*Supplementary Material*

# Proteomic analysis of *Pleurotus ostreatus* Grown on Glucose and Xylose Mixtures in Submerged Fermentation Provides Insights into Differentiated Mycelial Composition

**Table S1.** Enrichment analysis of Gene Ontology in biological processes that upregulate the different clusters of the HeatMap for proteomic analysis of *P. ostreatus* LGAM 1123 submerged cultivation using glucose, xylose and mixtures of them.

| Condition | Cluster | Type | Name | P value | Enrichment | Total | In cluster | Cluster size | Ben. Ho. FDR |
|---|---|---|---|---|---|---|---|---|---|
| 100% Glucose | Pink | GOBP name | cellular macromolecule biosynthetic process | 6E-12 | 1.45 | 133 | 114 | 1368 | 4E-09 |
| | | | macromolecule biosynthetic process | 4E-12 | 1.45 | 134 | 115 | | 5E-09 |
| | | | translation | 5E-09 | 1.44 | 101 | 86 | | 1E-06 |
| | | | cellular macromolecule metabolic process | 2E-06 | 1.20 | 305 | 216 | | 2E-04 |
| | | | macromolecule metabolic process | 4E-06 | 1.18 | 320 | 224 | | 4E-04 |
| | | | cellular protein metabolic process | 6E-05 | 1.23 | 165 | 120 | | 4E-03 |
| | | | protein metabolic process | 1E-04 | 1.20 | 189 | 134 | | 8E-03 |
| 100% Xylose | Blue | GOBP name | organic acid metabolic process | 3E-09 | 1.58 | 139 | 90 | 947 | 6E-07 |
| | | | cellular ketone metabolic process | 3E-09 | 1.59 | 137 | 89 | | 7E-07 |
| | | | oxoacid metabolic process | 3E-09 | 1.59 | 137 | 89 | | 9E-07 |
| | | | small molecule metabolic process | 7E-09 | 1.41 | 252 | 145 | | 1E-06 |
| | | | carboxylic acid metabolic process | 3E-09 | 1.59 | 137 | 89 | | 1E-06 |
| | | | cellular amino acid metabolic process | 2E-08 | 1.61 | 114 | 75 | | 3E-06 |
| | | | cellular amine metabolic process | 7E-08 | 1.58 | 116 | 75 | | 9E-06 |
| | | | amine metabolic process | 3E-07 | 1.54 | 121 | 76 | | 4E-05 |
| | | | small molecule biosynthetic process | 4E-06 | 1.57 | 87 | 56 | | 4E-04 |
| | | | cellular amino acid biosynthetic process | 8E-06 | 1.69 | 58 | 40 | | 7E-04 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | cellular nitrogen compound biosynthetic process | 1E-05 | 1.44 | 127 | 75 | | 7E-04 |
| | amine biosynthetic process | 2E-05 | 1.66 | 59 | 40 | | 1E-03 |
| | organic acid biosynthetic process | 2E-05 | 1.59 | 69 | 45 | | 1E-03 |
| | carboxylic acid biosynthetic process | 2E-05 | 1.59 | 69 | 45 | | 1E-03 |
| | acetyl-CoA metabolic process | 1E-04 | 2.06 | 19 | 16 | | 7E-03 |
| | cofactor metabolic process | 5E-04 | 1.51 | 60 | 37 | | 3E-02 |

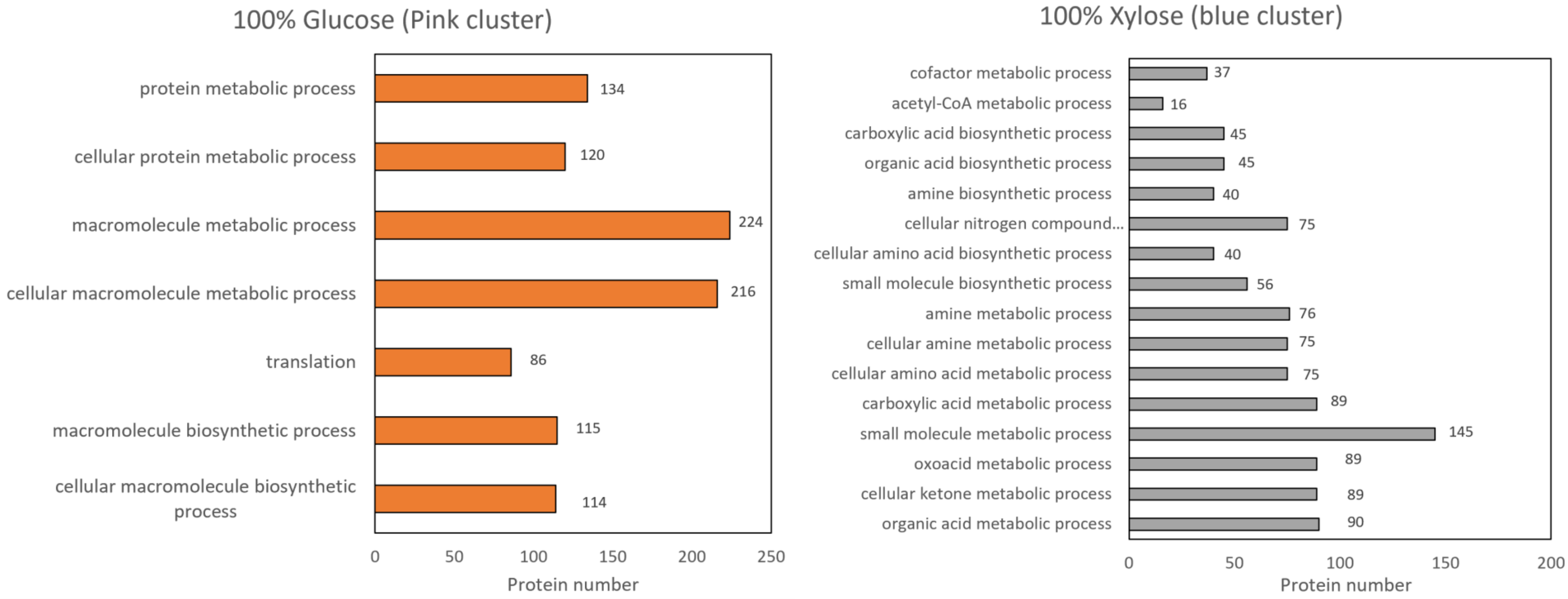

**Figure S1.** Enrichment analysis of Gene Ontology in biological processes that upregulate the different clusters of the HeatMap upregulated from glucose and xylose for proteomic analysis of *P. ostreatus* LGAM 1123 submerged cultivation using glucose, xylose and mixtures of them.

