

Figure S1. Effect of 2 μ M staurosporine (STA) on ABA/MeJA-induced stomatal closure and H₂O₂ production. (a) STA abolishes ABA/MeJA induced closure. (b) STA inhibits ABA/MeJA elevated ROS levels. Left, representative stomatal images; right, quantitative data. The pseudocolor key beside the lower right stomatal image indicates the increase of the fluorescence from bottom to top. At least 60 stomata were analyzed in each experiment and three replicate experiments were conducted. The quantitative data are shown as average ± standard deviation.

Figure S2

MS/MS spectra of ICAT identified ABA responsive cysteines

Twenty seven cysteines were mapped from ABA treated guard cells. The precursor of the cysteine-containing peptide and the fragmented ions were shown as the evidence for mapping.

Ribulose bisphosphate carboxylase large chain precursor GRPLLG<u>C</u>TIKPK

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	Protein Q	Jant				Protein ID	Spectra		Summary Statistics
Spectrum L	ist								
Spectrum	Time	Prec MW	/ Prec m/z	Prec z	Prot N	Best Sequence	△ Modifications	0	Conf Theor MW z
5.1.1.1821.4	34.2	28 1508.979	96 504.0005	3	2	GRPLLGCTIKPK	ICAT-C(C)@7		93 1508.8861 3
5.1.1.1822.2	34.2	80 1517.998	35 507.0068	3	2	GRPLLGCTIKPK	ICAT-C:13C(9)(C)@7		76 1517.9163 3
6.1.1.1691.2	30.2	53 1508.938	32 503.9867	3	2	GRPLLGCTIKPK	ICAT-C(C)@7		<1 1508.8861 3
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Peptide ID	- Hypotheses	5.1.1.1821.4	ļ					Precur	rsor MS Region
Conf ⊽ Sc	Prot N 🛆	Se	auence		Δ	Modifications	MW Theorm/z z ∆Mass		
93 13	2 GR	LLGCTIKPK			ICAT-0	C(C)@7 1508.	.8861 503.9693 3 0.0935	10	0 408 3168 503.9994 -507.0076
< 1 9	EDI	EHLQTLLQR				1508.	.7947 503.9388 3 0.1849	2 8	490.5100 502.3558 - 1 - 507.3398
< 1 9	KS	HQGNVKEE P	R			1508.	.7695 503.9305 3 0.2101	e se	0 507.6750
< 1 9	RL	QLFTTYLNK				1508.	.8715 503.9644 3 0.1081	트 4	0
< 1 9	SSI	ILLTENYRA	K		Deami	dated(N)@9 1508.	.7834 503.9351 3 0.1962	2	° 111 a
									0 114 114 144 144 144 144 144 144 144 14
Fragmentat	ion Evidence	for Peptide	!						
Fragmentat	ion Evidence PLLGC[C0]TIKPK	for Peptide	:						
Fragmentat GR Residue	ion Evidence PLLGC[C0]TIKPK b	for Peptide b+2	у						
Fragmentat GR G	ion Evidence PLLGC[C0]TIKPK b 58.0287	for Peptide b+2 29.5180 1	y 509.8934	50	o 1	y1 y2 1 3	y3 y5	у(6 y7
Fragmentat GR Residue	ion Evidence PLLGC[C0]TIKPK b 58.0287 214.1299	for Peptide	y 509.8934 452.8719	50	0	y1 y2 y b2 b5=8-2	y3 b67+2 b5 b6 594.40 b12+2	yt t	6 y7 b9 b11
Fragmentat GR Residue G R P	ion Evidence PLLGC[C0]TIKPK 58.0287 214.1299 311.1826	for Peptide b+2 29.5180 1 107.5686 1 156.0949 1	y 509.8934 452.8719 296.7708	50	0	y1 y2 y2 b2 b5-€8+2 244,18	y3 b b 7+2 b5 b6 594.40 b12+2 424.30 533 80	y¢ t	6 y7 b9 b11
Fragmentat G R P L	ion Evidence PLLGC[C0]TIKPK 58.0287 214.1299 311.1826 424.2667	for Peptide b+2 29.5180 1 107.5686 1 156.0949 1 212.6370 1	y 509.8934 452.8719 296.7708 (199.7180 (99.0214)	50 45 40	0 - 0 - 0 -	y1 y2 y b2 b5=±2+2 244.18	y3 bb7 +2 b5 b6 594.40 b12+2 537.39 -616.40	yt t	6 y7 b9 b11
Fragmentat G R P L L C	ion Evidence PLLGC[C0]TIKPK b 58.0287 214.1299 311.1826 424.2667 537.3507 E64.2727	for Peptide	y 509.8934 452.8719 296.7708 (199.7180 (86.6340) 97 7 640	50 45 40 35		y1 y2 y b2 b5 62 +2 244,18 129,11	y3 b67+2 b5 b6 594.40 b12+2 537.39 -616.40 663.44	y¢ E	6 y7 b9 b11
Fragmentat G R P L L G G CICOII	ion Evidence PLLGC[C0]TIKPK b 2 58.0287 214.1299 311.1826 424.2667 537.3507 594.3722 924.584	for Peptide 29.5180 11 107.5686 11 156.0949 11 212.6370 11 269.1790 11 297.6897 462 2578	y 509.8934 1 452.8719 1 296.7708 0 199.7180 0 086.6340 4 973.5499 4	50 45 40 35 ≩g30		y1 y2 b2 b5=8+2 244.18 129.11	y3 b67+2 -424.30 537,39 -616.40 663.44	y¢ b	6 y 7 b9 b11
Fragmentat G R P L L G C[C0I] T	ion Evidence PLLGC[C0]TIKPK b 2 58.0287 214.1299 311.1826 424.2667 537.3507 594.3722 924.5084 1025.5561	b+2 2 29.5180 1 107.5686 1 156.0949 1 212.6370 1 269.4790 1 297.6897 4 462.7578 5	y 509.8934 452.8719 296.7708 199.7180 086.6340 973.5499 916.5284 586.3923	50 45 40 35 ≩30 213 212 212		y1 y2 b5 b5 -2 244,118 129.11 226.17	y3 b6 7+2 b5 b6 594.40 b12+2 - 424.30 537.39 - 616.40 663.44	y¢ t	6 y7 b9 b11
Fragmentat G R P L L G C[C01] T T	ion Evidence PLLGC[C0]TIKPK b 2 58.0287 214.1299 311.1826 424.2667 537.3507 594.3722 924.5084 1025.5561 1138.6404	b+2 29.5180 11 107.5686 11 156.0949 11 212.6370 11 289.1790 11 297.6897 462.7578 513.2817 569.8237	y 509.8934 452.8719 296.7708 199.7180 086.6340 973.5499 916.5284 586.3923 485.3446	50 45 40 Aguup <u>1</u> 20		y1 y2 b2 b5 €8+2 244,18 129.11 226.17 396	y3 b67+2 b5 b6 594.40 b12+2 -424.30 537.39 -616.40 663.44	y¢ t	6 y7 b9 b11 1379.82
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Fragmentat GR R P L L G C[C0] T I K P	ion Evidence PLLGC[C0]TKPK 58.0287 214.1299 311.1826 424.2667 537.3507 594.3722 924.5084 1025.5561 1138.6401 1266.7351 1363.7879	b+2 29.5180 1 107.5686 1 156.0949 1 212.6370 1 209.5180 1 156.0949 1 212.6370 1 209.76897 1 209.5180 1 569.8237 1 633.8712 1 682.3976 1	y 509.8934 452.8719 296.7708 199.7180 086.6340 973.5499 916.5284 586.3923 485.3446 372.2605 244.1656	50 45 40 36 419 125 20 15		y1 y2 b5 b5 b2 +2 244,18 129,11 226.17 396 214,15 293 24	y3 b67+2 b5 b6 594.40 b12+2 - 424.30 537.39 - 616.40 663.44 1.30 746.50	907 879.56 825.52	6 y7 b9 b11 7.55 1138.69 1249.76 1332.95 1409.90
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Fragmentat GR Residue G R P L L L G C[C0I] T I K P K	ion Evidence PLLGC[C0]TIKPK 58.0287 214.1299 311.1826 424.2667 537.3607 594.3722 924.5084 1025.5661 1138.6401 1266.7351 1363.7879 1491.8828	b+2 2 29.5180 1 107.5686 1 156.0949 1 212.6370 1 269.1790 1 27.6897 1 269.8237 1 569.8237 1 633.8712 1 682.3976 1 746.4450 1	y 509.8934 452.8719 296.7708 199.7180 086.6340 973.5499 916.5284 586.3923 2485.3446 372.2605 244.1656 147.1128	50 45 40 35 32 30 20 15 10 5		y1 y2 b5 b5 b5 -2 244,18 129,11 226,17 214,15 293,24 136,08 214,15 293,24 136,08 2280,19 100	y3 bb7 +2 -424.30 537.39 -616.40 663.44 .30 746.50 400 500 600 700 400 500 500 500 500 500 500 5	907 879.56 825.52	6 y7 b9 b11 7 55 1138.69 1249.76 1332.95 1409.90 9 90.58 1077.71
Fragmentat GR R P L L L G C[C0I] T I K P K	ion Evidence PLLGC[C0]TIKPK 58 0287 214.1299 311.1826 424.2667 537.3607 594.3722 924.5084 1025.5661 1138.6401 1266.7351 1363.7879 1491.8828	b+2 2 29.5180 1 107.5686 1 156.0949 1 212.6370 1 207.6897 1 207.6897 1 203.8177 1 569.8237 1 633.8712 1 682.3976 1 746.4450 1	y 509.8934 452.8719 296.7708 199.7180 086.6340 973.5499 916.5284 586.3923 2485.3446 372.2605 244.1656 147.1128	50 45 40 35 225 20 15 10 5		y1 y2 b5 b5 b2 + 2 244,18 129,11 226,17 214,15 293,24 136,08 226,19 100 200 300	y3 b67+2 b5 b6 594.40 b12+2 -424.30 537.39 -616.40 663.44 .30 746.50 400 500 600 700 8 m/z, Da	907 879.56 825.52 800 90	6 y7 b9 b11 7 55 1138.69 1249.76 1332.95 1409.90 990.58 1077.71 100 100 1200 1300 1400 1500

Ribulose bisphosphate carboxylase large chain precursor <u>CYHIEPVPGEETQFIAY</u>

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	Protein (Juant					Protein ID			Spectra				Summa	ry Statis	tics	
Spectrum L	ist																
Spectrum	Time	Prec	MW F	Prec m/z	Prec z	Prot N	Best Sequen	ce 🗠			Modifica	tions			Conf	Theor MW	z 🔺
3.1˙1.15	40.	571 2222.	.0247	741.6821	3	2	2 CYHIEPVPGEETQFI	ΑY	ICAT-C(C)@1						99	2222.0354	3
3.1˙1.15	40.	528 2231.	.0327	744.6848	3	2	2 CYHIEPVPGEETQFI	ΑY	ICAT-C:13C(9)(C)@1					99	2231.0657	3
10.1˙1.1	41.	428 2221.	.9971	741.6730	3	2	2 CYHIEPVPGEETQFI	ΑY	ICAT-C(C)@1						99	2222.0354	3 👻
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Peptide ID	Hypotheses -	3.1dot;1.	1574.2.	.3										Precurs	sor MS R	egion	
Conf ⊽ Sc	Prot N A			s	equence		Δ	Modifi	cations /	Theor MW	Theor m/z	7 AMass				Js	
99 15	2 CY	HIEPVPGE	ETOFI	AY				ICAT-C:13C(9	J)(C)@1	2231.0657	744.6958	3 -0.0330		74	2.0170 -	745.019	3
< 1 11	GL	TITGVPVN	MAANTI	NVVTMGR				Oxidation(M)	@20	2231.1401	744.7207	3 -0.1076	-	100 -		745.69	00
< 1 10	HL	VWALRDSG	INVFK	DSFK						2231.1851	744.7357	3 -0.1525				/40.3	5/0
< 1 9	LA	CRTVGWGV	VGGLGI	PPLPR				ICAT-C(C)@3	1	2231.2361	744.7526	3 -0.2035		0-44	a da ha kata kata di ka Kata di kata di	mini na p atistika mini Da	Approx Apres
	en	CTRODULU	010077	тест				ICAT C:13C(N(C)@18	2231 1528	744 7249	3 0 1202				111/2, Da	
Fragmentat	ion Evidence	e for Pepti	ide														
Residue	b	b+2	У		24					1 1 11				1	I	1 1	
C[C91]	340.1736	170.5905	2232.0	0729 11	240	~1	y1 y2	-2 5 - 2 5 2		0.345.35	LC L7	y10		644 647			
Y	503.2370	252.1221	1892.5	9065 8	220	0	253.1	1 1	US @#	H2+2/10+200	00 07	00 09 01				014	
	752 2000	320.0510	1729.0	7042	200	0 -											
	882 4225	444 7440	1/170 2	7043 1	180	01											
	979.4753	490 2413	1350 /	6576													
v	1078.5437	539,7755	1253 (6048	160	1	102.00 28	118									
P	1175.5965	588.3019	1154.	5364	.≥ ¹⁴⁰	0	184.06				1078	.55					
G	1232.6179	616.8126	1057.4	4837 5	မ်း မြို့ 12(0 -		413.16									
E	1361.6605	681.3339	1000.4	4622 5	트 100	0											
E	1490.7031	745.8552	871.4	4196 4				496.2	'								
Т	1591.7508	796.3790	742.3	3770 3	80	0				882.40							
Q	1719.8094	860.4083	641.3	3293 3	60	0 1	20.08 230.11		514.21								
F	1866.8778	933.9425	513.2	2708 2	40	0-	29	5.16	^{044.27} 74	5.40 865.37	979.46	1061.51					
1	1979.9619	990.4846	366.2	2023 1	20	<u>_</u>			761 33		1	050.54		1490 72	1573.71	1866.87	
A	2050.9990	1026.0031	253.1	1183	20	11	10.07	اللبليل اس		1		1232.63 13	61.68		1701	.76	
Y	2214.0623	1107.5348	182.0	0812		0	100 200 300	400 500	600 700	800 900	1000 1	100 1200 1300	1400	1500 1	600 170	0 1800 1	1900
						Ĵ				m/	z, Da						
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Ribulose bisphosphate carboxylase large chain precursor VALEA<u>C</u>VQAR

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	Protein Qua	int				Protein ID			Spectra				Su	ummary	Statisti	ics	
Spectrum Lis	st																
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequen	nce 🗠			Modificat	ions				Conf	Theor MW	z 🔺
3.1˙1.14	. 28.250	1285.6472	643.8309	2	2	VALEACVKAR		ICAT-C(C)@6							32	1285.7177	2
3.1˙1.14	. 28.164	1294.6741	648.3443	2	2	VALEACVKAR		ICAT-C:13C(9)	(C)@6						97	1294.7478	2
9.1˙1.13	. 30.087	1285.6302	643.8224	2	2	VALEACVKAR		ICAT-C(C)@6							88	1285.7177	2
9.1˙1.13	. 30.044	1294.6531	648.3338	2	2	VALEACVKAR		ICAT-C:13C(9)	(C)@6						93	1294.7478	2 📼
10.1˙1.1	. 29.917	1285.6475	643.8310	2	2	VALEACVKAR		ICAT-C(C)@6							45	1285.7177	2 🔻
Peptide ID Hy	potheses - 2.	1dot;1.1399	.3.2										Р	recurso	r MS Re	egion	
Conf ⊽ Sc F	Prot N 🛆		:	Sequence		Δ	Modif	ications	A Theor MW	Theor m/z	z	∆Mass	Шг	1			
99 14	2 VALE	ACVKAR					ICAT-C:13C(9)(C)@6	1294.7478	648.3812	2	-0.0724		60 64	43.8265	648.3480	
99 14 9	94, 98, VALE	ACVQAR					ICAT-C:13C(9)(C)@6	1294.7114	648.3630	2	-0.0361		40	648	8499	
99 14	VAIE	ACVQAR					ICAT-C:13C(9)(C)@6	1294.7114	648.3630	2	-0.0361		20	- I	650.328	19
22 14	VALQ	ACVQAR					Deamidated(Q)@4, ICAT-C:	. 1294.7114	648.3630	2	-0.0361				A Martin A	e line hu
21 14	VAPE	ACVQAR					Oxidation(P)	@3, ICAT-C:13	1294.6750	648.3448	2	0.0003		640	645	650 655	660
															m/	/z, Da	
Fragmentatio	on Evidence fo	r Peptide															
Fragmentation	AC[C9]VQAR	or Peptide															
Fragmentation VALE	AC[C9]VQAR	or Peptide	у	y+2													
Fragmentation VALE	b I 100.0757 1	or Peptide	y 95.7187	y+2 648.3630	550	1	y1 y2 b2 y4+2 b3	y3 b4	y4 b5 v8+2	v10+2	уE	5 уб	у	y7 b8	у8	y9	
Residue V A	AC[C9I]VQAR b 100.0757 171.1128	b+2 50.5415 129 86.0600 119	y 95.7187 9 6.6503	y+2 648.3630 598.8288	550) [y1 y2 b3	y3 b4	y4 b5 y8+2 473.27	y10+2	уE	5 уб	у	y7 b8	у8	у9	
Residue V A L	b I 100.0757 1 171.1128 1 284.1969 1	or Peptide b+2 50.5415 125 86.0600 112 42.6021	y 95.7187 (96.6503 (25.6132 (y+2 648.3630 598.8288 563.3102	550 500 450		y1 y2 b2 y4+2 b3	y3 b4	y4 b5 473.27	y10+2	у£	5 y6	у	y7 b8	y8	у9	
Residue V A L E	b I 100.0757 1 171.1128 1 284.1969 1 413.2395 2	o+2 50.5415 129 86.0600 119 42.6021 111 07.1234 100	y 95.7187 9 96.6503 4 4 25.6132 4 4 12.5291 4 4	y+2 648.3630 598.8288 563.3102 506.7682	550 500 450		y1 y2 b2 y4+2 b3	y3 b4	y4 b5 y8+2 473.27	y10+2	уE	5 y 6 883.46	у	y7 b8	ув	y9	
Residue V A L E A	b 1 100.0757 1 284.1969 1 413.2395 2 484.2766 2	or Peptide 50,5415 125 86,0600 111 42,6021 111 07,1234 101 42,6419 88	y 95.7187 0 96.6503 8 25.6132 8 12.5291 8 33.4865 9	y+2 648.3630 598.8288 563.3102 506.7682 442.2469	550 500 450 400		y1 y2 b3	у3 _{b4}	y4 b5 y8+2 473.27	y10+2	уE	5 y6 883.46	у	y7 b8	у8	у9	
Residue V A L E A C[C9I]	b 1 100.0757 1 284.1969 1 413.2395 2 484.2766 2 823.4429 4	p+2 50.5415 125 86.0600 115 42.6021 111 07.1234 101 42.6419 88 12.2251 81	y 95.7187 0 96.6503 4 4 12.5291 4 4 12.4294 4 4	y+2 648.3630 598.8288 563.3102 506.7682 442.2469 406.7284	550 500 450 400 350		y1 y2 b3 b2 y4+2 b3 171 11 246.15	у3 _{b4}	y4 b5 y8+2 473.27	y10+2	у£	5 y6 883.46	у 10	y7 b8	у8	у9	
Residue V A L E A C[C9I] V	b 1 100.0757 1 284.1969 1 413.2395 2 484.2766 2 823.4429 4 922.5114 4	D+2 50.5415 125 86.0600 115 42.6021 111 07.1234 101 42.6419 88 12.2251 81 51.7533 47	y 95.7187 1 96.6503 4 4 25.6132 4 4 12.5291 4 4 12.4494 4 4 73.2831 5 4	y+2 648.3630 598.8288 563.3102 506.7682 442.2469 406.7284 237.1452	550 500 450 400 350 25 300		y1 y2 b3 b2 y4+2 b3 171 11 246.15	у3 _{b4}	y4 b5 y8+2 473.27	y10+2	γĔ	5 y6 883.46	у 10	y7 b8	у8	у9	
Fragmentation VALE. Residue V A L A C[C9I] V Q A	b I 100.0757 1 141.02757 1 141.32395 2 484.2766 2 823.4429 4 922.5114 4 1050.6599 5	D+2 50.5415 125 86.0600 115 42.6021 111 07.1234 101 42.6419 88 12.2251 84 81.7593 47 25.7866 29.07	y 95.7187 1 96.6503 8 2 1 12.5291 8 3 1 12.4494 4 4 1 73.2831 2 7 1 1	y+2 648.3630 598.8288 563.3102 506.7682 442.2469 406.7284 237.1452 187.6110 432.5247	550 500 450 400 350 253 300 E		y1 y2 b3 b2 y4+2 b3 171 11 246.15	y3 b4 374.21	y4 b5 y8+2 473.27	y10+2	yE	5 y6 883.46	y 10	y7 b8	у8	γ9	
Residue V A L E A C[C9I] V Q A P	b I 100.0757 1 100.0757 1 101.0757 1 101.0757 1 101.0757 1 101.0757 1 101.0757 1 101.0757 1 101.0757 1 102.0757 1 103.0359 2 1050.5699 5 1121.16070 5	Peptide 50.5415 125 86.0600 115 42.6021 111 07.1234 101 42.6419 88 12.2251 84 81.7593 41 25.786 31 91.3072 29.9577	y 95.7187 1 96.6503 2 12.5291 2 33.4865 2 12.4494 2 73.2831 2 74.2146 2 76.7561 2	y+2 648.3630 598.8288 563.3102 506.7682 442.2469 406.7284 237.1452 187.6110 123.5817 88.0634	550 500 450 450 450 350 250 250 200	143.12	y1 y2 b3 b2 y4+2 b3 171 11 246.15	y3 b4 374.21 54.13	y4 b5 y8+2 473.27	y10+2	у£ 81	5 y6 883.46 2.42	У 10	97 b8	у8	γ9	
Residue V A E A C[C9I] V A R	b I 100.0757 1 171.1128 1 413.2395 24 484.2766 2 823.4429 4 922.5114 44 1050.5699 5 1121.6070 5 1277.7082 6	Peptide 50.5415 122 86.0600 111 42.6021 111 07.1234 101 42.6419 88 12.2251 84 61.7593 41 25.786 31 61.3072 24 39.3577 11	y 955.7187 1 966.6503 2 12.5291 2 33.4865 2 12.4494 2 73.2831 2 74.2146 2 46.1561 2	y+2 648.3630 598.8288 563.3102 506.7682 442.2469 406.7284 237.1452 187.6110 123.5817 88.0631	550 500 450 450 350 250 250 200 150	143.12	y1 y2 b3 b2 y4+2 b3 171 11 246.15	y3 b4 374.21 54.13 284.20 205 45	y4 b5 y8+2 473.27	y10+2	у£ 81	5 y6 883.46 2.42	y 10 977.4	y7 b8	y8	γ9	
Residue V A L E A C[C9I] V Q A R	b I 100.0757 1 171.1128 1 413.2395 24 484.2766 2 823.4429 4 922.5114 4 1050.5699 5 1121.6070 56	Peptide 50.5415 1225 86.0600 1115 42.6021 1112 07.1234 1001 42.6129 88 12.2251 81 61.7593 47 25.7886 37 51.3072 24 39.3577 17	y	y+2 648.3630 598.8286 563.3102 506.7682 442.2469 406.7284 237.1452 187.6110 123.5817 88.0631	550 500 450 450 350 250 250 200 150 100	143.12	y1 y2 b3 b2 y4+2 b3 171 11 246.15	y3 b4 374.21 54.13 284.20 295.16 (, 323.15	y4 b5 y8+2 473.27	y10+2	у ^в 81 86	5 y6 883.46 2.42	977.4	y7 b8 012.51 48 995.49	y8 1125.63	γ9	
Fragmentation VALE Residue V A L E A C[C9I] V Q A R	b I 100.0757 1 284.1969 1 413.2395 2 484.2766 2 823.4429 4 922.5114 44 1050.5699 55 1121.6070 56 1277.7082 6	Peptide 0+2 50.5415 125 66.0600 115 42.6021 111 07.1234 101 42.6419 88 12.2251 81 51.7593 41 25.7886 33 51.3072 24 39.3577 11	Y Image: 200 minipage 955.7187 1minipage 966.6503 4minipage 25.6132 4minipage 12.5291 4minipage 33.4865 4minipage 12.4494 4minipage 73.2831 2minipage 146.1561 2minipage 75.1190 2minipage	y+2 648.3630 598.8288 506.7682 442.2469 406.7284 237.452 187.6110 123.5817 88.0631	550 500 450 450 350 <u>A</u> 350 <u>A</u> 300 250 200 150 100 50	143.12 157.13 129.10	y1 y2 b3 b2 y4+2 b3 171 11 246.15 ,2	y3 b4 374.21 54.13 284.20 295.16 323.15	y4 b5 y8+2 473.27 523.22	y10+2 563.31 648.	у£ 81 33 847.	5 y6 883.46 2.42 36.47 874 44 93	977.4 10 977.4	y7 b8 012.51 48 995.49 1066.	y8 1125.63	y9	
Fragmentation VALE Residue V A L E A C[C9I] V Q A R	b I 100.0757 1 284.1969 1 413.2395 2 484.2766 2 823.4429 4 922.5114 4 101.121.6070 5 1121.6070 5 1277.7082 6	P+2 50.5415 125 86.0600 115 42.6021 111 07.1234 101 42.6419 88 12.2251 84 51.7593 41 25.7886 33 31.3072 24 39.3577 11	y 955.7187 1 966.6503 4 255.6132 4 12.5291 4 33.4865 4 12.4494 4 73.2831 3 74.2146 4 75.1190 7	y+2 648.3630 598.8288 563.3102 506.7682 442.2469 406.7284 237.1452 187.6110 123.5817 88.0631	550 500 450 400 350 150 250 250 150 100 50 0	143.12 157.13 0 100	y1 y2 b3 b2 y4+2 b3 171 11 246.15 ,2 200	y3 b4 374.21 54.13 284.20 295.16 323.15 300 400	y4 b5 473.27 523.22 500	y10+2 563.31 648:	y£ 81 33 847.	5 y6 883.46 2.42 56.47 874 90 900	977.4 10 977.4 1.45 11	y7 b8 012.51 48 995.49 1066.	y8 1125.63	y9	
Fragmentation VALE Residue V A L E A C[C9I] V Q A R	b I 100.0757 1 120.0757 1 130.0757 1 141.32395 2 484.2766 2 823.4429 4 922.5114 4 101.050.5699 5 1121.6070 5 1277.7082 6	P+2 50.5415 125 86.0600 115 42.6021 111 97.1234 101 42.6419 88 12.2251 81 81.7593 47 25.7886 37 31.3072 24 39.3577 17	y 955.7187 1 966.6503 4 225.6132 4 12.5291 4 33.4865 4 12.4494 4 73.2831 3 74.2146 4 75.1190 5	y+2 648.3630 598.8288 563.3102 506.7682 442.2469 406.7284 237.1452 187.6110 123.5817 88.0631	550 500 450 400 350 250 250 150 100 50 0	143.12 157.13 129.10 0 100	y1 y2 b3 b2 y4+2 b3 171 11 246.15 ,2 200	y3 b4 374.21 54.13 284.20 295.16 323.15 300 400	y4 b5 473.27 523.22 500	y10+2 563.31 648. 600 70 m/z, Da	yf 81 33 847.	5 y6 883.46 2.42 56.47 874 90 900	977.4 10 977.4 1.45 10	y7 b8 012.51 48 995.49 1066. 1066.	y8 1125.63 51 1 1100	y9 192.66 1200	

Ribulose bisphosphate carboxylase large chain precursor WSPELAAA<u>C</u>EVWK

											_							
	Protei	n Quant				Protein ID			Spectra					Sum	mary St	tatistic	s	
Spectrum L	ist																	
Spectrum	Tir	ne Prec MW	Prec m/z	Prec z	Prot N	Best Sequen	ce 🛆			Modifica	tions				C	onf	Theor MV	Vz 🔺
2.1˙1.14.		39.017 1740.815	1 871.4148	2	2, 94,	WS PE LAAACEVWK		ICAT-C:13C(9)(C)@9, Oxidati	on(W)@12						21	1740.859	3 2
9.1˙1.14.		41.815 1732.769	867.3918	2	2, 94,	WS PE LAAACEVWK		ICAT-C:13C(9)(C)@9, Glu->H	is@10						<1	1732.880	6 2
9.1˙1.14.		40.221 1740.780	0 871.3973	2	2, 94,	WS PE LAAACEVWK		ICAT-C:13C(9)(C)@9, Oxidati	on(W)@12						60	1740.859	3 2
9.1˙1.14.		40.307 1731.754	6 866.8846	2		WSPELAAACEVWQ		ICAT-C(C)@9, (Oxidation(W)@	<u>0</u> 12						99	1731.792	6 2
9.1˙1.14.		37.482 1756.794	1 879.4043	2		WSPELAAASEVWKAI	ĸ	Val->Ala@11								13	1756.914	8 2 -
													_					
Peptide ID H	lypothese	s - 9.1dot;1.146	7.4.9											Prec	cursor N	AS Reg	gion	
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modif	ications /	Theor MW	Theor m/z	z	∆Mass		200	۲.		21	
99 17		WSPELAAACEVWQ					ICAT-C(C)@	9, Oxidation(W)	1731.7926	866.9036	2	-0.0380		20	۲]	871	.3955	
96 17	2, 94,	WSPELAAACEVWK					ICAT-C(C)@	9, Oxidation(W)	1731.8291	866.9218	2	-0.0744	=	40	86	7.3854		-871.8974
16 17		WSPELAAACEVGR	S				ICAT-C(C)@	9, Gly->Ser@12	1731.8251	866.9198	2	-0.0704		10	864.76	664		
14 17		WS PE IAAACQVWK					ICAT-C(C)@	9, Deamidated(1731.8291	866.9218	2	-0.0744					الالسوال	Human
13 17		WS PELAAAC QVWK	:				ICAT-C(C)@	9, Deamidated(1731.8291	866.9218	2	-0.0744			860	865	870	875
13 17		WS PELAAAC ZVWK					ICAT-C(C)@	9, Deamidated(1731.8291	866.9218	2	-0.0744	-			m	l/z, Da	
Fragmentati	on Evide	nce for Peptide																
Fragmentati	on Evide	nce for Peptide																
Fragmentati	on Evide	nce for Peptide																1 [
Fragmentati WS Residue	on Evide PELAAAC[C b	nce for Peptide DIJEVW[Oxi]K b+2	у	y+2	1.2													
Fragmentati WS Residue W	on Evide PELAAAC[C b 187.086	b+2 94.0469 17	y '32.8363 8	y+2 866.9218	1.20	54 1 y1 	b2	y2 y3 b3 v5+2 b4	+2 y4 b5	b6 b7	68 y	у5 у6	у7	у8	у9		y10	y11
Fragmentati	on Evide PELAAAC[C b 187.086 274.118	b+2 94.0469 17 137.5629 15	y 32.8363 8 46.7570 7	y+2 866.9218 773.8821	1.20	24 y1 24 y2+Br	b2 227.10	y2 b3 y5+2 p 7	+2 y4 b5	b6 b7	b8 y	y5 y6	у7	у8	у9		y10	y11
Fragmentati	on Evide PELAAAC[C b 187.086 274.118 371.171	b+2 0 94.0469 17 137.5629 16 186.0893 14	y 32.8363 8 46.7570 7 159.7250 7	y+2 866.9218 773.8821 730.3661	1.2¢ 1.1¢ 1.0¢	24 y1 24 - y2+ð 24 -	b2 227.10	y2 y3 b3 y5+2 p ₹	+2 y4 b5	b6 b7	b8 y	у5 у6	у7	у8	у9		y10	y11
Fragmentati	on Evide PELAAAC[C b 187.086 274.118 371.171 500.214	b+2 94.0469 17 137.5629 16 186.0893 14 200.000 1000	y 32.8363 8 46.7570 7 559.7250 7 662.6722 6	y+2 866.9218 773.8821 730.3661 581.8397	1.2¢ 1.1¢ 1.0¢ 9.0¢	24 y1 24 y2+ð 24 3	1 b2 227.10	y2 y3 y3 b3 y5+2 y 7	+2	b6 b7	b8 y	y5 y6	y7	у8	у9		y10	y11
Fragmentati	on Evide PELAAAC[C b 187.086 274.118 371.171 500.214 613.298	b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12	y 32.8363 88 46.7570 77 559.7250 77 662.6722 66 33.6296 66	y+2 866.9218 773.8821 730.3661 681.8397 617.3184	1.20 1.10 9.00 8.00	24 y1 24 y2+B 24 33 33	1 52 227.10	y2 y3 b3 y5+2 p 7	+2 y4 b5	b6 b7	b8 y	y5 y6	y7	у8	y9		y10	y11
Fragmentati	on Evide PELAAAC[C b 187.086 274.118 371.171 500.214 613.298 684.335	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11	y 32.8363 8 46.7570 7 62.6722 6 33.6296 6 20.5456 6	y+2 866.9218 773.8821 730.3661 881.8397 617.3184 560.7764	1.2¢ 1.1¢ 1.0¢ 9.0¢ 8.0¢ ≩7.0¢	24 y1 24 y2+8 33 33	1 b2 227.10	y2 y3 b3 y5+2 p 7	+2 y4 b5	b6 b7	b8	y5 y6	y7	у8	y9		y10	y11
Fragmentati	b PELAAAC[C b 187.086 274.118 371.171 500.214 613.298 684.335 755.372	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11 378.1898 10	y 32.8363 88 46.7570 77 59.7250 77 62.6722 66 33.6296 66 20.5456 68 49.5084 68	y+2 366.9218 773.8821 730.3661 581.8397 617.3184 560.7764 525.2579	1.20 1.10 9.00 8.00 ≩7.7.00 9.6.00	24 y1 24 y2+8 33 3 33 3 33 3	1 b2 227.10	y2 y3 b3 y5+2 p 7	+2 y4 b5	b6 b7	b8	y5 y6	y7	у8	y9		y10	y11
Fragmentati	PELAAAC[C PELAAAC[C 187.086 274.118 371.171 500.214 613.298 684.335 755.372 826.409	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11 378.1898 10 270.721 12	y 32.8363 88 46.7570 77 59.7250 77 62.6722 66 20.5456 68 49.5084 68 478.4713 4	y+2 366.9218 773.8821 730.3661 581.8397 617.3184 560.7764 525.2679 489.739	1.20 1.10 9.00 8.00 ≩7.700 9.6.00 100 100 100 100 100 100 100 100 100	94 y1 94 y2+8 94 33 93 33 93 199,10	1 b2 227.10	y2 y3 b3 y5+2 p 7	+2 y4 b5	b6 b7	b8 y	y5 y6	y7	у8	y9		y10	y11
Fragmentati WS Residue W S P E L A A C[C01]	PELAAAC[C PELAAAC[C 187.086 274.118 371.171 500.214 613.298 684.335 755.372 826.409 1156.545	b+2 137.5629 14 186.0893 14 250.6106 13 307.1527 12 342.6712 14 378.1898 10 413.7083 5 578.7764 5 578.7764 5	y 32.8363 88 46.7570 77 59.7250 77 62.6722 68 33.6296 68 20.5456 88 49.5084 88 778.4713 44	y+2 366.9218 773.8821 730.3661 581.8397 517.3184 560.7764 525.2579 489.7393 454.2207	1.20 1.10 9.00 8.00 5.00 5.00 4.00	24 y1 24 y2+b 33 33 33 33 33 33 33 33 33 33 33 33 33	b2 227.10	y2 y3 y3 b3 y5+2 y7	+2 y4 b5	b6 b7	b8)	y5 y6	y7	у8	y9		y10	y11
Fragmentati WS Residue W S P E L A A C[C0I] E	PELAAAC[C PELAAAC[C 187.086 274.118 371.171 500.214 613.298 684.335 755.372 826.409 1156.5458 1285.5458	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11 378.1898 10 413.7083 5 568.7264 5 643.2977 5	y 32.8363 88 46.7570 77 59.7250 77 62.6722 6 20.5456 6 49.5084 6 778.4713 4 07.4342 4 77.2980 2	y+2 366.9218 773.8821 730.3661 581.8397 517.3184 560.7764 525.2579 489.7393 454.2207 289.1527 289.1527	1.20 1.10 9.00 8.00 ₩ 5.00 4.00 3.00	24 y1 24 y2+b 33 3 33 3 33 199 10 33 199 10	1 b2 227.10	y2 y3 y3 b3 y5+2 y7 09 0	+2 y4 b5	b6 b7	b8)	y5 y6	y7	у8	y9		y10	y11
Fragmentati WS Residue W S P E L A A C[C0I] E V	PELAAAC[C PELAAAC[C 187.086 274.118 371.171 500.214 613.298 684.335 755.372 826.409 1156.545 1285.588 1384.656	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11 378.1898 10 413.7083 5 568.7724 5 643.2977 6 692.8319 4	y 32.8363 8 46.7570 7 59.7250 7 62.6722 6 20.5456 6 49.5084 6 178.4713 4 07.4342 4 48.2554 2	y+2 366.9218 773.8821 730.3661 581.8397 517.3184 560.7764 525.2579 489.7393 454.2207 289.1527 224.6314	1.20 1.10 9.00 8.000 ≥7.00 5.00 4.00 3.000 2.000	24 y1 24 y2+b 33 3 33 3 33 199 10 33 3	227.10	y2 y3 y3 b3 y5+2 y7 09 40.18 411.21	+2 y4 b5	b6 b7	b8 3 907.40	y5 y6	y7	y8 049.49	y9		y10	y11
Fragmentati WS Residue W S P E L A A C[C01] E V W[Oxi]	PELAAAC[C PELAAAC[C 187.086 274.118 371.171 500.214 613.298 684.335 755.372 826.409 1156.545 1285.588 1384.656 1384.656 1386.650	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11 378.1898 10 413.7083 5 564.32977 6 692.8319 4 793.8690 2	y 32.8363 8 46.7570 7 59.7250 7 62.6722 6 20.5456 5 49.5084 5 77.4342 4 67.72980 2 48.2554 2 49.1870 4	y+2 366.9218 773.8821 730.3661 581.8397 517.3184 560.7764 525.2579 489.7393 454.2207 289.1527 224.6314 175.072	1.20 1.10 9.00 8.00 20 5.00 4.00 3.00 2.00	24 y1 y2+b 33 33 33 33 33 33 33 33 33 33 33 33 33	1 b2 227.10 257.1 3	y2 y3 y3 b3 y5+2 y7 09 40.18 411.21 531.2	+2 y4 b5 3 559.26 585.	b6 b7	907.40 890.38	y5 y6	y7	y8 049.49 1120.5	y9) ;5		y10	y11
Fragmentati WS Residue W S P E L A A C[C0I] E V W V W[Oxi] K	Dependence of the second secon	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11 378.1898 10 413.7083 5 578.7764 5 643.2977 6 692.8319 4 793.8690 3	y 32.8363 8 46.7570 7 59.7250 7 62.6722 6 20.5456 5 49.5084 5 77.4342 4 677.2980 2 48.2554 2 44.1870 1	y+2 366.9218 773.8821 730.3661 581.8397 517.3184 560.7764 525.2579 489.7393 454.2207 289.1527 224.6314 175.0972 74.0600	1.20 1.10 9.00 8.00 € 6.00 5.00 4.00 3.00 2.00 1.00	24 y1 y2+b 33 33 33 33 33 33 33 33 33 33 33 33 33	1 b2 227.10 257.1 3	y2 y3 y3 b3 y5+2 y7 09 40.18 411.21 531.2	+2 y4 b5 3 559 26 585. 66	26 6.27 755.33	907.40 2 ^{907.40}	y5 y6	y7	y8 049.49 1120.5	y9) 1233		y10	y11
Fragmentati WS Residue W S P E L A A C[C0I] E V W[Oxi] K	PELAAAC[C PELAAAC[C 187.086 274.118 371.171 500.214 613.298 684.335 755.372 826.409 1156.545 1285.588 1384.656 1586.730 1714.825	Image: break with the second	y 32.8363 8 46.7570 7 559.7250 7 62.6722 6 20.5456 6 49.5084 6 778.4713 4 07.4342 4 477.2980 2 48.2554 2 449.1870 1 47.1128	y+2 366.9218 773.8821 730.3661 581.8397 517.3184 560.7764 525.2579 489.7393 454.2207 289.1527 224.6314 175.0972 74.0600	1.20 1.10 9.00 8.00 2.00 4.00 3.00 2.00 1.00	24 y1 y2+b 24 y2+b 33 3 33 199 10 33 199 10 33 130.07 176 33 0 100	1 b2 227.10 257.1 3.09 200 300	y2 y3 y3 b3 y5+2 y7 09 40.18 411.21 531.2 400 51	+2 y4 b5 3 559 26 585. 66 600	26 775.33	907.40 890.38	y5 y6	y7 14 1	y8 049.49 1120.5	y9 55 1233 1200	.55	y10 1459.) 140	y11
Fragmentati WS Residue W S P E L A C[C0I] E V W[Oxi] K	PELAAAC[C PELAAAC[C 187.086 274.118 371.171 500.214 613.298 684.335 755.372 826.409 1156.545 1285.588 1384.656 1586.730 1714.825	b+2 b+2 94.0469 17 137.5629 16 186.0893 14 250.6106 13 307.1527 12 342.6712 11 378.1896 10 413.7083 5 578.7764 5 643.2977 5 692.8319 4 793.8690 5	y 32.8363 8 46.7570 7 59.7250 7 62.6722 6 20.5456 6 20.5456 5 49.5084 5 778.4713 4 07.4342 4 477.2980 2 48.2554 2 449.1870 1 47.1128	y+2 366.9218 773.8821 730.3661 581.8397 517.3184 560.7764 525.2579 489.7393 454.2207 289.1527 224.6314 175.0972 74.0600	1.20 1.10 9.00 8.00 2.00 4.00 3.00 2.00 1.00	24 y1 y2+b 33 3 33 199 10 33 130.07 176 33 0 100	1 b2 227.10 257.1 257.1 200 300	y2 y3 y3 b3 y5+2 y7 09 40.18 411.21 531.2 400 50	+2 y4 b5 3 559 26 585. 66 20 600	26 b7 26 7 755.33 1.00 m/z, Da	907.40 890.38 2 010.001	y5 y6 978.4	y7 14 1 14 1	y8 049.49 1120.5	y9 55 1233 1200	.55	y10 1459.) 140	y11

Ribulose bisphosphate carboxylase large chain precursor YGRPLLG<u>C</u>TIKPK

	Protein G	uant				Protein ID			Spectra			Summ	ary Statist	ics	
Spectrum I	ist														
Spectrum	151														
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequen	ice 🗠			Modificatio	ons		Conf	Theor MW	z *
3.1˙1.14	26.	347 1671.9117	7 418.9852	4	2, 98,	YGRPLLGCTIKPK		ICAT-C(C)@8					< 1	1671.9495	4
9.1˙1.13	29.	035 16/1.8351	1 836.9248 9 941 4610	2	2, 98,	YGRPLLGCTIKPK		ICAT-C(C)@8	<u></u>				96	16/1.9495	2
10.1˙:1.13	29. 29	502 1671 8954	4 558 3057		2,90,	YGRPLIGCTIKPK		ICAT-C(C)@8	ഠയ്രം				99	1671 9495	2
11.1˙1.1	30.	393 1671.9034	4 558.3084	3	2, 98,	YGRPLLGCTIKPK		ICAT-C(C)@8					6	1671.9495	3 -
	1	- 1													
Pentide ID I		9 1dot-1 139	129									Broom	eor MS D	ogion	
i epude ib i	iypotiteses -	5.100,1.155	1.2.5									Flecu	501 W 5 K	egion	
Conf V Sc	Prot N 🛆		:	Sequence		Δ	Modif	ications /	Theor MW	Theor m/z	z 🛆 Mass 🔺	801	836.9336	944 4636	
99 17	2, 98, YG	RPLLGCTIKPK	7				ICAT-C:13C(9)(C)@8	1680.9796	841.4971	2 -0.0718	60		-041.4020	
99 17	YG	RPILGCTIKPK					ICAT-C:13C(9)(C)@8	1680.9796	841.4971	2 -0.0718	40		-041.970	50
99 17	YG	RPLLGCTIQPK	(7				ICAT-C:13C(9)(C)@8	1680.9432	841.4789	2 -0.0354	20 -	h. hu	045.40	50 L.h.
99 17	16	RPLLGCI 12 PK	7				ICAT-0:130(9)(C)@8	1680 9796	841 4071	2 -0.0354	0 ¹	IIYWWN JIMWY	11110NAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ha h
13 17	HG	RPLLGCTIKPK	r				Delta:H(2)C(2	2)(H)@1.ICAT	1680.9908	841.5027	2 -0.0830 -		835 84	0 845 m/z, Da	850
								-//·//e-////							
6															
Fragmentat	ion Evidence	for Peptide													
Fragmentat	ion Evidence RPLLGC[C9]]TIK	for Peptide													
Fragmentat	ion Evidence RPLLGC[C9]]TIK	for Peptide ж b+2	y	y+2											
Fragmentat	ion Evidence RPLLGC[C9][TIK b 164.0706	for Peptide % b+2 82.5389 16	y 581.9869 {	y+2 841.4971	160	,1 y1 ,	y2 y3	y4 y5			y7 y8 b0	y10		y13	
Fragmentat	ion Evidence RPLLGC[C9] TIK b 164.0706 221.0921	for Peptide ж 82.5389 16 111.0497 15	y 381.9869 518.9236	y+2 841.4971 759.9654	160	0 y 1 b2	y2 y3 2 b5+2 b7₩3 244.16	y4 y5 y6+2 b5	b6 b71	y1 8 3 2 2	y7 y8 b9	y10 b10	611 61	2 y13	
Fragmentat YG Residue Y G R	ion Evidence RPLLGC[C9][TIK b 164.0706 221.0921 377.1932	for Peptide ж 82.5389 16 111.0497 15 189.1002 14	y 581.9869 5 18.9236 5 1 61.9021 5 1	y+2 841.4971 759.9654 731.4547	160	0 y 1 b2	y2 y3 2 b5+2 b7 83 244.16	y4 y5 y6+2 b5	b6 b71	yi 18 3 1 2	y7 y8 b9	y10 b10	b11 b1	2 y13	
Fragmentati YG Residue Y G R P	b 164.0706 221.0921 377.1932 474.2459	for Peptide %	y 381.9869 518.9236 518.9021 305.8010 (1)	y+2 841.4971 759.9654 731.4547 653.4041	160 140	0 y1 b2	<mark>y2 y3</mark> 2 b5+2 b7 ⊎3 244.16	y4 y5 y6+2 b5	b6 b71	yi 13+42	y7 y8 b9 b9	y10 b10	Ы1 Ы	2 y13	
Fragmentat	ion Evidence RPLLGC[C9](TIK b 164.0706 221.0921 377.1932 474.2459 587.3300 779.441	for Peptide b+2	y 581.9869 5 518.9236 5 518.9256 5 518	y+2 841.4971 759.9654 731.4547 653.4041 604.8778	160 140 120	0 y 1 b2	<mark>y2 y3</mark> 2 b5+2 b7 *3 244.16	y4 y5 y6+2 b5	b6 b71	y169-92	y7 y8 b9 b9	y10 b10	611 61	2 y13	
Fragmentat	ion Evidence RPLLGC[C9] TIK b 164.0706 221.0921 377.1932 474.2459 587.3300 700.4141 757.4955	for Peptide b+2 82.5389 11 1.0497 15 189.1002 14 237.6266 13 294.1686 12 350.717 10	y 581.9869 4 518.9236 7 518.9236 7 505.8010 6 208.7482 6 995.6642 6	y+2 841.4971 759.9654 731.4547 653.4041 604.8778 548.3357 404.7923	160 140 120 ≩	0 - y1 b2 0 - b2 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 -	<mark>y2 y3</mark> 2 b5+2 b7#3 244.16	y4 y5 y6+2 b5	b6 b71	y/139-92	y7 y8 b9 b9	y10 b10	Ь11 Ь1	2 y13	
Fragmentat	ion Evidence RPLLGC[C9][TK b 164.0706 221.0921 377.1932 474.2459 587.3300 700.4141 757.4355 1096.5449	for Peptide b+2 16 111.0497 15 189.1002 14 237.6266 13 294.1686 12 350.7107 10 379.2214 8	y 581.9869 4 518.9236 7 461.9021 7 305.8010 6 208.7482 6 95.6642 5 882.5801 6 982.5805 6 982.	y+2 841.4971 759.9664 731.4547 653.4041 604.8778 548.3357 491.7937	160 140 120 ∑100	0 y1 b2 0 b2 0 b 0 b 0 b 0 b 0 b 0 b 0 b 0 b 0 b 0 b	<mark>y2 y3</mark> 2 b5+2 b7 ≋3 244.16	y 4 y5 y6+2 b5	b6 b71	y169-92	y7 y8 b8 b9	y10 b10	b11 b1	2 y13	
Fragmentati	ion Evidence RPLLGC[C9 T K b 164.0706 221.0921 377.1932 474.2459 587.3300 700.4141 757.4355 1096.6019 1197.6496	for Peptide ★	y 581.9869 4 518.9236 7 461.9021 7 305.8010 6 208.7482 6 95.6642 6 982.5801 4 225.5586 4	y+2 841.4971 759.9664 731.4547 653.4041 604.8778 548.3367 491.7937 463.2830 293.6988	160 140 120 <u>Atisungui</u> 80	0 y1 b2 0 0 0 0 0 0 0 0 226.15	y2 y3 2 b5+2 b7₩3 244.16 254.12	y 4 y5 y6+2 b5	b6 b71	y18 2 2	y7 y8 b8 b9	y10 b10	b11 b1	2 y13	
Fragmentat	ion Evidence RPLLGC[C9]TIK b 164.0706 221.0921 377.1932 474.2459 587.3300 700.4141 757.4355 1096.6019 1197.6496 1310.7336	for Peptide ★	y 581.9869 4 518.9236 7 461.9021 7 305.8010 6 208.7482 6 982.5801 4 225.5586 4 886.3923 2 485.3446 2	y+2 841.4971 759.9664 731.4547 653.4041 604.8778 548.3367 491.7937 445.2830 293.6998 243.1759	160 140 120 Atsuart 80 60	0 y1 b2 0 b2 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c	y2 y3 2 b5+2 b7₩3 244.16 ,254.12	y 4 y5 y6+2 b5	b6 b71	y18 2 2	y7 y8 b9 b9	y10 b10	b11 b1	2 y13	
Fragmentat	ion Evidence RPLLGC[C9]TK b 164.0706 221.0921 377.1932 474.2459 587.3300 700.4141 757.4355 1096.6019 1197.6496 1310.7336 1438.8286	for Peptide ★	y 581.9869 4 518.9236 7 461.9021 7 505.8010 6 008.7482 6 995.6642 8 982.5801 4 325.5586 4 586.3923 2 485.3446 2 372.2605 4	y+2 841.4971 759.9664 731.4547 653.4041 604.8778 548.3367 491.7937 463.2830 293.6998 243.1759 186.6339	160 140 120 ♪100 ♪100 ₽ ₽ ₽ 80 60 40	0 y1 b2 0 b2 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c	y2 y3 2 b5+2 b7⊌3 244.16 254.12	y4 y5 y6+2 b5	b6 b71	y189-92	y7 y8 b9 b9	y10 b10	b11 b1	2 y13	
Fragmentat YG Residue Y G R P L L G C[C9I] T I K P	b 1 164.0706 2 221.0921 377.1932 377.1932 474.2459 587.3300 700.4141 757.4355 1096.6019 1197.6496 1310.7336 1438.82866 1535.8814	for Peptide ** ** ** ** ** ** ** ** ** *	y 581.9869 8 518.9236 7 518.9236 7 505.8010 6 208.7482 6 995.6642 8 382.5801 4 325.5586 4 586.3923 2 485.3446 2 372.2605 7 244.1656 7	y+2 841.4971 759.9654 731.4547 653.4041 604.8778 548.3367 491.7937 463.2830 293.6998 243.1759 186.6339 122.5864	160 140 120 <u>Attenti</u> 80 60 40	0 y1 b2 0 b2 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c 0 c	y2 y3 2 b5+2 b7⊌3 244.16 254.12 254.12 377, 271.15	y4 y5 y6+2 b5	b6 b71	y18 2 2	y7 y8 b8 b9	y10 b10	b11 b1	2 y13 1681.92	
Fragmentat YG Residue Y G R P L G G C[C9I] T I K P K	b 1 164.0706 2 221.0921 377.1932 377.1932 474.2459 587.3300 700.4141 757.4355 1096.6019 1197.6496 1310.7336 1438.8286 1535.8814 1663.9763 3	for Peptide b+2 82.5389 161 11.0497 152 189.1002 141 237.6268 132 350.7107 103 379.2214 99 548.8046 99 565.8705 4 719.9179 3 768.4443 2 832.4918	y \$81.9869 \$451.9021 \$05.8010 \$08.7482 \$095.6642 \$82.5801 \$42.55586 \$44 \$25.5586 \$45 \$63.923 \$24.1656 \$44 \$72.2605 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$44 \$44.1656 \$45.16566 \$45.16566 \$45.16566 \$45.16566 \$45.165666 \$45.165666 \$45.1656666666666666666666666666666666666	y+2 841.4971 759.9664 731.4547 653.4041 604.8778 548.3367 491.7937 463.2830 293.6998 243.1759 186.6339 122.5864 74.0600	160 140 120 ≹suati 80 60 40 20	0 - y1 b2 0 - 226.15 0 - 226.15 0 - 129.10 0 - 115.09 183.11	y2 y3 2 b5+2 b7€3 244.16 254.12 271.15	y6+2 b5	b6 b71	yf 63-62	y7 y8 b9 b9	y10 b10	b11 b1	2 y13 1681.92 1664.90 553.86	
Fragmentation YG Residue Y G R P L L G C[C91] T I K P K	ion Evidence RPLLGC[C9]TIK b 164.0706 221.0921 377.1932 474.2459 587.3300 700.4141 757.4355 1096.6019 1197.6496 1310.7336 1438.8286 1535.8814 1663.9763	for Peptide b+2 82.5389 161 11.0497 151 189.1002 141 237.6266 133 294.1686 12350.7107 10379.2214 9 548.8046 99 565.8705 47 719.9179 37 68.4443 2 832.4918	y \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	y+2 841.4971 759.9654 731.4547 653.4041 604.8778 548.3367 491.7937 463.26398 243.1759 186.6339 122.5864 74.0600	160 140 120 <u>≵</u> 100 80 60 40 20	0 y1 b2 0 226.15 0 2226.15 0 129.10 0 115.09 11 11	y2 y3 2 b5+2 b7#3 244.16 244.16 254.12 377 5 5 0 300 4	y4 y5 y6+2 b5 .19 .19 .100 500 6	700.38 757	909.47 909.47 909.47	y7 y8 b9 b9	y10 b10	b11 b1	2 y13 2 1681.92 1664.90 553.86	
Fragmentation YG Residue Y G R P L L G C[C91] T I K P K	ion Evidence RPLLGC[C9]TIK b 164.0706 221.0921 377.1932 474.2459 587.3300 700.4141 757.4355 1096.6019 1197.6496 1310.7336 1438.8286 1535.8814 1663.9763	b+2 16 82.5389 16 111.0497 15 189.1002 14 237.6266 13 294.1686 12 350.717 10 379.2214 9 548.8046 9 559.3284 5 655.8705 4 719.9179 3 768.4443 2 832.4918 1	y 581.9869 518.9236 518.9236 518.9236 518.9236 518.923 5208.7482 6 995.6642 5 982.56586 4 925.5586 4 586.3923 2 1485.3446 2 372.2605 4 4 147.1128	y+2 841.4971 759.9664 731.4547 653.4041 604.8778 548.3367 491.7937 463.2830 293.6998 243.1759 186.6339 122.5864 74.0600	160 140 120 ∧tsup 100 60 40 20	0 - y1 b2 0 - 226.15 0 - 226.15 0 - 129.10 0 - 115.09 183.1 0 - 183.1 0 - 100 200	y2 y3 2 b5+2 b7%3 244.16 244.16 254.12 377 5 5 0 300 4	y4 y5 y6+2 b5 .19 .19	700.38 757	909.47 909.47 1 1 1	y7 y8 b9 b9 b9 b9 7 1051.58 1179.71 1000 1100 1200	y10 b10 1310.75	b11 b1	2 y13 1681.92 1664.90 553.86 0 1600	1700

Ribulose bisphosphate carboxylase large chain precursor GHYLNATAGT<u>C</u>EEMMK

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	Protein ()uant		Ĭ		Protein ID			Spectra		Ĭ	Summary	/ Statistics
Spectrum I	List												
Spectrun	n Time	Prec MV	V Prec m/z	Prec z	Prot N	Best Sequen	ce 🗸			Modifications			Conf Theor MW z 🔺
10.1˙1.	1 26.	523 2013.82	40 672.2819	9 3	98	GHYLNATAGTCEEMF	5	ICAT-C(C)@11,	Oxidation(M)	@14			99 2013.8925 3
10.1˙1.	1 27.	260 2013.82	65 672.2828	8 3	98	GHYLNATAGTCEEMF	(ICAT-C(C)@11,	Oxidation(M)	@14			99 2013.8925 3
10.1˙1.	1 26.	481 2022.85	63 675.2927	7 3	98	GHYLNATAGTCEEMF	(ICAT-C:13C(9)(C)@11, Oxida	tion(M)@14			99 2022.9226 3
10.1˙1.	1 27.	217 2022.86	675.2967	7 3	98	GHYLNATAGTCEEMFF	(ICAT-C:13C(9)(C)@11, Oxida	tion(M)@14			96 2022.9226 3
12.1˙1.	1 28.	466 2022.83	35 1012.42	. 2	2, 94,	GHYLNATAGTCEEMM	(ICAT-C:13C(9)(C)@11, Oxida	tion(M)@14, Oxida	tion(M)@15		<1 2022.8896 2 🔻
Peptide ID	Hypotheses -	10.1dot;1.1	302.3.10									Precurso	r MS Region
				•									
			TRACTICE.	Sequence		Δ	Modif	11 Ovidation/14	1 neor MW	FINEOR M/Z Z		1	672.6156 - 675.2891
99 10	5 90 GH	YLNA IAGICE	EMEK				ICAT-C(C)@	11, Oxidation(M	2013.0925	672.3047	3 -0.0005 =	100 -	675,9556
17 15	5 2, 34, Gn	VINA TACTOR	EMMZ				ICAT-C(C)@	11, Oxidation(M	2013.0554	672 2938	3 0.0355		harmonia a the lange shite of the
6 16	5 Gn	VINATACTOR	OMMZ				ICAT-C(C)@	11 Desmidsted	2013.8594	672.2038	3 .0.0355 -	0 1	m/z. Da
	- Gn	ILNAIAGICE	QUINK				10/1-0(0)@	ri, Deannoarea	2013.0004	072.2000	3 -0.0303 +		1112, Du
Fragmenta	tion Evidence	for Peptide	9										
GH	YLNATAGTC[C0	JEEM[Oxi]FK											
Desidue	h	h+2	v	V+2									'
G	58 0287	29.5180	2014 8997 1	1007 9535		y1	y2	y3 y4	y5		v8		
Н	195.0877	98.0475	1957.8783	979.4428		240 - yd:	₽+2 b 73	+2 b9+2b4 b!	5 b6 b7	7 b8 b9 b10			b14
Y	358.1510	179.5791	1820.8193	910.9133		220	195.09						
L	471.2350	236.1212	1657.7560	829.3816		200							
N	585.2780	293.1426	1544.6720	772.8396		180							
A	656.3151	328.6612	1430.6290	715.8182		160							
Т	757.3628	379.1850	1359.5919	680.2996		>							
A	828.3999	414.7036	1258.5442	629.7758		5 140 -	35	8.15					
G	885.4213	443.2143	1187.5071	594.2572		≝ ¹²⁰	269.11						
Т	986.4690	493.7381	1130.4857	565.7465		100 -	200.11						
C[C01]	1316.6052	658.8062	1029.4380	515.2226		80 -							
E	1445.6478	723.3275	699.3018	350.1545		60 167.09		441.19	5.32				
E	1574.6904	787.8488	570.2592	285.6332		40		574	739	.36	011.47 1088.43		
M[Oxi]	1721.7258	861.3665	441.2166	221.1119		136.08		J. J. S/1	f [*]	782.43 885.38	11153.47		1595 00 1721.63
F	1868.7942	934.9007	294.1812	147.5942		20		line alle in the line of the		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1000.00
к	1996.8892	998.9482	147.1128	74.0600		0 100	200 300	400 500	600 700	800 900 1	000 1100 1200	1300 1400	0 1500 1600 1700
										m/z, Da			

Ferredoxin FITPEGEQEVECDDDVYVLDAAEEAGIDLPYS<u>C</u>R

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	Protein	Quant				Protein ID		Spectra		Summary Statistics
Spectrum I	let									
Spectrum L	.151									
Spectrum	Time	Prec	MW Prec m	/z Prec z	Prot N	Best Seque	nce 🗠	Mo	odifications	Conf Theor MW 🔺
2.1˙1.16	52	2.014 4243	.8867 1061.9	7 4	47	FITPEGEQEVECDDDVYVLDA	AEEAGIDLPYSCR	ICAT-C(C)@12, ICAT-C(C)@3	33	99 4243.9092
•	1	1	1	1		1		1		
Peptide ID	Hypotheses	- 2.1dot;1.	1610.4.2							Precursor MS Region
Conf ⊽ Sc	Prot N A			Sequence		A	Modifications	Theor MW Theor m/z z	AMaee 🔺	40000000
99 14	47 F	ITPEGEOEN	ECDDDVYVU	DAAEEAGTD	LPYSCR	ICAT-0	C(C)@12. ICAT-C(C)	4243.9092 1061.9845	4 -0.0216	100 1062,7292
21 14	20 F	VTPEGEOEV	ECDDDVYVI	DAAEEAGID	LPYSCR	Val->L	eu@2, ICAT-C(C)@1	4243.9092 1061.9845	4 -0.0216	
	1					Derei		42422424 4004 0404	4 0.0740	
										/
Fragmentat	ion Evidend	e for Pept	ide							
FIT	PEGEQEVEC[C		DAAEEAGIDLP	YSC[C0]]R						
Residue	b	b+2	v	v+2	*					
D	1704.7421	852.8747	2656.2083	1328.6078		400 - v1	v2 v3	v4 v5 v6 v7	v8 v9 v10	
D	1819.7691	910.3882	2541.1814	1271.0943		380 - b4+2b2	b3 b9+2	b7 b8 b9 b10		
D	1934.7960	967.9017	2426.1544	1213.5808		360 -		852.38		
V	2033.8644	1017.4359	2311.1275	1156.0674		340				
Y	2196.9278	1098.9675	2212.0591	1106.5332		320				
V	2295.9962	1148.5017	2048.9957	1025.0015		300 -				
L	2409.0802	1205.0438	1949.9273	975.4673		280 -				
D	2524.1072	1262.5572	1836.8433	918.9253		260 233.16				
A	2595.1443	1298.0758	1721.8163	861.4118		240 1 ≿220 -				
A	2666.1814	1333.5943	1650.7792	825.8932		5240 - 261.16				
E	2795.2240	1398.1156	1579.7421	790.3747		±_180				
E	2924.2666	1462.6369	1450.6995	725.8534		160				
A	2995.3037	1498.1555	1321.6569	661.3321		140		965.47		
G	3052.3252	1526.6662	1250.6198	625.8135		120		1080.51		
	3165.4092	1583.2083	1193.5983	597.3028		100 245,09	286.14	1000.5		
	3280.4362	1640.7217	1080.5143	540.7608	=	80 201.09				
	3393.5203	1097.2038	905.4873	403.2473		60 187.08	362.20 516.25 755	835.35 870.39		
P V	3653 6363	1227 2240	755 3505	420.7053		40 171.11		1062.65	1250.69	1527 63 1674 57 1817.66 1988.79
s s	3740 6684	1870 8379	592 2872	206 6/72		201			1321.70	
CICOU	4070 8046	2036 9069	505 2554	250.0472		0 200	400 600	800 1000	1200 1400	1600 1800 2000
R	4226 9057	2113 9565	175,1190	88 0631				m/z, Da		
	4220.0001	2110.0000	113,1130	00.0001	-					

Ribulose bisphosphate carboxylase /oxygenase small subunit WIP<u>C</u>VEFELEHGFVYR

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Protein Quant	Protein ID	The second se	Spectra	Sumr	nary Statistics
Spectrum List					
Spectrum Time Prec MW Prec m/z	Prec z Prot N Bes	st Sequence 🗠	Mo	difications	Conf Theor MW 🔺
7.1˙1.16 45.801 2259.0684 754.030	1 3 7 WI PCVE FELEHGFVY	R	ICAT-C:13C(9)(C)@4		99 2259.1233
9.1˙1.15 46.637 2250.0010 751.007	6 3 7 WIPCVEFELEHGFVY	R	ICAT-C(C)@4		99 2250.0933 🗸
•					>
Peptide ID Hypotheses - 9.1dot;1.1526.3.9				Preci	ursor MS Region
Conf V Sc Prot N	Sequence 🛆	Modifications 🛆	Theor MW Theor m/z z	∆Mass 200	1 1
99 17 7 WI PCVE FELEHGFVYR		ICAT-C(C)@4	2250.0933 751.0383	3 -0.0921	751,3439
13 16 WVPCLEFELEHGFVYR		ICAT-C(C)@4	2250.0933 751.0383	3 -0.0921	
< 1 17 GWVPCLEFELEHGFVYR		Trp->Glu@2, ICAT-C(C)@5	2250.0779 751.0333	3 -0.0769 100	755.0161
<1 17 WI PCVELELEHGFVYR		ICAT-C(C)@4, Leu->Phe@7	2250.0933 751.0383	3 -0.0921 50	749.3541 759.3647
< 1 13 ASIGAN PQT FGGELQKYTLVF	1	Deamidated(N)@6	2250.1646 751.0621	3 -0.1634	ben in a summer a state of the
					745 750 755 760
					11/2, Da
Fragmentation Evidence for Peptide					
Residue b b+2 y	y+2 2 4e4 - 1 11	اعتدالات العاب الجاب ا		العفر الفقر المقر	v14 v15
W 187.0866 94.0469 2251.1005	1126.0539 2.464 91	y522 b976222 y9+2	b6 b7	yiu yii yiz	y14 y15
D 207 2224 100 1152 4054 0274	076 4722	272.17			
CICOII 727 3596 364 1834 1854 8843	927 9458				
V 826.4280 413 7176 1524 7482	762.8777				
E 955.4706 478.2389 1425.6797	713.3435 1.6e4 255	14			
F 1102.5390 551.7731 1296.6371	648.8222 ≥ 1.4e4				
E 1231.5816 616.2944 1149.5687	575.2880 § 1.2e4 -				
L 1344.6657 672.8365 1020.5261	510.7667 ^E 1.0e4				
E 1473.7083 737.3578 907.4421	454.2247 8.0e3				1051.97
H 1610.7672 805.8872 778.3995	389.7034 6.0e3 227.1		778.37		1951.07
G 1667.7886 834.3980 641.3406	321.1739 4 0e3 187.08	428,19 641.34	907.41		
F 1814.8571 907.9322 584.3191	292.6632 159.09	1584.32	1020.50	1425.61	1853.87 1934.85
V 1913.9255 957.4664 437.2507	219.1290 2.063 120.08		926.91 1149.5	7 1524.71	1755.79
Y 2076.9888 1038.9980 338.1823	169.5948 0.0e0 0 2	200 400 600	800 1000 12	200 1400 1600	1800 2000
R 2233.0899 1117.0486 175.1190	88.0631		m/z, Da		

Malate dehydrogenase, mitochondrial precursor GLNGVPDVVE<u>C</u>SYVQSTITELPFFASK

	Protein	Quant				Protein ID		Spectra		Summary Statistics
Spectrum I	ist									
						1				
Spectrum	n Time	Prec	MW Prec r	n/z Prec z	Prot N	Best Sequ	ance 🗠	N	odifications	Conf Theor MW 🔶
9.1˙1.15	i 52	.329 3135.	4971 1046.1	17 3	3	GLNGVPDVVECSYVQSTITE	.PFFASK	ICAT-C:13C(9)(C)@11		99 3135.5886
•			cool toto	- 11			III			4
Peptide ID	Hypotheses	- 9.1dot;1.′	1590.3.9							Precursor MS Region
Conf V Co	Drot N /			Formeroe		Δ.	Madifications	Theor MM Theor m/r		100 -
99 17	3 61	NCVDDVVF	CSWOSTIT	VIPUPPC	,	ICAT.	C:13C(9)(C)@11	3135 5886 1046 2035	3 -0.0904	
< 1 17		NGVPDVVE	CSYVOSTIT	FLPFFASK		lle->V	1/09 ICAT-C:13C(9)/	3135 5886 1046 2035	3 -0.0904	50 1 1046.5184
		NOVEDVIE		DEFF FAST				2425 5500 4040 4025	2 0.0005	
Fragmentat	ion Evidenc	e for Pepti	de							
GL	NGVPDVVEC[C	9IJSYVQSTIT	ELPFFASK							
Residue	b	b+2	у	y+2	*					
L	171.1128	86.0600	3079.5744	1540.2908		950 1	المبر الطبر ال	v5 v6 v7		v10 v11 v12 v13
N	285.1557	143.0815	2966.4903	1483.7488		900 - b3+2 b2	y532 b4 b5 y9+	206 95 96 97	b9 p10 y3	yio yii yiz yis
G	342.1772	171.5922	2852.4474	1426.7273		850 -	- 396.22	696.36 -		
V	441.2456	221.1264	2795.4259	1398.2166		800 -				
Р	538.2984	269.6528	2696.3575	1348.6824		750 -	413.24			
D	653.3253	327.1663	2599.3047	1300.1560		700	45	2.23		
V	752.3937	376.7005	2484.2778	1242.6425		650 - 245.13	271 14			
V	851.4621	426.2347	2385.2094	1193.1083	=	600	441	23		
E	980.5047	490.7560	2286.1410	1143.5741		550 254.1	2			
C[C9I]	1319.6711	660.3392	2157.0984	1079.0528		D 213.09	424.2		1039.53	
S	1406.7031	703.8552	1817.9320	909.4696		<u> 뿔</u> 450	312 16 46	53.22		
Y	1569.7665	785.3869	1730.9000	865.9536		400 197.16		809.4	14	
V	1668.8349	834.9211	1567.8366	784.4220		350	342.18	540.27		
Q	1796.8935	898.9504	1468.7682	734.8877		300 228.13				
S	1883.9255	942.4664	1340.7096	670.8585		250 - 172.07		550.26	938.47	
Т	1984.9732	992.9902	1253.6776	627.3424		200 -		565.28		
1	2098.0572	1049.5323	1152.6299	576.8186		150 143.12		573 25	862.40	
Т	2199.1049	1100.0561	1039.5459	520.2766		100 136.07		707.37 735.35	998.52	1152.63 1340.64 1449.71
E	2328.1475	1164.5774	938.4982	469.7527		50 -		de kilde i i de la k ilde i de se kilde i		1228.60
L	2441.2316	1221.1194	809.4556	405.2314		0 100 200	300 400 50	0 600 700 800	900 1000 1	100 1200 1300 1400
Р	2538.2843	1269.6458	696.3715	348.6894				m/z, Da		
F	2685.3527	1343.1800	599.3188	300.1630	-					

Cytosolic triosephosphatisomerase IIYGGSVNGGN<u>C</u>K

		-			
Protein Quant	Protein ID		Spectra		Summary Statistics
Spectrum List					
Spectrum Time Prec MW Prec m/z	Prec z Prot N Bes	st Sequence	4 M	odifications	Conf Theor MW 🔺
9.1˙1.13 28.790 1508.6750 755.3448	2 51 IIYGGSVNGGNCK		Deamidated(N)@8, ICAT-C(C	0)@12	98 1508.7294
9.1˙1.13 27.811 1516.7208 759.3677	2 51 IIYGGSVNGGNCK		ICAT-C:13C(9)(C)@12		88 1516.7755
9.1˙1.13 28.704 1517.6963 759.8554	2 51 IIYGGSVNGGNCK		Deamidated(N)@8, ICAT-C:13	3C(9)(C)@12	91 1517.7595
12.1˙1.1 29.839 1516.7283 759.3714	2 51 IIYGGSVNGGNCK		ICAT-C:13C(9)(C)@12		99 1516.7755 -
					F
Destide ID I have the see 0.4 dest1.4295.4.0					
Peptide ID Hypotheses - 9.1dot;1.1385.4.9					Precursor MS Region
Conf ⊽ Sc Prot N △	Sequence /	Modifications 🗠	Theor MW Theor m/z z	∠∆Mass	759 8594
98 15 51 IIYGGSVNGGNCK		Deamidated(N)@8, ICAT-C(1508.7294 755.3719	2 -0.0543	
<1 13 IIYGGSVTGANCK		ICAT-C(C)@12	1508.7657 755.3901	2 -0.0907	50 -
<1 10 DORU TOYOURGOUCK		Deamidated(N)@15	1508 7372 755 3759	2 0.0509	line in the second s
<1 10 MSRDSAAFASGGAGNK		Deamidated(N)@15	1508 6526 755 3336	2 0.0225	
		Dominantoa (11) (2010	1000.0020 100.0000	2 0.0220	/50 /55 /60 /65
		· · · · · · · · · · · · · · · · · · ·			m/z, Da
					m/z, Da
Fragmentation Evidence for Peptide					m/z, Da
Fragmentation Evidence for Peptide IYGGSVN[Dea]GGNC[C0]]K Residue b b+2 y I 114.0913 57.5493 1509.7366 I 227.1754 114.0913 1396.6525 Y 390.2387 195.6230 1283.5685 G 447.2602 224.1337 1120.5051 G 504.2817 252.6445 1063.4837 S 591.3137 296.1605 1006.4622 V 690.3821 345.6947 919.4302 N[Dea] 805.4090 403.2082 820.3618 G 919.4520 460.2296 648.3134 N 1033.4949 517.2511 591.2919 C[C0I] 1363.6311 682.3192 477.2490 K 1491.7260 746.3667 147.1128	y+2 6000 755.3719 5500 560.7562 4500 532.2455 4000 503.7347 23500 410.6845 2500 324.6603 2500 239.1281 1000 74.0600 500	y1 y22 p6+2 b830 y540 1 199.18 227.17 36.07 278.12 347.13 0 200 300 400	y3 y4 y5 y6 2 b611+2 y13+2 820 477.24 705.31 820 552.29 688.28 768.28 500 600 700 800 m/z. Da m/z. Da 800	y7 y8 y9 b10 .33 919.40 1006.44 900 1000	y10 y11 y12 1120.51 1183.61 1283.51 1100 1200 1300 1400 1500

Succinate dehydrogenase flavoprotein alpha subunit AAIGLSEHGFNTA<u>C</u>ITK

											_		_			- 8 >
	Protein	Quant		Ť	Protei	n ID	The second se		Spectra					Summary Sta	tistics	
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Spectrum L	ist															
Creation	Time	Dress	D	n In Dura a	Dest N	Dee			A		Mar all				Conf. These Mill	
9 18 dot:1 14	1 ime	703 1967	NIVV Prec n	1/Z Prec Z	10 42 DATCT	Des	t sequence		ICAT C:13	0.00/00/0014	Modif	Ications			00 1068 018	
3.10000,1.14		.703 1307.	.3050 050.3	300 3	10, 42, AAIGL	DERGENTAUTI			TOAT-0.15	0(3)(0)@14					55 1500.010	
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																-
Peptide ID I	lypotheses	- 9.1dot;1.	1425.3.9											Precursor M	S Region	
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modifica	tions 🛆	Theor MW	Theor m/z	z	∆Mass	- II	F 08	ls	
99 16	10, 42, A	AIGLSEHGF	NTACITK				ICAT-C:13C(9)(C)@14	1968.0186	657.0135	3	-0.0536		50 653 9985 .	656.9988	
< 1 12	G	LAAIVTSEL	ASAAHDTVS	R					1968.0276	657.0165	3	-0.0626		40	-657.6720	
< 1 11	A	LLMGQESP	AARAGQIAR				Deamidated(Q)	@7	1968.0211	657.0143	3	-0.0561		30 -	668.3201	1
<1 11	A	DAANKAL	AFHQTLAAR						1968.0541	657.0253	3	-0.0891		10	A Manual Lange	à. 📘
<1 11	57	/AHNFANTG	ALVTCVK				Deamidated(N)	@5, ICAT-C:	1968.0186	657.0135	3	-0.0536			T TILLER TITLER ALS A POINT AND A PARTY	44N 📗
	<u> </u>									. I.				650	655 660 665	
													- 11		111/2, Da	
Fragmentat	ion Evidend	e for Pepti	de													
	GLSEHGFNTA	C[C9I]ITK														
Residue	b	b+2	у	y+2												
A	72.0444	36.5258	1969.0259	985.0166	900 -	y1	y2 y3		y4 y5	y6 y7	y8 j	/9 y10		y12 y13y	14 y15	
A	143.0815	72.0444	1897.9888	949.4980	850	b4 962+ 2	b3 b4 b5	b11+2 y10+	2	y16+2	b	12				
1	256.1656	128.5864	1826.9516	913.9795	800 -		248.16									
G	313.1870	157.0972	1713.8676	857.4374	750 -											
L	426.2711	213.6392	1656.8461	828.9267	650									1	713.79	
S	513.3031	257.1552	1543.7620	772.3847	600		278.13									
E	642.3457	321.6765	1456.7300	728.8686	_ 550 -											
н	779.4046	390.2060	1327.6874	664.3474	155 500 1											
G	836.4261	418.7167	1190.6285	595.8179	± 450 ± 450			524.24								
F	983.4945	492.2509	1133.6070	567.3072	350 -		496	24						1695.81		
N	1097.5374	549.2724	986.5386	493.7730	300 -	230 1	5							1055.01	1826.89	
Т	1198.5851	599.7962	872.4957	436.7515	250 -	143.08	263.15			926.49				1543.77		
A	1269.6222	635.3148	771.4480	386.2277	200 -	110.07	124	581.27	700.38	872.47 986.53						
C[C9I]	1608.7886	804.8979	700.4109	350.7091	100	10.07	423		784.40	943.41	1	195.60	1526	6.72 1609.77	1809 91	
1	1721.8727	861.4400	361.2445	181.1259	50				111111		أساعا	133	5.68		111 11	
Т	1822.9203	911.9638	248.1605	124.5839	0 느	· · · · ·					L I L Hulu		الــــــــــــــــــــــــــــــــــــ		4000	-
К	1951.0153	976.0113	147.1128	74.0600		0 2	00 400	600	800	m/z, Da		1200	1400	1600	1800	
																-17

Vacuolar ATP synthase subunit A (VHA-A) YSNSDAVVYVG<u>C</u>GER

												-
	Protein C	uant				Protein ID		Spectra			Summary Sta	tistics
Spectrum L	ist											C
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Bes	st Sequence	Δ	N	Adifications		Conf Theor MW
12.1˙1.1	27.	17 3576.333	33 895.0906	6 4	7	YSMLSSAAVVT SPAQ	ATMVAPFTGLKSSSAFPVTR	Oxidation(M)	@3			< 1 3575.8003
2.1˙1.14	31.	76 1844.809	93 923.4119	9 2	8	YSNSDAVVYVGCGER		ICAT-C(C)@1	12			97 1844.8363
2.1˙1.14	k 31.	34 1853.849	99 927.9322	2 2	8	YSNSDAVVYVGCGER		ICAT-C:13C(9	9)(C)@12			99 1853.8665
3.1˙1.15	i 31.	09 1853.850	00 618.9573	3 3	8	YSNSDAVVYVGCGER		ICAT-C:13C(9	3)(C)@12			99 1853.8665
10.1˙1.1	32.	21 1844.802	29 923.4087	7 2	8	YSNSDAVVYVGCGER		ICAT-C(C)@1	12			45 1844.8363 -
•							III					4
Peptide ID	Hypotheses -	3.1dot;1.15(08.3.3								Precursor M	S Region
Conf V So	Drot N (Seguenee		A	Madificationa		boor m/z			
99 13	8 VS	SDAWWOO	GER	Sequence			ICAT-C:13C(9)(C)@12	1853,8665	618.9628	3 -0.0165	60 - 615	i.9370 618.9539
65 13	VS	ISNAVVYVGO	GER				Deamidated(N)@5.ICAT-C:	1853,8665	618,9628	3 -0.0165	40 - 616.6171	619.9520
2 12	YS	ISDGTVYVGC	GER				ICAT-C:13C(9)(C)@12	1853.8665	618.9628	3 -0.0165	20	630.7939
< 1 13	YS	SDTVVYVGC	GER				Thr->Ala@6, ICAT-C:13C(9)	1853.8665	618.9628	3 -0.0165	O WHEN INTER	INITAL III AVANAN KA MI MAAMAMAYAY
-1 12	NC:	CENTRALICO	CED					1052 0005	619 0619	2 0.0105		m/z, Da
							LITTLE SAME WALL FOR STOLEN					
Fragmentat	ion Evidence	for Peptide	•][
Fragmentat	ion Evidence	for Peptide	2								<u> </u>	
Fragmentat	ion Evidence NSDAVVYVGC[b	for Peptide	e V	y+2							II	
Fragmentat	ion Evidence NSDAVVYVGC[b 164.0706	for Peptide 99JGER b+2 82.5389 1	y 1854.8738	y+2 927.9405	1	300 - 136.08 y	/1 y3	у	*4 y5 y6	6 y7	y8	
Fragmentat YS Residue Y S	ion Evidence NSDAVVYVGC[b 164.0706 251.1026	for Peptide 900 900 900 900 900 900 900 90	y 1854.8738 1691.8105	y+2 927.9405 846.4089	T	300 - 136.08 y 280 -	/1 b2 y3 b4:9+2	b5 b8y11+	14 y6 y6 2 b7 b8	6 y7	y8	
Fragmentat	ion Evidence NSDAVVYVGC[164.0706 251.1026 365.1456	for Peptide 99/GER b+2 82.5389 1 126.0550 1 183.0764 1	y 1854.8738 1691.8105 1604.7784	y+2 927.9405 846.4089 802.8929	1	300 - 136.08 y 280 - 260 -	/1 b2 y3 b49+2	b5 b8y11+	14 y5 y6 2 b7 b8	6 y7	y8	
Fragmentat	ion Evidence NSDAVVYVGC[b 164.0706 251.1026 365.1456 452.1776	for Peptide 99/GER 82.5389 1 126.0550 1 183.0764 1 226.5924 1	y 1854.8738 1691.8105 1604.7784 1490.7355	y+2 927.9405 846.4089 802.8929 745.8714	T	300 136.08 y 280 260 240 -	/1 b2 y3 b49+2	b5 b8y11+	14 y5 y6 2 b7 b8	6 y7	y8	
Fragmentat	ion Evidence NSDAVVYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045	for Peptide 9)GER 225389 1 126.0550 1 183.0764 1 226.5924 1 284.1059 1	y x 1854.8738 x 1691.8105 x 1604.7784 x 1490.7355 x	y+2 927.9405 846.4089 802.8929 745.8714 702.3554		300 1 136.08 Y 280 2 260 2 240 2 200 2	/1 b2 y3 b49+2	b5 b8y11+	14 y/5 y/ 2 b7 b8 757,35	6 y7	y8	
Fragmentat	ion Evidence NSDAVVYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416	for Peptide 9)GER 22,5389 1 126.0550 1 183.0764 1 226.5924 1 284.1059 1 319.6245 1	y a 1854.8738 a 1691.8105 a 1604.7784 a 1490.7355 a 1288.6765 a	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419		300 136.08 2 280 2 260 2 240 2 200 2 210 2	/1 b2 y3 b49+2	b5 b8y11+	14 y/5 y/ 2 b7 b8 757,35	6 y7	y8	
Fragmentat	ion Evidence NSDAVVYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101	for Peptide sygGER b+2 82.5389 126.0550 1 183.0764 1 226.5924 1 284.1059 1 319.6245 1 369.1587 1	y x 1854.8738 1 1691.8105 1 1604.7784 1 1490.7355 1 1288.6765 1 1217.6394 1	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419 609.3233		300 136.08 280 260 240 220 200 200 210	/1 b2 y3 b49+2	b5 b8y11+	14 y/5 y/ 2 b7 b8 757,35	6 y7	y8	
Fragmentat	ion Evidence NSDAVVYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101 836.3785	for Peptide sygGER b+2 1 82.5389 1 126.0550 1 183.0764 1 226.5924 1 284.1059 1 319.6245 1 369.1587 1 418.6929 1	y x 1854.8738 x 1691.8105 x 1604.7784 x 1400.7355 x 1288.6765 x 1217.6394 x 1118.5710 x	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419 609.3233 559.7891		300 136.08 280 260 240 200 510 510 510 510 510 510 510 510 510 5	/1 b2 y3 b49+2 235.14	b5 b8y11+	14 y/5 y/ 2 b7 b8 757,35 85	6 y7 56.41	y8	
Fragmentat	ion Evidence NSDAVVYVGC[164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101 836.3785 999.4418	for Peptide sygGER b+2 1 82.5389 1 126.0550 1 183.0764 1 226.5924 1 284.1059 1 319.6245 1 369.1587 1 418.6929 1 500.2245 1	y 854.8738 691.8105 604.7784 1490.7355 1403.7035 1288.6765 1217.6394 1118.5710 1019.5026	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419 609.3233 559.7891 510.2549		300 136.08 280 260 240 200 200 160 140 120	1 b2 y3 b49+2 235.14 223.10	b5 b8y11+	14 y/5 y/c 2 b7 b8 757.35 85	6 y7 56.41 1019.49	y8	
Fragmentat	ion Evidence NSDAVVYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101 836.3785 999.4418 1098.5102	for Peptide sygGER 282.5389 1 126.0550 1 183.0764 1 284.1059 1 319.6245 1 369.1587 1 418.6929 1 500.2245 1 549.7587 1	y 854.8738 691.8105 604.7784 1490.7355 1403.7035 1288.6765 1217.6394 1118.5710 1019.5026 856.4393	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419 609.3233 559.7891 510.2549 428.7233		300 136.08 280 260 240 200 200 160 140 120 100	1 b2 y3 b49+2 235.14 223.10	b5 b8y11+	14 y/5 y/t 2 b7 b8 757.35 85	6 y7 56.41 1019.49	y8	
Fragmentat YS Residue Y S N S D A V V V Y V G	ion Evidence NSDAVVYYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101 836.3785 999.4418 1098.5102 1155.5317	for Peptide sygGER 282.5389 126.0550 1 126.0550 1 126.0550 1 126.0592 1 1 284.1059 1 319.6245 1 369.1587 1 418.6929 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 500.2245 1 1 1 1 1 1 1 1 1 1 1 1 1	y 1854.8738 1691.8105 1604.7784 1490.7355 1403.7035 1288.6765 1217.6394 1118.5710 1019.5026 856.4393 757.3708	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419 609.3233 559.7891 510.2549 428.7233 379.1891		300 136.08 280 260 240 200 200 200 200 200 200 200 200 20	1 b2 y3 b49+2 235.14 223.10 278.13	b5 b6y11+	14 y/5 y/c 2 b7 b8 757.35 85	5 y7 58.41 1019.49	y8	
Fragmentat YS Residue Y S D A V Y Y Q G C[C91]	ion Evidence NSDAVVYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101 836.3785 999.4418 1098.5102 1155.5317 1494.6980	for Peptide syger 82.5389 126.0550 1 126.0550 1 126.0524 1 126.5924 1 226.5924 1 226.5924 1 226.5924 1 226.5924 1 284.1059 1 319.6245 1 369.1587 1 500.2245 1 1 500.2245 1 1 500.2245 1 1 500.2245 1 1 1 1 1 1 1 1 1 1 1 1 1	y 1854.8738 1691.8105 1604.7784 1490.7355 1403.7035 1288.6765 1217.6394 1118.5710 1019.5026 856.4393 757.3708 700.3494	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419 609.3233 559.7891 510.2549 428.7233 379.1891 350.6783		300 136.08 280 260 240 200 200 160 160 140 120 100 80 60	1 b2 y3 b49+2 235.14 223.10 278.13 361.17 487.1	21 576 27 720.2	14 y/5 y/ 2 b7 b8 757.35 85	5 y7 56.41 1019.49 1002.45	y8	
Fragmentat YS Residue Y S D A V Y Y Q C[C9I] G C[C9I]	ion Evidence NSDAVVVVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101 836.3785 999.4418 1098.5102 1155.5317 1494.6980 1551.7195	for Peptide syger 82.5389 126.0550 1 126.0550 1 126.0520 1 123.0764 1 1226.5924 1 226.5924 1 226.5924 1 226.5924 1 239.1687 1 369.1687 1 500.2245 1 1 1 1 1 1 1 1 1 1 1 1 1	y y 1854.8738 1 1691.8105 1 1604.7784 1 1403.7035 1 1288.6765 1 1217.6394 1 1019.5026 8 856.4393 1 770.3494 3 361.1830 1	y+2 927.9405 846.4089 802.8929 745.8714 702.3654 644.8419 609.3233 559.7891 510.2549 428.7233 379.1891 350.6783 181.0951		300 136.08 280 260 240 200 160 160 140 120 100 80 60 40 20	1 b2 y3 b459+2 235.14 235.14 278.13 361.17 268.14	21 57 6.27 720.2	14 y/5 y/ 2 b7 b8 757.35 0.33	5 y7 56.41 1019.49 1002.45	y8	1477.63
Fragmentat YS Residue Y S D A V Y Y G C[C9I] G E	ion Evidence NSDAVVVYVGC[b 164.0706 251.1026 365.1456 452.1776 567.2045 638.2416 737.3101 836.3785 999.4418 1098.5102 1155.5177 1494.6980 1551.7195 1680.7621	for Peptide syger 82.5389 126.0550 1 126.0550 1 126.0550 1 126.0524 1 126.5924 1 226.5924 1 226.5924 1 226.5924 1 239.1687 1 369.1687 1 500.2245 1 500.2455 1 500.2455 1 500.2455 1 500.2455 1 50	y 1854.8738 1691.8105 1604.7784 1490.7355 1403.7035 1288.6765 1217.6394 1118.5710 1019.5026 856.4393 170.3494 361.1830 304.1615 1	y+2 927.9405 846.4089 802.8929 745.8714 702.3654 644.8419 609.3233 559.7891 510.2549 428.7233 379.1891 350.6783 181.0951 152.584		300 136.08 2 280 2 260 2 200 2 180 1 180 1 100 8 80 6 40 20 1 0 40 1 20 1 100 8 100 1 100 8 100 1 100 100 1 100 100 100 100 100 100 100 100 100 100	1 b2 y3 b459+2 235.14 235.14 223.10 278.13 361.17 268.14 487.1	21 740 576.27 720.2	14 y/5 y/c 2 b7 b8 757.35 0.33	5 y7 56.41 1019.49 1002.45 903.44 11	y8	1477.63
Fragmentat YS Residue Y S D A V Y Y C[C91] G E R	ion Evidence NSDAVVVVGC[251.1026 251.4066 251.4066 452.1776 567.2045 638.2416 737.3101 836.3785 999.4418 1098.5102 1155.5317 1494.6980 1551.7195 1680.7621 1836.8632	for Peptide 9)GER 2)E25389 126.0550 1 126.0550 1 126.0550 1 126.0524 1 226.5924 1 226.5924 1 226.5924 1 226.5924 1 239.1687 1 500.2245 1 5	y 1854.8738 1691.8105 1604.7784 1409.7355 1403.7035 1288.6765 1217.6394 118.5710 1019.5026 1856.4393 170.3494 361.1830 304.1615 175.1190	y+2 927.9405 846.4089 802.8929 745.8714 702.3554 644.8419 609.3233 559.7891 510.2549 428.7233 379.1891 350.6783 181.0951 152.5844 8.8.0631		300 280 260 240 200 3136.08 240 200 3180 300 200 3180 300 200 3180 300 200 300 200 300 200 200 200 200 20	1 b2 y3 b459+2 235.14 223.10 278.13 361.17 268.14 200 300 400 50	21 740 57 ¢.27 720.2	14 y/5 y/ 2 b7 b8 757.35 0.33 28 20 20 20 20 20 20 20 20 20 20 20 20 20	58.41 1019.49 1002.45 903.44 900 1000 1	y8 1118.60 101.55 1100 1200 13	1477.63 , , , , , , , , , , , , , , , , , , ,

Glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) SDLDIVSNAS<u>CTTNCLAPLAK</u>

																		- 8
	Protein	Quant				Protein	ID				Spectra				Su	immary St	atistics	
Spectrum I	let																	
Spectrum L	.151																	
Spectrum	Time	Prec	MW Prec	m/z Prec z	Prot N		Bes	t Sequen	ice		Δ		Modi	fications			Conf 1	Theor MW 🔺
12.1˙1.1	4().473 2588	3.1680 863.	7299 3	39	SDLNIV	SNASCTINC	LAPLAK			ICAT-C(C))@11, ICAT-(C(C)@15				99	2588.2937
12.1˙1.1	4	.156 2589	9.1445 864.	0555 3	39	SDLNIV	SNASCTTNCI	APLAK			ICAT-C(C))@11, ICAT-(C(C)@15				22	2588.2937 👻
•								P	11									4
Peptide ID I	Hypotheses	- 12.1dot:	1.1622.3.12												Р	recursor N	S Region	
																oouroor n	io nogion	
Conf ⊽ Sc	Prot N 🛆			Sequence	•		Δ	N	lodifica	tions 🗠	Theor MW	Theor m/z	z	🛆 Mass 🔺	1	00 - 864	0685	869.7440
99 14	39 S	DLNIVSNAS	SCTINCLAP:	LAK				ICAT-C(C)@11,	ICAT-C(C)	2588.2937	863.7719	3 3	-0.1259		861.35	58	
99 14	S	DINIVSNAS	SCTINCLAP	LAK				ICAT-C(C)@11,	ICAT-C(C)	2588.2937	863.7719) 3	-0.1259		0 -	a qua segue III from	њини ПРН иккери
	40							JOAT OF	0.044		3500 3770	004.0000	<u> </u>	4 40001				
Fragmentat	ion Evidenc	e for Pept	tide															
SDI	LNIVSNASCICO	ITTNCICOIL	APLAK															
100.			1															
Residue	b	b+2	У	y+2														
S	88.0393	44.5233	2589.3011	1295.1542		-	y1 1	/2 y3	y4	y5 y6		y7 y8	y9	y10	y.	11		
D	203.0662	102.0368	2502.2691	1251.6382		2400 -	D	205+2 03	105410	0+2 09+2 06	D/	99552 2						
	310,1503	150.5/00	2307.2421	1194.1247		2200 -				428.27								
	430.193Z	215.0003	2160 1151	1080 5612		2000												
V	642 3457	321 6765	2047 0311	1024 0192		2000												
S	729.3777	365 1925	1947.9627	974.4850		1800 -												
N	843.4207	422.2140	1860.9306	930,9690		1600 -												
A	914.4578	457.7325	1746.8877	873.9475		≥1400]												
s	1001.4898	501.2485	1675.8506	838.4289		elsi												
C[C0I]	1331.6260	666.3166	1588.8186	794.9129		<u>분</u> 1200 -		228.13										
Т	1432.6737	716.8405	1258.6824	629.8448		1000 -		245.09										
Т	1533.7213	767.3643	1157.6347	579.3210						499.30								
N	1647.7643	824.3858	1056.5870	528.7972		000 -												
C[C01]	1977.9005	989.4539	942.5441	471.7757		600 -		/	82.18	543.20								
L	2090.9845	1045.9959	612.4079	306.7076		400	200.14	2	9.09	515.26								
А	2162.0216	1081.5145	499.3239	250.1656			183.15			520.25								
Р	2259.0744	1130.0408	428.2867	214.6470		200 -	129.10			630.3	3 86	4.41 105	6.54	14	467 63	1657,73	1847.78	
L	2372.1585	1186.5829	331.2340	166.1206		₀ ⊥	h	Thirt and the second		LENGTHAL MAR PLAT		ىر يەلەقلىطىچىنا، مەرب	جار میں بار در	·····	1.	4000		
A	2443.1956	1222.1014	218.1499	109.5786			U 2	.00	400	600	800	1000 m/z. E	12)a	:00 1400		1600	1800	2000
К	2571.2905	1286.1489	147.1128	74.0600														

Putative transitional endoplasmic reticulum ATPase QSAP<u>C</u>VLFFDELDSIATQR

												_ 8 :
	Protein Quant			Protein	ID			Spectra			Summary St	tatistics
Spectrum L	ist											
Spectrum	n Time Prec	MW Prec m/	z Precz	Prot N	Best	Sequence		A		Modifications		Conf Theor MW 🔺
10.1˙1.1	I 57.341 2358	.1294 787.050	04 3	33 QSAPCV	LFFDELDSIAT	QR		Gln->pyro	-Glu@N-term,	ICAT-C:13C(9)(C)@5		99 2358.1614
5.1˙1.20	0 64.146 0	.0000 683.734	41 0	QSEMGI	FKILQGSLSGE	GGK		GIn->pyro	-Glu@N-term			< 1 2048.0249
•						111						
Peptide ID	Hypotheses - 10.1dot;1	1.1661.2.10									Precursor M	1S Region
Conf ⊽ Sc	Prot N A		Sequence		Δ	Modifie	ations	Theor MW	Theor m/z	7 (Mass	704 9700	
99 16	33 OSARCVIER	ELDSTATOR	Sequence		0	Sin->pyro-Glu	@N-term ICA	2358 1614	787.0610	3 -0.0319	20 - 1	, 787.3844
< 1 16	0SASCVLEFT	ELDSIATOR				Sin->pyro-Glu	@N-term. Ser-	2358.1614	787.0610	3 -0.0319	Atte up the	And the state of the
							ALICAT O	2257 4200	700 7440	2 4 0005		
Fragmentat	tion Evidence for Pept	ide										
PGQ QS	APC[C9I]VLFFDELDSIATQR											
Residue	b b+2	у	y+2									
Q	112.0393 56.5233	2359.1686	1180.0879	480	y1	y2	y3 y4	y5 y	y6 y7	ув у9	y10	
S	199.0713 100.0393	2248.1365	1124.5719	460		y4+2 b3	b4 y8+2	- 475.25	b5 b6	b14+2 b7 b8		
A	270.1084 135.5579	2161.1045	1081.0559	440								
Р	367.1612 184.0842	2090.0674	1045.5373	400								
C[C9I]	706.3276 353.6674	1993.0146	997.0110	380 -								
V	805.3960 403.2016	1653.8483	827.4278	340								
	918.4801 459.7437	1554.7798	777.8936	320 -								
F	1065.5485 533.2779	1441.6958	/21.3515	280 -					700	20		
	1212.6169 606.8121	1294.6274	04/.01/3	₹ <u>260</u>		245.07			790.	90		
	1327.0430 004.3250	1147.5590	5/4.2031	ta 240 - 1⊈ 220 -	120.08	245.07	13					
	1569 7705 785 3990	903 4894	452 2482	200	120.00	271	.15					
	1684 7974 842 9024	790.4054	395 7063	180			404.23		275 29	903.47		
S	1771 8295 886.4484	675.3784	338 1928	140				536.29	5/9.30			
	1884,9135 942,9604	588,3464	294,6768	120			437.22	588.35				
A	1955.9506 978.4790	475.2623	238,1348	100 -	175	.12	420.20	649.37	689.34			
T	2056.9983 1029.0028	404.2252	202.6162	60			367.17			917.44 1032.58	4050 54	
Q	2185.0569 1093.0321	303.1775	152.0924	40						850.47 962.50	1148.60 400	05.66
R	2341.1580 1171.0826	175.1190	88.0631	20							1140.09 128	1442.77
	1			Ť	100	200 300	400	500 600	700 80	00 900 1000	1100 1200 1	300 1400 1500
									m/z, Da			

Reversibly glycosylated polypeptide-1 NLL<u>C</u>PSTPFFFNTLYDPYR

											_							-	8 X
	Protein Qua	ant		T T		Protein ID				Spectr	a					Summary S	itatistics		
Spectrum L	.ist																	E	3
Spectrum	Time	Prec MW	Prec m/	z Prec z	Prot N	Be	st Sequen	се		Δ			Modif	ications			Conf	Theor MW	~
8.1˙1.14	50.599	2500.1655	5 834.39	58 3	28 1	NLLCPSTPFFFNTLY	DPYR			ICAT-C	(C)@4,	Phe->Let	u@9				99	2500.2461	
8.1˙1.14	50.556	2509.1816	5 837.40 ⁻	12 3	28 1	NLLCPSTPFFFNTLY	DPYR			ICAT-C	:13C(9)	(C)@4, P	he->Leu@	<u>)</u> 9			99	2509.2764	-
8.1˙1.14	51.491	2501.1628	8 834.72	82 3	1	NLLCPSTPHFFNTLY	DPYR			ICAT-C	(C)@4,	His->Asn	@9				62	2501.2048	-
•							11	1										- F	
															_	_			
Peptide ID I	Hypotheses - 8.	1dot;1.1422	2.3.8													Precursor	MS Regio	n	
Conf ⊽ Sc	Prot N 🛆			Sequence		1	M	odificatio	ns /	Theor M	W Th	eor m/z	z	∆Mass		400 1		- IN	
99 18	28 NLLC	PSTPFFFNT	LYDPYR				ICAT-C(C)@4, Phe	⊱>Leu@9	2500.24	61	834.4226	3	-0.0805		83	4.7326 -	837.7393	
37 18	NLLC	PSTPHFFNT	LYDPYR				ICAT-C(C)@4, His	->Leu@9	2500.24	61	834.4226	3	-0.0805		833	.4012	838.7371	
7 18	NLLC	PATPFFFNT	LYDPYR				ICAT-C(C)@4, Oxi	dation(P)	2500.24	61	834.4226	3	-0.0805	-	0 - 444-944	دارالين _{يس} ير	hell like here and all	54
										-									
Fragmentati	ion Evidence fo	r Pontido																	
riaginentat	Ton Lyndence id	n i chune																	-1
NLL	LC[C0]PSTPLFFNTL	YDPYR																	
Residue	b I	b+2	у	y+2															ר ר
N	115.0502	58.0287 25	01.2533	1251.1303		1.1e4 y1	y2	уЗ у	4 1	5 y6	y7 1	y8 y	/9 y1	0 y11	y12				
L	228.1343 1	14.5708 23	87.2104	1194.1088		b3+j23	622 b3 b3	06+2 - 43	5.22 b4	bb)/31+4942	b7	b8 b9	b10						
L	341.2183 1	71.1128 22	74.1264	1137.5668		1.064													
C[C0I]	671.3545 3	36.1809 21	61.0423	1081.0248		9.0e3 -													
P	768.4073 3	84.7073 18	30.9061	915.9567															
S	855.4393 42	28.2233 17	33.8533	867.4303		0.065													
Т	956.4870 4	78.7471 16	46.8213	823.9143		7.0e3 -													
Р	1053.5397 52	27.2735 15	45.7736	773.3905	≥	60-3													
	1166.6238 5	83.8155 14	48.7209	724.8641	ensi	5													
F	1313.6922 6	57.3497 13	35.6368	668.3220	Ĕ	5.0e3 -													
F	1460.7606 7	30.8840 11	88.5684	594.7878		1002													
N	1574.8036 7	87.9054 10	41.5000	521.2536		4.063	269.09												
T	1675.8512 8	38.4293 9	27.4571	464.2322		3.0e3 - 228 4	286.13												
L	1788.9353 8	94.9713 8	26.4094	413.7083		220.1			713.31	826 28	92	7.42							
Y	1951.9986 9	/6.5030 7	13.3253	357.1663		2.0e3 - 120.08		496.	23	020.00	1	041.48							
	2067.0256 10	34.0164 5	50.2620	275.6346		1.0e3 -		410.19	533.25	004 47	1 10	24 45					21	73.12	
P	2164.0783 10	82.5428 4	35.2350	218.1212				L. L. L.	al had to a l			. III ¹¹	130.56	35.61 1	527.72		- 1		
Ŷ	2327.1417 110	64.0745 3	38.1823	169.5948		0.0e0	200	400	600	800	10	00	1200	1400	1600	0 1800	2000	2200	
R	2483.2428 124	42.1250 1	75.1190	88.0631								m/z, Da							

Threonine synthase H<u>C</u>GISHTGSFK

				_												- 8
	Protein	Quant		Ĭ		Protein ID			Spectra					Summary	Statistics	
Spectrum L	ist															
Spectrum	Time	Prec N	IW Prec m/z	Prec z	Prot N	Bes	st Sequence	,	Δ		Modificat	tions			Conf	Theor MW 🔺
7.1˙1.17	63	.912 1421.7	7114 711.863	0 2		HATTLKAPASRGGR									< 1	1421.7852
9.1˙1.13	24	.586 1399.6	5583 700.836	4 2	77	HCGI SHTGS FK			ICAT-C(C)	@2					54	1399.6666
9.1˙1.13	24	.395 1408.6	3772 705.345	9 2	77	HCGISHTGSFK			ICAT-C:13	C(9)(C)@2					99	1408.6969
9.1&00t;1.13	25	828 0.0	0000 695 357	3 0	133	HCVNSVSIK	ONTOTOPECTU	CCD	IGAT-C:13	C(9)(C)@2					90	1221.0507
2 1˙:1 1F		530 0.0	000 613 295	9 0		HDODSAGUSCI OCAN	DDCD	GGK							21	1836 8351
•																•
														-		
Peptide ID	Hypotheses	- 9.1dot;1.1	356.2.9										ľ	Precursor	MS Regio	n
Conf V So	Drot N (Coguenes		A	Madif	instians A	Theor MM	Theor m/r	- 4	Maga				
99 19	77 H	GUSHIGS FR	ζ	Sequence	,	~	ICAT-C:13C(3)(C)@2	1408.6969	705.3557	2 -	-0.0196		150 7	00.8317 7	05.3439
< 1 13	II	SSENGPMGS	FK					1/10/62	1408.6769	705.3457	2	0.0003		100		
< 1 12	H	LGRLISFK					ICAT-C:13C(9)(C)@2	1408.8060	705.4103	2 -	-0.1288			· · · · · ·	09.8625
< 1 12	ম	AVFMLVVAM	IK				Oxidation(M	@11	1408.7611	705.3878	2 -	-0.0839		50 -		l non
< 1 11	H	VDLLQLLSE	ſΚ						1408.8079	705.4112	2 -	-0.1306		ANN A	hallhadllh	aad NaNaNNNN II
														0 11100	700 705	710 715
															m/z, [Da
Eragmontat	ion Evidenc	e for Pentic	lo													
Traymentar		e ioi i eput	10													
HC	C9IJGISHTGSFI	< C														
Residue	b	b+2	у	y+2		250 1										
Н	138.0662	69.5367	1409.7041	705.3557			b2+95+2	y3 y4 b2	y5 63	b4/11+2 b5	7 y8 b6	у9 b7	b8	b9	у10 b10	у11 b11
C[C9I]	477.2326	239.1199	1272.6452	636.8263		300 -									1	409.70
G	534.2540	267.6306	933.4789	467.2431		250 -		477	7.22							
	647.3381	324.1727	8/6.4574	438.7323	,	110.07	278.1	3 460 19	539.27							
<u>э</u> н	871 4290	436 2182	676 3413	338 6743	ensit	200	246.10	4.12				933.46				
Т	972.4767	486.7420	539.2824	270.1448	Ĕ	150 -		432 20						1098.51		1391.69
G	1029.4982	515.2527	438.2347	219.6210		100 -	207.09 294	.18			63.37	1 43	1011.4	6 1116.52		
S	1116.5302	558.7687	381.2132	191.1103		129.1	0	361.22		647.36 734.	35 843.4	3		1081.48	1245.62	1374.69
F	1263.5986	632.3029	294.1812	147.5942		50 120.08			599.	26	اليو. باير	L		dah k	լ հետ	
К	1391.6936	696.3504	147.1128	74.0600			200 3	וווווווווווווווווווווווווווווווווווו			400 800	900	1000	1100	1200 13	
						0 100	200 3				000	000		1100		00 1100

Oxalic acid oxidase SVQDF<u>C</u>VANLKR

																				-	ъ×
		Prote	in Quant			1		Protein ID	T			Spectra		T			Sum	mary Stati	istics		
												-									
Spectrun	n Li	st																		E	3
Spectr	rum	Ti	me Pi	rec MW	Prec m/z	Prec z	Prot N	Best Sequen	ce V				Modifica	tions				Conf	Theor	MW z 🔺	
9.1.1.141	7.3		33.512 1	614.7883	808.4014	4 2	4	SVQDFCVANLKR		ICAT-C:130	;(9)(C)@6						9	6 1614.	3599 2 🗆	5
12.1.1.15	23.3		35.294 10	614.7599	808.3872	2 2	4	SVQDFCVANLKR		ICAT-C:130	C(9)(C)@6						9	9 1614.	3599 2	
3.1.1.153	31.2		34.851 14	458.7555	730.3850) 2	4	SVQDFCVANLK		ICAT-C:130	;(9)(C)@6						7	/5 1458.7	7588 2	
7.1.1.153	6.2		35.640 1	458.7185	730.3665	5 2	4	SVQDFCVANLK		ICAT-C:130	;(9)(C)@6						2	8 1458.	7588 2	
9.1.1.143	34.4		35.998 14	458.6931	730.3538	2	4	SVQDFCVANLK		ICAT-C:130	;(9)(C)@6						7	2 1458.	7588 2	
011144	2.7		27.026 4	460.6040	720 0544	ป่าไ	4	CHODECIMANIA		Desmidator	1016	N2 ICAT C-12	C(0)(C)@6						2 4450	7400 0	- I
Peptide I	ID H	ypothes	es - 12.1.1	.1523.3													Prec	ursor MS	Region		
Conf ⊽	Sc	Prot N 🗠				Sequence		Δ	Modifi	cations	Δ.	Theor MW	Theor m/z	z	∆Mass			1	200 A	04.4	
99	16	4	SVQDFCVA	ANIKR					ICAT-C:13C(9)(C)@6		1614.8599	808.4373	2	-0.1000		30	808.908	81	011	
< 1	10		WKDRAYSI	LMMNGK					Oxidation(M)	<u>2</u> 9		1614.7646	808.3896	2	-0.0048		20	804.373	35 809	8962	
< 1	9		ENASLSNI	rvkr l <u>o</u> r	l							1614.8801	808.4474	2	-0.1203				- 003	.0302	
<1	9		GNAAFYQS	SRVVMKK	(Deamidated(N	1)@2, Oxidat	0	1614.8188	808.4167	2	-0.0590		10	- Mather of the	aallaataa	a la litta data a	
< 1	ŏ		NEYRNAH.	LARTDR								1614.7975	808.4060	2	-0.0376		0			III,III IIIII,	
																		800	810 m/z. Da	820	
																- 11					_
Fragmen	itatio	on Evide	ence for Pe	eptide																	
	0.10	DECICON																			- 1
	Isvu	DEC[Cal]V	ANLKK																		- 1
Residu	e	b	b+2		у	y+2		v1	v2	vall	الملر	vel lve	1	1	v7	vs	el .	vell v	10	1	
S		88.03	44.52	233 161	5.8672	808.4372	12	00 - b2	1 b3	b4 b7+	2 vi	3+2010+2011+1	2 v12+2	b6	,, b8	yu		b10		b12	
-		187.107	1 94.05	0/0 152	0.0352	704.9212	1 12	. 24	4.08 254.12												
		430 403	2 245 60	03 420	3.7007	651 3577	10	00 - 159.11 -													
F	_	577 264	7 280.13	45 148	6 6812	593 8442		175.11	278.	12											
01001		916.429	458 71	76 103	9.6128	520 3100	l ≩ 8	00 -													
V		1015 494	4 508.25	19 70	0.4464	350 7269	ţ,	oo]				601.37									
A		1086.533	6 543 77	04 60	1.3780	301,1926	5	~	35	2.19	530.3	12	772.35								
N		1200.576	600.79	19 53	0.3409	265.6741	4	00 - 420.07		430.17		700		952	.42 998.46	5					
L		1313.660	657.33	39 41	6.2980	208.6526		130.07	303.22	444.17	5	78.30			1 100	5 50					
к		1441.758	5 721.38	314 30	3.2139	152.1106	2	00 - 110.07	h ha	شا و اور ر	d L	593.87	831.38	895.40	109	0.00	1160.5	1 14	12.70	1511.69	
R		1597.856	6 799.43	19 17	5.1190	88.0631		126.05			11	did May ad an	da katika katika		li i i i i	La La La			ايدارا		
								0 100	200 300	400 5	00	600 70	0 800	900	1000 1	100	1200	1300 14	00 150	0 1600	
													m/z, Da								
L																					

