| No | Family name | Family Code | Positive | Negative |
| --- | --- | --- | --- | --- |
| 1 | 50S ribosome-binding GTPase | MMR\_HSR1 | 3084 | 3084 |
| 2 | Helicase conserved C-terminal domain | Helicase\_C | 2518 | 2518 |
| 3 | ATP synthase alpha/beta family, nucleotide-binding domain | ATP-synt\_ab | 2387 | 2387 |
| 4 | 7 transmembrane receptor (rhodopsin family) | 7tm\_1 | 1820 | 1820 |
| 5 | Amino acid kinase family | AA\_kinase | 1750 | 1750 |
| 6 | ATPase family associated with various cellular activities (AAA) | AAA | 1711 | 1711 |
| 7 | tRNA synthetases class I (I, L, M and V) | tRNA-synt\_1 | 1634 | 1634 |
| 8 | tRNA synthetases class II (D, K and N) | tRNA-synt\_2 | 1419 | 1419 |
| 9 | Major Facilitator Superfamily | MFS\_1 | 1303 | 1303 |
| 10 | Hsp70 protein | HSP70 | 1272 | 1272 |
| 11 | NADH-Ubiquinone/plastoquinone (complex I), various chains | Oxidored\_q1 | 1251 | 1251 |
| 12 | Histidine biosynthesis protein | His\_biosynth | 1248 | 1248 |
| 13 | TCP-1/cpn60 chaperonin family | Cpn60\_TCP1 | 1246 | 1246 |
| 14 | EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) | EPSP\_synthase | 1207 | 1207 |
| 15 | Aldehyde dehydrogenase family | Aldedh | 1200 | 1200 |
| 16 | Shikimate / quinate 5-dehydrogenase | Shikimate\_DH | 1128 | 1128 |
| 17 | GHMP kinases N terminal domain | GHMP\_kinases\_N | 1120 | 1120 |
| 18 | Ribosomal protein S2 | Ribosomal\_S2 | 1083 | 1083 |
| 19 | Ribosomal protein S4/S9 N-terminal domain | Ribosomal\_S4 | 1072 | 1072 |
| 20 | Ribosomal protein L16p/L10e | Ribosomal\_L16 | 1053 | 1053 |
| 21 | KOW motif | KOW | 1047 | 1047 |
| 22 | Uncharacterized protein family UPF0004 | UPF0004 | 1044 | 1044 |
| 23 | Ribosomal protein S12/S23 | Ribosom\_S12\_S23 | 1016 | 1016 |
| 24 | GHMP kinases C terminal | GHMP\_kinases\_C | 1011 | 1011 |
| 25 | Ribosomal protein S14p/S29e | Ribosomal\_S14 | 997 | 997 |
| 26 | Ribosomal protein S11 | Ribosomal\_S11 | 980 | 980 |
| 27 | UvrB/uvrC motif | UVR | 968 | 968 |
| 28 | Ribosomal protein L33 | Ribosomal\_L33 | 958 | 958 |
| 29 | BRCA1 C Terminus (BRCT) domain | BRCT | 956 | 956 |
| 30 | RF-1 domain | RF-1 | 950 | 950 |
| 31 | Ankyrin repeats (3 copies) | Ank\_2 | 944 | 944 |
| 32 | Ribosomal protein L20 | Ribosomal\_L20 | 932 | 932 |
| 33 | RNA polymerase beta subunit | RNA\_pol\_Rpb2\_1 | 912 | 912 |
| 34 | Ribosomal protein S18 | Ribosomal\_S18 | 908 | 908 |
| 35 | ATP synthase B/B CF(0) | ATP-synt\_B | 900 | 900 |
| 36 | Peptidase family M20/M25/M40 | Peptidase\_M20 | 889 | 889 |
| 37 | Ribosomal protein L18e/L15 | Ribosomal\_L18e | 887 | 887 |
| 38 | Glucose inhibited division protein A | GIDA | 886 | 886 |
| 39 | NADH-ubiquinone/plastoquinone oxidoreductase chain 4L | Oxidored\_q2 | 885 | 885 |
| 40 | lactate/malate dehydrogenase, NAD binding domain | Ldh\_1\_N | 880 | 880 |
| 41 | HD domain | HD | 879 | 879 |
| 42 | Ribosomal protein S10p/S20e | Ribosomal\_S10 | 873 | 873 |
| 43 | Pyridoxal-phosphate dependent enzyme | PALP | 870 | 870 |
| 44 | Ribosomal L18p/L5e family | Ribosomal\_L18p | 860 | 860 |
| 45 | Ribosomal protein L3 | Ribosomal\_L3 | 855 | 855 |
| 46 | tRNA synthetases class I (M) | tRNA-synt\_1g | 843 | 843 |
| 47 | UbiA prenyltransferase family | UbiA | 841 | 841 |
| 48 | Ribosomal protein L4/L1 family | Ribosomal\_L4 | 841 | 841 |
| 49 | Ribosomal protein S16 | Ribosomal\_S16 | 840 | 840 |
| 50 | Ribosomal protein S13/S18 | Ribosomal\_S13 | 840 | 840 |
| 51 | MraW methylase family | Methyltransf\_5 | 837 | 837 |
| 52 | Ribosomal L32p protein family | Ribosomal\_L32p | 825 | 825 |
| 53 | Elongation factor TS | EF\_TS | 819 | 819 |
| 54 | Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain | THF\_DHG\_CYH | 817 | 817 |
| 55 | ATP synthase delta (OSCP) subunit | OSCP | 813 | 813 |
| 56 | tRNA synthetases class I (C) catalytic domain | tRNA-synt\_1e | 812 | 812 |
| 57 | SecA Wing and Scaffold domain | SecA\_SW | 805 | 805 |
| 58 | Ribonuclease HII | RNase\_HII | 795 | 795 |
| 59 | Ribosomal protein L31 | Ribosomal\_L31 | 795 | 795 |
| 60 | Ribosomal L27 protein | Ribosomal\_L27 | 794 | 794 |
| 61 | IPP transferase | IPPT | 794 | 794 |
| 62 | GTP-binding protein LepA C-terminus | LepA\_C | 793 | 793 |
| 63 | Ribosomal protein L17 | Ribosomal\_L17 | 791 | 791 |
| 64 | Ribosomal protein L23 | Ribosomal\_L23 | 790 | 790 |
| 65 | Ribosomal protein L10 | Ribosomal\_L10 | 781 | 781 |
| 66 | Ribosomal protein L19 | Ribosomal\_L19 | 780 | 780 |
| 67 | Ribosomal protein S20 | Ribosomal\_S20p | 774 | 774 |
| 68 | Ribosomal protein L35 | Ribosomal\_L35p | 769 | 769 |
| 69 | Phosphoglucomutase/phosphomannomutase, C-terminal domain | PGM\_PMM\_IV | 768 | 768 |
| 70 | AMP-binding enzyme | AMP-binding | 767 | 767 |
| 71 | Ribosomal prokaryotic L21 protein | Ribosomal\_L21p | 766 | 766 |
| 72 | tRNA methyl transferase | tRNA\_Me\_trans | 759 | 759 |
| 73 | Ribosomal L29 protein | Ribosomal\_L29 | 757 | 757 |
| 74 | Glycosyl transferase family, a/b domain | Glycos\_transf\_3 | 754 | 754 |
| 75 | Translation initiation factor IF-2, N-terminal region | IF2\_N | 750 | 750 |
| 76 | Ribosomal L28 family | Ribosomal\_L28 | 749 | 749 |
| 77 | Glycosyl transferase family 4 | Glycos\_transf\_4 | 739 | 739 |
| 78 | tRNA synthetases class I (R) | tRNA-synt\_1d | 736 | 736 |
| 79 | Bacterial trigger factor protein (TF) C-terminus | Trigger\_C | 733 | 733 |
| 80 | Bacterial trigger factor protein (TF) | Trigger\_N | 731 | 731 |
| 81 | Ribosomal protein L34 | Ribosomal\_L34 | 731 | 731 |
| 82 | Ribosomal protein S9/S16 | Ribosomal\_S9 | 730 | 730 |
| 83 | Transcriptional regulator | Transcrip\_reg | 727 | 727 |
| 84 | NADH ubiquinone oxidoreductase, 20 Kd subunit | Oxidored\_q6 | 721 | 721 |
| 85 | Uncharacterised BCR, YhbC family COG0779 | DUF150 | 720 | 720 |
| 86 | Glycosyltransferase family 28 N-terminal domain | Glyco\_transf\_28 | 719 | 719 |
| 87 | tRNA synthetases class II (A) | tRNA-synt\_2c | 718 | 718 |
| 88 | SmpB protein | SmpB | 714 | 714 |
| 89 | Ribosome-binding factor A | RBFA | 714 | 714 |
| 90 | tRNA synthetases class I (W and Y) | tRNA-synt\_1b | 711 | 711 |
| 91 | Chorismate synthase | Chorismate\_synt | 707 | 707 |
| 92 | Ribosomal protein L13 | Ribosomal\_L13 | 705 | 705 |
| 93 | Holliday junction DNA helicase ruvB C-terminus | RuvB\_C | 700 | 700 |
| 94 | RNA polymerase Rpb6 | RNA\_pol\_Rpb6 | 700 | 700 |
| 95 | Holliday junction DNA helicase ruvB N-terminus | RuvB\_N | 698 | 698 |
| 96 | ATP synthase subunit C | ATP-synt\_C | 695 | 695 |
| 97 | CTP synthase N-terminus | CTP\_synth\_N | 687 | 687 |
| 98 | NADH dehydrogenase | NADHdh | 682 | 682 |
| 99 | FtsJ-like methyltransferase | FtsJ | 675 | 675 |
| 100 | PP-loop family | ATP\_bind\_3 | 674 | 674 |
| 101 | recA bacterial DNA recombination protein | RecA | 672 | 672 |
| 102 | tRNA (Guanine-1)-methyltransferase | tRNA\_m1G\_MT | 668 | 668 |
| 103 | Type II intron maturase | Intron\_maturas2 | 668 | 668 |
| 104 | rRNA small subunit methyltransferase G | GidB | 668 | 668 |
| 105 | SEC-C motif | SEC-C | 667 | 667 |
| 106 | MatK/TrnK amino terminal region | MatK\_N | 662 | 662 |
| 107 | HMGL-like | HMGL-like | 660 | 660 |
| 108 | Amidase | Amidase | 656 | 656 |
| 109 | DHHA1 domain | DHHA1 | 654 | 654 |
| 110 | Ribosomal protein S21 | Ribosomal\_S21 | 645 | 645 |
| 111 | Bacterial dnaA protein | Bac\_DnaA | 645 | 645 |
| 112 | Aconitase family (aconitate hydratase) | Aconitase | 643 | 643 |
| 113 | NAD-dependent glycerol-3-phosphate dehydrogenase N-terminus | NAD\_Gly3P\_dh\_N | 641 | 641 |
| 114 | Acetohydroxy acid isomeroreductase, catalytic domain | IlvN | 638 | 638 |
| 115 | Bacitracin resistance protein BacA | BacA | 638 | 638 |
| 116 | Acetohydroxy acid isomeroreductase, catalytic domain | IlvC | 637 | 637 |
| 117 | Respiratory-chain NADH dehydrogenase, 49 Kd subunit | Complex1\_49kDa | 636 | 636 |
| 118 | RecR protein | RecR | 635 | 635 |
| 119 | Predicted SPOUT methyltransferase | SPOUT\_MTase | 614 | 614 |
| 120 | Metalloenzyme superfamily | Metalloenzyme | 609 | 609 |
| 121 | Uncharacterised protein family (UPF0081) | UPF0081 | 607 | 607 |
