



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:46 PM UTC

PDB ID : 7DAF / pdb_00007daf
Title : IXA in complex with tubulin
Authors : Wu, C.; Wang, Y.
Deposited on : 2020-10-16
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

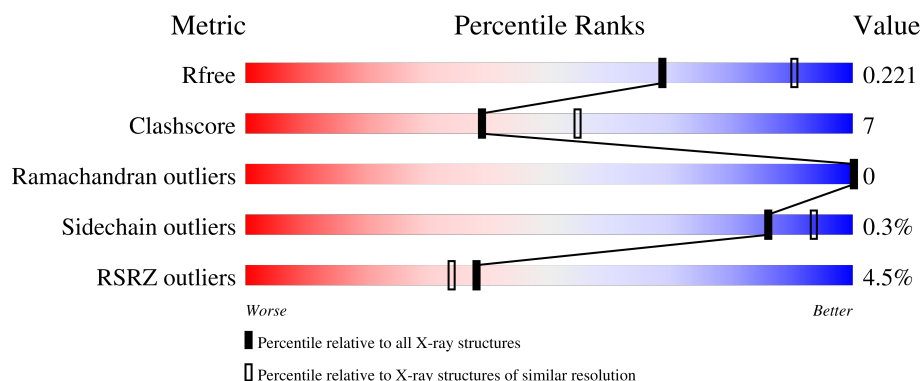
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	451	87% 11% .
1	C	451	83% 14% .
2	B	445	82% 13% 5%
2	D	445	4% 84% 12% .
3	E	143	4% 71% 15% 14%

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Mol	Chain	Length	Quality of chain
4	F	384	16% 76% 15% • 9%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 18541 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	442	Total	C	N	O	S	0	6	0
			3484	2204	591	665	24			
1	C	440	Total	C	N	O	S	0	11	0
			3479	2203	586	664	26			

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	423	Total	C	N	O	S	0	6	0
			3359	2114	568	650	27			
2	D	430	Total	C	N	O	S	0	5	0
			3395	2130	579	659	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	123	Total	C	N	O	S	0	3	0
			1031	636	187	203	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	initiating methionine	UNP P63042
E	4	ALA	-	expression tag	UNP P63042

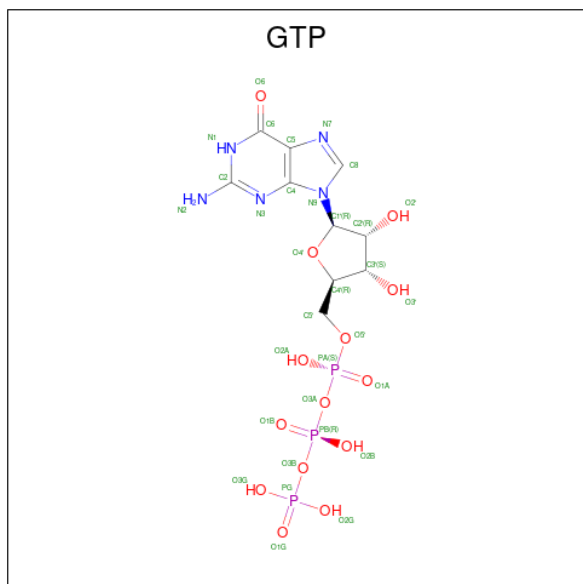
- Molecule 4 is a protein called Tubulin tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	351	Total	C	N	O	S	0	6	0
			2917	1874	501	526	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP E1BQ43
F	380	HIS	-	expression tag	UNP E1BQ43
F	381	HIS	-	expression tag	UNP E1BQ43
F	382	HIS	-	expression tag	UNP E1BQ43
F	383	HIS	-	expression tag	UNP E1BQ43
F	384	HIS	-	expression tag	UNP E1BQ43

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 32	C 10	N 5	O 14	P 3	0	0
5	C	1	Total 32	C 10	N 5	O 14	P 3	0	0

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		
6	B	2	Total	Mg	0	0
			2	2		
6	C	1	Total	Mg	0	0
			1	1		
6	D	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

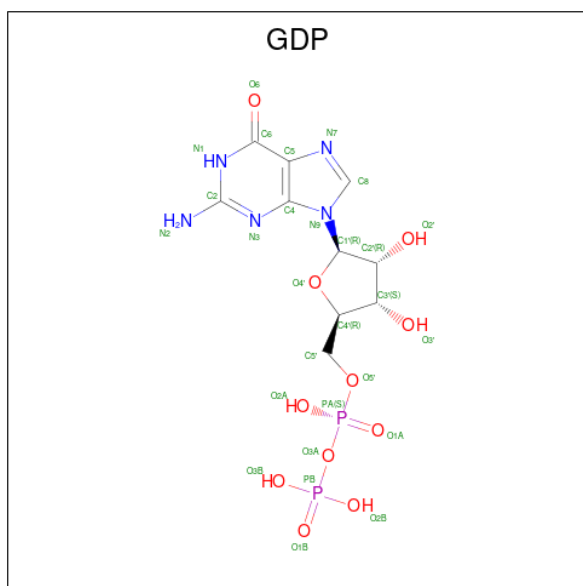
- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		
7	E	1	Total	Ca	0	0
			1	1		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Cl	0	0
			1	1		

- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



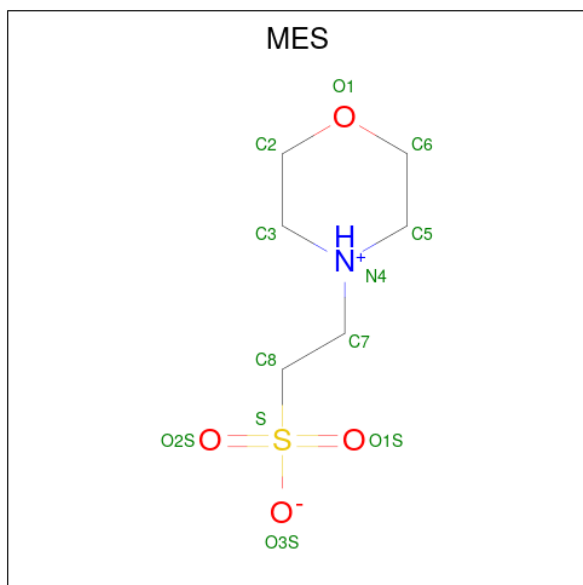
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

