



Supplementary Figure S4. Multiple sequence alignment of the 11 novel α -Enolase from *Anoplocephala perfoliata* (Apa-Enolase-1, 2 and 3). Secondary protein structure prediction using the PSIPRED Protein Analysis Workbench is presented below the alignment and comprises of 10 β -strands and 15 α -helices, highlighted in yellow and pink, respectively. The 5 essential residues necessary for proper catalytic function are highlighted in green (Pancholi, 2001). The predicted N- and C-terminal Enolase domain profiles are indicated by blue- and red-boxes, respectively.