| 122 | 4-phosphopantetheinyl transferase superfamily | ACPS | 602 | 602 |
| 123 | Glycosyl transferases group 1 | Glycos\_transf\_1 | 601 | 601 |
| 124 | Arginosuccinate synthase | Arginosuc\_synth | 597 | 597 |
| 125 | GTP-binding protein TrmE N-terminus | TrmE\_N | 594 | 594 |
| 126 | GrpE | GrpE | 591 | 591 |
| 127 | UvrC Helix-hairpin-helix N-terminal | UvrC\_HhH\_N | 588 | 588 |
| 128 | D-ala D-ala ligase C-terminus | Dala\_Dala\_lig\_C | 588 | 588 |
| 129 | Aminoacyl-tRNA editing domain | tRNA\_edit | 587 | 587 |
| 130 | Dehydratase family | ILVD\_EDD | 586 | 586 |
| 131 | D-ala D-ala ligase N-terminus | Dala\_Dala\_lig\_N | 586 | 586 |
| 132 | Zinc-binding dehydrogenase | ADH\_zinc\_N | 580 | 580 |
| 133 | YbaB/EbfC DNA-binding family | YbaB\_DNA\_bd | 579 | 579 |
| 134 | RecF/RecN/SMC N terminal domain | SMC\_N | 578 | 578 |
| 135 | Ribonuclease III domain | Ribonuclease\_3 | 578 | 578 |
| 136 | Nucleotidyl transferase | NTP\_transferase | 577 | 577 |
| 137 | Fatty acid synthesis protein | FA\_synthesis | 571 | 571 |
| 138 | Ketopantoate hydroxymethyltransferase | Pantoate\_transf | 565 | 565 |
| 139 | Putative methyltransferase | Methyltransf\_4 | 557 | 557 |
| 140 | tRNA (Uracil-5-)-methyltransferase | tRNA\_U5-meth\_tr | 556 | 556 |
| 141 | Pantoate-beta-alanine ligase | Pantoate\_ligase | 555 | 555 |
| 142 | TGS domain | TGS | 548 | 548 |
| 143 | Carboxyl transferase domain | Carboxyl\_trans | 548 | 548 |
| 144 | Imidazoleglycerol-phosphate dehydratase | IGPD | 542 | 542 |
| 145 | Queuine tRNA-ribosyltransferase | TGT | 537 | 537 |
| 146 | SAICAR synthetase | SAICAR\_synt | 536 | 536 |
| 147 | Iron-sulphur cluster biosynthesis | Fe-S\_biosyn | 536 | 536 |
| 148 | D-Tyr-tRNA(Tyr) deacylase | Tyr\_Deacylase | 532 | 532 |
| 149 | P-loop ATPase protein family | ATP\_bind\_2 | 532 | 532 |
| 150 | Queuosine biosynthesis protein | Queuosine\_synth | 530 | 530 |
| 151 | Prolipoprotein diacylglyceryl transferase | LGT | 529 | 529 |
| 152 | Glycine cleavage system P-protein | GDC-P | 529 | 529 |
| 153 | Glycoprotease family | Peptidase\_M22 | 528 | 528 |
| 154 | Actin | Actin | 527 | 527 |
| 155 | Peroxidase | peroxidase | 526 | 526 |
| 156 | ATP phosphoribosyltransferase | HisG | 526 | 526 |
| 157 | YgbB family | YgbB | 522 | 522 |
| 158 | Glu-tRNAGln amidotransferase C subunit | Glu-tRNAGln | 522 | 522 |
| 159 | TruB family pseudouridylate synthase (N terminal domain) | TruB\_N | 519 | 519 |
| 160 | Uncharacterized protein family UPF0054 | UPF0054 | 514 | 514 |
| 161 | Ribosomal protein L11 methyltransferase (PrmA) | PrmA | 512 | 512 |
| 162 | CrcB-like protein | CRCB | 512 | 512 |
| 163 | Survival protein SurE | SurE | 509 | 509 |
| 164 | Haemolytic domain | Haemolytic | 509 | 509 |
| 165 | mttA/Hcf106 family | MttA\_Hcf106 | 507 | 507 |
| 166 | Ribonuclease P | Ribonuclease\_P | 503 | 503 |
| 167 | Acetyltransferase (GNAT) family | Acetyltransf\_1 | 499 | 499 |
| 168 | Type III restriction enzyme, res subunit | ResIII | 497 | 497 |
| 169 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | IspD | 497 | 497 |
| 170 | Glycerol-3-phosphate acyltransferase | Acyltransferase | 497 | 497 |
| 171 | Cytidylate kinase | Cytidylate\_kin | 496 | 496 |
| 172 | NADH-ubiquinone/plastoquinone oxidoreductase, chain 3 | Oxidored\_q4 | 493 | 493 |
| 173 | Recombination protein O C terminal | RecO\_C | 492 | 492 |
| 174 | Respiratory-chain NADH dehydrogenase, 30 Kd subunit | Complex1\_30kDa | 490 | 490 |
| 175 | Transaldolase | Transaldolase | 486 | 486 |
| 176 | E1-E2 ATPase | E1-E2\_ATPase | 479 | 479 |
| 177 | Uncharacterised protein family UPF0102 | UPF0102 | 478 | 478 |
| 178 | KRAB box | KRAB | 478 | 478 |
| 179 | Phosphatidylserine decarboxylase | PS\_Dcarbxylase | 469 | 469 |
| 180 | AICARFT/IMPCHase bienzyme | AICARFT\_IMPCHas | 468 | 468 |
| 181 | Sugar (and other) transporter | Sugar\_tr | 467 | 467 |
| 182 | PUA domain | PUA | 467 | 467 |
| 183 | Ion transport protein | Ion\_trans | 467 | 467 |
| 184 | Acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit | ACCA | 464 | 464 |
| 185 | Binding-protein-dependent transport system inner membrane component | BPD\_transp\_1 | 462 | 462 |
| 186 | 60Kd inner membrane protein | 60KD\_IMP | 462 | 462 |
| 187 | DNA mismatch repair protein, C-terminal domain | DNA\_mis\_repair | 459 | 459 |
| 188 | ABC transporter transmembrane region | ABC\_membrane | 459 | 459 |
| 189 | Exonuclease | RNase\_T | 457 | 457 |
| 190 | Ribose 5-phosphate isomerase A (phosphoriboisomerase A) | Rib\_5-P\_isom\_A | 452 | 452 |
| 191 | Phage integrase family | Phage\_integrase | 449 | 449 |
| 192 | NAD dependent epimerase/dehydratase family | Epimerase | 447 | 447 |
| 193 | ThiC family | ThiC | 442 | 442 |
| 194 | Peptidase family M48 | Peptidase\_M48 | 440 | 440 |
| 195 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | DXP\_reductoisom | 440 | 440 |
| 196 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase C-terminal | DXP\_redisom\_C | 440 | 440 |
| 197 | GcpE protein | GcpE | 438 | 438 |
| 198 | ATP-NAD kinase | NAD\_kinase | 434 | 434 |
| 199 | MraZ protein | MraZ | 434 | 434 |
| 200 | LytB protein | LYTB | 434 | 434 |
| 201 | Exonuclease VII small subunit | Exonuc\_VII\_S | 432 | 432 |
| 202 | PPR repeat | PPR | 429 | 429 |
| 203 | Guanylate kinase | Guanylate\_kin | 425 | 425 |
| 204 | Mitochondrial carrier protein | Mito\_carr | 421 | 421 |
| 205 | Signal peptidase (SPase) II | Peptidase\_A8 | 419 | 419 |
| 206 | Exonuclease VII, large subunit | Exonuc\_VII\_L | 419 | 419 |
| 207 | Thiazole biosynthesis protein ThiG | ThiG | 413 | 413 |
| 208 | ubiE/COQ5 methyltransferase family | Ubie\_methyltran | 410 | 410 |
| 209 | Photosynthetic reaction centre protein | Photo\_RC | 410 | 410 |
| 210 | LysR substrate binding domain | LysR\_substrate | 410 | 410 |
| 211 | Acetokinase family | Acetate\_kinase | 409 | 409 |
| 212 | Cytidylyltransferase | CTP\_transf\_3 | 407 | 407 |
| 213 | Fructose-1-6-bisphosphatase | FBPase | 404 | 404 |
| 214 | Kinase/pyrophosphorylase | Kinase-PPPase | 403 | 403 |
| 215 | RadC-like JAB domain | RadC | 398 | 398 |
| 216 | Glycyl-tRNA synthetase alpha subunit | tRNA-synt\_2e | 393 | 393 |
| 217 | Hsp90 protein | HSP90 | 390 | 390 |
| 218 | Phosphoadenosine phosphosulfate reductase family | PAPS\_reduct | 387 | 387 |
| 219 | SNF2 family N-terminal domain | SNF2\_N | 381 | 381 |
| 220 | pfkB family carbohydrate kinase | PfkB | 378 | 378 |
| 221 | Ultra-violet resistance protein B | UvrB | 375 | 375 |
| 222 | Sodium:dicarboxylate symporter family | SDF | 375 | 375 |
| 223 | Tetraacyldisaccharide-1-P 4-kinase | LpxK | 374 | 374 |
| 224 | Toprim domain | Toprim | 369 | 369 |
| 225 | MoaC family | MoaC | 369 | 369 |
| 226 | Hsp20/alpha crystallin family | HSP20 | 368 | 368 |
| 227 | Preprotein translocase subunit SecB | SecB | 367 | 367 |
| 228 | Type III pantothenate kinase | Pan\_kinase | 364 | 364 |
| 229 | Septum formation topological specificity factor MinE | MinE | 364 | 364 |
| 230 | HrcA protein C terminal domain | HrcA | 364 | 364 |
| 231 | Protein of unknown function (DUF520) | DUF520 | 360 | 360 |
| 232 | SIS domain | SIS | 358 | 358 |
| 233 | Phosphoribosyl-AMP cyclohydrolase | PRA-CH | 358 | 358 |
| 234 | Intermediate filament protein | Filament | 356 | 356 |
| 235 | Enoyl-CoA hydratase/isomerase family | ECH | 350 | 350 |
| 236 | PCI domain | PCI | 348 | 348 |
| 237 | Glycyl-tRNA synthetase beta subunit | tRNA\_synt\_2f | 347 | 347 |
| 238 | K+ potassium transporter | K\_trans | 345 | 345 |
| 239 | Asp/Glu/Hydantoin racemase | Asp\_Glu\_race | 345 | 345 |
| 240 | Phosphoribosyl-ATP pyrophosphohydrolase | PRA-PH | 344 | 344 |
| 241 | Glycosyl transferase family 2 | Glycos\_transf\_2 | 344 | 344 |
| 242 | Uncharacterized ACR, COG1678 | DUF179 | 342 | 342 |
| 243 | Initiation factor 2 subunit family | IF-2B | 341 | 341 |
| 244 | Thiamine monophosphate synthase/TENI | TMP-TENI | 338 | 338 |
| 245 | Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT) | PCMT | 337 | 337 |
