

Supp. Info.SI1. Analysis of ATG genes homologs in *P. vulgaris*, *M. truncatula*, *G. max* in different databases. (A) Orthologous and paralogous, (B) Basic Local Alignment Search Tool -BLAST (C) KEGG (D)ENSEMBL (E)HMMER (F) INPARANOID (G) EGGNOG (H)PANTHER.

## A. Orthologous and paralogous

Orthologs		Paralogs		Orthologs		Paralogs		Orthologs		Paralogs	
<b>PvATG1t</b>	Phvul.010g120500	<b>PvATG1b</b>	Phvul.010g015100	<b>MtrATG1b</b>	Medtr8g024100	<b>MtrATG1t</b>	Medtr3g095620	<b>GmATG1c.II</b>	Glyma.01g099600	<b>GmATG1a.I</b>	Glyma.07g048400
<b>PvATG2</b>	Phvul.003g295800	<b>PvATG5</b>	Phvul.008g241000	<b>MtrATG1c</b>	Medtr4g019410	<b>MtrATG6</b>	Medtr3g018770	<b>GmATG7</b>	Glyma.12g010000	<b>GmATG1a.II</b>	Glyma.16g017300
<b>PvATG3</b>	Phvul.011g006500	<b>PvATG8c.I</b>	Phvul.003g079300	<b>MtrATG2</b>	Medtr4g086370	<b>MtrATG8c</b>	Medtr4g048510	<b>GmATG8b</b>	glyma.15g188600	<b>GmATG1b.I</b>	Glyma.03g069800
<b>PvATG4a</b>	Phvul.008g048900	<b>PvATG9a</b>	Phvul.001g159900	<b>MtrATG3</b>	Medtr4g036265	<b>MtrATG8f</b>	Medtr1g086310	<b>GmATG8c.III</b>	Gglyma.09g003900	<b>GmATG1b.II</b>	Glyma.01g099600
<b>PvATG6</b>	Phvul.005g029900	<b>PvATG9b</b>	Phvul.007g194300	<b>MtrATG4a</b>	Medtr7g081230	<b>MtrATG8g</b>	Medtr4g123760	<b>GmATG8c.V</b>	glyma.07g261000	<b>GmATG1t.I</b>	Glyma.06g150700
<b>PvATG7</b>	Phvul.011g010700	<b>PvATG18a</b>	Phvul.001g205000	<b>MtrATG5</b>	Medtr5g076920	<b>MtrATG9a</b>	Medtr7g096680	<b>GmATG8c.VI</b>	glyma.15g108200	<b>GmATG1t.II</b>	Glyma.04g215500
<b>PvATG8d</b>	Phvul.011g103300	<b>PvATG18c.II</b>	Phvul.007g196400	<b>MtrATG7</b>	Medtr0003s0540	<b>MtrATG9b</b>	Medtr1g070160	<b>GmATG8f</b>	glyma.17g140700	<b>GmATG2.I</b>	Glyma.02g133400
<b>PvATG8f.I</b>	Phvul.003g219600	<b>PvATG18f.I</b>	Phvul.011g140900	<b>MtrATG8e</b>	Medtr4g101090	<b>MtrATG11</b>	Medtr4g130370	<b>GmATG12b.I</b>	glyma.07g038100	<b>GmATG2.II</b>	Glyma.07g211600
<b>PvATG8f.II</b>	Phvul.002g062200	<b>PvATG18f.II</b>	Phvul.005g091300	<b>MtrATG10</b>	Medtr8g010140	<b>MtrATG13b.II</b>	Medtr3g095570	<b>GmATG12b.II</b>	glyma.16g007300	<b>GmATG3.I</b>	Glyma.12g005700
<b>PvATG8i</b>	Phvul.007g210800	<b>PvATG18g.II</b>	Phvul.007g183100	<b>MtrATG101</b>	Medtr8g079240	<b>MtrATG13c</b>	Medtr8g093050	<b>GmATG18a.II</b>	glyma.10g152500	<b>GmATG3.II</b>	Glyma.09g231000
<b>PvATG10</b>	Phvul.010g036300			<b>MtrATG12b</b>	Medtr8g020500	<b>MtrATG18a</b>	Medtr1g083230	<b>GmATG18a.II</b>	glyma.20g23500	<b>GmATG4a.I</b>	Glyma.18g248400
<b>PvATG11</b>	Phvul.003g153800			<b>MtrATG13a</b>	Medtr5g068710	<b>MtrATG18b</b>	Medtr4g0130190	<b>GmATG18c.I</b>	glyma.04g224300	<b>GmATG4a.II</b>	Glyma.09g244800
<b>PvATG12b</b>	Phvul.010g130300			<b>MtrATG14a</b>	Medtr5g061040	<b>MtrATG18c</b>	Medtr7g108520	<b>GmATG18c.III</b>	glyma.07g203900	<b>GmATG5.I</b>	Glyma.14g210200
<b>PvATG13</b>	Phvul.008g187800			<b>MtrATG16.II</b>	Medtr3g075400	<b>MtrATG18c.I</b>	Medtr1g088855	<b>GmATG18f.I</b>	glyma.12g214600	<b>GmATG5.II</b>	Glyma.02g240700
<b>PvATG13b</b>	Phvul.002g269600			<b>MtrATG16b</b>	Medtr4g104380	<b>MtrATG18e</b>	Medtr3g093590	<b>GmATG101</b>	glyma.17g180900	<b>GmATG6.I</b>	Glyma.11g153900
<b>PvATG14</b>	Phvul.008g169200			<b>MtrATG18f</b>	Medtr2g082770	<b>MtrATG18e</b>	Medtr3g093590			<b>GmATG6.II</b>	Glyma.04g141000
<b>PvATG16</b>	Phvul.003g207100			<b>MtrATG18g</b>	Medtr1g089110	<b>MtrATG18g</b>	Medtr1g082300			<b>GmATG8c.I</b>	Glyma.12g098400
<b>PvATG18b</b>	Phvul.003g152800									<b>GmATG8c.II</b>	Glyma.06g306300
<b>PvATG18c.I</b>	Phvul.009g041700									<b>GmATG8c.II</b>	Glyma.06g306300
<b>PvATG18g.I</b>	Phvul.001g146700									<b>GmATG8c.III</b>	Glyma.09g003900
<b>PvATG101</b>	Phvul.003g248000									<b>GmATG8c.III</b>	Glyma.09g003900

## B. Basic Local Alignment Search Tool (BLAST) of *P. vulgaris*, *M. truncatula*, *G.max* based in *A. thaliana*.

<i>Phaseolus vulgaris</i>			
<i>Arabidopsis Protein accession numbers</i>	<i>Phaseolus vulgaris Protein accession numbers</i>	Query Cover	Per. Ident
<i>At1g49180.1</i>	Phvul.010G120500	74	39.22
<i>At1g49180.2</i>	Phvul.010G120500	81	38.96
<i>At2g37840.1</i>	Phvul.010G015100	86	57.32

<i>At2g37840.2</i>	Phvul.010G015100	93	53.38
<i>At2g37840.3</i>	Phvul.010G015100	95	48.13
<i>At3g53930.1</i>	Phvul.010G015100	86	55.3
<i>At3g53930.2</i>	Phvul.010G015100	86	55.45
<i>At3g53930.3</i>	Phvul.010G015100	98	50
<i>At3g53930.4</i>	Phvul.010G015100	98	50.18
<i>At3g53930.5</i>	Phvul.010G015100	98	50
<i>At3g61960.1</i>	Phvul.010G120500	99	48.16
<i>At3g61960.2</i>	Phvul.010G120500	99	45.55
<i>At3g19190.1</i>	Phvul.003G295800	99	44.68
<i>At3g19190.2</i>	Phvul.003G295800	99	46.62
<i>At3g19190.3</i>	Phvul.003G295800	99	46.62
<i>At5g61500.1</i>	Phvul.011G006500	99	85.67
<i>At5g61500.2</i>	Phvul.011G006500	81	77.82
<i>At2g44140.1</i>	Phvul.008G048900	99	58.61
<i>At2g44140.2</i>	Phvul.008G048900	95	61.43
<i>At2g44140.3</i>	Phvul.008G048900	99	58.61
<i>At2g44140.4</i>	Phvul.008G048900	99	62.44
<i>At2g44140.5</i>	Phvul.008G048900	99	59.14
<i>At3g59950.1</i>	Phvul.008G048900	100	55.98
<i>At3g59950.2</i>	Phvul.008G048900	91	54.85
<i>At3g59950.3</i>	Phvul.008G048900	91	65.45
<i>At3g59950.4</i>	Phvul.008G048900	99	62.41
<i>At3g59950.5</i>	Phvul.008G048900	99	57.61
<i>At5g17290.1</i>	Phvul.008G241000	97	62.46
<i>At3g61710.1</i>	Phvul.005G029900	94	74.9
<i>At3g61710.2</i>	Phvul.005G029900	94	71.7
<i>At3g61710.3</i>	Phvul.005G029900	92	73.99
<i>At3g61710.4</i>	Phvul.005G029900	93	73.23
<i>At5g45900.1</i>	Phvul.011G010700	96	70.18
<i>At4g21980.1</i>	Phvul.011G103300	95	84.72
<i>At4g21980.2</i>	Phvul.011G103300	84	84.82
<i>At4g04620.1</i>	Phvul.003G079300	95	80.51
<i>At4g04620.2</i>	Phvul.003G079300	95	80.51
<i>At4g04620.3</i>	Phvul.003G079300	95	80.51
<i>At1g62040.1</i>	Phvul.011G103300	99	90.76
<i>At1g62040.2</i>	Phvul.011G103300	88	90.75
<i>At2g05630.1</i>	Phvul.011G103300	99	91.67
<i>At2g05630.2</i>	Phvul.011G103300	66	91.74
<i>At2g45170.1</i>	Phvul.003G219600	95	81.36
<i>At2g45170.2</i>	Phvul.003G219600	95	81.36

<i>At4g16520.1</i>	Phvul.003G219600	96	91.38
<i>At4g16520.1</i>	Phvul.002G062200	96	91.38
<i>At4g16520.2</i>	Phvul.003G219600	95	91.38
<i>At4g16520.3</i>	Phvul.003G219600	95	91.38
<i>At3g60640.1</i>	Phvul.003G219600	91	86.61
<i>At3g06420.1</i>	Phvul.007G210800	94	68.14
<i>At3g15580.1</i>	Phvul.007G210800	98	71.68
<i>At2g31260.1</i>	Phvul.001G159900	99	65.2
<i>At2g31260.1</i>	Phvul.007G194300	97	59.77
<i>At3g07525.1</i>	Phvul.010G036300	96	52.73
<i>At3g07525.2</i>	Phvul.010G036300	96	52.49
<i>At4g30790.1</i>	Phvul.003G153800	99	60.79
<i>At1g54210.1</i>	Phvul.010G130300	94	89.13
<i>At1g54210.2</i>	Phvul.010G130300	90	47.83
<i>At1g54210.3</i>	Phvul.010G130300	94	89.13
<i>At3g13970.1</i>	Phvul.010G130300	100	82.98
<i>At3g13970.2</i>	Phvul.010G130300	83	71.43
<i>At3g13970.3</i>	Phvul.010G130300	83	71.43
<i>At3g13970.4</i>	Phvul.010G130300	85	78.67
<i>At3g49590.1</i>	Phvul.008G187800	98	49.11
<i>At3g49590.2</i>	Phvul.008G187800	98	49.11
<i>At3g49590.3</i>	Phvul.008G187800	99	47.69
<i>At3g18770.1</i>	Phvul.002G269600	96	54.19
<i>AT1G77890.1</i>	Phvul.008G169200	96	51.21
<i>AT1G77890.2</i>	Phvul.008G169200	96	49.67
<i>AT1G77890.3</i>	Phvul.008G169200	96	51.21
<i>AT4G08540.1</i>	Phvul.008G169200	99	71.49
<i>At5g50230.1</i>	Phvul.003G207100	99	72.98
<i>At3g62770.1</i>	Phvul.007G196400	88	74.41
<i>At3g62770.1</i>	Phvul.001G205000	98	66.36
<i>At3g62770.3</i>	Phvul.007G196400	86	74.79
<i>At4g30510.1</i>	Phvul.003G152800	97	68.95
<i>At4g30510.2</i>	Phvul.003G152800	99	72.06
<i>At2g40810.1</i>	Phvul.009G041700	98	69.82
<i>At2g40810.2</i>	Phvul.009G041700	98	69.82
<i>At2g40810.3</i>	Phvul.009G041700	98	67.24
<i>At3g56440.1</i>	Phvul.009G041700	97	68.11
<i>At3g56440.2</i>	Phvul.009G041700	98	68.12
<i>At3g56440.3</i>	Phvul.009G041700	95	69.72
<i>At5g05150.1</i>	Phvul.009G041700	97	48.05
<i>At5g54730.1</i>	Phvul.005G091300	88	42.8

<i>At5g54730.2</i>	Phvul.011G140900	89	40.66
<i>At1g03380.1</i>	Phvul.001G146700	86	57.35
<i>At1g54710.1</i>	Phvul.007G183100	98	55.02
<i>At1g54710.2</i>	Phvul.007G183100	100	53.1
<i>At5g66930.1</i>	Phvul.003G248000	87	80.58
<i>At5g66930.2</i>	Phvul.003G248000	100	75.8
<i>At5g66930.3</i>	Phvul.003G248000	81	75

***Medicago truncatula***

<b>Arabidopsis Protein accession numbers</b>	<b><i>Medicago truncatula</i> Protein accession numbers</b>	<b>Query Cover</b>	<b>Per. Ident</b>
<i>At1g49180.1</i>	MTR_3g095620	62	57.65
<i>At1g49180.2</i>	MTR_3g095620	67	57.65
<i>At2g37840.1</i>	MTR_4g019410	97	63.5
<i>At2g37840.2</i>	MTR_4g019410	93	58.51
<i>At2g37840.3</i>	MTR_4g019410	95	53.47
<i>At3g53930.1</i>	MTR_4g019410	98	59.89
<i>At3g53930.2</i>	MTR_4g019410	98	59.94
<i>At3g53930.3</i>	MTR_4g019410	98	53.79
<i>At3g53930.4</i>	MTR_4g019410	98	53.87
<i>At3g53930.5</i>	MTR_4g019410	98	53.79
<i>At3g61960.1</i>	MTR_8g024100	98	49.71
<i>At3g61960.2</i>	MTR_8g024100	98	46.76
<i>At3g19190.1</i>	MTR_4g086370	99	43.74
<i>At3g19190.2</i>	MTR_4g086370	98	46.76
<i>At3g19190.3</i>	MTR_4g086370	99	45.9
<i>At5g61500.1</i>	MTR_4g036265	99	84.98
<i>At5g61500.2</i>	MTR_4g036265	80	76.65
<i>At2g44140.1</i>	MTR_7g081230	99	58.85
<i>At2g44140.2</i>	MTR_7g081230	96	60.38
<i>At2g44140.3</i>	MTR_7g081230	99	58.85
<i>At2g44140.4</i>	MTR_7g081230	99	62
<i>At2g44140.5</i>	MTR_7g081230	99	59.54
<i>At3g59950.1</i>	MTR_7g081230	99	56.26
<i>At3g59950.2</i>	MTR_7g081230	90	55.05
<i>At3g59950.3</i>	MTR_7g081230	91	63.01
<i>At3g59950.4</i>	MTR_7g081230	99	61.75
<i>At3g59950.5</i>	MTR_7g081230	99	57.36
<i>At5g17290.1</i>	MTR_5g076920	99	59.44
<i>At3g61710.1</i>	MTR_3g018770	99	74.27

<i>At3g61710.2</i>	MTR_3g018770	94	73.9
<i>At3g61710.3</i>	MTR_3g018770	92	77.36
<i>At3g61710.4</i>	MTR_3g018770	93	74.37
<i>At5g45900.1</i>	MTR_0003s0540	97	68.98
<i>At4g21980.1</i>	MTR_2g023430	95	84.75
<i>At4g21980.2</i>	MTR_2g023430	85	84.75
<i>At4g04620.1</i>	MTR_2g023430	96	82.35
<i>At4g04620.2</i>	MTR_2g023430	96	82.35
<i>At4g04620.3</i>	MTR_2g023430	96	82.35
<i>At1g62040.1</i>	MTR_4g048510	96	82.35
<i>At1g62040.1</i>	MTR_4g037225	95	60.87
<i>At1g62040.2</i>	MTR_2g023430	96	82.35
<i>At2g05630.1</i>	MTR_4g048510	98	90.76
<i>At2g05630.2</i>	MTR_4g048510	65	90.74
<i>At2g05630.1</i>	MTR_2g088230	98	72.88
<i>At2g45170.1</i>	MTR_4g101090	92	83.33
<i>At2g45170.2</i>	MTR_4g101090	92	83.33
<i>At4g16520.1</i>	MTR_4g101090	96	92.31
<i>At4g16520.2</i>	MTR_4g101090	96	92.31
<i>At4g16520.3</i>	MTR_4g101090	76	86.96
<i>At4g16520.1</i>	MTR_1g086310	96	53.85
<i>At3g60640.1</i>	MTR_4g101090	99	80.99
<i>At3g06420.1</i>	MTR_4g123760	96	73.04
<i>At3g15580.1</i>	MTR_4g123760	99	71.3
<i>At3g15580.1</i>	MTR_7g096540	98	79.03
<i>At2g31260.1</i>	MTR_7g096680	99	65.31
<i>At2g31260.1</i>	MTR_1g070160	98	65.22
<i>At3g07525.1</i>	MTR_8g010140	96	55.25
<i>At3g07525.2</i>	MTR_8g010140	96	54.09
<i>At4G30790.1</i>	MTR_4g130370	99	60.69
<i>At1g54210.1</i>	MTR_8g020500	94	91.3
<i>At1g54210.2</i>	MTR_8g020500	90	47.83
<i>At1g54210.3</i>	MTR_8g020500	94	91.3
<i>At3g13970.1</i>	MTR_8g020500	97	87.1
<i>At3g13970.2</i>	MTR_8g020500	80	76
<i>At3g13970.3</i>	MTR_8g020500	80	76.36
<i>At3g13970.4</i>	MTR_8g020500	80	76.36
<i>At3g49590.1</i>	MTR_5g068710	98	48.78
<i>At3g49590.2</i>	MTR_5g068710	98	48.78
<i>At3g49590.3</i>	MTR_5g068710	98	47.45
<i>At3g18770.1</i>	MTR_3g095570	95	50.16

