Table 1. Selection Analyses: *Psammophis mossambicus* monodomain Snake venom metalloproteinase (SVMP) propeptide

Model	Likelihood (ι)	$\omega_0{}^a$	Parameters	Sign.[b]	No. of Sites with $\omega > 1$[c]
					B.E.B
M0 (One ratio)	-894.467732	0.94	$= \omega_0$		-
M1 (Neutral)	-888.786682	0.71	P_0: 0.313 ω_0: 0.08 P_1: 0.686 $\omega 1$: 1.0		-
M2 (Selection)*	-883.578432	1.24	P_0: 0.238 ω_0: 0.05 P_1: 0.677 ω_1: 1.0 P_2: 0.08 ω_2: 6.56	$P < 0.01$	0 ($PP \geq 0.99$) 1 ($P \geq 0.95$)
M3 (Discrete)*	-883.453150	1.32	P_0: 0.357 ω_0: 0.17 P_1: 0.567 ω_1: 1.26 P_2: 0.075 ω_2: 7.19	$P \ll 0.001$	-
M7 (beta)	-888.908593	0.72	p: 0.04035 q: 0.01444 p_0: 0.914		-
M8 (beta and ω)*	-883.629400	1.23	p: 0.045 q: 0.01 p_1: 0.0853 ω: 6.46	$P < 0.01$	0 ($PP \geq 0.99$) 2 ($P > 0.95$)

Legend:

a: dn/ds (weighted average)

b: Significance of the model in comparison with the null model

c: Number of sites with $\omega > 1$ under the Bayes empirical Bayes approach with a posterior probability (PP) more than or equal to 0.99 and 0.95

* Models which allow $\omega > 1$

Table 2. Selection Analyses: *Echis* monodomain Snake venom metalloproteinase (SVMP) propeptide

Model	Likelihood (ι)	$\omega_0{}^a$	Parameters	Sign.[b]	No. of Sites with $\omega > 1$ [c] B.E.B
M0 (One ratio)	-777.728563	0.39	$= \omega_0$		-
M1 (Neutral)	-776.461469	0.34	P_0: 0.650 ω_0: 0.0 P_1: 0.349 ω_1: 1.0		-
M2 (Selection)*	-775.740783	0.52	P_0: 0.845 ω_0: 0.0 P_1: 0.0 ω_1: 1.0 P_2: 0.154 ω_2: 3.37	$P > 0.05^{N.S}$	0 (PP $\geq$ 0.99) 0 (P $\geq$ 0.95)
M3 (Discrete)*	-775.740783	0.52	P_0: 0.523 ω_0: 0.0 P_1: 0.322 ω_1: 0.0 P_2: 0.154 ω_2: 3.37	$P > 0.05^{N.S}$	-
M7 (beta)	-776.514054	0.40	p: 0.00500 q: 0.00758		-
M8 (beta and ω)*	-775.740783	0.52	p_0: 0.845 p: 0.005 q: 1.60 p_1: 0.154 ω: 3.37	$P > 0.05^{N.S}$	0 (PP $\geq$ 0.99) 0 (P $>$ 0.95)

Legend:

a: dn/ds (weighted average)

b: Significance of the model in comparison with the null model

c: Number of sites with $\omega > 1$ under the Bayes empirical Bayes approach with a posterior probability (PP) more than or equal to 0.99 and 0.95

* Models which allow $\omega > 1$

N. S: Not significant

Table 3. Selection Analyses: *Echis coloratus* multidomain Snake venom metalloproteinase (SVMP) propeptide