| 246 | Cytochrome C oxidase subunit II, transmembrane domain | COX2\_TM | 333 | 333 |
| 247 | Rnf-Nqr subunit, membrane protein | Rnf-Nqr | 329 | 329 |
| 248 | Peptide methionine sulfoxide reductase | PMSR | 326 | 326 |
| 249 | Acyltransferase | Acyltransferase | 326 | 326 |
| 250 | PHP domain | PHP | 325 | 325 |
| 251 | SPRY domain | SPRY | 324 | 324 |
| 252 | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase, LpxD | LpxD | 323 | 323 |
| 253 | Cytochrome b559, alpha (gene psbE) and beta (gene psbF)subunits | Cytochrom\_B559 | 322 | 322 |
| 254 | GlnD PII-uridylyltransferase | GlnD\_UR\_UTase | 320 | 320 |
| 255 | Protein of unknown function (DUF328) | DUF328 | 316 | 316 |
| 256 | UDP-3-O-acyl N-acetylglycosamine deacetylase | LpxC | 313 | 313 |
| 257 | Leucine Rich repeats (2 copies) | LRR\_4 | 312 | 312 |
| 258 | SET domain | SET | 310 | 310 |
| 259 | Formate--tetrahydrofolate ligase | FTHFS | 309 | 309 |
| 260 | Bacterial translation initiation factor IF-2 associated region | IF2\_assoc | 307 | 307 |
| 261 | Hsp33 protein | HSP33 | 302 | 302 |
| 262 | Sugar fermentation stimulation protein | SfsA | 299 | 299 |
| 263 | Leucyl/phenylalanyl-tRNA protein transferase | Leu\_Phe\_trans | 299 | 299 |
| 264 | Cadherin domain | Cadherin | 299 | 299 |
| 265 | Na+/H+ antiporter 1 | Na\_H\_antiport\_1 | 294 | 294 |
| 266 | Ubiquitin carboxyl-terminal hydrolase | UCH | 292 | 292 |
| 267 | NADH-Ubiquinone oxidoreductase (complex I), chain 5 N-terminus | Oxidored\_q1\_N | 292 | 292 |
| 268 | Thiamine biosynthesis protein (ThiI) | ThiI | 290 | 290 |
| 269 | Photosystem I psaA/psaB protein | PsaA\_PsaB | 288 | 288 |
| 270 | Photosystem II protein | PSII | 285 | 285 |
| 271 | Phosphoenolpyruvate carboxykinase | PEPCK\_ATP | 285 | 285 |
| 272 | S-Ribosylhomocysteinase (LuxS) | LuxS | 285 | 285 |
| 273 | CcmE | CcmE | 284 | 284 |
| 274 | ATP-dependent Clp protease adaptor protein ClpS | ClpS | 282 | 282 |
| 275 | Uncharacterized BCR, YaiI/YqxD family COG1671 | DUF188 | 280 | 280 |
| 276 | Protein of unknown function, DUF258 | DUF258 | 278 | 278 |
| 277 | Nucleotidyltransferase domain | NTP\_transf\_2 | 277 | 277 |
| 278 | Phosphotransferase enzyme family | APH | 277 | 277 |
| 279 | TOBE domain | TOBE\_2 | 276 | 276 |
| 280 | Global regulator protein family | CsrA | 276 | 276 |
| 281 | RecX family | RecX | 275 | 275 |
| 282 | Dephospho-CoA kinase | CoaE | 272 | 272 |
| 283 | RbsD / FucU transport protein family | RbsD\_FucU | 265 | 265 |
| 284 | Transglycosylase SLT domain | SLT | 264 | 264 |
| 285 | Major intrinsic protein | MIP | 262 | 262 |
| 286 | Uncharacterised protein family (UPF0075) | UPF0075 | 261 | 261 |
| 287 | ATP-grasp domain | ATP-grasp | 261 | 261 |
| 288 | Bacterial Fe(2+) trafficking | Iron\_traffic | 260 | 260 |
| 289 | Putative heavy-metal-binding | YbjQ\_1 | 259 | 259 |
| 290 | UreD urease accessory protein | UreD | 259 | 259 |
| 291 | Uncharacterized ACR, YdiU/UPF0061 family | UPF0061 | 259 | 259 |
| 292 | UDP-glucoronosyl and UDP-glucosyl transferase | UDPGT | 258 | 258 |
| 293 | Zinc finger C-x8-C-x5-C-x3-H type (and similar) | zf-CCCH | 257 | 257 |
| 294 | Molybdopterin oxidoreductase | Molybdopterin | 257 | 257 |
| 295 | Aromatic amino acid lyase | Lyase\_aromatic | 257 | 257 |
| 296 | Competence-damaged protein | CinA | 257 | 257 |
| 297 | Reverse transcriptase (RNA-dependent DNA polymerase) | RVT\_1 | 256 | 256 |
| 298 | Pyridoxal phosphate biosynthesis protein PdxJ | PdxJ | 255 | 255 |
| 299 | impB/mucB/samB family | IMS | 255 | 255 |
| 300 | Lipid-A-disaccharide synthetase | LpxB | 253 | 253 |
| 301 | Cytochrome C and Quinol oxidase polypeptide I | COX1 | 252 | 252 |
| 302 | bZIP transcription factor | bZIP\_1 | 252 | 252 |
| 303 | Protein phosphatase 2C | PP2C | 251 | 251 |
| 304 | Sodium/hydrogen exchanger family | Na\_H\_Exchanger | 249 | 249 |
| 305 | SNO glutamine amidotransferase family | SNO | 248 | 248 |
| 306 | Neurotransmitter-gated ion-channel ligand binding domain | Neur\_chan\_LBD | 246 | 246 |
| 307 | Spermine/spermidine synthase | Spermine\_synth | 245 | 245 |
| 308 | NADH-ubiquinone/plastoquinone oxidoreductase chain 6 | Oxidored\_q3 | 245 | 245 |
| 309 | Cobalamin-5-phosphate synthase | CobS | 245 | 245 |
| 310 | 3,4-dihydroxy-2-butanone 4-phosphate synthase | DHBP\_synthase | 242 | 242 |
| 311 | Smr domain | Smr | 240 | 240 |
| 312 | SelR domain | SelR | 240 | 240 |
| 313 | Quinolinate synthetase A protein | NadA | 240 | 240 |
| 314 | LamB/YcsF family | LamB\_YcsF | 238 | 238 |
| 315 | Carbon-nitrogen hydrolase | CN\_hydrolase | 237 | 237 |
| 316 | Glycosyl hydrolase family 3 N terminal domain | Glyco\_hydro\_3 | 236 | 236 |
| 317 | Coproporphyrinogen III oxidase | Coprogen\_oxidas | 236 | 236 |
| 318 | Protein of unknown function (DUF552) | DUF552 | 235 | 235 |
| 319 | S-adenosylmethionine decarboxylase | AdoMet\_dc | 235 | 235 |
| 320 | Neurotransmitter-gated ion-channel transmembrane region | Neur\_chan\_memb | 234 | 234 |
| 321 | XPG I-region | XPG\_I | 233 | 233 |
| 322 | PsbL protein | PsbL | 233 | 233 |
| 323 | Intracellular septation protein A | IspA | 232 | 232 |
| 324 | Transglycosylase | Transgly | 228 | 228 |
| 325 | Photosystem II reaction centre N protein (psbN) | PsbN | 228 | 228 |
| 326 | Phosphoenolpyruvate carboxylase | PEPcase | 228 | 228 |
| 327 | Histidinol dehydrogenase | Histidinol\_dh | 228 | 228 |
| 328 | GTP cyclohydrolase II | GTP\_cyclohydro2 | 228 | 228 |
| 329 | XPG N-terminal domain | XPG\_N | 224 | 224 |
| 330 | EamA-like transporter family | EamA | 224 | 224 |
| 331 | Potassium-transporting ATPase A subunit | KdpA | 223 | 223 |
| 332 | Bacterial regulatory proteins, gntR family | GntR | 223 | 223 |
| 333 | Protein of unknown function (DUF1328) | DUF1328 | 221 | 221 |
| 334 | Haemagglutinin | Hemagglutinin | 219 | 219 |
| 335 | ArgJ family | ArgJ | 219 | 219 |
| 336 | UreF | UreF | 218 | 218 |
| 337 | HAMP domain | HAMP | 218 | 218 |
| 338 | Uncharacterised BCR, YnfA/UPF0060 family | UPF0060 | 216 | 216 |
| 339 | Peptidase family M28 | Peptidase\_M28 | 216 | 216 |
| 340 | Nitrite and sulphite reductase 4Fe-4S domain | NIR\_SIR | 215 | 215 |
| 341 | HPr Serine kinase N terminus | Hpr\_kinase\_N | 214 | 214 |
| 342 | Thymidine kinase | TK | 213 | 213 |
| 343 | Ribosomal S3Ae family | Ribosomal\_S3Ae | 213 | 213 |
| 344 | RNA pseudouridylate synthase | PseudoU\_synth\_2 | 212 | 212 |
| 345 | Mammalian taste receptor protein (TAS2R) | TAS2R | 211 | 211 |
| 346 | Leucine carboxyl methyltransferase | LCM | 211 | 211 |
| 347 | K+-transporting ATPase, c chain | KdpC | 210 | 210 |
| 348 | Domain of unknown function (DUF3552) | DUF3552 | 210 | 210 |
| 349 | Cytochrome c oxidase subunit III | COX3 | 209 | 209 |
| 350 | Type I GTP cyclohydrolase folE2 | GCHY-1 | 208 | 208 |
| 351 | Receptor family ligand binding region | ANF\_receptor | 208 | 208 |
| 352 | Peptidase family M41 | Peptidase\_M41 | 207 | 207 |
| 353 | SOR/SNZ family | SOR\_SNZ | 206 | 206 |
| 354 | Cytidine and deoxycytidylate deaminase zinc-binding region | dCMP\_cyt\_deam\_1 | 206 | 206 |
| 355 | Protein kinase C terminal domain | Pkinase\_C | 205 | 205 |
| 356 | NOL1/NOP2/sun family | Nol1\_Nop2\_Fmu | 204 | 204 |
| 357 | JAB1/Mov34/MPN/PAD-1 ubiquitin protease | JAB | 204 | 204 |
| 358 | Homoserine O-succinyltransferase | HTS | 202 | 202 |
| 359 | Eukaryotic aspartyl protease | Asp | 202 | 202 |
| 360 | Putative undecaprenyl diphosphate synthase | Prenyltransf | 201 | 201 |
| 361 | NifU-like domain | NifU | 201 | 201 |
| 362 | Bacterial DNA polymerase III alpha subunit | DNA\_pol3\_alpha | 201 | 201 |
| 363 | tRNA pseudouridine synthase D (TruD) | TruD | 200 | 200 |
| 364 | ThiF family | ThiF | 200 | 200 |
| 365 | ATP-dependent protease La (LON) domain | LON | 199 | 199 |
| 366 | Ferric reductase like transmembrane component | Ferric\_reduct | 199 | 199 |
| 367 | ABC1 family | ABC1 | 199 | 199 |
| 368 | wnt family | wnt | 195 | 195 |
| 369 | Periviscerokinin family | Periviscerokin | 195 | 195 |
