

Table S2. GO Slim annotation of each module.

| GO Slim ID and assigned modules | GO Slim Term and GO IDs associated to GO Slim T No. GO Terms and GO Terms significantly enriched | |
|---------------------------------|--|--|
| Slim id: GO:0000003 | reproduction GO:0048700 GO:0048481 GO:0048437 GO:0048438 GO:0048440 GO:0048467 | acquisition of desiccation tolerance ovule development floral organ development floral whorl development carpel development gynoecium development |
| Slim id: GO:0005975 | carbohydrate metabolic process GO:0019253 GO:0019685 GO:0006096 GO:0010289 GO:0000271 GO:0005976 GO:0016051 GO:0033692 GO:0034637 GO:0044264 GO:0045488 GO:0045489 GO:0005998 GO:0005996 GO:0005997 GO:0016052 GO:0019323 GO:0044275 GO:0046365 GO:0010253 GO:0019299 GO:0019300 GO:0019319 GO:0033478 GO:0030244 GO:0030243 GO:0030244 GO:0000271 GO:0005976 GO:0030243 GO:0033692 GO:0034637 GO:0044264 GO:0019252 GO:0005982 GO:0010021 GO:0030244 GO:0009250 GO:0030243 GO:0005975 GO:0005986 GO:0005984 GO:0005985 GO:0009311 GO:0009312 GO:0016051 GO:0016137 GO:0016138 GO:0034637 GO:0046351 | reductive pentose-phosphate cycle photosynthesis, dark reaction glycolysis homogalacturonan biosynthetic process polysaccharide biosynthetic process polysaccharide metabolic process carbohydrate biosynthetic process cellular polysaccharide biosynthetic process cellular carbohydrate biosynthetic process cellular polysaccharide metabolic process pectin metabolic process pectin biosynthetic process xylulose catabolic process monosaccharide metabolic process xylulose metabolic process carbohydrate catabolic process pentose catabolic process cellular carbohydrate catabolic process monosaccharide catabolic process UDP-rhamnose biosynthetic process rhamnose metabolic process rhamnose biosynthetic process hexose biosynthetic process UDP-rhamnose metabolic process cellulose biosynthetic process cellulose metabolic process cellulose biosynthetic process polysaccharide biosynthetic process polysaccharide metabolic process cellulose metabolic process cellular polysaccharide biosynthetic process cellular carbohydrate biosynthetic process cellular polysaccharide metabolic process starch biosynthetic process starch metabolic process amylopectin biosynthetic process cellulose biosynthetic process glucan biosynthetic process cellulose metabolic process carbohydrate metabolic process sucrose biosynthetic process disaccharide metabolic process sucrose metabolic process oligosaccharide metabolic process oligosaccharide biosynthetic process carbohydrate biosynthetic process glycoside metabolic process glycoside biosynthetic process cellular carbohydrate biosynthetic process disaccharide biosynthetic process |
| Slim id: GO:0006091 | generation of precursor metabolites and energy GO:0042550 GO:0042548 GO:0043467 GO:0015980 GO:0045333 GO:0006096 GO:0009765 GO:0006091 GO:0009768 GO:0019684 GO:0009769 GO:0009765 GO:0006091 GO:0019684 GO:0009767 GO:0006091 GO:0019684 GO:0022900 GO:0009765 GO:0019684 GO:0006119 | photosystem I stabilization regulation of photosynthesis, light reaction regulation of generation of precursor metabolites and energy energy derivation by oxidation of organic compounds cellular respiration glycolysis photosynthesis, light harvesting generation of precursor metabolites and energy photosynthesis, light harvesting in photosystem I photosynthesis, light reaction photosynthesis, light harvesting in photosystem II photosynthesis, light harvesting generation of precursor metabolites and energy photosynthesis, light reaction photosynthetic electron transport chain generation of precursor metabolites and energy photosynthesis, light reaction electron transport chain photosynthesis, light harvesting photosynthesis, light reaction oxidative phosphorylation |
| Slim id: GO:0006139 | nucleobase, nucleoside, nucleotide and nucleic acid GO:0006556 GO:0009119 GO:0042278 GO:0046128 GO:0046500 GO:0006364 GO:0006396 GO:0016072 GO:0034470 GO:0034660 GO:0006355 GO:0051252 GO:0006418 GO:0006399 GO:0006431 GO:0034660 GO:0043039 GO:0016070 GO:0006396 GO:0006418 GO:0043039 GO:0010253 GO:0009226 GO:0033478 GO:0006139 GO:0090304 | S-adenosylmethionine biosynthetic process ribonucleoside metabolic process purine nucleoside metabolic process purine ribonucleoside metabolic process S-adenosylmethionine metabolic process rRNA processing RNA processing rRNA metabolic process ncRNA processing ncRNA metabolic process regulation of transcription, DNA-dependent regulation of RNA metabolic process tRNA aminoacylation for protein translation tRNA metabolic process methionyl-tRNA aminoacylation ncRNA metabolic process tRNA aminoacylation RNA metabolic process RNA processing tRNA aminoacylation for protein translation tRNA aminoacylation UDP-rhamnose biosynthetic process nucleotide-sugar biosynthetic process UDP-rhamnose metabolic process nucleobase, nucleoside, nucleotide and nucleic acid metabolic processes nucleic acid metabolic process |
| Slim id: GO:0006259 | DNA metabolic process GO:0015074 GO:0006268 GO:0006270 | DNA integration DNA unwinding involved in replication DNA-dependent DNA replication initiation |

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|---------------------|--|---|----|
| module_553 | GO:0006259 | DNA metabolic process | |
| module_553 | GO:0006260 | DNA replication | |
| module_553 | GO:0006261 | DNA-dependent DNA replication | |
| module_554 | GO:0006260 | DNA replication | |
| Slim id: GO:0006350 | | | |
| module_266 | transcription | | 1 |
| | GO:0006355 | regulation of transcription, DNA-dependent | |
| Slim id: GO:0006412 | | | 18 |
| module_113 | translation | | |
| module_237 | GO:0006413 | translational initiation | |
| module_285 | GO:0006412 | translation | |
| module_290 | GO:0006412 | translation | |
| module_290 | GO:0006414 | translational elongation | |
| module_293 | GO:0006418 | tRNA aminoacylation for protein translation | |
| module_293 | GO:0006431 | methionyl-tRNA aminoacylation | |
| module_313 | GO:0006412 | translation | |
| module_380 | GO:0006412 | translation | |
| module_41 | GO:0006412 | translation | |
| module_410 | GO:0006412 | translation | |
| module_414 | GO:0006412 | translation | |
| module_443 | GO:0006412 | translation | |
| module_480 | GO:0006412 | translation | |
| module_482 | GO:0006412 | translation | |
| module_491 | GO:0006418 | tRNA aminoacylation for protein translation | |
| module_529 | GO:0006412 | translation | |
| module_569 | GO:0006412 | translation | |
| Slim id: GO:0006464 | | | 18 |
| module_141 | protein modification process | | |
| module_271 | GO:0006468 | protein amino acid phosphorylation | |
| module_271 | GO:0018401 | peptidyl-proline hydroxylation to 4-hydroxy-L-proline | |
| module_271 | GO:0018208 | peptidyl-proline modification | |
| module_271 | GO:0019511 | peptidyl-proline hydroxylation | |
| module_391 | GO:0006468 | protein amino acid phosphorylation | |
| module_403 | GO:0017006 | protein-tetrapyrrole linkage | |
| module_403 | GO:0018298 | protein-chromophore linkage | |
| module_404 | GO:0006468 | protein amino acid phosphorylation | |
| module_404 | GO:0006464 | protein modification process | |
| module_404 | GO:0043687 | post-translational protein modification | |
| module_567 | GO:0043687 | post-translational protein modification | |
| module_567 | GO:0006464 | protein modification process | |
| module_567 | GO:0006468 | protein amino acid phosphorylation | |
| module_581 | GO:0006468 | protein amino acid phosphorylation | |
| module_581 | GO:0043687 | post-translational protein modification | |
| module_592 | GO:0006468 | protein amino acid phosphorylation | |
| module_592 | GO:0006464 | protein modification process | |
| module_592 | GO:0043687 | post-translational protein modification | |
| Slim id: GO:0006519 | | | 39 |
| module_12 | cellular amino acid and derivative metabolic process | | |
| module_12 | GO:0006556 | S-adenosylmethionine biosynthetic process | |
| module_12 | GO:0000097 | sulfur amino acid biosynthetic process | |
| module_12 | GO:0046500 | S-adenosylmethionine metabolic process | |
| module_142 | GO:0006656 | phosphatidylcholine biosynthetic process | |
| module_142 | GO:0006576 | cellular biogenic amine metabolic process | |
| module_142 | GO:0042439 | ethanolamine and derivative metabolic process | |
| module_142 | GO:0046470 | phosphatidylcholine metabolic process | |
| module_236 | GO:0009698 | phenylpropanoid metabolic process | |
| module_236 | GO:0006519 | cellular amino acid and derivative metabolic process | |
| module_236 | GO:0006575 | cellular amino acid derivative metabolic process | |
| module_236 | GO:0009699 | phenylpropanoid biosynthetic process | |
| module_236 | GO:0009812 | flavonoid metabolic process | |
| module_236 | GO:0009813 | flavonoid biosynthetic process | |
| module_236 | GO:0042398 | cellular amino acid derivative biosynthetic process | |
| module_249 | GO:0006558 | L-phenylalanine metabolic process | |
| module_249 | GO:0009698 | phenylpropanoid metabolic process | |
| module_249 | GO:0006519 | cellular amino acid and derivative metabolic process | |
