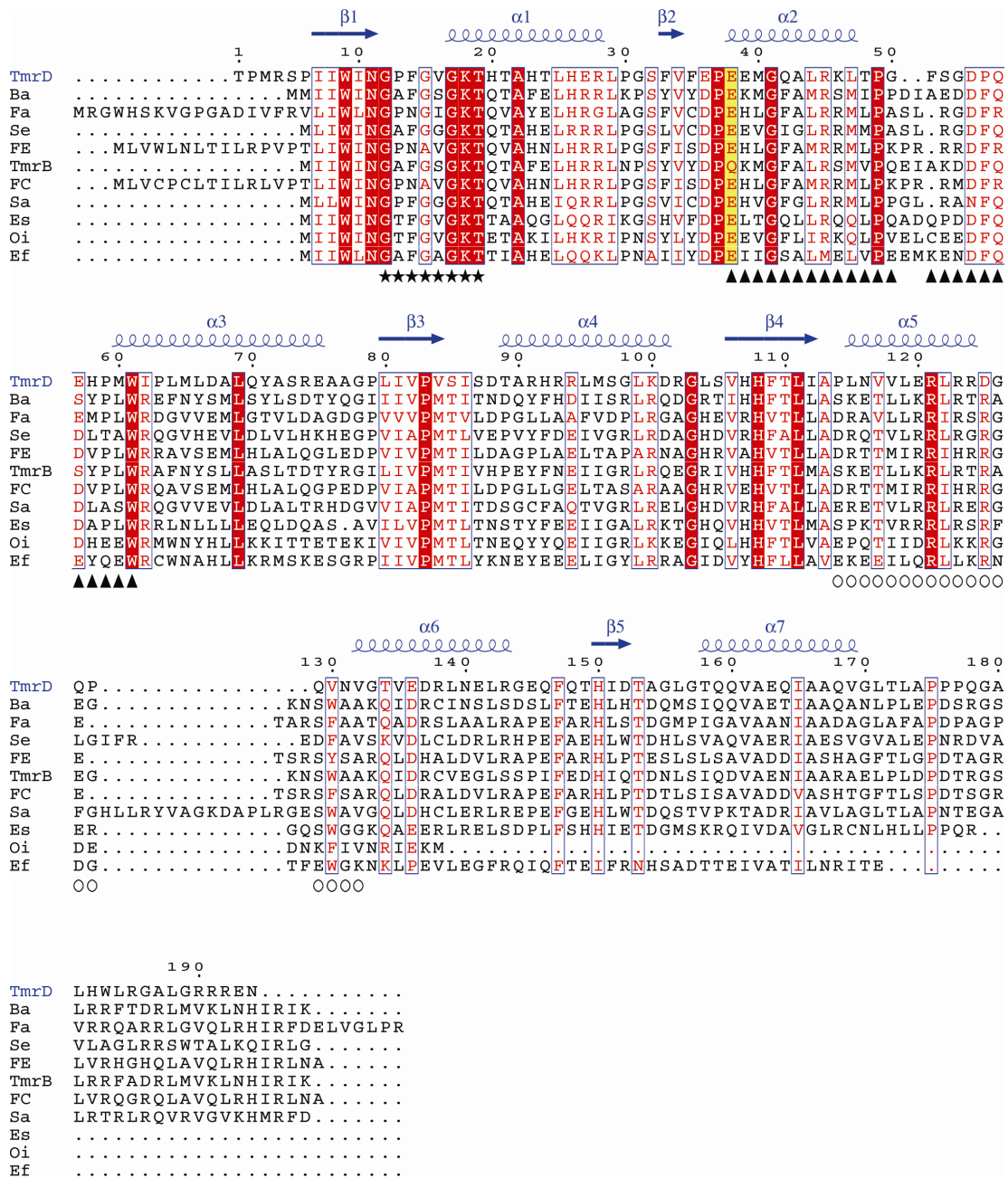


## Supplementary Figure 1



Multiple sequence alignment of TmrD with the first ten hits from a BLAST search: all ten are annotated as tunicamycin-resistance proteins or being related to tunicamycin resistance. The labels are: *Deinococcus radiodurans* (TmrD), *Bacillus amyloliquefaciens* (Ba), *Frankia alni* (Fa), *Saccharopolyspora erythraea* (Se), *Frankia* sp. EAN1pec (FE), *Bacillus subtilis* (TmrB), *Frankia* sp. strain Cc13 (FC), *Streptomyces avermitilis* (Sa), *Exiguobacterium sibiricum* (Es), *Oceanobacillus iheyensis* (Oi) and *Enterococcus faecalis* (Ef). All 11 representatives of the tunicamycin resistance family were aligned using the program *CLUSTALW*; the secondary-structure elements and the numbering of residues are according to the TmrD sequence in our crystal structure. Identical residues are shown in white text on red background and similar residues are shown in red text. For TmrD, residues that

form the Tn<sub>bind</sub> domain are marked with triangles and those that form the LID domain with circles. The predicted catalytic residue is shown in a yellow box. The individual *CLUSTALW* alignment scores against TmrD vary from 36 (for the *B. amyloliquefaciens* protein and corresponding to 39% identity over 186 matched residues) to 30 (for the *E. faecalis* corresponding protein and corresponding to 31% identity over 162 matched residues).