| 370 | Reprolysin family propeptide | Pep\_M12B\_propep | 195 | 195 |
| 371 | gag gene protein p24 (core nucleocapsid protein) | Gag\_p24 | 195 | 195 |
| 372 | Arginine-tRNA-protein transferase, C terminus | ATE\_C | 195 | 195 |
| 373 | Sir2 family | SIR2 | 194 | 194 |
| 374 | Arginine-tRNA-protein transferase, N terminus | ATE\_N | 194 | 194 |
| 375 | Putative SAM-dependent methyltransferase | SAM\_MT | 193 | 193 |
| 376 | Flagellar P-ring protein | FlgI | 191 | 191 |
| 377 | Thrombospondin type 1 domain | TSP\_1 | 190 | 190 |
| 378 | Voltage gated chloride channel | Voltage\_CLC | 189 | 189 |
| 379 | Demethylmenaquinone methyltransferase | Methyltransf\_6 | 189 | 189 |
| 380 | FAD binding domain | FAD\_binding\_3 | 188 | 188 |
| 381 | Protein of unknown function (DUF525) | DUF525 | 188 | 188 |
| 382 | DHHC palmitoyltransferase | zf-DHHC | 187 | 187 |
| 383 | B3 DNA binding domain | B3 | 187 | 187 |
| 384 | Protease inhibitor/seed storage/LTP family | Tryp\_alpha\_amyl | 184 | 184 |
| 385 | Predicted Permease Membrane Region | Asp-Al\_Ex | 184 | 184 |
| 386 | Malate:quinone oxidoreductase (Mqo) | Mqo | 183 | 183 |
| 387 | Protein of unknown function (DUF1698) | Methyltransf\_9 | 183 | 183 |
| 388 | Glutaminase | Glutaminase | 182 | 182 |
| 389 | Clp amino terminal domain | Clp\_N | 182 | 182 |
| 390 | CbiD | CbiD | 182 | 182 |
| 391 | Photosystem II reaction centre T protein | PsbT | 181 | 181 |
| 392 | 7 transmembrane receptor (Secretin family) | 7tm\_2 | 181 | 181 |
| 393 | TGF-beta propeptide | TGFb\_propeptide | 179 | 179 |
| 394 | Flagellar L-ring protein | FlgH | 179 | 179 |
| 395 | Domain of unknown function DUF | DUF204 | 179 | 179 |
| 396 | ZIP Zinc transporter | Zip | 178 | 178 |
| 397 | Viral (Superfamily 1) RNA helicase | Viral\_helicase1 | 178 | 178 |
| 398 | Prismane/CO dehydrogenase family | Prismane | 178 | 178 |
| 399 | HlyD family secretion protein | HlyD | 178 | 178 |
| 400 | Cytochrome oxidase assembly protein | COX15-CtaA | 177 | 177 |
| 401 | Diacylglycerol kinase catalytic domain | DAGK\_cat | 175 | 175 |
| 402 | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase | UbiD | 172 | 172 |
| 403 | Outer membrane lipoprotein carrier protein LolA | LolA | 172 | 172 |
| 404 | Cytochrome C assembly protein | Cytochrom\_C\_asm | 172 | 172 |
| 405 | Small Multidrug Resistance protein | Multi\_Drug\_Res | 171 | 171 |
| 406 | MatE | MatE | 171 | 171 |
| 407 | Protein of unknown function, DUF480 | DUF480 | 171 | 171 |
| 408 | Amidinotransferase | Amidinotransf | 171 | 171 |
| 409 | Virulence factor BrkB | Virul\_fac\_BrkB | 170 | 170 |
| 410 | Photosystem I reaction centre subunit IX / PsaJ | PSI\_PsaJ | 170 | 170 |
| 411 | Photosystem II reaction centre I protein (PSII 4.8 kDa protein) | PsbI | 170 | 170 |
| 412 | S-adenosylmethionine-dependent methyltransferase | Methyltrans\_SAM | 170 | 170 |
| 413 | MarR family | MarR | 170 | 170 |
| 414 | Influenza virus nucleoprotein | Flu\_NP | 170 | 170 |
| 415 | Urocanase | Urocanase | 168 | 168 |
| 416 | Cytochrome B6-F complex subunit 5 | PetG | 168 | 168 |
| 417 | G-patch domain | G-patch | 168 | 168 |
| 418 | Dehydrogenase E1 component | E1\_dh | 168 | 168 |
| 419 | SlyX | SlyX | 166 | 166 |
| 420 | DsrE/DsrF-like family | DrsE | 166 | 166 |
| 421 | Disulfide bond formation protein DsbB | DsbB | 164 | 164 |
| 422 | Cation efflux family | Cation\_efflux | 164 | 164 |
| 423 | Nicotinate phosphoribosyltransferase (NAPRTase) family | NAPRTase | 163 | 163 |
| 424 | S-adenosyl-L-methionine-dependent methyltransferase | Methyltransf\_30 | 163 | 163 |
| 425 | ROK family | ROK | 162 | 162 |
| 426 | Putative DNA-binding protein N-terminus | Put\_DNA-bind\_N | 162 | 162 |
| 427 | Outer membrane lipoprotein LolB | LolB | 162 | 162 |
| 428 | ARD/ARD family | ARD | 162 | 162 |
| 429 | Oxidoreductase family, NAD-binding Rossmann fold | GFO\_IDH\_MocA | 161 | 161 |
| 430 | NrdI Flavodoxin like | Flavodoxin\_NdrI | 161 | 161 |
| 431 | SRP54-type protein, GTPase domain | SRP54 | 160 | 160 |
| 432 | Phosphotransferase system, EIIC | PTS\_EIIC | 160 | 160 |
| 433 | Leucine rich repeat N-terminal domain | LRRNT\_2 | 159 | 159 |
| 434 | Protein of unknown function (DUF441) | DUF441 | 159 | 159 |
| 435 | SpoU rRNA Methylase family | SpoU\_methylase | 158 | 158 |
| 436 | Transcriptional regulator | Transcrip\_reg | 158 | 158 |
| 437 | Rab-GTPase-TBC domain | RabGAP-TBC | 158 | 158 |
| 438 | PsbJ | PsbJ | 158 | 158 |
| 439 | Tetraspanin family | Tetraspannin | 157 | 157 |
| 440 | DNA gyrase/topoisomerase IV, subunit A | DNA\_topoisoIV | 156 | 156 |
| 441 | Septum formation initiator | DivIC | 156 | 156 |
| 442 | SecY translocase | SecY | 155 | 155 |
| 443 | HIGH Nucleotidyl Transferase | HIGH\_NTase1 | 155 | 155 |
| 444 | PetN | PetN | 154 | 154 |
| 445 | Pyridoxal phosphate biosynthetic protein PdxA | PdxA | 154 | 154 |
| 446 | CheD chemotactic sensory transduction | CheD | 154 | 154 |
| 447 | ABC-2 type transporter | ABC2\_membrane | 154 | 154 |
| 448 | FAD binding domain | FAD\_binding\_2 | 153 | 153 |
| 449 | Domain of unknown function (DUF3410) | DUF3410 | 152 | 152 |
| 450 | ATP dependent DNA ligase C terminal region | DNA\_ligase\_A\_C | 152 | 152 |
| 451 | Aspartate-ammonia ligase | AsnA | 152 | 152 |
| 452 | Sodium:solute symporter family | SSF | 151 | 151 |
| 453 | SNARE domain | SNARE | 151 | 151 |
| 454 | Homeobox KN domain | Homeobox\_KN | 151 | 151 |
| 455 | Protein of unknown function (DUF489) | DUF489 | 151 | 151 |
| 456 | DNA ligase N terminus | DNA\_ligase\_A\_N | 151 | 151 |
| 457 | Ycf4 | Ycf4 | 150 | 150 |
| 458 | FtsX-like permease family | FtsX | 150 | 150 |
| 459 | FHA domain | FHA | 150 | 150 |
| 460 | AcrB/AcrD/AcrF family | ACR\_tran | 150 | 150 |
| 461 | Sulfatase | Sulfatase | 149 | 149 |
| 462 | Dihydrouridine synthase (Dus) | Dus | 149 | 149 |
| 463 | Succinylglutamate desuccinylase / Aspartoacylase family | AstE\_AspA | 149 | 149 |
| 464 | Natural resistance-associated macrophage protein | Nramp | 148 | 148 |
| 465 | Phosphatidylinositol 3- and 4-kinase | PI3\_PI4\_kinase | 147 | 147 |
| 466 | GDSL-like Lipase/Acylhydrolase | Lipase\_GDSL | 146 | 146 |
| 467 | DNA polymerase family B | DNA\_pol\_B | 146 | 146 |
| 468 | Cation transporting ATPase, C-terminus | Cation\_ATPase\_C | 146 | 146 |
| 469 | Pyridoxal-dependent decarboxylase conserved domain | Pyridoxal\_deC | 145 | 145 |
| 470 | NADPH-dependent FMN reductase | FMN\_red | 145 | 145 |
| 471 | Sulfurtransferase TusA | TusA | 144 | 144 |
| 472 | Putative N-acetylmannosamine-6-phosphate epimerase | NanE | 144 | 144 |
| 473 | Protein of unknown function (DUF494) | DUF494 | 144 | 144 |
| 474 | Chorismate lyase | Chor\_lyase | 144 | 144 |
| 475 | CemA family | CemA | 144 | 144 |
| 476 | Neuraminidase | Neur | 143 | 143 |
| 477 | NADH dehydrogenase subunit 2 C-terminus | NADH\_dehy\_S2\_C | 143 | 143 |
| 478 | Hydrogenase expression/synthesis hypA family | HypA | 143 | 143 |
| 479 | Protein of unknown function (DUF615) | DUF615 | 143 | 143 |
| 480 | 60s Acidic ribosomal protein | Ribosomal\_60s | 142 | 142 |
| 481 | Serine dehydratase alpha chain | SDH\_alpha | 141 | 141 |
| 482 | Prolyl oligopeptidase family | Peptidase\_S9 | 141 | 141 |
| 483 | Patatin-like phospholipase | Patatin | 141 | 141 |
| 484 | Gram positive anchor | Gram\_pos\_anchor | 141 | 141 |
| 485 | Glucokinase | Glucokinase | 141 | 141 |
| 486 | Bacterial protein of unknown function (DUF965) | DUF965 | 141 | 141 |
| 487 | Cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis | CIAPIN1 | 141 | 141 |
| 488 | RNA dependent RNA polymerase | RdRP\_2 | 140 | 140 |
| 489 | DNA polymerase family B, exonuclease domain | DNA\_pol\_B\_exo1 | 140 | 140 |
| 490 | Catalase-related immune-responsive | Catalase-rel | 140 | 140 |
| 491 | Putative exonuclease, RdgC | RdgC | 139 | 139 |
| 492 | Phosphomethylpyrimidine kinase | Phos\_pyr\_kin | 139 | 139 |
| 493 | Methyltransferase small domain N-terminal | MTS\_N | 139 | 139 |
| 494 | Flagellar hook-basal body complex protein FliE | FliE | 139 | 139 |
