

Arabidopsis Spot 35

[gi|15218112](#) **Mass:** 73895 **Score:** 76 **Queries matched:** 1 **emPAI:** 0.05

jacalin lectin family protein [Arabidopsis thaliana]

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 102	579.4990	1156.9834	1156.5764	0.4070	0	76	3.9e-06	1	K.TSSYFSVAAPK.D

[gi|15218112](#)
kinase (Experiment 3)
☐ Check to include this hit in error tolerant search or archive report

Top scoring peptide matches to query 102
File: 6H5.wiff, Sample: 6H5 (sample number 1), Elution: 20.64 min, Period: 1, Cycle(s): 407
Score greater than 23 indicates homology
Score greater than 35 indicates identity

Query	Score	Expect	Delta	Hit	Protein	Peptide
☒ 102	76.1	3.9e-06	0.4070	1	gi 15218112	K.TSSYFSVAAPK.D
	6.0	40	0.4135			K.LICQGFYTR.S
Protein	4.3	59	0.3522			M.TSSILRSHTTR.E

MS/MS Fragmentation of TSSYFSVAAPK

Found in [gi|15218112](#), jacalin lectin family protein [Arabidopsis thaliana]

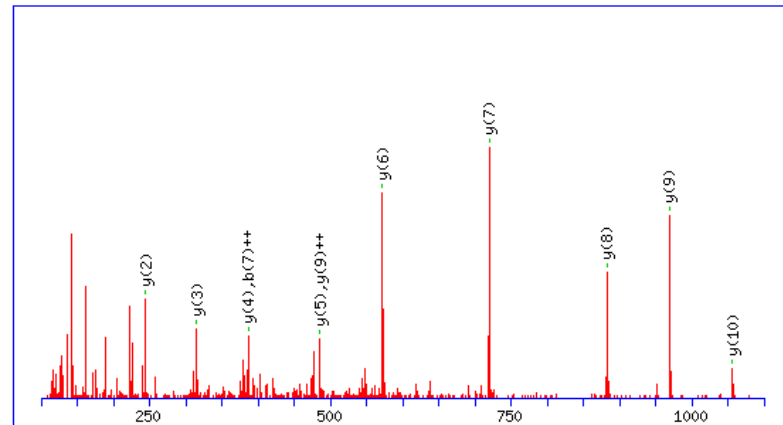
Match to Query 102: 1156.983450 from(579.499001,2+)

Title: File: 6H5.wiff, Sample: 6H5 (sample number 1), Elution: 20.64 min, Period: 1, Cycle(s): 407 (Experiment 3)

Data file C:\Documents and Settings\QStardata1\Desktop\Dai shaojun\dai search\20080414-6H5.mgf

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

Or, to Da



Arabidopsis Spot 515

[gi|417093](#) Mass: 24641 Score: 45 Queries matched: 1 emPAI: 0.15

Glutathione S-transferase (GST class-phi)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
138	482.7710	963.5275	963.5025	0.0250	0	45	0.026	1	K.VLDVYEAR.L

Top scoring peptide matches to query 138

Prot File: 13G4.wiff, Sample: 13G4 (sample number 1), Elution: 28.92 to 29 min, Period: 1, Cycle(s): 553-554 (Experiment 3)

[gi|4](#) Score greater than 42 indicates identity

glut

gi 2	Score	Expect	Delta	Hit	Protein	Peptide
Chai	45.0	0.026	0.0250	1+	gi 417093	K.VLDVYEAR.L
gi 3	26.8	1.8	0.0580			K.VLDVMDTR.L
T14P	17.5	15	0.0501			K.VIDNSNFR.N
gi 1	16.4	20	0.0097			K.VIDYIWR.E
gi 1	16.4	20	0.0758			K.VLDEMAMR.D
ATGS	14.3	31	-0.0590			K.IVDVHLLR.G
gi 1	13.8	35	0.0250			K.VLDFVESR.M
ATGS	13.8	35	0.0250			K.VLDIYEGR.L
gi 2	12.3	49	0.0692			R.VDIVDMEK.R
Atpm	12.3	49	0.0250			K.VDLVAYER.F

[gi|3](#)

MS/MS Fragmentation of VLDVYEAR

Found in [gi|417093](#), Glutathione S-transferase (GST class-phi)

