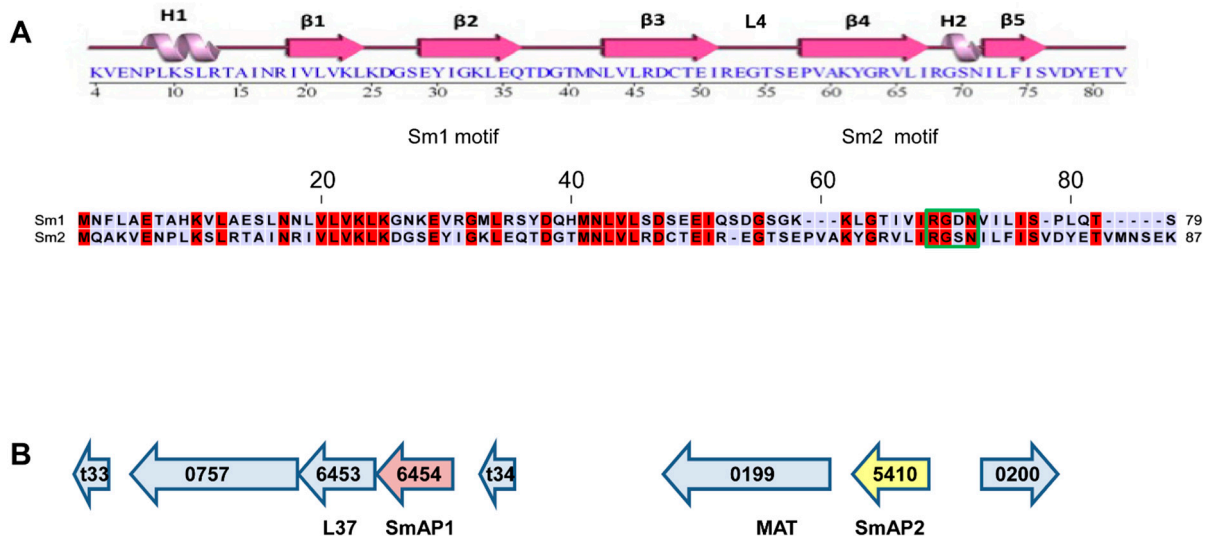
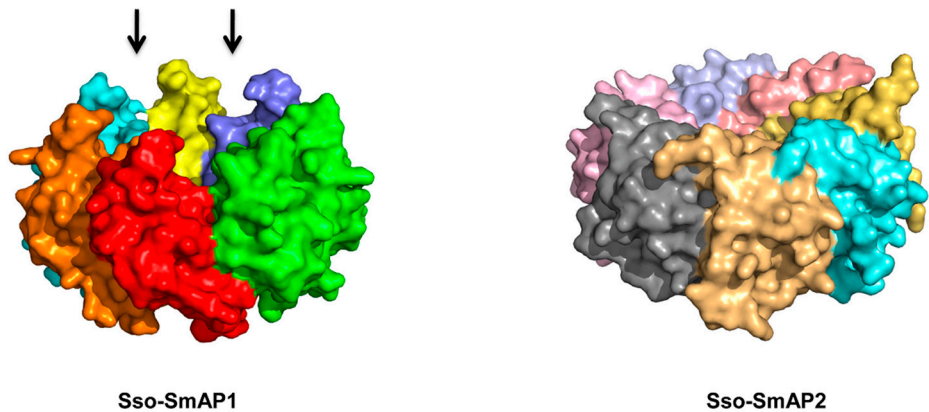


Supplementary Materials



**Figure S1.** Secondary structure and conservation of SmAP1 and SmAP2. **(A)** Upper panel, the secondary structure of Sso-SmAP1 is shown superposed on the primary amino-acid sequence.  $\beta$ -strands and helices are represented by arrows and bars, respectively. The N-terminal  $\alpha$ -helix is followed by five  $\beta$ -strands forming the continuous Sm-fold. The L4 loop links the Sm1 and Sm2 motif. Lower panel: conservation of Sso-SmAP1 and Sso-SmAP2. Like eukaryotic Sm proteins, both proteins contain a RGXX consensus sequence (green box), whereby X represents any charged amino acid. **(B)** Genomic organisation of the Sso-SmAP1 and Sso-SmAP2 gene loci. The Sso-SmAP1 gene (Sso 6453) is co-transcribed with ribosomal protein L37e gene and a spermidine synthetase gene. The Sso-SmAP1 operon is flanked by two tRNAs, t33 and t34, the latter of which contains an intron. The monocistronic Sso-SmAP2 (Sso 5410) transcript is transcribed in the same direction as a methionine adenosyl transferase (MAT) gene.



**Figure S2.** Representation of the Sso-SmAP1 and Sso-SmAP2 surfaces. The extended N-terminus of Sso-SmAP1 forms a protrusion on the L3 face/proximal site that results in distinct grooves (arrows) between the subunits (left panel) while Sso-SmAP2 displays a smoother surface (right panel). Each subunit is displayed in a different colour.

