Supplementary Materials:

Crystal structure of native *Anopheles gambiae* Serpin-2, a negative regulator of melanization in mosquitoes

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Supplementary figure legends

Table S1: Structural comparison of An. gambiae SRPN2 with other serpins

Figure S1: 2Fo-Fc electron density map of loop insertion in the P6₃ crystal form.

Figure S2: 2Fo-Fc electron density map of loop insertion in the *I*4₁32 crystal form.

Figure S3. The heparin binding site of ATIII is not conserved in SRPN2.

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. 2Fo-Fc electron density map contoured at 1σ for the $P6_3$ crystal form of the RCL residues (green) that are inserted between the two β-strands (magenta).

Figure S2. 2Fo-Fc electron density map contoured at 1σ for the $I4_132$ crystal form of SRPN2 showing the backbone trace of the loop insertion.

Figure S3. The heparin binding site of ATIII is not conserved in SRPN2. (A) Surface electrostatic potential representation of heparin bound ATIII (PDB: 2GD4). View is perpendicular to the heparin binding site of antithrombin III and the heparin is shown in green as a reference. (B) Surface electrostatic potential representation of Spn48 (PDB:3OZQ), view perpendicular to putative heparin-binding site, which is indicated by yellow arrowheads. Neither binding site is conserved in SRPN2 (C, D). Positive and negative charges are colored blue and red, respectively.

SUPPLEMENTARY TABLE

Table S1. Secondary structure comparison of $An.\ gambiae$ SRPN2 with other serpins.

Protein	Organism	PDB ID	Hinge insertion	RMSD (Å)
Serpin 1K	Manduca sexta	1K9O	no	1.72
Serpin 1B A353K	Manduca sexta	1SEK	no	1.65
Antithrombin III	Homo sapiens	1T1F	yes	1.71
Antithrombin-S195A	Homo sapiens	2GD4	no	1.66
Spn48	Tenebrio molitor	3OZQ	yes	1.56
Murine chymotrypsin	Mus musculus	1YXA	yes	1.62
heparin cofactor II	Homo sapiens	1 JMJ	yes	1.82

Figure S1

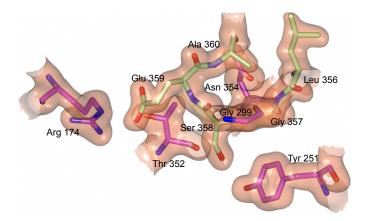


Figure S2

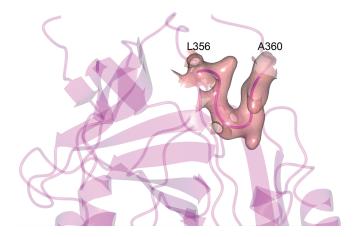


Figure S3

