

SUPPLEMENTAL MATERIAL**Table 1. CnTS crystallographic statistics as a function of resolution**

Resln. Low Å	Resln. High Å	R _{merge} %	Mult.	>3σ(I) %	% Complete	R _{cryst} %	R _{free} %
99.0	4.46	5.7	1.8	96.4	88.4	35.7	35.8
4.46	3.54	8.1	1.9	93.6	94.6	26.9	27.4
3.54	3.09	9.8	1.9	85.6	97.9	27.9	29.6
3.09	2.81	11.5	1.9	75.1	98.4	26.8	29.1
2.81	2.61	13.1	1.9	64.0	98.6	26.8	29.0
2.61	2.45	15.4	1.9	55.1	98.7	26.8	29.8
2.45	2.33	18.3	1.8	44.9	98.7	28.1	30.8
2.33	2.23	22.0	1.8	36.8	98.4	29.7	32.2
2.23	2.14	26.5	1.8	27.8	98.2	31.2	33.3
2.14	2.07	34.4	1.8	19.7	97.9	33.9	35.0

Table 2. EcTS-dUMP-GA9 crystallographic statistics as a function of resolution

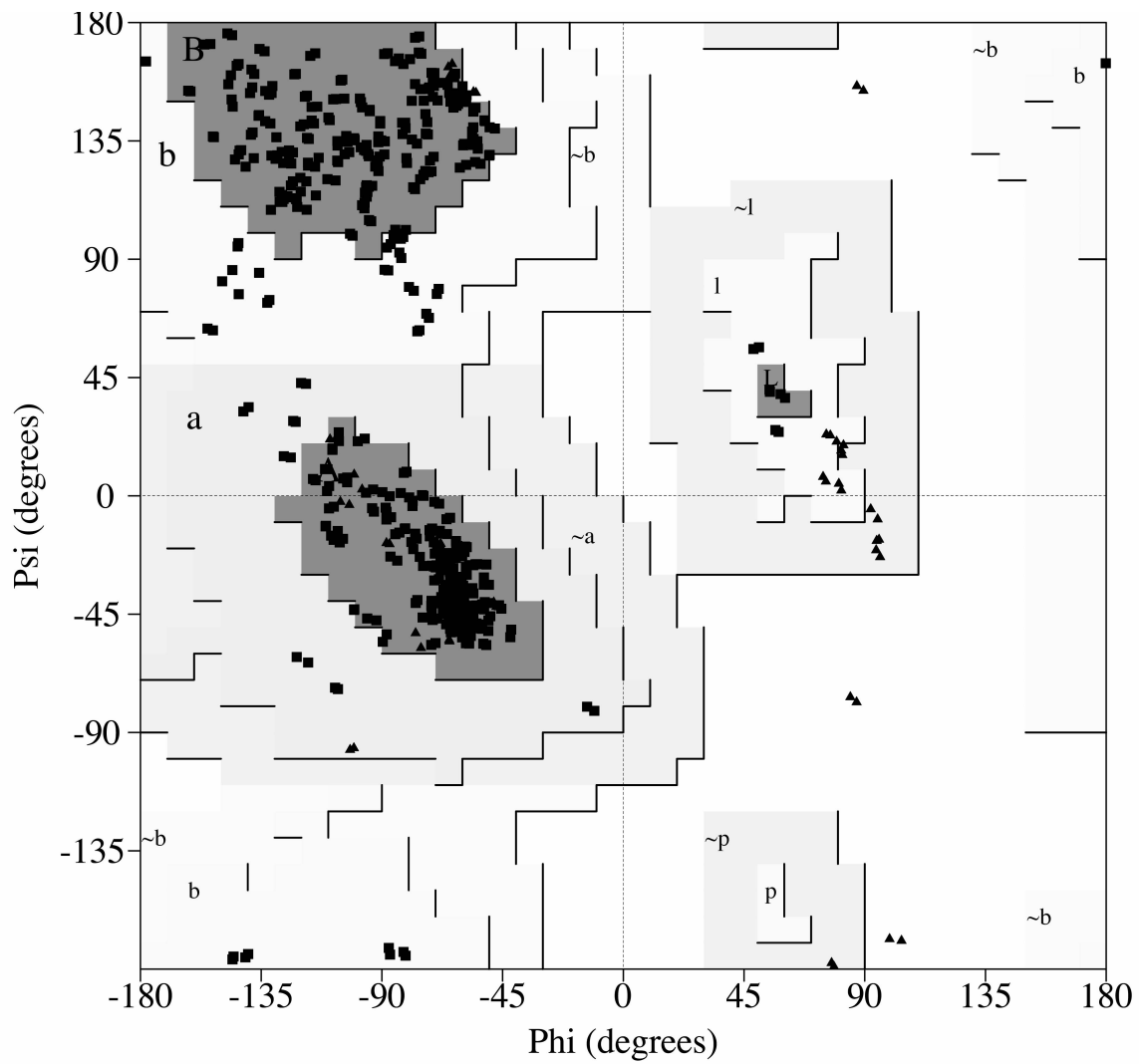
Resln. Low Å	Resln. High Å	R _{merge} %	Mult.	>3σ(I) %	% Complete	R _{cryst} %	R _{free} %
99.0	3.55	3.5	3.3	99.4	88.2	19.5	20.3
3.55	2.82	4.7	3.2	97.6	92.1	19.2	20.5
2.82	2.46	6.6	3.2	94.7	93.7	19.9	22.4
2.46	2.24	9.2	3.1	91.2	94.3	20.3	23.8
2.24	2.08	11.3	3.0	86.3	94.2	21.0	24.0
2.08	1.96	17.7	2.9	80.4	94.2	21.4	24.0
1.96	1.86	24.7	2.8	69.6	94.5	22.6	25.3
1.86	1.78	33.4	2.7	53.8	95.1	24.3	26.8
1.78	1.71	49.4	2.6	35.9	95.3	28.1	30.7
1.71	1.65	69.7	2.5	24.7	95.3	31.4	32.1