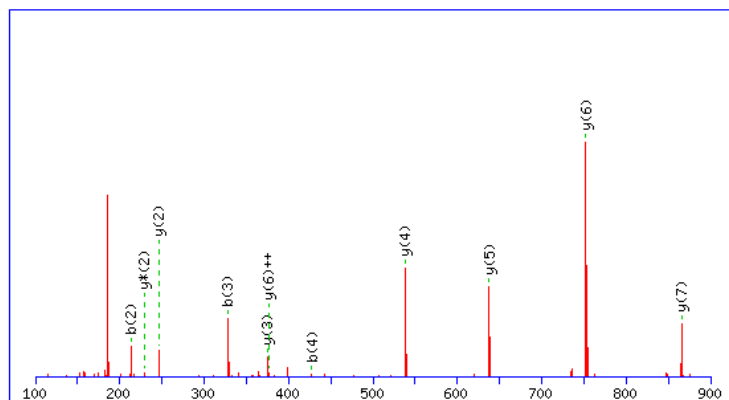
Match to Query 138: 963.527516 from(482.771034,2+)

Title: File: 13G4.wiff, Sample: 13G4 (sample number 1), Elution: 28.92 to 29 min, Period: 1, Cycle(s): 553-554 (Experiment 3)

Data file C:\Documents and Settings\QStardata1\Desktop\Dai shaojun\GAOJING-080625MODIFY\20080705\13E4.mgf

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Or, to Da



Thellungiella Spot 127

[gi|115473](#) **Mass:** 34888 **Score:** 77 **Queries matched:** 1

Carbonic anhydrase, chloroplast precursor (Carbonate dehydratase)

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 21	2056.0740	2055.0667	2055.0360	0.0307	0	77	9.2e-06	1	R.VCPSHVLNFQPGGEAFVVR.N

Top scoring peptide matches to query 21
Label: B6, Spot_Id: 29591, Peak_List_Id: 28525, MSMS Job_Run_Id: 10934, Comment:
Score greater than 39 indicates identity

Score	Expect	Delta	Hit	Protein	Peptide
76.8	9.2e-06	0.0307	1	gi 115473	R.VCPSHVLNFQPGGEAFVVR.N
51.5	0.0031	0.0307	2	gi 45451864	R.VCPSHVLNFQPGDAFIVR.N
24.0	1.7	-0.0057			R.VCPSHVLDFQPGKAFVVR.N
15.1	14	-0.0009			R.FLFXAEALFKAQAGTGEIK.G
12.7	24	0.1477			R.QPNFSADFSPECTLAPMTR.I
12.0	28	0.0790			K.LMSTCGRLNDVQTFER.E
11.9	29	0.2324			R.MAESSRMEEPPQMAGQASX.-
11.5	31	0.0500			K.TEMAALIQOPTNKQSSHR.R
9.7	47	0.1542			K.SGGNCNWVLPQYVCVMR.A
8.4	63	-0.0850			K.DLVGHSLSFLLVWTLISR.A

MS/MS Fragmentation of VCPSHVLNFQPGGEAFVVR

Found in [gi|115473](#), Carbonic anhydrase, chloroplast precursor (Carbonate dehydratase)

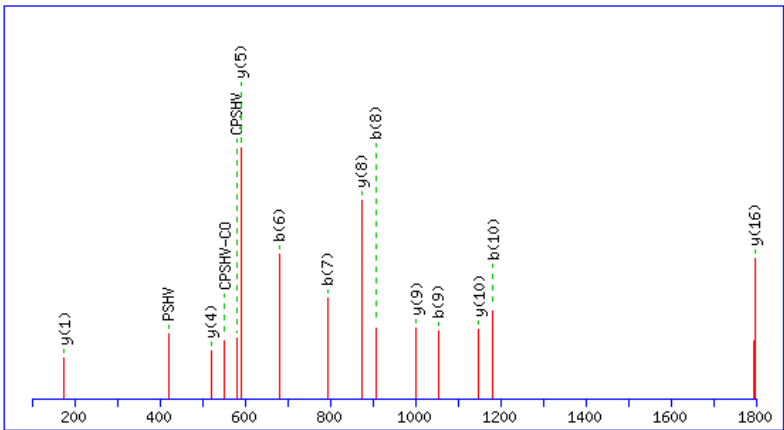
Match to Query 21: 2055.066724 from(2056.074000,1+) intensity(0.0000)

Title: Label: B6, Spot_Id: 29591, Peak_List_Id: 28525, MSMS Job_Run_Id: 10934, Comment:

Data file C:\Documents and Settings\QStardata1\Desktop\Dai shaojun-don't delete please\20080908-PANG-th\ppw_B6_122100963523.txt

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

Or, to Da



Thellungiella Spot 159

[gi|68131813](#) Mass: 29579 Score: 66 Queries matched: 1 emPAI: 0.13

dehydroascorbate reductase [Medicago truncatula]

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 114	540.2579	1078.5013	1078.4866	0.0148	0	66	0.00018	1	K.IGDCPFSQR.V

Top scoring peptide matches to query 114

[gi|9](#) File: Y2B7.wiff, Sample: Y2B7 (sample number 1), Elution: 14.92 min, Period: 1, Cycle(s): 334
dehy (Experiment 3)

