

A

SmanFPPS	1	
DmelFPPS	1	M F K L A R M L L P Q Q R I L A S P L R L Q R L I S T S D E V N A E P I I K S M D T I G G L P T
DrerFPPS	1	
HsapFPPS	1	M P L S R W L R S V G V F L L P A P Y W A P R E R W L G S L R R P S L V H G Y P V L A W H S A
PvivFPPS	1	
TbruFPPS	1	
XlaeFPPS	1	

SmanFPPS	1	
DmelFPPS	49	E L V N E Q K L K K T S R T L S T L Q N H S V P I A A R V T V S K D E S R D F M A V F F P D L V V R
DrerFPPS	1	
HsapFPPS	48	R C W C Q A W T E E P R A L C S S L R M N G D . . . Q N S D V Y A Q E K Q D F V Q H F S Q I V R
PvivFPPS	1	
TbruFPPS	1	
XlaeFPPS	1	

SmanFPPS	27	L L R H V H P K S . . . L E L A E Q H F Q N V T S Y N L S S G K R I R G V L V V L S Y M V F S N K
DmelFPPS	97	D I T T V T K A Y . N C S D A A K W F A Q V L Q Y N V P R G K K N R G I L T V L T Y K N L V P T
DrerFPPS	33	E L T E Q D F T D P V L S D A L N R L R E V L Q Y N A P G G K R N R G L S V I G S L R E L V S P
HsapFPPS	93	V L T E D E M G H P E I G D A I A R L K E V L E Y N A I G G K Y N R G L T V V V A F R E L V E P
PvivFPPS	30	H L N E Y S L E E E I K E H I S K Y Y K L L F D Y N C L G G K N N R G I L V I L I Y E Y V K N R
TbruFPPS	17	L L E E L E L K F D M D P N R V R Y L R K M M D T T C L G G K Y N R G L T V I D V A E S L L S L
XlaeFPPS	22	D L A A E D S G H P E V G D A I G R L K E V L O Y N T L G G K C N R G V T V L A S Y R E L L G P

FARM

SmanFPPS	73	N E N S R K N L S C V Y L I G W C V E L L H A G F L V L D D I I D N S T L R
DmelFPPS	144	Q D L T P E N I K L A Q Y L G W C V E M L Q S F F I I S D D V M D N S T T R
DrerFPPS	81	S E L P T E E V H R A L L V G W C I E L L Q A F F L V A D D I M D S S V T T R
HsapFPPS	141	R K Q D A D S L Q R A W T V G W C V E L L Q A F F L V A D D I M D S S L T T R
PvivFPPS	78	D I N S S E W E K A A C L A W C I E I L Q A A F L V A D D I M D K G E T T R
TbruFPPS	65	S P N N N G E E D D G A R R K R V L H D A C V C G W M I E F L Q A H Y L V E D D I M D N S V T R
XlaeFPPS	70	E L H K D G N L Q R A L A V G W C V E L L Q A F F L V A D D I M D N S V T R

SmanFPPS	111	R G Q P C W H C T Q I D S N R G L I G V N D G L H L I L S S K Y L I H S L F A E N Q S D V D S Y
DmelFPPS	182	R G Q P C W H K . . . V E N V G L T . A I N D A L M I E N A M Y A I L K K H F S H L D
DrerFPPS	119	R G Q P C W Y K . . . K E A I G L D . A I N D A F L L E G S I Y R L L R R H C R G Q P
HsapFPPS	179	R G Q J C W Y Q . . . K P G V G L D . A I N D A N L L E A C I Y R L L K E Y C R E Q P
PvivFPPS	115	R N K Y C W Y L . . . L K D V E T K N A V N D V L L L Y N S I Y K M L I E I Y L R N E S
TbruFPPS	113	R G K P C W Y R . . . H P G V T V Q C A I N D G L L L K S W T H M M A M H F F A D R P
XlaeFPPS	108	R G Q P C W Y R . . . K E G I G L D . A V N D S F L L E A C I Y R I L R K Y C R G K P

SmanFPPS	159	S W K D K N N V Y L K L C K L F D E I S Y K T C S G Q C L D V L S S N P N N Q C I L D
DmelFPPS	221 C Y V A L M E L F H E I T Y I T T C G Q S L D Q L N S
DrerFPPS	158 Y Y V H L L E L F T E S F Q T E L G Q A L D L M T A P P H
HsapFPPS	218 Y Y L N L I E L F L Q S S Y Q T E I G Q T L D L L T A P Q G
PvivFPPS	155 C Y V D V I A T F R D A T L K T I I G Q H L D T N I F S D K Y S D A H R E I D V N
TbruFPPS	153 F L Q D L L C R F N R V D Y T T A V G Q L Y D V T S M F D S N K L
XlaeFPPS	147 Y Y L S L L E L F L E T S Y Q T E L G Q A L D L L I T A Q P G

