**Table S2:**  Functional categories of thermo-regulated genes

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Functional Category** | **# of Genesa** | **% of Total genes** | **% of Genes Temperature Sensitiveb** | **Cold Induced** | **% of Cold Induced Genes** | **Hot Induced** | **% of Hot Induced Genes** |
| Type VI secretion system | 28 | 0.55 | 67.9 | 18 | 5.3 | 1 | 0.1 |
| QAC metabolism and transport | 42 | 0.82 | 66.7 | 5 | 1.5 | 23 | 2.1 |
| Toxin-Antitoxin system | 6 | 0.12 | 66.7 | 0 | 0.0 | 4 | 0.4 |
| Phytotoxin synthesis and transport | 23 | 0.45 | 60.9 | 14 | 4.1 | 0 | 0.0 |
| Cold shock proteins | 5 | 0.10 | 60.0 | 1 | 0.3 | 2 | 0.2 |
| Chaperones/Heat shock proteins | 28 | 0.55 | 57.1 | 1 | 0.3 | 15 | 1.4 |
| TAT secretion system | 10 | 0.20 | 50.0 | 0 | 0.0 | 5 | 0.5 |
| Plant-associated proteins | 11 | 0.22 | 45.5 | 0 | 0.0 | 5 | 0.5 |
| Amino acid metabolism and transport (GABA) | 7 | 0.14 | 42.9 | 0 | 0.0 | 3 | 0.3 |
| Phage & IS elements | 125 | 2.45 | 42.4 | 37 | 10.9 | 16 | 1.4 |
| Special | 12 | 0.24 | 41.7 | 0 | 0.0 | 5 | 0.5 |
| Transport (peptides) | 36 | 0.71 | 38.9 | 3 | 0.9 | 11 | 1.0 |
| Siderophore synthesis and transport | 76 | 1.49 | 38.2 | 10 | 3.0 | 19 | 1.7 |
| Polysaccharide synthesis and regulation | 49 | 0.96 | 36.7 | 11 | 3.3 | 7 | 0.6 |
| Type III secretion system | 49 | 0.96 | 36.7 | 0 | 0.0 | 18 | 1.6 |
| Carbohydrate metabolism and transport | 117 | 2.29 | 35.0 | 8 | 2.4 | 33 | 3.0 |
| Transcriptional regulation | 200 | 3.92 | 34.5 | 0 | 0.0 | 69 | 6.2 |
| Chemosensing & chemotaxis | 73 | 1.43 | 34.2 | 23 | 6.8 | 2 | 0.2 |
| Oxidative stress tolerance (Antioxidant enzyme) | 15 | 0.29 | 33.3 | 2 | 0.6 | 3 | 0.3 |
| Flagellar synthesis and motility | 48 | 0.94 | 33.3 | 15 | 4.4 | 1 | 0.1 |
| Outer membrane proteins | 24 | 0.47 | 33.3 | 4 | 1.2 | 4 | 0.4 |
| Fatty acid metabolism | 55 | 1.08 | 30.9 | 1 | 0.3 | 16 | 1.4 |
| Hypotheticalc | 1219 | 23.87 | 29.9 | 57 | 16.9 | 307 | 27.7 |
| Transport | 101 | 1.98 | 29.7 | 3 | 0.9 | 27 | 2.4 |
| Mechanosensitive ion channel | 7 | 0.14 | 28.6 | 0 | 0.0 | 2 | 0.2 |
| Secretion/Efflux/Export | 100 | 1.96 | 28.0 | 6 | 1.8 | 22 | 2.0 |
| Sulfur metabolism and transport | 61 | 1.19 | 27.9 | 0 | 0.0 | 17 | 1.5 |
| Secondary metabolism | 26 | 0.51 | 26.9 | 3 | 0.9 | 4 | 0.4 |
| Organic acid metabolism and transport | 105 | 2.06 | 26.7 | 4 | 1.2 | 24 | 2.2 |
| Cyclic di-GMP cyclase proteins | 34 | 0.67 | 26.5 | 2 | 0.6 | 7 | 0.6 |
| Compatible solute synthesis | 19 | 0.37 | 26.3 | 0 | 0.0 | 5 | 0.5 |
| Unannotatedd | 1007 | 19.72 | 26.2 | 36 | 10.7 | 226 | 20.4 |
| Pili synthesis and regulation | 51 | 1.00 | 25.5 | 2 | 0.6 | 11 | 1.0 |
