Additional Materials

>Lc1|*C. unicolor*|383410|pI: 5.21|Mw: 55.9 kDa

MSFNAAFATFLTLALAASVYAALGPVIDLHIVNT[35]NISTDGFTRPAVLAGGTFPGPVITAKKGDNFQVNVIDDLTNEAMLKSTSIHWHGLFQKGTNWADGP 100

AFVSQCPIISGNSFLYEFSVPDQAGTYWYHSHLSTQYCDGLRGVLVIYDPDDPHAGLYDVDDENTIITLADWYHTFARQIPGLPIADTTLINGLGRNH[199]NG 200

SADAELSVINVHAGKRYRFRLVSISCDPNYVFSIDDH[238]NMTVIEVEGTNVKPLTVDSIQIFAAQRYSFVLHADRPAGNYWIRANPSFGNTGFAGHINSAIL 300

RYDGAPCVEPHTRQTNSTKPLNEIDLHPLVPIPVPGKPYPGGVDVVKNLVFNFTDGHYTINNATFTPPSVPVLLQILSGTTSAQGLLPSGDVIELPLGKT 400

VEITLAAGVIGGPHPFHLHGHSFHVVRSACQNTSNYIDPIVRDTVNIGNMGDNVTIRFTTDNPGPWFLHCHIDWHLEAGFAVVLAEGMNETRAANPTPDE 500

WDSLCDTYNALPSGDQ* 516

>Lc2|*C. unicolor*|408157|pI: 5.13|Mw: 57.6 kDa

MGSKSSILTFTIFALALGSYAAIGPVADLHIVNKDLAPDGVTRPTILAGGTFPGPLITGQKGDNFKLNVIDELTDERMLTPTSIHWHGFFQKGTNWADGP 100

AFVNQCPIIPDNSFLYDFNVPDQAGTFWYHSHLSTQYCDGLRGAFVVYDPEDPHKDLYDVDDDSTVITLADWYHVLAPTVKFTATPDSTLINGLGRSHDG 200

PADAELAVIEVEQGKRYRFRLVNIGCFPNYDFSIDGH[238]NMTIIEVEGVNSQPHTVDSIQIFVAQRYSFVLNANQPVDNYWVKAVPNLGDKSTDGGINSAIL 300

RYKGAPVAEPKTRNVKSRMPLLETDLHPLERMPVPGRPVPGGADIVHLLDLSFSSDRFFI[361]NGSSYRDPPVPVLLQILSGVKTAQDLLPAGNVIGLELGKV 400

VEVIIPPRAHDGPHPFHLHGHNFWVVRSAGSKEYNFDDPILRDVVSIGGGNDEVTIRFVTDNAGPWFLHCHIDWHLEAGLAVVFAEGIESTAAANPTPQQ 500

WDELCPKYNALIQSQRALINNSTVN* 525

Figure S1 Protein sequences of Lc1 and Lc2 from *Cerrena unicolor*. Amino acids in bold indicate a putative signal peptide. Predicted N-glycosylation sites are in blue.