| 495 | Protein of unknown function, DUF576 | DUF576 | 138 | 138 |
| 496 | Putative zinc- or iron-chelating domain | CxxCxxCC | 138 | 138 |
| 497 | Succinylarginine dihydrolase | AstB | 138 | 138 |
| 498 | Photosystem II reaction centre M protein (PsbM) | PsbM | 137 | 137 |
| 499 | Protein of unknown function (DUF890) | Methyltransf\_10 | 135 | 135 |
| 500 | RasGEF domain | RasGEF | 134 | 134 |
| 501 | LrgA family | LrgA | 133 | 133 |
| 502 | Putative helix-turn-helix protein, YlxM / p13 like | UPF0122 | 132 | 132 |
| 503 | L-seryl-tRNA selenium transferase | SelA | 132 | 132 |
| 504 | MacB-like periplasmic core domain | MacB\_PCD | 132 | 132 |
| 505 | Endonuclease V | Endonuclease\_5 | 132 | 132 |
| 506 | SPFH domain / Band 7 family | Band\_7 | 131 | 131 |
| 507 | NQR2, RnfD, RnfE family | NQR2\_RnfD\_RnfE | 130 | 130 |
| 508 | Leucine rich repeat N-terminal domain | LRRNT | 130 | 130 |
| 509 | Glutamate-cysteine ligase family 2(GCS2) | GCS2 | 130 | 130 |
| 510 | Rhomboid family | Rhomboid | 129 | 129 |
| 511 | Sema domain | Sema | 128 | 128 |
| 512 | F-box associated | FBA\_1 | 128 | 128 |
| 513 | Protein of unknown function (DUF402) | DUF402 | 128 | 128 |
| 514 | Putative transcriptional regulators (Ypuh-like) | DUF387 | 128 | 128 |
| 515 | Cytochrome B6-F complex subunit VI (PetL) | PetL | 127 | 127 |
| 516 | NADH-Ubiquinone oxidoreductase (complex I) subunit C-terminus | Oxidored\_q1\_C | 127 | 127 |
| 517 | NAC domain | NAC | 127 | 127 |
| 518 | Ribose/Galactose Isomerase | LacAB\_rpiB | 127 | 127 |
| 519 | Influenza non-structural protein (NS1) | Flu\_NS1 | 127 | 127 |
| 520 | D-mannonate dehydratase (UxuA) | UxuA | 126 | 126 |
| 521 | Bacterial Na+/H+ antiporter B (NhaB) | NhaB | 126 | 126 |
| 522 | Photosystem II 4 kDa reaction centre component | PsbK | 125 | 125 |
| 523 | ParA/MinD ATPase like | ParA | 125 | 125 |
| 524 | Tetrahydrodipicolinate succinyltransferase N-terminal | DapH\_N | 125 | 125 |
| 525 | Lumenal portion of Cytochrome b559, alpha (gene psbE) subunit | Cytochrom\_B559a | 125 | 125 |
| 526 | Photosystem II 10 kDa phosphoprotein | PsbH | 124 | 124 |
| 527 | Influenza non-structural protein (NS2) | Flu\_NS2 | 124 | 124 |
| 528 | Dynamin family | Dynamin\_N | 124 | 124 |
| 529 | Protein of unknown function (DUF444) | DUF444 | 124 | 124 |
| 530 | HpcH/HpaI aldolase/citrate lyase family | HpcH\_HpaI | 123 | 123 |
| 531 | Protein of unknown function (DUF964) | DUF964 | 123 | 123 |
| 532 | Protein of unknown function (DUF1292) | DUF1292 | 123 | 123 |
| 533 | Transmembrane amino acid transporter protein | Aa\_trans | 123 | 123 |
| 534 | POT family | PTR2 | 122 | 122 |
| 535 | Insulinase (Peptidase family M16) | Peptidase\_M16 | 122 | 122 |
| 536 | Organic solvent tolerance protein | OstA\_C | 122 | 122 |
| 537 | FdhD/NarQ family | FdhD-NarQ | 122 | 122 |
| 538 | Brevenin/esculentin/gaegurin/rugosin family | Brevenin | 122 | 122 |
| 539 | TIR domain | TIR | 121 | 121 |
| 540 | DHH family | DHH | 121 | 121 |
| 541 | Ubiquinone biosynthesis protein COQ7 | COQ7 | 121 | 121 |
| 542 | Amino acid permease | AA\_permease | 121 | 121 |
| 543 | DNA topoisomerase | Topoisom\_bac | 120 | 120 |
| 544 | SCAN domain | SCAN | 120 | 120 |
| 545 | PMP-22/EMP/MP20/Claudin family | PMP22\_Claudin | 120 | 120 |
| 546 | Winged helix-turn-helix transcription repressor, HrcA DNA-binding | HrcA\_DNA-bdg | 120 | 120 |
| 547 | Complex 1 protein (LYR family) | Complex1\_LYR | 120 | 120 |
| 548 | Isocitrate dehydrogenase kinase/phosphatase (AceK) | AceK | 120 | 120 |
| 549 | Viral methyltransferase | Vmethyltransf | 119 | 119 |
| 550 | ScpA/B protein | ScpA\_ScpB | 119 | 119 |
| 551 | K-box region | K-box | 119 | 119 |
| 552 | Glutamate-cysteine ligase | Glu\_cys\_ligase | 119 | 119 |
| 553 | CorA-like Mg2+ transporter protein | CorA | 119 | 119 |
| 554 | Chlorophyll A-B binding protein | Chloroa\_b-bind | 119 | 119 |
| 555 | AUX/IAA family | AUX\_IAA | 119 | 119 |
| 556 | FtsK/SpoIIIE family | FtsK\_SpoIIIE | 118 | 118 |
| 557 | 37-kD nucleoid-associated bacterial protein | NA37 | 117 | 117 |
| 558 | PcrB family | PcrB | 116 | 116 |
| 559 | PAP2 superfamily | PAP2 | 116 | 116 |
| 560 | ATP synthase protein 8 | ATP-synt\_8 | 116 | 116 |
| 561 | ATP synthase (E/31 kDa) subunit | vATP-synt\_E | 115 | 115 |
| 562 | Snf7 | Snf7 | 115 | 115 |
| 563 | Periplasmic glucan biosynthesis protein, MdoG | MdoG | 115 | 115 |
| 564 | Retroviral envelope protein | GP41 | 115 | 115 |
| 565 | Influenza Matrix protein (M2) | Flu\_M2 | 115 | 115 |
| 566 | Domain of unknown function (DUF370) | DUF370 | 115 | 115 |
| 567 | RnfH family Ubiquitin | Ub-RnfH | 114 | 114 |
| 568 | Peptidase family M1 | Peptidase\_M1 | 114 | 114 |
| 569 | Proto-chlorophyllide reductase 57 kD subunit | PCP\_red | 114 | 114 |
| 570 | ATP synthase subunit D | ATP-synt\_D | 114 | 114 |
| 571 | L-arabinose isomerase | Arabinose\_Isome | 114 | 114 |
| 572 | Peptide hormone | Hormone\_2 | 113 | 113 |
| 573 | Dipeptidyl peptidase IV (DPP IV) N-terminal region | DPPIV\_N | 113 | 113 |
| 574 | Adaptin N terminal region | Adaptin\_N | 113 | 113 |
| 575 | Protein export membrane protein | SecD\_SecF | 112 | 112 |
| 576 | Ribosomal protein S8e | Ribosomal\_S8e | 112 | 112 |
| 577 | MHC\_I C-terminus | MHC\_I\_C | 112 | 112 |
| 578 | Glutathione peroxidase | GSHPx | 112 | 112 |
| 579 | Protein of unknown function (DUF1273) | DUF1273 | 112 | 112 |
| 580 | Polysaccharide deacetylase | Polysacc\_deac\_1 | 111 | 111 |
| 581 | ADAM cysteine-rich | ADAM\_CR | 111 | 111 |
| 582 | Malonate decarboxylase delta subunit (MdcD) | ACP | 111 | 111 |
| 583 | Plexin repeat | PSI | 110 | 110 |
| 584 | Myosin tail | Myosin\_tail\_1 | 110 | 110 |
| 585 | Isochorismatase family | Isochorismatase | 110 | 110 |
| 586 | FliW protein | FliW | 110 | 110 |
| 587 | Trans-2-enoyl-CoA reductase catalytic region | Enoyl\_reductase | 110 | 110 |
| 588 | Enoyl reductase FAD binding domain | Eno-Rase\_FAD\_bd | 110 | 110 |
| 589 | Connexin | Connexin | 110 | 110 |
| 590 | PEP-utilising enzyme, mobile domain | PEP-utilizers | 109 | 109 |
| 591 | Inositol monophosphatase family | Inositol\_P | 109 | 109 |
| 592 | Cytidine and deoxycytidylate deaminase zinc-binding region | dCMP\_cyt\_deam\_1 | 109 | 109 |
| 593 | Atrial natriuretic peptide | ANP | 109 | 109 |
| 594 | Ligand-gated ion channel | Lig\_chan | 108 | 108 |
| 595 | GRAM domain | GRAM | 108 | 108 |
| 596 | Influenza RNA-dependent RNA polymerase subunit PB2 | Flu\_PB2 | 108 | 108 |
| 597 | DNA gyrase B subunit, carboxyl terminus | DNA\_gyraseB\_C | 108 | 108 |
| 598 | 7 transmembrane sweet-taste receptor of 3 GCPR | 7tm\_3 | 108 | 108 |
| 599 | Triose-phosphate Transporter family | TPT | 107 | 107 |
| 600 | FtsH Extracellular | FtsH\_ext | 107 | 107 |
| 601 | Influenza RNA-dependent RNA polymerase subunit PB1 | Flu\_PB1 | 107 | 107 |
| 602 | Protein of unknown function (DUF904) | DUF904 | 107 | 107 |
| 603 | Uncharacterized protein conserved in bacteria (DUF2309) | DUF2309 | 107 | 107 |
| 604 | CDP-alcohol phosphatidyltransferase | CDP-OH\_P\_transf | 107 | 107 |
| 605 | Uncharacterised protein family (UPF0182) | UPF0182 | 106 | 106 |
| 606 | TonB dependent receptor | TonB\_dep\_Rec | 106 | 106 |
| 607 | Selenocysteine synthase N terminal | Se-cys\_synth\_N | 106 | 106 |
| 608 | von Willebrand factor type C domain | VWC | 105 | 105 |
| 609 | Salt stress response/antifungal | Stress-antifung | 105 | 105 |
| 610 | SpoVG | SpoVG | 105 | 105 |
| 611 | Pyruvate kinase, barrel domain | PK | 105 | 105 |
| 612 | Cell division protein FtsQ | FtsQ | 105 | 105 |
| 613 | Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold | eIF-5a | 105 | 105 |
| 614 | Trehalase | Trehalase | 104 | 104 |
| 615 | Ribosomal family S4e | Ribosomal\_S4e | 104 | 104 |
| 616 | Influenza RNA-dependent RNA polymerase subunit PA | Flu\_PA | 104 | 104 |
| 617 | YCF9 | Ycf9 | 103 | 103 |
| 618 | Ribonucleotide reductase, barrel domain | Ribonuc\_red\_lgC | 103 | 103 |
| 619 | PA domain | PA | 103 | 103 |
| 620 | Hormone receptor domain | HRM | 103 | 103 |
