Electronic Supplementary Material (ESI) for Molecular Systems Design & Engineering. This journal is © The Royal Society of Chemistry 2023

# 1 In vitro neutralisation of Zika virus by an engineered protein targeting the

2 viral envelope fusion loop

3 Isabelle F.T. Viana<sup>a,‡</sup>; Carlos H.B. Cruz<sup>a,b,‡</sup>; Diogo Athayde<sup>b,‡</sup>; W. Camilla S. Adan<sup>a,c</sup>; Lícya S.S. Xavier<sup>a</sup>; Margarida
 4 Archer<sup>b,\*</sup>; Roberto D. Lins<sup>a,c,\*</sup>

5

- <sup>a</sup>Department of Virology, Aggeu Magalhães Institute, Oswaldo Cruz Foundation, Recife, 507407 465, Brazil.
- 8 <sup>b</sup>Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, ITQB
- 9 NOVA, Oeiras, 2780-157, Portugal.
- 10 <sup>c</sup>Department of Fundamental Chemistry, Federal University of Pernambuco, Recife, 50740-540,
- 11 Brazil.
- 12 \*These authors contributed equally to this work, and therefore share primary authorship.
- 13 \*Corresponding authors: roberto.neto@fiocruz.br (ORCID 0000-0002-3983-8025);
  14 archer@itqb.unl.pt (ORCID 0000-0001-8419-5420)
- 15
- 16 SUPPLEMENTARY INFORMATION
- 17 Additional methods. Thermal unfolding of the ZIKV Env and ZVPA3 protein complex by18 circular dichroism
- 19 Supporting Figure S1. ZVPA3 production

20 **Supporting Figure S2.** Statistics of X-ray diffraction data collection/processing and 21 crystallographic refinement

- 22 Supporting Figure S3. Thermal stability of the ZIKV Env and ZVPA3 protein complex.
- 23 Supporting Figure S4. Assessment of flavivirus neutralization *in vitro*.

### 24 ADDITIONAL METHODS

#### 25 Thermal unfolding of the ZIKV Env and ZVPA3 protein complex by circular dichroism

26 The ZIKV Envelope and ZVPA3 proteins were diluted at the 1:3.75 ZVPA3:E<sub>(Dimer)</sub> ratio in 1X

27 PBS buffer and immediately used for the assay. The ZIKV Envelope protein alone was used as

- 28 control. Absorption spectra from 200 to 260 nm were acquired varing the temperature from 20 to
- 29 100 °C with a Jasco J-1100 spectropolarimeter coupled to a Peltier device. Spectra were acquired
- 30 at 1 °C intervals using a quartz cuvette of 0.1 cm path length and three accumulations. Ellipticity
- 31 at 222 nm was normalized, plotted against temperature, and fit by regression analysis using
- 32 Graphpad Prism v.7. to determine the melting temperature (T<sub>m</sub>) of the complex and the Env
- 33 protein.



35

36 Related to Method section: Production of ZVPA3

Supporting Figure S1. ZVPA3 production. (A) SEC chromatogram of ZVPA3 after affinity chromatography purification. UV absorbance at 280 nm (mAU) was monitored over time, and protein fractions were collected. (B) 15% SDS-PAGE of SEC eluted fractions showing a predominant band in all lanes around 20 kDa. The molecular weight marker (MWM) used was the PageRuler<sup>TM</sup> Plus Prestained Protein Ladder (ThermoFisher Scientific). a)

## b)

PDB entry		7ZFM
Data Collection	Isotropic	Anisotropic
Spacegroup	P 43212	P 43212
Cell Parameters		
a, b, c (Å)	81.62 81.62 113.28	81.62 81.62 113.28
$\alpha, \beta, \gamma$ (°)	90.0 90.0 90.0	90.0 90.0 90.0
Resolution (Å)	66.2-5.0 (1.88-1.85)	66.3-5.0 (1.80-1.71)
R <sub>merge</sub> (%)	4.4 (78.2)	4.5 (109.5)
R <sub>meas</sub> (%)	4.6 (83.5)	4.7 (118.0)
R <sub>pim</sub> (%)	1.2 (28.5)	1.3 (41.0)
CC(1/2) (%)	100 (80.5)	100 (58.0)
$Mean(I)/\sigma(I)$	31.3 (2.2)	28.4 (1.5)
Wilson B-factor	32.8	32.8
Completeness (spherical)	100 (100)	88.6 (31.0)
Completeness (ellipsoidal)		95.2 (54.9)
Number of Unique Reflections	33666	37153
Multiplicity	13.5 (8.1)	12.4 (7.6)
Refinement		.05.
Resolution (Å)	-	51.4 - 1.71
Number of Reflections	-	37150
Rwork (%)	-	17.6
Rfree(%)	-	21.1
No. atoms	-	3048
Protein	-	2618
Ligand/ion		135
Water	-	295
R.m.s. deviations		
Bond lengths (Å)	14	0.01
Bond angles (°)	-	1.75
Ramachandran plot(%)		
Favored	-	96.3
Outliers	-	0.31
Rotamer outliers (%)	-	1.03
MolProbity score	-	1.29
Clashscore	-	2.02
Mean B-factor (Å <sup>2</sup> )	-	40.28
Macromolecules	-	37.08
Ligands	-	80.63
Solvent	-	50.15



44 Related to Method section: Crystallization, data collection and structure determination

45 Supporting Figure S2. (A) Data Collection and refinement statistics of the ZVPA3 protein.

46 Statistics for the highest-resolution shell are shown in parentheses. 5% of reflections were

47 used to calculate  $R_{free}$ . (B) ZVPA3 crystals and (C) X-ray diffraction pattern.



#### 60 61

62 Related to the Additional Methods section: Thermal unfolding of the ZIKV Env and ZVPA3

- 63 protein complex by circular dichroism.
- 64 Supporting Figure S3. Thermal stability of the ZIKV Env and ZVPA3 protein complex. The

65 melting profile of the ZIKV Env – ZVPA3 complex was determined through CD experiments (in

- 66 purple) and compared to that obtained for the ZVPA3 protein alone (in green). The respective
- 67 melting temperatures are shown in the figure.
- 68
- 69





71 Related to Method section: Flavivirus-neutralising activity determination through plaque-72 reduction neutralization test (PRNT) and microneutralization (MN) test

73 Supporting Figure S4. Assessment of flavivirus neutralization in vitro. (A) Assessment of ZIKV (pink curve) neutralisation activity by microneutralization test. The assay was 74 performed in triplicates and the data is shown as the median plus standard deviation. The 75 ZVPA3 protein was used as a control (orange curve) and shows no unspecific binding with 76 77 the antibodies used to develop the assay. Dotted lines at 0 and 100% are shown for clarity. PRNT plates showing neutralization against ZIKV (B), DENV-1 (C) and DENV-2 (D) are 78 79 also shown. Highlighted in red and yellow are the negative and positive control wells, respectively. The dilution curve of ZVPA3 is represented in green in each plate. 80

81