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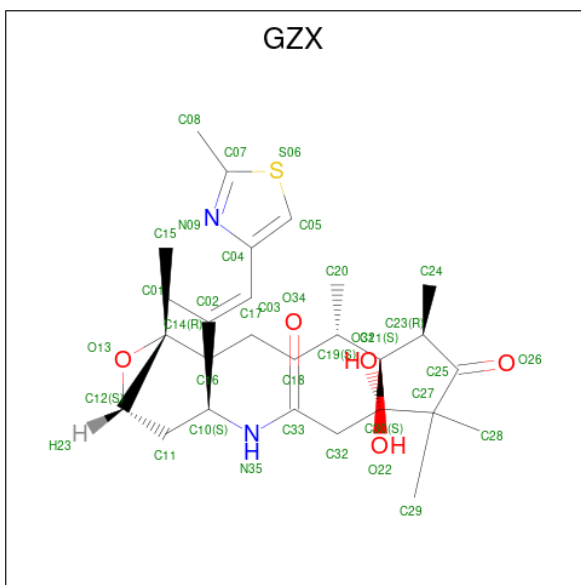
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 10 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



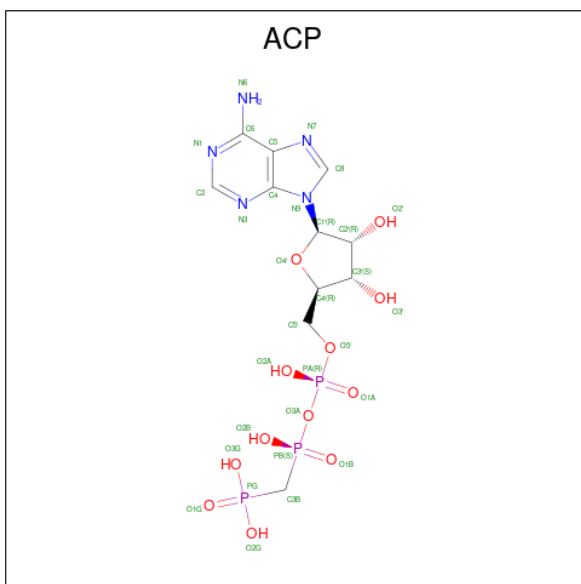
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
10	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 11 is (1 {S},3 {S},7 {S},10 {R},11 {S},12 {S},16 {R})-8,8,10,12,16-pentamethyl-3-[({E})-1-(2-methyl-1,3-thiazol-4-yl)prop-1-en-2-yl]-7,11-bis(oxidanyl)-17-oxa-4-azabicyclo[14.1.0]heptadecane-5,9-dione (CCD ID: GZX) (formula: C₂₇H₄₂N₂O₅S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	D	1	Total	C	N	O	S	0	0
			35	27	2	5	1		

- Molecule 12 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	F	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

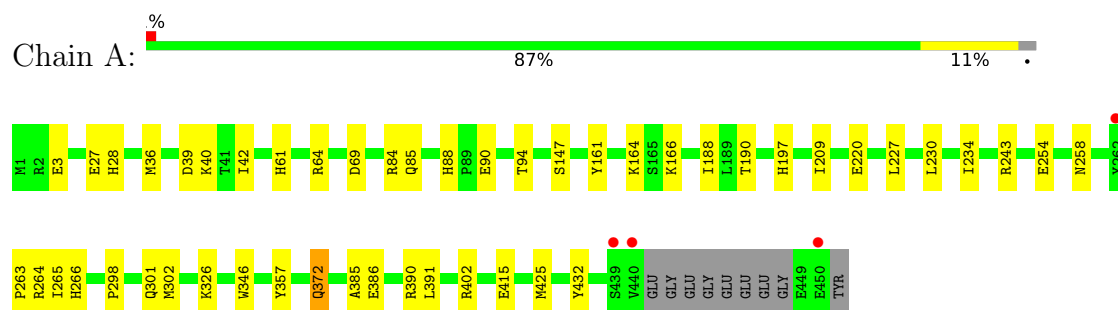
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	167	Total 167	O 167	0	0
13	B	117	Total 117	O 117	0	0
13	C	220	Total 220	O 220	0	0
13	D	65	Total 65	O 65	0	0
13	E	27	Total 27	O 27	0	0
13	F	59	Total 59	O 59	0	0

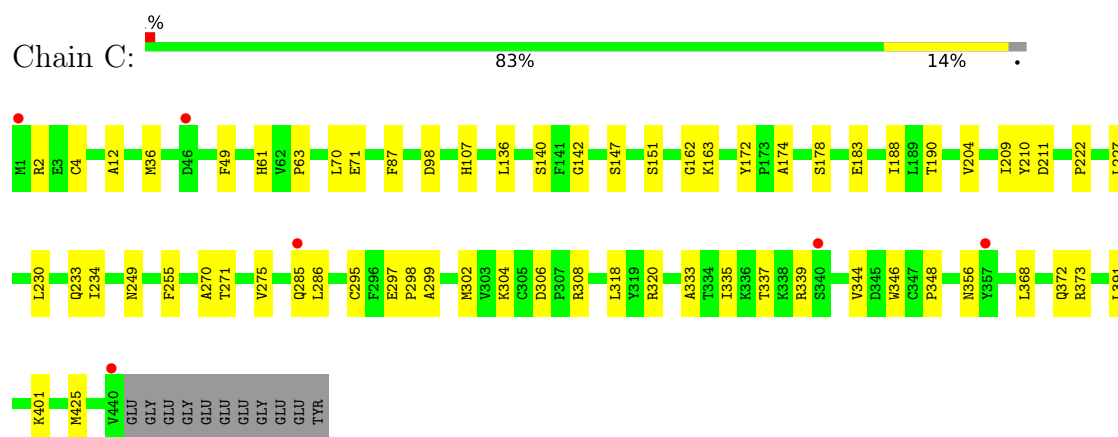
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