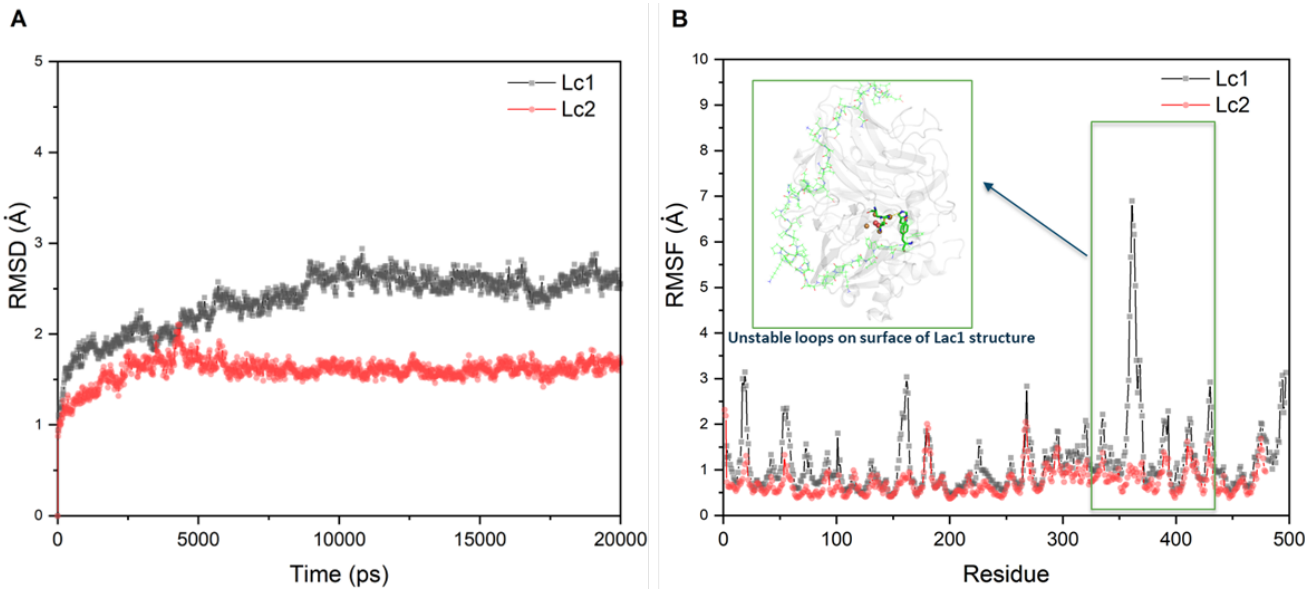

Figure S2 Time course of RMSD for Lc1 and Lc2 (A) and per-residue RMSF flexibility (B) of Lc1 and Lc2 for 50 ns of MD simulation at 333.15 K. The inset image shows the surface loop for which the RMSF larger in Lc1.

Table S1 Salt-bridge network analysis for structural models of Lc1 and Lc2. The analysis was conducted using VMD software. Salt bridges were as defined as a negatively charged oxygen atom of an acidic residue being within 3.2 Å of a positively charged nitrogen atom of basic residue.

Lc1: 35 salt-bridge bonds		**Lc2: 43 salt-bridge bonds**	
Non-homologous salt-bridges	**Homologous salt-bridges**	**Homologous salt-bridges**	**Non-homologous salt-bridges**
Asp_{63} - Lys_{60}	Asp_{122} - Lys_{92}	Asp_{122} - Lys_{92}	Asp_{35} - Arg_{77}
Asp_{122} - Lys_{61}	Asp_{139} - Arg_{43}	Asp_{139} - Arg_{43}	Asp_{35} - Lys_{34}
Asp_{151} - Lys_{61}	Asp_{149} - Lys_{61}	Asp_{149} - Lys_{61}	Asp_{75} - Arg_{77}
Asp_{159} - Lys_{215}	Asp_{152} - Arg_{218}	Asp_{152} - Arg_{218}	Asp_{117} - Lys_{66}
Asp_{236} - Arg_{273}	Asp_{159} - Arg_{216}	Asp_{159} - Arg_{216}	Asp_{156} - Arg_{216}
Asp_{236} - Arg_{313}	Asp_{161} - Arg_{218}	Asp_{161} - Arg_{218}	Asp_{156} - Lys_{155}
Asp_{272} - Arg_{273}	Asp_{161} - Arg_{220}	Asp_{161} - Arg_{220}	Asp_{203} - Arg_{196}
Asp_{325} - Lys_{319}	Asp_{171} - Arg_{142}	Asp_{171} - Arg_{142}	Asp_{231} - Lys_{289}
Asp_{515} - Lys_{80}	Asp_{235} - Arg_{281}	Asp_{235} - Lys_{281}	Asp_{231} - Lys_{316}
Glu_{76} - Lys_{80}	Asp_{255} - Lys_{319}	Asp_{255} - Arg_{318}	Asp_{276} - Lys_{311}
Glu_{245} - Arg_{264}	Asp_{344} - Lys_{337}	Asp_{344} - Arg_{337}	Asp_{292} - Arg_{313}
	Asp_{344} - Lys_{399}	Asp_{344} - Lys_{399}	Asp_{350} - Arg_{408}
	Asp_{438} - Lys_{250}	Asp_{438} - Arg_{331}	Asp_{356} - Lys_{181}
	Asp_{443} - Arg_{264}	Asp_{443} - Arg_{264}	Asp_{35} - Arg_{77}
	Asp_{452} - Arg_{427}	Asp_{452} -Arg_{427}	Asp_{35} - Lys_{34}
	Asp_{461} - Lys_{92}	Asp_{461} - Lys_{92}	Asp_{367} - Arg_{366}
	Glu_{243} - Arg_{218}	Glu_{243} - Arg_{218}	Asp_{437} - Arg_{331}
	Glu_{243} - Arg_{220}	Glu_{243} - Arg_{220}	Asp_{452} - Arg_{408}
	Glu_{245} - Arg_{442}	Glu_{245} - Arg_{442}	Asp_{452} - Lys_{432}
	Glu_{309} - Arg_{196}	Glu_{309} - Arg_{196}	
	Glu_{323} - Arg_{442}	Glu_{323} - Arg_{442}	
	Glu_{394} - Arg_{492}	Glu_{396} - Lys_{399}	
	Glu_{402} - Arg_{457}	Glu_{402} - Arg_{457}	
	Glu_{477} - Arg_{178}	Glu_{477} - Lys_{181}	