**Table S2.** Gene Ontology biological process categorization of up and down-regulated proteins when glucose condition compared to xylose one.

| ***Biological process*** | ***-Log(P-value)*** | ***Difference*** | ***Genes*** | ***Protein.Ids*** | ***First.Protein.Description*** |
|---|---|---|---|---|---|
| | | | **Up-regulated proteins** | | |
| ***Protein metabolic process*** | 6.05 | 1.02 | PLEOSDRAFT_1016358 | A0A067P077 | KOW domain-containing protein (Fragment) |
| | 2.96 | 0.33 | PLEOSDRAFT_1017509 | A0A067NGT0 | Ubiquitinyl hydrolase 1 (Fragment) |
| | 6.42 | 0.78 | PLEOSDRAFT_1025128 | A0A067NC11 | Ribosomal_L23eN domain-containing protein (Fragment) |
| | 1.49 | 0.70 | PLEOSDRAFT_1034155 | A0A067NVJ3 | S5 DRBM domain-containing protein |
| | 2.27 | 0.37 | PLEOSDRAFT_1034159 | A0A067P6Q1 | Protein-tyrosine-phosphatase |
| | 6.84 | 1.38 | PLEOSDRAFT_1038239 | A0A067NSE2 | 60S ribosomal protein L3 (Fragment) |
| | 1.23 | 0.22 | PLEOSDRAFT_1039283 | A0A067NY62 | Translational machinery component |
| | 3.42 | 1.45 | PLEOSDRAFT_1040237 | A0A067NZG0 | Ribosomal protein L7/L12 (Fragment) |
| | 1.67 | 0.59 | PLEOSDRAFT_1040256 | A0A067P1J9 | Peptidyl-prolyl cis-trans isomerase |
| | 4.44 | 0.43 | PLEOSDRAFT_1043668 | A0A067NSA2 | Ribosomal_L7Ae domain-containing protein |
| | 2.94 | 0.46 | PLEOSDRAFT_1044393 | A0A067NDS4 | Ribosomal protein S12 |
| | 8.38 | 1.23 | PLEOSDRAFT_1044894 | A0A067NGR8 | Ribos_L4_asso_C domain-containing protein |

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|---|---|---|---|---|---|
| | 2.46 | 0.26 | PLEOSDRAFT_1050854 | A0A067NG04 | Ribosomal_S10 domain-containing protein (Fragment) |
| | 4.75 | 1.47 | PLEOSDRAFT_1051587 | A0A067NX31 | Ribosomal protein L34e |
| | 3.86 | 0.65 | PLEOSDRAFT_1051744 | A0A067NYA3 | 60S ribosomal protein L20 |
| | 1.41 | 0.28 | PLEOSDRAFT_1052040 | A0A067P9U4 | HATPase_c domain-containing protein |
| | 3.56 | 0.28 | PLEOSDRAFT_1052167 | A0A067NZH9 | Glycosyltransferase family 15 protein |
| | 5.97 | 1.01 | PLEOSDRAFT_1053014 | A0A067NUU3 | 40S ribosomal protein S6 |
| | 3.36 | 0.91 | PLEOSDRAFT_1053176 | A0A067P7Q0 | Ribosomal_L18e/L15P domain-containing protein |
| | 3.12 | 0.70 | PLEOSDRAFT_1053876 | A0A067P2S5 | 60S ribosomal protein L16 |
| | 7.00 | 1.37 | PLEOSDRAFT_1053977 | A0A067P4P1 | Ribosomal_S17_N domain-containing protein |
| | 1.69 | 0.24 | PLEOSDRAFT_1054419 | A0A067NWH0 | Calnexin |
| | 3.65 | 0.77 | PLEOSDRAFT_1054560 | A0A067NTT4 | 60S ribosomal protein L21-A |
| | 6.14 | 0.90 | PLEOSDRAFT_1054562 | A0A067NUA5 | 40S ribosomal protein S9 |
| | 1.03 | 0.24 | PLEOSDRAFT_1054660 | A0A067NNT3 | Glycosyltransferase family 15 protein |
| | 4.32 | 0.99 | PLEOSDRAFT_1054789 | A0A067NXJ3 | 40S ribosomal protein S17 |
| | 0.97 | 0.35 | PLEOSDRAFT_1055283 | A0A067NMN7 | Ribosomal protein S18 |
| | 6.18 | 0.53 | PLEOSDRAFT_1055325 | A0A067NMS1 | 60S ribosomal protein L9-B |
| | 2.57 | 0.28 | PLEOSDRAFT_1055341 | A0A067NQV4 | 60S ribosomal protein L6 |
| | 7.55 | 1.11 | PLEOSDRAFT_1055401 | A0A067P0M5 | Ribosomal_L18_c domain-containing protein (Fragment) |
| | 3.67 | 0.64 | PLEOSDRAFT_1055807 | A0A067NP91 | Ribosomal protein |
| | 3.43 | 0.69 | PLEOSDRAFT_1056440 | A0A067NIT0 | Palmitoyl-protein thioesterase 1 |
| | 3.12 | 0.22 | PLEOSDRAFT_1056867 | A0A067NKK5 | CCT-theta |

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|---|---|---|---|---|---|
| | 5.32 | 0.99 | PLEOSDRAFT_1057271 | A0A067NFH4 | 40S ribosomal protein S15 |
| | 1.84 | 0.56 | PLEOSDRAFT_1060298 | A0A067N7L2 | Glycosyltransferase family 15 protein |
| | 4.27 | 1.03 | PLEOSDRAFT_1060402 | A0A067NX51 | 60S ribosomal protein L31 |
| | 3.70 | 0.81 | PLEOSDRAFT_1060439 | A0A067NX98 | Plus3 domain-containing protein |
| | 4.18 | 1.42 | PLEOSDRAFT_1062010 | A0A067NV33 | 60S ribosomal protein L39 |
| | 4.99 | 0.85 | PLEOSDRAFT_1062711 | A0A067P2W0 | Protein MEMO1 |
| | 3.46 | 0.54 | PLEOSDRAFT_1062741 | A0A067NS51 | KH type-2 domain-containing protein |
| | 1.66 | 0.39 | PLEOSDRAFT_1063308 | A0A067NWQ7 | 30S ribosomal protein S15 |
| | 4.97 | 0.64 | PLEOSDRAFT_1063630 | A0A067NZ52 | Ribosomal_L18e/L15P domain-containing protein |
| | 1.45 | 0.17 | PLEOSDRAFT_1063742 | A0A067NZE9 | Deoxyhypusine synthase |
| | 2.78 | 0.83 | PLEOSDRAFT_1063761 | A0A067NZG5 | 40S ribosomal protein S7 |
| | 1.65 | 0.22 | PLEOSDRAFT_1064317 | A0A067NR91 | Prefoldin beta-like protein |
| | 5.34 | 1.18 | PLEOSDRAFT_1064355 | A0A067P101 | Ribosomal_L2_C domain-containing protein |
| | 4.19 | 0.57 | PLEOSDRAFT_1064969 | A0A067NIF5 | Ribosomal_S7 domain-containing protein |
| | 1.13 | 0.24 | PLEOSDRAFT_1065027 | A0A067NIK0 | Ribosomal protein S9/S16 |
| | 3.74 | 1.21 | PLEOSDRAFT_1066156 | A0A067NFS2 | Ribosomal protein L37 |
| | 6.51 | 0.98 | PLEOSDRAFT_1066177 | A0A067NFT1 | 40S ribosomal protein S4 |
| | 3.92 | 0.61 | PLEOSDRAFT_1067221 | A0A067NJV4 | DnaJ_C domain-containing protein |
| | 2.61 | 0.56 | PLEOSDRAFT_1067469 | A0A067N9E0 | Protein arginine N-methyltransferase |
| | 2.66 | 0.12 | PLEOSDRAFT_1067547 | A0A067NCS9 | T-complex protein 1 subunit epsilon |
| | 2.45 | 0.56 | PLEOSDRAFT_1068380 | A0A067N6B7 | 60S ribosomal protein L38 |
| | 3.52 | 1.02 | PLEOSDRAFT_1068404 | A0A067NH17 | 40S ribosomal protein S14 |

