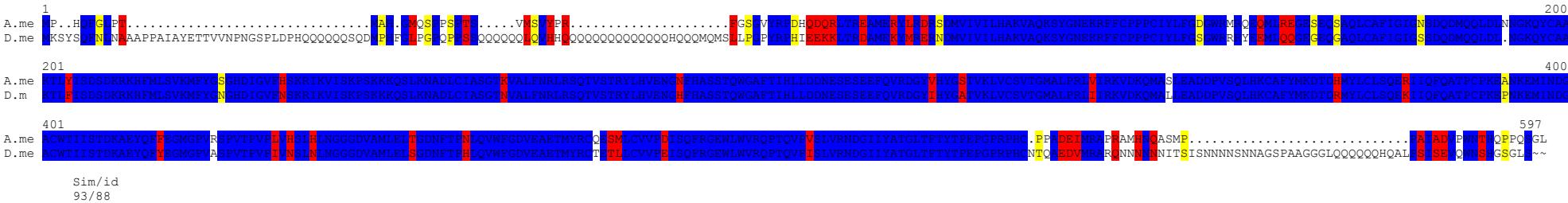
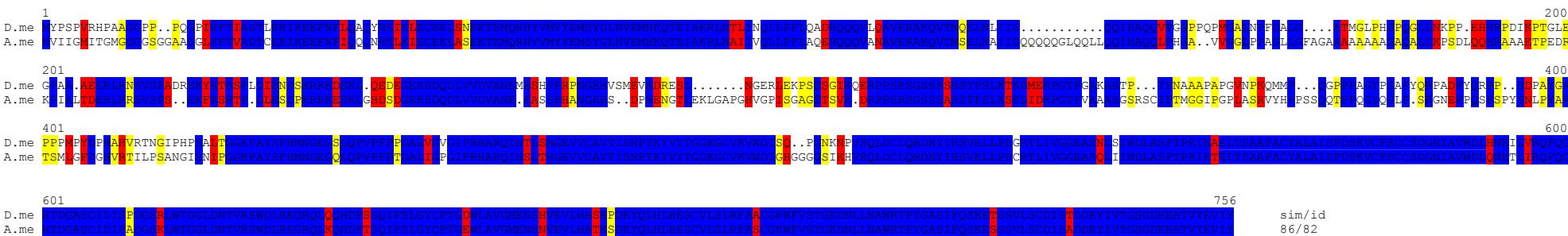


A) *D. melanogaster* and *A. mellifera* Notch orthologues

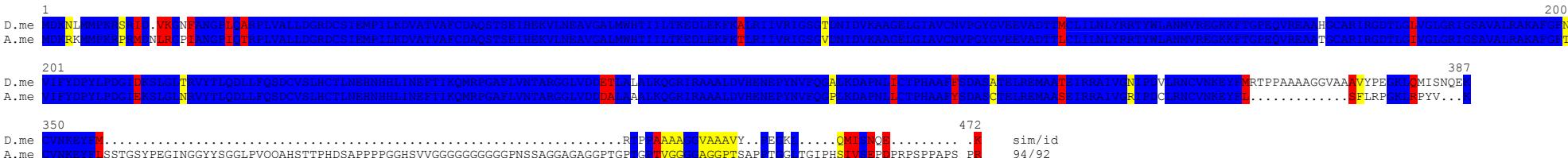
B) *D. melanogaster* and *A. mellifera* Su(H) orthologues



C) *D. melanogaster* and *A. mellifera* Groucho orthologues



D) *D. melanogaster* and *A. mellifera* CtBP orthologues



E) *D. melanogaster* and *A. mellifera* Mastermind orthologues

F) *D. melanogaster* and *A. mellifera* Vestigial orthologues

Detailed description: This figure shows a sequence alignment between *D. megaloptera* (top) and *A. megaloptera* (bottom). The alignment is color-coded by residue conservation. Regions 1-200, 201-400, and 401-482 are indicated with vertical bars on the left. The x-axis at the top indicates positions 1 through 200, 201 through 400, and 401 through 482. The x-axis at the bottom indicates positions 1 through 200, 201 through 400, and 401 through 482. The y-axis labels are 'D. me' and 'A. me'. Conservation is indicated by color: blue for identical residues, red for conservative substitutions, and black for non-conservative or gaps.

Figure S3**Conservation of Notch pathway components in honeybee.**

Single orthologues of Notch, Su(H), Gro, CtBP, Mam and Vg were identified in the honeybee genome. A.m. Protein sequences were deduced from genomic sequence and aligned with the respective *D. melanogaster* protein sequences. Blue, identical amino acids; red, highly similar amino acids; yellow, similar amino acids; dots represent gaps. Sequences similarities and identities are given in percent with respect to *D. melanogaster*. Gap in A.m.N is depicted by question marks.

Similarity and identity scores were calculated using BESTFIT (gap weight 1, length weight 1, maximum penalty length 30). Multi-alignments were done with PRRN with gap extension penalty 1 and the gap open penalty 9, apart for the Vestigial comparison, where gap open penalty 4 was applied.