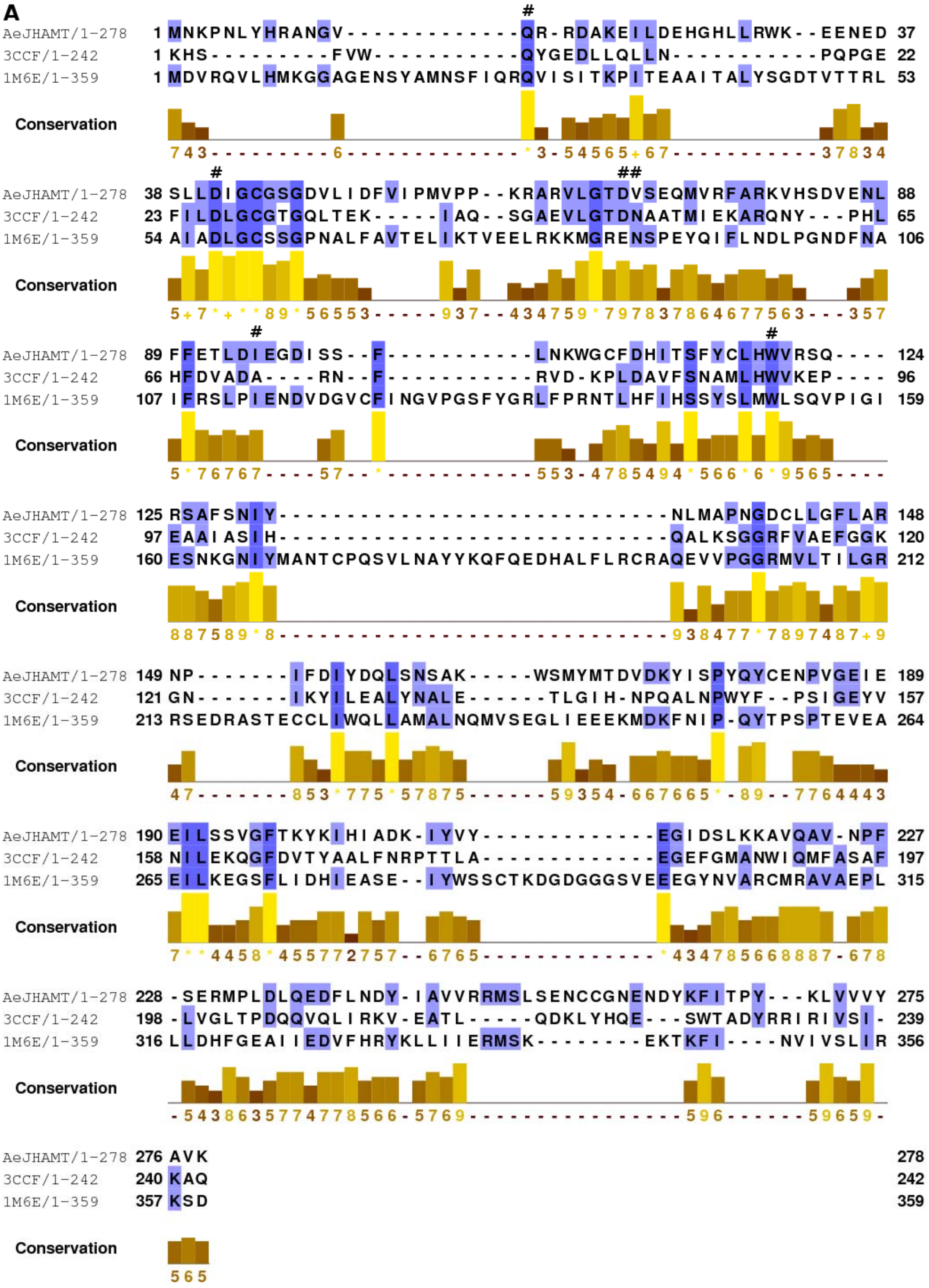
