**Table S8.** List of the main biological processes affected by iodine based on the GO terms enrichment analysis in root tissues (only genes regulated in NaI- and KI-treated plants, and not in KBr-treated plants, when compared with the control were analyzed). Data were extracted from Gorilla (http://cbl-gorilla.cs.technion.ac.il). In this analysis, DEGs with log2FC≥2.5 or log2FC≤-2.5 were used. 'P-value' is the enrichment p-value computed according to the mHG or HG model. This p-value is not corrected for multiple testing of 4037 GO terms. 'FDR q-value' is the correction of the above p-value for multiple testing using the Benjamini and Hochberg (1995) method (BH procedure). Namely, for the ith term (ranked according to p-value) the FDR q-value is (p-value \* number of GO terms) / i. Enrichment (N, B, n, b) is defined as follows: N - is the total number of genes; B - is the total number of genes associated with a specific GO term; n - is the number of genes in the top of the user's input list or in the target set when appropriate; b - is the number of genes in the intersection. Enrichment = (b/n) / (B/N). The genes classified in each GO term are also listed.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO term** | **Description** | [**P-value**](http://cbl-gorilla.cs.technion.ac.il/GOrilla/akje8mfg/GOResultsPROCESS.html#p_value_info) | [**FDR q-value**](http://cbl-gorilla.cs.technion.ac.il/GOrilla/akje8mfg/GOResultsPROCESS.html#fdr_info) | [**Enrichment (N, B, n, b)**](http://cbl-gorilla.cs.technion.ac.il/GOrilla/akje8mfg/GOResultsPROCESS.html#enrich_info)  | [**Genes**](http://cbl-gorilla.cs.technion.ac.il/GOrilla/akje8mfg/GOResultsPROCESS.html#genes_info)  |
| [GO:0050896](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0050896&view=details) | response to stimulus | 1.25E-11 | 5.03E-8 | 2.77 (11861,1303,161,49) | [-] Hide genesAT5G22530 - hypothetical proteinAT5G18470 - curculin-like (mannose-binding) lectin family proteinAT4G37290 - hypothetical proteinAT2G21210 - saur-like auxin-responsive proteinAT4G28460 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT1G68620 - probable carboxylesterase 6AT1G15010 - hypothetical proteinAT1G57630 - toll-interleukin-resistance domain-containing proteinAT4G36430 - peroxidase 49AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT1G35910 - probable trehalose-phosphate phosphatase dAT3G23170 - hypothetical proteinAT3G16530 - legume lectin-like proteinAT1G19020 - hypothetical proteinAT5G06730 - peroxidaseAT1G73805 - protein sar deficient 1AT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G05340 - peroxidase 52AT4G37710 - vq motif-containing proteinAT5G19880 - peroxidaseAT2G22880 - vq motif-containing proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G34510 - peroxidase 8AT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT3G21670 - nitrate transporter 1.3AT1G14540 - peroxidase 4AT5G39580 - peroxidase 62AT4G08780 - peroxidase 38AT4G23680 - polyketide cyclase/dehydrase and lipid transport superfamily proteinAT1G65500 - hypothetical proteinAT3G45710 - major facilitator superfamily proteinAT5G10760 - aspartyl protease family proteinAT3G28580 - aaa-type atpase family proteinAT2G38340 - dehydration-responsive element-binding protein 2eAT3G55790 - hypothetical proteinAT1G43910 - p-loop containing nucleoside triphosphate hydrolases superfamily proteinAT5G22270 - hypothetical proteinAT2G41380 - s-adenosyl-l-methionine-dependent methyltransferase-like proteinAT5G38710 - proline dehydrogenase 2AT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT4G37220 - cold acclimation protein wcor413AT5G38900 - thioredoxin superfamily proteinAT1G70880 - srpbcc domain-containing protein |
| [GO:0006950](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0006950&view=details) | response to stress | 3.23E-11 | 6.53E-8 | 3.23 (11861,890,161,39) | [-] Hide genesAT4G08780 - peroxidase 38AT5G22530 - hypothetical proteinAT4G23680 - polyketide cyclase/dehydrase and lipid transport superfamily proteinAT1G65500 - hypothetical proteinAT4G28460 - hypothetical proteinAT5G10760 - aspartyl protease family proteinAT1G66090 - tir-nbs class of disease resistance proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT3G28580 - aaa-type atpase family proteinAT4G36430 - peroxidase 49AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT1G35910 - probable trehalose-phosphate phosphatase dAT2G38340 - dehydration-responsive element-binding protein 2eAT3G55790 - hypothetical proteinAT3G23170 - hypothetical proteinAT1G19020 - hypothetical proteinAT5G06730 - peroxidaseAT5G22270 - hypothetical proteinAT1G73805 - protein sar deficient 1AT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G19880 - peroxidaseAT4G37710 - vq motif-containing proteinAT5G05340 - peroxidase 52AT5G38710 - proline dehydrogenase 2AT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G34510 - peroxidase 8AT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT5G38900 - thioredoxin superfamily proteinAT1G14540 - peroxidase 4AT5G39580 - peroxidase 62AT1G70880 - srpbcc domain-containing protein |