<i>AT1G77890.1</i>	MTR_5g061040	96	55.88
<i>AT1G77890.2</i>	MTR_5g061040	96	49.34
<i>AT1G77890.3</i>	MTR_5g061040	96	50.88
<i>AT4G08540.1</i>	MTR_5g061040	99	71.42
<i>At5g50230.1</i>	MTR_4g104380	99	67.19
<i>At5g50230.1</i>	MTR_4g007500	88	56.28
<i>At3g62770.1</i>	MTR_1g083230	88	73.49
<i>At3g62770.3</i>	MTR_1g083230	87	73.5
<i>At4g30510.1</i>	MTR_4g130190	99	68.71
<i>At4g30510.2</i>	MTR_4g130190	99	72.87
<i>At2g40810.1</i>	MTR_7g108520	88	62.00
<i>At2g40810.1</i>	MTR_3g093590	98	71.92
<i>At2g40810.2</i>	MTR_3g093590	98	71.92
<i>At2g40810.3</i>	MTR_3g093590	98	73.53
<i>At3g56440.1</i>	MTR_3g093590	96	74.23
<i>At3g56440.2</i>	MTR_3g093590	96	74.59
<i>At3g56440.3</i>	MTR_3g093590	97	74.66
<i>At3g56440.1</i>	MTR_1g088855	90	53.80
<i>At5g05150.1</i>	MTR_3g093590	96	48.16
<i>At5g54730.1</i>	MTR_3g093590	88	44.62
<i>At5g54730.2</i>	MTR_3g093590	89	43.11
<i>At3g56440.1</i>	MTR_2g082770	21	29.90
<i>At1g03380.1</i>	MTR_1g089110	86	58
<i>At1g54710.1</i>	MTR_1g082300	99	53.68
<i>At1g54710.2</i>	MTR_1g082300	100	52.44
<i>AT5G66930.1</i>	MTR_8g079240	75	83.33
<i>AT5G66930.2</i>	MTR_8g079240	100	75.34
<i>AT5G66930.3</i>	MTR_8g079240	81	74.52

#### Glycine max

<b>Arabidopsis Protein accession numbers</b>	<b><i>Glycine max</i> Protein accession numbers</b>	<b>Query Cover</b>	<b>Per. Ident</b>
<i>At1g49180.1</i>	GLYMA_04G215500	61	61.81
<i>At1g49180.2</i>	GLYMA_04G215500	61	61.81
<i>At2g37840.1</i>	GLYMA_03G069800	97	64.49
<i>At2g37840.2</i>	GLYMA_03G069800	93	58.89
<i>At2g37840.3</i>	GLYMA_03G069800	95	53.94
<i>At2g37840.1</i>	GLYMA_01G099600	97	63.99
<i>At2g37840.1</i>	GLYMA_06G150700	34	42.86

<i>At2g37840.1</i>	GLYMA_02G220700	98	49.84
<i>At3g53930.1</i>	GLYMA_03G069800	98	61.41
<i>At3g53930.2</i>	GLYMA_03G069800	98	61.83
<i>At3g53930.3</i>	GLYMA_03G069800	98	55.15
<i>At3g53930.4</i>	GLYMA_03G069800	98	55.72
<i>At3g53930.5</i>	GLYMA_03G069800	98	55.15
<i>At3g61960.1</i>	GLYMA_07G048400	98	52.71
<i>At3g61960.2</i>	GLYMA_07G048400	98	49.77
<i>At3g61960.1</i>	GLYMA_16G017300	98	50.82
<i>At3g19190.1</i>	GLYMA_02G133400	99	45.07
<i>At3g19190.2</i>	GLYMA_02G133400	99	47.13
<i>At3g19190.3</i>	GLYMA_02G133400	99	47.13
<i>At5g61500.1</i>	GLYMA_12G005700	99	87.22
<i>At5g61500.2</i>	GLYMA_12G005700	80	79.38
<i>At5g61500.1</i>	GLYMA_09G231000	99	78.21
<i>At2g44140.1</i>	GLYMA_09G244800	99	59.02
<i>At2g44140.2</i>	GLYMA_09G244800	96	61.12
<i>At2g44140.3</i>	GLYMA_09G244800	99	59.02
<i>At2g44140.4</i>	GLYMA_18G248400	99	62.84
<i>At2g44140.5</i>	GLYMA_09G244800	99	59.9
<i>At3g59950.1</i>	GLYMA_09G244800	99	56.22
<i>At3g59950.2</i>	GLYMA_09G244800	91	55.59
<i>At3g59950.3</i>	GLYMA_09G244800	91	65.04
<i>At3g59950.4</i>	GLYMA_09G244800	99	61.8
<i>At3g59950.5</i>	GLYMA_09G244800	99	58.23
<i>At5g17290.1</i>	GLYMA_14G210200	98	62.57
<i>At5g17290.1</i>	GLYMA_02G240700	98	62.68
<i>At3g61710.1</i>	GLYMA_11G153900	99	74.07
<i>At3g61710.2</i>	GLYMA_11G153900	94	72.8
<i>At3g61710.3</i>	GLYMA_11G153900	92	75.34
<i>At3g61710.4</i>	GLYMA_11G153900	93	74.14
<i>At3g61710.1</i>	GLYMA_04g141000	99	73.68
<i>At5g45900.1</i>	GLYMA_12G010000	98	70.52
<i>At4g21980.1</i>	GLYMA_15G108200	95	86.44
<i>At4g21980.2</i>	GLYMA_17G013000	95	79.55
<i>At4g04620.1</i>	GLYMA_15G108200	95	82.2
<i>At4g04620.2</i>	GLYMA_15G108200	95	82.2
<i>At4g04620.3</i>	GLYMA_15G108200	95	82.2
<i>At4g04620.1</i>	GLYMA_15G188600	56	74.29
<i>At1g62040.1</i>	GLYMA_12G098400	99	91.6
<i>At1g62040.2</i>	GLYMA_12G098400	88	91.6

<i>At1g62040.1</i>	GLYMA_06G306300	99	90.76
<i>At1g62040.1</i>	GLYMA_09G003900	97	88.89
<i>At1g62040.1</i>	GLYMA_07G261000	99	88.03
<i>At2g05630.1</i>	GLYMA_12G098400	99	90.83
<i>At2g05630.2</i>	GLYMA_12G098400	66	90.83
<i>At2g45170.1</i>	GLYMA_17G140700	92	84.21
<i>At2g45170.2</i>	GLYMA_17G140700	92	84.21
<i>At4g16520.1</i>	GLYMA_17G140700	95	93.16
<i>At4g16520.2</i>	GLYMA_17G140700	95	93.16
<i>At4g16520.3</i>	GLYMA_17G140700	75	88.04
<i>At3g60640.1</i>	GLYMA_17G140700	95	83.76
<i>At3g06420.1</i>	GLYMA_02G008800	94	68.14
<i>At3g15580.1</i>	GLYMA_02G008800	97	90.83
<i>At2g31260.1</i>	GLYMA_13G122200	99	84.21
<i>At2g31260.1</i>	GLYMA_03G162100	99	64.88
<i>At2g31260.1</i>	GLYMA_19G163500	99	64.88
<i>At3g07525.1</i>	GLYMA_03G097000	96	84.21
<i>At3g07525.2</i>	GLYMA_03G097000	96	93.16
<i>At4g30790.1</i>	GLYMA_17G071400	99	93.16
<i>At1g54210.1</i>	GLYMA_07G038100	94	88.04
<i>At1g54210.2</i>	GLYMA_16G007300	90	83.76
<i>At1g54210.3</i>	GLYMA_07G038100	94	68.14
<i>At3g13970.1</i>	GLYMA_07G038100	98	90.83
<i>At3g13970.2</i>	GLYMA_16G007300	79	71.68
<i>At3g13970.3</i>	GLYMA_16G007300	82	65.87
<i>At3g13970.4</i>	GLYMA_07G038100	85	65.89
<i>At3g49590.1</i>	GLYMA_14G187000	98	54.55
<i>At3g49590.2</i>	GLYMA_14G187000	98	53.64
<i>At3g49590.3</i>	GLYMA_14G187000	98	62.23
<i>At3g18770.1</i>	GLYMA_05G189000	96	90.22
<i>AT1G77890.1</i>	GLYMA_13G085400	96	50.22
<i>AT1G77890.2</i>	GLYMA_13G085400	96	49.12
<i>AT1G77890.3</i>	GLYMA_13G085400	96	50.22
<i>AT4G08540.1</i>	GLYMA_14G167200	99	70.53
<i>At5g50230.1</i>	GLYMA_05G043700	99	61.97
<i>At5g50230.1</i>	GLYMA_17G126200	99	73.43
<i>At3g62770.1</i>	GLYMA_20G235800	88	90.22
<i>At3g62770.3</i>	GLYMA_20G235800	87	82.98
<i>At3g62770.1</i>	GLYMA_10G152500	89	72.94
<i>At3g62770.1</i>	GLYMA_03G212100	99	68.94
<i>At3g62770.1</i>	GLYMA_19G209200	79	73.76



At4g30510.1	GLYMA_17G070200	99	74.07
At4g30510.2	GLYMA_17G070200	99	71.43
At2g40810.1	GLYMA_06G140400	99	78.67
At2g40810.2	GLYMA_06G140400	99	50.08
At2g40810.3	GLYMA_06G140400	99	50.08
At2g40810.1	GLYMA_10g126200	89	68.94
At2g40810.1	GLYMA_04g224300	96	73.76
At2g40810.1	GLYMA_07g203900	18	65.22
At3g56440.1	GLYMA_06G140400	97	48.42
At3g56440.2	GLYMA_06G140400	96	56.26
At3g56440.3	GLYMA_06G140400	93	73.57
At5g05150.1	GLYMA_06G140400	97	73.82
At5g05150.1	GLYMA_16g109400	60	25.43
At5g54730.1	GLYMA_13G287000	88	74.43
At5g54730.2	GLYMA_13G287000	89	70.65
At5g54730.1	GLYMA_12g214600	91	44.23
At5g54730.1	GLYMA_12g136000	88	43.33
At5g54730.1	GLYMA_06g267000	88	42.50
At1g03380.1	GLYMA_03G148700	86	75.00
At1g03380.1	GLYMA_19g152000	86	58.47
At1g03380.1	GLYMA_20g230900	75	56.93
At1g54710.1	GLYMA_10G157700	98	71.71
At1g54710.2	GLYMA_10G157700	99	71.71
AT5G66930.1	GLYMA_17G180900	87	82.01
AT5G66930.2	GLYMA_17G180900	100	76.71
AT5G66930.3	GLYMA_17G180900	81	75.96

B.KEGG Orthology analysis of *A. thaliana*, *P. vulgaris*, *M. truncatula*, and *G.max*.

KEGG ID	Arabidopsis thaliana	Phaseolus vulgaris	Medicago truncatula	Glycine max
GrpGenusOrganismK07204	ath	pvu	mtr	gmx *
(RAPTOR)[590]K07203	AT3G08850	PHAVU_008G08780	MTR_7g072330	100777178
	AT5G01770	PHAVU_008G08810		100779159
(MTOR)[616]K08266	AT1G50030	PHAVU_002G04990	MTR_5g005380	100816558
				100816446
(MLST8)[544]K08269	AT2G22040	PHAVU_006G17370	MTR_2g016690	100781599
	AT3G18140			100812024
(ULK2)[656]K08331	AT2G37840	PHAVU_010G01510	MTR_4g019410	100791596
	AT3G53930			
(ATG13)[641]K19730	AT3G18770	PHAVU_002G26960	MTR_8g093050	100778254
	AT3G49590	PHAVU_008G18780	MTR_5g068710	100798585
			MTR_3g095570	100818104
				100816476
(ATG101)[514]K08330	AT5G66930	PHAVU_003G24800	MTR_8g079240	100811916

(ATG11)[272]K17606	AT4G30790	PHAVU_003G15380	MTR_4g130370	100794018
(IGBP1)[592]K04382	AT5G53000	PHAVU_009G05190	MTR_3g091640	100792447
(PPP2C)[1332]K17907	AT1G10430	PHAVU_007G26220	MTR_1g050518	100780847
	AT1G59830	PHAVU_003G07260	MTR_8g085610	100807894
	AT1G69960	PHAVU_002G07880	MTR_5g037200	100783950
	AT2G42500	PHAVU_002G23540	MTR_8g062430	100784312
	AT3G58500	PHAVU_001G20030	MTR_7g107310	100794029
				100801108
				100807329
				100798408
				100817449
				100782279
				100775812
				100812326
(ATG9)[712]K17906	AT2G31260	PHAVU_007G19430	MTR_1g070160	100777405
		PHAVU_001G15990	MTR_7g096680	100779344
				100809347
				732654
(ATG2)[646]K17908	AT3G19190	PHAVU_003G29580	MTR_4g086370	100802641
(WIPI1_2)[751]K08334	AT4G30510	PHAVU_003G15280	MTR_4g130190	100805552
				100794908
				100803048
				100820465
				100816367
(BECN)[598]K00914	AT3G61710	PHAVU_005G02990	MTR_3g018770	100812721
(PIK3C3)[590]K08333	AT1G60490	PHAVU_002G07010	MTR_5g034120	732646
(PIK3R4)[527]K08336	AT4G29380	PHAVU_004G17510	MTR_6g088835	547983
(ATG12)[519]K08339	AT3G13970	PHAVU_010G13030	MTR_8g020500	100778348
	AT1G54210			100796837
(ATG5)[511]K17890	AT5G17290	PHAVU_008G24100	MTR_5g076920	100818467
				100527905
(ATG16L1)[426]K08337	AT5G50230	PHAVU_003G20710	MTR_3g075400	100527733
			MTR_4g104380	732567
			MTR_4g007500	100789045
(ATG7)[535]K17888	AT5G45900	PHAVU_011G01070	MTR_0003s0540	100806054
(ATG10L)[432]K08343	AT3G07525	PHAVU_010G03630	MTR_8g010140	100778336
				100781725
(ATG3)[588]K08341	AT5G61500	PHAVU_011G00650	MTR_4g036265	100786914
(GABARAP)[1655]K08342	AT2G05630	PHAVU_011G15160	MTR_4g101090	100808589
	AT4G16520	PHAVU_007G21080	MTR_4g048510	100787410
	AT4G04620	PHAVU_003G21960	MTR_7g096540	100814257
	AT4G21980	PHAVU_011G10330	MTR_2g023430	100301895
	AT1G62040	PHAVU_002G06220	MTR_1g086310	100499835
	AT2G45170	PHAVU_003G07930	MTR_4g123760	100527884
	AT3G60640		MTR_4g037225	100781703
	AT3G06420		MTR_2g088230	100818620
	AT3G15580			100818315
				100500165
				100305892
				100500023
				100527345
				100301894
				100784677
(ATG4)[1152]	AT2G44140	PHAVU_008G04890	MTR_7g081230	100809664
				100810317

\*

Glycine max gmx	Glycine max lds gmx
100777178	GLYMA_09G278500
100779159	GLYMA_18G210300
100816558	GLYMA_01G241300
100816446	GLYMA_11G002600
100781599	GLYMA_15G085200
100812024	GLYMA_13G227200
100791596	GLYMA_03G069800
100778254	GLYMA_02G220700
100798585	GLYMA_08G146700
100818104	GLYMA_14G187000
100816476	GLYMA_05G189000
100811916	GLYMA_17G180900
100794018	GLYMA_02G206500
100792447	GLYMA_17G071400
100780847	GLYMA_06G129600
100807894	GLYMA_04G234900
100783950	GLYMA_08G293400
100784312	GLYMA_01G038800
100794029	GLYMA_02G025900
100801108	GLYMA_02G169200
100807329	GLYMA_03G206900

# C.ENSEMBL Orthology analysis of *A. thaliana*, *P. vulgaris*, *M. truncatula*, and *G.max*.

ID Arabidopsis	Species	Type	Orthologue	dN/dS	Target %id	Query %id	GOC Score	WGA Coverage	High Confidence
At1g49180	Species without orthologues								
At2g37840	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_010G015100g Compare Regions (10:2,437,128-2,443,461:-1) View Sequence Alignments	n/a	53.40 %	47.20 %	n/a	93.18	Yes
At3g53930	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_010G015100g Compare Regions (10:2,437,128-2,443,461:-1) View Sequence Alignments	n/a	51.85 %	47.19 %	n/a	91.04	Yes
At3g61960	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_010G120500g Compare Regions (10:38,972,887-38,977,458:-1) View Sequence Alignments	n/a	46.41 %	46.49 %	n/a	85.79	Yes
At3g19190	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_003G295800g Compare Regions (3:52,098,694-52,109,253:1) View Sequence Alignments	n/a	44.76 %	46.78 %	n/a	95.15	No
At5g61500	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_011G006500g Compare Regions (11:475,609-480,221:1) View Sequence Alignments	0.043 84	85.67 %	85.94 %	n/a	100	No
At2g44140	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_008G048900g Compare Regions (8:4,303,200-4,308,640:1) View Sequence Alignments	n/a	57.87 %	60.60 %	n/a	93.4	No
At3g59950	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_008G048900g Compare Regions (8:4,303,200-4,308,640:1) View Sequence Alignments	n/a	55.83 %	57.23 %	n/a	93.29	No
At5g17290	haseolus vulgaris	1-to-1View Gene Tree	PHAVU_008G241000g Compare Regions (8:55,537,709-55,545,667:1) View Sequence Alignments	n/a	59.60 %	61.72 %	n/a	98.51	No
At3g61710	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_005G029900g Compare Regions (5:2,774,177-2,781,388:1) View Sequence Alignments	0.075 97	73.82 %	69.83 %	n/a	99.97	Yes
At5g45900	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_011G010700g Compare Regions (11:816,956-822,085:-1) View Sequence Alignments	n/a	68.57 %	68.87 %	n/a	98.91	No
At4g21980	Species without orthologues								
At4g04620	Species without orthologues								
At1g62040	Species without orthologues								
At2g05630	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_011G103300g Compare Regions (11:11,625,632-11,627,983:-1) View Sequence Alignments	0.026 28	89.17 %	65.24 %	n/a	80.07	Yes
At2g45170	Species without orthologues								
At4g16520	Species without orthologues								
At3g60640	Species without orthologues								
At3g06420	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_007G210800g Compare Regions (7:44,931,240-44,932,490:1) View Sequence Alignments	n/a	63.11 %	64.71 %	n/a	95.95	No
At3g15580	Species without orthologues								
At2g31260	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_001G159900g Compare Regions (1:41,950,751-41,958,196:1) View Sequence Alignments	n/a	65.34 %	64.67 %	n/a	98.58	No
	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_007G194300g Compare Regions (7:43,257,363-43,263,137:-1) View Sequence Alignments	n/a	58.19 %	58.66 %	n/a	79.44	No
At3g07525	Species without orthologues								
AT4G30790	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_003G153800g Compare Regions (3:35,797,412-35,804,197:-1) View Sequence Alignments	n/a	60.62 %	60.89 %	n/a	100	No
At1g54210	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_010G130300g Compare Regions (10:40,034,779-40,037,243:-1) View Sequence Alignments	n/a	87.23 %	85.42 %	n/a	89.65	Yes
	Phaseolus vulgaris	1-to-manyView Gene Tree	PHAVU_010G130300g Compare Regions (10:40,034,779-40,037,243:-1) View Sequence Alignments	n/a	82.98 %	82.98 %	n/a	90.45	Yes
At3g13970	Species without orthologues								
At3g49590	Species without orthologues								
At3g18770	Phaseolus vulgaris	1-to-1View Gene Tree	PHAVU_002G269600g Compare Regions (2:43,452,066-43,457,109:1) View Sequence Alignments	n/a	52.00 %	52.00 %	n/a	92.96	No
AT1G77890	Species without orthologues								
AT4G08540	Phaseolus vulgaris	1-to-manyView Gene Tree	03g22220	n/a	67.65 %	68.08 %	n/a	97.88	No



