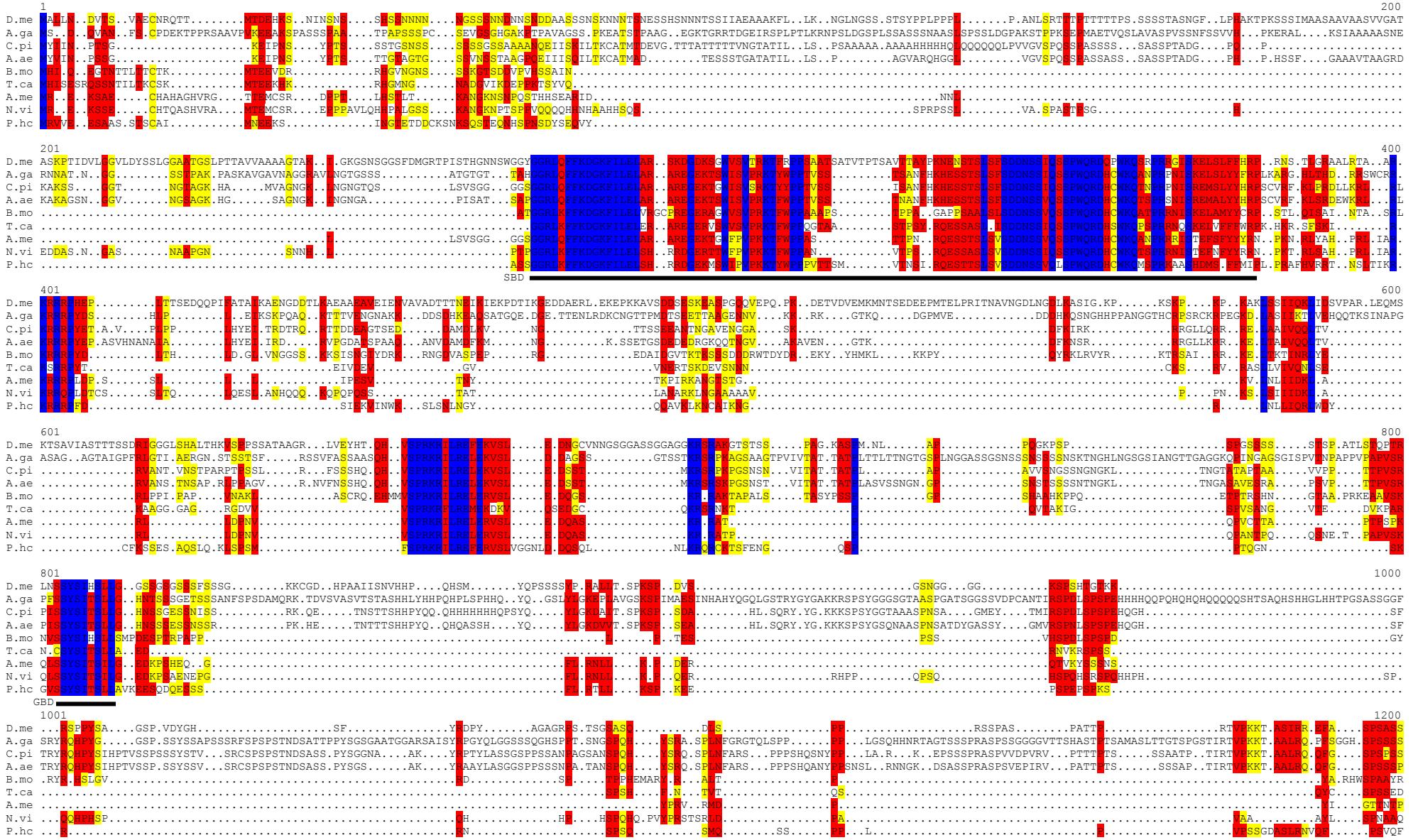


Figure S1

Multi-species alignment of H orthologues from Drosophilids

Hairless protein sequences were predicted from genomic sequences. SBD, GBD and CBD are underlined. H orthologues from Drosophilids contain each four introns at identical positions (arrowheads). Presumptive start methionines are shown in cyan. Green boxes: presumptive nuclear localization signals. Blue, identical amino acids; red, highly similar amino acids; yellow, similar amino acids; dots represent gaps. Similarities and identities with respect to the *D. melanogaster* sequence are given in percent. Sequencing gap in *D. ananassae* (D.an) is shown by question marks. D.me: *D. melanogaster*, D.se: *D. sechellia*, D.si: *D. simulans*, D.ya : *D. yakuba*, D.er : *D. erecta*, D.ps: *D. pseudoobscura*, D.pe: *D. persimilis*, D.wi: *D. willistoni*, D.mo: *D. mojavensis*, D.vi: *D. virilis*, D.hy: *D. hydei*, D.gr: *D. grimshawi*. The BESTFIT program was used for calculation of similarity and