Supplementary Table 1 Data collection, phasing and refinement statistics

	SAM complex	sinefungin complex
Data collection		
Cell dimensions (Å)	54.4, 140.9, 119.0	54.6, 141.0, 118.8
Wavelength (Å)	1	1
Resolution (Å)	30.0–2.50 (2.59–2.50)	50.0–2.17 (2.25–2.17)
R_{sym}	0.092 (0.426)	0.051 (0.352)
Mean I/σ	15.6 (2.6)	34.0 (3.4)
Completeness (%)	99.8 (99.3)	99.9 (99.8)
Redundancy	6.9 (5.5)	7.1 (5.9)
Refinement		
Resolution (Å)	30-2.50	50-2.17
No. reflections	16387	24710
$R_{\mathrm{work}}/R_{\mathrm{free}}$	0.185/0.225	0.186/0.219
Number of atoms		
Protein/ligand/ion/water	3170/27/21/53	3163/27/26/94
Average *B*-factors		
Protein/ligand/ion/water	44.2/43.7/65.9/38.5	46.0/37.9/72.6/46.0
Ramachandran favored/allowed (%)	98.2/1.8	97.9/2.1
Rmsd bond length (Å)/angles (°)	0.002/0.560	0.005/0.866
PDB ID	3AXT	3AXS

*Values in parentheses are for highest-resolution shell.