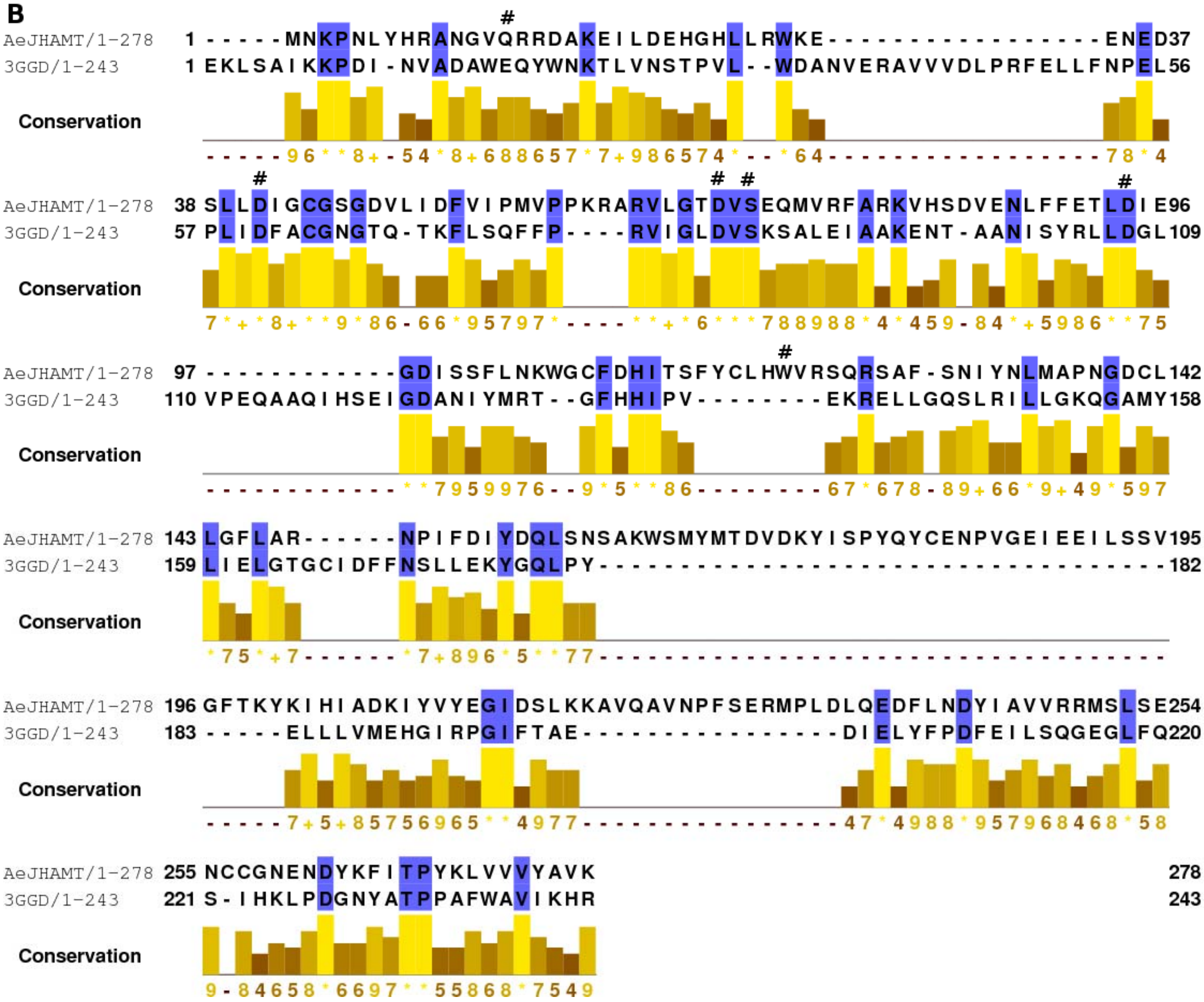
Supplementary figure 1





