## Additional file 5: Clusters of differential expressed genes in C. beijerinckii DSM6423 glucose fermentation

| ı | Clusters     | gen | es  |
|---|--------------|-----|-----|
| ı | name         | nb  | %   |
| ı | 6up++        | 18  | 44% |
| ı | 6up+         | 58  | 21% |
| ı | 6up          | 431 | 1%  |
| ı | 6down        | 203 | 21% |
| ı | 6down-       | 14  | 6%  |
| ı | 8up+         | 8   | 2%  |
| ı | 8up          | 206 | 0%  |
| ı | 8down        | 6   | 1%  |
| ı | 11up         | 23  | 1%  |
| ı | Unclassified | 20  | 2%  |
|   | TOTAL        | 987 |     |

Genes Cluster log2(FC vs T3h) functional annotation name T6/T3 T8/T3 T11/T3 T24/T3 function CIBE 0313 6up++ conserved protein of unknown function CIBE 0312 conserved protein of unknown function 6up++ CIBE\_0311 conserved protein of unknown function 6up++ CIBE\_0314 6up++ conserved protein of unknown function CIBE\_0315 6up++ Radical SAM-family protein CIBE\_0310 putative ABC transporter ATP-binding protein 6up++ CIBE\_3477 6up++ Accessory gene regulator B CIBE 3478 6up++ conserved membrane protein of unknown function CIBE 0316 6up++ conserved protein of unknown function CIBE 4430 6up++ putative permease CIBE\_4429 6up++ putative permease CIBE\_0280 6up++ conserved exported protein of unknown function CIBE\_3828 Glycosyl transferase 6up++ 2.7 CIBE 4431 6up++ conserved exported protein of unknown function CIBE\_4419 6up++ conserved exported protein of unknown function CIBF 4428 6up++ Transporter CIBE 4418 6up++ conserved exported protein of unknown function CIBE\_3476 conserved protein of unknown function 6up+ CIBE\_3751 6up+ conserved protein of unknown function CIBE\_3750 6up+ conserved protein of unknown function CIBE 4789 putative AgrB-like protein CIBE\_0824 6up+ Type 11 methyltransferase CIBE 3749 6up+ 2.8 2.7 Peptide synthetase CIBE 5303 conserved protein of unknown function 6up+ 2.8 CIBE 2622 NADPH-dependent butanol dehydrogenase 6up+ CIBE\_4040 Aliphatic sulfonates family ABC transporter, periplsmic ligand-binding protein 6up+ CIBE\_3079 6up+ 2.8 panD aspartate 1-decarboxylase CIBE\_4039 6up+ taurine transporter subunit; ATP-binding component of ABC superfamily CIBE\_3082 6up+ conserved protein of unknown function 2.1 CIBE 4610 6up+ Peptidase C1A, papain 2.2 CIBE 4417 6up+ conserved membrane protein of unknown function 2.8 CIBE 3475 Histidine kinase 6up+ CIBE\_4036 Thioredoxin reductase 6up+ CIBE\_3355 6up+ RNA polymerase sigma factor SigI CIBE\_3081 6up+ 2.8 panB ketopantoate hydroxymethyltransferase CIBE\_4038 2.8 3.3 3.6 4.5 3.4 2.8 3.1 3.3 3.3 2.7 3.8 3.3 3.6 Type I phosphodiesterase/nucleotide pyrophosphatase 6up+ CIBE 2623 6up+ conserved protein of unknown function 2.4 3.1 CIBE 5304 6up+ conserved protein of unknown function 2.9 CIBE 3537 6up+ putative transcriptional regulator CIBE\_5707 conserved protein of unknown function 6up+ CIBE\_0782 Nitrogenase 6up+ CIBE\_4041 6up+ taurine transporter subunit; membrane component of ABC superfamily CIBE\_2624 Sulfide dehydrogenase subunit alpha CIBE 3080 6up+ 2.3 panC pantothenate synthetase 3.4 3.4 2.7 3.2 CIBE 3353 6up+ Beta-glucanase (fragment) 1.9 1.2 CIBE 4861 6up+ conserved protein of unknown function CIBE 3700 6up+ YIEGIA protein 2.4 CIBE\_3753 protein of unknown function 6up+ CIBE\_3354 2.8 bglA 6up+ Beta-glucanase CIBE\_3748 3.7 4.3 3.3 3.5 2.8 putative cyclic peptide transporter 6up+ CIBE 4416 6up+ conserved membrane protein of unknown function CIBE\_1176 6up+ 4.3 3.2 50S ribosomal protein L25 CIBE 4788 6up+ CHAP domain containing protein CIBE 3357 6up+ Carbohydrate-binding family V/XII CIBE\_2891 Electron transport complex, RnfABCDGE type, D subunit 6up+ 3.5 3.9 3.3 2.8 3.0 2.9 2.9 CIBE\_6013 6up+ conserved protein of unknown function CIBE\_0281 6up+ conserved membrane protein of unknown function 1.8 CIBE 4862 2-hydroxyglutaryl-CoA dehydratase 6up+ CIBE 5605 6up+ conserved protein of unknown function 2.3 2.2 CIBE 2892 6up+ Electron transport complex, RnfABCDGE type, G subunit 3.8 3.0 CIBE 5208 6up+ Nucleotidyl transferase CIBE\_0725 6up+ cstA carbon starvation-induced membrane protein 3.0 CIBE\_3837 putative nuclease; skin element 6up+ vga. CIBE\_4414 6up+ Cell wall-associated hydrolase-like protein CIBE\_4037 6up+ Thioredoxin domain CIBE\_5606 6up+ Membrane spanning protein CIBE 3761 6up+ Multidrug transporter MatE 1.6 CIBE 3441 6up+ 2.4 ABC transporter substrate-binding protein CIBE 2221 ytfJ Uncharacterized spore protein YtfJ 6up+ CIBE\_2951 conserved protein of unknown function 6up+ CIBE 2222 6up+ conserved membrane protein of unknown function CIBE\_3534 putative DnaD-like protein, phage replisome organizer

| CIBE_4415<br>CIBE_0309  | 6up+<br>6up+ | 2.4<br>1.4 | 3.5<br>3.2 | 2.6<br>2.4 | 0.5<br>1.1  | -         | conserved protein of unknown function protein of unknown function                                     |
|-------------------------|--------------|------------|------------|------------|-------------|-----------|---|
| CIBE_3352               | 6up          | 3.7        | 3.0        | 2.1        | 3.2         | -         | conserved protein of unknown function   |
| CIBE_3401               | 6up          | 3.1        | 2.8        | 2.2        | 3.8         | -         | conserved protein of unknown function   |
| CIBE_3752               | 6up          | 2.9        | 3.4        | 2.3        | 3.1         | -         | protein of unknown function   |
| CIBE_2321               | 6up          | 3.6        | 2.6        | 2.5        | 2.7         | -         | Membrane-like protein   |
| CIBE_2893               | 6up          | 3.6        | 2.9        | 2.3        | 2.5         | -         | Electron transport complex subunit E  |
| CIBE_0460<br>CIBE 4600  | 6up          | 1.9<br>2.6 | 1.7<br>1.9 | 0.0<br>1.1 | -0.2<br>1.5 | -         | conserved protein of unknown function conserved protein of unknown function                           |
| CIBE_4000<br>CIBE_3469  | 6up<br>6up   | 2.0        | 2.8        | 2.6        | 2.5         | -         | conserved protein of unknown function   |
| CIBE_2894               | 6up          | 3.4        | 3.0        | 2.1        |             | rsxA      | putative inner membrane subunit of an electron transport system                                       |
| CIBE 4602               | 6up          | 2.8        | 1.3        | 0.9        | 0.0         | -         | ThiJ/Pfpl domain protein  |
| CIBE_2895               | 6up          | 3.5        | 2.8        | 2.1        | 2.2         | -         | Protein RnfB  |
| CIBE_3350               | 6up          | 3.9        | 2.3        | 2.0        | 2.4         | -         | Beta and gamma crystallin   |
| CIBE_3770               | 6up          | 3.2        | 2.8        | 2.7        | 1.8         |           | Multi-sensor signal transduction histidine kinase   |
| CIBE_3468               | 6up          | 2.6        | 2.6        | 2.5        |             | sudA      | Sulfide dehydrogenase subunit alpha   |
| CIBE_3356               | 6up          | 3.6        | 2.2        | 1.4<br>2.2 | 3.3<br>2.2  | -         | Glycoside hydrolase, family 18 (modular protein)  |
| CIBE_2889<br>CIBE_6055  | 6up<br>6up   | 3.2<br>2.7 | 2.0        | 1.6        |             | pdxS      | Positive regulator of sigma E, RseC/MucC glutamine amidotransferase for pyridoxal phosphate synthesis |
| CIBE_3769               | 6up          | 2.8        | 2.6        | 3.0        | 1.9         | -         | conserved protein of unknown function   |
| CIBE_4538               | 6up          | 2.4        | 2.2        | 2.7        | 2.9         | -         | RNA polymerase, sigma-24 subunit, ECF subfamily   |
| CIBE_5205               | 6up          | 2.9        | 2.5        | 2.8        | 1.9         | phnW      | 2-aminoethylphosphonatepyruvate transaminase  |
| CIBE_0282               | 6up          | 3.0        | 3.3        | 2.4        | 1.5         | -         | conserved membrane protein of unknown function  |
| CIBE_6021               | 6up          | 3.5        | 2.6        | 2.1        | 1.9         |           | conserved exported protein of unknown function  |
| CIBE_p0005              | 6up          | 3.8        | 2.5        | 1.8        | 2.0         |           | putative Peptidase M10A and M12B matrixin and adamalysin  |
| CIBE_3470               | 6up          | 2.6        | 2.4        | 2.5        | 2.4         | adh       | NADP-dependent isopropanol dehydrogenase  |
| CIBE_3827<br>CIBE_5206  | 6up<br>6up   | 3.1<br>2.8 | 3.2<br>2.5 | 1.7<br>2.6 | 2.0<br>2.0  | -         | protein of unknown function Phosphoenolpyruvate decarboxylase   |
| CIBE_3200<br>CIBE_3176  | 6up          | 2.8        | 2.5        | 2.0        | 2.7         |           | Coagulation factor 5/8 type domain protein  |
| CIBE_3835               | бир<br>6ир   | 2.8        | 3.2        | 1.8        | 2.7         |           | putative Phage replisome organizer  |
| CIBE_5855<br>CIBE_6054  | 6up          | 2.5        | 1.8        | 1.5        |             | pdxT      | glutamine amidotransferase for pyridoxal phosphate synthesis  |
| CIBE_3351               | 6up          | 3.4        | 2.5        | 2.0        | 1.9         | -         | Chitinase   |
| CIBE_3419               | 6up          | 3.5        | 2.5        | 2.0        | 1.7         | -         | conserved protein of unknown function   |
| CIBE_4603               | 6up          | 2.8        | 1.5        | 0.8        | 0.1         | -         | protein of unknown function   |
| CIBE_5207               | 6up          | 2.7        | 2.4        | 2.5        | 1.9         |           | Cytidyltransferase-related domain   |
| CIBE_0579               | 6up          | 1.7        | 2.9        | 2.7        |             | spolIID   | transcriptional regulator   |
| CIBE_2890               | 6up          | 3.1        | 2.3        | 2.0        |             | rnfC      | Electron transport complex subunit RnfC   |
| CIBE_0283<br>CIBE_3110  | 6up          | 2.6<br>3.2 | 3.1<br>2.6 | 2.5<br>0.9 | 2.9         | yybJ      | putative ATP-binding cassette protein protein of unknown function                                     |
| CIBE_3110<br>CIBE_3194  | 6up<br>6up   | 3.4        | 2.0        | 2.0        | 2.9         | -         | GCN5-related N-acetyltransferase  |
| CIBE_3909               | 6up          | 3.2        | 2.2        | 1.9        | 2.2         | _         | protein of unknown function   |
| CIBE_5701               | 6up          | 2.7        | 2.3        | 1.9        | 2.5         |           | Glutamine transport ATP-binding protein GInQ (fragment)   |
| CIBE_1173               | 6up          | 2.5        | 1.8        | 2.0        | 3.0         | -         | Membrane protein  |
| CIBE_6000               | 6up          | 2.6        | 2.3        | 2.5        | 1.9         | -         | GntR family transcriptional regulator   |
| CIBE_5300               | 6up          | 3.2        | 2.3        | 1.8        | 2.0         | -         | FHA domain containing protein   |
| CIBE_5290               | 6up          | 3.9        | 2.4        | 1.8        | 1.1         | -         | conserved protein of unknown function   |
| CIBE_2455               | 6up          | 2.2        | 3.4        | 1.7        | 1.9         |           | conserved protein of unknown function   |
| CIBE_2050<br>CIBE_3200  | 6up          | 3.5<br>3.5 | 2.5<br>2.3 | 1.6<br>1.8 | 1.6<br>1.5  |           | NADPH-dependent butanol dehydrogenase  Cytidine deaminase   |
| CIBE_3200<br>CIBE_0834  | 6up<br>6up   | 2.7        | 2.5        | 1.9        |             | amyA      | Alpha-amylase   |
| CIBE_1313               | 6up          | 3.3        | 2.5        | 2.1        | 1.3         | -         | conserved exported protein of unknown function  |
| CIBE_5299               | 6up          | 3.2        | 2.3        | 2.0        | 1.5         | -         | Protein phosphatase   |
| CIBE_misc_RNA_38        | 6up          | 2.8        | 2.5        | 1.9        | 1.8         | -         | TPP   |
| CIBE_3423               | 6up          | 3.0        | 1.9        | 1.8        | 2.3         | -         | Amino acid adenylation domain protein   |
|                         |              | 2.0        | 2.7        | 2.2        | 2.1         | -         | ydaO-yuaA   |
| CIBE_3421               | 6up          | 2.8        | 1.9        | 1.9        | 2.3         | -         | Long-chain-fatty-acid(Acyl-carrier-protein) ligase., 6-deoxyerythronolide-B synthase                  |
| CIBE_p0006<br>CIBE_3169 | 6up<br>6up   | 3.2        | 2.5<br>2.6 | 1.7<br>1.6 | 1.5         | -<br>ycbN | exported protein of unknown function putative ABC efflux transporter (ATP-binding protein)            |
| CIBE_3103               | 6up          | 3.5        | 2.4        | 1.3        | 1.5         |           | protein of unknown function   |
| CIBE_6115               | 6up          | 1.6        | 3.2        | 1.8        |             | yyaC      | conserved hypothetical protein  |
| CIBE_6012               | 6up          | 3.5        | 2.3        | 1.4        | 1.3         | -         | conserved protein of unknown function   |
| CIBE_3109               | 6up          | 2.9        | 2.0        | 0.9        | 2.9         | -         | conserved protein of unknown function   |
| CIBE_5297               | 6up          | 3.0        | 2.0        | 2.0        | 1.6         |           | Normocyte binding protein 2b  |
| CIBE_3434               | 6up          | 2.9        | 2.1        | 1.5        | 2.1         |           | L-lactate permease  |
| CIBE_5706               | 6up          | 2.4        | 2.5        | 2.2        |             | lagD      | Lactococcin-G-processing and transport ATP-binding protein LagD                                       |
| CIBE_5291               | 6up          | 3.4        | 2.0        | 1.9        | 1.2         | -         | conserved protein of unknown function   |
| CIBE_5288<br>CIBE_4321  | 6up<br>6up   | 3.4<br>1.9 | 2.2<br>2.2 | 1.8<br>2.3 | 1.2<br>2.1  | -         | conserved protein of unknown function RNA polymerase subunit sigma-24                                 |
| CIBE_4321<br>CIBE_6020  | бир<br>6ир   | 3.3        | 2.6        | 1.7        | 0.9         | -         | conserved protein of unknown function   |
| CIBE 3420               | 6up          | 3.1        | 2.1        | 1.8        | 1.5         |           | FMN-binding protein   |
| CIBE_0019               | 6up          | 1.9        | 3.1        | 1.8        | 1.6         |           | conserved protein of unknown function   |
| CIBE_4317               | 6up          | 2.8        | 2.1        | 1.5        | 2.0         |           | conserved protein of unknown function   |
| CIBE_5296               | 6up          | 3.2        | 2.2        | 1.9        | 1.2         | -         | conserved protein of unknown function   |
| CIBE_5286               | 6up          | 3.3        | 2.0        | 1.6        | 1.5         |           | YD repeat protein (fragment)  |
| CIBE_1337               | 6up          | 1.0        | 2.8        | 2.4        | 2.2         |           | conserved membrane protein of unknown function  |
| CIBE_4539               | 6up          | 2.1        | 1.6        | 2.2        | 2.5         |           | conserved protein of unknown function   |
| CIBE_5302               | 6up          | 3.2<br>1.5 | 2.2<br>3.3 | 1.6<br>1.2 | 1.4<br>2.4  |           | Heat shock protein DnaJ domain protein  |
| CIBE_1004<br>CIBE_5294  | 6up<br>6up   | 3.6        | 2.2        | 1.2        | 0.8         |           | conserved exported protein of unknown function conserved protein of unknown function                  |
| CIBE_5294<br>CIBE_6065  | бир<br>6ир   | 3.0        | 2.3        | 1.3        | 1.7         | _         | protein of unknown function   |
| CIBE_5999               | 6up          | 2.5        | 1.7        | 2.3        | 1.8         | -         | SAM-dependent methyltransferase   |
| CIBE_1287               | 6up          | 1.6        | 1.9        | 2.0        | 2.7         |           | Glycosyl transferase  |
| CIBE_1294               | 6up          | 1.7        | 2.0        | 2.1        | 2.6         |           | membrane protein of unknown function  |
| CIBE_3203               | 6up          | 3.3        | 2.0        | 1.4        | 1.5         |           | Valyl-tRNA synthetase (fragment)  |
| CIBE_3247               | 6up          | 2.9        | 1.8        | 1.8        | 1.8         |           | Acetolactate synthase   |
| CIBE_6011               | 6up          | 3.2        | 2.3        | 1.3        | 1.5         |           | conserved protein of unknown function   |
| CIBE_4689               | 6up          | 1.7        | 1.7        | 1.9        | 3.0         |           | Alcohol dehydrogenase GroES domain protein  |
| CIBE_5301               | 6up          | 2.9        | 2.2        | 1.6        | 1.5         |           | conserved protein of unknown function   |
| CIBE_1847               | 6up          | 2.6        | 3.3<br>2.2 | 1.6        | 0.5         | -         | putative pilus biogenesis protein   |
| CIBE_2425<br>CIBE_5287  | 6up<br>6up   | 2.7<br>3.1 | 1.9        | 1.5<br>1.7 | 1.7<br>1.4  | -         | putative molybdenum-pterin-binding protein conserved protein of unknown function                      |
| ISIDE_3207              | Jup          | 5.1        | 1.5        | 1.7        | 1.4         |           | conserved protein or unknown function   |

| CIBE_5705        | 6up   | 2.2 2.4 2.2 1.3 | -    | conserved protein of unknown function   |
|------------------|-------|-----------------|------|---|
| CIBE_3762        | 6up   | 3.0 2.0 1.4 1.7 |      | Helix-turn-helix-domain containing protein, AraC type                                       |
| CIBE_3641        | 6up   | 2.2 2.3 1.7 1.9 |      | conserved protein of unknown function   |
|                  |       |                 |      | ·   |
| CIBE_5295        | 6up   | 3.3 1.9 1.6 1.1 |      | Molecular chaperone   |
| CIBE_3766        | 6up   | 2.3 2.1 2.2 1.3 | -    | conserved protein of unknown function   |
| CIBE_5804        | 6up   | 2.0 2.6 1.6 1.8 | -    | protein of unknown function   |
| CIBE 4320        | 6up   | 1.8 2.0 2.1 1.9 |      | conserved protein of unknown function   |
| _                |       |                 |      | conserved membrane protein of unknown function  |
| CIBE_4537        | 6up   |                 |      | •   |
| CIBE_2940        | 6up   | 3.1 2.0 1.3 1.4 | -    | Lactate racemization operon protein LarA  |
| CIBE_0284        | 6up   | 2.3 3.0 2.4 0.2 | -    | conserved protein of unknown function   |
| CIBE_6001        | 6up   | 2.4 1.9 2.1 1.5 | -    | conserved protein of unknown function   |
| CIBE 5042        |       | 2.1 1.5 2.1 2.0 |      | Sulfate adenylyltransferase   |
| _                | 6up   |                 |      | ·   |
| CIBE_4315        | 6up   | 2.9 1.8 1.4 1.7 |      | conserved protein of unknown function   |
| CIBE_3435        | 6up   | 2.9 2.1 1.4 1.4 | -    | Electron transfer flavoprotein, alpha subunit-like protein                                  |
| CIBE_4919        | 6up   | 3.1 2.5 1.5 0.6 | -    | SAM-dependent methyltransferase   |
| CIBE 3422        | 6up   | 2.6 1.9 1.8 1.5 |      | Major facilitator superfamily MFS 1   |
| _                |       |                 |      | · · · · · · · · · · · · · · · · · · ·   |
| CIBE_3167        | 6up   | 2.7 1.8 1.1 2.1 |      | protein of unknown function   |
| CIBE_2391        | 6up   | 0.9 2.4 2.5 1.8 | xerD | Tyrosine recombinase XerD   |
| CIBE_1297        | 6up   | 1.6 2.2 1.9 1.8 | -    | Polysaccharide biosynthesis protein   |
| CIBE_4604        | 6up   | 3.6 2.4 0.9 0.7 | -    | conserved membrane protein of unknown function  |
| CIBE_0792        |       |                 | тссВ | cystathionine gamma-lyase and homocysteine gamma-lyase for reverse transsulfuration pathway |
|                  | 6up   |                 |      |   |
| CIBE_4729        | 6up   | 3.0 1.9 1.5 1.1 |      | conserved exported protein of unknown function  |
| CIBE_3637        | 6up   | 2.8 2.5 0.8 1.3 | -    | protein of unknown function   |
| CIBE_6002        | 6up   | 2.4 1.7 1.8 1.6 | -    | Membrane protein  |
| CIBE 4690        | 6up   | 1.8 1.4 1.7 2.5 |      | Aminotransferase class-III  |
| _                |       |                 |      |   |
| CIBE_5044        | 6up   | 2.0 1.4 2.1 2.0 |      | Adenylylsulfate reductase subunit beta  |
| CIBE_4730        | 6up   | 2.9 1.9 1.6 1.0 | 1-   | Transcriptional regulator, MerR family  |
| CIBE_5050        | 6up   | 1.8 1.4 2.1 2.1 | sbp  | sulfate transporter subunit; periplasmic-binding component of ABC superfamily               |
| CIBE 0829        | 6up   | 2.4 2.2 1.6 1.1 |      | conserved protein of unknown function   |
| _                |       |                 |      | ·   |
| CIBE_1292        | 6up   | 1.5 1.5 1.9 2.4 |      | Glycosyl transferase family 2   |
| CIBE_4168        | 6up   | 2.2 1.8 1.7 1.6 | -    | 4Fe-4S ferredoxin   |
| CIBE_0046        | 6up   | 0.6 2.4 2.2 2.1 | -    | conserved membrane protein of unknown function  |
| CIBE_3248        | 6up   | 2.7 1.4 1.8 1.4 | -    | NADH:flavin oxidoreductase/NADH oxidase   |
|                  |       | 2.3 1.9 1.5 1.6 |      |   |
| CIBE_4195        | 6up   |                 |      | conserved protein of unknown function   |
| CIBE_3197        | 6up   | 2.6 1.7 1.8 1.2 | -    | conserved exported protein of unknown function  |
| CIBE_3432        | 6up   | 2.8 1.8 1.3 1.3 | acdA | acyl-CoA dehydrogenase  |
| CIBE_5043        | 6up   | 2.0 1.3 2.0 2.0 | cysD | sulfate adenylyltransferase, subunit 2  |
| CIBE_1115        | 6up   | 2.7 2.2 1.2 1.1 |      | Fucose 4-O-acetylase  |
|                  |       |                 |      | ·   |
| CIBE_3343        | 6up   | 2.9 1.5 1.2 1.5 |      | protein of unknown function   |
| CIBE_0103        | 6up   | 0.7 2.5 2.2 1.8 | -    | YabP family protein   |
| CIBE_3086        | 6up   | 2.7 2.0 1.5 0.8 | fabG | 3-oxoacyl-[acyl-carrier-protein] reductase FabG   |
| CIBE_2160        | 6up   | 0.8 2.4 2.5 1.4 |      | Cobalamin synthesis protein, P47K   |
|                  |       |                 |      |   |
| CIBE_3344        | 6up   |                 |      | protein of unknown function   |
| CIBE_2454        | 6up   | 1.9 2.9 1.1 1.3 | -    | protein of unknown function   |
| CIBE_2805        | 6up   | 2.5 1.9 1.7 1.0 | -    | GCN5-related N-acetyltransferase  |
| CIBE_3747        | 6up   | 1.6 2.3 1.9 1.3 | grsB | Gramicidin S synthase 2   |
| CIBE 5298        |       | 2.5 1.8 1.6 1.2 | _    | Serine/threonine protein phosphatase  |
| _                | 6up   |                 |      |   |
| CIBE_3251        | 6up   | 3.5 2.1 1.1 0.4 |      | conserved exported protein of unknown function  |
| CIBE_4606        | 6up   | 3.2 2.7 2.6 2.5 | eutE | Ethanolamine utilization protein EutE   |
| CIBE_2390        | 6up   | 0.8 2.4 2.3 1.6 | -    | Sporulation stage II, protein M   |
| CIBE_3198        | 6up   | 3.2 2.2 0.1 1.6 |      | conserved exported protein of unknown function  |
|                  |       |                 |      |   |
| CIBE_3433        | 6up   | 2.7 1.8 1.3 1.3 |      | 2-hydroxy-acid oxidase  |
| CIBE_5289        | 6up   | 3.3 1.7 1.2 0.8 | -    | conserved protein of unknown function   |
| CIBE_2942        | 6up   | 2.3 2.0 1.4 1.3 | -    | Transcriptional regulator   |
| CIBE_1296        | 6up   | 1.6 1.7 1.7 2.0 | -    | Glycosyltransferase   |
| CIBE 5292        | 6up   | 3.1 1.8 1.5 0.6 |      | conserved protein of unknown function   |
| _                |       |                 |      | ·   |
| CIBE_1367        | 6up   | 1.5 1.8 1.9 1.7 | •    | Phosphate-specific transport system accessory protein PhoU homolog                          |
| CIBE_4731        | 6up   | 2.8 2.0 1.6 0.5 | -    | Acetyltransferase   |
| CIBE_3786        | 6up   | 2.0 1.9 1.4 1.7 | 1-   | Ser/Thr phosphatase family protein  |
| CIBE_1357        | 6up   |                 | sigG | RNA polymerase sporulation-specific sigma factor (sigma-G)                                  |
|                  |       |                 |      |   |
| CIBE_2403        | 6up   |                 | hyuA | D-stereospecific phenylhydantoinase   |
| CIBE_4820        | 6up   |                 | рерО | Neutral endopeptidase PepO  |
| CIBE_2751        | 6up   | 1.7 1.3 1.7 2.1 | yxjH | putative methyl-tetrahydrofolate methyltransferase  |
| CIBE_2420        | 6up   | 2.7 1.8 1.3 1.0 | 1-   | Molybdopterin binding domain  |
| CIBE_0299        | 6up   | 1.8 1.7 1.9 1.4 |      | conserved protein of unknown function   |
|                  |       |                 |      | protein of unknown function   |
| CIBE_3910        | 6up   |                 |      |   |
| CIBE_1633        | 6up   | 0.7 2.2 2.3 1.6 |      | Pyruvate kinase   |
| CIBE_3202        | 6up   | 2.9 1.5 1.1 1.3 | -    | ValyI-tRNA synthetase (fragment)  |
| CIBE_p0012       | 6up   | 2.8 2.0 0.9 1.0 | 1-   | conserved protein of unknown function   |
| CIBE 4173        | 6up   | 2.7 1.9 1.1 1.1 |      | Abortive infection protein  |
| _                |       |                 |      |   |
| CIBE_4540        | 6up   | 1.8 1.7 2.0 1.3 |      | Membrane protein  |
| CIBE_4251        | 6up   | 3.0 1.5 0.9 1.3 |      | conserved protein of unknown function   |
| CIBE_0481        | 6up   | 2.2 2.5 0.9 1.1 | -    | protein of unknown function   |
| CIBE_3195        | 6up   | 2.8 1.5 0.9 1.4 |      | Homocysteine S-methyltransferase  |
| CIBE 3788        |       | 2.9 1.8 1.1 0.7 |      | protein of unknown function   |
| _                | 6up   |                 |      | ·   |
| CIBE_3246        | 6up   | 2.4 1.5 1.2 1.5 |      | Carboxymuconolactone decarboxylase  |
| CIBE_0218        | 6up   | 0.4 2.4 2.0 1.8 | -    | Cell wall hydrolase, SleB   |
| CIBE_2419        | 6up   | 2.3 1.7 1.3 1.3 | -    | LysR family transcriptional regulator   |
| CIBE 4322        | 6up   | 2.0 1.6 1.6 1.4 |      | conserved exported protein of unknown function  |
| _                | •     |                 |      |   |
| CIBE_1363        | 6up   |                 | pstS | phosphate ABC transporter (binding lipoprotein)   |
