

## Supplementary Crystallographic Tables

*Table S1: Trehalose.*

Dataset name	Trehalose anhydrous (RT)	Trehalose anhydrous (100K)	Trehalose anhydrous (100K, high dose)	Trehalose dihydrate (100K)	Trehalose anhydrous (monoclinic, RT)
<b><i>Crystal data</i></b>					
Chemical formula	C <sub>12</sub> H <sub>22</sub> O <sub>11</sub> ·2(H <sub>2</sub> O)	C <sub>12</sub> H <sub>22</sub> O <sub>11</sub>			
M <sub>r</sub>	342.30	342.30	342.30	378.33	342.30
<b>Crystal system, space group</b>					
Collection temperature (K)	293	100	100	100	293
Transfer temperature (K)	293	293	293	100	293
a, b, c (Å)	6.8 (4), 11.6 (4), 18.5 (3)	6.7 (5), 11.6 (4), 18.5 (3)	6.8 (3), 11.6 (2), 18.5 (2)	7.50 (6), 12.08 (10), 17.67 (7)	6.75 (6), 8.19 (5), 12.94 (9)
α, β, γ (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90	90, 98.3 (2), 90
V (Å <sup>3</sup> )	1457 (103)	1442 (128)	1447 (79)	1602 (19)	708 (9)
Z	4	4	4	4	2
Radiation type	Electrons, λ = 0.0251 Å	Electrons, λ = 0.0251 Å			
<b><i>Data collection and processing</i></b>					
Diffractometer	Rigaku XtaLAB Synergy-ED	Rigaku XtaLAB Synergy-ED	Rigaku XtaLAB Synergy-ED	Rigaku XtaLAB Synergy-ED	Rigaku XtaLAB Synergy-ED
measured, independent, observed	6114, 2595, 980	5994, 2324, 985	6043, 2327, 1302	8500, 2835, 1758	3714, 2251, 1280
Resolution (Å)	0.80	0.80	0.80	0.80	0.80
Completeness (%)	86.7	79.1	78.7	84.6	75.6
Redundancy	4.0	4.4	4.4	5.3	3.2
R <sub>int</sub>	0.189	0.193	0.126	0.227	0.132
R <sub>pim</sub>	0.116	0.113	0.075	0.114	0.104
CC <sub>1/2</sub>	0.992	0.993	0.997	0.970	0.977
I/σ(I) [inf - 0.80 Å]	3.86	4.45	6.11	5.18	5.08
Total electron dose (e <sup>-</sup> /Å <sup>2</sup> )	0.18	0.18	0.54	0.18	0.18
Min, Max collection angle (°)	-50, +50	-50, +50	-50, +50	-60, +60	-60, +60

(sin $\theta/\lambda$ ) <sub>max</sub> ( $\text{\AA}^{-1}$ )	0.625	0.624	0.625	0.625	0.624
Detector distance (mm)	653	653	653	653	653
<b><u>Refinement</u></b>					
R <sub>1</sub> ,	0.117, 0.258	0.117, 0.294	0.106, 0.255	0.124, 0.280	0.129, 0.316
wR <sub>2</sub> [ $F^2 > 2\sigma(F^2)$ ]					
R <sub>1</sub> , wR <sub>2</sub> [all]	0.237, 0.319	0.216, 0.351	0.169, 0.285	0.174, 0.312	0.170, 0.346
S	1.01	1.04	1.19	1.09	1.22
No. of reflections	2595	2324	2327	2835	2251
No. of parameters	217	239	216	269	232
No. of restraints	177	332	178	335	189
$\Delta\rho_{\text{max}}, \Delta\rho_{\text{min}}$ (e $\text{\AA}^{-3}$ )	0.11, -0.12	0.12, -0.15	0.13, -0.12	0.13, -0.15	0.15, -0.14
CCDC number	-	-	2267656	2267657	2267654

Table S2: Tyrosine.

Dataset name	Tyrosine (initial)	Tyrosine (full kinematical)	Tyrosine (L, CAP)	Tyrosine (D, CAP)	Tyrosine (L, PETS2)	Tyrosine (D, PETS2)
<u>Crystal data</u>						
Chemical formula	C <sub>9</sub> H <sub>11</sub> NO <sub>3</sub>					
M <sub>r</sub>	181.2	181.2	181.2	181.2	181.2	181.2
Crystal system, space group	Orthorhombic, P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>					
Temperature (K)	293	293	293	293	293	293
a, b, c (Å)	5.85 (10), 6.97 (18), 21.24 (10)					
V (Å <sup>3</sup> )	866 (27)	866 (27)	866 (27)	866 (27)	866 (27)	866 (27)
Z	4	4	4	4	4	4
Radiation type	Electrons, λ = 0.0251 Å					
<u>Data collection and processing</u>						
Diffractometer	Rigaku XtaLAB					
	Synergy-ED	Synergy-ED	Synergy-ED	Synergy-ED	Synergy-ED	Synergy-ED
Processing program	CrysAlis <sup>Pro</sup>	CrysAlis <sup>Pro</sup>	CrysAlis <sup>Pro</sup>	CrysAlis <sup>Pro</sup>	PETS2	PETS2
Processed data type	Merged intensities	Merged intensities	Virtual frame intensities	Virtual frame intensities	Virtual frame intensities	Virtual frame intensities
measured, independent, observed	4026, 1550, 1102	4026, 1550, 1102	11915, 2680, 1337	11915, 2680, 1337	11488, 2593, 1690	11488, 2593, 1690
R <sub>int</sub>	0.084	0.084	-	-	-	-
CC <sub>1/2</sub>	0.994	0.994	-	-	-	-
Total electron dose (e/Å <sup>2</sup> )	10	10	10	10	10	10
(sin θ/λ) <sub>max</sub> (Å <sup>-1</sup> )	0.625	0.625	0.625	0.625	0.625	0.625
Detector distance (mm)	645	645	645	645	645	645
<u>Refinement</u>						
Refinement type	kinematical	kinematical	dynamical	dynamical	dynamical	dynamical
R <sub>1</sub> , wR <sub>2</sub> [F <sup>2</sup> >2σ(F <sup>2</sup> )]	0.144, 0.342	0.102, 0.236	0.076, 0.189	0.097, 0.241	0.097, 0.179	0.122, 0.230
R <sub>1</sub> , wR <sub>2</sub> [all]	0.170, 0.354	0.128, 0.249	0.113, 0.221	0.134, 0.268	0.126, 0.187	0.150, 0.237

