

**Table 2. Unidentified *Medicago truncatula* proteins responsive to *N*-acyl homoserine lactones (AHLs) and proteins affected only by high (50  $\mu$ M) concentrations of 3-oxo-C<sub>12</sub>-HL**

Putative identity	M. t. TC †	TOG §	pI/MW (kDa) ¶	C12** 50 $\mu$ M block 24h	C12 2 $\mu$ M block 24h	C12 100 nM spray 24h	C12 10 nM‡‡ spray 24h	C16 10 nM§§ block 24h	C16 1 nM§§ spray 24h	C12 50 $\mu$ M block 48	C12 2 $\mu$ M block 48h	C16 10 nM§§ spray 48h
<b>Flavonoid metabolism*</b>												
Chalcone isomerase	TC45048	131607	5.2 / 25	190‡‡	120	60	110	150	140	90	80	80
<b>Various metabolic functions</b>												
Glyceraldehyde-3-phosphate dehydrogenase	TC43151	126306	6.4 / 26	190	90	30	80	120	60	120	110	100
Glyceraldehyde-3-phosphate dehydrogenase	TC43151	126306	5.9 / 27	220	90	70	90	130	100	160	130	150
Malate dehydrogenase, cytosolic	TC43296	139607	6.2 / 40	160	60	30	50	120	60	240	190	90
Malate dehydrogenase, cytosolic	TC43296	139607	6.2 / 41	210	100	50	90	60	140	290	200	40
Malate dehydrogenase, cytosolic	TC43296	139607	6.5 / 40	180	60	30	90	140	130	440	100	70
12-oxophytodienoate reductase	TC43618	n/a	6.2 / 26	250	50	30	70	70	20	300	170	120
23 kDa polypeptide, oxygen evolving complex	TC43209	128629	5.3 / 23	310	60	70	50	130	130	30	70	70
<b>Unidentified proteins</b>												
Mta16 ‡			6.6 / 12	30	64	40	140	90	40	320	30	230
Mt110			4.8 / 41	90	50	20	40	100	60	110	110	150
Mt136			5.8 / 18	30	30	20	120	60	70	40	100	120
Mt13a			5.5 / 43	170	380	80	50	60	190	190	320	170
Mt142			6.3 / 29	80	40	30	50	90	60	80	90	100
Mt149			7.0 / 39	300	120	160	400	230	0	550	80	410
Mt182			5.6 / 23	340	290	100	80	120	360	220	110	120
Mt195			4.5 / 13	80	30	40	60	150	50	50	70	30
Mt20			5.1 / 43	160	80	60	60	140	90	140	130	60
Mt215			5.0 / 26	10	150	10	4	40	10	360	190	360
Mt217			5.1 / 30	240	70	100	80	150	110	160	100	40
Mt23			5.3 / 48	230	0	30	210	6	0	new	new	0
Mt24			5.4 / 50	210	90	70	70	120	130	40	100	50
Mt248			6.3 / 25	80	30	10	40	90	20	40	90	140
Mt250			6.6 / 38	40	20	7	50	40	1	1700	210	300
Mt266			4.8 / 22	110	20	8	20	100	30	20	50	0
Mt272			5.4 / 16	220	100	60	90	150	230	70	80	80
Mt312			4.6 / 29	140	210	140	90	140	280	410	110	100
Mt317			4.5 / 35	0	0	0	0	new	0	0	0	0
Mt331			4.5 / 52	0	240	270	0	860	0	new	0	0
Mt333			4.6 / 52	0	180	260	330	520	350	new	new	0
Mt336			4.75 / 54	130	0	10	90	80	10	0	50	30
Mt348			5.25 / 58	80	20	20	50	80	20	120	120	90
Mt351			5.0 / 31	180	60	80	50	150	70	250	210	90
Mt371			5.3 / 26	360	340	110	220	230	1100	140	150	140
Mt381			5.7 / 40	30	150	30	40	280	20	20	100	40
Mt394			5.9 / 60	440	0	0	0	40	0	0	0	new
Mt412			6.75 / 28	340	360	60	240	410	160	250	50	60
Mt416			6.6 / 22	6	100	50	230	130	80	170	30	110
Mt423			6.25 / 12	new	new	new	new	new	new	300	0	20
Mt447			5.8 / 35	150	50	60	50	50	10	150	120	140
Mt452			6.4 / 33	60	70	20	40	50	40	430	100	70
Mt53			5.6 / 27	50	30	10	30	70	30	80	70	90
Mt64			5.0 / 26	110	120	90	130	120	170	340	130	190
Mt65			5.0 / 25	120	170	110	140	140	220	500	140	220
Mt665			4.3 / 38	new	new	new	new	new	new	new	0	0
Mt666			6.4 / 43	110	20	10	30	70	3	150	110	190
Mt668			6.6 / 42	30	10	10	70	90	0	360	0	100
Mt69			6.2 / 21	70	30	30	60	120	10	40	110	80
Mt699			4.3 / 19	60	50	30	50	100	40	110	80	50
Mt724			5.5 / 10	250	520	250	610	250	940	90	80	90
Mt725			5.5 / 9.5	180	1400	390	2500	390	2800	130	20	50
Mt751			4.1 / 50	100	130	140	180	160	210	50	264	20
Mtx1			5.5 / 17	860	20	70	40	480	80	80	290	410

Mtx1a	5.4 / 17	130	330	80	370	420	790	160	160	130
Mtx2a	5.5 / 17	590	410	460	270	120	1100	110	60	150
Mtxx10	5.6 / 10	0	0	0	0	0	new	0	0	0

\*Proteins are grouped by putative function, recognizing that some functions may belong in more than one group.

†TCs = *M. truncatula* Tentative Clusters against which the proteins were matched by peptide mass fingerprinting. TCs can be accessed at <http://www.tigr.org/tdb/tgi/mtgi/>.

‡The unidentified proteins could not be matched to any TC in the *M. truncatula* database yet. Therefore, they are listed with a random identifier for internal reference.

§TOG indicates the Tentative Ortholog Group into which the *M. truncatula* TCs have been classified by The Institute for Genomic Research (TIGR), see <http://www.tigr.org/tdb/tgi/mtgi/>. N/a indicates that no TOG has been assigned to this TC.

¶The observed molecular weight (MW) and isoelectric point (pI) for each *M. truncatula* protein was determined from its position on the gels relative to known marker proteins.

\*\*C12 = 3-oxo-C<sub>12</sub>-HL; C16 = 3-oxo-C<sub>16:1</sub>-HL

††Relative accumulations are given in percent of the control level and are averages of results from three individual control gels and three individual treatment gels. Accumulation levels are also indicated by color code: yellow, a new protein not detected in controls; red, significantly increased; tan, nonsignificantly increased; pale green, nonsignificantly reduced; dark green, significantly reduced; blue, reduced below detection. *P* values for statistical significance of difference from control levels ranged from <0.001 to <0.05, but were <0.002 for over 90% of the proteins listed.

‡‡Only two gels were examined for proteins from roots exposed to the lowest concentration (10 nM) of 3-oxo-C<sub>12</sub>-HL.

§§Estimated concentration; see *Materials and Methods*.