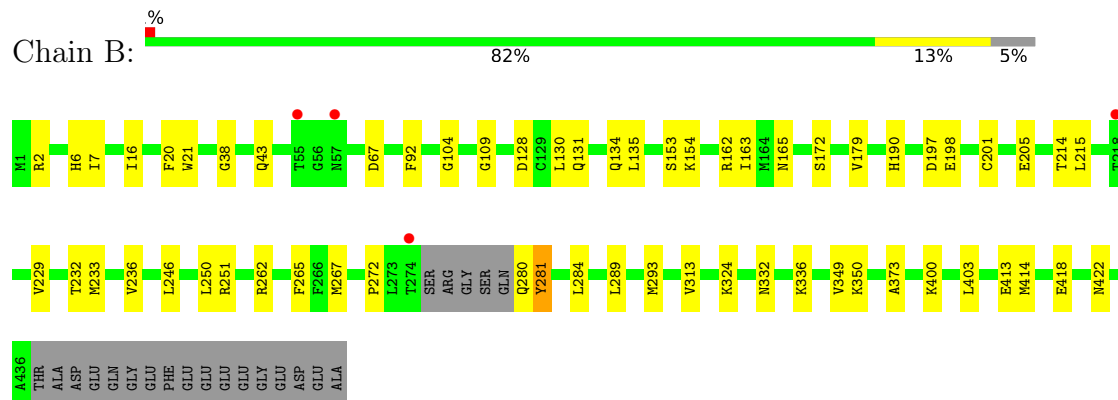
• Molecule 1: Tubulin alpha-1B chain



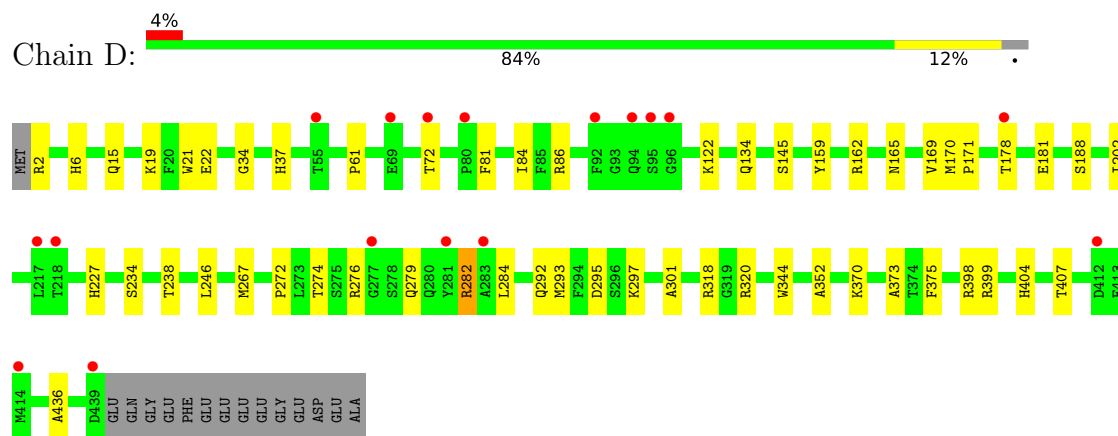
• Molecule 1: Tubulin alpha-1B chain



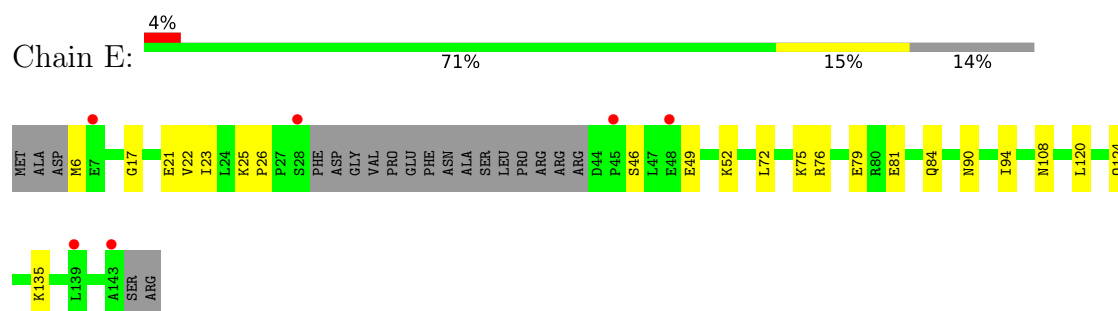
• Molecule 2: Tubulin beta chain



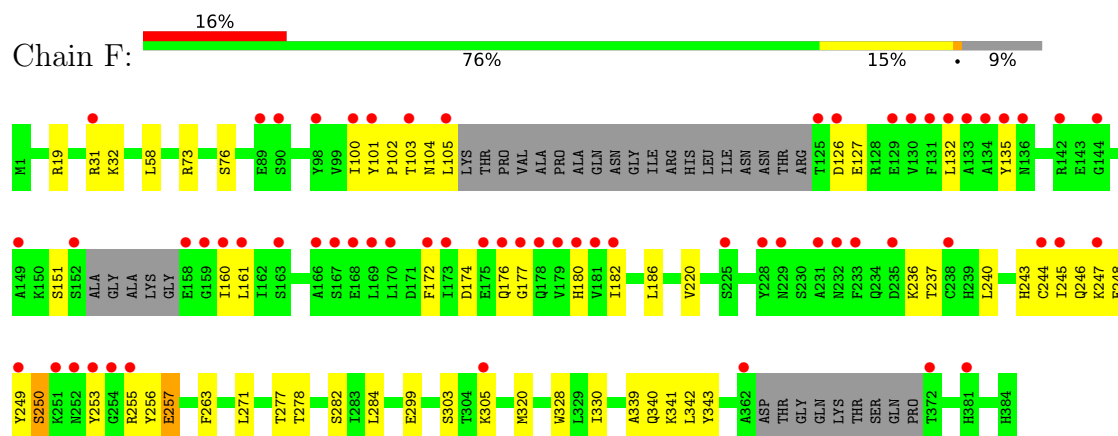
- Molecule 2: Tubulin beta chain



- Molecule 3: Stathmin-4



- Molecule 4: Tubulin tyrosine ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.16Å 158.18Å 181.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.50 – 2.40 35.50 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.0 (35.50-2.40) 99.4 (35.50-2.40)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.174 , 0.222 0.175 , 0.221	Depositor DCC
R_{free} test set	2000 reflections (1.67%)	wwPDB-VP
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18541	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GZX, MES, CL, MG, GDP, CA, ACP, GTP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.43	0/3579	0.63	0/4856
1	C	0.48	0/3587	0.67	0/4870
2	B	0.45	0/3448	0.63	0/4671
2	D	0.48	0/3484	0.66	1/4720 (0.0%)
3	E	0.44	0/1049	0.61	0/1393
4	F	0.37	0/3003	0.63	2/4056 (0.0%)
All	All	0.44	0/18150	0.65	3/24566 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	282	ARG	NE-CZ-NH2	6.38	124.94	119.20
4	F	250	SER	CA-C-N	6.26	129.82	120.31
4	F	250	SER	C-N-CA	6.26	129.82	120.31