S	1.84	1.29	1.19	1.44	2.85	3.62
No. of reflections	1550	1550	2680	2680	2593	2593
No. of parameters	54	121	156	156	181	181
No. of restraints	0	0	0	0	0	0
$\Delta\rho_{\max}$ , $\Delta\rho_{\min}$ (e $\text{\AA}^{-3}$ )	0.23, -0.14	0.12, -0.11	0.09, -0.09	0.12, -0.12	0.13, -0.12	0.19, -0.16

Table S3: Clarithromycin.

Dataset name	Clarithromycin (original)	Clarithromycin (inverted)
<u>Crystal data</u>		
Chemical formula	C <sub>38</sub> NO <sub>13</sub> (H atoms excluded)	C <sub>38</sub> NO <sub>13</sub> (H atoms excluded)
M <sub>r</sub>	678.4	678.4
Crystal system, space group	Orthorhombic, P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	Orthorhombic, P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>
Temperature (K)	293	293
a, b, c (Å)	8.8 (2), 20.1 (3), 23.91 (17)	8.8 (2), 20.1 (3), 23.91 (17)
V (Å <sup>3</sup> )	4230 (120)	4230 (120)
Z	4	4
Radiation type	Electrons, λ = 0.0251 Å	Electrons, λ = 0.0251 Å
<u>Data collection and processing</u>		
Diffractometer	Rigaku XtaLAB Synergy-ED	Rigaku XtaLAB Synergy-ED
Processing program	CrysAlis <sup>Pro</sup>	CrysAlis <sup>Pro</sup>
Processed data type	Virtual frame intensities	Virtual frame intensities
measured, independent, observed	20812, 6151, 1678	20812, 6151, 1678
Total electron dose (e/Å <sup>2</sup> )	10	10
(sin θ/λ) <sub>max</sub> (Å <sup>-1</sup> )	0.625	0.625
Detector distance (mm)	645	645
<u>Refinement</u>		
Refinement type	dynamical	dynamical
R <sub>1</sub> , wR <sub>2</sub> [F <sup>2</sup> > 2σ(F <sup>2</sup> )]	0.130, 0.220	0.167, 0.275
R <sub>1</sub> , wR <sub>2</sub> [all]	0.271, 0.257	0.311, 0.313
S	1.95	2.37
No. of reflections	6151	6151
No. of parameters	241	241
No. of restraints	0	0
Δρ <sub>max</sub> , Δρ <sub>min</sub> (e Å <sup>-3</sup> )	0.17, -0.17	0.25, -0.18

Table S4: Thaumatin.

Dataset name	Thaumatin
<u>Crystal data</u>	
Crystal system, space group	Tetragonal, $P4_12_12$
Temperature (K)	100
a, b, c (Å)	58.40(15), 58.40(15), 151.2(2)
$\alpha, \beta, \gamma$ (°)	90, 90, 90
<u>Data collection and processing</u>	
Radiation type	Electrons, $\lambda = 0.0251$ Å
Diffractometer	Rigaku XtaLAB Synergy-ED
Detector distance (mm)	1800
Total electron dose (e/(\AA <sup>2</sup> s))	10
Resolution range (Å)	16.14-2.15 (2.22-2.15)
# unique reflections	12870 (1081)
I/ $\sigma_i$	3.5 (1.2)
CC <sub>1/2</sub>	0.972 (0.603)
Completeness (%)	86.2 (86.0)
Multiplicity	6.4 (6.1)
R <sub>int</sub>	0.43 (1.90)
R <sub>wp</sub>	0.17 (0.74)
<u>Refinement</u>	
R <sub>work</sub> , R <sub>free</sub> (%)	19.5, 22.6
# atoms (protein, ligand, water)	1558, 10, 23
B-factors (protein, ligand, water) (Å <sup>2</sup> )	23.8, 7.2, 15.0
RMS bonds, angles	0.01, 1.86
Ramachandran outliers, favored (%)	0.0, 96.1
Rotamer outliers (%)	3.57
Cβ deviations	3
Clahscore	2.62
MolProbity score	1.73

*Table S5: Cystine.*

R <sub>1</sub> ,	0.164,	0.140,	0.122,	0.288,	0.227,	0.233,
wR <sub>2</sub> [F <sup>2</sup> > 2σ(F <sup>2</sup> )]	0.403	0.362	0.343	0.603	0.433	0.481
R <sub>1</sub> , wR <sub>2</sub> [all]	0.170, 0.406	0.160, 0.374	0.154, 0.365	0.308, 0.621	0.250, 0.443	0.292, 0.515
S	1.19	1.18	1.15	1.03	1.87	1.22
No. of reflections	880	882	877	393	375	365
No. of parameters	66	66	66	66	66	66
No. of restraints	75	39	0	75	75	75
Δρmax, Δρmin (e Å <sup>-3</sup> )	0.22, -0.18	0.20, -0.17	0.12, -0.15	0.14, -0.10	0.16, -0.17	0.15, -0.11
CCDC number	-	-	2267655	-	-	-