| module_249 | GO:0009072 | aromatic amino acid family metabolic process | |
| module_271 | GO:0018401 | peptidyl-proline hydroxylation to 4-hydroxy-L-proline | |
| module_271 | GO:0019471 | 4-hydroxyproline metabolic process | |
| module_293 | GO:0006418 | tRNA aminoacylation for protein translation | |
| module_293 | GO:0006431 | methionyl-tRNA aminoacylation | |
| module_293 | GO:0006520 | cellular amino acid metabolic process | |
| module_293 | GO:0043038 | amino acid activation | |
| module_293 | GO:0043039 | tRNA aminoacylation | |
| module_296 | GO:0006552 | leucine catabolic process | |
| module_413 | GO:0006573 | valine metabolic process | |
| module_419 | GO:0051555 | flavonol biosynthetic process | |
| module_419 | GO:0051552 | flavone metabolic process | |
| module_419 | GO:0051553 | flavone biosynthetic process | |
| module_419 | GO:0051554 | flavonol metabolic process | |
| module_491 | GO:0006418 | tRNA aminoacylation for protein translation | |
| module_491 | GO:0043038 | amino acid activation | |
| module_491 | GO:0043039 | tRNA aminoacylation | |
| module_502 | GO:0046274 | lignin catabolic process | |
| module_502 | GO:0046271 | phenylpropanoid catabolic process | |
| module_540 | GO:0006552 | leucine catabolic process | |
| module_557 | GO:0030418 | nicotianamine biosynthetic process | |
| module_557 | GO:0030417 | nicotianamine metabolic process | |
| Slim id: GO:0006629 | | | 28 |
| module_118 | lipid metabolic process | | |
| module_118 | GO:0019375 | galactolipid biosynthetic process | |
| module_118 | GO:0006643 | membrane lipid metabolic process | |
| module_118 | GO:0006664 | glycolipid metabolic process | |
| module_118 | GO:0009247 | glycolipid biosynthetic process | |
| module_118 | GO:0019374 | galactolipid metabolic process | |
| module_118 | GO:0046467 | membrane lipid biosynthetic process | |
| module_142 | GO:0006656 | phosphatidylcholine biosynthetic process | |
| module_142 | GO:0006644 | phospholipid metabolic process | |
| module_142 | GO:0006650 | glycerophospholipid metabolic process | |
| module_142 | GO:0008654 | phospholipid biosynthetic process | |
| module_142 | GO:0045017 | glycerolipid biosynthetic process | |
| module_142 | GO:0046470 | phosphatidylcholine metabolic process | |
| module_142 | GO:0046474 | glycerophospholipid biosynthetic process | |
| module_142 | GO:0046486 | glycerolipid metabolic process | |
| module_265 | GO:0006633 | fatty acid biosynthetic process | |
| module_265 | GO:0006631 | fatty acid metabolic process | |
| module_265 | GO:0008610 | lipid biosynthetic process | |
| module_265 | GO:0044255 | cellular lipid metabolic process | |
| module_315 | GO:0010025 | wax biosynthetic process | |
| module_315 | GO:0010166 | wax metabolic process | |
| module_433 | GO:0016119 | carotene metabolic process | |
| module_456 | GO:0045337 | farnesyl diphosphate biosynthetic process | |
| module_456 | GO:0016090 | prenol metabolic process | |
| module_456 | GO:0016091 | prenol biosynthetic process | |
| module_456 | GO:0016093 | polypropenol metabolic process | |
| module_456 | GO:0016094 | polypropenol biosynthetic process | |
| module_456 | GO:0045338 | farnesyl diphosphate metabolic process | |

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|---------------------|--------------------------------------|---|-----|
| module_476 | GO:0010143 | cutin biosynthetic process | |
| Slim id: GO:0006810 | transport | terpenoid transport | 8 |
| module_261 | GO:0046865 | isoprenoid transport | |
| module_261 | GO:0046864 | hexose phosphate transport | |
| module_375 | GO:0015712 | hexose transport | |
| module_375 | GO:0008645 | monosaccharide transport | |
| module_375 | GO:0015749 | malate transport | |
| module_538 | GO:0015743 | dicarboxylic acid transport | |
| module_538 | GO:0006835 | C4-dicarboxylate transport | |
| module_538 | GO:0015740 | | |
| Slim id: GO:0006811 | ion transport | | 2 |
| module_342 | GO:0015700 | arsenite transport | |
| module_544 | GO:0015706 | nitrate transport | |
| Slim id: GO:0006950 | response to stress | | 16 |
| module_277 | GO:0009408 | response to heat | |
| module_277 | GO:0042542 | response to hydrogen peroxide | |
| module_277 | GO:0000302 | response to reactive oxygen species | |
| module_277 | GO:0006950 | response to stress | |
| module_316 | GO:0016068 | type I hypersensitivity | |
| module_316 | GO:0002437 | inflammatory response to antigenic stimulus | |
| module_316 | GO:0002438 | acute inflammatory response to antigenic stimulus | |
| module_316 | GO:0002524 | hypersensitivity | |
| module_316 | GO:0002526 | acute inflammatory response | |
| module_319 | GO:0006979 | response to oxidative stress | |
| module_333 | GO:0009870 | defense response signaling pathway, resistance gene-dependent | |
| module_343 | GO:0009408 | response to heat | |
| module_343 | GO:0006950 | response to stress | |
| module_406 | GO:0009631 | cold acclimation | |
| module_406 | GO:0009414 | response to water deprivation | |
| module_448 | GO:0001666 | response to hypoxia | |
| Slim id: GO:0006996 | organelle organization | | 36 |
| module_167 | GO:0006334 | nucleosome assembly | |
| module_167 | GO:0006325 | chromatin organization | |
| module_167 | GO:0006333 | chromatin assembly or disassembly | |
| module_167 | GO:0006996 | organelle organization | |
| module_167 | GO:0031497 | chromatin assembly | |
| module_167 | GO:0034728 | nucleosome organization | |
| module_167 | GO:0051276 | chromosome organization | |
| module_286 | GO:0006334 | nucleosome assembly | |
| module_286 | GO:0006325 | chromatin organization | |
| module_286 | GO:0006333 | chromatin assembly or disassembly | |
| module_286 | GO:0006996 | organelle organization | |
| module_286 | GO:0031497 | chromatin assembly | |
| module_286 | GO:0034728 | nucleosome organization | |
| module_286 | GO:0051276 | chromosome organization | |
| module_400 | GO:0006334 | nucleosome assembly | |
| module_400 | GO:0006325 | chromatin organization | |
| module_400 | GO:0006333 | chromatin assembly or disassembly | |
| module_400 | GO:0006996 | organelle organization | |
| module_400 | GO:0031497 | chromatin assembly | |
| module_400 | GO:0034728 | nucleosome organization | |
| module_400 | GO:0051276 | chromosome organization | |
| module_408 | GO:0006334 | nucleosome assembly | |
| module_56 | GO:0006325 | chromatin organization | |
| module_56 | GO:0006333 | chromatin assembly or disassembly | |
| module_56 | GO:0006996 | organelle organization | |
| module_56 | GO:0031497 | chromatin assembly | |
| module_56 | GO:0034728 | nucleosome organization | |
| module_56 | GO:0051276 | chromosome organization | |
| module_598 | GO:0006334 | nucleosome assembly | |
| module_598 | GO:0006325 | chromatin organization | |
| module_598 | GO:0006333 | chromatin assembly or disassembly | |
| module_598 | GO:0006996 | organelle organization | |
| module_598 | GO:0031497 | chromatin assembly | |
| module_598 | GO:0034728 | nucleosome organization | |
| module_598 | GO:0051276 | chromosome organization | |
| Slim id: GO:0007005 | mitochondrion organization | | 1 |
| module_485 | GO:0007005 | mitochondrion organization | |
| Slim id: GO:0007010 | cytoskeleton organization | | 1 |
| module_408 | GO:0051225 | spindle assembly | |
| Slim id: GO:0007049 | cell cycle | | 3 |
| module_168 | GO:0007049 | cell cycle | |
| module_408 | GO:0051225 | spindle assembly | |
| module_408 | GO:0007049 | cell cycle | |
| Slim id: GO:0007275 | multicellular organismal development | | 9 |
| module_263 | GO:0048700 | acquisition of desiccation tolerance | |
| module_293 | GO:0048481 | ovule development | |
| module_293 | GO:0048437 | floral organ development | |
| module_293 | GO:0048438 | floral whorl development | |
| module_293 | GO:0048440 | carpel development | |
| module_293 | GO:0048467 | gynoecium development | |
| module_293 | GO:0048569 | post-embryonic organ development | |
| module_589 | GO:0010444 | guard mother cell differentiation | |
| module_589 | GO:0010440 | stomatal lineage progression | |
| Slim id: GO:0008150 | biological_process | | 361 |
| module_113 | GO:0006413 | translational initiation | |
| module_118 | GO:0042550 | photosystem I stabilization | |
| module_118 | GO:0019375 | galactolipid biosynthetic process | |
| module_118 | GO:0006643 | membrane lipid metabolic process | |
| module_118 | GO:0006664 | glycolipid metabolic process | |
| module_118 | GO:0009247 | glycolipid biosynthetic process | |
| module_118 | GO:0010109 | regulation of photosynthesis | |
| module_118 | GO:0019374 | galactolipid metabolic process | |
| module_118 | GO:0042548 | regulation of photosynthesis, light reaction | |
| module_118 | GO:0043467 | regulation of generation of precursor metabolites and energy | |
| module_118 | GO:0046467 | membrane lipid biosynthetic process | |
| module_12 | GO:0006556 | S-adenosylmethionine biosynthetic process | |
| module_12 | GO:0000097 | sulfur amino acid biosynthetic process | |
| module_12 | GO:0046500 | S-adenosylmethionine metabolic process | |
| module_125 | GO:0009853 | photorespiration | |
| module_125 | GO:0043094 | cellular metabolic compound salvage | |