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3484	0	3403	37	0
1	C	3479	0	3405	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3359	0	3241	42	0
2	D	3395	0	3273	47	0
3	E	1031	0	1048	18	0
4	F	2917	0	2900	48	0
5	A	32	0	12	0	0
5	C	32	0	12	0	0
6	A	1	0	0	0	0
6	B	2	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	F	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	E	1	0	0	0	0
8	A	1	0	0	0	0
9	B	28	0	12	0	0
9	D	28	0	12	0	0
10	B	24	0	24	4	0
11	D	35	0	0	2	0
12	F	31	0	13	1	0
13	A	167	0	0	2	0
13	B	117	0	0	2	0
13	C	220	0	0	3	0
13	D	65	0	0	5	0
13	E	27	0	0	0	0
13	F	59	0	0	0	0
All	All	18541	0	17355	241	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (241) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:103:THR:HG22	4:F:174:ASP:HB3	1.57	0.85
1:C:297:GLU:OE1	1:C:299:ALA:HB3	1.78	0.84
1:C:297:GLU:OE2	1:C:298:PRO:HD2	1.77	0.83
2:D:293:MET:HG2	2:D:375:PHE:HB2	1.65	0.79
4:F:320[B]:MET:HE2	4:F:330:ILE:HD11	1.65	0.78
1:C:297:GLU:OE2	1:C:298:PRO:CD	2.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:ILE:HG21	1:C:302[B]:MET:SD	2.25	0.77
1:A:230:LEU:O	1:A:234:ILE:HD12	1.84	0.76
2:D:276:ARG:HH11	2:D:276:ARG:HG3	1.50	0.76
1:C:297:GLU:OE2	1:C:298:PRO:N	2.21	0.73
1:C:297:GLU:OE1	1:C:299:ALA:CB	2.37	0.73
2:D:272:PRO:HG3	2:D:284:LEU:HD11	1.70	0.72
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.30	0.72
2:D:320:ARG:HH21	2:D:320:ARG:HG3	1.56	0.70
2:D:282:ARG:HH12	2:D:292:GLN:CD	1.97	0.70
2:D:398:ARG:HG3	2:D:399:ARG:HG3	1.74	0.69
1:A:27:GLU:OE2	1:A:243:ARG:NH2	2.25	0.68
1:C:297:GLU:CD	1:C:299:ALA:H	2.01	0.68
2:B:246:LEU:HD21	2:B:350:LYS:HB3	1.73	0.68
1:A:402:ARG:NH1	1:A:415:GLU:OE1	2.26	0.67
1:C:285:GLN:HE22	1:C:372:GLN:HE21	1.42	0.67
2:D:295:ASP:OD2	2:D:297:LYS:HE2	1.94	0.67
4:F:237:THR:HG21	4:F:250:SER:HB2	1.78	0.66
2:D:15:GLN:HE21	2:D:72:THR:HG23	1.62	0.65
4:F:277:THR:HG21	4:F:282:SER:HB3	1.77	0.65
4:F:186:LEU:HD22	4:F:320[B]:MET:HE3	1.79	0.64
2:D:2:ARG:N	13:D:603:HOH:O	2.29	0.64
2:B:272:PRO:HB3	2:B:284:LEU:HD22	1.80	0.63
2:B:422[A]:ASN:ND2	13:B:605:HOH:O	2.32	0.63
2:B:16[B]:ILE:HD13	2:B:229:VAL:HG11	1.81	0.63
2:D:238[B]:THR:HG21	2:D:318:ARG:HD2	1.80	0.62
2:D:19:LYS:NZ	13:D:602:HOH:O	2.29	0.62
1:C:306:ASP:OD1	1:C:308:ARG:HD3	1.99	0.62
4:F:248:GLU:HG3	4:F:249:TYR:CD1	2.35	0.61
2:D:34:GLY:HA2	2:D:84:ILE:HD11	1.82	0.61
1:A:84:ARG:HG3	1:A:85:GLN:N	2.16	0.61
2:D:272:PRO:HB2	13:D:601:HOH:O	1.99	0.61
2:D:276:ARG:HG3	2:D:276:ARG:NH1	2.16	0.60
2:D:274:THR:HB	2:D:279:GLN:HG2	1.84	0.60
3:E:6:MET:HE3	3:E:22:VAL:HG21	1.84	0.59
2:B:197:ASP:OD1	10:B:504:MES:H32	2.01	0.59
1:C:209:ILE:HG23	1:C:230:LEU:HD23	1.83	0.59
4:F:126:ASP:OD1	4:F:127:GLU:N	2.35	0.59
1:C:249:ASN:OD1	1:C:356:ASN:ND2	2.36	0.58
4:F:236:LYS:HE3	4:F:240:LEU:HD11	1.84	0.58
2:D:282:ARG:NH1	13:D:601:HOH:O	2.37	0.58
1:A:209:ILE:HD11	1:A:302:MET:SD	2.43	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:262:ARG:HH12	2:B:422[A]:ASN:HD21	1.51	0.57
4:F:161:LEU:HD22	4:F:172:PHE:CG	2.39	0.57
1:A:166:LYS:HE2	1:A:197:HIS:O	2.04	0.57
2:B:179:VAL:HG12	1:C:348:PRO:HG2	1.86	0.57
1:C:2:ARG:HH11	1:C:2:ARG:HG3	1.68	0.57
1:C:255:PHE:CZ	1:C:318:LEU:CD2	2.87	0.57
2:B:2:ARG:HE	2:B:128:ASP:HB3	1.69	0.57
2:B:214:THR:HG22	2:B:215:LEU:HD23	1.86	0.57
2:B:197:ASP:OD1	10:B:504:MES:H72	2.05	0.57
2:D:145[A]:SER:HB2	2:D:188:SER:OG	2.05	0.56
1:A:88:HIS:CE1	1:A:90:GLU:HG3	2.41	0.56
1:A:357:TYR:CE2	3:E:17:GLY:HA2	2.40	0.56
2:D:267:MET:HG3	2:D:301:ALA:HB3	1.87	0.56
4:F:160:ILE:O	4:F:161:LEU:HD12	2.04	0.56
1:A:220:GLU:HB3	2:B:324:LYS:HD3	1.88	0.56
3:E:25:LYS:HD3	3:E:26:PRO:O	2.05	0.56
2:D:320:ARG:HG3	2:D:320:ARG:NH2	2.20	0.55
1:C:255:PHE:CE2	1:C:318:LEU:CD2	2.89	0.55
1:A:166:LYS:NZ	1:A:197:HIS:O	2.38	0.55
2:B:163:ILE:HG21	2:B:250:LEU:HB3	1.89	0.55
4:F:132:LEU:HA	4:F:135:TYR:HB3	1.89	0.55
4:F:277:THR:HG22	4:F:278:THR:H	1.70	0.55
2:D:282:ARG:NH1	2:D:292:GLN:CD	2.65	0.55
1:C:270:ALA:HB3	1:C:302[B]:MET:SD	2.48	0.54
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.25	0.54
2:B:232:THR:O	2:B:236:VAL:HG13	2.07	0.54
4:F:247:LYS:HA	4:F:253:TYR:CD1	2.42	0.54
3:E:72:LEU:O	3:E:76:ARG:HG2	2.08	0.53
4:F:31:ARG:NE	4:F:32:LYS:H	2.06	0.53
1:C:204:VAL:HG22	1:C:302[B]:MET:HE3	1.89	0.53
1:A:88:HIS:HE1	1:A:90:GLU:HG3	1.72	0.53
1:C:172:TYR:CE2	1:C:391:LEU:HD22	2.43	0.53
2:B:6:HIS:CD2	2:B:21:TRP:HE1	2.26	0.53
4:F:237:THR:O	4:F:246:GLN:NE2	2.36	0.53
4:F:161:LEU:HD22	4:F:172:PHE:CB	2.39	0.53
1:C:204:VAL:HG22	1:C:302[B]:MET:CE	2.40	0.52
2:D:282:ARG:HD2	11:D:503:GZX:C08	2.39	0.52
12:F:402:ACP:H8	12:F:402:ACP:H5'2	1.91	0.52
2:B:284:LEU:HD23	2:B:289:LEU:HD23	1.92	0.52
1:C:285:GLN:HE21	1:C:373:ARG:HH22	1.57	0.52
4:F:101:TYR:N	4:F:126:ASP:OD2	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:LYS:HD3	3:E:76:ARG:CZ	2.39	0.52
2:D:159:TYR:HB3	2:D:162:ARG:HG3	1.91	0.52
4:F:237:THR:CG2	4:F:250:SER:HB2	2.40	0.52
2:B:67:ASP:O	2:B:92:PHE:HA	2.10	0.52
3:E:46:SER:OG	3:E:49:GLU:HG3	2.10	0.52
4:F:151:SER:HB3	4:F:180:HIS:NE2	2.24	0.52
4:F:299:GLU:OE2	4:F:305:LYS:NZ	2.43	0.52
1:A:166:LYS:CE	1:A:197:HIS:O	2.58	0.51
2:B:2:ARG:HB2	2:B:2:ARG:CZ	2.40	0.51
2:B:134:GLN:HA	2:B:165:ASN:O	2.10	0.51
1:C:255:PHE:CZ	1:C:318:LEU:HD22	2.45	0.51
2:B:332:ASN:ND2	2:B:336:LYS:HD2	2.26	0.51
1:A:209:ILE:HG22	1:A:227:LEU:HD22	1.92	0.51
2:D:19:LYS:HZ1	2:D:227:HIS:HD2	1.58	0.51
3:E:75:LYS:HE3	3:E:79:GLU:OE2	2.11	0.50
1:A:84:ARG:HG2	1:A:84:ARG:HH11	1.76	0.50
1:C:142:GLY:HA3	1:C:183:GLU:OE2	2.12	0.50
2:D:19:LYS:NZ	2:D:227:HIS:HD2	2.10	0.50
1:C:211[A]:ASP:OD2	1:C:304:LYS:NZ	2.45	0.50
4:F:102:PRO:HA	4:F:174:ASP:OD1	2.12	0.50
1:A:386:GLU:O	1:A:390[A]:ARG:HD3	2.12	0.50
2:D:134:GLN:HA	2:D:165:ASN:O	2.12	0.50
1:A:42:ILE:HD12	1:A:42:ILE:H	1.77	0.49
2:B:313:VAL:HB	2:B:349:VAL:HG22	1.93	0.49
1:C:368:LEU:HD22	13:C:724:HOH:O	2.12	0.49
4:F:339:ALA:HB3	4:F:342:LEU:HD12	1.92	0.49
1:C:255:PHE:CE2	1:C:318:LEU:HD21	2.47	0.49
4:F:151:SER:HB3	4:F:180:HIS:CD2	2.47	0.49
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.47	0.49
2:D:37:HIS:HB2	13:D:658:HOH:O	2.12	0.49
1:C:275:VAL:HG13	1:C:368:LEU:HD21	1.95	0.49
