# COG functional analysis between initial states

The proteins spectra quantifications were represented in krona plots, along with their **COG general function category (COG general)**, **COG functional category (COG functional)**, **COG protein description (COG description) and COG (COG ID)** – e.g. **METABOLISM**; **Energy production and conversion**; **Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit**; **COG1013**; **A0A090I6X8**.

Two types of representation were obtained:

1. Number of proteins – each protein is assigned the value of 1 in the plot, thus giving the same weight for each protein
2. Weighted – quantifies the differential expression of the proteins by two different methods, depending on whether the protein was detected on both conditions or only one
   1. Protein was only detected in one condition – the value associated is the spectra count for that protein
   2. Protein was detected in both conditions – the value associated is the % of under/overexpression from control to AC

138 proteins were only detected in control, 209 were underexpressed in AC, 68 were overexpressed in AC and 59 were only detected in AC.

## Only detected in control

The COG general categories of the proteins detected were as follow:

* 43% of proteins from METABOLISM – 12% related to amino acid transport and metabolism; 10% to Energy production and conversion, 9% to Coenzyme transport and metabolism and the remaining 12% to Nucleotide transport and metabolism, Carbohydrate transport and metabolism, Inorganic ion transport and metabolism, Lipid transport and metabolism and Secondary metabolites biosynthesis, transport and catabolism
* 23% from INFORMATION STORAGE AND PROCESSING – 15% related to Translation, ribosomal structure and biogenesis, 6% to Transcription and the remaining 2% to Replication, recombination and repair and Chromatin structure and dynamics
* 20% POORLY CHARACTERIZED
* 14% from CELLULAR PROCESSES AND SIGNALING – 6% related to Cell wall/membrane/envelope biogenesis, 4% to Posttranslational modification, protein turnover, chaperones and the remaining 4% to Signal transduction mechanisms, Intracellular trafficking, secretion, and vesicular transport and Defense mechanisms

When considering the spectra count, INFORMATION STORAGE AND PROCESSING accounts for 28% of spectra (with 23% of proteins) and some proteins from different pathways stand out in the data. Table 1 reports the proteins with 1% or more of spectra.

Table 1 - Most abundant proteins from those only detected in control

|  |  |  |  |
| --- | --- | --- | --- |
| **COG general** | **COG functional** | **COG description** | **% of spectra** |
| METABOLISM | Energy production and conversion | Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit | 3 |
| Fe-S oxidoreductases | 1 |
| Amino acid transport and metabolism | Transglutaminase-like enzymes, putative cysteine proteases | 2 |
| Coenzyme transport and metabolism | Delta-aminolevulinic acid dehydratase | 2 |
| Carbohydrate transport and metabolism | 2-phosphoglycerate kinase | 1 |
| Lipid transport and metabolism | Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases | 2 |
| INFORMATION STORAGE AND PROCESSING | Translation, ribosomal structure and biogenesis | Ribosomal protein L19E | 2 |
| Ribosomal protein S4 and related proteins | 2 |
| Prolyl-tRNA synthetase | 2 |
| Predicted exosome subunit | 1 |
| Ribosomal protein L16/L10E | 1 |
| Transcription | Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs | 2 |
| Transcription initiation factor TFIIIB, Brf1 subunit/Transcription initiation factor TFIIB | 2 |
| Replication, recombination and repair | DNA topoisomerase VI, subunit B | 2 |
| CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Predicted phosphosugar isomerases | 3 |
| Nucleoside-diphosphate-sugar epimerases | 1 |
| Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon) | 1 |
| ATPases of the AAA+ class | 2 |
| Signal recognition particle GTPase | 2 |
| Total | | | 34 |

## Underexpressed in AC

The COG general categories of the proteins underexpressed in AC were as follow:

* 41% of proteins from METABOLISM – 13% related to Energy production and conversion; 10% to Amino acid transport and metabolism; 8% to Coenzyme transport and metabolism and the remaining 10% to Nucleotide transport and metabolism, Lipid transport and metabolism, Inorganic ion transport and metabolism and Carbohydrate transport and metabolism
* 22% from INFORMATION STORAGE AND PROCESSING – 16% related to Translation, ribosomal structure and biogenesis; 4% to Transcription and the remaining 2% to Replication, recombination and repair
* 20% POORLY CHARACTERIZED
* 14% from CELLULAR PROCESSES AND SIGNALING – 7% related to Posttranslational modification, protein turnover, chaperones; 5% to Cell wall/membrane/envelope biogenesis and the remaining 5% to Cell cycle control, cell division, chromosome partitioning; Signal transduction mechanisms and Defense mechanisms

Table 2 reports the proteins with over 65% underexpression from control to AC.

Table 2 - Proteins with over 65% underexpression from control to AC

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COG general** | **COG functional** | **COG description** | **UniProt ID** | **% of underexpression** |
| METABOLISM | Lipid transport and metabolism | Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases | A0A090I3L1 | 88 |
| Amino acid transport and metabolism | Transglutaminase-like enzymes, putative cysteine proteases | A0A090I2R3 | 77 |
| Dihydrodipicolinate reductase | A0A090I521 | 67 |
| Coenzyme transport and metabolism | Tetrahydromethanopterin S-methyltransferase, subunit A | A0A090I2G3 | 72 |
| Inorganic ion transport and metabolism | ABC-type phosphate transport system, periplasmic component | A0A090JUG7 | 69 |
| Nucleotide transport and metabolism | Orotate phosphoribosyltransferase | A0A090I4T3 | 68 |
| INFORMATION STORAGE AND PROCESSING | Translation, ribosomal structure and biogenesis | Ribosomal protein S4E | A0A090I1H9 | 73 |
| Ribosomal protein L11 | A0A089ZEW4 | 72 |
| Ribosomal protein L6P/L9E | A0A090JTE0 | 67 |
| CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Putative peptidoglycan-binding domain-containing protein | A0A090I4G9 | 92 |
| Putative peptidoglycan-binding domain-containing protein | A0A090I9S3 | 85 |
| Membrane carboxypeptidase/penicillin-binding protein | A0A090I5J7 | 83 |
| Predicted sugar phosphate isomerase involved in capsule | A0A090JU20 | 75 |
| 20S proteasome, alpha and beta subunits | A0A090I2W9 | 70 |