| module_128 | GO:0006878 | cellular copper ion homeostasis | |
| module_128 | GO:0030005 | cellular di-, tri-valent inorganic cation homeostasis | |
| module_128 | GO:0055070 | copper ion homeostasis | |
| module_141 | GO:0006468 | protein amino acid phosphorylation | |
| module_142 | GO:0006656 | phosphatidylcholine biosynthetic process | |
| module_142 | GO:0006576 | cellular biogenic amine metabolic process | |

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| module_142 | GO:0006644 | phospholipid metabolic process |
| module_142 | GO:0006650 | glycerophospholipid metabolic process |
| module_142 | GO:0008654 | phospholipid biosynthetic process |
| module_142 | GO:0042439 | ethanolamine and derivative metabolic process |
| module_142 | GO:0045017 | glycerolipid biosynthetic process |
| module_142 | GO:0046470 | phosphatidylcholine metabolic process |
| module_142 | GO:0046474 | glycerophospholipid biosynthetic process |
| module_142 | GO:0046486 | glycerolipid metabolic process |
| module_167 | GO:0006334 | nucleosome assembly |
| module_167 | GO:0006323 | DNA packaging |
| module_167 | GO:0022607 | cellular component assembly |
| module_167 | GO:0031497 | chromatin assembly |
| module_167 | GO:0034621 | cellular macromolecular complex subunit organization |
| module_167 | GO:0034622 | cellular macromolecular complex assembly |
| module_167 | GO:0034728 | nucleosome organization |
| module_167 | GO:0044085 | cellular component biogenesis |
| module_167 | GO:0065003 | macromolecular complex assembly |
| module_167 | GO:0065004 | protein-DNA complex assembly |
| module_167 | GO:0071103 | DNA conformation change |
| module_170 | GO:0019253 | reductive pentose-phosphate cycle |
| module_170 | GO:0015979 | photosynthesis |
| module_170 | GO:0019685 | photosynthesis, dark reaction |
| module_180 | GO:0006084 | acetyl-CoA metabolic process |
| module_202 | GO:0033014 | tetrapyrrole biosynthetic process |
| module_202 | GO:0033013 | tetrapyrrole metabolic process |
| module_222 | GO:0006364 | rRNA processing |
| module_222 | GO:0006396 | RNA processing |
| module_222 | GO:0016072 | rRNA metabolic process |
| module_222 | GO:0022613 | ribonucleoprotein complex biogenesis |
| module_222 | GO:0034470 | ncRNA processing |
| module_222 | GO:0034660 | ncRNA metabolic process |
| module_222 | GO:0042254 | ribosome biogenesis |
| module_236 | GO:0009698 | phenylpropanoid metabolic process |
| module_236 | GO:0006725 | cellular aromatic compound metabolic process |
| module_236 | GO:0009699 | phenylpropanoid biosynthetic process |
| module_236 | GO:0009812 | flavonoid metabolic process |
| module_236 | GO:0009813 | flavonoid biosynthetic process |
| module_236 | GO:0019438 | aromatic compound biosynthetic process |
| module_236 | GO:0042398 | cellular amino acid derivative biosynthetic process |
| module_237 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_249 | GO:0006558 | L-phenylalanine metabolic process |
| module_249 | GO:0009698 | phenylpropanoid metabolic process |
| module_249 | GO:0019438 | aromatic compound biosynthetic process |
| module_249 | GO:0006725 | cellular aromatic compound metabolic process |
| module_249 | GO:0009072 | aromatic amino acid family metabolic process |
| module_249 | GO:0043648 | dicarboxylic acid metabolic process |
| module_259 | GO:0006511 | ubiquitin-dependent protein catabolic process |
| module_259 | GO:0019941 | modification-dependent protein catabolic process |
| module_259 | GO:0043632 | modification-dependent macromolecule catabolic process |
| module_259 | GO:0044248 | cellular catabolic process |
| module_259 | GO:0044257 | cellular protein catabolic process |
| module_259 | GO:0044265 | cellular macromolecule catabolic process |
| module_259 | GO:0051603 | proteolysis involved in cellular protein catabolic process |
| module_261 | GO:0046865 | terpenoid transport |
| module_261 | GO:0046864 | isoprenoid transport |
| module_263 | GO:0048700 | acquisition of desiccation tolerance |
| module_265 | GO:0006633 | fatty acid biosynthetic process |
| module_265 | GO:0006631 | fatty acid metabolic process |
| module_265 | GO:0016053 | organic acid biosynthetic process |
| module_265 | GO:0032787 | monocarboxylic acid metabolic process |
| module_265 | GO:0044255 | cellular lipid metabolic process |
| module_265 | GO:0046394 | carboxylic acid biosynthetic process |
| module_266 | GO:0006355 | regulation of transcription, DNA-dependent |
| module_266 | GO:0051252 | regulation of RNA metabolic process |
| module_271 | GO:0018401 | peptidyl-proline hydroxylation to 4-hydroxy-L-proline |
| module_271 | GO:0019471 | 4-hydroxyproline metabolic process |
| module_272 | GO:0006096 | glycolysis |
| module_277 | GO:0042542 | response to hydrogen peroxide |
| module_277 | GO:0006457 | protein folding |
| module_277 | GO:0000302 | response to reactive oxygen species |
| module_277 | GO:0010035 | response to inorganic substance |
| module_286 | GO:0006334 | nucleosome assembly |
| module_286 | GO:0006323 | DNA packaging |
| module_286 | GO:0022607 | cellular component assembly |
| module_286 | GO:0031497 | chromatin assembly |
| module_286 | GO:0034621 | cellular macromolecular complex subunit organization |
| module_286 | GO:0034622 | cellular macromolecular complex assembly |
| module_286 | GO:0034728 | nucleosome organization |
| module_286 | GO:0044085 | cellular component biogenesis |
| module_286 | GO:0065003 | macromolecular complex assembly |
| module_286 | GO:0065004 | protein-DNA complex assembly |
| module_286 | GO:0071103 | DNA conformation change |
| module_290 | GO:0042254 | ribosome biogenesis |
| module_290 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_290 | GO:0006414 | translational elongation |
| module_290 | GO:0009987 | cellular process |
| module_290 | GO:0022613 | ribonucleoprotein complex biogenesis |
| module_290 | GO:0044085 | cellular component biogenesis |
| module_290 | GO:0044237 | cellular metabolic process |
| module_290 | GO:0044249 | cellular biosynthetic process |
| module_290 | GO:0044260 | cellular macromolecule metabolic process |
| module_290 | GO:0044267 | cellular protein metabolic process |
| module_293 | GO:0006418 | tRNA aminoacylation for protein translation |
| module_293 | GO:0048481 | ovule development |
| module_293 | GO:0006399 | tRNA metabolic process |
| module_293 | GO:0006431 | methionyl-tRNA aminoacylation |
| module_293 | GO:0006520 | cellular amino acid metabolic process |
| module_293 | GO:0034660 | ncRNA metabolic process |
| module_293 | GO:0043038 | amino acid activation |
| module_293 | GO:0043039 | tRNA aminoacylation |
| module_293 | GO:0044106 | cellular amine metabolic process |
| module_293 | GO:0048437 | floral organ development |
| module_293 | GO:0048438 | floral whorl development |
| module_293 | GO:0048440 | carpel development |
| module_293 | GO:0048467 | gynoecium development |
| module_293 | GO:0048569 | post-embryonic organ development |
| module_296 | GO:0006552 | leucine catabolic process |
| module_303 | GO:0009765 | photosynthesis, light harvesting |
| module_303 | GO:0015979 | photosynthesis |
| module_303 | GO:0009768 | photosynthesis, light harvesting in photosystem I |
| module_303 | GO:0019684 | photosynthesis, light reaction |
| module_313 | GO:0044267 | cellular protein metabolic process |
| module_313 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_313 | GO:0044237 | cellular metabolic process |
| module_313 | GO:0044249 | cellular biosynthetic process |
| module_313 | GO:0044260 | cellular macromolecule metabolic process |
| module_315 | GO:0010025 | wax biosynthetic process |

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|------------|------------|---|
| module_315 | GO:0010166 | wax metabolic process |
| module_316 | GO:0016068 | type I hypersensitivity |
| module_316 | GO:0002250 | adaptive immune response |
| module_316 | GO:0002437 | inflammatory response to antigenic stimulus |
| module_316 | GO:0002438 | acute inflammatory response to antigenic stimulus |
| module_316 | GO:0002443 | leukocyte mediated immunity |
| module_316 | GO:0002449 | lymphocyte mediated immunity |
| module_316 | GO:0002460 | adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains |
| module_316 | GO:0002524 | hypersensitivity |
| module_316 | GO:0016064 | immunoglobulin mediated immune response |
| module_316 | GO:0019724 | B cell mediated immunity |
| module_317 | GO:0009769 | photosynthesis, light harvesting in photosystem II |
| module_317 | GO:0009765 | photosynthesis, light harvesting |
| module_317 | GO:0015979 | photosynthesis |
| module_317 | GO:0019684 | photosynthesis, light reaction |
| module_319 | GO:0006979 | response to oxidative stress |
| module_323 | GO:0009767 | photosynthetic electron transport chain |
| module_323 | GO:0015979 | photosynthesis |
| module_323 | GO:0019684 | photosynthesis, light reaction |
| module_333 | GO:0009870 | defense response signaling pathway, resistance gene-dependent |
| module_355 | GO:0010289 | homogalacturonan biosynthetic process |
| module_355 | GO:0033692 | cellular polysaccharide biosynthetic process |
