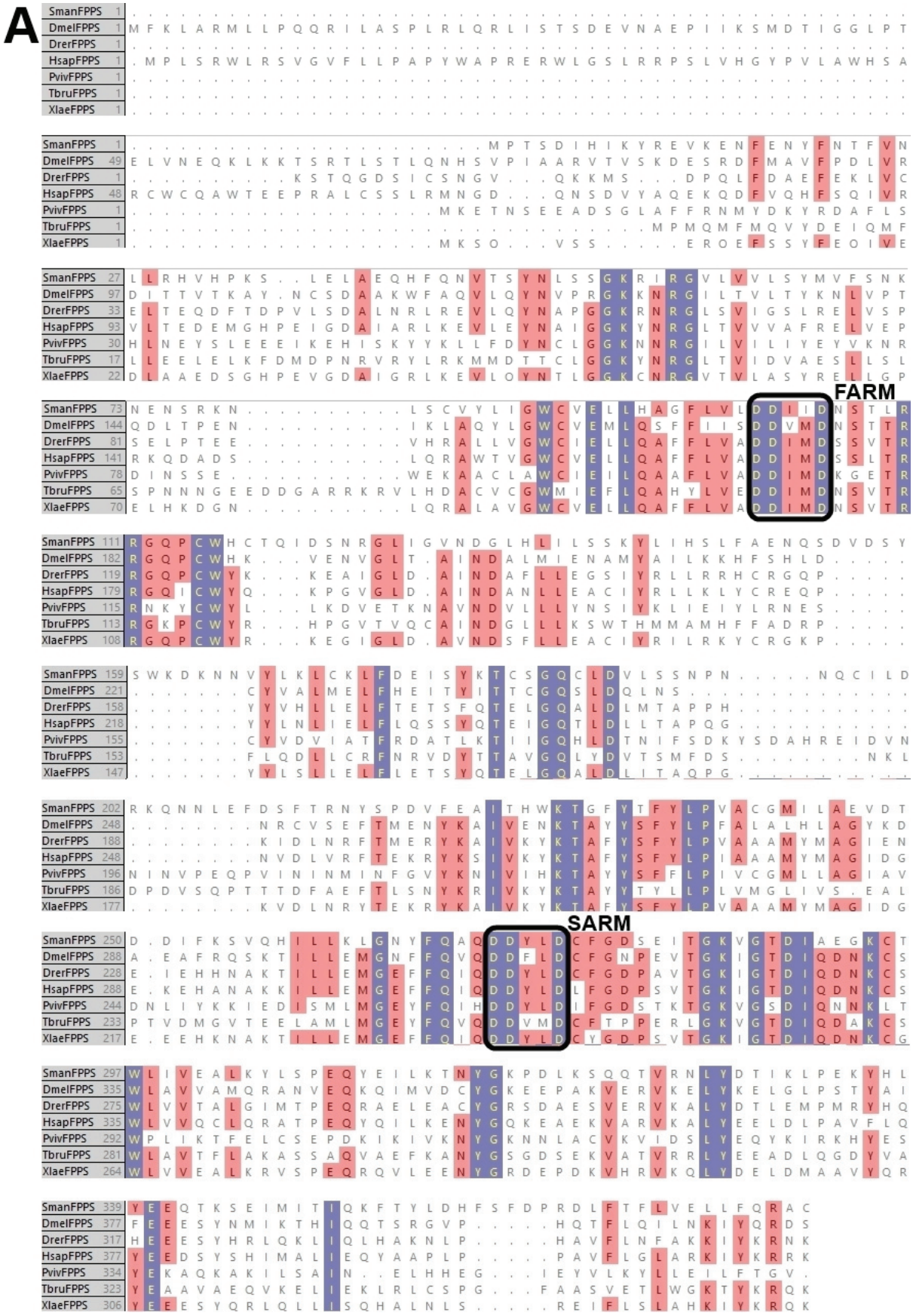
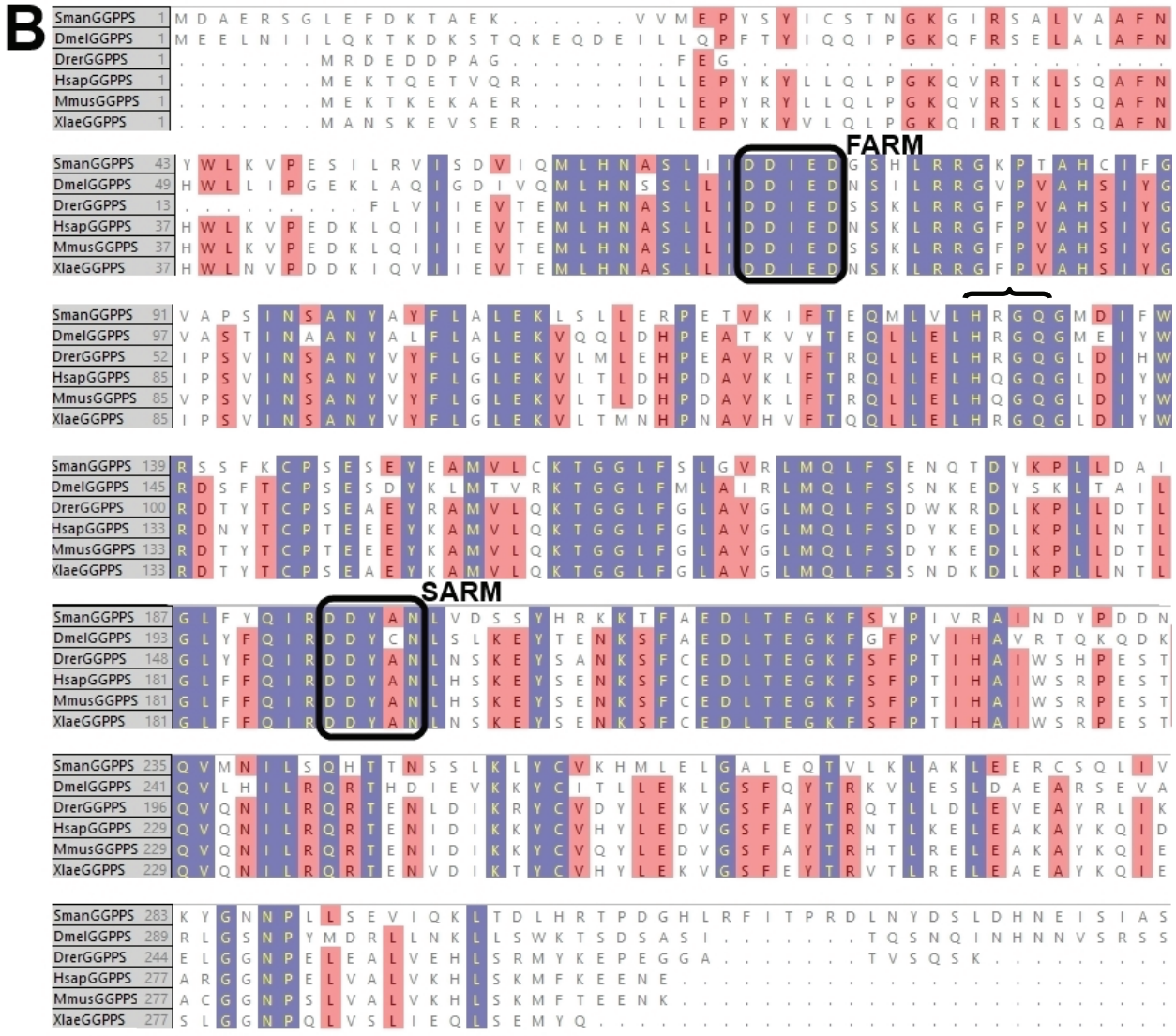
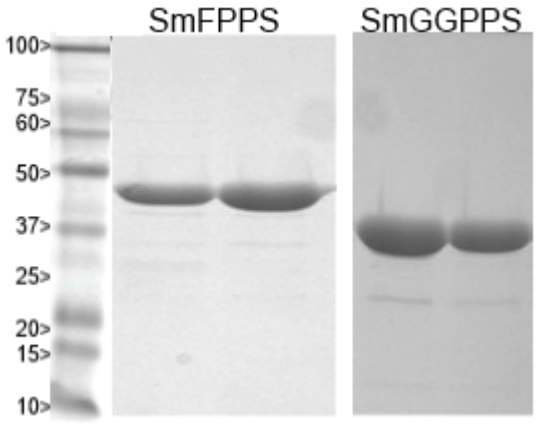

