

1 **Targeting the artemisinin resistant malaria by repositioning of the anti-hepatitis C virus drug**
2 **alisporivir**

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5 Ayushi Chaurasiya^{1#}, Geeta Kumari^{1#}, Swati Garg¹, Rumaisha Shoaib¹, Zille Anam¹, Nishant
6 Joshi², Jyoti Kumari², Jhalak Singhal¹, Niharika Singh¹, Shikha Kaushik¹, Amandeep Kaur
7 Kahlon¹, Neha Dubey³, Mukesh Kumar Maurya¹, Pallavi Srivastava¹, Manisha Marothia¹,
8 Gobardhan Das¹, Souvik Bhattacharjee¹, Shailja Singh^{1*} and Anand Ranganathan^{1*}

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11 ¹Special Centre for Molecular Medicine, Jawaharlal Nehru University, New Delhi, 110067 India

12 ²Department of Life Sciences, School of Natural Sciences, Shiv Nadar University, Greater Noida,
13 Uttar Pradesh, 201304 India

14 ³Department of Molecular Microbiology, Washington University in St. Louis, USA

15 # Co-first authors

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17 Running title: Antimalarial repositioning of Alisporivir

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19 Correspondence: anand.icgeb@gmail.com; shailja.jnu@gmail.com

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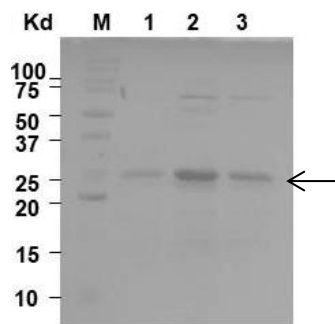
31 **TABLE S1** Primer sequences

<i>PfCyclophilin 19B For</i>	5'-AAGAATTCTACGTAACCTATTTTGATATAACTATC-3'
<i>PfCyclophilin 19B Rev</i>	5'-AAGAATTCTACGTACAATGGCAATTCTCCTGATTC-3'
<i>Pf18S For</i>	5'-CCGCCCGTCGCTCCTACCG-3'
<i>Pf18S Rev</i>	5'-CCTTGTTACGACTTCTCCTTCC-3'

