

Go term ID	Term	Observed Frequency
GO:0009828	plant-type cell wall loosening	4 out of 32 genes, 12.5%
GO:0009061	anaerobic respiration	3 out of 32 genes, 9.4%
GO:0009827	plant-type cell wall modification	4 out of 32 genes, 12.5%
GO:0009664	plant-type cell wall organization	4 out of 32 genes, 12.5%
GO:0007047	cellular cell wall organization	4 out of 32 genes, 12.5%
GO:0009831	plant-type cell wall modification involved in multid	3 out of 32 genes, 9.4%
GO:0042547	cell wall modification involved in multidimensional	3 out of 32 genes, 9.4%
GO:0045229	external encapsulating structure organization	4 out of 32 genes, 12.5%
GO:0015980	energy derivation by oxidation of organic compour	3 out of 32 genes, 9.4%
GO:0045333	cellular respiration	3 out of 32 genes, 9.4%
GO:0071669	plant-type cell wall organization or biogenesis	4 out of 32 genes, 12.5%
GO:0042545	cell wall modification	4 out of 32 genes, 12.5%
GO:0070882	cellular cell wall organization or biogenesis	4 out of 32 genes, 12.5%
GO:0071555	cell wall organization	4 out of 32 genes, 12.5%
GO:0006091	generation of precursor metabolites and energy	4 out of 32 genes, 12.5%
GO:0009826	unidimensional cell growth	4 out of 32 genes, 12.5%
GO:0060560	developmental growth involved in morphogenesis	4 out of 32 genes, 12.5%
GO:0006949	syncytium formation	2 out of 32 genes, 6.2%
GO:0048589	developmental growth	4 out of 32 genes, 12.5%
GO:0071554	cell wall organization or biogenesis	4 out of 32 genes, 12.5%
GO:0000902	cell morphogenesis	4 out of 32 genes, 12.5%
GO:0006098	pentose-phosphate shunt	2 out of 32 genes, 6.2%
GO:0006740	NADPH regeneration	2 out of 32 genes, 6.2%
GO:0016049	cell growth	4 out of 32 genes, 12.5%
GO:0032989	cellular component morphogenesis	4 out of 32 genes, 12.5%
GO:0044275	cellular carbohydrate catabolic process	3 out of 32 genes, 9.4%
GO:0006739	NADP metabolic process	2 out of 32 genes, 6.2%
GO:0016052	carbohydrate catabolic process	3 out of 32 genes, 9.4%
GO:0040007	growth	4 out of 32 genes, 12.5%
GO:0046496	nicotinamide nucleotide metabolic process	2 out of 32 genes, 6.2%
GO:0019362	pyridine nucleotide metabolic process	2 out of 32 genes, 6.2%
GO:0072524	pyridine-containing compound metabolic process	2 out of 32 genes, 6.2%
GO:0006733	oxidoreduction coenzyme metabolic process	2 out of 32 genes, 6.2%
GO:0009653	anatomical structure morphogenesis	4 out of 32 genes, 12.5%
GO:0048869	cellular developmental process	4 out of 32 genes, 12.5%

Expected Frequency	p-value	Genes
35 out of 24961 genes, 0.1%	3.79E-05	AT2G39700 AT2G03090 AT3G29030 AT3G45970
9 out of 24961 genes, 0%	3.80E-05	AT1G05575 AT1G19530 AT3G10020
47 out of 24961 genes, 0.2%	3.80E-05	AT2G39700 AT2G03090 AT3G29030 AT3G45970
69 out of 24961 genes, 0.3%	0.000122	AT2G39700 AT2G03090 AT3G29030 AT3G45970
74 out of 24961 genes, 0.3%	0.000127	AT2G39700 AT2G03090 AT3G29030 AT3G45970
26 out of 24961 genes, 0.1%	0.000225	AT2G03090 AT2G39700 AT3G29030
28 out of 24961 genes, 0.1%	0.000225	AT2G03090 AT2G39700 AT3G29030
95 out of 24961 genes, 0.4%	0.000225	AT2G39700 AT2G03090 AT3G29030 AT3G45970
34 out of 24961 genes, 0.1%	0.000309	AT1G05575 AT1G19530 AT3G10020
34 out of 24961 genes, 0.1%	0.000309	AT1G05575 AT1G19530 AT3G10020
118 out of 24961 genes, 0.5%	0.000342	AT2G39700 AT2G03090 AT3G29030 AT3G45970
136 out of 24961 genes, 0.5%	0.000538	AT2G39700 AT2G03090 AT3G29030 AT3G45970
151 out of 24961 genes, 0.6%	0.000739	AT2G39700 AT2G03090 AT3G29030 AT3G45970
163 out of 24961 genes, 0.7%	0.000918	AT2G39700 AT2G03090 AT3G29030 AT3G45970
182 out of 24961 genes, 0.7%	0.0013	AT1G05575 AT1G18270 AT1G19530 AT3G10020
189 out of 24961 genes, 0.8%	0.00141	AT2G39700 AT2G03090 AT3G29030 AT3G45970
206 out of 24961 genes, 0.8%	0.00183	AT2G39700 AT2G03090 AT3G29030 AT3G45970
14 out of 24961 genes, 0.1%	0.00213	AT2G39700 AT2G03090
219 out of 24961 genes, 0.9%	0.00213	AT2G39700 AT2G03090 AT3G29030 AT3G45970
236 out of 24961 genes, 0.9%	0.00259	AT2G39700 AT2G03090 AT3G29030 AT3G45970
247 out of 24961 genes, 1%	0.00261	AT2G39700 AT2G03090 AT3G29030 AT3G45970
17 out of 24961 genes, 0.1%	0.00261	AT1G13700 AT1G18270
18 out of 24961 genes, 0.1%	0.00261	AT1G13700 AT1G18270
251 out of 24961 genes, 1%	0.00261	AT2G39700 AT2G03090 AT3G29030 AT3G45970
247 out of 24961 genes, 1%	0.00261	AT2G39700 AT2G03090 AT3G29030 AT3G45970
101 out of 24961 genes, 0.4%	0.00263	AT1G18270 AT3G14210 AT1G13700
21 out of 24961 genes, 0.1%	0.00311	AT1G13700 AT1G18270
110 out of 24961 genes, 0.4%	0.00311	AT1G18270 AT3G14210 AT1G13700
294 out of 24961 genes, 1.2%	0.00406	AT3G29030 AT2G39700 AT2G03090 AT3G45970
27 out of 24961 genes, 0.1%	0.00452	AT1G13700 AT1G18270
31 out of 24961 genes, 0.1%	0.0055	AT1G13700 AT1G18270
31 out of 24961 genes, 0.1%	0.0055	AT1G13700 AT1G18270
39 out of 24961 genes, 0.2%	0.00814	AT1G13700 AT1G18270
371 out of 24961 genes, 1.5%	0.00814	AT3G29030 AT2G39700 AT2G03090 AT3G45970
378 out of 24961 genes, 1.5%	0.00846	AT3G29030 AT2G39700 AT2G03090 AT3G45970