| module_355 | GO:0034637 | cellular carbohydrate biosynthetic process |
| module_355 | GO:0044264 | cellular polysaccharide metabolic process |
| module_355 | GO:0045489 | pectin biosynthetic process |
| module_356 | GO:0009652 | thigmotropism |
| module_356 | GO:0009606 | tropism |
| module_357 | GO:0055062 | phosphate ion homeostasis |
| module_357 | GO:0030002 | cellular anion homeostasis |
| module_357 | GO:0030319 | cellular di-, tri-valent inorganic anion homeostasis |
| module_357 | GO:0030643 | cellular phosphate ion homeostasis |
| module_357 | GO:0055061 | di-, tri-valent inorganic anion homeostasis |
| module_357 | GO:0055081 | anion homeostasis |
| module_361 | GO:0010477 | response to sulfur dioxide |
| module_371 | GO:0016070 | RNA metabolic process |
| module_380 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_380 | GO:0044249 | cellular biosynthetic process |
| module_380 | GO:0044260 | cellular macromolecule metabolic process |
| module_380 | GO:0044267 | cellular protein metabolic process |
| module_391 | GO:0006468 | protein amino acid phosphorylation |
| module_400 | GO:0006334 | nucleosome assembly |
| module_400 | GO:0006323 | DNA packaging |
| module_400 | GO:0022607 | cellular component assembly |
| module_400 | GO:0031497 | chromatin assembly |
| module_400 | GO:0034621 | cellular macromolecular complex subunit organization |
| module_400 | GO:0034622 | cellular macromolecular complex assembly |
| module_400 | GO:0034728 | nucleosome organization |
| module_400 | GO:0044085 | cellular component biogenesis |
| module_400 | GO:0065003 | macromolecular complex assembly |
| module_400 | GO:0065004 | protein-DNA complex assembly |
| module_400 | GO:0071103 | DNA conformation change |
| module_403 | GO:0007600 | sensory perception |
| module_403 | GO:0010161 | red light signaling pathway |
| module_403 | GO:0003008 | system process |
| module_403 | GO:0050877 | neurological system process |
| module_403 | GO:0071491 | cellular response to red light |
| module_404 | GO:0006468 | protein amino acid phosphorylation |
| module_404 | GO:0006793 | phosphorus metabolic process |
| module_404 | GO:0006796 | phosphate metabolic process |
| module_404 | GO:0016310 | phosphorylation |
| module_406 | GO:0009961 | response to 1-aminocyclopropane-1-carboxylic acid |
| module_406 | GO:0009414 | response to water deprivation |
| module_406 | GO:0009737 | response to abscisic acid stimulus |
| module_406 | GO:0009415 | response to water |
| module_408 | GO:0007018 | microtubule-based movement |
| module_408 | GO:0051225 | spindle assembly |
| module_408 | GO:0007017 | microtubule-based process |
| module_41 | GO:0042254 | ribosome biogenesis |
| module_41 | GO:0022613 | ribonucleoprotein complex biogenesis |
| module_41 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_41 | GO:0044249 | cellular biosynthetic process |
| module_41 | GO:0044260 | cellular macromolecule metabolic process |
| module_41 | GO:0044267 | cellular protein metabolic process |
| module_410 | GO:0042254 | ribosome biogenesis |
| module_410 | GO:0022613 | ribonucleoprotein complex biogenesis |
| module_410 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_410 | GO:0044237 | cellular metabolic process |
| module_410 | GO:0044249 | cellular biosynthetic process |
| module_410 | GO:0044260 | cellular macromolecule metabolic process |
| module_410 | GO:0044267 | cellular protein metabolic process |
| module_413 | GO:0005998 | xylulose catabolic process |
| module_413 | GO:0006573 | valine metabolic process |
| module_413 | GO:0005996 | monosaccharide metabolic process |
| module_413 | GO:0005997 | xylulose metabolic process |
| module_413 | GO:0019323 | pentose catabolic process |
| module_413 | GO:0044275 | cellular carbohydrate catabolic process |
| module_413 | GO:0046365 | monosaccharide catabolic process |
| module_419 | GO:0051555 | flavonol biosynthetic process |
| module_419 | GO:0051552 | flavone metabolic process |
| module_419 | GO:0051553 | flavone biosynthetic process |
| module_419 | GO:0051554 | flavonol metabolic process |
| module_421 | GO:0006796 | phosphate metabolic process |
| module_421 | GO:0006793 | phosphorus metabolic process |
| module_429 | GO:0009765 | photosynthesis, light harvesting |
| module_429 | GO:0019684 | photosynthesis, light reaction |
| module_433 | GO:0016119 | carotene metabolic process |
| module_448 | GO:0001666 | response to hypoxia |
| module_448 | GO:0070482 | response to oxygen levels |
| module_456 | GO:0045337 | farnesyl diphosphate biosynthetic process |
| module_456 | GO:0016090 | prenol metabolic process |
| module_456 | GO:0016091 | prenol biosynthetic process |
| module_456 | GO:0016093 | polyprenol metabolic process |
| module_456 | GO:0016094 | polyprenol biosynthetic process |
| module_456 | GO:0045338 | farnesyl diphosphate metabolic process |
| module_467 | GO:0006457 | protein folding |
| module_467 | GO:0006779 | porphyrin biosynthetic process |
| module_467 | GO:0044237 | cellular metabolic process |
| module_467 | GO:0006778 | porphyrin metabolic process |
| module_467 | GO:0033013 | tetrapyrrole metabolic process |
| module_467 | GO:0033014 | tetrapyrrole biosynthetic process |
| module_467 | GO:0044267 | cellular protein metabolic process |
| module_471 | GO:0043086 | negative regulation of catalytic activity |
| module_471 | GO:0007186 | G-protein coupled receptor protein signaling pathway |
| module_471 | GO:0044092 | negative regulation of molecular function |
| module_473 | GO:0006396 | RNA processing |
| module_476 | GO:0010143 | cutin biosynthetic process |
| module_480 | GO:0034645 | cellular macromolecule biosynthetic process |

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|---------------------|-------------------|--|
| module_480 | GO:0044249 | cellular biosynthetic process |
| module_480 | GO:0044260 | cellular macromolecule metabolic process |
| module_480 | GO:0044267 | cellular protein metabolic process |
| module_491 | GO:0006418 | tRNA aminoacylation for protein translation |
| module_491 | GO:0043038 | amino acid activation |
| module_491 | GO:0043039 | tRNA aminoacylation |
| module_502 | GO:0046274 | lignin catabolic process |
| module_502 | GO:0046271 | phenylpropanoid catabolic process |
| module_521 | GO:0010253 | UDP-rhamnose biosynthetic process |
| module_521 | GO:0009226 | nucleotide-sugar biosynthetic process |
| module_521 | GO:0019299 | rhamnose metabolic process |
| module_521 | GO:0019300 | rhamnose biosynthetic process |
| module_521 | GO:0019319 | hexose biosynthetic process |
| module_521 | GO:0033478 | UDP-rhamnose metabolic process |
| module_529 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_529 | GO:0044249 | cellular biosynthetic process |
| module_529 | GO:0044260 | cellular macromolecule metabolic process |
| module_529 | GO:0044267 | cellular protein metabolic process |
| module_538 | GO:0051453 | regulation of intracellular pH |
| module_538 | GO:0030004 | cellular monovalent inorganic cation homeostasis |
| module_538 | GO:0030641 | regulation of cellular pH |
| module_540 | GO:0006552 | leucine catabolic process |
| module_543 | GO:0019379 | sulfate assimilation, phosphoadenylyl sulfate reduction by phosphoadenylyl-sulfate reductase (thioredoxin) |
| module_543 | GO:0019419 | sulfate reduction |
| module_544 | GO:0010167 | response to nitrate |
| module_548 | GO:0009834 | secondary cell wall biogenesis |
| module_548 | GO:0030244 | cellulose biosynthetic process |
| module_548 | GO:0009832 | plant-type cell wall biogenesis |
| module_548 | GO:0042546 | cell wall biogenesis |
| module_553 | GO:0006268 | DNA unwinding involved in replication |
| module_553 | GO:0006270 | DNA-dependent DNA replication initiation |
| module_553 | GO:0006260 | DNA replication |
| module_553 | GO:0006261 | DNA-dependent DNA replication |
| module_553 | GO:0032392 | DNA geometric change |
| module_553 | GO:0032508 | DNA duplex unwinding |
| module_553 | GO:0034641 | cellular nitrogen compound metabolic process |
| module_553 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_553 | GO:0044260 | cellular macromolecule metabolic process |
| module_553 | GO:0071103 | DNA conformation change |
| module_554 | GO:0006260 | DNA replication |
| module_557 | GO:0030418 | nicotianamine biosynthetic process |
| module_557 | GO:0030417 | nicotianamine metabolic process |
| module_56 | GO:0006334 | nucleosome assembly |
| module_56 | GO:0006323 | DNA packaging |
| module_56 | GO:0022607 | cellular component assembly |
| module_56 | GO:0031497 | chromatin assembly |
| module_56 | GO:0034621 | cellular macromolecular complex subunit organization |
| module_56 | GO:0034622 | cellular macromolecular complex assembly |
| module_56 | GO:0034728 | nucleosome organization |
| module_56 | GO:0044085 | cellular component biogenesis |
| module_56 | GO:0065003 | macromolecular complex assembly |
| module_56 | GO:0065004 | protein-DNA complex assembly |
| module_56 | GO:0071103 | DNA conformation change |
| module_563 | GO:0030244 | cellulose biosynthetic process |
| module_563 | GO:0009832 | plant-type cell wall biogenesis |
