

Additional file 8. The maximum likelihood tree of family PL1. The phylogenetic tree was constructed with PhyML3.0 based on a multiple sequence alignment generated with PSI-Coffee [53]. The midpoint rooted base tree was drawn using Interactive Tree Of Life Version 2.1.1 (<http://itol.embl.de/>). The p-values of approximate likelihood ratios (SH-aLRT) plotted as circle marks on the branches (only p-values >0.5 are indicated) and circle size is proportional to the p-values. Scale bars correspond to 0.2 amino acid substitutions per site.