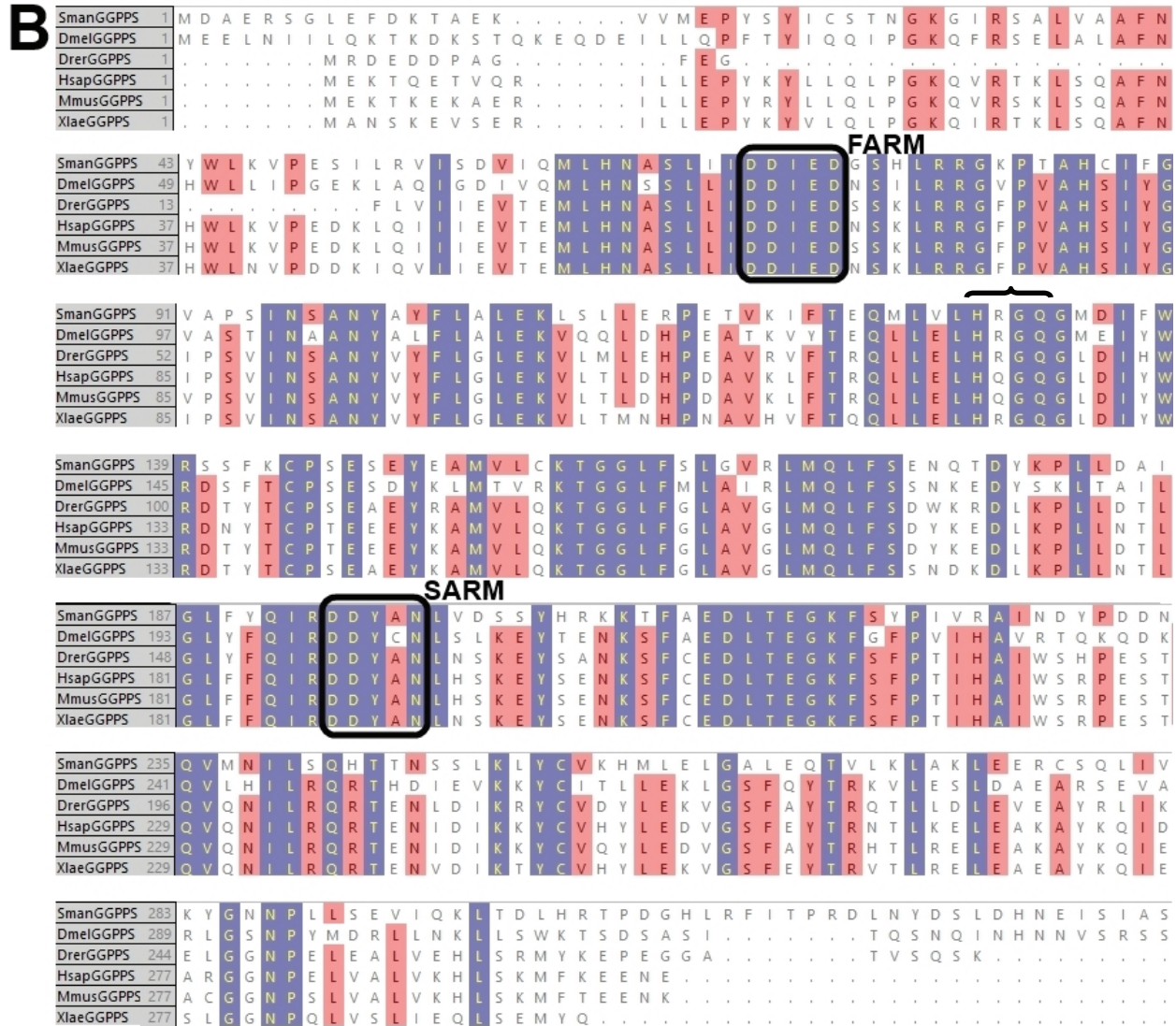
SmanFPPS	202	R K Q N N L E F D S F T R N Y S P D V F E A I T H W K T G F Y T F Y L P V A C G M I L A E V D T
DmelFPPS	248 N R C V S E F T M E N Y K A I V E N K T A Y Y S F Y L P F A A L A L H L A G Y K D
DrerFPPS	188 K I D L N R F T M E R Y K A I V K Y K T A F Y S F Y L P V A A A M Y M A G I E N
HsapFPPS	248 N V D L V R F T E K R Y K S I V K Y K T A F Y S F Y L P I A A A M Y M A G I D G
PvivFPPS	196	N I N V P E Q P V I N I M I N F G V Y K N I V I H K T A Y Y S F F L P I V C G M L L A G I A V
TbruFPPS	186	D P D V S Q P T T D A E F T L S N Y K R I V K Y K T A Y Y T Y L L P L V M G L L I V S . E A L
XlaeFPPS	177 K V D L N R Y T E K R Y K A I V K Y K T A Y Y S F Y L P V A A A M Y M A G I D G