| CIBE_misc_RNA_2  | 6up   | 1.5 1.7 1.1 2.2 |      | 6S  |
| CIBE_misc_RNA_44 | 4 6up | 1.8 1.9 1.7 1.2 | -    | Purine  |
| CIBE 4170        | 6up   | 2.0 1.5 1.4 1.6 |      | conserved protein of unknown function   |
| CIBE 2964        | 6up   | 1.7 2.1 1.5 1.2 |      | Aldehyde dehydrogenase  |
| _                |       |                 |      | · · · · · · ·   |
| CIBE_misc_RNA_11 |       | 1.5 1.5 1.2 2.3 |      | Glycine   |
| CIBE_2418        | 6up   | 1.8 1.7 1.9 1.1 | -    | Molybdopterin dehydrogenase, FAD-binding  |
| CIBE_0799        | 6up   | 0.7 2.3 2.1 1.4 | -    | 2', 3'-cyclic nucleotide 2'-phosphodiesterase   |
| CIBE 0476        | 6up   | 2.4 2.5 0.8 0.7 |      | protein of unknown function   |
| CIBE_3446        | 6up   | 1.8 1.9 1.7 1.1 |      | conserved protein of unknown function   |
|                  |       |                 |      | ·   |
| CIBE_2132        | 6up   | 1.6 1.6 1.9 1.3 |      | Single-stranded DNA-binding protein   |
| CIBE_0482        | 6up   | 2.4 2.5 0.8 0.6 | 1-   | protein of unknown function   |
| 1                |       |                 |      |   |

| CIBE 4468  |  |  |  |   |  |
|--|--|--|--|---|--|
| _  | 6up  | 1.9 1.6  | 1.5 1.   |   | Galactoside O-acetyltransferase  |
| CIBE_p0013   | 6up  | 2.7 1.5  | 1.2 0.   | 9 -   | conserved protein of unknown function  |
| CIBE_5803  | 6up  | 1.7 1.4  | 1.4 1.   | 8 -   | conserved protein of unknown function  |
| CIBE_5305  | 6up  | 2.4 1.5  | 1.4 1.   | 0 -   | conserved protein of unknown function  |
| CIBE_4198  | 6up  | 2.4 1.7  | 1.2 0.   | 9 -   | Acetyltransferase, GNAT family   |
| CIBE_4323  | 6up  | 2.1 1.5  | 1.4 1.   | 2 -   | conserved exported protein of unknown function   |
| CIBE 4174  | 6up  | 2.7 1.8  | 1.1 0.   | 6 -   | Methyltransferase type 12  |
| CIBE_4733  | 6up  | 3.1 1.9  | 1.1 0.   | 0 -   | Phosphinothricin N-acetyltransferase   |
| CIBE 0471  | 6up  | 2.3 2.4  | 0.7 0.   |   | conserved protein of unknown function  |
| CIBE 0444  | 6up  | 2.6 2.1  | 0.7 0.   |   | conserved protein of unknown function  |
| CIBE_2826  | 6up  | 1.8 2.3  |  | 8 glnH  | glutamine transporter subunit; periplasmic binding component of ABC superfamily  |
| CIBE 0250  | 6up  | 0.4 1.8  | 2.0 1.   | _   | Extracellular solute-binding protein, family 1   |
| CIBE 2017  | 6up  | 0.8 2.7  | 1.4 1.   |   | conserved protein of unknown function  |
| CIBE_3870  | 6up  | 2.7 1.7  | 1.1 0.   |   | Histidine triad (HIT) protein  |
| CIBE_3168  | 6up  | 2.8 2.3  | 0.8 0.   |   | conserved membrane protein of unknown function   |
|  |  | 1.7 1.3  | 1.5 1.   |   |  |
| CIBE_2878  | 6up  |  |  |   | Phospho-2-dehydro-3-deoxyheptonate aldolase  |
| CIBE_3782  | 6up  | 2.7 1.4  | 1.0 1.   |   | Acetyltransferase, GNAT family (fragment)  |
| CIBE_4171  | 6up  | 2.3 1.6  | 1.1 1.   |   | exported protein of unknown function   |
| CIBE_3324  | 6up  | 2.1 1.7  | 1.1 1.   |   | conserved protein of unknown function  |
| CIBE_3193  | 6up  | 2.6 1.2  | 1.3 0.   |   | conserved protein of unknown function  |
| CIBE_3287  | 6up  | 2.5 1.7  | 1.5 0.   |   | putative cell wall binding repeat-containing protein   |
| CIBE_4466  | 6up  | 2.3 1.6  | 1.4 0.   |   | conserved protein of unknown function  |
| CIBE_0470  | 6up  | 2.2 2.5  | 0.6 0.   |   | conserved protein of unknown function  |
| CIBE_0537  | 6up  | 0.6 2.2  | 1.8 1.   |   | conserved protein of unknown function  |
| CIBE_3640  | 6up  | 1.8 1.8  | 1.1 1.   |   | conserved protein of unknown function  |
| CIBE_2404  | 6up  | 1.6 1.6  | 1.8 0.   | 8 -   | YheO domain protein  |
| CIBE_3436  | 6up  | 2.5 1.6  | 0.9 0.   |   | Electron transfer flavoprotein, alpha/beta-subunit-like protein  |
| CIBE_4413  | 6up  | 0.6 2.5  | 1.7 1.   |   | conserved protein of unknown function  |
| CIBE_5285  | 6up  | 2.7 1.8  | 1.1 0.   |   | conserved protein of unknown function  |
| CIBE_1820  | 6up  | 2.0 2.1  | 1.4 0.   |   | conserved protein of unknown function  |
| CIBE_4252  | 6up  | 2.7 1.4  | 0.9 0.   | 9 -   | Radical SAM domain protein   |
| CIBE_3471  | 6up  | 2.3 1.4  | 1.3 0.   | 7 stc   | Signal-transduction and transcriptional-control protein  |
| CIBE_3899  | 6up  | 2.2 1.7  | 1.1 0.   | 8 -   | Glyoxalase/bleomycin resistance protein/dioxygenase  |
| CIBE_3787  | 6up  | 2.3 0.8  | 0.8 1.   | 9 -   | protein of unknown function  |
| CIBE_0473  | 6up  | 2.6 2.4  | 0.6 0.   | 2 -   | conserved protein of unknown function  |
| CIBE_2417  | 6up  | 1.7 1.5  | 1.6 1.   | 1 ndhS  | Nicotinate dehydrogenase small FeS subunit   |
| CIBE 0486  | 6up  | 2.4 2.8  | 0.7 -0.  |   | conserved protein of unknown function  |
| CIBE 3340  | 6up  | 2.3 1.3  | 1.1 1.   | _   | Elongation factor G, domain IV   |
| CIBE_3410  | 6up  | 2.2 1.3  | 1.4 0.   | _   | glycine betaine/carnitine/choline/choline sulfate ABC transporter (ATP-binding protein)  |
| CIBE_4467  | 6up  | 1.9 1.4  | 1.5 0.   |   | conserved protein of unknown function  |
| CIBE_2655  | 6up  | 2.4 1.7  | 1.4 0.   |   | Flavodoxin   |
| CIBE_0828  | 6up  | 2.2 1.9  | 0.9 0.   |   | putative AgrB-like protein 1   |
| CIBE_3868  | 6up  | 2.4 1.4  | 1.0 1.   |   | conserved protein of unknown function  |
| CIBE_3249  | 6up  | 2.2 1.1  | 1.5 1.   |   | Histidine kinase   |
| CIBE_3249<br>CIBE 4250   |  | 2.7 1.6  | 0.9 0.   |   | conserved protein of unknown function  |
| _  | 6up  | _  | 1.4 0.   |   | ·  |
| CIBE_6019  | 6up  | _  |  |   | Transcriptional regulator, RpiR family   |
| CIBE_4139  | 6up  | 2.8 1.8  | 0.9 0.   |   | Acetyltransferase  |
| CIBE_3347  | 6up  | 2.1 1.5  | 1.0 1.   |   | ATPase AAA (fragment)  |
|  |  |  |  |   |  |
| CIBE_0943  | 6up  | 2.0 0.8  | 0.8 2.   |   | O-acetylhomoserine aminocarboxypropyltransferase   |
| CIBE_2343  | 6up  | 2.3 1.2  | 1.0 1.   | 2 fldZ  | 2-enoate reductase FldZ  |
| CIBE_2343<br>CIBE_3199   |  | 2.3 1.2<br>2.7 1.5   | 1.0 1.<br>0.9 0.   | 2 fldZ<br>6 -   | 2-enoate reductase FldZ<br>Nicotinamidase-like amidase   |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773  | 6up<br>6up<br>6up                                    | 2.3 1.2<br>2.7 1.5<br>1.7 1.5  | 1.0 1.<br>0.9 0.<br>1.6 0.   | 2 fldZ<br>6 -<br>9 -  | 2-enoate reductase FldZ<br>Nicotinamidase-like amidase<br>Accessory gene regulator B   |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773<br>CIBE_1022   | 6up<br>6up<br>6up<br>6up                             | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0   | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.   | 2 fldZ<br>6 -<br>9 -<br>2 -   | 2-enoate reductase FldZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function   |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773<br>CIBE_1022<br>CIBE_3397  | 6up<br>6up<br>6up                                    | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7  | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.<br>0.9 0.   | 2 fldZ<br>6 -<br>9 -<br>2 -<br>6 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function   |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773<br>CIBE_1022<br>CIBE_3397<br>CIBE_2171   | 6up<br>6up<br>6up<br>6up                             | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1   | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.<br>0.9 0.<br>0.4 0.   | 2 fldZ<br>6 -<br>9 -<br>2 -<br>6 -<br>6 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family  |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773<br>CIBE_1022<br>CIBE_3397  | 6up<br>6up<br>6up<br>6up<br>6up                      | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0  | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.<br>0.9 0.   | 2 fldZ<br>6 -<br>9 -<br>2 -<br>6 -<br>6 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function   |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773<br>CIBE_1022<br>CIBE_3397<br>CIBE_2171<br>CIBE_3034<br>CIBE_1036   | 6up<br>6up<br>6up<br>6up<br>6up                      | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1  | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.<br>0.9 0.<br>0.4 0.<br>2.0 1.<br>1.8 1.   | 2 fldZ<br>6 -<br>9 -<br>2 -<br>6 -<br>6 -<br>2 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family  |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773<br>CIBE_1022<br>CIBE_3397<br>CIBE_2171<br>CIBE_3034  | 6up 6up 6up 6up 6up 6up 6up                          | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8  | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.<br>0.9 0.<br>0.4 0.<br>2.0 1.   | 2 fldZ<br>6 -<br>9 -<br>2 -<br>6 -<br>6 -<br>2 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function  |
| CIBE_2343<br>CIBE_3199<br>CIBE_3773<br>CIBE_1022<br>CIBE_3397<br>CIBE_2171<br>CIBE_3034<br>CIBE_1036   | 6up<br>6up<br>6up<br>6up<br>6up<br>6up<br>6up<br>6up | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1  | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.<br>0.9 0.<br>0.4 0.<br>2.0 1.<br>1.8 1.   | 2 fldZ<br>6 -<br>9 -<br>2 -<br>6 -<br>6 -<br>2 -<br>2 -<br>8 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458  | 6up<br>6up<br>6up<br>6up<br>6up<br>6up<br>6up<br>6up | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8  | 1.0 1.<br>0.9 0.<br>1.6 0.<br>1.9 1.<br>0.9 0.<br>0.4 0.<br>2.0 1.<br>1.8 1.<br>0.9 0.   | 2 fidZ<br>6 -<br>9 -<br>2 -<br>6 -<br>2 -<br>2 -<br>2 -<br>8 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773  | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5   | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1.  | 2 fldz<br>6 -<br>9 -<br>2 -<br>6 -<br>2 -<br>2 -<br>2 -<br>1 -<br>9 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_1458 CIBE_4773 CIBE_5284  | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0.  | 2 fidz 6 - 9 - 2 - 6 - 6 - 2 - 2 - 8 - 1 - 9 - 8 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment)  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_11036 CIBE_1458 CIBE_1458 CIBE_4525 CIBE_5284 CIBE_4253   | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5   | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 0.9 0. 0.9 0.  | 2 fidz 6 - 9 - 2 - 6 - 6 - 2 - 2 - 2 - 3 - 1 - 9 - 8 - 8 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_MISC_RNA_61   | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5<br>2.3 1.9  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 0.9 0. 0.9 0. 0.9 0. 0.9 0.   | 2 fidZ<br>6 -<br>9 -<br>6 -<br>6 -<br>2 -<br>2 -<br>3 8 -<br>1 1 -<br>9 -<br>8 8 -<br>8 -<br>2 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl   |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_misc_RNA_61 CIBE_4444   | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5<br>2.3 1.9<br>2.0 1.2   | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 0.6 0. 1.2 1.   | 2 fidz 6 - 9 - 9 - 6 - 2 - 2 - 2 - 2 - 3 - 9 - 8 - 1 - 9 - 8 - 2 - 0 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator   |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_4253 CIBE_misc_RNA_61 CIBE_18444 CIBE_2825  | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5<br>2.3 1.9<br>2.0 1.2<br>2.3 2.6  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 0.9 0. 1.2 1. 0.6 0.  | 2 fidz 6 - 9 - 2 - 6 - 2 - 2 - 2 - 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_1458 CIBE_4458 CIBE_4458 CIBE_4458 CIBE_4458 CIBE_4253 CIBE_misc_RNA_61 CIBE_4444 CIBE_2825 CIBE_4197   | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5<br>2.3 1.9<br>2.0 1.2<br>2.3 2.6<br>2.3 2.6<br>2.3 1.5  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 0.9 0. 0.6 0. 1.2 1. 0.6 0. 1.0 0.  | 2 fidz 6 - 9 - 2 - 6 - 2 - 2 - 8 - 1 - 9 - 8 - 2 - 7 - 7 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, FliA/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_11036 CIBE_1458 CIBE_1458 CIBE_1458 CIBE_4458 CIBE_4253 CIBE_misc_RNA_61 CIBE_4444 CIBE_2825 CIBE_4447 CIBE_3825 CIBE_4197 CIBE_3789  | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>0.5 2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5<br>2.3 1.9<br>2.0 1.2<br>2.3 2.6<br>2.3 1.5<br>2.3 1.4  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 0.9 0. 0.6 0. 1.2 1. 0.6 0. 1.0 0. 1.1 0.   | 2 fidz 6 - 9 - 2 - 6 - 6 - 2 - 2 - 3 - 5 - 8 - 9 - 8 - 8 - 2 - 7 - 7 bglF   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_miss_RNA_61 CIBE_4444 CIBE_2825 CIBE_4197 CIBE_3789 CIBE_3962   | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.4 2.4 1.5 2.3 1.5  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 2.0 1. 1.8 1. 0.9 0. 1.4 0. 0.9 0. 1.4 1. 0.9 0. 1.4 1. 0.9 0. 1.4 0. 1.0 0. 1.1 1. 0.1 1.0 0.  | 2 fidZ 6 - 9 - 9 - 6 - 2 - 2 - 2 - 3 - 9 - 8 - 1 - 9 - 8 - 7 - 7 bglF 1 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_MES_EXBA_63 CIBE_1825 CIBE_1825 CIBE_18389 CIBE_3789 CIBE_3962 CIBE_4196  | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>2.0<br>2.3 1.7<br>2.5 2.1<br>0.4 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5<br>2.3 1.9<br>2.0 1.2<br>2.3 2.6<br>2.3 1.5<br>2.3 1.5  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 1.4 1. 0.9 0. 1.4 1. 0.9 0. 1.1 1. 0.9 0. 1.1 1. 0.9 0. 1.1 1. 0.9 0. 1.1 1. 0.9 0. 1.1 1. 0.9 0. 1.1 1. 0.9 0. 1.1 1. 0.9 0. 1.1 1. 0.0 0. 1.1 0. 1.1 0. 1.1 0. 1.1 0.   | 2 fidz 6 - 9 - 9 - 2 - 6 - 6 - 2 - 2 - 7 - 7 bg F 1 - 4 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein Cots conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component Short-chain dehydrogenase  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_4253 CIBE_misc_RNA_61 CIBE_2825 CIBE_4197 CIBE_3789 CIBE_3789 CIBE_3962 CIBE_4196 CIBE_2591   | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.4 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.5 2.1  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 0.9 0. 0.6 0. 1.2 1. 0.6 0. 1.0 0. 1.1 0. 1.0 0. 1.1 0. 1.0 0.  | 2 fidZ 6 - 9 - 2 - 6 - 6 - 7 - 9 - 8 - 1 - 9 - 8 - 7 - 7 - 7 - 7 bglF 1 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein Cots conserved protein of unknown function conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function tonserved protein of unknown function suserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component Short-chain dehydrogenase conserved protein of unknown function   |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_1458 CIBE_4458 CIBE_4458 CIBE_4458 CIBE_4253 CIBE_misc_RNA_61 CIBE_18444 CIBE_2825 CIBE_4197 CIBE_3789 CIBE_3962 CIBE_4196 CIBE_2591 CIBE_0897  | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.4 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.1 1.5 2.5 2.1 2.0 1.5  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 0.4 0. 0.9 0. 1.4 1. 0.9 0. 1.0 0. 1.1 0. 1.0 0. 1.1 0. 1.0 0. 1.0 1.0 0. 1.0 1.0 1.0 0. 0.8 1.   | 2 fidz 6 - 9 - 2 - 6 - 6 - 2 - 2 - 3 - 5 - 7 - 7 - 7 bglF 1 - 1 - 2 - 1 - 2 - 2 - 3 - 4 - 1 - 2 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, FliA/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family   |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_11036 CIBE_1458 CIBE_1458 CIBE_1458 CIBE_4458 CIBE_4459 CIBE_3254 CIBE_4253 CIBE_162591 CIBE_3789 CIBE_3789 CIBE_3962 CIBE_4196 CIBE_2591 CIBE_0897 CIBE_0897 CIBE_0104   | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.4 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.1 1. | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 0.6 0. 1.2 1. 0.6 0. 1.0 0. 1.1 0. 1.0 0. 1.1 0. 1.0 0. 1.1 1. 0.5 0. 0.8 1. 1.6 1.   | 2 fidZ 6 - 9 - 9 - 6 - 2 - 2 - 2 - 2 - 3 - 5 - 7 - 7 bglF 1 - 4 - 1 - 2 - 1 - 1 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component; IIC component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ   |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_4253 CIBE_misc_RNA_61 CIBE_2825 CIBE_4197 CIBE_3962 CIBE_3962 CIBE_4196 CIBE_2591 CIBE_0897 CIBE_0897 CIBE_097 CIBE_0104 CIBE_4137  | 6up              | 2.3 1.2<br>2.7 1.5<br>1.7 1.5<br>2.0 0.5 2.0<br>0.5 2.1<br>1.2 2.8<br>2.0 1.1<br>2.3 1.4<br>2.4 1.5<br>2.3 1.9<br>2.0 1.2<br>2.3 2.6<br>2.3 1.5<br>2.3 1.5<br>2.5 2.1<br>2.0 1.5<br>2.7 1.6  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 1.4 1. 0.9 0. 1.5 1. 0.6 0. 1.2 1. 0.6 0. 1.0 0. 1.1 0. 1.0 0. 1.0 1. 0.5 0. 0.8 1. 1.6 1. 1.0 0.   | 2 fidZ 6 - 9 - 9 - 2 - 6 - 2 - 2 - 2 - 3 - 9 - 8 - 1 - 9 - 8 - 7 - 7 - 7 bg/F 1 - 1 - 1 - 1 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_MISC_RNA_61 CIBE_4253 CIBE_4253 CIBE_4197 CIBE_3789 CIBE_3789 CIBE_3789 CIBE_4196 CIBE_2591 CIBE_0887 CIBE_0887 CIBE_0897 CIBE_0897 CIBE_0104 CIBE_1137 CIBE_3826   | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.5 2.1 2.0 1.5 2.0 1. | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 1.4 1. 0.9 0. 1.4 1. 0.9 0. 1.4 1. 0.9 0. 1.0 0. 1.0 0. 1.1 0. 1.0 0. 1.0 1. 0.5 0. 0.8 1. 1.0 0. 0.4 0.  | 2 fidZ 6 - 9 - 2 - 6 - 6 - 2 - 2 - 7 - 7 - 7 bg F 1 - 2 - 1 - 1 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein Cots conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function tonserved protein of unknown function spl MarR family transcriptional regulator CAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function HAD hydrolase, family IA, variant 3   |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_misc_RNA_61 CIBE_4253 CIBE_misc_RNA_61 CIBE_3789 CIBE_3789 CIBE_3789 CIBE_3962 CIBE_4196 CIBE_2591 CIBE_0897 CIBE_0897 CIBE_10104 CIBE_1377 CIBE_3826 CIBE_4137 CIBE_3826 CIBE_4090   | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.1 1.5 2.5 2.1 2.0 1.5 0.4 2.2 2.7 1.6 2.9 2.0 1.6 1.5  | 1.0 1. 0.9 0. 1.6 0. 1.9 1. 0.9 0. 0.4 0. 2.0 1. 1.8 1. 0.9 0. 0.9 0. 0.9 0. 0.6 0. 1.2 1. 0.6 0. 1.1 0. 1.0 0. 1.1 0. 1.0 0. 1.1 0. 1.0 0. 1.1 0. 1.0 1. 0.5 0. 0.8 1. 1.6 1. 0.4 0. 1.6 0.   | 2 fidz 6 - 9 - 2 - 6 - 6 - 7 - 9 - 8 - 1 - 9 - 8 - 7 - 7 - 7 bglF 1 - 1 - 2 - 1 - 7 - 5 - 5 -   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function HAD hydrolase, family IA, variant 3 Cell wall-binding protein  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_1458 CIBE_4458 CIBE_4458 CIBE_4458 CIBE_485 CIBE_485 CIBE_486 CIBE_3284 CIBE_486 CIBE_4197 CIBE_3789 CIBE_3789 CIBE_3962 CIBE_4196 CIBE_2591 CIBE_0104 CIBE_4137 CIBE_3826 CIBE_4137 CIBE_3826 CIBE_4137 CIBE_3826 CIBE_4137 CIBE_3826 CIBE_4137 CIBE_3826 CIBE_4137 CIBE_3826 CIBE_41090 CIBE_1638   | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.4 2.3 1.5 2.3 1.4 2.1 1.5 2.3 1.6 2.1 1.5 2.1 1.5 1.8 1. | 1.0 1. 0.9 0. 1.6 0. 1.9 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0   | 2 fidZ 6 - 9 - 9 - 6 6 - 2 - 2 - 2 8 - 1 1 - 9 - 2 7 - 7 bglF 1 - 4 - 1 1 - 2 - 1 1 - 2 - 7 tglF 2 - 2 - 3 - 5 - 5 - 5 - 5 - 5 -  | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, FliA/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function HAD hydrolase, family IA, variant 3 Cell wall-binding protein Appr-1-p processing domain protein   |
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| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_36253 CIBE_36253 CIBE_36253 CIBE_362 CIBE_4197 CIBE_3826 CIBE_4196 CIBE_2591 CIBE_4196 CIBE_3826 CIBE_4196 CIBE_3826 CIBE_4197 CIBE_3826 CIBE_4197 CIBE_3826 CIBE_4090 CIBE_1638 CIBE_0407 CIBE_0477 CIBE_3902 CIBE_3338 CIBE_5293 CIBE_782 CIBE_782 CIBE_782 CIBE_1735 CIBE_1735 CIBE_1735 CIBE_1735 CIBE_174000 CIBE_1607 CIBE_3901   | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.1 2.0 1.6 1.5 1.7 1.7 2.6 2.6 2.2 2.3 2.2 1.1 1.3 1.3 2.2 1.3 2.6 1.5 2.0 1.9 2.8 2.2 2.0 1.6  | 1.0 1.0 0.9 0.0 1.1 1.0 0.1 1.0 0.1 1.0 0.1 1.0 0.1 1.0 0.1 1.0 0.1 1.1 1  | 2 fidz 6 - 9 - 9 - 1 6 - 2 7 - 2 8 - 1 1 - 9 8 8 - 2 7 0 - 7 bglF 1 - 1 - 2 1 - 7 tglF 2 - 7 tglF 3 - 7 tglF 5 - 7 tglF 6 tglF 7 tglF 7 tglF 7 tglF 7 tglF 7 tglF 8 | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein of unknown function conserved protein of unknown function Spore coat protein OctS conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component; IIC component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function HAD hydrolase, family IA, variant 3 Cell wall-binding protein Appr-1-p processing domain protein conserved protein of unknown function |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4173 CIBE_5284 CIBE_4253 CIBE_4253 CIBE_3789 CIBE_3789 CIBE_3789 CIBE_3789 CIBE_3826 CIBE_4197 CIBE_3826 CIBE_4196 CIBE_2591 CIBE_0897 CIBE_3826 CIBE_4196 CIBE_2591 CIBE_0897 CIBE_3826 CIBE_4196 CIBE_2591 CIBE_3826 CIBE_4196 CIBE_2591 CIBE_3826 CIBE_4196 CIBE_2591 CIBE_3826 CIBE_4196 CIBE_5291 CIBE_3826 CIBE_4196 CIBE_5291 CIBE_3826 CIBE_4090 CIBE_4090 CIBE_1638 CIBE_0477 CIBE_3382 CIBE_5293 CIBE_2782 CIBE_4735 CIBE_5293 CIBE_2782 CIBE_4735 CIBE_60020 CIBE_48001 CIBE_1607 CIBE_3901 CIBE_4712  | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 0.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.2 1.1 2.1 2.2 2.2 2.1 1.8 1.5 2.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.1 2.0 1.5 2.0 1.6 1.5 2.0 1.9 2.8 2.2 2.0 1.6  | 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0  | 2 fidz 6 - 9 - 9 - 16 - 2 - 2 - 2 - 3 - 9 - 8 - 1   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein CotS conserved protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component; IIC component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function HAD hydrolase, family IA, variant 3 Cell wall-binding protein Appr-1-p processing domain protein conserved protein of unknown function protein of unknown function Transcription activator, effector binding conserved membrane protein of unknown function putative lipoprotein protein of unknown function putative aminoacyloate CoA-transferase putative cell wall binding repeat-containing protein conserved protein of unknown function  |
| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_8253 CIBE_8255 CIBE_4197 CIBE_3789 CIBE_3789 CIBE_9104 CIBE_1036 CIBE_1496 CIBE_1496 CIBE_15897 CIBE_1097 CIBE_3892 CIBE_4196 CIBE_2591 CIBE_0897 CIBE_1044 CIBE_4137 CIBE_3826 CIBE_4196 CIBE_104 CIBE_4137 CIBE_3826 CIBE_4196 CIBE_1538 CIBE_5293 CIBE_4735 CIBE_1638 CIBE_5293 CIBE_4735 CIBE_64607 CIBE_4607 CIBE_4607 CIBE_4607 CIBE_49901 CIBE_46171 CIBE_3901 CIBE_46171 CIBE_3901 CIBE_3901 CIBE_3901 CIBE_3901 CIBE_3911  | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 0.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.1 2.0 1.5 0.4 2.2 2.7 1.6 2.9 2.0 1.6 1.5 1.7 1.7 2.6 2.6 2.3 2.2 1.1 1.8 1.3 3.1 1.3 2.1 1.3 2.2 1.3 2.2 1.3 2.2 1.3 2.2 1.3 2.2 1.3 2.2 1.3 2.2 1.3 2.3 1.5 2.0 1.6 2.9 2.0 2.9 2.0 2.9 2.0 2.0 1.6 1.5 2.1 1.7 1.7 2.6 2.6 2.6 2.2 2.3 2.2 1.1 2.2 2.3 2.2 1.1 2.3 1.3 1.3 2.4 1.3 2.6 1.5 2.0 1.6 2.0 1.6 2.0 1.6 2.0 1.6 2.0 1.6 2.0 1.4 2.7 1.4  | 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0  | 2 fidz 6 - 9 - 9 - 2 - 6 - 6 - 2 - 2 - 3 - 9 - 8 - 1 - 9 - 8 - 7 - 7 - 7 bglF 1 - 1 - 2 - 1 - 2 - 3 - 3 - 3 - 4 - 3 - 3 - 5 - 7 - 7 - 7 - 7 - 8 - 8 - 8 - 8 - 9 - 8 - 9 - 9 - 9 - 9 - 9 - 9 - 9 - 9 - 9 - 9   | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, Flia/WhiG family conserved protein of unknown function Spore coat protein of unknown function Conserved protein of unknown function Conserved protein of unknown function Wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cample-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component ; IIC component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function HAD hydrolase, family IA, variant 3 Cell wall-binding protein Appr-1-p processing domain protein conserved protein of unknown function protein of unknown function Transcription activator, effector binding conserved membrane protein of unknown function putative lipoprotein protein of unknown function putative aminoacyloate CoA-transferase putative cell wall binding repeat-containing protein conserved protein of unknown function Putative cell wall binding repeat protein (fragment)   |
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| CIBE_2343 CIBE_3199 CIBE_3773 CIBE_1022 CIBE_3397 CIBE_2171 CIBE_3034 CIBE_1036 CIBE_1458 CIBE_4773 CIBE_5284 CIBE_4253 CIBE_MSC_RNA_61 CIBE_3896 CIBE_3789 CIBE_3789 CIBE_0104 CIBE_1638 CIBE_0104 CIBE_1638 CIBE_0104 CIBE_1638 CIBE_0104 CIBE_3896 CIBE_3896 CIBE_3896 CIBE_3896 CIBE_3896 CIBE_3896 CIBE_3896 CIBE_3896 CIBE_3896 CIBE_5591 CIBE_0897 CIBE_0897 CIBE_0897 CIBE_0897 CIBE_1638 CIBE_1639 CIBE_3901 CIBE_3901 CIBE_3901 CIBE_3901 CIBE_3911 CIBE_5268  | 6up              | 2.3 1.2 2.7 1.5 1.7 1.5 0.5 2.0 2.3 1.7 2.5 2.1 0.4 2.0 0.5 2.1 1.2 2.8 2.0 1.1 2.3 1.4 2.4 1.5 2.3 1.9 2.0 1.2 2.3 2.6 2.3 1.5 2.3 1.5 2.3 1.5 2.3 1.5 2.1 1.0 2.8 1.5 2.7 1.6 2.9 2.0 1.6 1.5 1.7 1.7 2.6 2.6 2.2 2.3 2.2 1.1 1.8 1.3 3.1 1.3 2.2 1.3 3.1 1.3 2.2 1.3 3.1 1.3 2.2 1.3 2.6 1.5 2.0 1.9 2.8 2.2 2.0 1.6 2.0 1.9 2.8 2.2 2.0 1.6 2.0 1.9 2.8 2.2 2.0 1.6 2.0 1.4 2.0 1.2  | 1.0 1.0 1.0 9 0.1 1.6 0.1 1.0 1.0 1.0 1.0 1.0 1.0 1.1 1.1 1.1  | 2 fid2 6 - 9 - 9 - 1 6 - 2 7 - 2 8 - 1 1 - 9 8 8 - 2 7 7 - 1 bglF 1 - 1 - 2 - 3 3 - 3 - 3 3 - 3 3 - 3 3 - 3 3 - 3 3 - 3 3 - 3 7 - 5 5 - 7 7 - 7 7 - 8 8 - 8 8 - 8 9 - 8 | 2-enoate reductase FIdZ Nicotinamidase-like amidase Accessory gene regulator B conserved protein of unknown function conserved protein of unknown function RNA polymerase, sigma 28 subunit, FliA/WhiG family conserved protein of unknown function Spore coat protein of unknown function Spore coat protein of unknown function conserved protein of unknown function wall-associated protein WapA (fragment) 2-dehydropantoate 2-reductase Intron_gpl MarR family transcriptional regulator GntR family transcriptional regulator cAMP-binding protein conserved protein of unknown function fused beta-glucoside-specific PTS enzymes: IIA component; IIB component; IIC component Short-chain dehydrogenase conserved protein of unknown function Carbohydrate ABC transporter membrane protein 1, CUT1 family Spore cortex biosynthesis protein YabQ conserved protein of unknown function HAD hydrolase, family IA, variant 3 Cell wall-binding protein Appr-1-p processing domain protein conserved protein of unknown function putative ell wall binding repeat-containing protein conserved protein of unknown function Putative cell wall binding repeat protein (fragment) conserved protein of unknown function   |

|                        |     |     |     |      |      | •       |   |
|------------------------|-----|-----|-----|------|------|---------|---|
| CIBE_0450              | 6up | 2.3 | 2.0 | 0.4  | 0.5  |         | conserved protein of unknown function                             |