| module_563 | GO:0033692 | cellular polysaccharide biosynthetic process |
| module_563 | GO:0034637 | cellular carbohydrate biosynthetic process |
| module_563 | GO:0042546 | cell wall biogenesis |
| module_563 | GO:0044264 | cellular polysaccharide metabolic process |
| module_567 | GO:0006468 | protein amino acid phosphorylation |
| module_567 | GO:0006793 | phosphorus metabolic process |
| module_567 | GO:0006796 | phosphate metabolic process |
| module_567 | GO:0016310 | phosphorylation |
| module_567 | GO:0044267 | cellular protein metabolic process |
| module_569 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_569 | GO:0044267 | cellular protein metabolic process |
| module_581 | GO:0006468 | protein amino acid phosphorylation |
| module_581 | GO:0006793 | phosphorus metabolic process |
| module_581 | GO:0006796 | phosphate metabolic process |
| module_581 | GO:0016310 | phosphorylation |
| module_581 | GO:0034645 | cellular protein metabolic process |
| module_589 | GO:0044267 | cellular macromolecule biosynthetic process |
| module_589 | GO:0006468 | cellular protein metabolic process |
| module_589 | GO:0006793 | protein amino acid phosphorylation |
| module_592 | GO:0006796 | phosphorus metabolic process |
| module_592 | GO:0016310 | phosphate metabolic process |
| module_592 | GO:0006334 | phosphorylation |
| module_598 | GO:0006323 | nucleosome assembly |
| module_598 | GO:0022607 | DNA packaging |
| module_598 | GO:0031497 | cellular component assembly |
| module_598 | GO:0034621 | chromatin assembly |
| module_598 | GO:0034622 | cellular macromolecular complex subunit organization |
| module_598 | GO:0034728 | cellular macromolecular complex assembly |
| module_598 | GO:0044085 | nucleosome organization |
| module_598 | GO:0065003 | cellular component biogenesis |
| module_598 | GO:0065004 | macromolecular complex assembly |
| module_598 | GO:0071103 | protein-DNA complex assembly |
| module_603 | GO:0030244 | DNA conformation change |
| module_603 | GO:0009250 | cellulose biosynthetic process |
| module_606 | GO:0006465 | glucan biosynthetic process |
| module_606 | GO:0006518 | signal peptide processing |
| module_67 | GO:0008535 | peptide metabolic process |
| module_72 | GO:0009739 | respiratory chain complex IV assembly |
| module_82 | GO:0019915 | response to gibberellin stimulus |
| module_86 | GO:0006119 | lipid storage |
| module_94 | GO:0005986 | oxidative phosphorylation |
| module_94 | GO:0005984 | sucrose biosynthetic process |
| module_94 | GO:0005985 | disaccharide metabolic process |
| module_94 | GO:0016137 | sucrose metabolic process |
| module_94 | GO:0016138 | glycoside metabolic process |
| module_94 | GO:0034637 | glycoside biosynthetic process |
| module_94 | GO:0046351 | cellular carbohydrate biosynthetic process |
| Slim id: GO:0008152 | metabolic process | disaccharide biosynthetic process |
| module_118 | GO:0042550 | photosystem I stabilization |
| module_118 | GO:0019375 | galactolipid biosynthetic process |
| module_118 | GO:0006643 | membrane lipid metabolic process |
| module_118 | GO:0006664 | glycolipid metabolic process |
| module_118 | GO:0009247 | glycolipid biosynthetic process |
| module_118 | GO:0010109 | regulation of photosynthesis |
| module_118 | GO:0019374 | galactolipid metabolic process |
| module_118 | GO:0042548 | regulation of photosynthesis, light reaction |
| module_118 | GO:0043467 | regulation of generation of precursor metabolites and energy |
| module_118 | GO:0046467 | membrane lipid biosynthetic process |

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| module_12 | GO:0006556 | S-adenosylmethionine biosynthetic process |
| module_12 | GO:0000097 | sulfur amino acid biosynthetic process |
| module_12 | GO:0009119 | ribonucleoside metabolic process |
| module_12 | GO:0042278 | purine nucleoside metabolic process |
| module_12 | GO:0046128 | purine ribonucleoside metabolic process |
| module_12 | GO:0046500 | S-adenosylmethionine metabolic process |
| module_125 | GO:0009853 | photorespiration |
| module_125 | GO:0043094 | cellular metabolic compound salvage |
| module_141 | GO:0006468 | protein amino acid phosphorylation |
| module_142 | GO:0006656 | phosphatidylcholine biosynthetic process |
| module_142 | GO:0006576 | cellular biogenic amine metabolic process |
| module_142 | GO:0006644 | phospholipid metabolic process |
| module_142 | GO:0006650 | glycerophospholipid metabolic process |
| module_142 | GO:0008654 | phospholipid biosynthetic process |
| module_142 | GO:0019637 | organophosphate metabolic process |
| module_142 | GO:0042439 | ethanolamine and derivative metabolic process |
| module_142 | GO:0045017 | glycerolipid biosynthetic process |
| module_142 | GO:0046470 | phosphatidylcholine metabolic process |
| module_142 | GO:0046474 | glycerophospholipid biosynthetic process |
| module_142 | GO:0046486 | glycerolipid metabolic process |
| module_170 | GO:0019253 | reductive pentose-phosphate cycle |
| module_170 | GO:0015979 | photosynthesis |
| module_170 | GO:0015977 | carbon fixation |
| module_170 | GO:0019685 | photosynthesis, dark reaction |
| module_170 | GO:0071704 | organic substance metabolic process |
| module_180 | GO:0006084 | acetyl-CoA metabolic process |
| module_202 | GO:0033014 | tetrapyrrole biosynthetic process |
| module_202 | GO:0033013 | tetrapyrrole metabolic process |
| module_222 | GO:0006364 | rRNA processing |
| module_222 | GO:0006396 | RNA processing |
| module_222 | GO:0016072 | rRNA metabolic process |
| module_222 | GO:0034470 | ncRNA processing |
| module_222 | GO:0034660 | ncRNA metabolic process |
| module_236 | GO:0009698 | phenylpropanoid metabolic process |
| module_236 | GO:0006725 | cellular aromatic compound metabolic process |
| module_236 | GO:0009699 | phenylpropanoid biosynthetic process |
| module_236 | GO:0009812 | flavonoid metabolic process |
| module_236 | GO:0009813 | flavonoid biosynthetic process |
| module_236 | GO:0019438 | aromatic compound biosynthetic process |
| module_236 | GO:0042398 | cellular amino acid derivative biosynthetic process |
| module_237 | GO:0009059 | macromolecule biosynthetic process |
| module_237 | GO:0010467 | gene expression |
| module_237 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_249 | GO:0006558 | L-phenylalanine metabolic process |
| module_249 | GO:0009698 | phenylpropanoid metabolic process |
| module_249 | GO:0019438 | aromatic compound biosynthetic process |
| module_249 | GO:0006725 | cellular aromatic compound metabolic process |
| module_249 | GO:0009072 | aromatic amino acid family metabolic process |
| module_249 | GO:0043648 | dicarboxylic acid metabolic process |
| module_249 | GO:0044281 | small molecule metabolic process |
| module_259 | GO:0006511 | ubiquitin-dependent protein catabolic process |
| module_259 | GO:0009057 | macromolecule catabolic process |
| module_259 | GO:0019941 | modification-dependent protein catabolic process |
| module_259 | GO:0030163 | protein catabolic process |
| module_259 | GO:0043632 | modification-dependent macromolecule catabolic process |
| module_259 | GO:0044248 | cellular catabolic process |
| module_259 | GO:0044257 | cellular protein catabolic process |
| module_259 | GO:0044265 | cellular macromolecule catabolic process |
| module_259 | GO:0051603 | proteolysis involved in cellular protein catabolic process |
| module_265 | GO:0006633 | fatty acid biosynthetic process |
| module_265 | GO:0006631 | fatty acid metabolic process |
| module_265 | GO:0016053 | organic acid biosynthetic process |
| module_265 | GO:0032787 | monocarboxylic acid metabolic process |
| module_265 | GO:0044255 | cellular lipid metabolic process |
| module_265 | GO:0046394 | carboxylic acid biosynthetic process |
| module_266 | GO:0006355 | regulation of transcription, DNA-dependent |
| module_266 | GO:0051252 | regulation of RNA metabolic process |
| module_271 | GO:0018401 | peptidyl-proline hydroxylation to 4-hydroxy-L-proline |
| module_271 | GO:0019471 | 4-hydroxyproline metabolic process |
| module_272 | GO:0006096 | glycolysis |
| module_277 | GO:0006457 | protein folding |
| module_285 | GO:0010467 | gene expression |
| module_290 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_290 | GO:0010467 | gene expression |
| module_290 | GO:0009059 | macromolecule biosynthetic process |
| module_290 | GO:0006414 | translational elongation |
| module_290 | GO:0008152 | metabolic process |
| module_290 | GO:0043170 | macromolecule metabolic process |
| module_290 | GO:0044237 | cellular metabolic process |
| module_290 | GO:0044249 | cellular biosynthetic process |
| module_290 | GO:0044260 | cellular macromolecule metabolic process |
| module_290 | GO:0044267 | cellular protein metabolic process |
| module_293 | GO:0006418 | tRNA aminoacylation for protein translation |
| module_293 | GO:0006399 | tRNA metabolic process |
| module_293 | GO:0006431 | methionyl-tRNA aminoacylation |
| module_293 | GO:0006520 | cellular amino acid metabolic process |
| module_293 | GO:0034660 | ncRNA metabolic process |
| module_293 | GO:0043038 | amino acid activation |