SARM

SmanFPPS	250	D . D I F K S V Q H I L L K L G N Y F Q A Q D D Y L D C F G D S E I T G K V G T D I A E G K C T
DmelFPPS	288	A . E A F R Q S K T I L L E M G N F F Q V Q D D F L D C F G N P E V T G K I G T D I Q D N K C S
DrerFPPS	228	E . I E H H N A K T I L L E M G E F F Q I Q D D Y L D C F G D P A V T G K I G T D I Q D N K C S
HsapFPPS	288	E . K E H A N A K K I L L E M G E F F Q I Q D D Y L D L F G D P S V T G K I G T D I Q D N K C S
PvivFPPS	244	D N L I Y K K I E D I S M L M G E Y F Q I H D D Y L D I F G D S T K T G K V G S D I Q N N K L T
TbruFPPS	233	P T V D M G V T E E L A M L M G E Y F Q V Q D D V M D C F T P P E R L G K V G T D I Q D A K C S
XlaeFPPS	217	E . E E H K N A K T I L L E M G E F F Q I Q D D Y L D C Y G D P S V T G K I G T D I Q D N K C G

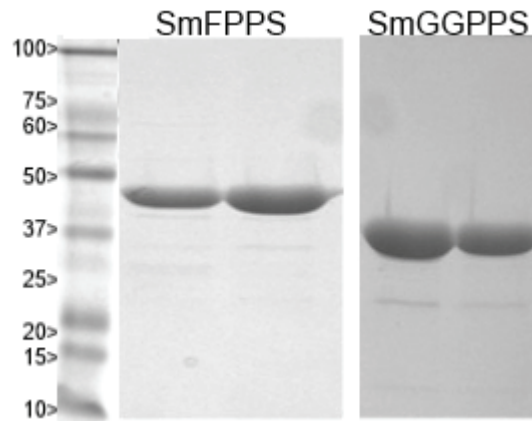
SmanFPPS	297	W L I V E A L K Y L S P E Q Y E I L K T N Y G K P D L K S Q Q T V R N L Y D T I K L P E K Y H L
DmelFPPS	335	W L A V V A M Q R A N V E Q K Q I M V D C Y G K E E P A K V E R V K E L Y K E L G L P S T Y A I
DrerFPPS	275	W L V V T A L G I M T P E Q R A E L E A C Y G R S D A E S V E R V K A L Y D T L E M P M R Y H Q
HsapFPPS	335	W L V V Q C L Q R A T P E Q Y Q I L K E N Y G Q K E A E K V A R V K A L Y E E L D L P A V F L Q
PvivFPPS	292	W P L I K T F E L C S E P D K I K I V K N Y G K N N L A C V K V I D S L Y E Q Y K I R K H Y E S
TbruFPPS	281	W L A V T F L A K A S S A Q V A E F K A N Y G S G D S E K V A T V R R L Y E E A D L Q G D Y V A
XlaeFPPS	264	W L V V E A L K R V S P E Q R Q V L E E N Y G R D E P D K V H R V K Q L Y D E L D M A A V Y Q R

SmanFPPS	339	Y E E Q T K S E I M I T I Q K F T Y L D H F S F D P R D L F T F L V E L L F Q R A C
DmelFPPS	377	F E E E S Y N M I K T H I Q Q T S R G V P H Q T F L Q I L N K I Y Q R R D S
DrerFPPS	317	Y E E E S Y H R L Q M L I Q L H A K N L P H A V F L N F A K K I Y K R R K
HsapFPPS	377	Y E E D S Y S H I X K L I E Q Y A A N P L P A V F L G L A R K I Y K R R K
PvivFPPS	334	Y E K A Q K A K I L S A I N . . . E L H H E G I E Y V L K Y L L E I L F T G V .
TbruFPPS	323	Y E A A V A E Q V K E L I E K L R L C S P G F A A S V E T L W G K T Y K R Q K
XlaeFPPS	306	Y E E E S Y Q R L Q L L I S Q H A L N L S R E I F L S L A H K I Y K R Q K