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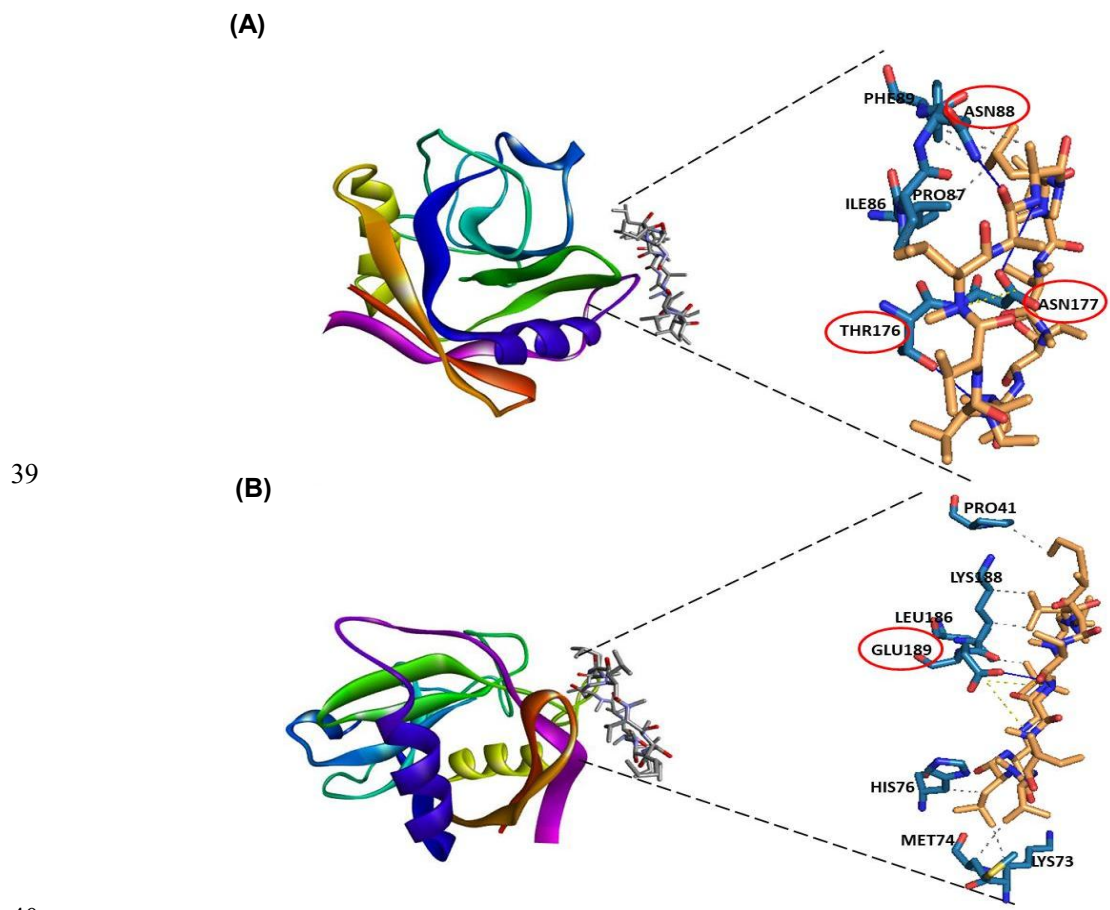
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36 **Supplementary Fig 1.** SDS-PAGE gel of purified *PfCyclophilin 19B* protein. Lane (1-3) show
37 purified recombinant *PfCyclophilin 19B* protein. Lane M shows the protein molecular weight
38 marker.