| module_293 | GO:0043039 | tRNA aminoacylation |
| module_293 | GO:0044106 | cellular amine metabolic process |
| module_296 | GO:0006552 | leucine catabolic process |
| module_303 | GO:0009765 | photosynthesis, light harvesting |
| module_303 | GO:0015979 | photosynthesis |
| module_303 | GO:0009768 | photosynthesis, light harvesting in photosystem I |
| module_303 | GO:0019684 | photosynthesis, light reaction |
| module_313 | GO:0044267 | cellular protein metabolic process |
| module_313 | GO:0009059 | macromolecule biosynthetic process |
| module_313 | GO:0010467 | gene expression |
| module_313 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_313 | GO:0043170 | macromolecule metabolic process |
| module_313 | GO:0044237 | cellular metabolic process |
| module_313 | GO:0044249 | cellular biosynthetic process |
| module_313 | GO:0044260 | cellular macromolecule metabolic process |
| module_315 | GO:0010025 | wax biosynthetic process |
| module_315 | GO:0010166 | wax metabolic process |
| module_317 | GO:0009769 | photosynthesis, light harvesting in photosystem II |
| module_317 | GO:0009765 | photosynthesis, light harvesting |
| module_317 | GO:0015979 | photosynthesis |
| module_317 | GO:0019684 | photosynthesis, light reaction |
| module_323 | GO:0009767 | photosynthetic electron transport chain |
| module_323 | GO:0015979 | photosynthesis |
| module_323 | GO:0019684 | photosynthesis, light reaction |
| module_323 | GO:0022900 | electron transport chain |
| module_355 | GO:0010289 | homogalacturonan biosynthetic process |
| module_355 | GO:0000271 | polysaccharide biosynthetic process |
| module_355 | GO:0005976 | polysaccharide metabolic process |
| module_355 | GO:0033692 | cellular polysaccharide biosynthetic process |

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| module_355 | GO:0034637 | cellular carbohydrate biosynthetic process |
| module_355 | GO:0044264 | cellular polysaccharide metabolic process |
| module_355 | GO:0045488 | pectin metabolic process |
| module_355 | GO:0045489 | pectin biosynthetic process |
| module_358 | GO:0019751 | polyol metabolic process |
| module_371 | GO:0016070 | RNA metabolic process |
| module_378 | GO:0015977 | carbon fixation |
| module_378 | GO:0071704 | organic substance metabolic process |
| module_380 | GO:0009059 | macromolecule biosynthetic process |
| module_380 | GO:0010467 | gene expression |
| module_380 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_380 | GO:0044249 | cellular biosynthetic process |
| module_380 | GO:0044260 | cellular macromolecule metabolic process |
| module_380 | GO:0044267 | cellular protein metabolic process |
| module_391 | GO:0006468 | protein amino acid phosphorylation |
| module_404 | GO:0006468 | protein amino acid phosphorylation |
| module_404 | GO:0006793 | phosphorus metabolic process |
| module_404 | GO:0006796 | phosphate metabolic process |
| module_404 | GO:0016310 | phosphorylation |
| module_404 | GO:0043412 | macromolecule modification |
| module_41 | GO:0009059 | macromolecule biosynthetic process |
| module_41 | GO:0010467 | gene expression |
| module_41 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_41 | GO:0043170 | macromolecule metabolic process |
| module_41 | GO:0044249 | cellular biosynthetic process |
| module_41 | GO:0044260 | cellular macromolecule metabolic process |
| module_41 | GO:0044267 | cellular protein metabolic process |
| module_410 | GO:0009059 | macromolecule biosynthetic process |
| module_410 | GO:0010467 | gene expression |
| module_410 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_410 | GO:0043170 | macromolecule metabolic process |
| module_410 | GO:0044237 | cellular biosynthetic process |
| module_410 | GO:0044249 | cellular macromolecule metabolic process |
| module_410 | GO:0044260 | cellular protein metabolic process |
| module_410 | GO:0044267 | cellular metabolic process |
| module_413 | GO:0005998 | cellular biosynthetic process |
| module_413 | GO:0006573 | xylulose catabolic process |
| module_413 | GO:0005996 | valine metabolic process |
| module_413 | GO:0005997 | monosaccharide metabolic process |
| module_413 | GO:0006066 | xylulose metabolic process |
| module_413 | GO:0019323 | alcohol metabolic process |
| module_413 | GO:0044275 | pentose catabolic process |
| module_413 | GO:0044282 | cellular carbohydrate catabolic process |
| module_413 | GO:0046164 | small molecule catabolic process |
| module_413 | GO:0046365 | alcohol catabolic process |
| module_419 | GO:0051555 | monosaccharide catabolic process |
| module_419 | GO:0051552 | flavonol biosynthetic process |
| module_419 | GO:0051553 | flavone metabolic process |
| module_419 | GO:0051554 | flavone biosynthetic process |
| module_421 | GO:0006796 | flavonol metabolic process |
| module_421 | GO:0006793 | phosphorus metabolic process |
| module_429 | GO:0009765 | photosynthesis, light harvesting |
| module_429 | GO:0019684 | photosynthesis, light reaction |
| module_433 | GO:0016119 | carotene metabolic process |
| module_433 | GO:0042440 | pigment metabolic process |
| module_456 | GO:0045337 | farnesyl diphosphate biosynthetic process |
| module_456 | GO:0016090 | prenol metabolic process |
| module_456 | GO:0016091 | prenol biosynthetic process |
| module_456 | GO:0016093 | polypropenol metabolic process |
| module_456 | GO:0016094 | polypropenol biosynthetic process |
| module_456 | GO:0045338 | farnesyl diphosphate metabolic process |
| module_467 | GO:0006457 | protein folding |
| module_467 | GO:0006779 | porphyrin biosynthetic process |
| module_467 | GO:0044237 | cellular metabolic process |
| module_467 | GO:0006778 | porphyrin metabolic process |
| module_467 | GO:0033013 | tetrapyrrole metabolic process |
| module_467 | GO:0033014 | tetrapyrrole biosynthetic process |
| module_467 | GO:0044267 | cellular protein metabolic process |
| module_471 | GO:0043086 | negative regulation of catalytic activity |
| module_473 | GO:0006396 | RNA processing |
| module_476 | GO:0010143 | cutin biosynthetic process |
| module_480 | GO:0009059 | macromolecule biosynthetic process |
| module_480 | GO:0010467 | gene expression |
| module_480 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_480 | GO:0043170 | macromolecule metabolic process |
| module_480 | GO:0044249 | cellular biosynthetic process |
| module_480 | GO:0044260 | cellular macromolecule metabolic process |
| module_480 | GO:0044267 | cellular protein metabolic process |
| module_491 | GO:0006418 | tRNA aminoacylation for protein translation |
| module_491 | GO:0043038 | amino acid activation |
| module_491 | GO:0043039 | tRNA aminoacylation |
| module_502 | GO:0046274 | lignin catabolic process |
| module_502 | GO:0046271 | phenylpropanoid catabolic process |
| module_521 | GO:0010253 | UDP-rhamnose biosynthetic process |
| module_521 | GO:0009226 | nucleotide-sugar biosynthetic process |
| module_521 | GO:0019299 | rhamnose metabolic process |
| module_521 | GO:0019300 | rhamnose biosynthetic process |
| module_521 | GO:0019319 | hexose biosynthetic process |
| module_521 | GO:0033478 | UDP-rhamnose metabolic process |
| module_529 | GO:0009059 | macromolecule biosynthetic process |
| module_529 | GO:0010467 | gene expression |
| module_529 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_529 | GO:0044249 | cellular biosynthetic process |
| module_529 | GO:0044260 | cellular macromolecule metabolic process |
| module_529 | GO:0044267 | cellular protein metabolic process |
| module_540 | GO:0006552 | leucine catabolic process |
| module_543 | GO:0019379 | sulfate assimilation, phosphoadenylyl sulfate reduction by phosphoadenylyl-sulfate reductase (thioredoxin) |
| module_543 | GO:0019419 | sulfate reduction |
| module_548 | GO:0030244 | cellulose biosynthetic process |
| module_548 | GO:0030243 | cellulose metabolic process |
| module_553 | GO:0006268 | DNA unwinding involved in replication |
| module_553 | GO:0006270 | DNA-dependent DNA replication initiation |
| module_553 | GO:0006260 | DNA replication |
| module_553 | GO:0006261 | DNA-dependent DNA replication |
| module_553 | GO:0006807 | nitrogen compound metabolic process |
| module_553 | GO:0009059 | macromolecule biosynthetic process |
| module_553 | GO:0034641 | cellular nitrogen compound metabolic process |
| module_553 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_553 | GO:0043170 | macromolecule metabolic process |
| module_553 | GO:0044260 | cellular macromolecule metabolic process |
| module_554 | GO:0006260 | DNA replication |
| module_557 | GO:0030418 | nicotianamine biosynthetic process |
| module_557 | GO:0030417 | nicotianamine metabolic process |
| module_563 | GO:0030244 | cellulose biosynthetic process |
| module_563 | GO:0000271 | polysaccharide biosynthetic process |
| module_563 | GO:0005976 | polysaccharide metabolic process |
| module_563 | GO:0030243 | cellulose metabolic process |

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| module_563 | GO:0033692 | cellular polysaccharide biosynthetic process |
| module_563 | GO:0034637 | cellular carbohydrate biosynthetic process |