Oxalic acid oxidase AETPAGYP<u>C</u>IRPIHVK

			_	_							-				
	Protein Qu	ant				Protein ID			Spectra			Summar	y Statist	ics	
Spectrum L	_ist														
Spectrum	n Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequen	ce 🛆			Modification	8		Conf	Theor MW	z 🔺
3.1˙1.22	2 60.06	4 1194.6041	598.3093	2		AETFGGEGGTAAK							< 1	1194.5516	2 📟
2.1˙1.15	5 28.21	1 1987.0409	497.7675	4	9	AETPAGYPCIRPIHV	K	ICAT-C:13C()(C)@9				1	1987.0760	4
10.1˙1.1	1 32.22	3 1986.9966	663.3395	3	9	AETPAGYPCIRPIHV	K	ICAT-C:13C())(C)@9				97	1987.0760	3
12.1˙1.1	1 29.20	3 1987.0282	497.7643	4	9	AETPAGYPCIRPIHV	K	ICAT-C:13C(S)(C)@9				47	1987.0760	4
12.1˙1.2	2 74.55	0.0000	717.6059	0		AETRLHSRHESFSAE	LPSVPSPY						< 1	2866.4111	4
La. 40. 400	00.70	0.0000	0044474					1						0700 0000	
															_
Peptide ID	Hypotheses - 1).1dot;1.153	5.3.10									Precurs	or MS R	egion	
Conf ⊽ So				Sequence		Δ.	Modif	icatione	A Theor MM	Theor m/z	7 (Maee A			ls.	
97 14	9 AFTE	AGYPCIEPTE	IVK	ocquence			ICAT-C:13C(9)(C)@9	1987.0760	663,3660	3 -0.0794	30 -	660.33	663.3394	
<1 11	Δ.F.MIX	EGTIVYTADS	NGER				Deamidated(N)@15	1986,8993	663,3071	3 0.0973	20 - 66	1.3167	663.9982	
<1 11	SEG	GLFYAVLASE	ASGNAK				,		1986.9873	663.3364	3 0.0093	10 - 11	. K	u d uluduru k	Աստեհես
<1 11	SLTS	TLSRGPEGAN	IKEIVK				Deamidated(N)@14	1987.0586	663.3601	3 -0.0620	o 120	30,730,00s		Lundar .
< 1 11	VAMY	NAEIFCETKN	IK				ICAT-C(C)@	10	1986.9543	663.3254	3 0.0423 -			m/z, Da	
Fragmentat	tion Evidence f	or Peptide													
AE	TPAGYPC[C91]IRPIH	VK													
Residue	b	h+2													
Δ		UT2	у	y+2											
	72.0444	36.5258 198	y 38.0833	y+2 994.5453	Γ.	800 y1	/2 y3	у5	y6 y7		y8 y9 y10	0y11 y12 3	/13 y14		'
E	72.0444 201.0870	36.5258 198 01.0471 191	y 38.0833 17.0462	y+2 994.5453 959.0267	1	800 y1 b2	/2 y3 2+2 b3 b4 201.08	b6 y5	y6 y7 y1)01+j21+2 b1	5+2	y8 y9 y10	0y11 y12 y	/13 y14		'
E T	72.0444 201.0870 302.1347	36.5258 198 01.0471 191 51.5710 178	y state 88.0833 state 17.0462 state 88.0036 state	y+2 994.5453 959.0267 894.5054		800 - y1 b26 600 -	/2 y3 2+2 b3 b4 201.08	b6	y6 y7 y1)01+j21+ 2 b1:	5+2	y8 y9 y10	0y11 y12 y	/13 y14		'
E T P	72.0444 201.0870 302.1347 399.1874	36.5258 198 01.0471 191 51.5710 178 00.0974 168	y state 88.0833 38.0833 17.0462 38.0036 36.9559 36.9559	y+2 994.5453 959.0267 894.5054 843.9816		800 - y1 600 - 400 -	/2 y3 (+2 b3 b4 201.08	b6 y5	y\$ y7 y1)0H¢2+2 b1:	5+2	y8 y9 y10	Dy11 y12 y	/13 y14		'
E T P A	72.0444 201.0870 302.1347 399.1874 470.2245	36.5258 198 01.0471 191 51.5710 178 00.0974 168 35.6159 158	y y 38.0833 3 17.0462 3 38.0036 3 36.9559 3 39.9032 3	y+2 994.5453 959.0267 894.5054 843.9816 795.4552		800 y1 b26	/2 y3 3+2 b3 b4 201.08	b6 y5	y¢ y7 y109¥£¥2+2 b1:	5+2	y8 y9 y10	Dy11 y12 y	/13 y14		-
E T P A G	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460	36.5258 198 01.0471 191 51.5710 178 00.0974 168 35.6159 158 64.1266 151	y 38.0833 17.0462 38.0036 36.9559 39.9032 18.8661	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367		800 y1 b26 600 400 - 200 -	/2 y3 →2 b3 b4 201.08	b6	y∳ y7 y1 01-92+2 +2 b1	5+2	y8 y9 y10	0y11 y12 j	/13 y14		1
E T P A G Y	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093	36.5258 198 01.0471 191 51.5710 178 00.0974 168 35.6159 158 64.1266 151 45.6583 146	y state 38.0833 3 17.0462 3 38.0036 3 36.9559 3 39.9032 3 51.8446 3	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259	1 1 1 1 1	800 - y1 600 - 400 - 200 - 000 -	/2 y3 +2 b3 b4 201.08 226.11	b6 y5	y¢ y7 y10+9+2+2 b1	5+2	y8 y9 y10	0y11 y12 y	y13 y14		-
С Е Т Р А G У Р	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621	36.5258 198 01.0471 191 51.5710 178 00.0974 168 35.6159 158 64.1266 154 45.6583 146 94.1847 125	y state 38.0833 38.0833 17.0462 38.0036 36.9559 39.9032 18.8661 31.8446 38.7813 39.7813	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943	1 1 1 1 1 1 1 1	800 y1 b2 600 400 - 200 - 000 -	72 y3 +2 b3 b4 201.08 226.11	у5 b6	yê y7 y1044942+2 b1	5+2	y8 y9 y10	0y11 y12 y	/13 y14		•
С С С С С С С С С С С С С С	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285	36.525 198 01.0471 191 51.5710 178 00.0974 168 35.6159 158 64.1266 151 94.1847 128 63.7679 122	y state 38.0833 17.0462 38.0036 38.0036 36.9559 39.9032 38.8661 36.7813 38.7813 11.7285	y+2 9994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679	1 1 1 1 1 1 1	800 y1 b20 600 400 200 000 173.09	72 y3 (+2 b3 b4 201.08 226.11 246.17	у5 b6	y∲ y7 y1¢H¢H2H2 b1	5+2	y8 y9 y10	0y11 y12 y	r13 y14		,
E T P A G V P C[C91] I	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125	36.525 198 01.0471 191 51.5710 178 00.0974 168 35.6159 158 64.1266 151 94.1847 122 20.3099 88	y y 88.0833 17.0462 38.0036 38.0036 36.9559 39.9032 38.8661 36.7813 30.7285 39.7624	y+2 9994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847	1 1 Iuteusity	800 y1 b20 600 - 400 - 200 - 800 - 800 - 173.09	72 y3 (+2 b3 b4 201.08 226.11 246.17 361.48	у5 b6	y¢i y7 y1¢14¢442+2 b1	5+2	y8 y9 y10	0∳11 y12 j	r13 y14		·
E F P A G Y P C[C91] I R	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136	36.525 198 36.525 198 01.0471 191 51.5710 178 00.0974 166 35.6159 156 64.1266 151 45.6583 146 94.1847 122 20.3099 86 98.3605 7	y 88.0833 17.0462 18.0036 16.9559 19.9032 18.8661 51.8446 18.7813 11.7285 52.6621 19.4781	y+2 9994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 6649.8943 601.3679 431.7847 375.2427	Intensity 1	800 y1 b20 600 - 400 - 200 - 800 - 800 - 173.09	72 y3 (+2 b3 b4 201.08 226.11 246.17 361.18	у5 b6	y¢ y7 y1¢H¢H2H2 b1	5+2	y8 y9 y10	0∳11 y12 _} .81	1686.88		
E T P A G V P C[C91] I R P	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664	36.525 198 36.525 198 01.0471 191 51.5710 178 00.0974 166 35.6159 156 64.1266 151 45.6583 146 94.1847 122 20.3099 86 98.3605 74 46.8868 55	y \$8.033	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921	Intensity 1 1	800 y1 b20 600 - 400 - 200 - 800 - 400 - 400 - 141 10 -	72 y3 (+2 b3 b4 201.06 226.11 246.17 361.18 389.1	5 b6 8	y¢ y7 1¢14¢442+2 b1	5+2	y8 y9 y10	0∳11 y12 .811589.84	y13 y14		·
E F P A G Y P C[C91] I R P I	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664 1605.8505	36.525 198 36.5258 198 01.0471 191 51.5710 178 00.0974 166 35.6159 156 64.1266 151 45.6583 146 94.1847 122 20.3099 86 98.3605 74 46.8868 55 03.4289 45	Y Hermitian 88.0833	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6657	Intensity 1 1	800 y1 b20 600 - 400 - 200 - 800 - 400 - 400 - 400 - 141.10 200 - 130.08 -	72 y3 2+2 b3 b4 201.06 226.11 246.17 361.18 389.1	b6 y5	y6 y7 1014942+2 b1	5+2	y8 y9 y10 1298.75 1518 152.66 1281 73	0 <mark>∲11 y12 _</mark> .81 1589.84	1686.88	7.91	·
E F P A G Y P C[C91] I R P I H	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664 1605.8505 1742.9094	36.525 198 36.525 198 01.0471 191 51.5710 176 00.0974 166 35.6159 158 64.1266 151 45.6583 146 94.1847 122 20.3099 86 98.3605 74 46.8868 55 03.4289 49 71.9583 3	Y Hermitian 88.033	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6667 192.1237	Intensity 1 1	800 y1 b20 600 400 200 173.09 600 400 173.09	72 y3 2+2 b3 b4 201.06 226.11 246.17 361.18 389.1	8 462.24 593.38	y6 y7 1904942+2 b1	5+2 1053.58 .53 11	y8 y9 y10 1298.75 1518 152.66 1281 73	0 ∲11 y12 .811589.84 1.73	1686.88	7.91	·
E T P A G Y P C[C91] I R P I H V	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664 1605.8505 1742.9094 1841.9778	D2 D3 36.525 198 01.0471 191 51.5710 175 00.0974 166 35.6159 155 64.1266 151 45.6583 146 94.1847 122 20.3099 86 98.3605 74 46.8868 55 03.4289 44 71.9583 38 21.4925 24	Y Hermitian 88.033	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6657 192.1237 123.5942	Intensity 1 1	800 600 400 200 000 173.09 600 141.10 130.08 0 200 0 0 0 0 0 0 0 0 0 0 0 0	72 y3 2+2 b3 b4 201.06 226.11 246.17 361.18 389.1	8 462.24 593.38	y6 y7 1904942+2 b1 731.41 862	5+2 1053.58 .53 11 11 11 1000	y8 y9 y10 1298.75 1518 152.66 1281 73 1200 1400	0 11 y12 3 .81 1589.84 1.73 1600	1686.88	7.91	
E F P A G Y P C[C91] I R P I H V K	72.0444 201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1492.7664 1605.8505 1742.9094 1841.9778 1970.0728	36.525 198 36.525 198 01.0471 191 51.5710 175 00.0974 166 35.6159 155 64.1266 151 45.6583 144 94.1847 122 20.3099 86 98.3605 74 46.8868 55 03.4289 48 71.9583 38 21.4925 24	Y Hermitian 88.033	y+2 994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6657 192.1237 123.5942 74.0600	Intensity 1 1	800 600 400 200 000 173.09 600 141.10 130.08 0 200 200	72 y3 2+2 b3 b4 201.06 226.11 246.17 361.18 389.1 0 400	8 462.24 593.38 600	y6 y7 y904942+2 b1 731.41 862	5+2 1053.58 .53 111 111 1000 m/z, Da	y8 y9 y10 1298.75 1518 152.66 1281 73 1200 1400	0 11 y12 3 .81 1589.84 1.73 1600	1686.88 178 178 178 178	7.91	

Initiation factor 5A-4, putative KLEDIVPSSHNCDVPHVNR

																- 8
	Protein	Quant			P	rotein ID			Spectra				S	ummary S	tatistics	
Spectrum Li	ist															
Spectrum	Time	Prec	MW Prec n	n/z Prec z	Prot N	Bes	st Sequence	Δ			Modifi	cations			Conf	Theor MW 🔶
11.1˙1.1.	3/	2.570 2393	.1709 599.3	000 4	63 KI	EDIVPSSHNCDVP	HVNR		ICAT-C:130	C(9)(C)@12					99	2394.2161
11 1˙ 1 1	3	2 379 2394	1587 799.0	602 31	63 KT	FDTVPSSHNCDVP			ICAT-C:130	C(9)(C)@12					99	2394 2161
Peptide ID H	lypotheses	- 11.1dot;1	.1494.4.11										Р	recursor I	IS Regior	1
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modification	s 🔺 7	Theor MW	Theor m/z	z	∆Mass ▲] [60 -	N	
99 16	63 K	LEDIVPSSH	INCDVPHVNR				ICAT-C:13C(9)(C)@	12	2394.2161	599.5613	4	-1.0453		40 -	91 - 59	39.8023
< 1 9	E	PMKLFCDNF	AAISIAHNR				ICAT-C:13C(9)(C)@7	7	2393.2395	599.3171	4	-0.0687		20 502 2/	120	609.9299
< 1 9	G	SPLDTAIGS	NLWKEQDGR	PPR					2393.2087	599.3094	4	-0.0379		20 - 593.30	23	601.5822
< 1 9	R	NSLAGMAWE	RSLSVIFVP	DK					2393.2678	599.3242	4	-0.0970			m/z D	aberation protential
<1 8	A	TEGDI.VAMT	T.E.PVAYWTR	MK					2393.2124	599.3104	4	-0.0415	J 🛛 L		11/2, 04	<u> </u>
Fragmentati	on Evideno	ce for Pept	ide													
Residue	b	b+2	У	y+2		4				_1		-	- [
ĸ	129.1022	65.0548	2395.2234	1198.1153	1:	300 - bi ^y	1 y2 y3	54 y4	ур уб с ьс	y/	5.12	у8	уa	y10	y11	y13
L	242.1663	121.5968	2267.1284	1134.0679	12	200 -	245.07	04 90 12:	5 00	, y i	0+2					
	3/1.2209	242 6246	2154.0444	10/7.5250	1	00-										
	400.2000	243.0310	1000.0749	055 4044			225.44									
V	698 4083	349 7078	1796 8908	898 9490	1		235.11									
P	795 4611	398 2342	1697.8224	849 4148	9	900			622.35							
S	882 4931	441.7502	1600.7696	800.8884		800 -	254.42									
s	969.5251	485.2662	1513.7376	757.3724	l st	700 -	204.12									
Н	1106.5841	553.7957	1426.7055	713.8564	<u><u><u></u></u></u>	soo 197.1	6 289 16	525 28								
N	1220.6270	610.8171	1289.6466	645.3269		129.1	358 15	020.20								
C[C9I]	1559.7933	780.4003	1175.6037	588.3055			550.15									
D	1674.8203	837.9138	836.4373	418.7223		100										
V	1773.8887	887.4480	721.4104	361.2088	:	110.07			701	39						
P	1870.9415	935.9744	622.3420	311.6746		200			12	~	000.27				16	597.73
н	2008.0004	1004.5038	525.2892	263.1482		00				836.40	7 35	1076.48 1	137.48	1426.70	1513 81	
V	2107.0688	1054.0380	388.2303	194.6188			la l					ով է հեն		L ì		
N	2221.1117	1111.0595	289.1619	145.0846		0 100	200 300 400	500 (600 700	800 90	0 1000) 1100 1	200 13	300 1400	1500 16	00 1700
R	2377.2128	1189.1101	175.1190	88.0631						m/z, Da						

Mitochondrial elongation factor Tu QVGVPSLV<u>C</u>FLNK

														_			-	8
	Protein Q	uant				Protein ID			Spectra					Sumn	nary Statis	stics		
Spectrum L	ist																	
Spectrum	Time	Prec MW	V Prec m/z	Prec z	Prot N	Best Sequen	ce 🗠			Modificat	tions				Conf	Theor MW	z /	<u> </u>
7.1˙1.17	51.2	81 1612.76	50 807.3898	8 2	75	QVGVPSLVCFLNK		GIn->pyro-Glu@	N-term, ICAT	-C(C)@9					24	1612.864	7 2	
7.1˙1.17	· 51.1	74 1621.79	65 811.9055	5 2	75	QVGVPSLVCFLNK		GIn->pyro-Glu@	N-term, ICAT	-C:13C(9)(C)@	<u>D</u> 9				99	1621.894	9 2	
7.1˙1.17	44.6	84 1629.78	97 815.9021	1 2	75	QVGVPSLVCFLNK		ICAT-C(C)@9							99	1629.891	2 2	
7.1˙1.17	44.8	35 1638.80	98 820.4122	2 2	75	QVGVPSLVCFLNK		ICAT-C:13C(9)(0	;)@9						99	1638.921	4 2 _	=
8.1˙1.15	i 30.3	61 1255.550	00 628.7823	3 2	105	QVISSEGQRPR									90	1255.663	3 2	-
L2 40 det 4 24		70 4202 64	42 042 2204	4 21		01113 03 31/017100										4202 725		_
Peptide ID	Hypotheses -	7.1dot;1.17(06.2.7										1	Precu	rsor MS I	Region		
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modif	ications 🗠	Theor MW	Theor m/z	z 2	∆Mass		4				
99 15	75 QV0	VPSLVCFLN	K				ICAT-C(C)@	9	1629.8912	815.9529	2	-0.1016		60 -	820	.9133	20.4061	
< 1 11	RKV	VML FQNCR					Deamidated(Q)@8, ICAT-C:	1629.8894	815.9520	2	-0.0998		40 -	815.902	9		
< 1 10	GAV	GVGSSLGGT	SELPDK						1629.8209	815.9178	2	-0.0313		20	816.4071			
< 1 10	GGI	.GVVAGGGGG	GGGWEMR						1629.7682	815.8914	2	0.0215			a lise of a sub-		in a spiller	4
< 1 10	INF	RPTSVFSVRV	GAK						1629.9315	815.9730	2	-0.1418		0-	810	815 820	825	- -
																m/z, Da		
<u> </u>																		
Fragmentat	ion Evidence	for Peptide	•															
av	GVPSLVC[C0I]FL	NK																-
Residue	b	b+2	У	y+2		1 11				-		_1	- 1	- 1				
Q	129.0659	65.0366 1	630.8985	815.9529	1	800 - y1 b1	y2 by24+203	y3 y4 b45+2 b5y7+2		у5	y6	у7 у	/8	y9	y10 y11		b13	
V	228.1343	114.5708 1	502.8399	751.9236	1	600 - 200.1	4 - 228.13											
G	285.1557	143.0815 1	1403.7715	702.3894		400	-2	85.15										
V	384.2241	192.615/ 1	1346.7501	673.8787		-												
Р С	401.2769	241.1421 1	1247.0017	024.3445 575.8184		200 211	10 2	07.14										
3	681 3930	341 2001 4	1063 5969	532,3024	l sit	000 -												
V	780 4614	390 7343	950.5128	475 7600	<u><u>t</u></u>	800 -				851	.41							
CICOII	1110,5976	555,8024	851,4444	426,2258														
F	1257.6660	629.3366	521.3082	261.1577		129 1								1247 6	1			
L	1370.7501	685.8787	374.2398	187.6235		400		461.17 534	591.29	834.39	950.47	070 45		1241.0				
N	1484.7930	742.9001	261.1557	131.0815		200 - 138.09			641.30	762.43		^{570.49} ,106	3.57	12	30.58	1612	2	
К	1612.8880	806.9476	147.1128	74.0600				<u>I thil this difference</u>			ا السبالا	ىلىپ لىس		_ألب	1403	.67		
						0 100	200 300	400 500	600 7	008 00	900 10	000 1100	1	200 1	300 140	0 1500	1600	
										m/z, Da								

60S ribosomal protein L2 SIPEGAVV<u>C</u>NVEHHVGDR

																			- 8	×
		Protein	Quant					Protein ID			Spectra					Summ	ary Statis	tics		
Spee	ctrum Li	ist																		
S	pectrum	Time	Prec	MW Pre	ec m/z	Prec z	Prot N	Best Sequen	ice 🗠			Modificat	tions				Conf	Theor MV	V z 🔺	I
5.18	˙1.17.	47	.960 0	0.0000 59	1.3188	0		SINVLISGVHE FODD	ATEGSSR	Deamidated(N)	<u>D</u> 3						< 1	2361.108	4 4	I
10.1	1˙1.1.	33	.565 2143	.9221 71	5.6480	3	69	SIPEGAVVCNVEHHV	GDR	ICAT-C(C)@9							99	2144.043	2 3	I
10.1	1˙1.1.	33	.608 2153	.0413 53	9.2676	4	69	SIPEGAVVCNVEHHV	GDR	ICAT-C:13C(9)(0	C)@9						99	2153.073	5 4	I
1.13	2 dot-1 17	E2	262 1070	2170 54	0.6660	2		CT CRUCCHCCDC									~ 1	1070 473	1 7	
																				÷
Pept	tide ID F	lypotheses	- 10.1dot;1	1.1548.3.1	10											Precu	rsor MS F	Region		I
Cor	nf⊽ Sc	Prot N 🛆			Se	equence		Δ	Modif	ications 🛛 🛆	Theor MW	Theor m/z	z	∆Mass		1		K		I
	99 16	69 SI	PEGAVVCN	VEHHVGD	R	-			ICAT-C:13C(9)(C)@9	2153.0735	539.2756	4	-0.0323	3	40 -	537.2651	539.51	32	
	< 1 16	SI	PEGAVVCN	VEQHVGD	R				ICAT-C:13C(9)(C)@9, GIn->	2153.0735	539.2756	4	-0.0323	3	30 -		540.02	70	
	<1 11	LS	GAPVPAPA	APVPE PE P	EEDR						2153.0640	539.2733	4	-0.0229	5	20 -	533,5345	540.9	005	
	< 1 10	Cł	AATQVPYE	PRRPAPPR					ICAT-C:13C(9)(C)@1, Deam	2153.1365	539.2914	4	-0.0951		10	. Lake	al finance		I
	<1 9	LI	QNIHAFRV	QREEEDR					Deamidated(N)@4	2153.0977	539.2817	4	-0.0566	5	0Щ	NINIIMMANNI		excelence of the second se	I
												1						m/z, Da		I
																				t
Frag	mentati	on Evidenc	e for Pept	ide																
	SIPE	EGAVVC[C9I]N	/EHHVGDR																	I
R	esidue	b	b+2	v		y+2														L
S		88.0393	44.5233	2154.08	08 107	77.5440		6500] v1	y2 y3	v4 v5	y6	y7 y8	y9		v	10 y11	y12 y1	13 14	y15	I
1		201.1234	101.0653	2067.04	87 103	34.0280		6000 - b4g	b6+2 b8+2					b10						I
Р		298.1761	149.5917	1953.96	47 97	77.4860		5500	173.12											I
E		427.2187	214.1130	1856.91	19 92	28.9596		5000												I
G		484.2402	242.6237	1727.86	93 86	64.4383		4500												
A		555.2773	278.1423	1670.84	78 83	35.9276		4000	199.10											
V		654.3457	327.6765	1599.81	07 80	00.4090		4000 -	1	446.22										
V		753.4141	377.2107	1500.74	23 75	50.8748	list,	3500 -	22/.10											
C[C	:91]	1092.5805	546.7939	1401.67	39 70	01.3406	Lite	3000 -	284,12											
Ν		1206.6234	603.8154	1062.50	75 53	31.7574		2500 -		583.30										
V		1305.6918	653.3496	948.46	46 47	74.7359		2000	254 12											
E		1434.7344	717.8709	849.39	6 2 42	25.2017		1500			720.24	849.37							833.82	
Н		1571.7933	786.4003	720.35	36 36	60.6804		1000	295.1	6	120.34		1062.49					111	033.02	
Н		1708.8523	854.9298	583.29	47 29	92.1510		1000 -	1 1 , 32	7.17 456.21		948.43				1500.70	1606.7	4 1727.80		
V		1807.9207	904.4640	446.23	58 22	23.6215		500		اللبيد اللب	771.30	00.00	11	32.51 1	281.57					
G		1864.9421	932.9747	347.16	74 17	74.0873					نېشلا يې د. د د	م مال دارية رال لية م	ني بايانانيو مم	<u>ші. і і і і</u>	. H .		4 4			
D		1979.9691	990.4882	290.14	59 14	45.5766		0 20	JU 4	00 600	800	u 10. m/z, Da	00	1200		1400	1600	18	00	
R		2136.0702	1068.5387	175.11	9 0 8	88.0631	-													

Ubiquitin extension protein (UBQ5) <u>C</u>GLTYVYQK

Protein Quant Protein ID Spectra Summary Statistics Spectrum List
Spectrum List Time Prec MW Prec m2 Pot N Best Sequence Modifications Conf 12:168.0r1.17 40.806 2104.0842 702.3867 3 4.94 CGINYQPETVYPGDLAX ICAT-C:13C(9)(C)@1, GIY-SPOQ2 09 51.8doc1:17 48.321 0.0000 524.7941 0 CGKLDDAMSLFYEVPR ICAT-C:13C(9)(C)@1, Oxidation(M/@8 < <1
Spectrum List Trice Prec m/z Prec m/z Prec m/z Prec m/z Prec m/z Prec m/z Red Sequence // Additional Conf 12.18dot1.1 40.666 2104.0842 702.3867 3 4.94 CGINYQPTVYRGGULAK ICAT-C13C(9)(C)(0)(1.0)/-Pro@2 99 15.18dot1.1 40.326 0.0000 524.7741 0 CextLDANSLFYEYR ICAT-C13C(9)(C)(0)(1.0)/-Pro@2 99 7.18dot1.18 33.382 1309.6002 65651 2 71 CeLTYYQK ICAT-C13C(9)(C)(0)(1 99 918dot1.28 66.616 0.0000 128.6651 0 CeStLDTRLIKLR ICAT-C13C(9)(C)(0)(1 99 918dot1.28 32.784 0.0000 128.6651 0 CeStLDTRLIKLR ICAT-C13C(9)(C)(0)(1 100 10 10 10 CeStLDTRLIKLR ICAT-C13C(9)(C)(0)(1 100.6677 665.8647 2 0.0786 4.1 10 CeLTYYQK ICAT-C13C(9)(C)(0)(1 100.66787 665.8647 2 0.0686 4.1 9 FESYHHSLYK
Spectrum Time Prec MW Prec MV Prec MV <th< td=""></th<>
12 124.040.t1.1 40.666 2104.0842 702.3871 3 4, 94 CGTNVDEPTVVEGGDLAK ICAT-C13C(9)(C)@1.GYv-Pro@2 99 5.18dot1.1.0 48.321 0.0000 524.7341 0 CGRLDDAMSLYEVPR ICAT-C13C(9)(C)@1.GYv-Pro@2 99 7.18dot1.6 33.352 1309.6502 656.2970 2 71 CGLTVVX0K ICAT-C(13C(9)(C)@1 99 9.18dot1.28 66.616 0.0000 718.5861 0 CGQLFTIGIDSVSSSYLGUVSSVLR ICAT-C(13C(9)(C)@1 <1
5 1360:1.17 48.321 0.0000 524.7941 0 CCKLDDASLEYEVER 10AT-C:13C(9)(C)(2):1.Oxidation(M)(2)8
7.18.0ct1.16 33.385 1300.6795 651.297 2 71 CCLTYVQK ICAT-C(1)C(9)(1) 99 7.18.0ct1.16 33.382 1309.8002 655.8074 2 71 CGLTYVQK ICAT-C(1)C(9)(1) 99 9.18.0ct1.18 65.616 0.0000 132.0382 0 CGLTYVQK ICAT-C(1)C(9)(1) <1
7.13640t.16 33.352 1309.6002 665.8074 2 71 GLTYVQK ICAT-C:13C(9)(C)@1 99 9.18dot.1.8 66.616 0.0000 718.5951 0 CGQALFTLGIDSVSSYLGUNGKUR ICAT-C:C)@1 <1
9:8:460±1.28 66:616 0.0000 718.6951 0 CCQALFTLGIDSVSSSYLGDVSGVLR ICAT-C(C)@1 <
5:84dot1.16 32.794 0.0000 432.0382 0 CGSLDITRLNKLR ICAT-C:13C(9)(C)@1 <
Image: Cont of the set of t
Peptide ID Hypotheses - 7.1dot;1.1604.2.7
Peptide ID Hypotheses - 7.1dot;1.1604.2.7
Conf v Sc Prot N Sequence Modifications Theor MW Theor m/z z AMass 99 13 71 CGLTYVYQK ICAT-C:13C(9)(C)@1 1309.6787 655.8467 2 -0.0786 <1
Image: Section of the sectio
<1
<1
<1
<1
Fragmentation Evidence for Peptide
ICIC9/JGLIYVYQK
Residue b b+2 v v+2
C[C9I] 340.1736 170.5905 1310.6860 655.8467 6000 y1 y2 y3 y4 y5 y6 y7 y8
G 397.1951 199.1012 971.5197 486.2635 y4+204+2 b2 y8+2 b3 b4 b5 b6
L 510.2792 255.6432 914.4982 457.7527 5000
T 611.3269 306.1671 801.4141 401.2107 ≥4000 254.12
Y 774.3902 387.6987 700.3665 350.6869
V 873.4586 437.2329 537.3031 269.1552 E 3000 - 20000 - 2000 - 2000 - 2000 - 200
Y 1036.5219 518.7646 438.2347 219.6210 2000 380.15 380.15
0 100 200 300 400 500 600 700 800 900 1000 1100 1200 1300

Early response to dehydration protein (ERD12) NPQQL<u>C</u>IGDLVPFTNK

															- 8
	Protein	Quant				Protein ID			Spectra					Summary Statistics	
Spectrum L	ist														
Spectrum	Time	Pre	CMW Prec	m/z Prec z	Prot N	Be	st Sequence	Δ			M	lodification	18		Conf
1.1˙1.19	/	1.206 142	1.7036 711.	.8591 2	00	NPNSTPVSIPPGSR				0					< 1
2.1˙1.16	4,	2.709 201	2.9910 672.	0405 0	89	NPQQLCIGDLVPFT	1K		ICAT-C(C)@	0					99
•		A RATE ALL	7101271 878		xu				LICAT CHREE	diri time					4
Peptide ID I	Hypotheses	- 2.1dot;1	.1661.2.2											Precursor MS Region	
Conf ⊽ Sc	Prot N 🛆			Sequence			 Mor 	difications 🗠	Theor MW	Theor m/z	z	∆Mass			
99 13	89 N	PQQLCIGD	LVPFTNK				ICAT-C(C)	@6	2013.0354	672.0190	3	-0.0444		672.3513 -	675.0233
<1 9	L	AKVADHVV	GAEAMTTKT	R			Oxidation	(M)@14	2013.0677	672.0298	3	-0.0767		1	-675.6834
<1 8	F	DVMSPFVT	GLDMC PK				ICAT-C(C)	@14	2012.9409	671.9876	3	0.0500		20 665.9707	
< 1 8	I	WAPISDKI	GSPTDMRVK						2013.0718	672.0312	3	-0.0807		10	. i. u a. i d.
< 1 7	С	AGASPPGR	VFRPKTSR				ICAT-C(C)	@1	2013.0691	672.0303	3	-0.0781			MAAN MAAMAN 💷
	II								II		I			665 670 675	5 680
														m/z, Da	
Fragmentat	ion Eviden	e for Pen	tido												
Truginentat			uuc												
NPC	QUCC[C0] GDL	VPFTNK													
Residue	b	b+2	у	y+2											
N	115.0502	58.028	7 2014.0426	1007.5249		110	y2 y3	y4 y5 y	6	y8 y9 y1	io				
Р	212.1030	106.5551	1899.9997	950.5035		245.10) b3	y8њ24 b5 −60	6.33 b14+2	y16+207 b8					
Q	340.1615	170.5844	1802.9469	901.9771		100 -									
Q	468.2201	234.6137	7 1674.8884	837.9478		90 -									
L	581.3042	291.1557	1546.8298	773.9185		80 -									
C[C01]	911.4404	456.2238	3 1433.7457	7 717.3765		70 -									
1	1024.5244	512.765	1103.6095	552.3084	sity	60									
G	1081.5459	541.2766	990.5255	495.7664	Inter	50									
D	1196.5728	598.790	933.5040	467.2556	-	5U -									
L	1309.6569	655.332	818.4771	409.7422		40	286.15	500 05 501 3	90	4 40					
V	1408.7253	704.8663	705.3930	353.2001		30 - 2	26.12 362.2	0 509.25 581.3	⁷⁴ 05	990.53					
Р	1505.7781	753.3927	606.3246	303.6659		20-	3	46.17 564.28	877.48	108	1 59	1177.60			
F	1652.8465	826.9269	509.2718	255.1396		146.07		650.3	8 730.35		1.00	00.111		1565.90	
Т	1753.8942	877.4507	362.2034	181.6053					lí in					1722.85	
N	1867.9371	934.4722	261.1557	131.0815		0 20	00 4	00 600	800	1000	120	00 0	1400	1600 1800	2000
К	1996.0321	998.5197	147.1128	3 74.0600						m/z, Da					
	ıl		1												

Stromal ascorbate peroxidase VDTSGPHE<u>C</u>PEEGRLPDAGPPSPANHLR

Protein Quant Protein ID Spectra Summary Statistics Spectrum List Spectrum Time Prec MW Prec m/z Prec z Prot N Best Sequence / Modifications O 10.18dot;1.1 30.934 3170.4314 793.6151 4 17 VDTSGPHECPEEGRLPDAGPPSPANHLR ICAT-C:13C(9)(C)@9 ICAT-C:13C(9)(C)@9 ICAT-C:13C(9)(C)@9 Peptide ID Hypotheses - 10.1dot;1.1524.4.10 III III III IIII IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	99 +
Spectrum List Time Prec MW Prec n/z Prec z Prot N Best Sequence // Modifications // 10.1˙11 30.934 3170.4314 793.6151 4 17 VDTSGPHEC PEEGRLPDA GPP SPANHLR ICAT-C:13C(9)(C)@9 1 <	■ onf 99 + >7.3443
Spectrum List Time Prec MW Prec m/z Prec z Prot N Best Sequence ✓ Modifications ✓ 10.1˙11 30.934 3170.4314 793.6161 4 17 VDTSGPHEC PEEGRLPDAGPP SPANHLR ICAT-C:13C(9)(C)@9 ICAT-C:	99 +
Spectrum Time Prec MW Prec m/z Prec z Prot N Best Sequence ✓ Modifications ✓ 10.1˙1.1 30.934 3170.4314 793.6151 4 17 VDTSGPHECPEEGRLPDAGPP SPANHLR ICAT-C:13C(9)(C)@9 ICAT-C:13C(9	onf ▲ 99 ★ ▶ 97.3443
Spectrum Free MV Prec MV	999 - - 97.3443
Image: Normal and the state of th	97.3443
Conf V Sc Prot N / Sequence / Modifications / Theor MW Theor m/z z AMass / 40 791.3445 793.6366 - 99 20 17 VDTSSCPHECPEEGRLEDAGEPE SPANHLR ICAT-C:13C(9)(C)@9 3170.5251 793.6385 4 -0.0937 -	97.3443
Conf ∑ Sc Prot N ∕ Sequence ✓ Modifications ✓ Theor MW Theor m/z z △Mass 40 791.3445 793.6866 - 99 20 17 VDTSGPHECPEEGRLEDAGEPSPANHLR ICAT-C:13C(9)(C)@9 3170.5251 793.6385 4 -0.0937 1 1 0 1 1 0 0	97.3443
Conf ⊽ Sc Prot N ∠ Sequence △ Modifications ✓ Theor MW Theor m/z z △Mass ↓	97.3443
Conf ⊽ Sc Prot N ∧ Sequence △ Modifications ✓ Theor MW Theor m/z z △Mass ↓	97.3443
Conf v Sc Prot N ≤ Sequence Modifications Theor MW Theor m/z z ΔMass 40 791.3445 793.8686 - 99 20 17 VDTSGPHECPEEGREPDAGPPSPANHLR ICAT-C:13C(9)(C)@9 3170.5251 793.6385 4 -0.0937 - <td>97.3443</td>	97.3443
991 201 171 VDTSGPHKCPKKGRLPDAGPPSPANHLR I ICAT-CT3CI91C009 I 3170.52511 793.53551 41 -0.09371	int Million (Mp)
	an antainte
Fragmontation Evidence for Pontide	
riaginentation Evidence for replice	
VDTSGPHEC[C9]]PEEGRLPDAGPPSPANHLR	
Residue b b+2 y y+2 ^	
V 100.0757 50.5415 3171.5323 1588.2698 1800 y1 y2 y3 y4 y5 y6 y7 y8 y910,11 y13 y15 y18 y19 y21	
D 215.1026 108.0550 30/2.4539 1536.7365 1700 y392-233 b7 b8 y2092 b14 b17 b19	
1 316.1503 158.5788 2957.4370 1479.2221 1600 -	
5 403.1823 202.0948 2856.3893 1428.6983 1500 -	
G 400.2030 230.0000 2709.3073 1385.1823 1400 -	
P 55/2506 2/9.1319 2/12.3356 1350.6715 1300 1/	
T 094,3155 347,5014 2015,2630 1306,1462 1200	
C(COII 4462 5344 561 7550 3340 4845 4475 0044 1100 -	
D 1250 5772 500 7003 2343.1010 1170.0944 ≥1000 5110 1170.0944	
F 1388 6108 604 8135 1012 002 0 66 0848 5 900 -	
E 1517.6524 759.3348 1783.9198 892.4635 E 800	
C 1574 6839 787 8456 1654 8772 827 9422 700 215.10 707 97	
B 1730 7850 865 8961 1597 8557 799 4315 600 - 235.11	
1 1843 8690 922 4382 1441 7546 721 3810 500 -	
P 1940 9218 970 9645 1328 6706 664 8389 400 187.10 254.13	
D 2055 9487 1028 4780 1231 6178 616 3125 300 169.10 169.10 988.53	
A 2126 9859 1063 9966 1116 5909 558 7991 200 200 200 200 200 200 200 200 200 20	
P 2281 0601 1141 0337 988 5323 494 7698	ц I
P 2378 1128 1189 5601 891 4795 446 2434 0 200 400 600 800 1000 1200 1400 1600 1800 2000 2200 2400 2600 2800	3000
m/z, Da	

Extensin-like protein IPASI<u>C</u>QLPK

					_ 8 >
Protein Quant	Protein ID		Spectra		Summary Statistics
Spectrum List	Prot N Bes	t Sequence		Modifications	Conf A
9.1˙:1.29 68.964 2722.1433 681.5431 4	TPALSBOVASECKGL	PLSLVTVGR	Deamidated(Q)@7.ICAT-C(C)@	12	<1
7.1˙1.16 34.035 1304.6754 653.3450 2	153 IPASICOLPK		ICAT-C:13C(9)(C)@6		24
3 18 dot 1 18 37 156 1061 //15 531 7280 2	THAVEFIND				
					· · ·
Peptide ID Hypotheses - 7.1dot;1.1608.4.7					Precursor MS Region
Conf ∇ Sc Prot N △ Sequence	Δ	Modifications 🛆	Theor MW Theor m/z z	∆Mass	
24 17 153 IPASICQLPK		ICAT-C:13C(9)(C)@6	1304.7573 653.3859	2 -0.0819	653.3513
24 17 LISAFVNRPIPK		Deamidated(N)@7	1304.7816 653.3981	2 -0.1062	50-
<1 13 EPSAPPTQRPPK		Deamidated(Q)@8	1304.6725 653.3435	2 0.0029	40 648.8374
<1 13 EVEKEPSAPPIK		Glu->pyro-Glu@N-term	1304.6976 653.3561	2 -0.0222	30
<1 12 IPKPQGKISLPK			1304.0100 053.4103	2 -0.1420	20 1 655.5966
					0 10 10 10 10 10 10 10 10 10 10 10 10 10 1
					m/z, Da
Fragmentation Evidence for Peptide					
IPASIC[C9I]QLPK					
Residue b b+2 y y+2 I 114.0913 57.5493 1305.7646 653.3859	8000 y1	y2 y3	y4	у5 у6	y7 y8 y9
P 211.1441 106.0757 1192.6805 596.8439	y,	244.16	05 y0+2 y10+2	00 07	00 09
A 282.1812 141.5942 1095.6278 548.3175	7000 -				
S 369.2132 185.1103 1024.5907 512.7990	6000 -				
1 402.2313 241.0523 937.5500 409.2030 C(C9I) 824.4637 411.2355 824.4746 412.7409	≥5000 -				
Q 949.5223 475.2648 485.3082 243.1577	12 4000 -				
L 1062.6063 531.8068 357.2496 179.1285	= 1000 ·				
P 1159.6591 580.3332 244.1656 122.5864	3000 -	256.12			
K 1287.7540 644.3807 147.1128 74.0600	2000 -	220.15	468.23		1192.66
	1000 - 141	10 357.23 45	1.19 581.31 1.19 482.28 694.86 733.2	824.44 3	⁷ 1061.55
	0 100	200 300 400	500 600 700 m/z, Da	800 900	1000 1100 1200 1300

Cell division protein FtsH GCLLVGPPGTGK

														- 5
	Protein Q	uant				Protein ID			Spectra			Summary Sta	tistics	
Spectrum L	ist													
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Bes	st Sequence	1	7		Modifications		Conf	Theor MW 🔺
8.1˙1.13	32.8	01 1324.6682	2 663.3414	2	125	GCLLVGPPGTGK			ICAT-C(C)	@2			76	1324.7173
8.1˙1.13	32.7	58 1333.6888	5 667.8515	2	125	GCLLVGPPGTGK			ICAT-C:13	C(9)(C)@2			93	1333.7476
12.1˙1.2.	74.1	81 0.000	0 685.1399	0		GCSGVKGDTVGPAGY	APVGLGTAF	GGSK	ICAT-C(C)	@2			< 1	2736.3540
12.1˙1.1.	36.0	14 3031.2231	1 1011.41	. 3	90	GCVEVNIGANPSAEE	GGEDEGVDD	SVEK	ICAT-C(C)	@2			99	3031.3201
12.1˙1.1.	35.9	28 3040.2380	0 1014.42	3	90	GCVEVNIGANPSAEE	GGEDEGVDD	SVEK	ICAT-C:13	C(9)(C)@2			99	3040.3503
7.1˙1.15.	32.8	09 0.000	0 432.6904	0		GCVNSPEEFIGAIR			ICAT-C:13	C(9)(C)@2			< 1	1726.8760
6.1˙1.17	55.9	87 0.000	0 699.2973	0		GDAAGRPAGLSRGGR							< 1	1396.7284 👻
•							111							-
Peptide ID H	Hypotheses -	8.1dot;1.1302	2.2.8									Precursor M	S Regior	1
Conf ⊽ Sc	Prot N 🛆			Sequence	•	<u> </u>	Mod	fications 🛛 🛆	Theor MW	Theor m/z	z 🛆 Mass 🔺	663.3	500	7.9660
93 14	125 GC1	LVGPPGTGK					ICAT-C:13C	(9)(C)@2	1333.7476	667.8810	2 -0.0591 ≘	50	00	7.0000
< 1 11	GAS	F FN SGG SQ FK					Deamidated	(N)@6	1333.5939	667.8042	2 0.0946	50	6	58.3588
< 1 11	LGI	QLIDNGPGPR					Deamidated	(Q)@4	1333.6990	667.8568	2 -0.0106	o Malahalal	haasin ,III Pila	Name and a second s
	1							I	1	1				
Fragmentati	ion Evidence (C91JLLVGPPGTG	for Peptide												
Residue	b	b+2	у	y+2										
G	58.0287	29.5180 13	34.7548	667.8810		1800 - y	1 y2	y3 y4 y	/5 y6	у7 у	8 y9 y10			
C[C9I]	397.1951	199.1012 12	77.7333	639.3703		1600	02+2	-254.12 D2	556	30	05			
L	510.2792	255.6432 9	38.5669	469.7871				-210.12						
L	623.3632	312.1853 8	25.4829	413.2451		1400				613.34				
V	722.4317	361.7195 7	12.3988	356.7030		1200 -		380.16	403.24					
G	779.4531	390.2302 6	13.3304	307.1688	4	1000			493.44					
Р	876.5059	438.7566 5	56.3089	278.6581				4	59.24					
Р	973.5586	487.2830 4	59.2562	230.1317	1	800 -	240.	3 335.14						
G	1030.5801	515.7937 3	62.2034	181.6053		600 -		535.14						
Т	1131.6278	566.3175 3	05.1819	153.0946		400			510.27	7	12.38 825.47			
G	1188.6492	594.8283 2	04.1343	102.5708		****]	175.09		467.28		93	8.55		
к	1316.7442	658.8757 1	47.1128	/4.0600		200 - 151.08	3		1	623.3	4 807.46 853.46	1053.58	1124.61	1221.72
						<u>م</u> 1	t dhilledd yr diae	lad bird, Doordood, da hall, da hi	la li dhuidh i a	ىتى ئاللاسى	بالبو مكابره وم	هر خارجت و معرول	Ĺ, L	L.,,
						0 100	200	300 400	500	600 7 m/z Do	00 800 900	1000 1100	1200	1300
										m/z, Da				
														37

Unnamed protein product LLI<u>C</u>GGSAYPR

									<u></u>
	Protein Qu	ant				Protein ID	Spectra		Summary Statistics
Spectrum Li	ist								
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW z
3.1.1.1960.2	34.43	0 849.5791	425.7968	2		LLGTRYK		< 1	849.5073 2
2.1.1.1674.4	35.65	9 1384.8097	693.4121	2		LLICGGSAYPR	ICAT-C:13C(9)(C)@4	62	1384.7584 2
5.1.1.1824.3	34.55	8 1295.8254	432.9491	3		LLIDNLIKAQR		2	1295.7925 3
				1 1		1			
Peptide ID H	lypotheses - 2	.1.1.1674.4						Precursor M	S Region
Conf ⊽ Sc	Prot N A	Sea	uence		4	Modifications 🛆 Theor MW	Theor m/z z AMass		
62 11	LLIC	GGSAYPR			ICAT-0	C:13C(9)(C)@4 1384.758	693.3865 2 0.0513	30 -	693.4087
< 1 8	ILI	TKKGTDIR				1384.840	693.4274 2 -0.0305	25 -	689.4020
< 1 8	LLQ	AIVDENNK			Deami	dated(Q)@3 1384.756	693.3854 2 0.0535	15 20 -	688.9115 694.4139 704.0970
< 1 8	LLS	SPPASIDQK			Deami	dated(Q)@12 1384.708	693.3616 2 0.1011	± 10 = 68	6.3860 701.5851
< 1 8	SYNS	PHQVSLPR			Deami	dated(N)@3 1384.673	693.3441 2 0.1361	5	
								0 111-11	690 695 700 705 m/z, Da
L									
Fragmentati	on Evidence f	or Peptide							
ILLIC	COIJGGSAYPR								
Residue	b	b+2	У	600					
L	114.0913	57.5493 13	85.7657		-	y1 y2	y3 y4 y5 y6 y7 7	07.38	y8 y9 y10
	227.1754	14.0913 12	/2.6816	500	7				
	340.2595	110.6334 11	09.5975 40.5425	500]				
C[Cal]	736 4473	040.2100 104	40.0135	450	1				
G	793 4688	397 2380	50 3257	400	1				
s	880 5008	40 7540 5	93.3042	<u></u> , 250	1				
A	951.5379	76.2726 5	06.2722	j j j 300	1				
Y	1114.6012	557.8043 4	35.2350	250					1046.56
P	1211.6540	306.3306 2	72.1717	200					1040.00
R	1367.7551	584.3812 1	75.1190	150					
				100 50		199.19 278.14 175.11 344.2	991.23 0 419.22 593.34 650.37 550.33 7	760.47 902.6	1028.54 1159.71 10_1143.74 1272.83
					0	100 200 300	400 500 600 700 m/z Da	800 900	1000 1100 1200 1300 1400

Figure S3

MS/MS spectra of ICAT identified MeJA responsive cysteines

Twenty one cysteines were mapped from MeJA treated guard cells. The precursor of the cysteine-containing peptide and the fragmented ions were shown as the evidence for mapping.

Ribulose bisphosphate carboxylase large chain precursor GHYLNATAGT<u>C</u>EEMMKR

														- 8 >			
	Protein Q	uant		1		Protein ID			Spectra			Summa	ry Statistics				
Spectrum L	ist																
Spectrum	Time	Prec MV	V Prec m/a	z Prec z	Prot N	Best Sequen	ce 🗠			Modifications	3		Conf Theor MW z	*			
4.1.1.1345.3	24.7	35 2179.09	81 727.373	33 3	2	GHYLNATAGTCEEMM	(R	ICAT-C:13C(9)(C)@11, Oxida	tion(M)@14, Oxida	ation(M)@15		99 2178.9907 3	5			
4.1.1.1344.3	24.8	88 2179.25	59 545.821	12 4	2	GHYLNATAGTCEEMM	(R	Thr->Lys@10,10	CAT-C(C)@11	, Methyl(E)@13			33 2179.0337 4	t			
5.1.1.1325.3	25.1	47 2170.05	05 724.357	74 3	2	GHYLNATAGTCEEMM	(R	ICAT-C:13C(9)(C)@11, Methy	l(E)@12, Lys->His(@16		99 2169.9805 3				
5.1.1.1324.2	24.9	57 2170.20	39 543.558	82 4	2	GHYLNATAGTCEEMM	(R	ICAT-C(C)@11,	Oxidation(M)	@14, Oxidation(M)	@15		97 2169.9604 4	4 -			
Peptide ID I	- Hypotheses	5.1.1.1325.3	3									Precurs	sor MS Region				
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modifi	ications 🛛 🛆	Theor MW	Theor m/z z	∆Mass ▲		4 797 909				
99 17	2 GH 3	LNATAGTCE	EMMKR				ICAT-C:13C(9)(C)@11, Met	2169.9805	724.3341	3 0.0699	100	724.6964 728.036	50 64			
73 15	GHY	LNATAGTCE	EMMKR				ICAT-C(C)@1	11, Oxidation(M	2169.9604	724.3275	3 0.0899		725.6849				
<1 11	LEI	LGIPKRYTH	FLTDPR						2170.1536	724.3918	3 -0.1031	50	728.70	<i>1</i> 0/			
< 1 11	MVV	KMMKWR PW P	PLVTR				Oxidation(M)	@5	2170.1731	724.3983	3 -0.1225	οщ	ւսվուսըումամիկինմիներիունեն	اللبيه			
<1 9	ATI	T.AGDSNGA P	LETVIOSH	R					2170.1130	724.3783	3 -0.0626 🔻		m/z, Da				
Fragmentat	ion Evidence	for Peptide	;														
GH	YLNATAGTC[C9]	E[1Me]EMMHR												_			
Residue	b	b+2	У	y+2													
G	58.0287	29.5180 2	2170.9878	1085.9975	2	200 - y1	y3	y5		y7	y8 y9 y10 y11 y1	12	y14 y15				
н	195.0877	98.0475 2	2113.9663	1057.4868		D2	003209+20	4 D5 y9+2/11	EZ DØ1892/18	5 1 /216+2							
Y	358.1510	179.5791 1	1976.9074	988.9573	4	.000]											
	471.2350	236.1212 1	1813.8441	907.4257	1	800 -											
N	585.2780	293.1426 1	1700.7600	850.8836	1	600 -											
A T	757 2628	270.4950	1500.7177	759 2420	· · ·	400											
	828 3000	414 7036	1414 6323	707 8109	Ť												
G	885 4243	443 2443	1343 5052	672 3042	tens	200 -											
т	986 4690	493 7381	1286 5737	643 7905	- E 1	000 -	358.18										
01001	1325 6354	663 3213	1185 5260	593 2667		800 -											
F[1Me]	1468 6936	734 8505	846 3597	423 6835		178.07											
E	1597,7362	799.3718	703.3014	352,1544		16	7.10										
M	1728,7767	864.8920	574,2588	287,6331		400 24	19.17	505.05					1812.00 1912.99				
M	1859.8172	930.4122	443.2183	222,1128		200 - 150.07		585.35 7	39.87 907.4	46 1104.54 ¹	150.70 1521.79 1619.70 1813.92 1512.55 2107.20						
H	1996.8761	998.9417	312.1779	156.5926		سال شير الم	dille dalle mi	el ili all'ha ma canti	a ha na h	بالعنال الاستامات							
R	2152.9772	1076.9922	175.1190	88.0631		0 200	400	600	800	1000 120	0 1400	1600	1800 2000				
										m/z, Da							

Ribulose bisphosphate carboxylase small chain LPLFG<u>C</u>TDSAQVLK

	Protein (Quant				Protein ID			Spectra					Summa	ary Stat	istics		
Speatrum I	lat																	
Spectrum L	.151																	
Spectrum	n Time	Prec N	/W Prec	m/z Prec	Prot N	Best Seq	uence	Δ		Мо	dificatio	ns				Conf	Theor M	w ^
4.1.1.1458.2	41	204 1734.0	0232 579	.0150	3 3	B LPLFGCTDSAQVLK		ICAT-C(C)@6, Ala->Ser	@10						55	1733.90	02:
4.1.1.1457.4	41	142 1743.0	0562 582	.0260	3 3	B LPLFGCTDSAQVLK		ICAT-C:13	3C(9)(C)@6, A	la->Ser@10						99	1742.93	32.
4.1.1.1526.2	51	199 1760.9	9393 881.	.4769	2 3	LPLFGCTDSAQVLK		Carbamyle	@N-term, ICAT	F-C(C)@6						96	1760.91	13 -
																		·
Peptide ID	Hypotheses	4.1.1.1526	5.2										_	Precur	sor MS	Regio	ı	_
Conf ⊽ Sc	Prot N 🗠			Sequer	се	Δ	Modificati	ons 🗠	Theor MW	Theor m/z	z	∆Mass						
96 14	3 LF	LFGCTDSAC	2VLK				Carbamyl@N-tern	n, ICAT-C(1760.9131	881.4638	2	0.0262		100 -		885.993	4	
< 1 7	18 GV	FQSLQPSDT	DLGAKV						1760.8945	881.4545	2	0.0448			881.4	792		
< 1 10	LE	LFGCTDSAC	2VLK				Leu->Phe@3, ICA	T-C:13C(9	1760.9219	881.4682	2	0.0175		50 -				
< 1 8	MI	AAGAKSLLG	GLSMAS PK				Oxidation(M)@14		1760.9529	881.4837	2	-0.0136			877.4	554	- 11.	
< 1 8	VS	EVSSLLGRA	AGTMGLGK						1760.9454	881.4800	2	-0.0062			at do Hilladori	ا الاسادار	nad Dialah	latel of
< 1 8	VS	SNSLCSLQG	SLTPK				Deamidated(N)@	4, ICAT-C(1760.8978	881.4562	2	0.0415		0-	875	880	885 890	0
																m/z. [)a	
													_ 11					
Eragmentat	ion Evidenc	for Pentir	do															4
Fragmentat	ion Evidenc	e for Peptic	de															
Fragmentat	ion Evidenc .FGC[C0]TDSA	e for Peptic	de															
Fragmentat	ion Evidenc .FGC[C0]TDSA	e for Peptic	de y	y+2														
Fragmentat CRM LPL Residue	ion Evidenc FGC[C0]TDSA4 b 157.0972	e for Peptic 2VLK b+2 79.0522	de <u>y</u> 1761.9204	y+2 4 881.463	8	550 1 y1	y2 3	y4 y5	y6 y7	y8		у9		y11		y13		
Fragmentat	ion Evidenc FGC[C0]TDSA b 157.0972 254.1499	e for Peptic XVLK b+2 79.0522 127.5786	de y 1761.9204 1605.8305	y+2 4 881.463 5 803.418	B 9	550 - y1 500 - b1	v2 v3 b8r02+2 b3 211.16	y4 y5	2 y6 y7 2 y1	3+2 y8		у9		y11		y13		
Fragmentat	ion Evidenc FGC[C0]/TDSA b 157.0972 254.1499 367.2340	e for Peptic 2VLK b+2 79.0522 127.5786 184.1206	y 1761.9204 1605.8305 1508.7777	y+2 881.463 803.418 7 754.892	B 9 5	550 - y1 500 - b1 450 -	y2 b8+ <u>y</u> 2+2 b3 211.16	y4 y5 y25+	2 y6 y7 y1:	3+2 y8		y9		y11		y13		
Fragmentat CRM LPL Residue L P L F	ion Evidenc FGC[C0IJTDSAI b 157.0972 254.1499 367.2340 514.3024	e for Peptic 2VLK 79.0522 127.5786 184.1206 257.6548	y 1761.9204 1605.8305 1508.7777 1395.6937	y+2 4 881.463 5 803.418 7 754.892 7 698.350	8 9 5 5	550 y1 500 b1 450 -	y2 y3 b8+y2+2 211.16 260.21	у4 у5 уд а -	2 y6 y7 y13	3+2 y8		уЭ		y11		y13		
Fragmentat CRM LPL Residue L P L F G	ion Evidenc FGC[C0IJTDSAI b 157.0972 254.1499 367.2340 514.3024 571.3239	e for Peptic 2VLK 79.0522 127.5786 184.1206 257.6548 286.1656	y 1761.9204 1605.8305 1508.7777 1395.6937 1248.6253	y+2 4 881.463 5 803.418 7 754.892 7 698.350 3 624.816	8 9 5 5 3	550 y1 500 b1 450 400 183.16	y2 b8+28+2 b3 211.16 260.21	y4 y5 y3	2 96 97 9 91	3+2 y8		у9		y11		y13		_
Fragmentat	ion Evidenc FGC[C0IJTDSA/ b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600	b+2 79.0522 127.5786 184.1206 257.6548 286.1656 451.2337	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6253 1191.6038	y+2 4 881.463 5 803.418 7 754.892 7 698.350 3 624.816 3 596.305	8 9 5 5 5 3 3	550 - y1 500 - b1 450 - 400 - 183.16 350 -	y2 b8+28+2 b3 211.16 260.21	y4 y5 y35+	2 96 97 9 91	3+2 y8		у9		y11		y13		
Fragmentat	ion Evidenc FGC[C0IJTDSA/ b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077	e for Peptic 2VLK 79.0522 127.5786 184.1206 257.6548 286.1656 451.2337 501.7575	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6263 1191.6038 861.4676	y+2 4 881.463 5 803.418 7 754.892 7 698.350 3 624.816 3 596.305 3 431.237	8 9 5 5 5 3 3 5	550 - y1 500 - b1 450 - 400 - 183.16 350 - 200 -	y2 b8+26+2 211.16 260.21 245.11	y4 y5 y3	2 96 97 9 91	3+2 y8		у9		y11		y13		
Fragmentat	ion Evidenc FGC[C0I]TDSA(b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347	b+2 2 127.5786 1 184.1206 2 257.6548 2 286,1656 4 501.7575 5 559.2710 1	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6263 1191.6036 861.4676 760.4195	y+2 4 881.463 5 803.418 7 754.892 7 698.350 3 624.816 3 596.305 3 431.237 3 380.713	8 9 5 5 5 5 8 9 8	550 - y1 500 - b1 450 - 400 - 183.16 350 - 183.16 350 - 183.16	y2 b8+26+2 211.16 260.21 245.11 289.11	y4 y5 y35+	2 96 97 9 91	3+2 y8		у9		y11		y13		
Fragmentat	ion Evidenc FGC[C0I]TDSA(b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347 1204.5667	b+2 2 127.5786 1 184.1206 2 257.6548 2 286,1656 4 501.7575 5 559.2710 6 602.7870 1	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6263 1191.6036 861.4676 760.4195 645.3930	y+2 4 881.463 5 803.418 7 754.892 7 698.360 3 624.816 3 596.305 4 31.237 3 380.713 3 323.200	8 9 5 5 5 4 6	550 y1 500 b1 450 400 183.16 350 400 183.16 350 400 183.16 200 147.12	y2 b8+26+2 b3 211.16 260.21 245.11 269.11	y4 y5 y35+	2 96 97 9 91	3+2 y8		у9		y11		y13		
Fragmentat	ion Evidenc FGC[C0I]TDSA/ b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347 1204.5667 1275.6038	b+2 2 79.0522 2 127.5786 2 184.1206 2 257.6548 2 286.1656 2 451.2337 5 501.7575 5 502.710 2 602.7870 3	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6263 1191.6036 861.4676 760.4195 645.3930 558.3610	y+2 4 881.463 5 803.418 7 754.892 7 698.350 3 624.816 3 596.305 3 431.237 9 380.713 9 323.200 9 279.684	8 9 5 5 5 3 6 4 6 1	550 y1 500 b1 460 183.16 350 <u>350 183</u> .16 <u>183</u> .16 <u>183</u> .16 <u>183</u> .16 250 1 200 147.12	y2 b8+26+2 b3 211.16 260.21 245.11 269.11	y4 y5 y35+	2 96 97 9 91	3+2 y8		y9		y11		y13		
Fragmentat	ion Evidenc FGC[C0I]TDSA b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347 1204.5667 1275.6038 1403.6624	b+2 2 127.5786 1 127.5786 2 127.5786 2 127.5786 2 127.5786 2 127.5786 2 127.5786 2 127.5786 2 127.5786 2 127.5786 2 559.2710 2 602.7870 2 638.3055 2 702.3348 2	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6265 1191.6038 861.4676 760.4195 645.3930 558.3610 487.3235	y+2 4 881.463 5 803.418 7 754.892 7 698.360 3 624.816 3 596.305 3 431.237 3 380.713 3 380.713 3 323.200 0 279.684 9 244.165	8 9 5 5 5 5 5 4 8 1 1 8	550 y1 500 b1 450 1 460 1 400 183.16 350 - 250 - 200 147.12 160 -	y2 y3 b3+25+2 b3 211.16 260.21 245.11 269.11 359.27 415	y4 y5 y25 5.25 472.23	2 96 97 9 91	3+2 y8 861.53		y9 1102.56		y11		y13		
Fragmentat	FGC[C0I]TDSA b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347 1204.5667 1275.6038 1403.6624 1502.7308	For Peptic DVLK 127.5786 127.5786 184.1206 257.6548 286.1656 451.2337 501.7576 559.2710 602.7870 638.3056 702.3348 751.8690	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6265 1191.6038 861.4676 760.4195 645.3930 558.3610 487.3235 359.2655	y+2 4 881.463 5 803.418 7 754.892 7 698.360 3 624.816 3 596.305 3 431.237 3 380.713 3 380.713 3 323.200 0 279.684 9 244.165 3 180.136	8 9 5 5 5 5 5 5 4 8 1 1 8 3 3	550 y1 500 b1 450 1 460 1 400 183.16 <u>56</u> 300 <u>56</u> 200 147.12 150 1 100 129.11	y2 b8+28+2 211.16 260.21 245.11 269.11 359.27 415 286.15	y4 y5 y3 5.25 472.23 487.3	2 <mark>96 97</mark> 913	3+2 y8 861.53 94	43.45	y9 1102.56	1247.5	y11		y13	92	
Fragmentat	ion Evidenc FGC[C0I]TDSA b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347 1204.5667 1275.6038 1403.6624 1502.7308 1615.8149	b+2 2 79.0522 2 127.5786 2 184.1206 2 257.6548 2 451.2337 2 501.7576 2 602.7870 2 638.3055 2 702.3348 2 808.4111 2	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6265 1191.6038 861.4676 760.4195 645.3930 558.3610 487.3235 359.2653 359.2653 260.1965	y+2 4 881.463 5 803.418 7 754.892 7 698.360 3 624.816 3 596.305 3 431.237 3 380.713 3 380.713 3 323.200 0 279.684 9 244.165 3 180.136 9 130.602	8 9 5 5 5 5 5 5 3 8 4 1 1 1	550 y1 500 b1 450 183.16 350 183.16 250 183.16 250 183.16 100 183.16 100 129.11 50 115.11	y2 b3+25+2 211.16 260.21 245.11 269.11 359.27 415 286.15	y4 y5 y3 5.25 472.23	2 <mark>96 97</mark> 91: 4 645.42	3+2 y8 861.53 94	43.45	y9 1102.56	1247.5	y11	1445.69	y13	92	
Fragmentat	FGC[C0I]TDSA b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347 1204.5667 1275.6038 1403.6624 1502.7308 1615.8149 1743.9098	For Peptic DVLK D+2 79.0522 127.5786 184.1206 257.6548 286.1656 451.2337 501.7575 559.2710 602.7870 638.3055 702.3348 751.8690 808.4111 872.4585	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6265 1191.6038 861.4676 760.4195 645.3930 558.3610 487.3235 359.2653 359.2653 260.1965 147.1128	y+2 4 881.463 5 803.418 7 754.892 7 698.360 3 624.816 3 596.305 3 431.237 3 380.713 3 380.713 3 380.713 3 380.713 3 380.713 3 380.713 3 380.713 3 130.602 3 130.602 3 74.060	8 9 5 5 5 5 5 5 8 4 8 1 1 5 3 3 1 1 0	550 y1 500 b1 450 183.16 350 250 183.16 200 147.12 150 115.11 0 0 100	y2 b3+25+2 211.16 260.21 245.11 259.11 259.27 415 286.15 200 300 400	y4 y5 y3 5.25 472.23 487.3 1487.3	2 <mark>96 97</mark> 913 4 645.42	3+2 y8 861.53 94 800 900	43.45	1102.56	1247.5	y11	1445.69 	y13 1605	.92 1760.93	, t
Fragmentat CRM LPL Residue L P L F G C[C01] T D S A Q V L K K	ion Evidenc FGC[C0I]TDSA/ b 157.0972 254.1499 367.2340 514.3024 571.3239 901.4600 1002.5077 1117.5347 1204.5667 1275.6038 1403.6624 1502.7308 1615.8149 1743.9098	For Peptic DVLK 127.5786 127.5786 184.1206 257.6548 286.1656 451.2337 501.7575 559.2710 602.7870 638.3055 702.3348 751.8690 808.4111 872.4585	y 1761.9204 1605.8306 1508.7777 1395.6937 1248.6265 1191.6038 861.4676 760.4195 645.3930 558.3610 487.3235 359.2653 260.1965 147.1128	y+2 881.463 803.418 7 754.892 7 698.360 3 624.816 3 380.713 380.713 380.713 323.200 279.684 244.165 3180.136 3130.602 374.060	8 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	550 500 450 400 183.16 350 200 147.12 160 100 115.11 0 100 100	y2 b8+25+2 211.16 260.21 245.11 259.11 259.27 416 286.15 200 300 400	y4 y5 y25 5.25 472.23 487.3 487.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.3 1497.4 140	2 <mark>96 97</mark> 913 4 645.42 600 700	3+2 y8 861.53 94 800 900 m/z, Da	43.45 4.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	y9 1102.56	1247.5	y11 59 1300 14	1445.69 ,	y13 1605 0 160	.92 1760.93	

Malate dehydrogenase, mitochondrial precursor GLNGVPDVVE<u>C</u>SYVQSTITELPFFASK

								_										-	8,
	Protein	Quant		T		Protein	ID				Spectra					Summary	/ Statistic	s	
Spectrum L	ist																	6	
Spectrum	Time	Prec	MW Prec n	n/z Prec z	Prot N		Best Se	equence	7	4			Modif	fications				Conf The	*
5.1.1.1546.2	5	4.223 3135	.6763 1046.2	23 3	12	GLNGVPI	DVVECSYVQS	TITELPFE	ASK	ICAT	-C:13C(9)(C)	@11						98 31;	-
•								111										+	
Peptide ID H	lypotheses	- 5.1.1.154	6.2													Precurso	or MS Reg	gion	_
Conf ⊽ Sc	Prot N 🛆			Sequence)		Δ	Mod	lifications	Δ.	Theor MW	Theor m/z	z	∆Mass	<u> </u>			1046 5601	
98 14	12 G	LNGVPDVVE	CSYVQSTIT	ELPFFASK				ICAT-C:130	C(9)(C)@11		3135.5886	1046.2035	3	0.0876		200 1		1047 5610	
33 14	17 G	LNGVPNVVE	CSFVQSTIT	ELPFFASK				Deamidate	d(N)@7, ICAT	-C:	3135.5886	1046.2035	3	0.0876		100 -	l I.	1047.5010	
5 14	G	LNGVPDVVE	CSYVQSTIT	ELPFFASK				ICAT-C(C)	@11, GIn->His	s@15	3135.5586	1046.1935	3	0.1175	-	مسل ہ	يبغ الالسعم محب	il III de la companya da pel de la	••
-	· · ·												· · · · · · · · · · · · · · · · · · ·						
Fragmentati	ion Evidend	ce for Pept	ide																
GLI	NGVPDVVEC[(:91JSYVQSTIT	ELPFFASK																_
Residue	b	b+2	у	y+2															
G	58.0287	29.5180	3136.5958	1568.8015		1700 -	y1	y2 y3	y4	y5	y6 y	7 y8	y9	y10 y1	1 y12	y13			
	1/1.1128	86.0600	30/9.5/44	1540.2908		1600 -	b3+2b2 254	b3 b4	b5 v9+2 396.24	6y1b 1 2	+2 b8	b9 b1	0						
N	265.1557	143.0815	2966.4903	1483.7488		1500 -		27	16 /		696.40								
G V	342.1112	171.0922	2052.4474	1209 2466		1400 -		245.13											
P	538 2084	221.1204	2606 3575	1348 6824	=	1300 -													
D	653 3253	327 1663	2599 3047	1300 1560		1200 -													
V	752,3937	376,7005	2484.2778	1242.6425		1100		234.15	112.27										
V	851.4621	426.2347	2385.2094	1193.1083		1000			413.21	125									
E	980.5047	490.7560	2286.1410	1143.5741		토 900 로		312.1	9	2.25									
C[C9I]	1319.6711	660.3392	2157.0984	1079.0528		Ĕ 800	213.0												
S	1406.7031	703.8552	1817.9320	909.4696		700	2.50		AA4	27			1039.57	'					
Y	1569.7665	785.3869	1730.9000	865.9536		600	197.17		441.	10.20	80	9.49							
V	1668.8349	834.9211	1567.8366	784.4220		500	172.08			10.23									
Q	1796.8935	898.9504	1468.7682	734.8877		400													
S	1883.9255	942.4664	1340.7096	670.8585		300	143.13			550	.30	0201	51						
Т	1984.9732	992.9902	1253.6776	627.3424		200	` `				678.39 80	0.42 020 5		1152.71					
1	2098.0572	1049.5323	1152.6299	576.8186		100	129.11				735.43	920.91	'	1228	3.70	1341.72		1750.00	
Т	2199.1049	1100.0561	1039.5459	520.2766		····					"hilling h					1450.93		1759.00	
E	2328.1475	1164.5774	938.4982	469.7527		0	0	200	400	600) 8	00	1000	1200		1400	1600	1800	
L	2441.2316	1221.1194	809.4556	405.2314								m/z, Da	a						
Р	2538.2843	1269.6458	696.3715	348.6894	-														

Malate dehydrogenase, mitochondrial precursor AGKGSATLSMAYAGALFADA<u>C</u>LK

																- 6
	Protein	Quant			Protein II)			S	pectra				Summan	y Statistics	
Spectrum L	.ist															
Spectrum	1 Time	Prec	MW Prec n	n/z Prec z	Prot N Be	st Sequen	ce	Trimethodd	10.00.0	1-1	Modifica	ations			Conf The	eor MW z
5.1.1.1343.4	35	2510	.4/49 83/.8	322 3	3 AGKGSATL	SMAYAGAI	-FADACLK	I rimetnyi(i	(K)@3, UXI	dation(M))@10,1CA1-0	0:130(9)(0)@21			99 25	10.2959 3
Peptide ID	Hypotheses	- 5.1.1.134	3.4											Precurso	or MS Regio	n
Carl V Ca	Dref N (0	-	Δ.			/ T L		There is to					
Conf V Sc	Prot N A	WCCATTCA	(1) V 1 (1) T (1) T	Sequence	e	~	Modif Trimethyl/K	Oxidation	- In	eor MW	1 neor m/z	Z ΔMass	Â.	50 835.	4891 -	338.1476
< 1 7		SDTGATLOP	WDCATI SAM	VETHD			Deamidated	(NI)@19	2	510.2303	837 7630	3 0.2049		031	1 8	342.1154
	A.	DI SARIMO	SKPGATLSAN	AF INK			Deannualeu	14)@13	23	10.2700	007.7039	0.2040		0 100 40		ay dia dia pangana sa p
Fragmentat	ion Evidenc	e for Pept	ide													
	KI3MelGSATLS	MIOxilAYAG	ALFADACIC9	ĸ												
				EIX												
Residue	b	b+2	У	y+2												
A	72.0444	36.5258	2511.3033	1256.1553	1700 -	y1 y	2	y3 y4	y5 y6	y7 y	y8 y9y10y11	y12				
G	129.0659	65.0366	2440.2662	1220.6367	1600	10					1033 63.					
K[3Me]	299.2078	150.1075	2383.2447	1192.1260	1000	02	00092-0200426	212 19209 1924 206	6 0/905+1 41	510 511	1000.001.001	4015				
G	356.2292	178.6183	2213.1028	1107.0550	1500 -											
S	443.2613	222.1343	2156.0813	1078.5443	1400 -											
A	514.2984	257.6528	2069.0493	1035.0283	1300											
T	615.3461	308.1767	1998.0122	999.5097	1200 -											
	728.4301	364./18/	1896.9645	948.9859	1100 -		5	11.32		962.58						
S MOvil	015,4021	406.2347	1/03.0004	892,4439	1000 -											
MUCXIJ	1033 5247	401.7524 547 2740	1090.0404	775 4404	200 s					944.54						
X X	1196 5980	598 8026	1478 7750	730.8016		235	5.11									
Α	1267.6351	634 3212	1315,7126	658 3599	700		481.79									
G	1324.6566	662.8319	1244.6755	622 8414	100				797 53	1	015.59					
A	1395.6937	698.3505	1187.6540	594,3306	600		254 15		151.55							
	1508,7777	754,8925	1116.6169	558,8121	500 -		399 27	72	28.49							
F	1655.8462	828.4267	1003.5328	502.2700	400											
A	1726.8833	863.9453	856.4644	428.7358	300 -	136.09					116/1/6	24.94				
D	1841.9102	921.4587	785.4273	393.2173	200 -	10000					13	1306.81 166	6.05	1996.19	9	0515 71
A	1912.9473	956.9773	670.4004	335.7038	100 120	.10	nia, julia/					1490.06		971.09	0000	2515./1
C[C9I]	2252.1137	1126.5605	599.3632	300.1853		<u> </u>		لإلك الجلالية	in a the second s				ĻĻĻļ	011.80	2282.	.81
L	2365.1978	1183.1025	260.1969	130.6021	Ŭ Ö	200	400	600	800	1000	1200	1400 1600	1800	0 2000	2200	2400
К	2493.2927	1247.1500	147.1128	74.0600							m/z, Da	1				

Malate dehydrogenase, mitochondrial precursor Y<u>C</u>PHALVNMISNPVNSTVPIAAEIFKK

													- 8 >
	Protein Q	uant		Ĭ		Protein ID			Spectra		Ĺ	Summary St	atistics
Spectrum L	ist												
Encotrum	Time	Dree MM	Drag m/s	Dree T	Drot N	Post Com				Mad	ifications		Conf. Theor MM A
5 1 1 1361 2	41.9	05 3198 902	PIEC III/2		PIOLN	VCDWAT WARTSNOWN	TUDIAR TEVE	LICAT-C(C)(an Ovidation	(MV@9	incations		00 3108 6570
0.1.1.1001.2	41.5	00 0100.002	.1 000.732	• •	5	TOPHADVNMIDNEVN	IVFIAALIFAA	10/1-0(0)@	gz, oxidation	(11)(200			33 3130.0370
Peptide ID H	lypotheses - !	5.1.1.1361.2										Precursor M	IS Region
Conf V So				Coguenee		4	Madifiaatia	-	Theor MM	Theor m/r			
	PIOL N C			AFTERV		-	ICAT-C(C)@2.0v	ris -	3198.6570	800.6715	4 0.2451	100 801	.2258 - 803.2105
10 17	VCD	OALVINTSNI	DVNSTVDT7	AFTERN			ICAT-C:13C(9)(C)	@2 Oxida	3198 6868	800.6790	4 0.2451		804.7240
	2 200	CONTRACTOR CONTRACTOR		TRACTOR OF			Esemul@httaam.h	LOAT(O)	2409.0570	000.0745	4 0.2454		
Fragmentati	on Evidence	for Peptide											
. raginentati	on Endende	ion i optide											
YC	COIPHALVNM[O>	ki]ISNPVNSTVP	NAAEIFKK										
Desidue		h.2											
Kesidue	164.0706	82 5380 - 3	y 100.6642	y+z 1600 3358	÷.	1 .1 -1	111011 11			.			
CICOII	494 2068	247 6070 3	036 6009	1518 8041		7000 - ^{y1} ^{y2}	у3 у4 у5 у	бу7 у8 у	y9 y10 y11	y18	y16		
P	591 2595	296.1334 2	706 4647	1353 7360		6500 - y4+2	b5 5/26242-29/12342	1)/125-1 2066 b	078+208 b9	b10 b11 b1:	2 b13 b14 b15		
	728.3185	364 6629 2	609 4120	1305 2096					1016.70				
A	799.3556	400.1814 2	472 3531	1236 6802		6000 -							
L	912.4396	456.7235 2	401.3159	1201.1616	=	5500 -							
V	1011.5080	506.2577 2	288.2319	1144.6196		5000 -							
N	1125.5510	563.2791 2	189.1635	1095.0854		4500 -							
M[Oxi]	1272.5864	636.7968 2	075.1205	1038.0639									
1	1385.6704	693.3389 1	928.0851	964.5462		<u>}</u> 4000 1	482.30						
S	1472.7025	736.8549 1	815.0011	908.0042		· 월 3500 -							
N	1586.7454	793.8763 1	727.9690	864.4882		3000			127	2.73			
Р	1683.7982	842.4027 1	613.9261	807.4667			4.22		1125.69				
V	1782.8666	891.9369 1	516.8734	758.9403		2500 - 3	1.23						
N	1896.9095	948.9584 1	417.8049	709.4061		2000 183.17 282	.21 563.1	15 912.5/	0				
S	1983.9415	992.4744 1	303.7620	652.3846		1500 -	501	43 806.5	3	15	86.88		
Т	2084.9892 1	1042.9982 1	216.7300	608.8686		1000	400 22				1569.86		
V	2184.0576 1	1092.5324 1	115.6823	558.3448				895.49			1782.06 2050	20	2005.64
Р	2281.1104 1	1141.0588 1	016.6139	508.8106		500 147.13	AL LUNDON DALLAR				1896.08	20	308.73 2300.04
1	2394.1944 1	1197.6009	919.5611	460.2842				<u> Andria Statica</u>					┵╌╍╨┵╌╌┥╴╴╽╏
A	2465.2316 1	1233.1194	806.4771	403.7422		0 200	400 600	800 1	000 1200	1400 m/z Da	1600 1800 2000	2200 2400	2600 2800
A	2536.2687 1	1268.6380	735.4400	368.2236	-					1102, Da			
-	0005.0440	000 4500	004 4000	000 7054									

ADP-glucose pyrophosphorylase small subunit S<u>C</u>ISEGAIIEDTLLMGADYYETDADR

												_ 8
	Protein	Quant				Protein ID			Spectra			Summary Statistics
Spectrum L	ist											
Spectrum	Time	Prec	MW Prec	m/z Prec z	Prot N	Best Sequ	ence 🗠			Modifie	cations	Conf Theor MW 🔺
6.1.1.1602.2	53	3.345 3102.	.6829 1035.	23 3	19	SCISEGAIIEDTLLM	GADYYETDADR	ICAT-C:130	C(9)(C)@2, Oxi	idation(D)@11		99 3102.4097 🚽
•	1	1				1						•
Peptide ID H	lypotheses	- 6.1.1.160	2.2									Precursor MS Region
Conf ⊽ Sc	Prot N 🛆			Sequence	,	Δ	Modificatio	ons 🛆	Theor MW	Theor m/z	z 🛆 Mass 🔺	
99 15	19 S	CISEGALLE	DTLLMGADY	YYETDADR			ICAT-C:13C(9)(C)	@2, Oxida	3102.4097	1035.1438	3 0.2731	50 - 1036.5636 - 1036.2362
12 14	S	CISEGALLE	DTLLMGAD	YYETDADR			ICAT-C:13C(9)(C)	@2, Oxida	3102.4097	1035.1438	3 0.2731	a terretari ante a seconda de la companya de
A							0	0(0)@1	2402 4402	4005 4400	2 2226 0	
Fragmentati	on Evidenc	e for Pepti Dxi]TLLMGAD	ide)YYETDADR									
Residue	b	b+2	v	v+2	*							
S	88.0393	44.5233	3103.4169	1552.2121		1 v1	v2 v3 1v4	↓ 5		ા આ ગ	9 v10 v11	1
C[C91]	427.2057	214.1065	3016.3849	1508.6961		140 - v3b2+2	b6+2b2b8+2	99-3210+124	bt45227	v17+b2 b9	b12	
1	540.2897	270.6485	2677.2185	1339.1129		130 -	254.15			- -		
S	627.3218	314.1645	2564.1345	1282.5709		120 -	441.22					
E	756.3644	378.6858	2477.1024	1239.0549								
G	813.3858	407.1966	2348.0598	1174.5336	=	110	391.19					
A	884.4229	442.7151	2291.0384	1146.0228		100 - 271.	18 361	.21				
1	997.5070	499.2571	2220.0013	1110.5043		90 - 243 45						
1	1110.5911	555.7992	2106.9172	1053.9622		× 80 -		577.34	883	.46		
E	1239.6337	620.3205	1993.8331	997.4202	1	175.1	†	1 20		869.45		
D[Oxi]	1370.6555	685.8314	1864.7905	932.8989		₽ ⁷⁰	50	7.25				
Т	1471.7032	736.3552	1733.7687	867.3880		60 -						
L	1584.7873	792.8973	1632.7210	816.8641		50			813.44	997.62		
L	1697.8713	849.4393	1519.6369	760.3221		40				10	51.70	1000.48
М	1828.9118	914.9595	1406.5529	703.7801		401			738.50	1	147.63 1454	1990.18
G	1885.9333	943.4703	1275.5124	638.2598		30 -		61	5.42		1177,45 1437.81	4470.00
A	1956.9704	978.9888	1218.4909	609.7491		20 162.11			719.41			14/3.68
D	2071.9973	1036.5023	1147.4538	574.2306		136.10					1359.78	1905.68
Y	2235.0607	1118.0340	1032.4269	516.7171		101						
Y	2398.1240	1199.5656	869.3636	435.1854								
E	2527.1666	1264.0869	706.3002	353.6538		0 20	J 400	600	800	m/z, Da	1200 1400	1600 1600 2000
Т	2628.2143	1314.6108	577.2576	289.1325	+							
	0740.0440	4070 4040	470.0400	000 0000								
Putative aldehyde dehydrogenase LGPALA<u>C</u>GNTVVLK

	Protein	Quant		1		Protein ID			Spectra				Summary Statistics
Spectrum Lis	st												
Spectrum	Time	Prec MW	Prec m/2	z Prec z	Prot N	Best Sequ	ence 🛆			Modi	fications		Conf Theor MW
4.1.1.1447.2	35	5.702 1582.104	41 528.375	53 3	31	LGPALACGNTVVLK		ICAT-C(C)	<u>@</u> 7				99 1581.8912
4.1.1.1446.3	35	5.597 1591.110	07 531.377	75 3	31	LGPALACGNTVVLK		ICAT-C:13C	C(9)(C)@7				74 1590.9214
4.1.1.1698.3	61	.379 972.461	17 487.238	81 2		LGQGLSGGER							< 1 972.4988
2 1 1 1855 2	50	445 1237 741	17 619 878	81 2	25	LORGSGEFTGTY							< 1 1237 5939
Peptide ID H	ypotheses	- 4.1.1.1447.2	2										Precursor MS Region
	,,											- II	
Conf ⊽ Sc	Prot N A			Sequence	•	Δ	Modificatio	ons 🗠	Theor MW	Theor m/z	z △Mass		531.3817
99 15	31 LG	FPALACGNTVV	LK				Oxidation(D)@7	Ovidation/	1581.8912	528.3044	3 0.2128		150 -
<1 9	50 AV	TEPORTGANG	STVK				Oxidation(D)@r,	JXIU8UUTI(1581 9454	528.3224	3 0.2427		100 528.3755
<1 9	NIN	ULTGT I PVEVG	OFK						1581.8727	528.2982	3 0.2315		E20 0207
<1 8	EF	KWETS DNP IVH	K						1581.7787	528.2668	3 0.3254		50 519.3219 536.3481
	I								11				📋 👌 հանաստություններին հատուների 📔
													520 530 540 m/z Da
												- 11	
Fragmentatio	on Evidenc	e for Peptide											
LGPA	LACICONGNT	VVLK											
Residue	b	b+2	y	y+2		v1	v2 v3	v4 1	v5 v6	v7	v8	v9	v12
	474 4429	57.5493 1	502.0905	791.9529		64 4 2	b6+123 y6+12 bi	/+265	ý í ý 13	6+2 b7	b8 b9	1	
P	268,1656	134 5864 4	412,7930	706 9001		2500 1	260.22						
A	339.2027	170.1050 1	315,7402	658.3738									
L	452.2867	226.6470 1	244.7031	622.8552		2000 -							
A	523.3239	262.1656 1	131.6191	566.3132	ĬŤ.	4500	200.42						
C[C01]	853.4600	427.2337 1	060.5819	530.7946	tens	1500 -	45.12						1296.85
G	910.4815	455.7444	730.4458	365.7265	-	4000							
N	1024.5244	512.7659	673.4243	337.2158		1000 - 14/.	286.16				938.53		
Т	1125.5721	563.2897	559.3814	280.1943		129.12				730.51			1310.87
V	1224.6405	612.8239	458.3337	229.6705		500 -	339.24	458.37 517.35	529.35	744.55	995.58 109	5.65 1.	199.84 1277.04 1449.81
V	1323.7089	662.3581	359.2653	180.1363		115.10	423.2	2 Millin	656.47	المراجب المراج	والمالية والمالية المرابي		13/7.91 1449.01
L	1436.7930	718.9001	260.1969	130.6021		0 100	200 300	400 500	600 7	00 800	900 1000 1	100	1200 1300 1400 1500 1600
К	1564.8880	782.9476	147.1128	74.0600		0.00				m/z, Da			

3-isopropylmalate dehydratase-like protein (small subunit) EHAPV<u>C</u>LGAAGAK

_	_										_		
	Protein	Quant			Prote	in ID		Spectra			Summ	ary Statistics	
Spectrum L	_ist												
Spectrum	n Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Δ		Modif	ications		Conf	Theor MW 🔺
5.1.1.1241.4	- 24	4.438 1458.967	9 487.3299	3	22 EHAPV	CLGAAGAK	ICAT-C:130	C(9)(C)@6				96	1458.7700
6.1.1.1771.2	6	7.797 1474.836	492.6193	3	22 EHAPV	CLGAAGAK	Oxidation(P)@4, ICAT-C	:13C(9)(C)@6			< 1	1474.7649
2.1.1.1865.2	5	1.921 1221.733	3 611.8739	2	EHDVL	PGFGAAK	Glu->pyro-	Glu@N-term				< 1	1221.6143
7 1 1 1721 2	3	8 259 1094 974	1 548 4943	2	FHFT.R							< 1	1094 5945
•													F
Peptide ID	Hypotheses	- 5.1.1.1241.4									Precu	rsor MS Regi	on
Conf V Sc	Prot N 🛆		:	Sequence		Modifica	tions 🗠	Theor MW	Theor m/z	z 🛆 Mass		N	
96 13	22 E	HAPVCLGAAGA	ĸ			ICAT-C:13C(9)(C)@6	1458.7700	487.2639	3 0.1978	80 -	485.3419 - 4	487.3327
< 1 8	16 P	AGN IQKDS PAA	KF			Oxidation(K)@7		1458.7467	487.2562	3 0.2212	60 -		
< 1 8	H	GKVYGSVAEKE	R					1458.7579	487.2599	3 0.2099	40 -		184.6570
< 1 8	I	QAIIQGMAASS:	LR			Deamidated(Q)	Q6	1458.7865	487.2694	3 0.1814	20		498.2935
< 1 7	A A	LQQRRTFVNAR						1458.8168	487.2795	3 0.1511	20	1 A	al i de la contra la fille i di la contra di l
< 1 7	L	ADTPCVVVTSK				ICAT-C(C)@6		1458.7753	487.2657	3 0.1926	0.4	480 485	490 495
												m/z,	Da
Fragmontat	tion Eviden	o for Dontido											
riaginentai		le ioi replide											
EH.	APVC[C9I]LGA	AGAK											
Residue	b	b+2	у	y+2			11 -1		_1			l	
E	130.0499	65.5286 1	459.7773	730.3923	4000 -	y1 y2 y3 b1 y54+22 b27+2	y4 y5 b3 474.30	y6 y7)- b5	7	b6 y8		y10	
Н	267.1088	134.0580 1	330.7347	665.8710	3500 -								
A	338.1459	169.5766 1	193.6758	597.3415									
P	435.1987	218.1030 1	122.6387	561.8230	3000 -	267.14							
V	534.2671	267.6372 1	025.5859	513.2966	_ 2500 -								
C[C9I]	873.4334	437.2204	926.5175	463.7624	ti ano	249.12							
L	986.5175	493.7624	587.3511	294.1792	±2000 1								1321.82
G	1043.5390	522.2731	474.2671	237.6372	1500 -	221.13	75.20	58	1.44				
A	1114.5761	557.7917	417.2456	209.1264	1000			488.30					
A	1185.6132	593.3102	346.2085	1/3.6079	1000 -	151.10 257.15		534.33		856.48	1002.67	1073.72	
G	1242.6347	621.8210	275.1714	138.0893	500 -	130.11			735.44	783.45 922	63 1019.68	1210.	79
A	1313.6718	657.3395	218.1499	109.5786			التقاولين والقار	يري الشاشماني .		المربط البالي المربية	i din hut		
к	1441.7667	/21.3870	147.1128	74.0600	<u> </u>	0 100 200 30	0 400	500	600 700	800 900	1000	1100 1200	1300
									m/z, Da				
1													

Aspartate aminotransferase Asp2 VGALSIV<u>C</u>K

														_ 8
	Protein Qua	nt				Protein ID			Spectra					Summary Statistics
Spectrum L	ist													
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Segu	ence 🗸			Modi	fications			Conf Theor MW
7.1.1.2046.2	63.491	0.0000	595.2124	4 0		VFNDTARYVDQGGGK	R	Deamidated	(Q)@11					< 1 1782.8649
4.1.1.1450.3	36.188	1117.7579	559.8862	2 2		VGALKFSPNGK		Deamidated	(N)@9					61 1117.6132
4.1.1.1427.2	32.747	1115.7665	558.8908	5 2	53	VGALSIVCK		ICAT-C(C)@	08					97 1115.6372 📼
7 <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>7</u> <u>1</u> <u>1</u> <u>1</u> <u>7</u> <u>1</u> <u>1</u> <u>1</u> <u>7</u> <u>1</u> <u>1</u> <u>1</u> <u>7</u> <u>2</u> <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>7</u> <u>2</u> <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>1</u> <u>7</u> <u>2</u> <u>1</u>	38 197	1088 7499	545 3822	2 2		VGAVEA SGLLR	111	1						< 1 1088 6343
Peptide ID H	-typotheses - 4.1	1.1.1427.2												Precursor MS Region
Conf V Sc	Prot N 🛆			Sequence		Δ	Modificati	ons 🛆	Theor MW	Theor m/z	z	∆Mass	1 📗	
97 13	53 VGALS	SIVCK					ICAT-C(C)@8		1115.6372	558.8259	2	0.1292		559.3735
< 1 10	GVRDI	VNTNK					Deamidated(N)@	9	1115.5935	558.8040	2	0.1730		200 - 549.3582 563,9100
< 1 10	INLLS	SKGMIK							1115.6737	558.8441	2	0.0928		559 8947
< 1 9	RRDSI	OGVVGR							1115.5796	558.7971	2	0.1869		100 550.3647 562.0146
<1 9	RVGDI	GRSIK					Oxidation(R)@7		1115.6411	558.8278	2	0.1253		
<1 9	VSKI	IVDKSK					L		1115.6914	558.8530	2	0.0750		550 560 570
														m/z, Da
Fragmentati	ion Evidence fo	r Peptide												
VG	ALSIVC[C0I]K													
Residue	b t	o+2	у	y+2										
V	100.0757	50.5415 111	6.6445	558.8259		8000 b1	y1 22	.8.15 2 b4	b5 y2	y3	3	/4 y	5	y6 y7 y8
G	157.0972	79.0522 101	7.5761	509.2917		7000								
A	228.1343 11	4.5708 96	0.5547	480.7810		/000			477	20				
L c	341.2183 1/	1.1128 88	9.5176	445.2624		6000 -			460.25	.20				
1	541.3344 27	1.1709 68	9.4015	345 2044	≩	5000 -	157.12		ì					
V	640.4028 32	20.7051 57	6.3174	288.6623	ensi	4000 -	2	.79.17						
C[C0I]	970.5390 48	35.7731 47	7.2490	239.1281	Ē	-				576.3	9			
К	1098.6340 54	9.8206 14	7.1128	74.0600		3000 -		286.16		550 36				
						2000 -	183 13	313.2	7			77	6.50	
						1000	173.15	413	.21 442.25	515.36		20 47		
							29.12	Lill Laker	India a land	Handan e	613.39		853.	.56 009.59 1017.67
						0 100	200	300	400	500 6	00	700	800	900 1000 1100
										m/z, Da				

Oxalic acid oxidase AETPAGYP<u>C</u>IRPIHVK

	Protein Qu	ant				Protein ID			Spectra					Summary Statistics
Spectrum L	ist													
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequ	ence 🛆			Modi	fications			Conf Theor MW 🔺
8.1.1.1747.3	31.47	0 1698.8354	850.425	0 2		AETAANSCLFSGHR		ICAT-C:13C	C(9)(C)@8					< 1 1698.8195
5.1.1.1278.3	29.86	4 1978.2782	495.576	8 4	6	AETPAGYPCIRPIHV	ĸ	ICAT-C(C)@	<u>n</u> 9					6 1978.0459
5.1.1.1278.2	29.82	1 1987.2930	497.830	5 4	6	AETPAGYPCIRPIHV	K	ICAT-C:13C	C(9)(C)@9					99 1987.0760
61114184	31.17	3 1978 1763	990 095	4 2	6	AFTPAGYPCTR PTHV		ICAT-C(C)@	70.9					99 1978 0459
														F
Peptide ID I	lypotheses - 5	.1.1.1278.2												Precursor MS Region
Conf V So	Drot N (Foguenee		6	Madificatio		Theor MW	Theor m/z	•	4 Maga	- II	
99 14	FIOL N 6 AFT		1772	Sequence		-	ICAT-C:13C(9)(C)	ନା ଃ ~ ଲବ	1987 0760	497 7763	4	0.2169		495.5794 - 497.8292
<1 8	DDH	VGHEVKAVAI	SDHK				10,11-0,100(0)(0)	@~	1987.0276	497,7642	4	0.2654		- 498.3338
<1 8	IVE	GOIEPAPSVI	LHMK						1988.0765	498.0264	4	-0.7836		496.0946 50 404.0574 500.0013
<1 7	AHW	TLGTKKPNNI	PAPK						1987.0640	497.7733	4	0.2290		50 - 491.8574
< 1 7	TRO	LTHTTLIPNY	TVK				Deamidated(N)@1	13	1987.0739	497.7757	4	0.2191		m/z. Da
													- 11	
Fragmentati	on Evidence	or Peptide												
AEI	PAGYPC[C9IJIRPI	IVK												
Residue	b	b+2	у	y+2										
A	72.0444													
E		36.5258 198	38.0833	994.5453		1.4e4		4 y5	y6 y7	1053.	.70 y8	y9	y10y	11 y12 y13
	201.0870	36.5258 198 101.0471 191	38.0833 17.0462	994.5453 959.0267		1.4e4 y1 1.3e4 b2	y2 y3 y b6 y 8+28 p4+2b5	4 y5 b6y8+g29+2	y6 y7 y1 1d#23+2 2	1053.	.70 y8	у9	y10y	'11 y12 y13
Т	201.0870 302.1347	36.5258 198 101.0471 197 151.5710 178	38.0833 17.0462 38.0036	994.5453 959.0267 894.5054		1.4e4 y1 1.3e4 b2 1.2e4 b2	yz y3 y b6 y8+ 28 p≇+2b5	4 y5 b6y8+g29+2	y6 y7 y1 1)d#23⊷ 22	1053.	.70 y8	y9	y10y	11 y12 y13
T P	201.0870 302.1347 399.1874	36.5258 198 101.0471 191 151.5710 176 200.0974 166	38.0833 17.0462 38.0036 36.9559	994.5453 959.0267 894.5054 843.9816		1.4e4 y1 1.3e4 1.2e4 1.1e4 136,09	y∠ y3 y b6 y 8+28 p4+2b5	4 y5 b6y8+g9+2	y6 y7 y1 1¢#23 ⊷22	1053.	.70 y8	у9	y10y	11 y12 y13
T P A	201.0870 302.1347 399.1874 470.2245	36.5258 198 101.0471 197 151.5710 176 200.0974 168 235.6159 156	38.0833 17.0462 38.0036 36.9559 39.9032	994.5453 959.0267 894.5054 843.9816 795.4552		1.4e4 y1 1.3e4 1 1.2e4 1 1.1e4 136.09 1.0e4 20	y2 y3 y b6 y2+2 8 y ₹+2b5	4 y5 b6y8+ <u>2</u> 9+2	y6 y7 y1)d#23+ 22	1053.	.70 y8	у9	y10y	11 y12 y13
T P A G	201.0870 302.1347 399.1874 470.2245 527.2460	36.5258 198 101.0471 19 151.5710 177 200.0974 168 235.6159 156 264.1266 157	38.0833 17.0462 88.0036 86.9559 89.9032 18.8661	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367		1.4e4 y1 1.3e4 1.2e4 1.1e4 136.09 1.0e4 20 9.0e3	y2 y3 y b6 y3+2 b5 n,10 246.20	4 y5 b6y8+ <u>2</u> 9+2 527.35	y6 y7 y1 1∮423-6 2	1053.	70 y8	у9	y10y	11 y12 y13
T P A G Y	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 155 264.1266 151 345.6583 146	38.0833 17.0462 38.0036 36.9559 39.9032 18.8661 51.8446	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259	sity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3	yz y b6 y2+2 3 y7+2 b5 1.10 246.20	4 y5 b6y8+ <u>9</u> 9+2 527.35	y6 y7 y1 1)d=123 +62	1053.	70 y8	y9 1298.93	y10y	11 y12 y13
Т Р А G Y Р	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621	36.5258 199 101.0471 191 151.5710 177 200.0974 169 235.6159 154 264.1266 157 345.6583 144 394.1847 129	38.0833 17.0462 38.0036 36.9559 39.9032 18.8661 61.8446 98.7813	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943	rtensity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 .	yz b6y 8+28 y 4 +2b5 1.10_246.20 1+226.13 509.27	4 y5 b6y8+ <u>2</u> 9+2 527.35	y6 y7 y1 9d+25+ 22	1025 70	70 y8	y9 1298.93 .90	y10y	11 y12 y13
T P A G Y P C[C91]	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285	36.5258 19 101.0471 19 151.5710 17 200.0974 16 235.6159 15 264.1266 15' 345.6583 14(394.1847 129 563.7679 120	88.0833 17.0462 88.0036 86.9559 89.9032 18.8661 61.8446 98.7813 01.7285	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679	Intensity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3	yz y3 y b6y8+28 y4+2b5 1.10 246.20 1+228.13 509.27	4 y5 b6y8+ <u>2</u> 9+2 527.35	y6 y7 y1 jdf25 +22	1053.	70 y8	y9 1298.93 .90	y10y	11 y12 y13
T P A G Y P C[C91] I	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 151 264.1266 151 345.6583 144 394.1847 122 563.7679 124 620.3099 84	88.0833 17.0462 88.0036 86.9559 89.9032 18.8661 61.8446 98.7813 01.7285 52.5621	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847	Intensity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3 5.0e3 5.0e3	yz y y b6y5+28 y7+2b5 1.10 246.20 1+226.13 509.27 278.16	4 y5 b6y8+ <u>2</u> 9+2 527.35 7	y6 y7 y1 ∮423 +22 97	1053.	70 y8 1281	y9 1298.93 .90	y10y	11 y12 y13
T P A G Y P C[C9I] I R	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 151 264.1266 157 345.6583 144 394.1847 124 563.7679 124 620.3099 80 698.3605 74	38.0833 17.0462 38.0036 36.9559 39.9032 18.8661 61.8446 98.7813 01.7285 52.5621 49.4781	994.5453 959.0267 894.5054 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427	Intensity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3 5.0e3 4.0e3 7.0e3	yz b6y5+28 1.10 246.20 1+226.13 509.27 278.16 , 302.19	4 y5 b6y8+ <u>2</u> 9+2 527.35 7	y6 y7 y1 ∮423 +2 97 862	1053. 1025.70	70 y8 1281 1152.83	y9 1298.93 .90	y10y	1565.95 1600.02
T P A G Y P C[C9I] I R P	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 151 264.1266 157 345.6583 144 394.1847 124 563.7679 124 620.3099 84 698.3605 74 746.8868 554	38.0833 17.0462 38.0036 38.0959 38.99032 18.8661 51.8446 98.7813 01.7285 52.5621 49.4781 33.3770	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921	Intensity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3 5.0e3 4.0e3 3.0e3 147.13	yz y y b6y5+28 y7+2b5 1.10 246.20 1 - 226.13 509.27 278.16 302.19	4 y5 b6y8+ <u>2</u> 9+2 527.35 7	y6 y7 y1 ∮423 +2 97 862	1053. 1025.70 .62	70 y8 1281 1152.83	y9 1298.93 .90	y10y	1565.95 1590.02
T P A G Y P C[C91] I R P I	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664 1605.8505	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 151 264.1266 157 345.6583 144 394.1847 124 563.7679 124 620.3099 84 698.3605 74 746.8868 54 803.4289 44	38.0833 38.0833 17.0462 38.0036 36.9559 39.9032 18.8661 31.8446 38.7813 101.7285 52.5621 49.4781 33.3770 96.3242	994.5453 955.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6657	Intensity	1.4e4 91 1.3e4 52 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3 5.0e3 4.0e3 3.0e3 147.13 2.0e3 147.13	yz y y b6y5+28 y7+2b5 1.10 246.20 - 226.13 509.27 278.16 302.19 361.23	4 y5 b6y8+ <u>2</u> 9+2 527.35 7	97 977 795 52	1053. 1025.70 .62	70 y8 1281 1152.83 1170.8	y9 1298.93 .90	y10y 1518.9	1565.95 1890.02 9 1687.18
Т Р G У Р С[С91] I R Р I H	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664 1605.8505 1742.9094	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 151 264.1266 157 345.6583 144 394.1847 122 663.7679 121 620.3099 84 698.3605 74 746.8868 54 803.4289 44 871.19583 3	38.0833 17.0462 38.0036 36.9559 39.9032 18.8661 51.8446 98.7813 11.7285 52.5621 49.4781 33.3770 96.3242 33.2401	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6657 192.1237	Intensity	1.4e4 91 1.3e4 52 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3 5.0e3 4.0e3 3.0e3 147.13 2.0e3 119.06 119.06	yz yy y b6y5+28 y7+2b5 1.10 246.20 - 226.13 509.27 278.16 302.19 361.23	4 y5 b6y8+ <u>2</u> 9+2 527.35 7	y6 y7 y1 j423 +2 97 795 52 751 49	1053. 1025.70 .62	70 y8 1281 1152.83 1170.8	y9 1298.93 .90 .5	y10y 1518.9 1410.95	1565.95 1690.02 9 1687.18 1671.10 1955.35
T P A G V P C[C91] I R R P I H V	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664 1605.8505 1742.9094 1841.9778	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 151 264.1266 157 345.6583 144 394.1847 122 563.7679 121 620.3099 84 698.3605 74 746.8868 54 803.4289 44 871.19583 34 921.4925 24	80.0833 17.0462 18.0036 36.9559 39.9032 18.8661 31.8446 98.7813 11.7285 52.5621 49.4781 33.3770 96.3242 33.2401 46.1812	994.5453 955.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6657 192.1237 123.5942	Intensity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3 5.0e3 4.0e3 3.0e3 147.13 2.0e3 119.06 119.06 0.0e0	yz yby y yby y y y y y y y y y y y y y y	4 y5 b6y8+ <u>2</u> 9+2 527.35 7 649.	y6 y7 y 19425 -22 97 862 795.52 751.49	1053.	70 y8 1281 1152.83 1170.8	y9 1298.93 .90	y10y 1518.9 1410.95	1565.95 1690.02 9 1687.18 167110 1955.35
T P A G V P C[C9I] I R P I H V K	201.0870 302.1347 399.1874 470.2245 527.2460 690.3093 787.3621 1126.5285 1239.6125 1395.7136 1492.7664 1605.8505 1742.9094 1841.9778 1970.0728	36.5258 191 101.0471 191 151.5710 177 200.0974 161 235.6159 151 264.1266 157 345.6583 144 394.1847 122 563.7679 121 520.3099 81 698.3605 77 746.8868 54 803.4289 44 871.19583 34 921.4925 24 985.5400 14	38.0833 17.0462 38.0036 36.9559 39.9032 18.8661 51.8446 308.7813 11.7285 52.5621 49.4781 33.3770 96.3242 33.2401 46.1812 47.1128	994.5453 959.0267 894.5054 843.9816 795.4552 759.9367 731.4259 649.8943 601.3679 431.7847 375.2427 297.1921 248.6657 192.1237 123.5942 74.0600	Intensity	1.4e4 y1 1.3e4 b2 1.2e4 136.09 1.0e4 20 9.0e3 8.0e3 7.0e3 6.0e3 5.0e3 4.0e3 3.0e3 147.13 2.0e3 119.06 0 0.0e0 0 2	yz yz yz yz yz yz yz yz yz yz	4 y5 b6y8+ <u>2</u> 9+2 527.35 7 649.	y6 y7 y1 9425 -22 97 862 795 52 751 49 800	1053. 1025.70 .62 1000 m/z. Da	70 y8 1261 1152.83 1170.8 1170.8 1170.8	y9 1298.93 .90 .5 .1 .1	y10y 1518.9 1410.95 1400	11 y12 y13 1565.95 1590.02 9 1687.18 1671.10 1955.35 1600 1800 2000

homocysteine S-methyltransferase <u>CVKPPVIYGDVSRPK</u>

																	- 8 :
	Protein Qu	ant				Protein ID			Spectra					Summary	Statistic	S	
Spectrum L	.ist																
Spectrum	n Time	Prec MW	Prec m/z	z Prec z	Prot N	Best Sequ	ence 🗸			Modi	fications	•			Cont	f Theor M	w 🔺
3.1.1.1812.3	56.47	6 2011.3837	671.468	5 3		CVCFIICKHHK		ICAT-C(C)@	21, ICAT-C(C)	@3, ICAT-C(C	c)@7				<	1 2011.03	317 🚥
5.1.1.1270.4	28.72	4 1884.2605	472.072	4 4	8	CVKPPVIYGDVSRPK		ICAT-C(C)@	<u>0</u> 1						9	95 1884.02	292
5.1.1.1269.4	28.57	6 1893.3053	474.333	6 4	8	CVKPPVIYGDVSRPK		ICAT-C:13C	(9)(C)@1						9	99 1893.05	593
8 1 1 2272 3	60.98	64 0 0000	742 740	05 0	25	CVREASEVAGVODI.GI	TLGR	ICAT-C:13C	(9)(C)ത1							<u>(1 2225 20</u>	139
																	·
														_			
Peptide ID	Hypotheses - 5	.1.1.1269.4												Precurso	r MS Reg	jion	
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modificati	ons 🗠	Theor MW	Theor m/z	z	∆Mass	ווו ר	1		N	
99 15	8 CAK	PVIYGDVSRE	9K				ICAT-C:13C(9)(C)	@1	1893.0593	474.2721	4	0.2459		100 4	64.8208	474.3300	
< 1 8	EFP	RASVLVLQQ	QQY				Deamidated(Q)@	15	1892.9633	474.2481	4	0.3420		#/2.		- 474.8393)
< 1 7	ARG	NSLIIPYSASN	IRFK						1893.0221	474.2628	4	0.2832		50 -		482.3	3360
< 1 7	DPL	LQFAFLGKVSF	RFR						1893.0625	474.2729	4	0.2428		اللبال ا	i para luti a na luti luti	line and the second	un halki
< 1 7	YVK	LGYHYLITHLE	rK 🛛						1894.0505	474.5199	4	-0.7453			m	/z, Da	
Eragmontat	ion Evidence	ior Pontido															
riaginentat	Ion Lyndence	or replice															
C[C	91JVKPPVIYGDVS	RPK															_
Residue	b	b+2	у	y+2													
C[C9I]	340.1736	170.5905 189	94.0666	947.5369		y1	y2	y3 y4	y5	y6 y7	у	8 y9	y1	0 y11	y12	y13	
V	439.2421	220.1247 158	54.9002	777.9538		1.8e4 -	b2 y2+2 y5+2 y6 y 2	+2 yd85+72+929+y	210 521 1 +212 52	y13+2	b6						
к	567.3370	284.1721 148	55.8318	728.4196		1.6e4 -	2/0.1	487.3	33								
Р	664.3898	332.6985 132	27.7369	664.3721													
Р	761.4426	381.2249 12 3	30.6841	615.8457		1.4e4											
V	860.5110	430.7591 113	33.6313	567.3193		1.2e4 -					9	21.54					
1	973.5950	487.3012 103	34.5629	517.7851	sitv	1.004	295.20										
Y	1136.6584	568.8328 92	21.4789	461.2431	L L L	1.004	254.15	23 19		758.48							
G	1193.6798	597.3435 78	58.4155	379.7114	-	8.0e3 -	244 18	422.20	6								
D	1308.7068	654.8570 7 0	01.3941	351.2007		6.0e3 136.	09 \										
V	1407.7752	704.3912 58	36.3671	293.6872		-		461.28	560.45			1034	.67		1327 0	0	
S	1494.8072	747.9072 48	37.2987	244.1530		4.0e3 -	197.15		00.01	445					1027.01	~	
R	1650.9083	825.9578 40	00.2667	200.6370		2.0e3 151 10		407.30	600.42	712.53	904.53	029.62	4.44		85	1477 16	
P	1747.9611	8/4.4842 24	14.1656	122.5864		101.10	h dhad a dhu dhu a dhu				Julio	920.03	118	00.62		14/1.10	
ĸ	1876.0560	938.5317 14	11128	/4.0600		0.0e0 0 100	200 300	400 50	0 600	700 80	0 90	0 1000	110	0 1200	1300	1400 15	500
									-	m/z, Da				-			

