1464.69	732.85	Y	**838.38**	419.70			820.37	410.69	7
14	***1553.73***	**777.37**	1536.71	768.86	1535.72	768.37	A	**675.32**	338.16			657.31	329.16	6

15	1666.82	833.91	1649.79	825.40	1648.81	824.91	L	**604.28**	302.64			586.27	293.64	5
16	***1781.85***	891.43	1764.82	882.91	1763.83	882.42	D	491.20	246.10			473.19	237.10	4
17	1910.89	**955.95**	1893.86	947.43	1892.88	946.94	E	376.17	188.59			358.16	179.58	3
18	2009.96	1005.48	1992.93	996.97	1991.95	996.48	V	**247.13**	124.07			229.12	115.06	2
19							E	**148.06**	74.53			130.05	65.53	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.3	2156.00	-0.00	NKVNYANVSTNNYALDEVE
6.7	2156.00	0.01	FLDFNSYYSCIALLCAKGE
4.3	2156.06	-0.06	QGPARSQLMSQSQGSSQGLPI
4.0	2156.07	-0.07	DLDMEEALGLTMHKKIPLC
3.0	2156.01	-0.01	FPLEFMREEDLRPAFME
1.7	2155.96	0.04	LMLANNARDDYFEDAADRG
0.4	2155.97	0.04	DEVLLDGFCDLSNESMLEK

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