At3g60640	Species without orthologues									
At3g06420	Medicago truncatula	1-to-many	View Gene Tree	MTR_4g123760 Compare Regions (4:51,007,802-51,010,377:-1) View Sequence Alignments	n/a	71.19 %	70.59 %	n/a	89.67	Yes
	Medicago truncatula	1-to-many	View Gene Tree	MTR_7g096540 Compare Regions (7:38,739,985-38,740,615:1) View Sequence Alignments	n/a	74.19 %	38.66 %	n/a	n/a	Yes
At3g15580	Species without orthologues									
At2g31260	Medicago truncatula	1-to-many	View Gene Tree	MTR_1g070160 Compare Regions (1:30,830,518-30,837,261:-1) View Sequence Alignments	n/a	63.39 %	63.39 %	n/a	81.43	No
	Medicago truncatula	1-to-many	View Gene Tree	MTR_7g096680 Compare Regions (7:38,799,346-38,805,558:1) View Sequence Alignments	n/a	62.49 %	64.43 %	n/a	99.56	No
At3g07525	Species without orthologues									
AT4G30790	Medicago truncatula	1-to-1	View Gene Tree	MTR_4g130370 Compare Regions (4:54,307,709-54,314,660:-1) View Sequence Alignments	n/a	60.57 %	60.89 %	n/a	100	No
At1g54210	Medicago truncatula	1-to-many	View Gene Tree	MTR_8g020500 Compare Regions (8:7,198,686-7,202,464:1) View Sequence Alignments	n/a	67.74 %	87.50 %	n/a	80.1	Yes
At1g54210	Medicago truncatula	1-to-many	View Gene Tree	MTR_8g020500 Compare Regions (8:7,198,686-7,202,464:1) View Sequence Alignments	n/a	65.32 %	86.17 %	n/a	82.59	Yes
At3g13970	Species without orthologues									
At3g49590	Species without orthologues									
At3g18770	Medicago truncatula	1-to-many	View Gene Tree	MTR_3g095570 Compare Regions (3:43,671,041-43,677,624:-1) View Sequence Alignments	n/a	46.45 %	47.04 %	n/a	97.3	No
	Medicago truncatula	1-to-many	View Gene Tree	MTR_8g093050 Compare Regions (8:38,885,014-38,889,871:1) View Sequence Alignments	n/a	44.43 %	41.44 %	n/a	87.12	No
AT1G77890	Species without orthologues									
AT4G08540	Medicago truncatula	1-to-many	View Gene Tree	MTR_5g061040 Compare Regions (5:25,385,477-25,394,644:-1) View Sequence Alignments	n/a	67.01 %	67.86 %	n/a	99.1	No
At5g50230	Medicago truncatula	1-to-many	View Gene Tree	MTR_3g075400 Compare Regions (3:34,315,394-34,318,708:-1) View Sequence Alignments	n/a	67.19 %	67.19 %	n/a	99.94	No
	Medicago truncatula	1-to-many	View Gene Tree	MTR_4g007500 Compare Regions (4:1,115,999-1,117,649:1) View Sequence Alignments	n/a	60.99 %	43.61 %	n/a	95.24	No
	Medicago truncatula	1-to-many	View Gene Tree	MTR_4g104380 Compare Regions (4:43,185,561-43,189,052:-1) View Sequence Alignments	n/a	69.65 %	70.33 %	n/a	99.22	No
At3g62770	Medicago truncatula	1-to-many	View Gene Tree	MTR_1g088855 Compare Regions (1:39,776,324-39,778,721:-1) View Sequence Alignments	n/a	61.30 %	51.06 %	n/a	94.59	No
	Medicago truncatula	1-to-many	View Gene Tree	MTR_7g108520 Compare Regions (7:44,206,217-44,209,925:1) View Sequence Alignments	n/a	64.11 %	63.06 %	n/a	99.43	No
At4g30510	Medicago truncatula	1-to-1	View Gene Tree	MTR_4g130190 Compare Regions (4:54,209,571-54,215,694:-1) View Sequence Alignments	n/a	66.13 %	67.21 %	n/a	90.93	No
At2g40810	Medicago truncatula	1-to-many	View Gene Tree	MTR_3g093590 Compare Regions (3:42,763,022-42,768,303:1) View Sequence Alignments	n/a	68.67 %	72.52 %	n/a	97.9	No
At3g56440	Medicago truncatula	1-to-many	View Gene Tree	MTR_3g093590 Compare Regions (3:42,763,022-42,768,303:1) View Sequence Alignments	0.11384	67.23 %	71.36 %	n/a	91.19	No
At5g05150	Species without orthologues									
At5g54730	Medicago truncatula	1-to-1	View Gene Tree	MTR_2g082770 Compare Regions (2:34,727,900-34,734,357:-1) View Sequence Alignments	n/a	34.41 %	40.63 %	n/a	85.36	No
At1g03380	Medicago truncatula	1-to-1	View Gene Tree	MTR_1g089110 Compare Regions (1:40,103,141-40,108,943:-1) View Sequence Alignments	0.19286	50.41 %	50.89 %	n/a	83.24	Yes
At1g54710	Medicago truncatula	1-to-1	View Gene Tree	MTR_1g082300 Compare Regions (1:36,587,909-36,596,198:-1) View Sequence Alignments	n/a	52.68 %	51.89 %	n/a	90.75	No
AT5G66930	Medicago truncatula	1-to-1	View Gene Tree	MTR_8g079240 Compare Regions (8:33,765,931-33,771,318:-1) View Sequence Alignments	n/a	70.64 %	61.35 %	n/a	92.37	No

<i>ID</i> <i>Arabidopsis</i>	<i>Species</i>	<i>Type</i>	<i>Orthologue</i>	<i>dN/dS</i>	<i>Target %id</i>	<i>Query %id</i>	<i>GOC Score</i>	<i>WGA Coverage</i>	<i>High Confidence</i>
<i>At1g49180</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_04G215500 Compare Regions (4:48,694,717-48,697,763:-1) View Sequence Alignments	n/a	43.09 %	38.97 %	n/a	<b>71.35</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_06G150700 Compare Regions (6:12,289,992-12,292,323:-1) View Sequence Alignments	0.192 2	44.66 %	33.82 %	n/a	<b>73.54</b>	No
<i>At2g37840</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_01G099600 Compare Regions (1:33,115,843-33,125,726:-1) View Sequence Alignments	0.182 38	60.00 %	59.35 %	n/a	<b>97.91</b>	Yes
	Glycine max	Many-to-manyView Gene Tree	GLYMA_03G069800 Compare Regions (3:15,703,649-15,719,178:-1) View Sequence Alignments	0.161 33	60.27 %	60.44 %	n/a	<b>97.92</b>	Yes
<i>At3g53930</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_01G099600 Compare Regions (1:33,115,843-33,125,726:-1) View Sequence Alignments	0.177 92	58.62 %	59.69 %	n/a	<b>96.24</b>	Yes
	Glycine max	Many-to-manyView Gene Tree	GLYMA_03G069800 Compare Regions (3:15,703,649-15,719,178:-1) View Sequence Alignments	0.160 97	58.23 %	60.11 %	n/a	n/a	Yes
<i>At3g61960</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_07G048400 Compare Regions (7:4,096,301-4,102,195:1) View Sequence Alignments	n/a	48.04 %	50.96 %	n/a	<b>87.4</b>	Yes
	Glycine max	1-to-manyView Gene Tree	GLYMA_16G017300 Compare Regions (16:1,519,674-1,525,290:1) View Sequence Alignments	n/a	45.04 %	50.00 %	n/a	<b>89.35</b>	Yes
<i>At3g19190</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_02G133400 Compare Regions (2:13,780,268-13,793,313:-1) View Sequence Alignments	n/a	45.42 %	47.46 %	n/a	<b>95.15</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_07G211600 Compare Regions (7:38,313,562-38,326,234:1) View Sequence Alignments	n/a	45.35 %	47.41 %	n/a	<b>95.29</b>	No
<i>At5g61500</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_09G231000 Compare Regions (9:45,443,954-45,447,812:-1) View Sequence Alignments	0.055 42	85.07 %	78.27 %	n/a	<b>90.02</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_12G005700 Compare Regions (12:433,113-437,871:1) View Sequence Alignments	0.041 54	87.22 %	87.22 %	n/a	<b>100</b>	No
<i>At2g44140</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_09G244800 Compare Regions (9:46,708,330-46,712,967:1) View Sequence Alignments	n/a	58.64 %	61.03 %	n/a	<b>92.57</b>	No
	Glycine max	Many-to-manyView Gene Tree	GLYMA_18G248400 Compare Regions (18:53,539,192-53,544,229:-1) View Sequence Alignments	n/a	59.18 %	61.46 %	n/a	<b>1.87</b>	No
<i>At3g59950</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_09G244800 Compare Regions (9:46,708,330-46,712,967:1) View Sequence Alignments	0.176 07	56.17 %	57.23 %	n/a	<b>93.33</b>	No
	Glycine max	Many-to-manyView Gene Tree	GLYMA_18G248400 Compare Regions (18:53,539,192-53,544,229:-1) View Sequence Alignments	0.188 77	55.67 %	56.60 %	n/a	<b>93.57</b>	No
<i>At5g17290</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_02G240700 Compare Regions (2:42,910,921-42,918,001:-1) View Sequence Alignments	n/a	59.71 %	62.02 %	n/a	<b>99.42</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_14G210200 Compare Regions (14:47,535,839-47,545,840:-1) View Sequence Alignments	n/a	60.17 %	62.31 %	n/a	<b>99.01</b>	No
<i>At3g61710</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_04G141000 Compare Regions (4:23,665,626-23,682,229:-1) View Sequence Alignments	n/a	72.69 %	71.57 %	n/a	<b>98.19</b>	Yes
	Glycine max	1-to-manyView Gene Tree	GLYMA_11G153900 Compare Regions (11:12,389,260-12,396,651:-1) View Sequence Alignments	0.085 4	72.89 %	71.76 %	n/a	<b>98.29</b>	Yes
<i>At5g45900</i>	Glycine max	1-to-1View Gene Tree	GLYMA_12G010000 Compare Regions (12:712,288-717,264:1) View Sequence Alignments	n/a	68.95 %	67.86 %	n/a	<b>98.09</b>	No
<i>At4g21980</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_15G188600 Compare Regions (15:19,737,953-19,738,255:-1) View Sequence Alignments	n/a	73.97 %	39.42 %	n/a	n/a	Yes
<i>At4g04620</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_15G188600 Compare Regions (15:19,737,953-19,738,255:-1) View Sequence Alignments	n/a	71.23 %	42.62 %	n/a	n/a	Yes
<i>At1g62040</i>	Species without orthologues								
<i>At2g05630</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_06G306300 Compare Regions (6:49,529,272-49,531,512:1) View Sequence Alignments	0.042 23	87.50 %	64.02 %	n/a	<b>88.13</b>	Yes
	Glycine max	1-to-manyView Gene Tree	GLYMA_12G098400 Compare Regions (12:8,463,842-8,466,127:-1) View Sequence Alignments	0.024 36	88.33 %	64.63 %	n/a	<b>88.97</b>	Yes
<i>At2g45170</i>	Species without orthologues								
<i>At4g16520</i>	Species without orthologues								
<i>At3g60640</i>	Species without orthologues								
<i>At3g06420</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_02G008800 Compare Regions (2:882,915-884,424:1) View Sequence Alignments	n/a	63.11 %	64.71 %	n/a	n/a	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_10G009300 Compare Regions (10:896,609-897,903:1) View Sequence Alignments	n/a	63.11 %	64.71 %	n/a	<b>73.91</b>	No

<i>At3g15580</i>	Species without orthologues								
<i>At2g31260</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_03G162100 Compare Regions (3:37,703,629-37,711,157:1) View Sequence Alignments	n/a	64.45 %	64.90 %	n/a	<b>81.59</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_10G035800 Compare Regions (10:3,130,966-3,138,037:1) View Sequence Alignments	n/a	65.82 %	65.59 %	n/a	<b>99.15</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_13G122200 Compare Regions (13:23,509,326-23,515,360:1) View Sequence Alignments	n/a	65.09 %	65.24 %	n/a	<b>96.58</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_19G163500 Compare Regions (19:42,435,811-42,443,348:1) View Sequence Alignments	n/a	63.52 %	63.74 %	n/a	<b>82.35</b>	No
<i>At3g07525</i>	Species without orthologues								
<i>AT4G30790</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_02G206500 Compare Regions (2:39,154,706-39,161,370:1) View Sequence Alignments	n/a	61.35 %	61.67 %	n/a	<b>99.74</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_17G071400 Compare Regions (17:5,578,787-5,585,492:-1) View Sequence Alignments	n/a	61.94 %	62.37 %	n/a	<b>97.89</b>	No
<i>At1g54210</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_07G038100 Compare Regions (7:3,134,753-3,137,886:1) View Sequence Alignments	n/a	88.30 %	86.46 %	n/a	<b>88.85</b>	Yes
	Glycine max	Many-to-manyView Gene Tree	GLYMA_16G007300 Compare Regions (16:599,220-602,627:1) View Sequence Alignments	n/a	67.37 %	66.67 %	n/a	<b>85.16</b>	Yes
<i>At3g13970</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_07G038100 Compare Regions (7:3,134,753-3,137,886:1) View Sequence Alignments	n/a	82.98 %	82.98 %	n/a	<b>89.56</b>	Yes
<i>At3g49590</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_16G007300 Compare Regions (16:599,220-602,627:1) View Sequence Alignments	n/a	63.16 %	63.83 %	n/a	n/a	Yes
<i>At3g49590</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_02G220700 Compare Regions (2:40,856,235-40,861,423:-1) View Sequence Alignments	n/a	46.80 %	44.98 %	n/a	<b>96.63</b>	Yes
	Glycine max	1-to-manyView Gene Tree	GLYMA_14G187000 Compare Regions (14:45,159,106-45,164,166:1) View Sequence Alignments	n/a	47.80 %	45.79 %	n/a	<b>97.4</b>	Yes
<i>At3g18770</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_05G189000 Compare Regions (5:37,485,611-37,491,652:1) View Sequence Alignments	n/a	54.05 %	53.44 %	n/a	<b>96.26</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_08G146700 Compare Regions (8:11,166,509-11,172,366:1) View Sequence Alignments	n/a	53.61 %	53.44 %	n/a	<b>98.06</b>	No
<i>AT1G77890</i>	Species without orthologues								
<i>AT4G08540</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_13G085400 Compare Regions (13:19,705,658-19,715,073:-1) View Sequence Alignments	n/a	67.51 %	67.65 %	n/a	<b>97.58</b>	No
	Glycine max	Many-to-manyView Gene Tree	GLYMA_14G167200 Compare Regions (14:41,352,672-41,365,398:-1) View Sequence Alignments	n/a	66.74 %	67.02 %	n/a	<b>98.11</b>	No
<i>At5g50230</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_05G043700 Compare Regions (5:3,901,985-3,905,389:1) View Sequence Alignments	n/a	72.37 %	73.08 %	n/a	<b>100</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_17G126200 Compare Regions (17:10,054,028-10,058,177:1) View Sequence Alignments	n/a	72.18 %	72.89 %	n/a	<b>99.54</b>	No
<i>At3g62770</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_03G212100 Compare Regions (3:41,817,313-41,820,500:1) View Sequence Alignments	n/a	66.19 %	65.88 %	n/a	<b>98.57</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_19G209200 Compare Regions (19:46,393,051-46,396,379:1) View Sequence Alignments	n/a	64.30 %	64.00 %	n/a	<b>90.99</b>	No
<i>At4g30510</i>	Glycine max	1-to-manyView Gene Tree	GLYMA_02G207500 Compare Regions (2:39,248,283-39,253,677:1) View Sequence Alignments	n/a	67.93 %	68.31 %	n/a	<b>93.81</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_10G126200 Compare Regions (10:33,430,366-33,432,117:-1) View Sequence Alignments	n/a	60.96 %	24.32 %	n/a	<b>69.62</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_16G109400 Compare Regions (16:23,481,725-23,483,856:-1) View Sequence Alignments	0.114 85	64.11 %	36.61 %	n/a	<b>83.4</b>	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_17G070200 Compare Regions (17:5,495,613-5,501,594:-1) View Sequence Alignments	n/a	68.56 %	69.13 %	n/a	<b>83.23</b>	No
	Glycine max	Many-to-manyView Gene Tree	GLYMA_04G224300 Compare Regions (4:49,475,519-49,486,851:1) View Sequence Alignments	0.105 99	68.50 %	73.03 %	n/a	<b>96.88</b>	No
	Glycine max	Many-to-manyView Gene Tree	GLYMA_06G140400 Compare Regions (6:11,446,439-11,452,684:-1) View Sequence Alignments	0.099 11	68.10 %	72.77 %	n/a	<b>98.94</b>	No
<i>At2g40810</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_04G224300 Compare Regions (4:49,475,519-49,486,851:1) View Sequence Alignments	0.105 99	68.50 %	73.03 %	n/a	<b>96.88</b>	No
	Glycine max	Many-to-manyView Gene Tree	GLYMA_06G140400 Compare Regions (6:11,446,439-11,452,684:-1) View Sequence Alignments	0.099 11	68.10 %	72.77 %	n/a	<b>98.94</b>	No
<i>At3g56440</i>	Glycine max	Many-to-manyView Gene Tree	GLYMA_04G224300 Compare Regions (4:49,475,519-49,486,851:1) View Sequence Alignments	0.127 83	65.87 %	70.59 %	n/a	<b>91.99</b>	No



At5g05150	Glycine max	Many-to-manyView Gene Tree	GLYMA_06G140400 Compare Regions (6:11,446,439-11,452,684:-1) View Sequence Alignments	0.126 3	65.71 %	70.59 %	n/a	4.52	No
	Species without orthologues								
At5g54730	Glycine max	1-to-manyView Gene Tree	GLYMA_06G267000 Compare Regions (6:45,497,961-45,504,163:-1) View Sequence Alignments	n/a	32.15 %	38.14 %	n/a	84.63	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_12G136000 Compare Regions (12:15,957,977-15,965,220:1) View Sequence Alignments	n/a	33.00 %	38.93 %	n/a	83.56	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_12G214600 Compare Regions (12:37,403,821-37,410,688:1) View Sequence Alignments	n/a	34.61 %	41.42 %	n/a	82.09	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_13G287000 Compare Regions (13:38,736,311-38,743,172:-1) View Sequence Alignments	n/a	34.91 %	41.55 %	n/a	85.17	No
At1g03380	Glycine max	1-to-manyView Gene Tree	GLYMA_03G148700 Compare Regions (3:36,433,817-36,440,498:-1) View Sequence Alignments	0.211 22	51.38 %	52.45 %	n/a	84.8	Yes
	Glycine max	1-to-manyView Gene Tree	GLYMA_19G152000 Compare Regions (19:41,245,379-41,252,443:-1) View Sequence Alignments	0.215 38	54.62 %	49.95 %	n/a	86.95	Yes
At1g54710	Glycine max	1-to-manyView Gene Tree	GLYMA_10G157700 Compare Regions (10:39,177,037-39,184,196:1) View Sequence Alignments	n/a	53.85 %	52.86 %	n/a	92.88	No
	Glycine max	1-to-manyView Gene Tree	GLYMA_20G230900 Compare Regions (20:46,480,639-46,484,770:-1) View Sequence Alignments	n/a	60.22 %	47.36 %	n/a	91.76	No
AT5G66930	Glycine max	1-to-1View Gene Tree	GLYMA_17G180900 Compare Regions (17:20,745,714-20,749,941:1) View Sequence Alignments	n/a	72.94 %	63.35 %	n/a	93.46	No