Streptomyces cyclase/dehydrase family protein SELAQSIAEFHTYHLGPGS<u>C</u>SSLHAQR

	Protein	Quant				Protein ID		Spectra			Summary Statistics
Spectrum L	ist										
				1 1							
Spectrum	n Time	Prec	MW Prec r	n/z Precz	Prot N	Best Sequence	<u>۸</u>		Modifi	cations	Conf Theor MW
1 1 1 1 1 3 1 8 4	ા ગ	5 8371 3161	86551 633 3	8041 51	4	/I SELLOS LAR ENTVHICOCSCO	III	_C:13C(9)(C)/@20			
Peptide ID	Hypotheses	- 5.1.1.131	8.4								Precursor MS Region
Conf V Sc	Prot N 🛆			Sequence		Δ	Modifications	△ Theor MW	Theor m/z	z 🛆 Mass 🔺	
99 16	47 S	ELAQSIAEF	HTYHLGPGS	CSSLHAQR		ICAT-(0:13C(9)(C)@20	3161.5400	633.3152	5 0.3255	50 631.7798 633.5732 632.6504 640.6500
< 1 8	49 S	LNIERPTYT	NLNRLVSQV	ISSLTASLR		Oxida	ion(R)@6, Deamic	late 3161.7043	633.3481	5 0.1610	
به این				00.07.112.02		Desmi		0 0400 5000	000 5404	5 0.0505 ¥	
Fragmentat	tion Evidend	ce for Pepti	ide								
SEI	LAQSIAEFHTY	HLGPGSC[C9	IJSSLHAQR								
Residue	b	b+2	у	y+2	*						
L	330.1660	165.5866	2946.4726	1473.7400		y1 y2 y3 y	4 y5 y6 y7	y8 y 91 0 y1	g12 y13 y14	y15	y19/20 y21
А	401.2031	201.1052	2833.3886	1417.1979		6000 - b4+82 10582b4 1	A####221+3#1249+25+	8/477/+28+/22642	y27+2		
Q	529.2617	265.1345	2762.3515	1381.6794		217.10					
S	616.2937	308.6505	2634.2929	1317.6501		5500 -					
1	729.3777	365.1925	2547.2608	1274.1341		5000 -					
A	800.4149	400.7111	2434.1768	1217.5920		-					
E	929.4575	465.2324	2363.1397	1182.0735		4500 5	11.31				
F	1076.5259	538.7666	2234.0971	1117.5522		4000 -					
н	1213.5848	607.2960	2087.0287	1044.0180							
Т	1314.6325	657.8199	1949.9697	975.4885	=	23500 - 189.10					
Y	1477.6958	739.3515	1848.9221	924.9647		<u>1</u> 3000 -					
Н	1614.7547	807.8810	1685.8587	843.4330		2500					
	1727.8388	864.4230	1548.7998	774.9036		2000					
G	1/84.8602	892.9338	1435./158	/18.3615		2000 -					
	1881.9130	941.4601	1378.6943	644 2244		4500					
6	1936,9345	1012 4000	1201.0415	612 0427		173.14					
CICOIL	2025.9005	1013.4009	1224.0201	612.013/ 560.2077		1000 -	709.40	13	78.83		
o[cai]	2305.1329	1226 5264	798 4247	300 71/1		154.07	623,43	886.47	1686.	.00	2434.33 2634.57
3 6	2402.1049	1220.0001	711 3896	356 1985		500 1			1580	0.93 2068.24	2/45.//
	2652 2810	1326 6441	624.3576	312 6824				INCONTROL OF A NUMBER OF A CONTROL OF		ىلىچىللىچىللار لىپ	
Н	2789 3399	1395 1736	511.2736	256 1404		0 200 400	600 800	1000 1200	1400 1600 m/z. Da	1800 2000 2200	2400 2600 2800 3000
A	2860.3770	1430 6921	374,2146	187 6110	+						
L ²	2000.0110	1400.0021	514.2140	107.0110							

Arabidopsis Rab GTPase homolog E1b HYAHVD<u>C</u>PGHADYVK

	Protein Qu	ant				Protein ID			Spectra					Summary St	atistics	
Spectrum L	ist															
Spectrum	Time	Prec MW	Prec m/a	z Prec z	Prot N	Best Sequ	ience	Δ		Modi	fications				Conf T	heor MW 🔺
5.1.1.1232.3	23.1	7 1938.2057	485.558	37 4	10, 48	HYAHVDCPGHADYVK		ICAT-C(C)	<u>@</u> 7						99	1937.8843
5.1.1.1232.2	23.1	5 1947.2229	487.813	30 4	10, 48	HYAHVDCPGHADYVK		ICAT-C:130	C(9)(C)@7						99	1946.9144 📼
6.1.1.1340.2	24.1	0 1938.2301	485.564	48 4	10, 48	HYAHVDCPGHADYVK		ICAT-C(C)	@7						99	1937.8843
3 1 1 1859 2	63.10	0.0000	740 920	กร กไ		TADGESSDIVSAODT	TRITTSSCTSA	C Deamidater	d(വ)@13						< 1	2959 4873
																,
Peptide ID	- typotheses - t	.1.1.1232.2												Precursor M	S Region	
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modifica	ations 🗠	Theor MW	Theor m/z	z	∆Mass	۳.	80 -	l.	
99 16	10, 48 HYA	IVDCPGHADY	VK				ICAT-C:13C(9)((C)@7	1946.9144	487.7359	4	0.3084		485.5543	3 - 487	.8158
< 1 11	EME	KEGAEKPNTTI	LFSR				Glu->pyro-Glu	@N-term	1947.9360	487.9913	4	-0.7132		00	- 48	8.3104
< 1 9	EQD	RFLPIANISR	IMK				Deamidated(N))@10, Oxidati	1947.0248	487.7635	4	0.1981		40 486.058	37 34	495.8165
< 1 8	SAN	/KLKAS PDTAI	NYDVR						1948.0013	488.0076	4	-0.7786				ditati na tantan 👘
< 1 8	TGN	TYNGENLNK	FHVK						1947.9802	488.0023	4	-0.7574		480	485 490	495
															m/z Da	
															11.12, Du	
															1112, Du	
Fragmentat	ion Evidence	or Peptide														
Fragmentat	ion Evidence	or Peptide														
Fragmentat	ion Evidence AHVDC[C9] PGHA b	for Peptide DYVK b+2	у	y+2	1	1			.dl +l	, el						
Fragmentat	AHVDC[C9]]PGHA	or Peptide	y 47.9217	y+2 974.4645	1	1800 - b242 t	b4+2 b26922421	y4∥y5 b8428+205	welyt	у8 t	57	у9	b11	b12		
Fragmentat	AHVDC[C9]]PGHA	Tor Peptide	y 47.9217 10.8628	y+2 974.4645 905.9351	-	1800 b262 t	b4+2 b2b6 923 42 464-2	b 84- 58+265 28 \ 509-28	ve v† biez +2	98 E	57	у9	ь11	b12		
Fragmentat	ion Evidence : AHVDC[C9]]PGHA 138.0662 301.1295 372.1666	or Peptide	y 47.9217 10.8628 47.7995	y+2 974.4645 905.9351 824.4034 700.00.00		1800 b2542 t 1600 -	b ^{Y2} b4+2 b2b6 983 ^{Y3} 481.2	<mark>, y4 y5</mark> b ∂+ 38+265 28 - 509.28	velv† biez+2	y8 t	57	у9	b11	b12		
Fragmentat	tion Evidence 1 AHVDC[C9]]PGHA 138.0662 301.1295 372.1666 509.2255 509.240	b+2 69.5367 19. 151.0684 18 18 18 186.5870 16. 255.1164 157	y 47.9217 10.8628 47.7995 76.7624 20.7025	y+2 974.4645 905.9351 824.4034 788.8848 720.2554		1800 b2542 t 1600 - 1400 -	<mark>¥2</mark> b4+2 b2b6 ¥23 ¹ 2 481.2	<mark>y4 y5</mark> b 5+3 8+265 28 − 1 509.28	velv† biez+2	у8 t	77	у9	Ь11	b12		
Fragmentat	tion Evidence 1 AHVDC[C9I]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3200	b+2 69.5367 19. 151.0684 18 18 18 255.1164 15 304.6506 14 304.6506 14 12 14	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8342		1800 - b2542 t 1600 - 1400 - 1200 -	y2 b4+2 b2b6 y23 42 481.2	<mark>y4 y5</mark> b 8428 4-265 28 - 1 509.28	vel v† telez-2	y8 t	07	y9	ь11	b12		
Fragmentat	tion Evidence : AHVDC[C9]]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873	b+2 69.5367 19. 151.0684 18 186.5870 16. 255.1164 15' 304.6506 14' 362.1641 13' 42' 40'	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077	sty	1800 - b292 t 1600 - 1400 - 1200 -	y2 b4+2 b2b6 y23 2 481,2 241,14	<mark>y4 y5</mark> b 8428 42b5 28 - 1 509.28	vel v† biez-2	y8 t	57	γ9	ь11	b12		
Fragmentat	tion Evidence : AHVDC[C9]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1155 6400	b+2 2 69.5367 19 151.0684 18 186.5870 16 255.1164 15' 304.6506 14' 362.1641 13' 531.7473 12'	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351 25.6081	y+2 974.4645 905.9351 824.4034 788.8848 670.8212 613.3077 613.3077	tensity	1800 - b292 b 1800 - 1400 - 1200 - 10000 - 10000 - 1000 - 1000 - 1000 - 1000 - 1000 - 1000 - 1000 -	y2 b4+2 b2b6 y23 2 431,2 241,14	<mark>y4 y5</mark> b 8 4284-205 28 - 1 509.28	ve vite	y8 E	57	γ9	Ь11	b12		
Fragmentat	tion Evidence : AHVDC[C9]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1159.5400 1216.5615	Tor Peptide DYVK 69.5367 19 151.0684 18 186.5870 16- 255.1164 15 304.6506 144 362.1641 13 362.1641 13 3631.7473 122 580.2737 88 808.7844 77	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351 25.6081 86.4417 89.3890	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077 443.7245 395.1881	Intensity	1800 - b2x2 t 1600 - 1400 - 1200 - 1000 - 800 - 255	241,14 241,18	<mark>y4 y5</mark> b84£88+265 28 − 1 509.28	ve vt	y8 E	77	γ9	Ь11	b12		
Fragmentat	tion Evidence : AHVDC[C9]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1159.5400 1216.5615 1353.6204	Tor Peptide DYVK b+2 69.5367 19. 151.0684 186.5870 16. 255.1164 153. 304.6506 14. 302.1641 13. 303.17473 122. 580.2737 88 508.7844 77. 577.3138 7.	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351 25.6081 86.4417 89.3890 32.3675	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077 443.7245 395.1981 366.6874	Intensity	1800 - b2x2 t 1600 - 1400 - 1200 - 1000 - 800 - 255 600 - 147.13	y2 b4+2 b2b6 y23+2 481,2 241,14 .14 301,18 3	<mark>y≰ y5</mark> b8488+205 28 - 1 509.28	ve vt	y8 E	77	γ9	ь11	b12		
Fragmentat	b 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1159.5400 1216.5615 1353.6204 1424.6575	The second secon	y 47.9217 10.8628 47.7995 56.7624 39.7035 40.6351 25.6081 36.4417 39.3890 32.3675 95.3086	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077 443.7245 395.1981 366.6874 298.1579	Intensity	1800 - b2x2 t 1600 - 1400 - 1200 - 1000 - 800 - 255 600 - 147,13	y2 b4+2 241,14 .14 301,18 3 400,2	<mark>y≰ y5</mark> b8488+205 28 - 509.28 21	yd yf bii2+2 723.40	y8 E	57	γ9	ь11	b12 1522.78 1589.84		
Fragmentat	AHVDC[C9]PGHA AHVDC[C9]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1159.5400 1216.5615 1353.6204 1424.6575 1539.6845	Tron Peptide	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351 25.6081 86.4417 89.3890 32.3675 95.3086 24.2715	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077 443.7245 395.1981 366.6874 298.1579 262.6394	Intensity	1800 - b2x2 t 1600 - 1400 - 1200 - 1000 - 800 - 255 600 - 147,13 400 - 129,12	y2 b4+2 b2b6 y23 +2 481,2 241,14 .14 301,18 3 400,2	21 608.3	ve vt	y8 t	47.64	у9 1308	b11	b12 1522.78 1539.84 1419.71		931.04
Fragmentat HY/ Residue H Y A H V D C[C9I] P G H A D Y	b 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1159.5400 1216.5615 1353.6204 1424.6575 1539.6845 1702.7478	Tron Peptide DYVK b+2 69.5367 19- 151.0684 186.5870 16- 255.1164 153 304.6506 144 362.1641 133 531.7473 122 580.2737 86 608.7844 77 12.8324 57 7712.8324 56 57 770.3459 56 851.8775 44	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351 25.6081 86.4417 89.3890 32.3675 95.3086 24.2715 09.2445	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077 443.7245 395.1981 366.6874 298.1579 262.6394 205.1259	Intensity	1800 - b2x2 t 1600 - 1400 - 1200 - 1000 - 800 - 129.12 200 - 110.00	y2 b4+2 b2b6 y23 +2 481,2 241,14 14 301,18 3 400,2	21 608.3	ve vt	y8 b 886.51 10-	47 64 1 60 115	у9 1308 9.74	b11	b12 1522.78 1539.84 1419.71 1630	.35 1	931.04
Fragmentat HY/ Residue H Y A H V D C[C9I] P G H A D V(C90) V	AHVDC[C9]PGHA AHVDC[C9]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1159.5400 1216.5615 1353.6204 1424.6575 1539.6845 1702.7478 1801.8162	b+2 2 69.5367 19 151.0684 18 186.5870 16 255.1164 15' 304.6506 14' 362.1641 13' 531.7473 12' 580.2737 8' 608.7844 7' 712.8324 5' 770.3459 5' 851.8775 4' 901.4117 2'	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351 25.6081 86.4417 89.3890 32.3675 95.3086 24.2715 09.2445	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077 443.7245 395.1981 366.6874 298.1579 262.6394 205.1259 123.5942	Intensity	1800 - bzłcz ł 1600 - 1400 - 1200 - 1000 - 255 600 - 147.13 400 - 129.12 200 - 110.00	241.14 241.14 3 400.2	21 608.3	vel v† bit2 -2 723.40 19 792.41	y8 b 886.51 10- 1 103	47 64 1 60 115	y9 9.74	b11	b12 1522.78 1539.84 1419.71 1630	,35 ¹	931.04
Fragmentat Residue H Y A H V D C[C9I] P G H Q Y K	AHVDC[C9]PGHA AHVDC[C9]PGHA 138.0662 301.1295 372.1666 509.2255 608.2940 723.3209 1062.4873 1159.5400 1216.5615 1353.6204 1424.6575 1539.6845 1702.7478 1801.8162 1929.9112	b+2 2000000000000000000000000000000000000	y 47.9217 10.8628 47.7995 76.7624 39.7035 40.6351 25.6081 86.4417 89.3890 32.3675 95.3086 24.2715 09.2445 46.1812 47.1128	y+2 974.4645 905.9351 824.4034 788.8848 720.3554 670.8212 613.3077 443.7245 395.1981 366.6874 298.1579 262.6394 205.1259 123.5942 74.0600	Intensity	1800 - b2H2 t 1600 - 1200 - 1400 - 255 600 - 147, 13 400 - 129, 12 200 - 147, 13 400 - 255 600 - 255 700 - 25	by2 b4+2 b2b6y22 481,2 241,14 .14 301,18 3 400,2 200 400	21 608.3	yd yf bil2 -2 723.40 19 40.41 10 10 10 10 800	y8 b 886.51 10. 103 1000	47.64	y9 9.74 1200	b11	b12 1522.78 1539.84 1419.71 1630 0 1600	.35 ¹	931.04

Arabidopsis Rab GTPase homolog E1b IVVELIVPVACEQGMR

													_	_ 8
	Protein Qu	ant		Ĭ		Protein ID			Spectra					Summary Statistics
Spectrum L	ist													
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequ	ence 🗠			Modi	ifications			Conf Theor MW
5.1.1.1444.3	53.69	5 2359.4600	787.493	9 3		IVVAVDIDEDMELLS	QRRSR	Oxidation(M)@11					< 1 2359.2166
1.1.1.1929.2	59.92	3 0.0000	700.182	0 0		IVVEGSDGSVRPGK								< 1 1398.7467 📼
5.1.1.1370.2	43.24	2007.2682	670.096	7 3	10	IVVELIVPVACEQGM	2	ICAT-C:130	C(9)(C)@11, C	xidation(M)@	15			99 2007.0944
6 1 1 1725 2	65.27	1 1247 0847	624 549	6 2		TUTUS DATARKND								< 1 1246 7034
Peptide ID	Hypotheses - 5.	1.1.13/0.2											_	Precursor MS Region
Conf ⊽ Sc	Prot N 4			Sequence		Δ	Modificatio	ons 🗠	Theor MW	Theor m/z	z	∆Mass	ן ר	50 1 1
99 19	10 IVVE	LIVPVACEQG	MR				ICAT-C:13C(9)(C)	@11, Oxid	2007.0944	670.0388	3	0.1738		40 667.4179 - 670.0965
< 1 8	39 ALDL	ASKPEGTGTF	TKDFK				Oxidation(F)@18	, Oxidation(2007.0160	670.0126	3	0.2522		30 6/0./661
< 1 8	IENA	PYSAQMCNIL	.GR				Deamidated(N)@3	3, ICAT-C(2006.9553	669.9924	3	0.3128		20 663.9225
< 1 8	QAKI	ESYAPSLSYA	PVGAR						2007.0425	670.0215	3	0.2257		
< 1 8	TQCP	APFTHGRSIS	LR				Deamidated(Q)@	2, ICAT-C:	2007.0408	670.0209	3	0.2275		665 670 675 680
< 1 8	VLLD	EKNHPLLIHC	.K				ICAT-C:13C(9)(C)	@14	2007.1387	670.0535	3	0.1296		m/z, Da
Fragmentat		or Peptide GM[Oxi]R												
Residue	b	b+2	у	y+2										
1	114.0913	57.5493 200	8.1017 1	1004.5545		5000 J y1	y2 y3 y	4 y5	HE72 . 2 1-9	y6 y7	у8 у	/9 y10	E.	y12
V	213.1598 1	07.0835 189	5.0176	948.0124		4500 -	213.18	72 UOY SYFED 60	WV3+2 D0	510			0	12
V	312.2282 1	56.6177 179	5.9492	898.4782		4000 - 185.18	229.14							
E	441.2708 2	21.1390 169	6.8808	848.9440		3500 -	1 223.14							
	554.3548 2	77.6811 156	4 75 44	/84.4227										
1 V	766 5072	09 7572 494	4.7541	674 2297	≩	3000 -	24245							
	863 5604	32 2837 424	12 6046	621 2045	ens	2500 -	243.15							
P V	962 6285	81 8170 444	5 5489	573 2784	Ĕ	2000	455.3	2 554.4				1242 70		
Δ	1033 6656	17 3364 404	16 4805	523 7439		199.18	342.24				11/8.7	/ 1242.79		
010911	1372 8320 6	86 9196 97	5 4434	488 2253		169.15		507.28 6	21.90	982.57	1046 59			
F	1501.8746 7	51 4409 63	6.2770	318 6421		1000 -		10 h 11.	636.35	-	1225.76			
Q	1629.9331	15.4702 50	7.2344	254.1208		500 136.10		Hell II	667.50	911.50	1127.67	1224.02		
G	1686.9546 8	43.9809 37	9.1758	190.0915			<u>, 1991 ya 11 (Jaharda Ka</u>			والمستعمل المسالية المراد		1324163		1566.96 1727.97 1859.93
M[Oxi]	1833.9900 9	17.4986 32	2.1544	161.5808		0 20	0 400	600	800	1000	120	0 1	400	1600 1800 2000
R	1990.0911 9	95.5492 17	5.1190	88.0631						m/z, Da				
L	L [_									

Multicatalytic endopeptidase complex ITQLTDNVYV<u>C</u>R

													-
	Protein Qua	int		<u> </u>		Protein ID	<u> </u>		Spectra				Summary Statistics
Spectrum L	ist												
		1											
Spectrum	Time	Prec MW	Prec m/z	2 Prec z	Prot N	Best Sequ	ence	A	140.00	Modif	fications		Conf Theor MW
3.1.1.1568.2	27.616	1015.5605	508.787	5 2	27	ITPVLGSSNK		Deamidated	d(N)@9				<1 1015.5550
4.1.1.1441.4	34.900	1660.0840	551.357	0 3	27	ITQLIDNVYVCR		ICAT-C(C)	ຍຼາງ ການເດັນສາງ				33 1650.0400
1 1 1 1565 2	27.04	1803.0051	602.009	0 3	38	TTUDDSINFFNDDLD		Oxidation(P)@5 Deamid	ated(N)@8_Ox	ridation/P	\@12	<1 1802.9163
•													4
Peptide ID I	Hypotheses - 4.	1.1.1441.3											Precursor MS Region
Conf ⊽ Sc	Prot N 🛆			Sequence		Δ	Modifica	tions 🛛 🛆	Theor MW	Theor m/z	z	∆Mass	s 100 - 1
99 15	27 ITQL	TDNVYVCR					ICAT-C:13C(9)(C)@11	1659.8701	554.2973	3	0.2138	38 550.3726 554.3672
< 1 9	FTSN	LPPKSMGAR	7R						1659.8879	554.3032	3	0.1961	61 551.3531
< 1 8	MVEI	SS LAE KVVA	ER				Oxidation(M)@	1	1659.9230	554.3149	3	0.1610	10 50 555.3367
< 1 8	QHIE.	VRLIEGDVP	R						1659.9056	554.3091	3	0.1783	83
< 1 8	QLVW	NKNYNVKPR					Deamidated(N)	@5, Deamid	1659.8733	554.2984	3	0.2107	545 550 555 560 56
													m/z, Da
Fragmentat	ion Evidence fo	or Peptide											
	LIDITY I YOLODIN	-			_								
Residue	114 0913	57 5403 16	y	930 9423		v v	1	v2	v3	v4 v5	v6	v7	v7 v8
T	215 1390 1	08.0731 15	47 7933	774 4003		1800 - b3+2	2 b2 y3+2 b3	y5+204 b	6.03		1 1 2	10	· · · · · · · · · · · · · · · · · · ·
Q	343,1976 1	72 1024 14	40.7457			4			90+2	D4 D8		69	
			46./45/1	723.8765		1600 -			90+2	776.48		69	
	456.2817 2	28.6445 13	18.6871	723.8765 659.8472		1600 -	230.12	514.3	3	776.48		69	
T	456.2817 2 557.3293 2	28.6445 13 79.1683 12	18.6871 05.6030	723.8765 659.8472 603.3052		1600 - 1400 -	230.12	514.3	3 613 45	776.48		69	
T D	456.2817 2 557.3293 2 672.3563 3	28.6445 13 79.1683 12 36.6818 11	46.7457 18.6871 05.6030 04.5553	723.8765 659.8472 603.3052 552.7813		1600 - 1400 - 1200 - 136.0	230.12 215.16	514.3	3 613.45	776.48		рэ	
T D N	456.2817 2 557.3293 2 672.3563 3 786.3992 3	28.6445 13 79.1683 12 36.6818 11 93.7032 9	18.6871 05.6030 04.5553 89.5284	723.8765 659.8472 603.3052 552.7813 495.2678	nsttv	1600 - 1400 - 1200 - 136.0	230.12 ₎₉ 215.16	514.3 497.30	3 613.45	0/ 08 776.48		D9	
	456.2817 2 557.3293 2 672.3563 3 786.3992 3 885.4676 4	28.6445 13 79.1683 12 36.6818 11 93.7032 9 43.2374 8	18.6871 05.6030 04.5553 89.5284 75.4855	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464	Intensity	1600 - 1400 - 1200 - 136.0 1000 -	230.12 215.16	514.3 497.30	3 613.45	07 776.48		09	
Т D N V Y	456.2817 2: 557.3293 2: 672.3563 3: 786.3992 3: 885.4676 4: 1048.5310 5:	28.6445 13 79.1683 12 36.6818 11 93.7032 9 43.2374 8 24.7691 7	40.7457 18.6871 05.6030 04.5553 89.5284 75.4855 76.4171	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464 388.7122	Intensity	1600 - 1400 - 1200 - 136.0 1000 - 800 -	230.12)9 215.16 187.16 249.16 843	514.3 497.30	3 613.45	07 Da 776.48		09	
T D N V Y V	456.2817 2: 557.3293 2: 672.3563 3: 786.3992 3: 885.4676 4 1048.5310 5: 1147.5994 5:	28.6445 13 79.1683 12 36.6818 11 93.7032 9 43.2374 8 24.7691 7 74.3033 6	40.7457 18.6871 05.6030 04.5553 89.5284 75.4855 76.4171 13.3537	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464 388.7122 307.1805	Intensity	1600 - 1400 - 1200 - 136.0 1000 - 800 - 600 -	230.12 215.16 187.16 249.16 343.	497.30 23	3 613.45	759.46		D9	
L T D V V V C[C91]	456.2817 2: 557.3293 2 672.3563 3 786.3992 3 885.4676 4 1048.5310 5 1147.5994 5 1486.7657 7	21.102+ 1+ 28.6445 13 79.1683 12 36.6818 11 93.7032 9 43.2374 8 24.7691 7 74.3033 6 43.8865 5	40.7457 18.6871 05.6030 04.5553 89.5284 75.4855 76.4171 13.3537 14.2853	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464 388.7122 307.1805 257.6463	Intensity	1600 - 1400 - 1200 - 136.0 1000 - 800 - 600 - 400 -	230.12 215.16 187.16 249.16 343.	497.30 497.42 444.27	3 613.45	о/а 776.48 759.46		D9	1308.78
L T D V V V C[C91] R	456.2817 2: 557.3293 2 672.3563 3 786.3992 3 885.4676 4 1048.5310 5 1147.5994 5 1486.7667 7 1642.8668 8	121.132 14 28.6445 13 79.1683 12 36.6818 11 93.7032 9 43.2374 8 24.7691 7 74.3033 6 43.8865 5 21.9371 1	40.7457 18.6871 05.6030 04.5553 89.5284 75.4855 76.4171 13.3537 14.2853 75.1190	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464 388.7122 307.1805 257.6463 88.0631	Intensity	1600 - 1400 - 1200 - 136.0 1000 - 800 - 600 - 400 - 119.09	230.12 215.16 187.16 249.16 343.	497.30 23 444.27 457.31	3 613.45	759.46	5.53	972.58	1308.78
L T D V Y V C[C9I] R	456.2817 2: 557.3293 2: 672.3563 3: 786.3992 3: 885.4676 4 1048.5310 5: 1147.5994 5: 1486.7657 7: 1642.8668 8:	11 12 28.6445 13 79.1683 12 36.6818 11 93.7032 9 43.2374 8 24.7691 7 74.3033 6 43.8865 5 21.9371 1	10.7457 18.6871 05.6030 04.5553 39.5284 75.4865 76.4171 13.3537 14.2853 75.1190	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464 388.7122 307.1805 257.6463 88.0631	Intensity	1600 - 1400 - 1200 - 136.0 1000 - 800 - 600 - 400 - 200 - 119.09	230.12 215.16 187.16 249.16 343.4	497.30 497.30 23 444.27 457.31	3 613.45	759.45 880.55	5.53	972.58	1308.78 1198.83 1427.84 1495.89
L T D V Y C[C9I] R	456.2817 2: 557.3293 2: 672.3663 3: 786.3992 3: 885.4676 4 1048.5310 5: 1147.5994 5: 1486.7657 7: 1642.8668 8:	121.102 14 28.6445 13 79.1683 12 36.6818 11 93.7032 9 43.2374 8 24.7691 7 74.3033 6 43.8865 5 21.9371 1	10.7457 18.6871 05.6030 04.5553 39.5284 75.4855 76.4171 13.3537 14.2853 75.4190	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464 388.7122 307.1805 257.6463 88.0631	Intensity	1600 - 1400 - 1200 - 136.0 1000 - 800 - 400 - 200 - 119.09 0 - 100	230.12 215.16 187.16 249.16 343. 200 300	497.30 497.30 444.27 457.31 457.31 400 500	613.45 600 70	759.46 880 840.55 840.55	5.53	972.58	1308.78 1198.83 1427.84 1495.89 100 1200 1300 1400 1500 1600
L T D V Y C[C91] R	456.2817 2: 557.3293 2: 672.3663 3: 786.3992 3: 885.4676 4 1048.5310 5: 1147.5994 5: 1486.7657 7: 1642.8668 8:	121.102 14 28.6445 13 79.1683 12 36.6818 11 39.7032 9 43.2374 8 24.7691 7 74.3033 6 43.8865 5 21.9371 1	10.7457 18.6871 05.6030 04.5553 39.5284 75.4855 76.4171 13.3537 14.2853 75.1190	723.8765 659.8472 603.3052 552.7813 495.2678 438.2464 388.7122 307.1805 257.6463 88.0631	Intensiţv	1600 - 1400 - 1200 - 136.0 1000 - 800 - 400 - 200 - 119.09 0 - 100	230.12 215.16 187.16 249.16 343. 249.16 343.	497.30 497.30 444.27 457.31 400 500	600 70	759.46 840.55 840.55 0 800 9 m/z, Da	5.53 1.1.1 1 900 10	972.58	1308.78 1198.83 1427.84 1495.89 14.11 1190 1200 1300 1400 1500 1600

Myrosinase QIIQDFKDYADL<u>C</u>FK

														-
	Protein Q	uant		Í		Protein ID			Spectra		1	S	ummary Statisti	cs
Spectrum L	ist													Ŀ
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequ	ence 🛆			Mod	lifications		Cor	f Theor MW
6.1.1.1579.2	51.0	49 2056.1816	686.4011	1 3	1	QIIQDFKDYADLCFK		Gln->pyro-G	lu@N-term,	ICAT-C(C)@1	3			99 2055.9976
6.1.1.1511.4	43.7	12 2082.2493	695.0904	4 3	1	QIIQDFKDYADLCFK		Deamidated(Q)@4, ICAT	-C:13C(9)(C)	@13			56 2083.0383
5.1.1.1423.2	51.0	11 2574.3772	859.1330	0 3	1	QIIQDFKDYADLCFK	EFGGK	GIn->pyro-G	lu@N-term,	ICAT-C(C)@1	3			99 2574.2466
151114233	51 (541 2583 4109	1 862 1443	21 31	11	OTTODEKDYADLCEK	FEGR	I GIn->nvro-G	lum/N-term	ICAT-C:13CO	4) (C)(7913		I	991 2583 2766
Peptide ID I	Hypotheses -	6.1.1.1579.2										Р	recursor MS Re	aion
														J
Conf ⊽ Sc	Prot N 🗠			Sequence		Δ	Modificatio	ons 🛆	Theor MW	Theor m/z	z ∆Mass		40 686.4039 ⁻	689.7630
99 15	1 QI .	QDFKDYADLCI	(K)				Gin->pyro-Giu@r	v-term, ICA	2055.9976	686 3314	3 0.1840		30 - 607 0707	690.4183
<1 10	OV	EDERDLADLCI	R				Deamidated(Q)@	1. Oxidatio	2055.9724	686.3347	3 0.1992		20 - 684.3768	697 6162
<1 9	MRI	TMOEVLDNLN	AIAOI				boundares (a) @	.,	2056.0444	686.3555	3 0.1370		10	Lurate to Lar
<1 9	TN	DAVVEPLDIC	KÖK.				ICAT-C:13C(9)(C)	@13, Dea	2056.0598	686.3605	3 0.1218		0	690 695
	II							I					000 003 m	/z, Da
Fragmentat	ion Evidence	for Pentide												
Truginentat		ior i cpude												
PGQ QII	QDFKDYADLC[C0	1JFK												
Residue	b	b+2	у	y+2										
Q	112.0393	56.5233 20	57.0048 1	1029.0061		1000 - y1	y2	y3	y4 y5	y6 y	7 y9 1	y10		
1	225.1234	113.0653 194	45.9728	973.4900			245.12	516.34	74 TZ 01	50	05 011			
1	338.2074	169.6074 183	32.8887	916.9480		900 -	- 269.13	510.54						
Q	466.2660	233.6366 17	19.8047	860.4060		800 -								
D	581.2930	291.1501 15	91.7461	796.3767		700 -	294.23							
F	/28.3614	304.6843 14	0.7192	738.8632	λ	600 -								
	000.4003	420.7310 13	1 5558	601 2815	tens	500 - 129.12		607.39		072 59			1702.96	
Y	1134,5466	567,7769 10	36.5288	543,7681	5	400	391.23	624	4.40 852 4	974.58 18				
A	1205.5837	603.2955 9	23.4655	462.2364										
D	1320.6107	660.8090 8	52.4284	426.7178		300 1			751 43					
L	1433.6947	717.3510 73	37.4015	369.2044		200 -			101.70	1051	.62 1134.71 1476.0	88	1586.82 1686.91	1958 16
C[C0I]	1763.8309	882.4191 6	24.3174	312.6623		100 101.08	المابية والمراجع المحاد المحاد		الدلار الل		400.00	"hlu	1797	96
F	1910.8993	955.9533 2	94.1812	147.5942		0				u llilli , di		PILII	III III II	
14	2022 0042	1020.0002 4.	17 4400	74.0600		0 20	00 400	600	800	1000	1200 140	0	1600 1800	2000
ĸ	2030.5545	1020.0000	17.1128	74.0000				000	000	m/z, Da		- -	1000 1000	

Myrosinase CSPMVDTKHR<u>C</u>YGGNSSTEPYIVAHNQLLAHATVVDLYR

										_ 8
	Protein	Quant				Protein ID	Spect	ra		Summary Statistics
Spectrum L	ist									
Spectrum	Time	Prec	MW Prec n	n/z Prec z	Prot N	Best Seque	nce 🔺		Modificat	tions
8.1.1.1887.2	4(0.952 4613	.3354 923.6	744 5	1	CS PMVDTKHRCYGGNS STEPY IV	AHNQLLAHATVVDLYR	Cys->Thr@1, Dioxidati	on(K)@8, ICAT-C:13	C(9)(C)@11
•										►
Peptide ID I	lypotheses	- 8.1.1.188	7.2							Precursor MS Region
Conf V Co	Drof N (6.			4	difications			
00 18			CVCCNCCTP	quence	T N U N T 17/7		tion/KV@8_ICAT_C:13C(9)/CV	@11_4611_268622	3 2610	40 922.2280 924.2460
29 17		SOUTHING	CODESTEDV				Debydrated(S)@2_ICAT_C-13	4011.2000 32.	3 6681	20 921.2534
•									E.	
L										
Fragmentat	ion Evidend	e for Pept	ide							
TSF	MVDTK[20x]H	RC[C9I]YGGN	ISSTEPYIVAH	NQLLAHATVV	/DLYR					
Residue	b	b+2	у	y+2	*					
Т	102.0550	51.5311	4612.2758	2306.6416		500]	اعدالتدا عداعات ا	404401 411 412	413 9154	16 v17
S	189.0870	95.0471	4511.2282	2256.1177		480 b4+2 b3 b4	8500+2+2 y14+25+2	y 99+2 yr y26+2	2	
P	286.1397	143.5735	4424.1961	2212.6017		400 - 204 10				
М	417.1802	209.0938	4327.1434	2164.0753		420				
V	516.2486	258.6280	4196.1029	2098.5551	=	400 -				
D	631.2756	316.1414	4097.0345	2049.0209		360 - 138.07				
Т	732.3233	366.6653	3982.0075	1991.5074		340				
K[2Ox]	892.4081	446.7077	3880.9599	1940.9836		320 - 269.12				
Н	1029.4670	515.2371	3720.8751	1860.9412		280 -				
R	1185.5681	593.2877	3583.8162	1792.4117		260				
C[C9I]	1524.7345	762.8709	3427.7150	1714.3612		240				
Y	1687.7978	844.4025	3088.5487	1544.7780		200				
G	1744.8192	872.9133	2925.4853	1463.2463		180				
G	1801.8407	901.4240	2868.4639	1434.7356		160				
N	1915.8836	958.4455	2811.4424	1406.2248		140 1 286.15				
S	2002.9157	1001.9615	2697.3995	1349.2034		100 451	30			
S	2089.9477	1045.4775	2610.3675	1305.6874		80	477.24 865.56	1074.66	1750	01
Т	2190.9954	1096.0013	2523.3354	1262.1714		60 1 40	673.39 936.6	1 1144.72	1/50	1921.17
E	2320.0380	1160.5226	2422.2878	1211.6475		20 115.05	748.40	1370.9	96 / 1464.08	2423.89
Р	2417.0907	1209.0490	2293.2452	1147.1262			11,1001104,0000,01111,0110,000,001,1111			
Y	2580.1541	1290.5807	2196.1924	1098.5998		0 200 400	600 800 1	000 1200 14 m/z.Da	00 1600 1	800 2000 2200 2400
1	2693.2381	1347.1227	2033.1291	1017.0682	-					
LV.	2702 2065	1206 6560	4020 0450	060 5261						

Extensin-like protein IPASI<u>C</u>QLPK

										_ B
	Proteir	n Quant		Prote	n ID	Spectra			Sumn	nary Statistics
						·				
Spectrum	List									
Time	Prec MW F	Prec m/z Prec	cz ProtN	Best S	quence /	7	Modif	ications		Conf Theor MW
32.537	1304.8840	653.4493	2 38	IPASICQLPK		ICAT-C:13C(9)(C)@6				99 1304.7573
42.205	695.4387	696.4459	1 48	IPDPVR						< 1 695.3966
65.934	1557.9241	779.9693	2	IPGNISGYTAGHSQR		Deamidated(N)@4				< 1 1557.7535
13 0.81	2212 4526 1	107.23	2	THUTEDBAOVENTOTUDBB						- 1 2212 2030
	Ŀ									
Peptide ID	Hypothese	s - 4.1.1.142	5.4						Precu	irsor MS Region
Conf ⊽ So	c Prot N 🗠		Sec	quence	△ Modific	ations 🖉 🛆	Theor MW	Theor m/z z		, ,
99 1	4 38	IPASICQLPK	:		ICAT-C:13C(9)(C)@6		1304.7573	653.3859 2	100	653.4483
< 1	9	ASPTASLSSL	EDK				1304.6460	653.3303 2		-
< 1	9	EGGLKKSVDM	NK				1304.6758	653.3452 2	80	648.0324
< 1	9	IENVLRVGYD	K				1304.7089	653.3617 2		040.5524
< 1	9	KDLEDMGIRT	K				1304.6758	653.3452 2	60	']
									40	654.4484
									20	654.9518
										, bilitetelle in het det der terbeitetelle
									0	650 660
4					1			•		m/z, Da
Fragmenta	tion Evider	ice for Pepti	de							
	ASICIC9/IQLPK	-								
Desidue		b .2								
Residue	114 0013	D+2	y 1305 7646	y+2	y1 +2 -2 +3 +3	y3 b7 ¥4 man	v10+2	у5	y6 y7	y8 y9 y10
	244 4444	106.0757	1192 6805	596 8439		UT UT THE TOP THE	y10+2			55
	282 4842	141 50/2	1095 6272	548 3175 3000 -		44.18				
<u>s</u>	360 2422	185 1102	1035.0270	512 7000 >2500 -						
	482 2072	241 6523	037 5596	469 2830						
CICOII	821 4637	411 2355	824 4746	412 7409						
0[031]	021.4037	411.2300	485 3082	243 1577 1000						
	1062 6063	531 8068	357 2406	179 1285	211.17 254.15	278.16 468.27				1192.89
	1159 6591	580 3332	244 1656	122 5864	171.12	351.23	581.40	819 48	32.59 102	4.09
ĸ	1287 7540	644,3807	147,1128	74 0600	0 100 200	300 400 500	600 7	00 800 90	0 1000	1100 1200 1300
IN	1201.1040	044.3007	147.1120	14.000	- 100 200 1	400 000	m/z, Da			1200 1200

Hypothetical protein M<u>CC</u>LFINDLDAGAGR

Protein Quant Spectrum List Time Prec MW Prec m/s		Protein II	D	Spectra						
Spectrum List				Spectra			Summary Statistics			
Time Prec MM/ Prec m/z	Spectrum List									
41.015 2086.1541 1044.08 30 475 1643 7676 548 9298	Prec z Prot N 2 29 M 3 M	Best Seque	ence /	Modifications Oxidation(M)@1,ICAT-C:13C(9)(C)@2,ICAT-C:13C(9)(C)@3			Conf Theor MW 99 2086.0144 <1			
Peptide ID Hypotheses - 5.1.1.		Precursor MS Region								
Conf ♥ Sc Prot N ∕ 99 15 29 MCCLFINI <1	Seque LDAGAGR SLRFLFSFS KNNSPEQAGR QAMTANLVAPR LKCAIDTNR VNDPFLGK	ence A	Modifice Oxidation(M)@1, ICAT-C:13 Deamidated(Q)@2 Deamidated(N)@1, Oxidation ICAT-C(C)@11, Deamidated ICAT-C:13C(9)(C)@4	itions A VC(9)(C)@2, ICAT-C:13C(Theor MW Theo 2086.0144 1044 2086.2344 1044 2086.0417 1044 2086.0630 1044 2086.0728 1044 2086.0525 1044	r m/z z 1.0145 2 1.1244 2 1.0281 2 1.0387 2 1.0387 2 1.0336 2 1.0336 2 1.0336 2	100 1035.5734 1044.0823 1045.0818 1045.6187 1046.6687 0 1040 1040 m/z, Da			
Fragmentation Evidence for Po	ptide GAGR									
Residue b b+2 M[Oxi] 148.0427 74.52 C[C9I] 487.2090 244.10 C[C9I] 826.3754 413.65 L 939.4595 470.22 F 1086.5279 543.76 I 1199.6120 6600.31 N 1313.6549 657.33 D 1428.6818 714.84 L 1541.7659 771.33 D 1656.7928 828.99 A 1727.8299 864.4' G 1784.8514 892.92 A 1855.8885 928.4' G 1912.9100 956.9 R 2069.0111 1035.0	y 50 2087.0217 11 82 1939.9863 9 13 1600.8199 4 34 1261.6535 6 76 1148.5695 5 96 1001.5010 8 11 888.4170 4 46 774.3741 3 36 431.2361 2 33 360.1990 7 33 360.1990 7 36 232.1404 7	y+2 2400 044.0145 2400 970.4968 2200 800.9136 2000 631.3304 1800 574.7884 1600 501.2542 1400 444.7121 1200 387.6907 1000 330.1772 800 273.6352 600 160.6031 400 162.0924 200 116.5738 0 88.0631 0	y1 y2 y3 y4 y5 b2+2 254.15 b43 276.15 232.16 295.20 175.14 151.10 360.24 151.40 400	y6 y7 y8 y9 3 28+27+2 b3 546.32 659.42 774.46 600 800	y10 y11 b4 1001.58 1148.7 984.54 1000 12 m/7 Da	y12 6 1261.83 1450. 200 1400	90 1649.03 1884.09 1966.13 1600 1800 2000			

Unknown protein LGA<u>C</u>VDLLGGLVK

													- 6
	Prote	ein Quant				Protein II	D	Spectra Summary Statistics					
Spectrum	List												
Time	Prec MW	Prec m/z	Prec z	Prot N		Best Seque	ence /		Mod	ifications			Conf Theor MW
36.614	0.0000	459.1318	0		LFPTEQIGIN	SR .		Deamidated(N)@10					< 1 1374.7144
63.764	1458.8007	730.4076	2		LFTGGGDPVI	ITGGR							< 1 1458.7831
44.721	1483.9393	742.9769	2	43	LGACVDLLGG	LVK		ICAT-C(C)@4					99 1483.8433
44.764	1492.9680	747.4913	2	43	LGACVDLLGG	LVK		ICAT-C:13C(9)(C)@4					99 1492.8734 🚽
•												•	
											_		
Peptide II	D Hypothes	ses - 4.1.1	.1508.3									Precursor N	IS Region
Conf ⊽	Sc Prot N 4			Sec	uence	Δ	Modific	ations 🗠	Theor MW	Theor m/z z	1	100 1	743 4741
99	16 43	LGACVDI	LLGGLVR	(ICAT-C:13C(9)(C)@4		1492.8734	747.4440 2		80 - 742	747 4937
< 1	8	AGRIEDO	GLTMFR	C					1492.7820	747.3983 2		60	141.4001
< 1	8	MKYLLV	INLSGNE	(Deamidated(N)@12		1492.8323	747.4235 2		00	755 4 470
< 1	8	SLDFSK	GKYLAHM	(1492.8038	747.4092 2		40 1	/55.1472
< 1	8	SLKEQLE	ENAFSVE	ζ			Deamidated(N)@8		1492.7773	747.3959 2		20	d da barran
												0 740	745 750 755
•										4	1.	140	m/z, Da
											1]
Fragment	ation Evid	ence for F	Peptide										
I	_GAC[C9I]VDI	LGGLVK											
Residue	e b	b+2		у	y+2								
L	114.09	13 57.	5493 14	493.8807	747.4440	900 -	y1 y2 y3	y4 y5 y6	y7 y 2 v13+2 b6	8 y9 b7 b8		y10	b12
G	171.11	28 86.0	0600 13	380.7966	690.9020	800	254.14	473.34					
A	242.14	99 121.8	5786 13	323.7752	662.3912								
C[C9I]	581.31	63 291.1	1618 12	252.7381	626.8727	700	228,16			913.65			
V	680.38	47 340.6	5960 9	913.5717	457.2895	≥600			2	14.58			
D	795.41	16 398.2	2095 8	314.5033	407.7553	500 -			0	17.00			
L	908.49	57 454.7	7515 6	699.4763	350.2418	Ĕ ₄₀₀	147 13 294	451.25					
L	1021.57	98 511.2	2935	586.3923	293.6998	300	141.10	586.47					
G	1078.60	12 539.8	3043 4	473.3082	237.1577	200	1/1.13	394.22 519.31					1 177 00
G	1135.62	27 568.3	3150 4	16.2867	208.6470	200 -) , .	699.	54 747 54	890.53 1018.6	0		1477.02
	1248.70	od 624.8	010	059.2653	180.1363	100 1	20.10		141,04		[™] 111	17.75 1220.85	
V V	1347.77	5Z 6/4.3	1207	46.1812	123.5942	وللبين				ւն ավերին փերիկինի։ Դուս որու	н Ц		
ĸ	14/5.8/	/38.4	136/	147.1128	74.0600	0	100 200 300	400 500 600	/00 8 m/z, Da	00 900 1000	110	JU 1200	1300 1400 1500

Figure S4

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to ABA treatment in guard cells by redox DIGE.

gi|109389998 Chloroplast chlorophyll a/b binding protein

Protein View

Match to: gi|109389998 Score: 127 chloroplast chlorophyll a/b binding protein [Brassica napus] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\8\E3 2365.wiff

Nominal mass (M_r): 28363; Calculated pI value: 5.48 NCBI BLAST search of <u>gi|109389998</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST), CyDye-Cy3 (C), CyDye-Cy5 (C), Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
```

Matched peptides shown in Bold Red

1 MAASTMALSS PAFAGKAVKL SPAASEVLGS GRVTMRKTVA KPKGPSGSPW 51 YGSERVKYLG PFSGEPPSYL TGEFPGDYGW DTAGLSADPE TFARNRELQV 101 IHCRWAMLGA LGCVFPELLA RNGVKFGEAV WFKAGSQIFS EGGLDYLGNP 151 SLVHAQSILA IWATQVILMG AVEGYRVAGD GPLGEAEDLL YPGGSFDPLG 201 LATDPEAFAE LKVKEIKNGR LAMFSMFGFF AQAIVTGKGP LENLADHLAD 251 PVNNNAWAFA TNFVPGK

Show predicted peptides also

Sort	Pe	ptides By	Resident line	lueNumber	Increasing Mass	ODecrease	sing Ma	ISS
Start	_	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44	-	55	640.2218	1278.4291	1278.5629	-0.1338	0	K.GPSGSPWYGSER.V (Ions score 73)
126	-	133	492.2274	982.4402	982.4913	-0.0510	0	K.FGEAVWFK.A (Ions score 54)

gi|131285 Photosystem II 44 kDa reaction center protein

Protein View

383 - 390 536.2895 1070.5644 1070.5145

```
Match to: gi | 131285 Score: 130
        Photosystem II 44 kDa reaction center protein (P6 protein) (CP43)
        Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff
        Nominal mass (Mr): 52213; Calculated pI value: 6.71
        NCBI BLAST search of gi|131285 against nr
        Unformatted sequence string for pasting into other applications
        Taxonomy: Secale cereale
        Links to retrieve other entries containing this sequence from NCBI Entrez:
        gi|12228 from Secale cereale
        Fixed modifications: Carbamidomethyl (C)
       Variable modifications: Oxidation (M), CyDye-Cy3 (C), CyDye-Cy5 (C), Oxidation (C)
        Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
        Sequence Coverage: 8%
        Matched peptides shown in Bold Red
             1 MKILYSLRRF YHVETLFNGT FVLAGRDOET TGFAWWAGNA RLINLSGKLL
            51 GAHVAHAGLI VFWAGAMNLF EVAHFVPEKP MYEQGLILLP HLATLGWGVG
           101 PGGEVLDTFP YFVSGVLHLI SSAVLGFGGI YHALLGPETL EESFPFFGYV
           151 WKDRNKMTTI LGIHLILLGL GAFLLVLKAL YFGGVYDTWA PGGGDVRKIT
           201 NLTLSPSVIF GYLLKSPFGG EGWIVSVDDL EDIIGGHVWL GFICVFGGIW
           251 HILTKPFAWA RRAFVWSGEA YLSYSLAALS VFGFIACCFV WFNNTAYSSE
           301 FYGPTGPEAS QAQAFTFLVR DORLGANVGS AQGPTGLGKY LMRSPTGEVI
           351 FGGETMRFWD LRAPWLEPLR GPNGLDLSRL KKDIOPWOER RSAEYMTHAP
           401 LGSLNSVGGV ATEINAVNYV SPRSWLSTSH FVLGFFPFVG HLWHAGRARA
           451 AAAGFEKGID RDLEPVLYMN PLN
                                            Delta Miss Sequence
Start - End
              Observed Mr(expt) Mr(calc)
 324 - 339 713.9294 1425.8442 1425.7576
                                             0.0866 0 R.LGANVGSAQGPTGLGK.Y (Ions score 53)
                                             0.0325
 344 - 357 748.8724 1495.7302 1495.6977
                                                       0 R.SPTGEVIFGGETMR.F Oxidation (M) (Ions score 41)
```

0.0499 0 K.DIQPWQER.R (Ions score 36)

gi|8745521 Ribulose bisphosphate carboxylase large chain precursor

Protein View

```
Match to: gi|1346967 Score: 220
Ribulose bisphosphate carboxylase large chain precursor (RuBisCO large subunit)
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff
```

Nominal mass (M_r): 53436; Calculated pI value: 5.88 NCBI BLAST search of <u>gi|1346967</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 11%

1	MSPQTETKAS	VGFKAGVKEY	KLNYYTPEYE	TKDTDILAAF	RVTPQPGVPP
51	EEAGAAVAAE	SSTGTWTTVW	TDGLTSLDRY	KGRCYHIEPV	PGEETQFIAY
101	VAYPLDLFEE	GSVTNMFTSI	VGNVFGFKAL	AALRLEDLRI	PPAYTKTFQG
151	PPHGIQVERD	KLNKYGRPLL	GCTIKPKLGL	SAKNYGRAVY	ECLRGGLDFT
201	KDDENVNSQP	FMRWRDRFLF	CAEAIYKSQA	ETGEIKGHYL	NATAGTCEEM
251	MKRAIFAREL	GVPIVMHDYL	TGGFTANTSL	AHYCRDNGLL	LHIHRAMHAV
301	IDRQKNHGMH	FRVLAKALR <mark>L</mark>	$\mathbf{S}\mathbf{G}\mathbf{G}\mathbf{D}\mathbf{H}\mathbf{V}\mathbf{H}\mathbf{A}\mathbf{G}\mathbf{T}$	VVGK LEGDRE	STLGFVDLLR
351	DDYVEKDRSR	GIFFTQDWVS	LPGVLPVASG	GIHVWHMPAL	TEIFGDDSVL
401	QFGGGTLGHP	WGNAPGAVAN	RVALEACVQA	RNEGRDLAVE	GNEIIREACK
451	WSPELAAACE	VWKEITFNFP	TIDKLDGQD		

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
22	-	32	710.8177	1419.6208	1419.6558	-0.0350	0	K.LNYYTPEYETK.D (Ions score 50)
195	-	213	729.3461	2185.0165	2184.9746	0.0419	1	R.GGLDFTKDDENVNSQPFMR.W Oxidation (M) (Ions score 51)
320	-	334	717.3900	1432.7654	1432.7423	0.0231	0	R.LSGGDHVHAGTVVGK.L (Ions score 55)
320	-	334	478.7023	1433.0850	1432.7423	0.3427	0	R.LSGGDHVHAGTVVGK.L (Ions score 34)
436	-	446	614.8159	1227.6173	1227.6459	-0.0286	0	R.DLAVEGNEIIR.E (Ions score 64)

gi|17855 Rubisco small subunit precursor

Protein View

Match to: gi|17855 Score: 181 rubisco ssu precursor [Brassica napus] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff

Nominal mass (M_r) : 20529; Calculated pI value: 7.63 NCBI BLAST search of <u>qi|17855</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 23%

Matched peptides shown in Bold Red

1 MAYSMLSSAA VVTSPAQATM VAPFTGLKSS SAFPVTRKAN NDITSIVSNG 51 GRVNSMQVWP PVGKKKFETL SYLPDLTEVE LGKEVDYLLR NKWIPCVEFE 101 LEHGFVYREH GSTPGYYDGR YWTMWKLPLF GCTDSAQVLK EVQECKTEYP 151 NAFIRIIGFD NNRQVQCISF IAYKPPSFTG A

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
84 - 90	454.2176	906.4206	906.4811	-0.0604	0	K.EVDYLLR.N (Ions score 34)
109 - 120	669.8454	1337.6763	1337.5636	0.1127	0	R.EHGSTPGYYDGR.Y (Ions score 53)
121 - 126	465.7598	929.5050	929.4106	0.0944	0	R.YWTMWK.L Oxidation (M) (Ions score 13)
147 - 155	555.8241	1109.6336	1109.5505	0.0831	0	K.TEYPNAFIR.I (Ions score 41)
156 - 163	474.7656	947.5166	947.4825	0.0341	0	R.IIGFDNNR.Q (Ions score 40)

gi|21839 Phosphoribulokinase; ribulose-5-phosphate kinase

Protein View

Match to: gi|21839 Score: 135 phosphoribulokinase; ribulose-5-phosphate kinase [Triticum aestivum] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B1 1546.wiff

Nominal mass (M_r) : 45406; Calculated pI value: 5.84 NCBI BLAST search of <u>gi|21839</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

Matched peptides shown in Bold Red

1	MAFCSPHSTT	SLRSPCTTIP	NSGFRQNQVI	LFTTRSSRRS	NTRHGARTFQ
51	VSCAVEQPIV	IGLAADSGCG	KSTFMRRLTS	VFGGAAEPPK	GGNPDSNTLI
101	SDTTTVICLD	DYHSLDRTGR	KEKGVTALDP	KANDFDLMYE	QVKAIKEGKA
151	IEKPIYNHVT	GLLDPAELIQ	PPKIFVIEGL	HPMYDERVRE	LLDFSIYLDI
201	SNEVKFAWKI	QRDMAERGHS	LESIKASIEA	RKPDFDAFIG	PQKQYADAVI
251	EVLPTQLIPD	DNEGKVLRVK	LIMKEGIKFF	NPVYLFDEGS	TINWIPCGRK
301	LTCSYPGIKF	SYGPDTYFGQ	EVSVLEMDGQ	FDRLDELIYV	ESHLSNLSTK
351	FYGEVTQQML	K HADFPGSNN	GTGLFQTIVG	LKIRDLYEQI	IAERAGVPAE
401	AAKV				

Show predicted peptides also

Sort Pontidos By

Solt i epildes by	Kesid	tue Number (Increasing Mass	Decrea	ising Ma	SS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
78 - 90	637.3328	1272.6511	1272.6714	-0.0203	0	R.LTSVFGGAAEPPK.G (Ions score 71)
351 - 361	680.8327	1359.6508	1358.6540	0.9967	0	K.FYGEVTQQMLK.H Oxidation (M) (Ions score 64)

D

gi|114420 ATP synthase subunit beta, mitochondrial precursor

Protein View

Match to: gi|l14420 Score: 139 ATP synthase subunit beta, mitochondrial precursor Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 103AMPLE3\F4 1223.wiff

Nominal mass (M_r): 59181; Calculated pI value: 6.01 NCBI BLAST search of <u>gi|114420</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Zea mays Links to retrieve other entries containing this sequence from NCBI Entres: gi|22173 from Zea mays gi|897618 from Zea mays

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

Matched peptides shown in Bold Red

1	MASRRVVSSL	LRSASRLRAA	SPAAPRPRAP	PHRPSPAGYL	FNRAAAYASS	
51	AAAQAAPATP	PPATGRTGGG	KITDEFTGAG	AIGQVCQVIG	AVVDVRFDEG	
101	LPPILTALEV	LDNNIRLVLE	VAQHLGENMV	RTIANDGTEG	LVRGQRVLNT	
151	GSPITVPVGR	ATLGRIINVI	GEPIDEKGDI	KINHFLPIHR	EAPAFVEQAT	
201	EQQILVTGIK	WOLLAPYOR	GGRIGLFGGA	GVGKTVLIME	LINNVAKAHG	
251	GESVEAGVGE	RTREGNDLYR	EMIESGVIKL	DDKQSESKCA	LVYGQMNEPP	
301	GARARVGLTG	LTVAEHFRDA	EGQDVLLFID	NIFRFTQANS	EVSALLGRIP	
351	SAVGYOPTLA	TDLGGLQERI	TTTKKGSITS	VQAIYVPADD	LTDPAPATTF	
401	AHLDATTVLS	RQISELGIYP	AVDPLDSTSR	MLSPHVLGED	HYNTARGVOR	
451	VLQNYKNLQD	IIAILGMDEL	SEDDKLTVAR	ARKIGRFLSQ	PFHVAEVFTG	
501	APGKYVELKE	SVKSFQGVLD	GKYDDLPEQS	FYMVGGIEEV	IAKAEKIAKE	
551	SAS					

Show predicted peptides also

Sort Peptides By

 Start - End
 Observed
 Mr(expt)
 Mr(calc)
 Delta
 Miss Sequence

 132 - 143
 639.8490
 1277.6834
 1277.6286
 0.0549
 0
 R.TIANDGTEGDVR.G
 Oxidation (M) (Ions score 67)

 211 - 220
 587.3486
 1172.6827
 1172.6553
 0.0274
 0
 K.VVDLLAPYQR.G
 (Ions score 37)

 224 - 234
 488.3454
 974.6762
 974.5549
 0.1213
 0
 K.IGLFGGA(VGK,T)
 (Ions score 36)

Residue Number Increasing Mass Decreasing Mass

gi|15219234 Vacuolar ATP synthase subunit A (VHA-A)

Match to: gi|15219234 Score: 368 VHA-A; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\B9 703.wiff

Nominal mass (M_r) : 69111; Calculated pI value: 5.11 NCBI BLAST search of <u>gi|15219234</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Links to retrieve other entries containing this sequence from NCBI Entrez: gi|79321468 from <u>Arabidopsis thaliana</u> gi|3334404 from <u>Arabidopsis thaliana</u> gi|3834305 from <u>Arabidopsis thaliana</u> gi|16649079 from <u>Arabidopsis thaliana</u> gi|1698899 from <u>Arabidopsis thaliana</u> gi|2553884 from <u>Arabidopsis thaliana</u> gi|27311967 from <u>Arabidopsis thaliana</u> gi|30725440 from <u>Arabidopsis thaliana</u> gi|110740311 from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 12%

1	MPAFYGGKLT	TFEDDEKESE	YGYVRKVSGP	VVVADGMAGA	AMYELVRVGH
51	DNLIGEIIRL	EGDSATIQVY	EETAGLTVND	PVLRTHKPLS	VELGPGILGN
101	IFDGIQRPLK	TIARISGDVY	IPRGVSVPAL	DKDCLWEFQP	NKFVEGDTIT
151	GGDLYATVFE	NTLMNHLVAL	PPDAMGKITY	IAPAGQYSLK	DTVIELEFQG
201	IKKSYTMLQS	WPVRTPRPVA	SKLAADTPLL	TGQRVLDALF	PSVLGGTCAI
251	PGAFGCGKTV	ISQALSKYSN	SDAVVYVGCG	ERGNEMAEVL	MDFPQLTMTL
301	PDGREESVMK	RTTLVANTSN	MPVAAREASI	YTGITIAEYF	RDMGYNVSMM
351	ADSTSRWAEA	LREISGRLAE	MPADSGYPAY	LAARLASFYE	RAGKVKCLGG
401	PERNGSVTIV	GAVSPPGGDF	SDPVTSATLS	IVQVFWGLDK	KLAQRKHFPS
451	VNWLISYSKY	STALESFYEK	FDPDFINIRT	KAREVLQRED	DLNEIVQLVG
501	KDALAEGDKI	TLETAKLLRE	DYLAQNAFTP	YDKFCPFYKS	VWMMRNIIHF
551	YNLANQAVER	AAGMDGQKIT	YTLIKHRLGD	LFYR LVSQKF	EDPAEGEDTL
601	VEKFKKLYDD	LNAGFRALED	ETR		

26 - 47 751.6538 2251.9397 2251.1341 0.8056 1 R.KVSGPVVVADGMAGAAMYELVR.V 2 0xidation (M) (Ions score 4) 204 - 214 692.3292 1382.6439 1382.6653 -0.0213 0 K.SYTMLQSWPVR.T 0xidation (M) (Ions score 49) 223 - 234 628.3441 1254.6737 1254.6932 -0.0195 0 K.LAADTPLLTGQR.V (Ions score 90) 259 - 267 473.8013 945.5881 945.5495 0.0386 0 K.TVISQALSK.Y (Ions score 63) 385 - 391 443.2615 884.5085 884.4392 0.0693 0 R.LASFYER.A (Ions score 43) 569 - 575 426.3156 850.6166 850.5164 0.1002 0 K.ITYTLIK.H (Ions score 34) 578 - 584 442.2734 882.5323 882.4599 0.0723 0 R.LGDLFYR.L (Ions score 47)	Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
204 - 214 692.3292 1382.6439 1382.6653 -0.0213 0 K.SYTMLQSWPVR.T Oxidation (M) (Ions score 49) 223 - 234 628.3441 1254.6737 1254.6932 -0.0195 0 K.LAADTPLLTGQR.V (Ions score 90) 259 - 267 473.8013 945.5881 945.5495 0.0386 0 K.TVISQALSK.Y (Ions score 63) 385 - 391 443.2615 884.5085 884.4392 0.0693 0 R.LASFYER.A (Ions score 43) 569 - 575 426.3156 850.6166 850.5164 0.1002 0 K.ITYTLIK.H (Ions score 34) 578 - 584 442.2734 882.5323 882.4599 0.0723 0 R.LGDLFYR.L (Ions score 47)	26	-	47	751.6538	2251.9397	2251.1341	0.8056	1	R.KVSGPVVVADGMAGAAMYELVR.V 2 Oxidation (M) (Ions score 44)
223 - 234 628.3441 1254.6737 1254.6932 -0.0195 0 K.LAADTPLLTGQR.V (Ions score 90) 259 - 267 473.8013 945.5881 945.5495 0.0386 0 K.TVISQALSK.Y (Ions score 63) 385 - 391 443.2615 884.5085 884.4392 0.0693 0 R.LASFYER.A (Ions score 43) 569 - 575 426.3156 850.6166 850.5164 0.1002 0 K.ITYTLIK.H (Ions score 34) 578 - 584 442.2734 882.5323 882.4599 0.0723 0 R.LGDLFYR.L (Ions score 47)	204	-	214	692.3292	1382.6439	1382.6653	-0.0213	0	K.SYTMLQSWPVR.T Oxidation (M) (Ions score 49)
259 - 267 473.8013 945.5881 945.5495 0.0386 0 K.TVISQALSK.Y (Ions score 63) 385 - 391 443.2615 884.5085 884.4392 0.0693 0 R.LASFYER.A (Ions score 43) 569 - 575 426.3156 850.6166 850.5164 0.1002 0 K.ITYTLIK.H (Ions score 34) 578 - 584 442.2734 882.5323 882.4599 0.0723 0 R.LGDLFYR.L (Ions score 47)	223	-	234	628.3441	1254.6737	1254.6932	-0.0195	0	K.LAADTPLLTGQR.V (Ions score 90)
385 - 391 443.2615 884.5085 884.4392 0.0693 0 R.LASFYER.A (Ions score 43) 569 - 575 426.3156 850.6166 850.5164 0.1002 0 K.ITYTLIK.H (Ions score 34) 578 - 584 442.2734 882.5323 882.4599 0.0723 0 R.LGDLFYR.L (Ions score 47)	259	-	267	473.8013	945.5881	945.5495	0.0386	0	K.TVISQALSK.Y (Ions score 63)
569 - 575 426.3156 850.6166 850.5164 0.1002 0 K.ITYTLIK.H (<u>lons score 34</u>) 578 - 584 442.2734 882.5323 882.4599 0.0723 0 R.LGDLFYR.L (<u>lons score 47</u>)	385	-	391	443.2615	884.5085	884.4392	0.0693	0	R.LASFYER.A (Ions score 43)
578 - 584 442.2734 882.5323 882.4599 0.0723 0 R.LGDLFYR.L (<u>Ions score 47</u>)	569	-	575	426.3156	850.6166	850.5164	0.1002	0	K.ITYTLIK.H (Ions score 34)
	578	-	584	442.2734	882.5323	882.4599	0.0723	0	R.LGDLFYR.L (Ions score 47)

gi|56384657 F1-ATPase alpha subunit

Protein View

Match to: gi|56384657 Score: 220
F1-ATPase alpha subunit [Brassica juncea]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\E2 1107.wiff

Nominal mass (M_r): 46684; Calculated pI value: 5.64 NCBI BLAST search of <u>gi|56384657</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica juncea

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 10%

Matched peptides shown in Bold Red

1 MELSPRAAEL TNLFESRIRN FYANFQVDEI GRVVSVGDGI AQVYGLNEIQ 51 AGEMVLFANG VKGMALNLEN ENVGIVVFGG DTAIKEGDLV KRTGSIVDVP 101 AGKAMLGRVV DAMGVPIDGR GALSDHEQRR VEVKAPGILE RKSVHEPMQT 151 GLKAVDSLVP IGRGQRELLI GDRQTGKTTI AIDTILNQKQ INSRATSESE 201 TMYCVYVAIG QKRSTVGQLI QTLEEANALE YSILVAATAS DPAPLQFLAP 251 YSGCAMGEYF RDNGMHALII YDDLSKQAVA YRQMSLLLRR PPGREASPGD 301 VFYLHSRLLE RAAKRSDQTG AGSLTALPVI ETQAGDVSAY IPTNVISITD 351 GQICLETELF YRGIRPAINV GLSVSRVGSA AQLKAMKQVC GSSKLELAQY 401 REVAAFAQFG SDLDALYEKR YVLSLKSEF

Show predicted peptides also

Son	Pe	plides by	Resid	ue Number () Increasing Mass	ODECTER	sing Mass
Start	_	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence
7	-	17	625.8285	1249.6425	1249.6302	0.0123	0 R.AAELTNLFESR.I (Ions score 82)
109	-	120	622.7948	1243.5750	1243.6231	-0.0481	0 R.VVDAMGVPIDGR.G Oxidation (M) (Ions score 56
154	-	163	513.7832	1025.5519	1025.5869	-0.0351	0 K.AVDSLVPIGR.G (Ions score 48)
363	-	376	480.3057	1437.8952	1437.8416	0.0537	0 R.GIRPAINVGLSVSR.V (Ions score 36)

gi|5708095 ATP synthase gamma chain, chloroplast precursor

Protein View

Match to: gi|5708095 Score: 112 ATP synthase gamma chain, chloroplast precursor [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1734.wiff

Nominal mass (M_r) : 33475; Calculated pI value: 6.12 NCBI BLAST search of <u>gi|5708095</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

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Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%
```

Matched peptides shown in Bold Red

```
1 RMKLVAAAKV RRAQEAVVNG RPFSETLVEV LYNINEQLQT DDVDVPLTKV
51 RPVKKVALVV VTGDRGLCGG FNNFIIKKAE ARIKELKGLG LEYTVISVGK
101 KGNSYFLRRP YIPVDKYLEA GTLPTAKEAQ AVADDVFSLF ISEEVDKVEL
151 LYTKFVSLVK SEPVIHTLLP LSPKGEICDI NGTCVDAAED EFFRLTTKEG
201 KLTVERETFR TPTADFSPIL LFEQDPVQIL DALLPLYLNS QILRALQESL
251 ASELAARMSA MSSASDNASD LKKSLSMVYN RKRQAKITGE ILEIVAGANA
301 QV
```

Show predicted peptides also

Sort Peptides By	Resid	lueNumber) Increasing Mass	O Decrea	sing Ma	ISS	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
56 - 65	514.8060	1027.5974	1027.6026	-0.0052	0	K.VALVVVTGDR.G	(Ions score 63)
117 - 127	582.2861	1162.5576	1162.6234	-0.0657	0	K.YLEAGTLPTAK.E	(Ions score 49)

gi|126896 Malate dehydrogenase, mitochondrial precursor

Protein View

Match to: gi|126896 Score: 66 Malate dehydrogenase, mitochondrial precursor Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\G8 1975.wiff

Nominal mass (M_r) : 36406; Calculated pI value: 8.88 NCBI BLAST search of <u>gi|126896</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Citrullus lanatus</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|18297</u> from <u>Citrullus lanatus var. lanatus</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1 MKASILRSVR SAVSRSSSSN RLLSRSFATE SVPERKVAVL GAAGGIGQPL 51 ALLMKLNPLV SKLALYDIAG TPGVAADVGH VNTRSEVTGY VGEEQLGKAL 101 EGSDVVIIPA GVPRKPGMTR DDLFNINAGI VKSLCTAIAK YCPNALINMI 151 SNPVNSTVPI AAEVFKKAGT YDEKKLFGVT TLDVVRAKTF YAGKANVPVA 201 EVNVPVIGGH AGITILPLFS QATPRANLSD DTIVALTKRT QDGGTEVVEA 251 KAGKGSATLS MAYAGALFAD ACLKGLNGVP DVVECSFVQS TVTELPFFAS 301 KVKLGKNGVE SVLDLGPLSD FEKEGLEKLK PELKASIEKG IQFANAN

Show predicted peptides also

Sort Peptides By © Residue Number © Increasing Mass © Decreasing Mass Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence 176 - 186 610.3730 1218.7314 1218.6972 0.0341 0 K.LFGVTTLDVVR.A (Ions score 66)

MS/MS Fragmentation of LFGVTTLDVVR

Found in gi 126896, Malate dehydrogenase, mitochondrial precursor

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	У	y++	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							11
2	261.1598	131.0835			F	1106.6204	553.8139	1089.5939	545.3006	1088.6099	544.8086	10
3	318.1812	159.5942			G	959.5520	480.2796	942.5255	471.7664	941.5415	471.2744	9
4	417.2496	209.1285			V	902.5306	451.7689	885.5040	443.2556	884.5200	442.7636	8
5	518.2973	259.6523	500.2867	250.6470	T	803.4621	402.2347	786.4356	393.7214	785.4516	393.2294	7
6	619.3450	310.1761	601.3344	301.1709	T	702.4145	351.7109	685.3879	343.1976	684.4039	342.7056	6
7	732.4291	366.7182	714.4185	357.7129	L	601.3668	301.1870	584.3402	292.6738	583.3562	292.1817	5
8	847.4560	424.2316	829.4454	415.2264	D	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
9	946.5244	473.7658	928.5138	464.7606	V	373.2558	187.1315	356.2292	178.6183			3
10	1045.5928	523.3001	1027.5823	514.2948	V	274.1874	137.5973	257.1608	129.0840			2
11					R	175.1190	88.0631	158.0924	79.5498			1

gi|15231715 Fructose-bisphosphate aldolase, putative

Protein View

Match to: gi|15231715 Score: 238 fructose-bisphosphate aldolase, putative [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B2 1550.wiff

Nominal mass (M_r): 38858; Calculated pI value: 6.05 NCBI BLAST search of <u>gi|15231715</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|7529717</u> from <u>Arabidopsis thaliana</u> <u>gi|15450683</u> from <u>Arabidopsis thaliana</u> <u>gi|16323105</u> from <u>Arabidopsis thaliana</u> <u>gi|17380610</u> from <u>Arabidopsis thaliana</u> <u>gi|21592946</u> from Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%
```

1	MSAFTSKFAD	ELIANAAYIG	TPGKGILAAD	ESTGTIGKRL	ASINVENVET
51	NRRNLRELLF	TAPGALPCLS	GVILFEETLY	QKSSDGKLFV	DILKEGGVLP
101	GIKVDKGTVE	LAGTDGETTT	QGLDGLGDRC	KKYYEAGARF	AKWRAVLKIG
151	ENEPSEHSIH	ENAYGLARYA	VICQENGLVP	IVEPEILVDG	SHDIQKCAAV
201	TERVLAACYK	ALSDHHVLLE	GTLLKPNMVT	PGSDSPKVSP	EVIAEHTVRA
251	LQRTVPAAVP	AIVFLSGGQS	EEEATRNLNA	MNQLKTKKPW	SLSFSFGRAL
301	QQSTLKTWAG	KEENVK AAQE	ALYVRCKANS	EATLGTYKGD	AKLGDGAAES
351	LHVKDYKY				

25 - 38 666.7997 1331.5848 1331	6933 -0.1084 0	K.GILAADESTGTIGK.R (Ions score 69)
88 - 94 424.2744 846.5343 846	0.5215 0.0128 0	K.LFVDILK.E (Ions score 34)
277 - 285 531.2674 1060.5202 1060	0.5335 -0.0133 0	R.NLNAMNQLK.T Oxidation (M) (Ions score 34)
317 - 325 511.2316 1020.4487 1019	0.5400 0.9087 0	K.AAQEALYVR.C (Ions score 51)
328 - 338 577.7809 1153.5472 1153	3.5615	K.ANSEATLGTYK.G (Ions score 52)

gi|15219721 Malate dehydrogenase, cytosolic, putative

Protein View

Match to: gi|15219721 Score: 246 malate dehydrogenase, cytosolic, putative [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\E4 1795.wiff

Nominal mass (M_r): 35890; Calculated pI value: 6.11 NCBI BLAST search of <u>gi|15219721</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|11133509</u> from <u>Arabidopsis thaliana</u> <u>gi|2341034</u> from <u>Arabidopsis thaliana</u> <u>gi|15215692</u> from <u>Arabidopsis thaliana</u> <u>gi|20148469</u> from <u>Arabidopsis thaliana</u> <u>gi|21593602</u> from <u>Arabidopsis thaliana</u> <u>gi|22137280</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%
```

Matched peptides shown in Bold Red

1MAKEPVRVLVTGAAGQIGYALVPMIARGIMLGADQPVILHMLDIPPAAEA51LNGVKMELIDAAFPLLKGVVATTDAVEGCTGVNVAVMVGGFPRKEGMERK101DVMSKNVSIYKSQAAALEKHAAPNCKVLVVANPANTNALILKEFAPSIPE151KNISCLTRLDHNRALGQISERLSVPVSDVKNVIIWGNHSSSQYPDVNHAK201VQTSSGEKPVRELVKDDAWLDGEFISTVQQRGAAIIKARKLSSALSAASS251ACDHIRDWVLGTPEGTFVSMGVYSDGSYSVPSGLIYSFPVTCRNGDWSIV301QGLPIDEVSRKKMDLTAEELKEEKDLAYSCLS

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
56	-	67	688.9003	1375.7860	1375.7421	0.0439	0	K.MELIDAAFPLLK.G Oxidation (M) (Ions score 73)
127	-	142	825.5131	1649.0117	1648.9876	0.0241	0	K.VLVVANPANTNALILK.E (Ions score 14)
127	-	142	550.7232	1649.1476	1648.9876	0.1601	0	K.VLVVANPANTNALILK.E (Ions score 40)
143	-	151	509.3646	1016.7147	1016.5178	0.1969	0	K.EFAPSIPEK.N (Ions score 27)
164	-	171	437.2560	872.4974	872.4716	0.0258	0	R.ALGQISER.L (Ions score 63)
172	-	180	472.3175	942.6205	942.5386	0.0819	0	R.LSVPVSDVK.N (Ions score 44)

gi|18391442 De-etiolated 3 (DET3)

Protein View

Match to: gi|18391442 Score: 137
DET3 (DE-ETIOLATED 3) [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B4 1571.wiff

Nominal mass (M_r) : 42878; Calculated pI value: 5.40 NCBI BLAST search of <u>gi|18391442</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|12585488</u> from <u>Arabidopsis thaliana</u> <u>gi|6636332</u> from <u>Arabidopsis thaliana</u> <u>gi|12248023</u> from <u>Arabidopsis thaliana</u> <u>gi|16649005</u> from <u>Arabidopsis thaliana</u> <u>gi|20259972</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%
```

Matched peptides shown in Bold Red

MTSRYWVVSL PVKDSASSLW NRLQEQISKH SFDTPVYRFN IPNLRVGTLD
 SLLALGDDLL KSNSFVEGVS QKIRRQIEEL ERISGVESNA LTVDGVPVDS
 YLTRFVWDEA KYPTMSPLKE VVDNIQSQVA KIEDDLKVRV AEYNNIRGQL
 NAINRKQSGS LAVRDLSNLV KPEDIVESEH LVTLLAVVPK YSQKDWLACY
 ETLTDYVVPR SSKKLFEDNE YALYTVTLFT RVADNFRIAA REKGFQVRDF
 EQSVEAQETR KQELAKLVQD QESLRSSLLQ WCYTSYGEVF SSWMHFCAVR
 TFAESIMRYG LPPAFLACVL SPAVKSEKKV RSILERLCDS TNSLYWKSEE
 DAGAMAGLAG DSETHPYVSF TINLA

start	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	s Sequence	
5	-	13	545.8074	1089.6003	1089.6223	-0.0219	0	R.YWVVSLPVK.D (Ions score 40)	
39	-	45	437.3059	872.5973	872.4868	0.1105	0	R.FNIPNLR.V (Ions score 37)	
112	-	119	476.7618	951.5091	951.4735	0.0355	0	K.YPTMSPLK.E Oxidation (M) (Ions score 13)
148	-	155	443.3184	884.6223	884.4828	0.1395	0	R.GQLNAINR.K (Ions score 48)	

gi|81621 Glyceraldehyde-3-phosphate dehydrogenase (NADP) B precursor

Protein View

Match to: gi 81621 Score: 220 glyceraldehyde-3-phosphate dehydrogenase (NADP) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B6 1581.wiff

Nominal mass (M_r) : 43168; Calculated pI value: 5.60 NCBI BLAST search of <u>gi|81621</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|336390</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 11%

1	MSSIGGEASF	FDAVAAQIIP	KAVTTSTPVR	GETVAKLKVA	INGFGRIGRN
51	FLRCWHGRKD	SPLEVVVLND	SGGVKNASHL	LKYDSMLGTF	KAEVK IVDNE
101	TISVDGKLIK	VVSNRDPLKL	PWAELGIDIV	IEGTGVFVDG	PGAGKHIQAG
151	ASKVIITAPA	KGADIPTYVM	GVNEQDYGHD	VANIISNASC	TTNCLAPFAK
201	VLDEEFGIVK	GTMTTTHSYT	GDQRLLDASH	RDLRRARAAA	${\bf LNIVPTSTGA}$
251	AKAVSLVLPQ	LK GKLNGIAL	RVPTPNVSVV	DLVINVEKKG	LTAEDVNEAF
301	RKAANGPMKG	ILDVCDAPLV	SVDFRCSDVS	TTIDSSLTMV	MGDDMVKVVA
351	WYDNEWGYSQ	RVVDLAHLVA	SKWPGAEAVG	SGDPLEDFCK	TNPADEECKV
401	YD				

\mathtt{Start}	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
96	-	107	645.3390	1288.6634	1288.6511	0.0124	0	K.IVDNETISVDGK.L (Ions score 95)
201	-	210	574.8050	1147.5954	1147.6125	-0.0170	0	K.VLDEEFGIVK.G (Ions score 52)
238	-	252	692.8460	1383.6774	1383.7722	-0.0947	0	R.AAALNIVPTSTGAAK.A (Ions score 35)
253	-	262	534.3020	1066.5894	1066.6750	-0.0856	0	K.AVSLVLPQLK.G (Ions score 38)

gi|14334740 Putative fructose bisphosphate aldolase

Protein View

Match to: gi|14334740 Score: 93 putative fructose bisphosphate aldolase [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D11 1762.wiff

Nominal mass (M_r) : 43033; Calculated pI value: 6.48 NCBI BLAST search of <u>gi|14334740</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

1	MASSTATMLK	ASPVKSDWVK	GQSLLLRQPS	SVSAIRSHVA	PSALTVRAAS
51	AYADELVKTA	KTIASPGHGI	MAMDESNATC	GKRLASIGLE	NTEANRQAYR
101	TLLVSAPGLG	QYISGAILFE	ETLYQSTTDG	KKMVDVLVEQ	NIVPGIKVDK
151	GLVPLVGSYD	ESWCQGLDGL	ASRTAAYYQQ	GARFAKWRTV	VSIPNGPSAL
201	AVKEAAWGLA	RYAAISQDSG	LVPIVEPEIM	LDGEHSIDRT	YDVAEKVWAE
251	VFFYLAQNNV	MFEGILLKPS	MVTPGAEATD	RATPEQVASY	TLK LLRNRIP
301	PAVPGIMFLS	GGQSGLEATL	NLNAMNQAPN	PWHVSFSYAR	ALQNTCLKTW
351	GGKEENVKAA	QDILLARAK <mark>A</mark>	NSLAQLGKYT	GEGESEEAKE	GMFVKGYTY

Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence	
282 - 293	654.3682	1306.7218	1306.6769	0.0449	0	R.ATPEQVASYTLK.L	(Ions score 45)
370 - 378	451.2774	900.5402	900.5029	0.0374	0	K.ANSLAQLGK.Y (]	lons score 48)

gi|15230595 Phosphoglycerate kinase 1 (PGK1)

Protein View

Match to: gi|15230595 Score: 142 PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B1 1546.wiff

Nominal mass (M_r) : 50195; Calculated pI value: 5.91 NCBI BLAST search of <u>qi|15230595</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
```

Matched peptides shown in Bold Red

1	MASAAASSAF	SLLKSTGAVA	SSAGTRARAS	LLPIPSTSVS	ARPLGFSATL
51	DSRRFSLHVA	SKVESVRGKG	SRGVVSMAKK	${\bf SVGDLTSADL}$	KGKKVFVRAD
101	LNVPLDDNQT	ITDDTRIRAA	IPTIKYLIEN	GAKVILSTHL	GRPKGVTPKF
151	SLAPLVPRLS	ELLGIEVTKA	DDCIGPEVES	LVASLPEGGV	LLLENVRFYK
201	EEEKNDPEFA	KKLASLADLY	VNDAFGTAHR	AHASTEGVTK	FLKPSVAGFL
251	LQKELDYLVG	AVSNPKRPFA	AIVGGSKVSS	KIGVIESLLE	KCDILLLGGG
301	MIFTFYKAQG	LSVGSSLVEE	DKLELATELL	AKAKAKGVSL	LLPTDVVVAD
351	KFAPDANSKI	VPASGIEDGW	MGLDIGPDSI	KTFNEALDTT	QTVIWNGPMG
401	VFEMEKFAAG	TEAIANKLAE	LSEKGVTTII	GGGDSVAAVE	K VGVAGVMSH
451	ISTGGGASLE	LLEGKVLPGV	IALDEAIPVT	v	

Show predicted peptides also

Or the Destidant Des

Soft Peptides By	Resid	ue Number	Increasing Mass	Decrea	asing M	ass
Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
81 - 91	553.3099	1104.6052	1104.5663	0.0389	0	K.SVGDLTSADLK.G (Ions score 49)
150 - 158	500.3133	998.6121	998.5913	0.0208	0	K.FSLAPLVPR.L (Ions score 46)
425 - 441	787.3732	1572.7319	1572.8359	-0.1040	0	K.GVTTIIGGGDSVAAVEK.V (Ions score 49)

gi|15240075 Succinate dehydrogenase 1-1 (SDH1-1)

Protein View

```
Match to: gi|15240075 Score: 192
SDH1-1 (Succinate dehydrogenase 1-1) [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\C4 794.wiff
```

Nominal mass (M_r) : 70240; Calculated pI value: 5.86 NCBI BLAST search of <u>gi|15240075</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

Residue Number Increasing Mass Decreasing Mass

Matched peptides shown in Bold Red

1	MWRCVSRGFR	APASKTSSLF	DGVSGSRFSR	FFSTGSTDTR	SSYTIVDHTY
51	DAVVVGAGGA	GLRAAIGLSE	HGFNTACITK	LFPTRSHTVA	AQGGINAALG
101	NMSEDDWRWH	MYDTVKGSDW	LGDQDAIQYM	CREAPKAVIE	LENYGLPFSR
151	TEEGKIYQRA	FGGQSLDFGK	GGQAYRCACA	ADRTGHALLH	TLYGQAMKHN
201	TQFFVEYFAL	DLLMASDGSC	QGVIALNMED	GTLHRFRSSQ	TILATGGYGR
251	AYFSATSAHT	CTGDGNAMVA	RAGLPLQDLE	FVQFHPTGIY	GAGCLITEGS
301	RGEGGILRNS	EGERFMERYA	PTAKDLASRD	VVSRSMTMEI	REGRGVGPHK
351	DHIYLHLNHL	PPEVLKERLP	GISETAAIFA	GVDVTKEPIP	VLPTVHYNMG
401	GIPTNYHGEV	VTIKGDDPDA	VIPGLMAAGE	AACASVHGAN	RLGANSLLDI
451	VVFGR ACANR	VAEISKPGEK	QKPLEKDAGE	KTIAWLDRLR	NSNGSLPTST
501	IRLNMQR IMQ	NNAAVFRTQE	TLEEGCQLID	KAWESFGDVQ	VKDRSMIWNS
551	DLIETLELEN	LLINASITMH	SAEARKESRG	AHAREDFTKR	EDGEWMKHTL
601	GYWEDEKVRL	DYRPVHMDTL	DDEIDTFPPK	ARVY	

Show predicted peptides also

Sort Peptides By

Start - End Observ	ved Mr(expt)	Mr(calc)	Delta	Miss	Sequence
160 - 170 563.79	65 1125.5785	1125.5455	0.0330	0	R.AFGGQSLDFGK.G (Ions score 51)
442 - 455 737.43	23 1472.8500	1472.8351	0.0149	0	R.LGANSLLDIVVFGR.A (Ions score 86)
508 - 517 590.31	.35 1178.6125	1178.5866	0.0259	0	R.IMQNNAAVFR.T Oxidation (M) (Ions score 56)

gi|3256066 Chloroplast NAD-dependent malate dehydrogenase

Protein View

Match to: gi|3256066 Score: 164 chloroplast NAD-MDH [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\H12 2051.wiff

Nominal mass (M_r): 42623; Calculated pI value: 8.48 NCBI BLAST search of <u>gi|3256066</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 10%
```

1	MATATSASLI	STVSSSYSKA	SSIPHSRLQS	VKFNSVPSFT	GLKSTSLISG		
51	SDSSSLTKTI	RGSVTNAQTS	DKKPYGFKIN	ASYKVAVLGA	AGGIGQPLSL		
101	LIKMSPLVS	LHLYDIANVK	GVAADLSHCN	TPSQVRDFTG	PSELADCLKD		
151	VNVVVIPAG	PRKPGMTRDD	LFNINANIVK	TLVEAVAENC	PNAFIHIISN		
201	PVNSTVPIA	A EVLKKKGVYD	PKKLFGVTTL	DVVRANTFVS	QKKNLKLIDV		
251	DVPVIGGHAG	; ITILPLLSKT	KPSVNFTDEE	IQELTVR <mark>IQN</mark>	AGTEVVDAKA		
301	GAGSATLSMA	YAAARFVESS	LRALDGDGDV	YECSFVESTL	TDLPFFASRV		
351	KIGKNGLEAV	/ IESDLQGLTE	YEQKALEALK	VELKASIDKG	VAFANKPAAA		
401	AAN						
Start -	- End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
150 ·	- 162	667.8972 1	.333.7799	1333.7718	0.0081	0	K.DVNVVVIPAGVPR.K (Ions score 50)
224 -	- 234	610.3568 1	218.6990	1218.6972	0.0017	0	K.LFGVTTLDVVR.A (Ions score 22)
288 -	- 299	622.7974 1	243.5803	1243.6408	-0.0605	0	R.IQNAGTEVVDAK.A (Ions score 51)
316 -	- 322	419.2391	836.4636	836.4392	0.0244	0	R.FVESSLR.A (Ions score 40)

gi|7769871 F12M16.14

Protein View

Match to: gi|7769871 Score: 86 F12M16.14 [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\2016.wiff

Nominal mass (M_r) : 37197; Calculated pI value: 8.54 NCBI BLAST search of <u>gi|7769871</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
```

```
1MFRSMLVRSS ASAKQAVIRR SFSSGSVPER KVAILGAAGG IGQPLALLMK51LNPLVSSLSL YDIANTPGVA ADVGHINTRSEVVGYMGDDNLAKALEGADL101VIIPAGVPRK PGMTRDDLFN INAGIVKNLCTAIAKYCPHA LINMISNPVN151STVPIAAEIF KKAGMYDEKKLFGVTTLDVVRARTFYAGKA NVPVAEVNVP201VIGGHAGVTILPLFSQVSSHFLSTQTVATPQANLSSDILT251TEVVEAKAGKGSATLSMAYAGALFADACLKGLNGVPDVIECSYVQSTITE301LPFFASKVRLGKNGVEEVLDLGPLSDFEKEGLEALKPELKSSIEKGVKFA351NQ
```

Start -	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
80 -	93	757.7786	1513.5427	1512.6766	0.8661	0	R.SEVVGYMGDDNLAK.A Oxidation (M) (Ions score 40)
171 -	181	610.3155	1218.6164	1218.6972	-0.0809	0	K.LFGVTTLDVVR.A (Ions score 47)

gi|904041 Adenosine triphosphatase

Protein View

Match to: gi|904041 Score: 130 adenosine triphosphatase Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\F4 1223.wiff

Nominal mass (M_r) : 53930; Calculated pI value: 5.05 NCBI BLAST search of <u>gi|904041</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Akebia quinata

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%
```

1	XXXXXXXXXXX	XXXXXXXXXXX	XXIAQIIGPV	LDVAFPPGKM	PNIYNALVVK
51	GRDTVDQQIN	VTCEVQQLLG	NNRVRAVAMS	ATDGLMRGMK	VIDTGAPLSV
101	PVGGATLGRI	FNVLGEPVDN	LXXXXXXTXS	PMHRSAPAFI	QLDTKLSIFE
151	TGIKVVDLLA	PYR RGGKIGL	FGGAGVGKTV	LIMELINNIA	KAHGGVSVFG
201	GVGERTREGN	DLYMEMKESG	VINEQNIPES	KVALVYGQMN	EPPGAR MRVG
251	LTALTMAEYF	RDVNEQDVLL	FIDNIFRFVQ	AGSEVSALLG	RXXSAVGYQP
301	TLSTEMGSLQ	ERITSTKEGS	ITSIQAVYVP	ADDLTDPAPA	TTFAHLDATT
351	VLSRGLAAKG	IYPAVDPLDS	TSTMLQPRIV	GEEHYETAQR	VKQTSQRYKE
401	LQDIIAILGL	DELSEDDRLT	VARARKIERF	LSQPFFVAEV	FTGSPGKYVG
451	LTETIRGFQL	ILSGELDGLP	EQAFYLVGNI	DEATAKAMNL	EVESNLKK

start	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
40	-	50	639.3996	1276.7847	1276.6849	0.0998	0	K.MPNIYNALVVK.G Oxidation (M) (Ions score 50)
155	-	163	523.3224	1044.6303	1044.5968	0.0335	0	K.VVDLLAPYR.R (Ions score 30)
168	-	178	488.3454	974.6762	974.5549	0.1213	0	K.IGLFGGAGVGK.T (Ions score 36)
232	-	246	809.3937	1616.7728	1616.7981	-0.0253	0	K.VALVYGQMNEPPGAR.M Oxidation (M) (Ions score 15)
gi|14423528 Putative fructokinase

Protein View

Match to: gi|14423528 Score: 123 putative fructokinase [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1913.wiff

Nominal mass (M_r) : 35405; Calculated pI value: 5.30 NCBI BLAST search of <u>gi|14423528</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: gi[22136070 from Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 10%
```

1	MASNGDKGLI	VSFGEMLIDF	VPTESGVSLA	EAPGFLK <mark>APG</mark>	GAPANVAIAV
51	SR LGGRSAFV	GKLGDDEFGH	MLAGILRKNG	VDDQGINFDT	GARTALAFVT
101	LRADGDREFM	FYHNPSADML	LRPDELNLDL	IRSAKVFHYG	SISLIVEPCR
151	SAHLKAMEVA	KEAGALLSYD	PNLREPLWPS	KEEAK TQIMS	IWDK AEIIKV
201	SDVELEFLTG	SNKIDDETAL	TLWHPNLKLL	LVTLGEKGCR	YYTKTFKGAV
251	DPFHVNAVDT	TGAGDSFVGA	LLNQIVDDRS	VLEDEERLRK	VLRFANACGA
301	ITTTKKGAIP	ALPSDAEVRS	FLEKK		

Start	-	End	C	bserved	Mr (expt)	Mr(calc)	Delta	Miss	Sequence						
38	-	52	6	575.8471	1349.6796	1349.7415	-0.0620	0	K.APGGAPANVAIA	VSR.L	(<u>Ion</u>	s sc	ore 34	<u>4</u>)	
186	-	194	5	69.2463	1136.4780	1136.5536	-0.0756	0	K.TQIMSIWDK.A	Oxidat	tion	(M)	(Ions	score	<u> 29</u>)
229	-	237	4	93.2918	984.5691	984.6219	-0.0528	0	K.LLLVTLGEK.G	(Ions	scor	e 60)		

gi|693690 Aspartate aminotransferase

Protein View

Match to: gi|693690 Score: 114 aspartate aminotransferase Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B6 1581.wiff

Nominal mass (M_r) : 44497; Calculated pI value: 6.80 NCBI BLAST search of <u>qi|693690</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

```
1 MDSVFSNVAR APEDPILGVT VAYNNDPSPV KINLGVGAYR TEEGKPLVLD
51 VVRKAEQQLV NDPSRVKEYI PIVGISDFNK LSAKLILGAD SPAITESRVT
101 TVQCLSGTGS LRVGAEFLKT HYHQSVIYIP KPTWGNHPKV FNLAGLSVEY
151 FRYYDPATRG LDFKGLLEDL GAAPSGAIVL LHACAHNPTG VDPTSEQWEQ
201 IRQLMRSKSL LPFFDSAYQG FASGSLDTDA QSVRTFVADG GECLIAQSYT
251 KNMGLYGERV GALSIVCKSA DVASKVESQV KLVVRPMYSS PPIHGASIVA
301 TILKSSDMYN NWTIELKEMA DRIKSMRQQL FEAIQARGTP GDWSHIIKQI
351 GMFTFTGLNK EQVEFMTKEF HIYMTSDGRI SMAGLSSKTV PHLADAMHAA
401 VTRLG
```

Start	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
32	-	40	481.7991	961.5837	961.5345	0.0492	0	K.INLGVGAYR.T (Ions score 62)
153	_	159	443.2554	884.4963	884.4028	0.0935	0	R.YYDPATR.G (Ions score 18)
252	_	259	478.2617	954.5089	954.4229	0.0860	0	K.NMGLYGER.V Oxidation (M) (Ions score 34)

gi|6966930 Glutamine synthetase

Protein View

```
Match to: gi|6966930 Score: 83
glutamine synthetase [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff
Nominal mass (M<sub>r</sub>): 47889; Calculated pI value: 6.37
NCBI BLAST search of <u>gi|6966930</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
Taxonomy: <u>Brassica napus</u>
Fixed modifications: Carbamidomethyl (C)
```

```
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

1	MAQILAASPT	CQMRLTKPSS	IASSKLWNSV	VLKQKKQSSS	KVRSFKVMAI
51	QSDNSTINRV	ESLLNLDTKP	FTDRIIAEYI	WYGGSGIDLR	SKSRTLEKPV
101	EDPSELPKWN	YDGSSTGQAP	GEDSEVILYP	QAIFRDPFRG	GNNILVICDT
151	YTPAGEPIPT	NKRAR AAEIF	SNK KVNEEIP	WFGIEQEYTL	LQPNVNWPLG
201	WPVGAYPGPQ	GPYYCGVGAE	KSWGRDISDA	HYKACLYAGI	NISGTNGEVM
251	PGQWEFQVGP	SVRIEAGDHV	WCARYLLERI	TEQAGVVLTL	DPKPIEGDWN
301	GAGCHTNYST	KSMREDGGFE	VIKKAILNLS	LRHMEHIIAY	GEGNERRLTG
351	KHETASIDQF	SWGVANRGCS	IRVGRDTEKK	GKGYLEDRRP	ASNMDPYIVT
401	SLLAETTLLW	EPTLEAEALA	AQKLSLKV		

Start -	- End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence				
95 -	- 108	528.0324	1581.0752	1580.8297	0.2455	0	R.TLEKPVEDPSEI	LPK.W	(Ions	score	<u>51</u>)
166 -	- 173	440.2458	878.4771	878.4498	0.0274	0	R.AAEIFSNK.K	(Ions	score	32)	

gi|1070000 Biotin carboxyl carrier protein

Protein View

Match to: gi|1070000 Score: 74 biotin carboxyl carrier protein [Brassica napus] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\A8 2106.wiff

Nominal mass (M_r) : 20791; Calculated pI value: 4.60 NCBI BLAST search of <u>gi|1070000</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Brassica napus</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|1589040</u> from <u>Brassica napus</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 12%

Matched peptides shown in Bold Red

1 SEGKDENSSK DPSSSTDLAT EESISEFLTQ VTTLVKLVDS RDIVELQLKQ 51 LDCELVIRKK EALPOPESPA QYVMMQOPNQ SSYVQSVAPP SAPAASPAPS

- 101 TPASSPTHLH YSSYSSLPTV KSPMAGTFYR SPGPGEPPFI KVGDKVQKGQ
- 151 VLCIVEAMKL MNEIESDNGT VVDIVAEMQP VSLDTPLFVV QP

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
37 - 49	509.9990	1526.9753	1526.8668	0.1085	1	K.LVDSRDIVELQLK.Q	(Ions score 31)
131 - 141	563.3258	1124.6370	1124.5866	0.0504	0	R.SPGPGEPPFIK.V (Ions score 43)

gi|15228194 Sedoheptulose bisphosphatase (SBPASE)

Protein View

Match to: gi | 15228194 Score: 208

```
SBPASE (sedoheptulose-bisphosphatase); phosphoric ester hydrolase [Arabidopsis thaliana]
    Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D12 1767.wiff
    Nominal mass (Mr): 42787; Calculated pI value: 6.17
    NCBI BLAST search of gi|15228194 against nr
    Unformatted sequence string for pasting into other applications
    Taxonomy: Arabidopsis thaliana
    Links to retrieve other entries containing this sequence from NCBI Entrez:
    gi|1173345 from Arabidopsis thaliana
    gi 786466 from Arabidopsis thaliana
    gi | 7263568 from Arabidopsis thaliana
    Fixed modifications: Carbamidomethyl (C)
    Variable modifications: Oxidation (M), CyDye-Cy3 (C), CyDye-Cy5 (C), Oxidation (C)
    Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
    Sequence Coverage: 13%
    Matched peptides shown in Bold Red
         1 METSIACYSR GILPPSVSSQ RSSTLVSPPS YSTSSSFKRL KSSSIFGDSL
        51 RLAPKSOLKA TKAKSNGAST VTKCEIGOSL EEFLAOATPD KGLRTLLMCM
       101 GEALRTIAFK VRTASCGGTA CVNSFGDEQL AVDMLADKLL FEALQYSHVC
       151 KYACSEEVPE LQDMGGPVEG GFSVAFDPLD GSSIVDTNFT VGTIFGVWPG
       201 DKLTGITGGD QVAAAMGIYG PRTTYVLAVK GFPGTHEFLL LDEGKWQHVK
       251 ETTEIAEGKM FSPGNLRATF DNSEYSKLID YYVKEKYTLR YTGGMVPDVN
       301 QIIVKEKGIF TNVTSPTAKA KLRLLFEVAP LGLLIENAGG FSSDGHKSVL
       351 DKTIINLDDR TQVAYGSKNE IIRFEETLYG TSRLKNVPIG VTA
Start - End
                Observed
                            Mr(expt)
                                        Mr(calc)
                                                     Delta
                                                              Miss Sequence
  223 - 230
                447.7505
                           893.4865
                                       893.5222
                                                   -0.0357
                                                                0 R.TTYVLAVK.G (Ions score 27)
                                       936.4487
                                                                0 K.MFSPGNLR.A Oxidation (M) (Ions score 24)
  260 - 267
                469.2111 936.4077
                                                   -0.0410
  268 - 277
                581.2725 1160.5304 1160.4986
                                                   0.0319
                                                                0 R.ATFDNSEYSK.L (Ions score 24)
  278 - 284
                457.2706 912.5266 912.4957
                                                   0.0309
                                                                0 K.LIDYYVK.E (Ions score 28)
  308 - 319
                618.3155 1234.6164 1234.6558
                                                   -0.0393
                                                                0
                                                                   K.GIFTNVTSPTAK.A (Ions score 58)
  374 - 383
                601.8135 1201.6124 1201.5615
                                                   0.0509
                                                                0 R.FEETLYGTSR.L (Ions score 48)
```

gi|1143445 Cinnamyl alcohol dehydrogenase

Protein View

Match to: gi|1143445 Score: 56 cinnamyl alcohol dehydrogenase [Eucalyptus gunnii] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D12 1767.wiff

Nominal mass (M_r) : 36053; Calculated pI value: 8.15 NCBI BLAST search of <u>gi|1143445</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Eucalyptus gunnii

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 2%

1	MSAAGGAGKV	VCVTGASRYI	ASWLVKLLLQ	RGYTVKASVR	DPNDPKKTEH
51	LLGLDGAKDR	LQLFKANLLE	EGSFDPIVEG	CAGVFHTASP	FYHDVKDPQA
101	ELLDPAVKGT	LNVLKSCSKA	PSLQRVVLTS	SMAAVAYNRQ	PRTPEVVVDE
151	SWFSDPDLCR	QTNAWYVLSK	TLAEDAAWKF	VKEKGIDMVT	INPAMVIGPL
201	LQPTLNTSAA	AIGNLINGAP	TFPNASFGWV	NVKDVANAHI	LAFEVPSASG
251	RYCLVERIAH	YSEIVRILRE	LYPSAQLPEK	SADDKPFVPI	YQVSKEKVKS
301	LGINYIPLEQ	NLKETVESLK	EKGFVKF		

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
171 - 179	502.7760	1003.5374	1003.4974	0.0400	0	K.TLAEDAAWK.F	(Ions score 56)

MS/MS Fragmentation of TLAEDAAWK

Found in gi 1143445, cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	Τ							9
2	215.1390	108.0731	197.1285	99.0679	L	903.4571	452.2322	886.4305	443.7189	885.4465	443.2269	8
3	286.1761	143.5917	268.1656	134.5864	Α	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	7
4	415.2187	208.1130	397.2082	199.1077	E	719.3359	360.1716	702.3093	351.6583	701.3253	351.1663	6
5	530.2457	265.6265	512.2351	256.6212	D	590.2933	295.6503	573.2667	287.1370	572.2827	286.6450	5
6	601.2828	301.1450	583.2722	292.1397	Α	475.2663	238.1368	458.2398	229.6235			4
7	672.3199	336.6636	654.3093	327.6583	Α	404.2292	202.6183	387.2027	194.1050			3
8	858.3992	429.7032	840.3886	420.6980	W	333.1921	167.0997	316.1656	158.5864			2
9					K	147.1128	74.0600	130.0863	65.5468			1

gi|15232763 Adenosine kinase 1 (ADK1)

Protein View

Match to: gi|15232763 Score: 59 ADK1 (ADENOSINE KINASE 1) [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D11 1762.wiff

Nominal mass (M_r) : 38268; Calculated pI value: 5.29 NCBI BLAST search of <u>qi|15232763</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|17367081</u> from <u>Arabidopsis thaliana</u> <u>gi|6681336</u> from <u>Arabidopsis thaliana</u> <u>gi|12017762</u> from <u>Arabidopsis thaliana</u> <u>gi|12017766</u> from <u>Arabidopsis thaliana</u> <u>gi|14030721</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%
```

1	MASSDFDGIL	LGMGNPLLDV	SAVVDQQFLD	KYDIK LNNAI	LAEDKHLPMY
51	DEMSQKFNVE	YIAGGATQNS	IKVAQWMLQV	PGATSYMGSI	GKDKYGEAMK
101	KDATAAGVYV	HYYEDEATPT	GTCGVCVLGG	ERSLIANLSA	ANCYKVEHLK
151	KPENWALVEK	AKFYYIAGFF	LTVSPESIQL	VREHAAANNK	VFTMNLSAPF
201	ICEFFKDVQE	KCLPYMDYIF	GNETEARTFS	RVHGWETDDV	EQIAIKMSQL
251	PKASGTYKRT	TVITQGADPV	VVAEDGKVKK	YPVIPLPKEK	LVDTNGAGDA
301	FVGGFLSQLV	HGKGIEECVR	AGCYASNVVI	QRSGCTYPEK	PDFN

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
36 - 45	550.7933	1099.5721	1099.5873	-0.0152	0	K.LNNAILAEDK.H	(Ions score 59)

MS/MS Fragmentation of LNNAILAEDK Found in gi|15232763, ADK1 (ADENOSINE KINASE 1) [Arabidopsis thaliana]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	228.1343	114.5708	211.10 77	106.0575			N	987.5106	494.2589	970.4840	485.7456	969.5000	485.2536	9
3	342.1772	171.5922	325.1506	163.0790			N	873.4676	437.2374	856.4411	428.7242	855.4571	428.2322	8
4	413.2143	207.1108	396.1878	198.5975			Α	7 59.424 7	380.2160	742.3981	371.7027	741.4141	371.2107	7
5	526.2984	263.6528	509.2718	255.1395			Ι	688.3876	344.6974	671.3610	336.1842	670.3770	335.6921	6
6	639.3824	320.1949	622.3559	311.6816			L	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
7	710.4196	355.7134	693.3930	347.2001			Α	462.2195	231.6134	445.1929	223.1001	444.2089	222.6081	4
8	839.4621	420.2347	822.4356	411.7214	821.4516	411.2294	E	391.1823	196.0948	374.1558	187.5815	373.1718	187.0895	3
9	954.4891	477.7482	937.4625	469.2349	936.4785	468.7429	D	262.139 7	131.5735	245.1132	123.0602	244.1292	122.5682	2
10							K	147.1128	74.0600	130.0863	65.5468			1

gi|1827677 Enoyl reductase

Protein View

228 - 239

```
Match to: gi | 1827677 Score: 66
      Chain , Brassica Napus Enoyl Acp ReductaseNADH BINARY COMPLEX AT Ph 8.0 And Room Temperature
      Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\G10 1989.wiff
     Nominal mass (Mr): 32983; Calculated pI value: 5.24
     NCBI BLAST search of gi 1827677 against nr
     Unformatted sequence string for pasting into other applications
     Taxonomy: Brassica napus
     Links to retrieve other entries containing this sequence from NCBI Entrez:
      gi|1827678 from Brassica napus
      Fixed modifications: Carbamidomethyl (C)
     Variable modifications: Oxidation (M), CyDye-Cy3 (C), CyDye-Cy5 (C), Oxidation (C)
     Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
      Sequence Coverage: 7%
     Matched peptides shown in Bold Red
          1 SESSESKASS GLPIDLRGKR AFIAGIADDN GYGWAVAKSL AAAGAEILVG
          51 TWVPALNIFE TSLRRGKFDQ SRVLPDGSLM EIKKVYPLDA VFDNPEDVPE
        101 DVKANKRYAG SSNWTVQEAA ECVRQDFGSI DILVHSLANG PEVSKPLLET
        151 SRKGYLAAIS ASSYSFVSLL SHFLPIMNPG GASISLTYIA SERIIPGYGG
         201 GMSSAKAALE SDTRVLAFEA GRKONIRVNT ISAGPLGSRA AKAIGFIDTM
         251 IEYSYNNAPI QKTLTADEVG NAAAFLVSPL ASAITGATIY VDNGLNSMGV
         301 ALDSPVFKDL DK
Start - End
               Observed
                           Mr(expt) Mr(calc)
                                                   Delta
                                                           Miss Sequence
  73 - 83 609.3338 1216.6531 1216.6373
                                                  0.0158
                                                             0 R.VLPDGSLMEIK.K Oxidation (M) (Ions score 16)
```

0 R.VNTISAGPLGSR.A (Ions score 49)

586.3465 1170.6785 1170.6357 0.0429

gi|18406430 Dihydrodipicolinate reductase family protein

Protein View

Match to: gi|18406430 Score: 70 dihydrodipicolinate reductase family protein [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1913.wiff

Nominal mass (M_r): 37754; Calculated pI value: 6.02 NCBI BLAST search of <u>gi|18406430</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|20197071</u> from <u>Arabidopsis thaliana</u> <u>gi|21536558</u> from <u>Arabidopsis thaliana</u> <u>gi|26452703</u> from <u>Arabidopsis thaliana</u> <u>gi|30793829</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

1	MATNGLMASS	SVFLHRPRIA	FASRTNQTVG	KYGKGRVSFM	GIGTRRLPVV
51	LSMTAMADSG	EEAVKSVLPG	NGISIMVNGC	SGKMGKAVIK	AADSAGVNIV
101	PISFGSAGED	GQRVEVCGKE	ITVHGPTERE	KVLSSVFEKH	PELIVVDYTI
151	PSAVNDNAEL	YSKVGVPFVM	GTTGGDRNKL	YETVEEAKIY	AVISPQMGKQ
201	VVAFLAAMEI	MAEQFPGAFS	GYSLDVMESH	QASKLDASGT	AKAVISCFQE
251	LGVSYDMDQI	QLIRDPKQQV	EMVGVPEEHI	SGHAFHLYHL	TSPDETVSFE
301	FOHNVCGRSI	YAEGTVDAVL	FLAKKIRLKA	DORIYNMIDV	LREGNMR

Start	- End	Observed	Mr(expt)	Mr(calc)	Delta Miss	Sequence
189	- 199	611.7644	1221.5142	1221.6427	-0.1285 0	K.IYAVISPQMGK.Q Oxidation (M) (Ions score 25)
334	- 342	576.7735	1151.5325	1151.6009	-0.0684 0	R.IYNMIDVLR.E Oxidation (M) (<u>Ions score 45</u>)

gi|2494843 Putative lactoylglutathione lyase (Methylglyoxalase)

