Supplementary Materials: Naja mossambica mossambica Cobra Cardiotoxin Targets Mitochondria to Disrupt Mitochondrial Membrane Structure and Function

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Table S1. Summary of the charged and polar groups of amino acid residues (a.a.r.) in the VII4 binding sites that interact with polar head groups of truncated CL. Hypothetical binding sites in VII4 that bind to the charged and polar groups of CL as determined by AutoDock modeling. Designation of PO^{4–} groups and carbon atoms in CO^{6–}, CO^{6–}C and C = O^{6–} in CL polar head is shown in Figure S1. Pb in NH_{pb}⁶⁺ denotes a peptide bond.

Site number	CL polar group	VII4 a.a.r. polar group	Bond type
	A PO4-	K12(N+H3) C38 (NHpb ^{d+})	Ionic, Ion-polar
Binding site 1	B PO ₄ -	K12(N+H ₃)	Ionic
Affinity: -4.2 kcal/mol	1 CO ⁵⁻ C	K35(N+H₃) Y22(OH ^{δ+})	Ion-polar, hydrogen
	2 C = O ^{δ-}	K35(N+H ₃)	Ion-polar
	A PO ₄ -	Y51(OH ^{δ+})	Ion-polar
	B PO ₄ -	K35(NH ₃ +) Y22(OH ⁶⁺)	Ionic, Ion-polar
Binding site 2	1 C = O ^{δ−}	$K44(NH_{pb^{\delta+}})$	hydrogen
Affinity -4.1 kcal/mal	CO ⁵⁻	K35(N+H3)	Ion-polar
Ammity. -4.1 Kcal/moi	3 CO ⁵⁻ C	K18(N+H ₃)	Ion-polar
	3 C = O ^{δ−}	K18(N+H3)	Ion-polar
	$4 \text{ C} = \text{O}^{\delta -}$	K12(N ⁺ H ₃) C38(NH _{pb} ^{δ+})	Ion-polar, hydrogen
Binding site 3 Affinity: -4.0 kcal/mol	A PO4-	K35(N ⁺ H ₃)	Ionic
	B PO ₄ -	C38(NH _{pb} ⁶⁺) K12(N ⁺ H ₃)	Ion-polar, ionic
	CO ^{δ-}	K35(N+H3) Y22(OH ⁶⁺)	Ion-polar, hydrogen
	2 C = O ^{δ-}	N40(NH $2^{\delta+}$)	hydrogen
	3 C = O ^{δ−}	K12(N+H ₃)	Ion-polar
	B PO ₄ -	K35(N+H ₃)	Ionic
Binding site 4	2 C = O ^{δ-}	K5(N+H3)	Ion-polar
Affinity: -3.7 kcal/mol	3 C = O ^{δ−}	K12(N+H ₃)	Ion-polar
	4 C = O ^{δ−}	$L6(NH_{pb}^{\delta+})$	Hydrogen
	A PO ₄ -	K18(N+H3)	Ionic
Binding site 5	B PO ₄ -	K12(N+H ₃)	Ionic
Affinity: -3.7 kcal/mol	2 CO ^{5–} C	K12(N+H ₃)	Ion-polar
	3 CO ⁵⁻ C	$L6(NH_{pb}^{\delta+})$	Hydrogen
Binding site 6 Affinity: -3.7 kcal/mol	A PO ₄ -	K35(N+H3) Y22(OH ⁵⁺)	Ionic, Ion-polar
	B PO ₄ -	Y51(OH ^{δ+})	Ion-polar
	1 C = O ^{δ−}	N40(NH2 ⁸⁺) K18(N ⁺ H3)	Hydrogen, Ion-polar,
	2 C = O ^{δ-}	K18(N+H ₃)	Ion-polar
	CO ⁵⁻	Y51(OH ^{δ+})	Hydrogen
	3 C = O ^{δ−}	S46(OH ^{δ+})	Hydrogen
	4 C = O ^{δ−}	K44(N+H3)	Ion-polar
Binding site 7 Affinity: -3.6 kcal/mol	A PO ₄ -	K12(N+H3)	Ionic
	B PO4-	$L6(NH_{pb}^{\delta+})$	Ion-polar

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	2 C = O ^{δ-}	K12(N+H ₃)	Ion-polar
	$3 \text{ C} = O^{\delta -}$	K12(N ⁺ H ₃) C38(NH _{pb} ^{δ+})	Ion-polar, hydrogen
Binding site 8 Affinity: -3.5 kcal/mol	B PO4-	Y51(OH ^{δ+})	Ion-polar
	1 C = O ^{δ−}	K35(N+H ₃)	Ion-polar
	$2 \text{ C} = \text{O}^{\delta -}$	K35(N+H ₃)	Ion-polar
	3 C = O ^{δ−}	Y51(OH ^{δ+})	Hydrogen
Binding site 9 Affinity: –3.5 kcal/mol	A PO4-	R36(= N+H ₂) R36(NH ₂ ^{δ+})	Ionic, ion-polar
	CO ^{δ-}	R36(NH ₂ ^{δ+})	Hydrogen
	4 CO ^{δ−} C	$R58(NH2^{\delta+})$	Hydrogen

