



Supplementary Figure 2.

Phylogenetic analysis of CG3921 isoform PB.

The phylogenetic study of CG3921 amino acid sequence (isoform B) using NCBI Blast search server (standard settings) and the MEGA 5.0 (1) alignment program, identified homologs in the following invertebrates and invertebrate-related animals: *Acyrthosiphon pisum* (pea aphid), *Aedes aegypti* (mosquito [vector of dengue virus]), *Anopheles gambiae* (mosquito [vector of malaria parasite]), *Ascaris suum* (nematode [causes ascariasis in pigs]) *Bombus terrestris* (bumblebee) *Branchiostoma floridae* (lancelet), *Caenorhabditis briggsae* (nematode), *Caenorhabditis elegans* (nematode), *Clonorchis sinensis* (Chinese fever fluke / liver fluke) *Culex quinquefasciatus* (southern house mosquito), *Daphnia pulex* (water flea), *Drosophila melanogaster*, *Drosophila sechellia*, *Harpegnathos saltator* (ant), *Ixodes scapularis* (blacklegged tick), *Megachile rotundata* (leafcutter bee), *Nasonia vitripennis* (wasp), *Pediculus humanus corporis* (body louse), *Trichinella spiralis* (nematode parasite, responsible for trichinosis). Database accession numbers are indicated.

REFERENCES:

1. Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S. (2011) MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol. Biol. Evol.* **28**, 2731-2739