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Supplementary Materials for

Human β-defensin 2 kills *Candida albicans* through phosphatidylinositol 4,5-bisphosphate–mediated membrane permeabilization

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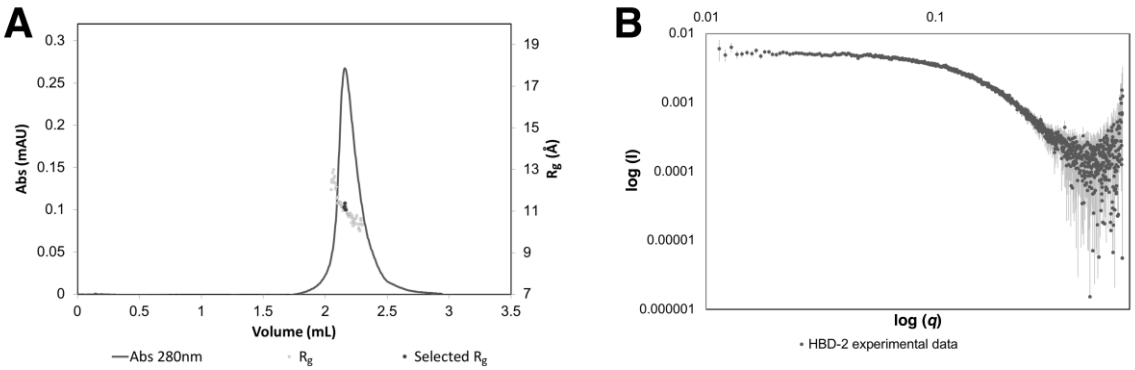

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Sample	I0	R_g (Å)	Guinier range	MW experimental (kDa)	Oligomerization
HBD-2	$0.013 \pm 4.9 \times 10^{-5}$	11 ± 0.36	10 to 146	5.68	1.3

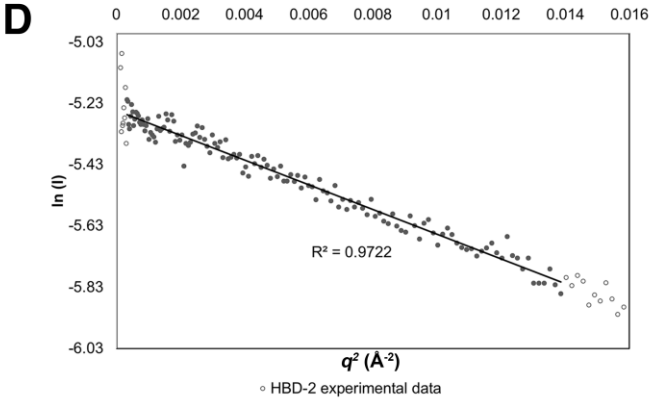

Fig. S1. SEC-SAXS analysis of HBD-2. (**A**) In-line size exclusion SAXS chromatogram of HBD-2. The dark dots represent the frames used for averaging the scattering profiles based on R_g (dots). (**B**) Log-log representation of HBD-2 scattering profile extracted from fractionated peaks obtained from in-line SEC-SAXS. (**C**) Oligomerization analyses of HBD-2 based on Guinier range. (**D**) Guinier plot of HBD-2 with Guinier range highlighted with dots.

