

Supplementary Material: rDromaserpin: A Novel Anti-Hemostatic Serpin, from the Salivary Glands of the Hard Tick *Hyalomma dromedarii*

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Table S1. GenBank accession numbers of serpins used in the phylogenetic analysis.

Serpin	Tick species	Accession number	% identity	% Coverage	References
Antithrombin III	<i>Homo sapiens</i>	AAB40025.1	31.32	92	[71]
AamS2	<i>Amblyomma americanum</i>	ABS87354.1	60.71	95	[72]
AamS6	<i>Amblyomma americanum</i>	ABS87358.1	45.87	92	[72]
AAS19	<i>Amblyomma americanum</i>	JAI08902.1	38.13	97	[73]
AAS27	<i>Amblyomma americanum</i>	JAI08961.1	39.84	92	[73]
HLS2	<i>Haemaphysalis longicornis</i>	BAD11156.1	45.59	98	[73]
HISerpin-a	<i>Haemaphysalis longicornis</i>	QFQ50847.1	39.84	92	[74]
HISerpin-b	<i>Haemaphysalis longicornis</i>	QFQ50848.1	33.69	91	[47]
Ipis-1	<i>Ixodes persulcatus</i>	BAP59746.1	37.07	91	[47]
Iripin-3	<i>Ixodes ricinus</i>	JAA69032.1	41.33	92	[75]
Iris	<i>Ixodes ricinus</i>	CAB55818.2	37.33	91	[76]
IRS-2	<i>Ixodes ricinus</i>	ABI94056.2	39.75	99	[50]
IxscS-1E1	<i>Ixodes scapularis</i>	AID54718.1	40.27	92	[77]
RAS-2	<i>Rhipicephalus appendiculatus</i>	AAK61376.1	33.24	87	[78]
RAS-1	<i>Rhipicephalus appendiculatus</i>	AAK61375.1	35.2	91	[78]
RAS-3	<i>Rhipicephalus appendiculatus</i>	AAK61377.1	45.06	97	[78]
RAS-4	<i>Rhipicephalus appendiculatus</i>	AAK61378.1	30.45	98	[78]
RmS-1	<i>Rhipicephalus microplus</i>	AHC98652.1	35.64	91	[34]
RmS3	<i>Rhipicephalus microplus</i>	AHC98654.1	47.73	95	[34]
RmS5	<i>Rhipicephalus microplus</i>	AHC98656.1	81.94	97	[34]
RmS-6	<i>Rhipicephalus microplus</i>	AHC98657.1	38.37	97	[34]
RmS-15	<i>Rhipicephalus microplus</i>	AHC98666.1	39.68	92	[34]
RmS-17	<i>Rhipicephalus microplus</i>	AHC98668.1	40.15	98	[34]
RHS-1	<i>Rhipicephalus haemaphysaloides</i>	AFX65224.1	84.51	97	[32]
RHS-2	<i>Rhipicephalus haemaphysaloides</i>	AFX65225.1	34.52	93	[32]
RHS-8	<i>Rhipicephalus haemaphysaloides</i>	QHU78941.1	38.9	98	[32]