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|---|---|---|---|---|---|
| | 2.49 | 0.34 | PLEOSDRAFT_1069349 | A0A067NYD8 | Dolichyl-phosphate-mannose--protein mannosyltransferase |
| | 4.41 | 0.68 | PLEOSDRAFT_1070466 | A0A067NT54 | 40S ribosomal protein S19 |
| | 3.94 | 1.39 | PLEOSDRAFT_1070894 | A0A067NMU9 | 60S ribosomal protein L36 |
| | 1.95 | 0.66 | PLEOSDRAFT_1075002 | A0A067NRN3 | 54S ribosomal protein L32, mitochondrial |
| | 2.42 | 0.43 | PLEOSDRAFT_1075166 | A0A067NVB4 | Nucleic acid-binding protein |
| | 5.57 | 0.72 | PLEOSDRAFT_1077025 | A0A067NV80 | FK506-binding protein |
| | 3.59 | 0.66 | PLEOSDRAFT_1077381 | A0A067NF01 | Dolichyl-diphosphooligosaccharide--protein glycotransferase |
| | 5.68 | 1.29 | PLEOSDRAFT_1077820 | A0A067NGT5 | 60S ribosomal protein L37a |
| | 1.43 | 0.43 | PLEOSDRAFT_1078384 | A0A067NPX4 | GPI transamidase component PIG-T |
| | 1.50 | 0.25 | PLEOSDRAFT_1087561 | A0A067PA83 | 40S ribosomal protein S30 |
| | 5.72 | 1.04 | PLEOSDRAFT_1087603 | A0A067NXY7 | 60S ribosomal protein L27 |
| | 1.70 | 0.65 | PLEOSDRAFT_1088048 | A0A067P4G1 | Ribosomal_S7 domain-containing protein |
| | 5.19 | 0.95 | PLEOSDRAFT_1088261 | A0A067NSE6 | Ribosomal protein L19 |
| | 2.13 | 0.60 | PLEOSDRAFT_1088477 | A0A067P470 | Ribosomal protein L22e |
| | 8.22 | 1.56 | PLEOSDRAFT_1088526 | A0A067P301 | Ribosomal protein L15 |
| | 5.79 | 1.76 | PLEOSDRAFT_1088565 | A0A067P4S5 | 60S ribosomal protein L13 |
| | 1.25 | 0.18 | PLEOSDRAFT_1088579 | A0A067P4U5 | Ribosomal protein S16 |
| | 6.85 | 0.77 | PLEOSDRAFT_1088906 | A0A067NZ20 | Ribosomal protein S8 |
| | 4.92 | 1.25 | PLEOSDRAFT_1089421 | A0A067NHZ5 | 40S ribosomal protein S8 |
| | 4.85 | 0.62 | PLEOSDRAFT_1089494 | A0A067NJ61 | Ribosomal protein S13 |
| | 1.43 | 0.31 | PLEOSDRAFT_1089639 | A0A067NX86 | 60S ribosomal protein L33-A |
| | 6.04 | 1.15 | PLEOSDRAFT_1089796 | A0A067NFC5 | 60S ribosomal protein L11 |
| | 8.25 | 1.41 | PLEOSDRAFT_1089909 | A0A067NTH6 | Ribosomal_L16 domain-containing protein |

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|---|---|---|---|---|---|
| | 4.47 | 0.42 | PLEOSDRAFT_1090454 | A0A067NCW3 | Protein phosphatase methylesterase 1 |
| | 1.49 | 0.17 | PLEOSDRAFT_1091494 | A0A067PAK1 | 50S ribosomal protein L27 |
| | 2.88 | 1.17 | PLEOSDRAFT_1091506 | A0A067P2K4 | KOW domain-containing protein |
| | 4.41 | 0.67 | PLEOSDRAFT_1091508 | A0A067PC57 | Glycylpeptide N-tetradecanoyltransferase |
| | 5.71 | 1.05 | PLEOSDRAFT_1091806 | A0A067NUF2 | Ribosomal_S13_N domain-containing protein |
| | 3.32 | 0.59 | PLEOSDRAFT_1092339 | A0A067NV44 | Ribosomal protein L4 |
| | 4.06 | 0.99 | PLEOSDRAFT_1093748 | A0A067NFL9 | Dolichyl-phosphate-mannose--protein mannosyltransferase |
| | 0.59 | 0.87 | PLEOSDRAFT_1096620 | A0A067NR16 | SWR1-complex protein 4 |
| | 3.03 | 1.43 | PLEOSDRAFT_1101344 | A0A067NR26 | Poly [ADP-ribose] polymerase |
| | 3.68 | 0.81 | PLEOSDRAFT_1111258 | A0A067NQM0 | 40S ribosomal protein S29 |
| | 2.96 | 0.53 | PLEOSDRAFT_1111462 | A0A067NUL4 | 50S ribosomal protein L17 (Fragment) |
| | 3.86 | 0.41 | PLEOSDRAFT_1111838 | A0A067P509 | Ribosomal_L2_C domain-containing protein |
| | 2.99 | 0.67 | PLEOSDRAFT_1112019 | A0A067NZB3 | 60S ribosomal protein L35 |
| | 2.13 | 1.29 | PLEOSDRAFT_1112555 | A0A067NKA1 | Prefoldin subunit 4 |
| | 3.91 | 1.33 | PLEOSDRAFT_1112875 | A0A067NWY0 | 40S ribosomal protein S23 |
| | 3.01 | 0.32 | PLEOSDRAFT_1113776 | A0A067NLD6 | Methionine aminopeptidase 2 |
| | 6.65 | 0.72 | PLEOSDRAFT_1113860 | A0A067NCB2 | Ribosomal_S10 domain-containing protein |
| | 1.79 | 0.45 | PLEOSDRAFT_1114678 | A0A067NG45 | Glycosyltransferase family 69 protein |