| [GO:0071453](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0071453&view=details) | cellular response to oxygen levels | 2.15E-10 | 2.89E-7 | 9.46 (11861,109,161,14) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT3G55790 - hypothetical proteinAT3G23170 - hypothetical protein |
| [GO:0071456](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0071456&view=details) | cellular response to hypoxia | 2.15E-10 | 2.17E-7 | 9.46 (11861,109,161,14) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT3G55790 - hypothetical proteinAT3G23170 - hypothetical protein |
| [GO:0036294](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0036294&view=details) | cellular response to decreased oxygen levels | 2.15E-10 | 1.74E-7 | 9.46 (11861,109,161,14) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT3G55790 - hypothetical proteinAT3G23170 - hypothetical protein |
| [GO:0001666](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0001666&view=details) | response to hypoxia | 2.75E-10 | 1.85E-7 | 9.29 (11861,111,161,14) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT3G55790 - hypothetical proteinAT3G23170 - hypothetical protein |
| [GO:0036293](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0036293&view=details) | response to decreased oxygen levels | 3.11E-10 | 1.79E-7 | 9.21 (11861,112,161,14) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT3G55790 - hypothetical proteinAT3G23170 - hypothetical protein |
| [GO:0070482](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0070482&view=details) | response to oxygen levels | 3.51E-10 | 1.77E-7 | 9.13 (11861,113,161,14) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT3G55790 - hypothetical proteinAT3G23170 - hypothetical protein |
| [GO:0042221](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0042221&view=details) | response to chemical | 3.43E-9 | 1.54E-6 | 3.58 (11861,577,161,28) | [-] Hide genesAT5G22530 - hypothetical proteinAT2G21210 - saur-like auxin-responsive proteinAT1G65500 - hypothetical proteinAT3G45710 - major facilitator superfamily proteinAT1G66090 - tir-nbs class of disease resistance proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT3G28580 - aaa-type atpase family proteinAT2G38340 - dehydration-responsive element-binding protein 2eAT3G55790 - hypothetical proteinAT3G23170 - hypothetical proteinAT3G16530 - legume lectin-like proteinAT1G43910 - p-loop containing nucleoside triphosphate hydrolases superfamily proteinAT1G19020 - hypothetical proteinAT1G73805 - protein sar deficient 1AT2G41380 - s-adenosyl-l-methionine-dependent methyltransferase-like proteinAT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT4G37710 - vq motif-containing proteinAT5G38710 - proline dehydrogenase 2AT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT3G21670 - nitrate transporter 1.3AT1G14550 - peroxidase 5AT4G37220 - cold acclimation protein wcor413AT1G14540 - peroxidase 4 |
| [GO:0070887](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0070887&view=details) | cellular response to chemical stimulus | 1.04E-8 | 4.2E-6 | 6.46 (11861,171,161,15) | [-] Hide genesAT1G19020 - hypothetical proteinAT3G45710 - major facilitator superfamily proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G15010 - hypothetical proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT3G55790 - hypothetical proteinAT3G23170 - hypothetical protein |