| 621 | Protein of unknown function (DUF1250) | DUF1250 | 103 | 103 |
| 622 | DHHA2 domain | DHHA2 | 103 | 103 |
| 623 | CsbD-like | CsbD | 103 | 103 |
| 624 | Coenzyme Q (ubiquinone) biosynthesis protein Coq4 | Coq4 | 103 | 103 |
| 625 | POTRA domain, FtsQ-type | POTRA\_1 | 102 | 102 |
| 626 | Latrophilin/CL-1-like GPS domain | GPS | 102 | 102 |
| 627 | Protein of unknown function (DUF1447) | DUF1447 | 102 | 102 |
| 628 | Ammonium Transporter Family | Ammonium\_transp | 102 | 102 |
| 629 | DJ-1/PfpI family | DJ-1\_PfpI | 101 | 101 |
| 630 | CutC family | CutC | 101 | 101 |
| 631 | Dolichyl-phosphate-mannose-protein mannosyltransferase | PMT | 100 | 100 |
| 632 | Malate synthase | Malate\_synthase | 100 | 100 |
| 633 | Laminin EGF-like (Domains III and V) | Laminin\_EGF | 100 | 100 |
| 634 | Bacterial flagellin N-terminal helical region | Flagellin\_N | 100 | 100 |
| 635 | FecCD transport family | FecCD | 100 | 100 |
| 636 | Uncharacterised ACR (DUF711) | DUF711 | 100 | 100 |
| 637 | Protein of unknown function (DUF1445) | DUF1445 | 100 | 100 |
| 638 | Thiopurine S-methyltransferase (TPMT) | TPMT | 99 | 99 |
| 639 | Syd protein (SUKH-2) | Syd | 99 | 99 |
| 640 | Prefoldin subunit | Prefoldin | 99 | 99 |
| 641 | Pectinesterase | Pectinesterase | 99 | 99 |
| 642 | Bacterial flagellin C-terminal helical region | Flagellin\_C | 99 | 99 |
| 643 | Protein of unknown function (DUF1414) | DUF1414 | 99 | 99 |
| 644 | Uncharacterized protein family, UPF0114 | UPF0114 | 98 | 98 |
| 645 | UAA transporter family | UAA | 98 | 98 |
| 646 | SAP domain | SAP | 98 | 98 |
| 647 | OstA-like protein | OstA | 98 | 98 |
| 648 | NADH dehydrogenase subunit 5 C-terminus | NADH5\_C | 98 | 98 |
| 649 | Protein of unknown function (DUF1342) | DUF1342 | 98 | 98 |
| 650 | Cadherin cytoplasmic region | Cadherin\_C | 98 | 98 |
| 651 | Uncharacterised protein family (UPF0154) | UPF0154 | 97 | 97 |
| 652 | Tryptophan 2,3-dioxygenase | Trp\_dioxygenase | 97 | 97 |
| 653 | Synaptobrevin | Synaptobrevin | 97 | 97 |
| 654 | Sodium:neurotransmitter symporter family | SNF | 97 | 97 |
| 655 | Sigma-70 region 3 | Sigma70\_r3 | 97 | 97 |
| 656 | Ribosomal protein L24e | Ribosomal\_L24e | 97 | 97 |
| 657 | Fz domain | Fz | 97 | 97 |
| 658 | chorismate binding enzyme | Chorismate\_bind | 97 | 97 |
| 659 | Formin Homology 2 Domain | FH2 | 96 | 96 |
| 660 | Uncharacterised protein family (UPF0270) | UPF0270 | 95 | 95 |
| 661 | Ribosomal L15 | Ribosomal\_L15e | 95 | 95 |
| 662 | Protein of unknown function DUF84 | NTPase\_I-T | 95 | 95 |
| 663 | LysE type translocator | LysE | 95 | 95 |
| 664 | JmjC domain, hydroxylase | JmjC | 95 | 95 |
| 665 | Glycosyl transferase family 8 | Glyco\_transf\_8 | 95 | 95 |
| 666 | DivIVA protein | DivIVA | 95 | 95 |
| 667 | Surface antigen | Bac\_surface\_Ag | 95 | 95 |
| 668 | Annexin | Annexin | 95 | 95 |
| 669 | MYND finger | zf-MYND | 94 | 94 |
| 670 | Cell division protein ZapA | ZapA | 94 | 94 |
| 671 | Nitrate reductase delta subunit | Nitrate\_red\_del | 94 | 94 |
| 672 | MIF4G domain | MIF4G | 94 | 94 |
| 673 | Branched-chain amino acid transport system / permease component | BPD\_transp\_2 | 94 | 94 |
| 674 | Septin | Septin | 93 | 93 |
| 675 | Photosystem I reaction centre subunit VIII | PSI\_8 | 93 | 93 |
| 676 | Glycosyl hydrolases family 35 | Glyco\_hydro\_35 | 93 | 93 |
| 677 | Ppx/GppA phosphatase family | Ppx-GppA | 92 | 92 |
| 678 | Phosphoenolpyruvate carboxykinase | PEPCK\_ATP | 92 | 92 |
| 679 | Uncharacterized protein conserved in bacteria (DUF2179) | DUF2179 | 92 | 92 |
| 680 | Respiratory-chain NADH dehydrogenase 51 Kd subunit | Complex1\_51K | 92 | 92 |
| 681 | Frog antimicrobial peptide | Antimicrobial\_2 | 92 | 92 |
| 682 | Ribosomal protein S6e | Ribosomal\_S6e | 91 | 91 |
| 683 | Carbohydrate kinase | Carb\_kinase | 91 | 91 |
| 684 | TYA transposon protein | TYA | 90 | 90 |
| 685 | Lactonase, 7-bladed beta-propeller | Lactonase | 90 | 90 |
| 686 | Protein of unknown function (DUF1450) | DUF1450 | 90 | 90 |
| 687 | YdjC-like protein | YdjC | 89 | 89 |
| 688 | Alpha conotoxin precursor | Toxin\_8 | 89 | 89 |
| 689 | Root hair defective 3 GTP-binding protein (RHD3) | RHD3 | 89 | 89 |
| 690 | Prefoldin subunit | Prefoldin | 89 | 89 |
| 691 | PAZ domain | PAZ | 89 | 89 |
| 692 | HB1, ASXL, restriction endonuclease HTH domain | HARE-HTH | 89 | 89 |
| 693 | FBD | FBD | 89 | 89 |
| 694 | Domain of unknown function (DUF3378) | DUF3378 | 89 | 89 |
| 695 | Maintenance of mitochondrial structure and function | MitMem\_reg | 88 | 88 |
| 696 | Fes/CIP4, and EFC/F-BAR homology domain | FCH | 88 | 88 |
| 697 | Protein of unknown function (DUF972) | DUF972 | 88 | 88 |
| 698 | ParB-like nuclease domain | ParBc | 87 | 87 |
| 699 | NLI interacting factor-like phosphatase | NIF | 87 | 87 |
| 700 | Cell cycle protein | FTSW\_RODA\_SPOVE | 87 | 87 |
| 701 | Protein involved in formate dehydrogenase formation | FdhE | 87 | 87 |
| 702 | Septation ring formation regulator, EzrA | ECF-ribofla\_trS | 87 | 87 |
| 703 | ECF-type riboflavin transporter, S component | ECF-ribofla\_trS | 87 | 87 |
| 704 | Conserved hypothetical protein 698 | Cons\_hypoth698 | 87 | 87 |
| 705 | Ribosomal S17 | Ribosomal\_S17e | 86 | 86 |
| 706 | FadR C-terminal domain | FadR\_C | 86 | 86 |
| 707 | Protein of unknown function (DUF3650) | DUF3650 | 86 | 86 |
| 708 | Uncharacterized protein conserved in bacteria (DUF2057) | DUF2057 | 86 | 86 |
| 709 | Telomere recombination | Sua5\_yciO\_yrdC | 85 | 85 |
| 710 | SNARE associated Golgi protein | SNARE\_assoc | 85 | 85 |
| 711 | Ribosomal protein L31e | Ribosomal\_L31e | 85 | 85 |
| 712 | Ribulose-1,5-bisphosphate carboxylase small subunit | RbcS | 85 | 85 |
| 713 | Phosphatidylinositol-specific phospholipase C, X domain | PI-PLC-X | 85 | 85 |
| 714 | Pancreatic hormone peptide | Hormone\_3 | 85 | 85 |
| 715 | Protein of unknown function (DUF496) | DUF496 | 85 | 85 |
| 716 | Tropomyosin | Tropomyosin | 84 | 84 |
| 717 | NADH-ubiquinone oxidoreductase chain 4, amino terminus | Oxidored\_q5\_N | 84 | 84 |
| 718 | Oligopeptide/dipeptide transporter, C-terminal region | oligo\_HPY | 84 | 84 |
| 719 | homogentisate 1,2-dioxygenase | HgmA | 84 | 84 |
| 720 | Beta-eliminating lyase | Beta\_elim\_lyase | 84 | 84 |
| 721 | Fumarylacetoacetate (FAA) hydrolase family | FAA\_hydrolase | 83 | 83 |
| 722 | eIF-6 family | eIF-6 | 83 | 83 |
| 723 | Plant protein of unknown function (DUF825) | DUF825 | 83 | 83 |
| 724 | Guanylyl transferase CofC like | CofC | 83 | 83 |
| 725 | Uncharacterised protein family (UPF0231) | UPF0231 | 82 | 82 |
| 726 | Papillomavirus helicase | PPV\_E1\_C | 82 | 82 |
| 727 | MCM2/3/5 family | MCM | 82 | 82 |
| 728 | Glycosyltransferase family 29 (sialyltransferase) | Glyco\_transf\_29 | 82 | 82 |
| 729 | Glycosyltransferase family 20 | Glyco\_transf\_20 | 82 | 82 |
| 730 | Galactosyltransferase | Galactosyl\_T | 82 | 82 |
| 731 | Acyltransferase family | Acyl\_transf\_3 | 82 | 82 |
| 732 | Uncharacterised protein family (UPF0227) | UPF0227 | 81 | 81 |
| 733 | Uncharacterised protein family (UPF0181) | UPF0181 | 81 | 81 |
| 734 | ENV polyprotein (coat polyprotein) | TLV\_coat | 81 | 81 |
| 735 | Thymidylate synthase complementing protein | Thy1 | 81 | 81 |
| 736 | Sigma-70 factor, region 1.2 | Sigma70\_r1\_2 | 81 | 81 |
| 737 | SecE/Sec61-gamma subunits of protein translocation complex | SecE | 81 | 81 |
| 738 | Domain of Unknown function (DUF542) | ScdA\_N | 81 | 81 |
| 739 | Pup-ligase protein | Pup\_ligase | 81 | 81 |
| 740 | Late Protein L2 | Late\_protein\_L2 | 81 | 81 |
| 741 | e3 binding domain | E3\_binding | 81 | 81 |
| 742 | Protein of unknown function, DUF412 | DUF412 | 81 | 81 |
| 743 | Putative integral membrane protein conserved region (DUF2404) | DUF2404 | 81 | 81 |
| 744 | Alpha crystallin A chain, N terminal | Crystallin | 81 | 81 |
| 745 | Insect cuticle protein | Chitin\_bind\_4 | 81 | 81 |
| 746 | VPR/VPX protein | VPR | 80 | 80 |
| 747 | Ureidoglycolate hydrolase | Ureidogly\_hydro | 80 | 80 |