Protein View

```
Match to: gi|2494843 Score: 58
   Putative lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase)
   Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\A10 2111.wiff
   Nominal mass (Mr): 31740; Calculated pI value: 5.19
   NCBI BLAST search of gi|2494843 against nr
   Unformatted sequence string for pasting into other applications
   Taxonomy: Brassica oleracea var. gemmifera
   Links to retrieve other entries containing this sequence from NCBI Entrez:
   gi|1469221 from Brassica oleracea var. gemmifera
   Fixed modifications: Carbamidomethyl (C)
   Variable modifications: Oxidation (M), CyDye-Cy3 (C), CyDye-Cy5 (C), Oxidation (C)
   Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
   Sequence Coverage: 7%
   Matched peptides shown in Bold Red
        1 MAENADLVEW PKKDKRRFLH VVYRVGDLDR TIQFYTECFG MKVLRKRDVP
       51 EEKYSNAFLG FGPETSNFVV ELTYNYGVSS YDIGTGFGHF AISTQDVSKM
      101 VEAVRAKGGN VTREPGPVKG GGSVIAFVKD PDGYTFELIQ RGPTPEPLCQ
      151 VMLRVGDLDR AVKFMEKALG MRLLRRIERP EYNTIGMMGY AEEYESIVLE
      201 LTYNYGVTEY TKGNAYAQIA IGTDDVYKSA EVVKIVNQEL GGKITREAGP
      251 LPGLGTKIVS FLDPDGWKQV LVDNEDFLKE LE
                   Observed Mr(expt)
                                              Mr(calc)
Start - End
                                                               Delta
                                                                         Miss Sequence
                   467.7795
                                933.5445
  120 - 129
                                              933.5284
                                                              0.0161
                                                                            0 K.GGGSVIAFVK.D
                                                                                                   (Ions score 22)
  247 - 257
                   520.2441 1038.4737 1038.5710
                                                                            0 R.EAGPLPGLGTK.I (Ions score 36)
                                                             -0.0973
```

gi|2499441 Proliferating cell nuclear antigen (PCNA)

Protein View

Match to: gi|2499441 Score: 62 Proliferating cell nuclear antigen (PCNA) Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\A8 2106.wiff

Nominal mass (M_r) : 29375; Calculated pI value: 4.61 NCBI BLAST search of <u>qi|2499441</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Brassica napus</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|408232</u> from <u>Brassica napus</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

1	MLELRLVQGS	LLKKVLESIK	DLVNDANFDC	STTGFSLQAM	DSSHVALVSL
51	LLRSEGFEHY	RCDRNLSMGM	NLGNMSKMLK	CAGNDDIITI	KADDGGDTVT
101	FMFESPKQDK	IADFEMKLMD	IDSEHLGIPD	AEYHSIVRMP	SNEFSRICKD
151	LSTIGDTVVI	SVTKEGVKFS	TAGDIGTANI	VLRQNTTVDK	PEDAIVIEMN
201	EPVSLSFALR	YMNSFTKATP	LSDTVTISLS	SELPVVVEYK	VAEMGYIRYY
251	LAPKIEEDEE	DKA			

\mathtt{Start}	-	End	 Observed	Mr	(expt)	Μ	fr(calc)	Delta	Miss	5	Sequence						
139	-	146	492.2267	982	2.4389	98	2.4178	0.0211	0		R.MPSNEFSR.I	Oxidat	tion	(M)	(Ions	score	<u>= 29</u>)
211	-	217	453.7513	905	5.4881	90	5.3953	0.0928	0		R.YMNSFTK.A	Oxidati	ion	(M)	(Ions	score	<u>33</u>)

gi|2501812 Glycolate oxidase

Protein View

Match to: gi|2501812 Score: 84 glycolate oxidase [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D11 1762.wiff

Nominal mass (M_r) : 28165; Calculated pI value: 9.52 NCBI BLAST search of <u>gi|2501812</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%
```

1	ATSSVEKIAS	TGPGIRFFQL	YVYKNRKVVE	QLVR KAEKAG	FKAIALTVNT
51	PRLGPKKSDI	KNRFTLPPNL	TLKNFEGLDL	GKMDEANDSG	LASYVAGQID
101	RTLSWKDIQW	LQTITNMPIL	VKGVLTGEDA	RIAIQAGAAG	IIVSNHGARQ
151	LDYVPATISA	LEEVVKATQG	GVPVFLDGGV	RRGTDVFKAL	ALGTSGIFIG
201	RPVVFALAAE	GEAGVKKVLQ	MLRDEFELTM	ALSGCRSISE	ITRNHIVTEW
251	DIPRHLPRL				

Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss Sequence	
28 - 34	422.2210	842.4274	841.5022	0.9253	0 K.VVEQLVR.K	(Ions score 44)
74 - 82	496.7563	991.4981	991.4975	0.0006	0 K.NFEGLDLGK.	M (Ions score 40)

gi|414550 Cytosolic triose phosphate isomerase

Protein View

196 - 206

Match to: gi|414550 Score: 118 cytosolic triose phosphate isomerase Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\C1 2227.wiff

Nominal mass (M_r): 27366; Calculated pI value: 5.24 NCBI BLAST search of <u>gi|414550</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|742408</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 12%
```

Matched peptides shown in Bold Red

552.7565 1103.4984 1103.5571

	1	MARKFFVGGN	WKCNGTAEEV	KKIVNTLNEA	QVPSQDVVEV	VVSPPYVFLP
	51	LVKSTLRSDF	FVAAQNCWVK	KGGAFTGEVS	AEMLVNLDIP	WVILGHSERR
	101	AILNESSEFV	GDKVAYALAQ	GLKVIACVGE	TLEEREAGST	MDVVAAQTKA
	151	IADRVTNWSN	VVIAYEPVWA	IGTGKVASPA	QAQEVHDELR	KWLAKNVSAD
	201	VAATTRIIYG	GSVNGGNCKE	LGGQADVDGF	LVGGASLKPE	FIDIIKAAEV
	251	NKSA				
Start -	- End	Observed	Mr(expt)	Mr(calc)	Delta Mi	ss Sequence
5 -	- 12	477.8052	953.5959	953.4760	0.1199	0 K.FFVGGNWK.C (Ions score 21)
136 -	- 149	712.3133	1422.6121	1422.6661	-0.0540	0 R.EAGSTMDVVAAQTK.A Oxidation (M) (Ions score 53)

0 K.NVSADVAATTR.I (Ions score 44)

-0.0587

gi|99805 Enoyl-[acyl-carrier-protein] reductase (NADH2) precursor

Protein View

Match to: gi|99805 Score: 67
enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9) precursor - rape
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\2016.wiff

Nominal mass (M_r) : 40633; Calculated pI value: 8.93 NCBI BLAST search of <u>gi|99805</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

1	MAATAAASSL	QMATTRPSIS	AASSKARTYV	VGANPRNAYK	IACTPHLSNL
51	GCLRNDSALP	ASKKSFSFST	KAMSESSESK	ASSGLPIDLR	GKRAFIAGIA
101	DDNGYGWAVA	KSLAAAGAEI	LVGTWVPALN	IFETSLRRGK	FDQSRVLPDG
151	SLMEIKKVYP	LDAVFDNPED	VPEDVKANKR	YAGSSNWTVQ	HAAECVRQDF
201	GSIDILVHSL	ANGPEVSKPL	LETSRKGYLA	AISASSYSFV	SLLSHFLPIM
251	NPGGASISLT	YIASERIIPG	YGGGMSSAKA	ALESDTRVLA	FEAGRKQNIR
301	VNTISAGPLG	SR AAKAIGFI	DTMIEYSYNN	APIQKTLTAD	EVGNAAAFLV
351	SPLASAITGA	TIYVDNGLNS	MGVALDSPVF	KDLNK	

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
81 - 90	514.7229	1027.4312	1027.5662	-0.1350	0	K.ASSGLPIDLR.G (1	ons score 18)
301 - 312	586.2406	1170.4666	1170.6357	-0.1691	0	R.VNTISAGPLGSR.A	(Ions score 49)

gi|780814 3-ketoacyl-acyl carrier protein synthase I

Protein View

Match to: gi|780814 Score: 52
3-ketoacyl-acyl carrier protein synthase I
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\H1 1431.wiff

Nominal mass (M_r) : 50890; Calculated pI value: 7.99 NCBI BLAST search of <u>gi|780814</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%
```

1	MQALQSSSLR	ASPPNPLRLP	SNRQSHQLIT	NARPLRRQQR	SFISASASTV
51	SAPKRETDPK	KRVVITGMGL	VSVCGNDVDA	YYEKLLSGES	GISLIDRFDA
101	SKFPTRFGGQ	IRGFSSEGYI	DGKNERRLDD	CLKYCIVAGK	KALESANLGG
151	DKLNTIDKRK	AGVLVGTGMG	GLTVFSEGVQ	NLIEKGHRRI	SPFFIPYAIT
201	NMGSALLAID	LGLMGPNYSI	STACATSNYC	FYAAANHNHR	GEADMMIAGG
251	TEAAIIPIGL	GGFVACRALS	QRNDDPQTAS	RPWDKARDGF	VMGEGAGVLV
301	MESLEHAMKR	GAPIVAEYLG	GAVNCDAHHM	TDPRADGLGV	SSCIERCLED
351	AGVSPEEVNY	INAHATSTLA	GDLAEINAIK	KVFKSTSGIK	INATKSMIGH
401	CLGAAGGLEA	IATVKAINTG	WLHPSINQFN	PEQAVDFDTV	PNEKKQHEVD
451	VAISNSFGFG	GHNSVVAFSA	FKP		

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
113 - 123	580.2990	1158.5835	1158.5193	0.0642	0	R.GFSSEGYIDGK.N (Ions score 20)
113 - 126	520.2567	1557.7483	1557.7059	0.0424	1	R.GFSSEGYIDGKNER.R (Ions score 24)

gi|1170506 Eukaryotic initiation factor 4A-2

Protein View

Match to: gi|1170506 Score: 95 Eukaryotic initiation factor 4A-2 (ATP-dependent RNA helicase eIF4A-2) (eIF-4A-2) Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\G7 1351.wiff

Nominal mass (M_r) : 47084; Calculated pI value: 5.38 NCBI BLAST search of <u>gi|1170506</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Nicotiana plumbaginifolia</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|19697</u> from <u>Nicotiana plumbaginifolia</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 8%

1	MAGSAPEGSQ	FDARQFDAKM	TELLGTEQEE	FFTSYDEVYD	SFDAMGLQEN
51	LLRGIYAYGF	EKPSAIQQRG	IVPFCKGLDV	IQQAQSGTGK	TATFCSGVLQ
101	QLDYSLVECQ	ALVLAPTREL	AQQIEKVMRA	LGDYLGVKVH	ACVGGTSVRE
151	DQRILQSGVH	VVVGTPGRVF	DMLRRQSLRP	DHIKMFVLDE	ADEMLSRGFK
201	DQIYDIFQLL	PPKIQVGVFS	ATMPPEALEI	TRKFMNKPVR	ILVKRDELTL
251	EGIKQFYVNV	DKEEWKLETL	CDLYETLAIT	QSVIFVNTRR	KVDWLTDKMR
301	SRDHTVSATH	GDMDQNTRDI	IMREFRSGSS	RVLITTDLLA	RGIDVQQVSL
351	VINYDLPTQP	ENYLHRIGRS	GRFGRKGVAI	NSVTKDDERM	LFDIQKFYNV
401	VIEELPANVA	DLL			

Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
54 - 69	609.9623 1	L826.8652	1826.9315	-0.0663	0	R.GIYAYGFEKPSAIQQR.G (Ions score 30)
77 - 90	701.3292 1	L400.6439	1400.7260	-0.0820	0	K.GLDVIQQAQSGTGK.T (Ions score 42)
390 - 396	455.7603	909.5061	909.4630	0.0431	0	R.MLFDIQK.F Oxidation (M) (Ions score 23)

gi|41352683 Putative proteasome 20S beta1 subunit

Protein View

Match to: gi|41352683 Score: 110 putative proteasome 20S beta1 subunit [Brassica napus] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\F11 2434.wiff

Nominal mass (M_r): 19000; Calculated pI value: 7.71 NCBI BLAST search of <u>gi|41352683</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 14%

Matched peptides shown in Bold Red

1 TSTGMYVANR ASDKITQLTD NVYVCRSGSA ADSQVVSDYV RYFLHQHTIQ 51 LGQPATVKVS ANLIRMLAYN NKNMLQTGLI VGGWDKYEGG KIYGIPLGGT 101 VVEQPFAIGG SGSSYLYGFF DQAWKENMTK EEAEQLVVKA VSLAIARDGA 151 SGGVVRTVII NSEGVTRNFY PGDKL

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence		
27 - 41	770.8111	1539.6076	1539.7165	-0.1089	0	R.SGSAADSQVVSDYVR.	(Ions score	<u>52</u>)
157 - 167	594.8033	1187.5921	1187.6510	-0.0589	0	R.TVIINSEGVTR.N (Ions score 58)	

gi|147801436 Hypothetical protein, containing elongation factor 1 domain

Protein View

```
Match to: gi|147801436 Score: 74
hypothetical protein [Vitis vinifera]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\H10 1421.wiff
```

Nominal mass (M_r) : 59829; Calculated pI value: 6.66 NCBI BLAST search of <u>qi|147801436</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Vitis vinifera

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 1%
```

MEDCRPPFGA	PSFLSFFAAH	LPAGRLFESQ	VLPPGWLLWN	QLSGIDGRMR
KRHQVGGYAE	DSESVMEGAL	AAGTFEDKRD	FQMSMNLGGC	VGHMGIKSTQ
QEIIVGQAST	SPGISGQIIQ	KSMCLSLLVK	GLLGKWPYES	QVGPSKTVWA
EEDEHRVTRA	HMGVASEGND	DYGTPPFNVE	QLVSLHGK TT	LTAAITRVLA
EEGKAKVVAL	DEIDKAPKEK	KRGITIATTH	IEYETAKRHC	DHVDCPGHAD
YVKNMITGAA	QMDGSIQETH	SSCVPEMEFR	ELLSFYEFPG	DEIPVIRGSA
ICVLQGTHEE	MRKQGCGTVA	IGRAEQGTIE	VGEDLRIWRG	TSALAEHMRW
KIAARRNQTV	IWVKPLTSDC	CIKKGTLVLN	LHSTDLMMVR	MLCGMLPNGT
LAQLLHDSTK	ISEYEPDWLT	RLTIATGVAE	GLAFLHHADY	DMVLGVLYRH
LSCLQDIVTA	VGRLRPIEPL	RQVTIRLRPP	FDQLDKRSGK	ERKSFCTLRL
VELNRLVGSS	SGSIGWAVFG	STTILFNLKP	FKQQV	
	MEDCRPPFGA KRHQVGGYAE QEIIVGQAST EEDEHRVTRA EEGKAKVVAL YVKNMITGAA ICVLQGTHEE KIAARRNQTV LAQLLHDSTK LSCLQDIVTA VELNRLVGSS	MEDCRPPFGA PSFLSFFAAH KRHQVGGYAE DSESVMEGAL QEIIVGQAST SPGISGQIIQ EEDEHRVTRA HMGVASEGND EEGKAKVVAL DEIDKAPKEK YVKNMITGAA QMDGSIQETH ICVLQGTHEE MRKQGCGTVA KIAARRNQTV IWVKPLTSDC LAQLLHDSTK ISEYEPDWLT LSCLQDIVTA VGRLRPIEPL VELNRLVGSS SGSIGWAVFG	MEDCRPPFGA PSFLSFFAAH LPAGRLFESQ KRHQVGGYAE DSESVMEGAL AAGTFEDKRD QEIIVGQAST SPGISGQIIQ KSMCLSLLVK EEDEHRVTRA HMGVASEGND DYGTPPFNVE EEGKAKVVAL DEIDKAPKEK KRGITIATTH YVKNMITGAA QMDGSIQETH SSCVPEMEFR ICVLQGTHEE MRKQGCGTVA IGRAEQGTIE KIAARRNQTV IWVKPLTSDC CIKKGTLVLN LAQLLHDSTK ISEYEPDWLT RLTIATGVAE LSCLQDIVTA VGRLRPIEPL RQVTIRLRPP VELNRLVGSS SGSIGWAVFG STTILFNLKP	MEDCRPPFGA PSFLSFFAAH LPAGRLFESQ VLPPGWLLWN KRHQVGGYAE DSESVMEGAL AAGTFEDKRD FQMSMNLGGC QEIIVGQAST SPGISGQIIQ KSMCLSLLVK GLLGKWPYES EEDEHRVTRA HMGVASEGND DYGTPPFNVE QLVSLHGK TT EEGKAKVVAL DEIDKAPKEK KRGITIATTH IEYETAKRHC YVKNMITGAA QMDGSIQETH SSCVPEMEFR ELLSFYEFPG ICVLQGTHEE MRKQGCGTVA IGRAEQGTIE VGEDLRIWRG KIAARRNQTV IWVKPLTSDC CIKKGTLVLN LHSTDLMMVR LAQLLHDSTK ISEYEPDWLT RLTIATGVAE GLAFLHHADY LSCLQDIVTA VGRLRPIEPL RQVTIRLRPP FDQLDKRSGK VELNRLVGSS SGSIGWAVFG STTILFNLKP FKQQV

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
189 - 197	474.2925	946.5704	946.5447	0.0257	0 K.TTLTAAITR.V	(Ions score 74)

MS/MS Fragmentation of **TTLTAAITR** Found in **gi**|**147801436**, hypothetical protein [Vitis vinifera]

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	Т							9
2	203.1026	102.0550	185.0921	93.0497	Т	846.5043	423.7558	829.4778	415.2425	828.4938	414.7505	8
3	316.1867	158.5970	298.1761	149.5917	L	745.4567	373.2320	728.4301	364.7187	727.4461	364.2267	7
4	417.2344	209.1208	399.2238	200.1155	Т	632.3726	316.6899	615.3461	308.1767	614.3620	307.6847	6
5	488.2715	244.6394	470.2609	235.6341	Α	531.3249	266.1661	514.2984	257.6528	513.3144	257.1608	5
6	559.3086	280.1579	541.2980	271.1527	Α	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	4
7	672.3927	336.7000	654.3821	327.6947	Ι	389.2507	195.1290	372.2241	186.615 7	371.2401	186.1237	3
8	773.4403	387.2238	755.4298	378.2185	Τ	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
9					R	175.1190	88.0631	158.0924	79.5498			1

gi|15218090 Mitochondrial processing peptidase alpha subunit

Protein View

```
Match to: gi|15218090 Score: 81
mitochondrial processing peptidase alpha subunit, putative [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\G7 1351.wiff
```

```
Nominal mass (M_r): 54539; Calculated pI value: 5.94
NCBI BLAST search of <u>gi|15218090</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

```
Taxonomy: <u>Arabidopsis thaliana</u>
Links to retrieve other entries containing this sequence from NCBI Entrez:
<u>qi|29839695</u> from <u>Arabidopsis thaliana</u>
<u>qi|4220446</u> from <u>Arabidopsis thaliana</u>
<u>qi|17529270</u> from <u>Arabidopsis thaliana</u>
<u>qi|20258957</u> from <u>Arabidopsis thaliana</u>
```

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%
```

1	MYRTAASRAR	ALKGVLTRSL	RPARYASSSA	VAETSSSTPA	YLSWLSGGSR
51	AALTSLDMPL	QGVSLPPPLA	DKVEPSKLQI	TTLPNGLKIA	SETTPNPAAS
101	IGLYVDCGSI	YEAPYFHGAT	HLLERMAFKS	TLNRTHFRLV	REIEAIGGNT
151	SASASREQMS	YTIDALKTYV	PEMVEVLIDS	VRNPAFLDWE	VNEELRKMKV
201	EIAELAKNPM	GFLLEAIHSA	GYSGPLASPL	YAPESALDRL	NGELLEEFMT
251	ENFTAARMVL	AASGVEHEEL	LKVAEPLTSD	LPNVPPQLAP	KSQYVGGDFR
301	QHTGGEATHF	AVAFEVPGWN	NEKEAVTATV	LQMLMGGGGS	FSAGGPGKGM
351	HSWLYRRVLN	EYQEVQSCTA	FTSIFNDTGL	FGIYGCSSPQ	FAAKAIELAA
401	KELKDVAGGK	VNQAHLDRAK	AATK <mark>SAVLMN</mark>	LESRMIAAED	IGR QILTYGE
451	RKPVDQFLKS	VDQLTLKDIA	DFTSKVISKP	LTMGSFGDVL	AVPSYDTISS
501	KFR				

Start - End	0bserved	Mr(expt)	Mr(calc)	Delta	Miss	Sequence					
425 - 434	568.2810	1134.5475	1134.5703	-0.0228	0	K.SAVLMNLESR.M	Oxidation	(M)	(Ions	score	<u>58</u>)
435 - 443	496.2299	990.4452	990.4804	-0.0352	0	R.MIAAEDIGR.Q	Oxidation	(M)	(Ions	score	24)

gi|510880 Putative aspartic protease

Protein View

Match to: gi|510880 Score: 51 putative aspartic protease [Brassica oleracea] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\H12 2051.wiff

Nominal mass (M_r) : 28008; Calculated pI value: 8.34 NCBI BLAST search of <u>gi|510880</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica oleracea

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%
```

Matched peptides shown in Bold Red

1	MGIYSKPVAV	SLIVSFLLFL	SASAERNDGT	FRVGLKKLKL	DRKSRIAARV
51	GSKQLKPLRG	YGLGDSGDAD	IVTLKNYLDA	QYYGEIAIGT	PPQKFTVVFD
101	TGSSNLWVPS	SKCYFSIACL	FHSKYKSSRS	STYEKNGKSA	AIHYGTGAIA
151	GFFSNDAVTV	GDLVVKDQEF	IEATKEPGIT	FVLAKFDGIL	GLGFQEISVG
201	NAAPVWYNML	KQGLYKEPVF	SFWLNRNAED	EEGGELVFGG	VDPNHYKGEH
251	IYVPV				

Show predicted peptides also

Sort Peptides By	Resid	ueNumber 🛛 🔊	Increasing Mass	Decrea	asing Mass	
Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss Sequence	
167 - 175	540.7669	1079.5192	1079.5135	0.0057	0 K.DQEFIEATK.E	(<u>Ions score 51</u>)

MS/MS Fragmentation of **DQEFIEATK**

Found in **gi510880**, putative aspartic protease [Brassica oleracea]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							9
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	965.4938	483.2506	948.4673	474.7373	947.4833	474.2453	8
3	373.1354	187.0713	356.1088	178.5581	355.1248	178.0661	E	837.4353	419.2213	820.4087	410.7080	819.4247	410.2160	7
4	520.2038	260.6055	503.1773	252.0923	502.1932	251.6003	F	708.3927	354.7000	691.3661	346.1867	690.3821	345.6947	6
5	633.2879	317.1476	616.2613	308.6343	615.2773	308.1423	Ι	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
6	762.3305	381.6689	745.3039	373.1556	744.3199	372.6636	E	448.2402	224.6237	431.2136	216.1105	430.2296	215.6185	4
7	833.3676	417.1874	816.3410	408.6742	815.3570	408.1821	A	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
8	934.4153	467.7113	917.3887	459.1980	916.4047	458.7060	Т	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
9							K	147.1128	74.0600	130.0863	65.5468			1

gi|127733 Myrosinase precursor

Protein View

Match to: gi|127733 Score: 330 Myrosinase precursor (Sinigrinase) (Thioglucosidase) Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\C3 778.wiff

Nominal mass (M_r) : 63266; Calculated pI value: 6.62 NCBI BLAST search of <u>gi|127733</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Brassica napus</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|22595</u> from <u>Brassica napus</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 14%

1	MKLLHGLALV	FLLAAASCKA	DEEITCEENN	PFTCSNTDIL	SSKNFGKDFI
51	FGVASSAYQI	EGGRGRGVNV	WDGFSHRYPE	KAGSDLKNGD	TTCESYTRWQ
101	KDVDVMGELN	ATGYR FSFAW	SRIIPKGKVS	RGVNQGGLDY	YHKLIDALLE
151	KNITPFVTLF	HWDLPQTLQD	EYEGFLDRQI	IQDFK DYADL	CFKEFGGKVK
201	HWITINQLYT	VPTRGYAIGT	DAPGRCSPMV	DTKHRCYGGN	SSTEPYIVAH
251	NQLLAHATVV	DLYRTKYKFQ	KGKIGPVMIT	RWFLPFDESD	PASIEAAERM
301	NQFFHGWYME	PLTKGR YPDI	MRQIVGSRLP	NFTEEEAELV	AGSYDFLGLN
351	YYVTQYAQPK	PNPYPSETHT	AMMDAGVKLT	YDNSRGEFLG	PLFVEDKVNG
401	NSYYYPKGIY	YVMDYFKTKY	GDPLIYVTEN	GFSTPSSENR	EQAIADYKRI
451	DYLCSHLCFL	RKVIKEKGVN	VRGYFAWALG	DNYEFCKGFT	VRFGLSYVNW
501	EDLDDRNLKE	SGKWYQRFIN	GTVKNAVKQD	FLRSSLSSQS	QKKRFADA

start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44	-	64	755.0270	2262.0590	2262.1069	-0.0479	1	K.NFGKDFIFGVASSAYQIEGGR.G (<u>lons score 34</u>)
116	-	122	450.7514	899.4883	899.4290	0.0593	0	R.FSFAWSR.I (Ions score 32)
179	-	185	446.2469	890.4792	890.4862	-0.0070	0	R.QIIQDFK.D (Ions score 35)
215	-	225	539.2561	1076.4977	1076.5251	-0.0274	0	R.GYAIGTDAPGR.C (Ions score 54)
274	-	281	451.7541	901.4936	901.5055	-0.0119	0	K.IGPVMITR.W Oxidation (M) (Ions score 67)
317	-	322	405.6933	809.3720	809.3742	-0.0021	0	R.YPDIMR.Q Oxidation (M) (Ions score 24)
408	-	417	657.3498	1312.6850	1313.6002	-0.9152	0	K.GIYYVMDYFK.T Oxidation (M) (Ions score 42)
441	-	448	469.2432	936.4719	936.4552	0.0167	0	R.EQAIADYK.R (Ions score 46)

gi|14764532 Monodehydroascorbate reductase

Protein View

Match to: gi|14764532 Score: 115 monodehydroascorbate reductase [Brassica rapa subsp. pekinensis] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\1370.wiff

Nominal mass (M_r) : 46604; Calculated pI value: 5.81 NCBI BLAST search of <u>gi|14764532</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica rapa subsp. pekinensis

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 10%
```

1	MAEKSFKYII	LGGGVSAGYA	AKEFASQGVK	PGELAVISKE	AVAPYERPAL
51	SKGYLFPEGA	ARLPGFHCCV	GSGGEKLLPE	SYKQKGIELI	LSTEIVKADL
101	AAKSLVSAAG	DVFKYETLII	ATGSTVLRLT	DFGVKGADSK	NILYLREIDD
151	ADKVVEAIQA	KKGGKAVVVG	GGYIGLELSA	ALRINNFDVT	MVFPEPWCMP
201	RLFTADIAAF	YETYYTNKGV	KIIKGTVASG	FTAHPNGEVN	EVQLKDGRSL
251	EADIVIVGVG	ARPLTALFKG	QVEEDKGGIK	TDAFFK TSVP	DVYAVGDVAT
301	FPLKMYGDMR	RVEHVDHSRK	SAEQAVKAIK	AAEGGGAVEE	YDYLPFFYSR
351	SFDLSWQFYG	DNVGDSVLFG	DSNPSNPKPR	FGAYWVQDGK	VVGAFMEGGS
401	GDENKALAKV	AKARPAAESL	EDLTKQGISF	AAKI	

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 39	587.3038	1758.8895	1758.9516	-0.0621	0	K.EFASQGVKPGELAVISK.E (Ions score 39)
53 - 62	540.7732	1079.5319	1079.5400	-0.0081	0	K.GYLFPEGAAR.L (Ions score 41)
287 - 304	627.2976	1878.8709	1877.9775	0.8934	0	K.TSVPDVYAVGDVATFPLK.M (Ions score 37)

gi|18141281 Senescence-associated cysteine protease

Protein View

Match to: gi|18141281 Score: 92 senescence-associated cysteine protease [Brassica oleracea] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\F7 2426.wiff

Nominal mass (M_r): 49581; Calculated pI value: 5.49 NCBI BLAST search of <u>qi|18141281</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica oleracea

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%
```

1	KFTAIALVTL	LVLLASSSLS	GVTAKADHRN	PEEVKMFERW	LVENHKNYNG
51	LGEKDKRFEI	FMDNLKFVQE	HNSVPNQSYE	LGLTRFADLT	NEEFRAIYLR
101	SKMERTRDSV	KSERYLHNVG	DKLPDEVDWR	AKGAVVPVKD	QGSCGSCWAF
151	SAIGAVEGIN	QIKTGELVSL	SEQELVDCDT	SYNNGCGGGL	MDYAFQFIIS
201	NGGIDTEEDY	PYTATDDNIC	NTDKKNTRVV	TIDGYEDVPE	NENSLKKALA
251	NQPISVAIEA	GGR GFQLYKS	GVFTGTCGTA	LDHGVVAVGY	GTSEGQDYWI
301	IRNSWGSNWG	ESGYIKLQRN	IKDSSGKCGV	AMMASYPTKS	SGSNPPKPPP
351	PAPVVCDKSY	TCPAKSTCCC	LYEYKGKCYS	WGCCPLESAT	CCEDGSSCCP
401	QAYPVCDLKA	GTCRMKADSP	LSVKALTRGP	ATATTKATNV	LVSSA

Start	-	End	Observ	ed Mr(expt)) Mr(calc)	Delta	Miss	Sequence	
247	-	263	565.95	05 1694.8297	1693.9475	0.8823	1	K.KALANQPISVAIEAGGR.G	(<u>Ions score 33</u>)
248	-	263	783.85	93 1565.7040	1565.8525	-0.1485	0	K.ALANQPISVAIEAGGR.G	(<u>Ions score 60</u>)
248	-	263	522.93	62 1565.7867	1565.8525	-0.0658	0	K.ALANQPISVAIEAGGR.G	(Ions score 36)

gi|15227987 Low expression of osmotically responsive genes 1 (LOS2) Protein View

Match to: gi|15227987 Score: 127 LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\F4 1223.wiff

Nominal mass (M_r): 47974; Calculated pI value: 5.54 NCBI BLAST search of <u>gi|15227987</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|119350</u> from <u>Arabidopsis thaliana</u> <u>gi|15983458</u> from <u>Arabidopsis thaliana</u> <u>gi|4581151</u> from <u>Arabidopsis thaliana</u> <u>gi|23297411</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
```

Matched peptides shown in Bold Red

1	MATITVVKAR	QIFDSRGNPT	VEVDIHTSNG	IKVTAAVPSG	ASTGIYEALE
51	LRDGGSDYLG	KGVSKAVGNV	NNIIGPALIG	KDPTQQTAID	NFMVHELDGT
101	QNEWGWCKQK	LGANAILAVS	LAVCKAGAVV	SGIPLYKHIA	NLAGNPKIVL
151	PVPAFNVING	GSHAGNKLAM	QEFMILPVGA	ASFKEAMKMG	VEVYHHLKSV
201	IKKKYGQDAT	NVGDEGGFAP	NIQENKEGLE	LLKTAIEKAG	YTGKVVIGMD
251	VAASEFYSED	KTYDLNFKEE	NNNGSQKISG	DALKDLYKSF	VAEYPIVSIE
301	DPFDQDDWEH	YAKMTTECGT	EVQIVGDDLL	VTNPKRVAKA	IAEKSCNALL
351	LKVNQIGSVT	ESIEAVKMSK	KAGWGVMTSH	RSGETEDTFI	ADLAVGLSTG
401	QIKTGAPCRS	ERLAKYNQLL	RIEEELGSEA	IYAGVNFRKP	VEPY

Show predicted peptides also

Sort Peptides By	Resid	ue Number 🛛 🔊	Increasing Mass	Decrea	using Mass
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence
126 - 137	587.9131	1173.8116	1173.6758	0.1358	0 K.AGAVVSGIPLYK.H (Ions score 34)
353 - 367	525.3462	1573.0169	1572.8359	0.1810	0 K.VNQIGSVTESIEAVK.M (<u>lons score 53</u>)
416 - 421	403.7902	805.5658	805.4446	0.1212	0 K.YNQLLR.I (Ions score 41)

gi|100554 14-3-3 protein homolog

Protein View

Match to: gi|100554 Score: 48
14-3-3 protein homolog - barley
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\A10 2111.wiff

Nominal mass (M_r) : 29361; Calculated pI value: 4.83 NCBI BLAST search of <u>gi|100554</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Hordeum vulgare</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|22607</u> from <u>Hordeum vulgare subsp. vulgare</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

MSTAEATREE NVYMAKLAEQ AERYEEMVEF MEKVAKTADV GELTVEERNL
 LSVAYKNVIG ARRASWRIIS SIEQKEESRG NEAYVASIKE YRTRIETELS
 KICDGILKLL DSHLVPSATA AESKVFYLKM KGDYHRYLAE FKAGAERKEA
 AENTLVAYKS AQDIALADLP TTHPIRLGLA LNFSVFYYEI LNSPDRACNL
 AKQAFDEAIA ELDSLGEESY KDSTLIMQLL RDNLTLWTSD NAEEGGDEIK
 EAASKPEGEG H

Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence	
49 - 56	454.2645	906.5144	906.5174	-0.0030	0	R.NLLSVAYK.N	(Ions score 48)

MS/MS Fragmentation of **NLLSVAYK** Found in **gi**|**100554**, 14-3-3 protein homolog - barley

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							8
2	228.1343	114.5708	211.1077	106.0575			L	7 93.481 8	397.2445	776.4553	388.7313	775.4713	388.2393	7
3	341.2183	171.1128	324.1918	162.5995			L	680.3978	340.7025	663.3712	332.1892	662.3872	331.6972	6
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	567.313 7	284.1605	550.2871	275.6472	549.3031	275.1552	5
5	527.3188	264.1630	510.2922	255.6497	509.3082	255.1577	V	480.2817	240.6445	463.2551	232.1312			4
6	598.3559	299.6816	581.3293	291.1683	580.3453	290.6763	Α	381.2132	191.1103	364.1867	182.5970			3
7	761.4192	381.2132	744.3927	372.7000	743.4087	372.2080	Y	310.1761	155.5917	293.1496	147.0784			2
8							K	147.1128	74.0600	130.0863	65.5468			1

gi|15242603 Calmodulin-binding protein

Protein View

Match to: gi|15242603 Score: 65 calmodulin-binding protein [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\H5 2546.wiff

Nominal mass (M_r) : 20718; Calculated pI value: 4.86 NCBI BLAST search of <u>gi|15242603</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|10177506</u> from <u>Arabidopsis thaliana</u> <u>gi|34098925</u> from <u>Arabidopsis thaliana</u> <u>gi|37202088</u> from <u>Arabidopsis thaliana</u> <u>gi|51968364</u> from <u>Arabidopsis thaliana</u> <u>gi|51969122</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%
```

Matched peptides shown in Bold Red

1 MSEGYAIELY FDPALENQVL KAWNVFARRQ ISTKLINTES RPHITLFSTS 51 FFDSTRLESV IKNFVSKQEP ISISFSTIGS FSSDNNVLFL SPTPSLSLLQ 101 LQTQLCDMLK KESVDIGEEY RVDSWVPFCP VALDVPKSRM AEAFSVLRDL 151 KLPVNGYGME IGLVEFSPVR EVFSFPLGNT LES

Start -	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence		
140 -	148	520.2466	1038.4786	1038.5168	-0.0382	0	R.MAEAFSVLR.D	Oxidation (M)	(Ions score 65)

MS/MS Fragmentation of MAEAFSVLR

Found in gi 15242603, calmodulin-binding protein [Arabidopsis thaliana]

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	У	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0427	74.5250			Μ							9
2	219.0798	110.0435			Α	892.488 7	446.7480	875.4621	438.2347	874.4781	437.7427	8
3	348.1224	174.5648	330.1118	165.5595	E	821.4516	411.2294	804.4250	402.7162	803.4410	402.2241	7
4	419.1595	210.0834	401.1489	201.0781	Α	692.4090	346.7081	675.3824	338.1949	674.3984	337.7028	6
5	566.2279	283.6176	548.2174	274.6123	F	621.3719	311.1896	604.3453	302.6763	603.3613	302.1843	5
6	653.2599	327.1336	635.2494	318.1283	S	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	4
7	752.3284	376.6678	734.3178	367.6625	V	387.2714	194.1394	370.2449	185.6261			3
8	865.4124	433.2098	847.4019	424.2046	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1

gi|19568098 Osmotic stress-activated protein kinase (OST1)

Protein View

Match to: gi|19568098 Score: 63 osmotic stress-activated protein kinase [Nicotiana tabacum] Found in search of E:\GC ABA DIGE SEARCH\G7 1351.wiff

Nominal mass (M_r) : 41399; Calculated pI value: 5.64 NCBI BLAST search of <u>gi|19568098</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Nicotiana tabacum

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Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%
```

Matched peptides shown in Bold Red

1	MDKYELVK <mark>DI</mark>	GSGNFGVARL	MRHKETKELV	AMKYIERGHK	IDENVAREII
51	NHRSLRHPNI	IRFKEVLVTP	THLAIVMEYA	AGGELFERIC	NAGRFSEDEA
101	RYFFQQLISG	VHYCHNMQIC	HRDLKLENTL	LDGSPAPRLK	ICDFGYSKSS
151	LLHSRPKSTV	GTPAYIAPEV	LSRREYDGKL	ADVWSCGVTL	YVMLVGAYPF
201	EDQEDPKNFR	KTIQRIMAVQ	YKIPDYVHIS	QDCRHLLSRI	FVANPARRIT
251	IKEIKSHPWF	LKNLPRELTE	AAQAAYYRRE	NPTFSLQSVE	EIMKIVEEAK
301	TPAPASRSVS	GFGWGGEEEE	EEKEGDVEEE	EEDEEEEDEY	EKQVKQAHES
351	GEVRLT				

Start - EndObservedMr(expt)Mr(calc)DeltaMissSequence9 - 19546.75841091.50231091.5360-0.03370K.DIGSGNFGVAR.L(Ions score 65)

MS/MS Fragmentation of **DIGSGNFGVAR**

Found in gi 19568098, osmotic stress-activated protein kinase [Nicotiana tabacum]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	у*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							11
2	229.1183	115.0628			211.1077	106.0575	Ι	977.5163	489.2618	960.4898	480.7485	959.5057	480.2565	10
3	286.1397	143.5735			268.1292	134.5682	G	864.4322	432.7198	847.4057	424.2065	846.4217	423.7145	9
4	373.1718	187.0895			355.1612	178.0842	S	807.4108	404.2090	790.3842	395.6958	789.4002	395.2037	8
5	430.1932	215.6003			412.1827	206.5950	G	720.3787	360.6930	703.3522	352.1797			7
6	544.2362	272.6217	527.2096	264.1084	526.2256	263.6164	Ν	663.3573	332.1823	646.330 7	323.6690			6
7	691.3046	346.1559	674.2780	337.6427	673.2940	337.1506	F	549.3144	275.1608	532.2878	266.6475			5
8	748.3260	374.6667	731.2995	366.1534	730.3155	365.6614	G	402.2459	201.6266	385.2194	193.1133			4
9	847.3945	424.2009	830.3679	415.6876	829.3839	415.1956	V	345.2245	173.1159	328.1979	164.6026			3
10	918.4316	459.7194	901.4050	451.2061	900.4210	450.7141	Α	246.1561	123.5817	229.1295	115.0684			2
11							R	175.1190	88.0631	158.0924	79.5498			1

gi|115468776 Os06g0597200, Serine/threonine phosphatases 2C (PP2C) family

Protein View

Match to: gi|115468776 Score: 51
Os06g0597200 [Oryza sativa (japonica cultivar-group)]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\500ug Prep Gel Plate 4 Q-Trap 33\B1 2630.wiff

Nominal mass (M_r) : 40100; Calculated pI value: 5.32 NCBI BLAST search of <u>qi|115468776</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Oryza sativa Japonica Group</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|50725574</u> from <u>Oryza sativa Japonica Group</u> <u>gi|113596027</u> from <u>Oryza sativa Japonica Group</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 4%

1	MEEHRLGGGG	GGGGGGGGRPP	IPGAAGRKLP	GLSRHASFVR	SPANSTKSGT
51	EKTFENMDAV	AYMPVVRSGG	WADIGSRHTM	EDVFICSDNL	MKEFGVESFE
101	DGPSAFYGVF	DGHGGKHAAD	FVCSNLARFI	VEDEDFPREI	EKALSSAFLQ
151	TDAAFADACS	VNSSLASGTT	ALAALVVGRS	LLVANAGDCR	AVLCCRGKAI
201	EMSRDHKPSC	NREKVRIEAS	GGYVYDGYLN	GQLNVARAIG	DWHMEGMKAC
251	DGLGPLSAEP	EVMIRNLTEE	DEFLIIGCDG	IWDVFRSQNA	VDFARRKLQE
301	HNDPVTCCKE	LVDEAIKRKS	GDNLSVVVIC	FNSRPPPVLT	TPRPRVQR <mark>SI</mark>
351	SAEGLRELOS	FLDSLAD			

Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss Se	equence					
41 - 47	432.2302	862.4459	863.2827	-0.8368	0 R.	.SPANSTK.S	2 Phospho	(ST)	(Ions	score	<u>15</u>)
349 - 356	416.7419	831.4693	831.4450	0.0243	0 R.	.SISAEGLR.E	(Ions sco	re 36	5)		

gi|62733113 Retrotransposon protein, putative

Protein View

Match to: gi | 62733113 Score: 49

retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa (japonica cultivar-group)] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\B8 663.wiff

Nominal mass (M_r) : 92125; Calculated pI value: 7.23 NCBI BLAST search of <u>gi|62733113</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

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Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%
```

1	MTSGNEINKI	SLEDLDVEAR	KITEECIKAI	TQEALMRSCF	RTHQGVVLKP
51	EPLIKPSFDM	HRPENMEELT	SIIIRDKFGI	EAMDRAREYQ	KSYPDYYDNI
101	PYPRGYRVPE	FTNFSGEDSR	TTWEYVAELN	DGSDCITSES	EIVLSPKIES
151	QINHVDVGKG	DDNVLRYSSE	IESKVAMHTY	QRPYPERIDL	VPYPQGFEVP
201	NFTKFTGEDA	RTTMEHICQF	IEQSGKTGSN	DLLKLKLFSL	SLSNFASIWY
251	SLLAPNSIST	WSQMEHEFHD	YFKDASLMEQ	NPIDNSSVTC	DTISVIPFAK
301	TRIVSNPLPI	SPIDLDNEKV	VIRPSQAEST	KGKCVIIGDL	RPKTRINNTK
351	ADDHKVVKDE	SSSFQKTKKL	NLTFEMLMAK	YKKGLAGQQF	DNQTSDLKRP
401	RSYRRKRFGQ	TPKQSEPSTI	PTPYKPPIVM	PWYPYPMSLY	GYPFMYYMPW
451	MPQPYMPFHQ	EWKQSSRSVP	SHSFNSSQDR	FPQKSRSGGS	KVKQVKKVWV
501	RKEAKAPEVV	TIKEESQDVQ	VPTRDAVKTI	QAKKTEADAV	TAKSGGLIET
551	AGWSDRR LAT	GLTGPRGWSD	RGALEKSGKC	GIHLAFEIVQ	SRKPILLGGQ
601	DINMLMKKSK	EMNNDGYNIT	SLSRRLLDAK	TRLLWEKYMK	GFVELINWPG
651	QRFVLIATDY	FIKWAEAVPL	KNITYTEANG	QAESSNKTLL	KLVEKEIEEH
701	QKKWHEVLSE	ALWTHRIFKH	GVTKVTSFEL	VCGQEAVLPI	EVNLGYLRYF
751	KQDDLSVEDY	KILMGGNFED	VIDKRLKTLK	EMDALQENNP	WEILEEILP

start	-	End	Obs	erved	Mr (e	expt)	Mr(cal	c) Delt	a Miss	Sequence			
22	-	28	426	.3209	850.0	6272	850.410	6 0.216	60	K.ITEECIK.A	Oxidation (C)	(Ions	score 19)
558	-	566	443	.2643	884.5	5140	884.508	0 0.006	0 0	R.LATGLTGPR.	G (Ions score	30)	
gi|15241472 Tubulin beta-4 chain(TUB4)

Protein View

253 - 262

381 - 390

```
Match to: gi|15241472 Score: 217
TUB4 (tubulin beta-4 chain) [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\F6 1237.wiff
Nominal mass (M<sub>r</sub>): 50361; Calculated pI value: 4.76
NCBI BLAST search of <u>gi|15241472</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
Taxonomy: <u>Arabidopsis thaliana</u>
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|27735260 from <u>Arabidopsis thaliana</u>
```

<u>gi|10176889</u> from <u>Arabidopsis thaliana</u> <u>gi|14334936</u> from <u>Arabidopsis thaliana</u> <u>gi|16323374</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%
```

		1	MREILHIQGG	QCGNQIGAKF	WEVICDEHGI	DHTGQYVGDS	PLQLERIDVY
		51	FNEASGGKYV	PRAVLMDLEP	GTMDSLRSGP	FGQIFRPDNF	VFGQSGAGNN
		101	WAKGHYTEGA	ELIDSVLDVV	RKEAENSDCL	QGFQVCHSLG	GGTGSGMGTL
		151	LISKIREEYP	DRMMMTFSVF	PSPKVSDTVV	EPYNATLSVH	QLVENADECM
		201	VLDNEALYDI	CFRTLKLANP	TFGDLNHLIS	ATMSGVTCCL	RFPGQLNSDL
		251	RKLAVNLIPF	PRLHFFMVGF	APLTSRGSQQ	YSALSVPELT	QQMWDAKNMM
		301	CAADPRHGRY	LTASAVFRGK	LSTKEVDEQM	MNIQNKNSSY	FVEWIPNNVK
		351	SSVCDIAPKG	LKMASTFIGN	STSIQEMFRR	VSEQFTAMFR	RKAFLHWYTG
		401	EGMDEMEFTE	AESNMNDLVA	EYQQYQDATA	GEEEYEEEEE	EYET
Start	_	End	Observed	Mr(expt)	Mr(calc)	Delta Mi	ss Sequence
47	-	58	650.2991	1298.5837 1	298.6143	-0.0306	0 R.IDVYFNEASGGK.Y (<u>Ions score 62</u>)
242	-	251	573.7901	1145.5656 1	145.5829	-0.0173	0 R.FPGQLNSDLR.K (Ions score 44)

```
      570.3348
      1138.6551
      1138.6862
      -0.0311
      0
      K.LAVNLIPFPR.L
      (Ions score 49)

      616.3009
      1230.5873
      1230.5703
      0.0170
      0
      R.VSEQFTAMFR.R
      Oxidation (M) (Ions score 63)
```

gi|4139264 Actin

Protein View

Match to: gi|4139264 Score: 298
actin [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B1 1546.wiff

Nominal mass (M_r) : 41888; Calculated pI value: 5.29 NCBI BLAST search of <u>gi|4139264</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 17%
```

1	MADGEDIQPL	VCDNGTGMVK	AGFAGDDAPR	AVFPSIVGRP	RHTGVMVGMG
51	QKDAYVGDEA	QSK RGILTLK	YPIEHGIVSN	WDDMENIWHH	TFYNELRVAP
101	EEHPVLLTEA	PLNPKANREK	MTHIMFETFN	VPAMYVAIQA	VLSLYASGRT
151	TGIVLDSGDG	VSHTVPIYEG	YALPHAILRL	DLAGRDLTDS	LMKILTERGY
201	MFTTTAEREI	VRDIKEKLAY	VALDYEQELE	TAKSSSSVEK	NYELPDGQVI
251	TIGAERFRCP	EVLFQPSLVG	MEAPGIHETT	YNSIMKCDVD	IRKDLYGNIV
301	LSGGSTMFPG	IADRMSKEIT	ALAPSSMKIK	VVAPPERKYS	VWIGGSILAS
351	LSTFQQMWIS	KGEYDESGPS	IVHRKCF		

Start	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
21	-	30	488.7436	975.4726	975.4410	0.0316	0	K.AGFAGDDAPR.A (Ions score 59)
21	-	30	488.7533	975.4920	975.4410	0.0510	0	K.AGFAGDDAPR.A (Ions score 23)
53	-	63	591.7711	1181.5276	1181.5200	0.0076	0	K.DAYVGDEAQSK.R (Ions score 37)
186	-	193	469.7407	937.4669	937.4426	0.0242	0	R.DLTDSLMK.I Oxidation (M) (Ions score 36)
199	-	208	588.7473	1175.4801	1175.5281	-0.0480	0	R.GYMFTTTAER.E (Ions score 23)
199	-	208	596.7648	1191.5151	1191.5230	-0.0079	0	R.GYMFTTTAER.E Oxidation (M) (Ions score 65)
241	-	256	887.9256	1773.8366	1773.8897	-0.0531	0	K.NYELPDGQVITIGAER.F (Ions score 72)
318	-	328	582.3145	1162.6145	1162.5903	0.0242	0	K.EITALAPSSMK.I Oxidation (M) (Ions score 28)

gi|14248550 Plastid-lipid associated protein PAP2

Protein View

Match to: gi|14248550 Score: 54 plastid-lipid associated protein PAP2 [Brassica rapa] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\D10 2330.wiff

Nominal mass (M_r): 34689; Calculated pI value: 4.79 NCBI BLAST search of <u>gi|14248550</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica rapa subsp. campestris

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%
```

1	MATVHSFNQF	PCKTRVQCPS	NSKPLSKPPS	SLVPMSALTR	RPSFSPGEFA
51	VSRSDFRVRV	IDAEDELDPE	TSEGGGSALL	MAEEAIESVE	ETEVLKR <mark>SLV</mark>
101	DSLYGTDRGL	SASSETRAEI	GDLITQLESK	NPTPAPTDAL	FLLNGKWILA
151	YTSFVGLFPL	LSRGIVPLVK	VDEISQTIDS	DNFTVENSVL	FAGPLATTSI
201	STNAKFEIRS	PKRVQIKFEE	GVIGTPQLTD	SIEIPEYVEF	LGQKIDLTPI
251	RGLLTSVQDT	ATSVARTISS	QPPLKFSLPG	DSAQSWLLTT	YLDKDIRISR
301	GDGGSVFVLI	KEGSPLLNP			

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
98 - 108	613.3112	1224.6079	1224.5986	0.0092	0	R.SLVDSLYGTDR.G	(Ions score 54)

MS/MS Fragmentation of **SLVDSLYGTDR**

Found in gi 14248550, plastid-lipid associated protein PAP2 [Brassica rapa]

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							11
2	201.1234	101.0653	183.1128	92.0600	L	1138.5739	569.7906	1121.5473	561.2773	1120.5633	560.7853	10
3	300.1918	150.5995	282.1812	141.5942	V	1025.4898	513.2485	1008.4633	504.7353	1007.4793	504.2433	9
4	415.2187	208.1130	397.2082	199.1077	D	926.4214	463.7143	909.3949	455.2011	908.4108	454.7091	8
5	502.2508	251.6290	484.2402	242.6237	S	811.3945	406.2009	794.3679	397.6876	793.3839	397.1956	7
6	615.3348	308.1710	597.3243	299.1658	L	724.3624	362.6849	707.3359	354.1716	706.3519	353.6796	6
7	778.3981	389.7027	760.3876	380.6974	Y	611.2784	306.1428	594.2518	297.6295	593.2678	297.1375	5
8	835.4196	418.2134	817.4090	409.2082	G	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
9	936.4673	468.7373	918.4567	459.7320	Τ	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
10	1051.4942	526.2508	1033.4837	517.2455	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
11					R	175.1190	88.0631	158.0924	79.5498			1

gi|14248552 Plastid-lipid associated protein PAP3

Protein View

Match to: gi|14248552 Score: 128 plastid-lipid associated protein PAP3 [Brassica rapa] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\H12 2051.wiff

Nominal mass (M_r) : 39278; Calculated pI value: 4.55 NCBI BLAST search of <u>gi|14248552</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica rapa subsp. campestris

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%
```

```
    MATLFTVTTT SRPFPANPSK TFSPSISLKP NALSFSLTHH RPPRPLRFSK
    IRSSLPSESD SEPEGGYSVT DEWGEQPAEP ESPPDNAPSA VSDEWGEKSE
    SVPEESVTRF AESDPPTNED EWEEREADDG VDKTWELKRC LADTVYGTEL
    GFRAGSEVRA EVLEIVNQLE ALNPTQAPVE NPELLDGNWV LLYTAFSELL
    PLLAAGSTPL LKVKSISQSI DTKSLSIDNS TTLSSPFADF SFSATASFEV
    RTPSRIEVSF KEGTLKPPEI KSSVDLPESV GVFGQEINLS FLKQSLNPLQ
    DVAANISRAI SGQPPLKLPF PGNRGSSWLL TTYLDKDLRI SRGDGGLFVL
    AREGSSLLEL
```

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence				
215 - 223	489.7758	977.5371	977.5029	0.0342	0	K.SISQSIDTK.S	(Ions	score	<u>58</u>)	
294 - 308	813.4080	1624.8014	1624.8533	-0.0518	0	K.QSLNPLQDVAANI	SR.A	(Ions	score	<u>48</u>)
309 - 317	455.7883	909.5620	909.5284	0.0337	0	R.AISGQPPLK.L	(Ions	score	22)	

gi|4469009 Putative protein, containing band 7 stomatin domain

Protein View

Match to: gi|4469009 Score: 75 putative protein [Arabidopsis thaliana] Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1577.wiff

Nominal mass (M_r) : 56003; Calculated pI value: 5.17 NCBI BLAST search of <u>gi|4469009</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|7269612</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%
```

1	MNHLVRKSSV	GYSALRSVSY	LRQSAVTSPP	PIFSAAASTV	RQFTSAGYPS
51	NSFQLTPPTN	WGIRIVPERK	AFVIERFGKY	ATTLPSGIHF	LIPFVDRIAY
101	VHSLKEEAIP	IPNQTAITKD	NVSIHIDGVL	YVKIVDPKLA	SYGVESPIYA
151	VVQLAQTTMR	SELGKITLDK	TFEERDTLNE	KIVEAINVAA	KDWGLQCLRY
201	EIRDIMPPHG	VRAAMEMQAE	AERKKRAQIL	ESEGERQSHI	NIADGKK <mark>SSV</mark>
251	ILASEAAKMD	QVNRAQGEAE	AILAR AQATA	KGLVLLSQSL	KETGGVEAAS
301	LRVAEQYITA	FGNIAKEGTI	MLLPSGASNP	ASMIAQALTM	YKSLVINGPS
351	KDHQETQALD	ETDLEELEDM	GEKHISEGSN	NRSGSISFDT	EKPALPIVSF
401	VFQTNPFNPK	TMGACASKPK	ESDIVEGSVS	TENAVVESKN	AATETDATLT
451	QEKKEESIEE	TKKEGETKED	SSEATKAEPT	PEAVKAEEKT	SSETEPPAQE
501	TTPAAKTDEA	PLVIL			

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
248 - 258	538.2852	1074.5558	1074.5921	-0.0362	0	K.SSVILASEAAK.M	(Ions score 43)
265 - 275	564.8173	1127.6200	1127.5934	0.0265	0	R.AQGEAEAILAR.A	(Ions score 32)

gi|585777 GTP-binding nuclear protein RAN1

Protein View

Match to: gi|585777 Score: 76 GTP-binding nuclear protein Ran1 Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\A10 2111.wiff

Nominal mass (M_r) : 25512; Calculated pI value: 6.25 NCBI BLAST search of <u>gi|585777</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Solanum lycopersicum</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>qi|453561</u> from <u>Solanum lycopersicum</u> <u>qi|77745509</u> from <u>Solanum tuberosum</u> <u>qi|82623375</u> from <u>Solanum tuberosum</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%
```

Matched peptides shown in Bold Red

1 MALPNQQTVD YPSFKLVIVG DGGTGKTTFV KRHLTGEFEK KYEPTIGVEV 51 HPLDFFTNCG KIRFYCWDTA GQEKFGGLRD GYYIHGQCAI IMFDVTARLT 101 YKNVPTWHRD LCRVCENIPI VLCGNKVDVK NRQVKAKQVT FHRKKNLQYY 151 EISAKSNYNF EKPFLYLARK LAGDGNLHFV ESPALAPPEV HIDLAAQALH 201 EEELQQAANQ PLPDDDDEAF E

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
16 - 26	508.2510	1014.4874	1014.5710	-0.0836	0	K.LVIVGDGGTGK.T	(<u>Ions score 40</u>)
146 - 155	614.7548	1227.4950	1227.6135	-0.1185	0	K.NLQYYEISAK.S	(Ions score 36)

Figure S5

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to ABA treatment in guard cells by ICAT.

gi|8745521 Ribulose-1,5-bisphosphate carboxylase / oxygenase large subunit

Proteins Detected											
Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*	
48.95	48.95	89.5	gi 414103	myrosinase, thioglucoside glucohydrolase[Brassi	Brassica napus	37					
27.81	27.81	84.3	gi 8745521	ribulose-1,5-bisphosphate carboxylase/oxygenas	Brassica napus	21					
11.79	11.79	88.3	gi 11972	ribulose bisphosphate carboxylase [Brassica rapa]	Brassica rapa	11				1	
10.55	10.55	56.0	gi 558479	tonoplast ATPase 70 kDa subunit		5				1	
10.27	10.27	54.6	gi 15226	putative triosephosphate isomerase [Arabidopsis	Arabidopsis thaliana	7				1	
10.21	10.21	64.2	gi 15229	glyceraldehyde-3-phosphate dehydrogenase Cs	Arabidopsis thaliana	6				-	
	Unu 48.95 27.81 11.79 10.55 10.27 10.21	Unu Total 48.95 48.95 27.81 27.81 11.79 11.79 10.55 10.55 10.27 10.21	Unu Total % Cov 48.95 48.95 89.5 27.81 27.81 84.3 11.79 11.79 88.3 10.55 10.55 56.0 10.27 10.27 54.6 10.21 10.21 64.2	Unu Total % Cov Accessio 48.95 48.95 89.5 gi 414103 27.81 27.81 84.3 gi 8745521 11.79 11.79 88.3 gi 11972 10.55 10.55 56.0 gi 558479 10.27 10.27 54.6 gi 15226 10.21 10.21 64.2 gi 15229	Unu Total % Cov Accessio Name 48.95 48.95 89.5 gil414103 myrosinase, thioglucoside glucohydrolase[Brassi 27.81 27.81 84.3 gil8745521 ribulose-1,5-bisphosphate carboxylase/oxygenas 11.79 11.79 88.3 gil11972 ribulose bisphosphate carboxylase [Brassica rapa] 10.55 10.55 56.0 gil558479 tonoplast ATPase 70 kDa subunit 10.27 10.27 54.6 gil15226 putative triosephosphate isomerase [Arabidopsis 10.21 10.22 64.2 gil2529 glyceraldehyde-3-phosphate dehydrogenase Cs	UnuTotal% CovAccessioNameSpecies48.9548.9589.5gil414103myrosinase, thioglucoside glucohydrolase[BrassiBrassica napus27.8127.8184.3gil8745521ribulose-1,5-bisphosphate carboxylase/oxygenasBrassica napus11.7911.7988.3gil11972ribulose bisphosphate carboxylase [Brassica rapa]Brassica rapa10.5510.5556.0gil558479tonoplast ATPase 70 kDa subunitArabidopsis thaliana10.2110.2254.6gil15226putative triosephosphate isomerase [ArabidopsisArabidopsis thaliana10.2110.2164.2gil15229glyceraldehyde-3-phosphate dehydrogenase CsArabidopsis thaliana	UnuTotal% CovAccessioNameSpeciesPeptides(95%)48.9548.9589.5gil414103myrosinase, thioglucoside glucohydrolase[BrassiBrassica napus3727.8127.8184.3gil8745521ribulose-1,5-bisphosphate carboxylase(bxygenasBrassica napus22111.7911.7988.3gil11972ribulose bisphosphate carboxylase [Brassica rapa]Brassica rapa11110.5510.5556.0gil558479tonoplast ATPase 70 kDa subunit56565610.2710.2754.6gil15226putative triosephosphate isomerase [ArabidopsisArabidopsis thaliana7710.2110.2164.2gil15229glyceraldehyde-3-phosphate dehydrogenase CsArabidopsis thaliana6	UnuTotal% CovAccessioNameSpeciesPeptides(95%)Biological Processes48.9548.9589.5gi 414103myrosinase, thioglucoside glucohydrolase[BrassiBrassica napus3727.8127.8184.3gi 8745521ribulose-1,5-bisphosphate carboxylase/oxygenasBrassica napus22111.7911.7988.3gi 11972ribulose bisphosphate carboxylase[Brassica rapa]Brassica rapa11110.5510.5656.0gi 558479tonoplast ATPase 70 kDa subunitBrassica rapa11510.2710.2754.6gi 15226putative triosephosphate isomerase[ArabidopsisArabidopsis thaliana7710.2110.2164.2gi 15229glyceraldehyde-3-phosphate dehydrogenase CsArabidopsis thaliana6	UnuTotal% CovAccessioNameSpeciesPeptides(95%)Biological ProcesseMolecular Functions48.9548.9589.5gi 414103myrosinase,thioglucoside glucohydrolase[BrassiBrassica napus373727.8127.8164.3gi 8745521ribulose-1,5-bisphosphate carboxylase(bxygenasBrassica napus22164.3611.7911.7988.3gi 11972ribulose bisphosphate carboxylase [Brassica rapa]Brassica rapa1116610.5510.5556.0gi 558479tonoplast ATPase 70 kDa subunitArabidopsis thaliana76610.2710.2754.6gi 15226putative triosephosphate dehydrogenase CsArabidopsis thaliana66610.2110.2164.2gi 15229glyceral dehyde-3-phosphate dehydrogenase CsArabidopsis thaliana666	UnuTotal% CovAccessioManeSpeciesPeptides(95%)Biological ProcesseMolecular FunctionsPANTHER ID48.9548.9589.5gi 41103myrosinase, thioglucoside glucohydrolase[BrassiBrassica napus337666627.8127.8184.3gi 874552ribulose-1,5-bisphosphate carboxylase@xygenasBrassica napus3216666611.7911.7988.3gi 11972ribulose bisphosphate carboxylase@Brassica rapaBrassica rapa111666	

Protein Group 2 - ribulose-1,5-bisphosphate carboxylase/oxygenase [Brassica napus]

				Pro	teins in Group					Peptides in Group				
N	Uni	u	Total	Accessio	Name	Species	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	: *
	2 27	7.81	27.81	gi 8745521	ribulose-1,5-bisphos	Brassica napus	2.00	99	CYHIEPVPGEETQFIAY	ICAT-C(C)@1	cleaved Y-V	0.1842	2222.25	=
	2 0).00	27.81	gi 30959	ribulose-1,5-bisphos	Brassica juncea				Deamidated(Q)@13				
	2 0	0.00	27.81	gi 30959	ribulose-1,5-bisphos	Brassica rapa	2.00	99	ELGVPIVMHDYLTGGFTAN	Oxidation(M)@8		0.4291	3207.97	
	2 0	0.00	27.81	gi 167157	ribulosebisphosphat					ICAT-C(C)@26				
	2 0	0.00	27.81	gi 1346967	Ribulose bisphosph	BRAOL	2.00	99	GHYLNATAGTCEEMMK	ICAT-C(C)@11 Oxidation(M)@14		0.1905	2014.04	
	0	0.00	26.10	gi 15732	ribulose-1,5-bisphosp	Brassica olerac				Oxidation(M)@15				
							2.00	99	LSGGDHVHAGTVVGKLEGDR		missed K-L	0.2717	2003.29	
							2.00	99	PLLGCTIKPK	ICAT-C:13C(9)(C)@5	cleaved R-P	0.1656	1304.95	
							2.00	99	TFQGPPHGIQVER			0.1852	1464.93	
							2.00	99	TKTFQGPPHGIQVER	Thr->Val@1	cleaved Y-T	0.1548	1692.06	
							2.00	99	VALEACVQAR	ICAT-C(C)@6		0.1551	1285.83	
							2.00	99	VAYPLDLFEEGSVTNMFTS	Oxidation(M)@16	cleaved Y-V	0.3629	3096.87	
							2.00	99	YGRPLLGCTIKPK	Gly->Pro@2 ICAT-C(C)@8		0.1914	1712.17	
							1.70	98	WS PE LAAACEVWK	ICAT-C(C)@9 Oxidation(W)@12		0.2116	1732.04	-
														Þ

Protein Sequence Coverage - ribulose-1,5-bisphosphate carboxylase/oxygenase [Brassica napus]

MSPQTETKASVGFKAGVKEYKLNYYTPEYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVPGEETQFIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFK ALAALRLEDLRIPPAYTKTFQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAIYKSQAETGEIKGHYLNATAGTCEEMMKRAIF ARELGVPIVMHDYLTGGFTANTSLAHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHVHAGTVVGKLEGDRESTLGFVDLLRDDYVEKDRSRGIFFTQDWVSLPGVLPVASGGIHV WHMPALTEIFGDDSVLQFGGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAVEGNEIIREACKWSPELAAACEVWKEITFNFPTIDKLDGQD

gi|119980 Ferredoxin

Pr	otei	ns Dete	ected								Ū	
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
	62	2.03	2.03	83.3	gi 119980	Ferredoxin	BRANA	1				
	63	2.02	2.02	39.3	gi 15231	putative protein [Arabidopsis thaliana]	Arabidopsisthaliana	1				
	64	2.02	2.02	51.1	gi 15235	leucyl aminopeptidase-like protein [Arabidopsis	Arabidopsis thaliana	2			c	_
Γ	65	2.02	2.02	44.6	gi 15222	6-phosphogluconate dehydrogenase, putative [A	Arabidopsisthaliana	1				
Γ	66	2.02	2.02	38.8	gi 15228	unknown protein [Arabidopsis thaliana]	Arabidopsis thaliana	1				÷
•		1				III			1		•	

Protein Group 62 - Ferredoxin

		P	roteins in Gr	oup				Peptides in Gr	oup						
N	Unu	Total	Accessio	Name	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
(62 2.03	2.03	gi 119980	Ferredoxin	1.70	98	FITPEGEQEVE CDDDVYVL	ICAT-C(C)@12 ICAT-C(C)@33		-0.0157	4243.89	4	14	4.1.1.1842.4	
					0.33	53	VVSGFVDQSDESFLDDDQI	Phe->Ser@5 ICAT-C(C)@27		0.0381	5214.46	5	14	3.1.1.1681.2	E
					0.00	<1	FITPEGEQEVECDDDVYVL	ICAT-C(C)@12	cleaved Y	-0.0196	3670.62	4	10	3.1.1.1801.3	
					0.00	<1	FITPEGEQEVECDDDVYVL	ICAT-C:13C(9)(C)@12	cleaved Y	-0.0185	3679.65	4	7	2.1.1.1686.4	
					0.00	<1	FITPEGEQEVE CDDDVYVL	Deamidated(Q)@8 ICAT-C(C)@12 ICAT-C(C)@33		0.9541	4245.84	5	7	3.1.1.1700.4	
					0.00	<1	FITPEGEQEVE CDDDVYVL	Deamidated(Q)@8 ICAT-C(C)@12 ICAT-C(C)@33		0.7723	4245.66	5	8	11.1.1.2011.2	1
					0.00	<1	FITPEGEQEVECDDDVYVL	Deamidated(Q)@8 ICAT-C:13C(9)(C)@12 ICAT-C:13C(9)(C)@33		0.0029	4262.95	4	7	2.1.1.1609.3	
					0.00	<1	FITPEGEQEVECDDDVYVL	Deamidated(Q)@8		-0.0879	4262.86	4	8	12.1.1.1977.2	-
•		1	11		•									•	

Protein Sequence Coverage - Ferredoxin

ATYKVKFITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGFVDQSDESFLDDDQIAEGFVLTCAAYPTSDVTIETHKEEELV

gi|15240013 33 kDa polypeptide of oxygen-evolving complex in photosystem II

Prote	ins Dete	ected								G	כ
N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
7	8.04	8.04	63.3	gi 15229	glyceraldehyde-3-phosphate dehydrogenase C	Arabidopsis thaliana	6			C	=
8	7.31	7.31	40.6	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsisthaliana	6				
9	6.90	6.90	57.5	gi 15227	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4				
10	6.62	6.62	80.4	gi 15240	33 kDa polypeptide of oxygen-evolving complex	Arabidopsis thaliana	7				
11	6.25	6.25	57.1	gi 15242	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	5				-
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Protein Group 10 - 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II (emb|CAA75629.1) [Arabidopsis thaliana]

		Р	roteins in Group					Peptides in Gr	oup						
N	Unu	Total	Accession #	Name	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
1	0 6.62	6.62	gi 15240013	33 kDa polypepti	2.00	99	FCFEPTSFTVK	ICAT-C(C)@2		-0.0741	1531.66	2	14	8.1.1.1354.4	
	0.00	6.61	gi]49359169	photosystem II pro	2.00	99	GTGTANQCPTIDGGSETFS	ICAT-C(C)@8		-0.0902	2626.14	3	20	11.1.1525.2	
	0.00	6.57	gi]45181461	photosystem II pro	2.00	99	KFCFEPTSFTVK	ICAT-C:13C(9)(C)@3	missed K-F	-0.0811	1668.78	2	16	9.1.1.1449.2	
	0.00	6.56	gi]5052366	33 kDa oxygen ev	0.55	72	KFCFEPTSF	ICAT-C:13C(9)(C)@3	cleaved F-T	-0.0628	1340.58	2	12	8.1.1.1348.2	
					0.02	5	ERVPFLFTVK	Glu->Ala@1	cleaved G-E	-0.0505	1176.65	2	13	7.1.1.1578.3	
					0.01	3	AD SV SKNAP PE FON TK	Ser->Oxoalanine(S)@3 Oxidation(P)@10	missed K-N	-0.0246	1745.79	2	12	12.1.1.1531.3	
					0.01	2	ENVKNTAASVGEITLKVTK	Dioxidation(K)@4 Deamidated(N)@5 Oxidation(K)@16	missed K-N	0.8785	2050.95	3	12	10.1.1.1403.3	
					0.01	2	SLQSTATFLQSAKIATAPS	Deamidated(R)@20 Phospho(S)@22	cleaved A	-0.2541	2795.14	3	11	12.1.1.1614.2	
					0.00	1	IAGFALATSALVVSGASAE	Formyl@N-term	missed K-R	-0.1842	2287.03	3	11	2.1.1.1424.4	Ŧ
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Protein Sequence Coverage - 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II (emb|CAA75629.1) [Arabidopsis thaliana]

MAASLQSTATFLQSAKIATAPSRGSSHLRSTQAVGKSFGLETSSARLTCSFQSDFKDFTGKCSDAVKIAGFALATSALVVSGASAEGAPKRLTYDEIQSKTYMEVKGTGTANQCPTIDGGSETFSFKP GKYAGKKFCFEPTSFTVKADSVSKNAPPEFQNTKLMTRLTYTLDEIEGPFEVASDGSVNFKEEDGIDYAAVTVQLPGGERVPFLFTVKQLDASGKPDSFTGKFLVPSYRGSSFLDPKGRGGSTGYDNA VALPAGGRGDEEELVKENVKNTAASVGEITLKVTKSKPETGEVIGVFESLQPSDTDLGAKVPKDVKIQGVWYGQLE

gi|17852 Ribulose bisphosphate carboxylase /oxygenase small subunit

P	rotei	ns Dete	cted									
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
Γ	5	8.96	8.96	68.9	gi 15226	putative triosephosphate isomerase [Arabidopsi	Arabidopsis thaliana	5				
	6	8.55	8.55	81.8	gi 17852	ribulose bisphosphate carboxylase/oxygenase s	Brassica napus	15				
Γ	7	8.04	8.04	63.3	gi 15229	glyceraldehyde-3-phosphate dehydrogenase C	Arabidopsis thaliana	6				
	8	7.31	7.31	40.6	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	6				
	9	6.90	6.90	57.5	gi 15227	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4				-
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Protein Group 6 - ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

		Р	roteins in Group					Peptides in Gr	oup						
N	Unu	Total	Accession #	Name	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
6	8.55	8.55	gi 17852	ribulose bisphos	2.00	99	LPLFGCTDSAQVLK	ICAT-C:13C(9)(C)@6		-0.1648	1726.77	2	22	8.1.1.1351.2	
6	0.00	8.55	gi 132091	Ribulose bisphos	2.00	99	NKWIPCVEFELEHGFVYR	Lys->Asn@2	missed K-W	-0.0485	2251.00	3	17	9.1.1.1534.3	
	0.00	8.55	gi)79013990	chloroplast ribulos	2.00			NUTCAT(C)@0		0.0499	2475.00	2	4.4	9.4.4.409.4	-
	0.00	8.55	gi]266891	Ribulose bisphosp	2.00		QVQCISTIAIKPPSTIGA	ICAT-C:13C(9)(C)@4		-0.0400	2175.00	2	14	0.1.1.1400.4	
	0.00	8.55	gi]17850	ribulose bisphospl	2.00	99	WI PCVE FELEHGFVYR	ICAT-C:13C(9)(C)@4		-0.0916	2259.03	3	21	9.1.1.1526.2	
	0.00	8.55	gi]119720808	ribulose bisphospl	0.51	69	CISFIAYKPPSFTGA	ICAT-C:13C(9)(C)@1	cleaved Q	-0.0564	1836.89	2	13	7.1.1.1580.2	
	0.00	8.54	gi]17855	rubisco ssu precur	0.02	5	CTDSAQVLK	ICAT-C(C)@1	cleaved G	-0.0234	1190.57	2	11	8.1.1.1226.2	
	0.00	8.54	gi\406727	ribulose-1,5-bisph	0.01	3	VSCMKVWPPVGKK	ICAT-C:13C(9)(C)@3 Oxidation(M)@4 Oxidation(K)@5 Lys->Asn@12	missed K-V	0.0720	1711.95	4	12	3.1.1.1505.3	
					0.01	2	QVQCISFIAYKPPSFTG	GIn->pyro-Glu@N-term ICAT-C:13C(9)(C)@4 Gly->GIn@17	cleaved G-A	-0.0488	2175.06	2	14	8.1.1.1408.4	
					0.00	< 1	PLFGCTDSAQVLK	Gly->Cys@4 ICAT-C:13C(9)(C)@4	cleaved L-P	-0.0784	1895.91	2	13	8.1.1.1434.4	Ŧ
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Protein Sequence Coverage - ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

MASSMLSSAAVVTSPAQATMVAPFTGLKSSAAFPVTRKANNDITSIASNGGRVSCMKVWPPVGKKKFETLSYLPDLTEVELGKEVDYLLRNKWIPCVEFELEHGFVYREHGSTPGYYDGRYWTMWKLP LFGCTDSAQVLKEVQECKTEYPNAFIRIIGFDNNRQVQCISFIAYKPPSFTGA

gi|15219234 ATPase 70 kDa subunit, putative

P	rotei	ns Dete	cted)
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT ^	
Г	10	6.62	6.62	80.4	gi 15240	33 kDa polypeptide of oxygen-evolving complex	Arabidopsis thaliana	7				a
Г	11	6.25	6.25	57.1	gi 15242	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	5				l
	12	6.02	6.02	48.0	gi 15224	cytoplasmic aconitate hydratase[Arabidopsis th	Arabidopsis thaliana	7				
	13	6.02	6.02	60.1	gi 15225	succinyl-CoAligase beta subunit [Arabidopsis th	Arabidopsis thaliana	4				
	14	6.01	6.01	58.6	gi 15219	ATPase 70 kDasubunit, putative [Arabidopsis th	Arabidopsis thaliana	6			+	
		T							1		•	

Protein Group 14 - ATPase 70 kDa subunit, putative [Arabidopsis thaliana]

			Pi	roteins in Group					Peptides in Gr	oup						
1	4 I	Jnu	Total	Accession #	Name	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
	14	6.01	6.01	gi 15219234	ATPase 70 kDa si	2.00	99	EDYLAQNAFTPYDKFCPFYK	ICAT-C(C)@16	missed K-F	-0.0349	2686.20	3	20	10.1.1.1471.3	=
		0.00	6.01	gi]558479	tonoplast ATPase	2.00	99	YSNSDAVVYVGCGER	ICAT-C:13C(9)(C)@12		-0.0148	1853.85	2	18	2.1.1.1420.3	
		0.00	6.01	gi]2493122	Vacuolar ATP syn	1.70	98	VLDALFPSVLGGTCAIPGA	ICAT-C(C)@14 ICAT-C(C)@22		-0.1051	2746.31	3	14	8.1.1.1414.3	
						0.29	49	VLDALFPSVLGGTCAIPGAF	ICAT-C(C)@14	cleaved F-G	-0.0744	2174.07	3	12	7.1.1.1671.2	
						0.01	2	LEGDSATIQVYEETAGLTV	Tyr->Gly@11 Oxidation(P)@22		-0.1709	2599.12	3	12	2.1.1.1510.3	
						0.00	1	NIIHFYNLANQAVER	Deamidated(N)@1 Ile->Val@3 Oxidation(N)@10		-0.1415	1803.74	3	11	2.1.1.1389.4	
						0.00	1	DALFPSVLGGTCAIPGAFG	Leu->His@8 ICAT-C:13C(9)(C)@12 ICAT-C:13C(9)(C)@20	cleaved L-D	0.9203	2577.22	3	12	8.1.1.1443.3	
						0.00	< 1	DGIQRPLK	Oxidation(D)@1	cleaved F-D	-0.0870	941.4424	2	7	6.1.1.1770.4	
						0.00	<1	DMGYNVSMMADSTSRWAEA	Oxidation(M)@2 Deamidated(N)@5 Dethiomethyl(M)@9	missed R-W	0.1046	2360.10	2	9	12.1.1.1680.3	Ŧ
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Protein Sequence Coverage - ATPase 70 kDa subunit, putative [Arabidopsis thaliana]

MPAFYGGKLTTFEDDEKESEYGYVRKVSGPVVVADGMAGAAMYELVRVGHDNLIGEIIRLEGDSATIQVYEETAGLTVNDPVLRTHKPLSVELGPGILGNIFDGIQRPLKTIARISGDVYIPRGVSVP ALDKDCLWEFQPNKFVEGDTITGGDLYATVFENTLMNHLVALPPDAMGKITYIAPAGQYSLKDTVIELEFQGIKKSYTMLQSWPVRTPRPVASKLAADTPLLTGQR**VLDALFPSVLGGTCAIPGAFGC** GKTVISQALSKYSNSDAVVYVGCGERGNEMAEVLMDFPQLTMTLPDGREESVMKRTTLVANTSNMPVAAREASIYTGITIAEYFRDMGYNVSMMADSTSRWAEALREISGRLAEMPADSGYPAYLAAR LASFYERAGKVKCLGGPERNGSVTIVGAVSPPGGDFSDPVTSATLSIVQVFWGLDKKLAQRKHFPSVNWLISYSKYSTALESFYEKFDPDFINIRTKAREVLQREDDLNEIVQLVGKDALAEGDKITL ETAKLLREDYLAQNAFTPYDKFCPFYKSVWMMRNIIHFYNLANQAVERAAGMDGQKITYTLIKHRLGDLFYRLVSQKFEDPAEGEDTLVEKFKKLYDDLNAGFRALEDETR

gi|15229231 Glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC)

Pro	otei	ns Dete	ected									
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
	4	9.45	9.45	66.2	gi 60686	oxalic acid oxidase [Brassica napus]	Brassica napus	6				
	5	8.96	8.96	68.9	gi 15226	putative triosephosphate isomerase [Arabidopsi	Arabidopsis thaliana	5				
	6	8.55	8.55	81.8	gi 17852	ribulose bisphosphate carboxylase/oxygenase s	Brassica napus	15				
	7	8.04	8.04	63.3	gi 15229	glyceraldehyde-3-phosphate dehydrogenase C	Arabidopsis thaliana	6				
	8	7.31	7.31	40.6	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	6				-
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Protein Group 7 - glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) [Arabidopsis thaliana]

			P	roteins in Group					Peptides in Gro	oup						
	N	Unu	Total	Accession #	Name	Con⊽	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
	7	8.04	8.04	gi 15229231	glyceraldehyde-3	2.00	99	DAPMFVVGVNEHEYK	Dethiomethyl(M)@4		-0.0091	1685.79	3	24	2.1.1.1413.3	
		0.00	8.04	gi]15222848	glyceraldehyde-3-	2.00	99	GGRAAS FNI IPSSTGAAK	Arg->GluSA(R)@3	missed R-A	-0.0465	1660.79	2	18	9.1.1.1433.3	
						2.00	99	SDLDIVSNASCTINCLAPL	ICAT-C(C)@11 ICAT-C(C)@15		-0.0993	2589.17	3	14	12.1.1.1641.2	
						2.00	99	TLLFGEKPVTVF		cleaved F-G	-0.0503	1349.70	2	15	7.1.1.1589.2	
						0.02	4	IRIGINGFGR	Arg->Asn@2	missed R-I@2	-0.0213	1059.56	2	11	7.1.1.1522.4	
						0.01	3	GGRAAS FNI IPSSTGAAKA	Deamidated(N)@8	missed R-A	-0.2246	2059.87	4	10	11.1.1.1446.4	
						0.01	2	KVVI SAPSK	Trimethyl(K)@1 Val->Arg@2	missed K-V	-0.0615	1026.59	2	13	8.1.1.1252.4	
						0.00	1	ADKKIR	Deamidated(R)@6	cleaved M	-0.0977	730.3361	1	6	5.1.1.2076.4	
						0.00	< 1	CLAPLAK	ICAT-C:13C(9)(C)@1	cleaved N-C	-0.0462	950.5209	2	10	8.1.1.1272.2	
						0.00	< 1	AASFNIIPSSTGAAK			-0.0378	1433.71	2	5	1.1.1.1942.3	
						0.00	< 1	AASFNIIPSSTGAAK			-0.0617	1433.68	2	7	2.1.1.1844.2	
						0.00	< 1	AASFNIIPSSTGAAK			0.1566	1433.90	2	5	5.1.1.1940.3	+
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Protein Sequence Coverage - glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) [Arabidopsis thaliana]

MADKKIRIGINGFGRIGRLVARVVLQRDDVELVAVNDPFITTEYMTYMFKYDSVHGQWKHNELKIKDEKTLLFGEKPVTVFGIRNPEDIPWAEAGADYVVESTGVFTDKDKAAAHLKGGAKKVVISAP SKDAPMFVVGVNEHEYKSDLDIVSNASCTTNCLAPLAKVINDRFGIVEGLMTTVHSITATQKTVDGPSMKDWRGGRAASFNIIPSSTGAAKAVGKVLPALNGKLTGMSFRVPTVDVSVVDLTVRLEKA ATYDEIKKAIKEESEGKLKGILGYTEDDVVSTDFVGDNRSSIFDAKAGIALSDKFVKLVSWYDNEWGYSSRVVDLIVHMSKA

gi|15232776 Putative transitional endoplasmic reticulum ATPase

Р	rotei	ns Dete	ected								[
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
Γ	17	4.49	4.49	62.1	gi 15240	succinate dehydrogenase flavoprotein alpha sub	Arabidopsis thaliana	5				_
	18	4.46	4.46	65.0	gi 15232	putative transitional endoplasmic reticulum ATP	Arabidopsis thaliana	2				
ľ	19	4.29	4.29	35.8	gi 15233	cytosolic triosephosphatisomerase [Arabidopsis	Arabidopsis thaliana	4				
	20	4.16	4.16	38.1	gi 15234	P-Protein - like protein [Arabidopsis thaliana]	Arabidopsis thaliana	1				
	21	4.15	6.75	53.1	gi 14722	unnamed protein product [Brassica napus]	Brassica napus	6				-
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Protein Group 18 - putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana]

			P	roteins in Group					Peptides in Gr	oup						
Γ	N	Unu	Total	Accession #	Name	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
	18	4.46	4.46	gi 15232776	putative transitio	2.00	99	GVLFYGPPGCGK	ICAT-C:13C(9)(C)@10		-0.0499	1429.69	2	14	8.1.1.1321.3	н
		0.00	4.31	gi]15242723	putative protein [A	2.00	99	QSAPCVLFFDELDSIATQR	GIn->pyro-Glu@N-term		0.0016	2358.16	3	16	10.1.1.1661.2	
		0.00	4.31	gi]15231775	CDC48 - like prote	0.31	E1	ADOCADOUT FEDELOCIAT	IGAT-C:13C(9)(C)@5	missed P.O.	0.0467	2259.16	2	12	10.1.1.1661.2	
						0.51	51	ARQSAFCVLFFDELDSIAI	Deamidated(R)@2 Deamidated(Q)@3 Pro->Ser@6 No ICAT(C)@7	111556014-Q	0.0407	2350.10	3	10	10.1.1.1001.2	
						0.14	28	FFDE LD SIATORGGGS GGD		cleaved L-F	-1.8506	2510.27	3	13	2.1.1.1590.4	
						0.01	2	DE LD SIATORGGGSGGDGG	Ser->Gly@14 Dehydrated(D)@23	cleaved F	-0.0222	2169.94	4	13	11.1.1.1456.3	
						0.00	1	DQLIYIPLPDEDSR	Deamidated(Q)@2 Oxidation(P)@7 Dehydrated(E)@11	cleaved L-D	0.1090	1671.90	4	11	2.1.1.1387.4	
						0.00	< 1	IIGATNR		cleaved F-I	-0.1011	743.3279	1	7	7.1.1.1690.2	
						0.00	<1	AALRKSPIAKDVDIGALAK	Oxidation(D)@13 Oxidation(K)@19	missed R-K	-0.1299	1968.00	3	8	3.1.1.1514.3	
	_					0.00	<1	AALRKSPIAKDVDIGALAK	Oxidation(P)@7	missed R-K	-0.1317	1968.00	3	9	2.1.1.1427.4	Ŧ
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Protein Sequence Coverage - putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana]

MSTPAESSDSKSKKDFSTAILERKKSPNRLVVDEAINDDNSVVSLHPATMEKLQLFRGDTILIKGKKRKDTVCIALADETCEEPKIRMNKVVRSNLRVRLGDVISVHQCPDVKYGKRVHILPVDDTVE GVTGNLFDAYLKPYFLEAYRPVRKGDLFLVRGGMRSVEFKVIETDPAEYCVVAPDTEIFCEGEPVKREDEERLDDVGYDDVGGVRKQMAQIRELVELPLRHPQLFKSIGVKPPKGILLYGPPGSGKTL IARAVANETGAFFFCINGPEIMSKLAGESESNLRKAFEEAEKNAPSIIFIDEIDSIAPKREKTNGEVERRIVSQLLTLMDGLKSRAHVIVMGATNRPNSIDPALRRFGRFDREIDIGVPDEIGRLEVL RIHTKNMKLAEDVDLERISKDTHGYVGADLAALCTEAALQCIREKMDVIDLEDDSIDAEILNSMAVTNEHFHTALGNSNPSALRETVVEVPNVSWNDIGGLENVKRELQETVQYPVEHPEKFEKFGMS PSKGVLFYGPPCCCKTLLAKAIANECQANFISVKGPELLTMWFGESEANVREIFDKARQSAPCVLFFDELDSIATQRGGGSGGDGGGAADRVLNQLLTEMDGMNAKKTVFIIGATNRPDIIDSALLRP GRLDQLIYIPLPDEDSRLNIFKAALRKSPIAKDVDIGALAKYTQGFSGADITEICQRACKYAIRENIEKDIEKEKRRSENPEAMEEDGVDEVSEIKAAHFEESMKYARRSVSDADIRKYQAFAQTLQQ SRGFGSEFRFENSAGSGATTGVADPFATSAAAAGDDDDLYN

gi|15233272 Cytosolic triosephosphatisomerase

Ρ	rotei	ns Dete	ected									
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*
	8	9.78	9.78	62.4	gi 8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	6				
I٢	9	8.91	8.91	68.9	gi 899226	malate dehydrogenase [Brassica napus]	Brassica napus	6				
	10	8.16	8.16	43.7	gi 15239	tubulin beta-6 chain (sp P29514) [Arabidopsis tha	Arabidopsis thaliana	4				7
	11	7.72	7.72	62.2	gi 15233	cytosolic triosephosphatisomerase [Arabidopsist	Arabidopsisthaliana	5				
ľ	12	7.46	7.46	40.9	gi 15222	tubulin alpha-2/alpha-4 chain, putative [Arabidops	Arabidopsis thaliana	4				7
	13	6.70	6.70	72.1	gi 15234	peptidylprolyl isomerase ROC1[Arabidopsis thali	Arabidopsis thaliana	4				-

Protein Group 11 - cytosolic triosephosphatisomerase [Arabidopsis thaliana]

			Prot	teins in Group				F	Peptides in Group				
N	Unu	Total	Accessio	Name	Species	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	; *
1	1 7.72	7.72	gi 15233	cytosolic triosephos	Arabidopsis th	2.00	99	IIYGGSVNGGNCK	Deamidated(N)@8 ICAT-C:13C(9)(C)@12		0.1993	1517.95	
						2.00	99	VAYALAQGLKVIACVGETL	Lys->Ser@10 ICAT-C(C)@14 Glu->Lys@21	missed K-V	0.2225	2517.58	Ш
						2.00	99	VIACVGETLEER	ICAT-C(C)@4 Glu->Gln@11		0.1885	1543.99	
						1.70	98	GKVASPAQAQEVHDELRK	Trimethyl(K)@2	cleaved T	0.2133	2004.28	
						0.02	4	VAYALAQGLK	Tyr->Trp@3 Deamidated(Q)@7		0.1042	1056.70	
						0.00	1	AKNVSADVAATTR	Deamidated(N)@3	cleaved L	0.1334	1303.80	
						0.00	1	IIYGGSVNGGNCKEL	Deamidated(N)@8 Cys->Pro@12	cleaved L	0.1863	1517.95	
						0.00	<1	ELGGQADVDGFLVGGASLKP	Deamidated(Q)@5	cleaved P	0.3087	1930.27	
						0.00	< 1	ELGGQADVDGFLVGGASLK			0.2530	2787.72	
						0.00	<1	ELGGOADVDGFLVGGASLK	Deamidated(Q)@5 Phe->Met@11	missed K-A	0.2447	3270.95	
						0.00	<1	IIYGGSVNGGNCK	Deamidated(N)@11 ICAT-C(C)@12		0.1796	1892.13	Ŧ
						•						•	

Protein Sequence Coverage - cytosolic triosephosphatisomerase [Arabidopsis thaliana]

MARKFFVGGNWKCNGTAEEVK<mark>KIVNTLNEAQVPSQDVVEVVVSPPYVFLP</mark>LVKSTLRSDFFVAAQNCWVKKGGAFTGEVSAEMLVNLDIP**WVILGHSERR**AILNESSEFVGDK**VAYALAQGLKVIACV** GETLEEREAGSTMDVVAAQTKAIADRVTNWSNVVIAYEPVWAIGTGKVASPAQAQEVHDELRKWLAKNVSADVAATTRIIYGGSVNGGNCKELGGQADVDGFLVGGASLKPEFIDIIKAAEVKKSA

gi|15237260 Succinyl-CoA synthetase, alpha subunit

Р	rotei	ns Dete	cted								G	
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
Γ	56	2.08	2.08	42.6	gi 15227	putative non-LTR retroelement reverse transcrip	Arabidopsis thaliana	1				
	57	2.07	2.07	60.7	gi 15237	succinyl-CoAsynthetase, alphasubunit [Arabido	Arabidopsis thaliana	2				
ľ	58	2.07	2.07	44.0	gi 15242	NADH dehydrogenase [Arabidopsis thaliana]	Arabidopsis thaliana	2				
Г	59	2.06	2.06	39.2	gi 15222	vacuolar ATP synthase subunit C, putative [Arab	Arabidopsis thaliana	1				
Г	60	2.03	2.03	56.6	gi 31043	glutamate-cysteine ligase [Brassica juncea]	Brassicajuncea	1				-
		1				"		1	1		Þ	

Protein Group 57 - succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana]

			Pr	roteins in Group					Peptides in Gro	oup						
1	I U	Jnu	Total	Accession #	Name	Con… ⊽	Conf V	Sequence 🗠	Modifications A	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
	57	2.07	2.07	gi 15237260	succinyl-CoA syr	2.00	99	LIGPNCPGIIKPGECK	ICAT-C:13C(9)(C)@6		-0.0740	2110.10	3	20	9.1.1.1409.2	_
\vdash		0.00	2.00	gi 15241592	succinyl-CoA-ligas	0.07	14	LLGS LRHSGGGCSGSSK	Gly->Ala@9 ICAT-C(C)@12	missed R-H	-0.1354	1842.80	2	12	11.1.1.1468.4	
						0.00	< 1	ENGTDKPVVAFIAGLTAPP			-0.2470	2108.87	3	8	10.1.1.1359.3	
						0.00	< 1	ENGTDKPVVAFIAGLTAPP	Glu->pyro-Glu@N-term	missed R-R	-0.2362	2246.97	3	8	12.1.1.1480.2	
						0.00	< 1	GHAGAIVSGGK		cleaved M	-0.0612	952.4479	2	7	7.1.1.1655.2	
						0.00	< 1	HS GGGC SGS SK	ICAT-C(C)@6		0.0712	1189.58	2	6	6.1.1.1717.4	
						0.00	<1	HS GGGC SGS SK	No ICAT(C)@6 Oxidation(K)@11		0.2425	978.6251	2	9	7.1.1.1607.3	
						0.00	<1	HS GGGC SGS SKVCS LT SLV	ICAT-C(C)@6 ICAT-C(C)@13 Deamidated(R)@22 Oxidation(F)@24	cleaved F	0.0279	2841.36	4	7	7.1.1.1834.2	
						0.00	< 1	IGEIGGTAEEDAAALI	Oxidation(D)@11	cleaved L-I	-0.0785	1544.67	2	7	9.1.1.1596.4	
						0.00	< 1	IGEIGGTAEEDAAALI	Oxidation(D)@11	cleaved L-I	-0.0538	1544.70	2	8	10.1.1.1745.2	Ŧ
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Protein Sequence Coverage - succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana]

MSRQVTRLLGSLRHSGGGCSGSSKVCSLTSLVQSRSFGTTPPPPAAVFVDKNTRVICQGITGKNGTFHTEQAIEYGTKMVAGVTPKKGGTEHLGLPVFNTVAEAKAETKANASVIYVPAPFAAAAIME GLAAELDLIVCITEGIPQHDMVRVKAALNSQSKTR**LIGPNCPGIIKPGECKIGIMPGYIHKPGKIGIVSRSGTLTYEAVF**QTTAVGLGQSTCVGIGGDPFNGTNFVDCLEKFFVDPQTEGIVL**IGEIG** GTAEEDAAALIKENGTDKPVVAFIAGLTAPPGRRMGHAGAIVSGGKGTAQDKIKSLRDAGVKVVESPAKIGAAMFELFQERGLLK

gi|899226 Malate dehydrogenase, mitochondrial precursor

P	rotei	ns Dete	ected								1	
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
I	1	45.88	45.88	90.5	gi 62131	myrosinase [Brassica rapa var. parachinensis]	Brassica rapa var. parachinensis	68				_
	2	27.80	27.80	67.6	gi 8745521	ribulose-1,5-bisphosphate carboxylase/oxygena	Brassica napus	31				
	3	10.32	10.32	86.5	gi 899226	malate dehydrogenase [Brassica napus]	Brassica napus	7				
ľ	4	9.45	9.45	66.2	gi 60686	oxalic acid oxidase [Brassica napus]	Brassica napus	6				
	5	8.96	8.96	68.9	gi 15226	putative triosephosphate isomerase [Arabidopsi	Arabidopsisthaliana	5				-
	•		i								•	

Protein Group 3 - malate dehydrogenase [Brassica napus]

		P	roteins in Group					Peptides in Gro	oup						
Ν	Unu	Total	Accession #	Name	Con	7 Conf ⊽	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
3	10.32	10.32	gi 899226	malate dehydrog	2.0	99	AGKGSATLSMAYAGALFAD	Ala->Gly@1	missed K	-0.0028	2550.19	3	22	9.1.1.1483.3	=
3	0.00	10.32	gi 2497857	Malate dehydrog				Phospho(S)@5							
								Oxidation(M)@10 ICAT-C:13C(9)(C)@21							
					2.0	99	GLNGVPDVVECSYVQSTIT	ICAT-C:13C(9)(C)@11		-0.0812	3135.50	3	15	9.1.1.1590.3	
					2.0	99	VAILGAAGGIGQPLALLMK	Oxidation(M)@18		-0.0257	1808.03	3	15	7.1.1.1602.4	
					2.0) 99	YCPHALVNMISNPVNSTVP	ICAT-C(C)@2 Oxidation(M)@9		-0.0637	3070.49	3	22	9.1.1.1517.2	
					2.0) 99	YCPHALVNMISNPVNSTVP	ICAT-C:13C(9)(C)@2 Oxidation(M)@9	missed K-K	-0.0154	3207.67	3	19	9.1.1.1493.3	
					0.2	9 49	SALVRSSASAKQSLLR	Lys->Allysine(K)@11 Deamidated(R)@16	missed R-S	-0.0954	1672.81	2	13	2.1.1.1574.2	
					0.0	2 3	AKYCPHALVNMISNPVNST	Formyl@N-term No ICAT(C)@4 Oxidation(M)@11	cleaved I-A	-0.0935	3070.46	4	16	9.1.1.1519.4	
					0.0) 1	RSALVRSSASAK	Arg->Thr@6	cleaved F	0.0228	1176.66	2	11	8.1.1.1309.2	Ŧ
		111		Þ	•									۱.	

Protein Sequence Coverage - malate dehydrogenase [Brassica napus]

MFRSALVRSSASAKQSLLRRSFSSGSVPERKVAILGAAGGIGQPLALLMKLNPLVSSLSLYDIANTPGVAADVGHINTRSQVVGYMGDDNLAKALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKN LWSAIAKYCPHALVNMISNPVNSTVPIAAEIFKKAGMYDEKKLFGVTTLDVVRVKTSYAGKANVPVAEVNVPAIVGHAGVTILPLFSQATPQAILSGDALTVTTKRTQDGGTEVEEAKAGKGSATLSM AYAGALFADACLKGLNGVPDVVECSYVQSTITELPFFASKVRLGKNGVEEVLDLGPLSDFEKEGLEALRPGIKSTIEKGVKFANQ

gi|15240075 Succinate dehydrogenase flavoprotein alpha subunit

Р	rotei	ns Dete	ected									
	Ν	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
ΙΓ	15	5.75	5.75	44.2	gi 15225	hypothetical protein [Arabidopsis thaliana]	Arabidopsisthaliana	4				_
Г	16	5.49	5.49	57.6	gi 15238	5-methyltetrahydropteroyltriglutamate-homocyst	Arabidopsis thaliana	5				
	17	4.49	4.49	62.1	gi 15240	succinate dehydrogenase flavoprotein alpha sub	Arabidopsis thaliana	5				
ľ	18	4.46	4.46	65.0	gi 15232	putative transitional endoplasmic reticulum ATP	Arabidopsis thaliana	2				
	19	4.29	4.29	35.8	gi 15233	cytosolic triosephosphatisomerase [Arabidopsis	Arabidopsis thaliana	4				-
	•	1				I III	i	i	Î		۱.	

Protein Group 17 - succinate dehydrogenase flavoprotein alpha subunit (emb|CAA05025.1) [Arabidopsis thaliana]

		F	roteins in Group					Peptides in Gro	oup						
N	Unu	. Total	Accession #	Name	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
1	4.4	4.49	gi 15240075	succinate dehydr	2.00	99	AAIGLSEHGFNTACITK	ICAT-C:13C(9)(C)@14		-0.0135	1968.00	3	14	2.1.1.1427.4	=
					2.00	99	TQET LEEGCQL IDK	ICAT-C(C)@9		-0.1059	1832.77	2	15	12.1.1.1529.3	
					0.29	49	PLODLEFVOFHPTGIYGAG	NeuAc(T)@13 ICAT-C(C)@20	cleaved L	-0.0542	3465.62	4	14	10.1.1.1567.4	
					0.11	22	AGLPLQDLEFVQFHPTGIY	Gly->Pro@2 ICAT-C:13C(9)(C)@23		-0.0572	3464.72	4	13	3.1.1.1675.2	
					0.06	13	GDDPDAVIPGLMAAGEAAC	Ile->Thr@8 Oxidation(M)@12 ICAT-C(C)@19		-0.0891	2795.17	3	13	11.1.1.1597.2	
					0.02	4	QKPLEKDAGEKTIAWL	Deamidated(Q)@1 Oxidation(P)@3	cleaved L	-0.1711	1842.80	2	11	11.1.1.1468.4	
					0.01	2	FRSSQTILATGGYGR	Ala->Val@9	missed R-S	-0.1549	1640.70	2	11	8.1.1.1324.3	
					0.00	99	AAIGLSEHGFNTACITK	Glu->Asp@7 Methyl(T)@12 ICAT-C:13C(9)(C)@14		-0.0117	1968.00	3	17	3.1.1.1514.3	
					0.00	96	AAIGLSEHGFNTACITK	ICAT-C:13C(9)(C)@14		-0.0488	1967.96	3	15	9.1.1.1425.3	-
•				+	•					0 4005	0000 11	•	-	•	

Protein Sequence Coverage - succinate dehydrogenase flavoprotein alpha subunit (emb|CAA05025.1) [Arabidopsis thaliana]

MWRCVSRGFRAPASKTSSLFDGVSGSRFSRFFSTGSTDTRSSYTIVDHTYDAVVVGAGGAGLRAAIGLSEHGFNTACITKLFPTRSHTVAAQGGINAALGNMSEDDWRWHMYDTVKGSDWLGDQDAIQ YMCREAPKAVIELENYGLPFSRTEEGKIYQRAFGGQSLDFGKGGQAYRCACAADRTGHALLHTLYGQAMKHNTQFFVEYFALDLLMASDGSCQGVIALNMEDGTLHRFRSSQTILATGGYGRAYFSAT SAHTCTGDGNAMVARAGLPLQDLEFVQFHPTGIYGAGCLITEGSRGEGGILRNSEGERFMERYAPTAKDLASRDVVSRSMTMEIREGRGVGPHKDHIYLHLNHLPPEVLKERLPGISETAAIFAGVDV TKEPIPVLPTVHYNMGGIPTNYHGEVVTIKGDDPDAVIPGLMAAGEAACASVHGANRLGANSLLDIVVFGRACANRVAEISKPGEKQKPLEKDAGEKTIAWLDRLRNSNGSLPTSTIRLNMQRIMQNN AAVFRTQETLEEGCQLIDKAWESFGDVQVKDRSMIWNSDLIETLELENLLINASITMHSAEARKESRGAHAREDFTKREDGEWMKHTLGYWEDEKVRLDYRPVHMDTLDDEIDTFPPKARVY

gi|15232865 Reversibly glycosylated polypeptide-1

Р	rotei	ns Dete	ected								G	3
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	•
Γ	6	8.55	8.55	81.8	gi 17852	ribulose bisphosphate carboxylase/oxygenase s	Brassica napus	15				
	7	8.04	8.04	63.3	gi 15229	glyceraldehyde-3-phosphate dehydrogenase C	Arabidopsis thaliana	6				
	8	7.31	7.31	40.6	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	6				
ľ	9	6.90	6.90	57.5	gi 15227	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4				
	10	6.62	6.62	80.4	gi 15240	33 kDa polypeptide of oxygen-evolving complex	Arabidopsis thaliana	7				+
E								1			4	

Protein Group 8 - reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

			Proteins in Group					Peptides in Gro	oup						
N	Unu.	Tota	Accession #	Name	Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	*
	8 7.3	31 7.3	1 gi 15232865	reversibly glycos	2.00	99	GT LF PMCGMNLAFDR	Oxidation(M)@6 ICAT-C:13C(9)(C)@7 Oxidation(N)@10		-0.0481	1939.85	2	16	8.1.1.1346.2	Ш
					2.00	99	NLLCPSTPFFFNTLYDPYR	Deamidated(N)@1 ICAT-C(C)@4 Phe->Leu@9		-0.0405	2501.18	3	17	8.1.1.1428.3	
					2.00	99	VICDHLGLGVK	ICAT-C(C)@3		-0.0337	1379.72	2	17	8.1.1.1295.3	
					1.30	95	YIFTIDDDCFVAK	ICAT-C:13C(9)(C)@9		-0.0702	1784.80	2	15	9.1.1.1496.3	
					0.01	2	ASCISFK	ICAT-C:13C(9)(C)@3		-0.0221	990.5035	2	9	8.1.1.1274.4	
					0.00	< 1	EKLSPIDPYFDK		missed K-L	-0.0118	1450.72	2	6	3.1.1.1892.2	
					0.00	<1	EPANTVGIPVNHI	Glu->pyro-Glu@N-term Deamidated(N)@4 Oxidation(P)@9	cleaved V	-0.0572	1358.62	2	8	9.1.1.1353.2	
					0.00	<1	EPANTVGIPVNHIP		cleaved V	-0.0411	1456.72	2	7	5.1.1.1981.4	
					0.00	<1	EPANTVGIPVNHIP		cleaved V	-0.0947	1456.67	2	6	6.1.1.1911.4	
					0.00	<1	EPANTVGIPVNHIP		cleaved V	-0.1213	1456.64	2	7	7.1.1.1808.3	Ŧ
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Protein Sequence Coverage - reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

MVEPANTVGIPVNHIPLLKDELDIVIPTIRNLDFLEMWRPFLQPYHLIIVQDGDPSKTIAVPEGFDYELYNRNDINRILGPKASCISFKDSACRCFGYMVSKKKYIFTIDDDCFVAKDPSGKAVNALE QHIKNLLCPSTPFFFNTLYDPYREGADFVRGYPFSLREGVSTAVSHGLWLNIPDYDAPTQLVKPKERNTRYVDAVMTIPKGTLFPMCGMNLAFDRELIGPAMYFGLMGDGQPIGRYDDMWAGWCIKVI CDHLGLGVKTGLPYIYHSKASNPFVNLKKEYKGIFWQEDIIPFFQSAKLTKEAVTVQQCYMELSKLVKEKLSPIDPYFDKLADAMVTWIEAWDELNPPTKA

gi|60686421 Oxalic acid oxidase

Р	rotei	ns Dete	ected								G	
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
Г	1	45.88	45.88	90.5	gi 62131	myrosinase [Brassica rapa var. parachinensis]	Brassica rapa var. parachinensis	68				_
Γ	2	27.80	27.80	67.6	gi 8745521	ribulose-1,5-bisphosphate carboxylase/oxygena	Brassica napus	31				
Γ	3	10.32	10.32	86.5	gi 899226	malate dehydrogenase [Brassica napus]	Brassica napus	7				
	4	9.45	9.45	66.2	gi 60686	oxalic acid oxidase [Brassica napus]	Brassica napus	6				
ľ	5	8.96	8.96	68.9	gi 15226	putative triosephosphate isomerase[Arabidopsi	Arabidopsis thaliana	5				-
	(1		•	

Protein Group 4 - oxalic acid oxidase [Brassica napus]

				Proteins in G	roup					Peptides in Group						
	N	Unu	Total	Accession #	Name		Con V	Conf V	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	*
	4	9.45	9.45	gi 60686421	oxalic acid oxidase [Bras	2.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		-0.0472	1987.02	4	15	3 =
		0.00	9.45	gi]914911	germin-like protein		2.00	99	PCIRPIHVK	ICAT-C:13C(9)(C)@2	cleaved Y-P	-0.0204	1297.75	2	14	2
		0.00	9.45	gi]1169941	Germin-like protein 1	BRA	2.00	99	RAETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@10	missed R-A	-0.0819	2143.09	3	16	1
		0.00	9.45	gi 15218535	germin-like protein [Ar	Arab	2.00	99	SVQDFCVANLKR	ICAT-C:13C(9)(C)@6	cleaved A-S	-0.0138	1614.84	3	15	2
							1.40	96	SVQDFCVANLK	ICAT-C:13C(9)(C)@6	cleaved A-S	-0.0641	1458.69	2	14	1
							0.05	11	GYPCIRPIHVK	Oxidation(P)@3 No ICAT(C)@4	cleaved A-G	0.0571	1297.75	2	15	2
							0.00	96	AETPAGYPCIRPIHVK	ICAT-C(C)@9		-0.0465	1977.99	4	13	3
							0.00	95	AETPAGYPCIRPIHVK	ICAT-C(C)@9		-0.0414	1978.00	3	13	1
							0.00	78	AETPAGYPCIRPIHVK	ICAT-C(C)@9		-0.0238	1978.02	4	12	2
							0.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		-0.0456	1987.03	4	14	2
							0.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		-0.0688	1987.00	3	16	1 👻
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Protein Sequence Coverage - oxalic acid oxidase [Brassica napus]

MLRIIFLLSLLFALSNA**SVQDFCVANLKRAETPAGYPCIRPIHVK**ASDFVFSLGTPGNTTNIISAAVT**PGFVAQFPALNGLGISTARLDLAPKGVI**PMHTHPGASEVLF**VLDGSITAGFISSANSVYV** QTLKPGQVMVFPQGLLHFQINAGKTPAAAFVTFSSASPGLQILDFALFANTLSTELVSATTFLPPATVKTLKGVLGGTG

gi|15233723 Threonine synthase

P	rotei	ns Dete	ected									C	
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	1	
	43	2.38	2.38	40.1	gi 15233	threonine synthase [Arabidopsis thaliana]	Arabidopsis thaliana	2					
ľ	44	2.29	2.29	49.6	gi 18266	chlorophyll a/b binding protein [Brassica oleracea]	Brassica oleracea	3					
	45	2.28	2.28	47.6	gi 15227	phosphoenolpyruvate carboxylase [Arabidopsist	Arabidopsis thaliana	1					
	46	2.27	2.27	33.9	gi 15222	elongation factor, putative [Arabidopsis thaliana]	Arabidopsis thaliana	1					
	47	2.25	2.25	45.4	gi 15223	phosphoglycerate kinase, putative [Arabidopsis t	Arabidopsis thaliana	1					
NUnuTotal% CovAccessioNameSpeciesPeptides(95%)Biological ProcessesMolecular FunctionsPertides(95%)432.382.3840.1gil1523threonine synthase [Arabidopsis thaliana]Arabidopsis thaliana2													
P	rotei	n Grou	p 43 -	threoni	ne synthas	e [Arabidopsis thaliana]							

				Proteins in G	roup					Peptides in Group						
	N	Unu	Total	Accession #	Name		Con⊽	Conf ∇	Sequence 🗠	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	
	43	2.38	2.38	gi 15233723	threonine synthase [Arab	2.00	99	HCGI SHTGS FK	ICAT-C:13C(9)(C)@2		-0.0203	1408.67	2	18	9 =
Г		0.00	2.20	gi]15218600	threonine synthase, p	Arab	0.20	38	VKHCGISHTGSFK	No ICAT(C)@4	cleaved W	-0.0390	1399.66	2	14	9
							0.14	27	NRSNAVNPFSAK	Deamidated(N)@1	missed R-S	0.0912	1304.73	3	11	7
							0.02	5	ADFGAVMDVLK	Oxidation(D)@8		-0.0736	1180.50	2	10	8
							0.02	4	KLRNQGVIAPTDR	Oxidation(R)@3 Oxidation(N)@4	cleaved F	-0.0627	1498.75	2	12	8
							0.00	< 1	TGVALTALFK	Thr->Pro@1	cleaved H	-0.0173	1015.58	2	11	7
							0.02 5 AD FGAVMDV LK Oxidation(D)@8 -0.073 0.02 4 KLRNQGVIAPTDR Oxidation(R)@3 Oxidation(N)@4 cleaved F -0.062 0.00 <1 TGVALTALFK Thr->Pro@1 cleaved H -0.0173 0.00 <1 DEARRNR Deamidated(R)@5 missed R-R 0.0483 0.00 <1 DEARNR Deamidated(R)@5 missed R-R 0.0594							2	5	1
							0.00	<1	DEARRNR	Deamidated(R)@5 Deamidated(N)@6 Deamidated(R)@7	missed R-R	0.0595	918.4751	2	6	7
							Oceanidateo(k)@/ Cleaved I-G 0.00 <1 DFKPMTASTTFASAIQI cleaved I-G							2	9	7
							0.00	-0.1048	1861.88	3	9	2 -				
-						- F	•									•

Protein Sequence Coverage - threonine synthase [Arabidopsis thaliana]

MASSCLFNASVSSLNPKQDPIRRHRSTSLLRHRPVVISCTADGNNIKAPIETAVKPPHRTEDNIR<mark>DEARRNRSNAVNPFSAK</mark>YVPFNAAPGSTESYSLDEIVYRSRSGGLLDVEHDMEALKRFDGAYW .FDSRVGKSTWPYGSGVWSKK<mark>EWVLPEIDDDDIVSAFEGNSNLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMK</mark>RPVVGVGCASTGDTSAALSAYCASAGIPSIVFLPA NKISMAQLVQPIANGAFVLSIDTDFDGCMKLIREITAELPIYLANSLNSLRLEGQKTAAIEILQQFDWQVPDWVIVPGGNLGNIYAFYKGFKMCQELGLVDRIPRMVCAQAANANPLYLHYKSGWKDF KPMTASTTFASAIQIGDPVSIDRAVYALKKCNGIVEEATEEELMDAMAQADSTGMFICPHTGVALTALFKLRNQGVIAPTDRTVVVSTAHGLKFTQSKIDYHSNAIPDMACRFSNPPVDVKADFGAVM DVLKSYLGSNTLTS

gi|15222741 Initiation factor 5A-4, putative

Pro	teins	s Dete	cted													
N	I U	nu	Total	% Cov	Accessi	o		Name			Specie	8	Peptides(95%)	Biological Processes	Molecular Functions	PANT 🔺
	75	2.01	2.01	39.0	gi 15222	initiatio	on factor 5A-4, p	utative	[Arabidop	sis thalia	Arabidopsis thalian	a	2			
•]									I		-		1	•
		~	76 1													
Pro	tein	Group	0/0-1	nitiatio	n factor	' SA-4, put	ative [Arabid	opsis	thaliana	J						
				Prot	eins in G	roup							Peptides in Gro	up		
N	I U	nu	Total	Acces	ssion #	N	lame	-	Con ⊽	Conf	Sequence		Modifications	Cleavages	∆Mass Prec MW	L SC 🔺
	75	2.01	2.01	gi 15222	2741	initiation	factor 5A-4,	A	2.00	99	KLEDIVPSSHNCDV	PHVNR	ICAT-C:13C(9)(C)(⊇12 missed K-L	-0.0069 2394.20	3 20 1
		0.00	2.01	gi 14532	24016	eukaryotic	translation i	A	0.00	1	EASESGASKTYPQS	AGNIR	Oxidation(Y)@11	cleaved F-E	0.0705 1969.95	3 11 8
		0.00	2 00	ail 15222	2317	Fukarvotic	initiation fa	4					Deamidated(N)@1			
																•
Pro	tein	Seque	ence C	overag	e - initi	ation facto	or 5A-4, puta	tive [/	Arabidop	sis thalia	ana]					
Me	חספיי		SPECE	GUTVD	OSACAT	PROCHTY		VSTC	KTCKHCH	AKCHEN	ATOTETAZ UL DOT	VDSSING	VDHUNDVOT	INTERCEVELTER	COTEDDI VI DIDDO	TTAONET
GF	DEGR	DIVV	SVMSS	MGEEO	ICAAKE ADVACINI	VGGGK	INNKPCKVVE	V 31 3	KI GKRGR	MNUTE V.	AIDICIAKKLEDI	VESSINCE	VYPRVIKVDIQL.	TOTIEDGE VOLLIDS	GGIKDDFKFLIDDG	LIAVIKL
				~												
Frag	gmei	ntatio	n Evid	ence												
		KLEDI	VPSSHN		PHVNR											
							_									
R	esidu	Ie	b	t	0+2	У	y+2		-	L. II		411-11		ابناما بنام		
K			129.104	22 12	05.0548	2395.2234	1198.1153		260 -	b3+2 b2	y2 y3 y4 y5 5+2 b3 b4 b5 yb	/or y/ 8+nµ21β+2¢n185+2	2y1 ÿ42 +2 99	b12 y14	y15 y16 y17	
			242.100	00 12	C 4494	2207.1204	1134.0079		240 -			84	19.39			
			486 25/	58 24	13 6316	2025.0018	1013.0045		220							
			599.339	99 30	0.1736	1909.9748	955.4911		200 -							
V			698.408	33 34	19.7078	1796.8908	898.9490		100							
P			795.46	11 39	08.2342	1697.8224	849.4148		100 -		622.3	2				
S			882.493	31 44	11.7502	1600.7696	800.8884		≥ ¹⁶⁰					1679.79		
S			969.528	51 48	35.2662	1513.7376	757.3724		8 140							
н			1106.584	41 55	53.7957	1426.7055	713.8564		트 120 -			/21.40	1075.50		2378.1	19
Ν			1220.627	70 61	0.8171	1289.6466	645.3269		100 -	197.	16 289.16			1796	5.85	
C[C9I]		1559.793	33 78	80.4003	1175.6037	588.3055		80			9	77.39		1919 80	
D			1674.820	03 83	37.9138	836.4373	418.7223		60						10.00	
V			1773.888	87 88	37.4480	721.4104	361.2088		<u> </u>					1409.86	2136.0	07
P			1870.941	15 93	35.9744	622.3420	311.6746		40 -				1134.00	6	2020.09 2268	05
н			2008.000	04 100	04.5038	525.2892	263.1482		20 -	أفلولوا			1289.			
V			2107.068	88 105	54.0380	388.2303	194.6188		م لب				1000 1200			-14
N			2221.111	17 111	1.0595	289.1619	145.0846		0	200	400 600	000	m/z, Da	1400 1000 18	00 2000 2200	2400
R			2377.212	28 118	39.1101	175.1190	88.0631									

gi|15236220 Mitochondrial elongation factor Tu

Р	rotei	ns Dete	ected								. (
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
	23	4.07	4.07	68.1	gi 15219	putative malate dehydrogenase[Arabidopsis tha	Arabidopsis thaliana	3				
ľ	24	4.06	4.06	56.8	gi 15236	mitochondrial elongation factor Tu [Arabidopsis t	Arabidopsis thaliana	4			C	
ľ	25	4.03	4.03	44.9	gi 15241	tubulin alpha-5 chain [Arabidopsis thaliana]	Arabidopsis thaliana	2				
	26	4.02	4.02	32.8	gi 15241	formate dehydrogenase (FDH) [Arabidopsis thali	Arabidopsis thaliana	7				
	27	3.90	3.90	57.0	gi 15237	H+-transporting ATPase chain E, vacuolar [Arab	Arabidopsis thaliana	3				
	28	3.60	3.60	44.5	gi 15220	putative alanine aminotransferase [Arabi	Arabidopsis thaliana	2				÷
	٠ 📃							•	•		Þ	

Protein Group 24 - mitochondrial elongation factor Tu [Arabidopsis thaliana]

				Proteins in Gr	oup					Peptides in Group						
N	Unu	u	Total	Accession #	Name		Con⊽	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	*
24	4 4	1.06	4.06	gi 15236220	mitochondrial elong	Arab	2.00	99	HSPFFAGYRPQFY		cleaved Y	-0.0365	1615.72	2	17	7
7	6 2	2.00	4.00	gi 15237059	translation elongatio	Arab	2.00	99	HYAHVDCPGHADYVK	ICAT-C:13C(9)(C)@7		-0.0307	1946.88	4	15	2
	-						2.00	99	QVGVPSLVCFLNK	GIn->pyro-Glu@N-term ICAT-C(C)@9		-0.0620	1612.80	2	14	8
							0.05	11	AEEGKAKAIAFDEIDK	Glu->Asn@3 Oxidation/D\@12	cleaved L	-0.0261	1734.85	3	13	1 🖵
•				III		- 1-	•									

Protein Sequence Coverage - mitochondrial elongation factor Tu [Arabidopsis thaliana]

MASVVLRNPSSKRLVPFSSQIYSRCGASVTSSYSISHSIGGDDLSSSTFGTSSFWRSMATFTRNKPHVNVGTIGHVDHGKTTLTAAITKVLAEEGKAKAIAFDEIDKAPEEKKRGITIATAHVEYETA KRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSGPDGPMPQTKEHILLARQVGVPSLVCFLNKVDVVDDPELLELVEMELRELLSFYKFPGDDIPIIRGSALSALQGTNDEIGRQAILKLMDAVDEY IPDPVRVLDKPFLMPIEDVFSIQGRGTVATGRIEQGVIKVGEEVEILGLREGGVPLKSTVTGVEMFKKILDNGQAGDNVGLLLRGLKREDIQRGMVIAKPGSCKTYKKFEAEIYVLTKDEGGRHTAFF SNYRPQFYLRTADITGKVELPENVKMVMPGDNVTAVFELIMPVPLETGQRFALREGGRTVGAGVVSKVMT

gi|15227954 60S ribosomal protein L2

Proteins Detected										
N Unu Total	% Cov Access	io	Na	ime		Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT ^
80 2.00 2.00	78.3 gi 1522	7 60Srib	osomal protein L	2 [Arabidopsis tl	naliana]	Arabidopsisthaliana	2			
		- 1 .	· ··· · · · ·		- 11	· · · · · · ·				- F
Protein Group 80	60S ribosomal	protein La	2 [Arabidopsis	thaliana]						
	Proteins in (Group					Peptides in Gro	an		
N Unu Total	Accession #		Name	▲ Con ∇	Conf	Sequence	Modifications	Cleavages	∆Mass Prec MW z	Sc 🔺
80 2.00 2.00	gi 15227954	60S ribos	omal protei A	2.00	99	SIPEGAVVCNVEHHVGDR	ICAT-C(C)@9		-0.0704 2143.97 4	16 2
0.00 2.00	gi 37731421	ribosomal	protein L2 [E	- 0.00	1	GAPLARVTFRHPFR	Deamidated(R)@6	missed R-V	-0.1644 1657.70 2	10 8 -
•	111		Þ	•						•
Protein Sequence	Coverage - 60S	ribosoma	l protein L2 [A	rabidopsis th	aliana]					
ASCDYATVTAHNP	VFKSHTHHRKG. SDTTRIKLPSG	PAKERSLD. SKRTVPSG	FGERNGYLKGV CRAMIGOVAGG	GRTEKPMLKA	GAPLAR GNAYHK	VTFRHPFRFKKQKELFVAAE YRVKRNSWPKVRGVAMNPVF	GMYTGQFLYCGK	KATLVVGNVLPLRSI HASTVRRDAPPGOKV	GLTAARRTGRIRGOA	AGVLAR
AD	obiikinbioo.	Sint (190	CIALITO VACO	ONIENTIMA	ONATIN	IRVIRIOWI RVROVALINI VL.	in noooniginto.	INDIVINIDALI OQIN	ODIAANNI ONDROQA	ANDAAL
Fragmentation Evi	lence									
SIPEGAVVC										
Residue b	b+2	v	v+2							
S 88.0	393 44.5233	2145.0506	1073.0289	2400 -	y1	y2y3 y4 y5 y6	y† y8 y9	y10 y11 y12	y13y14 y15	
I 201.1	234 101.0653	2058.0185	1029.5129	2200 -	b2+2 b	2 y5+b23 y7+b24 y9+b26 y10+2 y13	+915+2 018+2			
P 298.1	7 61 149.5917	1944.9345	972.9709	2000		261.16				
E 427.2	214.1130	1847.8817	924.4445	2000	18	3.15				
G 484.2	402 242.6237	1718.8391	859.9232	1800 -						
A 555.2	278.1423	1661.8176	831.4125	1600 -						
V 654.3	457 327.6765	1590.7805	795.8939	≥1400 -						
V 753.4	141 377.2107	1491.7121	746.3597	6 1200 -						
C[C0I] 1083.5	542.2788	1392.6437	696.8255	1000 ±	211.14					
V 1000 0	32 599.3003	048 4646	474 7350	1000		446.23 583.31				
F 1425.7	142 713 3558	849 3962	474.7359	800 -	141.1	0 0000000000000000000000000000000000000				
H 1562 7	32 781.8852	720.3536	360.6804	600		243.11 720.34	4 947 41		1733.69 1828.86	
H 1699.8	221 850.4147	583.2947	292.1510	400 -			867.35 104	4.48 1589 77	1677.70 20	073.98
V 1798.8	05 899.9489	446.2358	223.6215	200 -	157.06		11	58.45 1474.77	1845.94	
G 1855.9	119 928.4596	347.1674	174.0873	<u></u>			, palitika da Katara da 1	الليابة بالأف بيبية		
D 1970.9	389 985.9731	290.1459	145.5766	, v	o .	200 400 600 8	800 1000	1200 1400 10	600 1800 2000	
R 2127.0	1064.0236	175.1190	88.0631				m/z, Da			

gi|15228674 Peptidylprolyl isomerase ROC4

teir	ns Dete	ected									
N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PAN	*
49	2.19	2.19	30.6	gi 15227	enolase (2-phospho-D-glycerate hydroylase) [Ar	Arabidopsis thaliana	1				
50	2.17	2.17	28.0	gi 18141	senescence-associated cysteine protease[Bras	Brassica oleracea	2				_
51	2.16	2.16	62.7	gi 15228	peptidylprolyl isomerase ROC4[Arabidopsis thal	Arabidopsis thaliana	3				
52	2.15	2.15	44.4	gi 15219	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	2				
53	2.14	2.14	36.0	gi 31321	putative papillar cell-specific calnexin [Brassica	Brassica napus	1				-
			,							Þ	
	49 50 51 52 53	Unu 49 2.19 50 2.17 51 2.16 52 2.15 53 2.14	Unu Total 49 2.19 2.19 50 2.17 2.17 51 2.16 2.16 52 2.15 2.15 53 2.14 2.14	Unu Total % Cov 49 2.19 2.19 30.6 50 2.17 2.17 28.0 51 2.16 2.16 62.7 52 2.15 2.15 44.4 53 2.14 2.14 36.0	Vnu Total % Cov Accessio 49 2.19 2.19 30.6 gi 15227 50 2.17 2.17 28.0 gi 18141 51 2.16 2.16 62.7 gi 15219 52 2.15 2.15 44.4 gi 15219 53 2.14 2.14 36.0 gi 31321	Vnu Total % Cov Accessio Name 49 2.19 2.19 30.6 gi 15227 enolase (2-phospho-D-glycerate hydroylase)[Ar 50 2.17 2.17 28.0 gi 18141 senescence-associated cysteine protease[Bras 51 2.16 2.16 62.7 gi 15228 peptidylprolyl isomerase ROC4[Arabidopsis thal 52 2.15 2.15 44.4 gi 15219 hypothetical protein [Arabidopsis thaliana] 53 2.14 2.14 36.0 gi 31321 putative papillar cell-specific calnexin [Brassica	Vnu Total % Cov Accessio Name Species 49 2.19 2.19 30.6 gil15227 enolase (2-phospho-D-glycerate hydroylase)[Ar Arabidopsis thaliana 50 2.17 2.17 2.80 gil18141 senescence-associated cysteine protease[Bras Brassica oleracea 51 2.16 62.7 gil15228 peptidylprolyl isomerase ROC4[Arabidopsis thal Arabidopsis thaliana 52 2.15 2.14 gil15219 hypothetical protein [Arabidopsis thaliana] Arabidopsis thaliana 53 2.14 2.14 36.0 gil31321 putative papillar cell-specific calnexin [Brassica Brassica napus	Name Species Peptides(95%) 4 Vnu Total % Cov Accessio Name Species Peptides(95%) 49 2.19 2.19 30.6 gil15227 enolase (2-phospho-D-glycerate hydroylase)[Ar Arabidopsis thaliana 1 50 2.17 2.17 2.80 gil18141 senescence-associated cysteine protease[Bras Brassica oleracea 2 51 2.16 62.7 gil15228 peptidylprolyl isomerase ROC4[Arabidopsis thal Arabidopsis thaliana 3 52 2.15 2.44 gil15219 hypothetical protein [Arabidopsis thaliana] Arabidopsis thaliana 2 53 2.14 2.14 36.0 gil3321 putative papillar cell-specific cal nexin [Brassica Brassica napus 1	NameSpeciesPeptides(95%)Biological Processes4VnuTotal% CovAccessioNameSpeciesPeptides(95%)Biological Processes492.192.1930.6gi15227enolase (2-phospho-D-glycerate hydroylase)[ArArabidopsis thaliana1502.172.1728.0gi18141senescence-associated cysteine protease[BrasBrassica oleracea2512.1662.7gi15228peptidylprolyl isomerase ROC4[Arabidopsis thaliana]Arabidopsis thaliana3522.1544.4gi15219hypothetical protein [Arabidopsis thaliana]Arabidopsis thaliana2532.142.1436.0gi13131putative papillar cell-specific cal newin [BrassicaBrassica napus1	Vnu Yotal % Cov Accessio Name Species Peptides(95%) Biological Processes Molecular Functions 49 2.19 3.06 gi15227 enolase (2-phospho-D-glycerate hydroylase)[Ar Arabidopsis thaliana 1 50 2.17 2.17 2.80 gi118141 senescence-associated cysteine protease[Fas Brassica oleracea 2 2 3 3	Name Species Peptide(95%) Biological Processes Molecular Functions PANT 49 2.19 3.06 gi 15227 enolase (2-phospho-D-glycerate hydroylase)[Ar Arabidopsis thaliana 1

Protein Group 51 - peptidylprolyl isomerase ROC4 [Arabidopsis thaliana]

			Proteins in Gr	oup					Peptides in Group						
N	Unu	Total	Accession #	Name		Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	*
51	2.16	2.16	gi 15228674	peptidylprolyl isome	Arab	2.00	99	HTGPGILSMANAGPNTNGS	Oxidation(M)@9 ICAT-C:13C(9)(C)@24		-0.0962	3013.38	3	26	9
						0.11	23	SMAAEEEEVIE PQAKVTNK	Oxidation(M)@2 Glu->Ser@8 Deamidated(Q)@13	missed K-V	-0.0522	2076.93	3	13	1
						0.05	10	SMAAEEEEVIE	Phospho(S)@1	cleaved E	0.1681	1315.65	2	12	8
						0.00	< 1	FICTVK	ICAT-C:13C(9)(C)@3	cleaved F-F	-0.0322	945.5083	2	9	7
_						0.00	24	PT OWN IZ	ICAT CICIM3	cleaved F F	0 0208	3081 320	2	7	7 *
 _			111			•									Þ.

Protein Sequence Coverage - peptidylprolyl isomerase ROC4 [Arabidopsis thaliana]

MAS<mark>SSSMQMVHTSRSIAQIGFGVKSQLVSANRTTQSVCFGARSSGIALSSRLHYASPIKQFSGVYATTKHQRTACVKSMAAEEEEVIEPQAKVTNK</mark>VYFDVEIGGEVAGRIVMGLFGEVVPKTVENFR ALCTGEKKYGYKGSSFHRIIKDFMIQGGDFTEGNGTGGISIYGAKFEDENFTLKHTGPGILSMANAGPNTNGSQFFICTVKTSWLDNKHVVFGQVIEGMKLVRTLESQETRAFDVPKKGCRIYACGEL PLDA

gi|15228715 Ubiquitin extension protein (UBQ5)

Pro	Mins Detected Image: Species Peptides(95%) Biological Processes Molecular Functions PANT 1 152 152 52.9 g) (15228 ubiquitin extension protein (UBQ5) [Arabidopsis Arabidopsis thaliana 1 2 1.52 1.52 0.00 1.52 0.00 1.52 0.00 2 1.52 1.52 0.00 0.00 1.52 0.00 1.52 0.00 0.00 1.52 97 Coll YVYQK ICAT-C:13C(9)(C)(2) -0.0461 1309.63 2 1.8 9 -														
FIU	teins Detected Image: Species Peptides(95%) Biological Processes Molecular Functions PANT 99 1.52 1.52 62.9 gi(15228) ubiquitin extension protein (UBQ5) (Arabidopsis Arabidopsis thaliana 1 1 1 1 Image: Species Peptides(95%) Biological Processes Molecular Functions PANT Image: Species Peptides in Group Peptides in Group Image: Species Molecular Functions Image: Species Molecular Functions Species Peptides in Group Image: Species Molecular Functions Image: Species Molecular Functions Image: Species Molecular Functions Image: Species Image: Species														
N	Unu	Total	% Cov	Accessio		Na	ime			Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT 🔶	
	9 1.52	1.52	52.9	gi 15228	ubiquiti	n extension prot	ein (U	BQ5) [Arabi	dopsis	Arabidopsis thaliana	1			-	
र	Proteins in Group Peptides Peptides Mass Prec MW z Sc 99 1.52 1.52 0.00 1.52														
	leins Detected Junu Total % Cov Accessio Name Species Peptides(95%) Biological Processes Molecular Functions PANT 49 1.52 1.52 91/15228 ubiquitin extension protein (UBQ5) [Arabidopsis Arabidopsis thaliana 1														
Pro	ein Gro	up 99 - u	ıbiquiti	n extensi	on prote	in (UBQ5) [Ara	abido	opsis tha	liana]						
			Prot	eins in Gro	up						Peptides in Gro	up			
N	Unu	Total	Acces	sion #	N	ame		Con… ⊽	Conf	Sequence	Modifications	Cleavages	∆Mass Prec MW z	Sc 🔺	
	9 1.52	1.52	gi 15228	3715 I	ubiquitin e	extension p A		1.52	97	CGLTYVYQK	ICAT-C:13C(9)(C)@	21	-0.0461 1309.63 2	2 13 8	
	0.00	1.52	gi]15226	498	putative ub	oiquitin exte A	-	0.00	< 1	EGIPPDQQRLIFAGK		missed R-L	-0.1295 1667.77 3	3 8 9 -	
•															
MQ	otein Sequence Coverage - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] QIFVKTLIGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLVLRLRGGAKKRKKKTYTKPKKIKHKHKKVKLAVLQFYKIDGSGKVQRLRKECPNATCGA IFMASHFDRHYCGKCGLTYVYQKEGVEA														
Frag	0.00 1.52 git15226498 putative ubiquitin exte A 0.00 <1														
	C[CS	0]GLTYVY	′QK												
R	esidue	b	b)+2	у	y+2		9000 H		العرا العرالي	اعر العار	مراجرا إعلا			
C[(:91]	340.17	36 17	0.5905 13	310.6860	655.8467		8000		⁷ 'b2+2 y4 8 2 2 b2 ^y y8+2b	3 b4 y5	b5 b6 y yo			
G		397.19	51 19	9.1012	971.5197	486.2635	1	7000 -		278.12					
L		510.27	92 25	5.6432	914.4982	457.7527	Ę.	6000 -		254.12					
T		611.32	69 30	6.1671	801.4141	401.2107	teus	4000 -		204.12					
Y		774.39	02 38	7.6987	700.3665	350.6869	<u>-</u>	3000 -		438.22					
	0.00 1.52 gi15226498 putative ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] III otein Sequence Coverage - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] QIFVKTLTGKT ITLEVESSDT IDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLVLRLRGGAKKRKKT YTKPKKIKHKHKKVKLAVLQFYKIDGSGKVQRLRKECPNATCGA C[C9]IJTVVYQKEGVEA agmentation Evidence C[C9]IJTVVYQK 8000 Y102+2 Y42 y2 y2 y6 b y7 y8 (CG9)IJTVVYQK Residue b b+2 y y+2 9000 Y102+2 y42 y2 y2 y2 y8+243 b4 y5 b6 b6 y7 y8 307.195 199.0102 971.5197 488.2836 9000 7000 254.12 438.22 b2 y3 b4 y5 b6 b6 y7 y8 6000 937.6987 700.3686 380.6886 9000 136.07 176.08 438.22 b3.19 537.30 801.38 971.49														
	Image: Section 2 Proteins in Group Proteins in Group Peptides in Group 99 1.52 1.52 000 1.52 010 0.041 1309.65 2 1.52 90 0.00 1.52 015222715 ubiquitin extension pro A														
ĸ		1292 67	55 64	6.8414	147.1128	74.0600		0	100) 200 300 400 50	00 600 70	0 800 900	1000 1100 1200	1300	
Ľ	Proteins in Group Unu Total Accession # Name Con % Conf Sequence Modifications Cleavages Addass Prec MW z Sc A 152 152 gift2528715 ubiquitin extension p A A 152 97 CSLTYVYCK ICAT-C:13C(9)(O)@1 -0.0461 130e.85 2 13 8 P 0.00 1.52 gift228438 putative ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] Itein Sequence Coverage - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] Itein Sequence Coverage - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] Itein Sequence Modifications Modifications Modifications Itein Sequence Coverage - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] Itein Sequence Modifications Itein Sequence Modifications Itein Sequence Modifications Itein Sequence Coverage - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana] Itein Sequence Modifications Itein Sequence Modifications														

gi|157849770 Early response to dehydration protein (ERD12)

Р	rotei	ns Dete	ected									
Г	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
Г	68	2.02	2.02	70.9	gi 15236	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	4				
	69	2.02	2.02	37.9	gi 15784	ERD12 protein [Brassica rapa]	Brassica rapa	2				
	70	2.02	2.02	65.4	gi 83032	unknown [Brassica rapa]	Brassica rapa	0				_
	71	2.02	2.02	47.2	gi 6683965	cinnamyl alcohol dehydrogenase [Brassica rapa]	Brassica rapa	1				
	72	2.01	2.01	63.4	gi 15233	probable H+-transporting ATPase[Arabidopsis t	Arabidopsisthaliana	4				-
•		i				"		Î	Ì		Þ	

Protein Group 69 - ERD12 protein [Brassica rapa]

			Proteins	in Group				F	Peptides in Group				
N	Unu	Total	Accession #	Name	Species	Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	: *
6	2.02	2.02	gi 157849770	ERD12 protein [Bras	Brassica rapa	2.00	99	NPQQLCIGDLVPFTNK	ICAT-C:13C(9)(C)@6		-0.0663	2021.99	
			^			0.01	3	LFYTFYLK			-0.0139	1093.57	==
						0.01	2	NLRISSNGPALSARSR	Deamidated(R)@3 Deamidated(N)@7	cleaved H	-0.0595	1699.83	
						0.00	< 1	NEGDRHSPAVLK	Deamidated(N)@1 Deamidated(R)@5 Oxidation(H)@6	cleaved F	0.0131	1339.64	
						0.00	< 1	AITGGSGVFEGAYGQVK	Deamidated(Q)@15	cleaved L	-0.0338	1640.77	
						0.00	<1	EDTLLAITGGSGVF	Glu->pyro-Glu@N-term Oxidation(D)@2	cleaved Y	-0.0559	1376.62	
						0.00	<1	EDTLLATTGGSGVF	Glu->pvro-Glu@N-term	cleaved Y	-0.0310	1360.65	-
<					•								P

Protein Sequence Coverage - ERD12 protein [Brassica rapa]

MIMASSAAAASISLVRNLSRHHQTPLLGYSSSFH<mark>NLRISSNGPALSARSRSTTSSTPGFFRTMCNSSSENSR</mark>PTKIQELNVYEF**NEGDRHSPAVLK**LGK**NPQQLCIGDLVPFTNK**LYTGDLKKRVGIT AGLCVLIQHVPEKKGERFEASYSFYFGEYGHISVQGPYLTY**EDTLLAITGGSGVFEGAYGQVK**LRQLVYPTK**LFYTFYLK**GVVSDLPVELTGKHV**EPSK**DVKPAAELSCSARGHYHKLYRIIIIVSLR FLFSFSDL

gi|414103 Myrosinase, thioglucoside glucohydrolase

P	rotei	ins Dete	ected									
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*
	1	48.95	48.95	89.5	gi 414103	$myrosinase, thio glucoside glucohydrolase \cite{Brassi} \dots$	Brassica napus	37				
	2	27.81	27.81	84.3	gi 8745521	ribulose-1,5-bisphosphate carboxylase/oxygenas	Brassicanapus	21				
	3	11.79	11.79	88.3	gi 11972	ribulose bisphosphate carboxylase [Brassica rapa]	Brassica rapa	11				
I	4	10.55	10.55	56.0	gi 558479	tonoplast ATPase 70 kDa subunit		5				
	5	10.27	10.27	54.6	gi 15226	putative triosephosphate isomerase [Arabidopsis	Arabidopsis thaliana	7				
	6	10.21	10.21	64.2	gi 15229	glyceraldehyde-3-phosphate dehydrogenase Cs	Arabidopsis thaliana	6				-

Protein Group 1 - myrosinase, thioglucoside glucohydrolase [Brassica napus]

		Pi	roteins in Group					Peptides in Gr	oup						
N	Unu	. Total	Accession #	Na	Con… ⊽	Conf V	Sequence 🗸	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrum	× *
	1 48.95	5 48.95	gi 414103	myrosinas	2.00	99	ADEEITCEENNPFTCSNTD	Asp->Ser@2		0.3320	3058.70	3	17	1.1.1.1832.2	
1	7 5.68	8 47.03	gi 22595	myrosinas				Asn->Ser@11							
8	3 2.00	20.82	gi 12621052	myrosinas				ICAT-C(C)@15							
8	4 2.00	12.48	gi 159120044	myrosinas	2.00	99	DEEITCEENNPFTCSNTDI	ICAT-C(C)@6 ICAT-C(C)@14	cleaved A-D	0.2950	3042.63	3	15	2.1.1.1768.2	
10	4 1.64	4 19.61	gi 4033345	myrosinas	2.00	99	DYADLC FKE FGGK	ICAT-C(C)@6		0.2197	1719.01	2	15	6.1.1.1728.3	
10	5 1.59	32.24	gi 152207441	myrosinas	2.00	99	EEITCEENNPFTCSNTDIL	ICAT-C(C)@5 Asn->Ser@9 ICAT-C(C)@13	cleaved D-E	0.3060	2900.61	3	19	1.1.1.1805.2	
					2.00	99	ESDPASIEAAER		cleaved D-E	0.1546	1273.73	2	15	2.1.1.1660.2	
					2.00	99	FGLSYVNWEDLDDR			0.1653	1727.94	2	15	6.1.1.1796.4	
					2.00	99	IDYLCSHLCFLR	ICAT-C(C)@5 ICAT-C(C)@9		0.1662	1936.13	3	15	6.1.1.1739.2	
					2.00	99	ITINQLYTVPTR		cleaved W-I	0.1381	1417.93	2	15	7.1.1.1674.2	
					2.00	99	MNQFFHGWYMEPLTK	Oxidation(M)@1 Oxidation(W)@8 Met->Phe@10		0.1967	1976.08	2	22	7.1.1.1657.2	
					2.00	99	QIIQDFKDYADLCFK	Gin->pyro-Glu@N-term		0.1445	2065.17	2	23	6.1.1.1825.2	Ŧ
< .				•	•			III						•	

Protein Sequence Coverage - myrosinase, thioglucoside glucohydrolase [Brassica napus]

MKLLHGLALVFLLAAASCKADEEITCEENNPFTCSNTDILSSKNFGKDFLFGVASSAYQACRGVNVWDGFSHRYPEKSGSDLKNGDTTCESYTRWQKDVDVMGELNATGYRFSFAWSRIIPKGKVSRG VNQGGLDYYHKLIDALLEKNITPFVTLFHWDLPQTLQDEYEGFLDRQIIQDFKDYADLCFKEFGGKVKHWITINQLYTVPTRGYAVGTDAPGRCSPMVDTKHRCYGGNSSPEPYIVAHNQLLAHATVV DLYRTKYKFQKGKIGPVMITRWFLPFDESDPASIEAAERMNQFFHGWYMEPLTKGRYPDIMRQIVGSRLPNFTEEEAELVAGSYDFLGLNYYVTQYAQPKPNPYPSETHTAMMDAGVKLTYDNSRGEF LGPLFVEDEVNGNSYYYPKGIYYVMDYFKTKYGDPLIYVTENGFSTPSSENREQAIADYKRIDYLCSHLCFLRKVIKEKGVNVRGYFAWALGDNYEFCKGFTVRFGLSYVNWEDLDDRNLKESGKWYQ RFINGTVKNSAKQDFLRSSLSSQSQKKKLADA

gi|46093471 Stromal ascorbate peroxidase

Proteins Detected Biological Processes Molecular Functions % Cov Accessio... Peptides(95%) PANT 4 Unu... Total Name Species Ν 32 2.89 2.89 55.1 gi|15219... phosphoglycerate kinase, putative [Arabidopsis t. Arabidopsis thaliana 2 33 2.86 2.86 36.5 gi|15229... S-adenosyl-L-homocysteinas, putative [Arabidop. Arabidopsis thaliana 2 34 2.81 2.81 51.0 gi|15237... 3-oxoacyl-(acyl-carrier-protein) synthase I precu. Arabidopsis thaliana 35 2.80 2.80 78.9 gi|46093. stromal ascorbate peroxidase [Brassica oleracea] Brassica oleracea gi|15240.. 36 2.57 2.57 47.9 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3). Arabidopsis thaliana 111

Protein Group 35 - stromal ascorbate peroxidase [Brassica oleracea]

			Proteins	in Group				F	Peptides in Group				
N	Unu	Total	Accession #	Name	Species	Con⊽	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	: *
3	5 2.8	2.80	gi 46093471	stromal ascorbate pe	Brassica oler	2.00	99	VDTSGPHECPEEGRLPDAG	ICAT-C:13C(9)(C)@9	missed R-L	-1.1721	3169.35	Ξ
		-				0.80	84	FCHPILVR	ICAT-C(C)@2		-0.0302	1210.63	
						0.00	< 1	AANAGLVNALNLIKHIKDM		cleaved H	-0.5880	5014.04	
						0.00	< 1	AS LA LNTTMAS SLRTQVSA	Deamidated(N)@6	missed R-T	-0.1320	2607.28	
						0.00	< 1	EDIKELLNTKFCHPILVR	ICAT-C(C)@12	missed K-F	-0.1001	2394.20	
						0.00	< 1	EGPGAPGGQSWTPEWLKFD	Oxidation(P)@6	cleaved Y	-0.0339	2438.04	
						0.00	< 1	EGPGAPGGQSWTPEWLKFD	Oxidation(D)@19	cleaved Y	-0.0196	2438.06	
						0.00	< 1	ELKHAANAGLVNALNLIK	Oxidation(N)@12	cleaved I-E	-0.1255	1903.95	
						0.00	< 1	ERAS LA LNT TMASS LR TOV	Deamidated(R)@2	cleaved A	-0.0027	2356.15	-
•			III		•	•		III					Þ

Protein Sequence Coverage - stromal ascorbate peroxidase [Brassica oleracea]

MAERASLALNTTMASSLRTQVSAFRLLRFSSSGSKLSFPSSSLSFTRSLVSSPLLSQKRCQAALVNRSFSSAATTHCTAATDPEQLKSAREDIKELLNTKFCHPILVRLGWHDAGTYNKNISEWPQRG GANGSLRYEIELKHAANAGLVNALNLIKHIKDMYSGISYADLFQLASATAIEEAGGPKIPMKYGR**VDTSGPHECPEEGRLPDAGPPSPANHLR**EVFYRMGLDDKDIVALSGAHTLGRSRPERSGWGKP ETKYTKEGPGAPGGQSWTPEWLKFDNSYFTEIKEKRDEDLLVLPTDAAIFEDPSFKVYAEKYAADQDAFFKDYAESHAKLSNLGAKFNPPEGIII

gi|14764532 Monodehydroascorbate reductase

Pr	rotei	ns Dete	ected								G	
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
	57	2.07	2.07	60.7	gi 15237	succinyl-CoAsynthetase, alphasubunit [Arabido	Arabidopsis thaliana	2				
	58	2.07	2.07	44.0	gi 15242	NADH dehydrogenase [Arabidopsis thaliana]	Arabidopsis thaliana	2				
	59	2.06	2.06	39.2	gi 15222	vacuolar ATP synthase subunit C, putative [Arab	Arabidopsis thaliana	1			C	_
	60	2.03	2.03	56.6	gi 31043	glutamate-cysteineligase[Brassicajuncea]	Brassicajuncea	1				
	61	2.03	2.03	60.8	gi 14764	monodehydroascorbate reductase [Brassica rap	Brassica rapa subsp. pekinensis	2				-
•						' ''''					•	

Protein Group 61 - monodehydroascorbate reductase [Brassica rapa subsp. pekinensis]

				Proteins	in Group				I	Peptides in Group				
N	U	Jnu	Total	Accession #	Name	Species	Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	- ; A
	61	2.03	2.03	gi 14764532	monodehydroascorb	Brassica rapa	2.00	99	LPGFHCCVGSGGEK	ICAT-C:13C(9)(C)@6		-0.1058	1861.82	
		0.00	2.01	gi]46093475	monodehydroascorbat	Brassica olera	0.02	5	אידע ו קרע	10A1-0.130(9)(0)@/	cleaved G.	-0.0286	1015 58	-
		0.00	2.00	gi]15231702	monodehydroascorbat	Arabidopsis th	0.02	1	TYMYCDMPDUEUUDUSDUS	Deamidated(R)@9	cleaved DJ	-0.0200	3066.42	-
							0.01		LKHIGDMRKVENVDHSRRS	Phospho(S)@19 Oxidation(K)@25	Cleaved P-L	-0.0230	5000.42	
							0.00	< 1	AEKSFKYIILGGGVSAGYA		cleaved M	-0.1508	2129.00	
							0.00	< 1	ARPSAESLDELVKQGISFA	Oxidation(R)@2 Oxidation(F)@18	missed K-Q	-0.1556	2248.01	
							0.00	< 1	ARPSAESLDELVKQGISFA	Deamidated(R)@2 Deamidated(Q)@14	missed K-Q	-0.0389	2331.19	-
•						+	•							Þ

Protein Sequence Coverage - monodehydroascorbate reductase [Brassica rapa subsp. pekinensis]

MAEKSFKYIILGGGVSAGYAAKEFASQGVKPGELAVISKEAVAPYERPALSKGYLFPEGAARLPGFHCCVGSGGEKLLPESYKQKGIELILSTEIVKADLAAKSLVSAAGDVFKYETLIIATGSTVLR LTDFGVKGADSKNILYLREIDDADKVVEAIQAKKGGKAVVVGGGYIGLELSAALRINNFDVTMVFPEPWCMPRLFTADIAAFYETYYTNKGVKIIKGTVASGFTAHPNGEVNEVQLKDGRSLEADIVI VGVGARPLTALFKGQVEEDKGGIKTDAFFKTSVPDVYAVGDVATFPLKMYGDMRRVEHVDHSRKSAEQAVKAIKAAEGGGAVEEYDYLPFFYSRSFDLSWQFYGDNVGDSVLFGDSNPSNPKPRFGAY WVQDGKVVGAFMEGGSGDENKALAKVAKARPAAESLEDLTKQGISFAAKI

gi|15227559 Tubulin beta-7 chain

Р	rotei	ns Dete	ected									C
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	
	8	7.31	7.31	40.6	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	6				-
	9	6.90	6.90	57.5	gi 15227	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4				
ſ	10	6.62	6.62	80.4	gi 15240	33 kDa polypeptide of oxygen-evolving complex	Arabidopsisthaliana	7				
	11	6.25	6.25	57.1	gi 15242	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	5				
	12	6.02	6.02	48.0	gi 15224	cytoplasmic aconitate hydratase[Arabidopsis th	Arabidopsis thaliana	7				
ľ	•	1 1				"		1			÷.	

Protein Group 9 - tubulin beta-7 chain [Arabidopsis thaliana]

				Proteins	in Group				I	Peptides in Group				
N	U	nu	Total	Accession #	Name	Species	Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	: *
	9	6.90	6.90	gi 15227559	tubulin beta-7 chain [Arabidopsis t	2.00	99	EILHIQGGQCGNQIGSK	ICAT-C:13C(9)(C)@10		-0.0371	2017.00	
		0.00	6.90	gi]15239914	tubulin beta-6 chain (s	Arabidopsis th	2.00	99	RKLAVNLIPFPR	Lys->Ala@2	cleaved L-R	-0.0652	1365.75	
		0.00	6.90	gi]147224105	unnamed protein prod	Brassica napu	2.00	99	VNVYYNEASCGR	ICAT-C(C)@10		-0.0520	1600.67	
							0.57	73	VSDTVVEPYNATLSVHQLV	ICAT-C:13C(9)(C)@25 Oxidation(M)@26 ICAT-C:13C(9)(C)@37		-0.0716	4902.28	
							0.17	33	KLAVNLIPFPR	Oxidation(K)@1 Ala->Tyr@3	missed K-L	-0.0291	1374.77	
							0.10	20	QVCHSLGGGTGSGMGTLLI	ICAT-C(C)@3 Oxidation(H)@4 Dethiomethyl(M)@14	cleaved F-Q	-0.0116	2224.11	Ŧ
•				III		•	•							F

Protein Sequence Coverage - tubulin beta-7 chain [Arabidopsis thaliana]

MREILHIQGGQCGNQIGSKFWEVVNLEHGIDQTGRYVGDSELQLERVNVYYNEASCGRYVPRAVLMDLEPGTMDSVRSGPYGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELIDSVLDVVRKEAENCD CLQGFQVCHSLGGGTGSGMGTLLISKIREEYPDRMMMTFSVFPSPKVSDTVVEPYNATLSVHQLVENADECMVLDNEALYDICFRTLKLSTPSFGDLNHLISATMSGVTCCLRFPGQLNSDLRKLAVN LIPFPRLHFFMVGFAPLTSRGSQQYRNLTVPELTQQMWDAKNMMCAADPRHGRYLTASAMFRGKMSTKEVDEQMLNVQNKNSSYFVEWIPNNVKSTVCDIPPTGLKMASTFIGNSTSIQEMFRRVSEQ FTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQDATADEEGEYEEEEAEYEQEETY

gi|15235668 Extensin-like protein

Proteins D	etected												
N Unu	Total %	Cov Access	io		Name			Species	Peptide	s(95%) Biologica	I Processes	Molecular Func	tions PANT ^
81 2.0	00 2.00	27.4 gi 1523	5 extens	in-like protein	[Arabidopsis tha	iana]	Arabid	opsis thaliana		1			•
•													4
Protein Gr	oup 81 - ext	ensin-like p	rotein [Ara	bidopsis th	aliana]								
		Proteins	in Group						Рер	otides in Group			
N Unu	Total	Accession #	N	lame	Speci 🔺	Con	⊽ Conf	Sequence		Modifications	Cleav	ages ∆Mass	Prec MW
81 2.	00 2.00 gi	15235668	extensin-	like protein	Arabidops	2.0	0 99	IPASICQLPK	10	CAT-C:13C(9)(C)@	6	-0.0564	1304.70
0.0	00 2.00 gi)	15230120	disease re	sistance pro	Arabidopsi: 👻	0.0	10 1	MKKTIQILLF	D	ethiomethyl(M)@1	cleaved	IF-F0.1528	1202.57 👻
•	1 1-1				•	•							•
					,								
Protein Se	quence Cov	erage - exte	ensin-like p	orotein [Arab	oidopsis thali	ana]							
	<u> </u>	-											
MKKTIQII	LLFFFFLINI	TNALSISSI	DGGVLSDN	EVRHIQRRQI	LLEFAER <mark>SVK</mark> I	TVDPS	LNFENPR	LRNAYIALQAWKQAIL	LSDPNNF	TSNWIGSNVCNY	IGVFCSPAI	LDNRKIR TVAG	IDLNHADIAG
YLPEELGI	LLSDLALFHV	NSNRFCGT	PHRFNRL	KLLFELDLSN	NNRFAGKFPT	VLQLP:	SLKFLDL	RFNEFEGTVPKELFSK	KDLDAIF:	INHNRFRFELPE	NFGDSPVS	VIVLANNRFHG	CVPSSLVEMK
SESCORS	MNGLNSCLE 79 DD DDVV7TE	SDIGRLEN	/TVFDV5F1	NELVGPLPE: STDDTITSDI	SVGEMVSVEQI DDD SDDDDVV	NVAHN	MLSGKIP/ DDDDDVV	ASICQLPKLENFIISI	CNFFIGEA	APVCLRLPEFDD. DDDDDDDVVQDD	RKNCLPGRI	PAQKSPGQCKA DDV/VSDDDDDD	DEDEEDEVVSE
PPPPVYSS	SPPPPPSPAR	TPVYCTRPI	PPPPPHSPI	PPPQFSPPPI	PEPYYYSSPPI	PHSSP	PPHSPPPI	PHSPPPPIYPYLSPPP	PPTPVS	SPPPTPVYSPPP	PPPCIEPPI	PPPPCIEYSPP	PPPPVVHYSS
PPPPPVYY	YSSPPPPPVY	YSSPPPPP	PVHYSSPPI	PPEVHYHSPI	PPSPVHYSSPI	PPPSA	PCEESPPI	PAPVVHHSPPPPMVHH	ISPPPPV:	IHQSPPPPSPEY	EGPLPPVI	GVSYASPPPPP	FY
E 1	а. — Б. 14												
Fragmenta	ition Eviden	се											
IPA	ASIC[C9I]QLPK												
Residue	b	b+2	у	y+2									
1	114.0913	57.5493	1305.7646	653.3859			¥3+2 b2	y2 b3 y3 b66+2 b5	y8+2 y1	0+2 y5	yg7	y7 b8 y8 y	y9 b10
Р	211.1441	106.0757	1192.6805	596.8439	1.5e4 -			244.16					
A	282.1812	141.5942	1095.6278	548.3175				244.10					
S	369.2132	185.1103	1024.5907	512.7990	₩ 1.0e4 -								
1	482.2973	241.6523	937.5586	469.2830	te								
C[C9I]	821.4637	411.2355	824.4746	412.7409	=		226 15	256.12					107.60
Q	949.5223	475.2648	485.3082	243.1577	5.0e3 -		141 10	278.12	23 581 3	0		1024 57	192.09
L	1062.6063	531.8068	357.2496	179.1285				357.24		677.38 824	. ⁴⁴ 921.51	1024.5/	74.66
Р	1159.6591	580.3332	244.1656	122.5864	0.0e0 L			<u>المايمين المراجع الموالية الم</u>	<mark>Ակտեմիսեսի</mark> ս 500 - 00	<u>11 </u>	ىبلەللەتلىيىت بىلەل 2000		1200 1200
К	1287.7540	644.3807	147.1128	74.0600		U	100 20	0 300 400 8	500 60 r	n/z, Da	900	1000 1100	1200 1300

gi|15238333 Cell division protein FtsH

Р	rotei	ns Dete	ected															
	N	Unu	Total	% Cov	Accessio		Name				Species	Peptides(95%)	Biological Pro	cesses	Molecular Fur	octions	PANT	
	26	4.02	4.02	32.8	gi 15241	formate dehydrogena	ise (FDH) [Arabic	dopsis t	nali Ara	abido	psis thaliana	1	'					
	27	3.90	3.90	57.0	gi 15237	H+-transporting ATPa	ase chain E, vacu	uolar [A	rab Ara	abido	psis thaliana	3	}					
	28	3.60	3.60	44.5	gi 15220	putative alanine	aminotransfera	ase[Ara	bi Ara	abido	psis thaliana	2	2					
	29	3.58	3.58	57.8	gi 15224	3-isopropylmalate de	hydratase, smal	Isubunit	[A Ara	abido	psis thaliana	2	!					
	30	3.12	3.12	52.0	gi 15238	cell division protein F	tsH[Arabidopsis	s thaliana	a] Ara	abido	psis thaliana	1						
	31	3.09	44.66	89.0	gi 414103	myrosinase, thiogluc	oside glucohydro	olase (Bra	as Bra	assic	anapus	64	ł					
	32	2.89	2.89	55.1	gi 15219	phosphoglycerate kir	nase, putative[Ar	abidops	ist Ara	abido	psis thaliana	2	!					
	33	2 86	2.86	36.5	ail15229	S-adenosvi-L-homoc	vsteinas putativ	e [Arabid		abido	osis thaliana	5						-
									in,									
Protein Group 30 - cell division protein FtsH [Arabidopsis thaliana]																		
Pr	rotei	n Grou	р 30 - (cell divi	ision prote	in FtsH [Arabidops	is thaliana]											
					Proteins in C	Group						Peptides i	n Group					ר
	Ν	Unu	Total	Acces	sion #	Name	Species	Con.	V Co	nf	Sequence	Mo	difications	Cleava	ages ∆Mas	s Prec I	ww :	-
	30	3.12	3.12	gi 15238	3333 C	ell division protein	Arabidopsis t	2	2.00	99	GCLLVGPPGTGK	ICAT-C:	13C(9)(C)@2		-0.034	0 1333.	71	
		0.01	3.11	gi 15222	913 cl	hloroplast FtsH prote	Arabidopsis th	1	.10	92	PKGCLLVGPPGTGK	Cys->As	n@4	cleaved	II-P0.058	3 1333.	71	
								0).01	3	PLFIQNEILKAPSPK	Deamid Methyl(ated(N)@6 ()@10	cleaved	I S0.108	3 1708.	36	
								0	0.01	3	RGGQGGAGGPGGLGGP	Pro->py	ro-Glu(P)@16	cleaved	I F 0.080	7 1264.	67	
								0	0.01	2	GGQGGAGGPGGLGGPMD	FGR Leu->Va	l@12		0.053	8 1686.	30	
									0.00	1	AKSKAPCIVFIDEIDAV	7GR No ICAT Oxidatio Oxidatio Deamida	(C)@7 (D)@12 (n(D)@15 ated(R)@19	missed	K-S0.228	3 2347.9	98	
									0.00	<1	AATNRPDVLDSALLRPG	R Deamida	ated(N)@4	cleaved	IL-A0.140	3 1939.8	35	Ŧ

Protein Sequence Coverage - cell division protein FtsH [Arabidopsis thaliana]

MATTSSNPLLLSSNFLGSQIIISAPTPKTTKSLPFSVISRKRYQISQSEKLMKSLPSQAALAALLFSSSSPQALAVNEPVQPPAPTITAEAQSPNLSTFGQNVLMTAPNPQAQSSDLPDGTQWRYSE FLNAVKKGKVERVKFSKDGSVLQLTAVDNRRATVIVPNDPDLIDILAMNGVDISVSEGEGGNGLFDFIGNLLFPLLAFGGLFYLFRGGQGGAGGPGGLGGPMDFGRSKSKFQEVPETGVTFGDVAGAD QAKLELQEVVDFLKNPDKYTALGAKIPKGCLLVGPPGTGKTLLARAVAGEAGVPFFSCAASEFVELFVGVGASRVRDLFEKAKSKAPCIVFIDEIDAVGRQRGAGMGGNDEREQTINQLLTEMDGFS GNSGVIVLAATNRPDVLDSALLRPGRFDRQVTVDRPDVAGRVQILKVHSRGKAIGKDVDYEKVARRTPGFTGADLQNLMNEAAILAARRELKEISKDEISDALERIIAGPEKKNAVVSEEKKRLVAYH EAGHALVGALMPEYDPVAKISIIPRGQAGGLTFFAPSEERLESGLYSRSYLENQMAVALGGRVAEEVIFGDENVTTGASNDFMQVSRVARQMVERFGFSKKIGQVAVGGAGGNPFLGQSMSSQKDYSM ATADVVDAEVRELVEKAYVRAKEIITTQIDILHKLAQLLIEKETVDGEEFMSLFIDGQAELYVS

gi|134273558 Unnamed protein product

P	oteiı	ns Dete	ected													
Г	N	Unu	Total	% Cov	Accessio		Name			Species	Peptides(95%)	Biological Processes	Molecul	lar Funct	ions PAI	NT 🔺
	48	2.19	2.19	62.4	gi 13427	unnamed protein pro	duct [Brassica na	ipus]	Brassio	canapus	2					
_	49	2.19	2.19	30.6	gi 15227	enolase (2-phospho-	D-glycerate hydr	oylase) [Ar	. Arabid	opsis thaliana	1					
	50	2.17	2.17	28.0	gi 18141	senescence-associat	ted cysteine prot	ease (Bras	Brassio	ca oleracea	2					
	51	2.16	2.16	62.7	gi 15228	peptidylprolyl isomer	aseROC4[Arabi	dopsis thal	. Arabid	opsis thaliana	3					
	52	2.15	2.15	44.4	gi 15219	hypothetical protein [Arabidopsis thalia	ana]	Arabid	opsis thaliana	2					
	53	2.14	2.14	36.0	gi 31321	putative papillar cell-s	specificcalnexin	Brassica	Brassio	ca napus	1					
	54	2.12	2.12	45.1	gi 15222	putative calcium-bind	ing protein, calr	eticulin [Ara	. Arabid	opsis thaliana	2					
	55	2 12	2 12	47 1	ail28974	NAD-dependentisoc	itrate dehvdroge	nase beta	Brassie	ta napus	1					
Ľ	_								11							•
	oteii	n Grou	p 48 -	unname	ed protein	product [Brassica r Group	napus]				Peptides in	n Group				
	N	Unu	Total	Acces	ssion #	Name	Species	Con V	Conf	Sequence	Mod	difications Clea	avages	∆Mass	Prec MW	: 🔺
	48	2.19	2.19	gi 13427	73558 u	nnamed protein pro	Brassica napi	2.00	99	LLICGGSAYPR	ICAT-C:1	3C(9)(C)@4		-0.0835	1384.67	
┞		0.02	2.02	gi 15236	i375 hj	/droxymethyltransfer	Arabidopsis th	0.19	36	LCDLCNITLNK	ICAT-C: ICAT-C:	13C(9)(C)@2 13C(9)(C)@5		-0.0843	1720.85	
								0.02	4	EMPGFLMSEMK	Phospho	o(S)@8 cleav	ed Y	0.0348	1378.57	
								0.00	< 1	AGMI FYR	Gly->Pro Oxidatio	0@2 n(M)@3		-0.0253	912.4275	
								0.00	<1	AMDFRPKLLICGGSAY	PR Oxidatio Deamida Oxidatio ICAT-C(0	n(M)@2 misse ated(R)@5 n(P)@6 C)@11	ed K-L	-0.0459	2254.07	
	_							0.00	<1	AMDFRPKLLICGGSAY	PRD ICAT-C((Deamida	C)@11 misse	ed K-L	0.0635	3782.96	-
1	_				111			<								P

Protein Sequence Coverage - unnamed protein product [Brassica napus]

MDPVSSWGNTPLVTVDPEIHDLIEKEKRRQCRGIELIASENFTSFAVIEALGSALTNKYSEGMPGNRYYGGNEFIDQIENLCQSRALEAFRLESASWGVNVQPYSGSPANFAAYTALLQPHDRIMGLD LPSGGHLTHGYYTSGGKKISATSIYFESLPYKVNFTTGYIDYDKLEEKAMDFRPKLLICGGSAYPRDWDYARLRAVADKVGALLLCDMAHISGLVAAQEAANPFEYCDVVTTTHKSLRGPRAGMIFY RKGPKPPKKGQPEGAVYDFEDKINFAVFPALQGGPHNHQIGALAVALKQANTPGFKVYAKQVKANAVALANYLMGKGYSIVTGGTENHLVLWDLRPLGLTGNKVEKLCDLCNITLNKNAVFGDSSALA PGGVRIGTPAMTSRGLVEKDFEMIGEFLSRSVTLTLNIQKEHGKLLKDFNKGLVNNKEIEELKADVEKFSASYEMPGFLMSAMKYQD

Figure S6

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to MeJA treatment in guard cells by redox DIGE.
gi|109389998 Chlorophyll a/b binding protein

Protein View