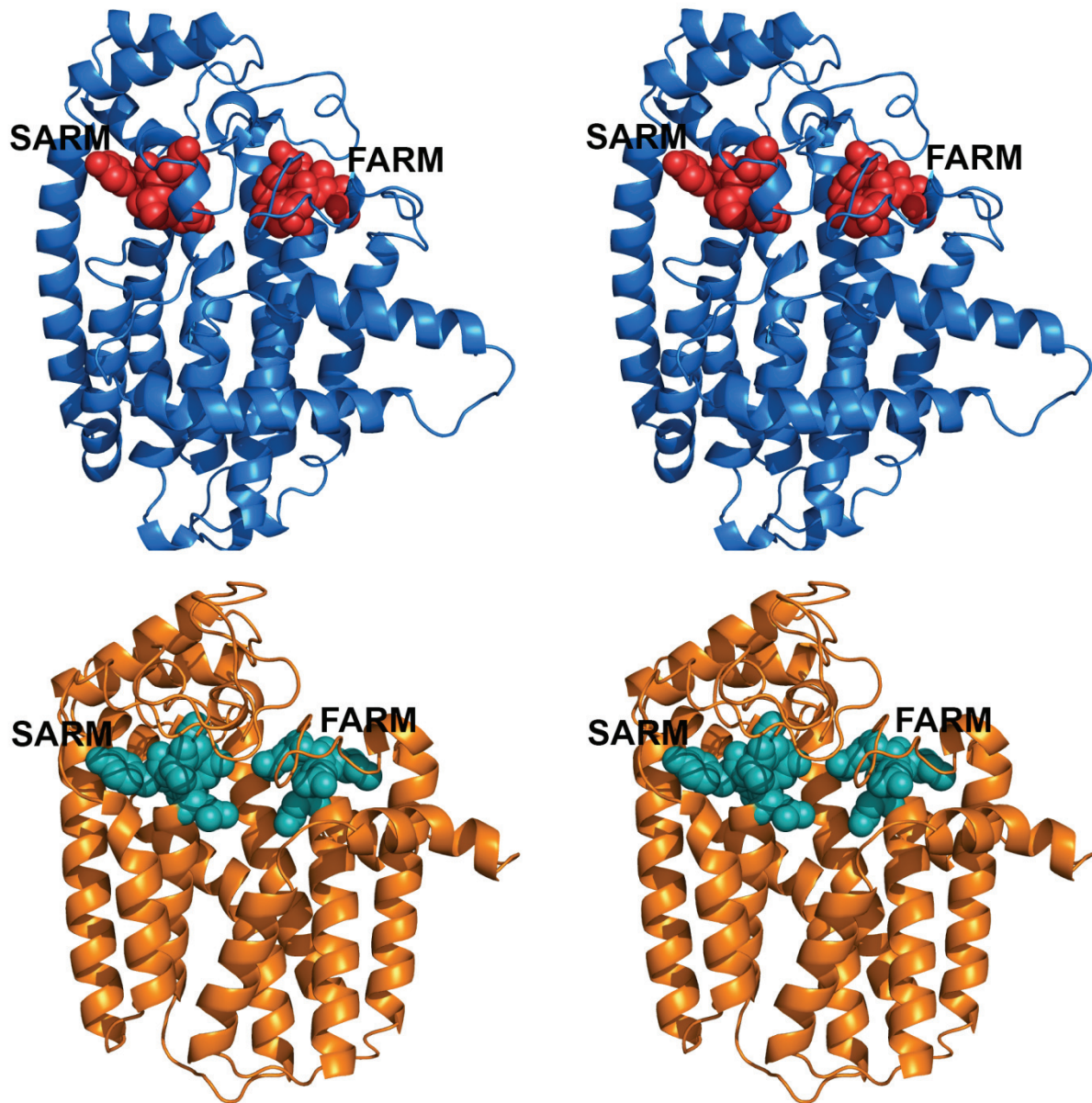


Supplemental FIG. S1: A. Multiple alignment of FPPS proteins. B. Multiple alignment of GGPPS proteins. Protein alignments were done with CLUSTAL W 2.0.12. Multiple alignment results are colored by sequence conserved. The boxed sequences indicate the predicted active sites, first aspartate-rich motif (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 *SmFPPS* and *SmGGPPS* 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) *SmFPPS* and B) *SmGGPPS*.

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.