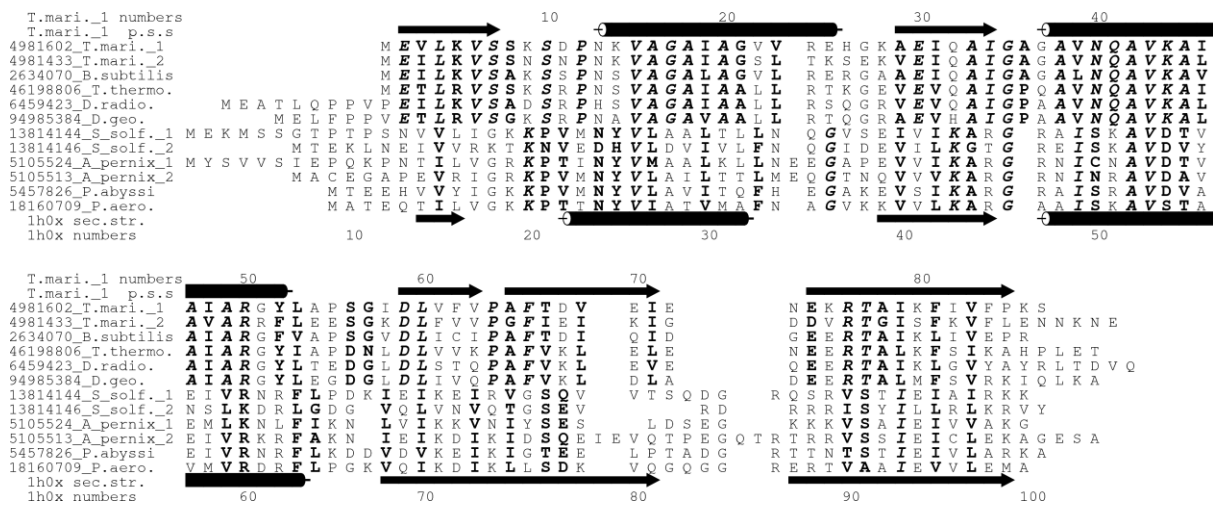


## Supplementary Figure 4: Sequence alignment of SpoVS and Alba family members.

Top 6 sequences are SpoVS family members from various bacteria and the bottom 6 sequences are Alba family members from various archaea. Sequences are annotated with their NCBI gene identification (gi) codes and abbreviated species names. The predicted secondary structure and numbering of the *Thermotoga maritima* SpoVS homologue subjected to comparative modeling are shown above the alignment while numbering and actual secondary structure for *Sulfolobus solfataricus* Alba (PDB code 1h0x) are shown below. Well conserved positions in each group are shown in bold, invariant residues additionally italicized. The figure was produced with ALSCRIPT (Barton, 1993).



## References

- Barton G. J. (1993) ALSCRIPT: a tool to format multiple sequence alignments. *Protein Eng.* 6, 37-40.
- Jones D. T. (1999) Protein secondary structure prediction based on position-specific scoring matrices. *J. Mol. Biol.* 292, 195-202.