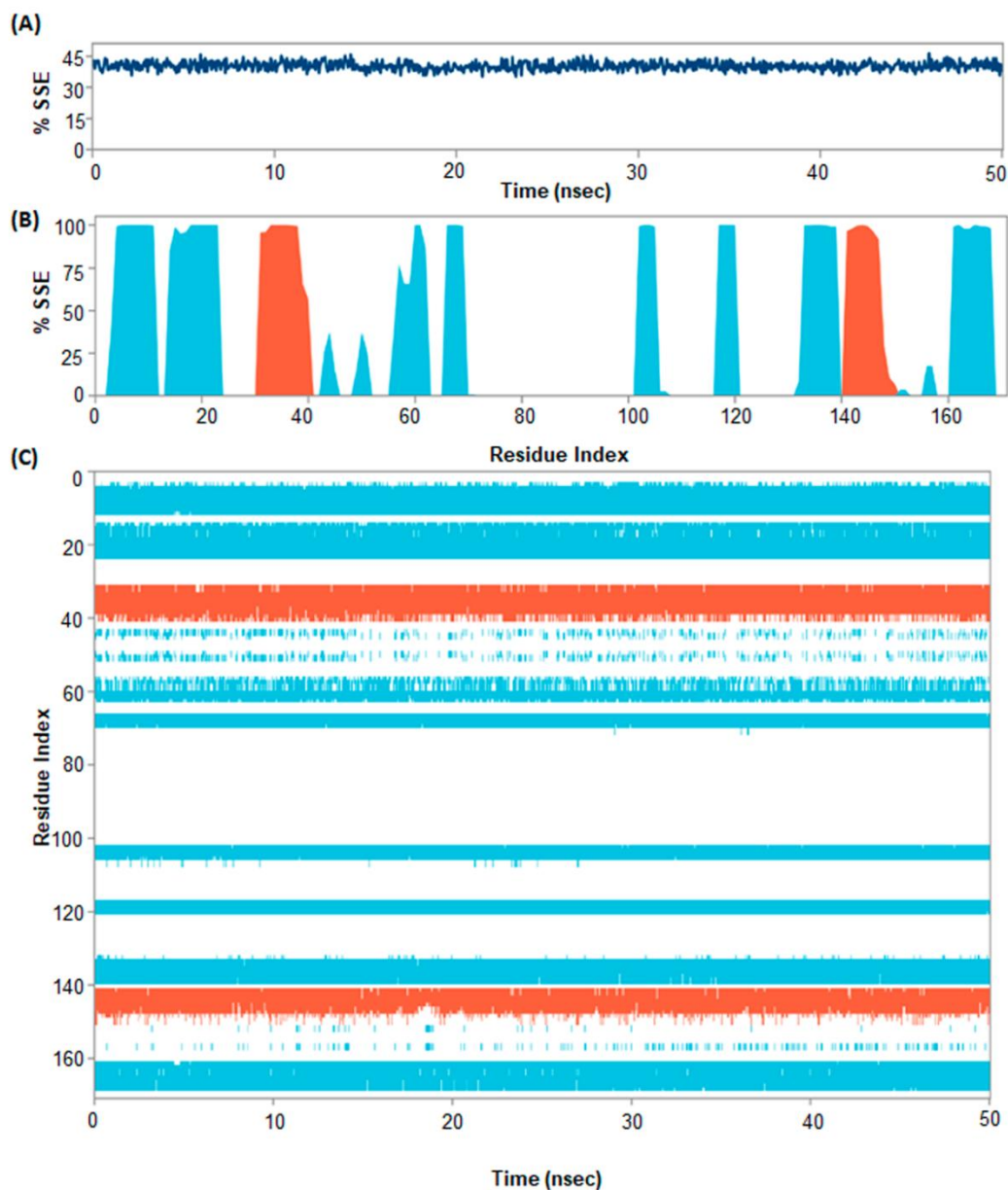


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Alisporivir- <i>PfCyclophilin 19B</i>								
Min. binding energy=-5.72Kcal/mol								
Index	Residue	AA	Distance H-A	Distance D-A	Donor Angle	Donor Atom	Acceptor Atom	
1	88	ASN	1.63	2.64	174.63	574 [Nam]	1610 [O3]	
2	176	THR	3.38	3.91	117.48	1400 [O3]	1568 [N3]	
3	177	ASP	3.36	3.93	116.66	1580 [N3]	1410 [O2]	
CyclosporinA- <i>PfCyclophilin 19B</i>								
Min. binding energy=-5.27Kcal/mol								
1	189	GLU	2.24	2.8	115.78	1605 [O3]	1528 [O2]	

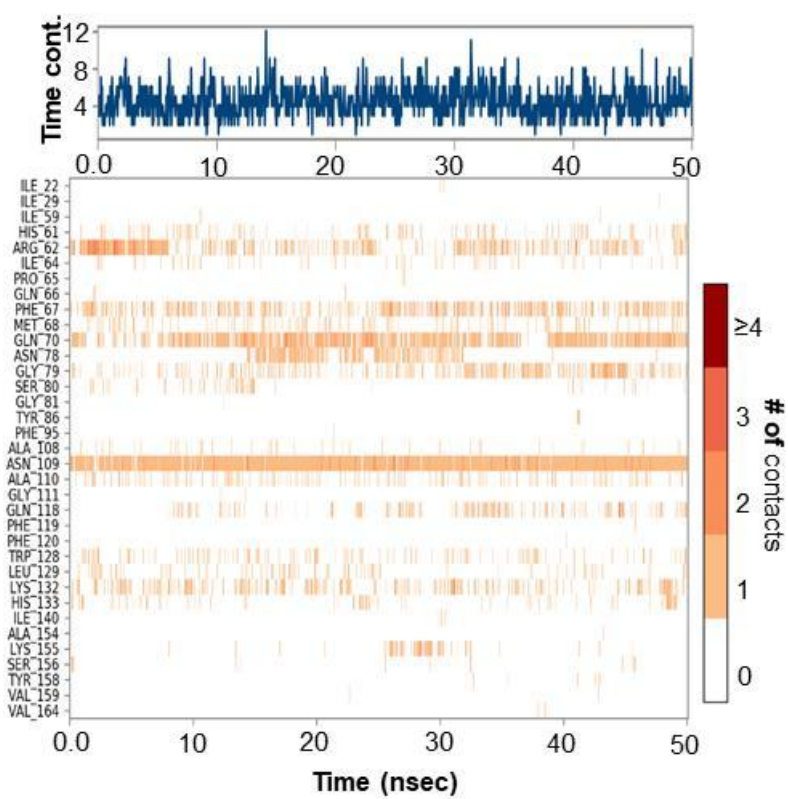
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42 **Supplementary Fig 2.** (A) The 3D ribbon model of alisporivir-*PfCyclophilin 19B* complex with
 43 interacting residues of drug and protein (B) The 3D ribbon model of cyclosporinA-
 44 *PfCyclophilin 19B* complex with interacting residues of drug and protein. Details of hydrogen
 45 binding residues of cyclosporinA-*PfCyclophilin 19B* and alisporivir-*PfCyclophilin 19B* complex.