identity scores (gap weight 1, length weight 1, maximum penalty length 30). The multi-alignment was performed with PRRN program. Parameters of multi-alignment were: gap extension penalty 1, gap open penalty 4.



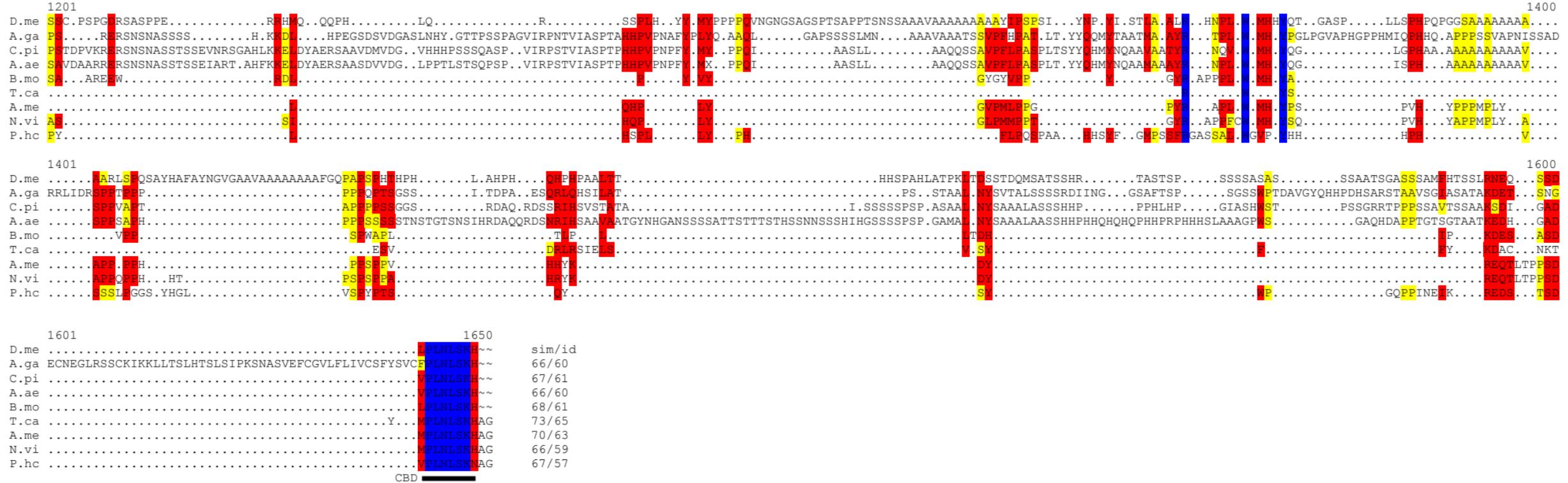


Figure S2

Multi-species alignment of H orthologues from different insects

Comparison of *Drosophila melanogaster* (*D.me.*), *Anopheles gambiae* (*A.ga.*), *Culex pipiens* (*C.pi*), *Aedes aegypti* (*A.ae*), *Bombyx mori* (*B.mo.*), *Tribolium castaneum* (*T.ca.*), *Apis mellifera* (*A.me.*), *Nasonia vitripennis* (*N.vi*) and *Pediculus humanus corporis* (*P.hc*) is shown. Protein sequences were predicted from genomic DNA apart from D.m.H and A.m.H. that are based on sequenced cDNAs. SBD, GBD and CBD are underlined. Sequence similarities and identities are given in percent with respect to the D.m.H. Blue, identical amino acids; red, highly similar amino acids; yellow, similar amino acids; dots represent gaps. For programs and parameters, see Figure S1.