| CIBE_2172              | 6up | 2.2 | 1.5 | 0.8  | 0.6  | -       | conserved protein of unknown function                             |
| CIBE_4143              | 6up | 3.0 | 2.1 | 0.7  | -0.7 | -       | ABC transporter related (fragment)                                |
| CIBE_3368              | 6up | 1.8 | 1.4 | 1.2  | 0.6  | -       | putative membrane protein   |
| CIBE_0472              | 6up | 2.1 | 2.1 | 0.6  | 0.3  | -       | Minor capsid  |
| CIBE_1572              | 6up | 1.7 | 1.2 | 0.9  |      | hisB    | imidazoleglycerol-phosphate dehydratase                           |
| CIBE 3903              | 6up | 2.4 | 1.4 | 0.7  | 0.5  |         | conserved protein of unknown function                             |
| _                      |     |     |     |      |      |         | ·   |
| CIBE_3639              | 6up | 2.0 | 1.6 | 1.3  | 0.1  | -       | GCN5-related N-acetyltransferase                                  |
| CIBE_2421              | 6up | 2.5 | 1.4 | 0.7  |      | moaA    | Cyclic pyranopterin monophosphate synthase                        |
| CIBE_4316              | 6up | 2.1 | 0.9 | 0.8  | 1.2  | -       | conserved exported protein of unknown function                    |
| CIBE_4608              | 6up | 3.1 | 2.5 | 2.4  | 2.8  | yodR    | putative acyloate-acetoacetate CoA-transferase                    |
| CIBE 0075              | 6up | 1.8 | 1.1 | 1.1  | 1.0  | leuA    | 2-isopropylmalate synthase 2                                      |
| CIBE_2021              | 6up | 1.6 | 2.4 | 0.8  | 0.2  | -       | Stage III sporulation protein AB                                  |
| CIBE 4445              |     | 1.7 | 1.3 | 1.1  | 0.9  |         | Beta-lactamase  |
| _                      | 6up |     |     |      |      | le E    |   |
| CIBE_5457              | 6up | 2.3 | 1.2 | 0.2  |      | yrbE    | putative oxidoreductase   |
| CIBE_3980              | 6up | 2.1 | 1.9 | 0.8  | 0.1  | -       | conserved protein of unknown function                             |
| CIBE_1281              | 6up | 1.9 | 1.0 | 0.4  | 1.6  | -       | ABC transporter   |
| CIBE_1570              | 6up | 1.5 | 0.9 | 1.3  | 1.2  | hisD    | histidinol dehydrogenase  |
| CIBE_6076              | 6up | 2.1 | 1.1 | 1.3  | 0.4  | -       | Acyl-CoA dehydrogenase  |
| CIBE_3245              | 6up | 2.1 | 1.3 | 0.1  | 1.4  | -       | PAS/PAC sensor signal transduction histidine kinase               |
| CIBE_0438              | 6up | 2.2 | 2.0 | 0.4  | 0.3  | -       | protein of unknown function                                       |
| CIBE_0994              | 6up | 2.5 | 1.5 | 0.5  |      | sigF    | RNA polymerase sporulation-specific sigma factor (sigma-F)        |
|                        |     |     |     |      |      | 31g1    |   |
| CIBE_3000              | 6up | 2.0 | 1.1 | 0.9  | 0.7  |         | Intermediate filament protein:ATP/GTP-binding site motif A        |
| CIBE_1450              | 6up | 0.2 | 1.7 | 1.6  |      | tepA    | protein export-enhancing protease                                 |
| CIBE_1240              | 6up | 1.7 | 1.0 | 1.1  | 0.9  | ilvE    | Branched-chain-amino-acid aminotransferase                        |
| CIBE_0055              | 6up | 0.4 | 1.9 | 1.5  | 0.9  | -       | Spore maturation protein  |
| CIBE_4472              | 6up | 2.5 | 1.5 | 0.6  | 0.1  | dkgB    | 2,5-diketo-D-gluconic acid reductase B                            |
| CIBE_1794              | 6up | 2.1 | 2.0 | 0.4  | 0.2  | -       | conserved protein of unknown function                             |
| CIBE 3780              | 6up | 2.0 | 1.3 | 0.9  | 0.5  | -       | membrane protein of unknown function                              |
| _                      |     |     | 1.1 |      | 0.5  |         | ·   |
| CIBE_2201              | 6up | 1.7 |     | 0.9  |      | -       | DegV domain-containing protein CA_C1624                           |
| CIBE_5267              | 6up | 1.9 | 1.1 | 0.7  | 1.0  | -       | YD repeat protein   |
| CIBE_0475              | 6up | 2.3 | 2.3 | 0.2  | -0.1 | -       | Bacteriophage Gp15 protein  |
| CIBE_0551              | 6up | 1.3 | 2.3 | 0.8  | 0.3  | -       | conserved protein of unknown function                             |
| CIBE 3869              | 6up | 2.2 | 0.9 | 0.6  | 0.9  | -       | Metal-dependent phosphohydrolase HD sub domain containing protein |
| CIBE_5423              | 6up | 1.6 | 1.4 | 1.1  | 0.5  | argC    | N-acetylglutamate gamma-semialdehyde dehydrogenase                |
| CIBE_5270              | 6up | 1.9 | 1.1 | 0.8  | 0.8  | -       | Pentapeptide repeat protein                                       |
| CIBE_4183              | 6up | 1.9 | 1.4 | 0.7  | 0.5  |         | Ketopantoate reductase ApbA/PanE, N-terminal domain protein       |
|                        |     |     |     |      |      | -       |   |
| CIBE_3908              | 6up | 2.4 | 1.6 | 0.6  | -0.2 | -       | Cyanophycinase  |
| CIBE_0918              | 6up | 2.5 | 1.8 | 0.1  | 0.1  | -       | ErfK/YbiS/YcfS/YnhG family protein                                |
| CIBE_1608              | 6up | 0.2 | 1.8 | 1.4  | 1.1  | -       | Membrane protein  |
| CIBE_3790              | 6up | 1.9 | 1.4 | 1.1  | 0.0  | -       | conserved protein of unknown function                             |
| CIBE_3396              | 6up | 2.0 | 1.3 | 0.8  | 0.3  | -       | conserved protein of unknown function                             |
| CIBE_0076              | 6up | 2.2 | 0.9 | 0.8  | 0.5  | _       | Aconitate hydratase   |
| CIBE_3877              | 6up | 2.2 | 1.1 | 0.9  | 0.2  |         | conserved protein of unknown function                             |
|                        |     |     |     |      |      |         | •   |
| CIBE_5882              | 6up | 2.1 | 1.6 | 0.4  | 0.3  | -       | conserved protein of unknown function                             |
| CIBE_2932              | 6up | 2.0 | 1.3 | 0.5  | 0.6  | -       | protein of unknown function                                       |
| CIBE_3201              | 6up | 2.4 | 1.0 | 0.7  | 0.4  | -       | conserved protein of unknown function                             |
| CIBE_3367              | 6up | 1.8 | 1.1 | 1.0  | 0.5  | -       | putative cell wall binding protein                                |
| CIBE_0479              | 6up | 1.9 | 2.0 | 0.4  | 0.0  | -       | Phage minor structural protein (modular protein)                  |
| CIBE 5271              | 6up | 1.7 | 1.0 | 0.9  | 0.7  | -       | conserved protein of unknown function                             |
| CIBE p0004             | 6up | 1.7 | 1.5 | 0.8  | 0.3  | -       | Putative cell wall binding protein (fragment)                     |
| CIBE_1609              | 6up | 2.3 | 1.4 | 0.4  | 0.2  |         | conserved protein of unknown function                             |
|                        |     | 2.4 | 1.3 | 0.6  |      | spollAA |   |
| CIBE_0992              | 6up |     |     |      |      |         | Anti-sigma F factor antagonist                                    |
| CIBE_1686              | 6up | 1.9 | 1.3 | 0.5  |      | kdpB    | potassium translocating ATPase, subunit B                         |
| CIBE_3185              | 6up | 1.6 | 1.1 | 1.0  | 0.6  | -       | conserved protein of unknown function                             |
| CIBE_6075              | 6up | 2.1 | 1.0 | 1.0  | 0.1  | -       | Beta-lactamase domain protein                                     |
| CIBE_4279              | 6up | 2.4 | 0.8 | 0.5  | 0.5  | -       | conserved protein of unknown function                             |
| CIBE_4736              | 6up | 2.3 | 1.6 | 0.7  | -0.3 | -       | conserved protein of unknown function                             |
| CIBE 3236              | 6up | 1.8 | 1.3 | 0.6  | 0.5  | -       | Alpha/beta hydrolase fold protein                                 |
| CIBE_3395              | 6up | 2.1 | 0.9 | 1.0  | 0.1  |         | N-acetylmuramoyl-L-alanine amidase family 2                       |
|                        |     |     |     |      |      | ymdB    |   |
| CIBE_5280              | 6up | 1.6 | 0.9 | 1.2  |      | yiiiub  | conserved hypothetical protein                                    |
| CIBE_4182              | 6up | 2.0 | 1.3 | 0.7  | 0.2  | -       | DNA mismatch repair protein MutS domain protein                   |
| CIBE_0487              | 6up | 2.1 | 2.1 | 0.4  | -0.4 | -       | conserved protein of unknown function                             |
| CIBE_1611              | 6up | 2.0 | 1.3 | 0.4  | 0.6  | -       | conserved exported protein of unknown function                    |
| CIBE_0457              | 6up | 1.7 | 1.7 | 0.4  | 0.3  | -       | conserved protein of unknown function                             |
| CIBE_5283              | 6up | 2.0 | 1.4 | 0.5  | 0.2  | -       | putative transcriptional regulatory protein, AsnC family          |
| CIBE_4142              | 6up | 2.5 | 1.2 | 0.3  | 0.0  | -       | ABC transporter (fragment)  |
| CIBE_1573              | 6up | 1.6 | 0.9 | 0.9  |      | hisH    | amidotransferase (glutaminase)                                    |
| CIBE_5881              | 6up | 1.8 | 1.3 | 0.5  |      | acpS    | holo-acyl carrier protein synthase                                |
| CIBE 0478              | 6up | 1.9 | 2.2 | 0.6  | -0.6 | -       | putative Phage tail component                                     |
| _                      |     | 1.6 | 1.5 | 0.8  | 0.0  |         | conserved protein of unknown function                             |
| CIBE_1335              | 6up |     |     |      |      |         |   |
| CIBE_4135              | 6up | 2.4 | 1.1 | 0.5  | 0.1  | -       | Phosphatidylethanolamine-binding protein                          |
| CIBE_0467              | 6up | 2.1 | 2.0 | 0.2  | -0.3 | -       | protein of unknown function                                       |
| CIBE_4734              | 6up | 2.1 | 1.2 | 0.7  | 0.1  | -       | conserved membrane protein of unknown function                    |
| CIBE_3290              | 6up | 1.7 | 1.2 | 0.7  | 0.4  | -       | conserved exported protein of unknown function                    |
| CIBE_4138              | 6up | 2.3 | 1.4 | 0.6  | -0.3 | -       | conserved membrane protein of unknown function                    |
| CIBE_1487              | 6up | 2.2 | 1.0 | 0.0  | 0.7  | -       | conserved protein of unknown function                             |
| CIBE_2304              | 6up | 2.0 | 0.9 | 0.6  | 0.5  | -       | conserved protein of unknown function                             |
| CIBE 0289              | 6up | 1.5 | 1.0 | 1.0  | 0.5  |         | Rubrerythrin  |
| _                      |     | 2.0 | 1.5 | 0.5  | 0.0  |         | conserved protein of unknown function                             |
| CIBE_2931              | 6up |     |     |      |      |         |   |
| CIBE_0461              | 6up | 2.0 | 1.9 | 0.2  | -0.2 | -       | conserved protein of unknown function                             |
| CIBE_4009              | 6up | 1.9 | 1.7 | 0.3  | 0.0  | -       | Membrane protein  |
| CIBE_5425              | 6up | 1.5 | 1.3 | 0.9  | 0.2  | argB    | Acetylglutamate kinase  |
| CIBE_3409              | 6up | 1.7 | 0.9 | 0.9  | 0.4  | -       | ABC transporter permease  |
| CIBE 0468              | 6up | 2.2 | 2.1 | 0.0  | -0.4 | -       | Phage coat protein  |
| CIBE_4134              | 6up | 2.2 | 1.3 | 0.3  | 0.1  | -       | GCN5 family acetyltransferase                                     |
| CIBE_4134<br>CIBE 5458 | 6up | 1.7 | 1.0 | 0.5  |      | iolD    | 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase              |
| _                      |     |     |     |      |      | .515    |   |
| CIBE_0445              | 6up | 2.1 | 1.6 | -0.1 | 0.2  | -       | Gp49 homologous (fragment)  |
| CIBE_1162              | 6up | 2.2 | 0.4 | 0.9  | 0.4  | l       | Polysaccharide biosynthesis protein                               |
| CIBE_3905              | 6up | 1.8 | 0.9 | 0.6  | 0.6  |         | Alpha/beta hydrolase fold   |
| CIBE_1398              | 6up | 0.4 | 2.1 | 0.9  | 0.4  | -       | Sporulation integral membrane protein YlbJ                        |
|                        |     |     |     |      |      |         |   |

| I   |   |  |  |  |   |   |
|---|---|--|--|--|---|---|
| CIBE_4367   | 6up   | 1.9  | 1.4  | 0.6  | -0.1 -  | DNA mismatch repair protein MutS (fragment)   |
| CIBE_2568   | 6up   | 2.1  | 1.7  | 0.2  | -0.3 -  | putative cell wall binding repeat-containing protein  |
| CIBE_0896   | 6up   | 2.0  | 1.4  | 0.7  | -0.4 -  | ABC transporter substrate-binding protein   |
| CIBE_3784   | 6up   | 2.1  | 0.9  | 0.5  | 0.0 -   | protein of unknown function   |
| CIBE_3281   | 6up   | 1.9  | 1.3  | 0.2  | 0.1 gldA  | glycerol dehydrogenase, NAD   |
| CIBE_3342   | 6up   | 1.9  | 0.7  | 0.5  | 0.3 -   | conserved protein of unknown function   |
| CIBE_0469   | 6up   | 2.0  | 2.1  | -0.1   | -0.4 -  | conserved protein of unknown function   |
| CIBE_3893   | 6up   | 2.0  | 0.9  | 0.6  | 0.0 pspB  | putative phosphoserine phosphatase 2  |
| CIBE_4609   | 6up   | 3.2  | 2.4  | 2.3  | 2.7 adc   | Acetoacetate decarboxylase  |
| CIBE_0993   | 6up   | 2.3  | 1.1  | 0.3  | -0.2 spolIAB  | anti-sigma factor (antagonist of sigma(F)) and serine kinase  |
| CIBE_2043   | 6up   | 1.7  | 1.2  | 0.5  | 0.1 -   | conserved protein of unknown function   |
| CIBE_0474   | 6up   | 2.0  | 1.8  | -0.1   | -0.3 -  | conserved protein of unknown function   |
| CIBE_3894   | 6up   | 2.1  | 1.2  | 0.5  | -0.4 -  | ADP-ribose pyrophosphatase  |
| CIBE_0594   | 6up   | 1.6  | 1.9  | 0.0  | -0.1 -  | conserved membrane protein of unknown function  |
| CIBE_0867   | 6up   | 1.7  | 0.7  | 0.4  | 0.5 -   | Histidine kinase  |
| CIBE 3172   | 6up   | 2.2  | 1.5  | 0.5  | -1.0 -  | conserved protein of unknown function   |
| CIBE_0751   | 6up   | 1.7  | 1.0  | 0.4  | 0.2 nth   | Endonuclease III  |
|   |   | 1.7  | 1.1  | 0.2  | 0.2 -   |   |
| CIBE_4366   | 6up   |  |  |  |   | DNA mismatch repair protein MutS (fragment)   |
| CIBE_3233   | 6up   | 1.9  | 1.1  | 0.6  | -0.4 -  | conserved protein of unknown function   |
| CIBE_3811   | 6up   | 1.9  | 0.8  | 0.4  | 0.0 -   | Fumarylacetoacetate (FAA) hydrolase   |
| CIBE_1605   | 6up   | 0.4  | 2.0  | 0.7  | 0.0 -   | Sporulation protein SpoVB   |
| CIBE_0462   | 6up   | 1.6  | 1.6  | 0.2  | -0.2 -  | putative SPP1 gp7 family phage head morphogenesis protein   |
| CIBE_2040   | 6up   | 3.0  | 0.9  | -0.3   | -0.6 -  | protein of unknown function   |
| CIBE_0416   | 6up   | 1.9  | 1.0  | 0.2  | -0.1 -  | Two component regulator three Y domain protein  |
| CIBE_2305   | 6up   | 1.8  | 0.5  | 0.3  | 0.3 -   | Methyl-accepting chemotaxis protein   |
| CIBE_3892   | 6up   | 2.2  | 0.6  | 0.2  | -0.2 -  | conserved protein of unknown function   |
| CIBE_4975   | 6up   | 1.8  | 0.9  | 0.1  | <b>0.1</b> hsp  | 18 kDa heat shock protein   |
| CIBE_0277   | 6up   | 1.9  | 0.8  | 0.8  | -0.5 -  | Cyclase   |
| CIBE_0357   | 6up   | 2.0  | 0.8  | 0.0  | 0.0 -   | protein of unknown function   |
| CIBE_4848   | 6up   | 2.1  | 1.1  | 0.1  | -0.5 -  | Methyl-accepting chemotaxis sensory transducer  |
| CIBE_2629   | 6up   | 1.5  | 1.2  | 0.3  | -0.2 -  | conserved protein of unknown function   |
| CIBE_5615   | 6up   | 1.8  | 0.9  | -0.1   | 0.2 -   | Cell wall hydrolase   |
| CIBE_2933   | 6up   | 1.8  | 0.7  | 0.2  | 0.1 -   | conserved protein of unknown function   |
| CIBE_2933<br>CIBE 5880  |   | 2.1  | 1.1  | -0.1   | -0.3 -  | Carbohydrate kinase   |
| CIBE_5880<br>CIBE_0488  | 6up   | 1.7  | 1.1  | -0.1   | -0.3 -  | Glycoside hydrolase, family 25  |
|   | 6up   |  |  |  |   |   |
| CIBE_3984   | 6up   | 1.6  | 0.7  | 0.1  | 0.2 -   | conserved protein of unknown function   |
| CIBE_4984   | 6up   | 1.6  | 0.7  | 0.4  | 0.0 -   | Alpha amylase, catalytic region   |
| CIBE_3783   | 6up   | 1.8  | 0.7  | 0.3  | -0.2 -  | conserved protein of unknown function   |
| CIBE_2783   | 6up   | 1.7  | 0.5  | 0.6  | -0.2 -  | conserved protein of unknown function   |
| CIBE_1355   | 6up   | 1.5  | 1.6  | 0.0  | -0.5 -  | Peptidase U4  |
| CIBE_2168   | 6up   | 1.6  | 0.7  | 0.3  | 0.0 -   | ATP-dependent DNA helicase RecQ   |
| CIBE_0435   | 6up   | 1.6  | 1.3  | 0.2  | -0.6 -  | conserved protein of unknown function   |
| CIBE_0974   | 6up   | 1.9  | 1.0  | 0.1  | -0.6 -  | Universal stress protein  |
| CIBE_0466   | 6up   | 1.8  | 1.8  | -0.4   | -1.0 -  | conserved protein of unknown function   |
| CIBE_4280   | 6up   | 1.9  | 0.8  | 0.3  | -0.6 -  | Metallo-beta-lactamase superfamily protein  |
| CIBE_4435   | 6up   | 1.8  | 0.9  | 0.6  | -1.0 -  | conserved protein of unknown function   |
| CIBE_5924   | 6up   | 1.8  | 0.8  | 0.0  | -0.4 glgC   | glucose-1-phosphate adenylyltransferase (ADP-glucose pyrophosphorylase) subunit alpha   |
| CIBE 2041   | 6up   | 2.0  | 0.6  | -0.1   | -0.3 spo0A  | response regulator  |
| CIBE 0456   | 6up   | 0.9  | 1.6  | -0.5   | 0.3 -   | conserved protein of unknown function   |
| CIBE_4732   | 6up   | 2.1  | 1.2  | 0.1  | -1.2 lepB   | Signal peptidase I  |
| CIBE_0831   | 6up   | 1.5  | 0.6  | 0.1  | 0.0 sudA  | Sulfide dehydrogenase subunit alpha   |
| CIBE_5056   |   | 2.0  | 0.5  | 0.2  | -0.6 -  | Isocitrate dehydrogenase [NADP]   |
| CIBE_4859   | 6up   | 1.8  | 0.3  | -0.2   | -0.3 -  |   |
|   | 6up   | 1.5  | 0.7  | 0.1  | -0.4 -  | Cell wall hydrolase/autolysin   |
| CIBE_0088   | 6up   | 1.8  | 0.7  |  |   | protein of unknown function Two component transcriptional regulator, LytTR family   |
| CIBE_0307   | 6up   |  |  | 0.1  | -0.3 -  | , , , , ,   |
| CIBE_2617   | 6up   | 1.9  | 1.0  | 0.1  | -1.0 -  | conserved protein of unknown function   |
| CIBE_3978   | 6up   | 1.8  | 1.1  | -0.4   | -0.7 -  | conserved protein of unknown function   |
| CIBE_5925   | 6up   | 1.6  | 0.5  | -0.2   | -0.2 -  | Alpha-amylase   |
| CIBE_3846   | 6up   | 1.6  | 0.4  | 0.1  | -0.5 thrZ   | threonyl-tRNA synthetase  |
| CIBE_5923   | 6up   | 1.9  | 0.7  | -0.3   | -0.8 -  | Glucose-1-phosphate adenylyltransferase   |
| CIBE_0279   | 6up   | 2.2  | 0.3  | 0.6  | -1.8 -  | Methyl-accepting chemotaxis sensory transducer  |
| CIBE_0628   | 6up   | 1.7  | 0.4  | -0.3   | -0.6 -  | protein of unknown function   |
| CIBE_0436   | 6up   | 1.5  | 1.1  | -0.7   | -0.8 -  | Excisionase family  |
| CIBE_3001   | 6up   | 1.6  | 0.1  | -0.2   | -0.4 ftnA   | Ferritin  |
| CIBE_0465   | 6up   | 1.8  | 1.5  | -0.6   | -1.6 -  | protein of unknown function   |
| CIBE_2317   | 6up   | 1.2  | 1.2  | -0.5   | -1.0 -  | conserved protein of unknown function   |
| CIBE_3891   | 6up   | 2.0  | 0.3  | -0.4   | -1.0 -  | conserved membrane protein of unknown function  |
| CIBE_0278   | 6up   | 1.9  | 0.0  | 0.3  | -2.5 -  | Transcriptional regulator   |
| CIBE tRNA57   | 6down   | -1.7   | -1.4   | -0.1   | 0.4 -   | Ala tRNA  |
| CIBE 4931   | 6down   | -1.7   | -1.2   | -0.4   | -0.3 ydaO   | Uncharacterized amino acid permease YdaO  |
| CIBE_1058   | 6down   | -1.6   | -0.5   | -0.9   | -0.9 amtB   | ammonium transporter  |
| CIBE_misc_RNA_81  |   | -1.6   | -1.5   | -0.9   | -0.4 -  | T-box   |
|   |   |  |  |  |   | 1 DON   |
|   |   |  |  |  |   | nutative enzyme   |
| CIBE_5854   | 6down   | -1.6   | -1.2   | -0.9   | -0.8 -  | putative enzyme   |
| CIBE_5854<br>CIBE_3636  | 6down<br>6down  | -1.6<br>-2.1   | -1.2<br>-1.4   | -0.9<br>-0.4   | -0.8 -<br>-0.7 -  | putative galactoside ABC transporter  |
| CIBE_5854<br>CIBE_3636<br>CIBE_tRNA46   | 6down<br>6down<br>6down   | -1.6<br>-2.1<br>-2.2   | -1.2<br>-1.4<br>-1.5   | -0.9<br>-0.4<br>-0.9   | -0.8 -<br>-0.7 -<br>0.0 -   | putative galactoside ABC transporter<br>Ile tRNA  |
| CIBE_5854<br>CIBE_3636<br>CIBE_tRNA46<br>CIBE_1055  | 6down<br>6down<br>6down<br>6down  | -1.6<br>-2.1<br>-2.2<br>-1.6   | -1.2<br>-1.4<br>-1.5<br>-1.3   | -0.9<br>-0.4<br>-0.9<br>-0.9   | -0.8 -<br>-0.7 -<br>0.0 -<br>-1.3 -   | putative galactoside ABC transporter<br>Ile tRNA<br>DNA topoisomerase   |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267   | 6down<br>6down<br>6down<br>6down  | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2   | -0.8 -<br>-0.7 -<br>0.0 -<br>-1.3 -<br>-0.9 glmS                                  | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing]  |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_1412   | 6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1   | -0.8 -<br>-0.7 -<br>0.0 -<br>-1.3 -<br>-0.9 glmS<br>-1.4 ffh                      | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase  |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870   | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down   | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.6<br>-1.9   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1   | -0.8 -<br>-0.7 -<br>0.0 -<br>-1.3 -<br>-0.9 glmS<br>-1.4 ffh<br>-0.5 -            | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function  |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529   | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.6<br>-1.9<br>-1.7   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1<br>-0.1   | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.4 -                                       | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase   |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_14870 CIBE_5529 CIBE_5213  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down   | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1   | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.2 -                                    | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function  |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529   | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.6<br>-1.9<br>-1.7   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1<br>-0.1   | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.4 -                                       | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase   |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_14870 CIBE_5529 CIBE_5213  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down                                     | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1<br>-0.1<br>-1.0                                 | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.2 -                                    | putative galactoside ABC transporter  Ile tRNA  DNA topoisomerase  Glutaminefructose-6-phosphate aminotransferase [isomerizing]  signal recognition particle-like (SRP) GTPase  conserved protein of unknown function  Glycosyl transferase  Sodium:dicarboxylate symporter   |
| CIBE_5854 CIBE_3636 CIBE_TRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5523 CIBE_5723   | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down                            | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1<br>-0.1<br>-1.0<br>-1.0                         | -0.80.7 - 0.01.30.9 gfms -1.4 ffh -0.51.41.20.8 -                                 | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase Sodium:dicarboxylate symporter conserved exported protein of unknown function   |
| CIBE_5854 CIBE_3636 CIBE_TRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5529 CIBE_5213 CIBE_5772 CIBE_5772   | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down                            | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.8   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7<br>-1.3   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1<br>-0.1<br>-1.0<br>-1.0<br>-0.9<br>-0.9         | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.20.81.4 -                              | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase Sodium:dicarboxylate symporter conserved exported protein of unknown function Methyl-accepting chemotaxis sensory transducer  |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5529 CIBE_5213 CIBE_5723 CIBE_5772 CIBE_2630                               | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down                   | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.8<br>-1.7   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7<br>-1.3<br>-1.5   | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1<br>-0.1<br>-1.0<br>-0.9<br>-0.9<br>-1.3         | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.21.2 -                                 | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase Sodium:dicarboxylate symporter conserved exported protein of unknown function Methyl-accepting chemotaxis sensory transducer conserved exported protein of unknown function   |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5523 CIBE_5723 CIBE_5723 CIBE_5772 CIBE_2630 CIBE_0191                     | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down          | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.8<br>-1.7   | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7<br>-1.3<br>-1.5<br>-1.4                                 | -0.9<br>-0.4<br>-0.9<br>-0.9<br>-1.2<br>-1.1<br>-0.1<br>-1.0<br>-0.9<br>-0.9<br>-1.3<br>-1.3 | -0.80.7 - 0.01.30.9 glmS -1.4 fffh -0.51.41.20.81.41.21.41.2 -                    | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase Sodium:dicarboxylate symporter conserved exported protein of unknown function Methyl-accepting chemotaxis sensory transducer conserved exported protein of unknown function methionine aminopeptidase   |
| CIBE_5854 CIBE_3636 CIBE_TRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5529 CIBE_5723 CIBE_5723 CIBE_5772 CIBE_637 CIBE_0191 CIBE_0637 CIBE_5709  | 6down             | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.8<br>-1.8                         | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7<br>-1.3<br>-1.5<br>-1.4<br>-1.6<br>-1.5                 | -0.9 -0.4 -0.9 -0.9 -1.2 -1.1 -0.1 -1.0 -0.9 -0.9 -1.3 -1.3 -1.1 -1.0                        | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.20.81.41.21.4 mapA -1.41.6 artQ        | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase Sodium:dicarboxylate symporter conserved exported protein of unknown function Methyl-accepting chemotaxis sensory transducer conserved exported protein of unknown function methionine aminopeptidase 2-nitropropane dioxygenase, NPD high affinity arginine ABC transporter (permease)   |
