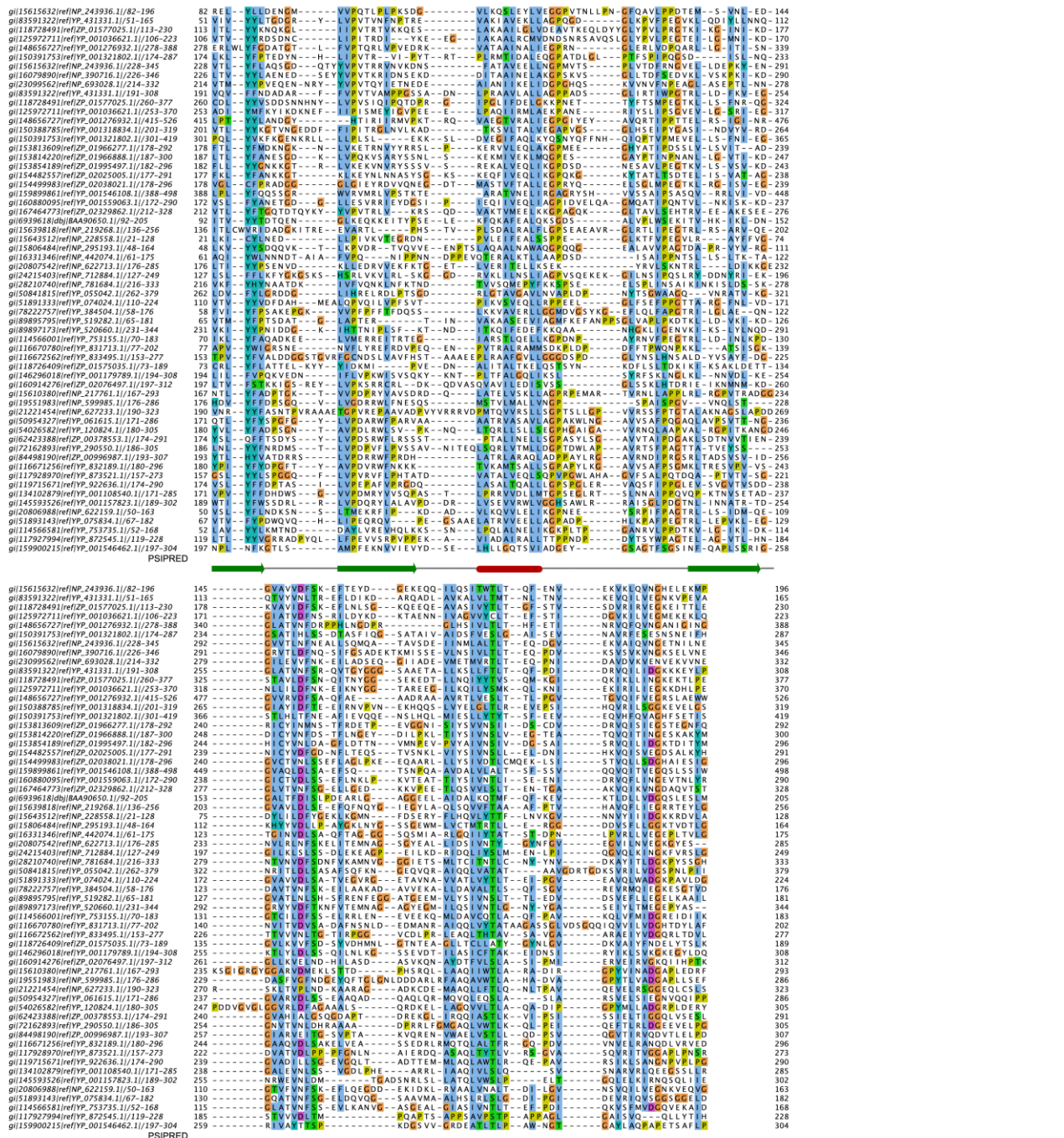


# Supplementary Figure 1: Sequence alignment of the GERMN domain.

The alignment was formatted with Jalview (Clamp *et al.*, 2004) and annotated with the PSIPRED (Jones, 1999) prediction for the top sequence. The sequences were extracted from a full alignment so that no pair shares more than 60% sequence identity. The sequences are sorted by domain context, from top to bottom, N-terminal domains from twin GERMN proteins (top 6 sequences), then C-terminal domains from twin GERMN proteins (17 sequences), domains from single GERMN proteins (19), domains from GERMN+GMAD1 proteins (13) and finally domains from GERMN+GMAD2 proteins (5).



## References

Clamp M., Cuff J., Searle S. M. & Barton G. J. (2004) The Jalview Java alignment editor. *Bioinformatics* 20, 426-427.

Jones D. T. (1999) Protein secondary structure prediction based on position-specific scoring matrices. *J. Mol. Biol.* 292, 195-202.