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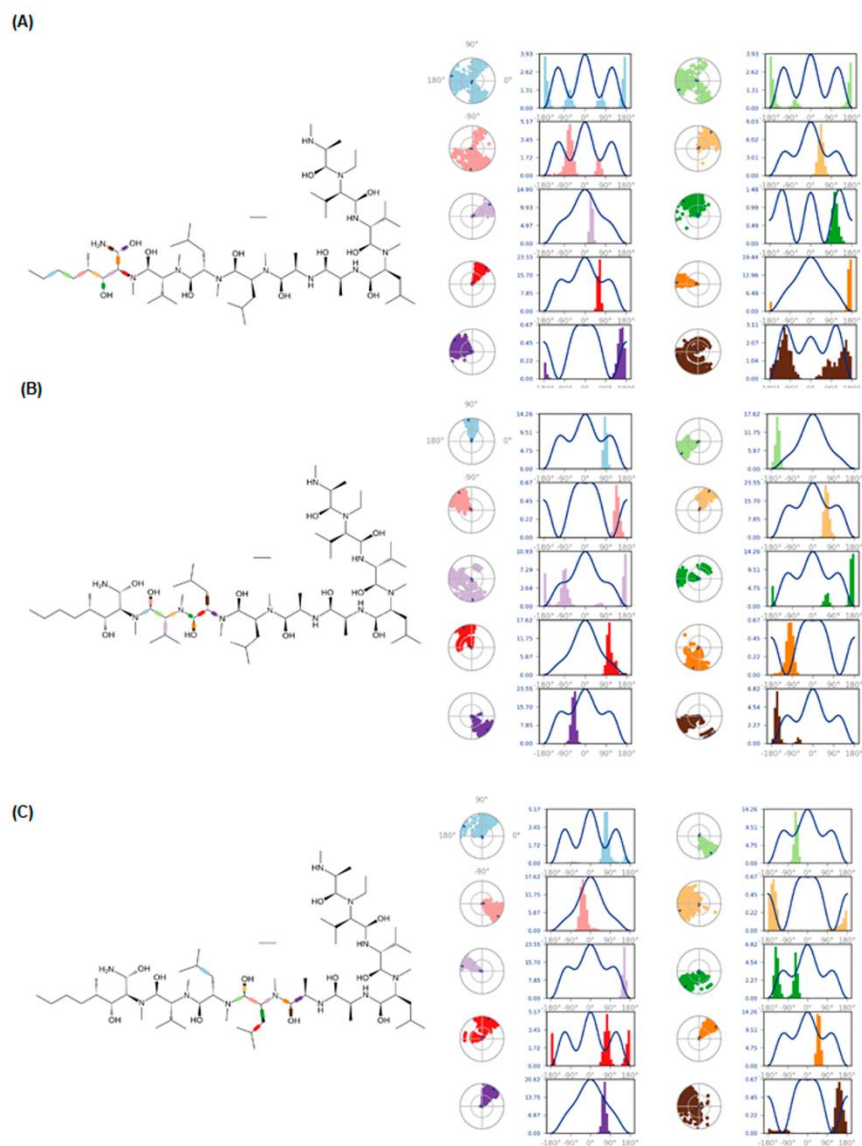
48 **Supplementary Fig 3.** Change in the overall secondary structure of *Pf*Cyclophilin 19B-
 49 alisporivir complex during 50 ns simulation. (A) The plot summarizes the secondary structure
 50 elements (SSE) composition for each trajectory frame over the course of the simulation. (B and
 51 C) the plot monitors each residue and its SSE assignment over time.