| CIBE_5854 CIBE_3636 CIBE_TRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5523 CIBE_5723 CIBE_5772 CIBE_630 CIBE_0191 CIBE_0637 CIBE_0637 CIBE_1369  | 6down | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.8<br>-1.7                 | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7<br>-1.3<br>-1.5<br>-1.4<br>-1.6<br>-1.5<br>-1.7         | -0.9 -0.4 -0.9 -0.9 -1.2 -1.1 -0.1 -1.0 -0.9 -0.9 -1.3 -1.3 -1.1 -1.0 -1.3                   | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.20.81.41.21.4 mapA -1.41.6 artQ -1.3 - | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase Sodium:dicarboxylate symporter conserved exported protein of unknown function Methyl-accepting chemotaxis sensory transducer conserved exported protein of unknown function methionine aminopeptidase 2-nitropropane dioxygenase, NPD high affinity arginine ABC transporter (permease) Fe-S oxidoreductase                                       |
| CIBE_5854 CIBE_3636 CIBE_tRNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5523 CIBE_5723 CIBE_5772 CIBE_6637 CIBE_0637 CIBE_0637 CIBE_1369 CIBE_0805 | 6down | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.7<br>-1.6<br>-1.9<br>-1.8<br>-1.7<br>-1.6<br>-1.8<br>-1.7<br>-1.8<br>-1.7<br>-1.8 | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7<br>-1.3<br>-1.5<br>-1.4<br>-1.6<br>-1.5<br>-1.7<br>-1.6 | -0.9 -0.4 -0.9 -0.9 -1.2 -1.1 -0.1 -1.0 -0.9 -0.9 -1.3 -1.3 -1.1 -1.0 -1.3 -1.2              | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.21.41.21.4 mapA -1.41.6 artQ -1.31.1 - | putative galactoside ABC transporter Ile tRNA DNA topoisomerase Glutaminefructose-6-phosphate aminotransferase [isomerizing] signal recognition particle-like (SRP) GTPase conserved protein of unknown function Glycosyl transferase Sodium:dicarboxylate symporter conserved exported protein of unknown function Methyl-accepting chemotaxis sensory transducer conserved exported protein of unknown function methionine aminopeptidase 2-nitropropane dioxygenase, NPD high affinity arginine ABC transporter (permease) Fe-S oxidoreductase conserved protein of unknown function |
| CIBE_5854 CIBE_3636 CIBE_HNA46 CIBE_1055 CIBE_0267 CIBE_1412 CIBE_4870 CIBE_5529 CIBE_5213 CIBE_5723 CIBE_5772 CIBE_2630 CIBE_0637 CIBE_0637 CIBE_1369            | 6down | -1.6<br>-2.1<br>-2.2<br>-1.6<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.7<br>-1.6<br>-1.9<br>-1.8<br>-1.7                 | -1.2<br>-1.4<br>-1.5<br>-1.3<br>-1.5<br>-1.2<br>-2.7<br>-1.3<br>-1.6<br>-1.7<br>-1.3<br>-1.5<br>-1.4<br>-1.6<br>-1.5<br>-1.7         | -0.9 -0.4 -0.9 -0.9 -1.2 -1.1 -0.1 -1.0 -0.9 -0.9 -1.3 -1.3 -1.1 -1.0 -1.3                   | -0.80.7 - 0.01.30.9 glmS -1.4 ffh -0.51.41.20.81.41.21.4 mapA -1.41.6 artQ -1.3 - | putative galactoside ABC transporter  Ile tRNA  DNA topoisomerase  Glutaminefructose-6-phosphate aminotransferase [isomerizing]  signal recognition particle-like (SRP) GTPase  conserved protein of unknown function  Glycosyl transferase  Sodium:dicarboxylate symporter  conserved exported protein of unknown function  Methyl-accepting chemotaxis sensory transducer  conserved exported protein of unknown function  methionine aminopeptidase  2-nitropropane dioxygenase, NPD  high affinity arginine ABC transporter (permease)  Fe-S oxidoreductase                         |

| CIBE 1411  | 6down   | -2.0   | -1.2   | -1.3   | -1.6  | ylxM   | conserved hypothetical protein   |
|--|---|--|--|--|---|--|--|
| CIBE_5007  | 6down   | -1.7   | -1.2   | -1.0   | -2.3  | -  | conserved protein of unknown function  |
| CIBE_5698  | 6down   | -2.2   | -1.4   | -1.3   | -1.2  | -  | Cation diffusion facilitator family transporter  |
| CIBE_5863  | 6down   | -1.9   | -1.8   | -1.1   |   | murB   | UDP-N-acetylenolpyruvoylglucosamine reductase  |
| CIBE_4421  | 6down   | -2.3   | -1.7   | -1.7   | -0.7  |  | transposase (fragment)   |
| CIBE_1001  | 6down   | -1.8   | -1.0   | -1.3   |   | rpsT   | ribosomal protein S20 (BS20)   |
| CIBE_0198  | 6down   | -1.5<br>-1.6   | -1.3<br>-1.8   | -1.5<br>-1.3   | -2.1<br>-1.7  | rpoA   | RNA polymerase (alpha subunit)   |
| CIBE_0566<br>CIBE 1624   | 6down<br>6down  | -1.6   | -1.5   | -1.5   | -1.7  | -  | conserved membrane protein of unknown function conserved protein of unknown function   |
| CIBE_1024<br>CIBE 4992   | 6down   | -1.7   | -1.5   | -1.6   |   | -<br>nupQ  | permease of ABC guanosine transporter  |
| CIBE_2872  | 6down   | -1.5   | -1.6   | -1.3   | -2.2  | -  | Ribose-phosphate pyrophosphokinase   |
| CIBE_5607  | 6down   | -1.8   | -1.3   | -1.5   | -2.1  | -  | Polysaccharide biosynthesis protein  |
| CIBE_0050  | 6down   | -1.7   | -1.4   | -1.6   | -2.0  | regA   | HTH-type transcriptional regulator RegA  |
| CIBE_1414  | 6down   | -1.6   | -1.5   | -1.6   | -2.0  | ylqC   | putative RNA binding protein   |
| CIBE_5948  | 6down   | -1.8   | -1.9   | -1.4   | -1.6  | -  | putative transcriptional regulator, TetR family  |
| CIBE_2478  | 6down   | -1.7   | -2.1   | -1.6   | -1.3  | -  | conserved protein of unknown function  |
| CIBE_4210  | 6down   | -1.1   | -0.3   | -2.4   | -3.0  | -  | Extracellular solute-binding protein, family 1   |
| CIBE_5783  | 6down   | -2.0   | -1.6   | -1.3   | -1.8  | -  | Dehydrogenase  |
| CIBE_2956<br>CIBE_4864   | 6down<br>6down  | -1.8<br>-2.5   | -1.5<br>-1.7   | -1.6<br>-1.3   | -1.8  | -<br>steT  | Polar amino acid ABC transporter, inner membrane subunit Serine/threonine exchanger SteT   |
| CIBE_4804<br>CIBE 1190   | 6down   | -1.9   | -1.7   | -1.7   | -1.3  | -  | Tetratricopeptide TPR 2 repeat protein   |
| CIBE_6107  | 6down   | -1.5   | -1.6   | -1.7   |   | rpsR   | ribosomal protein S18  |
| CIBE 6116  | 6down   | -2.3   | -1.5   | -1.4   | -1.7  | -  | transposase (fragment)   |
| CIBE 4945  | 6down   | -2.7   | -1.9   | -1.1   |   | ycaM   | putative transporter   |
| CIBE_4830  | 6down   | -1.8   | -1.5   | -1.6   | -1.9  | -  | Signal peptidase I   |
| CIBE_3454  | 6down   | -2.3   | -1.8   | -1.7   | -1.2  | -  | protein of unknown function  |
| CIBE_1330  | 6down   | -1.7   | -1.6   | -1.6   | -2.0  | rarA   | DNA-dependent ATPase   |
| CIBE_1490  | 6down   | -1.8   | -1.9   | -1.3   | -1.9  | kup  | putative potassium transport system protein kup  |
| CIBE_5914  | 6down   | -1.8   | -1.3   | -2.0   | -1.9  | -  | Peptidase A8   |
| CIBE_5729  | 6down   | -1.7   | -1.7   | -1.5   | -2.1  | -  | conserved protein of unknown function  |
| CIBE_5126  | 6down   | -1.5   | -2.1   | -1.6   | -1.7  | -  | Flagellar hook capping protein (fragment)  |
| CIBE_0735  | 6down   | -1.8   | -1.6   | -1.4   | -2.2  | -  | conserved protein of unknown function  |
| CIBE_1565  | 6down   | -1.9   | -1.9   | -1.4   | -1.9  |  | Cysteine desulfurase   |
| CIBE_1427  | 6down   | -1.7   | -1.4   | -1.5   | -2.4  | tsf  | elongation factor Ts   |
| CIBE_6030  | 6down   | -1.5   | -1.6   | -1.6   | -2.3  | -  | DEAD/DEAH box helicase domain protein  |
| CIBE_3635  | 6down   | -1.8<br>-3.1   | -1.2<br>-2.4   | -1.2<br>-0.9   | -2.9<br>-0.7  | -  | Rubrerythrin Purine  |
| CIBE_misc_RNA_4<br>CIBE_0162   | 6down   | -3.1   | -2.4   | -0.9   |   | rpsL   | ribosomal protein S12 (BS12)   |
| CIBE_0102<br>CIBE_2562   | 6down   | -1.6   | -1.8   | -1.8   |   | aspS   | AspartatetRNA ligase   |
| CIBE_0197  | 6down   | -1.8   | -1.6   | -1.7   |   | rpsD   | 30S ribosomal subunit protein S4   |
| CIBE_0679  | 6down   | -1.8   | -1.6   | -1.8   |   | rplU   | ribosomal protein L21 (BL20)   |
| CIBE_5784  | 6down   | -2.2   | -1.5   | -1.8   | -1.8  | -  | Xylose isomerase domain protein TIM barrel   |
| CIBE 4906  | 6down   | -3.5   | -1.9   | -0.9   | -1.0  | -  | conserved membrane protein of unknown function   |
| CIBE_1623  | 6down   | -1.9   | -1.7   | -1.8   | -2.0  | -  | conserved protein of unknown function  |
| CIBE_2076  | 6down   | -1.8   | -1.8   | -1.6   | -2.2  | -  | Rrf2 family transcriptional regulator  |
| CIBE_misc_RNA_4  | 5 6down   | -3.2   | -3.2   | -0.7   | -0.4  | -  | Purine   |
| CIBE_5855  | 6down   | -1.7   | -2.0   | -1.5   | -2.3  | pyk  | pyruvate kinase  |
|  |   |  |  |  |   |  |  |
| CIBE_0903  | 6down   | -2.1   | -2.4   | -1.3   | -1.7  | -  | FMN reductase  |
| CIBE_4960  | 6down   | -1.8   | -2.1   | -1.7   | -1.9  | ydeP   | Uncharacterized HTH-type transcriptional regulator YdeP  |
| CIBE_4960<br>CIBE_1566   | 6down<br>6down  | -1.8<br>-1.7   | -2.1<br>-2.0   | -1.7<br>-1.4   | -1.9<br>-2.4  | -<br>ydeP<br>trml  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification   |
| CIBE_4960<br>CIBE_1566<br>CIBE_5118  | 6down<br>6down<br>6down   | -1.8<br>-1.7<br>-1.6   | -2.1<br>-2.0<br>-2.0   | -1.7<br>-1.4<br>-2.0   | -1.9<br>-2.4<br>-2.0  | -  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB   |
| CIBE_4960<br>CIBE_1566<br>CIBE_5118<br>CIBE_4098   | 6down<br>6down<br>6down<br>6down  | -1.8<br>-1.7<br>-1.6<br>-1.6   | -2.1<br>-2.0<br>-2.0<br>-1.8   | -1.7<br>-1.4<br>-2.0<br>-2.5   | -1.9<br>-2.4<br>-2.0<br>-1.7  | -  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function   |
| CIBE_4960<br>CIBE_1566<br>CIBE_5118<br>CIBE_4098<br>CIBE_5130  | 6down<br>6down<br>6down<br>6down<br>6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2  | -  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein  |
| CIBE_4960<br>CIBE_1566<br>CIBE_5118<br>CIBE_4098<br>CIBE_5130<br>CIBE_0024   | 6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3  | -  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase  |
| CIBE_4960<br>CIBE_1566<br>CIBE_5118<br>CIBE_4098<br>CIBE_5130<br>CIBE_0024<br>CIBE_0680  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6  | trml -<br>-<br>-<br>-  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function  |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2  | -  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein)   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-1.8  | trml ykpA -  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-1.8  | trml -<br>-<br>-<br>-  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein)   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-1.8<br>-2.5  | trml ykpA -  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-1.8<br>-2.5<br>-2.4  | trml ykpA rpmF -   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0680 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5   | -2.1<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.6<br>-2.0<br>-1.7<br>-1.1   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -2.0 -0.7   | trml ykpA - rpmF fliG  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine  |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_0056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_5131 CIBE_misc_RNA_4 CIBE_2029  | 6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down<br>6down  | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -2.0 -0.7   | trml ykpA rpmF   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog  |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_5131 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120  | 6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5<br>-1.8<br>-2.3   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -2.0 -0.7 -1.7  | trml ykpA - rpmF fliG  | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease  |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_5131 CIBE_misc_RNA_4 CIBE_029 CIBE_4120 CIBE_4120 CIBE_5135   | 6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5<br>-1.9   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.5   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -2.0 -0.7 -1.7 -2.3   | trml ykpA rpmF   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB  |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1513 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_4120 CIBE_5135 CIBE_135 CIBE_135 CIBE_135 CIBE_135  | 6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5<br>-1.8<br>-2.0<br>-3.5<br>-1.8<br>-2.0   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.7   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -2.0 -0.7 -1.7 -2.3 -1.2  | trml ykpA rpmF   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_1403 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1331 CIBE_MISC_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_TRNA89 CIBE_1068  | 6down   | -1.8<br>-1.7<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5<br>-1.8<br>-2.3<br>-1.9<br>-2.9<br>-2.7   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.7   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -2.0 -0.7 -1.7 -2.3 -1.2 -0.4   | trml ykpA rpmF   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_0056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1268 CIBE_1335 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15136 CIBE_1608 CIBE_0298  | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.0 -3.5 -1.8 -2.3 -1.9 -2.7 -2.2  | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-1.8   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.0<br>-1.7<br>-1.1   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-1.8<br>-2.5<br>-2.4<br>-2.2<br>-2.0<br>-0.7<br>-1.7<br>-2.3<br>-1.2<br>-0.4<br>-1.9  | trmI ykpA fliG - nusB ydeD                                   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_5131 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_5135 CIBE_5135 CIBE_TRNA89 CIBE_1068 CIBE_0298 CIBE_1418  | 6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5<br>-1.8<br>-2.3<br>-1.9<br>-2.9<br>-2.9<br>-2.9   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-2.2   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.5<br>-1.3<br>-1.5<br>-1.1<br>-1.5<br>-1.5<br>-1.1<br>-1.5<br>-1.1   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-2.4<br>-2.2<br>-2.0<br>-0.7<br>-2.7<br>-1.7<br>-2.3<br>-1.2<br>-0.4<br>-1.9<br>-2.4  | trmI ykpA rpmF fliG - nusB ydeD rbgA                         | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A  |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_131 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_1368 CIBE_1068 CIBE_1068 CIBE_1068   | 6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5<br>-1.9<br>-2.9<br>-2.7<br>-2.9<br>-2.7<br>-1.8   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-2.0<br>-2.0<br>-2.1<br>-1.9   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.6   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-2.4<br>-2.2<br>-2.0<br>-0.7<br>-2.7<br>-1.7<br>-2.3<br>-2.6<br>-2.2<br>-2.0<br>-0.7<br>-2.7<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2  | trmI ykpA fliG - nusB ydeD rbgA obgE                         | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly   |
| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_0056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_131 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_4120 CIBE_5135 CIBE_168 CIBE_0028 CIBE_1068 CIBE_0028 CIBE_1418 CIBE_0082 CIBE_10682 CIBE_0158   | 6down   | -1.8 -1.7 -1.6 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.9 -2.7 -2.2 -1.9 -1.8 -1.9  | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-2.0<br>-2.0<br>-2.1<br>-1.5<br>-1.7<br>-2.5<br>-2.2<br>-1.7<br>-1.5<br>-1.7<br>-1.5<br>-1.7<br>-1.5<br>-1.7<br>-1.5<br>-1.7<br>-1.5<br>-1.7<br>-1.7<br>-1.7<br>-1.7<br>-1.7<br>-1.7<br>-1.7<br>-1.7   | 1.7<br>1.4<br>2.0<br>2.5<br>1.9<br>1.6<br>1.7<br>1.9<br>1.6<br>2.0<br>1.7<br>1.1<br>1.8<br>1.5<br>1.6<br>2.0<br>1.7<br>1.1<br>1.8<br>1.5<br>1.6<br>2.0<br>1.7<br>1.1<br>1.8<br>1.5<br>1.6<br>1.7<br>1.1<br>1.8<br>1.9<br>1.1<br>1.9<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0  | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-1.8<br>-2.5<br>-2.4<br>-2.2<br>-0.7<br>-1.7<br>-2.3<br>-1.2<br>-0.4<br>-1.9<br>-2.4<br>-2.9<br>-2.4<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9  | trmI ykpA fliG - nusB ydeD                                   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BLS)   |
| CIBE_4960 CIBE_1566 CIBE_1518 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5131 CIBE_1265 CIBE_135 CIBE_1412 CIBE_0682 CIBE_0682 CIBE_0682 CIBE_0158 CIBE_1419   | 6down   | -1.8<br>-1.7<br>-1.6<br>-1.6<br>-1.8<br>-2.1<br>-1.6<br>-2.0<br>-2.5<br>-1.6<br>-1.7<br>-1.8<br>-2.0<br>-3.5<br>-1.9<br>-2.9<br>-2.7<br>-2.9<br>-2.7<br>-1.8   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-2.0<br>-2.0<br>-2.1<br>-1.9   | -1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.6   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.5<br>-2.4<br>-2.2<br>-2.0<br>-0.7<br>-1.7<br>-2.7<br>-1.2<br>-0.4<br>-1.9<br>-2.4<br>-2.9<br>-2.6<br>-2.5<br>-2.5<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2  | trmI ykpA fliG - nusB ydeD rbgA obgE                         | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5)   |
| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_0056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_131 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_4120 CIBE_5135 CIBE_168 CIBE_0028 CIBE_1068 CIBE_0028 CIBE_1418 CIBE_0082 CIBE_10682 CIBE_0158   | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -1.8 -1.9 -2.2   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.2<br>-2.2<br>-2.3<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-1.9<br>-1.8<br>-1.7   | 1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.9<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.9<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.9<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>- | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-2.4<br>-2.2<br>-2.0<br>-0.7<br>-1.7<br>-2.7<br>-1.2<br>-2.4<br>-2.9<br>-2.5<br>-2.5<br>-2.4<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2  | trmI ykpA rmpF nusB ydeD rbgA obgE rplJ rnhB                 | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BLS)   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1085 CIBE_1418 CIBE_0682 CIBE_0682 CIBE_0158 CIBE_1419 CIBE_5117  | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.0 -3.5 -1.8 -2.3 -1.9 -2.9 -2.1 -1.8 -2.0 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -1.9 -2.1 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.9 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.9 -1.8 -1.8 -1.8 -1.8 -1.8 -1.8 -1.8 -1.8 | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.1<br>-1.8<br>-1.9<br>-2.2<br>-1.7<br>-2.5<br>-2.2<br>-1.7<br>-2.5<br>-2.2<br>-1.7<br>-2.5<br>-2.2<br>-1.7<br>-2.5<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0   | 1.7<br>-1.4<br>-2.0<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.1<br>-1.3<br>-1.5<br>-1.6<br>-1.7<br>-1.1<br>-1.5<br>-1.6<br>-1.7<br>-1.1<br>-1.1<br>-1.5<br>-1.6<br>-1.7<br>-1.1<br>-1.1<br>-1.5<br>-1.6<br>-1.7<br>-1.1<br>-1.1<br>-1.5<br>-1.6<br>-1.7<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>-1.1<br>- | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-2.4<br>-2.2<br>-2.0<br>-0.7<br>-1.7<br>-2.7<br>-1.2<br>-2.4<br>-2.9<br>-2.5<br>-2.5<br>-2.4<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2<br>-2.2  | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BLS) ribonuclease HII component of the flagellar export machinery  |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_5131 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_tRNA89 CIBE_1068 CIBE_0682 CIBE_0682 CIBE_0158 CIBE_0158 CIBE_1119 CIBE_5131 CIBE_1517 CIBE_5334  | 6down   | -1.8 -1.7 -1.6 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.0 -3.5 -1.8 -2.3 -1.9 -2.9 -2.9 -1.8 -1.9 -2.1 -1.6 -1.7 -1.8 -1.0 -1.5 -1.8 -1.3 -1.9 -1.9 -1.9 -1.9 -1.9 -1.9 -1.9 -1.9   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.3<br>-1.7<br>-2.5<br>-2.0<br>-2.0<br>-1.9<br>-1.7<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.1<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0   | -1.7<br>-1.4<br>-2.0<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.7<br>-1.9<br>-1.7<br>-1.9<br>-1.7<br>-1.9<br>-1.6<br>-2.3<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1   | -1.9<br>-2.4<br>-2.0<br>-1.7<br>-2.2<br>-2.3<br>-2.6<br>-2.2<br>-2.0<br>-2.7<br>-2.7<br>-1.7<br>-2.3<br>-1.2<br>-2.4<br>-2.9<br>-2.4<br>-2.9<br>-2.4<br>-2.9<br>-2.4<br>-2.9<br>-2.4<br>-2.9<br>-2.4<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9<br>-2.9  | trmI ykpA ffliG - nusB ydeD rbgA obgE rpIJ rnhB fflhA rbsA - | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BLS) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein)   |
| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0680 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_15131 CIBE_1655 CIBE_1513 CIBE_15135 CIBE_15135 CIBE_1668 CIBE_1068 CIBE_0298 CIBE_1418 CIBE_0298 CIBE_1418 CIBE_0158 CIBE_1419 CIBE_1517 CIBE_5117 CIBE_5334 CIBE_5117 CIBE_5334 CIBE_5122   | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -1.8 -1.9 -2.1 -1.6 -3.0 -1.6 -3.0 -1.6 -2.1 -2.1  | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-1.9<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.0<br>-2.2<br>-2.0<br>-2.2<br>-2.0<br>-2.2<br>-2.0<br>-2.0   | 1.7<br>1.4<br>2.0<br>2.5<br>1.4<br>1.5<br>1.9<br>1.6<br>2.0<br>1.1<br>1.8<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.1<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.5<br>1.6<br>1.7<br>1.1<br>1.5<br>1.6<br>1.7<br>1.1<br>1.5<br>1.6<br>1.7<br>1.1<br>1.5<br>1.6<br>1.7<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -0.7 -1.7 -2.3 -1.9 -2.4 -2.9 -2.4 -0.7 -2.9 -2.4 -2.9 -2.4 -2.9 -2.4 -2.9 -2.4 -2.9 -2.4 -2.9 -2.4 -2.9 -2.4   | trmI ykpA ffliG - nusB ydeD rbgA obgE rpIJ rnhB fflhA rbsA - | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar basal body-associated protein FliL  |
| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_131 CIBE_2029 CIBE_4120 CIBE_4120 CIBE_5135 CIBE_T418 CIBE_0298 CIBE_1418 CIBE_0682 CIBE_1418 CIBE_0682 CIBE_1517 CIBE_5117 CIBE_5117 CIBE_5134 CIBE_5334 CIBE_5334 CIBE_5534 CIBE_5532 CIBE_55132  | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -1.5 -1.7 -1.8 -2.0 -1.5 -1.7 -1.8 -2.0 -1.8 -2.3 -1.9 -2.9 -1.8 -1.9 -2.1 -1.6 -1.7 -1.8 -2.0 -1.6 -1.7 -1.8 -2.0 -1.6 -1.7 -1.8 -2.0 -1.6 -1.7 -1.8 -2.0 -1.6 -1.1 -1.1 -1.1 -1.1 -1.1 -1.1 -1.1  | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-1.9<br>-2.1<br>-2.5<br>-2.2<br>-2.0<br>-2.2<br>-2.2<br>-2.2<br>-2.3<br>-2.2<br>-2.2<br>-2.3<br>-2.2<br>-2.2   | 1.7<br>-1.4<br>-2.0<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.0<br>-1.7<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.6<br>-1.7<br>-1.9<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -0.7 -1.7 -1.7 -1.2 -0.4 -1.9 -2.6 -2.5 -2.4 -0.7 -2.7 -2.6 -2.6 -2.5 -2.4 -0.7 -2.7 -2.7 -2.8 -2.9 -2.0 -0.7 -2.7 -2.9 -2.0 -0.7 -2.9 -2.0   | trmI ykpA ffliG - nusB ydeD rbgA obgE rpIJ rnhB fflhA rbsA - | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein  |
| CIBE_4960 CIBE_1566 CIBE_1518 CIBE_4098 CIBE_5113 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1513 CIBE_1655 CIBE_1513 CIBE_1655 CIBE_1513 CIBE_165 CIBE_11418 CIBE_0298 CIBE_1419 CIBE_1419 CIBE_1419 CIBE_1419 CIBE_1419 CIBE_1419 CIBE_15135 CIBE_1419 CIBE_15135 CIBE_1419 CIBE_15135 CIBE_5135 C | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.0 -3.5 -1.8 -2.3 -1.9 -2.9 -2.7 -2.2 -1.9 -1.8 -1.9 -2.1 -1.6 -3.0 -1.6 -2.1 -2.1 -2.1 -2.0 -1.6   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-1.9<br>-2.1<br>-2.0<br>-2.0<br>-1.9<br>-2.0<br>-1.9<br>-2.0<br>-1.9<br>-2.0<br>-1.9<br>-2.0<br>-1.9<br>-2.0<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9   | 1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.7 -2.7 -2.7 -2.7 -1.2 -0.4 -1.9 -2.6 -2.5 -2.4 -0.7 -2.9 -2.0 -2.3 -3.1 -3.1  | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar basal body-associated protein FliL Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase  |
| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_131 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_14120 CIBE_5135 CIBE_14120 CIBE_15135 CIBE_1515 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15145 CIBE_55144 CIBE_5944   | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.9 -2.7 -2.2 -1.9 -2.1 -1.6 -3.0 -1.6 -2.1 -2.1 -2.1 -2.0 -1.6 -1.8   | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.2<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0   | 1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.9<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.5 -2.4 -2.2 -2.7 -2.7 -1.7 -1.7 -1.9 -2.4 -2.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -1.9 -2.6 -2.5 -2.4 -2.9 -2.0 -2.4 -2.9 -2.0 -2.4 -2.5 -2.4 -2.5 -2.4 -2.5 -2.4 -2.5 -2.4 -2.5 -2.4 -2.5 -2.4 -2.5 -2.4 -2.5 -2.4 -2.5 -2.5 -2.4 -2.5 -2.6 -2.5 -2.6 -2.6 -2.5 -2.6 -2.7 -2.9 -2.0 -2.1 -2.1 -2.2 -2.1 -2.2 -2.3 -2.3 -3.1 -2.5 | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar basal body-associated protein FliL Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase  |
| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_1265 CIBE_5135 CIBE_1419 CIBE_1418 CIBE_0682 CIBE_0682 CIBE_05158 CIBE_1419 CIBE_5117 CIBE_5334 CIBE_5137 CIBE_5334 CIBE_5132 CIBE_2477 CIBE_4853 CIBE_2477 CIBE_4853 CIBE_2477 CIBE_4853 CIBE_1444 CIBE_5944 CIBE_5073   | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -1.8 -1.9 -2.1 -1.6 -2.0 -1.6 -3.0 -1.6 -3.0 -1.6 -3.1 -3.1 -3.1 -3.1 -3.1 -3.1 -3.1 -3.1  | -2.1<br>-2.0<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.2<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-1.9<br>-1.8<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1   | 1.7<br>1.4<br>2.0<br>2.5<br>1.4<br>1.5<br>1.9<br>1.6<br>2.0<br>1.7<br>1.1<br>1.8<br>1.5<br>1.6<br>2.0<br>2.1<br>1.9<br>1.7<br>1.9<br>1.9<br>1.9<br>1.9<br>1.9<br>1.9<br>1.9<br>1.9   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -0.7 -1.7 -1.7 -2.3 -1.9 -2.4 -2.9 -2.5 -2.4 -0.7 -2.5 -2.4 -0.7 -2.5 -2.4 -0.7 -2.5 -2.4 -0.7 -2.5 -2.4 -0.7 -2.5 -2.4 -0.7 -2.9 -2.6 -2.5 -2.4 -2.3 -3.1 -3.5 -2.3  | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar hasal body-associated protein FliL Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase conserved membrane protein of unknown function   |