| Transcription - Sigma factor | 16 | 0.31 | 25.0 | 1 | 0.3 | 3 | 0.3 |
| Phosphate metabolism and transport | 20 | 0.39 | 25.0 | 2 | 0.6 | 3 | 0.3 |
| Amino acid metabolism and transport | 238 | 4.66 | 24.4 | 18 | 5.3 | 40 | 3.6 |
| Energy generation | 83 | 1.63 | 24.1 | 7 | 2.1 | 13 | 1.2 |
| LPS synthesis and transport | 38 | 0.74 | 23.7 | 1 | 0.3 | 8 | 0.7 |
| Nitrogen metabolism | 57 | 1.12 | 22.8 | 2 | 0.6 | 11 | 1.0 |
| Stress resistance | 41 | 0.80 | 22.0 | 0 | 0.0 | 9 | 0.8 |
| Polyamine metabolism and transport | 19 | 0.37 | 21.1 | 0 | 0.0 | 4 | 0.4 |
| Transport (inorganic ions) | 48 | 0.94 | 20.8 | 1 | 0.3 | 9 | 0.8 |
| Osmosensing & regulation | 5 | 0.10 | 20.0 | 1 | 0.3 | 0 | 0.0 |
| Degradation of xenobiotics | 15 | 0.29 | 20.0 | 0 | 0.0 | 3 | 0.3 |
| Transcription | 10 | 0.20 | 20.0 | 2 | 0.6 | 0 | 0.0 |
| RNA degradation | 16 | 0.31 | 18.8 | 3 | 0.9 | 0 | 0.0 |
| Cofactor metabolism | 152 | 2.98 | 18.4 | 1 | 0.3 | 27 | 2.4 |
| Transport (organic compounds) | 11 | 0.22 | 18.2 | 0 | 0.0 | 2 | 0.2 |
| Light and oxygen sensing | 11 | 0.22 | 18.2 | 0 | 0.0 | 2 | 0.2 |
| Proteases | 17 | 0.33 | 17.6 | 1 | 0.3 | 2 | 0.2 |
| Signal transduction mechanisms | 40 | 0.78 | 17.5 | 4 | 1.2 | 3 | 0.3 |
| Translation | 132 | 2.59 | 16.7 | 19 | 5.6 | 3 | 0.3 |
| Post-translational modification | 12 | 0.24 | 16.7 | 0 | 0.0 | 2 | 0.2 |
| Glutathione metabolism | 18 | 0.35 | 16.7 | 1 | 0.3 | 2 | 0.2 |
| Quorum regulation | 6 | 0.12 | 16.7 | 0 | 0.0 | 1 | 0.1 |
| Iron metabolism and transport | 27 | 0.53 | 14.8 | 0 | 0.0 | 4 | 0.4 |
| Phospholipid metabolism | 36 | 0.71 | 13.9 | 4 | 1.2 | 21 | 1.9 |
| Nucleotide metabolism and transport | 83 | 1.63 | 12.0 | 3 | 0.9 | 7 | 0.6 |
| Replication and DNA repair | 97 | 1.90 | 11.3 | 0 | 0.0 | 11 | 1.0 |
| Oxidative stress tolerance | 11 | 0.22 | 9.1 | 1 | 0.3 | 0 | 0.0 |
| Terpenoid backbone synthesis | 12 | 0.24 | 8.3 | 0 | 0.0 | 1 | 0.1 |
| Peptidoglycan/cell wall polymers | 29 | 0.57 | 6.9 | 0 | 0.0 | 2 | 0.2 |
| Iron-sulfur proteins | 14 | 0.27 | 0.0 | 0 | 0.0 | 0 | 0.0 |
| Oxidative stress tolerance (antioxidant enzyme) | 2 | 0.04 | 0.0 | 0 | 0.0 | 0 | 0.0 |
| Cell division | 21 | 0.41 | 0.0 | 0 | 0.0 | 0 | 0.0 |
| Total | 5106 | 100.0 | 28.3 | 338 | 100.0 | 1107 | 100.0 |

aTotal number of genes within functional category

bPercentage of functional category that is temperature sensitive

cHypothetical refers to predicted proteins with no discernable domain or motifs

dUnannotated refers to predicted proteins with discernable domains or motifs, but lack sufficient evidence to place within a functional category