(A) Sequence alignment between AeJHAMT, 3CCF and 1M6E. The alignment was performed using T-COFFEE (Poirot et al., 2003) and drawn with Jalview (Clamp et al., 2004). Residues shaded in blue are conserved (marked with * in the conservation panel). Residues shaded in light blue are semiconserved (marked with + in the conservation panel). Important residues interacting with SAM and the carboxylic acid in our docking simulations are marked with # (same residues highlighted in Figure 5). 9 to 0 values represent degree of conservation in all species. Conservation is measured as a numerical index reflecting the conservation of physicochemical properties in the alignment. Identities score the highest and the next most conserved group contain substitutions to amino acids included in the same physicochemical class as described by Livingstone, et al., 1993.

(B) Sequence alignment between AeJHAMT and 3GGD, an additional SAM-dependent methyltransferase, which was also evaluated to be used as a template. Note the absence in 3GGD of critical residues for substrate interaction such as Q14 and W120. Residues coding are the same as in A.

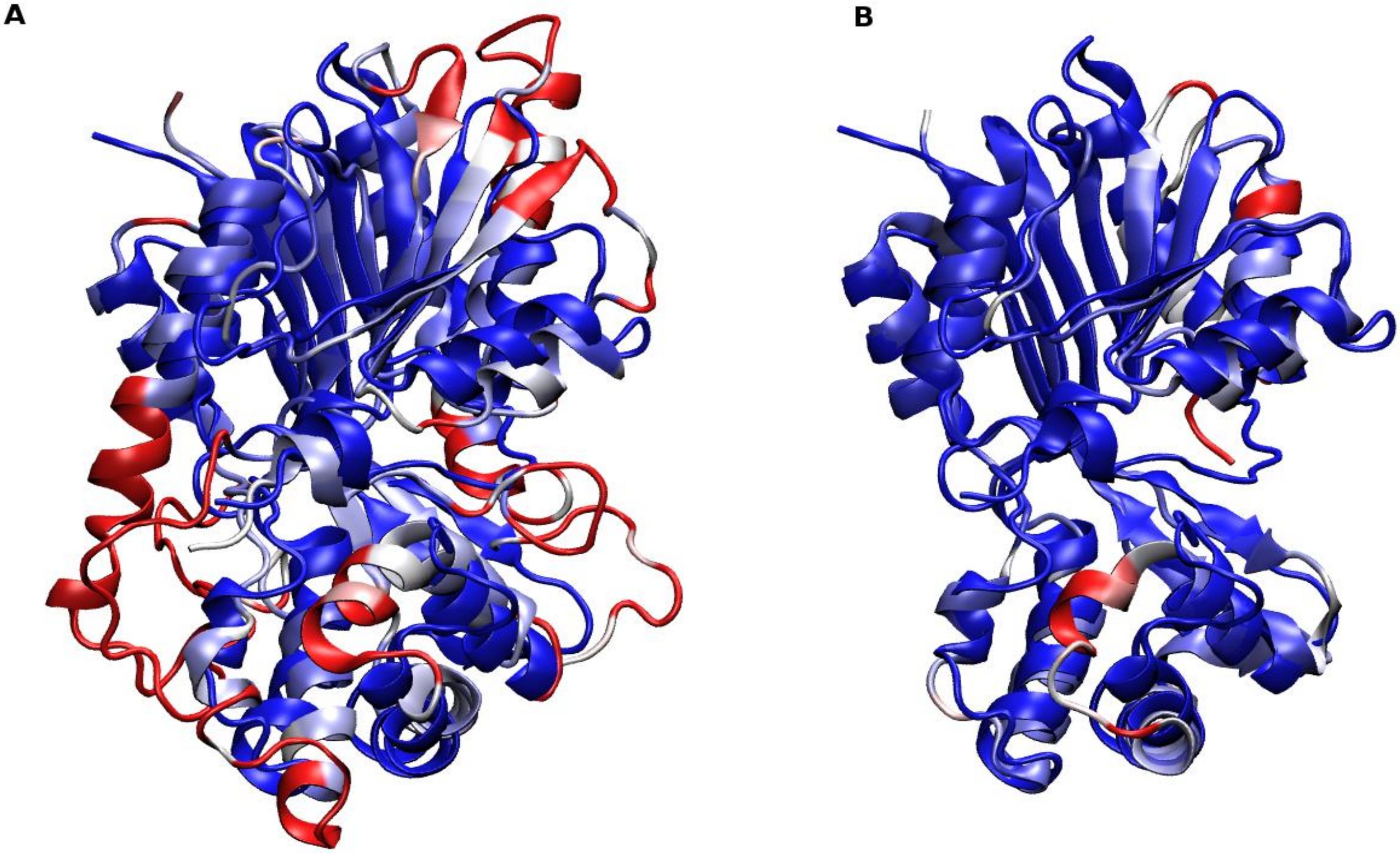
References

Clamp, M., Cuff, J., Searle, S. M., Barton, G. J. 2004. "The Jalview Java Alignment Editor". Bioinformatics 20, 426-7

Livingstone, C.D., Barton, G.J., 1993. Protein sequence alignments: a strategy for the hierarchical analysis of residue conservation. Comput. Appl. Biosci. 9, 745-756.