| [GO:0009628](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0009628&view=details) | response to abiotic stimulus | 3.07E-7 | 1.13E-4 | 3.36 (11861,504,161,23) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G73805 - protein sar deficient 1AT5G22270 - hypothetical proteinAT5G18470 - curculin-like (mannose-binding) lectin family proteinAT4G37290 - hypothetical proteinAT1G65500 - hypothetical proteinAT4G37710 - vq motif-containing proteinAT1G66090 - tir-nbs class of disease resistance proteinAT1G68620 - probable carboxylesterase 6AT1G15010 - hypothetical proteinAT1G57630 - toll-interleukin-resistance domain-containing proteinAT2G22880 - vq motif-containing proteinAT5G38710 - proline dehydrogenase 2AT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT1G35910 - probable trehalose-phosphate phosphatase dAT2G38340 - dehydration-responsive element-binding protein 2eAT1G14550 - peroxidase 5AT3G55790 - hypothetical proteinAT1G14540 - peroxidase 4AT3G23170 - hypothetical protein |
| [GO:0051704](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0051704&view=details) | multi-organism process | 5.26E-7 | 1.77E-4 | 4.80 (11861,230,161,15) | [-] Hide genesAT1G73805 - protein sar deficient 1AT4G28460 - hypothetical proteinAT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G10760 - aspartyl protease family proteinAT1G15010 - hypothetical proteinAT1G23160 - auxin-responsive gh3 family proteinAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT4G36430 - peroxidase 49AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT5G39580 - peroxidase 62AT5G38900 - thioredoxin superfamily proteinAT3G23170 - hypothetical proteinAT3G16530 - legume lectin-like protein |
| [GO:0006979](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0006979&view=details) | response to oxidative stress | 1.35E-6 | 4.2E-4 | 5.67 (11861,156,161,12) | [-] Hide genesAT4G08780 - peroxidase 38AT1G19020 - hypothetical proteinAT1G34510 - peroxidase 8AT5G06730 - peroxidaseAT3G28580 - aaa-type atpase family proteinAT4G36430 - peroxidase 49AT5G05340 - peroxidase 52AT5G19880 - peroxidaseAT1G35910 - probable trehalose-phosphate phosphatase dAT1G14550 - peroxidase 5AT1G14540 - peroxidase 4AT5G39580 - peroxidase 62 |
| [GO:0006952](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0006952&view=details) | defense response | 1.67E-6 | 4.81E-4 | 4.39 (11861,252,161,15) | [-] Hide genesAT4G23680 - polyketide cyclase/dehydrase and lipid transport superfamily proteinAT1G73805 - protein sar deficient 1AT4G28460 - hypothetical proteinAT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT1G66090 - tir-nbs class of disease resistance proteinAT5G10760 - aspartyl protease family proteinAT1G15010 - hypothetical proteinAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT5G39580 - peroxidase 62AT5G38900 - thioredoxin superfamily proteinAT1G70880 - srpbcc domain-containing proteinAT3G23170 - hypothetical protein |
| [GO:0051707](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0051707&view=details) | response to other organism | 1.91E-6 | 5.14E-4 | 4.65 (11861,222,161,14) | [-] Hide genesAT1G73805 - protein sar deficient 1AT4G28460 - hypothetical proteinAT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G10760 - aspartyl protease family proteinAT1G15010 - hypothetical proteinAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT4G36430 - peroxidase 49AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT5G39580 - peroxidase 62AT5G38900 - thioredoxin superfamily proteinAT3G23170 - hypothetical proteinAT3G16530 - legume lectin-like protein |
| [GO:0043207](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0043207&view=details) | response to external biotic stimulus | 2.48E-6 | 6.26E-4 | 4.54 (11861,227,161,14) | [-] Hide genesAT1G73805 - protein sar deficient 1AT4G28460 - hypothetical proteinAT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G10760 - aspartyl protease family proteinAT1G15010 - hypothetical proteinAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT4G36430 - peroxidase 49AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT5G39580 - peroxidase 62AT5G38900 - thioredoxin superfamily proteinAT3G23170 - hypothetical proteinAT3G16530 - legume lectin-like protein |
| [GO:0009607](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0009607&view=details) | response to biotic stimulus | 2.48E-6 | 5.9E-4 | 4.54 (11861,227,161,14) | [-] Hide genesAT1G73805 - protein sar deficient 1AT4G28460 - hypothetical proteinAT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G10760 - aspartyl protease family proteinAT1G15010 - hypothetical proteinAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT4G36430 - peroxidase 49AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT5G39580 - peroxidase 62AT5G38900 - thioredoxin superfamily proteinAT3G23170 - hypothetical proteinAT3G16530 - legume lectin-like protein |