☐ Check Score greater than 41 indicates identity

Query	Score	Expect	Delta	Hit	Protein	Peptide
11	66.3	0.00018	0.0148	1	gi 68131813	K.IGDCPFSQR.V
	66.3	0.00018	0.0148	2	gi 98978771	LGDCPFSQR
	35.8	0.2	-0.0580			K.LGFAGMPSRK.R
	28.3	1.1	-0.0434			K.IWGADFSVGK.R
Prot	16.3	18	-0.0645			R.LGDIGSYLNK.S
gi 1	16.2	19	-0.0506			R.ASAKANFSAGR.M
dehy	15.4	22	-0.0427			R.ILSXGTSSQR.T
gi 1	14.6	26	-0.0506			R.IQVSPHDGAR.T
hypo	14.2	29	0.0082			K.KSDDPFGEKG.D
	14.2	29	-0.0216			K.MRASPFNEK.S

MS/MS Fragmentation of **IGDCPFSQR**

Found in [gi|68131813](#), dehydroascorbate reductase [Medicago truncatula]

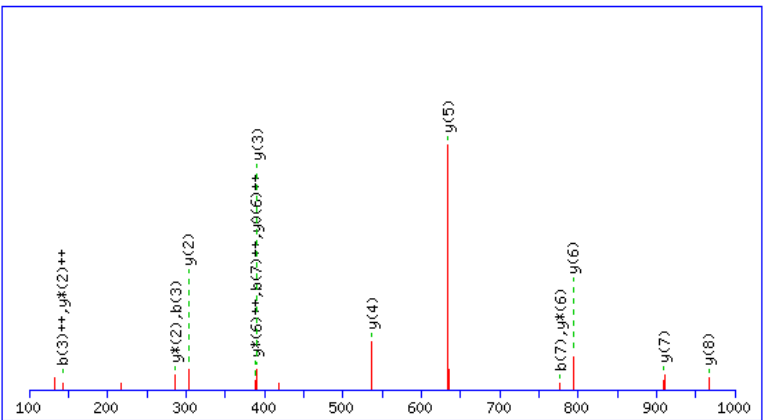
Match to Query 114: 1078.501340 from(540.257946,2+)

Title: File: Y2B7.wiff, Sample: Y2B7 (sample number 1), Elution: 14.92 min, Period: 1, Cycle(s): 334 (Experiment 3)

Data file C:\Documents and Settings\adg\Desktop\Pang\Y2B7.wiff

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

Or, to Da



Thellungiella Spot 160

[gi|15222089](#) **Mass:** 26148 **Score:** 63 **Queries matched:** 1
PR5 (PATHOGENESIS-RELATED GENE 5) [Arabidopsis thaliana]
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 12	1633.7457	1632.7384	1632.7672	-0.0287	0	63	0.00031	1	K.DFYDVSLVDGYNVK.L

ptide ma

Top scoring peptide matches to query 12
Label: A1, Spot_Id: 29562, Peak_List_Id: 28295, MSMS Job_Run_Id: 10934, Comment:
Score greater than 40 indicates identity

Query	Score	Expect	Delta	Hit	Protein	Peptide	
☒ 12	62.7	0.00031	-0.0287	1	gi 15222089	K.DFYDVSLVDGYNVK.L	EIR
☒ 12	23.7	2.4	-0.1498			R.GMEHLLISHTRAR.A	
☒ 12	17.0	11	-0.1352			R.SAVVALWDYRLQGR.H	+ Oxid
☒ 12	15.8	15	-0.1484			R.EIKNILMTVVNTSR.R	ELR
☒ 12	15.5	16	0.0870			R.EPYADSEMWNYYGR.D	ATKNLR
☒ 12	13.1	28	-0.0472			K.DSNLKSFDSSLHQR.T	KLR +
☒ 12	13.1	28	0.0434			K.ERMYDNSGYASGQR.S	ILEYCD
☒ 12	12.1	35	-0.0770			R.MSGLNHSGPSLVXAAR.L	QITEEE
☒ 12	12.0	36	-0.1100			R.NFYQSHVRTVLNR.V	
☒ 12	11.4	42	-0.0658			K.AQDYVCGLAPRIXR.L	

MS/MS Fragmentation of **DFYDVSLVDGYNVK**
Found in [gi|15222089](#), PR5 (PATHOGENESIS-RELATED GENE 5) [Arabidopsis thaliana]

Match to Query 12: 1632.738424 from(1633.745700,1+) intensity(0.0000)
Title: Label: A1, Spot_Id: 29562, Peak_List_Id: 28295, MSMS Job_Run_Id: 10934, Comment:
Data file C:\Documents and Settings\QStardata1\Desktop\Dai shaojun-don't delete please\20080908-PANG-th\ppw_A1_122100957100.txt

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