2:B:38:GLY:HA3	2:B:43:GLN:OE1	2.13	0.49
1:C:320:ARG:HA	1:C:356:ASN:O	2.13	0.49
4:F:243:HIS:CE1	4:F:247:LYS:HE2	2.48	0.49
4:F:303:SER:OG	4:F:305:LYS:HE3	2.13	0.49
2:D:282:ARG:NH1	2:D:292:GLN:NE2	2.61	0.48
4:F:340:GLN:HA	4:F:343:TYR:CD2	2.48	0.48
1:A:161:TYR:HB3	1:A:164:LYS:HD3	1.94	0.48
2:B:104:GLY:O	2:B:109:GLY:HA3	2.13	0.48
2:D:169:VAL:HA	2:D:202:ILE:O	2.14	0.48
2:B:165:ASN:OD1	2:B:198:GLU:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:19:ARG:HG2	4:F:19:ARG:HH11	1.79	0.48
1:C:255:PHE:CE2	1:C:318:LEU:HD22	2.48	0.47
1:C:339:ARG:O	13:C:601:HOH:O	2.20	0.47
1:A:264:ARG:NH1	13:A:603:HOH:O	2.25	0.47
2:B:190:HIS:NE2	2:B:422[B]:ASN:OD1	2.48	0.47
1:C:285:GLN:NE2	1:C:372:GLN:HE21	2.09	0.47
2:D:293:MET:SD	2:D:373:ALA:HB1	2.54	0.47
2:B:2:ARG:NH2	2:B:128:ASP:OD2	2.48	0.47
2:B:20:PHE:CD1	2:B:233:MET:HE2	2.49	0.47
1:C:333:ALA:O	1:C:337:THR:HG23	2.15	0.47
4:F:151:SER:HB3	4:F:180:HIS:CE1	2.50	0.47
2:D:279:GLN:NE2	11:D:503:GZX:O31	2.46	0.47
4:F:340:GLN:HA	4:F:343:TYR:HD2	1.79	0.47
2:D:398:ARG:HG3	2:D:399:ARG:N	2.30	0.47
1:C:285:GLN:NE2	1:C:373:ARG:HH12	2.13	0.47
1:C:209:ILE:HG22	1:C:227:LEU:HD22	1.97	0.46
1:C:297:GLU:CD	1:C:297:GLU:C	2.84	0.46
2:D:178:THR:O	2:D:181:GLU:HG3	2.14	0.46
1:C:188:ILE:HG13	1:C:425:MET:HG3	1.97	0.46
2:D:15:GLN:HE21	2:D:72:THR:CG2	2.26	0.46
4:F:244:CYS:SG	4:F:245:ILE:HG13	2.55	0.46
1:A:3:GLU:HG2	1:A:64:ARG:CZ	2.45	0.46
1:A:188:ILE:HG13	1:A:425:MET:HG3	1.98	0.46
4:F:263:PHE:CZ	4:F:341:LYS:HE3	2.50	0.46
1:A:263:PRO:O	1:A:266:HIS:HD2	1.98	0.46
1:A:357:TYR:CZ	3:E:17:GLY:HA2	2.50	0.46
2:B:267:MET:HE3	2:B:267:MET:HB2	1.66	0.46
2:D:22:GLU:HG2	2:D:81:PHE:CD1	2.51	0.46
4:F:100:ILE:HD13	4:F:182:ILE:HD12	1.98	0.46
1:A:147:SER:HB2	1:A:190:THR:HB	1.98	0.46
1:C:401:LYS:HG3	2:D:344:TRP:CE3	2.51	0.46
3:E:21:GLU:OE1	3:E:23:ILE:HD11	2.16	0.46
4:F:176:GLN:OE1	4:F:177:GLY:N	2.49	0.46
2:D:404:HIS:HA	2:D:407:THR:OG1	2.16	0.45
4:F:220[A]:VAL:HG12	4:F:263:PHE:CE2	2.51	0.45
13:C:764:HOH:O	3:E:108:ASN:HB2	2.16	0.45
4:F:161:LEU:HD22	4:F:172:PHE:HB2	1.98	0.45
2:B:7:ILE:O	2:B:135:LEU:HA	2.16	0.45
1:C:210:TYR:CZ	1:C:222:PRO:HD2	2.52	0.45
1:C:2:ARG:HG3	1:C:2:ARG:NH1	2.31	0.45
1:C:401:LYS:HE3	2:D:436:ALA:HB1	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:LYS:HD3	1:A:40:LYS:HA	1.77	0.45
4:F:244:CYS:SG	4:F:245:ILE:N	2.89	0.45
2:D:86:ARG:NH2	2:D:122:LYS:HE3	2.32	0.45
1:A:254:GLU:HG2	1:A:258:ASN:ND2	2.32	0.45
1:C:147:SER:HB2	1:C:190:THR:HB	1.99	0.45
1:A:84:ARG:HG2	1:A:84:ARG:NH1	2.31	0.44
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.53	0.44
2:B:332:ASN:CG	2:B:336:LYS:HD2	2.42	0.44
4:F:186:LEU:HD21	4:F:328:TRP:CG	2.52	0.44
2:B:403:LEU:HD23	2:B:403:LEU:HA	1.86	0.44
2:B:201:CYS:SG	2:B:265:PHE:HB3	2.58	0.44
4:F:102:PRO:HD2	4:F:105:LEU:HD13	2.00	0.44
1:A:391:LEU:HD12	1:A:391:LEU:HA	1.78	0.44
4:F:73:ARG:HG2	4:F:73:ARG:HH11	1.83	0.44
4:F:73:ARG:HB2	4:F:76:SER:OG	2.17	0.44
1:C:70:LEU:HD23	1:C:70:LEU:HA	1.78	0.44
2:B:414:MET:HE3	2:B:418:GLU:HG3	1.99	0.43
3:E:52:LYS:HA	3:E:52:LYS:HD3	1.65	0.43
1:C:285:GLN:HE22	1:C:372:GLN:NE2	2.13	0.43
2:D:284:LEU:HB3	2:D:370:LYS:NZ	2.33	0.43
1:A:69:ASP:O	1:A:94:THR:HA	2.18	0.43
1:C:107:HIS:HD2	1:C:151[A]:SER:OG	2.01	0.43
1:C:12:ALA:HB3	1:C:140:SER:HB3	2.00	0.43
2:D:170:MET:HG3	2:D:171:PRO:HD2	2.01	0.43
4:F:102:PRO:HB2	4:F:105:LEU:HD12	2.01	0.43
2:B:130:LEU:O	2:B:162:ARG:NH1	2.51	0.43
4:F:58:LEU:HD23	4:F:58:LEU:HA	1.85	0.43
1:A:326:LYS:HA	1:A:326:LYS:HD2	1.79	0.42
1:A:298:PRO:HA	1:A:301:GLN:CD	2.44	0.42
2:D:246:LEU:HD23	2:D:352:ALA:HB2	2.00	0.42
1:C:286:LEU:HD23	1:C:286:LEU:HA	1.72	0.42
1:C:163:LYS:CE	3:E:90[A]:ASN:OD1	2.67	0.42
3:E:81:GLU:HA	3:E:84:GLN:HG2	2.00	0.42
4:F:186:LEU:HD22	4:F:320[B]:MET:CE	2.49	0.42
4:F:256:TYR:HB2	4:F:257:GLU:OE2	2.19	0.42
1:A:346:TRP:CD1	1:A:346:TRP:H	2.37	0.42
2:B:172:SER:OG	2:B:205:GLU:OE1	2.33	0.42
1:C:162:GLY:HA2	3:E:94:ILE:HD11	2.01	0.42
1:C:271:THR:HG21	1:C:295:CYS:O	2.19	0.42
1:A:385:ALA:HB2	1:A:432:TYR:CG	2.55	0.42
1:C:174:ALA:O	1:C:178:SER:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:GLN:HG3	1:C:368:LEU:CD1	2.50	0.42
3:E:135:LYS:HE3	3:E:135:LYS:HB2	1.83	0.42
4:F:247:LYS:HD3	4:F:253:TYR:OH	2.20	0.42
1:C:210:TYR:CE1	1:C:222:PRO:HD2	2.55	0.41
2:D:21:TRP:CZ3	2:D:61:PRO:HB3	2.55	0.41
4:F:104:ASN:HD22	4:F:105:LEU:HG	1.84	0.41
1:A:36:MET:SD	1:A:39:ASP:HB2	2.60	0.41
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.56	0.41
1:A:372[B]:GLN:OE1	13:A:601:HOH:O	2.21	0.41
2:B:251:ARG:NH1	10:B:504:MES:O3S	2.52	0.41
4:F:284:LEU:HD12	4:F:284:LEU:HA	1.82	0.41
1:C:36:MET:HB3	1:C:61:HIS:CE1	2.55	0.41
1:C:36:MET:HE1	1:C:49:PHE:CE2	2.56	0.41
2:D:86:ARG:HH22	2:D:122:LYS:HE3	1.85	0.41
2:B:154:LYS:NZ	13:B:614:HOH:O	2.52	0.41
2:B:251:ARG:NH1	10:B:504:MES:O2S	2.50	0.41
2:B:400:LYS:HE2	2:B:413:GLU:OE1	2.21	0.41
2:D:234:SER:O	2:D:238[B]:THR:HG23	2.21	0.41
2:B:280:GLN:HG3	2:B:281:TYR:N	2.36	0.41
1:C:63:PRO:HG2	1:C:87:PHE:CE1	2.55	0.41
1:C:71:GLU:HG2	1:C:98:ASP:HB3	2.03	0.41
1:C:335:ILE:HG23	1:C:339:ARG:HG3	2.02	0.41
2:D:81:PHE:O	2:D:84:ILE:HG22	2.20	0.41
2:D:282:ARG:HH11	2:D:282:ARG:HD3	1.60	0.41
1:C:163:LYS:HE3	3:E:90[A]:ASN:OD1	2.21	0.40
3:E:120:LEU:O	3:E:124:GLN:HG3	2.21	0.40
1:A:28:HIS:O	1:A:36:MET:HE3	2.20	0.40
2:B:293:MET:HE3	2:B:373:ALA:HB1	2.04	0.40
4:F:105:LEU:HD11	4:F:177:GLY:O	2.22	0.40
2:B:153:SER:HB3	3:E:76:ARG:HH22	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	444/451 (98%)	430 (97%)	14 (3%)	0	100	100
1	C	448/451 (99%)	439 (98%)	9 (2%)	0	100	100
2	B	425/445 (96%)	415 (98%)	10 (2%)	0	100	100
2	D	432/445 (97%)	418 (97%)	14 (3%)	0	100	100
3	E	122/143 (85%)	119 (98%)	3 (2%)	0	100	100
4	F	349/384 (91%)	340 (97%)	9 (3%)	0	100	100
All	All	2220/2319 (96%)	2161 (97%)	59 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	379/379 (100%)	377 (100%)	2 (0%)	81	91
1	C	381/379 (100%)	381 (100%)	0	100	100
2	B	371/383 (97%)	369 (100%)	2 (0%)	81	91
2	D	375/383 (98%)	375 (100%)	0	100	100
3	E	113/127 (89%)	113 (100%)	0	100	100
4	F	323/342 (94%)	318 (98%)	5 (2%)	57	77
All	All	1942/1993 (97%)	1933 (100%)	9 (0%)	86	91

