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| --- | --- | --- |
| **Supplemental Table S5:** The analysis of differential abundance protein species (DAPS) identified by two-dimensional electrophoresis (2-DE) KEGG pathways of DAPS. | | |
| **Spot no.** | Description (Ricinus communisL.) | **Protein ID** |
|  |  |  |
| **Biosynthesis of secondary metabolites (2)** | | |
| 29 | Inositol-1-monophosphatase | XP\_002531606.1 |
| 41 | phospholipase D alpha | XP\_002517625.1 |
| **Ether lipid metabolism (1)** | | |
| 41 | phospholipase D alpha | XP\_002517625.1 |
| **Proteasome (5)** | | |
| 6 | 26S proteasome non ATPase regulatory subunit ribulose bisphosphat | XP\_002510253.1 |
| 32 | Proteasome subunit beta type | XP\_002527995.1 |
| 47 | Proteasome subunit beta type | XP\_002527995.1 |
| 57 | 26S proteasome non-atpase regulatory subunit | XP\_002518856.1 |
| 90 | proteasome subunit alpha type-3 | XP\_015583123.1 |
| **Selenocompound metabolism (1)** | | |
| 27 | Thioredoxin reductase NTRB | XP\_002528522.1 |
| **Carbon metabolism (10)** | | |
| 23 | Enolase | XP\_002510911.1 |
| 42 | Phosphoglycerate kinase | XP\_002513353.1 |
| 58 | Triosephosphate isomerase | XP\_002529248.1 |
| 71 | Isocitrate dehydrogenase | XP\_002528517.1 |
| 74 | Fructose-bisphosphate aldolase | XP\_002531508.1 |
| 86 | Enolase | XP\_002528580.1 |
| 87 | Malate dehydrogenase | XP\_002524262.1 |
| 91 | Cysteine synthase | XP\_002512253.1 |
| 93 | Enolase | XP\_002528580.1 |
| 96 | Malate dehydrogenase | XP\_002522546.1 |
| **Carbon fixation in photosynthetic organisms (5)** | | |
| 42 | Phosphoglycerate kinase | XP\_002513353.1 |
| 58 | Triosephosphate isomerase | XP\_002529248.1 |
| 74 | Fructose-bisphosphate aldolase | XP\_002531508.1 |
| 87 | Malate dehydrogenase | XP\_002524262.1 |
| 96 | Malate dehydrogenase | XP\_002522546.1 |
| **Biosynthesis of amino acids (8)** | | |
| 11 | S-adenosylmethionine synthase | XP\_015572366.1 |
| 23 | Enolase | XP\_002510911.1 |
| 42 | Phosphoglycerate kinase | XP\_002513353.1 |
| 58 | Triosephosphate isomerase | XP\_002529248.1 |
| 71 | Isocitrate dehydrogenase | XP\_002528517.1 |
| 74 | Fructose-bisphosphate aldolase | XP\_002531508.1 |
| 86 | Enolase | XP\_002528580.1 |
| 91 | cysteine synthase | XP\_002512253.1 |
| **Glycolysis/Gluconeogenesis (6)** | | |
| 11 | S-adenosylmethionine synthase | XP\_015572366.1 |
| 23 | Enolase | XP\_002510911.1 |
| 42 | Phosphoglycerate kinase | XP\_002513353.1 |
| 58 | Triosephosphate isomerase | XP\_002529248.1 |
| 71 | Isocitrate dehydrogenase | XP\_002528517.1 |
| 74 | Fructose-bisphosphate aldolase | XP\_002531508.1 |
| 86 | enolase | XP\_002528580.1 |
| **Oxidative phosphorylation (1)** | | |
| 61 | synthase delta chain, mitochondrial | XP\_002528798.1 |
| **Citrate cycle (TCA cycle) (3)** | | |
| 71 | Isocitrate dehydrogenase | XP\_002528517.1 |
| 87 | Malate dehydrogenase | XP\_002524262.1 |
| 96 | Malate dehydrogenase | XP\_002522546.1 |
| **Cysteine and methionine metabolism (6)** | | |
| 11 | S-adenosylmethionine synthase | XP\_015572366.1 |
| 42 | Phosphoglycerate kinase | XP\_002513353.1 |
| 80 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxyge | XP\_002517071.1 |