A
SmanFPPS
DmelFPPS
DrerFPPS
HsapFPPS
PvivFPPS
TbruFPPS
XlaeFPPS
FARM
SARM

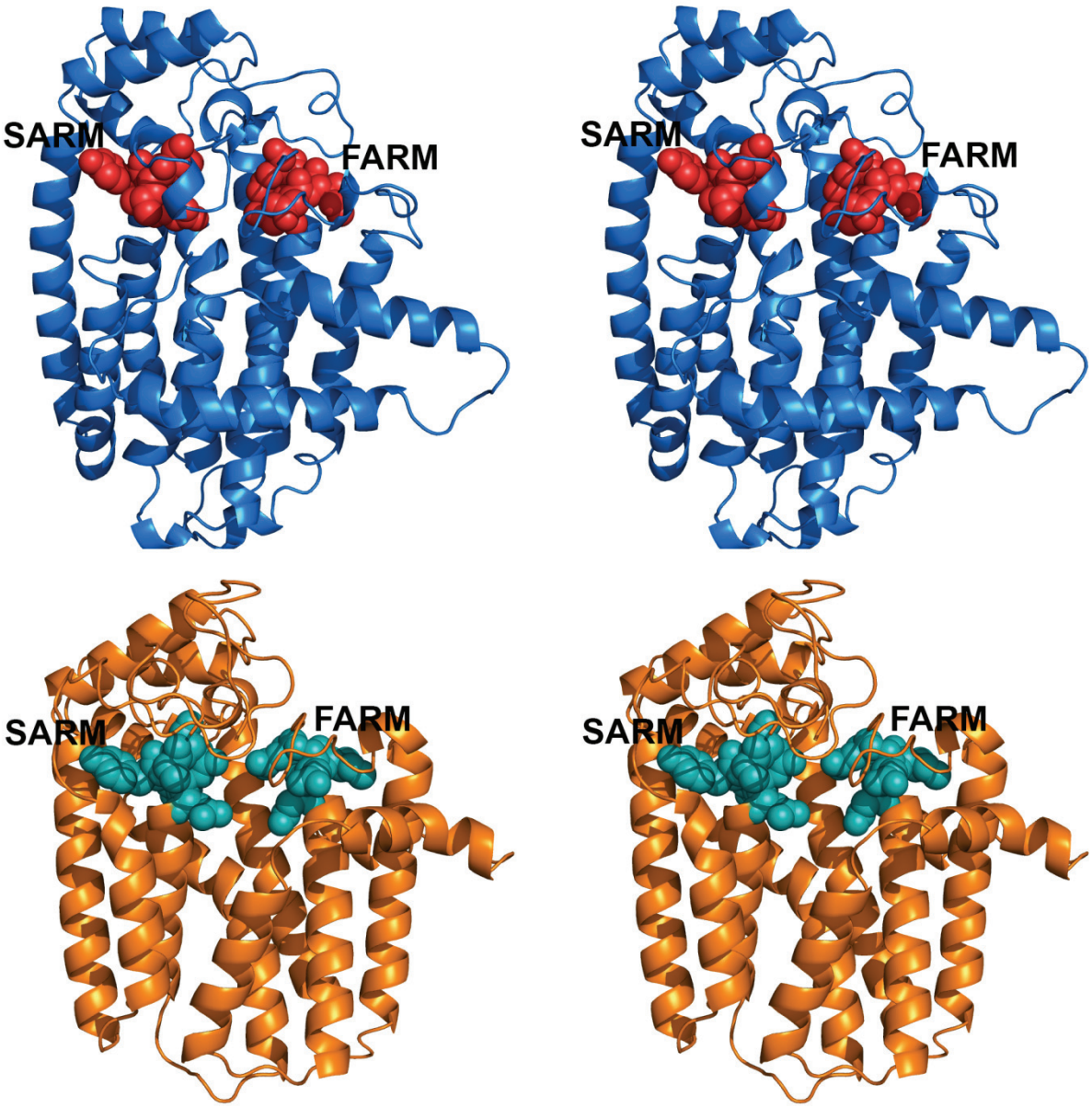


Supplemental FIG. S1: A. Multiple alignment of FPPS proteins. B. Multiple alignment of GGPPS proteins. Protein alignments were done with CLUSTAL W 2.0.12. Multiple alignment results are colored by sequence conserved. The boxed sequences indicate the predicted active sites, first aspartate-rich motif (FARM) and second aspartate-rich motif (SARM), which are highly conserved motifs. Residues determining product chain-length in GGPPS proteins are indicated with a bracket. Accession numbers for the sequences in the alignment are *Xenopus laevis* (Xlae), FPPS: NP_001084626 and GGPPS: NP_001091413; *Danio rerio* (Drer), FPPS: AAH83515 and GGPPS: XP_002664282; *Homo sapiens* (Hsap), FPPS: NP_001995 and GGPPS: NP_004828; *Trypanosoma brucei gambiense* (Tbru), FPPS: CBH12431; *Plasmodium vivax* (Pviv), FPPS: XP_001615401; *Mus musculus* (Mmus), GGPPS:

NP_034412; *Drosophila melanogaster* (Dmel), FPPS: NP_477380 and GGPPS: NP_523958; and *Schistosoma mansoni* (Sman), FPPS: CCD78373 and GGPPS: XP_002573680.



Supplemental FIG. S2: Analysis of purified recombinant *Schistosoma mansoni* FPPS and GGPPS. Recombinant *Sm*FPPS and *Sm*GGPPS were affinity purified on a nickel-affinity column and samples were analyzed by 16% SDS-PAGE with Coomassie stain. The two samples for each protein are the 300 mM imidazole elution fractions for both protein purifications.



Supplemental FIG. S3: Phyre2 (1) structure prediction for A) *Sm*FPPS and B) *Sm*GGPPS.

REFERENCES

1. **Kelley LA, Sternberg MJE.** 2009. Protein structure prediction on the web: a case study using the Phyre server. Nature Protocols. **4:**363-371.