Model	Likelihood (ι)	$\omega_0{}^a$	Parameters	Sign.[b]	No. of Sites with $\omega > 1{}^c$
					B.E.B
M0 (One ratio)	-1584.752493	0.39	$= \omega 0$		-
M1 (Neutral)	-1571.361292	0.43	P_0: 0.592 ω_o: 0.03 P_1: 0.407 ω_1: 1.0		-
M2 (Selection)*	-1570.667617	0.46	P_0: 0.603 ω_o: 0.05 P_1: 0.377 ω_1: 1.0 P_2: 0.018 ω_2: 3.11	$P > 0.05^{N.S}$	0 (PP $\geq$ 0.99) 0 (P $\geq$ 0.95)
M3 (Discrete)*	-1570.560349	0.45	P_0: 0.493 ω_o: 0.0 P_1: 0.462 ω_1: 0.74 P_2: 0.043 ω_2: 2.56	$P \ll 0.001$	-
M7 (beta)	-1570.973255	0.43	p: 0.02691 q: 0.03429 p_0: 0.972		-
M8 (beta and ω)*	-1570.607852	0.46	p: 0.119 q: 0.184 p_1: 0.027 ω: 2.84	$P > 0.05^{N.S}$	0 (PP $\geq$ 0.99) 0 (P > 0.95)

Legend:

a: dn/ds (weighted average)

b: Significance of the model in comparison with the null model

c: Number of sites with $\omega > 1$ under the Bayes empirical Bayes approach with a posterior probability (PP) more than or equal to 0.99 and 0.95

* Models which allow $\omega > 1$

N. S: Not significant

Table 4. Selection Analyses: *Echis coloratus* Snake venom metalloproteinase (SVMP) Peptidase M12B

Model	Likelihood (ι)	ω_0[a]	Parameters	Sign.[b]	No. of Sites with $\omega > 1$[c]
					B.E.B
M0 (One ratio)	-2897.950513	1.33	$= \omega 0$		-
M1 (Neutral)	-2900.490765	1.0	P_0: 1.0 ω_0: 1.0 P_1: 0.0 ω_1: 1.0		-
M2 (Selection)*	-2836.001209	1.60	P_0: 0.199 ω_0: 0.0 P_1: 0.476 ω_1: 1.0 P_2: 0.324 ω_2: 3.48	P << 0.001	5 (PP ≥ 0.99) 10 (P ≥ 0.95)
M3 (Discrete)*	-2834.118633	1.75	P_0: 0.305 ω_0: 0.11 P_1: 0.608 ω_1: 1.90 P_2: 0.086 ω_2: 6.55	P << 0.001	-
M7 (beta)	-2862.716038	0.71	p: 0.03801 q: 0.01372		-
M8 (beta and ω)*	-2836.004261	1.60	p_0: 0.672 p: 0.011 q: 0.005 p_1: 0.327 ω: 3.47	P << 0.001	14 (PP ≥ 0.99) 14 (P > 0.95)

Legend:

a: dn/ds (weighted average)

b: Significance of the model in comparison with the null model

c: Number of sites with $\omega > 1$ under the Bayes empirical Bayes approach with a posterior probability (PP) more than or equal to 0.99 and 0.95

* Models which allow $\omega > 1$

Table 5. Selection Analyses: *Echis coloratus* Snake venom metalloproteinase (SVMP) Disintegrin

Model	Likelihood (ι)	$\omega_0{}^a$	Parameters	Sign.[b]	No. of Sites with $\omega > 1$[c]
					B.E.B
M0 (One ratio)	-1014.038058	0.92	$= \omega 0$		-
M1 (Neutral)	-992.288438	0.52	P_0: 0.498 ω_0: 0.05 P_1: 0.501 $\omega 1$: 1.0		-
M2 (Selection)*	-980.305148	1.35	P_0: 0.537 ω_0: 0.16 P_1: 0.219 $\omega 1$: 1.0 P_2: 0.242 ω_2: 4.30	$P \ll 0.001$	3 (PP $\geq$ 0.99) 3 (P $\geq$ 0.95)
M3 (Discrete)*	-980.045669	1.32	P_0: 0.254 ω_0: 0.0 P_1: 0.488 $\omega 1$: 0.53 P_2: 0.257 ω_2: 4.15	$P \ll 0.001$	-
M7 (beta)	-992.774365	0.52	p: 0.02247 q: 0.01935 p_0: 0.746		-
M8 (beta and ω)*	-980.155609	1.33	p: 0.559 q: 0.958 p_1: 0.253 ω: 4.18	$P \ll 0.001$	4 (PP $\geq$ 0.99) 5 (P $>$ 0.95)