Poirot, O., O'Toole, E., Notredame, C. 2003. Tcoffee@igs: A web server for computing, evaluating and combining multiple sequence alignments. Nucleic Acids Res. 31, 3503-3506.

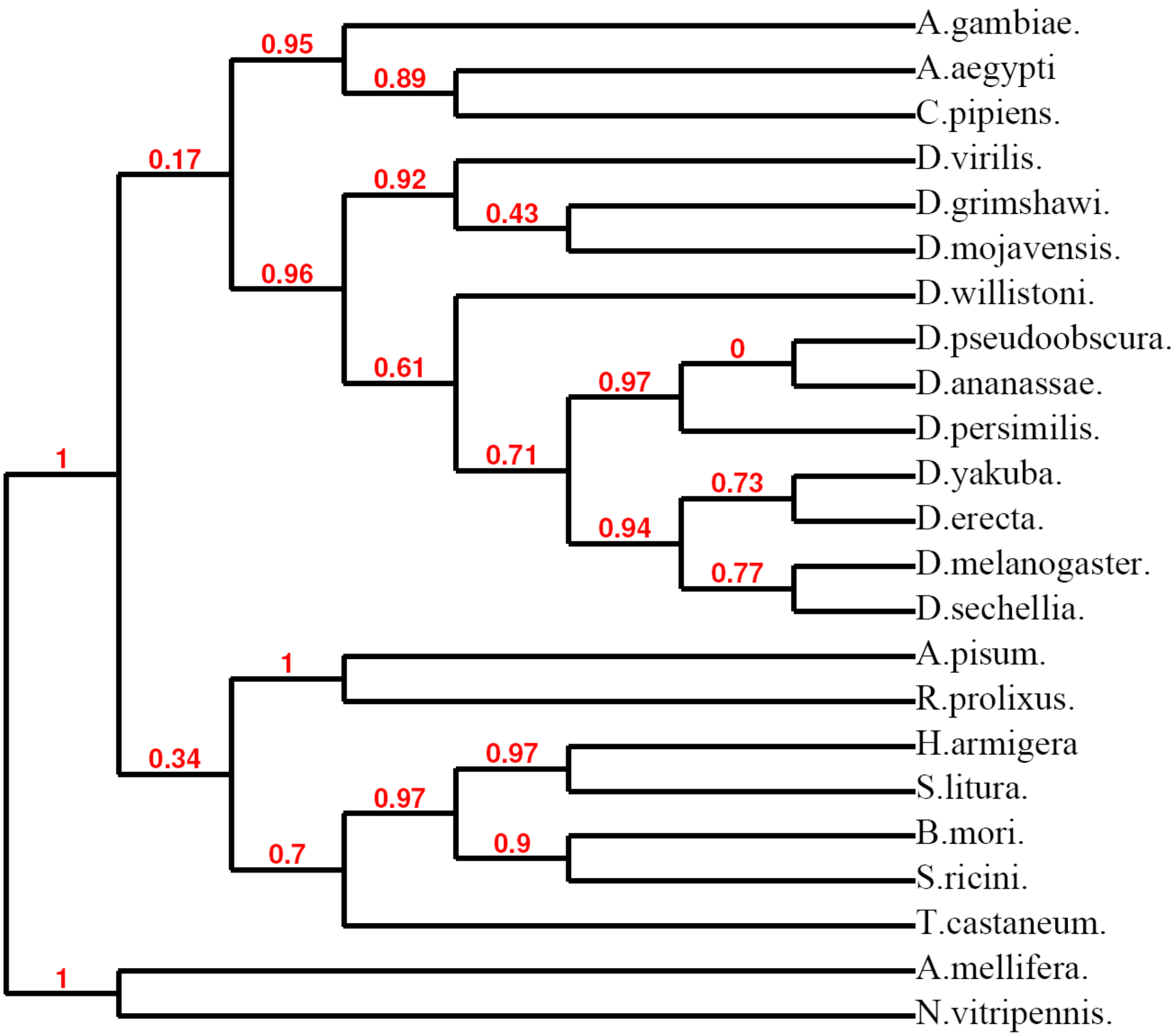
Supplementary figure 2



(A) Structural alignment between AeJHAMT and 1M6E colored showing the Root Mean Standard Deviation (RMSD) of the structurally aligned parts using AeJHAMT as a reference. Coloring goes form Blue as low RMSD to white as intermediate to red as high RMSD. (B) Same as (A) but between AeJHAMT and 3CCF. RMSD is a quantitative parameter used to estimate difference in the overall fold of proteins (Leach, 2001)

References: Leach, A. R. 2001. "Molecular Modeling, principles and applications, Second Edition", Pearson Prentice Hall, Essex, England.

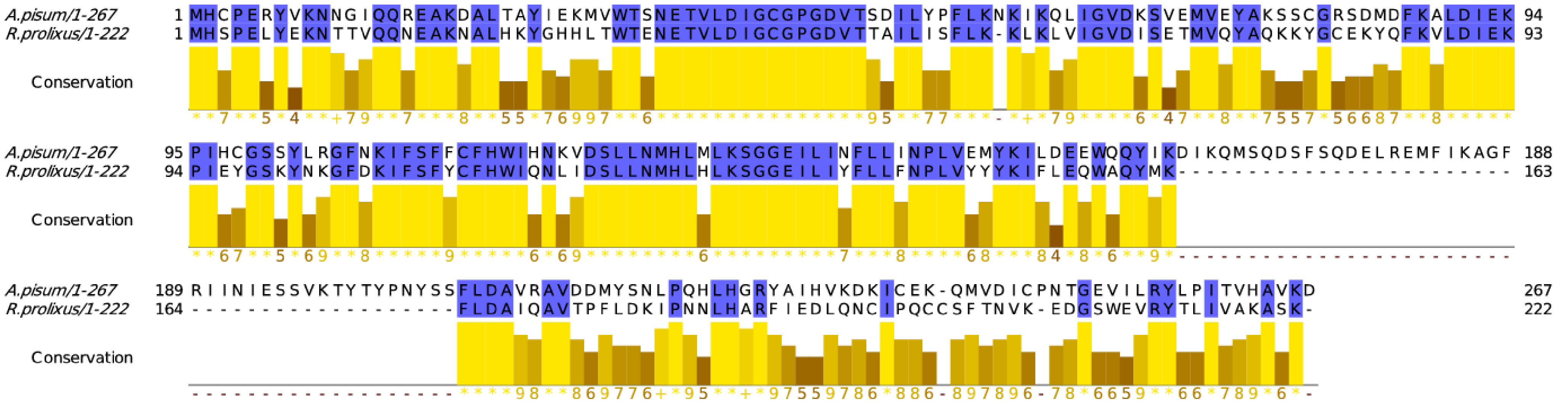
Supplementary figure 3



Phylogenetic analysis of the JHAMTs from different species of insects based on the primary amino acid sequences. Sequences are labeled with the species name. Phylogenetic analyses were done using Phylogeny.fr (Dereeper et al., 2008).

References: Dereeper A., Guignon V., Blanc G., Audic S., Buffet S., Chevenet F., Dufayard J.F., Guindon S., Lefort V., Lescot M., Claverie J.M., Gascuel O. (2008) Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Research. 2008 Jul 1; 36 (Web Server Issue):W465-9. Epub 2008 Apr 19).

Supplementary Fig. 4



Sequence alignment between JHAMTs from *Acyrthosiphon pisum* and *Rhodnius prolixus*. The alignment was performed using TCOFEE (Poirot et al., 2003) and drawn with Jalview (Clamp et al., 2004). Residues shaded in blue are conserved (marked with ***** in the conservation panel). Semiconserved residues are marked with **+** in the conservation panel. 9 to 0 values represent degree of conservation in both species. Conservation is measured as a numerical index reflecting the conservation of physicochemical properties in the alignment. Identities score the highest and the next most conserved group contain substitutions to amino acids included in the same physicochemical class as described by Livingstone, et al., 1993. References are the same as for Supplem. Fig. 1.