

SUPPLEMENTARY ONLINE DATA

The HicA toxin from *Burkholderia pseudomallei* has a role in persister cell formation

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Table S1 NMR assignment, structure calculation and validation statistics

Parameter	Values
Degree of assignment*	
Backbone (C α , C', N and H ^N) (%)	91.2
Side-chain H (%)	79.4
Side-chain non-H (%)	39.7
Number of restraints	
Distance restraints	
Intra-residue ($ i - j = 0$)	515
Sequential ($ i - j = 1$)	216
Medium range ($2 \leq i - j < 5$)	109
Long range ($ i - j \geq 5$)	172
Ambiguous	59
Total	1012
Dihedral angle restraints (Φ/Ψ)	94 (47/47)
Restraint statistics†	
RMSD of distance violations (Å)	0.019 ± 0.003
RMSD of dihedral violations (°)	0.27
Violations > 0.5 Å	0
Violations > 0.3 Å	0
Violations > 0.1 Å	9.8 ± 2.8
RMSD from idealized covalent geometry†	
Bonds (Å)	0.0031 ± 0.00017
Angles (°)	0.47 ± 0.0013
Impropers (°)	1.33 ± 4.97
Structural quality	
Ramachandran statistics*‡§	
Most favoured regions (%)	84.0/91.2
Allowed regions (%)	14.2/7.0
Generously allowed regions (%)	1.9/1.8
Disallowed regions (%)	0.0/0.0
CING ROG scores (R/O/G)* [1] (%)	20/22/58
Verify3D Z-score [2]	-2.57
Prosa II Z-score [3]	-0.74
Procheck Z-score (Φ/Ψ)‡ [4]	-1.14
Procheck Z-score (Φ/Ψ)‡ [4]	-1.71
MolProbity Z-score [5]	-1.57
Number of close contacts	2
Co-ordinates precision (RMSD)*§	
All backbone atoms (Å)	3.2/1.2/0.6
All heavy atoms (Å)	3.5/1.6/1.4

*Residues 5–59.

†Values reported by ARIA 2.3 [6].

‡Values reported by Procheck [4].

§Ordered residues (5–21, 23–32, 35–39 and 45–58) as calculated by PSVS 1.4 [3].

||Residues in secondary structure (6–12, 16–19, 24–28, 35–39 and 50–58) as determined by DSSP [7].

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The chemical shifts and structure reported for HicA toxin from *Burkholderia pseudomallei* will appear in the Biological Magnetic Resonance Data Bank (BMRB) under accession number 19464 and in the PDB under code 4C26 respectively.

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