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# Plant Defense Responses in Opium Poppy Cell Cultures Revealed by Liquid Chromatography-Tandem Mass Spectrometry Proteomics

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Molecular & Cellular Proteomics

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Table II. **Evidence for the identification of proteins with a single peptide match.** Theoretical/hypothetical pI values are shown for proteins identified from public databases, but could not be provided when matches were based on opium poppy EST information since most entries do not contain complete nucleotide sequence data.

Spot Number	Accession Number	Protein Name	m/z	Charge	Sequence	E-value	Species	pI
17	BAB02792	DNA damage inducible protein/Ub-like domain	712.87	2	AFVDSGAQSTIISK	1.20E06	<i>Arabidopsis thaliana</i>	4.9/5.1
19	CAA72741	DNA repair protein RAD23	477.87	2	LEAMGFDR	9.30E03	<i>Dacus carota</i>	4.6/4.8
23	gi009353	Curculin-like mannose binding lectin	622.4	2	DGNLVLADVDGR	9.80E03	<i>Papaver somniferum</i>	
24	gi009936	Oxidoreductase, 2OGFe(II) oxygenase family	636.92	2	GLGVEIDEATIR	5.50E06	<i>Papaver somniferum</i>	
25	P93373	Actin	596.88	2	GYMFTTTAER	2.00E03	<i>Nicotiana tabacum</i>	
33	Q42711	Monodehydroascorbate reductase	604.42	2	LSDFGVQGADAK	2.40E04	<i>Cucumis sativus</i>	5.3/5.5
34	O04866	Acetylnithine aminotransferase	843.03	2	VFFSNSGTEANEAAIK	5.40E04	<i>Alnus glutinosa</i>	8.6/5.6
							<i>Pelargonium</i>	
40	AAK08141	Chloroplast translational elongation factor Tu	593.41	2	IGETVEIVGLR	1.80E07	<i>graveolens</i>	6.1/5.8
42	EAZ21732	DEAD-box helicases	558.01	2	VLITDLLAR	7.20E03	<i>Oryza sativa</i>	5.5/5.8
42	P26301	Enolase	801.43	2	VNQIGSVTESIEAVR	4.90E06	<i>Zea mays</i>	5.3/5.8
45	AAK09225	Inosine monophosphate dehydrogenase	557.38	2	VAQGVVAVADK	6.00E03	<i>Oryza sativa</i>	6/5.6
45	gi002384	Alanine aminotransferase	457.98	2	LSQSLFILNXILS	3.00E05	<i>Papaver somniferum</i>	
54	A48788	Leucyl aminopeptidase	660.17	2	TIEVNNTDAEGR	1.90E04	<i>Solanum lycopersicum</i>	5.3/5.7
62	AAD25602	Dihydrolipoamide acetyltransferase	494.4	2	ISVNDLVVK	4.40E03	<i>Arabidopsis thaliana</i>	8.4/5.8
62	AAM60833	Phosphoglycerate dehydrogenase-like protein	599.94	2	LAVQLVAGGSGVK	2.60E03	<i>Arabidopsis thaliana</i>	6.8/5.8
		2,3-Bisphosphoglycerate-independent phosphoglycerate						
75	P35494	mutase	535.37	2	LDQVQLLLK	9.90E03	<i>Nicotiana tabacum</i>	6.0/5.4
75	O04059	3,4-Dihydroxy-2-butanone kinase	581.4	2	LNFGLAEEQAK	2.20E03	<i>Solanum lycopersicum</i>	5.2/5.4
76	gi010796	Heat shock protein 70	580.89	2	EIEDAISDLR	6.10E03	<i>Papaver somniferum</i>	5.3/5.5
76	CAB71138	Heat shock protein 70	428.86	2	IAGLDVLR	5.60E03	<i>Dunaliella salina</i>	
76	CAB37531	Heat shock protein 70	717.39	2	EVDEVLLVGGMTR	4.40E03	<i>Arabidopsis thaliana</i>	
77	AAO17017	Heat shock protein 70	618	2	VQEVVSEIFGK	2.80E03	<i>Oryza sativa</i>	5.3/5.5