#### D.HMMER analysis in *A. thaliana*, *P. vulgaris*, *M. truncatula*, and *G.max*.

<b>ID Arabidopsis</b>	<b>Target</b>	<b>Species</b>	<b>E-value</b>
AT1G49180.1	PHAVU_010G120500g	Phaseolus vulgaris	2.10E-71
AT1G49180.2	PHAVU_010G120500g	Phaseolus vulgaris	1.60E-71
AT2G37840.1	PHAVU_010G015100g	Phaseolus vulgaris	5.70E-211
AT2G37840.2	PHAVU_010G015100g	Phaseolus vulgaris	2.10E-162
AT2G37840.3	PHAVU_010G015100g	Phaseolus vulgaris	2.30E-104
AT3G53930.1	PHAVU_010G015100g	Phaseolus vulgaris	4.50E-194
AT3G53930.2	PHAVU_010G015100g	Phaseolus vulgaris	6.20E-196
AT3G53930.3	PHAVU_010G015100g	Phaseolus vulgaris	1.10E-132
AT3G53930.4	PHAVU_010G015100g	Phaseolus vulgaris	1.60E-134
AT3G53930.5	PHAVU_010G015100g	Phaseolus vulgaris	1.10E-132
AT3G61960.1	PHAVU_010G120500g	Phaseolus vulgaris	3.90E-180
AT3G61960.2	PHAVU_010G120500g	Phaseolus vulgaris	5.40E-163
AT3G19190.1	PHAVU_003G295800g	Phaseolus vulgaris	0.00E+00
AT3G19190.2	PHAVU_003G295800g	Phaseolus vulgaris	0.00E+00
AT3G19190.3	PHAVU_003G295800g	Phaseolus vulgaris	0.00E+00
AT5G61500.1	PHAVU_011G006500g	Phaseolus vulgaris	2.90E-184
AT5G61500.2	PHAVU_011G006500g	Phaseolus vulgaris	4.20E-132
AT2G44140.1	PHAVU_008G048900g	Phaseolus vulgaris	1.40E-184
AT2G44140.2	PHAVU_008G048900g	Phaseolus vulgaris	4.30E-171
AT2G44140.3	PHAVU_008G048900g	Phaseolus vulgaris	1.40E-184
AT2G44140.4	PHAVU_008G048900g	Phaseolus vulgaris	6.50E-166

AT2G44140.5	PHAVU_008G048900g	Phaseolus vulgaris	1.40E-151
AT3G59950.1	PHAVU_008G048900g	Phaseolus vulgaris	2.30E-177
AT3G59950.2	PHAVU_008G048900g	Phaseolus vulgaris	1.40E-114
AT3G59950.3	PHAVU_008G048900g	Phaseolus vulgaris	1.80E-105
AT3G59950.4	PHAVU_008G048900g	Phaseolus vulgaris	7.10E-167
AT3G59950.5	PHAVU_008G048900g	Phaseolus vulgaris	1.60E-147
AT5G17290.1	PHAVU_008G241000g	Phaseolus vulgaris	5.70E-144
AT3G61710.1	PHAVU_005G029900g	Phaseolus vulgaris	1.20E-250
AT3G61710.2	PHAVU_005G029900g	Phaseolus vulgaris	1.10E-171
AT3G61710.3	PHAVU_005G029900g	Phaseolus vulgaris	3.80E-139
AT3G61710.4	PHAVU_005G029900g	Phaseolus vulgaris	4.10E-216
AT5G45900.1	PHAVU_011G010700g	Phaseolus vulgaris	0.00E+00
AT4G21980.1	PHAVU_011G103300g	Phaseolus vulgaris	1.80E-60
AT4G21980.2	PHAVU_011G103300g	Phaseolus vulgaris	3.70E-60
AT4G04620.1	PHAVU_003G079300g	Phaseolus vulgaris	7.90E-59
AT4G04620.2	PHAVU_003G079300g	Phaseolus vulgaris	7.90E-59
AT4G04620.3	PHAVU_003G079300g	Phaseolus vulgaris	7.90E-59
AT1G62040.1	PHAVU_011G103300g	Phaseolus vulgaris	2.80E-66
AT1G62040.2	PHAVU_011G103300g	Phaseolus vulgaris	5.40E-66
AT2G05630.1	PHAVU_011G103300g	Phaseolus vulgaris	4.00E-67
AT2G05630.2	PHAVU_011G103300g	Phaseolus vulgaris	3.60E-60
AT2G45170.1	PHAVU_003G219600g	Phaseolus vulgaris	4.10E-60
AT2G45170.2	PHAVU_003G219600g	Phaseolus vulgaris	4.10E-60
AT4G16520.1	PHAVU_003G219600g	Phaseolus vulgaris	1.90E-65
AT4G16520.2	PHAVU_003G219600g	Phaseolus vulgaris	1.90E-65
AT4G16520.3	PHAVU_003G219600g	Phaseolus vulgaris	1.90E-65
AT3G60640.1	PHAVU_003G219600g	Phaseolus vulgaris	1.90E-60
AT3G06420.1	PHAVU_007G210800g	Phaseolus vulgaris	1.10E-30
AT3G15580.1	PHAVU_011G151600g	Phaseolus vulgaris	2.20E-39
AT2G31260.1	PHAVU_001G159900g	Phaseolus vulgaris	0.00E+00
AT3G07525.1	PHAVU_010G036300g	Phaseolus vulgaris	4.80E-68
AT3G07525.2	PHAVU_010G036300g	Phaseolus vulgaris	6.20E-67
AT4G30790.1	PHAVU_003G153800g	Phaseolus vulgaris	0.00E+00
AT1G54210.1	PHAVU_010G130300g	Phaseolus vulgaris	4.40E-50
AT1G54210.2	PHAVU_010G130300g	Phaseolus vulgaris	4.40E-50
AT1G54210.3	PHAVU_010G130300g	Phaseolus vulgaris	4.40E-50
AT3G13970.1	PHAVU_010G130300g	Phaseolus vulgaris	9.90E-49
AT3G13970.2	PHAVU_010G130300g	Phaseolus vulgaris	1.40E-20
AT3G13970.3	PHAVU_010G130300g	Phaseolus vulgaris	1.40E-20
AT3G13970.4	PHAVU_010G130300g	Phaseolus vulgaris	7.00E-34
AT3G49590.1	PHAVU_008G187800g	Phaseolus vulgaris	7.30E-157

AT3G49590.2	PHAVU_008G187800g	Phaseolus vulgaris	7.30E-157
AT3G49590.3	PHAVU_008G187800g	Phaseolus vulgaris	7.30E-157
AT3G18770.1	PHAVU_002G269600g	Phaseolus vulgaris	3.90E-173
AT1G77890.1	PHAVU_008G169200g	Phaseolus vulgaris	1.10E-125
AT1G77890.2	PHAVU_008G169200g	Phaseolus vulgaris	2.80E-116
AT1G77890.3	PHAVU_008G169200g	Phaseolus vulgaris	8.20E-124
AT4G08540.1	PHAVU_008G169200g	Phaseolus vulgaris	2.80E-222
AT5G50230.1	PHAVU_003G207100g	Phaseolus vulgaris	6.50E-257
AT4G30510.1	PHAVU_003G152800g	Phaseolus vulgaris	2.10E-132
AT4G30510.2	PHAVU_003G152800g	Phaseolus vulgaris	5.90E-112
AT3G62770.1	PHAVU_007G196400g	Phaseolus vulgaris	6.80E-186
AT3G62770.3	PHAVU_007G196400g	Phaseolus vulgaris	6.80E-186
AT2G40810.1	PHAVU_009G041700g	Phaseolus vulgaris	1.20E-183
AT2G40810.2	PHAVU_009G041700g	Phaseolus vulgaris	1.20E-183
AT2G40810.3	PHAVU_009G041700g	Phaseolus vulgaris	5.00E-104
AT3G56440.1	PHAVU_009G041700g	Phaseolus vulgaris	2.00E-179
AT3G56440.2	PHAVU_009G041700g	Phaseolus vulgaris	6.90E-166
AT3G56440.3	PHAVU_009G041700g	Phaseolus vulgaris	1.80E-148
AT5G05150.1	PHAVU_009G041700g	Phaseolus vulgaris	3.00E-110
AT5G54730.1	PHAVU_005G091300g	Phaseolus vulgaris	2.60E-160
AT5G54730.2	PHAVU_005G091300g	Phaseolus vulgaris	2.60E-160
AT1G03380.1	PHAVU_001G146700g	Phaseolus vulgaris	1.00E-297
AT1G54710.1	PHAVU_007G183100g	Phaseolus vulgaris	1.00E-302
AT1G54710.2	PHAVU_007G183100g	Phaseolus vulgaris	5.80E-252
AT5G66930.1	PHAVU_003G248000g	Phaseolus vulgaris	2.30E-70
AT5G66930.2	PHAVU_003G248000g	Phaseolus vulgaris	1.70E-106
AT5G66930.3	PHAVU_003G248000g	Phaseolus vulgaris	1.90E-98

<i>ID Arabidopsis</i>	<i>Target</i>	<i>Species</i>	<i>E-value</i>
AT1G49180.1	MTR_3g095620	Medicago truncatula	1.70E-94
AT1G49180.2	MTR_3g095620	Medicago truncatula	1.70E-94
AT2G37840.1	MTR_4g019410	Medicago truncatula	2.20E-284
AT2G37840.2	MTR_4g019410	Medicago truncatula	9.60E-195
AT2G37840.3	MTR_4g019410	Medicago truncatula	2.90E-126
AT3G53930.1	MTR_4g019410	Medicago truncatula	1.20E-260
AT3G53930.2	MTR_4g019410	Medicago truncatula	1.20E-262
AT3G53930.3	MTR_4g019410	Medicago truncatula	2.50E-158
AT3G53930.4	MTR_4g019410	Medicago truncatula	2.20E-160
AT3G53930.5	MTR_4g019410	Medicago truncatula	2.50E-158
AT3G61960.1	MTR_8g024100	Medicago truncatula	1.40E-184
AT3G61960.2	MTR_8g024100	Medicago truncatula	2.10E-170

AT3G19190.1	MTR_4g086370	Medicago truncatula	0.00E+00
AT3G19190.2	MTR_4g086370	Medicago truncatula	0.00E+00
AT3G19190.3	MTR_4g086370	Medicago truncatula	0.00E+00
AT5G61500.1	MTR_4g036265	Medicago truncatula	5.00E-181
AT5G61500.2	MTR_4g036265	Medicago truncatula	4.60E-129
AT2G44140.1	MTR_7g081230	Medicago truncatula	6.90E-186
AT2G44140.2	MTR_7g081230	Medicago truncatula	9.70E-172
AT2G44140.3	MTR_7g081230	Medicago truncatula	6.90E-186
AT2G44140.4	MTR_7g081230	Medicago truncatula	1.50E-166
AT2G44140.5	MTR_7g081230	Medicago truncatula	1.50E-152
AT3G59950.1	MTR_7g081230	Medicago truncatula	3.30E-176
AT3G59950.2	MTR_7g081230	Medicago truncatula	4.80E-113
AT3G59950.3	MTR_7g081230	Medicago truncatula	4.60E-104
AT3G59950.4	MTR_7g081230	Medicago truncatula	8.30E-166
AT3G59950.5	MTR_7g081230	Medicago truncatula	2.40E-146
AT5G17290.1	MTR_5g076920	Medicago truncatula	7.40E-138
AT3G61710.1	MTR_3g018770	Medicago truncatula	1.00E-258
AT3G61710.2	MTR_3g018770	Medicago truncatula	1.50E-175
AT3G61710.3	MTR_3g018770	Medicago truncatula	3.80E-144
AT3G61710.4	MTR_3g018770	Medicago truncatula	3.20E-218
AT5G45900.1	MTR_0003s0540	Medicago truncatula	0.00E+00
AT4G21980.1	MTR_2g023430	Medicago truncatula	2.90E-62
AT4G21980.2	MTR_2g023430	Medicago truncatula	5.90E-62
AT4G04620.1	MTR_2g023430	Medicago truncatula	2.30E-60
AT4G04620.2	MTR_2g023430	Medicago truncatula	2.30E-60
AT4G04620.3	MTR_2g023430	Medicago truncatula	2.30E-60
AT1G62040.1	MTR_4g048510	Medicago truncatula	6.10E-65
AT1G62040.2	MTR_4g048510	Medicago truncatula	1.10E-64
AT2G05630.1	MTR_4g048510	Medicago truncatula	2.70E-66
AT2G05630.2	MTR_4g048510	Medicago truncatula	2.00E-59
AT2G45170.1	MTR_4g101090	Medicago truncatula	4.70E-60
AT2G45170.2	MTR_4g101090	Medicago truncatula	4.70E-60
AT4G16520.1	MTR_4g101090	Medicago truncatula	2.60E-66
AT4G16520.2	MTR_4g101090	Medicago truncatula	2.60E-66
AT4G16520.3	MTR_4g101090	Medicago truncatula	2.60E-66
AT3G60640.1	MTR_4g101090	Medicago truncatula	9.30E-61
AT3G06420.1	MTR_4g123760	Medicago truncatula	5.90E-31
AT3G15580.1	MTR_4g123760	Medicago truncatula	3.40E-52
AT2G31260.1	MTR_1g070160	Medicago truncatula	0.00E+00
AT3G07525.1	MTR_8g010140	Medicago truncatula	3.50E-69
AT3G07525.2	MTR_8g010140	Medicago truncatula	2.20E-68

AT4G30790.1	MTR_4g130370	Medicago truncatula	0.00E+00
AT1G54210.1	MTR_8g020500	Medicago truncatula	7.40E-51
AT1G54210.2	MTR_8g020500	Medicago truncatula	7.40E-51
AT1G54210.3	MTR_8g020500	Medicago truncatula	7.40E-51
AT3G13970.1	MTR_8g020500	Medicago truncatula	7.40E-51
AT3G13970.2	MTR_8g020500	Medicago truncatula	6.50E-21
AT3G13970.3	MTR_8g020500	Medicago truncatula	6.50E-21
AT3G13970.4	MTR_8g020500	Medicago truncatula	8.10E-35
AT3G49590.1	MTR_5g068710	Medicago truncatula	1.30E-148
AT3G49590.2	MTR_5g068710	Medicago truncatula	1.30E-148
AT3G49590.3	MTR_5g068710	Medicago truncatula	1.30E-148
AT3G18770.1	MTR_3g095570	Medicago truncatula	4.50E-154
AT1G77890.1	MTR_5g061040	Medicago truncatula	4.80E-127
AT1G77890.2	MTR_5g061040	Medicago truncatula	1.30E-117
AT1G77890.3	MTR_5g061040	Medicago truncatula	3.80E-125
AT4G08540.1	MTR_5g061040	Medicago truncatula	3.00E-222
AT5G50230.1	MTR_4g104380	Medicago truncatula	4.40E-247
AT4G30510.1	MTR_4g130190	Medicago truncatula	2.40E-136
AT4G30510.2	MTR_4g130190	Medicago truncatula	1.80E-116
AT3G62770.1	MTR_1g083230	Medicago truncatula	6.00E-189
AT3G62770.3	MTR_1g083230	Medicago truncatula	6.00E-189
AT2G40810.1	MTR_3g093590	Medicago truncatula	4.10E-191
AT2G40810.2	MTR_3g093590	Medicago truncatula	4.10E-191
AT2G40810.3	MTR_3g093590	Medicago truncatula	7.70E-109
AT3G56440.1	MTR_3g093590	Medicago truncatula	9.10E-193
AT3G56440.2	MTR_3g093590	Medicago truncatula	5.20E-179
AT3G56440.3	MTR_3g093590	Medicago truncatula	4.30E-158
AT5G05150.1	MTR_3g093590	Medicago truncatula	1.40E-112
AT5G54730.1	MTR_2g082770	Medicago truncatula	4.30E-174
AT5G54730.2	MTR_2g082770	Medicago truncatula	4.30E-174
AT1G03380.1	MTR_1g089110	Medicago truncatula	6.40E-295
AT1G54710.1	MTR_1g082300	Medicago truncatula	7.90E-295
AT1G54710.2	MTR_1g082300	Medicago truncatula	6.50E-246
AT5G66930.1	MTR_8g079240	Medicago truncatula	3.80E-71
AT5G66930.2	MTR_8g079240	Medicago truncatula	3.80E-106
AT5G66930.3	MTR_8g079240	Medicago truncatula	1.00E-98

<i><b>ID Arabidopsis</b></i>	<i><b>Target</b></i>	<i><b>Species</b></i>	<i><b>E-value</b></i>
AT1G49180.1	GLYMA_04G215500	Glycine max	1.10E-95
AT1G49180.2	GLYMA_04G215500	Glycine max	6.20E-102
AT2G37840.1	GLYMA_03G069800	Glycine max	1.20E-288
AT2G37840.2	GLYMA_03G069800	Glycine max	3.90E-202
AT2G37840.3	GLYMA_03G069800	Glycine max	1.30E-130
AT3G53930.1	GLYMA_03G069800	Glycine max	2.10E-269
AT3G53930.2	GLYMA_03G069800	Glycine max	2.40E-271
AT3G53930.3	GLYMA_03G069800	Glycine max	1.20E-169
AT3G53930.4	GLYMA_03G069800	Glycine max	3.90E-171
AT3G53930.5	GLYMA_03G069800	Glycine max	1.20E-169
AT3G61960.1	GLYMA_07G048400	Glycine max	4.00E-195
AT3G61960.2	GLYMA_07G048400	Glycine max	1.30E-178
AT3G19190.1	GLYMA_02G133400	Glycine max	0.00E+00
AT3G19190.2	GLYMA_02G133400	Glycine max	0.00E+00
AT3G19190.3	GLYMA_02G133400	Glycine max	0.00E+00
AT5G61500.1	GLYMA_12G005700	Glycine max	1.20E-185
AT5G61500.2	GLYMA_12G005700	Glycine max	1.70E-133
AT2G44140.1	GLYMA_09G244800	Glycine max	1.70E-186
AT2G44140.2	GLYMA_09G244800	Glycine max	2.80E-171
AT2G44140.3	GLYMA_09G244800	Glycine max	1.70E-186
AT2G44140.4	GLYMA_09G244800	Glycine max	2.10E-166
AT2G44140.5	GLYMA_09G244800	Glycine max	7.60E-153
AT3G59950.1	GLYMA_09G244800	Glycine max	2.10E-176
AT3G59950.2	GLYMA_18G248400	Glycine max	2.60E-113
AT3G59950.3	GLYMA_18G248400	Glycine max	3.70E-105
AT3G59950.4	GLYMA_09G244800	Glycine max	2.60E-166
AT3G59950.5	GLYMA_18G248400	Glycine max	1.30E-146
AT5G17290.1	GLYMA_14G210200	Glycine max	5.70E-146
AT3G61710.1	GLYMA_11G153900	Glycine max	4.00E-258
AT3G61710.2	GLYMA_11G153900	Glycine max	2.20E-173
AT3G61710.3	GLYMA_11G153900	Glycine max	1.70E-141
AT3G61710.4	GLYMA_11G153900	Glycine max	8.90E-218
AT5G45900.1	GLYMA_12G010000	Glycine max	0.00E+00
AT4G21980.1	GLYMA_09G003900	Glycine max	1.40E-62
AT4G21980.2	GLYMA_07G261000	Glycine max	8.60E-64
AT4G04620.1	GLYMA_09G003900	Glycine max	4.50E-60
AT4G04620.2	GLYMA_09G003900	Glycine max	4.50E-60
AT4G04620.3	GLYMA_09G003900	Glycine max	4.50E-60
AT1G62040.1	GLYMA_12G098400	Glycine max	1.10E-66
AT1G62040.2	GLYMA_12G098400	Glycine max	2.10E-66