```
Match to: gi|109389998 Score: 65
chloroplast chlorophyll a/b binding protein [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2315DEC04.wiff
```

```
Nominal mass (M_r): 28363; Calculated pI value: 5.48
NCBI BLAST search of <u>qi|109389998</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%
```

- 1 MAASTMALSS PAFAGKAVKL SPAASEVLGS GRVTMRKTVA KPKGPSGSPW
- 51 YGSERVKYLG PFSGEPPSYL TGEFPGDYGW DTAGLSADPE TFARNRELQV
- 101 IHCRWAMLGA LGCVFPELLA RNGVKFGEAV WFKAGSQIFS EGGLDYLGNP
- 151 SLVHAQSILA IWATQVILMG AVEGYRVAGD GPLGEAEDLL YPGGSFDPLG
- 201 LATDPEAFAE LKVKEIKNGR LAMFSMFGFF AQAIVTGKGP LENLADHLAD
- 251 PVNNNAWAFA TNFVPGK

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
44 - 55	640.4367	1278.8588	1278.5629	0.2959	0 K.GPSGSPWYGSER.V	(Ions score 65)

Peptide View

MS/MS Fragmentation of GPSGSPWYGSER

Found in gi 109389998, chloroplast chlorophyll a/b binding protein [Brassica napus]

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							12
2	155.0815	78.0444			P	1222.5487	611. 7780	1205.5222	603.2647	1204.5382	602.7727	11
3	242.1135	121.5604	224.1030	112.5551	S	1125.4960	563.2516	1108.4694	554.7383	1107.4854	554.2463	10
4	299.1350	150.0711	281.1244	141.0659	G	1038.4639	519.7356	1021.4374	511.2223	1020.4534	510.7303	9
5	386.1670	193.5872	368.1565	184.5819	S	981.4425	491.2249	964.4159	482.7116	963.4319	482.2196	8
6	483.2198	242.1135	465.2092	233.1082	P	894.4104	447.7089	877.3839	439.1956	876.3999	438.7036	7
7	669.2991	335.1532	651.2885	326.1479	W	797.3577	399.1825	780.3311	390.6692	779.3471	390.1772	6
8	832.3624	416.6849	814.3519	407.6796	Y	611.2784	306.1428	594.2518	297.6295	593.2678	297.1375	5
9	889.3839	445.1956	871.3733	436.1903	G	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
10	976.4159	488.7116	958.4054	479.7063	S	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
11	1105.4585	553.2329	1087.4479	544.2276	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12					R	175.1190	88.0631	158.0924	79.5498			1

gi|4585935 Light harvesting chlorophyll A/B binding protein

Protein View

Match to: gi|4585935 Score: 75 putative chlorophyll a/b binding protein [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2200DEC04.wiff

Nominal mass (M_r) : 28659; Calculated pI value: 5.29 NCBI BLAST search of <u>qi|4585935</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

Matched peptides shown in Bold Red

1 MATSAIQQSS FAGQTALKPS SDLIQKVGVL GGGRVTMRRT VK**STPQSIWY** 51 GPDRPKYLGP FSENTPSYLT GEYPGDYGWD TAGLSADPET FAKNRELEVI 101 HSRWAMLGAL GCTFPEILSK NGVKFGEAVW FKAGSQIFSE GGLDYLGNPN 151 LIHAQSILAI WAVQVVLMGF IEGYRIGGGP LGEGLDPLYP GGAFDPLNLA 201 EDPEAFSELK VKELKNGRLA MFSMFGFFVQ AIVTGKGPIE NLFDHLADPV 251 ANNAWSYATN FVPGK

 Show predicted peptides also

 Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass
 Start - End
 Observed
 Mr (expt)
 Mr (calc)
 Delta
 Miss
 Sequence
 43 - 56
 816.5772
 1631.1399
 1630.8103
 0.3295
 K.STPQSIWYGPDRPK.Y
 (Ions score 75)

Peptide View

MS/MS Fragmentation of **STPQSIWYGPDRPK**

Found in gi 4585935, putative chlorophyll a/b binding protein [Arabidopsis thaliana]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	189.0870	95.0471			171.0764	86.0418	Τ	1544.7856	772.8964	1527.7591	764.3832	1526.7750	763.8912	13
3	286.1397	143.5735			268.1292	134.5682	P	1443.7379	722.3726	1426.7114	713.8593	1425.7274	713.3673	12
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	Q	1346.6852	673.8462	1329.6586	665.3329	1328.6746	664.8409	11
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	S	1218.6266	609.8169	1201.6000	601.3037	1200.6160	600.8116	10
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	Ι	1131.5946	566.3009	1114.5680	557.7876	1113.5840	557.2956	9
7	800.3937	400.7005	783.3672	392.1872	782.3832	391.6952	W	1018.5105	509.7589	1001.4839	501.2456	1000.4999	500.7536	8
8	963.4571	482.2322	946.4305	473.7189	945.4465	473.2269	Y	832.4312	416.7192	815.4046	408.2060	814.4206	407.7139	7
9	1020.4785	510.7429	1003.4520	502.2296	1002.4680	501.7376	G	669.3679	335.1876	652.3413	326.6743	651.3573	326.1823	6
10	1117.5313	559.2693	1100.5047	550.7560	1099.5207	550.2640	Р	612.3464	306.6768	595.3198	298.1636	594.3358	297.6715	5
11	1232.5582	616.7828	1215.5317	608.2695	1214.5477	607.7775	D	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	4
12	1388.6593	694.8333	1371.6328	686.3200	1370.6488	685.8280	R	400.2667	200.6370	383.2401	192.1237			3
13	1485.7121	743.3597	1468.6856	734.8464	1467.7015	734.3544	P	244.1656	122.5864	227.1390	114.0731			2
14							K	147.1128	74.0600	130.0863	65.5468			1

gi|1346967 Ribulose bisphosphate carboxylase large chain

Protein View

Match to: gi|1346967 Score: 535

RecName: Full=Ribulose bisphosphate carboxylase large chain; Short=RuBisCO large subunit; Flags: Precursor Found in search of C:\QStar Share Data\20091115MMZ\NOV26\850NOV26.wiff

Nominal mass (M_r) : 53436; Calculated pI value: 5.88 NCBI BLAST search of <u>gi|1346967</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica oleracea

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 21%

1	MSPQTETKAS	VGFKAGVKEY	KLNYYTPEYE	TKDTDILAAF	R VTPQPGVPP
51	EEAGAAVAAE	SSTGTWTTVW	TDGLTSLDRY	KGRCYHIEPV	PGEETQFIAY
101	VAYPLDLFEE	GSVTNMFTSI	VGNVFGFKAL	AALRLEDLRI	PPAYTK TFQG
151	PPHGIQVERD	KLNKYGRPLL	GCTIKPKLGL	SAKNYGRAVY	ECLRGGLDFT
201	KDDENVNSQP	FMRWRDRFLF	CAEAIYKSQA	ETGEIKGHYL	NATAGTCEEM
251	MKRAIFAREL	GVPIVMHDYL	TGGFTANTSL	AHYCRDNGLL	LHIHRAMHAV
301	IDRQKNHGMH	FRVLAKALRL	SGGDHVHAGT	VVGK LEGDRE	STLGFVDLLR
351	DDYVEKDRSR	GIFFTQDWVS	LPGVLPVASG	GIHVWHMPAL	TEIFGDDSVL
401	QFGGGTLGHP	WGNAPGAVAN	RVALEACVQA	RNEGRDLAVE	GNEIIREACK
451	WSPELAAACE	VWKEITFNFP	TIDKLDGOD		

start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
22	-	32	710.8920	1419.7694	1419.6558	0.1136	0	K.LNYYTPEYETK.D (Ions score 68)
33	-	41	511.3407	1020.6669	1020.5240	0.1429	0	K.DTDILAAFR.V (Ions score 50)
147	-	159	489.3349	1464.9828	1464.7474	0.2354	0	K.TFQGPPHGIQVER.D (Ions score 55)
195	-	213	724.0806	2169.2199	2168.9797	0.2403	1	R.GGLDFTKDDENVNSQPFMR.W (Ions score 64)
195	-	213	729.4117	2185.2132	2184.9746	0.2386	1	R.GGLDFTKDDENVNSQPFMR.W Oxidation (M) (Ions score 71)
202	-	213	726.9062	1451.7978	1451.5987	0.1991	0	K.DDENVNSQPFMR.W Deamidated (NQ) (Ions score 42)
202	-	213	734.3873	1466.7600	1466.6096	0.1504	0	K.DDENVNSQPFMR.W Oxidation (M) (Ions score 43)
320	-	334	717.4532	1432.8918	1432.7423	0.1495	0	R.LSGGDHVHAGTVVGK.L (Ions score 50)
340	-	350	625.4218	1248.8290	1248.6714	0.1576	0	R.ESTLGFVDLLR.D (Ions score 75)
436	-	446	614.9055	1227.7964	1227.6459	0.1505	0	R.DLAVEGNEIIR.E (Ions score 53)
464	-	474	662.9194	1323.8242	1323.6711	0.1531	0	K.EITFNFPTIDK.L (Ions score 62)
464	-	479	927.0402	1852.0658	1851.8891	0.1767	1	K.EITFNFPTIDKLDGQD (Ions score 10)

gi|18405145 Rubisco activase (RCA)

Protein View

Match to: gi|18405145 Score: 342
RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisp
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1378NOV26.wiff

Nominal mass (M_r) : 52347; Calculated pI value: 5.87 NCBI BLAST search of <u>gi|18405145</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%
```

1	MAAAVSTVGA	INRAPLSLNG	SGSGAVSAPA	STFLGKKVVT	VSRFAQSNKK
51	SNGSFKVLAV	KEDKQTDGDR	WRGLAYDTSD	DQQDITRGKG	MVDSVFQAPM
101	GTGTHHAVLS	SYEYVSQGLR	QYNLDNMMDG	FYIAPAFMDK	LVVHITKNFL
151	TLPNIKVPLI	LGIWGGKGQG	KSFQCELVMA	KMGINPIMMS	AGELESGNAG
201	EPAK LIRQRY	REAADLIKKG	KMCCLFINDL	DAGAGRMGGT	TQYTVNNQMV
251	NATLMNIADN	PTNVQLPGMY	NKEENARVPI	ICTGNDFSTL	YAPLIRDGRM
301	EKFYWAPTRE	DRIGVCKGIF	RTDKIKDEDI	VTLVDQFPGQ	SIDFFGALRA
351	RVYDDEVRKF	VESLGVEKIG	KRLVNSREGP	PVFEQPEMTY	EKLMEYGNML
401	VMEQENVKRV	QLAETYLSQA	ALGDANADAI	GRGTFYGKGA	QQVNLPVPEG
451	CTDPVAENFD	PTARSDDGTC	VYNF		

start	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
73	-	87	849.4554	1696.8962	1696.7540	0.1422	0	R.GLAYDTSDDQQDITR.G (Ions score 108)
182	-	204	779.4299	2335.2680	2335.0494	0.2186	0	K.MGINPIMMSAGELESGNAGEPAK.L 2 Oxidation (M) (Ions score 77)
182	-	204	784.7606	2351.2599	2351.0443	0.2156	0	K.MGINPIMMSAGELESGNAGEPAK.L 3 Oxidation (M) (Ions score 130)
393	-	408	659.3841	1975.1305	1974.8737	0.2568	0	K.LMEYGNMLVMEQENVK.R 3 Oxidation (M) (Ions score 55)
393	-	409	711.4039	2131.1898	2130.9748	0.2150	1	K.LMEYGNMLVMEQENVKR.V 3 Oxidation (M) (Ions score 51)

gi|15237225 High chlorophyll fluorescence 136 (HCF136)

Protein View

```
Match to: gi|15237225 Score: 118
HCF136 (High chlorophyll fluorescence 136) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1520NOV15.wiff
```

```
Nominal mass (M_r): 44133; Calculated pI value: 6.79
NCBI BLAST search of <u>gi|15237225</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

```
Taxonomy: <u>Arabidopsis thaliana</u>
Links to retrieve other entries containing this sequence from NCBI Entrez:
<u>gi|6016183</u> from <u>Arabidopsis thaliana</u>
<u>gi|3559807</u> from <u>Arabidopsis thaliana</u>
<u>gi|9759370</u> from <u>Arabidopsis thaliana</u>
<u>gi|15010780</u> from <u>Arabidopsis thaliana</u>
<u>gi|28416529</u> from Arabidopsis thaliana
```

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%
```

```
Matched peptides shown in Bold Red
```

'LLD 'NSI
NSI
KSA
TFS
ADG
IAAG
LLR

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
134 - 146	778.8692	1555.7239	1555.6790	0.0448	0	R.SIPSAEEEDFNYR.F	(Ions score 83)
370 - 382	667.3863	1332.7581	1332.7037	0.0544	0	K.AADNIAANLYAVK.F	(<u>Ions score 36</u>)

gi|18406661 Thylakoid lumenal 15 kDa protein, chloroplast

Protein View

Match to: gi|18406661 Score: 134 thylakoid lumenal 15 kDa protein, chloroplast [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2716.wiff

Nominal mass (M_r) : 24106; Calculated pI value: 7.55 NCBI BLAST search of <u>gi|18406661</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%
```

Matched peptides shown in Bold Red

1 MVILSNVSLF SCCNISQKPS LFSPSSRSSH CPIRCSQSQE GKEVVTSPLR 51 SVVWSLGEEV SKRSLFALVS ASLFFVDPAL AFKGGGPYGQ GVTRGQDLSG 101 KDFSGQTLIR QDFKTSILRQ ANFKGAKLLG ASFFDADLTG ADLSEADLRG 151 ADFSLANVTK VNLTNANLEG ATVTGNTSFK GSNITGADFT DVPLRDDQRV 201 YLCKVADGVN ATTGNATRDT LLCN

Show predicted peptides also

Sort Peptides By	Resid	ue Number 🛛 🔊	Increasing Mass	Decrea	asing M	ass
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
150 - 160	561.9037	1121.7929	1121.5717	0.2212	0	R.GADFSLANVTK.V (Ions score 60)
181 - 195	782.0118	1562.0091	1561.7737	0.2355	0	K.GSNITGADFTDVPLR.D (Ions score 74)

gi|21133 Oxygen-evolving complex of photosystem II

Protein View

Match to: gi|21133 Score: 135
oxygen-evolving complex of photosystem II [Sinapis alba]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2287.wiff

Nominal mass (M_r) : 28079; Calculated pI value: 6.84 NCBI BLAST search of <u>gi|21133</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: Sinapis alba

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 19%

Residue Number Increasing Mass Decreasing Mass

Matched peptides shown in Bold Red

1 MAYSACFLHQ SALASSTARS SPSSSSQRYV SISKLVCKAQ QTHEEDNSTV 51 SRRLALTLLV GAAAVGSKVS PADAAYGEAA NVFGKPKKNT DFTAYSGDGF 101 QVQVPAKWNP SREVEYPGQV LRYEDNFDAT SNLNVMVTPT DKKSITDYGS 151 PEEFLSQVNY LLGKQAYFGE TASEGGFDNN AVATANILET NIQDVGGKPY 201 YYLSVLTRTA DGDEGGKHQL ITATVNGGKL YICKAQAGDK RWFKGANKFV 251 EKAATSFSVA

Show predicted peptides also

Sort Peptides By

Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
88 - 107	725.4626	2173.3661	2173.0328	0.3333	1	K.KNTDFTAYSGDGFQVQVPAK.W Deamidated (NQ) (Ions score 10)
113 - 122	595.4251	1188.8356	1188.6139	0.2218	0	R.EVEYPGQVLR.Y (Ions score 29)
123 - 142	764.1269	2289.3589	2289.0107	0.3482	0	R.YEDNFDATSNLNVMVTPTDK.K Oxidation (M) (Ions score 64)
123 - 143	806.8225	2417.4458	2417.1057	0.3401	1	R.YEDNFDATSNLNVMVTPTDKK.S Oxidation (M) (Ions score 32)

gi|5748502 Precursor of the 33 kDa subunit of the oxygen evolving complex

Protein View

Match to: gi|5748502 Score: 158 precursor of the 33 kDa subunit of the oxygen evolving complex [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2073.wiff

Nominal mass (M_r) : 35226; Calculated pI value: 5.92 NCBI BLAST search of <u>qi|5748502</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 19%
```

1	MATSLQAAAT	FLQPAKIAAS	PSRNVHLRSN	QTVGKSFGLD	SSQARLTCSL
51	HSDLKDFAGK	CSDAAKIAGF	ALATSALVVS	GAGAEGAPKR	LTYDEIQSKT
101	YMEVKGTGTA	NQCPTIDGGS	ETFSFKAGKY	TGKKFCFEPT	SFTVKADSVS
151	KNAPPDFQNT	KLMTRLTYTL	DEIEGPFEVG	SDGSVKFKEE	DGIDYAAVTV
201	QLPGGERVPF	LFTVKQLEAS	GKPESFSGKF	LVPSYRGSSF	LDPKGR <mark>GGST</mark>
251	GYDNAVALPA	GGR GDEEELS	KENVKNTAAS	VGEITLKITK	SKPETGEVIG
301	VFESLQPSDT	DLGAKVPKDV	KIQGVWYGQI	E	

start	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
152	-	161	566.3993	1130.7840	1130.5356	0.2484	0	K.NAPPDFQNTK.L (Ions score 30)
247	-	263	781.9994	1561.9841	1561.7485	0.2357	0	R.GGSTGYDNAVALPAGGR.G (Ions score 53)
276	-	287	602.4497	1202.8848	1202.6507	0.2342	0	K.NTAASVGEITLK.I (Ions score 53)
291	-	315	868.8857	2603.6353	2603.2966	0.3387	0	K.SKPETGEVIGVFESLQPSDTDLGAK.V (Ions score 21)

gi|228403 Glycolate oxidase

Protein View

Match to: gi|228403 Score: 117 glycolate oxidase Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

Nominal mass (M_r) : 40907; Calculated pI value: 9.38 NCBI BLAST search of <u>gi|228403</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Lens culinaris

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

Matched peptides shown in Bold Red

MEITNVSEYE NVAKQKLPKM VFDYYASGAE DQWTLQENRN AFSRILFRPR
 ILIDVSKIDM TTTVLGFKIS MPIMIAPTAM QKMAHPEGEY ATARAASAAG
 TIMTLSSWAT SSVEEVASTG PGIRFFQLYV YKDRNVVAQL VRRAERAGFK
 AIALTVDTPR LGRREADIKN RFVLPPFLSL KNFEGLDLGK MDQANDSGLA
 SYVAGQIDRS LSWKDVKWLQ TITSLPILVK GVLTAEDARI AVQSGAAGII
 VSNHGARQLD YVLATISALE EVVKAAQGRV PVFLDGGVRR GTDVFKALAL
 GARGVFIGRP VVFSLAAEGE VGVKKVLQML RDEFEMTMTL SGCRSLKEIT
 REMIVADWDT PRIQPRALPR L

Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	liss	Sequence	
151 - 160	528.8606	1055.7066	1055.5975	0.1091	0	K.AIALTVDTPR.L	(Ions score 64)
182 - 190	496.8187	991.6228	991.4975	0.1254	0	K.NFEGLDLGK.M	(Ions score 53)

gi|15228194 Sedoheptulose-bisphosphatase (SBPASE)

Protein View

Match to: gi|15228194 Score: 251 SBPASE (SEDOHEPTULOSE-BISPHOSPHATASE); phosphoric ester hydrolase/ sedoheptulose-bisphosphatase [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1574NOV16.wiff

Nominal mass (M_r): 42787; Calculated pI value: 6.17 NCBI BLAST search of <u>gi|15228194</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|1173345</u> from <u>Arabidopsis thaliana</u> <u>gi|786466</u> from <u>Arabidopsis thaliana</u> <u>gi|7263568</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 15%

1	METSIACYSR	GILPPSVSSQ	RSSTLVSPPS	YSTSSSFKRL	KSSSIFGDSL
51	RLAPKSQLKA	TKAKSNGAST	VTKCEIGQSL	EEFLAQATPD	KGLRTLLMCM
101	GEALRTIAFK	VRTASCGGTA	CVNSFGDEQL	AVDMLADKLL	FEALQYSHVC
151	KYACSEEVPE	LQDMGGPVEG	GFSVAFDPLD	GSSIVDTNFT	VGTIFGVWPG
201	DKLTGITGGD	QVAAAMGIYG	PRTTYVLAVK	GFPGTHEFLL	LDEGKWQHVK
251	ETTEIAEGKM	FSPGNLRATF	DNSEYSKLID	YYVKE KYTLR	YTGGMVPDVN
301	QIIVKEKGIF	TNVTSPTAKA	KLRLLFEVAP	LGLLIENAGG	FSSDGHKSVL
351	DKTIINLDDR	TQVAYGSKNE	IIRFEETLYG	TSR LKNVPIG	VTA

Start	-	End	Observed	Mr (expt)	Mr(calc)	Delta	Miss	Sequence
223	-	230	447.8136	893.6127	893.5222	0.0905	0	R.TTYVLAVK.G (Ions score 40)
260	-	267	469.2334	936.4522	936.4487	0.0035	0	K.MFSPGNLR.A Oxidation (M) (Ions score 27)
278	-	284	457.2908	912.5671	912.4957	0.0715	0	K.LIDYYVK.E (Ions score 30)
291	-	305	550.6594	1648.9562	1648.8495	0.1068	0	R.YTGGMVPDVNQIIVK.E Oxidation (M) (Ions score 47)
308	-	319	618.3640	1234.7135	1234.6558	0.0577	0	K.GIFTNVTSPTAK.A (Ions score 58)
374	-	383	601.8144	1201.6142	1201.5615	0.0527	0	R.FEETLYGTSR.L (Ions score 48)

gi|114403 ATP synthase subunit alpha, mitochondrial

Protein View

```
Match to: gi | 114403 Score: 244
RecName: Full=ATP synthase subunit alpha, mitochondrial
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\708NOV26.wiff
```

Nominal mass (Mr): 55393; Calculated pI value: 6.23 NCBI BLAST search of gi | 114403 against nr Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ), Gln->pyro-Glu (N-term Q), Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%
```

	1 MELSPR <mark>AAEL TNLFESR</mark> IRN FYANFQVDEI GRVVSVGDGI AQVYGLNEIQ	
	51 AGEMVLFANG VKGMALNLEN ENVGIVVFGG DTAIKEGDLV KRTGSIVDVP	
	101 AGKAMLGRVV DAMGVPIDGR GALSDHEQRR VEVKAPGILE RKSVHEPMQT	
	151 GLK <mark>AVDSLVP IGR</mark> GQRELLI GDRQTGKTTI AIDTILNQKQ INSRATSESE	
	201 TMYCVYVAIG QKRSTVGQLI QTLEEANALE YSILVAATAS DPAPLQFLAP	
	251 YSGCAMGEYF RDNGMHALII YDDLSKQAVA YRQMSLLLRR PPGREAFPGD	
	301 VFYLHSRLLE RAAKRSDQTG AGSLTALPVI ETQAGDVSAY IPTNVISITD	
	351 GQICLETELF YRGIRPAINV GLSVSRVGSA AQLKAMKQVC GSSKLELAQY	
	401 REVAAFAQFG SDLDAATQAL LNRGARLTEV PK <mark>QPQYAPLP IEK</mark> QILVIYA	
	451 AVNGFCDRMP LDRISQYEKA IPNSVKPELL QALKGGLTNE RKMEPDAFLK	
	501 ERALRLI	
Start - End	Observed Mr(expt) Mr(calc) Delta Miss Sequence	
7 - 17	625.8907 1249.7669 1249.6302 0.1367 0 R.AAELTNLFESR.I (Ions score 77)	
109 - 120	614.8944 1227.7743 1227.6282 0.1461 0 R.VVDAMGVPIDGR.G (<u>lons score 36</u>)	
109 - 120	622.8902 1243.7658 1243.6231 0.1427 0 R.VVDAMGVPIDGR.G Oxidation (M) (<u>Ions score 62</u>)	
154 - 163	513.8775 1025.7405 1025.5869 0.1536 0 K.AVDSLVPIGR.G (<u>lons score 55</u>)	
		11 1

```
433 - 443
                                                    0 K.QPQYAPLPIEK.Q Gln->pyro-Glu (N-term Q) (Ions score 51)
         633.9125 1265.8104 1265.6656
                                        0.1448
433 - 443
          642.4151 1282.8157 1282.6921
                                         0.1236
                                                    0 K.QPQYAPLPIEK.Q (Ions score 32)
```

gi|75336517 ATP synthase subunit beta, chloroplastic

Protein View

```
Match to: gi|75336517 Score: 1158
RecName: Full=ATP synthase subunit beta, chloroplastic; AltName: Full=F-ATPase subunit beta
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1028NOV26.wiff
```

```
Nominal mass (M_r): 53740; Calculated pI value: 5.21
NCBI BLAST search of <u>gi|75336517</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 45%
```

1	MRINPTTSDP	AVSIREKNNL	GRIAQIIGPV	LDVAFPPGKM	PNIYNALVVK
51	GRDTLGQEIN	VTCEVQQLLG	NNRVRAVAMS	ATEGLKRGMD	VVDMGNPLSV
101	PVGGATLGRI	FNVLGEPVNN	LGPVDTLTTS	PIHK SAPAFI	DLDTTLSIFE
151	TGIKVVDLLA	PYR RGGKIGL	FGGAGVGKTV	LIMELINNIA	KAHGGVSVFG
201	GVGERTREGN	DLYMEMKESG	VINELNLADS	KVALVYGQMN	EPPGARMRVG
251	LTALTMAEYF	RDVNEQDVLL	FIDNIFRFVQ	AGSEVSALLG	R MPSAVGYQP
301	TLSAEMGSLQ	ERITSTKKGS	ITSIQAVYVP	ADDLTDPAPA	TTFAHLDATT
351	VLSRGLAAK <mark>G</mark>	IYPAVDPLDS	TSTMLQPRIV	GEEHYETAQQ	VK QTLQRYKE
401	LQDIIAILGL	DELSEEDRLT	VARARKIERF	LSQPFFVAEV	FTGSPGKYVG
451	LAETIRGFNL	ILSGEFDSLP	EQAFYLVGNI	DEATAKATNL	EMESKLKK

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
3 - 15	685.9302	1369.8459	1369.7201	0.1258	0	R.INPTTSDPAVSIR.E (Ions score 60)
40 - 50	631.4198	1260.8251	1260.6900	0.1351	0	K.MPNIYNALVVK.G (<u>Ions score 54</u>)
40 - 50	639.4316	1276.8487	1276.6849	0.1638	0	K.MPNIYNALVVK.G Oxidation (M) (Ions score 70)
76 - 86	539.3524	1076.6903	1076.5536	0.1367	0	R.AVAMSATEGLK.R (Ions score 83)
76 - 86	547.3542	1092.6938	1092.5485	0.1453	0	R.AVAMSATEGLK.R Oxidation (M) (<u>Ions score 38</u>)
76 - 86	547.3542	1092.6938	1092.5485	0.1453	0	R.AVAMSATEGLK.R Oxidation (M) (<u>Ions score 61</u>)
76 - 86	547.3542	1092.6938	1092.5485	0.1453	0	R.AVAMSATEGLK.R Oxidation (M) (Ions score 46)
76 - 86	547.3542	1092.6938	1092.5485	0.1453	0	R.AVAMSATEGLK.R Oxidation (M) (Ions score 64)
87 - 109	777.4621	2329.3644	2329.1519	0.2125	1	K.RGMDVVDMGNPLSVPVGGATLGR.I 2 Oxidation (M) (Ions score 63)
88 - 109	720.0981	2157.2725	2157.0559	0.2166	0	R.GMDVVDMGNPLSVPVGGATLGR.I Oxidation (M) (<u>lons score 51</u>)
88 - 109	725.4145	2173.2218	2173.0508	0.1710	0	R.GMDVVDMGNPLSVPVGGATLGR.I 2 Oxidation (M) (Ions score 61)
110 - 134	892.8789	2675.6150	2675.4170	0.1979	0	R.IFNVLGEPVNNLGPVDTLTTSPIHK.S Deamidated (NQ) (Ions score 82)
155 - 163	523.3724	1044.7303	1044.5968	0.1336	0	K.VVDLLAPYR.R (<u>lons score 44</u>)
168 - 178	488.3479	974.6813	974.5549	0.1263	0	K.IGLFGGAGVGK.T (<u>Ions score 56</u>)
179 - 191	744.9739	1487.9332	1487.8269	0.1063	0	K.TVLIMELINNIAK.A Deamidated (NQ); Oxidation (M) (Ions score 39
192 - 205	664.9092	1327.8039	1327.6633	0.1406	0	K.AHGGVSVFGGVGER.T (<u>lons score 65</u>)
208 - 217	615.3373	1228.6600	1228.5104	0.1496	0	R.EGNDLYMEMK.E (Ions score 50)
208 - 217	623.3247	1244.6349	1244.5053	0.1296	0	R.EGNDLYMEMK.E Oxidation (M) (<u>Ions score 44</u>)
208 - 217	631.3301	1260.6456	1260.5002	0.1454	0	R.EGNDLYMEMK.E 2 Oxidation (M) (Ions score 27)
218 - 231	744.9251	1487.8357	1487.7467	0.0890	0	K.ESGVINELNLADSK.V (Ions score 73)
232 - 246	801.4679	1600.9213	1600.8031	0.1182	0	K.VALVYGQMNEPPGAR.M (Ions score 104)
232 - 246	809.4494	1616.8842	1616.7981	0.0862	0	K.VALVYGQMNEPPGAR.M Oxidation (M) (Ions score 84)
249 - 261	744.4500	1486.8855	1486.7490	0.1365	0	R.VGLTALTMAEYFR.D Oxidation (M) (Ions score 80)
278 - 291	717.4532	1432.8918	1432.7674	0.1244	0	R.FVQAGSEVSALLGR.M (Ions score 68)
360 - 378	687.7553	2060.2440	2060.0248	0.2192	0	K.GIYPAVDPLDSTSTMLQPR.I (Ions score 98)
360 - 378	693.0804	2076.2195	2076.0198	0.1997	0	K.GIYPAVDPLDSTSTMLQPR.I Oxidation (M) (Ions score 88)
379 - 392	815.9650	1629.9155	1629.7998	0.1157	0	R.IVGEEHYETAQQVK.Q (Ions score 67)
379 - 392	544.3609	1630.0609	1629.7998	0.2611	0	R.IVGEEHYETAQQVK.Q (Ions score 48)

gi|558479 Tonoplast ATPase 70 kDa subunit

Protein View

Match to: gi|558479 Score: 545 tonoplast ATPase 70 kDa subunit Found in search of C:\QStar Share Data\20091115MMZ\NOV26\555NOV26.wiff

Nominal mass (M_r) : 69030; Calculated pI value: 5.19 NCBI BLAST search of <u>qi|558479</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 18%
```

1	MPAFYGGK LT	TFEDDEKESE	YGYVRKVSGP	VVVADGMAGA	AMYELVRVGH
51	DNLIGEIIRL	EGDSATIQVY	EETAGLTVND	PVLRTHKPLS	VELGPGILGN
101	IFDGIQRPLK	TIAKRSGDVY	IPRGVSVPAL	DKDCLWEFQP	KDFVEGDTIT
151	GGDLYATVFE	NSLMQHHVAL	PPDAMGK ITY	LAPAGQYSLK	DTVLELEFQG
201	VKKSFTMLQT	WPVRTPRPVA	SKLAADTPLL	TGQRVLDALF	PSVLGGTCAI
251	PGAFGCGKTV	ISQALSKYSN	SDAVVYVGCG	ERGNEMAEVL	MDFPQLTMTL
301	PDGREESVMK	RTTLVANTSN	MPVAAREASI	YTGITIAEYF	RDMGYNVSMM
351	ADSTSRWAEA	LREISGR LAE	MPADSGYPAY	LAARLASFYE	RAGKVKCLGG
401	PERNGSVTIV	GAVSPPGGDF	SDPVTSATLS	IVQVFWGLDK	KLAQRKHFPS
451	VNWLISYSK <mark>y</mark>	STALESFYEK	FDSDFIDIRT	KAREVLQRED	DLNEIVQLVG
501	KDALAEGDKI	TLETAKLLRE	DYLAQNAFTP	YDKFCPFYKS	VWMMRNIIHF
551	YNLANQAVER	GAGMDGQKIS	YSLIKHRLGD	LFYRLVSQKF	EDPAEGEDVL
601	VGKFKKLHDD	LTSGFRNLED	ETR		

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
9	-	25	694.3973	2080.1700	2079.9273	0.2427	1	K.LTTFEDDEKESEYGYVR.K (Ions score 59)
178	-	190	712.9645	1423.9144	1423.7711	0.1433	0	K.ITYLAPAGQYSLK.D (Ions score 47)
223	-	234	628.4396	1254.8646	1254.6932	0.1714	0	K.LAADTPLLTGQR.V (Ions score 72)
312	-	326	773.4842	1544.9538	1544.7981	0.1557	0	R.TTLVANTSNMPVAAR.E (Ions score 74)
312	-	326	773.4842	1544.9538	1544.7981	0.1557	0	R.TTLVANTSNMPVAAR.E (Ions score 67)
312	-	326	781.4751	1560.9357	1560.7930	0.1428	0	R.TTLVANTSNMPVAAR.E Oxidation (M) (Ions score 74)
342	-	356	840.9161	1679.8176	1679.6589	0.1587	0	R.DMGYNVSMMADSTSR.W Oxidation (M) (Ions score 59)
342	-	356	848.8960	1695.7775	1695.6539	0.1236	0	R.DMGYNVSMMADSTSR.W 2 Oxidation (M) (Ions score 38)
342	-	356	848.9090	1695.8035	1695.6539	0.1496	0	R.DMGYNVSMMADSTSR.W 2 Oxidation (M) (Ions score 67)
342	-	356	856.9136	1711.8127	1711.6488	0.1639	0	R.DMGYNVSMMADSTSR.W 3 Oxidation (M) (Ions score 74)
368	-	384	906.5095	1811.0044	1810.8559	0.1485	0	R.LAEMPADSGYPAYLAAR.L Oxidation (M) (Ions score 59)
460	-	470	669.4060	1336.7974	1336.6187	0.1788	0	K.YSTALESFYEK.F (Ions score 57)
502	-	516	787.9902	1573.9659	1573.8199	0.1460	1	K.DALAEGDKITLETAK.L (Ions score 103)

gi|1655480 Gamma subunit of mitochondrial F1-ATPase

Protein View

Match to: gi|1655480 Score: 83 gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1908DEC01.wiff

```
Nominal mass (M_r): 35597; Calculated pI value: 9.01
NCBI BLAST search of <u>qi|1655480</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
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Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%
```

1	MAMAVFRREG	RRLLPSIAAR	PIAAIRSPLS	SDQEEGLLGV	RSISTQVVRN
51	RMKSVKNIQK	ITKAMKMVAA	SKLRAVQGRA	ENSRGLWQPF	TALLGDNPSI
101	DVKKSVVVTL	SSDKGLCGGI	NSTVVKVSRA	LYKLNAGPEK	EVQFVIVGEK
151	AKAIMFRDSK	NDIVLSVTEL	NKNPLNYAQV	SVLADDILKN	VEFDALRIVY
201	NKFHSVVAFL	PTVSTVLSPE	IIEKESEIGG	KLGELDSYEI	EGGETKGEIL
251	QNLAEFQFSC	VMFNAVLENA	CSEMGARMSA	MDSSSRNAGE	MLDRLTLTYN
301	RTRQASITTE	LIEIISGASA	LEAAK		

Start - End	Observed	Mr (expt)	Mr(calc)	Delta	Miss Sequence
232 - 246	820.4725	1638.9304	1638.7624	0.1680	0 K.LGELDSYEIEGGETK.G (Ions score 83

Peptide View

MS/MS Fragmentation of LGELDSYEIEGGETK

Found in gi 1655480, gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	у*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							15
2	171.1128	86.0600			G	1526.6857	763.8465	1509.6591	755.3332	1508.6751	754.8412	14
3	300.1554	150.5813	282.1448	141.5761	E	1469.6642	735.3357	1452.6377	726.8225	1451.6536	726.3305	13
4	413.2395	207.1234	395.2289	198.1181	L	1340.6216	670.8144	1323.5951	662.3012	1322.6111	661.8092	12
5	528.2664	264.6368	510.2558	255.6316	D	1227.5376	614.2724	1210.5110	605.7591	1209.5270	605.2671	11
6	615.2984	308.1529	597.2879	299.1476	S	1112.5106	556.7589	1095.4841	548.2457	1094.5000	547.7537	10
7	778.3618	389.6845	760.3512	380.6792	Y	1025.4786	513.2429	1008.4520	504.7297	1007.4680	504.2376	9
8	907.4044	454.2058	889.3938	445.2005	E	862.4153	431.7113	845.3887	423.1980	844.4047	422.7060	8
9	1020.4884	510.7478	1002.4779	501.7426	Ι	733.3727	367.1900	716.3461	358.6767	715.3621	358.1847	7
10	1149.5310	575.2691	1131.5204	566.2639	E	620.2886	310.6479	603.2620	302.1347	602.2780	301.6427	6
11	1206.5525	603.7799	1188.5419	594.7746	G	491.2460	246.1266	474.2195	237.6134	473.2354	237.1214	5
12	1263.5739	632.2906	1245.5634	623.2853	G	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4
13	1392.6165	696.8119	1374.6060	687.8066	E	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
14	1493.6642	747.3357	1475.6536	738.3305	Τ	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
15					K	147.1128	74.0600	130.0863	65.5468			1

gi|166627 Nucleotide-binding subunit of vacuolar ATPase

Protein View

Match to: gi|166627 Score: 725 nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV16\842NOV16.wiff

Nominal mass (M_r): 54819; Calculated pI value: 4.98 NCBI BLAST search of <u>qi|166627</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 23%

1	MSLSVNMGTN	DLDIEEGTLE	IGMEYRTVSG	VAGPLVILDK	VKGPK YQEIV
51	NIR LGDGSTR	RGQVLEVDGE	KAVVQVFEGT	SGIDNKFTTV	QFTGEVLKTP
101	VSLDMLGRIF	NGSGKPIDNG	PPILPEAYLD	ISGSSINPSE	RTYPEEMIQT
151	GISTIDVMNS	IARGQKIPLF	SAAGLPHNEI	AAQICRQAGL	VKRLEKTVDL
201	LEDHGEDNFA	IVFAAMGVNM	ETAQFFKRDF	EENGSMERVT	LFLNLANDPT
251	IERIITPRIA	LTTAEYLAYE	CGKHVLVILT	DMSSYADALR	EVSAAREEVP
301	GRRGYPGYMY	TDLATIYERA	GRIEGRKGSI	TQIPILTMPN	DDITHPTPDL
351	TGYITEGQIY	IDRQLHNR <mark>QI</mark>	YPPINVLPSL	SR LMKSAIGE	GMTRKDHSDV
401	SNQLYANYAI	GK DVQAMKAV	VGEEALSSED	LLYLEFLDKF	ERKFVMQGAY
451	DTRNIFQSLD	LAWTLLRIFP	RELLHRIPAK	TLDQFYSRDS	TS

start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
46	-	53	517.8113	1033.6081	1033.5556	0.0525	0	K.YQEIVNIR.L (Ions score 42)
61	-	71	615.3594	1228.7043	1228.6412	0.0631	1	R.RGQVLEVDGEK.A (Ions score 79)
62	-	71	537.3120	1072.6095	1072.5401	0.0694	0	R.GQVLEVDGEK.A (Ions score 65)
72	-	86	521.9743	1562.9010	1562.7941	0.1070	0	K.AVVQVFEGTSGIDNK.F (Ions score 59)
87	-	98	685.3925	1368.7705	1368.7289	0.0416	0	K.FTTVQFTGEVLK.T (Ions score 63)
99	-	108	544.8297	1087.6449	1087.5696	0.0753	0	K.TPVSLDMLGR.I (Ions score 79)
229	-	238	607.2803	1212.5460	1212.4717	0.0743	0	R.DFEENGSMER.V (Ions score 65)
369	-	382	798.9929	1595.9712	1595.9035	0.0677	0	R.QIYPPINVLPSLSR.L (Ions score 48)
396	-	412	632.3287	1893.9643	1893.8857	0.0786	0	K.DHSDVSNQLYANYAIGK.D (Ions score 61)
443	-	453	444.5888	1330.7445	1330.6340	0.1105	1	R.KFVMQGAYDTR.N Oxidation (M) (Ions score 59)
444	-	453	602.3073	1202.6000	1202.5390	0.0609	0	K.FVMQGAYDTR.N Oxidation (M) (Ions score 55)
481	-	488	515.2851	1028.5556	1028.4927	0.0629	0	K.TLDQFYSR.D (Ions score 52)

gi|17939849 Mitochondrial F1 ATP synthase beta subunit

Protein View

Match to: gi|17939849 Score: 694 mitochondrial F1 ATP synthase beta subunit [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV16\905NOV15.wiff

Nominal mass (M_r): 63560; Calculated pI value: 6.52 NCBI BLAST search of <u>gi|17939849</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

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Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 26%
```

1	MTMITPSSNT	THYRESWYAC	RYRSGIPGST	HASVASRRVL	SSLLRSSSGR
51	SAAKLGNRNP	RLPSPSPARH	AAPCSYLLGR	VAEYATSSPA	SSAAPSSAPA
101	KDEGKKTYDY	GGKGAIGRVC	QVIGAIVDVR	FEDQEGLPPI	MTSLEVQDHP
151	TRLVLEVSHH	LGQNVVR TIA	MDGTEGLVRG	RKVLNTGAPI	TVPVGRATLG
201	RIMNVLGEPI	DERGEIKTEH	YLPIHRDAPA	LVDLATGQEI	LATGIKVVDL
251	LAPYQRGGKI	GLFGGAGVGK	TVLIMELINN	VAKAHGGFSV	FAGVGERTRE
301	GNDLYR <mark>EMIE</mark>	SGVIK LGEKQ	SESKCALVYG	QMNE PPGARA	RVGLTGLTVA
351	EYFRDAEGQD	VLLFIDNIFR	FTQANSEVSA	LLGRIPSAVG	YQPTLASDLG
401	ALQERITTTK	KGSITSVQAI	YVPADDLTDP	APATTFAHLD	ATTVLSRQIS
451	ELGIYPAVDP	LDSTSRMLSP	HILGEEHYNT	ARGVQKVLQN	YKNLQDIIAI
501	LGMDELSEDD	KLTVARARKI	QRFLSQPFHV	AEIFTGAPGK	YVDLKENINS
551	FQGLLDGKYD	DLSEQSFYMV	GGIDEVVAKA	EKIAKESAA	

start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
168	-	179	631.8573	1261.7001	1261.6336	0.0665	0	R.TIAMDGTEGLVR.G (Ions score 51)
168	-	179	639.8494	1277.6842	1277.6286	0.0556	0	R.TIAMDGTEGLVR.G Oxidation (M) (Ions score 73)
183	-	196	697.4355	1392.8565	1392.8089	0.0475	0	K.VLNTGAPITVPVGR.A (Ions score 69)
202	-	213	693.3860	1384.7575	1384.7020	0.0555	0	R.IMNVLGEPIDER.G (Ions score 46)
202	-	213	701.3786	1400.7426	1400.6969	0.0456	0	R.IMNVLGEPIDER.G Oxidation (M) (Ions score 63)
227	-	246	666.0608	1995.1606	1995.0888	0.0718	0	R.DAPALVDLATGQEILATGIK.V (Ions score 73)
247	-	256	587.3593	1172.7041	1172.6553	0.0488	0	K.VVDLLAPYQR.G (Ions score 53)
260	-	270	488.3183	974.6221	974.5549	0.0671	0	K.IGLFGGAGVGK.T (Ions score 48)
307	-	315	503.3072	1004.5998	1004.5212	0.0786	0	R.EMIESGVIK.L (Ions score 32)
307	-	315	511.3004	1020.5862	1020.5161	0.0700	0	R.EMIESGVIK.L Oxidation (M) (Ions score 37)
371	-	384	498.3023	1491.8851	1491.7681	0.1170	0	R.FTQANSEVSALLGR.I (Ions score 86)
385	-	405	729.4237	2185.2494	2185.1379	0.1115	0	R.IPSAVGYQPTLASDLGALQER.I (Ions score 85)
448	-	466	687.7084	2060.1035	2060.0426	0.0609	0	R.QISELGIYPAVDPLDSTSR.M (Ions score 56)
546	-	558	717.8957	1433.7768	1433.7150	0.0618	0	K.ENINSFQGLLDGK.Y (Ions score 50)

gi|18391442 De-etiolated 3 (DET3)

Protein View

Start - End

```
Match to: gi | 18391442 Score: 195
DET3 (DE-ETIOLATED 3) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1354NOV17.wiff
Nominal mass (Mr): 42878; Calculated pI value: 5.40
NCBI BLAST search of gi|18391442 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12585488 from Arabidopsis thaliana
gi|6636332 from Arabidopsis thaliana
gi|8698731 from Arabidopsis thaliana
gi|12248023 from Arabidopsis thaliana
gi|16649005 from Arabidopsis thaliana
gi|20259972 from Arabidopsis thaliana
gi|225897918 from Arabidopsis thaliana
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 10%
Matched peptides shown in Bold Red
     1 MTSRYWVVSL PVKDSASSLW NRLQEQISKH SFDTPVYRFN IPNLRVGTLD
    51 SLLALGDDLL KSNSFVEGVS QKIRRQIEEL ERISGVESNA LTVDGVPVDS
   101 YLTRFVWDEA KYPTMSPLKE VVDNIQSQVA KIEDDLKVRV AEYNNIRGQL
   151 NAINRKOSGS LAVRDLSNLV KPEDIVESEH LVTLLAVVPK YSOKDWLACY
   201 ETLTDYVVPR SSKKLFEDNE YALYTVTLFT RVADNFRIAA REKGFQVRDF
   251 EQSVEAGETR KOELAKLVOD GESLRSSLLO WCYTSYGEVF SSWMHFCAVR
   301 TFAESIMRYG LPPAFLACVL SPAVKSEKKV RSILERLCDS TNSLYWKSEE
   351 DAGAMAGLAG DSETHPYVSF TINLA
Observed
            Mr(expt) Mr(calc)
                                     Delta Miss Sequence
```

62 - 72	591.3256	1180.6367	1180.5724	0.0643	0	K.SNSFVEGVSQK.I (Ions score 49)
105 - 111	447.7664	893.5183	893.4283	0.0900	0	R.FVWDEAK.Y (Ions score 25)
112 - 119	476.7866	951.5587	951.4735	0.0851	0	K.YPTMSPLK.E Oxidation (M) (Ions score 51)
120 - 131	665.3813	1328.7480	1328.6936	0.0544	0	K.EVVDNIQSQVAK.I (Ions score 72)

gi|120675 Glyceraldehyde-3-phosphate dehydrogenase, cytosolic

Protein View

Match to: gi|120675 Score: 360
RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

Nominal mass (M_r) : 37015; Calculated pI value: 7.70 NCBI BLAST search of <u>gi|120675</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Sinapis alba</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|21143</u> from <u>Sinapis alba</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 22%

Matched peptides shown in Bold Red

1 MADKKIKIGI NGFGRIGRLV ARVILQRNDV ELVAVNDPFI TTEYMTYMFK 51 YDSVHGQWKH NELKVKDEKT LLFGEKPVTV FGIRNPEDIP WGEAGADFVV 101 ESTGVFTDKD KAAAHLKGGA KKVVISAPSK DAPMFVVGVN EHEYKSDLNI 151 VSNASCTTNC LAPLAKVIND RFGIVEGLMT TVHSITATQK TVDGPSMKDW 201 RGGRAASFNI IPSSTGAAKA VGKVLPQLNG KLTGMSFRVP TVDVSVVDLT 251 VRLEKAATYD EIKKAIKEES QGKLKGILGY TEDDVVSTDF VGDNRSSIFD 301 AKAGIALSDN FVKLVSWYDN EWGYSTRVVD LIIHMSKA

Show predicted peptides also

Sort Peptides By

Start	_	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8	-	15	417.2922	832.5699	832.4555	0.1143	0	K.IGINGFGR.I (Ions score 48)
131	-	145	579.0048	1733.9926	1733.8083	0.1843	0	K.DAPMFVVGVNEHEYK.S (Ions score 55)
131	-	145	584.3340	1749.9802	1749.8032	0.1770	0	K.DAPMFVVGVNEHEYK.S Oxidation (M) (Ions score 49)
205	-	219	717.9316	1433.8486	1433.7514	0.0971	0	R.AASFNIIPSSTGAAK.A (Ions score 57)
232	-	238	406.2593	810.5041	810.4058	0.0983	0	K.LTGMSFR.V (Ions score 44)
276	-	295	724.7294	2171.1663	2171.0019	0.1644	0	K.GILGYTEDDVVSTDFVGDNR.S (Ions score 84)
303	-	313	567.8663	1133.7181	1133.6081	0.1100	0	K.AGIALSDNFVK.L (Ions score 71)

gi|166702 Glyceraldehyde 3-phosphate dehydrogenase A subunit

Protein View

Match to: gi|166702 Score: 99 glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1619NOV15.wiff

Nominal mass (M_r) : 37937; Calculated pI value: 7.00 NCBI BLAST search of <u>gi|166702</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 7%

Matched peptides shown in Bold Red

1 MGSSGGYRKG VTEAKLKVAI NGFGRIGRNF LRCWHGRKDS PLDIIAINDT 51 GGVKQASHLL KYDSTLGIFD ADVKPSGETA ISVDGKIIQV VSNRNPSLLP 101 WKELGIDIVI EGTGVFVDRE GAGKHMEAGA KKVIITAPGK GDIPTYVVGV 151 NADAYSHDEP IISNASCTIN CLAPFVKVLD QKFGIIKGTM TTTHSYTGDQ 201 RLLDASHRDL RRARAAALNI VPTSTGAAKA VALVLPNLKG KLNGIALRVP 251 TPNVSVVDLV VQVSKKTFAE EVNAAFRDSA EKELKGILDV CDEPLVSVDF 301 RCSDFSTTID SSLTMVMGDD MVKVIAWYDN EWGYSQRVVD LADIVANNWK 351

Show predicted peptides also

	creasing Mass	Ising Mass
Start - End Observed Mr(expt) 215 - 229 692.9277 1383.8408 13 230 510 2768 1026 7201 10	Mr(calc) Delta 883.7722 0.0686	Miss Sequence 0 R.AAALNIVPTSTGAAK.A (<u>Ions score 48</u>)

gi|336390 Glyceraldehyde 3-phosphate dehydrogenase B subunit

Protein View

Match to: gi|336390 Score: 201 glyceraldehyde 3-phosphate dehydrogenase B subunit [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff

Nominal mass (M_r) : 43168; Calculated pI value: 5.60 NCBI BLAST search of <u>gi|336390</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 11%

Matched peptides shown in Bold Red

1	MSSIGGEASF	FDAVAAQIIP	KAVTTSTPVR	GETVAKLKVA	INGFGRIGRN
51	FLRCWHGRKD	SPLEVVVLND	SGGVKNASHL	LKYDSMLGTF	KAEVKIVDNE
101	TISVDGKLIK	VVSNRDPLKL	PWAELGIDIV	IEGTGVFVDG	PGAGKHIQAG
151	ASKVIITAPA	KGADIPTYVM	GVNEQDYGHD	VANIISNASC	TTNCLAPFAK
201	VLDEEFGIVK	GTMTTTHSYT	GDQRLLDASH	RDLRRARAAA	LNIVPTSTGA
251	AKAVSLVLPQ	LKGKLNGIAL	RVPTPNVSVV	DLVINVEKKG	LTAEDVNEAF
301	RKAANGPMKG	ILDVCDAPLV	SVDFRCSDVS	TTIDSSLTMV	MGDDMVKVVA
351	WYDNEWGYSQ	RVVDLAHLVA	SKWPGAEAVG	SGDPLEDFCK	TNPADEECKV
401	YD				

Show predicted peptides also

Sort Peptides By	Resid	🔋 💿 Residue Number 💿 Increasing Mass				155
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
83 - 91	539.3006	1076.5866	1076.4848	0.1017	0	K.YDSMLGTFK.A Oxidation (M) (Ions score 44)
96 - 107	645.3602	1288.7059	1288.6511	0.0549	0	K.IVDNETISVDGK.L (Ions score 89)
201 - 210	574.8553	1147.6961	1147.6125	0.0836	0	K.VLDEEFGIVK.G (Ions score 27)
238 - 252	692.9159	1383.8173	1383.7722	0.0451	0	R.AAALNIVPTSTGAAK.A (Ions score 41)

gi|15219412 Phosphoglycerate kinase (PGK)

```
Match to: gi | 15219412 Score: 129
PGK (PHOSPHOGLYCERATE KINASE) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1482NOV17.wiff
Nominal mass (M_): 42162; Calculated pI value: 5.49
NCBI BLAST search of gi|15219412 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|30699430 from Arabidopsis thaliana
gi|4835754 from Arabidopsis thaliana
gi 7839393 from Arabidopsis thaliana
gi|13194782 from Arabidopsis thaliana
gi|17065574 from Arabidopsis thaliana
gi|30725646 from Arabidopsis thaliana
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
Matched peptides shown in Bold Red
    1 MATKRSVGTL KEADLKGKSV FVRVDLNVPL DDNSNITDDT RIRAAVPTIK
    51 YLMGNGSRVV LCSHLGRPKG VTPKYSLKPL VPRLSELLGV EVVMANDSIG
   101 EEVOKLVAGL PEGGVLLLEN VRFYAEEEKN DPEFAKKLAA LADVYVNDAF
   151 GTAHRAHAST EGVAKFLKPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
   201 SKVSTKIGVI ESLLNTVDIL LLGGGMIFTF YKAQGLSVGS SLVEEDKLDL
   251 AKSLMEKAKA KGVSLLLPTD VVIADKFAPD ANSKIVPATA IPDGWMGLDI
   301 GPDSIKTFSE ALDTTKTIIW NGPMGVFEFD KFAAGTEAVA KQLAELSGKG
   351 VTTIIGGGDS VAAVEKVGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
   401 A
     Show predicted peptides also
```

Sort Peptides By

 Start - End
 Observed
 Mr(expt)
 Mr(calc)
 Delta
 Miss Sequence

 179 - 191
 694.9150
 1387.8154
 1387.7347
 0.0807
 0
 K.ELDYLVGAVANPK.K (Ions score 65)

 350 - 366
 787.4640
 1572.9135
 1572.8359
 0.0775
 0
 K.GVTTIIGGGDSVAAVEK.V (Ions score 63)

Residue Number O Increasing Mass O Decreasing Mass

gi|15230595 Phosphoglycerate kinase 1 (PGK1)

Protein View

Match to: gi|15230595 Score: 282
PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1324NOV15.wiff

Nominal mass (M_r) : 50195; Calculated pI value: 5.91 NCBI BLAST search of <u>gi|15230595</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 11%

Matched peptides shown in Bold Red

1	MASAAASSAF	SLLKSTGAVA	SSAGTRARAS	LLPIPSTSVS	ARPLGFSATL
51	DSRRFSLHVA	SKVESVRGKG	SRGVVSMAKK	SVGDLTSADL	KGKKVFVRAD
101	LNVPLDDNQT	ITDDTRIRAA	IPTIKYLIEN	GAKVILSTHL	GRPKGVTPKF
151	SLAPLVPRLS	ELLGIEVTKA	DDCIGPEVES	LVASLPEGGV	LLLENVRFYK
201	EEEKNDPEFA	KKLASLADLY	VNDAFGTAHR	AHASTEGVTK	FLKPSVAGFL
251	LQKELDYLVG	AVSNPKRPFA	AIVGGSKVSS	KIGVIESLLE	KCDILLLGGG
301	MIFTFYKAQG	LSVGSSLVEE	DKLELATELL	AKAKAKGVSL	LLPTDVVVAD
351	KFAPDANSKI	VPASGIEDGW	MGLDIGPDSI	KTFNEALDTT	QTVIWNGPMG
401	VFEMEKFAAG	TEAIANKLAE	LSEKGVTTII	GGGDSVAAVE	K VGVAGVMSH
451	ISTGGGASLE	LLEGKVLPGV	IALDEAIPVT	v	

Show predicted peptides also

Sort Peptides By

					-		-		
Start	; -	- End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
81	-	- 91	553.3233	1104.6320	1104.5663	0.0657	0	K.SVGDLTSADLK.G (Ions	score 81)
99) -	- 116	1008.5252	2015.0359	2014.9444	0.0916	0	R.ADLNVPLDDNQTITDDTR.I	(Ions score 70
407	-	- 417	546.8217	1091.6288	1091.5611	0.0677	0	K.FAAGTEAIANK.L (Ions	score 76)
425	j -	- 441	787.4640	1572.9135	1572.8359	0.0775	0	K.GVTTIIGGGDSVAAVEK.V	(Ions score 55)

gi 15219721 Malate dehydrogenase, cytosolic, putative

Protein View

Start - End

8 - 27