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|---|---|---|---|---|
| 2.65 | 0.25 | PLEOSDRAFT_160378 | A0A067ND40 | 54S ribosomal protein L4, mitochondrial |
| 3.16 | 0.88 | PLEOSDRAFT_4300 | A0A067NTP4 | 40S ribosomal protein S26 (Fragment) |
| 2.24 | 0.88 | PLEOSDRAFT_45869 | A0A067NBL2 | 60S ribosomal protein L44 |
| 4.52 | 1.02 | RPS1 | A0A067NQG0 | 40S ribosomal protein S1 |
| **Down Regulated proteins** | | | | |
| 2.88 | -0.43 | PLEOSDRAFT_1031207 | A0A067P1F8 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1 |
| 1.31 | -0.37 | PLEOSDRAFT_1034291 | A0A067P7C5 | Succinate dehydrogenase assembly factor 2, mitochondrial |
| 1.73 | -0.46 | PLEOSDRAFT_1036229 | A0A067NS63 | Peptidylprolyl isomerase |
| 0.97 | -0.44 | PLEOSDRAFT_1038094 | A0A067NLN1;A0A067NPU1;A0A067NPU1 | Transcription elongation regulator 1;Wheel domain-containing protein |
| 2.43 | -0.38 | PLEOSDRAFT_1039529 | A0A067NLK2 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 |
| 1.25 | -0.19 | PLEOSDRAFT_1044428 | A0A067NBT6 | Ribosomal_L5_C domain-containing protein |
| 2.96 | -0.53 | PLEOSDRAFT_1050332 | A0A067N320 | Ribosomal protein S8 |
| 1.88 | -0.38 | PLEOSDRAFT_1053360 | A0A067NVK7 | Hsp10-like protein |
| 3.99 | -0.54 | PLEOSDRAFT_1055766 | A0A067NPE8 | 40S ribosomal protein S12 |
| 4.75 | -0.82 | PLEOSDRAFT_1055883 | A0A067NTC8 | Signal peptidase subunit 3 |
| 3.77 | -0.91 | PLEOSDRAFT_1056572 | A0A067NV96 | Ribosomal protein S6 (Fragment) |
| 2.73 | -0.88 | PLEOSDRAFT_1057861 | A0A067NF07 | Peptidylprolyl isomerase |

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|---|---|---|---|---|---|
| | 4.18 | -0.92 | PLEOSDRAFT_1058252 | A0A067NRC4 | Peptidyl-prolyl cis-trans isomerase |
| | 2.79 | -0.86 | PLEOSDRAFT_1060916 | A0A067PBJ0 | Fe2OG dioxygenase domain-containing protein |
| | 1.88 | -0.18 | PLEOSDRAFT_1061882 | A0A067P5W8 | Glycosyltransferase family 24 protein |
| | 1.59 | -0.16 | PLEOSDRAFT_1062835 | A0A067NSI3 | 40S ribosomal protein S16 |
| | 4.57 | -0.44 | PLEOSDRAFT_1063833 | A0A067NLW0 | UBA_e1_C domain-containing protein |
| | 2.38 | -0.20 | PLEOSDRAFT_1069266 | A0A067NYF6 | PPIase cyclophilin-type domain-containing protein |
| | 2.65 | -0.30 | PLEOSDRAFT_1073596 | A0A067PAB9 | Heat shock protein 60, mitochondrial |
| | 0.51 | -0.82 | PLEOSDRAFT_1073749 | A0A067P036 | Alpha N-terminal protein methyltransferase 1 |
| | 3.87 | -0.99 | PLEOSDRAFT_1075979 | A0A067NZY1 | Mitochondrial ribosomal protein L11 |
| | 1.35 | -0.28 | PLEOSDRAFT_1089362 | A0A067NKE5 | Methyltransf_25 domain-containing protein |
| | 2.89 | -0.53 | PLEOSDRAFT_1089449 | A0A067NUF1 | SER_THR_PHOSPHATASE domain-containing protein |
| | 1.98 | -0.47 | PLEOSDRAFT_1090284 | A0A067NL79 | Peptidyl-prolyl cis-trans isomerase |
| | 2.53 | -0.53 | PLEOSDRAFT_1091212 | A0A067NY66 | BPL/LPL catalytic domain-containing protein |
| | 2.40 | -0.12 | PLEOSDRAFT_1091554 | A0A067P091 | T-complex protein 1 subunit alpha |
| | 2.35 | -0.84 | PLEOSDRAFT_1093200 | A0A067NK25 | Geranylgeranyl transferase type-2 subunit beta |
| | 5.14 | -0.57 | PLEOSDRAFT_1093556 | A0A067NJY1 | Heat shock protein 70 |

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|---|---|---|---|---|---|
|  | 2.56 | -0.45 | PLEOSDRAFT_1093970 | A0A067NBI1 | Protein-tyrosine-phosphatase |
|  | 1.61 | -0.43 | PLEOSDRAFT_1096304 | A0A067NX03 | Ribosomal_L28e domain-containing protein |
|  | 2.22 | -0.40 | PLEOSDRAFT_1096799 | A0A067NK42 | 60S ribosomal protein L23 |
|  | 3.82 | -0.26 | PLEOSDRAFT_1099644 | A0A067PCS0 | Mitochondrial protein import protein MAS5 |
|  | 3.80 | -1.13 | PLEOSDRAFT_1111975 | A0A067NLB5 | Signal peptidase complex catalytic subunit SEC11 |
|  | 0.70 | -0.43 | PLEOSDRAFT_1113129 | A0A067NR75;A0A067N860;A0A067NWI7;A0A067NZF5;A0A067P413;A0A067P7C4 | Ubiquitin-like domain-containing protein |
|  | 2.93 | -1.23 | PLEOSDRAFT_153711 | A0A067P9M6 | RRF domain-containing protein |
|  | 4.03 | -0.70 | PLEOSDRAFT_20477 | A0A067P2N5 | Translation protein |
|  | 3.35 | -0.90 | PLEOSDRAFT_30852 | A0A067NS41 | 54S ribosomal protein L49 |
|  | 2.20 | -0.26 | PLEOSDRAFT_40905 | A0A067NCV3 | PPM-type phosphatase domain-containing protein |
|  | 4.28 | -0.84 | PLEOSDRAFT_46396 | A0A067N9R6 | Peptide-methionine (S)-S-oxide reductase |
|  | 3.56 | -0.53 | PLEOSDRAFT_53382 | A0A067N4H8 | Peptidyl-prolyl cis-trans isomerase |
|  | 2.82 | -0.78 | PLEOSDRAFT_60840 | A0A067P1F7 | Peptidyl-prolyl cis-trans isomerase |
|  | 3.12 | -0.36 | RPS0 | A0A067NHP6 | 40S ribosomal protein S0 |
| ***Amino acid biosynthesis*** | **Down Regulated proteins** |  |  |  |  |
|  | 3.94 | -0.59 | ADI1 | A0A067P6R4 | Acireductone dioxygenase |
|  | 3.83 | -0.18 | ALA1 | A0A067NZQ8 | Alanine--tRNA ligase |
|  | 3.45 | -0.38 | BNA1 | A0A067N4U9 | 3-hydroxyanthranilate 3,4-dioxygenase |
|  | 3.82 | -0.60 | BNA5 | A0A067P9X7 | Kynureninase |

