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| **Select Polysaccharide Metabolism** **Gene/Protein Name**  |  **Source Organism** | **E-value** | **Fold of Increase** | **Comments on Function** |
| Exopolysaccharide phosphotransferase SCO6023 | *Streptomyces coelicolor* A3(2) | 6.00E-30 | 1.49591002 | Identified as a stealth protein. Stealth proteins are part of a protein family that is conserved from bacteria to higher eukaryotes. Family members were first identified in microbes as proteins that help pathogens to elude the host innate immune system. Microbial stealth proteins are involved in the biosynthesis of exopolysaccharides. Stealth proteins are predicted to function as hexose-1-phosphoryltransferases.Bentley et al. 2002<http://www.ncbi.nlm.nih.gov/protein/O69853> |
| Chitinase 1 | *Tulipa bakeri* | 2.00E-08 | 1.49591002 | Able to cleave glycolchitin.Yamagami et al. 2000<http://www.ncbi.nlm.nih.gov/protein/Q9SLP4> |
| Thermophilic beta-amylase | *Thermoanaerobacterium thermosulfurigenes* | 4.00E-89 | 1.49591002 | Hydrolysis of (1->4)-alpha-D-glucosidic linkages in polysaccharides so as to remove successive maltose units from the non-reducing ends of the chains.Kitamoto et al. 1988<http://www.ncbi.nlm.nih.gov/protein/p19584> |
| 42 kDa endochitinase | *Hypocrea lixii* | 2.00E-08 | 1.49591002 | Morphogenetic role during apical growth, cell division and differentiation (cell wall morphogenesis). Antifungal agent.Garcia et al. 1994<http://www.ncbi.nlm.nih.gov/protein/P48827> |
| Chitotriosidase-1 | *Mus musculus* | 1.00E-30 | 1.49591002 | Degrades chitin, chitotriose and chitobiose. May participate in the defense against nematodes and other pathogens.Zheng et al. 2005<http://www.ncbi.nlm.nih.gov/protein/Q9D7Q1> |
| Serine/threonine-protein phosphatase PP1-gamma catalytic subunit | *Xenopus (Silurana) tropicalis* | 3.00E-158 | 1.49591002 | Protein phosphatase 1 (PP1) is essential for cell division, and participates in the regulation of glycogen metabolism, muscle contractility and protein synthesis. Promotes nuclear envelope reassembly by targeting nuclear membrane vesicles to chromatin at the end of mitosis. Acts by dephosphorylating membrane proteins such as lamin B receptor (lbr) to regulate the binding of membrane proteins to chromatin.Direct submission<http://www.ncbi.nlm.nih.gov/protein/Q6NVU2> |
| UDP-galactose transporter | S*chizosaccharomyces pombe* 972h- | 3.00E-69 | 1.559645535 | Essential for the transport of UDP-galactose into the lumen of Golgi apparatus.Segawa et al. 1999<http://www.ncbi.nlm.nih.gov/protein/p87041> |
| UDP-3-O-acylglucosamine N-acyltransferase | *Brucella suis* 1330 | 1.00E-23 | 1.559645535 | Catalyzes the N-acylation of UDP-3-O-acylglucosamine using 3-hydroxyacyl-ACP as the acyl donor. Is involved in the biosynthesis of lipid A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer membrane of the cell.Paulsen et al. 2002<http://www.ncbi.nlm.nih.gov/protein/p0a3p5> |
| GPI mannosyltransferase 1 | *Arabidopsis thaliana* | 6.00E-103 | 1.559645535 | Mannosyltransferase involved in glycosylphosphatidylinositol-anchor biosynthesis. Transfers the first alpha-1,4-mannose to GlcN-acyl-PI during GPI precursor assembly.Tabata et al. 2000<http://www.ncbi.nlm.nih.gov/protein/q500w7> |
| 2-dehydro-3-deoxyphosphooctonate aldolase | *Arabidopsis thaliana* | 1.00E-19 | 1.559645535 | Synthesis of KDO 8-P which is required for lipid A maturation and cellular growth.Matsura et al. 2003<http://www.ncbi.nlm.nih.gov/protein/Q9AV97> |
| Glycogenin-2 | *Homo sapiens* | 2.00E-22 | 1.559645535 | Self-glucosylates, via an inter-subunit mechanism, to form an oligosaccharide primer that serves as substrate for glycogen synthase.Mu et al. 1997<http://www.ncbi.nlm.nih.gov/protein/o15488> |