AT2G05630.1	GLYMA_12G098400	Glycine max	1.10E-66
AT2G05630.2	GLYMA_12G098400	Glycine max	9.10E-60
AT2G45170.1	GLYMA_17G140700	Glycine max	1.50E-60
AT2G45170.2	GLYMA_17G140700	Glycine max	1.50E-60
AT4G16520.1	GLYMA_17G140700	Glycine max	8.10E-67
AT4G16520.2	GLYMA_17G140700	Glycine max	8.10E-67
AT4G16520.3	GLYMA_17G140700	Glycine max	8.10E-67
AT3G60640.1	GLYMA_17G140700	Glycine max	7.60E-61
AT3G06420.1	GLYMA_02G008800	Glycine max	6.40E-31
AT3G15580.1	GLYMA_02G008800	Glycine max	6.20E-51
AT2G31260.1	GLYMA_10G035800	Glycine max	0.00E+00
AT3G07525.1	GLYMA_07G124300	Glycine max	5.20E-68
AT3G07525.2	GLYMA_03G097000	Glycine max	4.60E-67
AT4G30790.1	GLYMA_17G071400	Glycine max	0.00E+00
AT1G54210.1	GLYMA_07G038100	Glycine max	9.70E-50
AT1G54210.2	GLYMA_07G038100	Glycine max	9.70E-50
AT1G54210.3	GLYMA_07G038100	Glycine max	9.70E-50
AT3G13970.1	GLYMA_07G038100	Glycine max	3.70E-48
AT3G13970.2	GLYMA_16G007300	Glycine max	3.70E-20
AT3G13970.3	GLYMA_16G007300	Glycine max	3.70E-20
AT3G13970.4	GLYMA_16G007300	Glycine max	2.10E-33
AT3G49590.1	GLYMA_14G187000	Glycine max	2.90E-160
AT3G49590.2	GLYMA_14G187000	Glycine max	2.90E-160
AT3G49590.3	GLYMA_14G187000	Glycine max	2.90E-160
AT3G18770.1	GLYMA_05G189000	Glycine max	8.40E-182
AT1G77890.1	GLYMA_14G167200	Glycine max	6.30E-127
AT1G77890.2	GLYMA_13G085400	Glycine max	1.20E-116
AT1G77890.3	GLYMA_14G167200	Glycine max	4.90E-125
AT4G08540.1	GLYMA_14G167200	Glycine max	8.70E-183
AT5G50230.1	GLYMA_05G043700	Glycine max	2.00E-256
AT4G30510.1	GLYMA_17G070200	Glycine max	2.40E-140
AT4G30510.2	GLYMA_17G070200	Glycine max	2.40E-140
AT3G62770.1	GLYMA_03G212100	Glycine max	7.00E-186
AT3G62770.3	GLYMA_03G212100	Glycine max	7.00E-186
AT2G40810.1	GLYMA_06G140400	Glycine max	8.60E-194
AT2G40810.2	GLYMA_06G140400	Glycine max	8.60E-194
AT2G40810.3	GLYMA_06G140400	Glycine max	2.70E-113
AT3G56440.1	GLYMA_06G140400	Glycine max	1.60E-19
AT3G56440.2	GLYMA_06G140400	Glycine max	9.40E-179
AT3G56440.3	GLYMA_06G140400	Glycine max	1.00E-157
AT5G05150.1	GLYMA_06G140400	Glycine max	3.20E-114

AT5G54730.1	GLYMA_13G287000	Glycine max	7.60E-172
AT5G54730.2	GLYMA_13G287000	Glycine max	7.60E-172
AT1G03380.1	GLYMA_03G148700	Glycine max	8.10E-306
AT1G54710.1	GLYMA_10G157700	Glycine max	1.60E-296
AT1G54710.2	GLYMA_10G157700	Glycine max	1.60E-296
AT5G66930.1	GLYMA_17G180900	Glycine max	7.70E-72
AT5G66930.2	GLYMA_17G180900	Glycine max	7.20E-108
AT5G66930.3	GLYMA_17G180900	Glycine max	8.80E-100

## E. Inparanoid

ID Arabidopsis	Homolog Gene . Primary Identifier	Gene Symbol	Gene Organism Name	Homolog Ortholog _ Gene . Primary Identifier	Ortholog _ Gene Organism Name	Homolog Relationship	Homolog Group Name
At1g49180	Species without orthologues						
At2g37840	AT2G37840		A. thaliana	Phvul.010G015100	P. vulgaris	many-to-one	442_167_2102
	AT2G37840		A. thaliana early-release	Phvul.010G015100	P. vulgaris	many-to-one	442_447_2103
At3g53930	AT3G53930		A. thaliana	Phvul.010G015100	P. vulgaris	many-to-one	442_167_2102
	AT3G53930		A. thaliana early-release	Phvul.010G015100	P. vulgaris	many-to-one	442_447_2103
At3g61960	AT3G61960		A. thaliana	Phvul.010G120500	P. vulgaris	one-to-one	442_167_4678
	AT3G61960		A. thaliana early-release	Phvul.010G120500	P. vulgaris	one-to-one	442_447_4677
At3g19190	AT3G19190	ATG2	A. thaliana	Phvul.003G295800	P. vulgaris	one-to-one	442_167_397
	AT3G19190	ATG2	A. thaliana early-release	Phvul.003G295800	P. vulgaris	one-to-one	442_447_310
At5g61500	AT5G61500	ATG3	A. thaliana	Phvul.011G006500	P. vulgaris	one-to-one	442_167_4852
	AT5G61500	ATG3	A. thaliana early-release	Phvul.011G006500	P. vulgaris	one-to-one	442_447_4852
At2g44140	AT2G44140		A. thaliana	Phvul.008G048900	P. vulgaris	many-to-one	442_167_4694
	AT2G44140		A. thaliana early-release	Phvul.008G048900	P. vulgaris	many-to-one	442_447_4694
At3g59950	AT3G59950		A. thaliana	Phvul.008G048900	P. vulgaris	many-to-one	442_167_4694
	AT3G59950		A. thaliana early-release	Phvul.008G048900	P. vulgaris	many-to-one	442_447_4694
At5g17290	AT5G17290	APG5	A. thaliana	Phvul.008G241000	P. vulgaris	one-to-one	442_167_6496
	AT5G17290	APG5	A. thaliana early-release	Phvul.008G241000	P. vulgaris	one-to-one	442_447_6506
At3g61710		ATG6	A. thaliana	Phvul.005G029900	P. vulgaris	one-to-one	442_167_2769
	AT3G61710	ATG6	A. thaliana early-release	Phvul.005G029900	P. vulgaris	one-to-one	442_447_2778
At5g45900	AT5G45900	APG7	A. thaliana	Phvul.011G010700	P. vulgaris	one-to-one	442_167_1340
	AT5G45900	APG7	A. thaliana early-release	Phvul.011G010700	P. vulgaris	one-to-one	442_447_1344
At4g21980	Species without orthologues						
At4g04620	Species without orthologues						
At1g62040	AT1G62040	ATG8C	A. thaliana	Phvul.011G103300	P. vulgaris	one-to-one	442_167_10280
	AT1G62040	ATG8C	A. thaliana early-release	Phvul.011G103300	P. vulgaris	one-to-one	442_447_10288
At2g05630	Species without orthologues						
At2g45170	AT2G45170	ATG8E	A. thaliana early-release	Phvul.002G062200	P. vulgaris	many-to-many	442_447_10594
	AT2G45170	ATG8E	A. thaliana early-release	Phvul.003G219600	P. vulgaris	many-to-many	442_447_10594
At4g16520	AT4G16520	ATG8F	A. thaliana	Phvul.002G062200	P. vulgaris	one-to-many	442_167_10328



At3g60640	AT4G16520	ATG8F	A. thaliana	Phvul.003G219600	P. vulgaris	one-to-many	442_167_10328
	AT3G60640	ATG8G	A. thaliana early-release	Phvul.002G062200	P. vulgaris	many-to-many	442_447_10594
	AT3G60640	ATG8G	A. thaliana early-release	Phvul.003G219600	P. vulgaris	many-to-many	442_447_10594
At3g06420	Species without orthologues						
At3g15580	AT3G15580	APG8H	A. thaliana	Phvul.007G210800	P. vulgaris	one-to-one	442_167_11037
At2g31260	AT3G15580	APG8H	A. thaliana early-release	Phvul.007G210800	P. vulgaris	one-to-one	442_447_11046
	AT2G31260	APG9	A. thaliana	Phvul.001G159900	P. vulgaris	one-to-one	442_167_1012
	AT2G31260	APG9	A. thaliana early-release	Phvul.001G159900	P. vulgaris	one-to-one	442_447_1023
At3g07525	AT3G07525	ATG10	A. thaliana	Phvul.010G036300	P. vulgaris	one-to-one	442_167_10197
	AT3G07525	ATG10	A. thaliana early-release	Phvul.010G036300	P. vulgaris	one-to-one	442_447_10203
At4G30790	AT4G30790		A. thaliana	Phvul.003G153800	P. vulgaris	one-to-one	442_167_523
	AT4G30790		A. thaliana early-release	Phvul.003G153800	P. vulgaris	one-to-one	442_447_528
At1g54210	AT1G54210	ATG12A	A. thaliana	Phvul.010G130300	P. vulgaris	many-to-one	442_167_11107
	AT1G54210	ATG12A	A. thaliana early-release	Phvul.010G130300	P. vulgaris	many-to-one	442_447_11118
At3g13970	AT3G13970	APG12B	A. thaliana	Phvul.010G130300	P. vulgaris	many-to-one	442_167_11107
	AT3G13970	APG12B	A. thaliana early-release	Phvul.010G130300	P. vulgaris	many-to-one	442_447_11118
At3g49590	AT3G49590	ATG13	A. thaliana early-release	Phvul.008G187800	P. vulgaris	one-to-one	442_447_5435
	AT3G49590		A. thaliana	Phvul.008G187800	P. vulgaris	one-to-one	442_167_5430
At3g18770	AT3G18770		A. thaliana	Phvul.002G269600	P. vulgaris	one-to-one	442_167_4855
	AT3G18770		A. thaliana early-release	Phvul.002G269600	P. vulgaris	one-to-one	442_447_4855
At4g08540	AT4G08540		A. thaliana	Phvul.008G169200	P. vulgaris	one-to-one	442_167_3451
At5g50230	AT5G50230		A. thaliana	Phvul.003G207100	P. vulgaris	one-to-one	442_167_2508
	AT5G50230		A. thaliana early-release	Phvul.003G207100	P. vulgaris	one-to-one	442_447_2513
At3g62770	Species without orthologues						
At4g30510	AT4G30510	ATG18B	A. thaliana	Phvul.003G152800	P. vulgaris	one-to-one	442_167_7006
	AT4G30510	ATG18B	A. thaliana early-release	Phvul.003G152800	P. vulgaris	one-to-one	442_447_6033
At2g40810	AT2G40810	ATG18C	A. thaliana	Phvul.009G041700	P. vulgaris	many-to-one	442_167_4857
	AT2G40810	ATG18C	A. thaliana early-release	Phvul.009G041700	P. vulgaris	many-to-one	442_447_4857
At3g56440	AT3G56440	ATG18D	A. thaliana	Phvul.009G041700	P. vulgaris	many-to-one	442_167_4857
	AT3G56440	ATG18D	A. thaliana early-release	Phvul.009G041700	P. vulgaris	many-to-one	442_447_4857
At5g05150	Species without orthologues						
At5g54730	AT5G54730	G18F	A. thaliana	Phvul.005G091300	P. vulgaris	one-to-many	442_167_5446
	AT5G54730	G18F	A. thaliana	Phvul.011G140900	P. vulgaris	one-to-many	442_167_5446
	AT5G54730	G18F	A. thaliana early-release	Phvul.005G091300	P. vulgaris	one-to-many	442_447_5452
	AT5G54730	G18F	A. thaliana early-release	Phvul.011G140900	P. vulgaris	one-to-many	442_447_5452
At1g03380	AT1G03380	ATG18G	A. thaliana	Phvul.001G146700	P. vulgaris	one-to-one	442_167_1655
	AT1G03380	ATG18G	A. thaliana early-release	Phvul.001G146700	P. vulgaris	one-to-one	442_447_1658
At1g54710	AT1G54710	ATG18H	A. thaliana	Phvul.007G183100	P. vulgaris	one-to-one	442_167_1517
	AT1G54710	ATG18H	A. thaliana early-release	Phvul.007G183100	P. vulgaris	one-to-one	442_447_1524
At5G66930	AT5G66930		A. thaliana	Phvul.003G248000	P. vulgaris	one-to-one	442_167_8650
	AT5G66930		A. thaliana early-release	Phvul.003G248000	P. vulgaris	one-to-one	442_447_8655

<i>ID Arabidopsis</i>	<i>Homolog Gene . Primary Identifier</i>	<i>Gene Symbol</i>	<i>Gene Organism Name</i>	<i>Homolog Ortholog _ Gene . Primary Identifier</i>	<i>Ortholog _ Gene Organism Name</i>	<i>Homolog Relationship</i>	<i>Homolog Group Name</i>
<i>At1g49180</i>	AT1G49180		A. thaliana	Medtr3g095620	M. truncatula	one-to-one	167_285_8624
<i>At2g37840</i>	AT2G37840		A. thaliana	Medtr4g019410	M. truncatula	many-to-one	167_285_1975
	AT2G37840		A. thaliana early- release	Medtr4g019410	M. truncatula	many-to-one	285_447_1979
<i>At3g53930</i>	AT3G53930		A. thaliana	Medtr4g019410	M. truncatula	many-to-one	167_285_1975
	AT3G53930		A. thaliana early- release	Medtr4g019410	M. truncatula	many-to-one	285_447_1979
<i>At3g61960</i>	AT3G61960		A. thaliana	Medtr8g024100	M. truncatula	one-to-one	167_285_4535
	AT3G61960		A. thaliana early- release	Medtr8g024100	M. truncatula	one-to-one	285_447_4536
<i>At3g19190</i>	AT3G19190	ATG2	A. thaliana	Medtr4g086370	M. truncatula	one-to-one	167_285_411
	AT3G19190	ATG2	A. thaliana early- release	Medtr4g086370	M. truncatula	one-to-one	285_447_309
<i>At5g61500</i>	AT5G61500	ATG3	A. thaliana	Medtr4g036265	M. truncatula	one-to-one	167_285_4887
	AT5G61500	ATG3	A. thaliana early- release	Medtr4g036265	M. truncatula	one-to-one	285_447_4890
<i>At2g44140</i>	AT2G44140		A. thaliana	Medtr7g081230	M. truncatula	many-to-one	167_285_4639
	AT2G44140		A. thaliana early- release	Medtr7g081230	M. truncatula	many-to-one	285_447_4647
<i>At3g59950</i>	AT3G59950		A. thaliana	Medtr7g081230	M. truncatula	many-to-one	167_285_4639
	AT3G59950		A. thaliana early- release	Medtr7g081230	M. truncatula	many-to-one	285_447_4647
<i>At5g17290</i>	AT5G17290	APG5	A. thaliana	Medtr5g076920	M. truncatula	one-to-one	167_285_6531
	AT5G17290	APG5	A. thaliana early- release	Medtr5g076920	M. truncatula	one-to-one	285_447_6546
<i>At3g61710</i>	AT3G61710	ATG6	A. thaliana	Medtr3g018770	M. truncatula	one-to-one	167_285_2512
	AT3G61710	ATG6	A. thaliana early- release	Medtr3g018770	M. truncatula	one-to-one	285_447_2523
<i>At5g45900</i>	AT5G45900	APG7	A. thaliana	Medtr0003s0540	M. truncatula	one-to-one	167_285_1357
	AT5G45900	APG7	A. thaliana early- release	Medtr0003s0540	M. truncatula	one-to-one	285_447_1362
<i>At4g21980</i>	AT4G21980	APG8A	A. thaliana	Medtr2g023430	M. truncatula	many-to-one	167_285_10350
	AT4G21980	APG8A	A. thaliana early- release	Medtr2g023430	M. truncatula	many-to-one	285_447_10362
<i>At4g04620</i>	AT4G04620	ATG8B	A. thaliana	Medtr2g023430	M. truncatula	many-to-one	167_285_10350
	AT4G04620	ATG8B	A. thaliana early- release	Medtr2g023430	M. truncatula	many-to-one	285_447_10362
<i>At1g62040</i>	AT1G62040	ATG8C	A. thaliana	Medtr4g048510	M. truncatula	one-to-one	167_285_10219
	AT1G62040	ATG8C	A. thaliana early- release	Medtr4g048510	M. truncatula	one-to-one	285_447_10225
<i>At2g05630</i>	Species without orthologues						
<i>At2g45170</i>	Species without orthologues						
<i>At4g16520</i>	AT4G16520	ATG8F	A. thaliana	Medtr4g101090	M. truncatula	one-to-one	167_285_10131
<i>At3g60640</i>	AT3G60640	ATG8G	A. thaliana early- release	Medtr4g101090	M. truncatula	one-to-one	285_447_10455
<i>At3g06420</i>	AT3G06420	ATG8H	A. thaliana	Medtr4g123760	M. truncatula	one-to-one	167_285_10842
	AT3G06420	ATG8H	A. thaliana early- release	Medtr4g123760	M. truncatula	one-to-one	285_447_10851
<i>At3g15580</i>	Species without orthologues						
<i>At2g31260</i>	AT2G31260	APG9	A. thaliana	Medtr1g070160	M. truncatula	one-to-many	167_285_963
	AT2G31260	APG9	A. thaliana	Medtr7g096680	M. truncatula	one-to-many	167_285_963
	AT2G31260	APG9	A. thaliana early- release	Medtr1g070160	M. truncatula	one-to-many	285_447_971
	AT2G31260	APG9	A. thaliana early- release	Medtr7g096680	M. truncatula	one-to-many	285_447_971

