**Table S4. List of 60 orthologsa unique to the ST36 ecotype.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Locus tag** | **Product** | **Length (aa)** | **Predicted functionb** |
| **VP10329\_14215** | **Hypothetical protein** | **109** | **Helix, transmembrane, signal peptide** |
| **VP10329\_14220** | **Hypothetical protein** | **220** | **Helix, transmembrane** |
| **VP10329\_14240** | **Hypothetical protein** | **189** | **None predicted** |
| **VP10329\_14265** | **Hypothetical protein** | **285** | **None predicted** |
| **VP10329\_14275** | **Hypothetical protein** | **428** | **Coil** |
| **VP10329\_14335** | **Hypothetical protein** | **830** | **None predicted** |
| **VP10329\_14380** | **Hypothetical protein** | **145** | **DHS-like NAD-binding domain** |
| **VP10329\_14405** | **Hypothetical protein** | **279** | **None predicted** |
| VP10329\_22853 | Chromosome partitioning ATPase | 277 | P-loop NTPase |
| VP10329\_22903 | Hypothetical protein | 101 | None predicted |
| VP10329\_22908 | Hypothetical protein | 145 | Helix, transmembrane, signal peptide |
| VP10329\_22963 | Hypothetical protein | 290 | Helix, transmembrane, signal peptide |
| VP10329\_22968 | Abortive infection protein | 376 | P-loop NTPase |
| VP10329\_22510 | Hypothetical protein | 141 | None predicted |
| VP10329\_04337 | Hypothetical protein | 163 | Signal peptide |
| VP10329\_05642 | Transcriptional regulator YidZ | 318 | HTH, LysR domains |
| VP10329\_05647 | Multidrug efflux protein MdtL | 402 | Transmembrane transport |
| VP10329\_05652 | Hypothetical protein | 201 | Signal peptide |
| VP10329\_05657 | Hypothetical protein | 739 | Endonuclease domain |
| VP10329\_03337 | Hypothetical protein | 62 | None predicted |
| VP10329\_03402 | DNA-damage-inducible protein | 287 | BRO N-terminal domain |
| VP10329\_19070 | Hypothetical protein | 222 | Bacteriophage T5 domain |
| VP10329\_01185 | HipA protein | 412 | Serine/threonin protease domain |
| VP10329\_01190 | Putative transcriptional activator | 105 | HTH DNA-binding domain |
| VP10329\_01195 | Hypothetical protein | 290 | HTH DNA-binding domain |
| VP10329\_01240 | Hypothetical protein | 583 | DNA helicase |
| *VP10329\_01520* | *Hypothetical protein* | *126* | *Capsule biosynthesis phosphotase* |
| *VP10329\_01535* | *Hypothetical protein* | *309* | *Pectin lyase fold virulence factor* |
| *VP10329\_01540* | *Hypothetical protein* | *271* | *None predicted* |
| *VP10329\_01550* | *Hypothetical protein* | *299* | *None predicted* |
| *VP10329\_01555* | *Hypothetical protein* | *187* | *None predicted* |
| *VP10329\_01560* | *Glycosyl transferase* | *287* | *Capsule biosynthesis* |
| *VP10329\_01565* | *Hypothetical protein* | *401* | *Helix, transmembrane* |
| *VP10329\_01570* | *Hypothetical protein* | *346* | *UDP-glycosyltransferase* |
| *VP10329\_01575* | *Glycosyl transferase* | *352* | *Capsule biosysnthesis* |
| VP10329\_19255 | Hypothetical protein | 249 | None predicted |
| VP10329\_19260 | Hypothetical protein | 123 | Helix, transmembrane |
| VP10329\_19265 | Hypothetical protein | 188 | Signal peptide |
| VP10329\_19295 | Hypothetical protein | 71 | Signal peptide |
| VP10329\_19300 | Hypothetical protein | 183 | Transmembrane beta-barrel OMP |
| VP10329\_19305 | Putative regulatory protein | 269 | HTH DNA-binding domain |
| VP10329\_19310 | Hypothetical protein | 162 | Helix, transmembrane |
| VP10329\_12474 | Hypothetical protein | 227 | Signal peptide, helix, transmembrane |
| VP10329\_12479 | Hypothetical protein | 82 | None predicted |
| VP10329\_12489 | Hypothetical protein | 249 | KilA-N DNA-binding domain |
| VP10329\_12494 | Hypothetical protein | 219 | Box inhibitor 1-related domain |
| VP10329\_12499 | Toxin resistance protein | 78 | Acyl-CoA N-acyltransferase |
| VP10329\_14045 | Hypothetical protein | 85 | Helix, transmembrane |
| VP10329\_16445 | Hypothetical protein | 336 | LysM domain |
| **VP10329\_18830** | **Hypothetical protein** | **155** | **Acyl-CoA N-acyltransferase** |
| **VP10329\_18870** | **Hypothetical protein** | **134** | **Helix, transmembrane** |
| **VP10329\_18885** | **Hypothetical protein** | **207** | **None predicted** |
| **VP10329\_18915** | **Hypothetical protein** | **185** | **None predicted** |
| **VP10329\_18920** | **Hypothetical protein** | **171** | **Helix, transmembrane** |
| **VP10329\_18925** | **Hypothetical protein** | **141** | **None predicted** |
| **VP10329\_18945** | **Hypothetical protein** | **197** | **Helix, transmembrane** |
| **VP10329\_18965** | **Hypothetical protein** | **356** | **None predicted** |
| **VP10329\_18980** | **Hypothetical protein** | **118** | **None predicted** |
| VP10329\_22973 | Hypothetical protein | 137 | None predicted |

aOrthologs located within the superintegron shown in bold font. Orthologs located within the capsular polysaccharide gene cluster shown in italic font.

bFunction predicted by InterPro protein sequence analysis. Protein domains and signature matches given when a function was not predicted.