## Overexpressed in AC

The COG general categories of the proteins overexpressed in AC were as follow:

* 57% of proteins from METABOLISM – 19% related to Energy production and conversion; 12% to Amino acid transport and metabolism; 7% to Coenzyme transport and metabolism; 6% to Carbohydrate transport and metabolism; 6% to Nucleotide transport and metabolism and the remaining 7% to Inorganic ion transport and metabolism and Lipid transport and metabolism
* 19% POORLY CHARACTERIZED
* 15% from INFORMATION STORAGE AND PROCESSING – 10% related to Translation and the remaining 4% to Transcription and Replication, recombination and repair
* 9% from CELLULAR PROCESSES AND SIGNALING – 6% related to Cell wall/membrane/envelope biogenesis and the remaining 2% to Cell cycle control, cell division, chromosome partitioning and Intracellular trafficking, secretion, and vesicular transport

Table 3 reports the proteins with over 65% underexpression from control to AC.

Table 1 - Most abundant proteins from those only detected in control

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **COG general** | **COG functional** | **COG description** | **UniProt ID** | **% of overexpression** |
| METABOLISM | Energy production and conversion | Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit | A0A090I431 | 106 |
| Formylmethanofuran dehydrogenase subunit E | A0A090I368 | 91 |
| Heterodisulfide reductase, subunit A and related polyferredoxins | A0A090I3G7 | 78 |
| Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) | A0A089ZG23 | 68 |
| Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) | A0A090I2F4 | 57 |
| Uncharacterized flavoproteins | A0A090I4R4 | 50 |
| Lipid transport and metabolism | Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain) | A0A090JTT4 | 62 |
| Inorganic ion transport and metabolism | ABC-type Fe3+-hydroxamate transport system, periplasmic component | A0A090I3I6 | 58 |
| POORLY CHARACTERIZED | General function prediction only | Protein containing a metal-binding domain shared with formylmethanofuran dehydrogenase subunit E | A0A090I5F3 | 900 |
| Predicted dinucleotide-binding enzymes | A0A090I4X8 | 150 |
| Predicted Fe-S oxidoreductases | A0A089Z928 | 106 |
| FOG: CBS domain | A0A090I314 | 82 |
| Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB) | A0A090I3C5 | 55 |

## Only detected in control

The COG general categories of the proteins only detected in AC were as follow:

* 49% of proteins from METABOLISM – 14% related to Amino acid transport and metabolism; 8% to Coenzyme transport and metabolism; 7% to Energy production and conversion, 7% to Nucleotide transport and metabolism; 5% to Inorganic ion transport and metabolism and the remaining 8% to Carbohydrate transport and metabolism, Secondary metabolites biosynthesis, transport and catabolism and Lipid transport and metabolism
* 14% from INFORMATION STORAGE AND PROCESSING – 7% related to Translation, ribosomal structure and biogenesis, 5% to Transcription and 2% to Replication, recombination and repair
* 25% POORLY CHARACTERIZED
* 12% from CELLULAR PROCESSES AND SIGNALING – 5% related to Cell wall/membrane/envelope biogenesis, and 2% related to each of Cell cycle control, cell division, chromosome partitioning, Intracellular trafficking, secretion, and vesicular transport, Posttranslational modification, protein turnover, chaperones and Signal transduction mechanisms

When considering the spectra count, INFORMATION STORAGE AND PROCESSING accounts for 28% of spectra (with 23% of proteins) and some proteins from different pathways stand out in the data. Table 1 reports the proteins with 1% or more of spectra.

Table 1 - Most abundant proteins from those only detected in AC

|  |  |  |  |
| --- | --- | --- | --- |
| **COG general** | **COG functional** | **COG description** | **% of spectra** |
| METABOLISM | Amino acid transport and metabolism | Carbamoylphosphate synthase large subunit (split gene in MJ) | 3 |
| Glutamate dehydrogenase/leucine dehydrogenase | 3 |
| Coenzyme transport and metabolism | Coenzyme F390 synthetase | 5 |
| Cobalamin biosynthesis protein CobN and related Mg-chelatases | 2 |
| Nucleotide transport and metabolism | Oxygen-sensitive ribonucleoside-triphosphate reductase | 4 |
| Energy production and conversion | Formylmethanofuran dehydrogenase subunit B | 3 |
| Uncharacterized flavoproteins | 2 |
| Lipid transport and metabolism | Acetyl/propionyl-CoA carboxylase, alpha subunit | 2 |
| INFORMATION STORAGE AND PROCESSING | Transcription | Rad3-related DNA helicases | 6 |
| Histone acetyltransferase | 5 |
| Translation, ribosomal structure and biogenesis | Methionyl-tRNA synthetase | 3 |
| Arginyl-tRNA synthetase | 2 |
| Replication, recombination and repair | Archaeal DNA polymerase II, large subunit | 5 |
| CELLULAR PROCESSES AND SIGNALING | Posttranslational modification, protein turnover, chaperones | La protein, small RNA-binding pol III transcript stabilizing protein and related La-motif-containing proteins involved in translation | 3 |
| Signal transduction mechanisms | FOG: CheY-like receiver | 3 |
| Total | | | 51 |