	AT2G31260	APG9	A. thaliana	Medtr1g070160	M. truncatula	one-to-many	167_285_963
	AT2G31260	APG9	A. thaliana	Medtr7g096680	M. truncatula	one-to-many	167_285_963
	AT2G31260	APG9	A. thaliana early-release	Medtr1g070160	M. truncatula	one-to-many	285_447_971
	AT2G31260	APG9	A. thaliana early-release	Medtr7g096680	M. truncatula	one-to-many	285_447_971
At3g07525	AT3G07525	ATG10	A. thaliana	Medtr8g010140	M. truncatula	one-to-one	167_285_9971
	AT3G07525	ATG10	A. thaliana early-release	Medtr8g010140	M. truncatula	one-to-one	285_447_9982
AT4G30790	AT4G30790		A. thaliana	Medtr4g130370	M. truncatula	one-to-one	167_285_526
	AT4G30790		A. thaliana early-release	Medtr4g130370	M. truncatula	one-to-one	285_447_528
At1g54210	AT1G54210	ATG12A	A. thaliana	Medtr8g020500	M. truncatula	many-to-one	167_285_11190
	AT1G54210	ATG12A	A. thaliana early-release	Medtr8g020500			
At3g13970	AT3G13970	APG12B	A. thaliana	Medtr8g020500	M. truncatula	many-to-one	167_285_11190
	AT3G13970	APG12B	A. thaliana early-release	Medtr8g020500	M. truncatula	many-to-one	285_447_11201
At3g49590	AT3G49590	ATG13	A. thaliana early-release	Medtr5g068710	M. truncatula	one-to-one	285_447_5668
	AT3G49590		A. thaliana	Medtr5g068710	M. truncatula	one-to-one	167_285_5658
At3g18770	AT3G18770		A. thaliana	Medtr3g095570	M. truncatula	one-to-one	167_285_5417
	AT3G18770		A. thaliana early-release	Medtr3g095570	M. truncatula	one-to-one	285_447_5424
AT4g08540	AT4G08540		A. thaliana	Medtr5g061040	M. truncatula	one-to-many	167_275_3592
At5g50230	AT5G50230		A. thaliana	Medtr3g075400	M. truncatula	one-to-many	167_285_2690
	AT5G50230		A. thaliana	Medtr4g104380	M. truncatula	one-to-many	167_285_2690
	AT5G50230		A. thaliana early-release	Medtr3g075400	M. truncatula	one-to-many	285_447_2698
	AT5G50230		A. thaliana early-release	Medtr4g104380	M. truncatula	one-to-many	285_447_2698
At3g62770	AT3G62770	AtATG18a	A. thaliana	Medtr1g083230	M. truncatula	one-to-one	167_285_4678
	AT3G62770	AtATG18a	A. thaliana early-release	Medtr1g083230	M. truncatula	one-to-one	285_447_4685
At4g30510	AT4G30510	ATG18B	A. thaliana	Medtr4g130190	M. truncatula	one-to-one	167_285_6727
	AT4G30510	ATG18B	A. thaliana early-release	Medtr4g130190	M. truncatula	one-to-one	285_447_5760
At2g40810	AT2G40810	ATG18C	A. thaliana	Medtr3g093590	M. truncatula	many-to-one	167_285_4491
	AT2G40810	ATG18C	A. thaliana early-release	Medtr3g093590	M. truncatula	many-to-one	285_447_4493
At3g56440	AT3G56440	ATG18D	A. thaliana	Medtr3g093590	M. truncatula	many-to-one	167_285_4491
	AT3G56440	ATG18D	A. thaliana early-release	Medtr3g093590	M. truncatula	many-to-one	285_447_4493
At5g05150	Species without orthologues						
At5g54730	AT5G54730	G18F	A. thaliana	Medtr2g082770	M. truncatula	one-to-one	167_285_4885
	AT5G54730	G18F	A. thaliana early-release	Medtr2g082770	M. truncatula	one-to-one	285_447_4888
At1g03380	AT1G03380	ATG18G	A. thaliana	Medtr1g089110	M. truncatula	one-to-one	167_285_1615
	AT1G03380	ATG18G	A. thaliana early-release	Medtr1g089110	M. truncatula	one-to-one	285_447_1623
At1g54710	AT1G54710	ATG18H	A. thaliana	Medtr1g082300	M. truncatula	one-to-one	167_285_1581
	AT1G54710	ATG18H	A. thaliana early-release	Medtr1g082300	M. truncatula	one-to-one	285_447_1588
At5G66930	AT5G66930		A. thaliana	Medtr8g079240	M. truncatula	one-to-one	167_285_8486
	AT5G66930		A. thaliana early-release	Medtr8g079240	M. truncatula	one-to-one	285_447_8493

<i>ID Arabidopsis</i>	<i>Homolog Gene . Primary Identifier</i>	<i>Gene Symbol</i>	<i>Gene Organism Name</i>	<i>Homolog Ortholog _ Gene . Primary Identifier</i>	<i>Ortholog _ Gene Organism Name</i>	<i>Homolog Relationship</i>	<i>Homolog Group Name</i>
AT1G49180	AT1G49180		A. thaliana	Glyma.04G215500	G. max	one-to-many	167_275_8523
	AT1G49180		A. thaliana	Glyma.06G150700	G. max	one-to-many	167_275_8523
At2g37840	AT2G37840		A. thaliana	Glyma.01G099600	G. max	many-to-many	167_275_2008
	AT2G37840		A. thaliana	Glyma.03G069800	G. max	many-to-many	167_275_2008
	AT2G37840		A. thaliana early-release	Glyma.01G099600	G. max	many-to-many	275_447_2016
	AT2G37840		A. thaliana early-release	Glyma.03G069800	G. max	many-to-many	275_447_2016
At3g53930	AT3G53930		A. thaliana	Glyma.01G099600	G. max	many-to-many	167_275_2008
	AT3G53930		A. thaliana	Glyma.03G069800	G. max	many-to-many	167_275_2008
	AT3G53930		A. thaliana early-release	Glyma.01G099600	G. max	many-to-many	275_447_2016
	AT3G53930		A. thaliana early-release	Glyma.03G069800	G. max	many-to-many	275_447_2016
At3g61960	AT3G61960		A. thaliana	Glyma.07G048400	G. max	one-to-many	167_275_4368
	AT3G61960		A. thaliana	Glyma.16G017300	G. max	one-to-many	167_275_4368
	AT3G61960		A. thaliana early-release	Glyma.07G048400	G. max	one-to-many	275_447_4383
	AT3G61960		A. thaliana early-release	Glyma.16G017300	G. max	one-to-many	275_447_4383
At3g19190	AT3G19190	ATG2	A. thaliana	Glyma.02G133400	G. max	one-to-many	167_275_380
	AT3G19190	ATG2	A. thaliana	Glyma.07G211600	G. max	one-to-many	167_275_380
	AT3G19190	ATG2	A. thaliana early-release	Glyma.02G133400	G. max	one-to-many	275_447_300
	AT3G19190	ATG2	A. thaliana early-release	Glyma.07G211600	G. max	one-to-many	275_447_300
At5g61500	AT5G61500	ATG3	A. thaliana	Glyma.12G005700	G. max	one-to-one	167_275_4956
	AT5G61500	ATG3	A. thaliana early-release	Glyma.12G005700	G. max	one-to-one	275_447_4964
At2g44140	AT2G44140		A. thaliana	Glyma.09G244800	G. max	many-to-many	167_275_4802
	AT2G44140		A. thaliana	Glyma.18G248400	G. max	many-to-many	167_275_4802
	AT2G44140		A. thaliana early-release	Glyma.09G244800	G. max	many-to-many	275_447_4808
	AT2G44140		A. thaliana early-release	Glyma.18G248400	G. max	many-to-many	275_447_4808
	AT3G59950		A. thaliana	Glyma.09G244800	G. max	many-to-many	167_275_4802
	AT3G59950		A. thaliana	Glyma.18G248400	G. max	many-to-many	167_275_4802
	AT3G59950		A. thaliana early-release	Glyma.09G244800	G. max	many-to-many	275_447_4808
	AT3G59950		A. thaliana early-release	Glyma.18G248400	G. max	many-to-many	275_447_4808
At3g59950	AT3G59950		A. thaliana	Glyma.09G244800	G. max	many-to-many	167_275_4802
	AT3G59950		A. thaliana	Glyma.18G248400	G. max	many-to-many	167_275_4802
	AT3G59950		A. thaliana early-release	Glyma.09G244800	G. max	many-to-many	275_447_4808
	AT3G59950		A. thaliana early-release	Glyma.18G248400	G. max	many-to-many	275_447_4808
At5g17290	AT5G17290	APG5	A. thaliana	Glyma.02G240700	G. max	one-to-many	167_275_6533
	AT5G17290	APG5	A. thaliana	Glyma.14G210200	G. max	one-to-many	167_275_6533
	AT5G17290	APG5	A. thaliana early-release	Glyma.02G240700	G. max	one-to-many	275_447_6550
	AT5G17290	APG5	A. thaliana early-release	Glyma.14G210200	G. max	one-to-many	275_447_6550
At3g61710	AT3G61710	ATG6	A. thaliana	Glyma.04G141000	G. max	one-to-many	167_275_2659
	AT3G61710	ATG6	A. thaliana	Glyma.11G153900	G. max	one-to-many	167_275_2659
	AT3G61710	ATG6	A. thaliana early-release	Glyma.04G141000	G. max	one-to-many	275_447_2674

<i>At5g45900</i>	AT3G61710	ATG6	A. thaliana early-release	Glyma.11G153900	G. max	one-to-many	275_447_2674
	AT5G45900	APG7	A. thaliana	Glyma.12G010000	G. max	one-to-one	167_275_1374
<i>At4g21980</i>	AT5G45900	APG7	A. thaliana early-release	Glyma.12G010000	G. max	one-to-one	275_447_1383
	AT4G21980	APG8A	A. thaliana	Glyma.07G261000	G. max	many-to-many	167_275_10571
	AT4G21980	APG8A	A. thaliana	Glyma.09G003900	G. max	many-to-many	167_275_10571
	AT4G21980	APG8A	A. thaliana	Glyma.15G108200	G. max	many-to-many	167_275_10571
	AT4G21980	APG8A	A. thaliana	Glyma.17G013000	G. max	many-to-many	167_275_10571
	AT4G21980	APG8A	A. thaliana early-release	Glyma.07G261000	G. max	many-to-many	275_447_10593
	AT4G21980	APG8A	A. thaliana early-release	Glyma.09G003900	G. max	many-to-many	275_447_10593
	AT4G21980	APG8A	A. thaliana early-release	Glyma.15G108200	G. max	many-to-many	275_447_10593
	AT4G21980	APG8A	A. thaliana early-release	Glyma.17G013000	G. max	many-to-many	275_447_10593
	AT4G04620	ATG8B	A. thaliana	Glyma.09G003900	G. max	many-to-many	167_275_10571
<i>At4g04620</i>	AT4G04620	ATG8B	A. thaliana	Glyma.15G108200	G. max	many-to-many	167_275_10571
	AT4G04620	ATG8B	A. thaliana	Glyma.17G013000	G. max	many-to-many	167_275_10571
	AT4G04620	ATG8B	A. thaliana early-release	Glyma.07G261000	G. max	many-to-many	275_447_10593
	AT4G04620	ATG8B	A. thaliana early-release	Glyma.09G003900	G. max	many-to-many	275_447_10593
	AT4G04620	ATG8B	A. thaliana early-release	Glyma.15G108200	G. max	many-to-many	275_447_10593
	AT1G62040	ATG8C	A. thaliana	Glyma.06G306300	G. max	one-to-many	167_275_10499
<i>At1g62040</i>	AT1G62040	ATG8C	A. thaliana	Glyma.12G098400	G. max	one-to-many	167_275_10499
	AT1G62040	ATG8C	A. thaliana early-release	Glyma.06G306300	G. max	one-to-many	275_447_10515
	AT1G62040	ATG8C	A. thaliana early-release	Glyma.12G098400	G. max	one-to-many	275_447_10515
<i>At2g05630</i>	Species without orthologues						
<i>At2g45170</i>	AT2G45170	ATG8E	A. thaliana early-release	Glyma.01G210200	G. max	many-to-many	275_447_10793
	AT2G45170	ATG8E	A. thaliana early-release	Glyma.05G058300	G. max	many-to-many	275_447_10793
	AT2G45170	ATG8E	A. thaliana early-release	Glyma.11G031800	G. max	many-to-many	275_447_10793
	AT2G45170	ATG8E	A. thaliana early-release	Glyma.17G140700	G. max	many-to-many	275_447_10793
<i>At4g16520</i>	AT4G16520	ATG8F	A. thaliana	Glyma.01G210200	G. max	one-to-many	167_275_10466
	AT4G16520	ATG8F	A. thaliana	Glyma.05G058300	G. max	one-to-many	167_275_10466
	AT4G16520	ATG8F	A. thaliana	Glyma.17G140700	G. max	one-to-many	167_275_10466
<i>At3g60640</i>	AT3G60640	ATG8G	A. thaliana early-release	Glyma.01G210200	G. max	many-to-many	275_447_10793
	AT3G60640	ATG8G	A. thaliana early-release	Glyma.05G058300	G. max	many-to-many	275_447_10793
	AT3G60640	ATG8G	A. thaliana early-release	Glyma.11G031800	G. max	many-to-many	275_447_10793
	AT3G60640	ATG8G	A. thaliana early-release	Glyma.17G140700	G. max	many-to-many	275_447_10793
<i>At3g06420</i>	Species without orthologues						
<i>At3g15580</i>	AT3G15580	APG8H	A. thaliana	Glyma.02G008800	G. max	one-to-many	167_275_11253
	AT3G15580	APG8H	A. thaliana	Glyma.10G009300	G. max	one-to-many	167_275_11253
	AT3G15580	APG8H	A. thaliana early-release	Glyma.02G008800	G. max	one-to-many	275_447_11278
	AT3G15580	APG8H	A. thaliana early-release	Glyma.10G009300	G. max	one-to-many	275_447_11278
<i>At2g31260</i>	AT2G31260	APG9	A. thaliana	Glyma.03G162100	G. max	one-to-many	167_275_968
	AT2G31260	APG9	A. thaliana	Glyma.10G035800	G. max	one-to-many	167_275_968
	AT2G31260	APG9	A. thaliana	Glyma.13G122200	G. max	one-to-many	167_275_968

<i>At3g07525</i>	AT2G31260	APG9	A. thaliana	Glyma.19G163500	G. max	one-to-many	167_275_968
	AT2G31260	APG9	A. thaliana early-release	Glyma.03G162100	G. max	one-to-many	275_447_977
	AT2G31260	APG9	A. thaliana early-release	Glyma.10G035800	G. max	one-to-many	275_447_977
	AT2G31260	APG9	A. thaliana early-release	Glyma.13G122200	G. max	one-to-many	275_447_977
	AT2G31260	APG9	A. thaliana early-release	Glyma.19G163500	G. max	one-to-many	275_447_977
<i>At4G30790</i>	AT3G07525	ATG10	A. thaliana	Glyma.03G097000	G. max	one-to-many	167_275_10381
	AT3G07525	ATG10	A. thaliana	Glyma.07G124300	G. max	one-to-many	167_275_10381
	AT3G07525	ATG10	A. thaliana early-release	Glyma.03G097000	G. max	one-to-many	275_447_10402
	AT3G07525	ATG10	A. thaliana early-release	Glyma.07G124300	G. max	one-to-many	275_447_10402
	AT4G30790		A. thaliana	Glyma.02G206500	G. max	one-to-many	167_275_515
<i>At1g54210</i>	AT4G30790		A. thaliana	Glyma.17G071400	G. max	one-to-many	167_275_515
	AT4G30790		A. thaliana early-release	Glyma.02G206500	G. max	one-to-many	275_447_519
	AT4G30790		A. thaliana early-release	Glyma.17G071400	G. max	one-to-many	275_447_519
	AT1G54210	ATG12A	A. thaliana	Glyma.07G038100	G. max	many-to-one	167_275_11360
	AT1G54210	ATG12A	A. thaliana early-release	Glyma.07G038100	G. max	many-to-one	275_447_11387
<i>At3g13970</i>	AT3G13970	APG12B	A. thaliana	Glyma.07G038100	G. max	many-to-one	167_275_11360
	AT3G13970	APG12B	A. thaliana early-release	Glyma.07G038100	G. max	many-to-one	275_447_11387
<i>At3g49590</i>	AT3G49590	ATG13	A. thaliana early-release	Glyma.02G220700	G. max	one-to-many	275_447_5383
	AT3G49590	ATG13	A. thaliana early-release	Glyma.14G187000	G. max	one-to-many	275_447_5383
	AT3G49590		A. thaliana	Glyma.02G220700	G. max	one-to-many	167_275_5368
	AT3G49590		A. thaliana	Glyma.14G187000	G. max	one-to-many	167_275_5368
<i>At3g18770</i>	AT3G18770		A. thaliana	Glyma.05G189000	G. max	one-to-many	167_275_4665
	AT3G18770		A. thaliana	Glyma.08G146700	G. max	one-to-many	167_275_4665
	AT3G18770		A. thaliana early-release	Glyma.05G189000	G. max	one-to-many	275_447_4677
	AT3G18770		A. thaliana early-release	Glyma.08G146700	G. max	one-to-many	275_447_4677
	AT4G08540		A. thaliana	Glyma.13G085400	G. max	one-to-many	167_275_3592
<i>At4g08540</i>	AT4G08540		A. thaliana	Glyma.14G167200	G. max	one-to-many	167_275_3592
	AT5G50230		A. thaliana	Glyma.05G043700	G. max	one-to-many	167_275_2616
	AT5G50230		A. thaliana	Glyma.17G126200	G. max	one-to-many	167_275_2616
<i>At3g62770</i>	AT5G50230		A. thaliana early-release	Glyma.05G043700	G. max	one-to-many	275_447_2629
	AT5G50230		A. thaliana early-release	Glyma.17G126200	G. max	one-to-many	275_447_2629
	AT3G62770	AtATG18a	A. thaliana	Glyma.03G212100	G. max	one-to-many	167_275_4880
	AT3G62770	AtATG18a	A. thaliana	Glyma.19G209200	G. max	one-to-many	167_275_4880
	AT3G62770	AtATG18a	A. thaliana early-release	Glyma.03G212100	G. max	one-to-many	275_447_4884
<i>At4g30510</i>	AT3G62770	AtATG18a	A. thaliana early-release	Glyma.19G209200	G. max	one-to-many	275_447_4884
	AT4G30510	ATG18B	A. thaliana	Glyma.02G207500	G. max	one-to-many	167_275_6877
	AT4G30510	ATG18B	A. thaliana	Glyma.17G070200	G. max	one-to-many	167_275_6877
	AT4G30510	ATG18B	A. thaliana early-release	Glyma.02G207500	G. max	one-to-many	275_447_5899
	AT4G30510	ATG18B	A. thaliana early-release	Glyma.17G070200	G. max	one-to-many	275_447_5899
<i>At2g40810</i>	AT2G40810	ATG18C	A. thaliana	Glyma.04G224300	G. max	many-to-many	167_275_4638
	AT2G40810	ATG18C	A. thaliana	Glyma.06G140400	G. max	many-to-many	167_275_4638