```
Match to: gi | 15219721 Score: 338
                     malate dehydrogenase, cytosolic, putative [Arabidopsis thaliana]
                      Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1509NOV15.wiff
                     Nominal mass (M_): 35890; Calculated pI value: 6.11
                     NCBI BLAST search of gi|15219721 against nr
                     Unformatted sequence string for pasting into other applications
                     Taxonomy: Arabidopsis thaliana
                     Links to retrieve other entries containing this sequence from NCBI Entrez:
                     gi|11133509 from Arabidopsis thaliana
                     gi|2341034 from Arabidopsis thaliana
                     gi|15215692 from Arabidopsis thaliana
                     gi|17473717 from Arabidopsis thaliana
                     gi|20148469 from Arabidopsis thaliana
                     gi|21593602 from Arabidopsis thaliana
                     gi|22137280 from Arabidopsis thaliana
                     Fixed modifications: Carbamidomethyl (C)
                     Variable modifications: Oxidation (M), Phospho (ST)
                     Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
                     Sequence Coverage: 23%
                     Matched peptides shown in Bold Red
                          1 MAKEPVRVLV TGAAGQIGYA LVPMIARGIM LGADQPVILH MLDIPPAAEA
                         51 LNGVKMELID AAFPLLKGVV ATTDAVEGCT GVNVAVMVGG FPRKEGMERK
                        101 DVMSKNVSIY KSQAAALEKH AAPNCKVLVV ANPANTNALI LKEFAPSIPE
                        151 KNISCLTRLD HNRALGOISE RLSVPVSDVK NVIIWGNHSS SOYPDVNHAK
                        201 VQTSSGEKPV RELVKDDAWL DGEFISTVQQ RGAAIIKARK LSSALSAASS
                        251 ACDHIRDWVL GTPEGTFVSM GVYSDGSYSV PSGLIYSFPV TCRNGDWSIV
                        301 QGLPIDEVSR KKMDLTAEEL KEEKDLAYSC LS
             Observed Mr(expt) Mr(calc) Delta Miss Sequence
             672.7596 2015.2569 2015.1238 0.1331
                                                          0 R.VLVTGAAGQIGYALVPMIAR.G Oxidation (M) (Ions score 67)
56 - 67 688.9147 1375.8149 1375.7421 0.0728 0 K.MELIDAAFPLLK.G Oxidation (M) (Ions score 62)
127 - 142 550.7117 1649.1134 1648.9876 0.1258 0 K.VLVVANPANTNALILK.E (<u>Ions score 61</u>)
143 - 151 509.3037 1016.5929 1016.5178
                                              0.0750 0 K.EFAPSIPEK.N (Ions score 54)
172 - 180 472.3134 942.6123 942.5386 0.0737 0 R.LSVPVSDVK.N (Ions score 46)
```

```
313 - 324
         484.6163 1450.8271 1450.6861
                                       0.1411 1 K.MDLTAEELKEEK.D Oxidation (M) (Ions score 50)
```

gi|18404382 Malate dehydrogenase (NAD), mitochondrial

Protein View

```
Match to: gi | 18404382 Score: 114
malate dehydrogenase (NAD), mitochondrial [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1737NOV15.wiff
Nominal mass (M_): 36010; Calculated pI value: 8.54
NCBI BLAST search of gi 18404382 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|11133715 from Arabidopsis thaliana
gi|11692836 from Arabidopsis thaliana
gi|12642848 from Arabidopsis thaliana
gi|3929649 from Arabidopsis thaliana
gi|17065008 from Arabidopsis thaliana
gi|22136210 from Arabidopsis thaliana
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
Matched peptides shown in Bold Red
     1 MFRSMLVRSS ASAKQAVIRR SFSSGSVPER KVAILGAAGG IGQPLALLMK
    51 LNPLVSSLSL YDIANTPGVA ADVGHINTRS EVVGYMGDDN LAKALEGADL
   101 VIIPAGVPRK PGMTRDDLFN INAGIVKNLC TAIAKYCPHA LINMISNPVN
   151 STVPIAAEIF KKAGMYDEKK LFGVTTLDVV RARTFYAGKA NVPVAEVNVP
   201 VIGGHAGVTI LPLFSQATPQ ANLSSDILTA LTKRTQDGGT EVVEAKAGKG
   251 SATLSMAYAG ALFADACLKG LNGVPDVIEC SYVQSTITEL PFFASKVRLG
   301 KNGVEEVLDL GPLSDFEKEG LEALKPELKS SIEKGVKFAN Q
```

Start -	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
80 -	93	749.3788	1496.7431	1496.6817	0.0614	0	R.SEVVGYMGDDNLAK.A	(Ions score 61)
116 -	127	659.8656	1317.7167	1317.6929	0.0239	0	R.DDLFNINAGIVK.N	Ions score 53)

gi|207667274 Chloroplast malate dehydrogenase

Protein View

Match to: gi|207667274 Score: 186 chloroplast malate dehydrogenase [Brassica rapa subsp. pekinensis] Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1660NOV16.wiff

Nominal mass (M_r) : 42520; Calculated pI value: 8.51 NCBI BLAST search of <u>gi|207667274</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica rapa subsp. pekinensis

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 8%

Matched peptides shown in Bold Red

1	MAAASSISIG	STVPRASSSS	SSSSLPQSRA	QAVNFNYSLP	RFTALRSSTL
51	LSGLDSSSFA	KSLRGSVTKP	QSTDTKPYGL	NINASYKVAV	LGAAGGIGQP
101	LSLLIKMSPL	VSTLHLYDIA	NVKGVAADLS	HCNTPSQVRD	FTGPAELADC
151	LKDVNVVVIP	AGVPRKPGMT	RDDLFNINAG	IVK TLVEAVA	DNCPNAFIHI
201	ISNPVNSTVP	IAAEVLRKKG	VYDPKKLFGV	TTLDVVRANT	FVSQKKNLKL
251	IDVDVPVIGG	HAGITILPLL	SKTKPSVSFT	DEEIEKLTVR	IQNAGTEVVD
301	AKAGAGSATL	SMAYAAARFV	ESSLRALDGD	GDVYECSFVD	STLTDLPFFA
351	SRIKIGRNGV	EAVIESDLQG	LTEYEHKALE	ALKPELKASI	EKGVAFANKP
401	AN				

Show predicted peptides also

Sort Peptides By	Resident of the second seco	tueNumber) Increasing Mass	Decrea	sing Ma	155	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
172 - 183	659.8771	1317.7396	1317.6929	0.0468	0	R.DDLFNINAGIVK.T	(<u>Ions score 42</u>)
227 - 237	610.3864	1218.7583	1218.6972	0.0610	0	K.LFGVTTLDVVR.A	(Ions score 75)
291 - 302	622.8679	1243.7212	1243.6408	0.0804	0	R.IQNAGTEVVDAK.A	(<u>Ions score 69</u>)

gi|15231715 Fructose-bisphosphate aldolase, putative

Protein View

Match to: gi|15231715 Score: 551
fructose-bisphosphate aldolase, putative [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff

Nominal mass (M_r) : 38858; Calculated pI value: 6.05 NCBI BLAST search of <u>gi|15231715</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 25%

Matched peptides shown in Bold Red

1	MSAFTSKFAD	ELIANAAYIG	TPGKGILAAD	ESTGTIGKRL	ASINVENVET
51	NRRNLRELLF	TAPGALPCLS	GVILFEETLY	QKSSDGKLFV	DILKEGGVLP
101	GIKVDKGTVE	LAGTDGETTT	QGLDGLGDRC	KKYYEAGARF	AKWRAVLKIG
151	ENEPSEHSIH	ENAYGLARYA	VICQENGLVP	IVEPEILVDG	SHDIQKCAAV
201	TERVLAACYK	ALSDHHVLLE	GTLLKPNMVT	PGSDSPKVSP	EVIAEHTVRA
251	LQRTVPAAVP	AIVFLSGGQS	EEEATRNLNA	MNQLKTKKPW	SLSFSFGRAL
301	QQSTLKTWAG	KEENVKAAQE	ALYVRCKANS	EATLGTYKGD	AKLGDGAAES
351	LHVKDYKY				

Show predicted peptides also

Sort Peptides By Residue Number Increasing 				O Decrea	sing Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 38	666.8790	1331.7435	1331.6933	0.0502	0	K.GILAADESTGTIGK.R (Ions score 109)
40 - 52	729.9181	1457.8217	1457.7474	0.0743	0	R.LASINVENVETNR.R (Ions score 93)
95 - 103	435.3007	868.5868	868.5018	0.0850	0	K.EGGVLPGIK.V (Ions score 45)
107 - 129	755.0596	2262.1570	2262.0612	0.0958	0	K.GTVELAGTDGETTTQGLDGLGDR.C (Ions score 77)
317 - 325	510.8160	1019.6174	1019.5400	0.0774	0	K.AAQEALYVR.C (Ions score 87)
328 - 338	577.8238	1153.6331	1153.5615	0.0716	0	K.ANSEATLGTYK.G (Ions score 79)
343 - 354	598.8503	1195.6861	1195.6197	0.0664	0	K.LGDGAAESLHVK.D (Ions score 62)
	Sort Peptides By Start - End 25 - 38 40 - 52 95 - 103 107 - 129 317 - 325 328 - 338 343 - 354	Sort Peptides By Reside Start - End Observed 25 - 38 666.8790 40 - 52 729.9181 95 - 103 435.3007 107 - 129 755.0596 317 - 325 510.8160 328 - 338 577.8238 343 - 354 598.8503	Sort Peptides By Residue Number Start - End Observed Mr (expt) 25 - 38 666.8790 1331.7435 40 - 52 729.9181 1457.8217 95 - 103 435.3007 868.5868 107 - 129 755.0596 2262.1570 317 - 325 510.8160 1019.6174 328 - 338 577.8238 1153.6331 343 - 354 598.8503 1195.6861	Sort Peptides By Residue Number Increasing Mass Start - End Observed Mr (expt) Mr (calc) 25 - 38 666.8790 1331.7435 1331.6933 40 - 52 729.9181 1457.8217 1457.7474 95 - 103 435.3007 868.5868 868.5018 107 - 129 755.0596 2262.1570 2262.0612 317 - 325 510.8160 1019.6174 1019.5400 328 - 338 577.8238 1153.6331 1153.5615 343 - 354 598.8503 1195.6861 1195.6197	Sort Peptides By Residue Number Increasing Mass Decrea Start - End Observed Mr (expt) Mr (calc) Delta 25 - 38 666.8790 1331.7435 1331.6933 0.0502 40 - 52 729.9181 1457.8217 1457.7474 0.0743 95 - 103 435.3007 868.5868 868.5018 0.0850 107 - 129 755.0596 2262.1570 2262.0612 0.0958 317 - 325 510.8160 1019.6174 1019.5400 0.0774 328 - 338 577.8238 1153.6331 1153.5615 0.0716 343 - 354 598.8503 1195.6861 1195.6197 0.0664	Sort Peptides By Residue Number Increasing Mass Decreasing Mass Start - End Observed Mr (expt) Mr (calc) Delta Miss 25 - 38 666.8790 1331.7435 1331.6933 0.0502 0 40 - 52 729.9181 1457.8217 1457.7474 0.0743 0 95 - 103 435.3007 868.5868 868.5018 0.0850 0 107 - 129 755.0596 2262.1570 2262.0612 0.0958 0 317 - 325 510.8160 1019.6174 1019.5400 0.0774 0 328 - 338 577.8238 1153.6331 1153.5615 0.0716 0 343 - 354 598.8503 1195.6861 1195.6197 0.0664 0

gi|14334740 Putative fructose bisphosphate aldolase

Protein View

Match to: gi|14334740 Score: 77 putative fructose bisphosphate aldolase [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1354NOV17.wiff

Nominal mass (M_r) : 43033; Calculated pI value: 6.48 NCBI BLAST search of <u>gi|14334740</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1	MASSTATMLK	ASPVKSDWVK	GQSLLLRQPS	SVSAIRSHVA	PSALTVRAAS
51	AYADELVKTA	KTIASPGHGI	MAMDESNATC	GKRLASIGLE	NTEANRQAYR
101	TLLVSAPGLG	QYISGAILFE	ETLYQSTTDG	KKMVDVLVEQ	NIVPGIKVDK
151	GLVPLVGSYD	ESWCQGLDGL	ASRTAAYYQQ	GARFAKWRTV	VSIPNGPSAL
201	AVKEAAWGLA	RYAAISQDSG	LVPIVEPEIM	LDGEHSIDRT	YDVAEKVWAE
251	VFFYLAQNNV	MFEGILLKPS	MVTPGAEATD	RATPEQVASY	TLKLLRNRIP
301	PAVPGIMFLS	GGQSGLEATL	NLNAMNQAPN	PWHVSFSYAR	ALQNTCLKTW
351	GGKEENVKAA	QDILLARAKA	NSLAQLGKYT	GEGESEEAKE	GMFVKGYTY

Show predicted peptides also

 Sort Peptides By
 Increasing Mass
 Decreasing Mass

 Start - End
 Observed
 Mr(expt)
 Mr(calc)
 Delta
 Miss Sequence

 282 - 293
 654.3844
 1306.7542
 1306.6769
 0.0773
 0
 R.ATPEQVASYTLK.L
 (Ions score 77)

Peptide View

MS/MS Fragmentation of ATPEQVASYTLK

Found in gi 14334740, putative fructose bisphosphate aldolase [Arabidopsis thaliana]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y++	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							12
2	173.0921	87.0497			155.0815	78.0444	T	1236.6470	618.8272	1219.6205	610.3139	1218.6365	609.8219	11
3	270.1448	135.5761			252.1343	126.5708	P	1135.5994	568.3033	1118.5728	559.7900	1117.5888	559.2980	10
4	399.1874	200.0974			381.1769	191.0921	E	1038.5466	519.7769	1021.5201	511.2637	1020.5360	510.7717	9
5	527.2460	264.1266	510.2195	255.6134	509.2354	255.1214	Q	909.5040	455.2556	892.4775	446.7424	891.4934	446.2504	8
6	626.3144	313.6608	609.2879	305.1476	608.3039	304.6556	V	781.4454	391.2264	764.4189	382.7131	763.4349	382.2211	7
7	697.3515	349.1794	680.3250	340.6661	679.3410	340.1741	A	682.3770	341.6921	665.3505	333.1789	664.3665	332.6869	6
8	784.3836	392.6954	767.3570	384.1821	766.3730	383.6901	S	611.3399	306.1736	594.3134	297.6603	593.3293	297.1683	5
9	947.4469	474.2271	930.4203	465.7138	929.4363	465.2218	Y	524.3079	262.6576	507.2813	254.1443	506.2973	253.6523	4
10	1048.4946	524.7509	1031.4680	516.2376	1030.4840	515.7456	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
11	1161.5786	581.2930	1144.5521	572.7797	1143.5681	572.2877	L	260.1969	130.6021	243.1703	122.0888			2
12							K	147.1128	74.0600	130.0863	65.5468			1

gi|34597330 Enolase

Protein View

Match to: gi|34597330 Score: 683
enolase [Brassica rapa]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\988NOV15.wiff

Nominal mass (M_r) : 47631; Calculated pI value: 5.46 NCBI BLAST search of <u>gi|34597330</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica rapa subsp. campestris

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 32%

1	MATITAVKAR	QIFDSRGNPT	VEVDVHTSSG	VKVTAAVPSG	ASTGIYEALE
51	LR DGGSDYLG	KGVSKAVGNV	NSIIGPASIG	KDPTQQTAID	NFMVHELDGT
101	QNEWGWCKQK	LGANAILAVS	LAVCKAGAVV	SGIPLYKHIA	NLAGNPKIVL
151	PVPAFNVING	GSHAGNKLAM	QEFMILPVGA	SSFKEAMKMG	VEVYHNLKSV
201	IKKKYGQDAT	NVGDEGGFAP	NIQENKEGLE	LLK TAIEKAG	YTGKVVIGMD
251	VAASEFYSSD	RTYDLNFREE	NNNGSQKISG	DALKDLYKSF	VAEYPIVSIE
301	DPFDQDDWEH	YAKMTAECGD	NVQIVGDDLL	VTNPKGVAKA	IAEKSCNALL
351	LKVNQIGSVT	ESIEAVKMSK	RAGWGVMASH	RSGETEDTFI	ADLSVGLSTG
401	QIKTGAPCRS	ERLAKYNQLL	RIEEELGSEA	VYAGANFRKP	VEPY

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
33	-	52	669.0596	2004.1568	2004.0528	0.1041	0	K.VTAAVPSGASTGIYEALELR.D (Ions score 117)
126	-	137	587.8896	1173.7646	1173.6758	0.0888	0	K.AGAVVSGIPLYK.H (Ions score 70)
168	-	184	634.3621	1900.0645	1899.9474	0.1171	0	K.LAMQEFMILPVGASSFK.E 2 Oxidation (M) (Ions score 55)
204	-	226	818.0831	2451.2276	2451.1302	0.0973	1	K.KYGQDATNVGDEGGFAPNIQENK.E (Ions score 68)
205	-	226	775.3973	2323.1700	2323.0353	0.1347	0	K.YGQDATNVGDEGGFAPNIQENK.E (Ions score 98)
227	-	233	401.2810	800.5475	800.4643	0.0832	0	K.EGLELLK.T (Ions score 56)
245	-	261	917.4693	1832.9241	1832.8502	0.0739	0	K.VVIGMDVAASEFYSSDK.T Oxidation (M) (Ions score 71)
262	-	277	634.3396	1899.9970	1899.8598	0.1372	1	K.TYDLNFKEENNNGSQK.I (Ions score 16)
353	-	367	787.4640	1572.9135	1572.8359	0.0776	0	K.VNQIGSVTESIEAVK.M (Ions score 83)
422	-	438	619.0080	1854.0022	1853.8795	0.1227	0	R.IEEELGSEAVYAGANFR.K (Ions score 51)
gi|18421656 EMB1467 (embryo defective 1467); NADH dehydrogenase

Protein View

```
Match to: gi|18421656 Score: 128
EMB1467 (EMBRYO DEFECTIVE 1467); NADH dehydrogenase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\385NOV17.wiff
```

Nominal mass (M_r): 82557; Calculated pI value: 6.24 NCBI BLAST search of <u>gi|18421656</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|55977290</u> from <u>Arabidopsis thaliana</u> <u>gi|15810151</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%
```

Matched peptides shown in Bold Red

1	MGLGILASRT	IRPASRLLQS	QTSNFFLRTI	VSKPELQSPE	SAAVSEPEPP
51	TQILPPRNPV	GGARVHFSNP	EDAIEVFVDG	YAVKVPKGFT	VLQACEVAGV
101	DIPRFCYHSR	LSIAGNCRMC	LVEVEKSPKP	VASCAMPALP	GMKIKTDTPI
151	AKKAREGVME	FLLMNHPLDC	PICDQGGECD	LQDQSMAFGS	DRGRFTEMKR
201	SVVDKNLGPL	VKTVMTRCIQ	CTRCVRFASE	VAGVQDLGIL	GRGSGEEIGT
251	YVEKLMTSEL	SGNVIDICPV	GALTSKPFAF	KARNWELKAT	ETIDVSDAVG
301	SNIRVDSRGP	EVMRIIPRLN	EDINEEWISD	KTRFCYDGLK	RQRLSDPMIR
351	DSDGRFKAVS	WRDALAVVGD	IIHQVKPDEI	VGVAGQLSDA	ESMMVLKDFV
401	NRMGSDNVWC	EGTAAGVDAD	LRYSYLMNTS	ISGLENADLF	LLIGTQPRVE
451	AAMVNARICK	TVRASNAKVG	YVGPPAEFNY	DCKHLGTGPD	TLKEIAEGRH
501	PFCTALKNAK	NPAIIVGAGL	FNRTDKNAIL	SSVESIAQAN	NVVRPDWNGL
551	NFLLQYAAQA	AALDLGLIQQ	SAKALESAKF	VYLMGADDVN	VDKIPKDAFV
601	VYQGHHGDKA	VYRANVILPA	SAFTEREGTY	ENTEGFTQQT	VPAVPTVGDA
651	RDDWKIVRAL	SEVSGVKLPY	NSIEGVRSRI	KSVAPNLVHT	DEREPAAFGP
701	SLKPECKEAM	STTPFQTVVE	NFYMTNSITR	ASKIMAQCSA	VLLKKPFV

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta Mis	Sequenc	e			
243	-	254	634.8344	1267.6543	1267.5932	0.0611 0	R.GSGEE	IGTYVEK. L	(Ions score	<u>58</u>)	
614	-	626	680.9005	1359.7865	1359.7398	0.0468 0	R.ANVIL	PASAFTEK.E	(Ions score	37)	
627	-	651	889.7737	2666.2993	2666.2460	0.0532 0	K.EGTYE	NTEGFTQQTVP	AVPTVGDAR.D	(Ions	score 35)

gi|3122572 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

Protein View

Match to: gi|3122572 Score: 135 RecName: Full=NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial; AltName: Full=76 kDa mitochondrial complex I subunit Found in search of C:\QStar Share Data\20091115MMZ\NOV15\333NOV15.wiff

Nominal mass (M_r): 80831; Calculated pI value: 5.87 NCBI BLAST search of <u>gi|3122572</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Solanum tuberosum</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi[758340</u> from <u>Solanum tuberosum</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

Matched peptides shown in Bold Red

1	MGLGLLASRA	LRSSRIIRNS	TRTIVSTPEL	KNADAAAAAA	AADAPSDLPK
51	RHPVGGARVH	LPNPEDVIEV	FVDGYPVKIP	KGMTVLQACE	IAGVDIPRFC
101	YHSRLSIAGN	CRMCLVEVEK	SPKPVASCAM	PALPGMKIKT	DTPIAKKARE
151	GVMEFLLMNH	PLDCPICDQG	GECDLQDQSM	AFGSDRGRFT	EMKRSVVDKN
201	LGPLVKTVMT	RCIQCTRCVR	FASEVAGVED	LGMLGRGSGE	EIGTYVEKLM
251	TSELSGNVID	ICPVGALTSK	PFAFKARNWE	LKGTESIDVT	DAVGSNIRID
301	SRGPEVMRVV	PRLNEDINEE	WISDKTRFFY	DGLKRQRLND	PMIRGADGRF
351	QAVSWRDALA	IVAEVMHQIK	PEEIVGVAGK	LSDAESMMAL	KDLLNKMGSN
401	NIFCEGNGMH	PNADLRSGYI	MNTSISGLEK	ADAFLLVGTQ	PRVEAAMVNA
451	RIHKTVKATN	AKVGYVGPAA	DFNYDHEHLG	TDPQTLVEIA	EGRHPFSSAL
501	KNAKNPVIIV	GAGVFDRDDK	DAVFAAVDTI	AKNNNVVRPD	WNGLNVLLLN
551	AAQVAALDLG	LVPESDKCIE	SAKFVYLMGA	DDVNLDKLPD	DAFVVYQGHH
601	GDRGVYRANV	ILPASAFTEK	EGIYENTEGC	AQITLPAVPT	VGDARDDWKI
651	VRALSEVAGV	GLPYDSLGAI	RSRIKTVAPN	LLEVDERQPA	TFSTSLRPEV
701	SQKVSATPFT	PAVENFYMTD	AITRASKIMA	QCSALLKK	

Start - H	Ind	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
237 - 2	248	634.8232	1267.6318	1267.5932	0.0386	0	R.GSGEEIGTYVEK.L (Ions score 47)
283 - 2	298	817.4321	1632.8496	1632.7955	0.0541	0	K.GTESIDVTDAVGSNIR.I (Ions score 22)
608 - 6	520	680.9005	1359.7865	1359.7398	0.0468	0	R.ANVILPASAFTEK.E (Ions score 67)

gi|15223753 Ferredoxin-NADP(+)-oxidoreductase 2 (FNR2)

Protein View

Match to: gi|15223753 Score: 66
FNR2 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 2); NADPH dehydrogenase/ oxidoreductase/ poly(U) binding [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1721NOV26.wiff

Nominal mass (M_r) : 41484; Calculated pI value: 8.51 NCBI BLAST search of <u>gi|15223753</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1 MATTMNAAVS LTSSNSSSFP ATSCAIAPER IRFTKGAFYY KSNNVVTGKR 51 VFSIKAQITT ETDTPTPAKK VEKVSKKNEE GVIVNRYRPK EPYTGKCLLN 101 TKITADDAPG ETWHMVFSHQ GEIPYREGQS VGVIADGIDK NGKPHKVRLY 151 SIASSALGDL GNSETVSLCV KRLVYTNDQG ETVKGVCSNF LCDLAPGSDV 201 KLTGPVGKEM LMPKDPNATV IMLATGTGIA PFRSFLWKMF FEKHDDYKFN 251 GLAWLFLGVP TTSSLLYQEE FDKMKAKAPE NFRVDYAISR EQANDKGEKM 301 YIQTRMAQYA AELWELLKKD NTFVYMCGLK GMEKGIDDIM VSLAANDGID 351 WFDYKKQLKK AEQWNVEVY

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
127 - 140	694.4326	1386.8506	1386.6991	0.1515	0	R.EGQSVGVIADGIDK.N	(Ions score 66)

Peptide View

MS/MS Fragmentation of **EGQSVGVIADGIDK** Found in gi[15223753, FNR2 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 2);

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y++	y *	y***	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	187.0713	94.0393			169.0608	85.0340	G	1258.6638	629.8355	1241.6372	621.3222	1240.6532	620.8302	13
3	315.1299	158.0686	298.1034	149.5553	297.1193	149.0633	Q	1201.6423	601.3248	1184.6157	592.8115	1183.6317	592.3195	12
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	S	1073.5837	537.2955	1056.5572	528.7822	1055.5732	528.2902	11
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	V	986.5517	493.7795	969.5251	485.2662	968.5411	484.7742	10
6	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	G	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	9
7	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	V	830.4618	415.7345	813.4353	407.2213	812.4512	406.7293	8
8	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	Ι	731.3934	366.2003	714.3668	357.6871	713.3828	357.1951	7
9	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	Α	618.3093	309.6583	601.2828	301.1450	600.2988	300.6530	6
10	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	D	547.2722	274.1397	530.2457	265.6265	529.2617	265.1345	5
11	1013.4898	507.2485	996.4633	498.7353	995.4793	498.2433	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
12	1126.5739	563.7906	1109.5473	555.2773	1108.5633	554.7853	Ι	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
13	1241.6008	621.3040	1224.5743	612.7908	1223.5903	612.2988	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
14							K	147.1128	74.0600	130.0863	65.5468			1

gi|15218869 NADP+ isocitrate dehydrogenase, putative

Match to: gi|15218869 Score: 130 isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (M_r) : 46059; Calculated pI value: 6.13 NCBI BLAST search of <u>gi|15218869</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|6227018</u> from <u>Arabidopsis thaliana</u> <u>gi|16930443</u> from <u>Arabidopsis thaliana</u> <u>gi|20453235</u> from <u>Arabidopsis thaliana</u> <u>gi|27311589</u> from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 9%

Matched peptides shown in Bold Red

```
1 MAFEKIKVAN PIVEMDGDEM TRVIWKSIKD KLITPFVELD IKYFDLGLPH
51 RDATDDKVTI ESAEATKKYN VAIKCATITP DEGRVTEFGL KQMWRSPNGT
101 IRNILNGTVF REPIICKNVP KLVPGWTKPI CIGRHAFGDQ YRATDAVIKG
151 PGKLTMTFEG KDGKTETEVF TFTGEGGVAM AMYNTDESIR AFADASMNTA
201 YEKKWPLYLS TKNTILKKYD GRFKDIFQEV YEASWKSKYD AAGIWYEHRL
251 IDDMVAYALK SEGGYVWACK NYDGDVQSDF LAQGFGSLGL MTSVLVCPDG
301 KTIEAEAAHG TVTRHFRVHQ KGGETSTNSI ASIFAWTRGL AHRAKLDDNA
351 KLLDFTEKLE AACVGTVESG KMTKDLALII HGSKLSRDTY LNTEEFIDAV
401 AAELKERLNA
```

Show predicted peptides also

Out Dustides Du

Soft Peptides By	Resid	lue Number () Increasing Mass	O Decrea	sing Ma	SS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 22	570.2836	1707.8290	1707.7444	0.0846	0	K.VANPIVEMDGDEMTR.V 2 Oxidation (M) (Ions score 51)
52 - 67	565.3055	1692.8948	1692.8054	0.0894	1	R.DATDDKVTIESAEATK.K (Ions score 61)
103 - 111	517.3137	1032.6129	1032.5716	0.0412	0	R.NILNGTVFR.E (Ions score 19)

gi|520478 Pyruvate dehydrogenase E1 beta subunit

Protein View

Match to: gi|8953766 Score: 223 pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (PDHE1-B) [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1378NOV26.wiff

Nominal mass (M_r): 39436; Calculated pI value: 5.67 NCBI BLAST search of <u>gi|8953766</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%
```

Matched peptides shown in Bold Red

```
1 MLGILRQRAI DGASTLRRTR FALVSARSYA AGAKEMTVRD ALNSAIDEEM
51 SADPKVFVMG EEVGQYQGAY KITKGLLEKY GPERVYDTPI TEAGFTGIGV
101 GAAYAGLKPV VEFMTFNFSM QAIDHIINSA AKSNYMSAGQ INVPIVFRGP
151 NGAAAGVGAQ HSQCYAAWYA SVPGLKVLAP YSAEDARGLL KAAIRDPDPV
201 VFLENELLYG ESFPISEEAL DSSFCLPIGK AKIEREGKDV TIVTFSKMVG
251 FALKAAEKLA EEGISAEVIN LRSIRPLDRA TINASVRKTS RLVTVEEGFP
301 QHGVCAEICA SVVEESFSYL DAPVERIAGA DVPMPYAANL ERLALPQIED
351 IVRASKRACY RSK
```

Sort Peptides By	Resid	lueNumber) Increasing Mass	O Decrea	sing Ma	ss
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
40 - 55	861.4540	1720.8935	1720.7461	0.1474	0	R.DALNSAIDEEMSADPK.V Oxidation (M) (Ions score 17)
177 - 187	596.3949	1190.7753	1190.5931	0.1822	0	K.VLAPYSAEDAR.G (Ions score 78)
259 - 272	757.5026	1512.9906	1512.8147	0.1759	0	K.LAEEGISAEVINLR.S (Ions score 100)
327 - 342	852.4895	1702.9645	1702.8348	0.1296	0	R.IAGADVPMPYAANLER.L Oxidation (M) (Ions score 28)

gi|15225353 Succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial

Protein View

Match to: gi|15225353 Score: 314 succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1297NOV26.wiff

Nominal mass (M_r) : 45602; Calculated pI value: 6.30 NCBI BLAST search of <u>gi|15225353</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 11%

Matched peptides shown in Bold Red

1	MRGLVNKLVS	RSLSISGKWQ	NQQLRRLNIH	EYQGAELMGK	YGVNVPKGVA
51	ASSLEEVKKA	IQDVFPNESE	LVVKSQILAG	GRGLGTFKSG	LKGGVHIVKR
101	DEAEEIAGKM	LGQVLVTKQT	GPQGKVVSKV	YLCEKLSLVN	EMYFSIILDR
151	KSAGPLIIAC	KKGGTSIEDL	AEKFPDMIIK	VPIDVFAGIT	DEDAAKVVDG
201	LAPKAADRKD	SIEQVKKLYE	LFRKTDCTML	EINPLAETST	NQLVAADAKL
251	NFDDNAAFRQ	KEVFAMRDPT	QEDPREVAAA	KVDLNYIGLD	GEIGCMVNGA
301	GLAMATMDII	KLHGGTPANF	LDVGGNASEH	QVVEAFKILT	SDDKVKAILV
351	NIFGGIMKCD	VIASGIVNAA	KEVALKVPVV	VRLEGTNVEQ	GKRILKESGM
401	KLITADDLDD	AAEKAVKALA	Н		

Sort Peptides By	Resid	lueNumber (Increasing Mass	Decrea	sing Ma	ss
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
110 - 118	502.8666	1003.7187	1003.5736	0.1451	0	K.MLGQVLVTK.Q Oxidation (M) (Ions score 50)
181 - 196	830.9909	1659.9673	1659.8356	0.1318	0	K.VPIDVFAGITDEDAAK.V (Ions score 102)
250 - 259	591.8577	1181.7008	1181.5465	0.1542	0	K.LNFDDNAAFR.Q (Ions score 71)
402 - 414	695.4093	1388.8040	1388.6671	0.1369	0	K.LITADDLDDAAEK.A (Ions score 91)

gi|15232763 Adenosine kinase 1 (ADK1)

Protein View

Match to: gi|15232763 Score: 149
ADK1 (ADENOSINE KINASE 1) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1354NOV17.wiff

Nominal mass (M_r): 38268; Calculated pI value: 5.29 NCBI BLAST search of <u>gi|15232763</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|17367081</u> from <u>Arabidopsis thaliana</u> <u>gi|6681336</u> from <u>Arabidopsis thaliana</u> <u>gi|12017762</u> from <u>Arabidopsis thaliana</u> <u>gi|12017766</u> from <u>Arabidopsis thaliana</u> <u>gi|14030721</u> from <u>Arabidopsis thaliana</u>

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%
```

Matched peptides shown in Bold Red

1	MASSDFDGIL	LGMGNPLLDV	SAVVDQQFLD	KYDIKLNNAI	LAEDKHLPMY
51	DEMSQKFNVE	YIAGGATQNS	IKVAQWMLQV	PGATSYMGSI	GKDKYGEAMK
101	KDATAAGVYV	HYYEDEATPT	GTCGVCVLGG	ERSLIANLSA	ANCYKVEHLK
151	KPENWALVEK	AKFYYIAGFF	LTVSPESIQL	VREHAAANNK	VFTMNLSAPF
201	ICEFFKDVQE	KCLPYMDYIF	GNETEARTFS	RVHGWETDDV	EQIAIKMSQL
251	PKASGTYKRT	TVITQGADPV	VVAEDGKVKK	YPVIPLPKEK	LVDTNGAGDA
301	FVGGFLSQLV	HGKGIEECVR	AGCYASNVVI	QRSGCTYPEK	PDFN

Sort F	Pe	ptides By	Resid	ueNumber	Increasing Mass	Decrease	sing Ma	ISS
Start	_	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36	-	45	550.8479	1099.6813	1099.5873	0.0940	0	K.LNNAILAEDK.H (Ions score 72)
260	-	277	600.6869	1799.0390	1798.9313	0.1077	0	R.TTVITQGADPVVVAEDGK.V (Ions score 77)

gi|1173347 Sedoheptulose-1,7-bisphosphatase

Protein View

Match to: gi|786466 Score: 310
sedoheptulose-1,7-bisphosphatase; SBPase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1569NOV26.wiff

Nominal mass (M_r) : 42787; Calculated pI value: 6.17 NCBI BLAST search of <u>gi|786466</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 17%

Matched peptides shown in Bold Red

1	METSIACYSR	GILPPSVSSQ	RSSTLVSPPS	YSTSSSFKRL	KSSSIFGDSL
51	RLAPKSQLKA	TKAKSNGAST	VTKCEIGQSL	EEFLAQATPD	KGLRTLLMCM
101	GEALRTIAFK	VRTASCGGTA	CVNSFGDEQL	AVDMLADKLL	FEALQYSHVC
151	KYACSEEVPE	LQDMGGPVEG	GFSVAFDPLD	GSSIVDTNFT	VGTIFGVWPG
201	DKLTGITGGD	QVAAAMGIYG	PRTTYVLAVK	GFPGTHEFLL	LDEGKWQHVK
251	ETTEIAEGKM	FSPGNLRATF	DNSEYSKLID	YYVKE KYTLR	YTGGMVPDVN
301	QIIVKEKGIF	TNVTSPTAKA	KLRLLFEVAP	LGLLIENAGG	FSSDGHKSVL
351	DKTIINLDDR	TQVAYGSKNE	IIRFEETLYG	TSRLKNVPIG	VTA

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start - 1	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
223 - 3	230	447.8325	893.6505	893.5222	0.1283	0	R.TTYVLAVK.G (Ions score 29)
260 - 3	267	469.3011	936.5876	936.4487	0.1389	0	K.MFSPGNLR.A Oxidation (M) (Ions score 32)
268 - 3	277	581.3380	1160.6615	1160.4986	0.1630	0	R.ATFDNSEYSK.L (Ions score 74)
278 - 3	284	457.3195	912.6244	912.4957	0.1288	0	K.LIDYYVK.E (Ions score 32)
291 - 3	305	825.4925	1648.9704	1648.8495	0.1209	0	R.YTGGMVPDVNQIIVK.E Oxidation (M) (Ions score 32)
308 - 3	319	618.4195	1234.8245	1234.6558	0.1687	0	K.GIFTNVTSPTAK.A (Ions score 59)
374 - 3	383	601.8691	1201.7237	1201.5615	0.1622	0	R.FEETLYGTSR.L (Ions score 53)

gi|15222241 Allene oxide cyclase 4 (AOC4)

Protein View

Match to: gi|15222241 Score: 75
AOC4 (ALLENE OXIDE CYCLASE 4); allene-oxide cyclase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2384.wiff

Nominal mass (M_r) : 27963; Calculated pI value: 9.15 NCBI BLAST search of <u>gi|15222241</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

Matched peptides shown in Bold Red

1	MIMASSAAAS	ISMITLRNLS	RNHQSHQSTF	LGFSRSFHNQ	RISSNSPGLS
51	TRARSTTSST	GGFFRTICSS	SSNDYSRPTK	IQELNVYEFN	EGDRNSPAVL
101	KLGKKPDQLC	LGDLVPFTNK	LYTGDLTKRI	GITAGLCVLI	QHVPEKKGDR
151	FEASYSFYFG	DYGHISVQGP	YLTYEDTFLA	ITGGSGVFEG	AYGQVKLRQL
201	VYPTKLFYTF	YLKGVAADLP	VELTGKHVEP	SKEVKPAAEA	QATQPGATIA
251	NFTN				

Sort Peptides By	Resid	lueNumber) Increasing Mass	Decrea Decrea	sing Ma	ISS	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	(<u>Ions score 75</u>)
81 - 94	863.4992	1724.9837	1724.8006	0.1832	O	K.IQELNVYEFNEGDR.N	

Peptide View

MS/MS Fragmentation of IQELNVYEFNEGDR

Found in gi 15222241, AOC4 (ALLENE OXIDE CYCLASE 4); allene-oxide cyclase [Arabidopsis thaliana]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y++	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					Ι							14
2	242.1499	121.5786	225.1234	113.0653			Q	1612.7238	806.8655	1595.6972	798.3523	1594.7132	797.8603	13
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	E	1484.6652	742.8362	1467.6387	734.3230	1466.6546	733.8310	12
4	484.2766	242.6419	467.2500	234.1287	466.2660	233.6366	L	1355.6226	678.3149	1338.5961	669.8017	1337.6121	669.3097	11
5	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	Ν	1242.5386	621.7729	1225.5120	613.2596	1224.5280	612.7676	10
6	697.3879	349.1976	680.3614	340.6843	679.3774	340.1923	V	1128.4956	564.7515	1111.4691	556.2382	1110.4851	555.7462	9
7	860.4512	430.7293	843.4247	422.2160	842.4407	421.7240	Y	1029.4272	515.2172	1012.4007	506.7040	1011.4167	506.2120	8
8	989.4938	495.2506	972.4673	486.7373	971.4833	486.2453	E	866.3639	433.6856	849.3373	425.1723	848.3533	424.6803	7
9	1136.5623	568.7848	1119.5357	560.2715	1118.5517	559.7795	F	737.3213	369.1643	720.2947	360.6510	719.3107	360.1590	6
10	1250.6052	625.8062	1233.5786	617.2930	1232.5946	616.8009	Ν	590.2529	295.6301	573.2263	287.1168	572.2423	286.6248	5
11	1379.6478	690.3275	1362.6212	681.8142	1361.6372	681.3222	E	476.2100	238.6086	459.1834	230.0953	458.1994	229.6033	4
12	1436.6692	718.8383	1419.6427	710.3250	1418.6587	709.8330	G	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
13	1551.6962	776.3517	1534.6696	767.8385	1533.6856	767.3464	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
14							R	175.1190	88.0631	158.0924	79.5498			1

gi|1526562 Glutamine synthetase

Protein View

Match to: gi|1526562 Score: 99
glutamine synthetase [Raphanus sativus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1509NOV15.wiff

Nominal mass (M_r) : 38722; Calculated pI value: 5.93 NCBI BLAST search of <u>gi|1526562</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Raphanus sativus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

Matched peptides shown in Bold Red

1	MSLLSDLVNL	NLSDSTEKII	AEYIWIGGSG	MDIRSKARTL	PGPVSDPSKL
51	PKWNYDGSST	GQAAGDDSEV	IIYPQAIFRD	PFRRGNNILV	MCDAYTPAGN
101	PIPTNKRHNA	AKIFSTSKVA	SEEPWYGIEQ	EYTLMQKGVN	WPIGWPVGGF
151	PGPQGPYYCG	VGADKAIGRD	IVDAHYKACL	YAGISISGVN	GEVMPGQWEF
201	QVGPVEGISA	GDQVWVARFL	LERITEISGV	NVSFDPKPVP	GDWNGAGAHC
251	NYSTKSMRND	GGLAVIKKAI	EKLQVKHKEH	IAAYGEGNER	RLTGKHETAD
301	INTFSWGVAN	RGASVRVGRD	TEKEGKGYFE	DRRPASNMDP	YVVTSMIAET
351	TILG				

Sort Pe	ptides By	Resid	ue Number	Increasing Mass	ODecrea	sing Ma	ISS
Start -	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
39 -	49	549.3403	1096.6660	1096.5764	0.0895	0	R.TLPGPVSDPSK.L (Ions score 57)
259 -	267	443.7891	885.5636	885.4920	0.0716	0	R.NDGGLAVIK.K (Ions score 43)

gi|1113783 Thi1 protein

Protein View

Match to: gi|1113783 Score: 206
Thi1 protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1791.wiff

Nominal mass (M_r) : 36755; Calculated pI value: 5.82 NCBI BLAST search of <u>gi|1113783</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%
```

Matched peptides shown in Bold Red

1	MAAIASTLSL	SSTKPQRLFD	SSFHGSAISA	APISIGLKPR	SFSVRATTAG
51	YDLNAFTFDP	IKESIVSREM	TRRYMTDMIT	YAETDVVVVG	AGSAGLSAAY
101	EISKNPNVQV	AIIEQSVSPG	GGAWLGGQLF	SAMIVRKPAH	LFLDEIGVAY
151	DEQDTYVVVK	HAALFTSTIM	SKLLARPNVK	LFNAVAAEDL	IVKGNRVGGV
201	VTNWALVAQN	HHTQSCMDPN	VMEAKIVVSS	CGHDGPFGAT	GVKRLKSIGM
251	IDHVPGMKAL	DMNTAEDAIV	RLTREVVPGM	IVTGMEVAEI	DGAPRMGPTF
301	GAMMISGQKA	GQLALKALGL	PNAIDGTLVG	NLSPELVLAA	ADSAETVDA

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
181	-	193	702.0289	1402.0433	1401.7867	0.2566	0	K.LFNAVAAEDLIVK.G (Ions score 46)
259	_	271	717.9794	1433.9442	1433.6820	0.2622	0	K.ALDMNTAEDAIVR.L Oxidation (M) (Ions score 107)
275	-	295	734.8228	2201.4466	2201.0708	0.3758	0	R.EVVPGMIVTGMEVAEIDGAPR.M 2 Oxidation (M) (Ions score 52)

gi|16394 Leucine aminopeptidase

Protein View

Match to: gi|16394 Score: 62 leucine aminopeptidase [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV26\828NOV26.wiff

Nominal mass (M_r) : 54760; Calculated pI value: 5.66 NCBI BLAST search of <u>gi|16394</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%
```

Matched peptides shown in Bold Red

1	MAHTLGLTQP	NSTEPHKISF	TAKEIDVIEW	KGDILVVGVT	EKDLAKDGNS
51	KFENPILSKV	DAHLSGLLAQ	VSSEEDFTGK	PGQSTVLRLP	GLGSKRIALI
101	GLGQSVSSPV	AFHSLGEAVA	TVSKASQSTS	AAIVLASSVS	DESKLSSVSA
151	LASGIVLGLF	EDGRYKSESK	KPSLKAVDII	GFGTGAEVEK	KLKYAEDVSY
201	GVIFGRELIN	SPANVLTPAV	LAEEAAKVAS	TYSDVFTANI	LNEEQCKELK
251	MGSYLAVAAA	SANPPHFIHL	VYKPPNGSVK	TKLALVGKGL	TFDSGGYNIK
301	TGPGCSIELM	KFDMGGSAAV	LGAAKAIGEI	KPPGVEVHFI	VAACENMISG
351	TGMRPGDVIT	ASNGKTIEVN	NTDAEGRLTL	ADALVYACNQ	GVDKIVDLAT
401	LTGACVIALG	TSMAGIYTPS	DELAKEVIAA	SERSGEKLWR	MPLEESYWEM
451	MKSGVADMVN	TGGRAGGSIT	AALFLKQFVS	EKVQWMHIDM	AGPVWNEKKK
501	SGTGFGVATL	VEWVQKNSSS			

Show predicted peptides also

Sort Peptides By Residue Number
 Increasing Mass
 Decreasing Mass
 Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
 366 - 377 659.9230 1317.8314 1317.6161 0.2153 0 K.TIEVNNTDAEGR.L (Ions score 62)

Peptide View

MS/MS Fragmentation of **TIEVNNTDAEGR** Found in **gi**|16394, leucine aminopeptidase [Arabidopsis thaliana]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	У	y++	y*	y***	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	Τ							12
2	215.1390	108.0731			197.1285	99.0679	Ι	1217.5757	609.2915	1200.5491	600.7782	1199.5651	600.2862	11
3	344.1816	172.5944			326.1710	163.5892	E	1104.4916	552.7494	1087.4651	544.2362	1086.4810	543.7442	10
4	443.2500	222.1287			425.2395	213.1234	V	975.4490	488.2281	958.4225	479.7149	957.4384	479.2229	9
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	Ν	876.3806	438.6939	859.3540	430.1807	858.3700	429.6887	8
6	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	Ν	762.3377	381.6725	745.3111	373.1592	744.3271	372.6672	7
7	772.3836	386.6954	755.3570	378.1821	754.3730	377.6901	Τ	648.2947	324.6510	631.2682	316.1377	630.2842	315.6457	6
8	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	D	547.2471	274.1272	530.2205	265.6139	529.2365	265.1219	5
9	958.4476	479.7274	941.4211	471.2142	940.4371	470.7222	Α	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
10	1087.4902	544.2487	1070.4637	535.7355	1069.4796	535.2435	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
11	1144.5117	572.7595	1127.4851	564.2462	1126.5011	563.7542	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1

gi|572517 Cysteine synthase

Protein View

Match to: gi|572517 Score: 198
cysteine synthase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1656NOV17.wiff

Nominal mass (M_r): **41976**; Calculated pI value: 8.13 NCBI BLAST search of <u>gi|572517</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 9%

Matched peptides shown in Bold Red

1 MAATSSSAFL LNPLTSRHRP FKYSPELSSL SLSSRKAAAF DVSSAAFTLK 51 RQSRSDVVCK AVSIKPEAGV EGLNIADNAA QLIGKTPMVY LNNVVKGCVA 101 SVAAKLEIME PCCSVKDRIG YSMITDAEEK GLITPGKSVL VESTSGNTGI 151 GLAFIAASKG YKLILTMPAS MSLERRVLLR AFGAELVLTE PAKGMTGAIQ 201 KAEEILKKTP NSYMLQQFDN PANPKIHYET TNPEIWEDTR GKIDILVAGI 251 GTGGTITGVG RFIKERKPEL KVIGVEPTES AILSGGKTGP HKIQGIGAGF 301 VPKNLDLAIV DEYIAISSEE AIETSKQLAL QEGLLVGISS GAAAAAAIQV 351 AKRPENAGKL IAVVFPSFGE RYLSTQLFQS IREECEQMQP EL

Sort Peptides By	Resid	lue Number) Increasing Mass	Oecrea	sing Ma	SS	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
119 - 130	678.8753	1355.7360	1355.6279	0.1081	0	R.IGYSMITDAEEK.G	(Ions score 58)
119 - 130	686.8658	1371.7171	1371.6228	0.0944	0	R.IGYSMITDAEEK.G	Oxidation (M) (Ions score 84)
163 - 175	747.4371	1492.8596	1492.7629	0.0967	0	K.LILTMPASMSLER.R	2 Oxidation (M) (Ions score 45)
181 - 193	673.4197	1344.8248	1344.7289	0.0959	0	R.AFGAELVLTEPAK.G	(Ions score 69)

gi|257676175 Unnamed protein product, containing CIMS (cobalamine independent methonine synthase) domain

Match to: gi|257676175 Score: 238
unnamed protein product [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\383NOV26.wiff

Nominal mass $(M_r): 84728;$ Calculated pI value: 6.05 NCBI BLAST search of <u>gi|257676175</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

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Matched peptides shown in Bold Red

1	MASHIVGYPR	MGPKRELKFA	LESFWDGKST	AEDLQKVSAD	IRSGIWKQMS
51	EAGTKYIPSN	TFAHYDQVLD	TTAMLGAVPP	RYGYTSGEIG	LDVYFSMARG
101	NASVPAMEMT	KWFDTNYHYI	VPELGPDVKF	SYASHKAVNE	YKEAKALGVD
151	TVPVLVGPVS	YLLLSKAAKG	VEKSFDLLSL	LPKILPVYKE	VITELKAAGA
201	TWIQLDEPVL	VMDLEGHKLQ	ALTGAYAELE	STLSGLNVLV	ETYFADIPAE
251	AYKTLTSLKG	VTAFGFDLVR	GTKTLDLVKA	GFPEGKYLFA	GVVDGRNIWA
301	NDFAASLSTL	EALEGVVGKD	KLVVSTSCSL	LHTAVDLVNE	TKLDDEIKSW
351	LAFAAQKIVE	VNALAKALAG	QKDEALFSAN	AAALASRRSS	PRVTNEGVQK
401	AAAALKGSDH	RRATNVSARL	DAQQKKLNLP	ILPTTTIGSF	PQTVELRRVR
451	REYKAKKVSE	EDYVKAMKEE	IKKVVDLQEE	LDIDVLVHGE	PERNDMVEYF
501	GEQLSGFAFT	ANGWVQSYGS	RCVKPPVIYG	DVSRPKAMTV	FWSAMAQSMT
551	SRPMKGMLTG	PVTILNWSFV	RNDQPRHETC	YQIALAIKDE	VEDLEKGGIG
601	VIQIDEAALR	EGLPLRKSEH	AFYLDWAVHS	FRITNCGVQD	TTQIHTHMCY
651	SHFNDIIHSI	IDMDADVITI	ENSRSDEKLL	SVFREGVKYG	AGIGPGVYDI
701	HSPRIPSTEE	IAERVNKMLA	VLEQNILWVN	PDCGLKTRKY	TEVKPALKNM
751	VDAAKLIRSQ	LASAK			

Show predicted peptides also

Sort Pentides By

l	Controphaco by		iue Number (Increasing Mass	Decrea	ising ivia	ISS
	Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
	100 - 111	626.3599	1250.7052	1250.5635	0.1417	0	R.GNASVPAMEMTK.W Oxidation (M) (Ions score 40)
	373 - 387	753.9561	1505.8976	1505.7474	0.1502	0	K.DEALFSANAAALASR.R (Ions score 85)
	458 - 465	484.8031	967.5915	967.4498	0.1417	0	K.VSEEDYVK.A (Ions score 53)
	705 - 714	572.8663	1143.7181	1143.5771	0.1409	0	R.IPSTEEIAER.V (Ions score 61)

gi|4803926 Putative triosephosphate isomerase

Protein View

Match to: gi|4803926 Score: 200 putative triosephosphate isomerase [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2073.wiff

Nominal mass (M_r) : 33553; Calculated pI value: 7.67 NCBI BLAST search of <u>gi|4803926</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%
```

Matched peptides shown in Bold Red

1	MAATSLTAPP	SFSGLRRISP	KLDAAAVSSH	QSFFHRVNSS	TRLVSSSSSS
51	HRSPRGVVAM	AGSGKFFVGG	NWKCNGTKDS	IAKLISDLNS	ATLEADVDVV
101	VSPPFVYIDQ	VKSSLTDRID	ISGQNSWVGK	GGAFTGEISV	EQLKDLGCKW
151	VILGHSERRH	VIGEKDEFIG	KKAAYALSEG	LGVIACIGEK	LEEREAGKTF
201	DVCFAQLKAF	ADAVPSWDNI	VVAYEPVWAI	GTGKVASPQQ	AQEVHVAVRG
251	WLKKNVSEEV	ASKTRIIYGG	SVNGGNSAEL	AKEEDIDGFL	VGGASLKGPE
301	FATIVNSVTS	KKVAA			

Sort Peptides By	Resid	tue Number	Increasing Mass	Decrea	easing Mass	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
131 - 144	718.4938	1434.9731	1434.7355	0.2376	0 K.GGAFTGEISVEQLK.D (<u>lons score 52</u>)	
235 - 249	540.4000	1618.1781	1617.8587	0.3194	0 K.VASPQQAQEVHVAVR.G (Ions score 72)	
255 - 263	481.8491	961.6836	961.4716	0.2120	0 K.NVSEEVASK.T (Ions score 57)	
298 - 311	725.9797	1449.9449	1449.7351	0.2098	0 K.GPEFATIVNSVTSK.K Deamidated (NQ) (Ions score	19)

gi|510880 Putative aspartic protease

Protein View

Match to: gi|510880 Score: 48 putative aspartic protease [Brassica oleracea] Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1748NOV15.wiff

Nominal mass (M_r) : 28008; Calculated pI value: 8.34 NCBI BLAST search of <u>gi|510880</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica oleracea

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1 MGIYSKPVAV SLIVSFLLFL SASAERNDGT FRVGLKKLKL DRKSRIAARV 51 GSKQLKPLRG YGLGDSGDAD IVTLKNYLDA QYYGEIAIGT PPQKFTVVFD 101 TGSSNLWVPS SKCYFSIACL FHSKYKSSRS STYEKNGKSA AIHYGTGAIA 151 GFFSNDAVTV GDLVVKDQEF IEATKEPGIT FVLAKFDGIL GLGFQEISVG 201 NAAPVWYNML KQGLYKEPVF SFWLNRNAED EEGGELVFGG VDPNHYKGEH 251 IYVPV



Peptide View

MS/MS Fragmentation of **EPGITFVLAK** Found in **gi**|**510880**, putative aspartic protease [Brassica oleracea]

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y++	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	227.1026	114.0550	209.0921	105.0497	P	945.5768	473.2920	928.5502	464.7788	927.5662	464.2867	9
3	284.1241	142.5657	266.1135	133.5604	G	848.5240	424.7656	831.4975	416.2524	830.5135	415.7604	8
4	397.2082	199.1077	379.1976	190.1024	Ι	791.5026	396.2549	774.4760	387.7416	773.4920	387.2496	7
5	498.2558	249.6316	480.2453	240.6263	T	678.4185	339.7129	661.3919	331.1996	660.4079	330.7076	6
6	645.3243	323.1658	627.3137	314.1605	F	577.3708	289.1890	560.3443	280.6758			5
7	744.3927	372.7000	726.3821	363.6947	V	430.3024	215.6548	413.2758	207.1416			4
8	857.4767	429.2420	839.4662	420.2367	L	331.2340	166.1206	314.2074	157.6074			3
9	928.5138	464.7606	910.5033	455.7553	Α	218.1499	109.5786	201.1234	101.0653			2
10					K	147.1128	74.0600	130.0863	65.5468			1

gi|1351856 Aconitate hydratase, cytoplasmic

Protein View

Match to: gi|1351856 Score: 79
RecName: Full=Aconitate hydratase, cytoplasmic; Short=Aconitase; AltName: Full=Citrate hydro-lyase
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\158NOV16.wiff

Nominal mass (M_r) : 98570; Calculated pI value: 5.74 NCBI BLAST search of <u>gi|1351856</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 2%

Matched peptides shown in Bold Red

1	MAAENPFKEN	LTSLPKPGGG	EFGKYYSLPS	LNDPRIDRLP	YSIRILLESA
51	IRNCDNFQVK	KEDVEKIIDW	ENSSPKQVEI	PFKPARVLLQ	DFTGVPAVVD
101	LACMRDAMNK	LGSDSNKINP	LVPVDLVIDH	SVQVDVARSE	NAVQANMELE
151	FQRNKERFAF	LKWGSNAFQN	MLVVPPGSGI	VHQVNLEYLG	RVVFNTSGLL
201	YPDSVVGTDS	HTTMIDGLGV	AGWGVGGIEA	EAAMLGQPMS	MVLPGVVGFK
251	LSGKLRNGVT	ATDLVLTVTQ	MLRKHGVVGK	FVEFYGDGME	ELSLADRATI
301	ANMSPEYGAT	MGFFPVDHVT	LQYLKLTGRS	DETVSMIEAY	LRANKMFVDY
351	KEPQQEKVYS	SYLQLDLTDV	EPCISGPKRP	HDRVPLKEMK	SDWHACLDNK
401	VGFKGFAIPK	EAQENVAKFS	FHGQPAELKH	GSVVIAAITS	CINISNPSVM
451	LGAALVAKKA	CELGLQVKPW	VKTSLAPGSG	VVTK YLLKSG	LQPYLNQQGF
501	HIVGYGCTTC	IGNSGDLDES	VSAAISDNDI	VAAAVLSGNR	NFEGRVHPLT
551	RANYLASPPL	VVAYALAGTV	DIDFEKEPIG	KGKDGKDVYF	RDIWPSTEEI
601	AEVVQSSVLP	DMFKSTYESI	TKGNPMWNQL	SVPSGTLYSW	DPNSTYIHEP
651	PYFKNMTMDP	PGAHGVKDAY	CLLNFGDSIT	TDHISPAGSI	HKDSPAAKYL
701	LERGVDRKDF	NSYGSRRGND	EVMARGTFAN	IRLVNKLLDG	EVGPKTVHVP
751	TGEKLSVFEA	AEKYKSAGQD	TIVLAGAEYG	SGSSRDWAAK	GPMLLGVKAV
801	IAKSFERIHR	SNLVGMGIIP	LCFKSGEDAD	SLGLTGHERY	TIDLPDDISK
851	IRPGQDVTVT	TDSGKSFTCT	VRFDTEVELA	YFNNGGILPY	VIRNLIKQ

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

 Start - End
 Observed
 Mr(expt)
 Mr(calc)
 Delta
 Miss
 Sequence

 473 - 484
 558.8498
 1115.6850
 1115.6187
 0.0664
 0
 K.TSLAPGSGVVTK.Y
 (Ions score 58)

 709 - 716
 473.3326
 944.6507
 944.3988
 0.2519
 0
 K.DFNSYGSR.R
 (Ions score 20)

gi|15235763 Cytosol aminopeptidase family protein

Match to: gi|15235763 Score: 212 cytosol aminopeptidase family protein [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\712NOV15.wiff

Nominal mass (M_r) : 61667; Calculated pI value: 6.62 NCBI BLAST search of <u>gi|15235763</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: gi|85700452 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 7%

Matched peptides shown in Bold Red

1	MAVTLVTSFA	SSSSRFHFRS	FSSSPSSLSS	CFVRFQFPSR	LRLAFAVTPL
51	YSSSRAMAHT	ISHATLGLTQ	ANSVDHPKIS	FSGKEIDVTE	WRGDILAVGV
101	TERDMAKDVN	SKFENPILKK	LDAHLGGLLA	DVSSEEDFSG	KPGQSTVLRL
151	PGLGSKRVGL	IGLGKSASTP	SAFQSLGEAV	AAAAKASQAS	SVAVVLASSE
201	SVSNESKLCS	ASAIASGTVL	GLFEDSRYKS	ESKKPSLKSV	DIIGFGSGPE
251	LEKKLKYAEH	VSYGVIFGKE	LVNSPANVLT	PAVLAEEALN	LASMYSDVMT
301	ANILNEEQCK	ELKMGSYLAV	AAASANPPHF	IHLIYKPSSG	PVKTKLALVG
351	KGLTFDSGGY	NIKTGPGCLI	ELMKFDMGGS	AAVLGAAKAI	GQIKPPGVEV
401	HFIVAACENM	ISGTGMRPGD	VLTASNGKTI	EVNNTDAEGR	LTLADALVYA
451	CNQGVDKVVD	LATLTGACII	ALGTSMAGIY	TPSDKLAKEV	IAASERSGEK
501	LWRMPMEESY	WEMMKSGVAD	MVNTGGRAGG	SITAALFLKQ	FVSEDVEWMH
551	IDMAGPVWNE	KKKAATGFGV	ATLVEWVQNH	SSS	

Show predicted peptides also

|--|

Residue Number O Increasing Mass O Decreasing Mass

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence 85 - 92 510.2915 1018.5684 1018.4971 0.0713 0 K.EIDVTEWK.G (Ions score 22) 0 K.GDILAVGVTEK.D (Ions score 41) 93 - 103 551.3405 1100.6664 1100.6077 0.0586 0 K.GLTFDSGGYNIK.T (Ions score 46) 352 - 363 636.3537 1270.6929 1270.6194 0.0735 375 - 388 655.8469 1309.6792 1309.6336 0.0455 0 K.FDMGGSAAVLGAAK.A Oxidation (M) (Ions score 104)

gi|195632542 Cytokinin-O-glucosyltransferase 1

Protein View

Match to: gi|195632542 Score: 47
cytokinin-O-glucosyltransferase 1 [Zea mays]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\343NOV15.wiff

Nominal mass (M_r) : 54361; Calculated pI value: 5.59 NCBI BLAST search of <u>gi|195632542</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Zea mays

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 1%

Matched peptides shown in Bold Red

1	MAAAVDTAAV	AGATGRLRVF	FLPSFIRGHL	IPQTDMACRV	AAARPAEVEA
51	TVVVTPANAA	LIAPTVARAA	AAGHAVRVLC	YPFPDVGLGE	GVECLATATA
101	RDAWRVYRAM	EVVQPSHESL	LRDHRPDAIV	ADVPFWWTTG	VAAELGVPRL
151	TFHPVGIFAL	LAMNSLFTIR	PDIIGRASSD	AAGTVLSVPG	LPGKEITIPV
201	SELPTFLVQD	DHLSKAWQRM	RACQLTGFGV	IVNTFADLEQ	PYCEEFSRVE
251	ARRAYFVGPL	GKPSRSTMHR	GGSGNADCLS	WLSTKPSRSV	VFVCFGSWAE
301	FSATQTRELA	LGLEASNQPF	LWVVRSNDSS	DDQWAPEGWE	QRVANRGLVV
351	HGWAPQLAVL	AHPSVGAFVT	HCGWNSVLEA	ASAGVPVLTW	PLVFEQFINE
401	RLATEVAAFG	VRLWDGGRRS	ERAEDAEIVP	AEAIARAVAG	FMEGGEQRDK
451	LNARAGELAE	RARAAVSEDG	SSWRDINRLI	DDLLQARASG	LPQMNSVQLE
501					

Show predicted peptides also

Sort Peptides By

 Start - End
 Observed
 Mr(expt)
 Mr(calc)
 Delta
 Miss Sequence

 455 - 463
 486.7905
 971.5665
 971.5148
 0.0517
 1
 R.AGELAERAR.A
 (Ions score 47)

 455 - 463
 486.8004
 971.5862
 971.5148
 0.0714
 1
 R.AGELAERAR.A
 (Ions score 47)

Residue Number
 Increasing Mass
 Decreasing Mass

gi|9757801 3-isopropylmalate dehydrogenase

Protein View

Match to: gi|9757801 Score: 88
3-isopropylmalate dehydrogenase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1908DEC01.wiff

Nominal mass (M_r) : 44305; Calculated pI value: 5.75 NCBI BLAST search of <u>gi|9757801</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%
```

Matched peptides shown in Bold Red

1	MAAFLQTNIS	LNAIKIVPGK	YSSLTDHQFR	APYRIRCAAA	SPGKKRYNIA
51	LLPGDGIGPE	VISVAKNVLQ	KAGSLEGLEF	DFKEMPVGGA	ALDLVGVPLP
101	EETFTAAKLS	DAILLGAIGG	YKWDKNEKHL	RPEMALFYLR	RDLKVFANLR
151	PATVLPQLVD	ASTLKKEVAE	GVDMMIVREL	TGGIYFGEPR	GITINENGEE
201	VGVSTEIYAA	HEIDRIARVA	FETARKRRGK	LCSVDKANVL	DASILWRKRV
251	TALASEYPDV	ELSHMYVDNA	AMQLIRDPKQ	FDTIVTNNIF	GDILSDEASM
301	ITGSIGMLPS	ASLGESGPGL	FEPIHGSAPD	IAGQDKANPL	ATILSAAMLL
351	KYGLGEEKAA	KRIEDAVVDA	LNKGFRTGDI	YSPGNKLVGC	KEMGEEVLKS
401	VESKVPATV				

Sort Peptides B	y Resid 	lueNumber	Increasing Mass	Decrea	sing Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
47 - 66	1013.6636	2025.3127	2025.1146	0.1980	0	R.YNIALLPGDGIGPEVISVAK.N (Ions score 27)
191 - 215	906.1869	2715.5390	2715.2987	0.2403	0	R.GITINENGEEVGVSTEIYAAHEIDR.I (<u>lons score 61</u>)

gi|15221044 Dihydrolipoamide dehydrogenase 1, mitochondrial

Match to: gi|15221044 Score: 141 dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1) [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\753NOV15.wiff

Nominal mass (M_r) : 54239; Calculated pI value: 6.96 NCBI BLAST search of <u>gi|15221044</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|30694221</u> from <u>Arabidopsis thaliana</u> <u>gi|75264759</u> from <u>Arabidopsis thaliana</u> <u>gi|12323085</u> from <u>Arabidopsis thaliana</u> <u>gi|12704696</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 6%

Matched peptides shown in Bold Red

1	MAMASLARRK	AYFLTRNLSN	SPTDALRFSF	SLSRGFASSG	SDENDVVIIG
51	GGPGGYVAAI	KASQLGLKTT	CIEKRGALGG	TCLNVGCIPS	KALLHSSHMY
101	HEAKHSFANH	GIKVSSVEVD	LPAMLAQKDN	AVKNLTRGIE	GLFKKNKVTY
151	VKGYGKFISP	NEVSVETIDG	GNTIVKGKHI	IVATGSDVK <mark>S</mark>	LPGITIDEKK
201	IVSSTGALSL	SEVPKKLIVI	GAGYIGLEMG	SVWGRLGSEV	TVVEFAGDIV
251	PSMDGEIRKQ	FQRSLEKQKM	KFMLKTKVVS	VDSSSDGVKL	TVEPAEGGEQ
301	SILEADVVLV	SAGRTPFTSG	LDLEKIGVET	DKAGRILVND	RFLSNVPGVY
351	AIGDVIPGPM	LAHKAEEDGV	ACVEFIAGKH	GHVDYDKVPG	VVYTHPEVAS
401	VGKTEEQLKK	EGVSYRVGKF	PFMANSRAKA	IDNAEGLVKI	LADKETDKIL
451	GVHIMAPNAG	ELIHEAVLAI	NYDASSEDIA	RVCHAHPTMS	EALKEAAMAT
501	YDKPIHI				

Show predicted peptides also

Sort Pontidos By

JUIL FE	plides by	Residue Number Increasing Mass			Decreasing Mass			
Start -	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
190 -	199	536.8258	1071.6370	1071.5812	0.0559	0	K.SLPGITIDEK.K	(Ions score 56)
315 -	325	604.3467	1206.6788	1206.6132	0.0656	0	R. TPFTSGLDLEK. I	(Ions score 39)
430 -	439	515.3155	1028.6164	1028.5502	0.0662	0	K.AIDNAEGLVK.I	(Ions score 46)

gi|9755610 Reversibly glycosylated polypeptide-2 (AtRGB)

Protein View

Match to: gi|9755610 Score: 78
reversibly glycosylated polypeptide-2 (AtRGB) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1378NOV26.wiff

Nominal mass (M_r) : 41377; Calculated pI value: 5.76 NCBI BLAST search of <u>gi|9755610</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

Matched peptides shown in Bold Red

1	MVEPANTVGL	PVNPTPLLKD	ELDIVIPTIR	NLDFLEMWRP	FLQPYHLIIV
51	QDGDPSKKIH	VPEGYDYELY	NRNDINRILG	PKASCISFKD	SACRCFGYMV
101	SKKKYIFTID	DDCFVAKDPS	GKAVNALEQH	IKNLLCPSSP	FFFNTLYDPY
151	REGADFVRGY	PFSLREGVST	AVSHGLWLNI	PDYDAPTQLV	KPKERNTRYV
201	DAVMTIPKGT	LFPMCGMNLA	FDRDLIGPAM	YFGLMGDGQP	IGRYDDMWAG
251	WCIKVICDHL	SLGVKTGLPY	IYHSKASNPF	VNLKKEYKGI	FWQEEIIPFF
301	QNAKLSKEAV	TVQQCYIELS	KMVKEKLSSL	DPYFDKLADA	MVTWIEAWDE
351	LNPPAASGKA				

Sort Peptides By	Resid	lueNumber	Increasing Mass	Decrea	sing Ma	ISS	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
199 - 208	576.8799	1151.7453	1151.5896	0.1557	0	R.YVDAVMTIPK.G	Oxidation (M) (<u>Ions score 35</u>)
327 - 336	592.8789	1183.7433	1183.5761	0.1672	0	K.LSSLDPYFDK.L	(Ions score 43)

gi|1710838 S-adenosyl-L-homocysteine hydrolase

Protein View

Match to: gi|1710838 Score: 252
RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\842NOV16.wiff

Nominal mass (M_r): 53744; Calculated pI value: 5.69 NCBI BLAST search of <u>gi|1710838</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Medicago sativa</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|535584</u> from <u>Medicago sativa</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 8%

Matched peptides shown in Bold Red

1	MALLVETTTS	GREYKVKDMS	QADFGRLEIE	LAEVEMPGLM	SCRTEFGPSQ
51	PFKGARITGS	LHMTIQTAVL	IETLTALGAE	VRWCSCNIFS	TQDHAAAAIA
101	RDSAAVFAWK	GETLQEYWWC	SERALDWGPG	GGPDLIVDDG	GDVTLLIHEG
151	VKAEEVFEKT	GQLPDPSSTD	NAEMQIVLTI	IRDGLKTDPK	RYQKMKTRIV
201	GVSEETTTGV	K RLYQMQASG	TLLFPAINVN	DSVTKSKFDN	LYGCRHSLPD
251	GLMRATDVMI	AGKVAVVCGY	GDVGKGCAAA	LKQGGARVIV	TEIDPICALQ
301	ALMEGLQVLT	LEDVISEADI	FVTTTGNKDI	IMVSDMKKMK	NNAIVCNIGH
351	FDNEIDMHGL	ETYPGVKRIT	IKPQTDRWVF	PETKSGIIVL	AEGRLMNLGC
401	ATGHPSFVMS	CSFTNQVIAQ	IELWKEKTSG	KAEKKAAATb	KHLDEKVAAL
451	HLGQLGAKLT	KLSKDQADYI	SVPVEGPYKP	AHYRY	

Show predicted peptides also

Oast Destides De

Soft Peptides By	Resid	lue Number () Increasing Mass	O Decrea	sing Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 53	569.3139	1136.6133	1136.5502	0.0631	0	R.TEFGPSQPFK.G (Ions score 19)
102 - 110	497.7843	993.5540	993.4920	0.0621	0	R.DSAAVFAWK.G (Ions score 52)
199 - 211	660.3703	1318.7260	1318.6980	0.0280	0	R.IVGVSEETTTGVK.R (Ions score 81)
385 - 394	507.8339	1013.6533	1013.5869	0.0664	0	K.SGIIVLAEGR.L (Ions score 100)

gi|15223574 Isoflavone reductase, putative

Protein View

Match to: gi|15223574 Score: 112
isoflavone reductase, putative [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1791.wiff

Nominal mass (M_r) : 34515; Calculated pI value: 5.44 NCBI BLAST search of <u>gi|15223574</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
```

Matched peptides shown in Bold Red

1	MTSKILVIGA	TGLIGKVLVE	ESAKSGHATF	ALVREASLSD	PVKAQLVERF
51	KDLGVTILYG	SLSDKESLVK	AIKQVDVVIS	AVGRFQTEIL	NQTNIIDAIK
101	ESGNVKRFLP	SEFGNDVDRT	VAIEPTLSEF	ITKAQIRRAI	EAAKIPYTYV
151	VSGCFAGLFV	PCLGQCHLRL	RSPPRDKVSI	YDTGNGKAIV	NTEEDIVAYT
201	LKAVDDPRTL	NKILYIHPPN	YIVSQNDMVG	LWEEKIGKTL	EKTYVSEEEL
251	LK TIQESKPP	MDFLVGLIHT	ILVKSDFTSF	TIDPSFGVEA	SELYPEVKYT
301	SVDEFLNRFI				

Sort Peptides By	Resid	lueNumber	Increasing Mass	ODecrea	sing Mass
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence
108 - 119	698.4615	1394.9085	1394.6467	0.2618	0 R.FLPSEFGNDVDR.T (Ions score 75)
243 - 252	605.9390	1209.8634	1209.6129	0.2505	0 K.TYVSEEELLK.T (Ions score 37)

gi|15242822 Glutamate-1-semialdehyde-2,1-aminomutase (GSA1)

Protein View

```
Match to: gi|15242822 Score: 211
GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMINOMUTASE); glutamate-1-semialdehyde 2,1-aminomutase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff
```

Nominal mass (M_r) : 50737; Calculated pI value: 6.43 NCBI BLAST search of <u>gi|15242822</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 12%

Matched peptides shown in Bold Red

1	MSATLTGSGT	ALGFSCSSKI	SKRVSSSPAS	NRCCIKMSVS	VDEKKKSFSL
51	QKSEEAFNAA	KNLMPGGVNS	PVRAFKSVGG	QPVLIDSVKG	SKMWDIDGNE
101	YIDYVGSWGP	AIIGHADDEV	LAALAETMKK	GTSFGAPCLL	ENVLAEMVIS
151	AVPSIEMVRF	VNSGTEACMG	VLRLARAFTN	KEKFIKFEGC	YHGHANAFLV
201	KAGSGVATLG	LPDSPGVPKA	ATSDTLTAPY	NDLEAVEKLF	AAHKGEISAV
251	ILEPVVGNSG	FIPPTPEFIN	GLRQLTKDNG	VLLIFDEVMT	GFRLAYGGAQ
301	EYFGITPDLT	TLGKIIGGGL	PVGAYGGRRD	IMEMVAPAGP	MYQAGTLSGN
351	PLAMTAGIHT	LKRLKQAGTY	EYLDKITKEL	TNGILEAGKK	TGHPMCGGYI
401	SGMFGFFFAE	GPVYNFADSK	KSDTEKFGRF	FRGMLEEGVY	FAPSQFEAGF
451	TSLAHTPEDI	QLTIAAAERV	LSRI		

Sort Peptides By	Residue Number	Increasing Mass	Decreasing Mass	

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence
62	-	73	628.8537	1255.6929	1255.6343	0.0585	0 K.NLMPGGVNSPVR.A Oxidation (M) (Ions score 57)
77	-	89	649.9043	1297.7941	1297.7242	0.0699	0 K.SVGGQPVLIDSVK.G (Ions score 71)
202		219	811.9660	1621.9175	1621.8676	0.0499	0 K.AGSGVATLGLPDSPGVPK.A (<u>lons score 44</u>)
315	i –	328	643.8869	1285.7592	1285.7143	0.0449	0 K.IIGGGLPVGAYGGR.R (<u>Ions score 40</u>)

gi|15226618 Fumarate hydratase (FUM1)

Protein View

Match to: gi|15226618 Score: 102
FUM1 (FUMARASE 1); fumarate hydratase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1102NOV15.wiff

Nominal mass (M_r) : 53479; Calculated pI value: 8.01 NCBI BLAST search of <u>gi|15226618</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 4%

Matched peptides shown in Bold Red

1	MSIYVASRRL	SGGTTVTALR	YATSLRSYST	SFREERDTFG	PIQVPSDKLW
51	GAQTQRSLQN	FEIGGERERM	PEPIVRAFGV	LKKCAAKVNM	EYGLDPTIGK
101	AIMQAAQEVA	EGKLNDHFPL	VVWQTGSGTQ	SNMNANEVIA	NRAAEILGRK
151	RGEKCVHPND	HVNRSQSSND	TFPTVMHIAA	ATEINSRLIP	SLKTLHSTLE
201	SKSFEFKDIV	KIGRTHTQDA	TPLTLGQEFG	GYATQVKYGL	NRVTCTLPRL
251	YQLAQGGTAV	GTGLNTKKGF	DVKIAAAVAE	ETNLPFVTAE	NKFEALAAHD
301	ACVETSGSLN	TIATSLMKIA	NDIRFLGSGP	RCGLGELVLP	ENEPGSSIMP
351	GKVNPTQCEA	LTMVCAQVMG	NHVAVTVGGS	NGHFELNVFK	PVIASALLHS
401	VRLIADASAS	FEKNCVRGIE	ANRERISKLL	HESLMLVTSL	NPKIGYDNAA
451	AVAKKAHKEG	CTLKEAALNL	GVLTAEEFDT	LVVPEKMIGP	SD

Sort Peptides By	Resid	lueNumber) Increasing Mass	Decrea	sing Ma	155	
Start - End 57 - 67 444 - 454	Observed 625.3436 546.8217	Mr(expt) 1248.6727 1091.6288	Mr(calc) 1248.6098 1091.5611	Delta 0.0628 0.0677	Miss O O	Sequence R.SLQNFEIGGER.E K.IGYDNAAAVAK.K	(<u>Ions score 39</u>) (Ions score 63)

gi|461461 Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic

Protein View

Match to: gi|461461 Score: 191
RecName: Full=Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic; AltName: Full=NADH-dependent enoyl-ACP reductase;
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1791.wiff

Nominal mass (M_r) : 40625; Calculated pI value: 8.78 NCBI BLAST search of <u>gi|461461</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%
```

Matched peptides shown in Bold Red

1	MAATAAASSL	QMATTRPSIS	AASSKARTYV	VGANPRNAYK	IACTPHLSNL
51	GCLRNDSALP	ASKKSFSFST	KAMSESSESK	ASSGLPIDLR	GKRAFIAGIA
101	DDNGYGWAVA	KSLAAAGAEI	LVGTWVPALN	IFETSLRRGK	FDQSRVLPDG
151	SLMEIKKVYP	LDAVFDNPED	VPEDVKANKR	YAGSSNWTVQ	EAAECVRQDF
201	GSIDILVHSL	ANGPEVSKPL	LETSRKGYLA	AISASSYSFV	SLLSHFLPIM
251	NPGGASISLT	YIASERIIPG	YGGGMSSARA	ALESDTRVLA	FEAGRKQNIR
301	VNTISAGPLG	SR AAKAIGFI	DTMIEYSYNN	APIQKTLTAD	EVGNAAAFLV
351	SPLASAITGA	TIYVDNGLNS	MGVALDSPVF	KDLNK	

Show predicted peptides also

Sort Peptides By	Resid	tueNumber	Increasing Mass	Oecrea	ising Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
81 - 90	514.8900	1027.7654	1027.5662	0.1992	0	K.ASSGLPIDLR.G (Ions score 55)
146 - 156	609.4493	1216.8841	1216.6373	0.2468	0	R.VLPDGSLMEIK.K Oxidation (M) (Ions score 42)
267 - 279	627.4328	1252.8511	1252.6122	0.2390	0	R.IIPGYGGGMSSAK.A Oxidation (M) (Ions score 57)
301 - 312	586.4401	1170.8657	1170.6357	0.2300	0	R.VNTISAGPLGSR.A (Ions score 37)

gi|5881963 Dihydrolipoamide S-acetyltransferase

Protein View

Match to: gi|5881963 Score: 64 dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1001NOV26.wiff

Nominal mass (M_r): 50106; Calculated pI value: 8.33 NCBI BLAST search of <u>gi|5881963</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%
```

Matched peptides shown in Bold Red

1	MAVSSSSFLS	TASLTNSKSN	ISFASSVSPS	LRSVVFRSTT	PATSHRRSMT
51	VRSKIREIFM	PALSSTMTEG	KIVSWIKTEG	EKLAKGESVV	VVESDKADMD
101	VETFYDGYLA	AIVVGEGETA	PVGAAIGLLA	ETEAEIEEAK	SKAASKSSSS
151	VAEAVVPSPP	PVTSSPAPAI	AQPAPVTAVS	DGPRKTVATP	YAKKLAKQHK
201	VDIESVAGTG	PFGRITASDV	ETAAGIAPSK	SSIAPPPPPP	PPVTAKATTT
251	NLPPLLPDSS	IVPFTAMQSA	VSKNMIESLS	VPTFRVGYPV	NTDALDALYE
301	K VKPKGVTMT	ALLAKAAGMA	LAQHPVVNAS	CKDGKSFSYN	SSINIAVAVA
351	INGGLITPVL	QDADKLDLYL	LSQKWKELVG	KARSKQLQPH	EYNSGTFTLS
401	NLGMFGVDRF	DAILPPGQGA	IMAVGASKPT	VVADKDGFFS	VKNTMLVNVT
451	ADHRIVYGAD	LAAFLQTFAK	IIENPDSLTL		

Show predicted peptides also

Sort Peptides By
 Residue NumberIncreasing MassDecreasing MassStart - EndObservedMr(expt)Mr(calc)DeltaMissSequence57 - 71837.46341672.91221672.76880.14340R.EIFMPALSSTMTEGK.I2 Oxidation (M) (Ions score 21)286 - 301884.50851767.00251766.87270.12980R.VGYPVNTDALDALYEK.V(Ions score 43)

gi|7329685 Transketolase-like protein

Protein View

433 - 447

Match to: gi|7329685 Score: 280
transketolase-like protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\NOV28\374NOV28.wiff

Nominal mass (M_r) : 81937; Calculated pI value: 5.80 NCBI BLAST search of <u>gi|7329685</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),mBBr (C),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 6%

Matched peptides shown in Bold Red

	1 MASTSSLALS	QALLARAISH HGSDQRGSL	P AFSGLKSTGS	RASASSRRRI
	51 AQSMTKNRSL	RPLVRAAAVE TVEPTTDSS	I VDKSVNSIRF	LAIDAVEKAK
1	01 SGHPGLPMGC	APMAHILYDE VMRYNPKNP	Y WFNRDRFVLS	AGHGCMLLYA
1	51 LLHLAGYDSV	QEEDLKQFRQ WGSKTPGHP	E NFETPGIEVT	TGPLGQGIAN
2	01 AVGLALAEKH	LAARFNKPDA EVVDHYTYA	I LGDGCQMEGI	SNEACSLAGH
2	51 WGLGKLIAFY	DDNHISIDGD TEIAFTENV	D QRFEALGWHV	IWVKNGNTGY
3	01 DEIRAAIKEA	KTVTDKPTLI KVTTTIGYG	S PNKANSYSVH	GAALGEKEVE
3	51 ATRNNLGWPY	EPFQVPDDVK SCLDDLLFD	L HFSSHWSRHT	PEGATLESDW
4	01 SAKFAAYEKK	YPEEASELKS IITGELPAG	W EKALPTYTPE	SPGDATRNLS
4	51 QQCLNALAKV	VPGFLGGSAD LASSNMTLL	K AFGDFQKATP	EERNLRFGVR
5	01 EHGMGAICNG	IALHSPGLIP YCATFFVFT	D YMRGAMRISA	LSEAGVIYVM
5	51 THDSIGLGED	GPTHQPIEHI ASFRAMPNT	L MFRPADGNET	AGAYKIAVTK
6	01 RKTPSILALS	RQKLPHLPGT SIEGVEKGG	Y TISDDSSGNK	PDVILIGTGS
6	51 ELEIAAQAAE	VLRKDGKTVR VVSFVCWEL	F DEQSDEYKES	VLPSDVSARV
7	01 SIEAASTFGW	GKIVGGKGKS IGINSFGAS	A PAPLLYKEFG	ITVEAVVDAA
7	51 KSFF			
Start - End Ob	served Mr	(expt) Mr(calc)	Delta Mis	ss Sequence
90 - 98 50	3.3773 1004	.7400 1004.5542	0.1858 (D R.FLAIDAVEK.A (Ions score 37)
295 - 304 57	0.3582 1138	.7019 1138.4891	0.2129 (D K.NGNTGYDEIR.A Deamidated (NQ) (Ions score 78)
322 - 333 61	9.4190 1236	.8235 1236.6350	0.1884 (D K.VTTTIGYGSPNK.A (Ions score 86)

```
788.4915 1574.9685 1574.7576 0.2109 0 K.ALPTYTPESPGDATR.N (<u>Ions score 80</u>)
```

gi|7385217 Beta-ketoacyl-ACP synthetase 1

Protein View

Match to: gi|7385217 Score: 168
beta-ketoacyl-ACP synthetase 1 [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (M_r) : 32334; Calculated pI value: 9.47 NCBI BLAST search of <u>gi|7385217</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 8%

Matched peptides shown in Bold Red

1	MQALQSSSLR	ASPPNPLRTP	SNRQSHQITN	ARPTTRRSFI	SASASVSAPK
51	RETDPKKRVV	ITGMGLVSVF	GNDVDAYYEK	LLSGESGISL	IDRFDASKFP
101	TRFGGQIRGF	SSEGYIDGKN	ERRLDDCLKY	CIVAGKKALE	SANLGGDKLN
151	TIDKQKAGVL	VGTGMGGLTV	FSDGVQALVE	KGHRRISPFF	IPYAITNMGS
201	ALLAIDLGLM	GPNYSISTAC	ATSNYCFYAA	ANHIRRGEAD	MMVAGGTEAA
251	IIPIGWEVLL	LVGHCRREMM	TLKRLQGHGI	NREMALSWVK	ELVFW

Sort Peptides By	Resident of the second seco	tueNumber) Increasing Mass	Decrea	sing Mass	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sec	guence
81 - 93	680.3881	1358.7617	1358.7405	0.0212	0 K.I	LSGESGISLIDR.F (Ions score 107)
109 - 119	580.2945	1158.5744	1158.5193	0.0551	0 R.C	FSSEGYIDGK.N (Ions score 61)

gi|7671449 Oligopeptidase A-like protein

Protein View

Match to: gi|7671449 Score: 63
oligopeptidase A-like protein [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\370NOV15.wiff

Nominal mass (M_r): 81777; Calculated pI value: 5.39 NCBI BLAST search of <u>gi|7671449</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 1%

Matched peptides shown in Bold Red

1	MASEDTLSSN	PLLQNFDFPP	FDSVDAHHVR	PGIRALLQQL	EAELEQLEKA
51	VEPSWPKLVE	PLEKIIDRLS	VVWGMINHLK	AVKDTPELRA	AIEEVQDSFS
101	CFPNNTFIYT	LQPEKVKFQL	RLGQSKPIYN	AFKAIRESPD	WNSLSEAPQI
151	KEAVLSGIAL	EDDKREEFNK	IEQELEKLSH	KFSENVLDAT	K KFEKLITDK
201	KEIEGLPPSA	LGLFAQAAVS	KGHETATADT	GPWLITLDAP	SYLPVMQHAK
251	NRALREEVYR	AYLSRASSGD	LDNTAIIDQI	LKLRLEKAKL	LGYRNYAEVS
301	MATKMATVEK	ADELLEKLRS	ASWDPAVQDI	EDLKSFAKNQ	GAAEADSLTH
351	WDITFWSERL	RESKYDINEE	ELRPYFSLPK	VMDALFGLAK	TLFGIDVVPA
401	DGVAPVWNSD	VRFYCVKDSS	GNPTAYFYFD	PYSRPSEKRD	GAWMDEVFSR
451	SRVMAQKGSS	VRLPVAQMVC	NQTPPVGDKP	SLMTFREVET	VFHEFGHALQ
501	HMLTKEDEGL	VAGIRNIEWD	AVELPSQFME	NWCYHRDTLM	SIAKHYQTGE
551	TLPENVYKKL	LAARTFRAGS	LSLRQLKFAT	VDLELHTKYM	PGGAETIYEV
601	DQRVSIKTQV	IPPLPEDRFL	CSFSHIFAVC	FTCSPSHVLS	GGYAAGYYSY
651	KWAEVLSADA	FSAFEDAGLD	DIKAVKETGQ	RFRNTILALG	GGKAPLKVFV
701	EFRGREPSPE	PLLRHNGLLA	ASA		

Show predicted peptides also

Sort Peptides By OResidue Number OIncreasing Mass ODecreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
182 - 191	562.3165	1122.6184	1122.5557	0.0627	0	K.FSENVLDATK.K	(Ions score 63)

Peptide View

MS/MS Fragmentation of **FSENVLDATK** Found in **gi**|7671449, oligopeptidase A-like protein [Arabidopsis thaliana]

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	У	y++	y*	y***	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							10
2	235.1077	118.0575			217.0972	109.0522	S	976.4946	488.7509	959.4680	480.2376	958.4840	479.7456	9
3	364.1503	182.5788			346.1397	173.5735	E	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	8
4	478.1932	239.6003	461.1667	231.0870	460.1827	230.5950	N	760.4199	380.7136	743.3934	372.2003	742.4094	371.7083	7
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	V	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
6	690.3457	345.6765	673.3192	337.1632	672.3352	336.6712	L	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
7	805.3727	403.1900	788.3461	394.6767	787.3621	394.1847	D	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4
8	876.4098	438.7085	859.3832	430.1952	858.3992	429.7032	A	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
9	977.4575	489.2324	960.4309	480.7191	959.4469	480.2271	Τ	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468			1
gi|7688095 ADP-glucose pyrophosphorylase small subunit

Protein View

Match to: gi|7688095 Score: 182
ADP-glucose pyrophosphorylase small subunit [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1006NOV26.wiff

Nominal mass (M_r) : 57294; Calculated pI value: 5.87 NCBI BLAST search of <u>gi|7688095</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%
```

Matched peptides shown in Bold Red

1	MATMAAIGSL	KVPSSSSNHT	RRLSSSSQRK	TLSFSSSSLT	GEKLNPTQEI
51	IISNLPRGNE	RRTPSIVSPK	AVSDSQNSQT	CLDPDASRSV	LGIILGGGAG
101	TRLYPLTKKR	AKPAVPLGAN	YRLIDIPVSN	CLNSNISKIY	VLTQFNSASL
151	NRHLSRAYAS	NMGGYKNEGF	VEVLAAQQSP	ENPNWFQGTA	DAVRQYLWLF
201	EEHNVLEFLV	LAGDHLYRMD	YEKFIQAHRE	TDADITVAAL	PMDEKRATAF
251	GLMKIDDEGR	IIEFAEKPKG	EQLKAMKVDT	TILGLDDERA	KEMPFIASMG
301	IYVVSKNVML	DLLRDQFPGA	NDFGSEVIPG	ATDLGLRVQA	YLYDGYWEDI
351	GTIEAFYNAN	LGITKKPVPD	FSFYDRSAPI	YTQPRYLPPS	KMLDADVTDS
401	VIGEGCVIKN	CKIHHSVIGL	RSCISEGAII	EDTLLMGADY	YETDADRTLL
451	AAKGSIPIGI	GRDSHIKRAI	IDKNARIGDN	VKIINTDNVQ	EAARETDGYF
501	IKSGIVTVIK	DALIPSGTVI			

Sort Peptides By	Resid	lueNumber) Increasing Mass	Decrea	asing Mass	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
278 - 289	673.9179	1345.8213	1345.6725	0.1487	0 K.VDTTILGLDDER.A	(Ions score 112)
483 - 494	672.4238	1342.8331	1342.6841	0.1490	0 K.IINTDNVQEAAR.E	(Ions score 74)

gi|780814 3-ketoacyl-acyl carrier protein synthase I

Protein View

Match to: gi|780814 Score: 379
3-ketoacyl-acyl carrier protein synthase I
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1001NOV26.wiff

Nominal mass (M_r) : 50890; Calculated pI value: 7.99 NCBI BLAST search of <u>gi[780814</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%
```

Matched peptides shown in Bold Red

1	MQALQSSSLR	ASPPNPLRLP	SNRQSHQLIT	NARPLRRQQR	SFISASASTV
51	SAPKRETDPK	KRVVITGMGL	VSVCGNDVDA	YYEKLLSGES	GISLIDRFDA
101	SKFPTRFGGQ	IRGFSSEGYI	DGKNERRLDD	CLKYCIVAGK	KALESANLGG
151	DKLNTIDKRK	AGVLVGTGMG	GLTVFSEGVQ	NLIEKGHRRI	SPFFIPYAIT
201	NMGSALLAID	LGLMGPNYSI	STACATSNYC	FYAAANHNHR	GEADMMIAGG
251	TEAAIIPIGL	GGFVACRALS	QRNDDPQTAS	RPWDKARDGF	VMGEGAGVLV
301	MESLEHAMKR	GAPIVAEYLG	GAVNCDAHHM	TDPRADGLGV	SSCIERCLED
351	AGVSPEEVNY	INAHATSTLA	GDLAEINAIK	KVFKSTSGIK	INATKSMIGH
401	CLGAAGGLEA	IATVKAINTG	WLHPSINQFN	PEQAVDFDTV	PNEKKQHEVD
451	VAISNSFGFG	GHNSVVAFSA	FKP		

Show predicted peptides also

Sort Peptides By

Start -	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
85 -	97	680.4580	1358.9014	1358.7405	0.1609	0	K.LLSGESGISLIDR.F (Ions score 100)
113 -	123	580.3375	1158.6605	1158.5193	0.1411	0	R.GFSSEGYIDGK.N (Ions score 59)
142 -	152	537.8606	1073.7066	1073.5353	0.1713	0	K.ALESANLGGDK.L (Ions score 68)
142 -	158	587.0564	1758.1475	1757.9159	0.2316	1	K.ALESANLGGDKLNTIDK.R (Ions score 68)
273 -	285	765.4231	1528.8317	1528.6906	0.1411	0	R.NDDPQTASRPWDK.A (Ions score 57)
273 -	285	510.6545	1528.9418	1528.6906	0.2512	0	R.NDDPQTASRPWDK.A (Ions score 40)
288 -	309	785.7613	2354.2621	2354.0593	0.2028	0	R.DGFVMGEGAGVLVMESLEHAMK.R 3 Oxidation (M) (Ions score 29)

gi|84579412 9-cis-epoxycarotenoid dioxygenase 4

Protein View

Match to: gi|84579412 Score: 53 Lactuca sativa 9-cis-epoxycarotenoid dioxygenase 4 Found in search of C:\QStar Share Data\20091115MMZ\NOV15\92NOV15.wiff

Nominal mass (M_r) : 64534; Calculated pI value: 7.65 NCBI BLAST search of <u>gi|84579412</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Lactuca sativa

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 1%

Matched peptides shown in Bold Red

1	MDTSVTLTRC	STATLVRIST	RPSVTCIIQI	NHHPTTNTPP	HISKPPKIKP
51	TSKSLPELTT	VSPPQLNPFQ	KLAASALDFV	ERSLNVLEND	QKRSHQADPA
101	VQLMGNFAPV	PECPVHHGLE	VIGEIPNDLN	GFYLRNGANP	MFKPTGGHHL
151	FDGDGMIHAV	KLGPKNKASY	CSRFTRTSRL	KQELSLGRPY	FPKPIGELHG
201	HLGLARLALF	YARGVAGLLD	TAHGIGVANA	GLVYFNGRLL	AMSEDDLPYS
251	INIKRDGDLA	TDGRFDYDGQ	VNCPLIAHPK	VDPVTGELFS	LSYDVLKKPY
301	LKFFSFEKNG	KKSREVSISL	NQPTMIHDFA	ITQSHIVIPD	HQVVFKLSEM
351	VQGKSPVLLD	PNKVSRYGIL	PKSVKNESSI	QWIDVPDCFC	YHLWNAWEEV
401	DVKGDQIIVV	IGSRMTPPDA	IFNEINFDLL	RSELTEIRLN	RTTGQSTQRV
451	LVSGINLDAG	NVNKKLLGRK	TRFVYLAIVE	PWPKCNGMAK	VDLETGVVSK
501	LFYGNGRFGG	EPCFIPVEGS	DKEDEGYIMS	YVRDEAMERS	ELVIVEASSM
551	KEIGIVRLTG	RVPYGFHGTF	VSTHDLAN		

Sort Peptides By	🖉 💿 Residi	Residue Number			sing Mass	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
432 - 438	424.2605	846.5065	846.4447	0.0618	0 R.SELTEIR.L	(Ions score 54)

Peptide View

MS/MS Fragmentation of SELTEIR

Found in gi 84579412, Lactuca sativa 9-cis-epoxycarotenoid dioxygenase 4

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	У	y++	y*	y***	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							7
2	217.0819	109.0446	199.0713	100.0393	E	760.4199	380.7136	743.3934	372.2003	742.4094	371.7083	6
3	330.1660	165.5866	312.1554	156.5813	L	631.3 774	316.1923	614.3508	307.6790	613.3668	307.1870	5
4	431.2136	216.1105	413.2031	207.1052	Т	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
5	560.2562	280.6318	542.2457	271.6265	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
6	673.3403	337.1738	655.3297	328.1685	Ι	288.2030	144.6051	271.1765	136.0919			2
7					R	175.1190	88.0631	158.0924	79.5498			1

gi|89274227 Streptomyces cyclase/dehydrase family protein

Protein View

Match to: gi|89274227 Score: 90
Streptomyces cyclase/dehydrase family protein [Brassica oleracea]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2529.wiff

Nominal mass (M_r) : 32680; Calculated pI value: 6.61 NCBI BLAST search of <u>gi|89274227</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica oleracea

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 9%

Matched peptides shown in Bold Red

1 MPSELTQEER SKLTQSISEF HTYHLGPGSC SSLHAQRIHA PPEIVWSVVR 51 QFDKPQTYKH FIKSCSVEEG FEMRVGCTRD VIVISGLPAN TSTERLDMLD 101 DERRVTGFSI IGGEHRLKNY KSVTTVHRFE RERRIWTVVL ESYVVDMPEG 151 NSEDDTRMFA DTVVKLNLQK LATVTEAMAR NAGDGRGSRE TTCRESFHLI 201 TAFEKQRQIT EPTVYQNPPY HTGMTPEPRT STVFIELEDH RTLPGNLTPT 251 TEEHLQRMYQ RFWGIRQLQR PRQSFGERQS I

Sort Peptides By	Resid	lueNumber	Increasing Mass	Decrea	sing Ma	SS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
80 - 95	836.5593	1671.1041	1670.8839	0.2202	0	R.DVIVISGLPANTSTER.L (Ions score 38)
171 - 180	539.8813	1077.7480	1077.5488	0.1991	0	K.LATVTEAMAR.N Oxidation (M) (Ions score 52)

gi|938021 Delta1-pyrroline-5-carboxylate synthetase

Match to: gi|938021 Score: 108
delta1-pyrroline-5-carboxylate synthetase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\386NOV17.wiff

Nominal mass (M_r) : 78170; Calculated pI value: 6.00 NCBI BLAST search of <u>gi|938021</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1	MEELDRSRAF	ARDVKRIVVK	VGTAVVTGKG	GRLALGRLGA	LFEQLAELNS
51	DGFKVILVSS	GAVGLGRQRL	RYRQLVNSSF	ADLQKPQTEL	DGKACAGVGQ
101	SSLMAYYETM	FDQLDVTAAQ	LLVNDSSFRD	KDFRKQLNET	VKSMLDLRVI
151	PIFNENDAIS	TRRAPYQDSS	GIFWDNDSLA	ALLALELKAD	LLILLSDVEG
201	LYTGPPSDPN	SKLIHTFVKE	KHQDEITFGD	KSRLGRGGMT	AKVKAAVNAA
251	YAGIPVIITS	GYSAENIDKV	LRGLRVGTLF	HQDARLWAPI	TDSNARDMAV
301	AARESSRKLQ	ALSSEDRKKI	LLDIADALEA	NVTTIKAENE	LDVASAQEAG
351	LEESMVARLV	MTPGKISSLA	ASVRKLADME	EPIGRVLKKT	EVADGLVLEK
401	TSSPLGVLLI	VFESRPDALV	QIASLAIRSG	NGLLLKGGKE	ARRSNAILHK
451	VITDAIPETV	GGKLIGFVTS	REEIPDLLKL	DDVIDLVIPR	GSNKLVTQIK
501	NTTKIPVLGH	ADGICHVYVD	KACDTDMAKR	IVSDAKLDYP	AACNAMETLL
551	VHKDLEQNAV	LNELIFALQS	NGVTLYGGPR	ASKILNIPEA	RSFNHEYCAK
601	ACTVEVVEDV	YGAIDHIHRH	GSAHTDCIVT	EDHEVAELFL	RQVDSAAVFH
651	NASTRFSDGF	RFGLGAEVGV	STGRIYARGP	VGVEGLLTTR	WIMRGKGQVV
701	DGDNGIVYTH	QDIPIQA			

Sort Peptides By	Resident of the second seco	lueNumber) Increasing Mass	O Decrea	sing Ma	ISS	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
451 - 463	650.3937	1298.7729	1298.7082	0.0647	0	K.VITDAIPETVGGK.L	(Ions score 63)
679 - 690	599.8776	1197.7406	1197.6718	0.0689	0	R.GPVGVEGLLTTR.W	(Ions score 45)

gi|223530647 Aldo-keto reductase, putative

Protein View

Match to: gi|223530647 Score: 118
aldo-keto reductase, putative [Ricinus communis]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1660NOV16.wiff

Nominal mass (M_r) : 36795; Calculated pI value: 5.49 NCBI BLAST search of <u>gi|223530647</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Ricinus communis

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%
```

Matched peptides shown in Bold Red

MANEIRFFEL NTGAKMPSVG LGTWQAEPGL VGAAVDAAIK IGYRHIDCAQ
 AYNNEKEIGS VLKKLFEDGV VKREDLFITS KLWCSNHDPE DVVKALEGTL
 QDLQLDYIDL YLIHWPVKMK KESVTLEPEN FDQPDIPRTW RAMEALYNSG
 KARAIGLSNF STKKLADLLE VARIPPAVNQ VECHPSWQQA KLREFCQSKG
 VHLSGYSPLG SPGTTWLKSD VLKNPVLNMV AEKLGKTPAQ VALCWGLQMG
 HSVLPKSTNE ERIKENFDVF QWSIPDDLFA KFSEIEQAST FISHGSNIAR
 LITGTFFVSE KFGPYKSIEE LWDGEI

Sort Peptides By	Resid	ueNumber) Increasing Mass	Decrea	sing Ma	SS			
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence			
7 - 15	513.8067	1025.5989	1025.5182	0.0807	0	R.FFELNTGAK.M	(Ions s	core 58	3)
165 - 173	500.3272	998.6399	998.5760	0.0639	0	K.LADLLEVAR.I	(Ions s	core 60)

gi|15235745 Serine hydroxymethytransferase 1 (SHM1)

Protein View

Match to: gi|15235745 Score: 198
SHM1 (SERINE HYDROXYMETHYLTRANSFERASE 1); glycine hydroxymethyltransferase/ poly(U) binding [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\905NOV15.wiff

Nominal mass (M_r) : 57535; Calculated pI value: 8.13 NCBI BLAST search of <u>gi|15235745</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 11%

Matched peptides shown in Bold Red

1	MAMAMALRRL	SSSIDKPIRP	LIRSTSCYMS	SLPSEAVDEK	ERSRVTWPKQ
51	LNAPLEEVDP	EIADIIEHEK	ARQWKGLELI	PSENFTSVSV	MQAVGSVMTN
101	KYSEGYPGAR	YYGGNEYIDM	AETLCQKRAL	EAFRLDPEKW	GVNVQPLSGS
151	PANFHVYTAL	LKPHERIMAL	DLPHGGHLSH	GYQTDTKKIS	AVSIFFETMP
201	YRLDESTGYI	DYDQMEKSAT	LFRPKLIVAG	ASAYARLYDY	ARIRKVCNKQ
251	KAVMLADMAH	ISGLVAANVI	PSPFDYADVV	TTTTHKSLRG	PRGAMIFFRK
301	GVKEINKQGK	EVLYDFEDKI	NQAVFPGLQG	GPHNHTITGL	AVALKQATTS
351	EYKAYQEQVL	SNSAKFAQTL	MERGYELVSG	GTDNHLVLVN	LKPKGIDGSR
401	VEKVLEAVHI	ASNKNTVPGD	VSAMVPGGIR	MGTPALTSRG	FVEEDFAKVA
451	EYFDKAVTIA	LKVKSEAQGT	KLKDFVSAME	SSSTIQSEIA	KLRHEVEEFA
501	KQFPTIGFEK	ETMKYKN			

Show predicted peptides also

Sort Poptidos By

• Residue Number © Increasing Mass					Increasing Mass	Decreasing Mass				
	Start	- End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence		
	203	- 217	911.9070	1821.7995	1821.7615	0.0381	0	R.LDESTGYIDYDQMEK.S Oxidation (M) (Ions score 26)		
	311	- 319	579.3056	1156.5966	1156.5288	0.0678	0	K.EVLYDFEDK.I (Ions score 32)		
	415	- 430	529.3124	1584.9153	1584.7930	0.1223	0	K.NTVPGDVSAMVPGGIR.M Oxidation (M) (Ions score 61)		
	440	- 448	521.2810	1040.5474	1040.4815	0.0660	0	R.GFVEEDFAK.V (Ions score 33)		
	502	- 510	533.8099	1065.6053	1065.5495	0.0558	0	K.QFPTIGFEK.E (Ions score 48)		

gi|18407710 Nucleotide-rhamnose synthase/epimerase-reductase (NRS/ER)

Protein View

Match to: gi|18407710 Score: 140
NRS/ER (NUCLEOTIDE-RHAMNOSE SYNTHASE/EPIMERASE-REDUCTASE) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1737NOV15.wiff

Nominal mass (M_r) : 33861; Calculated pI value: 5.73 NCBI BLAST search of <u>gi|18407710</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|8493590</u> from <u>Arabidopsis thaliana</u> <u>gi|12083298</u> from <u>Arabidopsis thaliana</u> <u>gi|41080591</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 10%

Matched peptides shown in Bold Red

1	MVADANGSSS	SSFNFLIYGK	TGWIGGLLGK	LCEAQGITYT	YGSGRLQDRQ
51	SIVADIESVK	PSHVFNAAGV	TGRPNVDWCE	SHKVETIRTN	VAGTLTLADI
101	CREKGLVLIN	YATGCIFEYD	SGHPLGSGIG	FKEEDTPNFT	GSFYSKTKAM
151	VEELLKNYEN	VCTLRVRMPI	SSDLTNPRNF	ITKIARYEKV	VDIPNSMTIL
201	DELLPISIEM	AKRNLTGIYN	FINPGVVSHN	EILEMYRDYI	DPSFTWKNFT
251	LEEQARVIVA	PRSNNELDAT	KLKTEFPELM	SIKESLIKFV	FEPNKKTEVK
301	Α				

Sort Peptides By Residue Number Increasing Mass) Increasing Mass	s 💿 Decreasing Mass				
Start	- End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence		
133	- 146	811.3683	1620.7220	1620.6944	0.0276	0	K.EEDTPNFTGSFYSK.T (Ions score 74)		
149	- 156	474.7905	947.5665	947.4997	0.0667	0	K.AMVEELLK.N Oxidation (M) (Ions score 44)		
248	- 256	540.3066	1078.5986	1078.5295	0.0692	0	K.NFTLEEQAK.V (Ions score 23)		

gi|17865468 Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic

Match to: gi | 17865468 Score: 222

RecName: Full=Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic; AltName: Full=Alpha-D-glucose-1-phosphate adenyl transferase Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1051NOV17.wiff

Nominal mass (M_r): 57294; Calculated pI value: 5.87 NCBI BLAST search of <u>gi|17865468</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: <u>Brassica napus</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi[7688095</u> from <u>Brassica napus</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 9%

Matched peptides shown in Bold Red

```
1 MATMAAIGSL KVPSSSSNHT RRLSSSSQRK TLSFSSSSLT GEKLNPTQEI
51 IISNLPRGNE RRTPSIVSPK AVSDSQNSQT CLDPDASRSV LGIILGGGAG
101 TRLYPLTKKR AKPAVPLGAN YRLIDIPVSN CLNSNISKIY VLTQFNSASL
151 NRHLSRAYAS NMGGYKNEGF VEVLAAQQSP ENPNWFQGTA DAVRQYLWLF
201 EEHNVLEFLV LAGDHLYRMD YEKFIQAHRE TDADITVAAL PMDEKRATAF
251 GLMKIDDEGR IIEFAEKPKG EQLKAMKVDT TILGLDDERA KEMPFIASMG
301 IYVVSKNVML DLLRDQFPGA NDFGSEVIPG ATDLGLRVQA YLYDGYWEDI
351 GTIEAFYNAN LGITKKPVPD FSFYDRSAPI YTQPRYLPPS KMLDADVTDS
401 VIGEGCVIKN CKIHHSVIGL RSCISEGAII EDTLLMGADY YETDADRTLL
451 AAKGSIPIGI GRDSHIKRAI IDKNARIGDN VKIINTDNVQ EAARETDGYF
501 IKSGIVTVIK DALIPSGTVI
```

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start	- End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
230	- 245	867.9254	1733.8363	1733.8029	0.0334	0	R.ETDADITVAALPMDEK.R Oxidation (M) (Ions score 1	<u>(8</u>
278	- 289	673.8716	1345.7286	1345.6725	0.0560	0	K.VDTTILGLDDER.A (Ions score 109)	
483	- 494	672.3775	1342.7405	1342.6841	0.0564	0	K.IINTDNVQEAAR.E (Ions score 78)	
511	- 520	493.3126	984.6106	984.5492	0.0614	0	K.DALIPSGTVI (Ions score 18)	

gi|18404212 3-chloroallyl aldehyde dehydrogenase

Match to: gi|18404212 Score: 60

ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD) [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\753NOV15.wiff

Nominal mass (M_r) : 54782; Calculated pI value: 5.47 NCBI BLAST search of <u>gi|18404212</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|118595574</u> from <u>Arabidopsis thaliana</u> <u>gi|9294041</u> from <u>Arabidopsis thaliana</u> <u>gi|15912241</u> from <u>Arabidopsis thaliana</u> <u>gi|20530143</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 1%

Matched peptides shown in Bold Red

```
1 MENGKCNGAT TVKLPEIKFT KLFINGQFID AASGKTFETI DPRNGEVIAT
51 IAEGDKEDVD LAVNAARYAF DHGPWPRMTG FERAKLINKF ADLIEENIEE
101 LAKLDAVDGG KLFQLGKYAD IPATAGHFRY NAGAADKIHG ETLKMTRQSL
151 FGYTLKEPIG VVGNIIPWNF PSIMFATKVA PAMAAGCTMV VKPAEQTSLS
201 ALFYAHLSKE AGIPDGVLNI VTGFGSTAGA AIASHMDVDK VSFTGSTDVG
251 RKIMQAAAAS NLKKVSLELG GKSPLLIFND ADIDKAADLA LLGCFYNKGE
301 ICVASSRVFV QEGIYDKVVE KLVEKAKDWT VGDPFDSTAR QGPQVDKRQF
351 EKILSYIEHG KNEGATLLTG GKAIGDKGYF IQPTIFADVT EDMKIYQDEI
401 FGPVMSLMKF KTVEEGIKCA NNTKYGLAAG ILSQDIDLIN TVSRSIKAGI
451 IWVNCYFGFD LDCPYGGYKM SGNCRESGMD ALDNYLQTKS VVMPLHNSPW
501 M
```