| module_563 | GO:0044264 | cellular polysaccharide metabolic process |
| module_567 | GO:0006468 | protein amino acid phosphorylation |
| module_567 | GO:0006793 | phosphorus metabolic process |
| module_567 | GO:0006796 | phosphate metabolic process |
| module_567 | GO:0016310 | phosphorylation |
| module_567 | GO:0043412 | macromolecule modification |
| module_567 | GO:0044267 | cellular protein metabolic process |
| module_569 | GO:0009059 | macromolecule biosynthetic process |
| module_569 | GO:0010467 | gene expression |
| module_569 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_569 | GO:0043170 | macromolecule metabolic process |
| module_569 | GO:0044267 | cellular protein metabolic process |
| module_581 | GO:0006468 | protein amino acid phosphorylation |
| module_581 | GO:0006793 | phosphorus metabolic process |
| module_581 | GO:0006796 | phosphate metabolic process |
| module_581 | GO:0016310 | phosphorylation |
| module_589 | GO:0019252 | starch biosynthetic process |
| module_589 | GO:0005982 | starch metabolic process |
| module_589 | GO:0010021 | amylopectin biosynthetic process |
| module_592 | GO:0006468 | protein amino acid phosphorylation |
| module_592 | GO:0006793 | phosphorus metabolic process |
| module_592 | GO:0006796 | phosphate metabolic process |
| module_592 | GO:0016310 | phosphorylation |
| module_603 | GO:0030244 | macromolecule modification |
| module_603 | GO:0009250 | cellulose biosynthetic process |
| module_603 | GO:0030243 | glucan biosynthetic process |
| module_606 | GO:0006465 | cellulose metabolic process |
| module_606 | GO:0006518 | signal peptide processing |
| module_606 | GO:0016485 | peptide metabolic process |
| module_606 | GO:0051604 | protein processing |
| module_606 | GO:0051605 | protein maturation |
| module_86 | GO:0006119 | protein maturation by peptide bond cleavage |
| module_94 | GO:0005986 | oxidative phosphorylation |
| module_94 | GO:0005984 | sucrose biosynthetic process |
| module_94 | GO:0005985 | disaccharide metabolic process |
| module_94 | GO:0016137 | sucrose metabolic process |
| module_94 | GO:0016138 | glycoside metabolic process |
| module_94 | GO:0034637 | glycoside biosynthetic process |
| module_94 | GO:0046351 | cellular carbohydrate biosynthetic process |
| Slim id: GO:0008283 | cell proliferation | 1 |
| module_553 | GO:0008283 | cell proliferation |
| Slim id: GO:0009056 | catabolic process | 22 |
| module_259 | GO:0006511 | ubiquitin-dependent protein catabolic process |
| module_259 | GO:0009056 | catabolic process |
| module_259 | GO:0009057 | macromolecule catabolic process |
| module_259 | GO:0019941 | modification-dependent protein catabolic process |
| module_259 | GO:0030163 | protein catabolic process |
| module_259 | GO:0043632 | modification-dependent macromolecule catabolic process |
| module_259 | GO:0044248 | cellular catabolic process |
| module_259 | GO:0044257 | cellular protein catabolic process |
| module_259 | GO:0044265 | cellular macromolecule catabolic process |
| module_259 | GO:0051603 | proteolysis involved in cellular protein catabolic process |
| module_272 | GO:0006096 | glycolysis |
| module_296 | GO:0006552 | leucine catabolic process |
| module_413 | GO:0005998 | xylulose catabolic process |
| module_413 | GO:0016052 | carbohydrate catabolic process |
| module_413 | GO:0019323 | pentose catabolic process |
| module_413 | GO:0044275 | cellular carbohydrate catabolic process |
| module_413 | GO:0044282 | small molecule catabolic process |
| module_413 | GO:0046164 | alcohol catabolic process |
| module_413 | GO:0046365 | monosaccharide catabolic process |
| module_502 | GO:0046274 | lignin catabolic process |
| module_502 | GO:0046271 | phenylpropanoid catabolic process |
| module_540 | GO:0006552 | leucine catabolic process |
| Slim id: GO:0009058 | biosynthetic process | 99 |
| module_118 | GO:0019375 | galactolipid biosynthetic process |
| module_118 | GO:0009247 | glycolipid biosynthetic process |
| module_118 | GO:0046467 | membrane lipid biosynthetic process |
| module_12 | GO:0006556 | S-adenosylmethionine biosynthetic process |
| module_12 | GO:0000097 | sulfur amino acid biosynthetic process |
| module_125 | GO:0009853 | photorespiration |
| module_125 | GO:0043094 | cellular metabolic compound salvage |
| module_142 | GO:0006656 | phosphatidylcholine biosynthetic process |
| module_142 | GO:0008654 | phospholipid biosynthetic process |
| module_142 | GO:0045017 | glycerolipid biosynthetic process |
| module_142 | GO:0046474 | glycerophospholipid biosynthetic process |
| module_170 | GO:0019253 | reductive pentose-phosphate cycle |
| module_170 | GO:0019685 | photosynthesis, dark reaction |
| module_202 | GO:0033014 | tetrapyrrole biosynthetic process |
| module_236 | GO:0009699 | phenylpropanoid biosynthetic process |
| module_236 | GO:0009813 | flavonoid biosynthetic process |
| module_236 | GO:0019438 | aromatic compound biosynthetic process |
| module_236 | GO:0042398 | cellular amino acid derivative biosynthetic process |
| module_237 | GO:0009059 | macromolecule biosynthetic process |
| module_237 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_249 | GO:0019438 | aromatic compound biosynthetic process |
| module_265 | GO:0006633 | fatty acid biosynthetic process |
| module_265 | GO:0008610 | lipid biosynthetic process |
| module_265 | GO:0016053 | organic acid biosynthetic process |
| module_265 | GO:0046394 | carboxylic acid biosynthetic process |
| module_266 | GO:0006355 | regulation of transcription, DNA-dependent |
| module_290 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_290 | GO:0009059 | macromolecule biosynthetic process |
| module_290 | GO:0006414 | translational elongation |
| module_290 | GO:0009058 | biosynthetic process |
| module_290 | GO:0044249 | cellular biosynthetic process |
| module_313 | GO:0009058 | biosynthetic process |
| module_313 | GO:0009059 | macromolecule biosynthetic process |
| module_313 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_313 | GO:0044249 | cellular biosynthetic process |
| module_315 | GO:0010025 | wax biosynthetic process |
| module_355 | GO:0010289 | homogalacturonan biosynthetic process |
| module_355 | GO:0000271 | polysaccharide biosynthetic process |
| module_355 | GO:0016051 | carbohydrate biosynthetic process |
| module_355 | GO:0033692 | cellular polysaccharide biosynthetic process |
| module_355 | GO:0034637 | cellular carbohydrate biosynthetic process |
| module_355 | GO:0045489 | pectin biosynthetic process |
| module_380 | GO:0009058 | biosynthetic process |
| module_380 | GO:0009059 | macromolecule biosynthetic process |
| module_380 | GO:0034645 | cellular macromolecule biosynthetic process |
| module_380 | GO:0044249 | cellular biosynthetic process |

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|---------------------|--|---|---|
| module_41 | GO:0009058 GO:0009059 GO:0034645 GO:0044249 GO:0009058 GO:0009059 GO:0034645 GO:0044249 GO:0051555 GO:0051553 GO:0045337 GO:0016091 GO:0016094 GO:0006779 GO:0033014 GO:0010143 GO:0009058 GO:0009059 GO:0034645 GO:0044249 GO:0010253 GO:0009226 GO:0019300 GO:0019319 GO:0009058 GO:0009059 GO:0034645 GO:0044249 GO:0030244 GO:0006268 GO:0006270 GO:0006260 GO:0006261 GO:0009059 GO:0034645 GO:0006260 GO:0030418 GO:0030244 GO:0000271 GO:0033692 GO:0034637 GO:0009059 GO:0034645 GO:0019252 GO:0010021 GO:0030244 GO:0009250 GO:0005986 GO:0009312 GO:0016051 GO:0016138 GO:0034637 GO:0046351 | biosynthetic process macromolecule biosynthetic process cellular macromolecule biosynthetic process cellular biosynthetic process biosynthetic process macromolecule biosynthetic process cellular macromolecule biosynthetic process cellular biosynthetic process flavonol biosynthetic process flavone biosynthetic process farnesyl diphosphate biosynthetic process prenol biosynthetic process polypropenol biosynthetic process porphyrin biosynthetic process tetrapterrole biosynthetic process cutin biosynthetic process biosynthetic process macromolecule biosynthetic process cellular macromolecule biosynthetic process cellular biosynthetic process UDP–rhamnose biosynthetic process nucleotide–sugar biosynthetic process rhamnose biosynthetic process hexose biosynthetic process biosynthetic process macromolecule biosynthetic process cellular macromolecule biosynthetic process cellular biosynthetic process cellulose biosynthetic process DNA unwinding involved in replication DNA-dependent DNA replication initiation DNA replication DNA-dependent DNA replication macromolecule biosynthetic process cellular macromolecule biosynthetic process cellular biosynthetic process cellulose biosynthetic process polysaccharide biosynthetic process cellular polysaccharide biosynthetic process cellular carbohydrate biosynthetic process macromolecule biosynthetic process cellular macromolecule biosynthetic process starch biosynthetic process amylopectin biosynthetic process cellulose biosynthetic process glucan biosynthetic process sucrose biosynthetic process oligosaccharide biosynthetic process carbohydrate biosynthetic process glycoside biosynthetic process cellular carbohydrate biosynthetic process disaccharide biosynthetic process | |