<i>At3g56440</i>	AT2G40810	ATG18C	A. thaliana early-release	Glyma.04G224300	G. max	many-to-many	275_447_4651
	AT3G56440	ATG18D	A. thaliana	Glyma.04G224300	G. max	many-to-many	167_275_4638
	AT3G56440	ATG18D	A. thaliana	Glyma.06G140400	G. max	many-to-many	167_275_4638
	AT3G56440	ATG18D	A. thaliana early-release	Glyma.04G224300	G. max	many-to-many	275_447_4651
	AT3G56440	ATG18D	A. thaliana early-release	Glyma.06G140400	G. max	many-to-many	275_447_4651
<i>At5g05150</i>	Species without orthologues						
<i>At5g54730</i>	AT5G54730	G18F	A. thaliana	Glyma.06G267000	G. max	one-to-many	167_275_5202
	AT5G54730	G18F	A. thaliana	Glyma.12G136000	G. max	one-to-many	167_275_5202
	AT5G54730	G18F	A. thaliana	Glyma.12G214600	G. max	one-to-many	167_275_5202
	AT5G54730	G18F	A. thaliana	Glyma.13G287000	G. max	one-to-many	167_275_5202
	AT5G54730	G18F	A. thaliana early-release	Glyma.06G267000	G. max	one-to-many	275_447_5215
<i>At1g03380</i>	AT5G54730	G18F	A. thaliana early-release	Glyma.12G136000	G. max	one-to-many	275_447_5215
	AT5G54730	G18F	A. thaliana early-release	Glyma.12G214600	G. max	one-to-many	275_447_5215
	AT5G54730	G18F	A. thaliana early-release	Glyma.13G287000	G. max	one-to-many	275_447_5215
	AT1G03380	ATG18G	A. thaliana	Glyma.03G148700	G. max	one-to-many	167_275_1595
	AT1G03380	ATG18G	A. thaliana	Glyma.19G152000	G. max	one-to-many	167_275_1595
<i>At1g54710</i>	AT1G03380	ATG18G	A. thaliana early-release	Glyma.03G148700	G. max	one-to-many	275_447_1602
	AT1G03380	ATG18G	A. thaliana early-release	Glyma.19G152000	G. max	one-to-many	275_447_1602
	AT1G54710	ATG18H	A. thaliana	Glyma.10G157700	G. max	one-to-many	167_275_1666
	AT1G54710	ATG18H	A. thaliana	Glyma.20G230900	G. max	one-to-many	167_275_1666
	AT1G54710	ATG18H	A. thaliana early-release	Glyma.10G157700	G. max	one-to-many	275_447_1676
<i>AT5G66930</i>	AT1G54710	ATG18H	A. thaliana early-release	Glyma.20G230900	G. max	one-to-many	275_447_1676
	AT5G66930		A. thaliana	Glyma.17G180900	G. max	one-to-one	167_275_8781
	AT5G66930		A. thaliana early-release	Glyma.17G180900	G. max	one-to-one	275_447_8795

## F. EGGNOG analysis of *A. thaliana*, *P. vulgaris*, *M. truncatula*, and *G. max*.

Gene accession numbers	KOG	Organism	#Seq	Members	Close homologs in this group (preferred gene names)
<i>At2g37840</i>	<b>KOG0595</b>	<i>Phaseolus vulgaris</i>	3 seqs	3885.XP_007134050.1,	3885.XP_007134050.1,
<i>At3g53930</i>				3885.XP_007135333.1,	3885.XP_007135333.1,
<i>At3g61960</i>				3885.XP_007134049.1	3885.XP_007134049.1
<i>At3g19190</i>	<b>KOG2993</b>	<i>Phaseolus vulgaris</i>		3885.XP_007156552.1	3885.XP_007156552.1
<i>At5g61500</i>	<b>KOG2981</b>	<i>Phaseolus vulgaris</i>		3885.XP_007131351.1	3885.XP_007131351.1
<i>At2g44140</i>	<b>KOG2674</b>	<i>Phaseolus vulgaris</i>		3885.XP_007139667.1	3885.XP_007139667.1
<i>At3g59950</i>					
<i>At5g17290</i>	<b>KOG2976</b>	<i>Phaseolus vulgaris</i>		3885.XP_007141966.1	3885.XP_007141966.1
<i>At3g61710</i>	<b>KOG2751</b>	<i>Phaseolus vulgaris</i>		3885.XP_007148972.1	3885.XP_007148972.1
<i>At5g45900</i>	<b>COG0476</b>	<i>Phaseolus vulgaris</i>	12 seqs	3885.XP_007141506.1, 3885.XP_007142173.1, 3885.XP_007133804.1, 3885.XP_007160018.1, 3885.XP_007146816.1,	3885.XP_007141506.1, 3885.XP_007142173.1, 3885.XP_007133804.1, 3885.XP_007160018.1, 3885.XP_007146816.1, CNX5,

				3885.XP_007142325.1, 3885.XP_007160019.1, 3885.XP_007131401.1, 3885.XP_007133324.1, 3885.XP_007154113.1, 3885.XP_007155550.1, 3885.XP_007132545.1	3885.XP_007160019.1, 3885.XP_007131401.1, 3885.XP_007133324.1, 3885.XP_007154113.1, 3885.XP_007155550.1, 3885.XP_007132545.1
At4g21980	<b>KOG1654</b>	<i>Phaseolus vulgaris</i>	6 seqs	3885.XP_007155648.1,	3885.XP_007155648.1,
At4g04620				3885.XP_007157342.1,	3885.XP_007157342.1,
At1g62040				3885.XP_007133099.1,	3885.XP_007133099.1,
At2g05630				3885.XP_007145111.1,	3885.XP_007145111.1,
At2g45170				3885.XP_007153954.1,	3885.XP_007153954.1,
At4g16520				3885.XP_007132541.1	3885.XP_007132541.1
At3g60640					
At3g06420					
At3g15580					
At2g31260	<b>KOG2173</b>	<i>Phaseolus vulgaris</i>	2 seqs	3885.XP_007162532.1, 3885.XP_007144916.1	3885.XP_007162532.1, 3885.XP_007144916.1
At3g07525	<b>KOG4741</b>	<i>Phaseolus vulgaris</i>		3885.XP_007134309.1	3885.XP_007134309.1
AT4G30790	<b>ENOG5028M XS</b>	<i>Phaseolus vulgaris</i>		3885.XP_007154860.1	3885.XP_007154860.1
At1g54210	<b>KOG3439</b>	<i>Phaseolus vulgaris</i>		3885.XP_007135446.1	3885.XP_007135446.1
At3g13970					
At3g49590	<b>KOG4573</b>	<i>Phaseolus vulgaris</i>	2 seqs	3885.XP_007159813.1, 3885.XP_007141345.1	3885.XP_007159813.1, 3885.XP_007141345.1
At3g18770					
AT1G77890	<b>KOG2351</b>	<i>Phaseolus vulgaris</i>	2 seqs	3885.XP_007147572.1, 3885.XP_007134240.1	3885.XP_007147572.1, 3885.XP_007134240.1
AT4G08540					
At5g50230	<b>KOG0288</b>	<i>Phaseolus vulgaris</i>		3885.XP_007155503.1	3885.XP_007155503.1
At4g30510	<b>KOG2110</b>	<i>Phaseolus vulgaris</i>		3885.XP_007154849.1	3885.XP_007154849.1
At3g62770	<b>KOG2111</b>	<i>Phaseolus vulgaris</i>	3 seqs	3885.XP_007144942.1, 3885.XP_007163087.1, 3885.XP_007136398.1	3885.XP_007144942.1, 3885.XP_007163087.1, 3885.XP_007136398.1
At2g40810	<b>KOG2111</b>				
At3g56440	<b>KOG2111</b>				
At5g05150	<b>KOG2111</b>				
At5g54730	<b>KOG2109</b>	<i>Phaseolus vulgaris</i>	4 seqs	3885.XP_007162375.1, 3885.XP_007149695.1, 3885.XP_007144768.1, 3885.XP_007132977.1	3885.XP_007162375.1, 3885.XP_007149695.1, 3885.XP_007144768.1, 3885.XP_007132977.1
At1g03380					
At1g54710					
AT5G66930	<b>KOG4493</b>	<i>Phaseolus vulgaris</i>		3885.XP_007155972.1	3885.XP_007155972.1



Gene accession numbers	KOG	Organism	#Seq	Members*	Close homologs in this group (preferred gene names)*
At2g37840 At3g53930 At3g61960 At3g19190	KOG0595	Medicago truncatula	2 seqs	3880.AES72802, 3880.AES72806	11420712, 11418929
At5g61500	KOG2993	Medicago truncatula	2 seqs	3880.AES90192, 3880.AES90193	3880.AES90192, 11441425
At2g44140	KOG2981			x	
At3g59950	KOG2674	Medicago truncatula		3880.AES80500	ATG4
At5g17290	KOG2674				
At3g61710	KOG2976	Medicago truncatula		3880.AES99130	11433638
At5g45900	KOG2751	Medicago truncatula		3880.AES68897	11414676
	COG0476	Medicago truncatula	9 seqs	3880.AES92586, 3880.AES98758, 3880.AES88130, 3880.AET00579, 3880.AES73061, 3880.AES65672, 3880.AES98760, 3880.AET02216, 3880.AET00193	11436326, 3880.AES98758, 11444042, CNX5, 11431238, 11418341, 11409554, 25501072, 11431855
At4g21980 At4g04620 At1g62040 At2g05630 At2g45170 At4g16520 At3g60640 At3g06420 At3g15580	KOG1654	Medicago truncatula	4 seqs	3880.AES61582, 3880.AES92053, 3880.AES67226, 3880.AES90925	11443804, 11424644, 11431581, 11410993
At2g31260	KOG2173			x	
At3g07525	KOG4741			x	
AT4G30790	ENOG5028MX S	Medicago truncatula		3880.AES92467	11428392
At1g54210 At3g13970	KOG3439	Medicago truncatula		3880.AET01741	ATG12
At3g49590 At3g18770	KOG4573	Medicago truncatula	4 seqs	3880.AES72801, 3880.AET04691, 3880.AES98447,	11424978, 3880.AET04691, 11426224, 11432206
AT1G77890 AT4G08540	KOG2351	Medicago truncatula	2 seqs	3880.AET01383, 3880.AES64594	11418894, 11416659
At5g50230	KOG0288			x	
At4g30510	KOG2110	Medicago truncatula		3880.AES92450	11446800
At3g62770 At2g40810 At3g56440	KOG2111	Medicago truncatula	2 seqs	3880.AES61388, 3880.AES82117	11416663, 11431898

At5g05150	<b>KOG2109</b>	<i>Medicago truncatula</i>	4 seqs	3880.AES61860,	3880.AES61860, 11407930, 11413910, 11426407
At5g54730				3880.AES66872,	
At1g03380				3880.AES61823,	
At1g54710				3880.AES61302	
AT5G66930	<b>KOG4493</b>	<i>Medicago truncatula</i>		3880.AET04015	11406119

NCBI ID	ID
3880.AES61302	Medtr1g082300.1
3880.AES61388,	Medtr1g083230.1
3880.AES61582,	Medtr1g086310.1
3880.AES61823,	Medtr1g089110.1
3880.AES62926,	Medtr1g113830.1
3880.AES65672,	Medtr2g045230.1
3880.AES66872,	Medtr2g082770.1
3880.AES67226,	Medtr2g088230.1
3880.AES68897	Medtr3g018770.1
3880.AES72801,	Medtr3g095570.1
3880.AES72806	Medtr3g095620.1
3880.AES72850,	Medtr3g096100.1
3880.AES72851,	Medtr3g096110.1
3880.AES73061,	Medtr3g099240.1
3880.AES74138,	Medtr3g116250.1
3880.AES88130,	Medtr4g048220.1
3880.AES89060,	Medtr4g068580.1
3880.AES90192,	Medtr4g086350
3880.AES90193	Medtr4g086370.1
3880.AES90925	Medtr4g101090.1
3880.AES92053,	Medtr4g123760.1
3880.AES92450	Medtr4g130190.1
3880.AES92467	Medtr4g130370.1
3880.AES92586,	Medtr4g131690.1
3880.AES93602,	Medtr5g005380.1
3880.AES95122,	Medtr5g022000.1
3880.AES96176,	Medtr5g034120.1
3880.AES96520,	Medtr5g038110.1
3880.AES98447,	Medtr5g068710.1
3880.AET04707	Medtr5g068710.1
3880.AES98760,	Medtr5g072480.1
3880.AES99130	Medtr5g076920.1
3880.AET00193	Medtr5g089330.1

3880.AET00579,	Medtr5g093580.1
3880.AES79768	Medtr7g072330.1
3880.AES80500	Medtr7g081230.1
3880.AES82117	Medtr7g108520.1
3880.AET01741	Medtr8g020500.1
3880.AET04015	Medtr8g079240.1
3880.AET04691,	Medtr8g093050.1
3880.AET04735	Medtr8g093570.1
3880.AES61860,	MTR_1g089540
3880.AES64594	MTR_2g027530
3880.AET01383	MTR_8g011890

<i>Gene accession numbers</i>	<i>KOG</i>	<i>Organism</i>	<i>#Seq</i>	<i>Members</i>	<i>Close homologs in this group (preferred gene names)</i>
<i>At2g37840</i> <i>At3g53930</i> <i>At3g61960</i>	<b>KOG0595</b>	<i>Glycine max</i>	6 seqs	3847.GLYMA01G24510.1, 3847.GLYMA16G01970.2, 3847.GLYMA07G05400.3, 3847.GLYMA03G11280.1, 3847.GLYMA04G39350.1, 3847.GLYMA06G15570.2	3847.GLYMA01G24510.1, 3847.GLYMA16G01970.2, 3847.GLYMA07G05400.3, 3847.GLYMA03G11280.1, 3847.GLYMA04G39350.1, 3847.GLYMA06G15570.2
<i>At3g19190</i>	<b>KOG2993</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA07G33400.4, 3847.GLYMA02G15050.3	3847.GLYMA07G33400.4, 3847.GLYMA02G15050.3
<i>At5g61500</i>	<b>KOG2981</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA09G36540.1, 3847.GLYMA12G00830.1	3847.GLYMA09G36540.1, GMATG3A
<i>At2g44140</i> <i>At3g59950</i>	<b>KOG2674</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA18G48380.1, 3847.GLYMA09G38000.1	3847.GLYMA18G48380.1, 3847.GLYMA09G38000.1
<i>At5g17290</i>	<b>KOG2976</b>	<i>Glycine max</i>	3 seqs	3847.GLYMA10G30170.1, 3847.GLYMA02G40770.1, 3847.GLYMA14G39095.1	3847.GLYMA10G30170.1, ATG5, 3847.GLYMA14G39095.1
<i>At3g61710</i>	<b>KOG2751</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA04G26840.1, 3847.GLYMA11G21490.1	3847.GLYMA04G26840.1, ATG6
<i>At5g45900</i>	<b>COG0476</b>	<i>Glycine max</i>	21 seqs	3847.GLYMA05G03350.1, 3847.GLYMA12G01250.1, 3847.GLYMA12G10540.1, 3847.GLYMA12G36450.1, 3847.GLYMA06G46210.1, 3847.GLYMA14G37610.1, 3847.GLYMA13G27140.1, 3847.GLYMA18G06620.1, 3847.GLYMA02G46300.1, 3847.GLYMA05G38190.1, 3847.GLYMA07G38770.1, 3847.GLYMA17G01940.4, 3847.GLYMA14G02410.1, 3847.GLYMA07G12250.1, 3847.GLYMA14G02260.1, 3847.GLYMA17G13940.1, 3847.GLYMA11G29302.1, 3847.GLYMA14G04000.1, 3847.GLYMA02G39495.2,	3847.GLYMA05G03350.1, GMATG7, 3847.GLYMA12G10540.1, 3847.GLYMA12G36450.1, 3847.GLYMA06G46210.1, 3847.GLYMA14G37610.1, 3847.GLYMA13G27140.1, 3847.GLYMA18G06620.1, 3847.GLYMA02G46300.1, 3847.GLYMA05G38190.1, 3847.GLYMA07G38770.1, 3847.GLYMA17G01940.4, 3847.GLYMA14G02410.1, 3847.GLYMA07G12250.1, 3847.GLYMA14G02260.1, 3847.GLYMA17G13940.1, 3847.GLYMA11G29302.1, 3847.GLYMA14G04000.1, 3847.GLYMA02G39495.2,

<i>At4g21980</i>	<b>KOG1654</b>	<i>Glycine max</i>	13 seqs	3847.GLYMA02G44730.1,	3847.GLYMA02G44730.1,
<i>At4g04620</i>				3847.GLYMA08G01440.1	3847.GLYMA08G01440.1
<i>At1g62040</i>				3847.GLYMA10G01220.1,	3847.GLYMA10G01220.1,
<i>At2g05630</i>				3847.GLYMA17G14970.1,	3847.GLYMA17G14970.1,
<i>At2g45170</i>				3847.GLYMA09G00630.3,	3847.GLYMA09G00630.3,
<i>At4g16520</i>				3847.GLYMA07G39090.1,	3847.GLYMA07G39090.1,
<i>At3g60640</i>				3847.GLYMA12G10510.1,	ATG8d, ATG8i,
<i>At3g06420</i>				3847.GLYMA02G01180.1,	3847.GLYMA05G04540.1,
<i>At3g15580</i>				3847.GLYMA05G04540.1,	3847.GLYMA11G03460.1,
<i>At2g31260</i>	<b>KOG2173</b>	<i>Glycine max</i>	4 seqs	3847.GLYMA11G03460.1,	3847.GLYMA15G11510.1,
				3847.GLYMA15G11510.1,	3847.GLYMA01G41910.2,
				3847.GLYMA01G41910.2,	3847.GLYMA17G01650.1,
<i>At3g07525</i>	<b>KOG4741</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA17G01650.1,	3847.GLYMA06G46270.3,
				3847.GLYMA06G46270.3,	3847.GLYMA15G21427.1
				3847.GLYMA15G21427.1	
<i>AT4G30790</i>	<b>KOG2173</b>	<i>Glycine max</i>	4 seqs	3847.GLYMA13G18300.2,	3847.GLYMA13G18300.2,
				3847.GLYMA19G34630.1,	ATG9,
				3847.GLYMA10G04120.1,	3847.GLYMA10G04120.1,
<i>At1g54210</i>	<b>KOG4741</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA03G31890.3	3847.GLYMA03G31890.3
<i>At3g13970</i>				3847.GLYMA07G12280.2,	3847.GLYMA07G12280.2,
<i>At3g49590</i>				3847.GLYMA03G23850.2	3847.GLYMA03G23850.2
<i>At3g18770</i>	<b>ENOG5028MXS</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA02G36800.2,	3847.GLYMA02G36800.2,
<i>AT1G77890</i>				3847.GLYMA17G07920.1	3847.GLYMA17G07920.1
<i>AT4G08540</i>	<b>KOG3439</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA16G00940.2,	3847.GLYMA16G00940.2,
<i>At5g50230</i>				3847.GLYMA07G04250.1	3847.GLYMA07G04250.1
<i>At4g30510</i>					
<i>At3g62770</i>	<b>KOG4573</b>	<i>Glycine max</i>	4 seqs	3847.GLYMA05G32250.1,	3847.GLYMA05G32250.1,
<i>At2g40810</i>				3847.GLYMA08G15500.2,	3847.GLYMA08G15500.2,
<i>At3g56440</i>				3847.GLYMA14G36553.2, 3847.	3847.GLYMA14G36553.2,
<i>At5g05150</i>	<b>KOG2351</b>	<i>Glycine max</i>	6 seqs	.1	3847.GLYMA02G38530.1
				3847.GLYMA08G15515.1,	3847.GLYMA08G15515.1,
				3847.GLYMA09G01880.2,	3847.GLYMA09G01880.2,
	<b>KOG0288</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA15G12830.1,	3847.GLYMA15G12830.1,
				3847.GLYMA16G09890.1,	3847.GLYMA16G09890.1,
				3847.GLYMA03G22220.1,	3847.GLYMA03G22220.1,
	<b>KOG2110</b>	<i>Glycine max</i>	4 seqs	3847.GLYMA05G32260.1	3847.GLYMA05G32260.1
<i>At3g62770</i>	<b>KOG0288</b>	<i>Glycine max</i>	2 seqs	3847.GLYMA17G13520.2,	3847.GLYMA17G13520.2,
<i>At2g40810</i>				3847.GLYMA05G02850.1	3847.GLYMA05G02850.1
<i>At3g56440</i>					
<i>At5g05150</i>	<b>KOG2110</b>	<i>Glycine max</i>	4 seqs	3847.GLYMA02G36960.4,	3847.GLYMA02G36960.4,
				3847.GLYMA10G25246.1,	3847.GLYMA10G25246.1,
				3847.GLYMA17G07800.2,	3847.GLYMA17G07800.2,
	<b>KOG2111</b>	<i>Glycine max</i>	6 seqs	3847.GLYMA16G20500.2	3847.GLYMA16G20500.2
				3847.GLYMA10G29320.1,	3847.GLYMA10G29320.1,
				3847.GLYMA19G39660.1,	3847.GLYMA19G39660.1,
	<b>KOG2111</b>	<i>Glycine max</i>	6 seqs	3847.GLYMA06G14550.2,	3847.GLYMA06G14550.2,
				3847.GLYMA03G37030.1,	3847.GLYMA03G37030.1,
				3847.GLYMA04G40230.2,	3847.GLYMA04G40230.2,
	<b>KOG2111</b>	<i>Glycine max</i>	6 seqs	3847.GLYMA20G37960.1	3847.GLYMA20G37960.1

G.PANTHER analysis of *A. thaliana*, *P. vulgaris*, *M. truncatula*, and *G.max*.

