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Supplementary Table 1. Data collection and refinement statistics.

	Anisomycin (ANI)	Blasticidin S (BLA)	CCA	Cryptopleurine (CRY)	Cycloheximide (CHX)
Data collection					
Space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions					
a, *b*, *c* (Å)	436.68 287.99 304.76	435.64 286.76 303.26	436.02 287.59 304.52	435.15 287.07 303.24	436.43 288.22 305.08
a, *b*, *g* (°)	90.0 99.0 90.0	90.0 98.7 90.0	90.0 99.0 90.0	90.0 98.9 90.0	90.0 98.9 90.0
Resolution (Å)	99.795-3.00 (3.10-3.00)*	299.756-3.45 (3.55-3.45)*	49.817-3.20 (3.30-3.20)*	99.87-3.20 (3.30-3.20)*	267.37-2.90 (3.00-2.90)*
R_{meas} **	30 (274.7)	44.8 (317.9)	30.8 (166.4)	36.7 (266.4)	39.6 (390.9)
I/s*I*	8.36 (1.09)	5.96 (1.01)	6.46 (1.22)	8.09 (1.02)	8.62 (1.11)
Completeness (%)	99.98 (100)	99.97 (100)	99.95 (100)	100 (100)	100 (100)
Redundancy	13.58 (12.94)	12.12 (11.29)	6.13 (6.22)	12.54 (9.71)	19.07 (17.89)
Refinement					
Resolution (Å)	99.795-3.00	299.756-3.45	49.817-3.20	99.87-3.20	267.37-2.90
No. reflections	1479278	963190	1214336	1205793	1639498
R_{work} / R_{free}	0.1985/0.2453	0.1960/0.2595	0.1814/0.2366	0.1938/0.2460	0.2042/0.2448
Total No. atoms	411203	411215	411287	411207	411203
Average B-factor	74.79	93.13	70.5	88.02	66.29
R.m.s deviations					
Bond lengths (Å)	0.013	0.012	0.011	0.013	0.012
Bond angles (º)	1.700	1.590	1.518	1.650	1.577

	Deoxynivalenol (DON)	Edeine (EDE)	Geneticin (GEN)	Homoharringtonine (HHT)	Lactimidomycin (LTM)
Data collection					
Space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions					
a, *b*, *c* (Å)	435.84 286.77 303.77	434.77 287.66 303.84	437.00 286.75 305.18	436.25 286.92 303.84	436.64 287.69 304.39
a, *b*, *g* (°)	90.0 99.0 90.0	90.0 98.9 90.0	90.0 99.2 90.0	90.0 98.8 90.0	90.0 98.9 90.0
Resolution (Å)	49.702-3.30 (3.40-3.30)*	73.94-3.10 (3.20-3.10)*	135.58-3.60 (3.70-3.60)*	49.69-3.00 (3.10-3.00)*	300.66-2.80 (2.90-2.80)*
R_{meas} **	31.2 (191.6)	41.1 (178.8)	51.7 (330.3)	34.1 (352.7)	26.5 (252.7)
I/s*I*	5.80 (0.99)	6.52 (0.88)	5.77 (0.96)	7.13 (0.88)	11.25 (1.20)
Completeness (%)	99.42 (99.1)	99.96 (100)	99.97 (100)	98.8 (98.2)	99.57 (95.1)
Redundancy	5.86 (5.73)	9.74 (5.20)	15.07 (13.52)	9.38 (9.37)	15.13 (11.25)
Refinement					
Resolution (Å)	49.702-3.30	73.94-3.10	135.58-3.60	49.69-3.00	300.66-2.80
No. reflections	1095281	1329330	854944	1451074	1805175
R_{work} / R_{free}	0.2016/0.2553	0.2035/0.2515	0.1898/0.2667	0.2079/0.2546	0.2084/0.2458
Total No. atoms	411182	411257	411096	411244	411229
Average B-factor	90.07	74.66	115.57	74.00	60.48
R.m.s deviations					
Bond lengths (Å)	0.012	0.013	0.018	0.012	0.012
Bond angles (º)	1.576	1.649	2.256	1.616	1.684

	Lycorine (LYC)	Nagilactone C (NAG)	Narciclasine (NAR)	Pactamycin (PAC)	Phyllanthoside (PHY)
Data collection					
Space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions					
a, *b*, *c* (Å)	435.26 287.54 304.02	435.39 286.22 303.33	435.34 287.00 303.36	436.92 288.52 305.75	434.98 287.50 303.22
a, *b*, *g* (°)	90.0 98.9 90.0	90.0 98.9 90.0	90.0 98.9 90.0	90.0 99.0 90.0	90.0 98.8 90.0
Resolution (Å)	73.99-3.00 (3.10-3.00)*	299.62-3.00 (3.10-3.00)*	49.18-3.20 (3.30-3.20)*	267.96-3.20 (3.30-3.20)*	299.60-3.10 (3.20-3.10)*
R_{meas} **	29.5 (241.5)	27.3 (224)	30.3 (218.9)	39.3 (246.5)	36.9 (291.1)
I/s*I*	7.02 (0.97)	8.57 (1.26)	6.47 (0.91)	8.71 (0.86)	7.22 (0.90)
Completeness (%)	100 (100)	99.97 (100)	99.93 (99.9)	100 (100)	99.96 (99.9)
Redundancy	7.52 (7.45)	11.17 (10.40)	6.37 (6.46)	17.78 (7.71)	12.78 (11.37)
Refinement					
Resolution (Å)	73.99-3.00	299.62-3.00	49.18-3.20	267.96-3.20	299.60-3.10
No. reflections	1468778	1459232	1205277	1226129	1327202
R_{work} / R_{free}	0.2115/0.2588	0.2068/0.2576	0.2043/0.2525	0.1928/0.2453	0.2015/0.2520
Total No. atoms	411209	411206	411179	411224	411277
Average B-factor	64.88	66.50	80.80	81.49	76.86
R.m.s deviations					
Bond lengths (Å)	0.012	0.014	0.012	0.013	0.012
Bond angles (º)	1.637	1.817	1.590	1.660	1.620

	T2-Toxin (T2T)	Verrucarin (VER)
Data collection		
Space group	$P2_12_12_1$	$P2_12_12_1$
Cell dimensions		
a, *b*, *c* (Å)	436.64 287.69 304.39	434.39 285.58 303.06
a, *b*, *g* (°)	90.0 98.9 90.0	90.0 98.9 90.0
Resolution (Å)	300.66-3.10 (3.20-3.10)*	49.88-3.20 (3.30-3.20)*
R_{meas} **	40.1 (194.9)	34.5 (223.7)
I/s*I*	4.19 (1.05)	5.59 (0.95)
Completeness (%)	98.70 (99.5)	99.86 (99.9)
Redundancy	5.69 (5.38)	4.068 (4.11)
Refinement		
Resolution (Å)	300.66-3.10	49.88-3.20
No. reflections	1320886	1194740
R_{work} / R_{free}	0.1978/0.2467	0.2122/0.2619
Total No. atoms	415053	411230
Average B-factor	71.82	72.42
R.m.s deviations		
Bond lengths (Å)	0.011	0.011
Bond angles (º)	1.513	1.546

* Highest resolution shell is shown in parenthesis.
** The elevated Rmeas is attributed to the high number of data-sets that were used and to the method of data collection which results in a large number of relatively weak measurements of each reflection. The quality of individual measurements might be relatively low but the merged result has a higher signal to noise ratio due to averaging.