| 748 | Ribosomal L39 protein | Ribosomal\_L39 | 80 | 80 |
| 749 | E1 Protein, N terminal domain | PPV\_E1\_N | 80 | 80 |
| 750 | O-methyltransferase | Methyltransf\_2 | 80 | 80 |
| 751 | Eukaryotic and archaeal DNA primase small subunit | DNA\_primase\_S | 80 | 80 |
| 752 | CoA-transferase family III | CoA\_transf\_3 | 80 | 80 |
| 753 | Caveolin | Caveolin | 80 | 80 |
| 754 | Zona pellucida-like domain | Zona\_pellucida | 79 | 79 |
| 755 | Ycf1 | Ycf1 | 79 | 79 |
| 756 | Ribosomal protein L37e | Ribosomal\_L37e | 79 | 79 |
| 757 | HSF-type DNA-binding | HSF\_DNA-bind | 79 | 79 |
| 758 | E7 protein, Early protein | E7 | 79 | 79 |
| 759 | Uncharacterised protein, DegV family COG1307 | DegV | 79 | 79 |
| 760 | Condensation domain | Condensation | 79 | 79 |
| 761 | Der GTPase activator (YihI) | YihI | 78 | 78 |
| 762 | VHS domain | VHS | 78 | 78 |
| 763 | TENA/THI-4/PQQC family | TENA\_THI-4 | 78 | 78 |
| 764 | Surface antigen variable number repeat | Surf\_Ag\_VNR | 78 | 78 |
| 765 | E2 (early) protein, N terminal | PPV\_E2\_N | 78 | 78 |
| 766 | Peptidase family M50 | Peptidase\_M50 | 78 | 78 |
| 767 | Mononegavirales RNA dependent RNA polymerase | Mononeg\_RNA\_pol | 78 | 78 |
| 768 | MoaE protein | Mononeg\_RNA\_pol | 78 | 78 |
| 769 | Uncharacterized protein conserved in bacteria (DUF2129) | DUF2129 | 78 | 78 |
| 770 | Uncharacterised protein family (UPF0223) | UPF0223 | 77 | 77 |
| 771 | GlcNAc-PI de-N-acetylase | PIG-L | 77 | 77 |
| 772 | Met-10+ like-protein | Met\_10 | 77 | 77 |
| 773 | KicB killing factor | KicB | 77 | 77 |
| 774 | Envelope glycoprotein GP120 | GP120 | 77 | 77 |
| 775 | Fusaric acid resistance protein family | FUSC | 77 | 77 |
| 776 | Ferric uptake regulator family | FUR | 77 | 77 |
| 777 | NADP oxidoreductase coenzyme F420-dependent | F420\_oxidored | 77 | 77 |
| 778 | Early Protein (E6) | E6 | 77 | 77 |
| 779 | Cytochrome c552 | Cytochrom\_C552 | 77 | 77 |
| 780 | ATP:dephospho-CoA triphosphoribosyl transferase | CitG | 77 | 77 |
| 781 | von Willebrand factor type D domain | VWD | 76 | 76 |
| 782 | Ribosomal L40e family | Ribosomal\_L40e | 76 | 76 |
| 783 | Ribosomal protein L21e | Ribosomal\_L21e | 76 | 76 |
| 784 | REV protein (anti-repression trans-activator protein) | REV | 76 | 76 |
| 785 | Phospholipase D Active site motif | PLDc | 76 | 76 |
| 786 | 3C cysteine protease (picornain 3C) | Peptidase\_C3 | 76 | 76 |
| 787 | MukB N-terminal | MukB | 76 | 76 |
| 788 | Negative regulator of genetic competence (MecA) | MecA | 76 | 76 |
| 789 | Lipase (class 3) | Lipase\_3 | 76 | 76 |
| 790 | Domain found in IF2B/IF5 | eIF-5\_eIF-2B | 76 | 76 |
| 791 | Piwi domain | Piwi | 75 | 75 |
| 792 | Peptidase family S51 | Peptidase\_S51 | 75 | 75 |
| 793 | Myosin tail | Myosin\_tail\_1 | 75 | 75 |
| 794 | IBR domain | IBR | 75 | 75 |
| 795 | Histidine phosphatase superfamily (branch 2) | His\_Phos\_2 | 75 | 75 |
| 796 | Dynamin GTPase effector domain | GED | 75 | 75 |
| 797 | Flagella basal body rod protein | Flg\_bb\_rod | 75 | 75 |
| 798 | Dynamin central region | Dynamin\_M | 75 | 75 |
| 799 | Uncharacterized protein conserved in bacteria (DUF2317) | DUF2317 | 75 | 75 |
| 800 | Coiled coil | Coiled | 75 | 75 |
| 801 | Anthranilate synthase component I, N terminal region | Anth\_synt\_I\_N | 75 | 75 |
| 802 | Huwentoxin-II family | Toxin\_20 | 74 | 74 |
| 803 | GINS complex protein | Sld5 | 74 | 74 |
| 804 | Ribosomal protein L32 | Ribosomal\_L32e | 74 | 74 |
| 805 | Ethanolamine ammonia-lyase light chain (EutC) | EutC | 74 | 74 |
| 806 | Putative esterase | Esterase | 74 | 74 |
| 807 | Ecotin | Ecotin | 74 | 74 |
| 808 | Protein of unknown function (DUF3461) | DUF3461 | 74 | 74 |
| 809 | Exportin 1-like protein | Xpo1 | 73 | 73 |
| 810 | Phosphate-starvation-inducible E | PsiE | 73 | 73 |
| 811 | Peptidase family M3 | Peptidase\_M3 | 73 | 73 |
| 812 | Phospholipid methyltransferase | PEMT | 73 | 73 |
| 813 | OmpA family | OmpA | 73 | 73 |
| 814 | Fatty acid hydroxylase superfamily | FA\_hydroxylase | 73 | 73 |
| 815 | Transactivating regulatory protein (Tat) | Tat | 72 | 72 |
| 816 | Fe-S metabolism associated domain | SufE | 72 | 72 |
| 817 | L-rhamnose isomerase (RhaA) | RhaA | 72 | 72 |
| 818 | Eukaryotic translation initiation factor 3 subunit G | eIF3g | 72 | 72 |
| 819 | Domain of unknown function (DUF947) | DUF947 | 72 | 72 |
| 820 | Protein of unknown function (DUF445) | DUF445 | 72 | 72 |
| 821 | Protein of unknown function DUF134 | DUF134 | 72 | 72 |
| 822 | CRISPR associated protein Cas2 | CRISPR\_Cas2 | 72 | 72 |
| 823 | Cecropin family | Cecropin | 72 | 72 |
| 824 | African swine fever virus multigene family 360 protein | ASFV\_360 | 72 | 72 |
| 825 | Calpain family cysteine protease | Peptidase\_C2 | 71 | 71 |
| 826 | Organiser of macrodomain of Terminus of chromosome | MatP | 71 | 71 |
| 827 | Glycosyl transferase WecB/TagA/CpsF family | Glyco\_tran\_WecB | 71 | 71 |
| 828 | Negative factor, (F-Protein) or Nef | F-protein | 71 | 71 |
| 829 | Eukaryotic translation initiation factor eIF2A | eIF2A | 71 | 71 |
| 830 | Domain of unknown function (DUF336) | DUF336 | 71 | 71 |
| 831 | Carboxymuconolactone decarboxylase family | CMD | 71 | 71 |
| 832 | Glycoprotein VP7 | VP7 | 70 | 70 |
| 833 | Sulfate transporter family | Sulfate\_transp | 70 | 70 |
| 834 | Ribosomal protein S24e | Ribosomal\_S24e | 70 | 70 |
| 835 | Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 | PTS\_EIIA\_2 | 70 | 70 |
| 836 | Major prion protein bPrPp - N terminal | Prion\_bPrPp | 70 | 70 |
| 837 | Alpha/beta hydrolase of unknown function (DUF1100) | DUF1100 | 70 | 70 |
| 838 | DEAD\_2 | DEAD\_2 | 70 | 70 |
| 839 | CUE domain | CUE | 70 | 70 |
| 840 | Cytidylyltransferase family | CTP\_transf\_1 | 70 | 70 |
| 841 | Basic region leucine zipper | bZIP\_2 | 70 | 70 |
| 842 | AsnC family | AsnC\_trans\_reg | 70 | 70 |
| 843 | Adaptor complexes medium subunit family | Adap\_comp\_sub | 70 | 70 |
| 844 | Tim17/Tim22/Tim23/Pmp24 family | Tim17 | 69 | 69 |
| 845 | Cell division inhibitor SulA | SulA | 69 | 69 |
| 846 | Phosphatidylinositol-specific phospholipase C, Y domain | PI-PLC-Y | 69 | 69 |
| 847 | Type I phosphodiesterase / nucleotide pyrophosphatase | Phosphodiest | 69 | 69 |
| 848 | Fungalysin metallopeptidase (M36) | Peptidase\_M36 | 69 | 69 |
| 849 | UNC-6/NTR/C345C module | NTR | 69 | 69 |
| 850 | MBOAT, membrane-bound O-acyltransferase family | MBOAT | 69 | 69 |
| 851 | Flagellar transcriptional activator (FlhD) | FlhD | 69 | 69 |
| 852 | Firmicute fructose-1,6-bisphosphatase | FBPase\_2 | 69 | 69 |
| 853 | DsrH like protein | DsrH | 69 | 69 |
| 854 | CPSF A subunit region | CPSF\_A | 69 | 69 |
| 855 | N2,N2-dimethylguanosine tRNA methyltransferase | TRM | 68 | 68 |
| 856 | Pescadillo N-terminus | Pescadillo\_N | 68 | 68 |
| 857 | Homeobox associated leucine zipper | HALZ | 68 | 68 |
| 858 | F-actin capping protein alpha subunit | F-actin\_cap\_A | 68 | 68 |
| 859 | Protein of unknown function (DUF986) | DUF986 | 68 | 68 |
| 860 | Protein of unknown function (DUF436) | DUF436 | 68 | 68 |
| 861 | Uncharacterised protein family (UPF0259) | UPF0259 | 67 | 67 |
| 862 | Toxin with inhibitor cystine knot ICK or Knottin scaffold | Toxin\_35 | 67 | 67 |
| 863 | RNA 2-phosphotransferase, Tpt1 / KptA family | PTS\_2-RNA | 67 | 67 |
| 864 | Photosystem II complex subunit Ycf12 | PSII\_Ycf12 | 67 | 67 |
| 865 | Protein of unknown function (DUF1253) | DUF1253 | 67 | 67 |
| 866 | DNA polymerase (viral) N-terminal domain | DNA\_pol\_viral\_N | 67 | 67 |
| 867 | DNA polymerase (viral) C-terminal domain | DNA\_pol\_viral\_C | 67 | 67 |
| 868 | DisA bacterial checkpoint controller nucleotide-binding | DisA\_N | 67 | 67 |
| 869 | Inhibitor of apoptosis-promoting Bax1 | Bax1-I | 67 | 67 |
| 870 | Outer Capsid protein VP4 (Hemagglutinin) | VP4\_haemagglut | 66 | 66 |
| 871 | Retroviral Vif (Viral infectivity) protein | Vif | 66 | 66 |
| 872 | Uncharacterised protein family (UPF0253) | UPF0253 | 66 | 66 |
| 873 | Uncharacterised protein family UPF0052 | UPF0052 | 66 | 66 |