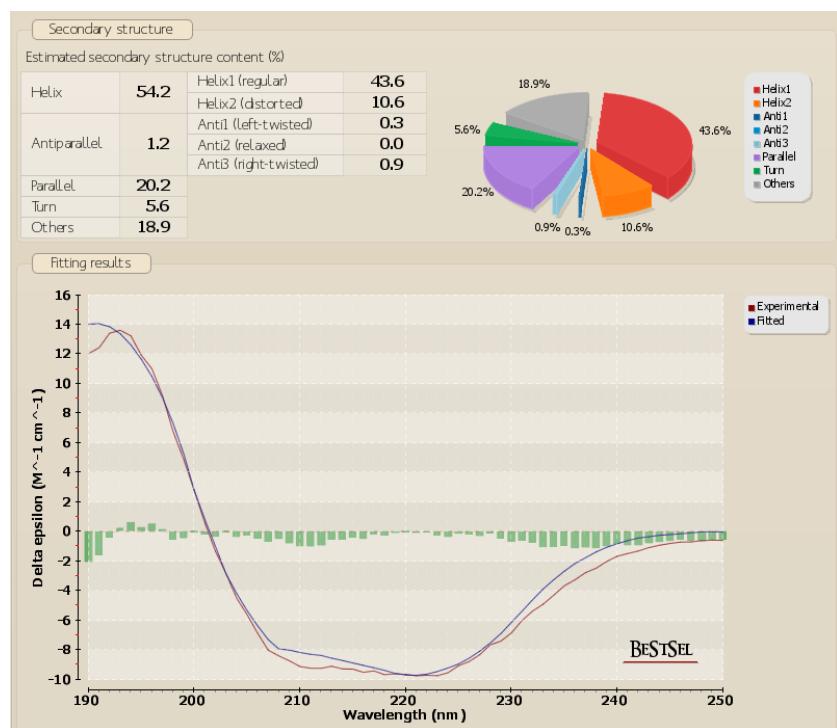


Figure S1. Circular dichroism (CD) spectrum analysis by the BesSel program. Above is described the estimated secondary structure content (%) in rDromaserpin. Below are shown the experimental and predicted CD spectrum by BestSel.

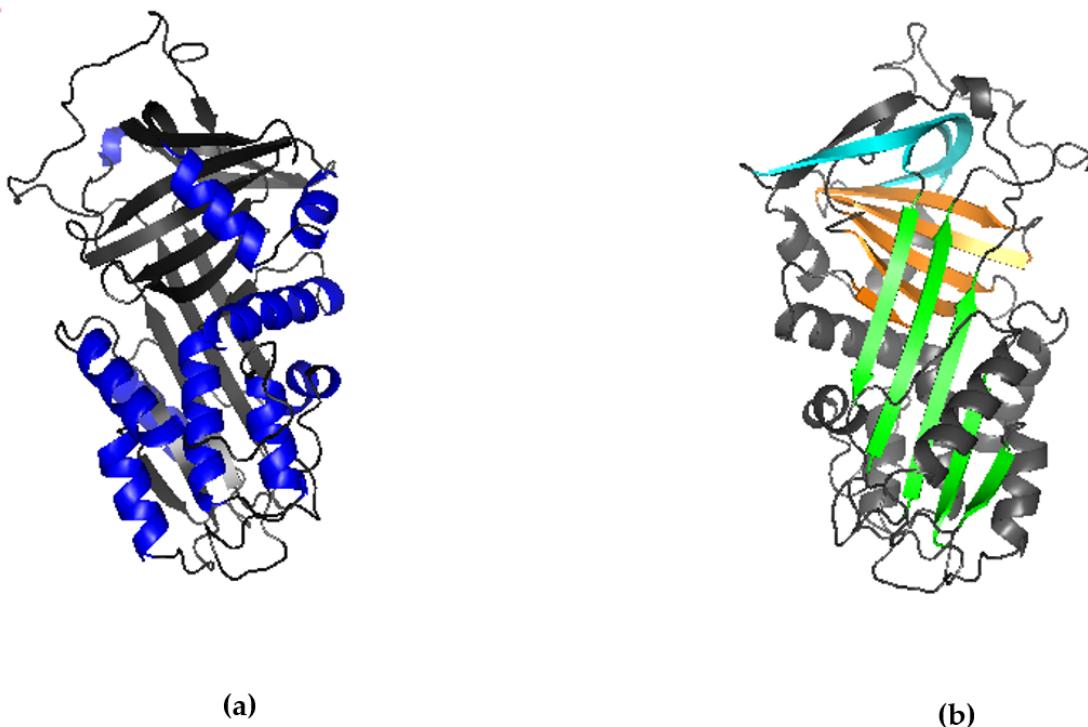


Figure S2. Cartoon representations of the secondary elements in the active model of Dromaserpin. (a) Overall structure of Dromaserpin model adopting a typical serpin fold composed of 8 α -helices colored blue. (b) Rotation 180 ° left of (a) highlighting 3 large β -sheets: β -sheet A is green, β -sheet B is orange, β -sheet C is cyan. Loops are colored grey.

