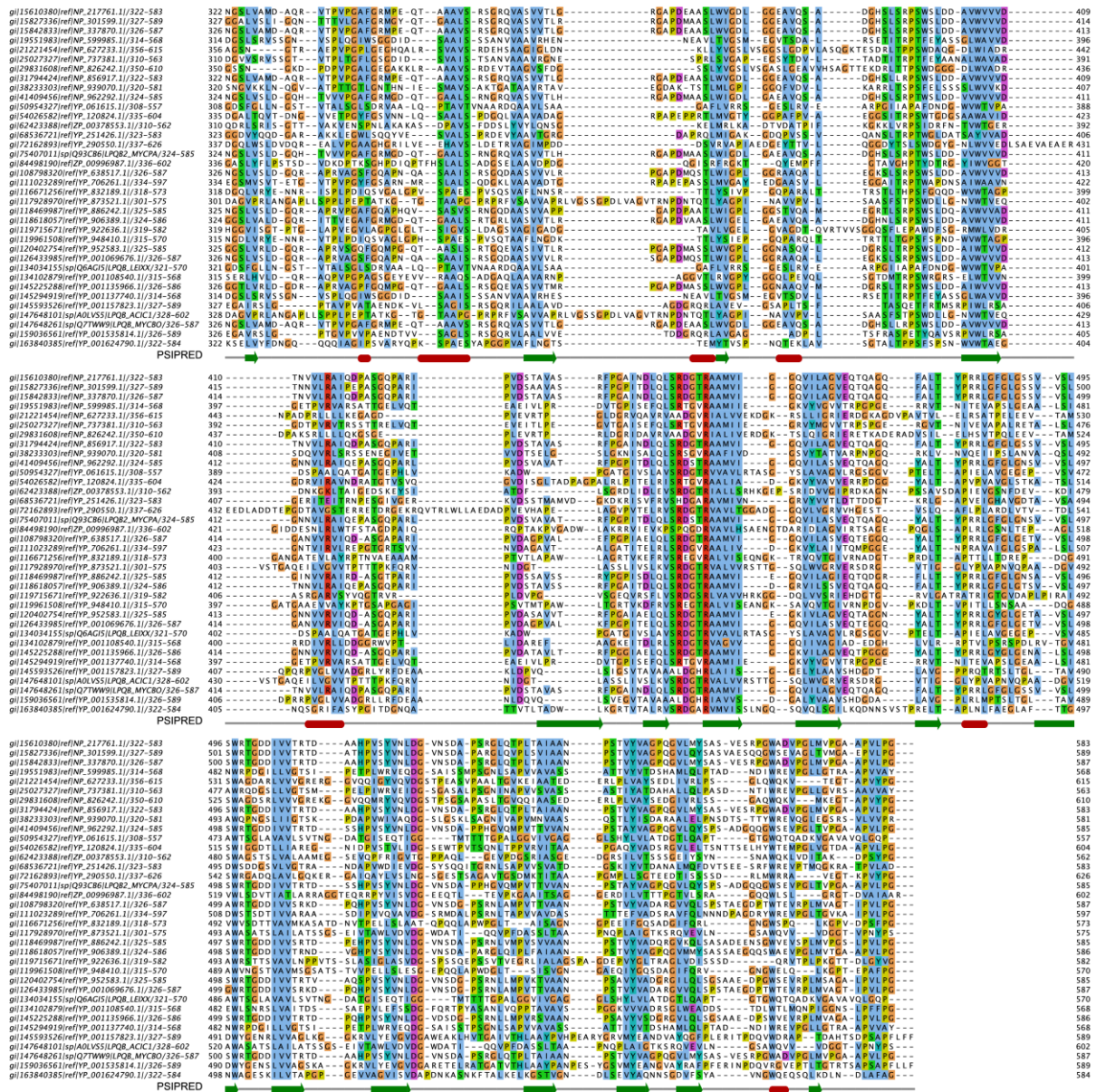


Supplementary Figure 2: Sequence alignment of the GMAD1 domain.

The alignment was formatted with Jalview (Clamp *et al.*, 2004) and annotated with the PISPRED (Jones, 1999) prediction for the top sequence.



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.