

**Table S1. Summary of X-Ray Diffraction Data and Structure Refinement Statistics, Related to Figure 1**

**Summary of diffraction data**

Crystal	Se-NtDRM + sinefungin	NtDRM + sinefungin	NtDRM-M5 + sinefungin
Beamline	SSRF-BL17U	APS-24ID-E	APS-24ID-E
Wavelength (Å)	0.9795	0.9792	0.9792
Space group	$P4_3$	$P3_121$	$P6_5$
Cell parameters			
<i>a</i> , <i>b</i> (Å)	83.8	153.3	131.5
<i>c</i> (Å)	154.9	149.0	88.2
Resolution (Å)	50.0-3.3 (3.42-3.30) <sup>a</sup>	50.0-2.8 (2.90-2.80)	50.0-2.5 (2.59-2.50)
$R_{\text{merge}}$ (%)	14.7 (68.4)	12.2 (72.3)	7.1 (69.4)
Observed reflections	97,226	348,674	335,243
Unique reflections	15,822	49,582	30,076
Redundancy	6.1 (6.4)	7.0 (7.3)	11.1 (11.2)
Average $I/\sigma(I)$	21.4 (3.6)	24.2 (2.6)	45.6 (3.7)
Completeness (%)	99.5 (100.0)	99.9 (100.0)	100.0 (100.0)

**Refinement and structure model**

$R$ factor / Free $R$ factor (%)	20.1 / 22.1	18.5 / 23.0
Number of non-H atoms	5,386	5,301
Protein	5,332	5,134
Sinefungin	54	54
Water	-	113
Average B factors (Å <sup>2</sup> )	81.5	62.6
Protein	81.1	62.6
Sinefungin	115.4	85.9
Water	-	53.3
RMS deviations		
Bond lengths (Å)	0.007	0.015
Bond angles (°)	1.288	1.410

<sup>a</sup> Values in parentheses are for highest-resolution shell.

**Table S2. List of Primers Used for Cloning NtDRM, NtDRM-M5, AtDRM2 and AtDRM2-M5. Related Figures 3 and 5**

Name	Primer sequences from 5' to 3'
NtDRM point mutation R309S F310S	TCTTTGTACGATATTGAGCCAGAGTTTG AGAAGAAATTGTGTCCCACACAC
NtDRM point mutation Y590S D591S	TCTTATGTTCCGGATATTGGACTTGGTC AGAAAATAGGGAAGACTCTTTGCC
NtDRM point mutation E283S	CAAGCTGTTGGACCCCCGTTTTTC AGAGGGAAGAGTTCTTCGAACCATTG
NtDRM 255-608 cDNA cloning into pENTR/D	CACCGAGACAATTCGTTTGCCCAAACC CTAATGTTTATGTCTGGACATTATGG
Full length genomic AtDRM2 cloning into pENTR/D	CACCGTAATGGAGATAGCTTCTCAGGATTATC AACCAGATTGGGGCAATATACATATAGAAGAGCC
AtDRM2 point mutation primer 1	CACATAGATCGCTTCCATCGTTAGCCCCGAGGGCCAC
AtDRM2 point mutation primer 2	GTTTGGGAGACTATTTCCAG <sub>ctc</sub> CTTGTTTCGAGATCCCACCTG
AtDRM2 point mutation primer 3	CTTGAAGGTGATCAATCTTCGTTGTTCT <sub>cTtc</sub> GTATTGCCGTATTC TAG
Quikchange primers to destroy EcoR I site of AtDRM2	CTAAAAATTCTCTGGGTATTCCGCCCTTACT CTAGTAAGGGCGAATACCCAGAGAATTTTGTAG