



Suppl. Fig. 1: The predicted structure of the SPRY domain of Fsn is similar to that of Gus and those of the SSB proteins.

- (A) Representation of the solved crystal structures of Gus (left), SSB1 (middle) and SSB2 (right) in complex with a 20-residue Vasa peptide (yellow). The SPRY domains are shown with transparent surfaces, ribbons (main chains) and sticks (side chains). PDB accession codes of the structures are 2IHS for Gus, 3F2O for SSB1 and 3EMW for SSB2.
- (B) Multiple sequence alignment of *Drosophila* Gus and Fsn with those SSB family proteins whose crystal structure has been determined. Residues marked in red are conserved between all five proteins while those in yellow are conserved between four out of the five proteins.
- (C) Superposition of the predicted Fsn structure with the crystal structures of Gus and SSB2 suggests that the SPRY domains of these proteins are highly similar. The side chains of the Vas-binding pocket-forming residues are shown as stick models, those of Fsn are labeled. Y239 is highlighted.