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6 Suppl. fig. S3

7 A, Structure of SmNck2 (Smp 014850) analyzed by SMART showing three SH3 domains (SH3) 8 and one SH2 (SH2) domain.

9 B, Phylogenetic analysis using the Neighbor-Joining method [1-4]. Besides SmNck2 (SmaNck2) the analysis involved the following 15 amino acid sequences of orthologs of 10 organisms of different phylogenetic origins such as Drosophila melanogaster (DmDreadlocks; 11 NP 722657), Homo sapiens (HsNck2; NP 003572), Xenopus laevis (XINck2; NP 001083313), 12 Loa loa (LloNck2; XP 003137411), Ascaris suum (AsuNck2; ERG86028), Caenorhabditis 13 elegans (CeNck1; NP 508706), Necator americanus (NamNck2; ETN84925), Haemonchus 14 contortus (HcoNck2; CDJ85790), Hydra vulgaris (HvNck2; XP 002160090), Clonorchis sinensis 15 (CsiNck2; GAA50029), Hymenolepis microstoma (HmiNck2; CDS31037), Echinococcus 16 17 multilocularis (EmuNck2; CDJ02918), Strongylocentrotus purpuratus (SpNck2; XP_011668987), and two amino acid sequences coding for SH2- and SH3-domains containing 18

- 19 proteins of Schistosoma mansoni (SmaTK5; AAF64151) and Homo sapiens (HsFyn; P06241)
- 20 serving as out-groups. All positions containing gaps and missing data were eliminated. In
- 21 Planaria, the free-living class of the phylum platyhelminthes, doing BLAST analyses, there was
- 22 no homolog found. Parasite species names were abbreviated with the first two letters, free-
- 23 living with the first.
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