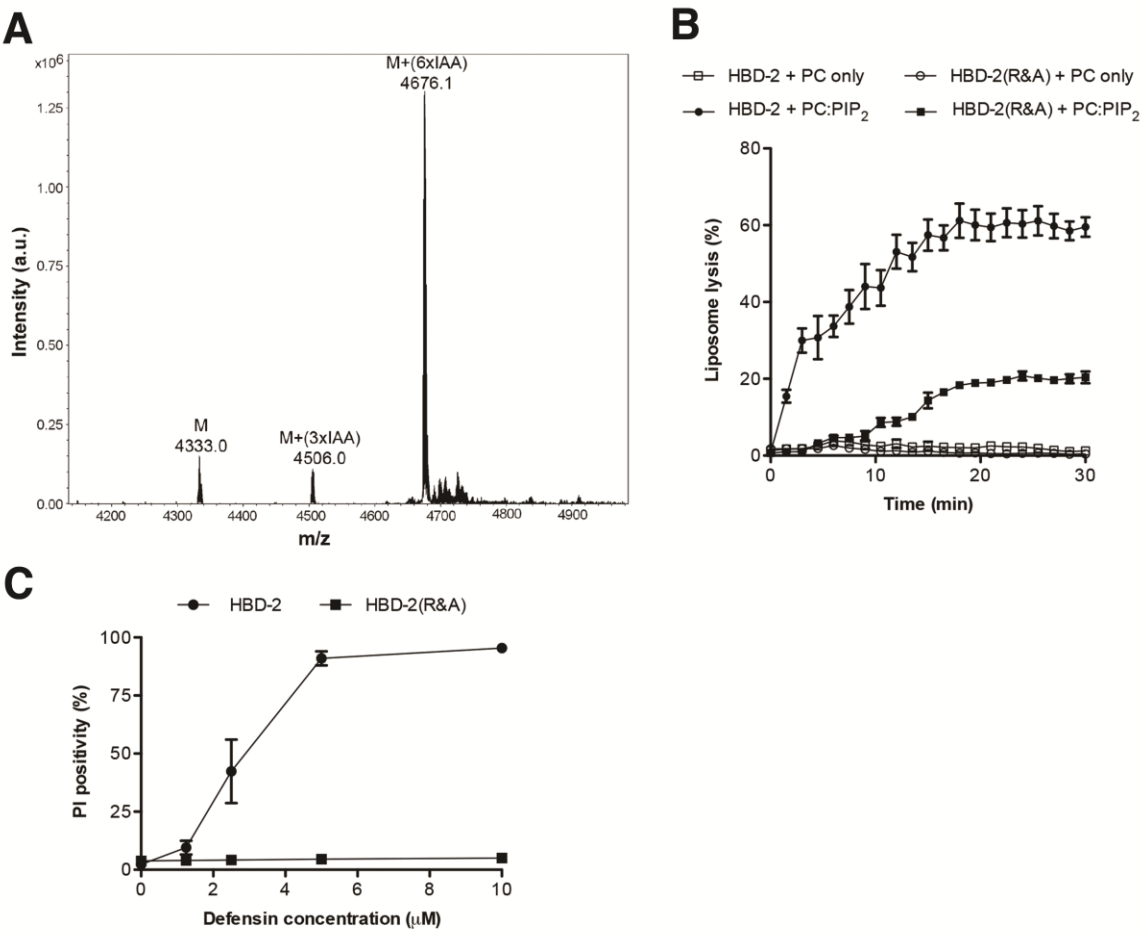

Fig. S2. The three-dimensional structure of HBD-2 is important for its antifungal activity and liposome permeabilization. (**A**) ESI-Q-TOF mass spectrum of reduced and alkylated HBD-2 (HBD-2(R&A)) sample with masses (M) and number of conjugated iodoacetamide (IAA) explicitly indicated. (**B**) Fungal cell permeabilization by HBD-2(R&A) in comparison to HBD-2. *C. albicans* was treated with defensins at indicated concentrations for 30 min, followed by PI staining prior to flow cytometry analysis. (**C**) Liposome lysis with 50 μM HBD-2 or HBD-2(R&A) using calcein-encapsulated PC only or PC:PIP_2 liposomes. Lyposome lysis was normalized against triton X-100 treatment. Data in (B) and (C) represent mean±SEM of three independent experiments.

Table S1. SAXS data collection and scattering-derived parameters.

	HBD-2
Data collection parameters	
Instrument	SAXS/WAXS beamline, Australian Synchrotron
Beam geometry (μm)	250 x 450
Fractional sample flow rate	0.5
Wavelength (keV)	12
Flux (ph.s^{-1})	6 x 10^{12}
q range (Å^{-1})	0.011-0.65
Exposure time (s)	1 (detector integration)
Temperature (K)	299.15
Structural parameters †	
I (0) (from Guinier) (cm^{-1})	0.013 ± 4.85 x 10-5
R_g (from Guinier) (Å)	11.00 ± 0.36
Molecular-mass determination†	
Partial specific volume (cm^3 g^{-1})	0.739
Contrast ($\Delta\rho \times 10^{10}$ cm^{-2}) §	2.897
Molecular mass M_r [from I (0)] (kDa) §	5.68
Calculated monomeric M_r from sequence (kDa)	4.33
Software employed	
Primary data reduction	SAXS/WAXS beamline software
Data processing	*PRIMUS*
Theoretical scattering calculations	*CRYSOL*
Three-dimensional graphics representation	*PyMOL*
Graphics representation	*EXCEL*

† Reported for peaks (Fig. S1) § Determined with MULCh (Whitten *et al.*, 2008)