| CIBE_4960 CIBE_1566 CIBE_1518 CIBE_4098 CIBE_5113 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_0056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_5135 CIBE_1419 CIBE_0682 CIBE_058 CIBE_1419 CIBE_5137 CIBE_5334 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5144 CIBE_5144 CIBE_5944 CIBE_5944 CIBE_5073 CIBE_0074   | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.0 -3.5 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -1.8 -1.9 -2.1 -2.1 -2.0 -1.6 -3.0 -1.6 -3.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2  | -2.1<br>-2.0<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.8<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.8<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.8<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.8<br>-2.0<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.8<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.8<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.8<br>-2.1   | 1.7<br>1.4<br>2.0<br>2.5<br>1.4<br>1.5<br>1.9<br>1.6<br>2.0<br>1.7<br>1.1<br>1.8<br>1.5<br>1.6<br>2.3<br>3.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>1.1<br>1.1<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.1<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.1<br>1.1<br>1.1<br>1.1<br>1.1<br>1.1   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -2.8 -2.5 -2.4 -2.2 -2.0 -2.0 -1.7 -2.7 -1.7 -2.3 -1.9 -2.4 -0.7 -2.9 -2.4 -2.9 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0   | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar ha-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase conserved membrane protein of unknown function Anaerobic ribonucleoside-triphosphate reductase   |
| CIBE_4960 CIBE_1566 CIBE_1518 CIBE_4098 CIBE_5118 CIBE_0024 CIBE_0680 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1513 CIBE_MISC_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_11418 CIBE_0682 CIBE_1419 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5144 CIBE_5135 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5135 CIBE_5135 CIBE_5144 CIBE_5136 CIBE_5137 | 6down   | -1.8 -1.7 -1.6 -1.6 -1.8 -2.1 -1.6 -2.0 -1.5 -1.7 -1.8 -2.0 -1.5 -1.8 -2.3 -1.9 -2.9 -1.8 -1.9 -2.9 -1.8 -1.9 -2.1 -1.6 -1.6 -1.7 -1.8 -2.0 -1.6 -1.7 -1.8 -2.0 -1.6 -1.1 -1.1 -1.1 -1.8 -3.3  | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.2<br>-2.2<br>-2.3<br>-2.6<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1<br>-2.1 | 1.7<br>-1.4<br>-2.0<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-1.7<br>-1.9<br>-1.7<br>-1.9<br>-1.7<br>-1.9<br>-1.6<br>-2.3<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.9<br>-1.0<br>-1.7<br>-1.9<br>-1.0<br>-1.7<br>-1.9<br>-1.9<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -2.0 -0.7 -2.7 -1.7 -2.3 -1.2 -2.9 -2.6 -2.4 -0.7 -2.7 -2.3 -1.2 -2.9 -2.6 -2.4 -2.9 -2.6 -2.4 -2.9 -2.6 -2.1 -2.9 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1  | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FIBB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine Nutilization substance protein B homolog putative permease Flagellar basal body rod protein FIgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell 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| CIBE_4960 CIBE_1566 CIBE_1518 CIBE_4098 CIBE_5118 CIBE_0024 CIBE_0680 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_131 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_1149 CIBE_5135 CIBE_1149 CIBE_1513 CIBE_1419 CIBE_5153 CIBE_1419 CIBE_5125 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1419 CIBE_5135 CIBE_1418 CIBE_0298 CIBE_1419 CIBE_5137 CIBE_85334 CIBE_5144 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5134 CIBE_5144 CIBE_5944 CIBE_2073 CIBE_2073 CIBE_2073 CIBE_0074 CIBE_2295 CIBE_2930  | 6down   | -1.8 -1.7 -1.6 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.9 -2.7 -2.2 -1.9 -1.8 -1.9 -2.1 -1.6 -3.0 -1.6 -2.1 -2.1 -2.1 -2.0 -1.6 -1.8 -2.1 -2.1 -2.0 -1.6 -1.8 -2.1 -2.1 -2.0 -1.6 -1.8 -2.1 -2.1 -2.0 -1.6 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -2.0 -1.6 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1  | -2.1<br>-2.0<br>-2.0<br>-2.0<br>-1.8<br>-1.9<br>-2.2<br>-2.0<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-1.8<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0   | 1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -2.4 -2.2 -0.7 -2.7 -2.7 -2.7 -2.7 -2.4 -1.9 -2.6 -2.5 -2.4 -2.9 -2.6 -2.5 -2.4 -2.9 -2.6 -2.5 -2.4 -2.9 -2.6 -2.5 -2.4 -2.9 -2.6 -2.5 -2.1 -2.5 -2.1 -2.5 -2.1 -2.5 -2.3 -3.1 -2.5 -2.3 -3.1 -2.5 -2.3 -2.7 -1.6 -2.3  | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function 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| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_133 CIBE_1265 CIBE_135 CIBE_14120 CIBE_5135 CIBE_14120 CIBE_5135 CIBE_14120 CIBE_5135 CIBE_15135 CIBE_1418 CIBE_0298 CIBE_1418 CIBE_0534 CIBE_1517 CIBE_5334 CIBE_5132 CIBE_1517 CIBE_5334 CIBE_5144 CIBE_5247 CIBE_2477 CIBE_5485 CIBE_1440 CIBE_2073 CIBE_0074 CIBE_2073 CIBE_0074 CIBE_2295 CIBE_2930 CIBE_4105  | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -3.5 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -2.1 -1.6 -3.0 -1.6 -3.1 -1.1 -1.1 -1.1 -1.1 -1.1 -1.1 -1.1  | -2.1<br>-2.0<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.2<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0   | 1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.9<br>-2.0<br>-2.1<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>-1.0<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -0.7 -1.7 -1.7 -1.2 -0.4 -1.9 -2.6 -2.5 -2.4 -0.7 -2.7 -2.7 -2.6 -2.5 -2.4 -2.3 -2.7 -2.6 -2.3 -2.1 -2.3 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -1.7   | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar basal body-associated protein FliL Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase conserved membrane protein of unknown function Anaerobic ribonucleoside-triphosphate reductase putative transporter Zinc chelation protein SecC Phage-like element pbsx protein XkdK   |
| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5135 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_1265 CIBE_131 CIBE_MISC_RNA_4 CIBE_2029 CIBE_135 CIBE_135 CIBE_1418 CIBE_0682 CIBE_1418 CIBE_0682 CIBE_1418 CIBE_0682 CIBE_1535 CIBE_1419 CIBE_5137 CIBE_5334 CIBE_5137 CIBE_5334 CIBE_5137 CIBE_5334 CIBE_5149 CIBE_5149 CIBE_5140 CIBE_5140 CIBE_5140 CIBE_5140 CIBE_5140 CIBE_5140 CIBE_5140 CIBE_5140 CIBE_5140 CIBE_2073 CIBE_2073 CIBE_2073 CIBE_2073 CIBE_2075 CIBE_2090 CIBE_2090 CIBE_4105 CIBE_4283   | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -2.1 -1.6 -3.0 -1.6 -3.0 -1.6 -3.1 -2.1 -2.1 -2.0 -1.6 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.9 -2.2   | -2.1 -2.0 -2.0 -1.8 -2.2 -1.7 -1.5 -2.0 -2.0 -2.3 -2.6 -1.7 -2.5 -2.2 -2.0 -2.0 -1.9 -1.8 -1.7 -2.3 -2.6 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1   | 1.7<br>1.4<br>2.0<br>2.5<br>1.4<br>1.5<br>1.9<br>1.6<br>2.0<br>1.1<br>1.8<br>1.5<br>1.6<br>2.0<br>2.1<br>1.9<br>1.0<br>1.1<br>1.1<br>1.2<br>1.3<br>1.0<br>1.1<br>1.3<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -0.7 -1.7 -1.2 -1.4 -2.9 -2.4 -0.7 -2.3 -3.1 -2.5 -2.4 -2.3 -3.1 -2.1 -1.6 -2.3 -2.7 -2.9 -2.9 -2.9 -2.9 -2.9 -2.9 -2.9 -2.9                | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase conserved membrane protein of unknown function Anaerobic ribonucleoside-triphosphate reductase putative transporter Zinc chelation protein SecC Phage-like element pbsx protein XkdK conserved protein of unknown function  |
| CIBE_4960 CIBE_1566 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_0056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_5135 CIBE_133 CIBE_1068 CIBE_0682 CIBE_0158 CIBE_1419 CIBE_5137 CIBE_5334 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5144 CIBE_5944 CIBE_5944 CIBE_5944 CIBE_295 CIBE_2930 CIBE_295 CIBE_2930 CIBE_295 CIBE_2930 CIBE_4105 CIBE_4105 CIBE_4283 CIBE_1059  | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -1.5 -1.7 -1.8 -2.0 -1.5 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -1.8 -1.9 -2.1 -1.6 -3.0 -1.6 -3.1 -1.1 -2.1 -2.1 -2.0 -1.6 -1.8 -3.3 -2.4 -1.9 -2.9 -1.8  | -2.1 -2.0 -2.0 -2.0 -1.8 -2.2 -1.7 -1.5 -2.0 -2.0 -2.3 -2.6 -1.7 -2.5 -2.2 -1.8 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0 -2.0  | 1.7<br>1.4<br>2.0<br>2.5<br>1.4<br>1.5<br>1.9<br>1.6<br>2.0<br>1.7<br>1.1<br>1.8<br>1.5<br>1.6<br>2.0<br>2.1<br>1.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.8<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.8<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.1<br>1.9<br>2.0<br>2.0<br>1.0<br>2.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>2.0<br>1.0<br>1.0<br>1.0<br>2.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1  | -1.9 -2.4 -2.0 -1.7 -1.2 -2.3 -2.6 -2.2 -2.0 -2.7 -1.7 -2.3 -1.6 -2.9 -2.4 -2.9 -2.4 -2.9 -2.4 -2.9 -2.6 -2.5 -2.4 -2.7 -1.6 -2.3 -2.7 -1.6 -2.3 -2.7 -1.2 -2.8   | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar basal body-associated protein FliL Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase conserved membrane protein of unknown function Anaerobic ribonucleoside-triphosphate reductase putative transporter Zinc chelation protein SecC Phage-like element pbsx protein XkdK conserved protein of unknown function Methyl-accepting chemotaxis protein   |
| CIBE_4960 CIBE_1566 CIBE_1518 CIBE_4098 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0680 CIBE_1655 CIBE_1655 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_1313 CIBE_misc_RNA_4 CIBE_2029 CIBE_4120 CIBE_5135 CIBE_1418 CIBE_0682 CIBE_1418 CIBE_0682 CIBE_1419 CIBE_5117 CIBE_5314 CIBE_5117 CIBE_5314 CIBE_5117 CIBE_5135 CIBE_1419 CIBE_5117 CIBE_5334 CIBE_1419 CIBE_5117 CIBE_5334 CIBE_5144 CIBE_5122 CIBE_2477 CIBE_4853 CIBE_1512 CIBE_2477 CIBE_4853 CIBE_1512 CIBE_2477 CIBE_4853 CIBE_1512 CIBE_2477 CIBE_4853 CIBE_1512 CIBE_2477 CIBE_4853 CIBE_5144 CIBE_295 CIBE_2930 CIBE_2073 C | 6down   | -1.8 -1.7 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.7 -2.2 -1.9 -2.1 -1.6 -3.0 -1.6 -3.0 -1.6 -3.1 -2.1 -2.1 -2.0 -1.6 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.9 -2.2   | -2.1 -2.0 -2.0 -1.8 -2.2 -1.7 -1.5 -2.0 -2.0 -2.3 -2.6 -1.7 -2.5 -2.2 -2.0 -2.0 -1.9 -1.8 -1.7 -2.3 -2.6 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1   | 1.7<br>1.4<br>2.0<br>2.5<br>1.4<br>1.5<br>1.9<br>1.6<br>2.0<br>1.1<br>1.8<br>1.5<br>1.6<br>2.0<br>2.1<br>1.9<br>1.0<br>1.1<br>1.1<br>1.2<br>1.3<br>1.0<br>1.1<br>1.3<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0<br>1.0   | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -0.7 -1.7 -1.2 -1.4 -2.9 -2.4 -0.7 -2.3 -3.1 -2.5 -2.4 -2.3 -3.1 -2.1 -1.6 -2.3 -2.7 -2.9 -2.9 -2.9 -2.9 -2.9 -2.9 -2.9 -2.9                | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase conserved membrane protein of unknown function Anaerobic ribonucleoside-triphosphate reductase putative transporter Zinc chelation protein SecC Phage-like element pbsx protein XkdK conserved protein of unknown function  |
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1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.2 -1.8 -2.5 -2.4 -2.2 -0.7 -2.7 -1.7 -1.2 -0.4 -1.9 -2.6 -2.5 -2.4 -2.9 -2.6 -2.5 -2.1 -2.5 -2.1 -2.5 -2.1 -2.5 -2.1 -2.5 -2.1 -2.5 -2.1 -2.5 -2.1 -2.5 -2.3 -3.1 -2.5 -2.3 -1.7 -1.6 -2.3 -1.7 -1.6 -2.3 -1.7 -1.6 -2.3 -1.7 -2.8 -2.6 -2.8 -2.6   | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein 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| CIBE_4960 CIBE_1566 CIBE_5118 CIBE_4098 CIBE_5130 CIBE_0024 CIBE_0680 CIBE_0025 CIBE_6056 CIBE_1403 CIBE_5945 CIBE_1265 CIBE_1265 CIBE_131 CIBE_1265 CIBE_5131 CIBE_1265 CIBE_5135 CIBE_14120 CIBE_5135 CIBE_14120 CIBE_5135 CIBE_14120 CIBE_5135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15135 CIBE_15140 CIBE_5117 CIBE_5334 CIBE_5122 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5132 CIBE_5144 CIBE_5144 CIBE_5944 CIBE_2073 CIBE_2073 CIBE_2073 CIBE_2073 CIBE_2095 CIBE_21059 CIBE_21059 CIBE_21059 CIBE_21059 CIBE_21059 CIBE_1059 CIBE_3093 CIBE_1059 CIBE_3093 CIBE_4060   | 6down | -1.8 -1.7 -1.6 -1.6 -1.8 -2.1 -1.6 -2.0 -2.5 -1.6 -1.7 -1.8 -2.3 -1.9 -2.9 -2.7 -2.2 -1.9 -2.1 -1.6 -3.0 -1.6 -2.1 -2.1 -2.1 -2.0 -1.6 -1.8 -2.1 -1.8 -2.1 -1.8 -2.1 -1.9 -2.2 -1.9 -2.2 -1.9 -2.2 -1.9 -2.2 -1.9 -2.2 -1.9 -2.2 -1.9 -2.2 -1.9 -2.2 -1.9 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1 -2.1  | -2.1<br>-2.0<br>-2.0<br>-1.8<br>-2.2<br>-1.7<br>-1.5<br>-2.0<br>-2.2<br>-2.3<br>-2.6<br>-1.7<br>-2.5<br>-2.2<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0<br>-2.0   | 1.7<br>-1.4<br>-2.0<br>-2.5<br>-1.4<br>-1.5<br>-1.9<br>-1.6<br>-2.0<br>-1.7<br>-1.1<br>-1.8<br>-1.5<br>-1.6<br>-2.3<br>-3.0<br>-2.1<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>-1.9<br>- | -1.9 -2.4 -2.0 -1.7 -2.2 -2.3 -2.6 -2.5 -2.4 -2.2 -0.7 -1.7 -1.7 -1.9 -2.4 -1.9 -2.6 -2.5 -2.4 -2.2 -2.6 -2.7 -2.7 -2.7 -1.7 -1.7 -1.9 -2.6 -2.5 -2.4 -2.9 -2.0 -2.4 -2.3 -1.7 -0.2 -2.4 -2.3 -2.7 -2.9 -2.0 -2.4 -2.3 -2.7 -2.9 -2.0 -2.4 -2.3 -2.7 -2.2 -2.8 -2.3 -2.7 -2.2 -2.8 -2.6 -2.1  | trmI   | Uncharacterized HTH-type transcriptional regulator YdeP persulfide ATP pyrophosphatase involved in tRNA modification Flagellar biosynthetic protein FlhB conserved protein of unknown function Flagellar biosynthesis/type III secretory pathway-like protein Haloacid dehalogenase conserved protein of unknown function ABC efflux transporter (ATP-binding protein) RNA methyltransferase ribosomal protein L32 Adenosylhomocysteine nucleosidase conserved exported protein of unknown function flagellar motor switching and energizing component Purine N utilization substance protein B homolog putative permease Flagellar basal body rod protein FlgB Asp tRNA conserved protein of unknown function conserved protein of unknown function ribosome biogenesis GTPase A ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly ribosomal protein L10 (BL5) ribonuclease HII component of the flagellar export machinery ribose ABC transporter (ATP-binding protein) Flagellar basal body-associated protein FliL Flagellar M-ring protein Zinc chelation protein SecC Methyl-accepting chemotaxis protein dTDP-4-deoxyrhamnose-3,5-epimerase tRNA threonylcarbamoyladenosine dehydratase conserved membrane protein of unknown function Anaerobic ribonucleoside-triphosphate reductase putative transporter Zinc chelation protein SecC Phage-like element pbsx protein XkdK conserved protein of unknown function Methyl-accepting chemotaxis protein Chemotaxis protein Sigma54 specific transcriptional regulator, Fis family |

| CIBE_0642<br>CIBE_1639<br>CIBE_5123<br>CIBE_0159 | 6down<br>6down<br>6down | -2.0<br>-1.8<br>-2.5 | -2.2<br>-2.1<br>-1.7 | -2.7<br>-2.4 | -2.0<br>-2.6 |   | Radical SAM domain protein<br>Metallophosphoesterase                                     |
|--|-------------------------|----------------------|----------------------|--------------|--------------|---|--|
| CIBE_1639<br>CIBE_5123<br>CIBE_0159              |                         |                      |                      |              |              |   | Metallophosphoesterase   |
| CIBE_5123<br>CIBE_0159                           | 6down                   | -2 5                 | -17                  |              |              |   |  |
| CIBE_0159  |                         |                      |                      | -1.9         | -2.9         |   | conserved protein of unknown function  |
|  | 6down                   | -1.6                 | -2.1                 | -2.0         | -3.2         |   | putative flagellar protein   |
| CIBE 2115  | 6down                   | -1.8                 | -2.0                 | -2.1         | -3.1         | rplL                                    | ribosomal protein L12 (BL9)  |
|  | 6down                   | -3.0                 | -2.5                 | -2.5         | -0.9         | •                                       | protein of unknown function  |
| CIBE_misc_RNA_56                                 |                         | -2.3                 | -2.1                 | -1.8         | -2.8         |   | L10_leader   |
| _  | 6down                   | -0.4                 | -2.2                 | -2.7         |              | dhaS                                    | 3-hydroxypropionaldehyde dehydrogenase   |
| _  | 6down                   | -2.3                 | -2.3                 | -1.7         | -2.7         |   | Metal-dependent hydrolase of the beta-lactamase superfamily                              |
| _  | 6down                   | -2.2                 | -2.5                 | -2.0         | -2.4         | •                                       | conserved membrane protein of unknown function   |
| _  | 6down                   | -2.2                 | -2.2                 | -2.8         | -1.9         | •                                       | FMN-binding protein  |
| _  | 6down                   | -2.6                 | -2.1                 | -1.9         | -2.5         |   | Major facilitator superfamily MFS_1  |
| _  | 6down                   | -2.2                 | -2.5                 | -2.1         | -2.4         | •                                       | Glycosyltransferase, group 2 family protein  |
| _  | 6down                   | -3.3                 | -2.2                 | -2.5         | -1.2         |   | Phe tRNA   |
| _  | 6down                   | -0.6                 | -2.4                 | -2.9         | -3.3         | SUTB                                    | FeS cluster formation protein  |
| _  | 6down                   | -2.2                 | -2.3                 | -2.1         | -2.6         | •                                       | protein of unknown function  |
| _  | 6down                   | -2.0                 | -2.3                 | -2.0         | -2.9         | •                                       | Group 2 glycosyl transferase   |
| _  | 6down                   | -1.9                 | -1.9                 | -1.8         | -3.6         |   | Asn tRNA   |
| _  | 6down                   | -2.1                 | -2.1                 | -2.2         | -2.9         |   | ribosomal protein L19  |
| _  | 6down                   | -1.7                 | -1.8                 | -2.2         | -3.6         | -                                       | proton/sodium-glutamate symport protein  |
| _  | 6down                   | -1.9                 | -2.4                 | -1.5<br>-2.3 | -3.5<br>-3.2 |   | MotA/ToIQ/ExbB proton channel  |
| _  | 6down                   | -1.5                 | -2.4                 | -2.3<br>-2.2 |              |   | Thioredoxin reductase  |
| _  | 6down                   | -2.7                 | -2.4                 |              | -2.1         | •                                       | putative hydrogenase, 4Fe-4S ferredoxin-type component                                   |
| _  | 6down                   | -1.8                 | -2.7<br>-2.0         | -1.9<br>-2.3 | -3.0         |   | conserved protein of unknown function ribosomal protein L27 (BL24)                       |
| _  | 6down                   | -2.1<br>-2.3         | -2.0<br>-2.5         | -2.3<br>-2.5 | -3.0<br>-2.1 | rpmA                                    |  |
| _  | 6down                   |                      |                      |              |              | nvrG                                    | Membrane protein CTP synthetase  |
| _  | 6down                   | -2.4<br>-2.6         | -2.2<br>-2.2         | -2.1<br>-2.3 | -2.8<br>-2.4 | pyrG<br>amtB                            | •  |
| _  | 6down                   | -2.6                 | -2.2<br>-2.1         | -2.3<br>-2.3 | -2.4         |   | ammonium transporter   |
| _  | 6down                   | -2.1<br>-1.9         | -2.1<br>-2.3         | -2.3<br>-2.5 | -3.0<br>-2.9 | -                                       | HAD family hydrolase   |
| _  | 6down<br>6down          | -1.9<br>-2.8         | -2.3<br>-2.6         | -2.5<br>-1.9 | -2.9<br>-2.3 |   | Sulfatase  Membrane protein  |
|  |                         | -2.8                 | -2.6                 | -2.5         | -2.3<br>-2.9 | hca A                                   | putative bacillithiol peroxidase   |
| _  | 6down<br>6down          | -2.0<br>-2.0         | -2.3<br>-2.3         | -2.5<br>-2.1 | -2.9<br>-3.2 | usam<br>-                               | putative bacilithiol peroxidase  Flavin reductase domain protein, FMN-binding            |
|  | 6down                   | -2.0<br>-2.3         | -2.3<br>-2.7         | -2.1<br>-2.3 | -3.2<br>-2.4 | -                                       |  |
| _  | 6down                   | -2.3                 | -2.7<br>-2.6         | -2.3<br>-3.1 | -2.4         |   | conserved exported protein of unknown function sulfur mobilizing ABC protein, ATPase     |
| _  | 6down                   | -0.7                 | -2.6<br>-2.9         | -3.1         | -3.4         | -<br>-                                  | conserved exported protein of unknown function   |
| _  | 6down                   | -2.3                 | -1.9                 | -2.2<br>-2.2 | -3.7         |   | Cof-like hydrolase   |
|  | 6down                   | -2.1                 | -3.1                 | -2.7         | -2.1         |   | SCP-like extracellular protein   |
|  | 6down                   | -2.1                 | -2.5                 | -2.7         | -3.3         | •                                       | Haloacid dehalogenase  |
| _  | 6down                   | -2.3                 | -2.9                 | -2.0         | -2.3         |   | HD family phosphohydrolase   |
|  | 6down                   | -1.9                 | -2.7                 | -2.1         | -2.9         |   | Ig-like domain-containing protein, putative cell wall binding protein (fragment)         |
|  | 6down                   | -1.7                 | -2.7                 | -2.7         | -3.4         |   | conserved protein of unknown function  |
|  | 6down                   | -1.9                 | -2.3                 | -3.3         | -2.7         |   | conserved protein of unknown function  |
|  | 6down                   | -2.3                 | -2.8                 | -2.0         | -3.1         |   | flagellar component of cell-proximal portion of basal-body rod                           |
|  | 6down                   | -2.0                 | -2.1                 | -2.9         | -3.3         | iigC<br>-                               | Uncharacterized glutaredoxin-like 8.6 kDa protein in rubredoxin operon                   |
|  | 6down                   | -2.6                 | -2.7                 | -2.3         |              | yfmM                                    | putative ATP-binding protein   |
|  | 6down                   | -2.4                 | -2.6                 | -2.3         | -3.1         | y 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | Methyl-accepting chemotaxis sensory transducer   |
| _  | 6down                   | -2.4                 | -2.6                 | -2.5         | -2.9         |   | Secretion protein HIyD family protein  |
|  | 6down                   | -1.8                 | -2.2                 | -3.4         | -3.0         |   | protein of unknown function  |
|  | 6down                   | -2.3                 | -2.8                 | -1.9         | -3.4         |   | conserved protein of unknown function  |
| _  | 6down                   | -2.3                 | -2.7                 | -2.2         | -3.5         |   | Flagellin  |
|  | 6down                   | -2.3                 | -2.0                 | -2.7         | -3.7         |   | Methyl-accepting chemotaxis protein  |
|  | 6down                   | -3.1                 | -2.7                 | -2.2         | -2.7         |   | Asn tRNA   |
| _  | 6down                   | -2.3                 | -2.5                 | -2.2         | -3.8         | _                                       | Glycosyltransferase  |
|  | 6down                   | -2.8                 | -2.6                 | -1.4         | -3.9         |   | OmpA/MotB domain protein   |
|  | 6down                   | -2.9                 | -2.6                 | -2.0         | -3.3         | hnt                                     | Hypoxanthine phosphoribosyltransferase   |
|  | 6down                   | -2.5                 | -2.6                 | -3.7         | -2.0         | -                                       | exported protein of unknown function   |
|  | 6down                   | -2.2                 | -2.4                 | -2.0         | -4.0         | fliF                                    | Flagellar hook-basal body complex protein FliE   |
|  | 6down                   | -2.2                 | -2.8                 | -2.5         | -3.4         |   | Methyl-accepting chemotaxis sensory transducer   |
|  | 6down                   | -2.4                 | -2.3                 | -2.9         | -3.2         |   | putative Methyl-accepting chemotaxis protein   |
|  | 6down                   | -3.2                 | -3.6                 | -2.0         | -2.2         |   | GMP synthetase   |
| _  | 6down                   | -1.6                 | -2.5                 | -3.1         | -3.8         | -                                       | Glutathione peroxidase   |
|  | 6down                   | -2.3                 | -2.8                 | -2.8         | -3.1         | -                                       | S-layer domain-containing protein (fragment)   |
|  | 6down                   | -2.4                 | -2.8                 | -2.6         | -3.2         |   | Methyl-accepting chemotaxis protein  |
|  | 6down                   | -2.3                 | -2.3                 | -3.2         | -3.3         |   | Chemotaxis protein CheA  |
|  | 6down                   | -1.7                 | -2.4                 | -3.5         | -3.6         |   | L-aspartase (aspartate ammonia lyase)  |
|  | 6down                   | -2.2                 | -3.1                 | -2.5         | -3.5         |   | Murein hydrolase transporter LrgA  |