| Slim id: GO:0009605 | response to external stimulus GO:0009652 GO:0009606 GO:0009612 | 3 | thigmotropism tropism response to mechanical stimulus |
| Slim id: GO:0009628 | response to abiotic stimulus GO:0009411 GO:0009408 GO:0009644 GO:0009266 GO:0009628 GO:0009642 GO:0010114 GO:0010218 GO:0009637 GO:0009408 GO:0009266 GO:0009628 GO:0009652 GO:0009612 GO:0010201 GO:0010203 GO:0010161 GO:0055122 GO:0071491 GO:0009631 GO:0009414 GO:0009415 GO:0009644 GO:0009416 GO:0009314 | 25 | response to UV response to heat response to high light intensity response to temperature stimulus response to abiotic stimulus response to light intensity response to red light response to far red light response to blue light response to heat response to temperature stimulus response to abiotic stimulus thigmotropism response to mechanical stimulus response to continuous far red light stimulus by the high–irradiance response system response to very low fluence red light stimulus red light signaling pathway response to very low light intensity stimulus cellular response to red light cold acclimation response to water deprivation response to water response to high light intensity response to light stimulus response to radiation |
| Slim id: GO:0009719 | response to endogenous stimulus GO:0009961 GO:0009737 GO:0009739 | 3 | response to 1–aminocyclopropane–1–carboxylic acid response to abscisic acid stimulus response to gibberellin stimulus |
| Slim id: GO:0009790 | embryo development GO:0009790 | 1 | embryo development |
| Slim id: GO:0016043 | cellular component organization GO:0006334 GO:0006323 GO:0016043 GO:0022607 GO:0031497 GO:0034621 GO:0034622 GO:0034728 GO:0043933 GO:0065003 GO:0065004 GO:0006334 GO:0006323 GO:0016043 GO:0022607 GO:0031497 GO:0034621 GO:0034622 GO:0034728 GO:0043933 GO:0065003 GO:0065004 | 56 | nucleosome assembly DNA packaging cellular component organization cellular component assembly chromatin assembly cellular macromolecular complex subunit organization cellular macromolecular complex assembly nucleosome organization macromolecular complex subunit organization macromolecular complex assembly protein–DNA complex assembly nucleosome assembly DNA packaging cellular component organization cellular component assembly chromatin assembly cellular macromolecular complex subunit organization cellular macromolecular complex assembly nucleosome organization macromolecular complex subunit organization macromolecular complex assembly protein–DNA complex assembly |

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| module_400 | GO:0006334 | nucleosome assembly |
| module_400 | GO:0006323 | DNA packaging |
| module_400 | GO:0022607 | cellular component assembly |
| module_400 | GO:0031497 | chromatin assembly |
| module_400 | GO:0034621 | cellular macromolecular complex subunit organization |
| module_400 | GO:0034622 | cellular macromolecular complex assembly |
| module_400 | GO:0034728 | nucleosome organization |
| module_400 | GO:0043933 | macromolecular complex subunit organization |
| module_400 | GO:0065003 | macromolecular complex assembly |
| module_400 | GO:0065004 | protein-DNA complex assembly |
| module_408 | GO:0051225 | spindle assembly |
| module_56 | GO:0006334 | nucleosome assembly |
| module_56 | GO:0006323 | DNA packaging |
| module_56 | GO:0016043 | cellular component organization |
| module_56 | GO:0022607 | cellular component assembly |
| module_56 | GO:0031497 | chromatin assembly |
| module_56 | GO:0034621 | cellular macromolecular complex subunit organization |
| module_56 | GO:0034622 | cellular macromolecular complex assembly |
| module_56 | GO:0034728 | nucleosome organization |
| module_56 | GO:0043933 | macromolecular complex subunit organization |
| module_56 | GO:0065003 | macromolecular complex assembly |
| module_56 | GO:0065004 | protein-DNA complex assembly |
| module_598 | GO:0006334 | nucleosome assembly |
| module_598 | GO:0006323 | DNA packaging |
| module_598 | GO:0016043 | cellular component organization |
| module_598 | GO:0022607 | cellular component assembly |
| module_598 | GO:0031497 | chromatin assembly |
| module_598 | GO:0034621 | cellular macromolecular complex subunit organization |
| module_598 | GO:0034622 | cellular macromolecular complex assembly |
| module_598 | GO:0034728 | nucleosome organization |
| module_598 | GO:0043933 | macromolecular complex subunit organization |
| module_598 | GO:0065003 | macromolecular complex assembly |
| module_598 | GO:0065004 | protein-DNA complex assembly |
| module_67 | GO:0008535 | respiratory chain complex IV assembly |
| Slim id: GO:0019538 | protein metabolic process | 31 |
| module_259 | GO:0006511 | ubiquitin-dependent protein catabolic process |
| module_259 | GO:0006508 | proteolysis |
| module_259 | GO:0019941 | modification-dependent protein catabolic process |
| module_259 | GO:0030163 | protein catabolic process |
| module_259 | GO:0044257 | cellular protein catabolic process |
| module_259 | GO:0051603 | proteolysis involved in cellular protein catabolic process |
| module_277 | GO:0006457 | protein folding |
| module_290 | GO:0019538 | protein metabolic process |
| module_290 | GO:0044267 | cellular protein metabolic process |
| module_313 | GO:0044267 | cellular protein metabolic process |
| module_313 | GO:0019538 | protein metabolic process |
| module_380 | GO:0019538 | protein metabolic process |
| module_380 | GO:0044267 | cellular protein metabolic process |
| module_41 | GO:0019538 | protein metabolic process |
| module_41 | GO:0044267 | cellular protein metabolic process |
| module_410 | GO:0019538 | protein metabolic process |
| module_410 | GO:0044267 | cellular protein metabolic process |
| module_467 | GO:0006457 | protein folding |
| module_467 | GO:0044267 | cellular protein metabolic process |
| module_480 | GO:0019538 | protein metabolic process |
| module_480 | GO:0044267 | cellular protein metabolic process |
| module_529 | GO:0019538 | protein metabolic process |
| module_529 | GO:0044267 | cellular protein metabolic process |
| module_567 | GO:0019538 | protein metabolic process |
| module_567 | GO:0044267 | cellular protein metabolic process |
| module_569 | GO:0019538 | protein metabolic process |
| module_569 | GO:0044267 | cellular protein metabolic process |
| module_606 | GO:0006465 | signal peptide processing |
| module_606 | GO:0016485 | protein processing |
| module_606 | GO:0051604 | protein maturation |
| module_606 | GO:0051605 | protein maturation by peptide bond cleavage |
| Slim id: GO:0019725 | cellular homeostasis | 8 |
| module_128 | GO:0006878 | cellular copper ion homeostasis |
| module_128 | GO:0030005 | cellular di-, tri-valent inorganic cation homeostasis |
| module_357 | GO:0030002 | cellular anion homeostasis |
| module_357 | GO:0030319 | cellular di-, tri-valent inorganic anion homeostasis |
| module_357 | GO:0030643 | cellular phosphate ion homeostasis |
| module_538 | GO:0051453 | regulation of intracellular pH |
| module_538 | GO:0030004 | cellular monovalent inorganic cation homeostasis |
| module_538 | GO:0030641 | regulation of cellular pH |
| Slim id: GO:0019748 | secondary metabolic process | 13 |
| module_236 | GO:0009698 | phenylpropanoid metabolic process |
| module_236 | GO:0009699 | phenylpropanoid biosynthetic process |
| module_236 | GO:0009812 | flavonoid metabolic process |
| module_236 | GO:0009813 | flavonoid biosynthetic process |
| module_236 | GO:0019748 | secondary metabolic process |
| module_249 | GO:0009698 | phenylpropanoid metabolic process |
| module_419 | GO:0051555 | flavonol biosynthetic process |
| module_419 | GO:0051552 | flavone metabolic process |
| module_419 | GO:0051553 | flavone biosynthetic process |
| module_419 | GO:0051554 | flavonol metabolic process |
| module_433 | GO:0016119 | carotene metabolic process |
| module_502 | GO:0046274 | lignin catabolic process |
| module_502 | GO:0046271 | phenylpropanoid catabolic process |
| Slim id: GO:0030154 | cell differentiation | 1 |
| module_589 | GO:0010444 | guard mother cell differentiation |
| Slim id: GO:0044238 | primary metabolic process | 5 |
| module_266 | GO:0006355 | regulation of transcription, DNA-dependent |
| module_266 | GO:0051252 | regulation of RNA metabolic process |
| module_290 | GO:0044238 | primary metabolic process |
| module_313 | GO:0044238 | primary metabolic process |
| module_410 | GO:0044238 | primary metabolic process |
| Slim id: GO:0050789 | regulation of biological process | 8 |
| module_118 | GO:0042550 | photosystem I stabilization |
| module_118 | GO:0010109 | regulation of photosynthesis |
| module_118 | GO:0042548 | regulation of photosynthesis, light reaction |
| module_118 | GO:0043467 | regulation of generation of precursor metabolites and energy |
| module_266 | GO:0006355 | regulation of transcription, DNA-dependent |
| module_266 | GO:0051252 | regulation of RNA metabolic process |
| module_333 | GO:0009870 | defense response signaling pathway, resistance gene-dependent |
| module_471 | GO:0043086 | negative regulation of catalytic activity |