| [GO:0098542](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0098542&view=details) | defense response to other organism | 4.51E-6 | 1.01E-3 | 5.05 (11861,175,161,12) | [-] Hide genesAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT1G73805 - protein sar deficient 1AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G12200 - putative flavin monooxygenase.AT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G65600 - concanavalin a-like lectin kinase-like proteinAT4G28460 - hypothetical proteinAT5G10760 - aspartyl protease family proteinAT1G15010 - hypothetical proteinAT5G38900 - thioredoxin superfamily proteinAT5G39580 - peroxidase 62AT3G23170 - hypothetical protein |
| [GO:0051716](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0051716&view=details) | cellular response to stimulus | 7.74E-6 | 1.64E-3 | 3.48 (11861,360,161,17) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G73805 - protein sar deficient 1AT3G45710 - major facilitator superfamily proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G15010 - hypothetical proteinAT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT2G38340 - dehydration-responsive element-binding protein 2eAT1G14550 - peroxidase 5AT3G55790 - hypothetical proteinAT1G14540 - peroxidase 4AT3G23170 - hypothetical protein |
| [GO:0009605](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0009605&view=details) | response to external stimulus | 2.47E-5 | 4.99E-3 | 3.51 (11861,315,161,15) | [-] Hide genesAT1G73805 - protein sar deficient 1AT4G28460 - hypothetical proteinAT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G10760 - aspartyl protease family proteinAT1G15010 - hypothetical proteinAT3G28580 - aaa-type atpase family proteinAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT4G36430 - peroxidase 49AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT1G12200 - putative flavin monooxygenase.AT5G65600 - concanavalin a-like lectin kinase-like proteinAT5G39580 - peroxidase 62AT5G38900 - thioredoxin superfamily proteinAT3G23170 - hypothetical proteinAT3G16530 - legume lectin-like protein |
| [GO:0033554](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0033554&view=details) | cellular response to stress | 2.97E-5 | 5.71E-3 | 3.45 (11861,320,161,15) | [-] Hide genesAT1G19020 - hypothetical proteinAT1G66090 - tir-nbs class of disease resistance proteinAT4G37710 - vq motif-containing proteinAT1G68620 - probable carboxylesterase 6AT1G15010 - hypothetical proteinAT1G57630 - toll-interleukin-resistance domain-containing proteinAT1G26380 - fad-binding and bbe domain-containing proteinAT1G72910 - toll-interleukin-resistance domain-containing proteinAT1G26410 - fad-binding and bbe domain-containing proteinAT1G72940 - toll-interleukin-resistance domain-containing proteinAT2G38340 - dehydration-responsive element-binding protein 2eAT1G14550 - peroxidase 5AT3G55790 - hypothetical proteinAT1G14540 - peroxidase 4AT3G23170 - hypothetical protein |
| [GO:0018958](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0018958&view=details) | phenol-containing compound metabolic process | 4.76E-5 | 8.74E-3 | 36.84 (11861,6,161,3) | [-] Hide genesAT1G64160 - dirigent-like protein dir5AT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G63560 - hxxxd-type acyl-transferase-like protein |
| [GO:0002239](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0002239&view=details) | response to oomycetes | 5.53E-5 | 9.7E-3 | 8.84 (11861,50,161,6) | [-] Hide genesAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT1G73805 - protein sar deficient 1AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G65600 - concanavalin a-like lectin kinase-like proteinAT3G16530 - legume lectin-like protein |
| [GO:0002229](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0002229&view=details) | defense response to oomycetes | 1.94E-4 | 3.26E-2 | 9.21 (11861,40,161,5) | [-] Hide genesAT2G29250 - concanavalin a-like lectin protein kinase-like proteinAT1G73805 - protein sar deficient 1AT2G29220 - putative inactive l-type lectin-domain containing receptor kinase iii.1AT4G10500 - oxidoreductase, 2og-fe(ii) oxygenase family proteinAT5G65600 - concanavalin a-like lectin kinase-like protein |
| [GO:0046189](http://www.godatabase.org/cgi-bin/amigo/go.cgi?query=GO:0046189&view=details) | phenol-containing compound biosynthetic process | 5.44E-4 | 8.79E-2 | 49.11 (11861,3,161,2) | [-] Hide genesAT1G64160 - dirigent-like protein dir5AT5G63560 - hxxxd-type acyl-transferase-like protein |