79	ABN05716	Heat shock protein 70	717.45	2	DIDEVLLVGGMTR	2.30E03	<i>Medicago truncatula</i>	5.9/5.4
79	gi010796	Heat shock protein 70	561.34	2	SSGGLSESEIR	6.40E04	<i>Papaver somniferum</i>	

82	Q42434	Heat shock protein 70	725.95	2	VQQLLKEFFNGK	6.10E03	<i>Spinacia oleracea</i>	5.0/5.4
90	gi011206	Heat shock protein 70	410.3	2	SSXFLVR	4.50E03	<i>Papaver somniferum</i>	
92	CAA94389	Heat shock protein 70	668.88	2	ILTEFFGKEPR	5.30E03	<i>Arabidopsis thaliana</i>	5.1/5.5
112	AAT02533	NADP-malic enzyme	672.43	2	NIEVIVVTDGER	4.30E03	<i>Hydrilla verticillata</i>	5.7/6.3
112	gi010075	NADP-malic enzyme	490.32	2	AYELGVATR	3.90E03	<i>Papaver somniferum</i>	
115	NP_195146	Phosphoglycerate dehydrogenase-like protein	599.97	2	LAVQLVAGGSGVK	1.10E03	<i>Arabidopsis thaliana</i>	6.2/5.9
117	gi008122	Protein kinase, GroEL-like chaperone, ATPase	651.95	2	ALSTQVTENXTK	7.20E03	<i>Papaver somniferum</i>	
119	AAL09728	Chaperonin	624.4	2	SVAAGVNVMDLR	3.30E05	<i>Arabidopsis thaliana</i>	7.6/6.1
119	gi002402	Chaperonin	580.96	2	VGGASEAEVGER	1.10E06	<i>Papaver somniferum</i>	
120	ABD96914	Chaperonin	633.32	2	GIDPPSLDLLAR	1.60E03	<i>Cleome spinosa</i>	6.0/6.3
121	NP_187789	Chaperonin	661.31	2	GGADQFIEEAER	2.60E03	<i>Arabidopsis thaliana</i>	6.0/6.2
124	AAL73395	26S Proteasome regulatory subunit	619.36	2	AVANSTSATFLR	1.60E03	<i>Tortula ruralis</i>	8.2/6.2
132	gi000360	Glutathione reductase	664.45	2	LNLEAVGVELDR	3.30E05	<i>Papaver somniferum</i>	
147	P48498	SAM synthetase	751.81	2	TN <u>M</u> VMVFGEITTK	3.10E04	<i>Petunia x hybrida</i>	5.5/6.5
152	P49611	SAM synthetase	716.42	2	FVIGGPDGDAGLTGR	3.60E04	<i>Brassica juncea</i>	5.5/6.1
163	gi002567	SAM synthetase	751.94	2	TN <u>M</u> VMVFGEITTK	4.70E05	<i>Papaver somniferum</i>	
164	gi001599	12-Oxophytodienoate reductase	725.47	2	AITSNSADLVVFR	4.80E07	<i>Papaver somniferum</i>	
169	gi004434	Alcohol dehydrogenase	540.38	2	GV <u>M</u> LDGQSR	3.60E04	<i>Papaver somniferum</i>	
169	gi005842	Alcohol dehydrogenase	662.41	2	GPIILE <u>M</u> DTYR	2.50E03	<i>Papaver somniferum</i>	
171	CAB83039	SAM synthetase	751.88	2	TN <u>M</u> VMVFGEITTK	3.20E04	<i>Camellia sinensis</i>	5.3/6.2
178	gi001912	Proteasome regulatory subunit	687.4	2	AVQEEDELSPEK	1.00E02	<i>Papaver somniferum</i>	
179	gi009016	Hypothetical protein/cyclase family	507.77	2	LVGSEGSPLR	4.30E03	<i>Papaver somniferum</i>	
180	NP_001051818	Electron transfer flavoprotein $\alpha$ subunit	950.98	2	AAVDAGFVPNELQVGQTGK	2.80E03	<i>Oryza sativa</i>	6.1/6.3
181	CAL49971	Aldose reductase	435.36	2	TPAQIALR	6.90E03	<i>Ostreococcus tauri</i>	10.2/6.2
181	NP_195146	Phosphoglycerate dehydrogenase-like protein	599.92	2	LAVQLVAGGSGVK	1.30E03	<i>Arabidopsis thaliana</i>	8.7/6.2
189	P48534	Ascorbate peroxidase	439.24	2	TGGPFGTIK	5.40E03	<i>Pisum sativum</i>	5.5/6.1
191	NP_197745	26S Proteasome regulatory subunit	687.42	2	AVQEEDELSPEK	5.10E03	<i>Arabidopsis thaliana</i>	6.3/6.2
