

Figure S1. Amino acid sequence alignment for CaNs of *O. furnacalis* and other species. The black, dark grey, light gray and colourless areas respectively indicate the 90–100%, 80–90%, 60–80% and lower than 60% similarity/identity. Specific names and GenBank IDs: *O. furnacalis*, XP_028156950.1; *Helicoverpa armigera*, XP_021181213.1; *Spodoptera frugiperda*, XP_035436316.1; *Manduca sexta*, XP_030032629.1; *Bombyx mori*, NP_001037025.1; *Leptinotarsa decemlineata*, XP_023017364.1; *Tribolium castaneum*, EEZ99522.2; *Aedes aegypti*, XP_021707011.1; *Drosophila melanogaster*, NP_001259622.1; *Araneus ventricosus*, GBL91594.1; *Schistosoma japonicum*, KAH8863363.1; *Homo sapiens*, NP_001124163.1; *Oryctolagus cuniculus*, NP_001076196.1; *Mus musculus*, NP_001280551.1; *Gallus gallus*, XP_040527134.1; *Anas platyrhynchos*, EOB04152.1; *Aspergillus fumigatus*, KAF4282405.1.

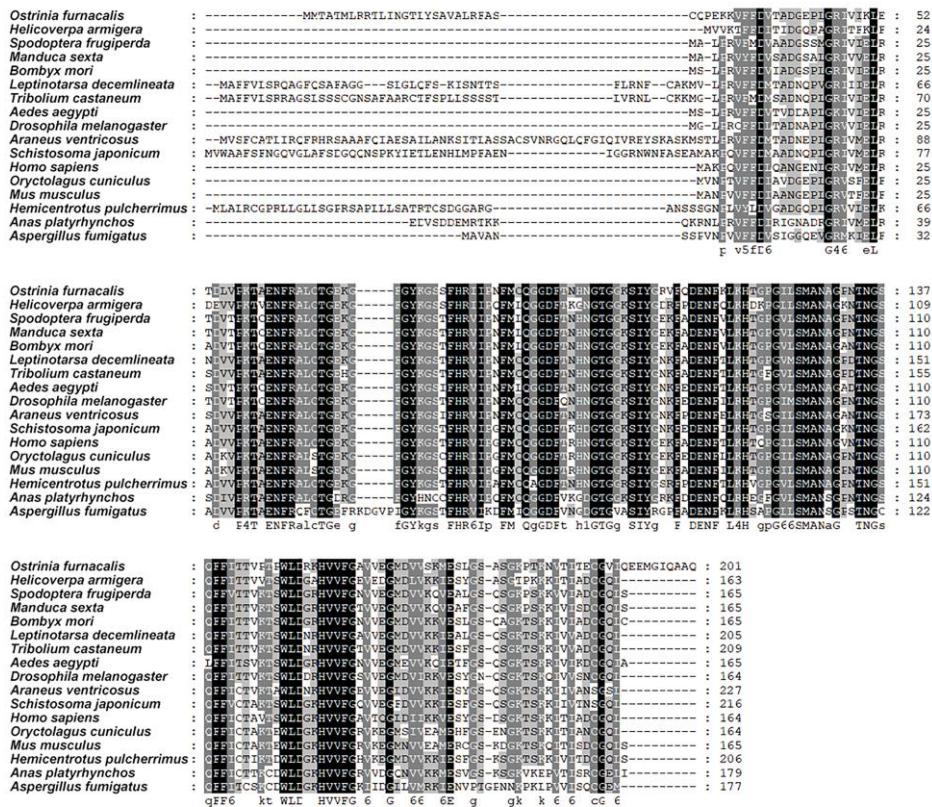


Figure S2. Amino acid sequence alignment for cyclophilins of *O. furnacalis* and other species. The similarity/identity of amino acid sequences of 90–100%, 80–90%, 60–80% and lower than 60% were respectfully displayed with black, dark grey, light gray

and colourless areas. Specific names and GenBank IDs: *O. furnacalis*, XP_028172843.1; *H. armigera*, XP_021200657.1; *S. frugiperda*, XP_035453679.1; *M. sexta*, XP_030031426.1; *B. mori*, NP_001037301.1; *L. decemlineata*, XP_023012814.1; *T. castaneum*, EEZ98965.2; *A. aegypti*, ABF18058.1; *D. melanogaster*, NP_523366.2; *Araneus ventricosus*, GBL90912.1; *S. japonicum*, AAA29863.1; *H. sapiens*, AAC51927.1; *O. cuniculus*, AAF22215.1; *M. Musculus*, NP_598845.1; *Hemicentrotus pulcherrimus*, AAB37708.1; *A. platyrhynchos*, AJR16770.1; *A. fumigatus*, CAI78448.1.