Table S2. Summary of the charged and polar groups of amino acid residues (a.a.r.) in the VII4 binding sites that interact with polar head groups of complete CL molecule. Hypothetical binding sites in VII4 that bind to the charged and polar groups of CL as determined by AutoDock modeling. Designation of PO^{4–} groups and carbon atoms in CO^{6–}, CO^{6–}C and C = O^{6–} in CL polar head is shown in Figure S1. Pb in NH_{Pb}⁶⁺ denotes a peptide bond.

Site number	CL polar group	1CDT a.a.r. polar group	Bond type
Binding site 1	A PO ₄ -	R58(NH2 ⁸⁺)	Ion-polar
Affinity: -4.2	1 C = O ^{δ−}	K23(N+H3) R36(NH2 ⁰⁺)	Ion-polar,
kcal/mol			Hydrogen
	$3 \text{ C} = 0^{\circ}$	$19(NH_{Pb}^{\delta+})$	hydrogen
Binding site 2	CO ⁸⁻	$R58(NH_{2^{0+}}) R58(= N^{+}H_{2})$	Hydrogen, ion-polar
Affinity: –4.2	3 CO⁵-C	$R36(NH_{2^{5+}})$	Hydrogen
kcal/mol	$3 \text{ C} = O^{\delta - 1}$	$R36(=N+H_2)$	Ion-polar
Binding site 3			
Affinity; –4.1 kcal/mol	A PO₄⁻	K23(N+H ₃) R36(NH ₂ ⁸⁺)	Ionic, Ion-polar
	B PO4-	K23(N+H ₃)	Ionic
	3 CO ^o -C	R36(NH2 ^{δ+})	Hydrogen
Din din a site 4	A PO4-	K35(N+H ₃)	Ionic
Binding site 4	B PO ₄ -	L6(NH _{pb} ^{δ+}) K12(N ⁺ H ₃)	Ion-polar, ionic
Affinity: -4.0	CO ⁸⁻	Y22(OH ^{δ+})	Hydrogen
Kcal/mol	$1 \text{ C} = O^{\delta -}$	K18(N+H ₃)	Ion-polar
Binding site 5 Affinity: -3.9 kcal/mol	3 C = O ^{δ-}	C42(NH _{pb} ^{δ+})	Hydrogen
Binding site 6			
Affinity: –3.9 kcal/mol	A PO ₄ -	K12(N+H ₃) R36(NH ₂ ⁵⁺)	Ionic, Ion-polar
	2 C = O ^{δ-}	$R36(=N^{+}H_{2})$	Ion-polar
	3 C = O ^{δ−}	$I9(NH_{pb^{\delta+}})$	hydrogen
Binding site 7 Affinity: -3.8 kcal/mol Binding site 8	A PO4-	R36(= N+H2) R36(NH2 ⁵⁺) K23(N+H3)	Ionic, Ion-polar, ionic
Affinity: -3.8 kcal/mol	A PO4-	$R36(NH_{2^{\delta+}})$	Ion-polar
Binding site 9	2 CO ⁸⁻ C	R36(= N ⁺ H ₂) R36(NH ₂ ^{δ+})	Ion-polar, hydrogen
Affinity: -3.8 kcal/mol	A PO4-	$I9(NH_{pb}^{\delta +})$	Ion-polar
	B PO₄⁻	K12(N+H ₃)	Ionic
	CO ⁸⁻	$L6(NH_{pb}^{\delta+})$	Hvdrogen
	3 C = O ^{δ−}	R36(NH _{pb} ^{δ+})	Hydrogen

Table S3. Summary of the charged and polar groups of amino acid residues (a.a.r.) in the VII4 binding sites that interact with polar head groups of truncated PC. Hypothetical binding sites in VII4 that bind to the charged and polar groups of PC as determined by AutoDock modeling. Designation of carbon atoms in CO^{b–}C and C = O^{b–} in PC polar head is shown in Figure S1. Pb in NH_{Pb}^{b+} denotes a peptide bond.