Legend:

a: dn/ds (weighted average)

b: Significance of the model in comparison with the null model

c: Number of sites with $\omega > 1$ under the Bayes empirical Bayes approach with a posterior probability (PP) more than or equal to 0.99 and 0.95

* Models which allow $\omega > 1$

Table 6. Selection Analyses: *Echis coloratus* Snake venom metalloproteinase (SVMP) Cysteine-rich Domain

Model	Likelihood (ι)	$\omega_0{}^a$	Parameters	Sign.[b]	No. of Sites with $\omega > 1$[c]
					B.E.B
M0 (One ratio)	-1591.157230	0.97	$= \omega 0$		-
M1 (Neutral)	-1553.512752	0.60	P_0: 0.407 ω_0: 0.02 P_1: 0.592 ω_1: 1.0		-
M2 (Selection)*	-1537.293303	1.43	P_0: 0.320 ω_0: 0.0 P_1: 0.466 ω_1: 1.0 P_2: 0.212 ω_2: 4.57	$P \ll 0.001$	4 (PP $\geq$ 0.99) 4 (P $\geq$ 0.95)
M3 (Discrete)*	-1537.259170	1.49	P_0: 0.327 ω_0: 0.0 P_1: 0.471 ω_1: 1.08 P_2: 0.201 ω_2: 4.87	$P \ll 0.001$	-
M7 (beta)	-1553.495533	0.61	p: 0.02894 q: 0.01687 p_0: 0.788		-
M8 (beta and ω)*	-1537.298493	1.44	p: 0.007 q: 0.005 p_1: 0.211 ω: 4.6	$P \ll 0.001$	6 (PP $\geq$ 0.99) 9 (P $>$ 0.95)

Legend:

a: dn/ds (weighted average)

b: Significance of the model in comparison with the null model

c: Number of sites with $\omega > 1$ under the Bayes empirical Bayes approach with a posterior probability (PP) more than or equal to 0.99 and 0.95

* Models which allow $\omega > 1$

Table 7. Selection Analyses: *Echis coloratus* Snake venom metalloproteinase (SVMP), entire toxin

Model	Likelihood (ι)	ω_0 [a]	Parameters	Sign. [b]	No. of Sites with $\omega > 1$ [c]
					B.E.B
M0 (One ratio)	-7582.537380	0.89	$= \omega 0$		-
M1 (Neutral)	-7417.733058	0.57	P_0: 0.440 ω_0: 0.03 P_1: 0.559 ω_1: 1.0		-
M2 (Selection)*	-7362.356460	1.16	P_0: 0.373 ω_0: 0.0 P_1: 0.421 ω_1: 1.0 P_2: 0.204 ω_2: 3.59	$P \ll 0.001$	9 ($PP \geq 0.99$) 18 ($P \geq 0.95$)
M3 (Discrete)*	-7361.284591	1.20	P_0: 0.496 ω_0: 0.10 P_1: 0.440 ω_1: 1.77 P_2: 0.063 ω_2: 5.88	$P \ll 0.001$	-
M7 (beta)	-7418.843502	0.60	p: 0.02705 q: 0.01615		-
M8 (beta and ω)*	-7362.406809	1.15	p_0: 0.788 p: 0.026 q: 0.023 p_1: 0.211 ω: 3.51	$P \ll 0.001$	14 ($PP \geq 0.99$) 20 ($P > 0.95$)

Legend:

a: dn/ds (weighted average)

b: Significance of the model in comparison with the null model

c: Number of sites with $\omega > 1$ under the Bayes empirical Bayes approach with a posterior probability (PP) more than or equal to 0.99 and 0.95

* Models which allow $\omega > 1$