| | | | | 8 |
|----------|---------|----------|---|---|
| | | | sulfur compound metabolic process (GO:0006790) | 0 |
| | | | regulation of sister chromatid cohesion (GO:0007063) | |
| | | | regulation of MHC class II biosynthetic process (GO:0045346) | |
| | | | post-embryonic development (GO:0009791) | |
| | | | oocyte development (GO:0048599) | 6 |
| | | | negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator (GO:1902254) | |
| | | | macrophage differentiation (GO:0030225) | |
| | | | linoleic acid metabolic process (GO:0043651) | |
| | | | histone H4 deacetylation (GO:0070933) | 4 |
| | | | granulocyte differentiation (GO:0030851) | 4 |
| | | | fatty acid beta-oxidation using acyl-CoA oxidase (GO:0033540) | |
| | | | embryo development (GO:0009790) | |
| | | | alpha–linolenic acid metabolic process (GO:0036109) | |
| | | | anatomical structure arrangement (GO:0048532) | 2 |
| | | | pyridine nucleotide metabolic process (GO:0019362) | _ |
| | | | nicotinamide nucleotide metabolic process (GO:0046496) | |
| | | | monosaccharide catabolic process (GO:0046365) | |
| | | | hexose catabolic process (GO:0019320) | |
| | | | hexose biosynthetic process (GO:0019319) | 0 |
| | | | glycolytic process (GO:0006096) | |
| | | | cellular aldehyde metabolic process (GO:0006081) | |
| | | | gluconeogenesis (GO:0006094) | |
| | | | synaptic vesicle maturation (GO:0016188) | |
| | | | protein palmitoylation (GO:0018345) | |
| | | | pentose–phosphate shunt (GO:0006098) | |
| | | | NADPH regeneration (GO:0006740) | |
| | | | glucose catabolic process (GO:0006007) | |
| | | | NADP metabolic process (GO:0006739) | |
| | | | midbrain development (GO:0030901) | |
| | | | forebrain morphogenesis (GO:0048853) | |
| | | | lateral ventricle development (GO:0021670) | |
| | | | proteolysis involved in cellular protein catabolic process (GO:0051603) | |
| | | | ubiquitin-dependent protein catabolic process (GO:0006511) | |
| | | | modification-dependent macromolecule catabolic process (GO:0043632) | |
| | | | modification-dependent protein catabolic process (GO:0019941) | |
| | | | energy derivation by oxidation of organic compounds (GO:0015980) | |
| | | | energy reserve metabolic process (GO:0006112) | |
| | | | insulin secretion (GO:0030073) | |
| | | | signal release (GO:0023061) | |
| | | | regulation of peptide secretion (GO:0002791) | |
| | | | regulation of peptide hormone secretion (GO:0090276) | |
| | | | regulation of insulin secretion (GO:0050796) carbohydrate homeostasis (GO:0033500) | |
| | | | glucose homeostasis (GO:0033500) | |
| | | | | |
| | | | amide transport (GO:0042886) peptide transport (GO:0015833) | |
| | | | peptide secretion (GO:0002790) | |
| | | | peptide secretion (GO:0002730) peptide hormone secretion (GO:0030072) | |
| | | | hormone secretion (GO:0046879) | |
| | | | hormone transport (GO:0009914) | |
| | | | positive regulation of GTP catabolic process (GO:0033126) | |
| | | | positive regulation of GTPase activity (GO:0043547) | |
| | | | regulation of small GTPase mediated signal transduction (GO:0051056) | |
| | | | small GTPase mediated signal transduction (GO:0007264) | |
| | | | filopodium assembly (GO:0046847) | |
| | | | regulation of Cdc42 GTPase activity (GO:0043088) | |
| | | | multicellular organismal development (GO:0007275) | |
| | | | regulation of Rho GTPase activity (GO:0032319) | |
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