Site number	PC polar group	1CDT a.a.r. polar group	Bond type
Dia dia 5 site 1	PO4-	K12(N+H3) C38 (NHpb ^{b+})	Ionic, Ion-polar
Affinity: –3.9 kcal/mol	1 CO ⁵⁻ C	K12(N+H ₃)	Ion-polar
	1 C = O ^{δ−}	$L6(NH_{pb}^{\delta+})$	Hydrogen
Dinding site 2	PO4 ⁻	K12(N+H ₃)	Ionic
Affinity 2.0 keel/mel	1 C = O ^{δ−}	R36 (NH _{pb} ^{δ+})	Hydrogen
Annity: -3.9 Kcal/mol	2 C = O ^{δ-}	K12(N ⁺ H ₃) C38(NH _{pb} ^{δ+})	Ion-polar, hydrogen
Binding site 3 Affinity: -3.7 kcal/mol	PO ₄ -	K12(N+H ₃)	Ionic
	1 C = O ^{δ−}	$L6(NH_{pb}^{\delta+})$	Hydrogen
	2 C = O ^{δ-}	K12(N ⁺ H ₃) C38(NH _{pb} ^{δ+})	Ion-polar, hydrogen
Binding site 4	PO ₄ -	K18(N+H3) N40(NH2 ⁵⁺)	Ionic, ion-polar
Affinity: -3.7 kcal/mol	1 C = O ^{δ−}	K35(N+H ₃)	Ion-polar
Binding site 5	PO ₄ -	$K12(N^{+}H_{3}) C38(NH_{pb}^{\delta+})$	Ionic, ion-polar
Affinity: -3.6 kcal/mol	1 C = O ^{δ−}	K12(N+H ₃)	Ion-polar
Binding site 6 Affinity: -3.5 kcal/mol	PO4 ⁻	$K12(N^{+}H_{3}) C38(NH_{Pb}^{\delta^{+}})$	Ionic, ion-polar
Binding site 7 Affinity: –3.4 kcal/mol	PO ₄ -	I7(NH _{pb} ^{δ+}) L6(NH _{pb} ^{δ+})	Ion-polar
	1 C = O ^{δ−}	$R36(NH_{2^{\delta+}})$	Hydrogen
	2 C = O ^{δ-}	K12(N+H3)	Ion-polar
Binding site 8 Affinity: -3.4 kcal/mol	PO4-	$R58(NH_{2^{\delta+}})$	Ion-polar
	2 CO ^{5–} C	$R58(NH_{2^{\delta+}}) R58(= N^+H_2)$	Hydrogen, ion-polar
Binding site 9 Affinity: -3.4 kcal/mol	PO ₄ -	R36(= N+H ₂) R36(NH ₂ $^{\delta+}$)	Ionic, ion-polar

Table S4. Summary of the charged and polar groups of amino acid residues (a.a.r.) in the VII4 binding sites that interact with polar head groups of complete PC. Hypothetical binding sites in VII4 that bind to the charged and polar groups of PC as determined by AutoDock modeling. Designation of carbon atoms in $CO^{b-}C$ and $C = O^{b-}$ in PC polar head is shown in Figure S1. Pb in NH_{Pb}^{b+} denotes a peptide bond.

Site number	PC polar group	1CDT a.a.r. polar group	Bond type
Binding site 1	PO -	K12(N+H3) K18(N+H3) C38	Ionic, ionic, ion-
Affinity: -4.4	ΓO_4	$(\mathrm{NH}_{\mathrm{pb}^{\delta+}})$	polar
kcal/mol	2 CO ^{8–} C	K35(N+H ₃)	Ion-polar
Binding site 2	PO ₄ -	Y51(OH ^{δ+})	Ion-polar
Affinity: -4.3	2 CO ^{8–} C	K35(N+H ₃)	Ion-polar
kcal/mol	1 C = O ^{δ-}	K35(N+H ₃)	Ion-polar
Binding site 3			
Affinity: -4.2	PO ₄ -	R36(= N+H2) R36(NH2 ^{δ+})	Ionic, ion-polar
kcal/mol			
Binding site 4	PO ₄ -	K35(N+H ₃)	Ionic
Affinity: -4.1	$2CO^{b-C}$	V25/NI+LI_)	Ion nolar
kcal/mol	200°C	K35(IN ⁺ H3)	ion-polar
Binding site 5	PO ₄ -	R36(NH ₂ ⁵⁺)	Ion-polar

Affinity –4.1 kcal/mol	2 CO ^s -C	R36(= N+H ₂)	Ion-polar
Binding site 6			
Affinity -4.0	1 C = O ^{δ−}	K44(N+H ₃)	Ion-polar
kcal/mol			
Binding site 7			
Affinity: -4.0	PO ₄ -	S46(OH ⁶⁺)	Ion-polar
kcal/mol			
Binding site 8			
Affinity: -4.0	PO ₄ -	K50(N+H ₃)	Ionic
kcal/mol			
	2 CO⁵-C	N45(NH _{pb$^{\delta+}$})	Hydrogen
Binding site 9			
Affinity: -4.0	PO ₄ -	K29(N+H ₃)	Ionic
kcal/mol			
	2 CO⁵-C	K29(N+H ₃)	Ion-polar



Figure S1. The marking of the charged and polar groups in the CL polar head.



Figure S2. The marking of the charged and polar groups in the PC polar head.