195	gi001085	Malate dehydrogenase	494.88	2	LSVQISDVK	3.90E03	<i>Papaver somniferum</i>	
199	AAF19790	Fructose 1,6-bisphosphatase	843.42	2	LIGLAGETNVQGEEQK	2.20E04	<i>Lactuca sativa</i>	5.2/6.0
205	AAB61672	Type-IIIa membrane protein cpwap13	559.86	2	YVDAVLTIPK	2.30E03	<i>Vigna unguiculata</i>	6.2/5.8

207	NP_172447	U2A' (U2 small nuclear ribonucleoprotein A)	811.03	2	LVNLVEIDPLASIPK	7.70E03	<i>Arabidopsis thaliana</i>	5.8/5.8
207	gi004600	Oxidoreductase, 2OGFe(II) oxygenase family	707.43	2	GTSVLEMVSAFEK	9.00E03	<i>Papaver somniferum</i>	
207	gi009936	Oxidoreductase, 2OGFe(II) oxygenase family	636.9	2	GLGVEIDEATIR	1.30E04	<i>Papaver somniferum</i>	
209	gi011914	Catalytic coenzyme binding protein	905.48	2	AEQYLADSGIPYTIIR	3.90E03	<i>Papaver somniferum</i>	
214	gi001863	NADPH thioredoxin reductase	553.85	2	GVFAAGDVQDK	4.20E03	<i>Papaver somniferum</i>	
214	gi008536	NADPH thioredoxin reductase	676.4	2	FGTEIITETVNK	9.50E03	<i>Papaver somniferum</i>	
217	AAB61672	Type-IIIa membrane protein cpwap13	559.87	2	YVDAVLTIPK	2.30E03	<i>Vigna unguiculata</i>	6.2/5.7
222	ABE85940	Isoflavone reductase-like protein	715.37	2	FFPSEFGNDVDR	6.80E03	<i>Medicago truncatula</i>	6.6/5.5
227	gi004645	Adenosine kinase	870.51	2	IAVISQGADPVVVATDGK	1.20E03	<i>Papaver somniferum</i>	
232	ABE86848	Inorganic pyrophosphatase	535.77	2	IVAISLDDPK	5.90E03	<i>Medicago truncatula</i>	6.0/5.4
239	O82530	20S Proteasome $\alpha$ subunit C	787.93	2	AAAIGANNQAAQSM <del>L</del> KLK	1.20E04	<i>Petunia x hybrida</i>	6.6/5.6
248	BAC78570	Nascent polypeptide associated complex $\alpha$ chain	757.93	2	SPTSPTYVIFGEAK	1.40E05	<i>Oryza sativa</i>	4.3/4.5
249	gi009925	Glutathione S-transferase	641.47	2	VIDPAEIVANIK	1.80E03	<i>Papaver somniferum</i>	
255	AAM60833	Phosphoglycerate dehydrogenase-like protein	599.94	2	LAVQLVAGGSGVK	9.90E04	<i>Arabidopsis thaliana</i>	6.2/5.1
261	gi006444	Cytidine deaminase	758.03	2	GVDNGDGGPFGAVVVR	8.90E07	<i>Papaver somniferum</i>	
262	gi009009	Early tobacco anther 1	512.86	2	AAEAIQFFK	5.20E03	<i>Papaver somniferum</i>	
263	gi002777	Early tobacco anther 1	513	2	AAEAIQFFK	5.90E03	<i>Papaver somniferum</i>	
265	gi002777	Early tobacco anther 1	512.89	2	AAEAIQFFK	1.30E03	<i>Papaver somniferum</i>	
266	gi004261	Early tobacco anther 1	512.87	2	AAEAIQFFK	4.90E03	<i>Papaver somniferum</i>	
266	gi006161	Unknown protein	743.41	2	ADQELPSVVS <del>A</del> ELK	3.30E03	<i>Papaver somniferum</i>	
270	gi006948	Glutathione dehydrogenase	579.91	2	LFGSFVTF <del>L</del> K	3.20E03	<i>Papaver somniferum</i>	
270	gi006815	Glutathione S-transferase	774.97	2	NVEFEVIVPVDL <del>M</del> K	3.60E05	<i>Papaver somniferum</i>	
272	gi002674	Triosphosphate isomerase	559.9	2	NVSAEVAATTR	8.40E05	<i>Papaver somniferum</i>	
272	gi004193	Proteosome $\alpha$ subunit	587.87	2	AVDNSGTVIGIK	4.20E03	<i>Papaver somniferum</i>	