| 87 | Malate dehydrogenase | XP\_002524262.1 |
| 91 | cysteine synthase | XP\_002512253.1 |
| 96 | Malate dehydrogenase | XP\_002522546.1 |
| **Stilbenoid, diarylheptanoid and gingerol biosynthesis (1)** | | |
| 12 | O-methyltransferase | XP\_002522586.1 |
| **mRNA surveillance pathway (1)** | | |
| 48 | Polyadenylate-binding protein | XP\_002513523.1 |
| **Pyrimidine metabolism (1)** | | |
| 60 | UMP-CMP kinase | XP\_002526510.1 |
| **Peroxisome (2)** | | |
| 16 | Tubulin alpha chain | XP\_002512288.1 |
| 95 | Superoxide dismutase [Cu-Zn] | XP\_002512288.1 |
| **Purine metabolism (1)** | | |
| 25 | Inosine triphosphate pyrophosphatase | XP\_015574043.1 |
| **Inositol phosphate metabolism (1)** | | |
| 29 | Inositol-1-monophosphatase | XP\_002531606.1 |
| **Phosphatidylinositol signaling system (1)** | | |
| 29 | Inositol-1-monophosphatase | XP\_002531606.1 |
| **Ascorbate and aldarate metabolism (1)** | | |
| 29 | Inositol-1-monophosphatase | XP\_002531606.1 |
| **Protein processing in endoplasmic reticulum (5)** | | |
| 1 | Heat shock protein | XP\_002526446.1 |
| 28 | Protein transport protein sec13 | XP\_002515980.1 |
| 40 | Transitional endoplasmic reticulum ATPase | XP\_002519500.1 |
| 68 | Heat shock protein | XP\_002527736.1 |
| 94 | Protein disulfide isomerase | XP\_002515309.1 |
| **Spliceosome (3)** | | |
| 1 | Heat shock protein | XP\_002526446.1 |
| 48 | Polyadenylate-binding protein | XP\_002513523.1 |
| 68 | Heat shock protein | XP\_002527736.1 |
| **Endocytosis (3)** | | |
| 1 | Heat shock protein | XP\_002526446.1 |
| 41 | phospholipase D alpha | XP\_002517625.1 |
| 68 | Heat shock protein | XP\_002527736.1 |
| **RNA degradation (4)** | | |
| 3 | Rubiscosu bunit binding protein beta subunit | XP\_002523404.1 |
| 20 | Heat shock protein | XP\_002518324.1 |
| 23 | Enolase | XP\_002510911.1 |
| 86 | enolase | XP\_002528580.1 |
| **Glutathione metabolism (2)** | | |
| 24 | Glutathione-s-transferase omega | XP\_002525204.1 |
| 89 | Glutathione s-transferase | XP\_002532823.1 |
| **RNA transport (2)** | | |
| 28 | Protein transport protein sec13 | XP\_002515980.1 |
| 48 | Polyadenylate-binding protein | XP\_002513523.1 |
| **Metabolic pathways (10)** | | |
| 14 | Oxygen-evolving enhancer protein 1 | XP\_002522386.1 |
| 25 | Inosine triphosphate pyrophosphatase | XP\_015574043.1 |
| 29 | Inositol-1-monophosphatase | XP\_002531606.1 |
| 39 | Oxygen-evolving enhancer protein 1 | XP\_002522386.1 |
| 41 | phospholipase D alpha | XP\_002517625.1 |
| 42 | Phosphoglycerate kinase | XP\_002513353.1 |
| 60 | UMP-CMP kinase | XP\_002526510.1 |
| 61 | synthase delta chain, mitochondrial | XP\_002528798.1 |
| 80 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxyge | XP\_002517071.1 |
| 86 | enolase | XP\_002528580.1 |
| **Photosynthesis (2)** | | |
| 14 | Oxygen-evolving enhancer protein 1 | XP\_002522386.1 |
| 39 | Oxygen-evolving enhancer protein 1 | XP\_002522386.1 |
| **Ubiquitin mediated proteolysis (1)** | | |
| 34 | Ubiquitin-conjugating enzyme rad6 | XP\_002520127.1 |
| **Ribosome (1)** | | |
| 64 | 40S ribosomal protein S12 | XP\_002521598.1 |
| **Glycerophospholipid metabolism (1)** | | |
| 41 | phospholipase D alpha | XP\_002517625.1 |