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|---|---|---|---|---|---|
| | 5.96 | -4.35 | MET3 | A0A067NI66 | Sulfate adenylyltransferase |
| | 2.98 | -0.28 | PLEOSDRAFT_1031798 | A0A067NYQ3 | Methylenetetrahydrofolate reductase |
| | 5.20 | -0.18 | PLEOSDRAFT_1032700 | A0A067NY97 | Threonine--tRNA ligase |
| | 3.48 | -0.49 | PLEOSDRAFT_1034365 | A0A067NVT6 | Homoserine dehydrogenase |
| | 0.86 | -0.29 | PLEOSDRAFT_1035599 | A0A067P2X6 | AB hydrolase-1 domain-containing protein |
| | 2.32 | -0.18 | PLEOSDRAFT_1036478 | A0A067NS28 | Imidazole glycerol phosphate synthase hisHF |
| | 6.41 | -0.90 | PLEOSDRAFT_1037212 | A0A067P3F9 | Gamma-glutamyltranspeptidase |
| | 4.51 | -0.72 | PLEOSDRAFT_1037674 | A0A067NT30 | Glutamate--tRNA ligase |
| | 1.05 | -0.15 | PLEOSDRAFT_1039266 | A0A067NRV8 | Aspartate-semialdehyde dehydrogenase |
| | 1.83 | -0.25 | PLEOSDRAFT_1039721 | A0A067NY57 | Acetylornithine transaminase (Fragment) |
| | 2.20 | -0.64 | PLEOSDRAFT_1043258 | A0A067NSI6 | Pantoate--beta-alanine ligase |
| | 6.45 | -0.88 | PLEOSDRAFT_1046785 | A0A067NLR9 | Homocitrate synthase |
| | 5.89 | -0.66 | PLEOSDRAFT_1048814 | A0A067N889 | Phospho-2-dehydro-3-deoxyheptonate aldolase |
| | 3.03 | -0.15 | PLEOSDRAFT_1049175 | A0A067NHD2 | Glycine--tRNA ligase |
| | 4.64 | -0.54 | PLEOSDRAFT_1052049 | A0A067P1S4 | Aspartate aminotransferase |
| | 6.40 | -0.58 | PLEOSDRAFT_1052256 | A0A067NZB1 | S-adenosylmethionine synthase |
| | 5.24 | -0.65 | PLEOSDRAFT_1059326 | A0A067NG42 | N-acetyltransferase domain-containing protein |
| | 8.86 | -1.43 | PLEOSDRAFT_1059932 | A0A067N3J5 | Serine hydroxymethyltransferase |
| | 4.67 | -0.43 | PLEOSDRAFT_1061805 | A0A067P5K9 | Lysine--tRNA ligase |

| | | | | | |
|---|---|---|---|---|---|
| | 5.41 | -1.46 | PLEOSDRAFT_1063015 | A0A067P3T1 | Glycine cleavage system P protein |
| | 2.26 | -0.56 | PLEOSDRAFT_1063885 | A0A067NY76 | AA_TRNA_LIGASE_II domain-containing protein |
| | 6.15 | -1.32 | PLEOSDRAFT_1063965 | A0A067NM77 | 3-isopropylmalate dehydratase |
| | 6.27 | -0.89 | PLEOSDRAFT_1064157 | A0A067P0J4 | 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase |
| | 3.56 | -0.90 | PLEOSDRAFT_1064990 | A0A067NIH2 | Carbamoyl-phosphate synthase (glutamine-hydrolyzing) |
| | 4.00 | -0.50 | PLEOSDRAFT_1066801 | A0A067ND08 | Dihydroxy-acid dehydratase |
| | 0.69 | -0.58 | PLEOSDRAFT_1067181 | A0A067NJR8 | Arginase |
| | 3.45 | -0.67 | PLEOSDRAFT_1074654 | A0A067P2X0 | Branched-chain-amino-acid aminotransferase |
| | 1.68 | -0.21 | PLEOSDRAFT_1077525 | A0A067NFL4 | Methylenetetrahydrofolate reductase |
| | 4.82 | -0.48 | PLEOSDRAFT_1078749 | A0A067NCL8 | Aminomethyltransferase |
| | 0.80 | -0.54 | PLEOSDRAFT_1083989 | A0A067NJN9 | Tyrosine--tRNA ligase |
| | 7.68 | -1.22 | PLEOSDRAFT_1087775 | A0A067NZQ5 | Arginase |
| | 4.77 | -0.85 | PLEOSDRAFT_1088122 | A0A067NVE7 | Methionine adenosyltransferase 2 subunit beta |
| | 3.40 | -0.48 | PLEOSDRAFT_1088157 | A0A067NVM8 | Serine--tRNA ligase |
| | 2.19 | -0.18 | PLEOSDRAFT_1088517 | A0A067NUP7 | Aspartate aminotransferase |
| | 7.43 | -0.83 | PLEOSDRAFT_1089099 | A0A067NQW2 | Glutamine synthetase |
| | 6.52 | -1.32 | PLEOSDRAFT_1090361 | A0A067N929 | Ketol-acid reductoisomerase, mitochondrial |

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| | 4.56 | -0.95 | PLEOSDRAFT_1091635 | A0A067P0T1 | 3-hydroxyisobutyrate dehydrogenase |
| | 4.18 | -0.62 | PLEOSDRAFT_1091773 | A0A067P1I6 | Cyclase |
| | 2.39 | -0.28 | PLEOSDRAFT_1092046 | A0A067NQJ8 | Arginine biosynthesis bifunctional protein ArgJ, mitochondrial |
| | 7.21 | -1.22 | PLEOSDRAFT_1092197 | A0A067NR84 | Branched-chain-amino-acid aminotransferase |
| | 2.86 | -0.35 | PLEOSDRAFT_1092207 | A0A067NRA4 | Saccharopine dehydrogenase [NAD(+), L-lysine-forming] |
| | 3.63 | -0.84 | PLEOSDRAFT_1093046 | A0A067NNB7 | ThrRS/AlaRS common domain-containing protein |
| | 3.52 | -1.25 | PLEOSDRAFT_1093081 | A0A067NNJ6 | PAPS_reduct domain-containing protein |
| | 3.38 | -0.32 | PLEOSDRAFT_1093381 | A0A067NLG7 | PALP domain-containing protein |
| | 5.77 | -0.83 | PLEOSDRAFT_1094120 | A0A067NNX9 | Phospho-2-dehydro-3-deoxyheptonate aldolase |
| | 4.02 | -0.30 | PLEOSDRAFT_1094347 | A0A067NC64 | Valine--tRNA ligase |
| | 2.85 | -0.33 | PLEOSDRAFT_1094403 | A0A067N9H4 | Methionine--tRNA ligase |
| | 3.14 | -1.21 | PLEOSDRAFT_1095075 | A0A067NFB4 | O-acetylhomoserine (Thiol)-lyase |
| | 1.17 | -0.24 | PLEOSDRAFT_1098775 | A0A067NXK2 | Threonine synthase |
| | 2.33 | -0.34 | PLEOSDRAFT_1103406 | A0A067NZ19 | Histidine biosynthesis trifunctional protein |
| | 3.94 | -0.67 | PLEOSDRAFT_1104435 | A0A067NI99 | Dihydroxy-acid dehydratase |
| | 1.18 | -0.53 | PLEOSDRAFT_1107098 | A0A067NDY7 | Anthranilate phosphoribosyltransferase |
| | 4.36 | -0.64 | PLEOSDRAFT_1107467 | A0A067NLQ7 | Homoaconitase, mitochondrial |