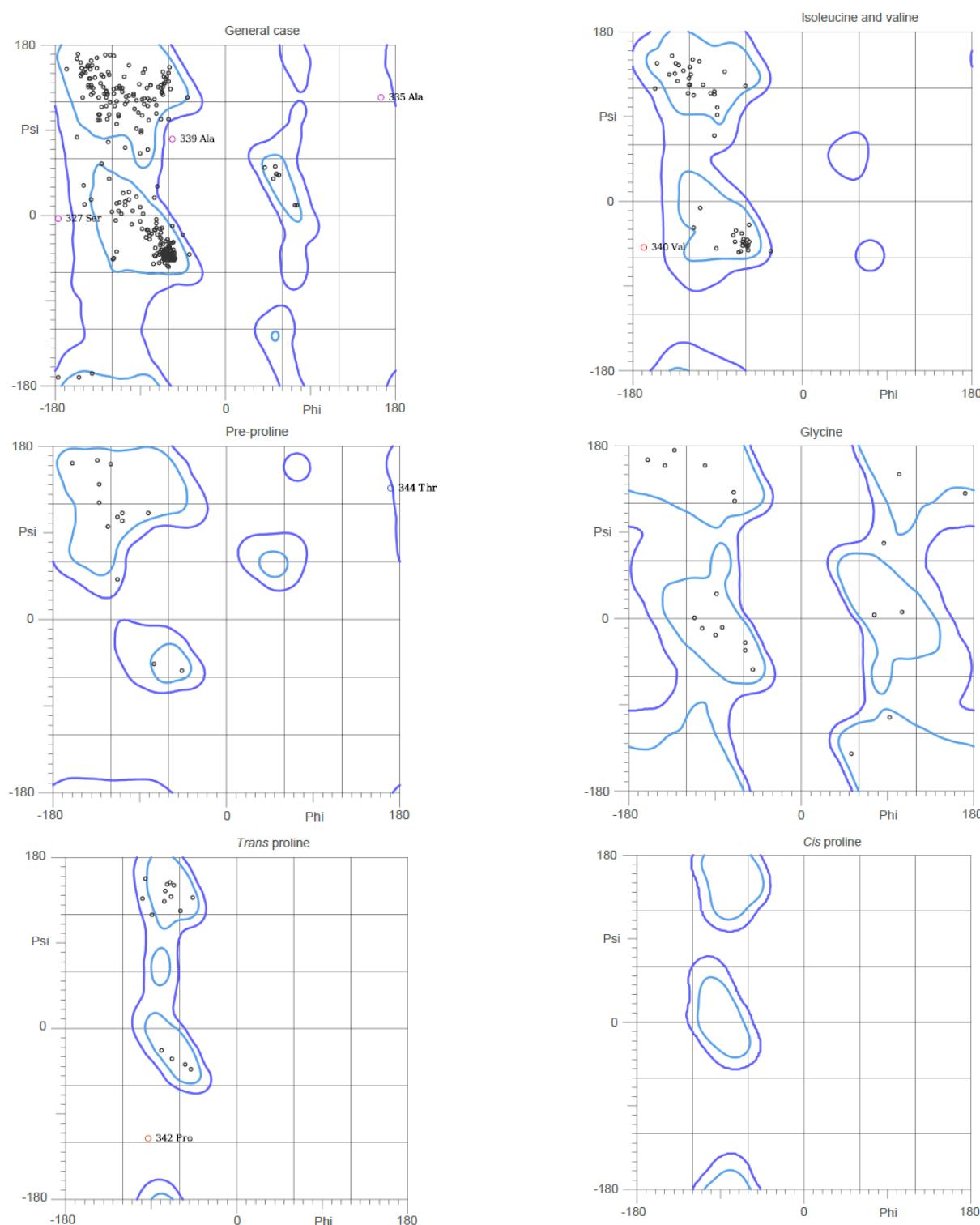


Figure S3. Ramachandran plot of Dromaserpin Model with an exposed reactive center loop (RCL) generated by MolPro-bity program. 91.9% (340/370) of all residues were in favored (98%) regions. 98.4% (364/370) of all residues were in allowed (>99.8%) regions. There were 6 outliers (phi, psi): 327 Ser (-177.1, -3.9), 335 Ala (165.3, 125.3), 339 Ala (-56.3, 81.9), 340 Val (-169.4, -49.3), 342 Pro (-93.7, -116.9), and 344 Thr (171.9, 137.7).