Sort Peptides By	/ 💿 Resid	tueNumber) Increasing Mass	Decrea	ising Mass	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
308 - 317	599.3420	1196.6694	1196.6077	0.0617	0 R.VFVOEGIYDK.V	(Ions score 61)

Peptide View

MS/MS Fragmentation of VFVQEGIYDK Found in gi|18404212, ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1);

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y++	y *	y*++	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	247.1441	124.0757					F	1098.5466	549.7769	1081.5201	541.2637	1080.5360	540.7717	9
3	346.2125	173.6099					V	951.4782	476.2427	934.4516	467.7295	933.4676	467.2375	8
4	474.2711	237.6392	457.2445	229.1259			Q	852.4098	426.7085	835.3832	418.1953	834.3992	417.7032	7
5	603.3137	302.1605	586.2871	293.6472	585.3031	293.1552	E	724.3512	362.6792	707.3246	354.1660	706.3406	353.6740	6
6	660.3352	330.6712	643.3086	322.1579	642.3246	321.6659	G	595.3086	298.1579	578.2821	289.6447	577.2980	289.1527	5
7	773.4192	387.2132	756.3927	378.7000	755.4087	378.2080	Ι	538.2871	269.6472	521.2606	261.1339	520.2766	260.6419	4
8	936.4825	468.7449	919.4560	460.2316	918.4720	459.7396	Y	425.2031	213.1052	408.1765	204.5919	407.1925	204.0999	3
9	1051.5095	526.2584	1034.4829	517.7451	1033.4989	517.2531	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
10							K	147.1128	74.0600	130.0863	65.5468			1

gi|219914490 Unnamed protein product, containing chalcone-flavanone isomerase domain

Protein View

Match to: gi|219914490 Score: 125 unnamed protein product [Brassica napus] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2287.wiff

Nominal mass (M_r) : 23362; Calculated pI value: 4.91 NCBI BLAST search of <u>gi|219914490</u> against nr Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 14%
```

Matched peptides shown in Bold Red

1 MGTEMVMVHE VPFPPQIITS KPFSLLGQGI TDIEIHFLQV KFTAIGVYLD 51 PSDVKTHLDK WKGKTGKDLA GDDDFFDALA SGEIEKVIRV VVIKEIKGAQ 101 YGVQLENSVR DRLAAEDKYE EEEETELEKV VGFFQSKYFK THSIITYRFS 151 AKDGICEIGF ETEGKEEEKL KVENANVVGM MQKWYLSGSR GVSPSTIVSL 201 ADSLSAVLT

Sort Peptides By	Resident	lueNumber) Increasing Mass	Decrea	ising Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
98 - 110	710.9753	1419.9361	1419.7106	0.2254	0	K.GAQYGVQLENSVR.D (Ions score 67)
113 - 129	685.7666	2054.2779	2053.9215	0.3564	1	R.LAAEDKYEEEEETELEK.V (Ions score 58)

gi|15237059 Arabidopsis Rab GTPase homolog E1b (AtRABE1b/AtRab8D)

Protein View

Match to: gi|15237059 Score: 106 AtRABE1b/AtRab8D (Arabidopsis Rab GTPase homolog E1b); translation elongation factor [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1158NOV15.wiff

Nominal mass (M_r) : 51883; Calculated pI value: 5.84 NCBI BLAST search of <u>gi|15237059</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 5%

Matched peptides shown in Bold Red

1	MAISAPAACS	SSSRILCSYS	SPSPSLCPAI	STSGKLKTLT	LSSSFLPSYS
51	LTTTSASQST	RRSFTVRAAR	GKFERKKPHV	NIGTIGHVDH	GKTTLTAALT
101	MALASIGSSV	AKKYDEIDAA	PEERARGITI	NTATVEYETE	NRHYAHVDCP
151	GHADYVKNMI	TGAAQMDGAI	LVVSGADGPM	PQTKEHILLA	KQVGVPDMVV
201	FLNKEDQVDD	AELLELVELE	VRELLSSYEF	NGDDIPIISG	SALLAVETLT
251	ENPKVKRGDN	KWVDKIYELM	DAVDDYIPIP	QRQTELPFLL	AVEDVFSITG
301	RGTVATGRVE	RGTVKVGETV	DLVGLRETRS	YTVTGVEMFQ	KILDEALAGD
351	NVGLLLRGIQ	KADIQRGMVL	AKPGSITPHT	KFEAIIYVLK	KEEGGRHSPF
401	FAGYRPQFYM	RTTDVTGKVT	KIMNDKDEES	KMVMPGDRVK	IVVELIVPVA
451	CEQGMRFAIR	EGGKTVGAGV	IGTILE		

Sort Peptides By	Resid	lueNumber	Increasing Mass	Decrea	sing Mass
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence
1 - 14	898.1555	1794.2965	1794.4598	-0.1633	0MAISAPAACSSSSR.I 5 Phospho (ST) (Ions score 14
316 - 326	579.3486	1156.6826	1156.6452	0.0374	0 K.VGETVDLVGLR.E (Ions score 92)

gi|295789 Elongation factor 1-alpha

Protein View

Match to: gi|295789 Score: 199
elongation factor 1-alpha [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1103NOV16.wiff

Nominal mass (M_r) : 49799; Calculated pI value: 9.19 NCBI BLAST search of <u>gi|295789</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 8%

Matched peptides shown in Bold Red

1	MGKEKFHINI	VVIGHVDSGK	STTTGHLIYK	LGGIDKRVIE	RFEKEAAEMN
51	KRSFKYAWVL	DKLKAERDRG	ITIDIALWKF	ETTKYYCTVI	DAPGHRDFIK
101	NMITGTSQAD	CAVLIIDSTT	GGFEAGISKD	GQTREHALLA	FTLGVKQMIC
151	CCNKMDATTP	KYSKARYDEI	IKEVSSYLKK	VGYNPDKIPF	VPISGFEGDN
201	MIERSTNLDW	YKGPTLLEAL	DQINEPKRPS	DKPLRLPLQD	VYKIGGIGTV
251	PVGRVETGMI	KPGMVVTFAP	TGLTTEVKSV	EMHHESLLEA	LPGDNVGFNV
301	KNVAVKDLKR	GYVASNSKDD	PAKGAANFTS	QVIIMNHPGQ	IGNGYAPVLD
351	CHTSHIAVKF	SEILTKIDRR	SGKEIEKEPK	FLKNGDAGMV	KMTPTKPMVV
401	ETFSEYPPLG	RFAVRDMRQT	VAVGVIKSVD	KKDPTGAKVT	KAAVKKGAK

Sort Peptides By	Resid	lue Number	Increasing Mass	Decrea	ising Ma	155
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
205 - 212	513.7865	1025.5584	1025.4818	0.0766	0	R.STNLDWYK.G (Ions score 33)
236 - 243	488.3183	974.6221	974.5437	0.0784	0	R.LPLQDVYK.I (Ions score 60)
244 - 254	513.3515	1024.6884	1024.6030	0.0854	0	K.IGGIGTVPVGR.V (Ions score 58)
419 - 427	457.8256	913.6366	913.5597	0.0769	0	R.QTVAVGVIK.S (Ions score 49)

gi|303844 Eukaryotic initiation factor 4A

Protein View

Match to: gi|303844 Score: 155 eukaryotic initiation factor 4A [Oryza sativa Japonica Group] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (M_r) : 47187; Calculated pI value: 5.29 NCBI BLAST search of <u>gi|303844</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Oryza sativa Japonica Group</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|12381900</u> from <u>Oryza sativa</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 10%

Matched peptides shown in Bold Red

1	MAGMAPEGSQ	FDAKHYDSKM	QELLNQGETE	EFFTSYDEVH	ESFDDMGLQE
51	NLLRGIYAYG	FEKPSAIQQR	GIVPFCKGLD	VIQQAQSGTG	KTATFCSGIL
101	QQLDYAVVEC	QALVLAPTRE	LAQQIEKVMR	ALGDYLGVKV	HACVGGTSVR
151	EDQRILASGV	HVVVGTPGRV	FDMLRRQSLR	PDYIKMFVLD	EADEMLSRGF
201	KDQIYDIFQL	LPSKIQVGVF	SATMPPEALE	ITRKFMNKPV	RILVKRDELT
251	LEGIR QFYVN	VEKEEWKLDT	LCDLYETLAI	TQSVIFVNTR	KVDWLTDKMR
301	GRDHTVSATH	GDMDQNTRDI	IMREFRSGSS	RVLITTDLLA	RGIDVQQVSL
351	VINYDLPTQP	ENYLHRIGRS	GRFGRKGVAI	NFVTRDDERM	LFDIQRFYNV
401	VIEELPANVA	DLL			

Show predicted peptides also

Sort Peptides By

Start	_	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
78	-	91	701.3904	1400.7662	1400.7260	0.0402	0	K.GLDVIQQAQSGTGK.T (Ions score 27)
131	-	139	468.2959	934.5772	934.5124	0.0649	0	R.ALGDYLGVK.V (Ions score 37)
247	-	255	509.3037	1016.5929	1016.5390	0.0539	0	R.DELTLEGIK.Q (Ions score 35)
332	-	341	557.8688	1113.7230	1113.6758	0.0473	0	R.VLITTDLLAR.G (Ions score 56)

gi|2494261 Elongation factor Tu, chloroplastic

Protein View

Match to: gi|2494261 Score: 79
RecName: Full=Elongation factor Tu, chloroplastic; Short=EF-Tu; Flags: Precursor
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1193NOV15.wiff

Nominal mass (M_r) : 52177; Calculated pI value: 6.21 NCBI BLAST search of <u>gi|2494261</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Glycine max</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|18776</u> from <u>Glycine max</u> <u>gi|448921</u> from <u>Glycine max</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 2%

Matched peptides shown in Bold Red

1	MAVSSATASS	KLILLPHASS	SSSLNSTPFR	SSTTNTHKLT	PLSSSFLHPT
51	TVLRRTPSST	TTPRRTFTVR	AARGKFERKK	PHVNIGTIGH	VDHGKTTLTA
101	ALTMALAALG	NSAPKKYDEI	DAAPEERARG	ITINTATVEY	ETENRHYAHV
151	DCPGHADYVK	NMITGAAQMD	GAILVVSGAD	GPMPQTKEHI	ILAKQVGVPN
201	MVVFLNKQDQ	VDDEELLQLV	EIEVRDLLSS	YEFPGDDTPI	VSGSALLALE
251	ALMANPAIKR	GDNEWVDKIF	QLMDEVDNYI	PIPQRQTDLP	FLLAVEDVFS
301	ITGRGTVATG	RVERGTIKVG	ETVDLVGLRE	TRNTTVTGVE	MFQKILDEAL
351	AGDNVGLLLR	GVQKTDIQRG	MVLAKPGTIT	PHTKFSAIVY	VLKKEEGGRH
401	SPFFAGYRPQ	FYMRTTDVTG	KVTSIMNDKD	EESTMVLPGD	RVKMVVELIV
451	PVACEQGMRF	AIREGGKTVG	AGVIQSIIE		

Show predicted peptides also

Sort Peptides By Sort Peptides By
Residue Number Increasing Mass
Decreasing Mass
Start - End Observed Mr(expt) Mr(calc)
Delta Miss Sequence
319 - 329
579.3593
1156.7041
1156.6452
0.0589
0 K.VGETVDLVGLR.E (<u>Ions score 79</u>)

gi|40805177 Eukaryotic translation initiation factor-5A

Protein View

Match to: gi|40805177 Score: 210 eukaryotic translation initiation factor-5A [Brassica napus] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2529.wiff

Nominal mass (M_r) : 17315; Calculated pI value: 5.71 NCBI BLAST search of <u>gi|40805177</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 21%

Matched peptides shown in Bold Red

1 MSDEEHHFES SDAGASKTYP QQAGNIRKGG HIVIKGRPCK VVEVSTSKTG 51 KHGHAKCHFV AIDIFTAKKL EDIVPSSHNC DVPHVNRIDY QLIDISENGF 101 VSLLTDSGGT KDDLKLPTDD NLSALMKSGF EEGKDVVVSV MSSMGEEQIC 151 AVKEVGGGK

Sort Peptides By Residue Number Increasing Mass 					O Decreasing Mass				
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence			
18 - 27	574.3952	1146.7758	1146.5782	0.1977	0	K.TYPQQAGNIR.K (Ions score 50)			
41 - 48	424.8308	847.6470	847.4651	0.1819	0	K.VVEVSTSK.T (Ions score 47)			
112 - 127	602.4168	1804.2286	1803.8924	0.3362	1	K.DDLKLPTDDNLSALMK.S Oxidation (M) (Ions score 5	0		
116 - 127	667.4440	1332.8735	1332.6595	0.2140	0	K.LPTDDNLSALMK.S Oxidation (M) (Ions score 64)			

gi|9755847 Translation initiation factor 3, subunit g (eIF3g)

Protein View

Match to: gi|9755847 Score: 142 translation initiation factor 3, subunit g (eIF3g) [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1831.wiff

Nominal mass (M_r) : 32865; Calculated pI value: 8.31 NCBI BLAST search of <u>gi|9755847</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%
```

Matched peptides shown in Bold Red

1 MTIDSQQKTS KFRWGEMDED EDLDFLLPPK QVIGPDENGL KTTIEYKFND 51 EENKVKITTR TRVRKLASAR LNKRAMERRN WPKFGDAANE EAGSHLTMVS 101 TEEILLERPR APGTKADESK ATGDGLSQLG KGGAVLMVCR ICHKKGDHWT 151 SKCPYKDLAA PTDVFIDKPP TGESSTMSAA PGTGKAAYVP PSMRAGADRS 201 AVGSDMRRRN DENSVRVTNL SEDTREPDLM ELFHPFGAVT RVYVAIDQKT 251 GVSRGFGFVN FVSREDAQRA INKLNGYGYD NLILRVEWAT PRPT

Sort Peptides By	Resid	lueNumber) Increasing Mass	Decrea	asing Mass	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
242 - 249	468.3539	934.6932	934.5124	0.1808	<pre>0 R.VYVAIDQK.T (Ions score 35)</pre>	
274 - 285	706.4832	1410.9518	1410.7143	0.2375	0 K.LNGYGYDNLILR.V Deamidated (NQ) (<u>lons score 10</u>)	<u>8</u>)

gi|3775985 RNA helicase

Protein View

Match to: gi|3775985 Score: 156
RNA helicase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (M_r) : 44634; Calculated pI value: 5.52 NCBI BLAST search of <u>gi|3775985</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|9294443</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 8%

Matched peptides shown in Bold Red

1	MDDDKLVFET	TDGIEPITSF	NDMGIKEDVL	RGVYEYGFEK	PSAIQQRAVM
51	PILQGRDVIA	QAQSGTGKTS	MIALSVCQVV	DTSSREVQAL	ILSPTRELAT
101	QTEKTIQAIG	LHANIQAHAC	IGGNSVGEDI	RKLEHGVHVV	SGTPGRVCDM
151	IKRRSLRTRA	IKLLILDESD	EMLSRGFKDQ	IYDVYRYLPP	DLQVCLVSAT
201	LPHEILEMTS	KFMTEPVKIL	VKRDELTLEG	IR QFFVAVEK	EEWKFDTLCD
251	LYDTLTITQA	VIFCNTKRKV	DYLSEKMRSH	NFTVSSMHGD	MPQKERDAIM
301	NEFRSGDSRV	LITTDVWARG	IDVQQVSLVI	NYDLPNNREL	YIHRIGRSGR
351	FGRKGVAINF	VKSDDIKILR	DIEOYYSTOI	DEMPMNVADL	I

Show predicted peptides also

Sort Pontidos By

ι	Soft Peptides Dy	Resid	tue Number	Increasing Mass	Decrease	sing Ma	ISS	
	Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
	86 - 96	613.8765	1225.7384	1225.7030	0.0354	0	R.EVQALILSPTR.E (Ions score 55)	
	163 - 175	775.4470	1548.8794	1548.7705	0.1089	0	K.LLILDESDEMLSR.G Oxidation (M)	(Ions score 67)
	224 - 232	509.3037	1016.5929	1016.5390	0.0539	0	R.DELTLEGIK.Q (Ions score 35)	

gi|17819 Glycine-rich RNA binding protein

Protein View

Match to: gi|17819 Score: 260 glycine-rich RNA binding protein [Brassica napus] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2716.wiff

Nominal mass (M_r): 16351; Calculated pI value: 5.56 NCBI BLAST search of <u>gi|17819</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 44%

Matched peptides shown in Bold Red

- 1 MSEVEYRCFV GGLAWATGDA ELERTFSQFG EVIDSKIIND RETGRSRGFG
- 51 FVTFKDEKSM KDAIDEMNGK ELDGRTITVN EAQSRGGGGG GGRGGGGGGGG
- 101 RGGGGYGGGG GGYGDRRGGG GYGSGGGGRG GGGYGSGGGG YGGGGGGRRDG
- 151 GGYGGGDGGY GGGSGGGGW

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start -	- 1	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 -	- 1	36	679.4453	1356.8760	1356.6562	0.2199	0	R.TFSQFGEVIDSK.I (Ions score 61)
62 -	- '	75	527.3423	1579.0052	1578.6831	0.3220	1	K.DAIDEMNGKELDGR.T Deamidated (NQ); Oxidation (M) (Ions score 31)
76 -	-	85	559.9056	1117.7966	1117.5727	0.2238	0	R.TITVNEAQSR.G (Ions score 60)
130 -	- :	147	693.9151	1385.8156	1385.5709	0.2447	0	R.GGGGYGSGGGGGGGGGGGR.R (Ions score 79)
149 -	- 1	169	852.4374	1702.8602	1702.6245	0.2357	0	R.DGGGYGGGDGGYGGGSGGGGW (Ions score 29)

gi|15237716 KH domain-containing protein NOVA, putative

Protein View

```
Match to: gi|15237716 Score: 91
KH domain-containing protein NOVA, putative [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1509NOV15.wiff
```

```
Nominal mass (M_r): 33857; Calculated pI value: 5.70
NCBI BLAST search of <u>gi|15237716</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

```
Taxonomy: <u>Arabidopsis thaliana</u>
Links to retrieve other entries containing this sequence from NCBI Entrez:
<u>gi|14030641</u> from <u>Arabidopsis thaliana</u>
<u>gi|21554568</u> from <u>Arabidopsis thaliana</u>
<u>gi|23507775</u> from <u>Arabidopsis thaliana</u>
```

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%
```

Matched peptides shown in Bold Red

```
1 MESTESYAAG SPEELAKRSP EPHDSSEADS AEKPTHIRFL VSNAAAGSVI
51 GKGGSTITEF QAKSGARIQL SRNQEFFPGT TDRIIMISGS IKEVVNGLEL
101 ILDKLHSELH AEDGNEVEPR RRIRLVVPNS SCGGIIGKGG ATIKSFIEES
151 KAGIKISPLD NTFYGLSDRL VTLSGTFEEQ MRAIDLILAK LTEDDHYSQN
201 VHSPYSYAAG YNSVNYAPNG SGGKYQNHKE EASTTVTIGV ADEHIGLVLG
251 RGGRNIMEIT QMTGARIKIS DRGDFMSGTT DRKVSITGPQ RAIQQAETMI
301 KQKVDSATER TTD
```

Sort Peptides By	Resid	lueNumber	Increasing Mass	Decrea	ising Ma	155	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
53 - 63	569.8253	1137.6361	1137.5666	0.0695	0	K.GGSTITEFQAK.S	(Ions score 35)
73 - 83	656.3271	1310.6396	1310.5891	0.0505	0	R.NQEFFPGTTDR.I	(Ions score 56)

gi|9758155 40S ribosomal protein S3

Protein View

```
Match to: gi|9758155 Score: 154
40S ribosomal protein S3 [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1831.wiff
```

Nominal mass (M_r) : 27612; Calculated pI value: 9.57 NCBI BLAST search of <u>gi|9758155</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%
```

Matched peptides shown in Bold Red

1 MATQISKKRK FVADGVFYAE LNEVLTR**ELA EDGYSGVEVR** VTPMRTEIII 51 RATRTQNVLG EKGRRIR**ELT SLVQK**RFK**FP QDSVELYAEK** VANRGLCAIA 101 QAESLRYKLL GGLAVRRACY GVLRFVMESG AKGCEVIVSG KLRAARAKSM 151 KFKDGYMVSS GQPTKEYIDA AVRHVLLRQG VLGLKVKIML DWDPKGKQGP 201 MTPLPDVVII HTPKEDDVYI APAQVVTQAA FVPEAPLTTT DYPAMPVA

Sort Peptides By	Resid	Residue Number			Decreasing Mass			
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence		
28 - 40	712.4520	1422.8895	1422.6627	0.2268	0	R.ELAEDGYSGVEVR.V (Ions score 93)		
68 - 75	459.3551	916.6956	916.5229	0.1727	0	R.ELTSLVQK.R (Ions score 36)		
79 - 90	713.4652	1424.9158	1424.6823	0.2334	0	K.FPQDSVELYAEK.V (Ions score 24)		

gi|6729494 60S ribosomal protein L12-like

Protein View

Match to: gi|6729494 Score: 128
60S RIBOSOMAL PROTEIN L12-like [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2605.wiff

Nominal mass (M_r) : 18073; Calculated pI value: 9.05 NCBI BLAST search of <u>gi|6729494</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 26%
```

Matched peptides shown in Bold Red

1 MPPKLDPSQI VDVYVRVTGG EVGAASSLAP KIGPLGLAPK KIGEDIAKET 51 AKEWKGLRVT VKLTVQNRQA KVTVVPSAAA LVIKALKEPE RDRKKVKNIK 101 HNGNISFDDV TEIARIMRPR SIAKELSGTV REILGTCVSV GCTVDGKDPK 151 DLQQEIQEGE IEIPEN

Sort Peptides By	Resid	lueNumber	Decreasing Mass			
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
17 - 31	672.4817	1342.9489	1342.7092	0.2396	0	R.VTGGEVGAASSLAPK.I (Ions score 53)
72 - 84	634.5083	1267.0020	1266.7911	0.2109	0	K.VTVVPSAAALVIK.A (Ions score 47)
151 - 166	942.5582	1883.1019	1882.8796	0.2223	0	K.DLQQEIQEGEIEIPEN (Ions score 28)

gi|550544 RIbosomal protein L16

Protein View

Match to: gi|550544 Score: 118 ribosomal protein L16 [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2420.wiff

Nominal mass (M_r) : 21033; Calculated pI value: 9.94 NCBI BLAST search of <u>gi|550544</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 14%
```

Matched peptides shown in Bold Red

1 MASEKKLSNP MRDIKVQKLV LNISVGESGD RLTRASKVLE QLSGQTPVFS 51 KARYTVRSFG IRRNEKIACY VTVRGEKAMQ LLESGLKVKE YELLRRNFSD 101 TGCFGFGIQE HIDLGIKYDP STGIYGMEFY VVLERPGYRV ARRRCKTRV 151 GIQHRVTKDD AMKWFQVKYE GVILNKSQNI TG

Sort Peptides By	Resid	tueNumber) Increasing Mass	Decrea	sing Ma	SS	
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
19 - 31	679.9806	1357.9467	1357.7201	0.2266	0	K.LVLNISVGESGDR.L	(Ions score 77)
38 - 51	767.0295	1532.0444	1531.8246	0.2198	0	K.VLEQLSGQTPVFSK.A	(Ions score 41)

gi|30692346 Ribosomal protein S1; RNA binding

Match to: gi|30692346 Score: 272
RPS1 (ribosomal protein S1); RNA binding [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1259NOV16.wiff

Nominal mass (M_r) : 45310; Calculated pI value: 5.13 NCBI BLAST search of <u>gi|30692346</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 12%

Matched peptides shown in Bold Red

1	MASLAQQFSG	LRCSPLSSSS	RLSRRASKNF	PQNKSASVSP	TIVAAVAMSS
51	GQTKERLELK	KMFEDAYERC	RTSPMEGVAF	TVDDFAAAIE	QYDFNSEIGT
101	RVKGTVFKTD	ANGALVDISA	KSSAYLSVEQ	ACIHRIKHVE	EAGIVPGMVE
151	EFVIIGENES	DDSLLLSLRN	IQYELAWERC	RQLQAEDVIV	KAKVIGANKG
201	GLVALVEGLR	GFVPFSQISS	KAAAEELLEK	EIPLKEVEVD	EEQTKLVLSN
251	RKAVADSQAQ	LGIGSVVLGV	VQSLKPYGAF	IDIGGINGLL	HVSQISHDRV
301	SDIATVLQPG	DTLKVMILSH	DRDRGRVSLS	TKKLEPTPGD	MIRNPKLVFE
351	KAEEMAQTFR	QRIAQAEAMA	RADMLRFQPE	SGLTLSSDGI	LGPLGSELPD
401	DGVDLTVDDI	PSAVDI			

Į	Sort Peptides By	Resid	ue Number	Increasing Mass	Decrease	sing Ma	155
	Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
	109 - 121	637.8523	1273.6900	1273.6514	0.0386	0	K.TDANGALVDISAK.S (Ions score 65)
	211 - 221	598.8503	1195.6861	1195.6237	0.0623	0	R.GFVPFSQISSK.A (Ions score 35)
	222 - 230	487.3028	972.5910	972.5127	0.0783	0	K.AAAEELLEK.E (Ions score 62)
	222 - 230	487.3028	972.5910	972.5127	0.0783	0	K.AAAEELLEK.E (Ions score 23)
	236 - 245	612.3180	1222.6214	1222.5717	0.0496	0	K.FVEVDEEQTK.L (Ions score 51)
	352 - 360	541.7810	1081.5475	1081.4862	0.0613	0	K.AEEMAQTFR.Q (Ions score 59)

gi|13194778 Putative ATP-dependent Clp protease proteolytic subunit ClpP6

Protein View

Match to: gi|13194778 Score: 77 putative ATP-dependent Clp protease proteolytic subunit ClpP6 [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2352DEC04.wiff

Nominal mass (M_r) : 29534; Calculated pI value: 9.38 NCBI BLAST search of <u>gi|13194778</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%
```

Matched peptides shown in Bold Red

1 MAGLAISPPL GLSFSSRTRN PKPTSFLSHN QRNPIRRIVS ALQSPYGDSL 51 KAGLSSNVSG SPIKIDNKAP RFGVIEAKKG NPPVMPSVMT PGGPLDLSSV 101 LFRNRIIFIG QPINAQVAQR VISQLVTLAS IDDKSDILMY LNCPGGSTYS 151 VLAIYDCMSW IKPKVGTVAF GVAASQGALL LAGGEKGMRY AMPNTRVMIH 201 QPQTGCGGHV EDVRRQVNEA IEARQKIDRM YAAFTGQPLE KVQQYTERDR 251 FLSASEALEF GLIDGLLETE Y

Sort Peptides By	Resid	tueNumber) Increasing Mass	Decrease Decrease	sing Ma	ISS			
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence			
165 - 186	672.8175	2015.4305	2015.1051	0.3254	0	K.VGTVAFGVAASQGALLLAGGEK.G	(Ions	score	77)

Peptide View

MS/MS Fragmentation of VGTVAFGVAASQGALLLAGGEK

Found in gi 13194778, putative ATP-dependent Clp protease proteolytic subunit ClpP6 [Arabidopsis thaliana]

#	b	b++	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y**	y*	y***	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							22
2	157.0972	79.0522					G	1917.0440	959.0256	1900.0175	950.5124	1899.0334	950.0204	21
3	258.1448	129.5761			240.1343	120.5708	Τ	1860.0225	930.5149	1842.9960	922.0016	1842.0120	921.5096	20
4	357.2132	179.1103			339.2027	170.1050	V	1758.9749	879.9911	1741.9483	871.4778	1740.9643	870.9858	19
5	428.2504	214.6288			410.2398	205.6235	A	1659.9064	830.4569	1642.8799	821.9436	1641.8959	821.4516	18
6	575.3188	288.1630			557.3082	279.1577	F	1588.8693	794.9383	1571.8428	786.4250	1570.8588	785.9330	17
7	632.3402	316.6738			614.3297	307.6685	G	1441.8009	721.4041	1424.7744	712.8908	1423.7904	712.3988	16
8	731.4087	366.2080			713.3981	357.2027	V	1384.7795	692.8934	1367.7529	684.3801	1366.7689	683.8881	15
9	802.4458	401.7265			784.4352	392.7212	A	1285.7110	643.3592	1268.6845	634.8459	1267.7005	634.3539	14
10	873.4829	437.2451			855.4723	428.2398	A	1214.6739	607.8406	1197.6474	599.3273	1196.6634	598.8353	13
11	960.5149	480.7611			942.5043	471.7558	S	1143.6368	572.3220	1126.6103	563.8088	1125.6262	563.3168	12
12	1088.5735	544.7904	1071.5469	536.2771	1070.5629	535.7851	Q	1056.6048	528.8060	1039.5782	520.2928	1038.5942	519.8007	11
13	1145.5950	573.3011	1128.5684	564.7878	1127.5844	564.2958	G	928.5462	464 .77 6 7	911.5197	456.2635	910.5356	455.7715	10
14	1216.6321	608.8197	1199.6055	600.3064	1198.6215	599.8144	A	871.5247	436.2660	854.4982	427.7527	853.5142	427.2607	9
15	1329.7161	665.3617	1312.6896	656.8484	1311.7056	656.3564	L	800.4876	400.7475	783.4611	392.2342	782.4771	391.7422	8
16	1442.8002	721.9037	1425.7736	713.3905	1424.7896	712.8985	L	687.4036	344.2054	670.3770	335.6921	669.3930	335.2001	7
17	1555.8843	778.4458	1538.8577	769.9325	1537.8737	769.4405	L	574.3195	287.6634	557.2930	279.1501	556.3089	278.6581	6
18	1626.9214	813.9643	1609.8948	805.4510	1608.9108	804.9590	A	461.2354	231.1214	444.2089	222.6081	443.2249	222.1161	5
19	1683.9428	842.4751	1666.9163	833.9618	1665.9323	833.4698	G	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	4
20	1740.9643	870.9858	1723.9377	862.4725	1722.9537	861.9805	G	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
21	1870.0069	935.5071	1852.9803	926.9938	1851.9963	926.5018	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
22							K	147.1128	74.0600	130.0863	65.5468			1

gi|4105131 ClpC protease

Match to: gi|4105131 Score: 97
ClpC protease [Spinacia oleracea]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\273NOV26.wiff
Nominal mass (M_r): 99588; Calculated pI value: 8.78
NCBI BLAST search of gi|4105131 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Spinacia oleracea

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 2%

Matched peptides shown in Bold Red

1	MAGALIQSTN	IPSLAYKVNG	QFQRSDKGNK	AVKMMASLQD	PGYRMRTFSG
51	VRGGNALDTL	GTTSECFYSK	MRAVLSVRKG	TASRGVVRAM	FERFTEKAIK
101	VIMLAQEEAR	RLGHNFVGTE	QILLGLIGEG	TGIAAKVLKS	MGINLKDARV
151	EVEKIIGRGS	GFVAVEIPFT	PRAKRVLELS	LEEARQLGHN	YIGSEHLLLG
201	LLREGEGVAA	RVLENLGADP	SNIRTQVIRM	VGENTEAVGA	GVGGGTTGNK
251	MPTLEEYGTN	LTKLAEEGKL	DPVVGRQAQI	ERVTQILGRR	TKNNPCLIGE
301	PGVGKTAIAE	GLAQRIATGD	VPETIEGKKV	ITLHMGLLVA	GTKYRGEFEE
351	RIKKIMEEIK	QSDEIILFID	EVHTLIGAGA	AEGAIDRANI	LKPRFRRGEL
401	QCIGATTLDE	YRKHIEKDPA	LERRFQPVKV	PEPTVDETIQ	ILKGLRERYE
451	IHHKLRYTDE	ALVAAAQLSY	QYISDRFLPD	KAIDLIDEAG	SRVLPSSLKK
501	LESWLQHEKE	LRQLTKEKNE	AVRGQDFEKA	GELRDREMDL	KAQISALVEK
551	KKEMSKAETE	AGDVGPMVTE	SDIQHIVSSW	TGIPVEKVST	DESDRLLKME
601	DTLHTRVIGQ	DEAVKAISRA	IRRARVGLKN	PNRPIASFIF	SGPTGVGKSE
651	LAKALAAYYF	GSEEAMIRLD	MSEFMERHTV	SKLIGSPPGY	VGYTEGGQLT
701	EAVRRRPYTV	VLFDEIEKAH	PDVFNMMLQI	LEDGRLTDSK	GRTADFKNTL
751	LIMTSNVGSS	VIEKGGRRIG	FDLDYDEKDS	SYNRIKSLVT	EELKQYFRPE
801	FLNRLDEMIV	FRQLTKLEVK	EIADIMLKEV	FGRLKNKEIE	LQVTERFRDR
851	VVDEGYNPSY	GARPLRRAIM	RLLEDSMAEK	MLARKSKRVI	Q

Show predicted peptides also

Sort Peptides By
 • Residue Number

 • Increasing Mass

 • Decreasing Mass

 • Decreasing MassStart - End

 212 - 224

 316 - 328Observed

 • Mr(expt)

 1328.7940Mr(calc)

 1328.6824Delta

 Miss

 • Decreasing Mass

 • Decreasing Mass

 • Decreasing Mass

 • Delta

 Miss

 • Sequence

 • R.VLENLGADPSNIR.T

 (Ions score 40)

 (Ions score 57)

gi|15232123 Cyclophilin 38 (CYP38); peptidyl-prolyl cis-trans isomerase

Match to: gi|15232123 Score: 126 CYP38 (CYCLOPHILIN 38); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

```
Nominal mass (M<sub>r</sub>): 48180; Calculated pI value: 5.06
NCBI BLAST search of <u>gi|15232123</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

```
Taxonomy: <u>Arabidopsis thaliana</u>
Links to retrieve other entries containing this sequence from NCBI Entrez:
<u>gi|75266250</u> from <u>Arabidopsis thaliana</u>
<u>gi|6016707</u> from <u>Arabidopsis thaliana</u>
<u>gi|14532438</u> from <u>Arabidopsis thaliana</u>
<u>gi|21360549</u> from <u>Arabidopsis thaliana</u>
<u>gi|21593368</u> from <u>Arabidopsis thaliana</u>
gi|45680876 from Arabidopsis thaliana
```

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%
```

Matched peptides shown in Bold Red

1	MAAAFASLPT	FSVVNSSRFP	RRRIGFSCSK	KPLEVRCSSG	NTRYTKQRGA
51	FTSLKECAIS	LALSVGLMVS	VPSIALPPNA	HAVANPVIPD	VSVLISGPPI
101	KDPEALLRYA	LPIDNKAIRE	VQKPLEDITD	SLKIAGVKAL	DSVERNVRQA
151	SRTLQQGKSI	IVAGFAESKK	DHGNEMIEKL	EAGMQDMLKI	VEDRKRDAVA
201	PKQKEILKYV	GGIEEDMVDG	FPYEVPEEYR	NMPLLKGRAS	VDMKVKIKDN
251	PNIEDCVFRI	VLDGYNAPVT	AGNFVDLVER	HFYDGMEIQR	SDGFVVQTGD
301	PEGPAEGFID	PSTERTRTVP	LEIMVTGEKT	PFYGSTLEEL	GLYKAQVVIP
351	FNAFGTMAMA	REEFENDSGS	SQVFWLLKES	ELTPSNSNIL	DGRYAVFGYV
401	TDNEDFLADL	KVGDVIESIQ	VVSGLENLAN	PSYKIAG	

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta Mi	SS	Sequence				
291 - 315	860.4586	2578.3539	2578.1711	0.1827	0	R.SDGFVVQTGDPEGPAEGFIDE	STEK.T	(Ions	score	46
379 - 393	816.4624	1630.9103	1630.7798	0.1305	0	K.ESELTPSNSNILDGR.Y (]	lons scor	<u>e 80</u>)		

gi|405131 Cyclophilin

Protein View

Match to: gi|405131 Score: 116
cyclophilin
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2222.wiff

Nominal mass (M_r) : 28532; Calculated pI value: 8.83 NCBI BLAST search of <u>gi[405131</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 12%
```

Matched peptides shown in Bold Red

1 MASSSSMQMV HTSRSIAQIG FGVKSQLVSA NRTTQSVCFG ARSSGIALSS 51 RLHYASPIKQ FSGVYATTKH QRTACVKSMA AEEEEVIEPQ AKVTNKVYFD 101 VEIGGEVAGR IVMGLFGEVV PKTVENFRAL CTGEKKYGYK GSSFHRIIKD 151 FMIQGGDFTE GNGTGGISIY GAKFEDENFT LKHTGPGILS MANAGPNTNG 201 SQFFICTVKT SWLDNKHVVF GQVIEGMKLV RTLESQETRA FDVPKKGCRI 251 YACGELPLDA

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
150 - 173	818.1597	2451.4574	2451.0900	0.3674	0	K.DFMIQGGDFTEGNGTGGISIYGAK.F Deamidated (NQ); Oxidation (M) (Ions score 74)
174 - 182	571.8838	1141.7530	1141.5291	0.2239	0	K.FEDENFTLK.H (Ions score 41)

gi|15218090 Mitochondrial processing peptidase alpha subunit, putative

Match to: gi | 15218090 Score: 302 mitochondrial processing peptidase alpha subunit, putative [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1102NOV15.wiff

Nominal mass (M_): 54539; Calculated pI value: 5.94 NCBI BLAST search of gi 15218090 against nr Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 10%

Matched peptides shown in Bold Red

1	MYRTAASRAR	ALKGVLTRSL	RPARYASSSA	VAETSSSTPA	YLSWLSGGSR
51	AALTSLDMPL	QGVSLPPPLA	DKVEPSKLQI	TTLPNGLKIA	SETTPNPAAS
101	IGLYVDCGSI	YEAPYFHGAT	HLLERMAFKS	TLNRTHFRLV	REIEAIGGNT
151	SASASREQMS	YTIDALKTYV	PEMVEVLIDS	VRNPAFLDWE	VNEELRKMKV
201	EIAELAKNPM	GFLLEAIHSA	GYSGPLASPL	YAPESALDRL	NGELLEEFMT
251	ENFTAARMVL	AASGVEHEEL	LKVAEPLTSD	LPNVPPQLAP	KSQYVGGDFR
301	QHTGGEATHF	AVAFEVPGWN	NEKEAVTATV	LQMLMGGGGS	FSAGGPGKGM
351	HSWLYRRVLN	EYQEVQSCTA	FTSIFNDTGL	FGIYGCSSPQ	FAAKAIELAA
401	KELKDVAGGK	VNQAHLDRAK	AATKSAVLMN	LESRMIAAED	IGRQILTYGE
451	R KPVDQFLKS	VDQLTLKDIA	DFTSKVISKP	LTMGSFGDVL	AVPSYDTISS
501	KFR				

Show predicted peptides also

Sort Peptides By

Start	; -	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
142	- 1	156	731.8974	1461.7802	1461.7059	0.0742	0	R.EIEAIGGNTSASASR.E (Ions score 84)
157	-	167	657.8490	1313.6834	1313.6173	0.0661	0	R.EQMSYTIDALK.T Oxidation (M) (Ions score 60)
425	j —	434	560.3282	1118.6418	1118.5754	0.0664	0	K.SAVLMNLESR.M (Ions score 57)
425	j —	434	568.3238	1134.6331	1134.5703	0.0628	0	K.SAVLMNLESR.M Oxidation (M) (Ions score 64)
435	j —	443	496.2815	990.5485	990.4804	0.0681	0	R.MIAAEDIGR.Q Oxidation (M) (Ions score 52)
444	- 1	451	490.3031	978.5916	978.5134	0.0782	0	R.QILTYGER.K (Ions score 43)

gi|38154485 Molecular chaperone Hsp90-2

Protein View

Match to: gi|38154485 Score: 145
molecular chaperone Hsp90-2 [Nicotiana benthamiana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\389NOV15.wiff

Nominal mass (M_r): 80430; Calculated pI value: 4.98 NCBI BLAST search of <u>gi|38154485</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Nicotiana benthamiana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1	MAEAETFAFQ	AEINQLLSLI	INTFYSNKEI	FLRELISNSS	DALDKIRFES
51	LTDKSKLDAQ	PELFIHIIPD	KTNNTLTIID	SGIGMTKADL	VNNLGTIARS
101	GTKEFMEALA	AGADVSMIGQ	FGVGFYSAYL	VAERVVVTTK	HNDDEQYVWE
151	SQAGGSFTVT	RDTSGENLGR	GTKITLFLKE	DQLEYLEERR	LKDLVKKHSE
201	FISYPISLWV	EKTIEKEISD	DEDEEEKKDE	EGKVGEVDEE	KEKEEKKKKK
251	IKEVSNEWSL	VNKQKPIWMR	KPEEITKEEY	AAFYKSLTND	WEEHLAVKHF
301	SVEGQLEFKA	VLFVPKRAPF	DLFDTKKKPN	NIKLYVRRVF	IMDNCEELIP
351	EYLSFVKGIV	DSEDLPLNIS	REMLQQNKIL	KVIRKNLVKK	CIELFFEIAE
401	NKEDYDKFYE	AFSKNLKLGI	HEDSQNRSKF	AELLRYHSTK	SGDEMTSLKD
451	YVTRMKEGQN	DIYYITGESK	KAVENSPFLE	KLKKKGYEVL	YMVDAIDEYS
501	VGQLKEFEGK	KLVSATKEGL	KLDESEDEKK	KHEELKEKFE	GLCKVIKDVL
551	GDKVEKVVVS	DRVVDSPCCL	VTGEYGWTAN	MERIMKAQAL	RDTSMAGYMS
601	SKKTMEINPE	NAIMEELRKR	ADADKNDKSV	KDLVLLLFET	ALLTSGFSLD
651	EPNTFGNRIH	RMLKLGLSID	EDCGDAEADM	PPLEDPEADA	EGSKMEEVD

Show predicted peptides also

Sort Peptides By
 • Residue Number Increasing Mass
 • Decreasing Mass
 • Decreasing Mass
 • Delta Miss Sequence
 • Observed Mr(expt) Mr(calc)
 • Delta Miss Sequence
 • 0.0496
 • 0 R.ELISNSSDALDK.I (Ions score 73)
 • 189
 • 662.3333
 • 1322.6521
 • 1322.5990
 • 0.0531
 • K.EDQLEYLEER.R (Ions score 72)
 • Oken vectors
 • O

gi|15222729 Chaperonin 60 beta (CPN60B)

Protein View

Match to: gi|15222729 Score: 185 CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding / unfolded protein binding [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\712NOV15.wiff

Nominal mass (M_r): 64169; Calculated pI value: 6.21 NCBI BLAST search of <u>gi|15222729</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 8%

Matched peptides shown in Bold Red

1	MASTFTATSS	IGSMVAPNGH	KSDKKLISKL	SSSSFGRRQS	VCPRPRRSSS
51	AIVCAAKELH	FNKDGTTIRR	LQAGVNK LAD	LVGVTLGPKG	RNVVLESKYG
101	SPRIVNDGVT	VAREVELEDP	VENIGAKLVR	QAAAKTNDLA	GDGTTTSVVL
151	AQGFIAEGVK	VVAAGANPVL	ITRGIEKTAK	ALVTELKKMS	KEVEDSELAD
201	VAAVSAGNND	EIGNMIAEAM	SKVGRKGVVT	LEEGKSAENN	LYVVEGMQFD
251	RGYISPYFVT	DSEKMSVEFD	NCKTTTADKK	ITNARDLVGV	LEDAIRGGYP
301	ILIIAEDIEQ	EALATLVVNK	LRGTLKIAAL	RAPGFGERKS	QYLDDIAILT
351	GATVIREEVG	LSLDKAGKEV	LGNASKVVLT	KETSTIVGDG	STQDAVKKRV
401	TQIKNLIEQA	EQDYEKEKLN	ERIAKLSGGV	AVIQVGAQTE	TELKEKKLRV
451	EDALNATKAA	VEEGIVVGGG	CTLLRLASKV	DAIKATLDND	EEKVGADIVK
501	RALSYPLKLI	AKNAGVNGSV	VSEKVLSNDN	VKFGYNAATG	KYEDLMAAGI
551	IDPTKVVRCC	LEHAASVAKT	FLMSDCVVVE	IKEPEPVPVG	NPMDNSGYGY
601					

Show predicted peptides also

Sort Peptides By	Resid	ue Number (Increasing Mass	Oecrea	sing Ma	SS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
78 - 89	591.8794	1181.7442	1181.7020	0.0422	0	K.LADLVGVTLGPK.G (Ions score 50)
114 - 127	771.4247	1540.8348	1540.7620	0.0727	0	R.EVELEDPVENIGAK.L (Ions score 37)
357 - 365	495.2876	988.5606	988.5077	0.0529	0	R.EEVGLSLDK.A (Ions score 54)
382 - 398	579.3163	1734.9272	1734.8636	0.0636	1	K.ETSTIVGDGSTQDAVKK.R (Ions score 43)

gi|2511578 20S proteasome beta subunit; multicatalytic endopeptidase

Protein View

Match to: gi|2511578 Score: 179
multicatalytic endopeptidase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2119.wiff

Nominal mass (M_r) : 29847; Calculated pI value: 6.66 NCBI BLAST search of <u>gi|2511578</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%
```

Matched peptides shown in Bold Red

1 MSQSTVDVPP KGGFSFDLCK RNDMLTPKGL KAPSFLKTGT TIVGLIFKDG 51 VILGADTRAT EGPIVADKNC EKIHYMAPNI YCCGAGTAAD TEAVTDMVSS 101 QLRLHRYQTG RDSRVITALT LLKKHLFSYQ GHVSAALVLG GVDITGPHLH 151 TIYPHGSTDT LPFATMGSGS LAAMSVFEAK YKEGLTRDEG IKLVAESICS 201 GIFNDLGSGS NVDICVITKG NKEYLRNYME PNPRTYVSSK GYSFTKKTEV 251 LLTKITPLLE RVEITEVGEA MEE

l	Sort Peptides By	Resident of the second seco	tue Number (Increasing Mass	Decrea	sing Ma	SS		
	Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence		
	49 - 58	508.8807	1015.7468	1015.5298	0.2170	0	K.DGVILGADTR.A	(Ions score 40)	
	59 - 68	500.8666	999.7186	999.5237	0.1949	0	R.ATEGPIVADK.N	(Ions score 71)	
	115 - 123	486.4262	970.8378	970.6427	0.1951	0	R.VITALTLLK.K	(Ions score 39)	
	262 - 273	676.4117	1350.8089	1350.5861	0.2228	0	R.VEITEVGEAMEE.	- Oxidation (M)	(Ions score 29)

gi|3421087 20S proteasome subunit PAE1

Protein View

Match to: gi|3421087 Score: 61
20S proteasome subunit PAE1 [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2315DEC04.wiff

Nominal mass (M_r) : 26102; Calculated pI value: 4.70 NCBI BLAST search of <u>gi|3421087</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%
```

Matched peptides shown in Bold Red

1 MFLTRTEYDR GVNTFSPEGR LFQVEYAIEA IKLGSTAIGV KTKEGVVLAV 51 EKRITSPLLE PSSVEKIMEI DDHIGCAMSG LIADARTLVE HARVETQNHR 101 FSYGEPMTVE STTQALCDLA LRFGEGEEES MSRPFGVSLL IAGHDENGPS 151 LYYTDPSGTF WQCNAKAIGS GSEGADSSLQ EQFNKDLSLQ EAETIAVSIL 201 KQVMEEKVTP NNVDIAKVAP AYHLYTPQEV EAVIARL

Sort Peptides By	Resid	lueNumber	Increasing Mass	Decrea	sing Ma	155
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
54 - 66	700.5512	1399.0879	1398.7606	0.3273	0	R.ITSPLLEPSSVEK.I (Ions score 51)
167 - 185	963.1168	1924.2191	1923.8810	0.3381	0	K.AIGSGSEGADSSLQEQFNK.D (Ions score 10)
gi|166830 Proteasome

Protein View

Match to: gi|166830 Score: 243 proteasome Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1944.wiff

Nominal mass (M_r) : 30685; Calculated pI value: 4.99 NCBI BLAST search of <u>gi|166830</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 19%
```

Matched peptides shown in Bold Red

1 MFRNQYDTDV TTWSPTGRLF QVEYAMEAVK QGSAAIGLRS RSHVVLACVN 51 KAQSELSSHQ RKIFKVDDHI GVAIAGLTAD GRVLSRYMRS ESINHSFTYE 101 SPLPVGRLVV HLADKAQVCT QRSWKRPYGV GLLVGGLDES GAHLYYNCPS 151 GNYFEYQAFA IGSRSQAAKT YLERRFESFG DSSREDLIKD AILAVRETLQ 201 GETLKSSLCT VAILGVDEPF HFLDQEAIQK VIDTFEKVPE EEEGEGEAGE 251 GEAEAAEAAF AERGGGVAGD QDVAPMEM

	Sort Peptides By	Resid	tue Number (Increasing Mass	ODecrea	sing Ma	ISS
st	tart - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
	4 - 18	871.0187	1740.0228	1739.7751	0.2477	0	R.NQYDTDVTTWSPTGR.L (Ions score 61)
	19 - 30	714.4790	1426.9435	1426.7166	0.2269	0	R.LFQVEYAMEAVK.Q (Ions score 46)
	19 - 30	722.4839	1442.9532	1442.7115	0.2417	0	R.LFQVEYAMEAVK.Q Oxidation (M) (Ions score 40)
	66 - 82	560.7403	1679.1992	1678.8639	0.3353	0	K.VDDHIGVAIAGLTADGR.V (Ions score 80)
	197 - 205	509.8781	1017.7417	1017.5342	0.2074	0	R.ETLQGETLK.S (Ions score 56)

gi|22331799 ATPDIL1-3 (PDI-LIKE 1-3); thiol-disulfide exchange intermediate

Match to: gi|22331799 Score: 135
ATPDIL1-3 (PDI-LIKE 1-3); thiol-disulfide exchange intermediate [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\333NOV15.wiff

Nominal mass (M_r): 64400; Calculated pI value: 4.74 NCBI BLAST search of <u>gi|22331799</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|18072841</u> from <u>Arabidopsis thaliana</u> <u>gi|20260432</u> from <u>Arabidopsis thaliana</u> gi|23197928 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1	MASSSTSISL	LLFVSFILLL	VNSRAENASS	GSDLDEELAF	LAAEESKEQS
51	HGGGSYHEEE	HDHQHRDFEN	YDDLEQGGGE	FHHGDHGYEE	EPLPPVDEKD
101	VAVLTKDNFT	EFVGNNSFAM	VEFYAPWCGA	CQALTPEYAA	AATELKGLAA
151	LAKIDATEEG	DLAQKYEIQG	FPTVFLFVDG	EMRKTYEGER	TKDGIVTWLK
201	KKASPSIHNI	TTKEEAERVL	SAEPKLVFGF	LNSLVGSESE	ELAAASRLED
251	DLSFYQTASP	DIAKLFEIET	QVKRPALVLL	KKEEEKLARF	DGNFTKTAIA
301	EFVSANKVPL	VINFTREGAS	LIFESSVKNQ	LILFAKANES	EKHLPTLREV
351	AKSFKGKFVF	VYVQMDNEDY	GEAVSGFFGV	TGAAPKVLVY	TGNEDMRKFI
401	LDGELTVNNI	KTLAEDFLAD	K LKPFYKSDP	LPENNDGDVK	VIVGNNFDEI
451	VLDESKDVLL	EIYAPWCGHC	QSFEPIYNKL	GKYLKGIDSL	VVAKMDGTSN
501	EHPRAKADGF	PTILFFPGGN	KSFDPIAVDV	DRTVVELYKF	LKKHASIPFK
551	LEKPATPEPV	ISTMKSDEKI	EGDSSKDEL		

Show predicted peptides also

 Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass
 Start - End
 Observed
 Mr(expt)
 Mr(calc)
 Delta
 Miss
 Sequence
 154 - 165
 645.3376
 1288.6606
 1288.6147
 0.0459
 K.IDATEEGDLAQK.Y
 (Ions score 72)
 412 - 421
 561.8191
 1121.6236
 1121.5604
 0.0631
 K.TLAEDFLADK.L
 (Ions score 64)

gi|219687002 Daikon cysteine protease RD21

Protein View

Match to: gi|219687002 Score: 218
daikon cysteine protease RD21 [Raphanus sativus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1767NOV26.wiff

Nominal mass (M_r) : 32085; Calculated pI value: 4.57 NCBI BLAST search of <u>gi|219687002</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Raphanus sativus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%
```

Matched peptides shown in Bold Red

1	DAIPESVDWR	KEGAVAAVKD	QGSCGSCWAF	STIGAVEGIN	KIVTGDLISL
51	SEQELVDCDT	SYNQGCNGGL	MDYAFEFIIK	NGGIDTEEDY	PYK AADGRCD
101	QNRKNAK VVT	IDAYEDVPEN	NEAALKKALA	NQPISVAIEA	GGRAFQLYSS
151	GVFDGTCGTE	LDHGVVAVGY	GTENGKDYWI	VRNSWGGSWG	ESGYIKMARN
201	IAEATGKCGI	AMEASYPIKK	GQNPPQPGPS	PPSPIKPPTQ	CDKYYSCPEG
251	NTCCCLFKYG	KYCFGWGCCP	LEAATCCDDN	TSCCPHEYP	

Sort Peptides By Residue Number Increasing Mass 				Decrea	sing Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
81 - 93	750.8949	1499.7752	1499.6416	0.1336	0	K.NGGIDTEEDYPYK.A (Ions score 74)
81 - 93	751.3842	1500.7539	1500.6256	0.1283	0	K.NGGIDTEEDYPYK.A Deamidated (NQ) (Ions score 61)
108 - 126	697.4237	2089.2493	2089.0215	0.2278	0	K.VVTIDAYEDVPENNEAALK.K (Ions score 56)
128 - 143	783.9479	1565.8813	1565.8525	0.0288	0	K.ALANQPISVAIEAGGR.A (Ions score 15)
128 - 143	784.0104	1566.0063	1565.8525	0.1538	0	K.ALANQPISVAIEAGGR.A (Ions score 89)

gi|13124444 Phospholipase D alpha 1 (PLD1)

Match to: gi|13124444 Score: 270
RecName: Full=Phospholipase D alpha 1; Short=PLD 1; AltName: Full=Choline phosphatase 1
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\322NOV15.wiff

Nominal mass (M_r) : 92236; Calculated pI value: 5.52 NCBI BLAST search of <u>gi|13124444</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica oleracea var. capitata

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 7%

Matched peptides shown in Bold Red

1	MAQHLLHGTL	HATIYEVDDL	HTGGLRSGFF	GKILANVEET	IGVGKGETQL
51	YATIDLQRAR	VGRTRKIKDE	AKNPKWYESF	HIYCAHLASD	IIFTVKDDNP
101	IGATLIGRAY	VPVDQVIHGE	EVDQWVEILD	NDRNPIHGGS	KIHVKLQYFG
151	VEADRNWNQG	IKSAKFPGVP	YTFFSQRQGC	KVSLYQDAHI	PDNFVPRIPL
201	AGGKNYEPQR	CWEDIFDAIS	NAQHMIYITG	WSVYTEIALV	RDSRRPKPGG
251	DVTVGELLKK	KASEGVRVLL	LVWDDRTSVD	VLKKDGLMAT	HDEETENFFR
301	GSDVHCILCP	RNPDDGGSIV	QNLQVSAMFT	HHQKIVVVDS	EMPSRGGSQM
351	RRIVSFVGGI	DLCDGRYDTP	FHSLFRTLDT	VHHDDFHQPN	FTGAAITKGG
401	PREPWHDIHS	RLEGPIAWDV	LYNFEQRWSK	QGGKDILVKL	RELSDIIITP
451	SPVMFQEDHD	VWNVQLFRSI	DGGAAAGFPE	SPEAAAEAGL	VSGKDNIIDR
501	SIQDAYIHAI	RRAKDFIYIE	NQYFLGSSFA	WAADGITPED	INALHLIPKE
551	LSLKIVSKIE	KGEKFRVYVV	VPMWPEGLPE	SASVQAILDW	QRRTMQMMYK
601	DIVQALRAQG	LEEDPRNYLT	FFCLGNREVK	KEGEYEPAER	PDADSSYMKA
651	QEARRFMIYV	HTKMMIVDDE	YIIIGSANIN	QRSMDGARDS	EIAMGGYQPH
701	HLSHRQPARG	QIHGFRMSLW	YEHLGMLDET	FLDPSSVECI	EKVNRISDKY
751	WDLYSSESLE	HDLPGHLLRY	PVDVDGEGDV	TEFPGFEFFP	DTKARILGTK
801	SDYLPPILTT				

Sort Peptides By	Resid	lueNumber) Increasing Mass	Decrea	sing Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
97 - 108	621.3648	1240.7150	1240.6412	0.0738	0	K.DDNPIGATLIGR.A (Ions score 80)
146 - 155	599.3311	1196.6476	1196.5826	0.0650	0	K.LQYFGVEADR.N (Ions score 82)
469 - 494	787.0882	2358.2429	2358.1339	0.1090	0	R.SIDGGAAAGFPESPEAAAEAGLVSGK.D (Ions score 73)
801 - 810	560.3387	1118.6629	1118.5859	0.0769	0	K.SDYLPPILTT (Ions score 35)

gi|30690210 Arabidopsis thaliana MAP kinase 12 (ATMPK12); MAP kinase

Protein View

Match to: gi|30690210 Score: 131
ATMPK12 (Arabidopsis thaliana MAP kinase 12); MAP kinase/ kinase
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1193NOV15.wiff

Nominal mass (M_r): 42904; Calculated pI value: 8.05 NCBI BLAST search of <u>gi|30690210</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|75151485</u> from <u>Arabidopsis thaliana</u> <u>gi|26449987</u> from <u>Arabidopsis thaliana</u> <u>gi|90093312</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 7%

Matched peptides shown in Bold Red

1 MSGESSSGST EHCIKVVPTH GGRYVQYNVY GQLFEVSRKY VPPIRPIGRG 51 ACGIVCAAVN SVTGEKVAIK KIGNAFDNII DAKRTLREIK LLRHMDHENV 101 ITIKDIVRPP QRDIFNDVYI VYELMDTDLQ RILRSNQTLT SDQCRFLVYQ 151 LLRGLKYVHS ANILHRDLRP SNVLLNSKNE LKIGDFGLAR TTSDTDFMTE 201 YVVTRWYRAP ELLLNCSEYT AAIDIWSVGC ILGEIMTGQP LFPGKDYVHQ 251 LRLITELVGS PDNSSLGFLR SDNARRYVRQ LPRYPKQQFA ARFPKMPTTA 301 IDLLERMLVF DPNRRISVDE ALGHAYLSPH HDVAKEPVCS TPFSFDFEHP 351 SCTEEHIKEL IYKESVKFNP DH

Sort Pe	eptides By	Resid	lueNumber) Increasing Mass	Decrease	sing Ma	SS	
Start -	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
72 -	83	645.8593	1289.7041	1289.6615	0.0425	0	K.IGNAFDNIIDAK.R (Ions score 72)	
191 -	205	891.4123	1780.8100	1780.7826	0.0274	0	R.TTSDTDFMTEYVVTR.W Oxidation (M) (Ions se	<u>core 59</u>)

gi|395072 Guanine nucleotide regulatory protein (Ran2)

Protein View

```
Match to: gi|395072 Score: 89
guanine nucleotide regulatory protein [Vicia faba]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1944.wiff
Nominal mass (M<sub>x</sub>): 25616; Calculated pI value: 6.39
NCBI BLAST search of <u>gi|395072</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
Taxonomy: <u>Vicia faba</u>
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%
Matched peptides shown in Bold Red
```

1 MALPNQQTVD YPSFKLVIVG DGGTGKTTFV KRHLTGEFEK KYEPTIGVEV 51 HPLDFFTNCG KIRFYCWDTA GQEKFGGLRD GYYIHGQCAI IMFDVTARLT 101 YKNVPTWHRD LCRVCENIPI VLCGNKVDVK NRQVKAKQVT FHRKKNLQYY 151 EISAKSNYNF EKPFLYLARK LAGDANLHFV ESPALAPPEV QIDIALQQRH 201 ENEILEAANQ PLPDDDDDAF E

Sort Peptides By	Resid	Residue Number O Increasing Mass			sing Ma		
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
16 - 26	508.3974	1014.7803	1014.5710	0.2093	0	K.LVIVGDGGTGK.T	(Ions score 62)
146 - 155	614.9276	1227.8407	1227.6135	0.2272	0	K.NLQYYEISAK.S	(Ions score 28)

gi|159462486 Predicted protein, containing calcium binding motif Protein View

```
Match to: gi|159462486 Score: 67
predicted protein [Chlamydomonas reinhardtii]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\153NOV15.wiff
```

```
Nominal mass (M_r): 36689; Calculated pI value: 8.61
NCBI BLAST search of <u>gi|159462486</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

```
Taxonomy: <u>Chlamydomonas reinhardtii</u>
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi[158283461 from Chlamydomonas reinhardtii
```

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%
```

Matched peptides shown in Bold Red

1	MQLARTLNFG	ARPRAISQRA	CIAPARIRTR	VVRCRADGKE	TDSKTDSKKL
51	DSLLDELQKS	GVDSKKAQAV	LKKWKELGVE	DSEQLRKLLV	KRSLRPAGIV
101	AFQAALDGLA	CWGGFYTSGL	IADSPPFTGQ	FPLQLLASFF	GFYYVLQGLL
151	NLSVASTLAF	TAYKYGTNSV	ELLAAVQQLA	GPATGLNVLD	RAQVGRGVNT
201	LKVLQTLDEI	AELLKNMSFA	SSQRSTLQNL	SAYLQLSHAR	ETLGFDPARY
251	GLTAAEAGEI	AYVFSCYDKN	EDYRLELSEV	KR LCQDLGKE	LSDEEYKEAL
301	RLLDTSKNGF	VEFDEFCAWW	TKSKGAATTA		

Show predicted peptides also

Sort Peptides By	Residue	e Number 🔘 I	Increasing Mass	Oecreas	ing Ma	SS	
Start - End (275 - 282 4	Observed 487.3028	Mr(expt) 972.5910	Mr(calc) 972.5604	Delta 0.0307	Miss 1	Sequence R.LELSEVKR.L	(<u>Ions score 67</u>)
275 - 282 4	487.3028	972.5910	972.5604	0.0307	1	R.LELSEVKR.L	(Ions score 67)

gi|1063415 Potassium channel protein

Protein View

Match to: gi|1063415 Score: 62 K+ channel protein Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1771NOV17.wiff

Nominal mass (M_r): 36596; Calculated pI value: 8.22 NCBI BLAST search of <u>gi|1063415</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 3%

Matched peptides shown in Bold Red

1 MQYKNLGKSG LKVSTLSFGA WVTFGNQLDV KEAKSILQCC RDHGVNFFDN 51 AEVYANGRAE EIMGQAIREL GWRRSDIVIS TKIFWGGPGP NDKGLSRKHI 101 VEGTKASLKR LDMDYVDVLY CHRPDASTPI EEAVRAMNYV IDKGWAFYWG 151 ISEWSAQQIT EAWGAADRLD LVGPIVEQPE YNMFARHKVE TEFLPLYTNH 201 GIGLTTWSPL ASGVLTGKYN KGAIPSDSRF ALENYKNLAN RSLVDDVLRK 251 VSGLKPIAGE LGVTLAQLAI AWCASNPNVS SVITGATRGS QIQENMKAVD 301 VIPLLTPIVL DKIEQVIQSK PKRPESYR

Show predicted peptides also

 Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

 Start - End Observed Mr(expt) Mr(calc)
 Delta Miss Sequence
 59 - 68
 567.3452
 1132.6758
 1132.5546
 1122
 R.AEEIMGQAIR.E
 Oxidation (M) (Ions score 62)

 Increasing Mass

Peptide View

MS/MS Fragmentation of **AEEIMGQAIR** Found in **gi**|1063415, K+ channel protein

#	b	b ⁺⁺	b*	b* ⁺⁺	ь ⁰	b ⁰⁺⁺	Seq.	у	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					Α							10
2	201.0870	101.0471			183.0764	92.0418	E	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	9
3	330.1296	165.5684			312.1190	156.5631	E	869.4839	435.2456	852.4574	426.7323	851.4734	426.2403	8
4	443.2136	222.1105			425.2031	213.1052	Ι	740.4414	370.7243	723.4148	362.2110			7
5	526.2508	263.6290			508.2402	254.6237	Μ	627.3573	314.1823	610.3307	305.6690			6
6	583.2722	292.1397			565.2617	283.1345	G	544.3202	272.6637	527.2936	264.1504			5
7	711.3308	356.1690	694.3043	347.6558	693.3202	347.1638	Q	487.2987	244.1530	470.2722	235.6397			4
8	782.3679	391.6876	765.3414	383.1743	764.3573	382.6823	Α	359.2401	180.1237	342.2136	171.6104			3
9	895.4520	448.2296	878.4254	439.7164	877.4414	439.2243	Ι	288.2030	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1

gi|123656 Chloroplast envelope membrane 70 kDa heat shock-related protein

Match to: gi|123656 Score: 65 RecName: Full=Chloroplast envelope membrane 70 kDa heat shock-related protein Found in search of C:\QStar Share Data\20091115MMZ\NOV15\478NOV15.wiff

Nominal mass (M_r): 72143; Calculated pI value: 5.34 NCBI BLAST search of <u>gi|123656</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Spinacia oleracea</u> Links to retrieve other entries containing this sequence from NCBI Entrez: gi|21338 from Spinacia oleracea

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 1%

Matched peptides shown in Bold Red

1	MAGKGEGPAI	GIDLGTTYSR	VGVWQHDRVE	IIANDQGNRT	TPSYVAFTDS
51	ERLIGDAAKN	QVAMNPINTV	FDAKRLIGRR	FSDASVQADM	KHRPFKVVSG
101	PGEKPMIGVN	YKGEEKQFAA	EEISSMVLTK	MKEIAEAYLG	STVKNAVVTV
151	PAYFNDSQRQ	ATKDAGVISG	LNVMRIINEP	TAAAIAYGLD	KKATSVGEKN
201	VLIFDLGGGT	FDVSLLTIEE	GIFEVKATAG	DTHLGGEDFD	NRMVNHSLQE
251	FKRKNKKDIM	ETPGHIRRLR	TACERAKRTL	SSTAQTTIEI	DSLYEGVDFY
301	SPITRARFEE	LNIDLFRKCM	EPVEKCLRDA	KMDKSTVHDV	VLVGGSTRIP
351	KVQQLLQDFF	NGKELCKSIN	PDEAVAYGAA	VQAAILSGEG	NEKVQDLLLL
401	DVTPLSLGLE	TAGGVMTVLI	PRNTTIPTKK	EQVFSTYSDN	QPGVLIQVYE
451	GERTRTRDNN	LLGKFELSGI	PPGPRGVPQI	NVCFDIDANG	ILNVSAEDKT
501	TGQKNKIRIT	NDKGRLSKEE	IEKMVQEAEK	YKSEDEEHKK	KVESKNALEN
551	YAYNMRNIVK	DEKIGAKLSE	ADKKKIEEAI	DASIQWLDGN	QLAEADEFDD
601	KMKELESICN	PIIAKMYQGA	GGDMGGGMED	EGPTSGGGAG	PKIEECRLSC
651	HFF				

Show predicted peptides also

Sort Peptides By OResidue Number OIncreasing Mass ODecreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence	
40 - 52	737.3904	1472.7663	1472.6783	0.0879	0 R.TTPSYVAFTDSER.L	(Ions score 65)

Peptide View

MS/MS Fragmentation of TTPSYVAFTDSER

Found in gi|123656, RecName: Full=Chloroplast envelope membrane 70 kDa heat shock-related protein

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	у	y++	y*	y*++	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	Τ							13
2	203.1026	102.0550	185.0921	93.0497	Τ	1372.6379	686.8226	1355.6114	678.3093	1354.6274	677.8173	12
3	300.1554	150.5813	282.1448	141.5761	P	1271.5903	636.2988	1254.5637	627.7855	1253.5797	627.2935	11
4	387.1874	194.0974	369.1769	185.0921	S	1174.5375	587.7724	1157.5109	579.2591	1156.5269	578.7671	10
5	550.2508	275.6290	532.2402	266.6237	Y	1087.5055	544.2564	1070.4789	535.7431	1069.4949	535.2511	9
6	649.3192	325.1632	631.3086	316.1579	V	924.4421	462.7247	907.4156	454.2114	906.4316	453.7194	8
7	720.3563	360.6818	702.3457	351.6765	A	825.3737	413.1905	808.3472	404.6772	807.3632	404.1852	7
8	867.4247	434.2160	849.4141	425.2107	F	754.3366	377.6719	737.3101	369.1587	736.3260	368.6667	6
9	968.4724	484.7398	950.4618	475.7345	T	607.2682	304.1377	590.2416	295.6245	589.2576	295.1325	5
10	1083.4993	542.2533	1065.4888	533.2480	D	506.2205	253.6139	489.1940	245.1006	488.2100	244.6086	4
11	1170.5313	585.7693	1152.5208	576.7640	S	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
12	1299.5739	650.2906	1281.5634	641.2853	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13					R	175.1190	88.0631	158.0924	79.5498			1

gi|14596025 P-Protein - like protein

```
Match to: gi|14596025 Score: 69
P-Protein - like protein [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\158NOV16.wiff
```

```
Nominal mass (M_r): 113852; Calculated pI value: 6.51
NCBI BLAST search of <u>gi|14596025</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 1%

Matched peptides shown in Bold Red

1	MERARRLAYR	GIVKRLVNDT	KRHRNAETPH	LVPHAPARYV	SSLSPFISTP
51	RSVNHTAAFG	RHQQTRSISV	DAVKPSDTFP	RRHNSATPDE	QTHMAKFCGF
101	DHIDSLIDAT	VPKSIRLDSM	KFSKFDAGLT	ESQMIQHMVD	LASKNKVFKS
151	FIGMGYYNTH	VPTVILRNIM	ENPAWYTQYT	PYQAEISQGR	LESLLNFQTV
201	ITDLTGLPMS	NASLLDEGTA	AAEAMAMCNN	ILKGKKKTFV	IASNCHPQTI
251	DVCKTRADGF	DLKVVTSDLK	DIDYSSGDVC	GVLVQYPGTE	GEVLDYAEFV
301	KNAHANGVKV	VMATDLLALT	VLKPPGEFGA	DIVVGSAQRF	GVPMGYGGPH
351	AAFLATSQEY	KRMMPGRIIG	ISVDSSGKQA	LRMAMQTREQ	HIRRDKATSN
401	ICTAQALLAN	MAAMYAVYHG	PAGLKSIAQR	VHGLAGIFSL	GLNKLGVAEV
451	QELPFFDTVK	IKCSDAHAIA	DAASKSEINL	RVVDSTTITA	SFDETTTLDD
501	VDKLFKVFAS	GKPVPFTAES	LAPEVQNSIP	SSLTRESPYL	THPIFNMYHT
551	EHELLRYIHK	LQSKDLSLCH	SMIPLGSCTM	KLNATTEMMP	VTWPSFTDIH
601	PFAPVEQAQG	YQEMFENLGD	LLCTITGFDS	FSLQPNAGAA	GEYAGLMVIR
651	AYHMSRGDHH	RNVCIIPVSA	HGTNPASAAM	CGMKIITVGT	DAKGNINIEE
701	VRKAAEANKD	NLAALMVTYP	STHGVYEEGI	DEICNIIHEN	GGQVYMDGAN
751	MNAQVGLTSP	GFIGADVCHL	NLHKTFCIPH	GGGGPGMGPI	GVKNHLAPFL
801	PSHPVIPTGG	IPQPEKTAPL	GAISAAPWGS	ALILPISYTY	IAMMGSGGLT
851	DASKIAILNA	NYMAKRLEKH	YPVLFRGVNG	TVAHEFIIDL	RGFKNTAGIE
901	PEDVAKRLMD	YGFHGPTMSW	PVPGTLMIEP	TESESKAELD	RFCDALISIR
951	EEIAQIEKGN	ADVQNNVLKG	APHPPSLLMA	DTWKKPYSRE	YAAFPAPWLR
1001	SSKFWPTTGR	VDNVYGDRKL	VCTLLPEEEQ	VTAAVSA	

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence			
951 - 958	480.3021	958.5896	958.4971	0.0925	0	R.EEIAQIEK.G	(Ions	score 3	2)
959 - 969	586.3428	1170.6711	1170.5993	0.0718	0	K. GNADVQNNVLK.	G (I	ons scor	e 38)

gi|223638918 Unnamed protein product, containing pfam00153 domain

Protein View

Match to: gi|223638918 Score: 122
unnamed protein product [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1767NOV26.wiff

Nominal mass (M_r) : 32397; Calculated pI value: 9.35 NCBI BLAST search of <u>gi|223638918</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%
```

Matched peptides shown in Bold Red

1 MAEEKKVAPI GVWNTVKPFV NGGASGMLAT CVIQPIDMIK VRIQLGQGSA 51 VSVTKNMLKN DGIGAFYKGL SAGLLRQATY TTARLGSFKM LTAKAIEAND 101 GKPLPLYQKA LCGLTAGAIG ACVGSPADLA LIRMQADNTL PLAQRRNYTN 151 AFHALYRISA DEGVLALWKG CGPTVVRAMA LNMGMLASYD QSAEYMRDNL 201 GLGETSTVVG ASAVSGFCAA ACSLPFDFVK TQIQKMQPDA QGKYPYTGSL 251 DCAMQTLKSG GPLKFYTGFP VYCVRIAPHV MMTWIFLNQI TKFQKTIGL

Sort Peptides By	Resid	lue Number 🏾	Dincreasing Mass	O Decrease	sing Ma	SS			
Start - End	Observed	Mr(expt)	Mr (calc)	Delta	Miss	Semence			
43 - 55	644.4307	1286.8468	1286.7194	0.1274	0	R. IOLGOGSAVSVTK.N	(Ions scor	e 49)	
134 - 145	687.4158	1372.8171	1372.6769	0.1402	0	R.MQADNTLPLAQR.R	Oxidation (M) (Ions	score 73)

gi|11119229 2-Cys peroxiredoxin

Protein View

```
Match to: gi|11119229 Score: 210
2-Cys peroxiredoxin [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2405.wiff
```

Nominal mass (M_r) : 29708; Calculated pI value: 5.81 NCBI BLAST search of <u>gi|11119229</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 21%
```

Matched peptides shown in Bold Red

1	MASLASTTTL	ISSSSVLLPS	KPSPFSPAAS	FLRTLPSTSV	STSSSLRSCF
51	SSISPLTCIR	SSSRPSFAVK	AQADDLPLVG	NK APDFEAEA	VFDQEFIKVK
101	LSEYIGKKYV	ILFLYPLDFT	FVCPTEITAF	SDRYEEFEKL	NTEVLGVSVD
151	SVFSHLAWVQ	TERKSGGLGD	LNYPLVSDIT	RSISKSFGVL	IPDQGIALRG
201	LFIIDKKKGVI	QHSTINNLGI	GRSVDETMRT	LQALQYVQEN	PDEVCPAGWK
251	PGEKSMKPDP	KLSKEYFSAI			

Show predicted peptides also

Sort Peptides By

Residue Number O Increasing Mass O Decreasing Mass

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
71	-	82	620.9309	1239.8472	1239.6459	0.2013	0	K.AQADDLPLVGNK.A (Ions score 57)
165	-	181	875.0547	1748.0949	1747.8992	0.1957	0	K.SGGLGDLNYPLVSDITK.S (Ions score 71)
186	-	199	743.5368	1485.0591	1484.8351	0.2240	0	K.SFGVLIPDQGIALR.G (Ions score 54)
207	-	222	854.4979	1706.9812	1706.9427	0.0384	1	K.KGVIQHSTINNLGIGR.S Deamidated (NQ) (Ions score 28)

gi|227247694 Unnamed protein product, containing cd03013 domain

Protein View

```
Match to: gi|227247694 Score: 178
unnamed protein product [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2559.wiff
```

```
Nominal mass (M<sub>r</sub>): 21623; Calculated pI value: 8.97
NCBI BLAST search of <u>gi|227247694</u> against nr
Unformatted <u>sequence string</u> for pasting into other applications
```

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 25%
```

Matched peptides shown in Bold Red

1	MAMSILKLRN	SPALRSAASI	ARIGVSSRAF	SKLSEGTDIT	SAAPGVSLQR
51	ARSWDEGVSS	KFSTTPLSDI	FKGKKVVIFG	LPGAYTGVCS	QQHVPSYKSH
L01	MDKFKAKGID	SVICVSVNDP	YTLNGWAEKI	GAKDAIEFYG	DFDGKFHKSL
151	GLDKDLSAAL	LGPRSERWSA	YVEDGKVKAV	NVEEAPSDFK	VTGAEVILGQ
201	I				

Sort Pept	tides By	Residu	e Number 🔘	Increasing Mass	Decrease	sing Ma	SS
Start - E	Ind O	bserved	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
33 - 5	iO 88	87.5647	1773.1148	1772.9156	0.1992	0	K.LSEGTDITSAAPGVSLQK.A (Ions score 31)
62 - 7	2 62	28.4284	1254.8422	1254.6496	0.1926	0	K.FSTTPLSDIFK.G (Ions score 50)
179 - 1	.90 63	53.4255	1304.8365	1304.6248	0.2116	0	K.AVNVEEAPSDFK.V (Ions score 71)
191 - 2	201 53	50.4185	1098.8224	1098.6285	0.1939	0	K.VTGAEVILGQI (Ions score 26)

gi|14764532 Monodehydroascorbate reductase

Match to: gi | 14764532 Score: 410 monodehydroascorbate reductase [Brassica rapa subsp. pekinensis] Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff

Nominal mass (M_): 46604; Calculated pI value: 5.81 NCBI BLAST search of gi|14764532 against nr Unformatted sequence string for pasting into other applications

Taxonomy: Brassica rapa subsp. pekinensis

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 22%

Matched peptides shown in Bold Red

1	MAEKSFKYII	LGGGVSAGYA	AKEFASQGVK	PGELAVISKE	AVAPYERPAL
51	SKGYLFPEGA	ARLPGFHCCV	GSGGEKLLPE	SYK QKGIELI	LSTEIVKADL
101	AAKSLVSAAG	DVFKYETLII	ATGSTVLRLT	DFGVKGADSK	NILYLREIDD
151	ADKVVEAIQA	KKGGKAVVVG	GGYIGLELSA	ALRINNFDVT	MVFPEPWCMP
201	RLFTADIAAF	YETYYTNKGV	KIIKGTVASG	FTAHPNGEVN	EVQLKDGRSL
251	EADIVIVGVG	ARPLTALFKG	QVEEDKGGIK	TDAFFKTSVP	DVYAVGDVAT
301	FPLKMYGDMR	RVEHVDHSRK	SAEQAVKAIK	AAEGGGAVEE	YDYLPFFYSR
351	SFDLSWQFYG	DNVGDSVLFG	DSNPSNPKPR	FGAYWVQDGK	VVGAFMEGGS
401	GDENKALAKV	AKARPAAESL	EDLTKQGISF	AAKI	

Show predicted peptides also

Sort Peptides By

Residue Number
 Increasing Mass
 Decreasing Mass

Stai	rt ·	- End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
- 1	23 -	- 39	587.3593	1759.0562	1758.9516	0.1046	0	K.EFASQGVKPGELAVISK.E (Ions score 51)
4	10 ·	- 52	477.6350	1429.8832	1429.7565	0.1267	0	K.EAVAPYERPALSK.G (Ions score 27)
	53 ·	- 62	540.8152	1079.6158	1079.5400	0.0758	0	K.GYLFPEGAAR.L (Ions score 51)
	17 ·	- 83	425.2817	848.5489	848.4643	0.0846	0	K.LLPESYK.Q (Ions score 37)
10	04 -	- 114	547.3333	1092.6520	1092.5815	0.0705	0	K.SLVSAAGDVFK.Y (Ions score 40)
14	17 ·	- 161	548.6604	1642.9594	1642.8414	0.1181	1	R.EIDDADKVVEAIQAK.K (Ions score 56)
- 38	31 ·	- 390	585.8241	1169.6336	1169.5506	0.0831	0	R.FGAYWVQDGK.V (Ions score 64)
39	91 ·	- 405	748.8657	1495.7168	1495.6613	0.0554	0	K.VVGAFMEGGSGDENK.A (Ions score 75)
39	91 ·	- 405	756.8638	1511.7131	1511.6562	0.0569	0	K.VVGAFMEGGSGDENK.A Oxidation (M) (Ions score 86)

gi|15227987 Low expression of osmotically responsive genes 1 (LOS2)

Match to: gi|15227987 Score: 344 LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1102NOV15.wiff

Nominal mass (M_r) : 47974; Calculated pI value: 5.54 NCBI BLAST search of <u>gi|15227987</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 19%

Matched peptides shown in Bold Red

1	MATITVVKAR	QIFDSRGNPT	VEVDIHTSNG	IKVTAAVPSG	ASTGIYEALE
51	LRDGGSDYLG	KGVSKAVGNV	NNIIGPALIG	K DPTQQTAID	NFMVHELDGT
101	QNEWGWCKQK	LGANAILAVS	LAVCKAGAVV	SGIPLYKHIA	NLAGNPKIVL
151	PVPAFNVING	GSHAGNKLAM	QEFMILPVGA	ASFKEAMKMG	VEVYHHLKSV
201	IKKKYGQDAT	NVGDEGGFAP	NIQENKEGLE	LLKTAIEKAG	YTGKVVIGMD
251	VAASEFYSED	KTYDLNFKEE	NNNGSQKISG	DALKDLYKSF	VAEYPIVSIE
301	DPFDQDDWEH	YAKMTTECGT	EVQIVGDDLL	VTNPKRVAKA	IAEKSCNALL
351	LKVNQIGSVT	ESIEAVKMSK	KAGWGVMTSH	RSGETEDTFI	ADLAVGLSTG
401	QIKTGAPCRS	ERLAKYNQLL	RIEEELGSEA	IYAGVNFRKP	VEPY

Sort	Sort Peptides By Residue Number Increasing Mass 			Decrease Decrease	sing Ma	ISS		
Start	_	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
33	-	52	669.0596	2004.1568	2004.0528	0.1041	0	K.VTAAVPSGASTGIYEALELR.D (Ions score 117)
66	-	81	517.3442	1549.0107	1548.8988	0.1119	0	K.AVGNVNNIIGPALIGK.D (Ions score 44)
126	-	137	587.8679	1173.7213	1173.6758	0.0455	0	K.AGAVVSGIPLYK.H (Ions score 57)
205	-	226	775.3848	2323.1327	2323.0353	0.0974	0	K.YGQDATNVGDEGGFAPNIQENK.E (Ions score 61)
353	-	367	787.4640	1572.9135	1572.8359	0.0776	0	K.VNQIGSVTESIEAVK.M (Ions score 65)

gi|14248550 Plastid-lipid associated protein PAP2

Protein View

Match to: gi|14248550 Score: 61 plastid-lipid associated protein PAP2 [Brassica rapa] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2199DEC04.wiff

Nominal mass (M_r): 34689; Calculated pI value: 4.79 NCBI BLAST search of <u>gi|14248550</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica rapa subsp. campestris

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%
```

Matched peptides shown in Bold Red

1 MATVHSFNQF PCKTRVQCPS NSKPLSKPPS SLVPMSALTR RPSFSPGEFA 51 VSRSDFRVRV IDAEDELDPE TSEGGGSALL MAEEAIESVE ETEVLKRSLV 101 DSLYGTDRGL SASSETRAEI GDLITQLESK NPTPAPTDAL FLLNGKWILA 151 YTSFVGLFPL LSRGIVPLVK VDEISQTIDS DNFTVENSVL FAGPLATTSI 201 STNAKFEIRS PKRVQIKFEE GVIGTPQLTD SIEIPEYVEF LGQKIDLTPI 251 RGLLTSVQDT ATSVARTISS QPPLKFSLPG DSAQSWLLTT YLDKDIRISR 301 GDGGSVFVLI KEGSPLLNP

Show predicted peptides also

Sort Peptides ByIncreasing MassDecreasing MassStart - EndObservedMr(expt)Mr(calc)DeltaMiss Sequence252 - 266760.08481518.15511517.80490.35020R.GLLTSVQDTATSVAR.T(Ions score 61)

Peptide View

MS/MS Fragmentation of GLLTSVQDTATSVAR

Found in gi|14248550, plastid-lipid associated protein PAP2 [Brassica rapa]

#	b	b ⁺⁺	b*	b* ⁺⁺	ь ⁰	b ⁰⁺⁺	Seq.	у	y++	y*	y***	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							15
2	171.1128	86.0600					L	1461.7908	731.3990	1444.7642	722.8857	1443.7802	722.3937	14
3	284.1969	142.6021					L	1348.7067	674.8570	1331.6801	666.3437	1330.6961	665.8517	13
4	385.2445	193.1259			367.2340	184.1206	T	1235.6226	618.3149	1218.5961	609.8017	1217.6121	609.3097	12
5	472.2766	236.6419			454.2660	227.6366	S	1134.5749	567.7911	1117.5484	559.2778	1116.5644	558.7858	11
6	571.3450	286.1761			553.3344	277.1709	V	1047.5429	524.2751	1030.5164	515.7618	1029.5323	515.2698	10
7	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	Q	948.4745	474.7409	931.4480	466.2276	930.4639	465.7356	9
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	D	820.4159	410.7116	803.3894	402.1983	802.4054	401.7063	8
9	915.4782	458.2427	898.4516	449.7295	897.4676	449.2375	T	705.3890	353.1981	688.3624	344.6849	687.3784	344.1928	7
10	986.5153	493.7613	969.4888	485.2480	968.5047	484.7560	A	604.3413	302.6743	587.3148	294.1610	586.3307	293.6690	6
11	1087.5630	544.2851	1070.5364	535.7719	1069.5524	535.2798	T	533.3042	267.1557	516.2776	258.6425	515.2936	258.1504	5
12	1174.5950	587.8011	1157.5685	579.2879	1156.5844	578.7959	S	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
13	1273.6634	637.3354	1256.6369	628.8221	1255.6529	628.3301	V	345.2245	173.1159	328.1979	164.6026			3
14	1344.7005	672.8539	1327.6740	664.3406	1326.6900	663.8486	Α	246.1561	123.5817	229.1295	115.0684			2
15							R	175.1190	88.0631	158.0924	79.5498			1

gi|15241115 Early-responsive to dehydration 8 (HSP81-2)

Match to: gi|15241115 Score: 586 HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP binding [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV15\336NOV15.wiff

Nominal mass (M_r) : 80299; Calculated pI value: 4.95 NCBI BLAST search of <u>gi|15241115</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 15%

Matched peptides shown in Bold Red

1	MADAETFAFQ	AEINQLLSLI	INTFYSNKEI	FLRELISNSS	DALDKIRFES
51	LTDKSKLDGQ	PELFIHIIPD	K TNNTLTIID	SGIGMTKADL	VNNLGTIARS
101	GTKEFMEALA	AGADVSMIGQ	FGVGFYSAYL	VADKVVVTTK	HNDDEQYVWE
151	SQAGGSFTVT	RDTSGETLGR	GTKMVLYLKE	DQLEYLEERR	LKDLVKKHSE
201	FISYPISLWI	EKTIEKEISD	DEEEEEKKDE	EGKVEEVDEE	KEKEEKKKKK
251	IKEVSHEWDL	VNKQKPIWMR	KPEEINK EEY	AAFYKSLSND	WEEHLAVKHF
301	SVEGQLEFKA	ILFVPKRAPF	DLFDTKKKPN	NIKLYVRRVF	IMDNCEDIIP
351	EYLGFVKGIV	DSEDLPLNIS	RETLQQNKIL	KVIRKNLVKK	CLELFFEIAE
401	NKEDYNK FYE	AFSKNLKLGI	HEDSQNRTKI	AELLRYHSTK	SGDELTSLKD
451	YVTRMKEGQN	DIFYITGESK	KAVENSPFLE	K LKKKGIEVL	YMVDAIDEYA
501	IGQLKEFEGK	KLVSATKEGL	KLDETEDEKK	KKEELKEKFE	GLCKVIKDVL
551	GDKVEKVIVS	DRVVDSPCCL	VTGEYGWTAN	MERIMKAQAL	RDSSMAGYMS
601	SKKTMEINPE	NSIMDELRKR	ADADKNDKSV	KDLVLLLFET	ALLTSGFSLD
651	EPNTFGSRIH	RMLKLGLSID	DDDAVEADAE	MPPLEDDADA	EGSKMEEVD

Show predicted peptides also

Sort Peptides By OResidue Number OIncreasing Mass ODecreasing Mass

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
57	-	71	579.0155	1734.0248	1733.9352	0.0896	0	K.LDGQPELFIHIIPDK.T (Ions score 43)
88	-	99	628.8761	1255.7376	1255.6884	0.0492	0	K.ADLVNNLGTIAR.S (Ions score 77)
180	-	189	662.3218	1322.6291	1322.5990	0.0302	0	K.EDQLEYLEER.R (Ions score 74)
278	-	285	510.7756	1019.5367	1019.4600	0.0767	0	K.EEYAAFYK.S (Ions score 37)
318	-	326	527.3013	1052.5881	1052.5179	0.0702	0	R.APFDLFDTK.K (Ions score 50)
358	-	371	764.4354	1526.8563	1526.7940	0.0623	0	K.GIVDSEDLPLNISR.E (Ions score 85)
408	-	414	446.2563	890.4981	890.4174	0.0807	0	K.FYEAFSK.N (Ions score 33)
441	-	449	475.2867	948.5589	948.4764	0.0825	0	K.SGDELTSLK.D (Ions score 74)
457	-	470	800.9120	1599.8094	1599.7417	0.0677	0	K.EGQNDIFYITGESK.K (Ions score 59)
472	-	481	567.3239	1132.6333	1132.5764	0.0569	0	K.AVENSPFLEK.L (Ions score 59)

gi|2655420 Heat shock cognate protein HSC70

Protein View

```
Match to: gi|2655420 Score: 459
heat shock cognate protein HSC70 [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\379NOV17.wiff
```

Nominal mass (M_r) : 71129; Calculated pI value: 5.08 NCBI BLAST search of <u>gi|2655420</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 18%
```

Matched peptides shown in Bold Red

1	MSGKGEGPAI	GIDLGTTYSC	VGVWQHDRVE	IIANDQGNR T	TPSYVAFTDS
51	ERLIGDAAKN	QVAMNPINTV	FDAKRLIGRR	FSDSSVQSDM	K LWPFKIIAG
101	PAEKPMIVVN	YKGEEKQFAA	EEISSMVLIK	MREIAEAYLG	VTIKNAVVTV
151	PAYFNDSQRQ	ATKDAGVIAG	LNVMRIINEP	TAAAIAYGLD	KKATSVGEKN
201	VLIFDLGGGT	FDVSLLTIEE	GIFEVKATAG	DTHLGGEDFD	NRMVNHFVQE
251	FKRKSKKDIT	GNPRALRRLR	TACERAKRTL	SSTAQTTIEI	DSLFEGIDFY
301	SALTRARFEE	LNMDLFRKCM	EPVEKCLRDA	KMDKSTVHDV	VLVGSTRIPK
351	VQQLLQDFFN	GKELCKSINP	DEAVAYGAAV	QGAILSGEGN	EKVQDLLLLD
401	VTPLSLGLET	AGGVMTTLIA	RNTTIPTKKE	QVFSTYSDNQ	PGVLIQVFEG
451	ERARTKDNNL	LGKFELSGIP	PAPRGVPQIT	VCFDIDANGI	LNVSAEDKTT
501	GQKNKITITT	DKGRLSKDDI	EKMVQEAEKY	KSEDEEHKKK	VEAKNALENY
551	AYNMRNTIQD	EKIGEKLPAA	DKKKIEDAIE	QAIQWLENNQ	LGEADEFEDK
601	MKELESICNP	IIAKMYQGAG	GEAAGMDDDA	PPASGGAGPK	IEEVD

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
40	-	52	737.3662	1472.7178	1472.6783	0.0395	0	R.TTPSYVAFTDSER.L (Ions score 82)
60	-	74	831.4414	1660.8682	1660.8243	0.0439	0	K.NQVAMNPINTVFDAK.R (Ions score 39)
81	-	91	615.8024	1229.5903	1229.5234	0.0669	0	R.FSDSSVQSDMK.L (Ions score 39)
145	-	159	560.9835	1679.9286	1679.8267	0.1019	0	K.NAVVTVPAYFNDSQR.Q (Ions score 49)
164	-	175	608.3919	1214.7692	1214.6441	0.1250	0	K.DAGVIAGLNVMR.I (Ions score 57)
164	-	175	616.3564	1230.6983	1230.6391	0.0593	0	K.DAGVIAGLNVMR.I Oxidation (M) (Ions score 49)
227	-	242	559.2825	1674.8258	1674.7234	0.1024	0	K.ATAGDTHLGGEDFDNR.M (Ions score 56)
308	-	317	665.3352	1328.6559	1328.6071	0.0488	0	R.FEELNMDLFR.K Oxidation (M) (Ions score 72)
615	-	640	804.0228	2409.0464	2408.9849	0.0615	0	K.MYQGAGGEAAGMDDDAPPASGGAGPK.I 2 Oxidation (M) (Ions score 69)

gi|1755154 Germin-like protein

Protein View

Match to: gi|1755154 Score: 79
germin-like protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2274DEC04.wiff

Nominal mass (M_r): 22020; Calculated pI value: 6.81 NCBI BLAST search of <u>gi|1755154</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 17%
```

Matched peptides shown in Bold Red

1 MKMIIQIFFI ISLISTISFA SVQDFCVADP KGPQSPSGYS CKNPDQVTEN 51 DFAFTGLGKA GNTSNIIKAA VTPAFAPAYA GINGLGVSLA RLDLAGGGVI 101 PLHTHPGASE VLVVIQGTIC AGFISSANKV YLKTLNRGDS MVFPQGLLHF 151 QLNSGKGPAL AFVAFGSSSP GLQILPFALF ANDLPSELVE ATTFLSDAEV 201 KKLKGVLGGT N

Show predicted peptides also

Sort Peptides By

 Residue Number
 Increasing Mass
 Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
43 - 59	618.4750	1852.4032	1852.8479	-0.4447	0	K.NPDQVTENDFAFTGLGK.A Deamidated (NQ) (Ions score 32)
43 - 59	927.6111	1853.2077	1852.8479	0.3597	0	K.NPDQVTENDFAFTGLGK.A Deamidated (NQ) (Ions score 34)
138 - 156	697.8482	2090.5227	2091.0095	-0.4868	0	R.GDSMVFPQGLLHFQLNSGK.G Deamidated (NQ); Oxidation (M) (Ions score 46)

gi|24421231 Ascorbate peroxidase

Protein View

Match to: gi|24421231 Score: 142
ascorbate peroxidase [Brassica juncea]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2119.wiff

Nominal mass (M_r) : 27726; Calculated pI value: 5.73 NCBI BLAST search of <u>gi|24421231</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica juncea

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 20%
```

Matched peptides shown in Bold Red

1	MTKSYPTVSE	DYOKAIEKCK	RKLRGLIAEK	NCAPIMVRLA	WHSAGTFDCA
51	SKTGGPFGTM	R FDAEQGHGA	NSGIHIALRL	LDPIREQFPA	ISFADFHQLA
101	GVVAVEVTGG	PEIPFHPGRE	DKPQPPPEGR	LPDATKGCDH	LRQVFTKQMG
151	LSDKDIVALS	GAHTLGRCHK	DRSGFEGAWT	SNPLIFDNSY	FKELLTGEKE
201	GLLQLVSDKA	LLDDPVFRPL	VEKYAADEEA	FFADYAEAHL	K LSELGFADA
251					

Show predicted peptides also

U	Sort Peptides B	y Resid 	lueNumber	Increasing Mass	O Decrea	sing Ma	ISS
	Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
	4 - 14	658.9142	1315.8139	1315.5932	0.2207	0	K.SYPTVSEDYQK.A (Ions score 19)
	53 - 61	470.3170	938.6195	938.4280	0.1915	0	K.TGGPFGTMR.F Oxidation (M) (Ions score 55)
	210 - 223	538.0780	1611.2122	1610.9032	0.3090	0	K.ALLDDPVFRPLVEK.Y (Ions score 50)
	224 - 241	687.7787	2060.3142	2059.9163	0.3980	0	K.YAADEEAFFADYAEAHLK.L (Ions score 18)

gi|169244541 Putative manganese superoxide dismutase 1

Protein View

Match to: gi|169244541 Score: 83 putative manganese superoxide dismutase 1 [Brassica napus] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2384.wiff

Nominal mass (M_r) : 25499; Calculated pI value: 8.47 NCBI BLAST search of <u>gi|169244541</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%
```

Matched peptides shown in Bold Red

1 MAIRSLASRR TLAGLKETSS RLLGLRSIQT FTLPDLPYDY SALEPAISGE 51 IMQIHHQKHH QAYVTNYNNA LEQLDQAVNK GDASTVVKLQ SAIKFNGGGH 101 VNHSIFWKNL APVKEGGGEP PKGALGGAID THFGSLEGLV KKMSAEGAAL 151 QGSGWVWLGL DKELKTLVVD TTANQDPLVT KGGSLVPLVG IDVWEHAYYL 201 QYKNVRPEYL KNVWKVINWK YASEVYEKEC K

Sort Peptides By	Resid	ueNumber	Increasing Mass	O Decrease	sing Ma	155
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
123 - 141	614.7727	1841.2962	1840.9683	0.3278	0	K.GALGGAIDTHFGSLEGLVK.K (Ions score 40)
166 - 181	858.0770	1714.1395	1713.9149	0.2246	0	K.TLVVDTTANQDPLVTK.G (Ions score 43)

gi|15224810 Late embryogenesis abundant (LEA) family protein

Protein View

Match to: gi|15224810 Score: 72 late embryogenesis abundant family protein / LEA family protein [Arabidopsis thaliana] Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

Nominal mass (M_r) : 36185; Calculated pI value: 4.69 NCBI BLAST search of <u>gi|15224810</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: <u>Arabidopsis thaliana</u> Links to retrieve other entries containing this sequence from NCBI Entrez: <u>gi|30689599</u> from <u>Arabidopsis thaliana</u> <u>gi|3212877</u> from <u>Arabidopsis thaliana</u> <u>gi|89000943</u> from <u>Arabidopsis thaliana</u>

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M), Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 6%

Matched peptides shown in Bold Red

1 MSTSEDKPEI ISRVVHQEGD VEIVDRSQKD KDEEKEEGKG GFLDKVKDFI 51 HDIGEKLEGT IGFGKPTADV SAIHIPKINL ERADIVVDVL VKNPNPVPIP 101 LIDVNYLVES DGRKLVSGLI PDAGTLKAHG EETVKIPLTL IYDDIKSTYN 151 DINPGMIIPY RIKVDLIVDV PVLGRLTLPL EKCGEIPIPK KPDVDIEKIK 201 FQKFSLEETV AILHVRLQNM NDFDLGLNDL DCEVWLCDVS IGKAEIADSI 251 KLDKNGSGLI NVPMTFRPKD FGSALWDMIR GKGTGYTIKG NIDVDTPFGA 301 MKLPIIKEGG ETRLKKEDDD DDDEE

Sort Peptides By	Resident	lueNumber	Increasing Mass	Decrease	sing Ma	ISS
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
115 - 127	642.4378	1282.8610	1282.7496	0.1113	O	K.LVSGLIPDAGTLK.A (<u>Ions score 34</u>)
176 - 182	407.3127	812.6109	812.5007	0.1101	O	R.LTLPLEK.C (<u>Ions score 37</u>)

gi|9082317 Actin

Protein View

Match to: gi|9082317 Score: 547
actin [Helianthus annuus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1297NOV26.wiff

Nominal mass (M_r) : 41934; Calculated pI value: 5.64 NCBI BLAST search of <u>gi|9082317</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Helianthus annuus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 27%

Matched peptides shown in Bold Red

1	MAHEGEIQPL	VCDNGTGMVK	AGFAGDDAPR	AVFPSIVGRP	RHTGVMVGMG
51	QKDAYVGDEA	QSKRGILTLK	YPIEHGIVSN	WDDMERIWHH	TFYNELRVAP
101	EEHPVLLTEA	PLNPKANREK	MTQIMFETFN	VPAMYVAIQA	VLSLYASGRT
151	TGIVLDSGDG	VSHTVPIYKG	YALPHAILRL	DLAGRDLTDS	LMRILTERGY
201	MFTTTAEREI	VRDMKEKLAY	VALDYEQELE	TAKSSSSVEK	NYELPDGQVI
251	TIGAERFRCP	EVLFQPSLIG	MEAAGIHETT	YNSIMKCDVD	IRKDLYGNIV
301	LSGGSTMFPG	IADRMSKEIT	ALAPSSMKIK	VVAPPERKYS	VWIGGSILAS
351	LSTFQQMWIS	KGEYDESGPS	IVHRKCF		

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
21	-	30	488.8018	975.5890	975.4410	0.1480	0	K.AGFAGDDAPR.A (Ions score 71)
21	-	30	488.8018	975.5890	975.4410	0.1480	0	K.AGFAGDDAPR.A (Ions score 63)
71	-	86	645.0428	1932.1064	1931.8723	0.2341	0	K.YPIEHGIVSNWDDMEK.I (Ions score 59)
71	-	86	650.3824	1948.1253	1947.8673	0.2580	0	K.YPIEHGIVSNWDDMEK.I Oxidation (M) (Ions score 46)
98	-	115	652.1025	1953.2857	1953.0571	0.2286	0	R.VAPEEHPVLLTEAPLNPK.A (Ions score 62)
186	-	193	461.7980	921.5815	921.4477	0.1338	0	R.DLTDSLMK.I (Ions score 42)
186	-	193	469.8041	937.5936	937.4426	0.1510	0	R.DLTDSLMK.I Oxidation (M) (Ions score 20)
199	- 1	208	588.8424	1175.6703	1175.5281	0.1422	0	R.GYMFTTTAER.E (Ions score 49)
199		208	596.8529	1191.6912	1191.5230	0.1682	0	R.GYMFTTTAER.E Oxidation (M) (Ions score 60)
241	-	256	888.0302	1774.0459	1773.8897	0.1561	0	K.NYELPDGQVITIGAER.F (Ions score 96)
318	-	328	574.3738	1146.7330	1146.5954	0.1376	0	K.EITALAPSSMK.I (Ions score 60)
318	-	328	582.3717	1162.7289	1162.5903	0.1386	0	K.EITALAPSSMK.I Oxidation (M) (Ions score 41)
362	-	374	723.4081	1444.8016	1444.6583	0.1433	0	K.GEYDESGPSIVHR.K (Ions score 97)
362	-	374	482.6431	1444.9075	1444.6583	0.2492	0	K.GEYDESGPSIVHR.K (Ions score 71)

gi|15241472 TUB4 (tubulin beta-4 chain)

Match to: gi|15241472 Score: 427
TUB4 (tubulin beta-4 chain) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\916NOV17.wiff

Nominal mass (M_r) : 50361; Calculated pI value: 4.76 NCBI BLAST search of <u>gi|15241472</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 24%

Matched peptides shown in Bold Red

1	MREILHIQGG	QCGNQIGAKF	WEVICDEHGI	DHTGQYVGDS	PLQLERIDVY
51	FNEASGGRYV	PRAVLMDLEP	GTMDSLRSGP	FGQIFRPDNF	VFGQSGAGNN
101	WAKGHYTEGA	ELIDSVLDVV	RKEAENSDCL	QGFQVCHSLG	GGTGSGMGTL
151	LISKIREEYP	DRMMMTFSVF	PSPKVSDTVV	EPYNATLSVH	QLVENADECM
201	VLDNEALYDI	CFRTLKLANP	TFGDLNHLIS	ATMSGVTCCL	RFPGQLNSDL
251	RKLAVNLIPF	PRLHFFMVGF	APLTSRGSQQ	YSALSVPELT	QQMWDAKNMM
301	CAADPRHGRY	LTASAVFRGK	LSTKEVDEQM	MNIQNKNSSY	FVEWIPNNVK
351	SSVCDIAPKG	LKMASTFIGN	STSIQEMFRR	VSEQFTAMFR	RKAFLHWYTG
401	EGMDEMEFTE	AESNMNDLVA	EYQQYQDATA	GEEEYEEEEE	EYET

Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start	-	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
47	-	58	650.3596	1298.7046	1298.6143	0.0904	0	R.IDVYFNEASGGK.Y (Ions score 80)
63	-	77	824.4539	1646.8933	1646.8008	0.0925	0	R.AVLMDLEPGTMDSLR.S (Ions score 56)
63	-	77	832.4457	1662.8768	1662.7957	0.0811	0	R.AVLMDLEPGTMDSLR.S Oxidation (M) (Ions score 36)
63	-	77	560.6558	1678.9455	1678.7906	0.1549	0	R.AVLMDLEPGTMDSLR.S 2 Oxidation (M) (Ions score 43)
242	-	251	573.8497	1145.6848	1145.5829	0.1019	0	R.FPGQLNSDLR.K (Ions score 58)
253	-	262	570.4009	1138.7872	1138.6862	0.1010	0	K.LAVNLIPFPR.L (Ions score 39)
310	-	318	514.3330	1026.6515	1026.5498	0.1016	0	R.YLTASAVFR.G (Ions score 42)
325	-	336	498.9403	1493.7990	1493.6490	0.1500	0	K.EVDEQMMNIQNK.N Oxidation (M) (Ions score 26)
337	-	350	848.9741	1695.9336	1695.8257	0.1079	0	K.NSSYFVEWIPNNVK.S (Ions score 27)
363	-	379	651.3504	1951.0293	1950.8815	0.1478	0	K.MASTFIGNSTSIQEMFR.R 2 Oxidation (M) (Ions score 42)
381	-	390	616.3454	1230.6762	1230.5703	0.1059	0	R.VSEQFTAMFR.R Oxidation (M) (Ions score 58)

gi|34733239 Putative tubulin alpha-2/alpha-4 chain

Protein View

Match to: gi|34733239 Score: 250 putative tubulin alpha-2/alpha-4 chain [Brassica napus] Found in search of C:\QStar Share Data\20091115MMZ\NOV17\897NOV17.wiff

Nominal mass (M_r) : 50089; Calculated pI value: 4.91 NCBI BLAST search of <u>gi|34733239</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C) Variable modifications: Oxidation (M),Phospho (ST) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 14%

Matched peptides shown in Bold Red

1	MGECISIHMG	QAGIQVGNAC	WELYCLEHGI	QPDGQMPGDK	TVGGGDDAFN
51	TFFSETGAGK	HVPRAVEVDL	EPTVIDEVRT	GTYRQLFHPE	QLISGKEDAA
101	NNFARGHYTI	GKEIVDLCLD	RIRKLADNCT	GLQGFLVFNA	VGGGTGSGLG
151	SLLLERLSVD	YGKKSKLGFT	VYPSPQVSTS	VVEPYNSVLS	THSLLEHTDV
201	SILLDNEAIY	DICRRSLNIE	RPTYTNLNRL	VSQVISSLTA	SLRFDGALNV
251	DVTEFQTNLV	PYPRIHFMLS	SYAPVISAEK	AFHEQLSVAE	ITNSAFEPAS
301	MMAKCDPRHG	KYMACCLMYR	GDVVPK DVNA	AVGTIKTKRT	IQFVDWCPTG
351	FKCGINYQPP	TVVPGGDLAK	VQRAVCMISN	STSVAEVFPR	IDHKFDLMYA
401	KRAFVHWYVG	EGMEEGEFSE	AREDLAALEK	DYEEVGAEGG	DDVDDEGEEY
451					

Sor	t Peptides B	Resid	lue Number	Increasing Mass	Decrea	ising Ma	155
Star	t - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
41	L - 60	660.0147	1977.0223	1976.8752	0.1471	0	K.TVGGGDDAFNTFFSETGAGK.H (Ions score 64)
63	5 - 79	851.4992	1700.9839	1700.8985	0.0854	0	R.AVFVDLEPTVIDEVR.T (Ions score 71)
210	5 - 229	564.3507	1690.0303	1689.8798	0.1505	0	R.SLNIERPTYTNLNR.L (Ions score 23)
321	7 - 336	494.3343	986.6541	986.5397	0.1144	0	K.DVNAAVGTIK.T (Ions score 42)
423	3 - 430	444.7865	887.5584	887.4600	0.0984	0	R.EDLAALEK.D (Ions score 51)

gi|408232 Proliferating cell nuclear antigen

Protein View

Match to: gi|408232 Score: 226
PCNA [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1856DEC04.wiff

Nominal mass (M_r) : 29375; Calculated pI value: 4.61 NCBI BLAST search of <u>gi|408232</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Brassica napus

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 29%
```

Matched peptides shown in Bold Red

1 MLELRLVQGS LLKKVLESIK DLVNDANFDC STTGFSLQAM DSSHVALVSL 51 LLRSEGFEHY RCDRNLSMGM NLGNMSKMLK CAGNDDIITI KADDGGDTVT 101 FMFESPKQDK IADFEMKLMD IDSEHLGIPD AEYHSIVRMP SNEFSRICKD 151 LSTIGDTVVI SVTKEGVKFS TAGDIGTANI VLRQNTTVDK PEDAIVIEMN 201 EPVSLSFALR YMNSFTKATP LSDTVTISLS SELPVVVEYK VAEMGYIRYY 251 LAPKIEEDEE DKA

Sort P	eptides By	Resid	ueNumber	Increasing Mass	Decrea	sing Ma	SS
Start -	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
92 -	107	866.9919	1731.9693	1731.7298	0.2395	0	K.ADDGGDTVTFMFESPK.Q Oxidation (M) (Ions score 36)
150 -	164	774.5522	1547.0899	1546.8454	0.2445	0	K.DLSTIGDTVVISVTK.E (Ions score 58)
169 -	183	768.0436	1534.0726	1533.8151	0.2575	0	K.FSTAGDIGTANIVLR.Q (Ions score 68)
218 -	240	816.8961	2447.6666	2447.3047	0.3619	0	K.ATPLSDTVTISLSSELPVVVEYK.V (Ions score 23)
255 -	263	539.3420	1076.6695	1076.4509	0.2186	1	K.IEEDEEDKA (Ions score 41)

gi|15238284 CBS domain-containing protein

Protein View

Match to: gi | 15238284 Score: 205 CBS domain-containing protein [Arabidopsis thaliana] Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2559.wiff

Nominal mass (M_): 22829; Calculated pI value: 9.10 NCBI BLAST search of gi|15238284 against nr Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C) Variable modifications: Deamidated (NQ), Gln->pyro-Glu (N-term Q), Oxidation (M) Cleavage by Trypsin: cuts C-term side of KR unless next residue is P Sequence Coverage: 15%

Matched peptides shown in Bold Red

1 MQGVIRSFVS GGNVVKGSVL QHLRVINPAI QPSVFCSRSE STQPARMEES 51 GFESTTISDV MKSKGKSADG SWLWCTTDDT VYDAVKSMTQ HNVGALVVVK 101 PGEQQALAGI ITERDYLRKI IVQGRSSKST KVGDIMTEEN KLITVTPETK 151 VLRAMOLMTD NRIRHIPVIK DKGMIGMVSI GDVVRAVVHE HREELORLNA 201 YIQGGY

Show predicted peptides also

Sort Peptide:	в Ву	Residue Number Output Description Second State Second Second State Second St	r 💿 Increasing Mass	Decrease	sing Ma	SS			
Start - End	Obse	erved Mr(ex	pt) Mr(calc)	Delta	Miss	Sequence			
132 - 141	568	.3664 1134.71	82 1134.5227	0.1956	0	K.VGDIMTEENK.L	(Ions score 58))	
132 - 141	576	.3654 1150.71	63 1150.5176	0.1987	0	K.VGDIMTEENK.L	Oxidation (M)	(Ions	score 62)
142 - 150	501	.3762 1000.73	79 1000.5805	0.1574	0	K.LITVTPETK.V	(Ions score 58)		
173 - 185	667	.4555 1332.89	65 1332.6894	0.2071	0	K.GMIGMVSIGDVVR.	A (Ions score	78)	
173 - 185	683	.4539 1364.89	33 1364.6792	0.2141	0	K.GMIGMVSIGDVVR	A 2 Oxidation	(M)	(Ions scor

(Ions score 87)

gi|147799132 Hypothetical protein

Protein View

Match to: gi|147799132 Score: 55
hypothetical protein [Vitis vinifera]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\343NOV15.wiff

Nominal mass (M_r) : 41562; Calculated pI value: 8.77 NCBI BLAST search of <u>gi|147799132</u> against nr Unformatted <u>sequence string</u> for pasting into other applications

Taxonomy: Vitis vinifera