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| | 1.42 | -1.60 | PLEOSDRAFT_1107468 | A0A067NKB6 | Trimethyllysine dioxygenase |
| | 5.03 | -1.22 | PLEOSDRAFT_1109836 | A0A067NF57 | MR_MLE domain-containing protein |
| | 3.74 | -0.78 | PLEOSDRAFT_1110444 | A0A067NZ33 | Phosphoserine transaminase |
| | 4.39 | -0.52 | PLEOSDRAFT_1110544 | A0A067PAE8 | Pyruvate carboxyltransferase domain-containing protein |
| | 3.71 | -0.56 | PLEOSDRAFT_1112872 | A0A067NM83 | Threonine dehydratase |
| | 2.37 | -0.30 | PLEOSDRAFT_158438 | A0A067NUA3 | Isoleucine--tRNA ligase |
| | 2.20 | -0.68 | PLEOSDRAFT_158524 | A0A067NIA8 | Glutathione hydrolase |
| | 3.78 | -0.62 | PLEOSDRAFT_166222 | A0A067P394 | Phosphoglycerate dehydrogenase |
| | 2.41 | -1.67 | PLEOSDRAFT_173727 | A0A067NVB1 | Phenylalanine ammonia-lyase |
| | 3.22 | -0.27 | PLEOSDRAFT_176102 | A0A067P0Q8 | Glutaminyl-tRNA synthetase |
| | 2.14 | -0.30 | PLEOSDRAFT_21709 | A0A067P1C4 | Prephenate/arogenate dehydrogenase domain-containing protein |
| | 2.90 | -0.19 | PLEOSDRAFT_36220 | A0A067N573 | Alpha-aminoadipate reductase |
| | 4.48 | -0.40 | PLEOSDRAFT_37280 | A0A067P023 | Leucine--tRNA ligase |
| | 2.47 | -0.15 | PLEOSDRAFT_37432 | A0A067PBX9 | Glutamate--tRNA ligase |
| | 9.42 | -1.97 | PLEOSDRAFT_40761 | A0A067NBU9 | NAD-specific glutamate dehydrogenase |
| | 3.48 | -0.58 | PLEOSDRAFT_42813 | A0A067NYT2 | Acetolactate synthase |
| | 1.51 | -0.13 | PLEOSDRAFT_49024 | A0A067P897 | Ornithine carbamoyltransferase |
| | 5.08 | -0.48 | PLEOSDRAFT_50455 | A0A067NR73 | 3-isopropylmalate dehydrogenase |

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| 2.70 | -0.21 | PLEOSDRAFT_51354 | A0A067NSH3 | Glutamate-5-semialdehyde dehydrogenase |
| 5.48 | -1.67 | PLEOSDRAFT_51396 | A0A067NS81 | Flavodoxin-like domain-containing protein |
| 5.25 | -0.47 | PLEOSDRAFT_61563 | A0A067NP59 | Multifunctional fusion protein |
| | | **Up-regulated proteins** | | |
| 1.76 | 0.52 | BNA4 | A0A067NYR6 | Kynurenine 3-monooxygenase |
| 4.63 | 0.54 | PLEOSDRAFT_1033198 | A0A067PBU4 | Imidazoleglycerol-phosphate dehydratase |
| 0.32 | 0.21 | PLEOSDRAFT_1033366 | A0A067P9T8 | Pyrroline-5-carboxylate reductase |
| 0.91 | 0.26 | PLEOSDRAFT_1035435 | A0A067NR52 | Homoserine kinase |
| 4.57 | 0.30 | PLEOSDRAFT_1036410 | A0A067P591;A0A067N687;A0A067P591 | HGTP_anticodon domain-containing protein (Fragment);Histidine--tRNA ligase (Fragment) |
| 6.22 | 0.83 | PLEOSDRAFT_1037028 | A0A067NW13 | NAD_binding_2 domain-containing protein |
| 2.30 | 0.22 | PLEOSDRAFT_1041271 | A0A067NUX8 | Acetohydroxy-acid synthase small subunit |
| 1.06 | 0.26 | PLEOSDRAFT_1041369 | A0A067NHS3 | PALP domain-containing protein |
| 4.05 | 0.29 | PLEOSDRAFT_1042472 | A0A067NMV8 | Asparagine--tRNA ligase |
| 1.63 | 0.37 | PLEOSDRAFT_1044117 | A0A067NIB0 | Aspartate kinase |
| 6.25 | 0.58 | PLEOSDRAFT_1053009 | A0A067P5M7 | Arginine--tRNA ligase |
| 4.48 | 0.36 | PLEOSDRAFT_1056503 | A0A067NLU8 | Multifunctional tryptophan biosynthesis protein |
| 1.53 | 0.37 | PLEOSDRAFT_1061666 | A0A067PCD4 | AA_kinase domain-containing protein |

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| | 1.45 | 0.17 | PLEOSDRAFT_1063742 | A0A067NZE9 | Deoxyhypusine synthase |
| | 2.20 | 0.27 | PLEOSDRAFT_1076641 | A0A067NKB9 | Cysteine--tRNA ligase |
| | 0.90 | 0.26 | PLEOSDRAFT_1088869 | A0A067NLD0 | Glutaminase |
| | 1.45 | 0.24 | PLEOSDRAFT_1091418 | A0A067PA74 | Phenylalanine--tRNA ligase |
| | 4.98 | 0.30 | PLEOSDRAFT_1092280 | A0A067P4F3 | Aspartate--tRNA ligase |
| | 1.62 | 1.45 | PLEOSDRAFT_1097003 | A0A067NV26 | PLP-dependent transferase (Fragment) |
| | 3.30 | 0.57 | PLEOSDRAFT_1099891 | A0A067P0U5 | Tryptophan--tRNA ligase |
| | 4.40 | 0.76 | PLEOSDRAFT_1111305 | A0A067P3I4 | Prenylcys_lyase domain-containing protein |
| | 2.10 | 0.27 | PLEOSDRAFT_1113928 | A0A067NMD2 | CTP synthase |
| | 3.64 | 1.22 | PLEOSDRAFT_14441 | A0A067P4P8 | Asparagine--tRNA ligase (Fragment) |
| | 1.19 | 0.25 | PLEOSDRAFT_48944 | A0A067P7U7 | MR_MLE domain-containing protein |
| | 4.89 | 0.64 | PLEOSDRAFT_49322 | A0A067P3V0 | Beta_elim_lyase domain-containing protein |
| | 2.38 | 0.24 | PLEOSDRAFT_49987 | A0A067NYP3 | S-methyl-5'-thioadenosine phosphorylase |
| | 1.47 | 0.26 | PLEOSDRAFT_51281 | A0A067NTC0 | Phosphoribosylformylglycinamidine synthase |
| | | | **Down Regulated proteins** | | |
| ***Carbohydrates biosynthetic process*** | 5.53 | -0.92 | PLEOSDRAFT_1044084 | A0A067NS78 | Phosphomannomutase |
| | 3.37 | -0.40 | PLEOSDRAFT_1058940 | A0A067N730 | Glycosyltransferase family 20 protein |
| | 4.46 | -0.80 | PLEOSDRAFT_1089538 | A0A067NUZ3;A0A067NWF1;A0A067NUZ3 | Phosphoenolpyruvate carboxykinase (ATP) (Fragment);Phosphoenolpyruvate carboxykinase (ATP) (Fragment) |