| Methionine adenosyltransferase 2 subunit beta | *Danio rerio* | 2.00E-22 | 1.559645535 | Non-catalytic regulatory subunit of S-adenosylmethionine synthetase 2 (MAT2A), an enzyme that catalyzes the formation of S-adenosylmethionine from methionine and ATP. Regulates the activity of S-adenosylmethionine synthetase 2 by changing its kinetic properties, rendering the enzyme more susceptible to S-adenosylmethionine inhibition.Direct submission<http://www.ncbi.nlm.nih.gov/protein/Q5BJJ6> |
| 3-deoxy-D-manno-octulosonic-acid transferase | *Haemophilus influenzae* Rd KW20 | 5.00E-15 | 1.559645535 | Essential step in lipopolysaccharides biosynthesis. Acts at transfer of 3-deoxy-D-mono octulonic acid (KDO) from CMP-KDO to a tetraacyldisaccharide 1,4'-bisphosphate precursor of lipid A (lipid IVA). Transfers a single molecule of KDO to lipid IVA. Brabetz et al. 2000<http://www.ncbi.nlm.nih.gov/protein/P44806> |
| Lipid-A-disaccharide synthase | *Nitrobacter winogradskyi* Nb-255 | 2.00E-16 | 1.559645535 | Condensation of UDP-2,3-diacylglucosamine and 2,3-diacylglucosamine-1-phosphate to form lipid A disaccharide, a precursor of lipid A, a phosphorylated glycolipid that anchors the lipopolysaccharide to the outer membrane of the cell.Sterkenburg et al. 2006<http://www.ncbi.nlm.nih.gov/protein/Q3SRI5> |
|  Feruloyl esterase A | *Aspergillus awamori* | 8.00E-06 | 1.585726564 | Involved in the degradation of plant cell walls. Hydrolyzes the feruloyl-arabinose ester bond in arabinoxylans, and the feruloyl-galactose ester bond in pectin. Active against methyl ferulate, methyl sinapate, methyl caffeate, and alpha-naphthyl esters with chains containing 2 to 8 carbons (C2-C8). Inactive against alpha-naphthyl esters with longer chains (C10 or more).Koseki et al. 2005<http://www.ncbi.nlm.nih.gov/protein/q9p979> |
| Carbohydrate-binding domain-containing protein C2E1P3.05c | *Schizosaccharomyces pombe* 972h- | 2.00E-12 | 1.49591002 | Carbohydrate-binding module (CBM) is a [protein domain](http://en.wikipedia.org/wiki/Protein_domain) found in [carbohydrate](http://en.wikipedia.org/wiki/Carbohydrate)-active enzymes (for example [glycoside hydrolases](http://en.wikipedia.org/wiki/Glycoside_hydrolases)). The majority of these domains have carbohydrate-binding activity.Wood et al. 2002<http://www.ncbi.nlm.nih.gov/protein/q9p7f1> |
| Serine/threonine-protein phosphatase PP1-alpha catalytic subunit | *Mus musculus* | 4.00E-116 | 1.585726564 | Protein phosphatase that associates with over 200 regulatory proteins to form highly specific holoenzymes which dephosphorylate hundreds of biological targets. Essential for cell division, and participates in the regulation of glycogen metabolism, muscle contractility and protein synthesis. Involved in regulation of ionic conductances and long-term synaptic plasticity. May play an important role in dephosphorylating substrates such as the postsynaptic density-associated Ca(2+)/calmodulin dependent protein kinase II. Component of the PTW/PP1 phosphatase complex, which plays a role in the control of chromatin structure and cell cycle progression during the transition from mitosis into interphase. Regulates NEK2 function in terms of kinase activity and centrosome number and splitting, both in the presence and absence of radiation-induced DNA damage. Regulator of neural tube and optic fissure closure, and enteric neural crest cell (ENCCs) migration during development.Carninci et al. 2005<http://www.ncbi.nlm.nih.gov/protein/P62137> |

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