| 874 | Ribosomal L37ae protein family | Ribosomal\_L37ae | 66 | 66 |
| 875 | Eukaryotic porin | Porin\_3 | 66 | 66 |
| 876 | Transcription termination factor nusG | NusG | 66 | 66 |
| 877 | Sodium/calcium exchanger protein | Na\_Ca\_ex | 66 | 66 |
| 878 | Flavoprotein | Flavoprotein | 66 | 66 |
| 879 | Ferredoxin-dependent bilin reductase | Fe\_bilin\_red | 66 | 66 |
| 880 | Pre-mRNA cleavage complex II protein Clp1 | Clp1 | 66 | 66 |
| 881 | CHD5-like protein | CHD5 | 66 | 66 |
| 882 | Cellulose synthase | Cellulose\_synt | 66 | 66 |
| 883 | WH2 motif | WH2 | 65 | 65 |
| 884 | Major surface antigen from hepadnavirus | vMSA | 65 | 65 |
| 885 | TFIIE alpha subunit | TFIIE\_alpha | 65 | 65 |
| 886 | TatD related DNase | TatD\_DNase | 65 | 65 |
| 887 | Oxysterol-binding protein | Oxysterol\_BP | 65 | 65 |
| 888 | OTU-like cysteine protease | OTU | 65 | 65 |
| 889 | Flavin-binding monooxygenase-like | FMO-like | 65 | 65 |
| 890 | FATC domain | FATC | 65 | 65 |
| 891 | Peptidase | DUF3663 | 65 | 65 |
| 892 | Defensin propeptide | Defensin\_propep | 65 | 65 |
| 893 | Magi peptide toxin family | Toxin\_22 | 64 | 64 |
| 894 | Nine Cysteines Domain of family 3 GPCR | NCD3G | 64 | 64 |
| 895 | Sugar efflux transporter for intercellular exchange | MtN3\_slv | 64 | 64 |
| 896 | Miro-like protein | Miro | 64 | 64 |
| 897 | Putative methyltransferase | Methyltransf\_16 | 64 | 64 |
| 898 | Flagellar protein FliT | FliT | 64 | 64 |
| 899 | Domain of unknown function (DUF3393) | DUF3393 | 64 | 64 |
| 900 | Cullin family | Cullin | 64 | 64 |
| 901 | ATP synthase (F/14-kDa) subunit | ATP-synt\_F | 64 | 64 |
| 902 | 7tm Odorant receptor | 7tm\_6 | 64 | 64 |
| 903 | AN1-like Zinc finger | zf-AN1 | 63 | 63 |
| 904 | Tagatose 6 phosphate kinase | Tagatose\_6\_P\_K | 63 | 63 |
| 905 | X-Pro dipeptidyl-peptidase (S15 family) | Peptidase\_S15 | 63 | 63 |
| 906 | Glucose-regulated metallo-peptidase M90 | Peptidase\_M90 | 63 | 63 |
| 907 | Antimicrobial peptide resistance and lipid A acylation protein PagP | PagP | 63 | 63 |
| 908 | Protein of unknown function, DUF440 | DUF440 | 63 | 63 |
| 909 | Protein of unknown function (DUF1656) | DUF1656 | 63 | 63 |
| 910 | Protein of unknown function DUF111 | DUF111 | 63 | 63 |
| 911 | Transcriptional regulator Crl | Crl | 63 | 63 |
| 912 | Universal stress protein B (UspB) | UspB | 62 | 62 |
| 913 | Tryptophan/tyrosine permease family | Trp\_Tyr\_perm | 62 | 62 |
| 914 | SEA domain | SEA | 62 | 62 |
| 915 | Ribosomal protein S28e | Ribosomal\_S28e | 62 | 62 |
| 916 | Melibiase | Melibiase | 62 | 62 |
| 917 | KR domain | KR | 62 | 62 |
| 918 | Hypoxia induced protein conserved region | HIG\_1\_N | 62 | 62 |
| 919 | Protein of unknown function (DUF1054) | DUF1054 | 62 | 62 |
| 920 | Coronavirus nucleocapsid protein | Corona\_nucleoca | 62 | 62 |
| 921 | Amiloride-sensitive sodium channel | ASC | 62 | 62 |
| 922 | Bacterial extracellular solute-binding protein | SBP\_bac\_1 | 61 | 61 |
| 923 | GRAS domain family | GRAS | 61 | 61 |
| 924 | Eukaryotic translation initiation factor 3 subunit 7 (eIF-3) | eIF-3\_zeta | 61 | 61 |
| 925 | Protein of unknown function (DUF359) | DUF359 | 61 | 61 |
| 926 | Double-stranded DNA-binding domain | dsDNA\_bind | 61 | 61 |
| 927 | Cytochrome C biogenesis protein transmembrane region | DsbD | 61 | 61 |
| 928 | Cysteine-rich domain | CCG | 61 | 61 |
| 929 | VWA domain containing CoxE-like protein | VWA\_CoxE | 60 | 60 |
| 930 | Deuterolysin metalloprotease (M35) family | Peptidase\_M35 | 60 | 60 |
| 931 | Porphyromonas-type peptidyl-arginine deiminase | PAD\_porph | 60 | 60 |
| 932 | Memo-like protein | Memo | 60 | 60 |
| 933 | LMBR1-like membrane protein | LMBR1 | 60 | 60 |
| 934 | Fusion glycoprotein F0 | Fusion\_gly | 60 | 60 |
| 935 | L-fucose isomerase, second N-terminal domain | Fucose\_iso\_N2 | 60 | 60 |
| 936 | L-fucose isomerase, first N-terminal domain | Fucose\_iso\_N1 | 60 | 60 |
| 937 | CutA1 divalent ion tolerance protein | CutA1 | 60 | 60 |
| 938 | 2-phosphosulpholactate phosphatase | 2-ph\_phosp | 60 | 60 |
| 939 | Uncharacterised protein family (UPF0370) | UPF0370 | 59 | 59 |
| 940 | SRP19 protein | SRP19 | 59 | 59 |
| 941 | Pup-like protein | Pup | 59 | 59 |
| 942 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | PhosphMutase | 59 | 59 |
| 943 | Peptidase family C54 | Peptidase\_C54 | 59 | 59 |
| 944 | Nucleosome assembly protein (NAP) | NAP | 59 | 59 |
| 945 | Protein of unknown function (DUF3582) | DUF3582 | 59 | 59 |
| 946 | Cut8 six-helix bundle | Cut8\_C | 59 | 59 |
| 947 | Apoptosis regulator proteins, Bcl-2 family | Bcl-2 | 59 | 59 |
| 948 | ArsC family | ArsC | 59 | 59 |
| 949 | Permease family | Xan\_ur\_permease | 58 | 58 |
| 950 | WzyE protein | WzyE | 58 | 58 |
| 951 | Reticulon | Reticulon | 58 | 58 |
| 952 | Peptidase S7, Flavivirus NS3 serine protease | Peptidase\_S7 | 58 | 58 |
| 953 | Na(+)-translocating NADH-quinone reductase subunit A (NQRA) | NQRA | 58 | 58 |
| 954 | 4-alpha-L-fucosyltransferase glycosyl transferase group 56 | Glyco\_transf\_56 | 58 | 58 |
| 955 | Frizzled/Smoothened family membrane region | Frizzled | 58 | 58 |
| 956 | Iron-containing alcohol dehydrogenase | Fe-ADH | 58 | 58 |
| 957 | Eukaryotic translation initiation factor 3 subunit 8 N-terminus | eIF-3c\_N | 58 | 58 |
| 958 | Domain of unknown function DUF108 | DUF108 | 58 | 58 |
| 959 | Chlorite dismutase | Chlor\_dismutase | 58 | 58 |
| 960 | Animal haem peroxidase | An\_peroxidase | 58 | 58 |
| 961 | Tubulin-tyrosine ligase family | TTL | 57 | 57 |
| 962 | D-aminoacyl-tRNA deacylase | tRNA\_deacylase | 57 | 57 |
| 963 | RUN domain | RUN | 57 | 57 |
| 964 | Ribosomal protein S27 | Ribosomal\_S27e | 57 | 57 |
| 965 | L-rhamnose-proton symport protein (RhaT) | RhaT | 57 | 57 |
| 966 | Phosphate acetyl/butaryl transferase | PTA\_PTB | 57 | 57 |
| 967 | Lipopolysaccharide-assembly | LptE | 57 | 57 |
| 968 | Integrin alpha | Integrin\_alpha2 | 57 | 57 |
| 969 | Indigoidine synthase A like protein | Indigoidine\_A | 57 | 57 |
| 970 | Plasma-membrane choline transporter | Choline\_transpo | 57 | 57 |
| 971 | Auxin response factor | Auxin\_resp | 57 | 57 |
| 972 | S-adenosylmethionine synthetase (AdoMet synthetase) | AdoMet\_Synthase | 57 | 57 |
| 973 | SigmaW regulon antibacterial | YdfA\_immunity | 56 | 56 |
| 974 | Trans-activation protein X | X | 56 | 56 |
| 975 | Viral family 110 | v110 | 56 | 56 |
| 976 | Sec1 family | Sec1 | 56 | 56 |
| 977 | Regulator of RNA polymerase sigma(70) subunit, Rsd/AlgQ | Rsd\_AlgQ | 56 | 56 |
| 978 | Ribosomal protein L34e | Ribosomal\_L34e | 56 | 56 |
| 979 | Viral RNA dependent RNA polymerase | RdRP\_3 | 56 | 56 |
| 980 | Poly(ADP-ribose) polymerase catalytic domain | PARP | 56 | 56 |
| 981 | Myc amino-terminal region | Myc\_N | 56 | 56 |
| 982 | MerR family regulatory protein | MerR | 56 | 56 |
| 983 | Haemagglutinin-neuraminidase | HN | 56 | 56 |
| 984 | Galactose binding lectin domain | Gal\_Lectin | 56 | 56 |
| 985 | Intermediate filament head (DNA binding) region | Filament\_head | 56 | 56 |
| 986 | Uncharacterized protein conserved in bacteria (DUF2312) | DUF2312 | 56 | 56 |
| 987 | Protein of unknown function (DUF1507) | DUF1507 | 56 | 56 |
| 988 | Protein of unknown function (DUF1283) | DUF1283 | 56 | 56 |
| 989 | DNA polymerase family A | DNA\_pol\_A | 56 | 56 |
| 990 | Putative cyclase | Cyclase | 56 | 56 |
| 991 | Cathelicidin | Cathelicidins | 56 | 56 |
| 992 | Calcitonin / CGRP / IAPP family | Calc\_CGRP\_IAPP | 56 | 56 |
| 993 | Histone-binding protein RBBP4 or subunit C of CAF1 complex | CAF1C\_H4-bd | 56 | 56 |
| 994 | 7tm Chemosensory receptor | 7tm\_7 | 56 | 56 |
| 995 | 3-hydroxyanthranilic acid dioxygenase | 3-HAO | 56 | 56 |
| 996 | Papain like viral protease | Viral\_protease | 55 | 55 |
| 997 | Uncharacterised protein family (UPF0262) | UPF0262 | 55 | 55 |
| 998 | Trehalose-phosphatase | Trehalose\_PPase | 55 | 55 |
| 999 | GTPase-activator protein for Ras-like GTPase | RasGAP | 55 | 55 |
| 1000 | Coronavirus endopeptidase C30 | Peptidase\_C30 | 55 | 55 |