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|---|---|---|---|---|---|
|  | 2.19 | -0.43 | PLEOSDRAFT_1089539 | A0A067NIV8;A0A067NWF1;A0A067NIV8 | Phosphoenolpyruvate carboxykinase [ATP];Phosphoenolpyruvate carboxykinase [ATP] |
|  | 3.43 | -0.85 | PLEOSDRAFT_1091186 | A0A067NYY4;A0A067P8J0 | 1,3-beta-glucan synthase |
|  | 3.60 | -0.17 | PLEOSDRAFT_1091820 | A0A067NUJ5 | Glycosyltransferase family 20 protein |
|  | 3.97 | -0.30 | PLEOSDRAFT_1112299 | A0A067NNJ9 | 1,4-alpha-glucan-branching enzyme (Fragment) |
|  | 3.59 | -0.62 | PLEOSDRAFT_1114673 | A0A067NG33 | Glycogen [starch] synthase |
|  | **Up-regulated proteins** |  |  |  |  |
|  | 3.52 | 0.68 | PLEOSDRAFT_1060638 | A0A067PAN8 | GDP-L-fucose synthase |
|  | 4.82 | 0.39 | PLEOSDRAFT_1064869 | A0A067NV87 | Glucose-6-phosphate isomerase |
|  | 6.87 | 1.14 | PLEOSDRAFT_1090849 | A0A067NI38 | Triosephosphate isomerase |
| ***Lipid biosynthesis*** | **Down Regulated proteins** |  |  |  |  |
|  | 2.16 | -0.58 | PLEOSDRAFT_1050437 | A0A067N3Z0 | Acyl-CoA desaturase |
|  | 2.49 | -0.44 | PLEOSDRAFT_1056854 | A0A067NKI4 | Terpenoid synthase |
|  | 2.24 | -0.53 | PLEOSDRAFT_1060887 | A0A067NYS6 | CDP-diacylglycerol--inositol 3-phosphatidyltransferase |
|  | 4.02 | -2.20 | PLEOSDRAFT_1062065 | A0A067P6D9 | PSDC domain-containing protein |
|  | 2.71 | -0.70 | PLEOSDRAFT_1064420 | A0A067NNF3 | 1-acyl-sn-glycerol-3-phosphate acyltransferase |
|  | 2.58 | -1.84 | PLEOSDRAFT_1068722 | A0A067N2Z9 | Ceramide very long chain fatty acid hydroxylase |
|  | 1.25 | -0.55 | PLEOSDRAFT_1088060 | A0A067PCQ7 | Fatty acid hydroxylase domain-containing protein |
|  | 2.46 | -0.26 | PLEOSDRAFT_1113039 | A0A067NEB3 | Terpenoid synthase |

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| | 4.47 | -0.48 | PLEOSDRAFT_154934 | A0A067NTA0 | Leuk-A4-hydro_C domain-containing protein |
| | 3.17 | -0.46 | PLEOSDRAFT_171277 | A0A067N6D1 | Sphingolipid C9-methyltransferase |
| | 5.70 | -0.55 | PLEOSDRAFT_50927 | A0A067NIY8 | Very-long-chain 3-oxoacyl-CoA reductase |
| | 1.82 | -0.37 | PSD1 | A0A067P1J4 | Phosphatidylserine decarboxylase proenzyme 1, mitochondrial |
| | 3.91 | -0.29 | PSD2 | A0A067NDV1 | Phosphatidylserine decarboxylase proenzyme 2 |
| | | | **Up Regulated proteins** | | |
| | 7.42 | 2.56 | PLEOSDRAFT_1056866 | A0A067NN68 | Inositol-3-phosphate synthase |
| | 1.48 | 1.64 | PLEOSDRAFT_1069395 | A0A067PBH4 | CDP-diacylglycerol--serine O-phosphatidyltransferase |
| | 5.38 | 1.24 | PLEOSDRAFT_1071633 | A0A067NFE3 | Hydroxymethylglutaryl-CoA synthase |
| | 1.67 | 0.37 | PLEOSDRAFT_1092315 | A0A067NV02 | Isopentenyl-diphosphate Delta-isomerase |
| | 3.18 | 0.24 | PLEOSDRAFT_1093271 | A0A067NKJ0 | Diphosphomevalonate decarboxylase |
| | 1.10 | 0.21 | PLEOSDRAFT_1111461 | A0A067NRY0 | Acyl carrier protein |
| | 6.15 | 0.30 | PLEOSDRAFT_33075 | A0A067NAR2 | Fatty acid synthase subunit alpha |
| ***Stress responce*** | | | **Down Regulated proteins** | | |
| | 2.78 | -0.22 | PLEOSDRAFT_1038295 | A0A067NM20 | Actin-related protein 4 |
| | 5.59 | -0.66 | PLEOSDRAFT_1041327 | A0A067NUQ4 | UV excision repair protein RAD23 |

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| 1.14 | -0.63 | PLEOSDRAFT_1045135 | A0A067NCL6 | AAA_23 domain-containing protein |
| 4.18 | -0.62 | PLEOSDRAFT_1045442 | A0A067NMH7 | Structural maintenance of chromosomes protein |
| 7.39 | -1.11 | PLEOSDRAFT_1062334 | A0A067P2Z7 | Thioredoxin reductase |
| 2.27 | -0.26 | PLEOSDRAFT_1079704 | A0A067N5M9 | DNA_MISMATCH_REPAIR_2 domain-containing protein |
| 5.07 | -0.46 | PLEOSDRAFT_1097379 | A0A067NG67 | XPGI domain-containing protein |
| 1.17 | -1.05 | PLEOSDRAFT_1101314 | A0A067P1S3 | ATP-dependent DNA helicase II subunit 2 |
| 2.61 | -1.51 | PLEOSDRAFT_176186 | A0A067NP48 | RTA1-domain-containing protein |
| 4.89 | -0.95 | PLEOSDRAFT_23768 | A0A067NST4 | BRCA-2_OB1 domain-containing protein |
| 4.70 | -3.94 | VP3 | A0A067NKY1 | Peroxidase |
| **Up Regulated proteins** |  |  |  |  |
| 3.86 | 0.69 | CCP | A0A067NK95 | Peroxidase |
| 2.96 | 0.29 | NDUFA6 | A0A067NKS2 | NDUFA6, NADH-ubiquinone oxidoreductase 14.8 kDa |
| 3.29 | 0.36 | PIM1 | A0A067N8L4 | Lon protease homolog, mitochondrial |
| 2.92 | 0.59 | PLEOSDRAFT_1008602 | A0A067NTM0 | Actin-like protein arp5 (Fragment) |
| 3.56 | 2.23 | PLEOSDRAFT_1057999 | A0A067NFJ2 | Thiamine thiazole synthase |
| 5.32 | 0.78 | PLEOSDRAFT_1067519 | A0A067NA41 | Survival factor 1 |
| 1.12 | 0.53 | PLEOSDRAFT_1085502 | A0A067N876;A0A067N876;A0A067NYK8;A0A067N876;A0A067P833 | Heme peroxidase;Heme peroxidase;Heme peroxidase |
| 3.11 | 0.41 | PLEOSDRAFT_1090305 | A0A067NBV4 | Glutathione peroxidase |
| 6.36 | 2.21 | PLEOSDRAFT_1090819 | A0A067NHY5 | Catalase |