275	1TP9_A	Thioredoxin-independent peroxidase	517.3	2	FALLVDDLK	4.80E03	<i>Populus trichocarpa</i>	5.6/6.4
277	AAF74983	Methionine synthase	565.81	2	IPSTEEIADR	6.10E04	<i>Solanum tuberosum</i>	5.7/6.6
277	gi008399	Methionine synthase	490.3	2	GDYAVEIGR	4.10E03	<i>Papaver somniferum</i>	
282	gi002674	Triosphosphate isomerase	559.91	2	NVSAEVAATTR	4.70E05	<i>Papaver somniferum</i>	
283	gi004264	Triosphosphate isomerase	725.43	2	ALLNESNEFVGEK	2.10E06	<i>Papaver somniferum</i>	
286	gi000716	Proteosome $\beta$ subunit	554.36	2	DTIDL <del>F</del> VER	5.00E03	<i>Papaver somniferum</i>	

287	gi000902	Proteosome $\beta$ subunit	400.78	2	AVSLAIAR	4.00E03	<i>Papaver somniferum</i>	
292	gi007329	Pathogenesis-related protein	559.93	2	TITVNEAQRSR	3.90E03	<i>Papaver somniferum</i>	
293	BAB02391	Unknown protein/contains calcium binding domain	506.77	2	GSFSSVVS DK	9.20E03	<i>Papaver somniferum</i>	
296	gi009265	Eukaryotic transcription initiation factor	671.46	2	LPTDDVVL TQIK	9.60E04	<i>Papaver somniferum</i>	
300	AAM77651	Chaperonin 10-kDa subunit	483.82	2	TGAQVIYSK	4.20E03	<i>Gossypium hirsutum</i>	7.8/5.7
300	gi009570	Unknown protein	645.42	2	ETAGGLLL TEASK	3.60E03	<i>Papaver somniferum</i>	
301	AAT57642	NIM1-like protein	657.92	2	GLSSSM YPTVR	7.70E03	<i>Helianthus annuus</i>	5.6/5.8
302	gi008637	Triosphosphate isomerase	725.39	2	ALLNESNEFVGEK	4.40E05	<i>Papaver somniferum</i>	
302	gi002674	Triosphosphate isomerase	559.86	2	NVSAEVAATTR	4.30E05	<i>Papaver somniferum</i>	
304	gi002674	Triosphosphate isomerase	559.9	2	NVSAEVAATTR	8.60E05	<i>Papaver somniferum</i>	
304	gi004264	Triosphosphate isomerase	725.92	2	ALLNESNEFVGEK	3.50E04	<i>Papaver somniferum</i>	
306	gi002674	Triosphosphate isomerase	559.84	2	NVSAEVAATTR	2.40E05	<i>Papaver somniferum</i>	
306	gi004264	Triosphosphate isomerase	725.38	2	ALLNESNEFVGEK	2.40E05	<i>Papaver somniferum</i>	
307	CAB50768	Cytochrome P450	555.26	3	LFLQTHEAVSFNTR	1.00E02	<i>Cicer arietinum</i>	9.1/5.6
308	ABH08430	Integrase	454.32	2	YIKELLK	5.90E03	<i>Beta vulgaris</i>	8.0/5.6
312	gi008967	Unknown protein	545.87	2	VFEDNV LVR	2.40E03	<i>Papaver somniferum</i>	
315	gi004973	Thioredoxin	474.39	2	LTNVLFLK	4.20E03	<i>Papaver somniferum</i>	
325	gi003295	Pathogenesis-related protein	623.33	2	GDTVLN EEEIK	2.30E03	<i>Papaver somniferum</i>	
327	gi002777	Early tobacco anther 1	512.33	2	AAEAIQFFK	1.50E03	<i>Papaver somniferum</i>	
328	gi002777	Early tobacco anther 1	513.35	2	AAEAIQFFK	6.10E03	<i>Papaver somniferum</i>	
329	CAA67923	Ubiquitin-like protein	584.87	2	GQDGNEVFFR	1.00E02	<i>Arabidopsis thaliana</i>	5.3/5.0
333	gi003966	Calcium binding protein	596.42	2	ISSTELSDVLK	5.20E03	<i>Papaver somniferum</i>	
334	gi003966	Calcium binding protein	596.39	2	ISSTELSDVLK	2.10E04	<i>Papaver somniferum</i>	
339	gi002775	Copper chaperone	734.99	2	TNLAPDVVLQTVAK	5.50E05	<i>Papaver somniferum</i>	