

Table III. Proteins induced by fungal elicitor treatment of opium poppy cell cultures.
Determined by comparing spot intensity on two-dimensional gels containing total protein extracts from control and elicitor-treated opium poppy cell cultures.

Spot	EST	Protein Name	Spot	EST	Protein Name
8		Heat shock protein 70	235		Not identified
9		26S Proctosome regulatory subunit	236		Not identified
10	EST	Calreticulin precursor	245		Not identified
28		Not identified	247		Not identified
30		Not identified	248		Nascent polypeptide associated complex α -
44		Root phototropism 3; ATPase	249	EST	Glutathione S-transferase
81	EST	Heat shock protein 70	252		Not identified
82		Heat shock protein 70	258		Not identified
83	EST	Heat shock protein 70	259		Not identified
84	EST	Heat shock protein 70	260		Not identified
85	EST	Heat shock protein 70	262	EST	Early tobacco anther 1
86	EST	Heat shock protein 70	263	EST	Early tobacco anther 1
87	EST	Heat shock protein 70	264		Not identified
88	EST	Heat shock protein 70	265	EST	Early tobacco anther 1
89		Not identified	266	EST	Early tobacco anther 1
112	EST	NADP-malic enzyme	267	EST	Glutathione S-transferase
113		NADP-malic enzyme	270		Dirigent-like protein
141	EST	ATP synthase	270	EST	Glutathione S-transferase
149		Not identified	271	EST	Glutathione S-transferase
151	EST	SAM synthetase	271		Sorbitol-like transporter
152	EST	SAM synthetase	276		Not identified
160	EST	SAM synthetase	278	EST	Pathogenesis-related protein
160		ATP-dependent protease	278	EST	Eukaryotic initiation factor
166	EST	Glutamate dehydrogenase	288	EST	Dirigent-like protein
168	EST	Phenylalanine ammonia lyase	289		Not identified
168	EST	Mitochondrial elongation factor Tu	291		Pathogenesis-related protein
179	EST	Putative cyclase family protein	295	EST	Pathogenesis-related protein
182	EST	Pyridine nucleotide cytochrome reductase	296	EST	Eukaryotic translation initiation factor
184	EST	Dirigent-like protein	297		Not identified
191	EST	26S Proctosome regulatory subunit	298		Not identified
193		Malate dehydrogenase	302		Glutathione S-transferase
193	EST	ATP synthase	302	EST	Triosephosphate isomerase
193		F-box family protein	309	EST	ATP synthase D chain-related
194	EST	ATP synthase	310		Not identified
194	EST	(<i>R,S</i>)-norcoclaurine 6- <i>O</i> -methyltransferase	311	EST	Pathogenesis-related protein Bet v 1
194		Proteosome, non-ATPase	312		Dimethylmenaquinone methyltransferase family
196		ATP synthase	313		Not identified
196	EST	(<i>R,S</i>)-norcoclaurine 6- <i>O</i> -methyltransferase	319		Not identified
196		Malate dehydrogenase	320		Plant lipase-like protein
196		Eukaryotic translation initiation factor	320	EST	Non-symbiotic haemoglobin
200		Not identified	321		Not identified
204		Not identified	324	EST	Non-symbiotic haemoglobin
209	EST	Catalytic/coenzyme binding protein	326		Not identified
211		Not identified	327	EST	Early tobacco anther 1
212		Cysteine synthase	332	EST	Profilin
225	EST	Isoflavone reductase-like	333	EST	Calcium binding protein
226	EST	Isoflavone reductase-like	335		Not identified
228	EST	Fructokinase	336	EST	Calmodulin
230	EST	Catalytic/coenzyme binding protein	337	EST	Calmodulin
232		Inorganic pyrophosphatase	338		Not identified
232	EST	Nucleic acid binding protein	339	EST	Copper chaperone
234		Not identified	340		Not identified