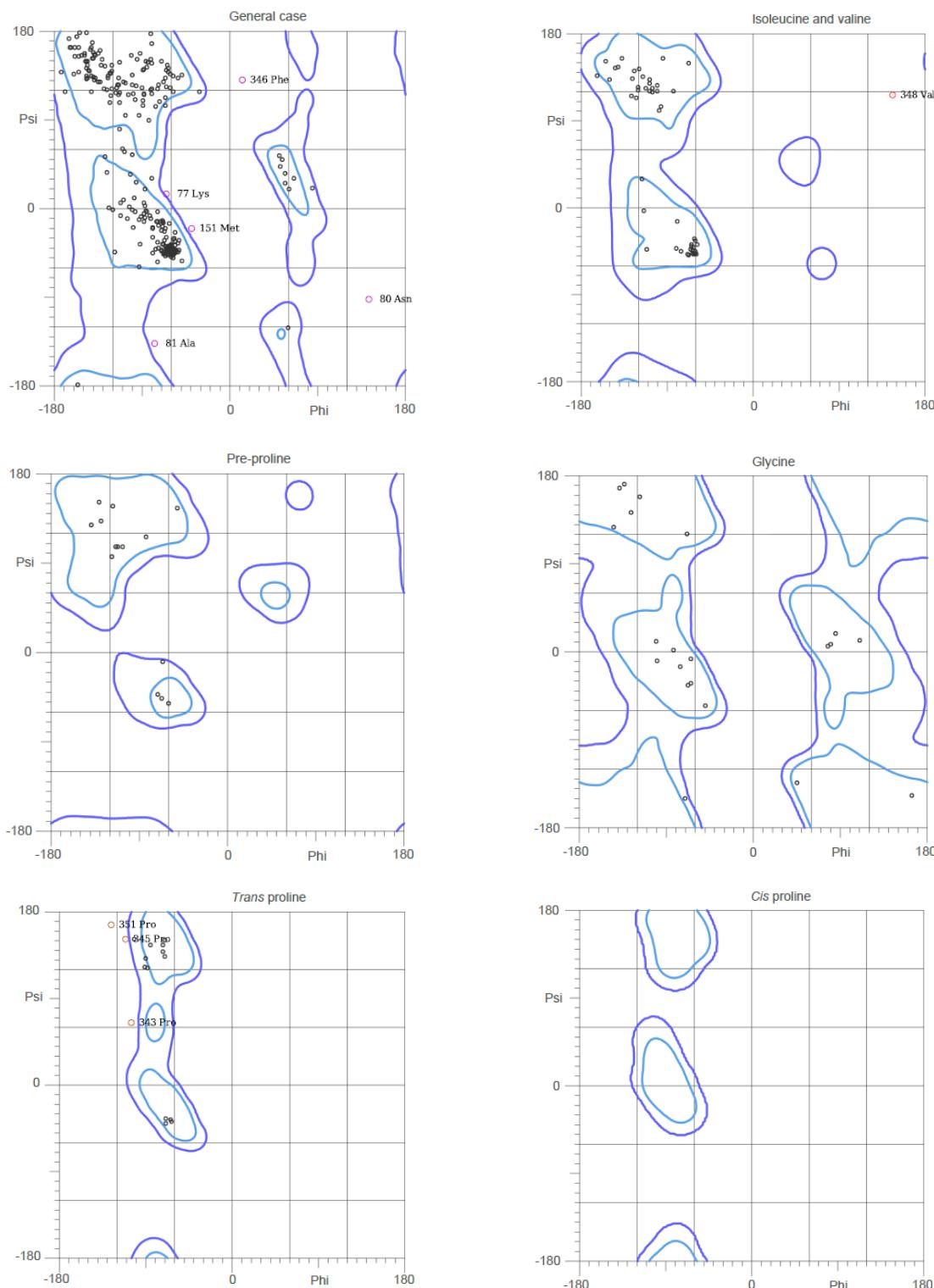


Figure S4. Ramachandran plot of Dromaserpin Model with an inserted RCL generated by MolProbity program. 92.2% (341/370) of all residues were in favored (98%) regions. 97.6% (361/370) of all residues were in allowed (>99.8%) regions. There were 9 outliers (phi, psi): 77 Lys (-65.9, 15.3), 80 Asn (143.2, -92.8), 81 Ala (-77.7, -137.1), 151 Met (-39.8, -20.3), 343 Pro (-105.9, 66.0), 345 Pro (-111.8, 152.5), 346 Phe (13.1, 131.3), 348 Val (146.9, 117.8), and 351 Pro (-126.6, 167.7).

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