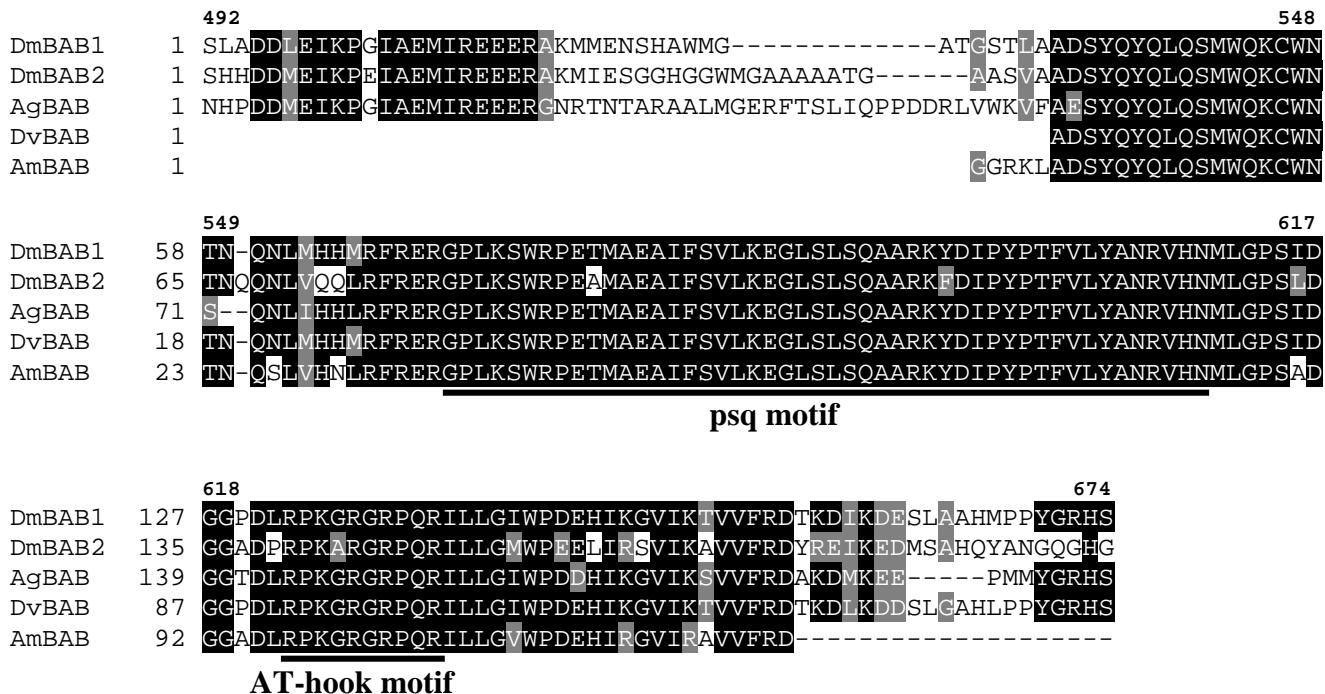


## Supplementary data for online-only publication



### Multiple sequence alignment of BabCD motifs.

Amino acid sequences of the BabCD of the BAB proteins of *D. melanogaster* Bab1 (AJ252082.1), *D. melanogaster* Bab2 (AJ252173.1), *D. virilis* (AJ544785), *A. gambiae* (AAAB01008960.1) and *A. mellifera* (BB170013A10G09) have been aligned. Amino acid residues that are identical in all the sequences are shaded black. Amino acid positions with conservative changes are shaded gray. The position of the psq and the AT-Hook domains is indicated. Numbers above the sequence indicate the amino acid positions respective to the BAB1 protein.

### Supplemental data