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Supporting information for article:

**1.45 Å resolution structure of SRPN18 from the malaria vector
*Anopheles gambiae***

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Supporting information

Table S1 Selected top hits of SRPN 18 against the DALI database.

Protein	Source	PDB ID	RMSD (Å)	Residues Aligned	Sequence Identity (%)
Antithrombin	<i>Homo Sapiens</i>	1AZX	2.3	347	18
Alaserpin	<i>Manduca sexta</i>	1K9O	2.2	343	22
Antithrombin III	<i>Homo Sapiens</i>	1NQ9	2.3	343	19
Serpin K	<i>Manduca sexta</i>	1SEK	2.3	376	22
Neuroserpin	<i>Homo Sapiens</i>	3F5N	2.3	364	19
Serpin 2	<i>Anopholes gambiae</i>	3PZF	2.2	369	16
Serpin peptidase inhibitor	<i>Danio rerio</i>	4DTE	2.4	374	22
Protease Nexin-1	<i>Homo Sapiens</i>	4DY7	2.2	378	20
Serpin B1	<i>Homo Sapiens</i>	4GA7	2.3	369	22

Figure S1 Ribbon diagram of the NCS dimer of SRPN18 showing chain A (cyan) and chain B (magenta). The area highlighted with a solid box is magnified in the panel below and highlights the resolved residues of the RCL (red). In chain A, residues G344-P352 were disordered, while in chain B only G342 and S343 were disordered (dashed lines).