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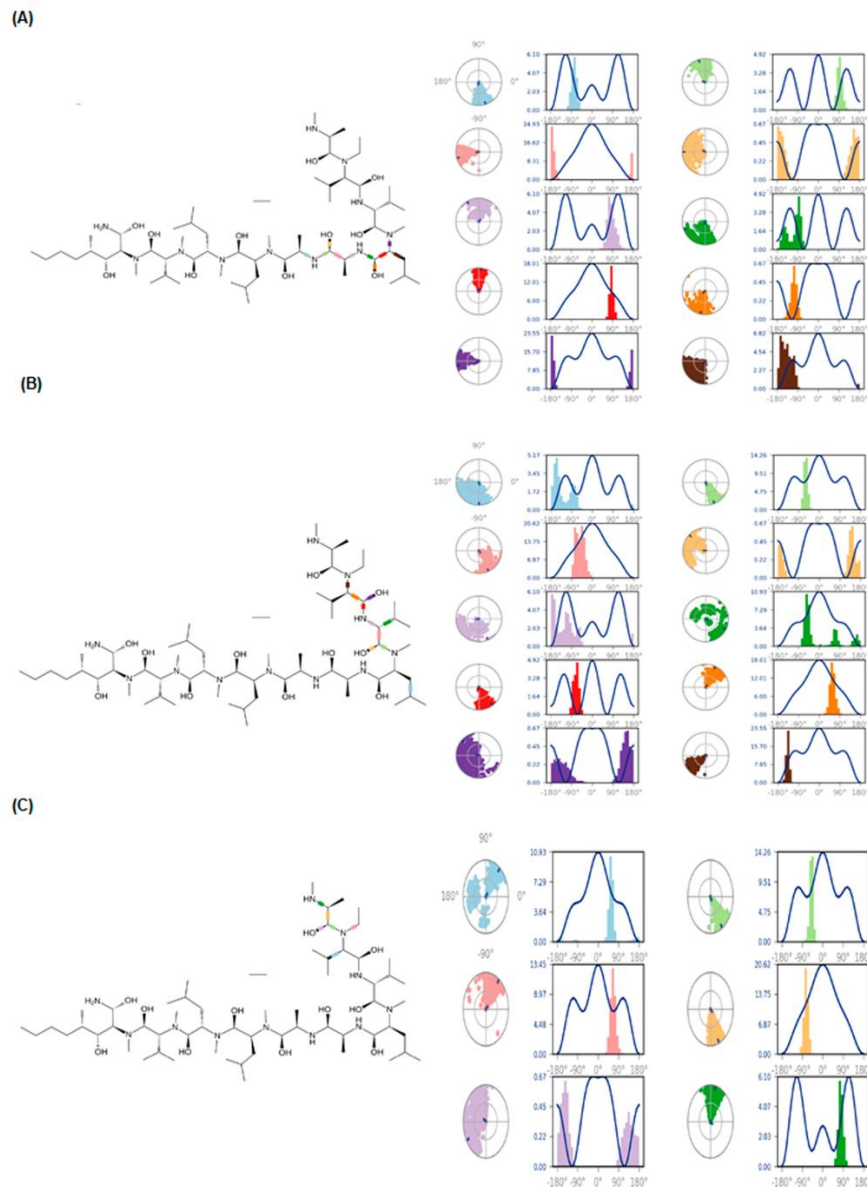
53 **Supplementary Fig 4.** Analysis of total contacts formed between *Pf*Cyclophilin 19B residues

54 and alisporivir during MD simulation.