|  | 6down                   | -2.8                 | -3.1                 | -2.9         | -2.5         |   | Molybdopterin-guanine dinucleotide biosynthesis protein B                                |
|  | 6down                   | -2.6                 | -2.2                 | -3.6         | -2.8         | mglB                                    | methyl-galactoside transporter subunit; periplasmic-binding component of ABC superfamily |
|  | 6down                   | -2.4                 | -3.1                 | -3.8         | -2.0         | -                                       | ApbE family lipoprotein  |
|  | 6down                   | -2.8                 | -2.8                 | -2.4         | -3.5         |   | Methyl-accepting chemotaxis protein  |
|  | 6down                   | -3.2                 | -3.3                 | -2.4         | -2.7         | fruK                                    | fructose-1-phosphate kinase  |
|  | 6down                   | -3.4                 | -2.7                 | -3.0         | -2.5         |   | Methyl-accepting chemotaxis protein  |
|  | 6down                   | -3.0                 | -3.2                 | -3.0         | -2.5         | -                                       | conserved protein of unknown function  |
|  | 6down                   | -2.2                 | -3.7                 | -2.6         | -3.3         |   | protein of unknown function  |
| CIBE_2185  | 6down                   | -2.8                 | -3.3                 | -2.5         | -3.3         | fruR                                    | transcriptional regulator (DeoR family)  |
| CIBE_4551  | 6down                   | -3.3                 | -3.4                 | -2.6         | -2.6         | -                                       | Molybdenum cofactor biosynthesis protein   |
| _  | 6down                   | -3.0                 | -3.5                 | -2.6         | -2.9         | fruA                                    | phosphotransferase system (PTS) fructose-specific enzyme IIABC component                 |
| _  | 6down                   | -1.6                 | -2.6                 | -3.1         | -4.6         | -                                       | Cation transporter   |
| CIBE_5785  | 6down                   | -2.0                 | -3.0                 | -3.2         | -3.8         | -                                       | Oxidoreductase   |
| _  | 6down                   | -3.2                 | -3.0                 | -2.7         |              | maeB                                    | NADP-dependent malic enzyme (conversion of malate into pyruvate)                         |
| _  | 6down                   | -2.8                 | -3.1                 | -3.4         | -3.4         |   | regulator of chemotaxis and motility   |
| _  | 6down                   | -2.6                 | -2.6                 | -3.0         | -4.6         |   | Ribonucleoside-diphosphate reductase subunit beta  |
| _  | 6down                   | -2.0                 | -3.7                 | -3.4         | -4.0         |   | FMN-binding domain protein   |
| _  | 6down                   | -2.5                 | -3.3                 | -3.0         | -4.5         |   | protein of unknown function  |
| _  | 6down                   | -2.7                 | -3.4                 | -3.5         | -3.9         |   | repressor of copper utilisation proteins - Cu(I)   |
| _  | 6down                   | -3.0                 | -3.4                 | -2.6         | -4.5         |   | Transferase  |
| _  | 6down                   | -3.0                 | -3.2                 | -3.5         |              | nrdA                                    | Ribonucleoside-diphosphate reductase subunit alpha                                       |
| _  | 6down-                  | -3.8                 | -4.0                 | -1.9         | -2.2         |   | conserved membrane protein of unknown function   |
| _  | 6down-                  | -4.1                 | -3.5                 | -2.9         | -2.1         |   | Glycoside hydrolase, family 18   |
| CIBE_4547  | 6down-                  | -2.3                 | -4.2                 | -3.2         | -3.4         | hndD                                    | NADP-reducing hydrogenase subunit HndC   |

| College  | CIDE 4540              | Cdown  | 2.0          | 4.5          | 2.0          | 204    | idh D | Dratain EdhD hamalag                                    |
|--|------------------------|--------|--------------|--------------|--------------|--------|-------|---|
| March   Marc | CIBE_4549<br>CIBE_2868 | 6down- | -2.8<br>-4.1 | -4.5<br>-4.5 | -3.0<br>-2.0 |        |       | Protein FdhD homolog xanthine phosphorihosyltransferase |
| Control   Cont |                        |        |              | _            |              |        |       |   |
| Description   Company    |                        | 6down- | -3.5         | -3.6         | -3.9         | -4.5 f | dhF   |   |
| Description   Column   |                        |        |              |              |              |        |       |   |
| Contract and making persons in active and m |                        |        | _            |              |              |        |       | ·   |
| Table  |                        |        |              |              |              |        | git i |   |
| Control   Cont |                        |        |              |              |              |        |       | ·   |
| Control   Cont |                        |        |              |              |              |        |       |   |
| Col. 1.712   Super   Col. 2   2   4   5   5   7   2   2   1   1   1   1   1   1   1   1  |                        | -      |              |              |              |        |       | ·   |
| Columb   |                        | •      |              |              |              |        |       | ,                 |
| Cut 2327   |                        | •      | _            |              |              |        | , iad |   |
| Control   Cont | _                      |        |              |              |              |        |       |   |
| Dec.   2006   Dec.   2007    |                        |        |              | _            |              |        | /xdL  |   |
| Company   Comp |                        |        |              |              |              |        | •     | ·   |
| Section   Sect | _                      |        |              |              |              |        |       |   |
| Cold   1977   20   |                        |        |              |              |              |        |       | ·   |
| Cut 1 1781   |                        |        |              |              |              |        |       |   |
| Code 1,7556 Big 0  | CIBE_3697              | 8up    | 0.1          |              |              |        |       | conserved protein of unknown function                   |
| Cost   |                        | •      |              |              |              |        |       | = : :   |
| CIEL 1978  |                        |        |              |              |              |        |       |   |
| Description    |                        |        | _            |              |              |        |       | ·   |
| Description    |                        |        |              |              |              |        |       | ·   |
| CRE_5555   Superior   Superior  | CIBE_4568              | 8up    | 0.7          |              | 3.5          | 3.3    | /vcR  | putative ABC transporter (ATP-binding protein)          |
| Cold   2008  |                        |        |              |              |              |        |       | ·   |
| Dall 1848  |                        |        |              |              |              |        |       |   |
| CRE_1734   Sup   |                        |        |              |              |              |        |       |   |
| Des.   1974  |                        |        |              |              |              |        |       | ·   |
| CRE_1373   |                        |        | -0.5         |              | 4.0          | 4.7 r  | psD   | 30S ribosomal protein S4 B                              |
| Dec   1733   Sup   |                        |        |              |              |              |        |       |   |
| Colleg 5955   Sup  | _                      |        |              |              |              |        |       | · · · · · · · · · · · · · · · · · · ·                   |
| Dec   2775   Sup   | _                      | •      |              |              |              |        | /ra⊦  |   |
| College   Coll |                        |        |              |              |              |        |       |   |
| Cell    | _                      |        |              |              |              |        |       |   |
| OBE   Collect   Collect  |                        | 8up    |              |              |              |        |       | conserved protein of unknown function                   |
| Conf.   2045   Sup   13   2.8   2.9   2.1   Connerved protein of unknown function  |                        |        |              |              |              |        | celB  |   |
| Conserved protein of unknown function   Cons | _                      |        |              |              |              |        |       |   |
| ORE     150   Sup     12     23   41   30  |                        |        |              |              | _            |        |       |   |
| CRE_5220   Sup   | _                      |        |              |              |              |        |       | ·   |
| CRE 5-517   Sup  |                        |        | -0.5         | 2.1          | 4.3          | 3.0 -  |       | Coat F domain protein                                   |
| CRE_5128  Sup  | _                      |        |              |              |              |        |       | · · · ·   |
| CRE_0127   |                        |        |              |              |              |        |       | · ·   |
| CHE   CHE  |                        |        |              |              |              |        | norV  | •   |
| CIBE_ 0098   Sup   |                        |        |              |              |              |        |       |   |
| CRIE   1944   Sup  |                        |        | -0.2         |              |              | 2.4    | spoVT |   |
| CBE 3528   Sup   |                        |        | _            |              |              |        |       | ·   |
| Cube   |                        |        |              |              |              |        |       |   |
| CIBE 50-56   |                        |        |              |              |              |        |       | ·   |
| CIBE 2057   8up  |                        |        |              |              |              |        |       | ·   |
| CIBE _ 3642  | CIBE_5454              | 8up    | 0.6          | 2.1          | 3.2          | 2.3    | /ngF  | putative Methylglutaconyl-CoA hydratase                 |
| CIBE 5938   Sup  |                        |        |              |              |              |        |       | • •   |
| CIBE 5420  |                        |        |              |              |              |        |       |   |
| CIBE _ 2858  |                        |        |              |              |              |        |       | · ·   |
| CIBE _ 1750   Sup  |                        |        |              |              |              |        | oglB  | ·   |
| CIBE 2002  | CIBE_2362              |        | -0.3         | 2.0          | 3.3          | 3.1    |       | CBS domain-containing protein YhcV                      |
| CIBE_4218  |                        |        |              |              |              |        |       | ·   |
| CIBE_4745  |                        |        |              |              |              |        | ncdA  |   |
| CIBE_1188  | _                      |        |              |              |              |        |       | · · · · · · · · ·                                       |
| CIBE_1188  |                        |        |              |              |              |        |       |   |
| CIBE_4567 8up 0.4 2.1 2.5 2.8 - conserved membrane protein of unknown function CIBE_1757 8up 0.6 2.2 3.0 2.1 - conserved protein of unknown function CIBE_1745 8up 0.9 1.5 4.1 3.1 - conserved protein of unknown function CIBE_1266 8up 0.4 2.1 2.8 2.4 - conserved protein of unknown function CIBE_1734 8up 0.3 1.5 3.4 2.9 adhB putative oxidoreductase CIBE_1734 8up 0.3 2.7 2.3 - FAD-dependent oxidoreductase CIBE_1669 8up 0.3 2.1 3.1 2.6 amyC putative starch degradation products transport system permease protein AmyC CIBE_1669 8up 0.3 2.1 3.1 2.6 amyC putative starch degradation products transport system permease protein AmyC CIBE_3927 8up 0.1 2.6 2.2 2.8 - conserved protein of unknown function CIBE_10306 8up 0.7 1.9 3.6 2.6 adhE fused acetaldehyde-CoA dehydrogenase ; iron-dependent alcohol dehydrogenase ; pyruvate-formate lyase deactivase CIBE_1229 8up 0.8 2.3 3.1 2.8 - Stage V sporulation protein AF CIBE_1244 8up 0.2 1.7 3.0 2.5 - Ferredoxin hydrogenase CIBE_1494 8up 0.2 1.3 3.2 2.9 - Protein CA_C1420 CIBE_15646 8up 0.3 2.3 2.7 1.9 - conserved membrane protein of unknown function CIBE_20307 8up 0.5 1.5 3.1 3.1 3.1 - Conserved membrane protein of unknown function CIBE_20307 8up 0.5 1.5 3.1 3.1 3.1 - Conserved membrane protein of unknown function CIBE_20307 8up 0.5 1.5 3.1 3.1 3.1 - Conserved membrane protein of unknown function CIBE_20307 8up 0.5 1.5 3.1 3.1 3.1 - Conserved membrane protein of unknown function  | _                      |        | _            |              |              |        |       | •   |
| CIBE_1757 8up  |                        |        |              |              |              |        |       | ·   |
| CIBE_12745 8up   |                        |        |              |              |              |        |       | ·   |
| CIBE_1226 8up 0.4 2.1 2.8 2.4 - conserved protein of unknown function CIBE_0065 8up 0.4 2.3 2.7 2.3 - conserved exported protein of unknown function CIBE_1734 8up -0.3 1.5 3.4 2.9 4nb putative oxidoreductase CIBE_3627 8up -0.2 1.9 3.2 2.7 - FAD-dependent oxidoreductase CIBE_1669 8up -0.3 2.1 3.1 2.6 amyC putative starch degradation products transport system permease protein AmyC CIBE_5518 8up -0.6 1.9 3.7 2.5 - Coat F domain protein CIBE_3927 8up -0.1 2.6 2.2 2.8 - conserved protein of unknown function CIBE_0306 8up -0.7 1.9 3.6 2.6 alb fused acetaldehyde-CoA dehydrogenase; iron-dependent alcohol dehydrogenase; pyruvate-formate lyase deactivase CIBE_1229 8up -0.8 2.3 3.1 2.8 - Stage V sporulation protein AF CIBE_4835 8up -0.4 2.3 3.2 2.5 - Ferredoxin hydrogenase CIBE_2743 8up -0.4 2.3 3.2 2.9 - Ferredoxin hydrogenase CIBE_1494 8up -0.2 1.3 3.2 2.9 - Protein CA_C1420 CIBE_5646 8up -0.9 1.6 3.6 3.0 dacf D-alanyl-D-alanine carboxypeptidase Dacf CIBE_2307 8up -0.5 1.5 3.1 3.1 conserved exported protein of unknown function  |                        |        |              |              |              |        |       | ·   |
| CIBE_1065  |                        |        |              |              |              |        |       | ·   |
| CIBE_1669  | CIBE_0065              |        | 0.4          | 2.3          | 2.7          | 2.3 -  |       |   |
| CIBE_1669  |                        |        |              |              |              |        | adhB  |   |
| CIBE_5518 8up  |                        |        |              |              |              |        | amvC  |   |
| CIBE_3927 8up  |                        |        |              |              |              |        | annyC |   |
| CIBE_0306         8up         -0.7         1.9         3.6         2.6         adhE         fused acetaldehyde-CoA dehydrogenase; iron-dependent alcohol dehydrogenase; pyruvate-formate lyase deactivase           CIBE_1229         8up         -0.8         2.3         3.1         2.8         -         Stage V sporulation protein AF           CIBE_4835         8up         0.2         1.7         3.0         2.5         -         Ferredoxin hydrogenase           CIBE_2743         8up         -0.4         2.3         3.2         2.2         -         conserved protein of unknown function           CIBE_1494         8up         -0.2         1.3         3.2         2.9         -         Protein CA_C1420           CIBE_1494         8up         0.3         2.3         2.7         1.9         -         conserved membrane protein of unknown function           CIBE_2218         8up         -0.9         1.6         3.6         3.0         dacF         D-alanyl-D-alanine carboxypeptidase DacF           CIBE_2307         8up         -0.5         1.5         3.1         3.1         -         conserved exported protein of unknown function  | _                      |        |              |              |              |        |       | ·   |
| CIBE_1229  |                        |        |              |              | _            |        | adhE  | · ·   |
| CIBE_2743 8up  |                        |        |              |              |              |        |       |   |
| CIBE_1494       8up       -0.2       1.3       3.2       2.9       - Protein CA_C1420         CIBE_5646       8up       0.3       2.3       2.7       1.9       - conserved membrane protein of unknown function         CIBE_2218       8up       -0.9       1.6       3.6       3.0       dacF       D-alanyl-D-alanine carboxypeptidase DacF         CIBE_2307       8up       -0.5       1.5       3.1       3.1       - conserved exported protein of unknown function  |                        |        |              |              |              |        |       | • =   |
| CIBE_5646         8up         0.3         2.3         2.7         1.9         -         conserved membrane protein of unknown function           CIBE_2218         8up         -0.9         1.6         3.6         3.0         dacF         D-alanyl-D-alanine carboxypeptidase DacF           CIBE_2307         8up         -0.5         1.5         3.1         3.1         -         conserved exported protein of unknown function  |                        |        |              |              |              |        |       |   |
| CIBE_2218         8up         -0.9         1.6         3.6         3.0 dacF         D-alanyl-D-alanine carboxypeptidase DacF           CIBE_2307         8up         -0.5         1.5         3.1         3.1         -         conserved exported protein of unknown function   |                        |        |              |              |              |        |       |   |
|  |                        |        |              |              |              |        | dacF  | · · · · · · · · · · · · · · · · · · ·                   |
| CIBE_5419 8up -1.0 1.7 2.9 3.6 - conserved protein of unknown function   |                        |        |              |              |              |        |       | · · ·   |
|  | CIBE_5419              | 8up    | -1.0         | 1.7          | 2.9          | 3.6    |       | conserved protein of unknown function                   |

| CIBE_2131  | 8up  | 0.4 2.0   |   | 2.2 -  | Deacetylase  |
|--|--|---|---|--|--|
| CIBE_2056  | 8up  | -0.2 1.9  | 3.2   | 2.2 -  | conserved protein of unknown function  |
| CIBE_3019  | 8up  | -0.9 2.2  | 3.6   | 2.2 -  | conserved protein of unknown function  |
| CIBE_3504  | 8up  | -1.1 0.8  | 3.4   | 4.0 -  | conserved exported protein of unknown function   |
| CIBE_1735  | 8up  | -0.1 1.9  | 2.8   | 2.5 -  | Spore coat protein   |
| CIBE_2566  | 8up  | 0.3 2.0   |   | 2.0 -  | conserved protein of unknown function  |
| CIBE_1545  | 8up  | 0.3 1.8   |   | 2.2 -  | conserved protein of unknown function  |
|  | _  |   |   |  | ·  |
| CIBE_1683  | 8up  |   | _   | 2.0 -  | conserved protein of unknown function  |
| CIBE_3923  | 8up  | 0.1 1.6   | _   | 2.6 -  | Spore cortex-lytic protein   |
| CIBE_1309  | 8up  | -0.8 2.4  |   | 2.9 -  | protein of unknown function  |
| CIBE_5365  | 8up  | -0.9 0.8  | 3.2   | 3.7 -  | Methyl-accepting chemotaxis sensory transducer   |
| CIBE_5656  | 8up  | -1.3 2.5  | 3.0   | 2.6 -  | Lipopolysaccharide biosynthesis protein  |
| CIBE_5686  | 8up  | -0.6 1.1  | 3.1   | 3.2 -  | conserved protein of unknown function  |
| CIBE_2493  | 8up  | -0.3 1.8  | 2.7   | 2.5 -  | Extracellular solute-binding protein, family 3   |
| CIBE_5100  | 8up  | -0.6 1.9  |   | 2.8 ydaM   | putative glycosyltransferase associated to biofilm formation   |
| CIBE_4957  | 8up  | 0.0 1.9   |   | 2.3 -  | conserved protein of unknown function  |
| CIBE_0510  | _  | -0.9 1.9  |   | 2.7 -  | Endothelin-converting enzyme 1   |
|  | 8up  |   | _   |  |  |
| CIBE_3002  | 8up  | -1.1 1.5  | _   | 2.8 -  | conserved protein of unknown function  |
| CIBE_3935  | 8up  | -0.3 1.3  | _   | 2.7 -  | Small, acid-soluble spore protein beta   |
| CIBE_1670  | 8up  | -0.2 1.6  | _   | 2.4 -  | Alpha-glucosidase 2  |
| CIBE_3149  | 8up  | -0.1 1.4  | 2.8   | 2.4 yodR   | putative acyloate-acetoacetate CoA-transferase   |
| CIBE_1312  | 8up  | -0.4 0.8  | 2.8   | 3.2 -  | Autolysin (fragment)   |
| CIBE_4642  | 8up  | 0.0 3.3   | 1.4   | 1.7 -  | conserved membrane protein of unknown function   |
| CIBE_5644  | 8up  | 0.0 2.1   | 2.3   | 1.9 -  | Glycosyl transferase, family 2   |
| CIBE 3150  | 8up  | -0.2 1.4  | _   | 2.4 atoA   | acetoacetyl CoA-transferase (subunit A)  |
| CIBE 4958  | 8up  | -0.2 1.7  | _   | 2.2 -  | conserved protein of unknown function  |
| CIBE 0741  | 8up  | 0.2 1.8   |   | 2.1 -  | conserved protein of unknown function  |
| _  | _  | -1.0 2.2  |   | 2.1 -  | protein of unknown function  |
| CIBE_2744  | 8up  |   | _   |  | •  |
| CIBE_1671  | 8up  | 0.1 1.6   | _   | 2.0 malL   | Oligo-1,6-glucosidase  |
| CIBE_2745  | 8up  | -0.7 2.2  |   | 1.7 rbr3A  | Reverse rubrerythrin-1   |
| CIBE_0064  | 8up  | 0.1 1.8   | _   | 1.8 -  | conserved protein of unknown function  |
| CIBE_6033  | 8up  | -1.1 1.6  | 3.1   | 2.5 -  | Phosphohydrolase   |
| CIBE_2316  | 8up  | 0.0 2.0   | 2.2   | 1.8 -  | CarD family transcriptional regulator  |
| CIBE 4956  | 8up  | 0.1 1.7   | 2.3   | 2.0 -  | Amine oxidase  |
| CIBE_1748  | 8up  | -0.8 1.7  | _   | 1.7 -  | conserved exported protein of unknown function   |
| CIBE_4402  | 8up  | -0.8 1.7  | _   | 2.5 -  | Dual specificity protein phosphatase   |
| CIBE 5066  | 8up  | 0.2 2.2   | _   | 1.3 -  | protein of unknown function  |
| _  |  |   | _   |  | ·  |
| CIBE_3516  | 8up  |   |   | 1.9 -  | conserved protein of unknown function  |
| CIBE_5436  | 8up  | -0.8 1.6  |   | 2.3 -  | Amino acid permease-associated region  |
| CIBE_3517  | 8up  | -0.1 1.6  | _   | 1.8 -  | Rubrerythrin   |
| CIBE_2560  | 8up  | -0.5 1.1  | 2.9   | 2.4 -  | conserved exported protein of unknown function   |
| CIBE_2662  | 8up  | -0.1 2.7  | 2.1   | 1.0 -  | protein of unknown function  |
| CIBE_1668  | 8up  | -0.6 1.6  | 2.7   | 2.0 amyD   | putative starch degradation products transport system permease protein AmyD  |
| CIBE_5692  | 8up  | -0.7 1.7  | 2.5   | 2.3 -  | Glycosyl transferase   |
| CIBE 2939  | 8up  | -0.1 1.6  |   | 2.0 -  | D-galactose-binding protein  |
| CIBE_3567  | 8up  | 0.3 1.8   |   | 1.4 -  | Ni/Fe hydrogenase  |
| CIBE 2039  |  | -1.1 1.7  | _   | 2.5 spolVE   |  |
| _  | 8up  |   |   |  |  |
| CIBE_3924  | 8up  | -0.2 1.5  |   | 2.0 -  | Methyltransferase type 11  |
| CIBE_0742  | 8up  | 0.1 1.8   |   | 1.6 -  | conserved protein of unknown function  |
| CIBE_3256  | 8up  | 0.1 1.8   | _   | 1.7 -  | Sugar transporter  |
| CIBE_1500  | 8up  | -0.5 1.2  | 3.1   | 2.0 -  | Ferredoxin   |
| CIBE_2196  | 8up  | -0.9 1.1  | 2.8   | 2.7 nifJ   | Pyruvate-flavodoxin oxidoreductase   |
| CIBE_5643  | 8up  | 0.0   | 2.3   | 1.6 -  | Glycosyl transferase, group 1  |
| CIBE 4055  | 8up  | -1.1 1.5  | 2.6   | 2.7 -  | putative galactoside ABC transporter   |
| CIBE_2661  | 8up  | -0.1 2.€  | 2.0   | 1.1 -  | protein of unknown function  |
| CIBE_1667  | 8up  | -0.9 1.4  | _   | 2.2 -  | ABC transporter substrate-binding protein  |
| CIBE 4880  | 8up  | -0.6 1.4  |   | 2.2 -  | Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein   |
| _  |  |   | 2.7   |  | Small, acid-soluble spore protein 1  |
| CIBE_0641  | 8up  |   | 2.0   |  | Sitiali, acid-soluble spore protein 1  |
| CIBE 0047  |  | -0.6 0.7  | _   | 2.4 ssp  |  |
| _  | 8up  | -0.6 0.7<br>0.0 1.9   | 2.0   | 2.4 ssp<br>1.4 -   | conserved protein of unknown function  |
| CIBE_0738  | 8up<br>8up   | -0.6 0.7<br>0.0 1.9<br>-0.1 1.3   | 2.0<br>2.3  | 2.4 ssp<br>1.4 -<br>1.8 -  | conserved protein of unknown function conserved protein of unknown function  |
| CIBE_0738<br>CIBE_1081   | 8up<br>8up<br>8up  | -0.6 0.7<br>0.0 1.9<br>-0.1 1.3<br>-1.4 1.5   | 2.0<br>2.3<br>2.7   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -   | conserved protein of unknown function<br>conserved protein of unknown function<br>conserved exported protein of unknown function   |
| CIBE_0738<br>CIBE_1081<br>CIBE_4034  | 8up<br>8up   | -0.6 0.7<br>0.0 1.9<br>-0.1 1.3<br>-1.4 1.5<br>-0.4 2.1   | 2.0<br>2.3<br>2.7<br>2.3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -  | conserved protein of unknown function conserved protein of unknown function  |
| CIBE_0738<br>CIBE_1081   | 8up<br>8up<br>8up  | -0.6 0.7<br>0.0 1.9<br>-0.1 1.3<br>-1.4 1.5   | 2.0<br>2.3<br>2.7<br>2.3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -   | conserved protein of unknown function<br>conserved protein of unknown function<br>conserved exported protein of unknown function   |
| CIBE_0738<br>CIBE_1081<br>CIBE_4034  | 8up<br>8up<br>8up<br>8up   | -0.6 0.7<br>0.0 1.9<br>-0.1 1.3<br>-1.4 1.5<br>-0.4 2.1   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -  | conserved protein of unknown function<br>conserved protein of unknown function<br>conserved exported protein of unknown function<br>conserved membrane protein of unknown function   |