Table 3. Top native Patterson peaks, P4₁ crystal form of CnTS

	x (frac.)	y (frac.)	z (frac.)	Height(σ)
1	0.0000	0.0000	0.0000	212.8
2	0.5000	0.5000	0.0221	68.9
3	0.0000	0.0346	0.0105	14.3
4	0.0000	0.0000	0.0545	5.1
5	0.0000	0.0667	0.0035	5.1
6	0.0302	0.0917	0.0000	4.7
7	0.0000	0.0917	0.0085	3.9
8	0.0289	0.0289	0.0556	3.9
9	0.4618	0.5000	0.0111	3.7
10	0.1000	0.1000	0.0000	3.5

Table 4. Top native Patterson peaks, C2 crystal form CnTS

	x (frac.)	y (frac.)	z (frac.)	Height(σ)
1	0.0000	0.0000	0.0000	650.7
2	0.5000	0.0199	0.0319	84.5
3	0.4800	0.0000	0.0313	42.9
4	0.0010	0.0151	0.9927	38.7
5	0.0037	0.0148	0.0062	36.0
6	0.4792	0.0000	0.9685	31.7
7	0.0184	0.0000	0.0002	29.8
8	0.0013	0.0000	0.0154	20.0
9	0.0000	0.0000	.0646	16.6
10	0.0199	0.0153	0.9886	15.2