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| | 1.60 | 0.44 | PLEOSDRAFT_1091949 | A0A067N876;A0A067P833;A0A067P833 | Heme peroxidase;Cytochrome P450 |
| | 3.82 | 0.26 | PLEOSDRAFT_1099644 | A0A067PCS0 | Mitochondrial protein import protein MAS5 |
| | 4.28 | 0.84 | PLEOSDRAFT_46396 | A0A067N9R6 | Peptide-methionine (S)-S-oxide reductase |
| | 1.49 | 0.57 | PLEOSDRAFT_53109 | A0A067N2Y0 | DNA_mis_repair domain-containing protein |
| ***Redox processes*** | **Down Regulated proteins** | | | | |
| | 1.77 | -0.29 | PLEOSDRAFT_1042143 | A0A067NUT8 | Glutaredoxin domain-containing protein |
| | 4.25 | -1.24 | PLEOSDRAFT_1043990 | A0A067NFU9 | Glutaredoxin domain-containing protein (Fragment) |
| | 2.26 | -0.28 | PLEOSDRAFT_1061347 | A0A067P361 | PITH domain-containing protein |
| | 7.39 | -1.11 | PLEOSDRAFT_1062334 | A0A067P2Z7 | Thioredoxin reductase |
| | 3.30 | -0.55 | PLEOSDRAFT_61361 | A0A067NXK3 | Thioredoxin-domain-containing protein |
| | **Up Regulated proteins** | | | | |
| | 3.69 | 2.02 | PLEOSDRAFT_1054608 | A0A067P6N3 | Glutaredoxin domain-containing protein |
| | 4.70 | 0.47 | PLEOSDRAFT_1064231 | A0A067NPJ6;A0A067NR11;A0A067NR11 | Protein disulfide-isomerase;Protein disulfide-isomerase |
| | 3.14 | 0.48 | PLEOSDRAFT_1089747 | A0A067NQN6 | Thioredoxin domain-containing protein |
| | 4.02 | 0.99 | PLEOSDRAFT_1090141 | A0A067NQ75 | Thioredoxin domain-containing protein |

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| | 3.50 | 0.28 | PLEOSDRAFT_1102085 | A0A067P5E3 | Thioredoxin domain-containing protein |
| | 1.27 | 0.27 | PLEOSDRAFT_1114009 | A0A067NA98 | Thioredoxin domain-containing protein |
| | 5.33 | 1.02 | PLEOSDRAFT_40885 | A0A067NNU1 | Thioredoxin domain-containing protein |
| | 2.60 | 0.42 | PLEOSDRAFT_62289 | A0A067N5Y3 | Dihydrolipoyl dehydrogenase |
| | | | **Down Regulated proteins** | | |
| ***Nucleotide biosynthetic process*** | 2.86 | -0.21 | ATP3 | A0A067P946 | ATP synthase subunit gamma (Fragment) |
| | 1.62 | -0.16 | ATP5 | A0A067NUN8 | ATP synthase subunit 5, mitochondrial |
| | 1.76 | -0.52 | BNA4 | A0A067NYR6 | Kynurenine 3-monooxygenase |
| | 1.69 | -0.22 | PLEOSDRAFT_1049922 | A0A067N3P6 | Orotate phosphoribosyltransferase |
| | 3.59 | -0.60 | PLEOSDRAFT_1066023 | A0A067NFT2 | Dihydroorotate dehydrogenase (quinone), mitochondrial |
| | 1.77 | -0.41 | PLEOSDRAFT_1066756 | A0A067NNI7 | AMP deaminase |
| | 3.88 | -0.52 | PLEOSDRAFT_1088731 | A0A067P636 | ATP synthase subunit e, mitochondrial |
| | 3.20 | -0.24 | PLEOSDRAFT_1091324 | A0A067NYD2 | Mitochondrial ATP synthase epsilon chain |
| | 2.06 | -0.58 | PLEOSDRAFT_1093786 | A0A067NT11 | Glutamine-dependent NAD(+) synthetase |
| | 1.68 | -0.20 | PLEOSDRAFT_1110948 | A0A067NUN3 | Plasma membrane ATPase |
| | 2.10 | -0.27 | PLEOSDRAFT_1113928 | A0A067NMD2 | CTP synthase |
| | 1.50 | -0.24 | PLEOSDRAFT_159224 | A0A067NIR6 | dTMP kinase |

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| | 3.47 | -1.09 | PLEOSDRAFT_49162 | A0A067NQC4 | DHO_dh domain-containing protein |
| | 1.47 | -0.26 | PLEOSDRAFT_51281 | A0A067NTC0 | Phosphoribosylformylglycinamidine synthase |
| | **Up Regulated proteins** | | | | |
| | 4.88 | 0.57 | ADK1 | A0A067P416 | Adenylate kinase |
| | 3.39 | 0.47 | ATP16 | A0A067NL68 | ATP synthase subunit delta, mitochondrial |
| | 1.28 | 0.29 | ATP4 | A0A067NEH1 | ATP synthase subunit 4 |
| | 2.28 | 0.29 | ATP7 | A0A067NMW7 | ATP synthase subunit d, mitochondrial |
| | 3.45 | 0.38 | BNA1 | A0A067N4U9 | 3-hydroxyanthranilate 3,4-dioxygenase |
| | 3.82 | 0.60 | BNA5 | A0A067P9X7 | Kynureninase |
| | 1.17 | 0.26 | PLEOSDRAFT_1039444 | A0A067NNN3 | Phosphoribosylaminoimidazole-succinocarboxamide synthase |
| | 2.29 | 0.20 | PLEOSDRAFT_1052542 | A0A067PBA8 | Nucleoside diphosphate kinase |
| | 0.92 | 0.86 | PLEOSDRAFT_1065222 | A0A067NWB4 | ATP-NAD kinase |
| | 3.19 | 0.67 | PLEOSDRAFT_1078660 | A0A067NC97 | Nicotinate phosphoribosyltransferase |
| | 3.03 | 0.61 | PLEOSDRAFT_1090538 | A0A067NLS5 | ATP synthase subunit g, mitochondrial |
| | 3.22 | 0.53 | PLEOSDRAFT_1090677 | A0A067NAX7 | Inosine-5'-monophosphate dehydrogenase |
| | 4.54 | 0.47 | PLEOSDRAFT_159040 | A0A067NG73 | MGS-like domain-containing protein |
| | 2.36 | 0.56 | PLEOSDRAFT_26417 | A0A067NNI2 | Thymidylate synthase |
| | 0.86 | 0.63 | PLEOSDRAFT_28785 | A0A067NKR9 | ATP-NAD kinase |
| | 2.86 | 0.52 | PLEOSDRAFT_52752 | A0A067NI42 | Adenylosuccinate lyase |