| CIBE_0738<br>CIBE_1081<br>CIBE_4034<br>CIBE_0740   | 8up<br>8up<br>8up<br>8up<br>8up                                    | -0.6 0.7<br>0.0 1.9<br>-0.1 1.3<br>-1.4 1.5<br>-0.4 2.1<br>-0.2 1.5   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr   | conserved protein of unknown function<br>conserved protein of unknown function<br>conserved exported protein of unknown function<br>conserved membrane protein of unknown function<br>Rubrerythrin   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000  | 8up<br>8up<br>8up<br>8up<br>8up<br>8up                             | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.2<br>2.4  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879  | 8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up                      | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.2<br>2.4<br>2.4   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -   | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807  | 8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up               | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.2   | 2.4 ssp<br>1.8 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -   | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_0231  | 8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up        | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>3.5<br>2.5  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_0231 CIBE_2101  | 8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up        | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 0.1 1.6  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>3 2.5<br>5 2.0   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.3 -   | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_0231 CIBE_2101 CIBE_3953  | 8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up<br>8up | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 -0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.2<br>3.5<br>2.0<br>1.6   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_0739  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.3 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 0.1 1.6 -0.1 1.6 -0.1 1.6 -0.1 1.6 -0.1 1.6 -0.1 1.9   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.6<br>2.2  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 0.1 1.6 -0.1 1.6 -0.1 1.6 -0.1 1.6 -0.2 1.2  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.0<br>1.6<br>2.2<br>2.2  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>3.0 -   | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_5000 CIBE_1807 CIBE_1807 CIBE_1201 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_0739 CIBE_5688 CIBE_5774  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>2.4<br>3.0  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>3.0 -<br>1.5 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of runknown function putative manganese catalase   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 0.0 1.5  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.2<br>2.4<br>2.4<br>2.5<br>2.0<br>1.6<br>2.2<br>2.2<br>2.2<br>2.2<br>2.3<br>2.4<br>2.4<br>2.5<br>2.0<br>2.0<br>2.0<br>2.0<br>2.0<br>2.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>3.0 -   | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_5000 CIBE_1807 CIBE_1807 CIBE_1201 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_0739 CIBE_5688 CIBE_5774  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.3 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 0.0 1.9 -0.4 1.2   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.2<br>2.4<br>2.4<br>2.5<br>2.0<br>1.6<br>2.2<br>2.2<br>2.2<br>2.2<br>2.3<br>2.4<br>2.4<br>2.5<br>2.0<br>2.0<br>2.0<br>2.0<br>2.0<br>2.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>3.0 -<br>1.5 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of runknown function putative manganese catalase   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 0.0 1.5  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.6<br>2.2<br>3.0<br>2.4<br>3.0<br>2.3   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>3.0 -<br>1.5 -<br>1.4 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_1807 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_0737  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.3 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 0.0 1.9 -0.4 1.2   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>2.4<br>3.0<br>2.2<br>2.4<br>3.0<br>3.0<br>3.1  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>1.5 -<br>1.4 -<br>1.7 prkA  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_5000 CIBE_5073 CIBE_4879 CIBE_1807 CIBE_2101 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_0737 CIBE_2348 CIBE_2348 CIBE_2879  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 0.1 1.6 -0.1 1.9 -0.9 0.4 -0.7 1.1 0.0 1.5 -0.4 1.2 -1.7 1.6 -0.5 1.0  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.2<br>3.0<br>2.0<br>2.3<br>3.0<br>2.2<br>2.3<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>3.0 -<br>1.5 -<br>1.4 -<br>1.7 prkA<br>1.8 -<br>2.0 -   | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein in funknown function serine protein in funknown function serine protein in funknown function Cytochrome b5  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_1807 CIBE_1807 CIBE_1201 CIBE_3953 CIBE_2101 CIBE_3953 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_0737 CIBE_2348 CIBE_2879 CIBE_5642  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 0.0 1.9 -0.4 1.2 -1.7 1.6 -0.5 1.0 -0.7 1.7   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>2.4<br>3.0<br>2.0<br>2.3<br>3.0<br>2.2<br>2.3   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.5 -<br>1.6 -<br>3.0 -<br>1.5 -<br>1.4 -<br>1.7 prkA<br>1.8 -<br>1.8 -<br>1.8 rbr  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Serine protein for unknown function Serine protein for unknown function Serine protein for unknown function Cytochrome b5 Polysaccharide biosynthesis protein  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_0737 CIBE_2348 CIBE_2348 CIBE_2879 CIBE_26642 CIBE_2769   | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.3 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.3 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 -0.0 1.5 -0.4 1.2 -1.7 1.6 -0.5 1.7 -0.5 1.7 -0.5 1.7 -0.5 1.7 -0.5 1.7 -0.5 1.7 -0.5 1.7 -0.5 1.7 -0.5 1.6   | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>3.0<br>2.0<br>2.3<br>3.0<br>2.3<br>3.1<br>2.2<br>2.3   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.3 -<br>1.6 -<br>1.6 -<br>1.5 -<br>1.4 -<br>1.7 prkA<br>1.8 -<br>1.8 -<br>1.8 rbr  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Serine protein in funknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_2311 CIBE_2101 CIBE_353 CIBE_5774 CIBE_5774 CIBE_3314 CIBE_0737 CIBE_2348 CIBE_2879 CIBE_5642 CIBE_2769 CIBE_4807   | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 0.0 1.5 -0.4 1.2 -1.7 1.6 -0.5 1.0 -0.7 1.7 -0.3 1.6 -0.3 1.6  | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>2.2<br>2.3<br>3.1<br>2.2<br>2.3<br>3.1<br>2.2<br>2.3<br>3.1<br>2.2<br>2.3<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>1.6 -<br>1.7 prkA<br>1.8 -<br>2.0 -<br>1.8 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.0 -<br>1. | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_2331 CIBE_9739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_2348 CIBE_2879 CIBE_2769 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_0538  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 -0.5 1.6 -0.5 1.6 -0.1 1.6 -0.1 1.6 -0.1 1.6 -0.1 1.6 -0.1 1.6 -0.7 1.1 -0.5 1.6 -0.7 1.1 -0.5 1.6 -0.7 1.7 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6   | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.2<br>2.4<br>3.0<br>2.0<br>2.3<br>3.1<br>2.2<br>2.4<br>3.0<br>2.1<br>3.0<br>2.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>1.7 prkA<br>1.8 -<br>2.0 -<br>1.8 -<br>1.8 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.0 -<br>1. | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sexported protein of unknown function exported protein of unknown function sporulation-specific protease  |
| CIBE_0738 CIBE_1081 CIBE_40740 CIBE_5000 CIBE_5000 CIBE_0773 CIBE_1807 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_2348 CIBE_2348 CIBE_2348 CIBE_2469 CIBE_5642 CIBE_2769 CIBE_4807 CIBE_4807 CIBE_45538 CIBE_2224  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 -0.5 1.0 -0.5 1.0 -0.7 1.7 -0.3 1.6   | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.6<br>2.0<br>2.0<br>2.1<br>3.0<br>2.0<br>2.1<br>3.0<br>2.0<br>2.1<br>4.1<br>7.1<br>7.1<br>7.1<br>7.1<br>7.1<br>7.1<br>7.1  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>3.0 -<br>1.5 -<br>1.4 -<br>1.7 prkA<br>1.8 -<br>2.0 -<br>1.8 -<br>1.8 -<br>1.8 rbr<br>1.1 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>1.7 -<br>1.8 -<br>1.8 -<br>1.8 -<br>1.8 -<br>1.8 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.7 -<br>1.8 -     | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein in funknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_22101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_3314 CIBE_2487 CIBE_2487 CIBE_2487 CIBE_25642 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_1771  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 -0.5 1.6 -0.5 1.6 -0.1 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.1 0.3 -0.1 0.3 -0.1 0.3   | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.0<br>1.6<br>2.2<br>2.4<br>3.0<br>2.0<br>2.3<br>3.1<br>2.2<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.7<br>2.1<br>3.0<br>2.1<br>3.0<br>2.1<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0   | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.5 -<br>1.6 -<br>1.6 -<br>1.5 -<br>1.4 -<br>1.7 prkA<br>1.8 -<br>1.8 -<br>1.8 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.0 -<br>1. | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function sporulation-specific protease conserved protein of unknown function   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_3314 CIBE_2348 CIBE_2879 CIBE_2879 CIBE_26642 CIBE_2769 CIBE_4807 CIBE_0538 CIBE_2224 CIBE_1771 CIBE_4865   | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 -0.5 1.6 -0.7 1.7 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.1 0.9 -0.4 1.2 -1.7 1.6 -0.5 1.0 -0.7 1.7 -0.8 1.6 -0.9 1.8 -0.9 1.8 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 1.9 -0.9 1.9 1.9 1.9  | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>2.3<br>3.0<br>2.0<br>2.3<br>3.1<br>2.2<br>2.3<br>3.1<br>2.2<br>2.3<br>3.1<br>2.3<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>1.6 -<br>1.7 prkA<br>1.8 -<br>1.7 prkA<br>1.8 -<br>2.0 -<br>1.8 -<br>1.8 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.0 -    | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function experved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_22101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_3314 CIBE_2487 CIBE_2487 CIBE_2487 CIBE_25642 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_5038 CIBE_1771  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 -0.5 1.6 -0.5 1.6 -0.1 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.1 0.3 -0.1 0.3 -0.1 0.3   | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>2.3<br>3.0<br>2.0<br>2.3<br>3.1<br>2.2<br>2.3<br>3.1<br>2.2<br>2.3<br>3.1<br>2.3<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3.1<br>3  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.5 -<br>1.6 -<br>1.6 -<br>1.5 -<br>1.4 -<br>1.7 prkA<br>1.8 -<br>1.8 -<br>1.8 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.0 -<br>1. | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function sporulation-specific protease conserved protein of unknown function   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_3314 CIBE_2348 CIBE_2879 CIBE_2879 CIBE_26642 CIBE_2769 CIBE_4807 CIBE_0538 CIBE_2224 CIBE_1771 CIBE_4865   | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 -0.5 1.6 -0.7 1.7 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.1 0.9 -0.4 1.2 -1.7 1.6 -0.5 1.0 -0.7 1.7 -0.8 1.6 -0.9 1.8 -0.9 1.8 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 1.9 -0.9 1.9 1.9 1.9  | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.2<br>2.5<br>2.0<br>1.2<br>2.0<br>2.0<br>2.0<br>2.0<br>2.1<br>2.1<br>1.7<br>2.1<br>1.7<br>2.1<br>2.1<br>2.2  | 2.4 ssp<br>1.4 -<br>1.8 -<br>2.4 -<br>1.3 -<br>1.8 rbr<br>1.1 -<br>1.4 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.6 -<br>1.6 -<br>1.6 -<br>1.7 prkA<br>1.8 -<br>1.7 prkA<br>1.8 -<br>2.0 -<br>1.8 -<br>1.8 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.9 -<br>1.0 -    | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function experved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_0773 CIBE_5007 CIBE_1807 CIBE_1807 CIBE_1231 CIBE_2101 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_23314 CIBE_2348 CIBE_2879 CIBE_5642 CIBE_1771 CIBE_10738 CIBE_1771 CIBE_1865 CIBE_1771 CIBE_1865 CIBE_5903  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.7 1.1 -0.1 1.9 -0.4 1.2 -1.7 1.6 -0.5 1.0 -0.7 1.1 -0.3 1.6 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9 -0.9 1.9  | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.0<br>2.0<br>2.0<br>2.0<br>2.1<br>2.1<br>1.7<br>2.1<br>1.6<br>2.1<br>1.6<br>2.4<br>1.7<br>2.1  | 2.4 ssp 1.4 - 1.8 - 2.4 - 1.3 - 1.8 rbr 1.1 - 1.4 - 1.9 - 1.9 - 1.6 - 1.6 - 3.0 - 1.5 - 1.4 - 1.7 prkA 1.8 - 2.0 - 1.8 - 1.8 yabG 2.2 - 0.8 - 2.2 - 1.4 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function Sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase conserved protein of unknown function  |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_5000 CIBE_0773 CIBE_2201 CIBE_1807 CIBE_2201 CIBE_3953 CIBE_5688 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_2379 CIBE_248 CIBE_2769 CIBE_5642 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_15588 CIBE_2769 CIBE_5642 CIBE_1771 CIBE_4865 CIBE_1771 CIBE_4865 CIBE_5903 CIBE_5903 CIBE_5903 CIBE_1043 CIBE_3965  | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 -0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 -0.5 1.0 -0.7 1.7 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.1 0.3  | 2.0<br>2.3<br>2.7<br>2.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.0<br>1.6<br>2.0<br>2.0<br>2.1<br>2.1<br>1.7<br>2.1<br>1.6<br>3.3<br>1.7<br>2.1<br>1.6<br>3.3<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.4<br>2.5<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0   | 2.4 ssp 1.4 - 1.8 - 2.4 - 1.3 - 1.8 rbr 1.1 - 1.4 - 1.9 - 1.9 - 1.6 - 1.6 - 3.0 - 1.5 - 1.4 - 1.7 prkA 1.8 - 2.0 - 1.8 - 1.8 yabG 2.2 - 0.8 - 2.2 - 1.4 - 1.7 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase conserved protein of unknown function Peptidase S8 and S53, subtilisin, kexin, sedolisin Spore protein  |
| CIBE_0738 CIBE_1081 CIBE_4074 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_0231 CIBE_2101 CIBE_3953 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_2374 CIBE_2348 CIBE_2879 CIBE_2879 CIBE_2879 CIBE_2879 CIBE_4807 CIBE_224 CIBE_1771 CIBE_4865 CIBE_5903 CIBE_1903 CIBE_1903 CIBE_1903 CIBE_1903 CIBE_1903 CIBE_1903 CIBE_1903 CIBE_1903 CIBE_1043 CIBE_3965 CIBE_4722   | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.9 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.4<br>2.5<br>2.0<br>1.6<br>2.2<br>2.4<br>3.0<br>2.0<br>2.3<br>3.1<br>2.2<br>2.7<br>1.7<br>2.0<br>1.7<br>1.7<br>2.1<br>1.6<br>2.3<br>2.4<br>2.4<br>2.4<br>2.4<br>2.4<br>2.5<br>3.0<br>2.0<br>2.0<br>2.0<br>2.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3.0<br>3 | 2.4 ssp 1.4 - 1.8 - 2.4 - 1.3 - 1.8 rbr 1.1 - 1.4 - 1.9 - 1.9 - 1.9 - 1.3 - 1.6 - 1.6 - 1.7 prkA 1.8 - 2.0 - 1.8 - 1.8 yabG 2.2 - 1.4 - 1.7 - 1.6 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase conserved protein of unknown function Peptidase S8 and S53, subtilisin, kexin, sedolisin Spore protein putative galactoside ABC transporter   |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_5000 CIBE_0773 CIBE_5000 CIBE_0773 CIBE_22101 CIBE_3953 CIBE_2101 CIBE_3953 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_3314 CIBE_27348 CIBE_2879 CIBE_26642 CIBE_2769 CIBE_4807 CIBE_0538 CIBE_1771 CIBE_4865 CIBE_1771 CIBE_4865 CIBE_5903 CIBE_1043 CIBE_1043 CIBE_3965 CIBE_3965 CIBE_3965 CIBE_3965 CIBE_3965 CIBE_3722 CIBE_5648   | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.1 1.9 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.7 1.1 -0.5 1.6 -0.7 1.7 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 0.6 -0.5 1.3  | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.5<br>2.5<br>2.0<br>1.6<br>2.2<br>2.3<br>3.0<br>2.0<br>2.3<br>3.1<br>2.2<br>2.7<br>2.1<br>7<br>2.0<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.6<br>1.7<br>1.7<br>1.6<br>1.6<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7<br>1.7                      | 2.4 ssp 1.4 - 1.8 - 2.4 - 1.3 - 1.8 rbr 1.1 - 1.4 - 1.9 - 1.9 - 1.9 - 1.6 - 1.6 - 1.6 - 1.7 prkA 1.8 - 2.0 - 1.8 yabG 2.2 - 0.8 - 1.3 - 1.6 - 1.3 - 1.6 - 1.8 yabG 2.2 - 1.4 - 1.3 - 1.6 - 1.8 - 1.7 prkA 1.8 - 1.8 yabG 2.1 - 1.8 yabG 2.2 - 1.8 yabG 2.2 - 1.8 yabG 2.2 - 1.8 yabG 2.1 - 1.8 - 1.8 - 1.8 -   | conserved protein of unknown function conserved exported protein of unknown function conserved exported protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase conserved protein of unknown function Peptidase S8 and S53, subtilisin, kexin, sedolisin Spore protein putative galactoside ABC transporter Glycosyl transferase family 1                               |
| CIBE_0738 CIBE_10738 CIBE_1081 CIBE_40740 CIBE_5000 CIBE_5000 CIBE_5000 CIBE_1807 CIBE_1807 CIBE_2231 CIBE_2101 CIBE_3553 CIBE_9739 CIBE_5688 CIBE_5688 CIBE_5774 CIBE_3314 CIBE_2348 CIBE_2348 CIBE_2348 CIBE_2769 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_4807 CIBE_1771 CIBE_4865 CIBE_5903 CIBE_1043 CIBE_3905 CIBE_1043 CIBE_3648 CIBE_1722 CIBE_5648 CIBE_15648 CIBE_15648 CIBE_15648   | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 -0.2 1.7 -0.1 1.6 -0.5 1.6 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.1 1.6 -0.1 1.9 -0.2 1.3 -0.9 0.4 -0.7 1.1 -0.5 1.6 -0.7 1.7 -0.5 1.6 -0.7 1.7 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.5 0.6 -0.5 0.6 -0.5 0.6 -0.5 0.6 -0.5 0.6 -0.5 0.6   | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.0<br>2.0<br>2.0<br>2.1<br>2.1<br>1.7<br>2.1<br>1.7<br>2.1<br>1.6<br>2.4<br>1.8<br>2.4<br>1.8<br>2.4<br>1.8<br>2.4<br>1.8<br>2.4<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8   | 2.4 ssp 1.4 - 1.8 - 2.4 - 1.3 - 1.8 rbr 1.1 - 1.4 - 1.9 - 1.9 - 1.3 - 1.6 - 1.6 - 3.0 - 1.5 - 1.4 - 1.7 prkA 1.8 - 2.0 - 1.8 s 2.0 - 1.8 yabG 2.2 - 0.8 - 2.2 - 0.8 - 1.3 - 1.6 - 1.8 yabG 2.1 - 1.7 - 1.6 - 1.8 yabG 2.1 - 1.8 - 1.9 -  | conserved protein of unknown function conserved protein of unknown function conserved exported protein of unknown function conserved membrane protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved exported protein of unknown function Stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase conserved protein of unknown function Peptidase S8 and S53, subtilisin, kexin, sedolisin Spore protein putative galactoside ABC transporter Glycosyl transferase family 1 Calcium-transporting ATPase 1 |
| CIBE_0738 CIBE_1081 CIBE_4034 CIBE_0740 CIBE_5000 CIBE_0773 CIBE_4879 CIBE_1807 CIBE_2101 CIBE_3953 CIBE_0739 CIBE_5688 CIBE_5688 CIBE_5774 CIBE_2348 CIBE_2348 CIBE_2879 CIBE_5642 CIBE_2649 CIBE_4807 CIBE_0538 CIBE_2769 CIBE_4807 CIBE_0538 CIBE_1043 CIBE_1044 CIBE_1 | 8up                            | -0.6 0.7 0.0 1.9 -0.1 1.3 -1.4 1.5 -0.4 2.1 -0.2 1.5 0.2 1.7 -0.1 1.6 -0.5 1.4 -0.1 1.9 -0.2 1.2 -0.6 1.3 -0.1 1.6 -0.7 1.1 -0.5 1.6 -0.7 1.7 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.3 1.6 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 1.0 -0.5 0.6 -0.5 1.3  | 2.0<br>2.3<br>2.7<br>2.2<br>2.2<br>2.4<br>2.4<br>2.2<br>2.5<br>2.0<br>1.0<br>2.0<br>2.0<br>2.1<br>2.1<br>1.7<br>2.1<br>1.7<br>2.1<br>1.6<br>2.4<br>1.8<br>2.4<br>1.8<br>2.4<br>1.8<br>2.4<br>1.8<br>2.4<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8<br>1.8   | 2.4 ssp 1.4 - 1.8 - 2.4 - 1.3 - 1.8 rbr 1.1 - 1.4 - 1.9 - 1.9 - 1.9 - 1.6 - 1.6 - 1.6 - 1.7 prkA 1.8 - 2.0 - 1.8 yabG 2.2 - 0.8 - 1.3 - 1.6 - 1.3 - 1.6 - 1.8 yabG 2.2 - 1.4 - 1.3 - 1.6 - 1.8 - 1.7 prkA 1.8 - 1.8 yabG 2.1 - 1.8 yabG 2.2 - 1.8 yabG 2.2 - 1.8 yabG 2.2 - 1.8 yabG 2.1 - 1.8 - 1.8 - 1.8 -   | conserved protein of unknown function conserved exported protein of unknown function conserved exported protein of unknown function Rubrerythrin conserved protein of unknown function conserved protein of unknown function Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit Sporulation protein conserved protein of unknown function Lactate utilization protein B/C conserved protein of unknown function Stage V sporulation protein R conserved protein of unknown function stage V sporulation protein R conserved protein of unknown function putative manganese catalase conserved protein of unknown function serine protein kinase conserved protein of unknown function Cytochrome b5 Polysaccharide biosynthesis protein conserved protein of unknown function exported protein of unknown function sporulation-specific protease conserved protein of unknown function Membrane protein Glycosyl transferase conserved protein of unknown function Peptidase S8 and S53, subtilisin, kexin, sedolisin Spore protein putative galactoside ABC transporter Glycosyl transferase family 1          |

| CIBE_3011  |  |  |  |   |  |  |  |
|--|--|--|--|---|--|--|--|
|  | 8up  | -0.6   | 1.0  | 2.4   | 1.3 -  |  | conserved exported protein of unknown function   |
| CIBE_3600  | 8up  | -0.3   | 1.4  | 1.8   | 1.3 fc   | da   | Fructose-bisphosphate aldolase class 1   |
| CIBE_0206  | 8up  | -0.8   | 0.8  | 2.0   | 1.9 -  |  | N-acetylmuramoyl-L-alanine amidase CwlD  |
| CIBE_3070  | 8up  | -0.5   | 0.5  | 2.2   | 1.7 -  |  | Serine acetyltransferase-related protein   |
| CIBE_3462  | 8up  | -0.1   | 1.5  | 1.3   | 1.1 -  |  | Sodium:proton antiporter   |
| CIBE_2293  | 8up  | 0.0  | 0.1  | 1.7   | 1.9 -  |  | FAD-dependent oxidoreductase   |
| CIBE 0419  | 8up  | -0.3   | 1.4  | 1.4   | 1.1 nt   | nfsB   | NAD(P)H-flavin oxidoreductase (nitroreductase)   |
| CIBE_3541  | 8up  | 0.1  | 0.1  | 1.6   | 1.8 yı   | rkC  | putative dioxygenase; cupin family   |
| CIBE 2065  | 8up  | -0.7   | 1.3  | 2.0   | 0.9 az   |  | FMN-dependent NADH-azoreductase  |
| CIBE_4640  | 8up  | -0.1   | 1.8  | 1.1   | 0.7 -  |  | conserved protein of unknown function  |
| CIBE_0807  | 8up  | -1.1   | 1.1  | 2.6   | 1.0 -  |  | conserved protein of unknown function  |
| CIBE 1557  | 8up  | -0.4   | 1.7  | 1.5   | 0.5 -  |  | conserved protein of unknown function  |
| CIBE_4641  | 8up  | -0.4   | 2.2  | 0.7   | 0.6 y  | n/rH   | two-component response regulator YvrH involved in cell wall processes [YvrG]   |
|  |  | 0.0  | 1.6  | 1.3   | 0.5 -  | VIII   |  |
| CIBE_5966  | 8up  |  |  |   | 1.0 -  |  | conserved protein of unknown function conserved protein of unknown function  |
| CIBE_0428  | 8up  | -0.6   | 1.0  | 1.9   |  |  | ·  |
| CIBE_5684  | 8up  | -0.7   | 0.2  | 2.3   | 1.5 -  |  | conserved protein of unknown function  |
| CIBE_3428  | 8up  | -0.2   | 1.5  | 1.5   | 0.5 -  |  | conserved protein of unknown function  |
| CIBE_3620  | 8up  | -0.7   | 1.2  | 1.6   | 0.9 -  |  | Uncharacterized NAD(P)H oxidoreductase HI_1544   |
| CIBE_0581  | 8up  | -0.8   | 1.2  | 1.8   | 0.8 -  |  | conserved protein of unknown function  |
| CIBE_2121  | 8up  | -1.0   | 0.7  | 2.1   | 1.1 -  |  | conserved membrane protein of unknown function   |
| CIBE_3649  | 8up  | -1.2   | 0.5  | 1.8   | 1.8 -  |  | Small acid-soluble spore protein, alpha/beta type  |
| CIBE_0042  | 8up  | 0.0  | 1.9  | 0.8   | 0.3 -  |  | conserved membrane protein of unknown function   |
| CIBE_1741  | 8up  | -0.5   | 0.1  | 1.6   | 1.8 -  |  | conserved protein of unknown function  |
| CIBE_0040  | 8up  | -0.5   | 0.0  | 1.7   | 1.8 -  |  | Peptidoglycan-binding domain 1 protein   |
| CIBE 1558  | 8up  | -0.3   | 1.6  | 1.3   | 0.4 -  |  | Lysophospholipase  |
| CIBE_3057  | 8up  | -0.8   | -0.1   | 1.6   | 2.0 -  |  | Glycosyl transferase, family 2   |
| CIBE_0672  | 8up  | -0.2   | 1.5  | 0.9   | 0.5 -  |  | Peptidase M50  |
| CIBE_1544  | 8up  | -0.9   | 0.9  | 1.4   | 1.1 -  |  | Lipase   |
| CIBE 5092  | 8up  | -0.5   | 1.1  | 1.2   | 0.8 -  |  | Sporulation protein YunB   |
| CIBE_0547  | 8up  | -0.3   | 0.8  | 1.3   | 1.2 is   | snF  | 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase   |
| CIBE_0754  | 8up  | -0.2   | 1.4  | 1.0   | 0.2 m  |  | putative manganese efflux pump MntP  |
|  |  |  | 1.2  |   |  | IIIICF   |  |
| CIBE_1646  | 8up  | -0.4   |  | 1.1   | 0.5 -  |  | Permease   |
| CIBE_1682  | 8up  | -0.7   | 0.9  | 1.2   | 0.7 -  |  | Peptidase S8 and S53, subtilisin, kexin, sedolisin   |
| CIBE_5685  | 8up  | -1.4   | 0.0  | 2.2   | 1.1 -  |  | conserved protein of unknown function  |
| CIBE_2775  | 8up  | -1.3   | 0.3  | 1.7   | 1.3 -  |  | Small, acid-soluble spore protein beta   |
| CIBE_4959  | 8up  | -0.6   | 1.2  | 1.2   | <b>0.2</b> m   | nntR   | Transcriptional regulator MntR   |
| CIBE_3698  | 8up  | -0.8   | -0.1   | 1.7   | 0.8 -  |  | Small acid-soluble spore protein, alpha/beta type  |
| CIBE_0673  | 8up  | -0.4   | 1.3  | 0.5   | -0.1 -   |  | conserved protein of unknown function  |
| CIBE_2216  | 8up  | -0.4   | 1.2  | 1.3   | -0.9 -   |  | conserved protein of unknown function  |
| CIBE_5060  | 8up  | -0.9   | 1.1  | 0.8   | 0.2 -  |  | Abortive infection protein   |
| CIBE_2258  | 8down  | -0.7   | -0.5   | -2.3  | -2.6 -   |  | conserved protein of unknown function  |
| CIBE_4352  | 8down  | 0.1  | -2.0   | -2.1  | -2.8 -   |  | Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein   |
| CIBE_5053  | 8down  | 0.6  | -1.3   | -1.9  | -4.3 -   |  | Ferrous iron transport protein B   |
| CIBE_5055  | 8down  | 0.4  | -1.6   | -1.5  | -4.9 -   |  | FeoA family protein  |
| CIBE 5054  | 8down  | 0.4  | -2.1   | -1.8  | -4.7 -   |  | FeoA family protein  |
| CIBE_1056  | 11up   | -0.9   | -0.3   | 1.8   | 2.3 yl   | rhxC   | putative oxidoreductase  |
| CIBE 2329  | 11up   | -0.8   | -0.2   | 1.7   | 2.1 -  | TIAC   | conserved protein of unknown function  |
| CIBE 4882  | 11up   | -0.5   | -0.2   | 1.6   | 1.7 -  |  | Metallophosphoesterase   |