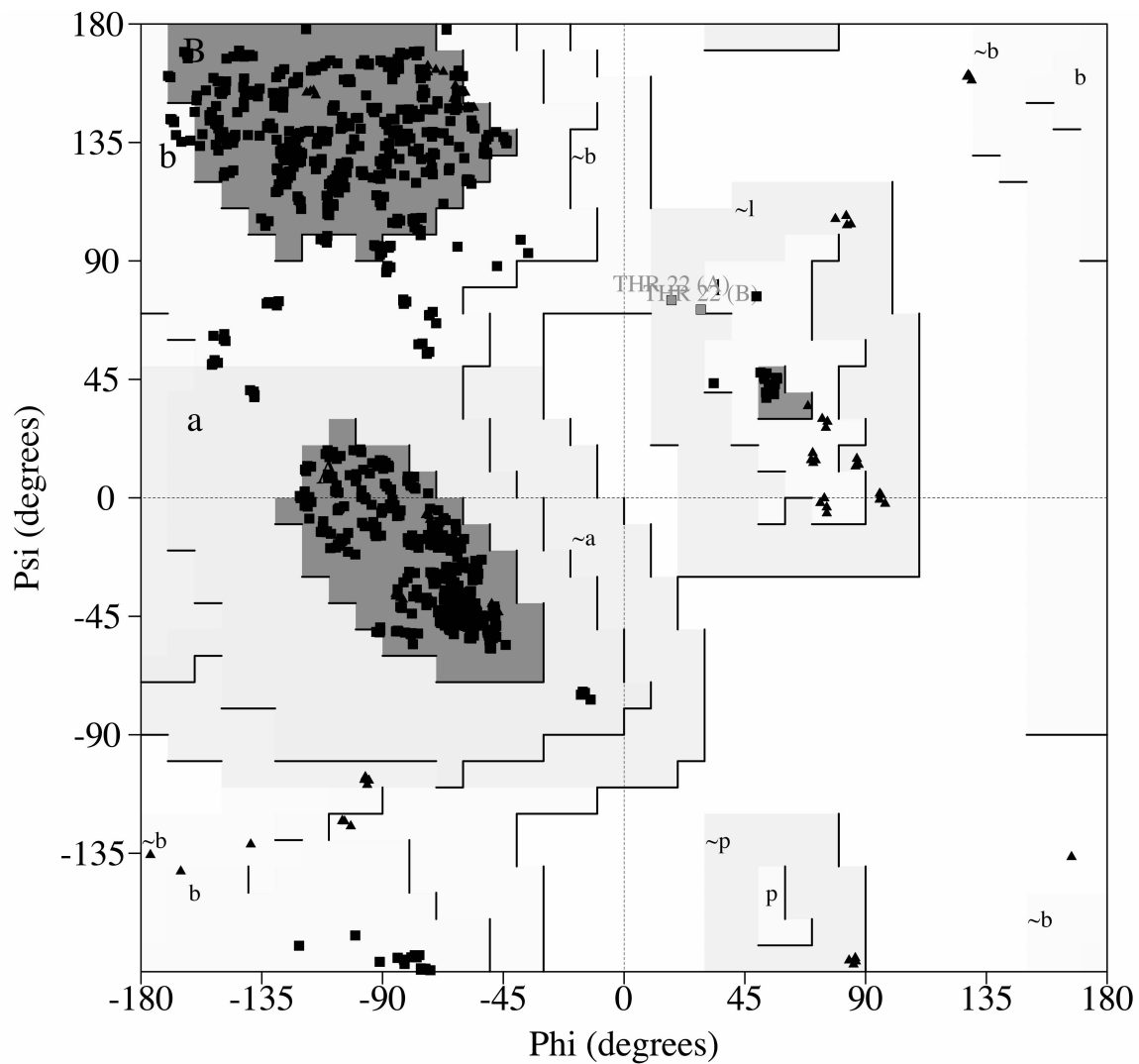


Plot statistics

Residues in most favoured regions [A,B,L]	449	88.0%
Residues in additional allowed regions [a,b,l,p]	61	12.0%
Residues in generously allowed regions [-a,~b,~l,~p]	0	0.0%
Residues in disallowed regions	0	0.0%

Number of non-glycine and non-proline residues	510	100.0%
Number of end-residues (excl. Gly and Pro)	4	
Number of glycine residues (shown as triangles)	52	
Number of proline residues	44	

Ramachandran plot for *C. neoformans* TS-dUMP-CB3717 complex, C2 cell



Plot statistics

Residues in most favoured regions [A,B,L]	855	92.5%
Residues in additional allowed regions [a,b,l,p]	67	7.3%
Residues in generously allowed regions [-a,-b,-l,-p]	2	0.2%
Residues in disallowed regions	0	0.0%

Number of non-glycine and non-proline residues	924	100.0%
Number of end-residues (excl. Gly and Pro)	8	
Number of glycine residues (shown as triangles)	72	
Number of proline residues	56	

Total number of residues	1060	

Ramachandran plot for E. coli TS-dUMP-CB3717 complex