```
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%
```

Matched peptides shown in Bold Red

1	MKDPRCMRPL	DTSSFILFER	NRFRTSKSKA	LANRLNQLGY	RSTSYSFPIE
51	VRLRDTKKPY	LSSNGLPFLN	QGICLHGKDN	ETIVEMITRF	TDLVNGLEAL
101	GKTYEESXKR	HTKVTAVQEA	KYLTKLPLEE	LIGSLMTYEI	NLVKKQQEGE
151	DKKKKSIALK	VTTKEEEEVE	EDKQSEKDED	LIIITRKFNK	FMRDERFKGR
201	RCKKLGHIKY	DCPFYKSKAK	KRKKKAMMAT	WSESEDESSK	EENEKEVANM
251	CFMVIDELDE	VNSNISDEDI	HDVFQELYED	LEKLGLKNAS	TKKKKAŐŐTEK
301	ELGEDKYVTH	LGSFRPDQDK	FRLASKVRGS	PSSTRSDKID	SLGSLDSQSG
351	RSVQSSL				

Sort Peptides By	Resid	tueNumber) Increasing Mass	Decrea	sing Ma	ISS			
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Dheenhe	(67)	(7
103 - 110	547.3124	1092.6102	1092.4488	0.1614	1	K.TIEESTKR.H	Pnospno	(51)	(lons score 26)
103 - 110	554.3108	1106.6070	1106.4281	0.1789	1	K. TYEESDKR. H	Phospho	(ST)	(Ions score 20)
103 - 110	554.3108	1106.6070	1106.4281	0.1789	1	K. TYEESDKR. H	Phospho	(ST)	(Ions score 29)

Figure S7

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to MeJA treatment in guard cells by ICAT.

gi|8745521 Ribulose-1,5-bisphosphate carboxylase / oxygenase

Р	rotei	ns Dete	ected																	
Lг	N	Unu	Total	% Cov	Ac	cessio		Name		Species	Peptides	(95%) Biol	ogical Proce	sses Mol	ecula	r Fur	nctions	PANTI	IER ID	
	1	18.20	18.20	86.7	giļ	22595	myrosina	se [Brassica napus]	Bras	sica napus		28								
	2	10.86	10.86	61.2	gi	8745521	ribulose-	1,5-bisphosphate carboxylase/oxygena	Bras	ssica napus		10								
	3	8.09	8.09	95.0	gili	266891	Ribulose	bisphosphate carboxylasesmall chain,	BRA	NA		10								Ŧ
Р	rotei	n Grou	ıp 2 - r	ibulose	-1,5	5-bispho	sphate o	carboxylase/oxygenase [Brassica	napı	us]										
		Proteir	ns in Gr	oup						Peptid	es in Gro	up								
	N	Unu	Total	Accessi	io	Con V	Conf	Sequence		Modificat	ions	Cleavage	s ∆Mass	Prec MV	/ z	Sc	Spe	ctrum	Туре	~
	2	10.86	10.86	gi 87458	521	2.00	99	CYHIEPVPGEETQFIAY		ICAT-C(C)@1		cleaved Y-V	0.1280	2222.16.	2	15	5.1.1.1	448.2	Winner	
	2	0.00	10.86	gi 30959	9	2.00	99	ELGVPIVMHDYLTGGFTANTSLAHYC	R	Oxidation(M)@	8 (C)@26		0.1033	3216.68.	4	16	5.1.1.1	445.3	Winner	
	2	0.00	10.86	gi 30959	9	2.00	99	GHYLNATAGTCEEMMK		ICAT-C(C)@11			0.1280	2013.98.	3	16	5.1.1.1	333.2	Winner	
۱ŀ	2	0.00	10.86	gi 16/18	57 967					Oxidation(M)@ Oxidation(M)@)14)15									
ŀ	-	0.00	10.86	gi 15732	2	2.00	99	GHYLNATAGTCEEMMKR		ICAT-C:13C(9) Oxidation(M)@ Oxidation(M)@	(C)@11)14)15	missed K-R	0.1073	2179.09.	3	21	4.1.1.1	345.3	Winner	
						2.00	99	VALEACVQAR		ICAT-C(C)@6			0.0746	1285.75.	2	14	5.1.1.1	359.2	Winner	
						0.52	70	PLLGCTIKPK		ICAT-C(C)@5		cleaved R-F	P 0.0758	1295.83.	3	13	5.1.1.1	354.2	Winner	
						0.14	27	NEGRDLAVEGNEIIR		Gly->Ser@3 Oxidation(N)@	<u>)</u> 11	missed R-D	0.1797	1730.03.	3	13	6.1.1.1	559.2	Winner	
						0.07	14	AVYECLR		ICAT-C:13C(9)	(C)@5		0.0037	1088.57.	2	10	4.1.1.1	377.4	Winner	
						0.05	10	FLFCAEAIYK		ICAT-C:13C(9)	(C)@4		0.0439	1439.80.	2	10	4.1.1.1	462.4	Winner	
						0.04	9	GRCYHIEPVPGEETQFIAY		Oxidation(R)@ Cys->Thr@3	2	cleaved Y-V	0.0990	2222.16.	2	16	5.1.1.1	448.2	Winner	
						0.04	9	YGRPLLGCTIKPK		ICAT-C(C)@8 Thr->Pro@9 Methyl(I)@10			0.0771	1682.04.	4	13	5.1.1.1	357.2	Winner	
	1				F	0.00	1	AVYECLRGGL		No ICAT(C)@5		cleaved L-D	0.1125	1079.65.	2	10	4.1.1.1	380.4	Winner	-
Ľ					_															

Protein Sequence Coverage - ribulose-1,5-bisphosphate carboxylase/oxygenase [Brassica napus]

MSPQTETKASVGFKAGVKEYKLNYYTPEYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVPGEETQFIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFK ALAALRLEDLRIPPAYTKTFQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAIYKSQAETGEIKGHYLNATAGTCEEMMKRAIF ARELGVPIVMHDYLTGGFTANTSLAHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHVHAGTVVGKLEGDRESTLGFVDLLRDDYVEKDRSRGIFFTQDWVSLPGVLPVASGGIHV WHMPALTEIFGDDSVLQFGGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAVEGNEIIREACKWSPELAAACEVWKEITFNFPTIDKLDGQD

gi|17852 Ribulose bisphosphate carboxylase small chain, chloroplast precursor

Р	rotei	ns Dete	ected									
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	-
Γ	2	10.86	10.86	61.2	gi 8745521	ribulose-1,5-bisphosphate carboxylase/oxygena	Brassica napus	10				
	3	8.09	8.09	95.0	gi 266891	${\sf Ribulose} \ {\sf bisphosphate} \ {\sf carboxylasesmall} \ {\sf chain}, \ldots$	BRANA	10				
Ιſ	4	6.02	6.02	69.4	gi 15224	cytoplasmic aconitate hydratase[Arabidopsis th	Arabidopsis thaliana	4				1
	5	5.00	5.00	42.0	gi 15237	translation elongation factor EF-Tu precursor, ch	Arabidopsis thaliana	3				1
	6	4.77	4.77	78.7	gi 60686	oxalic acid oxidase [Brassica napus]	Brassica napus	4				1
	7	4.29	4.29	55.5	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	2				1
	8	4.11	4.11	68.9	gi 15238	5-methyltetrahydropteroyltriglutamate-homocyst	Arabidopsis thaliana	4				1
	9	4.04	4.04	62.4	gi 15222	glyceraldehyde-3-phosphate dehydrogenase, pu	Arabidopsis thaliana	2				1
	10	4.01	4.01	70.8	gi 15219	ATPase 70 kDasubunit, putative [Arabidopsis th	Arabidopsis thaliana	4				1
	11	4.00	4.00	79.3	gi 8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	4				1
	12	3.71	3.71	86.8	gi 899226	malate dehydrogenase [Brassica napus]	Brassica napus	3				-

Protein Group 3 - Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit)

	Proteins in Group Peptides in Group													
N	Unu	Total	Accessio	Na 🔦	Con… ⊽	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectr 🔺
	3 8.09	8.09	gi 266891	Ribulose bi 😑	2.00	99	KLPLFGCTDSAQVLK	ICAT-C:13C(9)(C)@7	cleaved W	0.1191	1855.15	3	15	5.1.1.141
:	3 0.00	8.09	gi 17850	ribulose bi:	2.00	99	LPLFGCTDSAQVLK	ICAT-C(C)@6		-0.0471	1717.86	2	21	4.1.1.145
	0.00	8.09	gi]11972	ribulose bis	2.00	99	QVQCISFIAYKPPSFTGA	ICAT-C(C)@4		0.0669	2183.17	3	14	4.1.1.147
	0.00	8.09	gi 17855	rubisco ssu	2.00	99	WI PCVE FELEHGFVYR	ICAT-C:13C(9)(C)@4		0.1311	2259.25	3	19	5.1.1.148
	0.00	0.00	~170/12	ablaraplaat	0.00	10	FILOP CUTEV DNA FT D	10AT 0420/01/01/85	missed KT	0.0760	2062.40	2	44	E 4 4 490

Protein Sequence Coverage - ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

MASSMLSSAAVVTSPAQATMVAPFTGLKSSAAFPVTRKANNDITSIASNGGRVSCMKVWPPVGKKKFETLSYLPDLTEVELGKEVDYLLRNKWIPCVEFELEHGFVYREHGSTPGYYDGRYWTMWKLP LFGCTDSAQVLKEVQECKTEYPNAFIRIIGFDNNRQVQCISFIAYKPPSFTGA

gi|8745523 ATP synthase beta subunit

P	Proteins Detected												
Γ	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*	
	10	4.01	4.01	70.8	gi 15219	ATPase 70 kDasubunit, putative [Arabidopsis th	Arabidopsis thaliana	4				1	
	11	4.00	4.00	79.3	gi 8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	4					
	12	3.71	3.71	86.8	gi 899226	malate dehydrogenase [Brassica napus]	Brassica napus	3				1	
	13	3.61	3.61	57.1	gi 15226	putative triosephosphate isomerase [Arabidopsi	Arabidopsis thaliana	3				1	
	14	3.41	3.41	37.8	gi 14722	unnamed protein product [Brassica napus]	Brassica napus	3				1	
l	15	3.10	3.10	63.4	gi 15233	cytosolic triosephosphatisomerase [Arabidopsis	Arabidopsis thaliana	2				-	

Protein Group 11 - ATP synthase beta subunit [Brassica napus]

Proteins in Group					Peptides in Group									
N	Unu	Total	Accessio	Name	Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectr 🔺
11	4.00	4.00	gi 8745523	ATP synthase	2.00	99	DTLGQEINVTCEVQQLLGNNR	ICAT-C:13C(9)(C)@11		0.0170	2579.32	3	15	5.1.1.152 E
11	0.00	4.00	gi 75336	ATP synthase	2.00	99	GRDTLGQEINVTCEVQQLLGNNR	ICAT-C:13C(9)(C)@13	missed R-D	0.0801	2792.50	3	17	4.1.1.148
	0.00	4.00	gi]56675	atp synthase bi	0.00	1	GRIAQIIGPVLDVAFPPGK	Asp->Leu@12	cleaved L	-0.0296	1945.15	3	12	3.1.1.170
	0.00	4.00	gi]14717	ATP synthase I	0.00	< 1	AVAMSATDGLKR	Dethiomethyl(M)@4 Oxidation(D)@8 Oxidation(R)@12	missed K-R	0.0599	1202.68	2	9	3.1.1.175
					0.00	< 1	AVAMSATDGLKR	Phospho(T)@7	missed K-R	0.2260	1298.83	2	7	3.1.1.171
					0.00	< 1	AVAMSATDGLKR	Leu->Asp@10	missed K-R	0.2337	1220.81	2	10	2.1.1.187
					0.00	< 1	AVAMSATEGLKR	Leu->Thr@10	missed K-R	0.1973	1220.81	2	9	2.1.1.187
					0.00	< 1	DEATAKATNLEMESKLK	Deamidated(N)@9	cleaved I-D	-0.0173	1878.90	2	5	4.1.1.166
					0.00	99	DTLGQEINVTCEVQQLLGNNR	ICAT-C(C)@11		0.0915	2570.36	3	17	6.1.1.169
					0.00	97	DTLGQEINVTCEVQQLLGNNR	ICAT-C:13C(9)(C)@11		1.1182	2580.42	3	14	5.1.1.153
4					• 0 00							٦	8	1 1 1 153

Protein Sequence Coverage - ATP synthase beta subunit [Brassica napus]

MRINPTTSDPAVSIREKNNLGRIAQIIGPVLDVAFPPGKMPNIYNALVVKGRDTLGQEINVTCEVQQLLGNNRVRAVAMSATEGLKRGMDVVDMGNPLSVPVGGATLGRIFNVLGEPVNNLGPVDTLT TSPIHKSAPAFIDLDTTLSIFETGIKVVDLLAPYRRGGKIGLFGGAGVGKTVLIMELINNIAKAHGGVSVFGGVGERTREGNDLYMEMKESGVINELNLADSKVALVYGQMNEPPGARMRVGLTALTM AEYFRDVNEQDVLLFIDNIFRFVQAGSEVSALLGRMPSAVGYQPTLSAEMGSLQERITSTKKGSITSIQAVYVPADDLTDPAPATTFAHLDATTVLSRGLAAKGIYPAVDPLDSTSTMLQPRIVGEEH YETAQQVKQTLQRYKELQDIIAILGLDELSEEDRLTVARARKIERFLSQPFFVAEVFTGSPGKYVGLAETIRGFNLILSGEFDSLPEQAFYLVGNIDEATAKATNLEMESKLKK
gi|899226 Malate dehydrogenase, mitochondrial precursor

Р	rotei	ns Dete	ected									
	N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*
Γ	1	18.08	18.08	75.4	gi 22595	myrosinase[Brassica napus]	Brassica napus	26				
	2	10.54	10.54	70.6	gi 8745521	ribulose-1,5-bisphosphate carboxylase/oxygenas	Brassica napus	7				
	3	8.04	8.04	71.6	gi 899226	malate dehydrogenase [Brassica napus]	Brassica napus	4				
	4	6.02	6.02	66.9	gi 406727	ribulose-1,5-bisphosphate carboxylase /oxygenas	Brassica napus	7				
	5	5.40	5.40	41.0	gi 8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	8				
Ľ	6	5.22	5.22	38.5	gi 15218	germin-like protein [Arabidopsis thaliana]	Arabidopsis thaliana	4				-

Protein Group 3 - malate dehydrogenase [Brassica napus]

			1	Proteins in G	roup					Peptides in Gro	up					
1	4	Unu	Total	Accessio	Name		Con∇	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrui 🔺
	3	8.04	gi 899226	malate dehydrogena	E	2.00	99	AGKGSATLSMAYAGALFAD	Trimethyl(K)@3	missed K	0.1788	2510.47	3	19	5.1.1.1343.4	
	3	0.00	8.04	gi 2497857	Malate dehydrogena	E				ICAT-C:13C(9)(C)@21						E
							2.00	99	GLNGVPDVVECSYVQSTIT	Deamidated(N)@3 ICAT-C(C)@11		0.2775	3127.81	3	15	5.1.1.1468.
							2.00	99	YCPHALVNMISNPVNSTVP	ICAT-C:13C(9)(C)@2 Oxidation(M)@9		0.2152	3079.80	3	15	5.1.1.1381.4
							2.00	99	YCPHALVNMISNPVNSTVP	ICAT-C(C)@2 Oxidation(M)@9	missed K-K	0.2451	3198.90	4	18	5.1.1.1361.:
							0.02	5	AKYCPHALVNMISNPVNST	Formyl@N-term No ICAT(C)@4 Oxidation(M)@11	cleaved I-A	0.2451	3198.90	4	19	5.1.1.1361.:
							0.02	4	SMAYAGALFADACLK	Oxidation(M)@2 ICAT-C:13C(9)(C)@13	cleaved L	0.2089	1783.08	3	11	4.1.1.1477.4
							0.00	1	LNPLVSSLSLYDIANTPGV	Methylthio(N)@2 Oxidation(N)@27		-0.8863	3067.67	4	12	5.1.1.1361.:
٠				111	Þ		•									•

Protein Sequence Coverage - malate dehydrogenase [Brassica napus]

MFRSALVRSSASAKQSLLRRSFSSGSVPERKVAILGAAGGIGQPLALLMKLNPLVSSLSLYDIANTPGVAADVGHINTRSQVVGYMGDDNLAKALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKN LWSAIAKYCPHALVNMISNPVNSTVPIAAEIFKKAGMYDEKKLFGVTTLDVVRVKTSYAGKANVPVAEVNVPAIVGHAGVTILPLFSQATPQAILSGDALTVTTKRTQDGGTEVEEAKAGKGSATLSM AYAGALFADACLKGLNGVPDVVECSYVQSTITELPFFASKVRLGKNGVEEVLDLGPLSDFEKEGLEALRPGIKSTIEKGVKFANQ

gi|13487709 ADP-glucose pyrophosphorylase small subunit

Р	rotei	ns Dete	ected									
Γ	Ν	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*
I	16	3.56	3.56	58.1	gi 15224	cytoplasmic aconitate hydratase[Arabidopsis thal	Arabidopsis thaliana	3				
	17	3.47	3.47	83.3	gi 49359	photosystem II protein [Brassica oleracea]	Brassica oleracea	5				
	18	3.40	3.40	53.9	gi 15239	translation elongation factor eEF-1 alpha chain (g	Arabidopsis thaliana	2				
	19	3.22	3.22	69.0	gi 13487	ADP-glucose pyrophosphorylase small subunit [B	Brassica rapa sub	1				
	20	2.80	2.82	80.3	gi 15226	putative triosephosphate isomerase[Arabidopsis	Arabidopsis thaliana	1				
	21	2.78	2.97	63.8	gi 6503064	myrosinase[Brassica napus]	Brassica napus	2				-

Protein Group 19 - ADP-glucose pyrophosphorylase small subunit [Brassica rapa subsp. pekinensis]

				Proteins in Group					Peptides in Gro	up					
	N	Unu	Total	Accession #	Name	Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrui 🔺
	19	3.22	3.22	gi 13487709	ADP-glucose pyro	2.00	99	SCISEGAIIEDTLLMGADY	ICAT-C:13C(9)(C)@2 Oxidation(D)@11		0.2731	3102.68	3	15	6.1.1.1602.1 E
┢		0.00	3.22	gi 7688090	ADP-giucose pyrop	1.22	94	LIDIPVSNCLNSNISK	ICAT-C:13C(9)(C)@9		0.1620	1965.22	3	13	5.1.1.1346.
┝		0.00	3.22	gi 17000400	Giucose-1-priospria	0.00	< 1	NRHLSRAYASNMGGYK	Oxidation(M)@12	cleaved L-N	0.2279	1840.10	3	10	5.1.1.1255.4
						0.00	<1	ANRAVPLGANYRLIDIPVS	Deamidated(R)@3 ICAT-C(C)@21 Deamidated(N)@25 Deamidated(N)@36 Deamidated(N)@41	missed R-A	0.6523	4850.15	5	8	7.1.1.1833.:
						0.00	< 1	ATAFGLMKIDDEGRIIEFA		missed K-I	0.3819	3464.20	6	3	7.1.1.2014.4
						0.00	< 1	AVPLGANYR	Deamidated(N)@7		0.1738	960.6767	2	5	3.1.1.1789.4
						0.00	< 1	DEGR		cleaved D-D	0.1235	475.3261	1	3	4.1.1.1451.4
						0.00	< 1	DEGR		cleaved D-D	0.1481	475.3508	1	4	3.1.1.1658.
						0.00	< 1	ET DA DI TVAAL PMDEK			0.3268	1718.13	3	9	4.1.1.1484.: 👻
-			1	1	F.	•			III						4

Protein Sequence Coverage - ADP-glucose pyrophosphorylase small subunit [Brassica rapa subsp. pekinensis]

MATMAAIGSLKVPSSSSNHTRRLSSSSQRKTLSFSSSSLTGEKLNPTQEIIISNLPRWQREKNAIDSPKAVSDSQNSQTCLDPDASRSVLGIILGGGAGTRLYPLTKKRANRAVPLGANYRLIDIPVS NCLNSNISKIYVLTQFNSASLNRHLSRAYASNMGGYKNEGFVEVLAAQQSPENPNWFQGTADAVRQYLWLFEEHNVLEFLVLAGDHLYRMDYEKFIQAHRETDADITVAALPMDEKRSTAFGLMKIDD EGRIIEFAEKPKGEQLKAMKVDTTILGLDDERAKEIPFIASMGIYVVSKNVMLDLLRDQFPGANDFGSEVIPGATDLGLRVQAYLYDGYWEDIGTIEAFYNANLGITKKPVPDFSFYGRSAPIYTQPR YLPPSKMLDADVTDSVIGEGCVIKNCKIHHSVIGLR**SCISEGAIIEDTLLMGADYYETDADR**TLLAAKGRVPIGIGENSHIKRAIIDKNARIGDNVKIINTDNVQEAARETDGYFIKSGIVTVIKDAL IPSGTVI

gi|15220881 Putative aldehyde dehydrogenase

Prote	ins Dete	ected									
N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*
28	2.06	2.06	57.1	gi 15233	probable H+-transporting ATPase[Arabidopsis th	Arabidopsis thaliana	2				
29	2.02	2.02	60.3	gi 15225	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	1				
30	2.01	2.01	63.3	gi 15236	hydroxymethyltransferase [Arabidopsis thaliana]	Arabidopsis thaliana	2				
31	2.01	2.01	46.7	gi 15220	putative aldehyde dehydrogenase[Arabidopsis th	Arabidopsisthaliana	1				
32	2.01	2.01	67.1	gi 15231	monodehydroascorbate reductase (NADH) - like	Arabidopsisthaliana	1				7
- 33	2.00	2.00	63.9	gi 15231	CDC48 - like protein [Arabidopsis thaliana]	Arabidopsis thaliana	1				-

Protein Group 31 - putative aldehyde dehydrogenase [Arabidopsis thaliana]

				Proteins in Group					Peptides in Gro	up					
	N I	Unu	Total	Accession #	Name	Con ⊽	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	Spectrui 🔺
	31	2.01	2.01	gi 15220881	putative aldehyde	2.00	99	LGPA LACGNTVVLK	ICAT-C(C)@7		0.2128	1582.10	3	15	4.1.1.1447.; 🗐
						0.01	3	LIGGR		cleaved L-L	0.0175	514.3402	1	6	8.1.1.2230.:
						0.00	< 1	AKARALKRNVGDPF		cleaved F	0.0535	1541.93	3	5	5.1.1.1649.:
						0.00	<1	AKARALKRNVGDPFK	Deamidated(R)@8 Deamidated(N)@9	missed K-A	0.1476	1672.08	4	8	5.1.1.1257.:
						0.00	< 1	ALKRNVGDPFKSGIEQGPQ	Phospho(S)@22	missed K-R	0.1973	3067.67	4	7	5.1.1.1361.:
						0.00	<1	ANNSRYGLAAGVFTQNLDT	Oxidation(R)@5 Deamidated(R)@22	missed R-Y	-0.2665	2792.11	5	6	6.1.1.1682.:
						0.00	<1	ANNSRYGLAAGVFTQNLDT	Deamidated(R)@5 Deamidated(N)@16	missed R-Y	0.7611	3118.35	6	4	7.1.1.2000.:
						0.00	< 1	ATDEIFGPVQTILK	Oxidation(F)@6	cleaved I-A	0.1056	1546.92	3	8	6.1.1.1343.:
						0.00	< 1	AVEN	Deamidated(N)@4	cleaved A	0.1171	432.3027	1	3	1.1.1.1724.:
						0.00	< 1	DEGPWPKMTAYERSKILFR		cleaved F	0.8030	4834.18	5	4	7.1.1.1831.:
						0.00	24	DI DEL CADA DI CDVCI AA C		minood D A	0 5764	2000 00	c		044 3400 -
•			1	11	1				111						•

Protein Sequence Coverage - putative aldehyde dehydrogenase [Arabidopsis thaliana]

MNRGAQRYSNLAAAVENTITPPVKVEHTQLLIGGRFVDAVSGKTFPTLDPRNGEVIAQVSEGDAEDVNRAVAAARKAFDEGPWPKMTAYERSKILFRFADLIEKHNDEIAALETWDNGKPYEQSAQIE VPMLARVFRYYAGWADKIHGMTMPGDGPHHVQTLHEPIGVAGQIIPWNFPLLMLSWKLGPALACGNTVVLKTAEQTPLSALLVGKLLHEAGLPDGVVNIVSGFGATAGAAIASHMDVDKVAFTGSTDV GKIILELASKSNLKAVTLELGGKSPFIVCEDADVDQAVELAHFALFFNQGQCCCAGSRTFVHERVYDEFVEK<mark>AKARALKRNVGDPFKSGIEQGPQVDSEQFNKILK</mark>YIKHGVEAGATLQAGGDRLGSK GYYIQPTVFSDVKDDMLIATDEIFGPVQTILKFKDLDEVIARANNSRYGLAAGVFTQNLDTAHRLMRALRVGTVWINCFDVLDASIPFGGYKMSGIGREKGIYSLNNYLQVKAVVTSLKNPAWL

gi|15239772 Aspartate aminotransferase Asp2

Pro	teins Det	tected														
N	Unu	. Total	% Cov A	ccessio		N	lame			Species	Peptides(95%)	Biological Processes	Molecular Fun	ctions	PANTHEF	R ID 🔺
	52 1.52	2 1.52	57.5 g	ji 15231	ketol-a	cid reductoisom	erase [Arabic	lopsis thalia	na] Ara	bidopsis thaliana	1					
	53 1.52	2 1.52	57.8 g	gi 15239	asparta	ate aminotransfe	rase Asp2[Ar	abidopsis th	Ara	bidopsis thaliana	1					Ŧ
•									111							P.
Pro	tein Gro	up 53 - a	aspartate	aminotra	ansfera	se Asp2 [Ara	bidopsis tł	naliana]								
			Pro	oteins in G	roup						Pe	ptides in Group				
N	Unu	. Total	Access	sion #		Name	Spec	Con⊽	Conf	Sequ	ence	Modifications	Cleavages	∆Mas	s Prec MV	v 🔺
	53 1.52	1.52	gi 152397	72	aspartat	e aminotran	Arabidop	1.52	97	VGALSIVCK		ICAT-C(C)@8		0.129	2 1115.76.	
	0.00	0 1.52	gi 1523907	78	aspartate	e aminotransf	Arabidops	0.00	< 1	GVTVAY			cleaved L-G	0.086	608.403	31
								0.00	< 1	AMADRIISMR	KOLFEALRTR	Oxidation(D)@4	missed R-I	0.13	3 2438.41	
•							•	•								•
MD IY MG RI	SVFSNVA IPKPTWG LYGERVG SMAGLSS	ARAPEDF SNHPKVF SALSIVC SKTVPHL	ILGVTVI NLAGLS KSADVA: ADAMHAJ	AYNNDPS VEYFRYY SKVESQVI AVTRLG	PVKINI DPATRO KLVVRI	LGVGAYRTEEG SLDFKGLLEDI PMYSSPPIHGA	KPLVLDVV GAAPSGAI ASIVATILM	Y <mark>RKAEQQI</mark> IVLLHAC <i>I</i> KSSDMYNN	ANN DPS ANN PTG WTIEI	RVKEYIPIVG] WDPTSEQWEQI KEMADRIKSME	ISDFNKLSAKI IRQLMRSK <mark>SLI</mark> RQQLFEAIQAF	ILGADSPAITESRVT PFFDSAYQGFASGSL GTPGDWSHIIKQIGM	TVQCLSGTGS: DTDAQSVRTF FTFTGLNKEQ	LRVGA VADGG VEFMT	EFLKTHYF ECLIAQS KEFHIYMI	HQSV YAKN ISDG
Frag	gmentati	on Evide	ence													
	VGA	LSIVC[CO	јк													
R	esidue	b	b+2	2	у	y+2			v1	228 15	2	v3 v4	v5 v6	v7	v8	
V		100.075	50.	5415 111	6.6445	558.8259	7000 -	b1	b#2-2	y2326+2 b4	b5 y8+2	b6	,.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		,,,	
G		157.097	2 79.0	0522 101	7.5761	509.2917	6000 -				477.29					
A		228.134	3 114.8	5708 96	0.5547	480.7810	₹5000		157.1	2	460.25					
L		341.218	3 171.	1128 88	9.5176	445.2624	နှို 4000 -			279.17						
S	N Unu Total % Cov Accessio Name 52 1.52 1.52 57.5 gi 15231 ketol-acid reductoisomeral 53 1.52 1.52 57.8 gi 15239 aspartate aminotransferase correction Group 53 1.52 1.52 57.8 gi 15239 aspartate aminotransferase rotein Group 53 - aspartate aminotransferase Aspartate aminotransferase N Unu Total Accession # Name aspartate aminotransferase 53 1.52 gi 15239772 aspartate aminotransf Ar 0.00 1.52 gi 15239078 aspartate aminotransferase Aspartate aminotransferase 4 III III III III IIII IIII IIII rotein Sequence Coverage - aspartate aminotransferase Asportage IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII						3000 -]			269.12		576.39	770 50			
	N Unu Total % Cov Accessio Name 52 1.52 1.52 57.5 gi 15231 ketol-acid reductoisomera 53 1.52 1.52 57.8 gi 15239 aspartate aminotransferase 63 1.52 1.52 57.8 gi 15239 aspartate aminotransferase Proteins in Group N Unu Total Accession # Name 53 1.52 1.52 gi 15239772 aspartate aminotransferase 63 1.52 1.52 gi 15239772 aspartate aminotransf Ar 0.00 1.52 gi 15239078 aspartate aminotransferase Ar Total Accession # Name A 63 1.52 1.52 gi 15239772 aspartate aminotransferase Ar 0.00 1.52 gi 15239772 aspartate aminotransferase Ar Totein Sequence Coverage - aspartate aminotransferase Ar DSVFSNVARAPEDPILGVTVAYNNDFSPVKINLGVGAYRTEEGKE TYPHYPWSMHPKVFNLAGLSVEYFNYDPATRGLDFKGLLEDLGA GELYGEKVGALSIVCKSADVASKVESQVKLVVRPMYSSPPIHGASI <						2000 -			31	13.27 410.28		//6.50			
V		640.402	8 320.7	7051 57	6.3174	288.6623	1000 -	129.1	2	l i dan di C	424.28	689.47	889.	59	1017.67	
C[(C0I]	970.539	485.7	7731 47	7.2490	239.1281	0	0 10		200 300	400 50	մետուկենցեր երկենցերի է։ 0 600 700	پلیانی <u>، مساملی</u> ۵۵۵ م	14-1-1-1-1- 10	1000 1	100
K		1098.634	0 549.8	8206 14	7.1128	74.0600		0 10	~	200 300	400 50	m/z Da	000 30	~	1000 1	100

gi|15231608 3-isopropylmalate dehydratase-like protein (small subunit)

F	rote	ns Dete	ected													
1	N	Unu	Total	% Cov	Accessio.		Nam	e	Species	Peptides(95%)	Biological Processes	Molecular Fund	tions	P	ANTHER ID	*
	66	1.53	1.53	74.7	gi 28974	NAD-depend	entisocitrate	dehydrogenase beta s	Brassica napus	1						
	67	1.53	1.53	62.8	gi 15231	3-isopropylm	alate dehydr:	atase-like protein (smal	Arabidopsis tha	liana 1						
	68	1.52	1.58	36.8	gi 15239	aspartate amir	notransferas	e Asp2[Arabidopsis th	Arabidopsis tha	liana 1						-
F	rote	n Grou	p 67 -	3-isopro	opylmalat	e dehydratase	e-like prote	in (small subuni) [Arabidopsis tl	aliana]						
ſ			Pr	oteins in	Group					Peptides in	Group					
	Ν	Unu	Total	Acces	sion #	Name	Con⊽	Conf ⊽ S	equence 🗠	Modifications	△ Cleavages △	Mass Prec MW	z	Sc	Spectrum	*
	67	1.53	1.53	gi 15231	608 3	-isopropylmala	1.52	97 EHAPVCI	GAAGAK	ICAT-C:13C(9)(C)@6	6	0.1858 1458.95.	. 3	13	5.1.1.1265.3	
		0.00	1.52	gi]15224	221	3-isopropyImalate	0.01	2 EKLGSF		Oxidation(F)@6	cleaved F	0.0430 695.392) 1	7	1.1.1.1829.4	
		0.00	1.52	gi 15224	222	3-isopropyImalate	0.00	<1 EDGSSLI	INHTTRK	Glu->pyro-Glu@N-te Deamidated(N)@9	erm missed R-K	0.0192 1552.80.	. 3	7	3.1.1.1864.2	.
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	13.77.0	OOFT			INICOTT O	COPEL OF WORK	TENUT	T0003TT TTD1/33		FUCT OF UT VONT D	POTTDEPOTTE	TREPRENTOS				IDC
	MATS EMKS ragn	QQFLNI KYSVII	PTLFKS	ELASSN GCGSS ence	KNSCTLCI REHAPVC	PSPFLQLKSAS LGAAGAKAVVA	TIFNYKPL ESYARIFF	TSSSATIITRVAP RNCVATGEIFPLE	SSSDSGESITRET SEVRICDECKTGI	FHGLCFVLKDNIDI VVTIEHKEDGSSLI	TDQIIPAEYGTLIPS LINHTTRKEYKLKPI	IPEDREKLGSI GDAGPVIDAG(ALNG	SL PE (ARE	KFYNERFVV KAGMIPSA	7PG
	MATS EMKS	QQFLNE KYSVII nentatio	ON Evid	GCGSS GCGSS ence GAAGAM	KNSCTLC: REHAPVC	PSPFLQLKSAS LGAAGAKAVVA	TIFNYKPL ESYARIFF	TSSSATIITRVAF RNCVATGEIFPLE	SSSDSGESITRET SEVRICDECKTGI	FHGLCFVLKDNIDJ	FDQIIPAEYGTLIPS LINHTTRKEYKLKPI	IPEDREKLGSI GDAGPVIDAGO	TALNG	SL PF (ARF	KFYNERFVV KAGMIPSA	7PG
F	MATS EMKS ragn Res	QQFLNE KYSVII nentatio EHAP	PTLFKS IGGDNF on Evid VC[C9]]L b	GCGSS ence GAAGAk	KNSCTLC: REHAPVC:	SPFLQLKSAS GAAGAKAVVA y y+	TIFNYKPL ESYARIFF 2	TSSSATIITRVA# RNCVATGEIFPLE	SSSDSGESITRET	FHGLCFVLKDNIDI	TDQIIPAEYGTLIPS	GDAGPVIDAG	ALNG	ARP	KFYNERFVV KAGMIPSA	/PG
	MATS EMKS ragn Res E	QQFLNH KYSVII nentatio EHAP	PTLFKS IGGDNH on Evid VC[C9]L b 130.04	ELASSIN FGCGSS ence GAAGAM b 99 6	KNSCTLC: REHAPVC: ()+2)5.5286 1:	PSPFLQLKSAS GAAGAKAVVA y y+ 159.7773 730	TIFNYKPL ESYARIFF 2 3923	TSSSATIITRVAP RNCVATGEIFPLE	SSSDSGESITRET SEVRICDECKTGI	FHGLCFVLKDNID VVTIEHKEDGSSLI	rDQIIPAEYGTLIPS LINHTTRKEYKLKPI y13+2 b6 98	GDAGPVIDAGO	'ALNG (IFA) (11	ARF	KFYNERFVV KAGMIPSA	7PG
F	MATS EMKS ragn Res E H	QQFLNH KYSVII nentatio EHAP	PTLFKS IGGDNF on Evid VC[C9]L b 130.04 267.10	GCGSS GCGSS ence GAAGAk 99 6 88 13	KNSCTLC: REHAPVC: 55.5286 11 4.0580 11	y y+ 459.7773 730 330.7347 665	Z 2 3923 8710	TSSSATIITRVAP RNCVATGEIFPLE 1800 - b 1600 -	SSSDSGESITRET SEVRICDECKTGI	y5 v6 v10 v7	Y13+2 b6 y8	GDAGPVIDAGO	'ALNG (IFA)	SL PF	KFYNERFVV KAGMIPSA	7PG
F	ragn Res E H A	QQFLNH KYSVII nentatio EHAP	PTLFKS IGGDNF IGGDNF VC[C9]L b 130.04 267.10 338.14	ELASSN FGCGSS ence GAAGAH 99 6 88 13 59 16	KNSCTLC: REHAPVC: (((((((((((((((((((y y+ 159.7773 730 330.7347 665 193.6758 597	TIFNYKPL ESYARIFF 2 3923 8710 3415	1800 - b 1600 - 1400 - b	SSSDSGESITRET SEVRICDECKTGI	FHGLCFVLKDNID VVTIEHKEDGSSLI y5 b4 y6 y19 c 2 2 2 2 2 487.29	y13+2 b6 y8	GDAGPVIDAGO	*ALNG *IFAY	SL PF	KFYNERFVV KAGMIPSA	7PG
F	Res E H A P	QQFLNH KYSVII nentatio	PTLFKS IGGDNF IGGDNF VC[C9]L b 130.04 267.10 338.14 435.19	CGCGSS CGCGSS ence GAAGAk 99 6 88 13 59 16 87 21	KNSCTLC: REHAPVC: ++2 55.5286 1: 4.0580 1: 9.5766 1 8.1030 1:	2SPFLQLKSAS GAAGAKAVVA 459.7773 730 330.7347 665 193.6758 597 122.6387 561	2 3923 8710 3415 8230	1800	SSSDSGESITRET SEVRICDECKTGI	FHGLCFVLKDNIDI VVTIEHKEDGSSLI y5 46 y199 21-2 474.30 487.29	Y13+2 b6 y8	gdagpvidago y10 y	7ALNG 51 FA3	SL PP ZARP	KFYNERFVV KAGMIPSA	/PG
F	Res E H A P V	QQFLNE KYSVII nentatio EHAP	PTLFKS IGGDNF On Evid VC[C9]L b 130.04 267.10 338.14 435.19 534.26	ELASSN GCGSS ence GAAGAH 99 6 88 133 59 16 87 21 71 26	KNSCTLC: REHAPVC: 55.5286 1: 4.0580 1: 9.5766 1 8.1030 1: 7.6372 1:	y y+ 159.7773 730 330.7347 665 193.6758 597 122.6387 561 325.5859 513	2 3923 8710 3415 8230 2966	1800 - b 1400 - 1200 - b 1000 - 1200 - b	SSSDSGESITRET SEVRICDECKTGI	Y5 Y6 Y7 474.30 487.29	y13+2 b6 y8	gdagpvidago y10 y	TALNG SIFAS	SL PP VARE	KFYNERFVV KAGMI PSA	/PG
F	MATS EMKS EMKS E H A A P V C[C9	QQFLNR KYSVII EHAP idue	PTLFKS IGGDNF on Evid VC[C9]L 267.10 338.14 435.19 534.26 873.43	ELASSN GCGSS ence GAAGAA 99 6 88 13 59 16 87 21 71 26 34 43 34 43	KNSCTLC: REHAPVC: 55.5286 1. 4.0580 1. 9.5766 1. 8.1030 1. 7.6372 1. 7.2204 .	y y+ y59.7773 730 330.7347 665 193.6758 597 122.6387 561 326.5175 463	2 3923 8710 3415 8230 2966 7624	1800 - b 1600 - 1200 - 200 -	SSSDSGESITRET SEVRICDECKTGI	y6 y7 y5 y6 y7 y6 y1000222 y7 474.30 487.29 487.29	y13+2 b6 y8	y10	7ALNG (IFA) 711	SL PP VARP	b13 321.84	/PG
F	MATS EMKS E Res E H A P V C[C9 L	QQFLNE KYSVII eentatio EHAP idue	PTLFKS IGGDNF on Evid VC[C9]L b 130.04 267.10 338.14 435.19 534.26 873.43 986.51	CGCGSS ence GAAGAK 99 6 88 13 59 16 87 21 71 26 34 43 75 49	KNSCTLC: REHAPVC: 5.5286 1 4.0580 1 9.5766 1 8.1030 1 7.6372 1 7.2204 2 3.7624 2	y y+ y59.7773 730 330.7347 665 193.6758 597 122.6387 561 326.5175 463 367.3511 294	2 3923 8710 3415 8230 2966 7624 1792	1800	SSSDSGESITRET SEVRICDECKTGI	y5 y6 y7 b4 y7 y7 474.30 487.29 10 29	y13+2 b6 y8	y10	TALNG DIFAY	SLPP (ARE	b13	/PG
F	Res E H A C[C9 L G	QQFLNH KYSVII nentatio EHAP idue	PTLFKS IGGDNF IGGDNF 130.04 267.10 338.14 435.19 534.26 873.43 986.51 1043.53	ELASSN GCGSS ence GAAGAA 99 € € 88 13 59 16 87 21 71 26 34 43 75 49 90 52 81 55	KNSCTLC REHAPVC 5.5286 1 4.0580 1 9.5766 1 8.1030 1 7.6372 1 7.2204 1 3.7624 1 2.22731 1 7.7917	y y+ 159.7773 730 330.7347 665 193.6768 597 122.6387 561 326.5175 463 387.3511 294 174.2671 237	2 3923 8710 3415 8230 2966 7624 1792 6372	TSSSATIITRVAA RNCVATGEIFPLE	SSSDSGESITRET SEVRICDECKTGI	FHGLCFVLKDNID VVTIEHKEDGSSLI y5 y6 y19962+2 474.30 487.29 10 .29 587.43	y13+2 b6 y8	y10 1073.71	ALNG SIFAY	LPP (ARE	6FYNERFVV (AGMIPSA b13 321.84 .1338.82	2 PG
F	Res E H A P V C[C9 L G A A	QQFLNH KYSVII Tentatio	PTLFKS IGGDNF IGGDNF VC[C9]L b 130.04 267.10 338.14 435.19 534.26 873.43 986.51 1043.53 1114.57	CGCGSS CGCGS CGC	KNSCTLC: REHAPVC: 55.5286 1: 4.0580 1: 9.5766 1 8.1030 1 7.2204 1 3.7624 1 2.2731 1 7.7917 1 3.3102 1	y y+ 459.7773 730 330.7347 665 193.6758 597 122.6387 561 326.5175 463 587.3511 294 474.2671 237 117.2456 209	2 3923 8710 3415 8230 2966 7624 1792 6372 1264 6079	TSSSATIITRVAA RNCVATGEIFPLE	SSSDSGESITRET SEVRICDECKTGI 249.12 249.12 249.12 292. 249.12 292. 249.12 292.	FHGLCFVLKDNID VVTIEHKEDGSSLI y5 b4 y6 y1 b7 b4 y6 y1 b7 2 2 2 487.29 10 587.43 138.18 104.25	y13+2 b6 y8	y10 1002.66	*ALNG	JL PP (ARE	kFYNERFVV (AGMIPSA b13 321.84 1338.82	2 2
F	Res E H A P V C[C9 L G A A A G	QQFLNE KYSVII EHAP idue	PTLFKS IGGDNI IGGDNI VC[C9]L b 130.04 267.10 338.14 435.19 534.26 873.43 986.51 1043.53 1114.57 1185.61 1242.63	SLASSN GCGSS ence GAAGAH 99 6 88 13 59 16 87 21 71 26 34 43 75 90 52 61 55 32 59	KNSCTLC: REHAPVC: REHAPVC: 5.5286 1: 4.0580 1: 9.5766 1: 8.1030 1: 7.6372 1: 7.6372 1: 7.7204 2: 3.7624 2: 2.2731 2: 7.7917 2: 3.3102 2: 1.8210 2:	y y+ 159.7773 730 330.7347 665 193.6758 597 122.6387 561 326.5175 463 387.3511 294 474.2671 237 117.2456 209 346.2085 173 725.1744 138	2 3923 8710 3415 8230 2966 7624 1792 6372 1264 6079 0893	TSSSATIITRVAA RNCVATGEIFPLE 1800 - 1600 - 1200 - ↓ 1200 - ↓ 1200 - ↓ 1200 - ↓ 1200 - ↓ 1200 - ↓ 1000 - 110.09 \	SSSDSGESITRET SEVRICDECKTGI 1 92-2 92-2 53 249.12 292 221.12 44 51.10 44	y6 y7 b4 y7 b4 y7 b4 y7 b4 y7 10 587.43 138.18 104.26	y13+2 b6 y8 811.47 856.48 783.44 1	y10 1 1002.66 1 1073.71	ALNG SIFAY 111 04.73 1193 7	JLPP (ARE 1	6FYNERFVV (AGMIPSA b13 321.84 1338.82 1403.63	2 2
	ragn Res E H A P V C[C9 L G A A A G A	QQFLNR KYSVII EHAP idue	PTLFK8 IGGDNE on Evid VC[C9]L b 130.04 267.10 338.14 435.19 534.26 873.43 986.51 1043.53 1114.57 1185.61 1242.63 1313.67	SLASSN GCGSS ence GAAGAM 99 68 30 67 71 26 34 43 75 90 52 61 52 61 32 47 62	KNSCTLC: REHAPVC: S5.5286 1 4.0580 1 9.5766 1 8.1030 1 7.2204 1 3.7624 1 2.2731 1 7.7917 1 3.3102 1 1.8210 1 7.3395 1	y y+ 459.7773 730 330.7347 665 193.6758 597 122.6387 561 326.5175 463 326.5175 463 387.3511 294 474.2671 237 147.2456 209 346.2085 173 275.1714 138 218.1499 109	2 3923 8710 3415 8230 2966 7624 1792 6372 1264 6079 0893 5786	TSSSATIITRVAP RNCVATGEIFPLE	SSSDSGESITRET SEVRICDECKTGI 249.12 249.12 249.12 292. 221.12 44	y5 y6 y7 b4 y1000000000000000000000000000000000000	y13+2 b6 y8 811.47 856.48 783.44 9	1073.71 1002.66	ALNG EIFAY 04.73 1193.7	1 1	6FYNERFVV (AGMI PSA b13 321.84 1338.82 1403.63	2 2

gi|60686421 Oxalic acid oxidase

Prote	ins Dete	ected									
N	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*
4	6.02	6.02	69.4	gi 15224	cytoplasmic aconitate hydratase[Arabidopsis th	Arabidopsis thaliana	4				
5	5.00	5.00	42.0	gi 15237	translation elongation factor EF-Tu precursor, ch	Arabidopsis thaliana	3				
6	4.77	4.77	78.7	gi 60686	oxalic acid oxidase [Brassica napus]	Brassica napus	4				
7	4.29	4.29	55.5	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	2				1
8	4.11	4.11	68.9	gi 15238	5-methyltetrahydropteroyltriglutamate-homocyst	Arabidopsis thaliana	4				1
9	4.04	4.04	62.4	gi 15222	glyceraldehyde-3-phosphate dehydrogenase, pu	Arabidopsis thaliana	2				-

Protein Group 6 - oxalic acid oxidase [Brassica napus]

			Proteins in Group				Pept	ides in Group					
N	Unu	Tot	Accession #	Name	Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	S 🔺
	6 4.7	7 4.	7 gi 60686421	oxalic acid oxidase [2.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.0222	1987.09	2	2 =
	0.(0 4.	77 gi]15218535	germin-like protein [Ar	2.00	99	SVQDFCVANLKR	ICAT-C(C)@6	cleaved A-S	0.0935	1605.92	3	1
	0.	0 4.	77 gi]914911	germin-like protein	0.77	83	SVQDFCVANLK	ICAT-C(C)@6	cleaved A-S	0.0221	1449.75	2	1
	0.(0 4.	77 gi]1169941	Germin-like protein 1.	0.00	71	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.1912	1987.26	4	1
					0.00	99	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.1294	1978.17	4	1
					0.00	32	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.1842	1978.23	4	1
					0.00	< 1	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9 His->GIn@14		0.1668	1978.24	4	1
					0.00	34	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.2004	1987.27	4	1
					0.00	1	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.1966	1978.24	4	
					0.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.1601	1987.23	4	1
					0.00	29	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.2246	1978.27	4	1 🚽
•			III	- F	•								Þ.

Protein Sequence Coverage - oxalic acid oxidase [Brassica napus]

MLRIIFLLSLLFALSNASVQDFCVANLKRAETPAGYPCIRPIHVKASDFVFSLGTPGNTTNIISAAVTPGFVAQFPALNGLGISTARLDLAPKGVIPMHTHPGASEVLFVLDGSITAGFISSANSVYV QTLKPGQVMVFPQGLLHFQINAGKTPAAAFVTFSSASPGLQILDFALFANTLSTELVSATTFLPPATVKTLKGVLGGTG

gi|15238686 Homocysteine S-methyltransferase

Р	rotei	ns Dete	ected									
Γ	Ν	Unu	Total	% Cov	Accessio	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID	*
Γ	4	6.02	6.02	69.4	gi 15224	cytoplasmic aconitate hydratase[Arabidopsis th	Arabidopsis thaliana	4				
Γ	5	5.00	5.00	42.0	gi 15237	translation elongation factor EF-Tu precursor, ch	Arabidopsis thaliana	3				
Γ	6	4.77	4.77	78.7	gi 60686	oxalic acid oxidase [Brassica napus]	Brassica napus	4				
	7	4.29	4.29	55.5	gi 15232	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	2				
	8	4.11	4.11	68.9	gi 15238	5-methyltetrahydropteroyltriglutamate-homocyst	Arabidopsisthaliana	4				
Ľ	9	4.04	4.04	62.4	gi 15222	glyceraldehyde-3-phosphate dehydrogenase, pu	Arabidopsis thaliana	2				

Protein Group 8 - 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Arabidopsis thaliana]

				Proteins in Group				Pepti	des in Group					
	Ν	Unu	Total	Accession #	Name	Con… ⊽	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	S 🔺
	8	4.11	4.11	gi 15238686	5-methyltetrahydrop	2.00	99	CVKPPVIYGDVSRPK	ICAT-C(C)@1		0.1550	1884.18	4	1 E
Γ		0.00	4.00	gi]15228634	putative methionine sy	2.00	99	HETCYQIALAIKDEVEDLEK	ICAT-C(C)@4		0.2187	2573.48	4	1
						0.11	22	VNRMLAVLEONILWVNPDCGLK	Oxidation(N)@2 Deamidated(Q)@10 Trp->Phe@14 ICAT-C:13C(9)(C)@19	missed K	-0.0736	2710.37	3	1
						0.00	< 1	VPELGPEVKFSYASHK	Oxidation(K)@16	cleaved I-V	-0.1436	1802.77	2	1
						0.00	<1	AAKGVDKSFELLSLLPKILP	Oxidation(F)@9 Oxidation(P)@20	cleaved P-I	-0.0548	2170.20	4	
						0.00	<1	AAKGVDKSFELLSLLPKILP	Oxidation(F)@9 Oxidation(P)@20	cleaved P-I	-0.0575	2170.20	4	
						0.00	< 1	AAKGVDKSFELLSLLPKILPIYKEVITEL	Oxidation(K)@3	cleaved E	-0.4370	4526.09	5	
						0.00	<1	AAKGVDKSFELLSLLPKILPIYKEVITEL	Oxidation(P)@42 Oxidation(K)@52	missed K	-0.1811	5751.98	6	Ţ
•					•	<			0.11.0 0005		0.4000	0.000 (D	-	Þ

Protein Sequence Coverage - 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Arabidopsis thaliana]

MASHIVGYPRMGPKRELKFALESFWDGKSTAEDLQKVSADLRSSIWKQMSAAGTKFIPSNTFAHYDQVLDTTAMLGAVPPRYGYTGGEIGLDVYFSMARGNASVPAMEMTKWFDTNYHYIVPELGPEV NFSYASHKAVNEYKEAKALGVDTVPVLVGPVSYLLLSKAAKGVDKSFELLSLLPKILPIYKEVITELKAAGATWIQLDEPVLVMDLEGQKLQAFTGAYAELESTLSGLNVLVETYFADIPAEAYKTLT SLKGVTAFGFDLVRGTKTLDLVKAGFPEGKYLFAGVVDGRNIWANDFAASLSTLQALEGIVGKDKLVVSTSCSLLHTAVDLINETKLDDEIKSWLAFAAQKVVEVNALAKALAGQKDEALFSANAAAL ASRRSSPRVTNEGVQKAAAALKGSDHRRATNVSARLDAQQKKLNLPILPTTTIGSFPQTVELRRVRREYKAKKVSEEDYVKAIKEEIKKVVDLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTAN GWVQSYGSR**CVKPPVIYGDVSRPKAM**TVFWSAMAQSMTSRPMKGMLTGPVTILNWSFVRNDQPR**HETCYQIALAIKDEVEDLEK**GGIGVIQIDEAALREGLPLRKSEHAFYLDWAVHSFRITNCGVQD STQIHTHMCYSHFNDIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYGAGIGPGVYDIHSPRIPSEEIADRVNKMLAVLEQNILWVNPDCGLKTRKYTEVKPALKNMVDAAKLIRSQLASAK

gi|89257688 Streptomyces cyclase / dehydrase family protein

Pro	oteins	Dete	cted																					G	
	N U	nu	Total	% Cov	Ac	cession #			Name					:	Spec	ies	F	Peptides(95%	b) Bi	ological P	rocesses	Molecular	Functions	PANT	*
	46	2.00	2.00	56.4	gi 1578	49770	ERD12 pr	otein [Brass	sicarapa]			E	Brassi	ica ra	ра			1	-					
	47	2.00	2.00	55.0	gi 8925	7688	Streptomy	ces cyclas	e/dehyd	rasefa	mily pr	otein [. E	Brassi	ica o	leracea			1						_
	48	1.88	3.88	56.8	gi 1523	6220	mitochon	drial elong	ation fac	tor Tu [Arabido	opsis th.	/	Arabid	dops	is thalian	na		3						÷
•			,																			,		4	
Pro	otein	Grou	p 47 -	Strepto	myces	cyclase/de	hydrase fa	nily prot	ein (Bra	assica	a ole	racea]												6	٦
				Proteins	s in Grou	p										Р	Pept	tides in Grou	p						٦
	N U	nu	Total	Acce	ssion #		Name	Con⊽	Conf		:	Sequen	nce			Mo	odifi	ications	CI	eavages	∆Mass	Prec MW	z Sc	Spectr	~
	47	2.00	2.00	gi 8925	7688	Strepton	yces cycla:	2.00	99	SEL	AQSI	AE FH T	YHI	GPG	S	ICAT-C:	:130	C(9)(C)@20			0.3255	3161.86	. 5 16	5.1.1.131	-
								0.00	1	MP S	LTP	EER				Oxidatio	ion(l	M)@1			0.1901	1203.73	. 2 9	5.1.1.124	-
•							•	•								Deamid	later	d(C))@4						Þ	
Pro	otein	Sequ	ence (Coveraç	je - Str	eptomyces	cyclase/de	hydrase	family	prote	in (B	rassic	ca o	lera	cea]										
М	SOLT	PFFR	SELA	STAR	HTYHL	POSCSSLB	AORTHAPP	FTVWSVV	BBEDK	POTY	KHET	KSCSI	VFD	GFEI	MRV	CTRAN	UNU	TSGLPANT	STE	RLDTLDI	FRRVTG	FSTIGGE	HRLTNYK	SVTTVHE	
FF	CKERF	IWTV	VLESI	VVDMF	EGNSEI	DDTRMFADT	VVKLNLQK	LATVTEA	MARNA	GDGS	GAQV	T	* 11 12	01.01		JOINA.		IDODIANI	DIL						<u></u>
																									_
Fra	igmei	ntatio	n Evid	ence																					
		SELA	SIAEF	ITYHLGF	GSCIC91	SSLHAQR																			_
							_																		_
	Residu	ie	b	77 20	0+2	y	y+2		1	المت	الطرحيا	ا ا س	والط	-		الما ا	ala	بالاقتنا طيسا	a	.el		atolari			
L L			800.44	11 J	0 7111	2047.2000	1214.1341	60	000	b4+52	y2 y - p832	1091 <u>0</u>	₹9216		516212	428 y 2042	2	y27+2	~ y	15	y 13	20 92 1			
F			929.45	75 40	35 2324	2363 1397	1182 0735				217	10													
			1076 52	59 5	38 7666	2234 0971	1117.5522																		
H			1213.58	48 6	07.2960	2087.0287	1044.0180	50	00																
Т			1314.63	25 6	57.8199	1949.9697	975.4885	48	500 -			511.3	1												
Y			1477.69	58 73	39.3515	1848.9221	924.9647	40	00 -																
н			1614.75	47 80	07.8810	1685.8587	843.4330	₹38	189	.10															
L			1727.83	88 86	64.4230	1548.7998	774.9036	tens																	
G			1784.86	02 8	92.9338	1435.7158	718.3615	르이	~																
P			1881.91	30 94	41.4601	1378.6943	689.8508	28	00																
G			1938.93	45 90	69.9709	1281.6415	641.3244	20	00																
S			2025.96	65 10	13.4869	1224.6201	612.8137	18	500 -		26	9.15													
С	[C9I]		2365.13	29 11	33.0701	1137.5880	569.2977	10	000									1270 02							
S			2452.16	49 122	26.5861	798.4217	399.7145				40	2.21		198.	49 8	86.47		13/0.03	86.00)		2434.33	2634.57	_	
s			2539.19	69 12	70.1021	711.3896	356.1985		- 00			ما الس ا	ĽĬĬ	T.			և			206	5.24	ار ار	2727.3	8	
L			2652.28	10 13	26.6441	624.3576	312.6824		04	20	0 4	00 9	300			000 42	141.41 200	1400 160	 0 19	100 2000 300 2000	2200	11 11 11 11 11 2400 2600	2800 3	000	
H			2789.33	99 13	95.1736	511.2736	256.1404	-	0	20	4			000	· 1	000 12	200	m/z, D	a id	2000	2200	2400 2000	, 2000 3		
1				1	11		+																		

gi|15235668 Extensin-like protein

Prote	ins Dete	ected														
N 38 39 ∢	Unu 2.00 2.00	Total 2.00 2.00	% Cov 40.5 gi 1 62.0 gi 1	Accession # 5235668 5224339	extensin-lik unknown p	N ke protein (A rotein (Arabi	ame rabidops dopsis t	sis thaliana] naliana] III	Specie Arabidopsis Arabidopsis	thaliana thaliana	Peptides(95%) 1 1	Biological F	Processes	Molecular Fi	Inctions	PANT ~
Prote	in Grou	p 38 - e	xtensin-lik	e protein [Arat	oidopsis tha	liana]										
			Proteins in	Group						Pe	eptides in Group)				
N	Unu	Total	Accessio	n# 1	Name 🔺	Con⊽	Conf	Sequen	се	Mo	odifications	Cleavage	s ∆Mass	Prec MW	z So	: Sper 🔺
38	3 2.00	2.00	gi 15235668	extensin-	like protei	2.00	99	IPASICQLPK		ICAT-C	:13C(9)(C)@6		0.126	7 1304.88	2 14	4 4.1.1.1
	0.00	2.00	gi 15230120	disease re	esistance p 👻	0.00	< 1	ADIGRLKNVTVF		Deamid	lated(R)@5	cleaved P-A	0.161	8 1349.88	2 10	0 3.1.1.1
٩ 🗖		in	I		•	I ■										•
Prote MKK YLPI NLNI	FIQILLE EELGLLS EIIFMNN	FFFFLI SDLALF	NLTNALSI HVNSNRFC	extensin-like pr SSDGGVLSDNE GTVPHRFNRLK	vrhigrrgl	idopsis th LEFAER <mark>SV</mark> NRFAGKFE	aliana] KITVD TVVLQ	PSLNFENPRLRN LPSLKFLDLRFN	AYIALQAWI Efegivpki	KQAILS Elfsk <mark>i</mark>	SDPNNFTSNWI DLDAIFINHNR	GSNVCNYT(FR FELPEN)	GVFCSPA1 FGDSPVSV	LDNRKIRTV	AGIDL	NHADIAG
SFS(PPP) PPP)	CGRSVSI PVYSSPI PPVYYSS	PRPPVV PPPPSP SPPPPP	TPLPPPSL APTPVYCT VYYSSPPP	RNVIVFDVSFN PSPPPPAPIFS RPPPPPPHSPP PPPVHYSSPPP	ELVGPLPES TPPTLTSPP PPQFSPPPP PEVHYHSPP	VGEMVSVE PPSPPPPV EPYYYSSE PSPVHYSS	QLNVA YSPPP PPPPHS PPPPPP	HNMLSGKIPASI PPPPPPPVYSPP SPPPHSPPPPHS SAPCEESPPPAP	CQLPKLEN PPPPPPPP PPPPIYPY VVHHSPPP	FTYSYN PPVYSI LSPPPI PMVHHS	NFFTGEAPVCL PPPPPPPPPP PTPVSSPPPT SPPPPVIHQSP	RLPEFDDRI PPVYSPPP PVYSPPPP PPPSPEYE(RNCLPGRI PSPPPPPI PPCIEPPI GPLPPVI(PAQRSPGQC PPVYSPPPI PPPPCIEYS GVSYASPPI	KAFLS PPPPP PPPPP PPPFY	RPPVNCG PPPVYSP PVVHYSS
SFS(PPP) PPP) Fragr	CGRSVSI PVYSSPI PPVYYS: mentatio	PRPPVV PPPPSP SPPPPP on Evide	TPLPPPSL APTPVYCT VYYSSPPP ence	REPERENTIAL	ELVGPLPES TPPTLTSPP PPQFSPPPP PEVHYHSPP	VGEMVSVE PPSPPPV EPYYYSSE PSPVHYSS	QLNVA YSPPP PPPHS PPPPP	HNMLSGK IPASI PPPPPPPVSPP SPPPHSPPPPHS SAPCEESPPPAP	CQLPKLEN PPPPPPPP PPPPIYPY VVHHSPPP	FTYSYN PPVYSI LSPPPI PMVHHS	NFFTGEAPVCL PPPPPPPPPP PTPVSSPPPT SPPPPVIHQSP	RLPEFDDRI PPVYSPPPI PVYSPPPPI PPPSPEYE(RNCLPGRI PSPPPPPI PPCIEPPI GPLPPVI(PAQRSPGQC PPVYSPPPI PPPPCIEYS GVSYASPPI	KAFLS PPPPP PPPPP PPFY	RPPVNCG PPPVYSP PVVHYSS
SFS(PPP) PPP) Fragr	CGRSVSI PVYSSPI PPVYSS mentatio	PRPPVV PPPPSP SPPPPP on Evide C(C9)JQLP	TPLPPPSL APTPVYCT VYYSSPPP ence	RNVIVFDVSFN PSPPPPAPIFS RPPPPPPHSPP PPPVHYSSPPP	ELVGPLPES TPPTLTSPP PPQFSPPPP PEVHYHSPP	VGEMVSVE PPSPPPV EPYYYSSE PSPVHYSS	QLNVA YSPPP PPPHS PPPPP	HNMLSGK IPASI PPPPPPPVSPP SPPPHSPPPPHS SAPCEESPPPAP	CQLPKLEN PPPPPPP PPPPIYPY VVHHSPPP	FTYSYN PPVYSI LSPPPI PMVHHS	NFFTGEAPVCL PPPPPPPPP PTPVSSPPPT SPPPPVIHQSP	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(RNCLPGRI PSPPPPP PPCIEPPI GPLPPVI(PAQRSPGQ0 PPVYSPPPI PPPPCIEYS GVSYASPPI	KAFLS PPPPP PPPPP PPFY	RPPVNCG PPPVYSP PVVHYSS
SFS(PPP) PPP) Fragr	CGRSVSI PVYSSPI PPVYSS mentatio IPASK	PRPPVV PPPPSP SPPPPP on Evide C[C9]QLP b	TPLPPPSL APTPVYCT VYYSSPPP ence % b+2	PSPPPPAPIFS RPPPPPPHSPP PPPVHYSSPPP	PPQFSPPP PPQFSPPP PEVHYHSPP y+2	VGEMVSVE PPSPPPPV EPYYYSSE PSPVHYSS	QLNVA YSPPP PPPHS PPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPP:	FTYSYN PPVYSE LSPPPE PMVHHS	VFFTGEAPVCL PPPPPPPPPP PPTPVSSPPPT SPPPPVIHQSP	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(NCLPGRI PSPPPPP PPCIEPPI GPLPPVI(PAQRSPGQ PPVYSPPPP PPPPCIEY: GVSYASPPI	KAFLS PPPPP PPPPP PPPFY	RPPVNCG PPPVYSP PVVHYSS
SFS(PPP) PPP) Fragi	CGRSVSI PVYSSPI PPVYSS nentatio IPASK sidue	PRPPVV PPPPSP SPPPPP on Evide C[C9]JQLP b 114.091	TPLPPPSL APTPVYCT VYYSSPPP ence K b+2 13 57.54	PSPPPPAPIFS RPPPPPPHSPP PPPVHYSSPPP 93 1305.7646	PPTLTSPP PPQFSPPPP PEVHYHSPP y+2 653.3859	VGEMVSVE PPSPPPPV EPYYYSSE PSPVHYSS 3500	QLNVA YYSPPP PPPHS SPPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP	CQLPKLEN PPPPPPPP PPPPIYPY VVHHSPPP	FTYSYN PPVYSE LSPPPF PMVHHS	PFFTGEAPVCL PPPPPPPPPP PPTPVSSPPPT SPPPPVIHQSP P22 y10+2	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(V87	PAQRSPGQ PPVYSPPPP PPPPCIEYS GVSYASPPI	YPPPP SPPPPP SPPPPY PPPFY y9	PPPVNCG PPPVYSP PVVHYSS y10
SFS(PPP) PPP) Fragi Rei I P	CGRSVSI PVYSSPI PPVYYSS mentatio IPASK sidue	PRPPVV PPPPSP SPPPPP on Evide C[C9]QLP b 114.091 211.144	нг рыррокы АРТРУУСТ VYYSSPPP ence ж b+2 13 57.54 11 106.07	y 93 1305.7646 57 1192.6805	ELVGPLPES TPPTLTSPP PPQFSPPP PEVHYHSPP 653.3859 596.8439	VGEMVSVE PPSPPPV EPYYYSSE PSPVHYSS 3500 3000	QLNVA YYSPPP PPPHS PPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPPI 3 4 244.18	FTYSYN PPVYSE LSPPPE PMVHHS	PFFIGEAPVCL PPPPPPPPPP PFTPVSSPPPT SPPPPVIHQSP P2 y10+2	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(V8	PAQRSPGQ PPVYSPPPP PPPPCIEYS GVSYASPPI	YPPPP PPPPP PPPFY YPPFY	PPPVNCG PPPVYSP PVVHYSS y10
Fragi Res A	CGRSVSI PVYSSPI PPVYSS mentatio 	PRPPVV PPPPSP SPPPPP on Evide C[C9]QLP b 114.091 211.144 282.181	нг рыррока артрууст чуузэррр епсе ж b+2 13 57.54 14 106.07 12 141.59	y 93 1305.7646 57 1192.6805 42 1095.6278	y+2 596.8439 548.3175	VGEMVSVE PPSPPPV EPYYYSSE PSPVHYSS 3500 - 3000 - 2500 -	QLNVA YYSPPP PPPHS PPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPP: 244.18	FTYSYN PPVYSI LSPPPI PMVHHS	PFFIGEAPVCL PPPPPPPPPP PTPVSSPPPT SPPPPVIHQSP P2 y10+2	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(V ⁸⁷	PAQRSPGQ PPVYSPPPP PPPPCIEYS GVSYASPPI	YPPPP PPPPP PPPFY y9	PPPVNCG PPPVYSP PVVHYSS y10
Fragi PPP) Fragi I P A S	CGRSVSI PVYSSPI PPVYSS mentatio pipASK sidue	PRPPVV PPPPSP SPPPPP C[C9]QLP b 114.091 211.144 282.181 369.213	b+2 3 57.54 11 106.07 12 141.59 32 185.11	y y y 93 1305.7646 57 1192.6805 42 1095.6278 03 1024.5907	y+2 596.8439 548.3175 512.7990	VGEMVSVE PPS PPPPV EPYYYSSE PSPVHYSS 3500 - 3000 - 2500 - 2500 - 2500 - 2500 -	QLNVA YSPPP PPPHS SPPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPP: 244.18	FTYSYN PPVYSI LSPPPI PMVHHS	PFFIGEAPVCL PPPPPPPPPP PTPVSSPPPT SPPPPVIHQSP P	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(V ⁶⁷	PAQRSPGQ PPVYSPPPP PPPPCIEYS GVSYASPPP y7 b8 y8	YPPPP YPPPP YPPFY y9 y9	PPPVNCG PPPVYSP PVVHYSS y10
Fragi PPP) Fragi Re: 1 P A S 1	CGRSVSI PVYSSPI PPVYSS mentatio 	PRPPVV PPPPSP SPPPPP C[C9]JQLP b 114.091 211.144 282.181 369.213 482.297	b+2 3 57.54 11 106.07 12 141.59 13 21.65	y y	y+2 653.3859 596.8439 548.3175 512.7990 469.2830	VGEMVSVE PPSPPPPV EPYYYSSE PSPVHYSS 3500 - 3000 - 2500 - 2500 - 2500 - 1500 - 1500 -	QLNVA YSPPP PPPHS PPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP	CQLPKLEN PPPPPPPP PPPPIYPY VVHHSPPP	FTYSYN PPVYSI LSPPPP PMVHHS	PFFIGEAPVCL PPPPPPPPPP PTPVSSPPPT SPPPPVIHQSP P P P P P P P P P P P P P	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(Y ⁶⁷	PAQRSPGQ PPVYSPPPP PPPPCIEYS GVSYASPPP y7 b8 y8	y9	PPPVNCG PPPVYSP PVVHYSS y10
Fragi Fragi	CGRSVSI PVYSSPI PPVYSS mentatio 	PRPPVV PPPPSP SPPPPP C[C9JJQLP b 114.091 211.144 282.181 369.213 482.297 821.463	b+2 3 57.54 11 106.07 12 141.59 32 185.11 73 241.65 37 411.23	y 93 1305.7646 57 1192.6805 42 1095.6278 03 1024.5907 23 937.5586 55 824.4746	y+2 653.3859 596.8439 548.3175 512.7990 469.2830 412.7409	VGEMVSVE PPSPPPPV EPYYYSSE PSPVHYSS 3500 3000 2500 2500 1500 1500	QLNVA YSPPP PPPHS PPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPP: VVHHSPPP: 254.15	FTYSYN PPVYSI LSPPPF PMVHHS	PFFFGEAPVCL PPPPPPPPPP PTPVSSPPPT SPPPPVIHQSP P2 y10+2	RLPEFDDR PPVYSPPP PVYSPPPP PPPSPEYE(Y67	PAQRSPGQ PPVYSPPPP PPPPCIEYS GVSYASPPI	y9	PPPVNCG PPPVYSP PVVHYSS y10
Fragr Fragr Res I P A S I C[CS Q	CGRSVSI PVYSSPI PPVYSS nentatio	PRPPVV PPPPSP SPPPPP on Evide C[C9]QLP b 114.091 211.144 282.181 369.213 482.297 821.463 949.522	b+2 3 57.54 12 141.59 32 185.11 73 241.65 37 411.23 23 475.26	y 93 1305.7646 57 1192.6805 42 1095.6278 03 1024.5907 23 937.5586 55 824.4746 48 485.3082	y+2 653.3859 596.8439 548.3175 512.7990 469.2830 412.7409 243.1577	VGEMVSVE PPSPPPV EPYYYSSE PSPVHYSS 3500 3000 2500 2500 1500 1000 5555 1000	QLNVA YSPPP PPPHS PPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP V84+2 1242 2 1	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPP: 244.18 254.15 271.19	FTYSYN PPVYSE LSPPPE PMVHHS	PPPPPPPPPP PPTPVSSPPPT SPPPPVIHQSP	y5	ygr	PAQRSPGQ PPVYSPPPP PPPPCIEY: GVSYASPPI	y9 1192.8	PPPVNCG PPPVYSP PVVHYSS y10 39
Fragr Fragr Res I P A S I C(CS Q L	CGRSVSI PVYSSPI PPVYSS nentatio	PRPPVV PPPPSP SPPPPP on Evide C[C9]QLP b 114.091 211.144 282.181 369.213 482.297 821.463 949.522 1062.606	b+2 3 57.54 41 106.07 12 141.59 32 185.11 73 241.65 37 411.23 23 475.26 33 531.80	y 93 1305.7646 57 1192.6805 42 1095.6278 03 1024.5907 23 937.5586 55 824.4746 48 485.3082 68 357.2496	y+2 653.3859 596.8439 548.3175 512.7990 469.2830 412.7409 243.1577 179.1285	VGEMVSVE PPSPPPV EPYYYSSE PSPVHYSS 3500 3000 2500 2500 1000 1000 500	QLNVA YSPPP PPPHS PPPPP	HIMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP VB4+2 02 42 b 141.12	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPP: 244.18 254.15 271.19	468 27	PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	819.48 9	V8	PAQRSPGQ PPVYSPPPP PPPPCIEYS GVSYASPPI	y9 y9 1192.8	PPPVNCG PPPVYSP PVVHYSS y10 39
Fragr Fragr Re: I P A S I C[CS Q L P	CGRSVSE PVYSSPE PPVYSS nentatio	PRPPVV PPPPSP SPPPPP on Evide C[C9]OLP b 114.091 211.144 282.181 369.213 482.297 821.463 949.522 1062.606 1159.655	b+2 3 57.54 11 106.07 12 141.59 32 185.11 73 241.65 37 411.23 23 57.56 365.11 57.54 37 57.54 365.11 57.54 37 57.54 38 531.80 31 580.33	y 93 1305.7646 57 1192.6805 42 1095.6278 03 1024.5907 23 937.5586 55 824.4746 48 485.3082 68 357.2496 32 244.1656	y+2 653.3859 596.8439 548.3175 512.7990 469.2830 412.7409 243.1577 179.1285 122.5864	VGEMVSVE PPSPPPV EPYYYSSE PSPVHYSS 3500 3000 2500 2500 1500 1000 500 0	QLNVA YSPPP PPPHS PPPPP	HNMLSGKIPASI PPPPPPPVSPP SPPPHSPPPHS SAPCEESPPPAP VB4+2 1242 12 100 200	CQLPKLEN: PPPPPPPP PPPPIYPY: VVHHSPPPI 244.18 254.15 271.19 300 400	FTYSYN PPVYSE LSPPPF PMVHH3 b7-425-42 468 27 	PFFTGEAPVCL PPPPPPPPPP PPPPVSSPPT SPPPVIHQSP SPPVIHQSP SPVIHQSP SPVIHQSP	819.48 9	VB	PAQRSPGQC PPVYSPPPP PPPPCIEY: GVSYASPPI 900 900 900 900 900 900 900 900 900 90	y9 1192.8	PPPVNCG PPPVYSP PVVHYSS y10 39 0 1300

gi|15235889 Multicatalytic endopeptidase complex, beta subunit

Pr	otei	ns Dete	ected								[
Г	N	Unu	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT	*
	26	2.20	2.20	39.1	gi 15231715	fructose bisphosphate aldolase-like protein [Ara	Arabidopsis thaliana	1				
	27	2.07	2.07	43.3	gi 15235889	multicatalytic endopeptidase complex, proteasom	Arabidopsisthaliana	1				
	28	2.06	2.06	57.1	gi 15233891	probable H+-transporting ATPase[Arabidopsis th	Arabidopsis thaliana	2				
	29	2.02	2.02	60.3	gi 15225545	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	1				
	30	2.01	2.01	63.3	gi 15236375	hydroxymethyltransferase [Arabidopsis thaliana]	Arabidopsis thaliana	2				
	31	2.01	2.01	46.7	gi 15220881	putative aldehyde dehydrogenase[Arabidopsis th	Arabidopsis thaliana	1				
	32	2.01	2.01	67.1	gi 15231702	monodehydroascorbate reductase (NADH) - like	Arabidopsis thaliana	1				
	22	2.00	2.00	63.0	ail15231775	CDC/8_like protein [Arabidonsis thaliana]	Arabidoneis thaliana	1				*
											•	

Protein Group 27 - multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana]

			Proteins in Gro	up					Peptides in Group						
N	Unu	Total	Accession #	Name		Con V	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	Sc	*
27	2.07	2.07	gi 15235889	multicatalytic endop	Ara	2.00	99	ITQLTDNVYVCR	ICAT-C:13C(9)(C)@11		0.2138	1660.08	3	15	4
	0.00	2.07	gi]41352685	putative proteasome 2	Bra	0.07	15	TSTGMYVANRASDK	Deamidated(R)@10	missed R-A	0.3015	1516.98	3	11	4 ≘
	0.00	2.07	gi]41352683	putative proteasome 2	Bra	0.00	- 1	A CONTROL TONIARIOD CC C	Oxidation(K)@14	missed K I	0.0502	2594 74	6	5	6
						0.00	~ 1	ASDKIIQLIDNVIVCKS65	ICAT-C:13C(9)(C)@15	1115560144	0.5550	3004.71	Ů	5	•
						0.00	< 1	AVSLAIARDGASGGVVR	Deamidated(R)@8	missed R-D	0.0814	1598.95	2	7	3
						0.00	< 1	AVSLAIARDGASGGVVRTV	Methyl(R)@8	missed R-D	0.0276	3602.94	4	8	e
						0.00	33	ITQLTDNVYVCR	ICAT-C(C)@11		0.2110	1651.05	3	11	4
						0.00	< 1	LNLDAPHSMGTTII	Oxidation(D)@4	cleaved D	-0.0227	1497.72	2	7	2 -
•					- F	•									Þ

Protein Sequence Coverage - multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana]

MD**LNLDAPHSMGTTII**GVTY<mark>NGGVVLGADSRTSTGMYVANRASDKITQLTDNVYVCRSGSAADSQVVSDYVR</mark>YFLHQHTIQHGQPATVKVSANLIRMLAYNNKNMLQTGLIVGGWDKYEGGKIYGIPL GGTVVEQPFAIGGSGSSYLYGFFDQAWKDNMTKEEAEQLVVK**AVSLAIARDGASGGVVRTVIINSEGVTRNFYPGDK**LQLWHEELEPQNSLLDILNAAGPEPMAM

gi|15237059 Translation elongation factor EF-Tu precursor, chloroplast

Ρ	rotei	ns Dete	ected									E]
	N	Unu	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER	ID 🔺	
	4	6.02	6.02	69.4	gi 15224580	cytoplasmic aconitate hydratase[Arabidopsis th	Arabidopsisthaliana	4					2
Ũ	5	5.00	5.00	42.0	gi 15237059	translation elongation factor EF-Tu precursor, ch	Arabidopsisthaliana	3					
Γ	6	4.77	4.77	78.7	gi 60686421	oxalic acid oxidase [Brassica napus]	Brassica napus	4					
Γ	7	4.29	4.29	55.5	gi 15232865	reversibly glycosylated polypeptide-1 [Arabidops	Arabidopsis thaliana	2					
	8	4.11	4.11	68.9	gi 15238686	5-methyltetrahydropteroyltriglutamate-homocyst	Arabidopsis thaliana	4				-	,
	۰ 📃					III						Þ	

Protein Group 5 - translation elongation factor EF-Tu precursor, chloroplast [Arabidopsis thaliana]

		1	Proteins in Group				Pept	ides in Group					
N	Unu	Total	Accession #	Name	Con⊽	Conf	Sequence	Modifications	Cleavages	∆Mass	Prec MW	z	S 🔶
	5 5.00	5.00	gi 15237059	translation elongatio	2.00	99	HSPFFAGYRPQFY		cleaved Y	0.1247	1615.88	3	1
					2.00	99	HYAHVDCPGHADYVK	ICAT-C(C)@7		0.1966	1938.08	4	2
					1.00	90	IVVE LIVPVACEQGMR	ICAT-C:13C(9)(C)@11 Oxidation(M)@15		0.1306	2007.22	3	1=
					0.00	<1	AGDNVGLLLRGIQKADIQR	Deamidated(N)@4 Deamidated(R)@10 Oxidation(K)@14 Oxidation(R)@19	cleaved L	-0.0319	2070.07	3	
					0.00	<1	AISAPAACSSSSR	Protein Terminal Acetyl@N-term Oxidation(P)@5 ICAT-C:13C(9)(C)@8 Oxidation(R)@13	cleaved M	0.2280	1516.95	3	
					0.00	< 1	EEGGR			0.1384	546.3782	1	
					0.00	< 1	EEGGR			0.0780	546.3178	1	-
•				•	•		Ш						Þ

Protein Sequence Coverage - translation elongation factor EF-Tu precursor, chloroplast [Arabidopsis thaliana]

M**AISAPAACSSSSR**ILCSYSSPSPSLCPAISTSGKLKTLTLSSSFLPSYSLTTSASQSTRRSFTVRAARGKFERKKPHVNIGTIGHVDHGKTTLTAALTMALASIGSSVAKKYDEIDAAPEERARGI TINTATVEYETENR**HYAHVDCPGHADYVK**NMITGAAQMDGAILVVSGADGPMPQTK**EHILLAKQVGVPDMVVF**LNKEDQVDDAELLELVEL**EVRELLSSYEFNGDDIPIISGSALLAVETLTENPK**VK RGDNKWVDKIYELMDAVDDYIPIPQ<mark>RQTELPFLLAVEDVFSITGR</mark>GTVATGRVERGTVKVGETVDLVGLRETRSYTVTGVEMFQKILDEAL<mark>AGDNVGLLLRGIQKADIQR</mark>GMVLAKPGSITPHTKFEA IIYVLKK**EEGGRHSPFFAGYRPQFYMRTTDVTGKVTKIMNDKDEESKMVMPGDRVKIVVELIVPVACEQGMRFAIREGGKTVGAGVI**GTILE

gi|414103 Myrosinase

Proteins Detected									
N Unu Total % Cov Accession	# myrosipasell	Name	Species Brassics papus	Peptides(95%)	Biological Proces	sses Molecular F	unctions	PANTHER I	D
2 10.86 10.86 61.2 gi 8745521	ribulose-1,5-b	isphosphate carboxylase/oxygena	Brassica napus	10					-
•		III	J.					,	•
Protein Group 1 - myrosinase [Brassic	a napus]								
Proteins in Group			Pept	ides in Group					
N Unu Total Accession #	Con⊽ Con	Sequence	Mo	difications	Cleavages 🛆	Mass Prec MW	z Sc	Spectrum	-
1 18.20 18.20 gi 22595 m	2.00	9 ADEEITCEENNPFTCSNTDILS	SK Asp->S ICAT-C	er@2 (C)@7	0	.2045 3058.57	3 17	1.1.1.1849.3	
39 1.55 3.57 gi 15239559 m			Asn->S ICAT-C	er@11 (C)@15					
	2.00	9 AG SD LKNGD TT CE S YTR	Deamid ICAT-C	ated(N)@7 :13C(9)(C)@12	missed K-N 0	.1313 2054.06	3 18	4.1.1.1358.2	
	2.00	9 CSPMVDTKHRCYGGNSSTEPYI	VAHNQLL No ICA Oxidati Oxidati ICAT-C	T(C)@1 on(M)@4 on(H)@9 (C)@11	missed K-H 1	.2442 4605.44	4 21	5.1.1.1437.2	
	2.00	9 DEEITCEENNPFTCSNTDILSS	K ICAT-C Deamid Asn->S ICAT-C	:13C(9)(C)@6 ated(N)@9 er@10 :13C(9)(C)@14	cleaved A0	.8251 3033.55	3 18	1.1.1.1826.2	
	2.00	9 IDYLCSHLCFLR	ICAT-C	(C)@5 (C)@9	C	.1146 1936.08	3 16	4.1.1.1460.2	
	2.00	9 QI IQDFKDYAD LCFK	Gin->py ICAT-C	ro-Glu@N-term (C)@13	0	.0482 2056.04	2 21	5.1.1.1513.4	
	2.00	9 QI IQDFKDYAD LCFKEFGGK	Gin->py ICAT-C	/ro-Glu@N-term :13C(9)(C)@13	0	.0141 2583.29	3 27	5.1.1.1523.2	
	1.52	7 CSQWVDKRCYGGDSSTEPYIVA	HNQLLAH ICAT-C Oxidati ICAT-C Asp->G	C)@1 on(W)@4 (C)@9 Iy@13	missed K-R0	.6790 4605.56	4 17	4.1.1.1454.4	
	1.52	7 NGDTTCESYTR	ICAT-C	:13C(9)(C)@6	0	.0651 1481.71	2 13	5.1.1.1316.3	-
4	•		III						•

Protein Sequence Coverage - myrosinase [Brassica napus]

MKLLHGLALVFLLAAASCKADEEITCEENNPFTCSNTDILSSKNFGKDFIFGVASSAYQIEGGRGRGVNVWDGFSHRYPEKAGSDLKNGDTTCESYTRWQKDVDVMGELNATGYRFSFAWSRIIPKGK VSRGVNQGGLDYYHKLIDALLEKNITPFVTLFHWDLPQTLQDEYEGFLDRQIIQDFKDYADLCFKEFGGKVKHWITINQLYTVPTRGYAIGTDAPGRCSPMVDTKHRCYGGNSSTEPYIVAHNQLLAH ATVVDLYRTKYKFQKGKIGPVMITRWFLPFDESDPASIEAAERMNQFFHGWYMEPLTKGRYPDIMRQIVGSRLPNFTEEEAELVAGSYDFLGLNYVTQYAQPKPNPYPSETHTAMMDAGVKLTYDNS RGEFLGPLFVEDKVNGNSYYYPKGIYYVMDYFKTKYGDPLIYVTENGFSTPSSENREQAIADYKRIDYLCSHLCFLRKVIKEKGVNVRGYFAWALGDNYEFCKGFTVRFGLSYVNWEDLDDRNLKESG KWYQRFINGTVKNAVKQDFLRSSLSSQSQKKRFADA

gi|4928472 Type 2 peroxiredoxin

Prot	eins De	tected														
N	Unu	Total	% ⊽	Access	ion #		Name			Species	Peptides(95%)	Biological P	rocesses	Molecular Fu	nctions	PANTHER ID 🔺
	37 1.72	1.72	93.8	gi 11998	0 F	Ferredoxin			BRA	ANA	1					
	34 2.00	2.00	92.6	gi 83032	224 u	unknown [Brassio	ca rapa]		Bra	ssica rapa	1					
1	28 2.00	2.00	91.5	gi 15231	702 r	monodehydroas	corbate reductase	e (NADH) - like	e Ara	bidopsisthaliana	1					-
•																•
Prot	ein Gro	up 34 - i	unknow	vn (Brass	sica rap	a]										
				Proteins	in Group)					Pe	ptides in Gro	up			
N	Unu	Total	Acces	ssion #		Name	Specie 🔺	Con V	Conf		Sequence		Modi	fications	Cleavag	es 🛆 Mass 🔺
:	34 2.00	2.00	gi 83032	2224	unknow	/n [Brassica r	Brassica ra 😑	2.00	99	VILFGVPGAF	TPTCSMK		ICAT-C:13	C(9)(C)@14		0.1046
	34 0.00	2.00	gi 49284	472	type 2 p	eroxiredoxin	Brassica ra	0.00	< 1		DOSTSPEDENDO		Oxidation	(111)@16	cleaved M	- 0 3695
	0.00	2.00	gi]15218	3877	type 2 pe	eroxiredoxin,	Arabidopsis	0.00	< 1	AFIAVODVVFI	HVKEVADGSGEV	THLIGLE	Oxidation	(H)@11	missed K-	-0.0163 -
	0.00	1 2 001	m17039/	1786	TDV1 /T	HIOREDOVIN	Arshidonsis	•		- month - Dirite		11100000	A		1	•
Prot MAI RFZ	ein Seq	uence (VPDGSI .KVTVAI	Coverag ISFFDE IVESGG	ie - type NDQLQT EFTVSS	2 perox VSVHSL ADDILK	tiredoxin [Brand AAGKKVILFG AL	ssica rapa sub /PGAFTPTCSM	osp. pekir KHVPGFII	iensis] E <mark>k</mark> aeei	KSKGVDEIIC	FSVNDPFVMKA	WGKTYPENF	KHVKFVA	DGSGEYTKL	LGLELDL	KDKGLGVRSR
Frag	jmentati 	on Evid	lence TPTC[C9]	SM[Oxi]K												
R	esidue	b	t	0+2	v	v+2										
V		100.07	57 5	50.5415	2020.069	3 1010.5383	4500 -	y1		y2 y3	у4	y5 y6	y7	y8 y10	y11	
1		213.15	98 10	07.0835	1921.000	9 961.0041	-	У	3+202 bi	6+8308/ 69/8 8-4977-28 - 4 7	5 by811+2b7	b9b16+b2115	x 420 b 11 318 48			
L		326.24	38 16	63.6255	1807.916	8 904.4621	4000 -		105	5.17						
F		473.31	22 23	37.1598	1694.832	8 847.9200	3500 -			226.13						
G		530.33	37 26	65.6705	1547.764	4 774.3858										
V		629.40	21 31	15.2047	1490.742	9 745.8751	3000 -			261.17						
Р		726.45	49 36	53.7311	1391.674	5 696.3409	₹ 2500 -					854 49				
G		783.47	63 39	92.2418	1294.621	7 647.8145	te -					UT. TU				
A		854.51	35 42	27.7604	1237.600	2 619.3038	= 2000 -			318.22						
F		1001.58	19 50	1.2946	1166.563	583.7852	1500 -			474.2	6					
		1102.62	3 5 55	01.0104	049.447	0 450,7070	-	120.	09	389.28	516.34	901.46			1391.76	
۲ ۲		1300.73	23 60	50 8696	916.447	3 414 2002	1000 -			304 20	502.35 696 38					
	:911	1630.20	64 22	20.4518	720 349	6 360 6760	500 -				664.40	837.48	1019.55	132	27.79	
	~1	1726.03	84 84	3 9678	381 180	2 191.0938		130.11		10 I.U., U.I., U.I.	Mark I. I. I.		1	147.69		1645.83
MIC	Dxil	1873.96	38 91	37.4855	294.148	2 147 5777	0-	0	200		600		1000	1200	1400	1600
K	- And	2002.05	87 100	1.5330	147,112	8 74.0600			200	400	000	m/z, Da	.000	1200	1400	1000
		2002.00	100			. 4.0000										

gi|15225545 Hypothetical protein

F	rotei	ns Dete	ected														
	N	Unu	Total	% Cov	Accession #		N	ame			Species	Peptides(95%)	Biological Processes	Molecular Funct	tions	PANTHER ID	-
	21	2.06	2.06	51.9	gi 15240264	NADH dehydrogena	ase	(ubiquin	one)(EC	1.6.5.3)	Arabidopsisthaliana	1					
	22	2.02	2.02	73.3	gi 15225545	hypothetical proteir	n [A	rabidops	is thaliana)		Arabidopsisthaliana	1					
	23	2.02	2.02	54.2	gi 15241492	formate dehydroger	nas	e (FDH)	[Arabidop	sis thali	Arabidopsisthaliana	2					
	24	2.01	2.01	61.8	gi 15242723	putative protein [Ara	abid	lopsis th	aliana]		Arabidopsisthaliana	1					
	25	2.01	2.01	67.3	gi 4704613	monodehydroasco	rba	te reduct	ase (Brass	ica jun	Brassicajuncea	1					Ξ
	26	2.01	2.01	41.0	gi 15239843	cytosolic malate del	hyd	Irogenas	e [Arabido	psis th	Arabidopsisthaliana	2					
	27	2.00	2.00	74.5	gi 15233891	probable H+-transp	orti	ng ATPa	se[Arabid	opsis t	Arabidopsisthaliana	3					
	28	2.00	2.00	91.5	gi 15231702	monodehydroasco	rba	te reduct	ase (NADH	H) - like	Arabidopsisthaliana	1					
	29	2.00	2.00	50.8	gi 15235763	leucyl aminopeptida	ase	-likepro	tein [Arab	dopsis	Arabidopsisthaliana	1					.
	•															•	
F	rotei	n Grou	ip 22 -	hypothe	etical protein	Arabidopsis thali	an	a]									
				Protei	ns in Group							Peptides	in Group				
	N	Unu	Total	Acces	sion #	Name		Con… ⊽	Conf		Sequence		Modifications	Cleavages	∆Mass	Prec MW	
	22	2.02	2.02	gi 1522	5545 hypot	thetical protein A		2.00	99	MCCLF	INDLDAGAGR		Oxidation(M)@1 ICAT-C:13C(9)(C)@2 ICAT-C:13C(9)(C)@3		0.0897	2086.10	
								0.02	5	SFQCE	LVMAK		ICAT-C:13C(9)(C)@4 Oxidation(M)@8		0.0538	1406.75	
								0.00	<1	APLSL	NGSGSGAVSAPASTF	LGKKVVTVS	Deamidated(N)@6	cleaved L	0.5910	4527.00	-

Protein Sequence Coverage - hypothetical protein [Arabidopsis thaliana]

MAAAVSTVGAINRAPLSLNGSGSGAVSAPASTFLGKKVVTVSRFAQSNKKSNGSFKVLAVKEDKQTDGDRWRGLAYDTSDDQQDITRGKGMVDSVFQAPMGTGTHHAVLSSYEYVSQGLRQYNLDNMM DGFYIAPAFMDKLVVHITKNFLTLPNIKVPLILGIWGGKGQGKSFQCELVMAKMGINPIMMSAGELESGNAGEPAKLIRQRYREAADLIKKGKMCCLFINDLDAGAGRMGGTTQYTVNNQMVNATLMN IADNPTNVQLPGMYNKEENARVPIICTGNDFSTLYAPLIRDGRMEKFYWAPTREDRIGVCKGIFRTDKIKDEDIVTLVDQFPGQSIDFFGALRARVYDDEVRKFVESLGVEKIGKRLVNSREGPPVFE QPEMTYEKLMEYGNMLVMEQENVKRVQLAETYLSQAALGDANADAIGRGTFYGKTEEKEPSK

gi|15227359 Unknown protein

Protein	s Detec	cted											
N L	Jnu 1	Total	% Cov	Accessio	n#		Name		Species	Peptides(95%)	Biological Processes	Molecular Function	IS PANTHER ID
32	2.00	2.00	80.4	gi 1522738	59 unk	(nown protein [A	vrabidopsis th	naliana]	Arabidopsisthaliana	2			
33	2.00	2.00	39.1	gi 5874349)5 Put	ative Acttin-relat	ed protein 4 ((ARP4) [Brassic	Brassica oleracea	1			T
•													Þ
Protein	Group	p 32 - u	nknow	n protein	[Arabid	opsis thaliana	a]						
			Protein	s in Group)					Peptides	in Group		
N L	Jnu 1	Total	Access	sion #	N	ame	Con⊽	Conf	Sequence		Modifications	Cleavages AM	lass Prec MW
32	2.00	2.00	gi 15227	359 I	Inknown	protein [Ar A	2.00	99 LGAC	VD LLGGLVK	1	ICAT-C:13C(9)(C)@4	0	0487 1492.92
•						•	1			III.			1001 1010 00 V
												VDVT DVDDVTVDV	
MDSSK PPVTV TLKLK	LSSLSI PKLPVI ALDLNI	SLCLFL VPPVTV NLYVPV	ICII YI PKLPLE ALQLLI	PQHSLA PISGLP: LTCGKNP	CGSCNPF LPPVVGF PPGYTCS	REGENTSPRAF	KLPVPPVI GPILPPGI	TVPKLPVPPVT TTPPATGGKDC	VPKLPVPPVTVPKL PPPPGSVKPPSGGG	KATCPIDTLKL	GACVDLLGGLVKIGL	GDPAVNKCCPLLK	LPVPPVTVPKLPV GLVEVEAAACLCT
MDSSK PPVTV TLKLK Fragme	LSSLSI PKLPVF ALDLNI entation	SLCLFL PPVTV ILYVPV n Evide [C9]/VDL	ICIIYI PKLPLE ALQLLI ence LGGLVK	PQHSLA PISGLP TCGKNP	CGSCNPF IPPVVGF PPGYTCS	RKGGKHSPKAF PNLPLPPLPIV SI	PKLPVPPVI GPILPPGI	IVPKLPVPPVT ITPPATGGKDC	PPELEVEPVEVEVELE	KATCPIDTLKL	GACVDLLGGLVKIGL	GDPAVNKCCPLLK	GLVEVEAAACLCT
MDSSK PPVTV TLKLK Fragme Resid	LSSLSI PKLPVI ALDLNI entation	SLCLFL VPPVTV ILYVPV n Evide [C9][VDL] b	ICIIYI PKLPLE ALQLLI ence LGGLVK	PQHSLA PISGLP TCGKNP	CGSCNPF IPPVVGF PPGYTCS	RKGGKHSPKAF PNLPLPPLPIV 31 y+2	YKLPVPPVI 7GPILPPGI	TYPKLPVPPVT TTPPATGGKDC	PPPPGSVKPPSGGG	KATCPIDILKL	GACVDLLGGLVKIGL	GDPAVNKCCPLLK	GLVEVEAAACLCT
MDSSK PPVTV TLKLK Fragme Resid	LSSLSI PKLPVF ALDLNI entation LGAC[0	ELCLFL VPPVTV ILYVPV n Evide (C9IJVDLI b 114.091	ICIIYI PKLPLE ALQLLI ence LGGLVK 3 5	+2 7.5493	y 493.8807	RKGGKHSPKAE PNLPLPPLPIV SI y+2 747.4440	2500	VPKLPVPPVT TTPPATGGKDC	PPPPGSVKPPSGGG	VEPTIERLE KATCPIDTLKL	GACVDLLGGLVRIGL	GDPAVNKCCPLLK	y ¹² b ^y ¹⁸
MDSSK PPVTV TLKLK Fragme Resid	LSSLSI PKLPVF ALDLNI entation LGAC[0	BLCLFL VPPVTV ILYVPV n Evide (C9)VDL b 114.091 171.112	ICIIYI PKLPLE ALQLII Ence LGGLVK 3 5 88 8	+2 7.5493 1 6.0600 1	y 493.8807 380.7966	y+2 747.4440 690.9020	2500 -	Y142 y5	VPKLPVPPVTVPKL PPPPGSVKPPSGGG +2 y3 y4 y5 278.15	VE TOPIDILKL	PPVIVPKLEVPPVI GACVDLLGGLVKIGL	b9 b10 y10	y12 y18 b13
MDSSK PPVTV TLKLK Fragme Resid L G A	LSSLSI PKLPVF ALDLNI entation LGAC[C	ELCLFL /PPVTV /LYVPV. n Evide (C9)/VDL b 114.091 171.112 242.149	ICIIYI PKLPLE ALQLII LGGLVK 3 5 18 8 12	+2 6.0600 1.5786 1.5786 1.5786 +2 1.5786	CGSCNPF IPPVVGE PPGYTCS 493.8807 380.7966 323.7752	y+2 747.4440 690.9020 662.3912	2500 - 2000 -	VPKLPVPPVT TTPPATGGKDC V122VE 246.1	VPKLPVPPVTVPKL PPPPGSVKPPSGGG +2 +2 +2 +2 +2 +2 +2 +2 +2 +2 +2 +2 +2 +	y6 y6 y6 3	PPVIVPKLEVPPVI GACVDLLGGLVKIGL	b9 b10 y10	y ¹² b ^y 3 ⁸
MDSSK PPVTV TLKLK Fragme Resid L G A C[C9I]	LSSLSI PKLPVI ALDLNI entation LGAC(C	ELCLFL 7PPVTV ILYVPV. (C9I/VDLI (C9I/VDLI 114.091 171.112 242.149 581.316	ICIIYI PKLPLE ALQLLI LGGLVK 3 5 88 80 99 12 33 29	+2 7.5493 1.5786 1.1618 1.200 1.1618 1.200 1	CGSCNPF IPPVVGE PPGYTCS y 493.8807 380.7966 323.7752 252.7381	y+2 747.4440 690.9020 662.3912 626.8727 626.8727	2500 - 2000 -	VPKLPVPPVT TTPPATGGKDC V1 _{b2} y5 246.1	VPKLPVPPVTVPKL PPPPGSVKPPSGGG 278.15 473.3	ys +21+2 /13-	2 b ^y ⁸ b ^y ⁹ b ^y	b9 b10 y10	y12 y18 b13
MDSSK PPVTV TLKLK Fragme Resid L G A C[C9I] V	LSSLSI PKLPVI ALDLNI entation LGAC[0	LCLFL /PPVTV /LYVPV. n Evide [C9]/VDL b 114.091 171.112 242.149 581.316 680.384	ICIIYI PKLPLE ALQLII LGGLVK b 3 57 8 8 9 12 3 29 7 340	+2 7.5493 1.5786 1.1618 1.0.6960 1.15786 1.1618	CGSCNPF IPPVVGF PPGYTCS y 493.8807 380.7966 323.7752 252.7381 913.5717	y+2 747.4440 690.9020 662.3912 626.8727 457.2895	2500 - 2000 - 2000 -	Y12y5 246.1	PPPPGSVKPPSGGG 278.15 9	ух ⁸ нд +2 /7з-	-2 be 8 b7 913.61	b9 b10 y10	y12 y13 b13
MDSSK PPVTV TLKLK Fragme Resid L G A C[C9I] V D	LSSLSI PKLPVI ALDLNI entation LGAC[0	LCLFL /PPVTV ILYVPV. n Evide (C9)/VDL b 114.091 171.112 242.149 581.316 680.384 795.411	ICIIYI PKLPLE ALQLII LGGLVK b 3 5 28 8 9 12 33 29 17 344 6 394	+2 7.5493 1 6.0600 1 1.5786 1 1.1618 1 0.6960 5 8.2095 5	CGSCNPF IPPVVGF PPGYTCS 493.8807 380.7966 323.7752 252.7381 913.5717 814.5033	y+2 747.4440 690.9020 662.3912 626.8727 457.2895 407.7553	2500 - 2000 - 2000 -	y12y5 246.1	VPKLPVPPVTVPKL PPPPGSVKPPSGGG 278.15 473.3	y 26 +2 13+	-2 b ^X ⁸ b ^{Y9} 913.61	b9 b10 y10	y ¹² b ^y ¹⁸
MDSSK PPVTV TLKLK Fragme L G A C[C9I] V D L	LSSLSI PKLPVI ALDLNI entation LGAC[0	LCLFL VPPVTV ILYVPV. n Evide (C9)VDL b 114.091 171.112 242.149 581.316 680.384 795.411 908.495	ICIIYI PKLPLE ALQLLI ALQLLI COLORN ALQLLI ALQLLI ALQLLI ALQLI A	+2 7.5493 1.5786 1.1618 1.2095 4.7515	CGSCNPF IPPVVGE PPGYTCS 493.8807 380.7966 323.7752 252.7381 913.5717 814.5033 599.4763	y+2 747.4440 690.9020 662.3912 626.8727 457.2895 407.7553 350.2418	2500 - 2000 - 2000 - 2000 -	VPKLPVPPVT ГТРРАТGGKDC У12у 246.1 228.15	VPKLPVPPVTVPKL PPPPGSVKPPSGGGI 278.15 473.3 295.19	y ⁶ 13	2 b ⁸ b ⁹ 913.61 814.54	b9 b10 y10	y12 by38
MDSSK PPVTV TLKLK Fragme L G A C[C9I] V D L L	LSSLSI PKLPVI ALDLNI entation LGAC[0 ue	LCLFL VPPVTV ILYVPV. n Evide (C9I/VDLI 114.091 171.112 242.149 581.316 680.384 795.411 908.495 1021.579	ICIIYI PKLPLE ALQLLI ALQLLI COLORN ALQLLI ALQLLI ALQLLI ALQLLI ALQLLI ALQLLI ALQLI	+2 7.5493 1 1.5786 1 1.1618 1 0.6960 2 4.7515 1 1.2935 2	CGSCNPF IPPVVGE PPGYTCS 493.8807 380.7966 323.7752 252.7381 913.5717 814.5033 599.4763 586.3923	y+2 747.4440 690.9020 662.3912 626.8727 457.2895 407.7553 350.2418 293.6998	2500 - 2000 - 2000 - 2000 -	VPKLPVPPVT ГТРРАТGGKDC У122уб 246.1 228.15	VPKLPVPPVTVPKL PPPPGSVKPPSGGGI 278.15 473.3 295.19 451.23	yon -21+2 /13+	2 b ⁸ b ⁹ 913.61 814.54	b9 b10 y10	y12 by38
MDSSK PPVTV TLKLK Fragme L G A C[C9I] V D L L G	LSSLSI PKLPVF ALDLNI entation LGAC[0 ue	LCLFL 7PPVTV ILYVPV n Evide (C9I)VDLI (C9I)VDLI 114.091 171.112 242.149 581.316 680.384 795.411 908.495 1021.579 1078.601	ICIIYI PKLPLE ALQLLI ALQLLI COCC IGGLVK IGGLVK IGGLVK IGG IC IC IC IC IC IC IC IC IC IC IC IC IC	+2 7.5493 1.5786 1.1618 1.2095 3.2095 1.2935 9.8043	CGSCNPF IPPVVGE PPGYTCS 493.8807 380.7966 323.7752 252.7381 913.5717 814.5033 589.4763 586.3923 473.3082	y+2 747,4440 690,9020 662,3912 626.8727 457,2895 407,7553 350,2418 293,6998 237,1577	2500 - 2000 - 2000 - 500 - 1000 -	VPKLPVPPVT TTPPATGGKDC 91 246.1 228.15 171.1	VPKLPVPPVTVPKL PPPPGSVKPPSGGGI 278.15 473.3 295.19 451.23 3 416.32	xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	2 b ⁸ b ⁹ 913.61 814.54	b9 b10 y10	y12 b13 ⁸
MDSSK PPVTV TLKLK Fragme L G A C[C9I] V D L L G G G	LSSLSI PKLPVF ALDLNI entation LGAC(C ue	LCLFL 7PPVTV ILYVPV. n Evide (C9IJVDLI 114.091 171.112 242.149 581.316 680.384 795.411 908.495 1021.579 1078.601 1135.622	ICIIYI PKLPLE ALQLLI ALQLLI CGGLVK 3 5: 88 88 99 12: 53 29: 53 29: 53 29: 53 29: 53 29: 53 29: 53 29: 53 29: 53 29: 53 29: 54 50: 55 10: 55 10: 56 10: 55 10	+2 7.5493 1.1618 1.2935 4.7515 9.8043 8.3150	CGSCNPF IPPVVGE PPGYTCS 493.8807 380.7966 323.7752 252.7381 913.5717 814.5033 589.4763 586.3923 473.3082 416.2867	y+2 747.4440 690.9020 662.3912 626.8727 457.2895 407.7553 350.2418 293.6998 237.1577 208.6470	2500 - 2000 - 2000 - 1000 - 1000 - 500 -	y122yE 246.1 228.15 171.1	VPKLPVPPVTVPKL PPPPGSVKPPSGGG 278.15 473.3 295.19 451.23 416.32 51	y 240 +21 +2 13- 33 586.46	2 b 8 b 7 9 10 4.1 54 1004.1 52 778.42 1004.1	60 b10 y10 b10 b10 b10 b10 b10 b10 b10 b10 b10 b	y12 y18 b138
MDSSK PPVTV TLKLK Fragme G A C[C9I] V D L L C G G L	LSSLSI PKLPVI ALDLNI entation LGAC[0 ue	LCLFL 7PPVTV ILYVPV n Evide (C9IJVDLI b 114.091 171.112 242.149 581.316 680.384 795.411 908.495 1021.579 1078.601 1135.622 1248.706	ICIIYI PKLPLE ALQLLI CGGLVK IGGLVK 3 57 88 81 99 122 53 299 17 340 6 390 17 340 6 390 7 450 8 511 12 533 7 566 88 624	+2 7.5493 1.60600 1.5786 1.1618 1.2935 4.7515 9.8043 8.3150 4.8570	CGSCNPF IPPVVGF PPGYTCS 493.8807 380.7966 323.7752 252.7381 913.5717 814.5033 599.4763 586.3923 473.3082 416.2867 359.2653	y+2 747.4440 690.9020 662.3912 457.2895 407.7553 350.2418 293.6998 237.1577 208.6470 180.1363	2500 - 2000 - 2000 - 2000 - 1000 - 500 -	y12yE 246.1 228.1E 171.1 129.11	VPKLPVPPVTVPKL PPPPGSVKPPSGGGI 2 y3 y4 y5 9 278.15 473.3 2 295.19 451.23 3 416.32 51	yxxx yxxx 33 586.46 15.33 699.1	2 b 8 b 9 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	60 b10 y10 b10 b10 b10 b10 b10 b10 b10 b10 b10 b	y12 y13 b1390.92
MDSSK PPVTV TLKLK Fragme G C[C9I] V D L L G G G L V V	LSSLSI PKLPVI ALDLNI entation LGAC[0 ue	LCLFL 7PPVTV ILYVPV. (C9I/VDLI 114.091 171.112 242.149 581.316 680.384 795.411 908.495 1021.579 1078.601 1135.622 1248.706 1347.775	ICIIYI PKLPLE ALQLII	+2 7.5493 1 6.0600 1 1.5786 1 1.618 1 0.6960 3 8.2095 3 4.7515 3 1.2935 3 8.3150 4 4.8570 3 4.3912 3	y 493.8807 380.7966 323.7752 252.7381 913.5717 814.5033 586.3923 4416.2867 359.2653 246.1812	y+2 747.4440 690.9020 662.3912 626.8727 457.2895 407.7553 350.2418 293.6998 237.1577 208.6470 180.1363 123.5942	2500 - 2000 - 2000 - 2000 - 1000 - 500 - 0	VPKLPVPPVT TTPPATGGKDC V1c2 ys 246.1 228.16 171.1 129.11 0 20	VPKLPVPPVTVPKL PPPPGSVKPPSGGG 278.15 473.3 295.19 451.23 416.32 51 00 400	xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	PPVIVPRLEVPPVI GACVDLLGGLVRIGL 12 b6 b7 913.61 913.61 814.54 1004.1 52 778.42 1004.1 1000 1000	61 1077.67	y12 b13 1390.92 1400



Figure S8. Histogram of measured ICAT ratio distribution of each experiment. (a)-(c) ICAT replicates 1, 2 and 3 of ABA treated guard cells. The overall average of the ABA-ICAT ratio is 1.023 and 71.27% of the peptides fall into the range of 0.8-1.2. (d)-(e) ICAT replicates 1, 2, and 3 of MeJA treated guard cells. The overall average of the MeJA-ICAT ratio is 1.031 and 69.54% of the peptides fall into the range of 0.8-1.2. In all six experiments, the average ICAT ratio is 1.024. Nearly 70% of the ICAT labeled peptides have the ratio within the range of 0.8-1.2. Therefore, a cut-off value of 20% change of the ICAT ion intensity (red dash in figure) was chosen to reflect the genuine quantitative differences.