| CIBE_4882<br>CIBE_1066   | 11up<br>11up   | -0.5   | -0.2   | 1.4   | 1.7  |  | putative ABC transporter, periplasmic-binding  |
| CIDE 1000  |  |  | -0.5   | 1.7   | 1.6 -  |  |  |
|  |  |  | 0.2  |   | 1.0 -  |  | conserved protein of unknown function Glycosyl transferase, group 1  |
| CIBE_5950  | 11up   | -1.0   | -0.2   |   |  |  |  |
| CIBE_5950<br>CIBE_0536   | 11up<br>11up   | -1.0<br>-0.9   | -0.3   | 1.3   | 1.4 -  |  |  |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532  | 11up<br>11up<br>11up   | -1.0<br>-0.9<br>-1.4   | -0.3<br>-0.5   | 1.3<br>1.5  | 1.4 -<br>1.9 -   |  | Glycosyl transferase, group 1  |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532<br>CIBE_5516   | 11up<br>11up<br>11up<br>11up                                 | -1.0<br>-0.9<br>-1.4<br>-1.0   | -0.3<br>-0.5<br>-0.3   | 1.3<br>1.5<br>2.1   | 1.4 -<br>1.9 -<br>0.6 tl   | lp   | Glycosyl transferase, group 1<br>Protein Tlp homolog   |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532<br>CIBE_5516<br>CIBE_0533  | 11up<br>11up<br>11up<br>11up<br>11up                         | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.0   | -0.3<br>-0.5<br>-0.3<br>-0.5   | 1.3<br>1.5<br>2.1<br>1.5  | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -  | lp   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein   |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532<br>CIBE_5516<br>CIBE_0533<br>CIBE_4006   | 11up<br>11up<br>11up<br>11up                                 | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.0   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5   | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -   |  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function   |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532<br>CIBE_5516<br>CIBE_0533<br>CIBE_4006<br>CIBE_4742  | 11up<br>11up<br>11up<br>11up<br>11up                         | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.0<br>-1.1   | -0.3<br>-0.5<br>-0.3<br>-0.5   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4  | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -   | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein   |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532<br>CIBE_5516<br>CIBE_0533<br>CIBE_4006<br>CIBE_4742<br>CIBE_3050   | 11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.0<br>-1.1<br>-1.1   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0   | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -<br>1.5 yi   | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein VisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase   |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532<br>CIBE_5516<br>CIBE_0533<br>CIBE_4006<br>CIBE_4742  | 11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up         | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4  | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -<br>1.5 yi<br>1.9 fc   | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY   |
| CIBE_5950<br>CIBE_0536<br>CIBE_0532<br>CIBE_5516<br>CIBE_0533<br>CIBE_4006<br>CIBE_4742<br>CIBE_3050   | 11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.0<br>-1.1<br>-1.1   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0   | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -<br>1.5 yi<br>1.9 fc<br>0.9 -<br>0.7 -   | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein VisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736  | 11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3  | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -<br>1.5 yi<br>1.9 fo<br>0.9 -<br>0.7 -<br>0.7 -  | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein VisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951  | 11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4   | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -<br>1.5 yi<br>1.9 fc<br>0.9 -<br>0.7 -<br>0.7 -<br>0.3 -   | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913  | 11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4   | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -<br>1.5 yi<br>1.9 fo<br>0.9 -<br>0.7 -<br>0.7 -  | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_0736 CIBE_2913 CIBE_2913 CIBE_1674  | 11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up<br>11up | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2  | 1.4 -<br>1.9 -<br>0.6 tl<br>1.4 -<br>1.6 -<br>1.5 yi<br>1.9 fc<br>0.9 -<br>0.7 -<br>0.7 -<br>0.3 -   | risY   | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_9736 CIBE_1951 CIBE_1913 CIBE_1674 CIBE_3604  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2<br>-0.9   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2   | 1.4 - 1.9 - 0.6 tl 1.4 - 1.6 - 1.5 yi 1.9 fc 0.9 - 0.7 - 0.7 - 0.3 - 1.5 -   | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein B homolog (fragment)   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_1 | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2<br>-0.9<br>-1.5   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1   | 1.4 - 1.9 - 0.6 tl 1.4 - 1.5 yi 1.9 fc 0.7 - 0.7 - 0.3 - 1.5 - 0.6 -   | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1RNA28 CIBE_1RNA28 CIBE_1RNA28 CIBE_3605  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-0.8   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1  | 1.4 - 1.9 - 0.6 tl 1.4 - 1.5 yi 1.9 fc 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bi  | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tip homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein VisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_9736 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1RNA28 CIBE_1RNA28 CIBE_4841 CIBE_3605 CIBE_3603  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.5<br>-1.5<br>-1.5<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.6<br>0.2   | 1.4 - 1.9 - 0.6 tl 1.4 - 1.6 - 1.5 yi 1.9 fc 0.9 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bt 1.0 - 1.0 - 1.0 -  | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1684 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3603 CIBE_4869  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9<br>-1.5   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.6<br>0.2   | 1.4 - 1.9 - 0.6 tl 1.4 - 1.5 yi 1.9 fc 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bi 1.0 - 1.00.4 -   | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3605 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3603 CIBE_4869 CIBE_4341  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.5<br>-1.5<br>-1.5<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9<br>-1.5   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-1.7<br>-1.7<br>-2.5   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.6<br>0.2<br>0.2   | 1.4 - 1.9 - 0.6 tl 1.4 - 1.5 yi 1.9 fc 0.7 - 0.7 - 0.3 - 1.5 - 0.0 bi 1.0 - 0.4 - 2.1 - 2.1 -  | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tip homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_9736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3605 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3603 CIBE_4869 CIBE_4841 CIBE_3505  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9<br>-1.5<br>-4.7<br>4.2  | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.1<br>0.2<br>0.2<br>1.9<br>1.5   | 1.4 - 1.9 - 0.6 tll 1.4 - 1.5 yi 1.9 fc 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bl 1.0 - 1.0 - 1.0 - 1.2 3 - 2.3 - | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function   |
| CIBE_5950 CIBE_0536 CIBE_0536 CIBE_0533 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3604 CIBE_1RNA28 CIBE_4RN41 CIBE_3605 CIBE_3603 CIBE_3603 CIBE_4869 CIBE_4841 CIBE_3250 CIBE_3250 CIBE_3258   | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9<br>-1.5<br>-4.7<br>-4.2   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.9<br>-1.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7<br>-1.7<br>-2.5<br>-3.0<br>-2.5<br>-3.0   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.6<br>0.2<br>1.9<br>1.5  | 1.4 - 1.9 - 0.6 tll 1.4 - 1.6 - 1.5 yi 1.9 fo 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bl 1.0 - 1.0 - 1.0 - 1.2 3 - 3.9   | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC  |
| CIBE_5950 CIBE_0536 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_1674 CIBE_3606 CIBE_3603 CIBE_4869 CIBE_4869 CIBE_4341 CIBE_3401 CIBE_3500 CIBE_3501 CIBE_3550 CIBE_3258 CIBE_3259  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9<br>-1.5<br>4.7<br>4.2<br>-1.6<br>-2.1   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5<br>2.4<br>1.6   | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.6<br>0.2<br>0.2<br>1.5<br>1.5<br>1.4<br>1.4<br>1.2<br>1.2<br>1.3   | 1.4 - 1.9 - 0.6 tl. 1.4 - 1.5 yi fc 0.9 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bl. 1.0 - 0.4 - 2.1 - 2.1 - 2.3 - 3.9 - 3.8  | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acryl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS mallose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_4841 CIBE_3605 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3505 CIBE_3503 CIBE_4859 CIBE_3258 CIBE_3258 CIBE_3258 CIBE_3258 CIBE_3259 CIBE_0988  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9<br>-1.5<br>4.7<br>4.2<br>-2.1   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5<br>2.4<br>1.6<br>1.7  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4   | 1.4 - 1.9 - 0.6 tt 1.4 - 1.5 yi fc 1.9 fc 0.9 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bt 1.0 - 0.4 - 2.1 - 2.3 - 3.9 - 0.8 - | risY<br>dtB  | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_3050 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3250 CIBE_3259 CIBE_3259 CIBE_3259 CIBE_0988 CIBE_0920  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.6 -3.0 -2.9 -1.5 4.7 4.2 -1.6 -2.1 0.1  | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.4<br>-0.8<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5<br>2.4<br>1.6<br>1.7<br>1.3   | 1.3<br>1.5<br>2.1<br>1.5<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.1<br>0.2<br>1.9<br>1.5<br>4.7<br>4.7  | 1.4 - 1.9 - 0.6 ti 1.4 - 1.5 yi 1.9 fc 0.9 - 0.7 - 0.3 - 1.5 - 0.6 - 1.0 - 1.0 - 2.1 - 2.3 - 3.9 3.8 0.8 0.2 -   | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein VisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_3050 CIBE_3050 CIBE_3050 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3605 CIBE_3603 CIBE_3603 CIBE_34841 CIBE_3605 CIBE_3503 CIBE_3259 CIBE_3259 CIBE_0988 CIBE_0988 CIBE_0988 CIBE_0080   | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0<br>-0.9<br>-1.4<br>-1.0<br>-1.1<br>-1.1<br>-1.5<br>-1.5<br>-1.2<br>-1.7<br>-1.3<br>-2.6<br>-1.7<br>-1.6<br>-3.0<br>-2.9<br>-1.5<br>-4.7<br>4.2<br>-1.6<br>-2.1<br>0-2.1   | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.8<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7<br>-1.7<br>-2.5<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0<br>-3.0       | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.3<br>0.3  | 1.4 - 1.9 - 0.6 tt 1.4 - 1.5 yi 1.9 fc 1.5 yi 1.9 fc 1.5 yi 1.9 fc 1.5 yi 1.9 fc 1.5 yi 1.5 c 1.5 yi 1.5  | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase   |
| CIBE_5950 CIBE_0536 CIBE_0536 CIBE_0533 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3604 CIBE_1805 CIBE_3604 CIBE_3605 CIBE_3605 CIBE_3605 CIBE_3605 CIBE_3503 CIBE_4869 CIBE_4841 CIBE_3500 CIBE_3503 CIBE_3503 CIBE_3503 CIBE_3500 CIBE_3500 CIBE_3259 CIBE_0988 CIBE_0988 CIBE_0920 CIBE_0080 CIBE_5443  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -1.7 -1.6 -3.0 -2.9 -1.5 -4.7 -4.2 -1.6 -2.1 0.1 -0.5 -0.8 -1.0  | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.6<br>-0.4<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5<br>2.4<br>1.6<br>1.7<br>1.3<br>1.0<br>0.9   | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.5<br>0.3<br>0.3  | 1.4 - 1.9 - 0.6 ttl 1.4 - 1.5 yi 1.9 fc 0.7 - 0.3 - 1.5 - 0.6 - 0.0 - 1.0 - 2.1 - 2.3 - 3.9 - 3.80.8 - 0.2 - 0.3 yi -0.3 -   | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BglG   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_3050 CIBE_736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3505 CIBE_3603 CIBE_4869 CIBE_3250 CIBE_0920 CIBE_0928 CIBE_0920 CIBE_0920 CIBE_0080 CIBE_0080 CIBE_0080 CIBE_05325 CIBE_0080  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.5 -1.5 -1.2 -1.7 -1.6 -3.0 -2.9 -1.5 -4.7 -4.2 -1.6 -2.1 -0.5 -0.1 -1.1 -1.5 -1.1 -1.5 -1.1 -1.1 -1.5 -1.1 -1.1  | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.4 -0.8 -0.2 -0.9 -1.5 -0.9 -1.7 -1.7 -2.5 3.0 2.5 2.4 1.6 1.7 1.3 1.0 0.9 0.8  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>1.5<br>4.7<br>4.4<br>0.5<br>0.3<br>0.3<br>0.3   | 1.4 - 1.9 - 0.6 til 1.4 - 1.5 yi fc 0.9 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bi 6.0 - 0.4 - 0.2 1 - 2.3 - 0.8 - 0.2 - 0.3 yi - 0.3 - 1.3  | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS mallcose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_3050 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_4841 CIBE_3605 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_4841 CIBE_3505 CIBE_3603 CIBE_4869 CIBE_4841 CIBE_3505 CIBE_0505 CIBE_0525 CIBE_0525 CIBE_0988 CIBE_0920 CIBE_0080 CIBE_5443 CIBE_0080 CIBE_5443 CIBE_00308   | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.6 -3.0 -2.9 -1.5 -4.7 -4.2 -1.6 -2.1 0.1 -0.5 -0.8 -1.0 -1.1  | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.4<br>-0.8<br>-0.2<br>-0.9<br>-1.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5<br>2.4<br>1.6<br>1.7<br>1.3<br>1.0<br>0.9<br>0.9<br>0.9<br>0.9<br>0.9<br>0.9<br>0.9<br>0  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.1<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.5<br>0.3<br>0.3<br>0.3<br>0.3<br>0.3   | 1.4 - 1.9 - 0.6 tt 1.4 - 1.6 - 1.5 yi 1.9 fc 0.9 - 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bt 1.0 - 2.3 - 0.3 - 0.3 - 0.3 - 0.3 - 0.3 yi - 0.3 - | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Small, acid-soluble spore protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_7365 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3605 CIBE_3600 CIBE_4841 CIBE_3605 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3603 CIBE_4859 CIBE_3259 CIBE_3258 CIBE_3259 CIBE_920 CIBE_0988 CIBE_9434 CIBE_0080 CIBE_5443 CIBE_1643 CIBE_1643 CIBE_1643 CIBE_1643 CIBE_16080 CIBE_5443 CIBE_16080 CIBE_5443 CIBE_16080 CIBE_5443 CIBE_16080 CIBE_1 | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -1.7 -1.6 -3.0 -2.9 -1.5 -4.7 -4.2 -1.6 -2.1 -0.5 -0.8 -1.0 -1.1 -0.5 -0.8 -1.0 -7   | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.4 -0.8 -0.2 -0.9 -1.5 -0.9 -0.8 -1.7 -1.7 -2.5 3.0 2.5 2.4 1.6 1.7 1.3 1.0 0.9 0.8 -0.3 0.9  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.6<br>0.2<br>1.9<br>1.5<br>4.7<br>4.7<br>4.4<br>0.5<br>0.3<br>0.3<br>0.3<br>0.3<br>-0.7<br>-1.1   | 1.4 - 1.9 - 0.6 tl 1.4 - 1.5 yi 1.9 fc 1.5 yi 1.9 fc 1.7 - 0.7 - 0.7 - 0.7 - 0.7 - 0.7 - 0.3 - 1.5 - 2.3 - 0.8 - 0.2 - 0.3 yi 1.3 - 0.2 - 0.3 yi 1.3 - 0.2 - 0.3 - 1.3 - 0.2 - 0.3 - 1.3 - 0.8 - 1.6 - | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tip homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_3050 CIBE_3050 CIBE_3050 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3605 CIBE_3603 CIBE_34841 CIBE_3605 CIBE_3503 CIBE_4869 CIBE_3450 CIBE_3259 CIBE_3259 CIBE_3259 CIBE_0988 CIBE_3259 CIBE_0988 CIBE_5443 CIBE_5443 CIBE_5443 CIBE_5443 CIBE_0107 CIBE_0008 CIBE_5197 CIBE_0019   | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -1.7 -1.6 -3.0 -2.9 -1.5 -4.7 -4.2 -1.6 -2.1 0.1 -0.5 -0.8 -1.0 1.1 1.5 -0.7 -0.8  | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.8 -0.2 -0.9 -1.5 -0.9 -0.8 -1.7 -1.7 -2.5 3.0 2.5 2.4 1.6 1.7 1.3 1.0 0.9 0.8 -0.9 1.4   | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.3<br>0.3<br>0.3<br>0.3<br>0.3<br>-0.7<br>-1.1<br>-0.6  | 1.4 - 1.9 - 0.6 ti 1.4 - 1.5 yi 1.9 fc 0.9 - 0.7 - 0.3 - 1.5 - 0.0 bi 1.0 - 0.4 - 2.1 - 2.3 - 0.8 - 0.8 - 0.2 - 0.3 yi 0.3 - 0 | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I  Sugar-binding protein conserved protein of unknown function PTS mallose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function protein of unknown function   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_7736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3605 CIBE_1674 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4841 CIBE_3505 CIBE_3603 CIBE_4869 CIBE_4341 CIBE_3250 CIBE_3259 CIBE_0928 CIBE_0920 CIBE_0920 CIBE_0920 CIBE_0920 CIBE_09308 CIBE_0107 CIBE_0308 CIBE_0107 CIBE_0308 CIBE_1070 CIBE_0107 CIBE_0107 CIBE_0107 CIBE_01091 CIBE_2260  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -2.1 -1.6 -3.0 -2.9 -1.5 -1.5 -1.5 -1.6 -2.1 -1.6 -2.1 -1.6 -2.1 -0.5 -0.8 -1.0 -1.1 -0.5 -0.8 -1.0 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8  | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.4 -0.2 -0.9 -1.5 -0.9 -1.7 -1.7 -2.5 3.0 2.5 2.4 1.6 1.7 1.3 0.9 0.8 -0.9 1.4 0.2  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.5<br>0.3<br>0.3<br>-1.0<br>-0.7<br>-1.1<br>-0.6<br>-1.5  | 1.4 - 1.9 - 0.6 tt 1.4 - 1.5 yi fc 1.9 fc 1.0 - 1.0 - 1.0 - 1.0 - 1.0 - 1.0 - 1.0 - 1.0 - 1.0 yi fc 1 | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein TJp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I  Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function protein of unknown function   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_3050 CIBE_736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3606 CIBE_4841 CIBE_3605 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4869 CIBE_4869 CIBE_4869 CIBE_4841 CIBE_3250 CIBE_05080 CIBE_0920 CIBE_0920 CIBE_0920 CIBE_0980 CIBE_5197 CIBE_0308 CIBE_5197 CIBE_0308 CIBE_5197 CIBE_0919 CIBE_0919 CIBE_0919 CIBE_2260 CIBE_2260 CIBE_22839   | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -1.7 -1.6 -3.0 -2.9 -1.5 -2.1 0.1 -0.5 -0.8 -1.0 -1.1 -1.5 -0.7 -0.8 -0.0 0.2  | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.2<br>-0.9<br>-0.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5<br>2.4<br>1.6<br>1.7<br>1.3<br>1.0<br>0.9<br>0.8<br>-0.9<br>-0.8<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0. | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.1<br>0.2<br>1.9<br>1.5<br>4.7<br>0.3<br>0.3<br>0.3<br>0.3<br>0.3<br>0.7<br>-1.1<br>-0.6<br>-1.5<br>-1.5  | 1.4 - 1.9 - 0.6 tt 1.4 - 1.6 - 1.5 yi 1.9 fc 0.9 - 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bt 1.0 - 2.1 - 2.3 - 0.8 - 0.2 - 0.3 yi 1.5 - 0.8 - 1.3 - 0.8 - 1.6 - 1.3 - 1.3 - 1.4 - 1.7 - 1 | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function protein of unknown function protein of unknown function  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_3050 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3603 CIBE_1674 CIBE_3603 CIBE_34841 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3250 CIBE_3258 CIBE_3259 CIBE_0500 CIBE_5443 CIBE_0500 CIBE_5443 CIBE_0080 CIBE_5443 CIBE_0080 CIBE_5443 CIBE_00919 CIBE_00919 CIBE_00919 CIBE_00919 CIBE_00919 CIBE_2260 CIBE_2260 CIBE_2260 CIBE_2227  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -2.1 -1.6 -3.0 -2.9 -1.5 -1.5 -1.5 -1.6 -2.1 -1.6 -2.1 -1.6 -2.1 -0.5 -0.8 -1.0 -1.1 -0.5 -0.8 -1.0 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8 -1.0 -0.8  | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.4 -0.2 -0.9 -1.5 -0.9 -1.7 -1.7 -2.5 3.0 2.5 2.4 1.6 1.7 1.3 0.9 0.8 -0.9 1.4 0.2  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.5<br>0.3<br>0.3<br>-1.0<br>-0.7<br>-1.1<br>-0.6<br>-1.5  | 1.4 - 1.9 - 0.6 tt 1.4 - 1.5 yi 1.9 ft 6 - 1.5 yi 1.9 ft 6 - 0.7 - 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bt 1.0 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.4 - 1.4 - 1.7 - 1.2 xi   | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein TJp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I  Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function protein of unknown function   |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_3050 CIBE_736 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3606 CIBE_4841 CIBE_3605 CIBE_3605 CIBE_4841 CIBE_3605 CIBE_4869 CIBE_4869 CIBE_4869 CIBE_4841 CIBE_3250 CIBE_05080 CIBE_0920 CIBE_0920 CIBE_0920 CIBE_0980 CIBE_5197 CIBE_0308 CIBE_5197 CIBE_0308 CIBE_5197 CIBE_0919 CIBE_0919 CIBE_0919 CIBE_2260 CIBE_2260 CIBE_22839   | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -1.7 -1.6 -3.0 -2.9 -1.5 -2.1 0.1 -0.5 -0.8 -1.0 -1.1 -1.5 -0.7 -0.8 -0.0 0.2  | -0.3<br>-0.5<br>-0.3<br>-0.5<br>-0.6<br>-0.8<br>-0.2<br>-0.9<br>-0.5<br>-0.9<br>-0.8<br>-1.7<br>-1.7<br>-2.5<br>3.0<br>2.5<br>2.4<br>1.6<br>1.7<br>1.3<br>1.0<br>0.9<br>0.8<br>-0.9<br>-0.8<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0.9<br>-0. | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.1<br>0.2<br>1.9<br>1.5<br>4.7<br>0.3<br>0.3<br>0.3<br>0.3<br>0.3<br>0.7<br>-1.1<br>-0.6<br>-1.5<br>-1.5  | 1.4 - 1.9 - 0.6 tt 1.4 - 1.6 - 1.5 yi 1.9 fc 0.9 - 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bt 1.0 - 2.1 - 2.3 - 0.8 - 0.2 - 0.3 yi 1.5 - 0.8 - 1.3 - 0.8 - 1.6 - 1.3 - 1.3 - 1.4 - 1.7 - 1 | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function protein of unknown function protein of unknown function  |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_3050 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_1674 CIBE_3603 CIBE_1674 CIBE_3603 CIBE_34841 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3505 CIBE_3250 CIBE_3258 CIBE_3259 CIBE_0500 CIBE_5443 CIBE_0500 CIBE_5443 CIBE_0080 CIBE_5443 CIBE_0080 CIBE_5443 CIBE_00919 CIBE_00919 CIBE_00919 CIBE_00919 CIBE_00919 CIBE_2260 CIBE_2260 CIBE_2260 CIBE_2227  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.6 -3.0 -2.9 -1.5 -1.7 -1.6 -3.0 -2.9 -1.5 -1.7 -1.6 -3.0 -2.9 -1.5 -0.8 -1.0 -1.1 -0.5 -0.8 -1.0 -0.1 -0.5 -0.8 -1.0 -0.1 -0.5 -0.8 -1.0 -0.1 -0.5 -0.8 -1.0 -0.1 -0.5 -0.8 -1.0 -0.1 -0.5 -0.8 -0.0  | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.4 -0.8 -0.2 -0.9 -1.5 -0.9 -0.8 -1.7 -1.7 -2.5 3.0 2.5 2.4 1.6 1.7 1.3 1.0 0.9 0.8 -0.3 0.9 1.4 0.2 0.6 0.1  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.1<br>0.6<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.5<br>0.3<br>0.3<br>0.3<br>0.3<br>0.1<br>0.5<br>1.6<br>1.6<br>1.6<br>1.6<br>1.6<br>1.6<br>1.6<br>1.6<br>1.6<br>1.6            | 1.4 - 1.9 - 0.6 tt 1.4 - 1.5 yi 1.9 ft 6 - 1.5 yi 1.9 ft 6 - 0.7 - 0.7 - 0.7 - 0.3 - 1.5 - 0.6 - 0.0 bt 1.0 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.3 - 1.4 - 1.4 - 1.7 - 1.2 xi   | risY<br>dtB<br>buk                                       | Glycosyl transferase, group 1 Protein Tlp homolog Spore cost protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function                    |
| CIBE_5950 CIBE_0536 CIBE_0532 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_7365 CIBE_3951 CIBE_2913 CIBE_1674 CIBE_3604 CIBE_4674 CIBE_3605 CIBE_3603 CIBE_4841 CIBE_3605 CIBE_3505 CIBE_3505 CIBE_3603 CIBE_4869 CIBE_34341 CIBE_3250 CIBE_3259 CIBE_0808 CIBE_5250 CIBE_3259 CIBE_0920 CIBE_0080 CIBE_5443 CIBE_5443 CIBE_5443 CIBE_5443 CIBE_1077 CIBE_0308 CIBE_5197 CIBE_0919 CIBE_2260 CIBE_22839 CIBE_2277 CIBE_0350  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -1.7 -1.6 -3.0 -2.9 -1.5 -1.7 -1.6 -3.0 -2.9 -1.5 -1.7 -1.6 -3.0 -2.9 -1.5 -0.8 -1.0 -1.1 -0.5 -0.8 -1.0 -1.1 -1.1 | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.9 -1.5 -0.9 -1.7 -1.7 -2.5 -0.9 -1.6 -1.7 -1.7 -2.5 -0.9 -1.4 -0.9 -0.8 -0.1 -4.7  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.3<br>0.3<br>0.3<br>0.3<br>0.3<br>-0.7<br>-1.1<br>-0.6<br>-1.5<br>-1.5   | 1.4 - 1.9 - 0.6 ti 1.4 - 1.5 yi 1.9 f  | risY<br>dtB<br>buk<br>wkoT                               | Glycosyl transferase, group 1 Protein Tlp homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoacyl-acyl-carrier-protein synthase I Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS IIA-like nitrogen-regulatory protein PtsN TspO conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved protein of unknown function |
| CIBE_5950 CIBE_0536 CIBE_0536 CIBE_0533 CIBE_5516 CIBE_0533 CIBE_4006 CIBE_4742 CIBE_3050 CIBE_0736 CIBE_3951 CIBE_2913 CIBE_2913 CIBE_3604 CIBE_1674 CIBE_3605 CIBE_3605 CIBE_3605 CIBE_3441 CIBE_3605 CIBE_3469 CIBE_4869 CIBE_4869 CIBE_4869 CIBE_4869 CIBE_3259 CIBE_0988 CIBE_3259 CIBE_0988 CIBE_5443 CIBE_0080 CIBE_5443 CIBE_0107 CIBE_0308 CIBE_5443 CIBE_0107 CIBE_0308 CIBE_5429 CIBE_0919 CIBE_2260 CIBE_2277 CIBE_0919 CIBE_2277 CIBE_0350 CIBE_2740  | 11up 11up 11up 11up 11up 11up 11up 11up                      | -1.0 -0.9 -1.4 -1.0 -1.1 -1.1 -1.5 -1.5 -1.2 -1.7 -1.3 -2.6 -1.7 -1.6 -3.0 -2.9 -1.5 -4.7 -4.2 -1.6 -2.1 0.1 -0.5 -0.8 -1.0 1.1 -0.5 -0.8 -1.0 0.1 -1.1 -0.5 -0.8 -1.0 -1.1 -1.2 -1.1 -1.2   | -0.3 -0.5 -0.3 -0.5 -0.6 -0.8 -0.6 -0.4 -0.2 -0.9 -1.5 -0.9 -1.7 -1.7 -2.5 3.0 2.5 2.4 1.6 1.7 1.3 1.0 0.9 0.8 -0.3 0.9 1.4 0.2 0.6 0.1 -4.7 -3.2  | 1.3<br>1.5<br>2.1<br>1.5<br>1.4<br>1.0<br>1.3<br>1.4<br>1.2<br>1.2<br>1.3<br>0.1<br>0.6<br>0.2<br>0.2<br>1.9<br>1.5<br>4.7<br>4.4<br>0.3<br>0.3<br>0.3<br>0.3<br>-0.7<br>-1.1<br>-0.6<br>-1.5<br>-2.1<br>-1.5<br>-1.5<br>-1.5<br>-1.5<br>-1.5<br>-1.5<br>-1.5<br>-1 | 1.4 - 1.9 - 0.6 tt 1.4 - 1.5 yi 1.9 fc 1.5 yi 1.9 y | risY<br>dtB<br>buk<br>vkoT<br>kkdU<br>uuaB<br>reA<br>reP | Glycosyl transferase, group 1 Protein Tip homolog Spore coat protein conserved protein of unknown function AB hydrolase superfamily protein YisY dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase conserved protein of unknown function Spore protein Small, acid-soluble spore protein beta Small, acid-soluble spore protein beta Ferrous iron transport protein B homolog (fragment) Gly tRNA branched-chain fatty-acid kinase Ferrous iron transport protein B homolog (fragment) Iron transporter FeoA Beta-ketoayl-acyl-carrier-protein synthase I  Sugar-binding protein conserved protein of unknown function PTS maltose transporter subunit IIBC putative PTS INA-like nitrogen-regulatory protein PtsN TspQ conserved protein of unknown function putative glycosyltransferase Transcription antiterminator BgIG Sporulation protein Signal transduction histidine kinase regulating citrate/malate metabolism conserved exported protein of unknown function putative phage protein XkdU inosine-monophosphate dehydrogenase trehalose-6-phosphate hydrolase                                    |