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	372[A]	GLN
1	A	372[B]	GLN
2	B	131	GLN
2	B	281	TYR

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Mol	Chain	Res	Type
4	F	255[A]	ARG
4	F	255[B]	ARG
4	F	257	GLU
4	F	271[A]	LEU
4	F	271[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	88	HIS
1	A	128	GLN
1	A	216	ASN
1	A	258	ASN
1	A	301	GLN
1	A	393	HIS
2	B	280	GLN
2	B	291	GLN
2	B	347	ASN
2	B	383	GLN
2	B	432	GLN
1	C	35	GLN
1	C	85	GLN
1	C	107	HIS
1	C	256	GLN
1	C	285	GLN
1	C	372	GLN
1	C	393	HIS
2	D	8	GLN
2	D	14	ASN
2	D	15	GLN
2	D	134	GLN
2	D	165	ASN
2	D	227	HIS
2	D	329	GLN
3	E	124	GLN
4	F	104	ASN
4	F	234	GLN
4	F	260	ASN
4	F	269	GLN
4	F	348	GLN
4	F	379	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 11 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
9	GDP	D	501	6	29,30,30	1.19	3 (10%)	45,47,47	1.69	6 (13%)
10	MES	B	505	-	12,12,12	4.58	7 (58%)	15,16,16	2.09	4 (26%)
5	GTP	C	501	6	33,34,34	0.85	1 (3%)	50,54,54	1.64	13 (26%)
12	ACP	F	402	6	31,33,33	3.26	11 (35%)	47,52,52	2.19	15 (31%)
5	GTP	A	501	6	33,34,34	0.97	3 (9%)	50,54,54	1.54	9 (18%)
10	MES	B	504	-	12,12,12	4.63	7 (58%)	15,16,16	2.59	5 (33%)
9	GDP	B	501	6	29,30,30	1.27	5 (17%)	45,47,47	1.76	9 (20%)
11	GZX	D	503	-	36,37,37	1.98	8 (22%)	47,56,56	3.03	11 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GDP	D	501	6	-	4/16/32/32	0/3/3/3
10	MES	B	505	-	-	0/6/14/14	0/1/1/1
5	GTP	C	501	6	-	7/22/38/38	0/3/3/3
12	ACP	F	402	6	-	1/19/38/38	0/3/3/3
5	GTP	A	501	6	-	5/22/38/38	0/3/3/3
10	MES	B	504	-	-	2/6/14/14	0/1/1/1
9	GDP	B	501	6	-	3/16/32/32	0/3/3/3
11	GZX	D	503	-	-	10/51/59/59	0/2/3/3