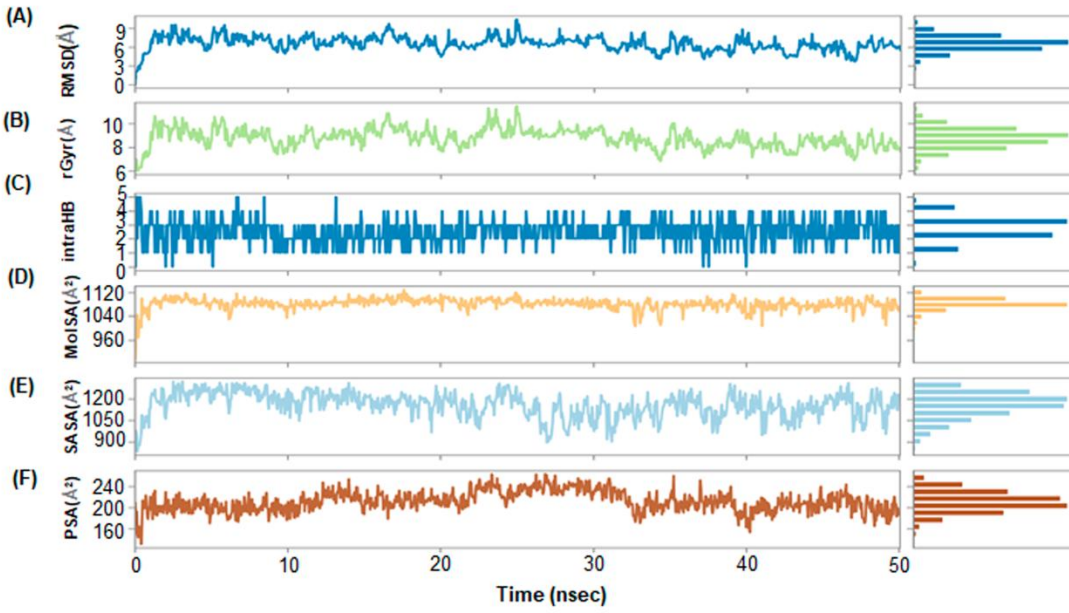
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56 **Supplementary Fig 5.** Ligand alisporivir properties during simulation. (A, B and C). The
 57 rotatable bonds in alisporivir has been showed in different colors in the alisporivir structure (ten
 58 bonds at a time) is shown in left. Analysis of torsional degree of freedom during MD simulation
 59 trajectory for the rotatable bonds present in the alisporivir. The dial plots of the angle of each
 60 corresponding rotatable bond after simulations are displayed in the left, and the bar charts of the
 61 torsional probability as a function of angle are shown in the right.



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63 **Supplementary Fig 6.** Ligand alisporivir properties during simulation. (A, B and C). The
 64 rotatable bonds in alisporivir has been showed in different colors in the alisporivir structure (ten
 65 bonds at a time) is shown in left. Analysis of torsional degree of freedom during MD simulation
 66 trajectory for the rotatable bonds present in the alisporivir. The dial plots of the angle of each
 67 corresponding rotatable bond after simulations are displayed in the left, and the bar charts of the
 68 torsional probability as a function of angle are shown in the right.



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70 **Supplementary Fig 7.** Fluctuations in the alisporivir properties over 50 ns simulation. (A)
 71 Ligand RMSD (B) Radius of gyration (C) Intramolecular Hydrogen Bonds (D) Molecular
 72 surface area (E) Solvent accessible surface area (F) Polar surface area.

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