<b>Gene accession numbers</b>	<b>PANTHER</b>	<b>Description</b>
<i>At2g37840</i>	PTHR24348:SF26	PROTEIN KINASE FAMILY PROTEIN
<i>At3g53930</i>	PTHR24348:SF26	PROTEIN KINASE FAMILY PROTEIN
<i>At3g61960</i>	PTHR24348:SF26	PROTEIN KINASE FAMILY PROTEIN
<i>At3g19190</i>	PTHR13190	FAMILY NOT NAMED
<i>At5g61500</i>	PTHR12866:SF2	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG3
<i>At2g44140</i>	PTHR22624	APG4 AUTOPHAGY 4-RELATED
<i>At3g59950</i>	PTHR22624	APG4 AUTOPHAGY 4-RELATED
<i>At5g17290</i>	PTHR13040	AUTOPHAGY PROTEIN 5
<i>At3g61710</i>	PTHR12768	BECLIN 1
<i>At5g45900</i>	PTHR10953:SF3	UBIQUITIN-LIKE MODIFIER-ACTIVATING ENZYME ATG7
<i>At4g21980</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>At4g04620</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>At1g62040</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>At2g05630</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>At2g45170</i>	PTHR10969:SF39	AUTOPHAGY-RELATED PROTEIN 8F
<i>At4g16520</i>	PTHR10969:SF39	AUTOPHAGY-RELATED PROTEIN 8F
<i>At3g60640</i>	PTHR10969:SF31	AUTOPHAGY-RELATED PROTEIN 8G
<i>At3g06420</i>	PTHR10969:SF36	AUTOPHAGY-RELATED PROTEIN 8H
<i>At3g15580</i>	PTHR10969:SF25	AUTOPHAGY-RELATED PROTEIN 8I
<i>At2g31260</i>	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
<i>At3g07525</i>	PTHR12866:SF5	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG10
<i>At4G30790</i>	PTHR13222:SF1	RB1-INDUCIBLE COILED-COIL PROTEIN 1
<i>At1g54210</i>	PTHR13385	AUTOPHAGY PROTEIN 12
<i>At3g13970</i>	PTHR13385	AUTOPHAGY PROTEIN 12
<i>At3g49590</i>	PTHR13430:SF3	AUTOPHAGY-RELATED PROTEIN 13
<i>At3g18770</i>	PTHR13430	UNCHARACTERIZED
<i>At5g50230</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>At3g62770</i>	PTHR11227:SF18	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3
<i>At4g30510</i>	PTHR11227:SF17	AUTOPHAGY-SPECIFIC GENE 18, ISOFORM E
<i>At2g40810</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>At3g56440</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>At5g05150</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>At5g54730</i>	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F
<i>At1g03380</i>	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
<i>At1g54710</i>	PTHR13268:SF0	BREAST CARCINOMA-AMPLIFIED SEQUENCE 3

AT5G66930	PTHR13292:SF0	AUTOPHAGY-RELATED PROTEIN 101
AT1G50030	PTHR11139:SF9	SERINE/THREONINE-PROTEIN KINASE MTOR
AT3G08850	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
AT5G01770	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
AT2G22040	PTHR19842	G BETA-LIKE PROTEIN GBL
AT3G18140	PTHR19842	G BETA-LIKE PROTEIN GBL
<b>Gene accession numbers</b>	<b>PANTHER</b>	<b>Description</b>
Phvul.010G120500	PTHR24348:SF26	PROTEIN KINASE FAMILY PROTEIN
Phvul.010G015100	PTHR24348	PROTEIN KINASE FAMILY PROTEIN
Phvul.003G295800	PTHR13190	FAMILY NOT NAMED
Phvul.011G006500	PTHR12866:SF2	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG3
Phvul.008G048900	PTHR22624:SF34	AUTOPHAGY-SPECIFIC GENE 4, ISOFORM A
Phvul.008G241000	PTHR13040:SF2	AUTOPHAGY PROTEIN 5
Phvul.005G029900	PTHR12768:SF4	BECLIN 1
Phvul.011G010700	PTHR10953:SF3	UBIQUITIN-LIKE MODIFIER-ACTIVATING ENZYME ATG7
Phvul.003G079300	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
Phvul.011G103300	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
Phvul.006G149640	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
Phvul.011G151600	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
Phvul.003G219600	PTHR10969:SF39	AUTOPHAGY-RELATED PROTEIN 8F
Phvul.002G062200	PTHR10969:SF39	AUTOPHAGY-RELATED PROTEIN 8F
Phvul.007G210800	PTHR10969:SF25	AUTOPHAGY-RELATED PROTEIN 8I
Phvul.001G159900	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
Phvul.007G194300	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
Phvul.010G036300	PTHR12866:SF5	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG10
Phvul.003G153800	PTHR13222:SF1	RB1-INDUCIBLE COILED-COIL PROTEIN 1
Phvul.010G130300	PTHR13385	AUTOPHAGY PROTEIN 12
Phvul.008G187800	PTHR13430:SF3	AUTOPHAGY-RELATED PROTEIN 13
Phvul.002G269600	PTHR13430	UNCHARACTERIZED
Phvul.003G207100	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
Phvul.002G020500	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
Phvul.003G245800	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
Phvul.007G196400	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
Phvul.001G205000	PTHR11227:SF18	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3
Phvul.003G152800	PTHR11227:SF17	AUTOPHAGY-SPECIFIC GENE 18, ISOFORM E
Phvul.009G041700	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
Phvul.005G091300	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F
Phvul.001G146700	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
Phvul.011G140900	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F

<i>Phvul.007G183100</i>	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
<i>Phvul.003G24800</i>	PTHR13292:SF0	AUTOPHAGY-RELATED PROTEIN 101
<i>Phvul.002G04990</i>	PTHR11139:SF9	SERINE/THREONINE-PROTEIN KINASE MTOR
<i>Phvul.008G08780</i>	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
<i>Phvul.008G8810</i>	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
<i>Phvul.006G17370</i>	PTHR19842	G BETA-LIKE PROTEIN GBL
<b>Gene accession numbers</b>	<b>PANTHER</b>	<b>Description</b>
<i>Medtr3g095620</i>	PTHR24348:SF24	PROTEIN KINASE FAMILY PROTEIN
<i>Medtr4g019410</i>	PTHR24348	SERINE/THREONINE-PROTEIN KINASE UNC-51-RELATED
<i>Medtr8g024100</i>	PTHR24348	SERINE/THREONINE-PROTEIN KINASE UNC-51-RELATED
<i>Medtr4g086370</i>	PTHR13190	FAMILY NOT NAMED
<i>Medtr4g036265</i>	PTHR12866:SF2	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG3
<i>Medtr7g081230</i>	PTHR22624	APG4 AUTOPHAGY 4-RELATED
<i>Medtr5g076920</i>	PTHR13040	AUTOPHAGY PROTEIN 5
<i>Medtr3g018770</i>	PTHR12768	BECLIN 1
<i>Medtr0003s0540</i>	PTHR10953:SF3	UBIQUITIN-LIKE MODIFIER-ACTIVATING ENZYME ATG7
<i>Medtr2g023430</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>Medtr4g048510</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>Medtr4g037225</i>	PTHR10969:SF61	AUTOPHAGY-RELATED PROTEIN 8C
<i>Medtr2g88230</i>	PTHR10969:SF74	AUTOPHAGY-RELATED PROTEIN
<i>Medtr4g101090</i>	PTHR10969:SF39	AUTOPHAGY-RELATED PROTEIN 8F
<i>Medtr4g123760</i>	PTHR10969:SF36	AUTOPHAGY-RELATED PROTEIN 8H
<i>Medtr7g096540</i>	PTHR10969:SF36	AUTOPHAGY-RELATED PROTEIN 8H
<i>Medtr1g086310</i>	PTHR10969:SF25	AUTOPHAGY-RELATED PROTEIN 8I
<i>Medtr7g096680</i>	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
<i>Medtr1g070160</i>	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
<i>Medtr8g010140</i>	PTHR12866:SF5	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG10
<i>Medtr4g130370</i>	PTHR13222:SF1	RB1-INDUCIBLE COILED-COIL PROTEIN 1
<i>Medtr8g020500</i>	PTHR13385	AUTOPHAGY PROTEIN 12
<i>Medtr5g068710</i>	PTHR13430:SF3	AUTOPHAGY-RELATED PROTEIN 13
<i>MTR_8g011890</i>	PTHR21297	DNA-DIRECTED RNA POLYMERASE II
<i>MTR_2g027530</i>	PTHR21297:SF2	DNA-DIRECTED RNA POLYMERASES IV AND V SUBUNIT 4
<i>Medtr3g095570</i>	PTHR13430	UNCHARACTERIZED
<i>Medtr8g093050</i>	PTHR13430	UNCHARACTERIZED
<i>Medtr4g104380</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>Medtr3g075400</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>Medtr4g007500</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>MTR_6g27280</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE

<i>Medtr1g083230</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>Medtr3g093590</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>Medtr1g088855</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>Medtr7g108520.</i>	PTHR11227:SF18	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3
<i>Medtr4g130190</i>	PTHR11227:SF17	AUTOPHAGY-SPECIFIC GENE 18, ISOFORM E
<i>Medtr2g082770</i>	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F
<i>Medtr1g089110</i>	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
<i>Medtr1g082300</i>	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
<i>Medtr8g079240</i>	PTHR13292:SF0	AUTOPHAGY-RELATED PROTEIN 101
<i>Medtr5g005380</i>	PTHR11139:SF9	SERINE/THREONINE-PROTEIN KINASE MTOR
<i>Medtr7g072330</i>	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
<i>Medtr2g016690</i>	PTHR19842	G BETA-LIKE PROTEIN GBL

<b>Gene accession numbers</b>	<b>PANTHER</b>	<b>Description</b>
<i>Glyma.04G215500</i>	PTHR24348	SERINE/THREONINE-PROTEIN KINASE UNC-51-RELATED
<i>Glyma.06G150700</i>	PTHR24348	SERINE/THREONINE-PROTEIN KINASE UNC-51-RELATED
<i>Glyma.03G069800</i>	PTHR24348	SERINE/THREONINE-PROTEIN KINASE UNC-51-RELATED
<i>Glyma.07G048400</i>	PTHR24348	SERINE/THREONINE-PROTEIN KINASE UNC-51-RELATED
<i>GLYMA_01G099600</i>	PTHR24348:SF22	SERINE/THREONINE-PROTEIN KINASE ULK3
<i>GLYMA_15G088500</i>	PTHR24348:SF22	SERINE/THREONINE-PROTEIN KINASE ULK3
<i>GLYMA_03G069800</i>	PTHR24348:SF22	SERINE/THREONINE-PROTEIN KINASE ULK3
<i>GLYMA_14G026700</i>	PTHR24348:SF22	SERINE/THREONINE-PROTEIN KINASE ULK3
<i>GLYMA_20G031300</i>	PTHR24348:SF22	SERINE/THREONINE-PROTEIN KINASE ULK3
<i>GLYMA_16G017300</i>	PTHR24348:SF39	AUTOPHAGY-RELATED 1, ISOFORM B
<i>Glyma.02G133400</i>	PTHR13190	FAMILY NOT NAMED
<i>Glyma.07G211600</i>	PTHR13190	FAMILY NOT NAMED
<i>Glyma.12G005700</i>	PTHR12866:SF2	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG3
<i>Glyma.09G231000</i>	PTHR12866:SF2	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG3
<i>Glyma.18G248400</i>	PTHR22624	APG4 AUTOPHAGY 4-RELATED
<i>Glyma.09G244800</i>	PTHR22624	APG4 AUTOPHAGY 4-RELATED
<i>Glyma.14G210200</i>	PTHR13040	AUTOPHAGY PROTEIN 5
<i>GLYMA.01G231500</i>	PTHR13040:SF2	glyma_14G187000
<i>Glyma.02G240700</i>	PTHR13040:SF2	AUTOPHAGY PROTEIN 5
<i>Glyma.11G153900</i>	PTHR12768	BECLIN 1
<i>Glyma.04G141000</i>	PTHR12768	BECLIN 1
<i>Glyma.12G010000</i>	PTHR10953:SF3	UBIQUITIN-LIKE MODIFIER-ACTIVATING ENZYME ATG7
<i>glyma.15G108200</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>glyma.17G013000</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>glyma.12G098400</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED



<i>Glyma.06G306300</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>Glyma.07G261000</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>Glyma.09G003900</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>Glyma.15G188600</i>	PTHR10969:SF43	AUTOPHAGY-RELATED PROTEIN 8A-RELATED
<i>glyma.17G140700</i>	PTHR10969:SF39	AUTOPHAGY-RELATED PROTEIN 8F
<i>GLYMA.05G058300</i>		AUTOPHAGY-RELATED PROTEIN 8F (PTHR10969:SF58)
<i>GLYMA.1G210200</i>		AUTOPHAGY-RELATED PROTEIN 8F (PTHR10969:SF58)
<i>GLYMA.11G031800</i>		AUTOPHAGY-RELATED PROTEIN 8F (PTHR10969:SF58)
<i>Glyma.10G009300</i>	PTHR10969:SF25	AUTOPHAGY-RELATED PROTEIN 8I
<i>glyma.02G008800</i>	PTHR10969:SF25	AUTOPHAGY-RELATED PROTEIN 8I
<i>glyma.13G122200</i>	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
<i>Glyma.03G162100.</i>	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
<i>Glyma.19G163500.</i>	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
<i>Glyma.10G035800.</i>	PTHR13038:SF10	AUTOPHAGY-SPECIFIC GENE 9
<i>glyma.03G097000</i>	PTHR12866:SF5	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG10
<i>Glyma.07G124300</i>	PTHR12866:SF5	UBIQUITIN-LIKE-CONJUGATING ENZYME ATG10
<i>glyma.17G071400</i>	PTHR13222:SF1	RB1-INDUCIBLE COILED-COIL PROTEIN 1
<i>Glyma.02G206500</i>	PTHR13222:SF1	RB1-INDUCIBLE COILED-COIL PROTEIN 1
<i>glyma.16G007300</i>	PTHR13385	AUTOPHAGY PROTEIN 12
<i>glyma.07G038100</i>	PTHR13385	AUTOPHAGY PROTEIN 12
<i>glyma.14G187000</i>	PTHR13430:SF3	AUTOPHAGY-RELATED PROTEIN 13
<i>glyma.05G189000</i>	PTHR13430	UNCHARACTERIZED
<i>Glyma.08G146700</i>	PTHR13430	UNCHARACTERIZED
<i>Glyma.02G220700</i>	PTHR13430:SF3	AUTOPHAGY-RELATED PROTEIN 13
<i>GLYMA_15G121800</i>	PTHR21297:SF2	DNA-DIRECTED RNA POLYMERASES IV AND V SUBUNIT 4
<i>GLYMA_16G084800</i>	PTHR21297	DNA-DIRECTED RNA POLYMERASE II
<i>GLYMA_03G088500</i>	PTHR21297	DNA-DIRECTED RNA POLYMERASE II
<i>GLYMA_09G016100</i>	PTHR21297:SF2	DNA-DIRECTED RNA POLYMERASES IV AND V SUBUNIT 4
<i>GLYMA_08G146800</i>	PTHR21297	DNA-DIRECTED RNA POLYMERASE II
<i>GLYMA_05G189100</i>	PTHR21297	DNA-DIRECTED RNA POLYMERASE II
<i>glyma.05G043700</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>Glyma.05G090500</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>Glyma.17G176300</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>Glyma.17G126200</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>Glyma.11G057700</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>Glyma.01G184500</i>	PTHR19878	AUTOPHAGY PROTEIN 16-LIKE
<i>glyma.20G235800</i>	PTHR11227:SF18	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3
<i>Glyma.19G209200</i>	PTHR11227:SF18	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3
<i>Glyma.10G152500.</i>	PTHR11227:SF18	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3

<i>Glyma.03G212100</i>	PTHR11227:SF18	WD REPEAT DOMAIN PHOSPHOINOSITIDE-INTERACTING PROTEIN 3
<i>Glyma.17G070200</i>	PTHR11227:SF17	AUTOPHAGY-SPECIFIC GENE 18, ISOFORM E
<i>Glyma.02G207500</i>	PTHR11227:SF17	AUTOPHAGY-SPECIFIC GENE 18, ISOFORM E
<i>Glyma.16G109400</i>	PTHR11227:SF17	AUTOPHAGY-SPECIFIC GENE 18, ISOFORM E
<i>Glyma.10G126200</i>	PTHR11227:SF17	AUTOPHAGY-SPECIFIC GENE 18, ISOFORM E
<i>glyma.06G140400</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>Glyma.04G224300</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>Glyma.07G203900</i>	PTHR11227:SF25	AUTOPHAGY-RELATED PROTEIN 18C-RELATED
<i>glyma.13G287000</i>	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F
<i>Glyma.12G214600</i>	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F
<i>Glyma.12G136000</i>	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F
<i>Glyma.06G267000</i>	PTHR13268:SF1	AUTOPHAGY-RELATED PROTEIN 18F
<i>glyma.03G148700</i>	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
<i>Glyma.20G230900</i>	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
<i>Glyma.19G152000</i>	PTHR13268:SF2	AUTOPHAGY-RELATED PROTEIN 18G
<i>glyma.10G157700</i>	PTHR13268:SF0	BREAST CARCINOMA-AMPLIFIED SEQUENCE 3
<i>Glyma.17G180900</i>	PTHR13292:SF0	AUTOPHAGY-RELATED PROTEIN 101
<i>Glyma.01G241300</i>	PTHR11139:SF9	SERINE/THREONINE-PROTEIN KINASE MTOR
<i>Glyma.11G002600</i>	PTHR11139:SF9	SERINE/THREONINE-PROTEIN KINASE MTOR
<i>Glyma.09G278500</i>	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
<i>Glyma.18G210300</i>	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
<i>Glyma.U032100.1.p</i>	PTHR12848:SF16	REGULATORY-ASSOCIATED PROTEIN OF MTOR
<i>Glyma.15G085200</i>	PTHR19842	G BETA-LIKE PROTEIN GBL
<i>Glyma.13G227200</i>	PTHR19842	G BETA-LIKE PROTEIN GBL