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	F	402	ACP	O4'-C1'	8.95	1.62	1.42
10	B	505	MES	C7-N4	-8.74	1.27	1.47
10	B	504	MES	O1S-S	8.02	1.67	1.45
10	B	504	MES	C7-N4	-7.96	1.29	1.47
11	D	503	GZX	C33-N35	7.43	1.49	1.34
10	B	505	MES	O2S-S	7.37	1.65	1.45
10	B	505	MES	O1S-S	7.34	1.65	1.45
10	B	504	MES	O2S-S	7.18	1.65	1.45
12	F	402	ACP	C2'-C1'	-6.90	1.31	1.53
12	F	402	ACP	PB-O3A	6.89	1.66	1.58
12	F	402	ACP	O4'-C4'	-6.32	1.31	1.45
12	F	402	ACP	PA-O3A	6.02	1.66	1.59
10	B	504	MES	C8-S	5.77	1.85	1.77
10	B	504	MES	O3S-S	4.99	1.66	1.47
10	B	505	MES	O3S-S	4.87	1.65	1.47
10	B	505	MES	C8-S	4.71	1.84	1.77
12	F	402	ACP	C6-N6	4.54	1.45	1.34
11	D	503	GZX	C03-C04	3.89	1.56	1.41
11	D	503	GZX	C27-C25	3.33	1.59	1.54
9	D	501	GDP	C5-C4	3.21	1.47	1.38
12	F	402	ACP	O2'-C2'	3.10	1.50	1.43
10	B	505	MES	C5-N4	-3.04	1.38	1.46
11	D	503	GZX	C01-C02	3.00	1.56	1.50
10	B	504	MES	C5-N4	-2.81	1.39	1.46
10	B	505	MES	C3-N4	-2.80	1.39	1.46
9	B	501	GDP	PA-O3A	2.78	1.62	1.59
12	F	402	ACP	O3'-C3'	-2.76	1.36	1.43
11	D	503	GZX	C05-C04	2.73	1.41	1.36
5	A	501	GTP	PA-O3A	2.72	1.62	1.59
5	C	501	GTP	PB-O3B	2.71	1.62	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	504	MES	C3-N4	-2.64	1.39	1.46
9	B	501	GDP	C5-C4	2.63	1.45	1.38
12	F	402	ACP	C5-C4	-2.58	1.34	1.39
11	D	503	GZX	O31-C30	-2.52	1.39	1.43
9	D	501	GDP	C6-N1	-2.50	1.34	1.38
12	F	402	ACP	C5-N7	-2.48	1.34	1.39
9	B	501	GDP	C6-N1	-2.44	1.34	1.38
11	D	503	GZX	C32-C33	2.39	1.56	1.51
9	B	501	GDP	C4-N9	-2.37	1.32	1.38
5	A	501	GTP	PB-O3B	2.29	1.62	1.59
12	F	402	ACP	C8-N9	-2.23	1.33	1.37
9	B	501	GDP	C5-N7	-2.14	1.34	1.39
11	D	503	GZX	C04-N09	-2.10	1.33	1.38
5	A	501	GTP	C2-N3	2.03	1.38	1.33
9	D	501	GDP	C5-N7	-2.01	1.35	1.39

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	503	GZX	C16-C14-C12	11.44	137.84	118.95
11	D	503	GZX	O13-C14-C16	-10.20	96.34	114.22
11	D	503	GZX	C15-C14-C16	-6.64	107.23	116.11
11	D	503	GZX	C11-C12-C14	6.03	136.67	125.65
12	F	402	ACP	C5-C4-N3	-5.98	118.48	126.72
9	D	501	GDP	C5-C4-N3	-5.75	119.24	128.39
12	F	402	ACP	N3-C2-N1	-5.57	120.15	128.58
10	B	504	MES	C5-N4-C3	5.23	120.11	108.84
9	B	501	GDP	C2-N3-C4	5.15	121.16	112.30
9	B	501	GDP	C5-C4-N3	-4.94	120.53	128.39
10	B	504	MES	O3S-S-C8	4.79	115.38	106.00
10	B	504	MES	C2-C3-N4	4.76	117.35	110.12
10	B	505	MES	C5-N4-C3	4.59	118.72	108.84
5	C	501	GTP	C2-N3-C4	4.58	120.18	112.30
9	D	501	GDP	C2-N3-C4	4.56	120.16	112.30
12	F	402	ACP	N6-C6-N1	-4.53	108.30	118.38
5	A	501	GTP	C2-N3-C4	4.46	119.98	112.30
5	A	501	GTP	C5-C4-N3	-4.43	121.34	128.39
9	D	501	GDP	N9-C4-N3	4.27	134.50	125.95
11	D	503	GZX	C04-C05-S06	-4.24	104.58	111.44
11	D	503	GZX	O13-C12-C11	-4.20	107.49	116.53
11	D	503	GZX	C15-C14-C12	-4.02	113.59	121.67
10	B	505	MES	C2-C3-N4	4.01	116.21	110.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	F	402	ACP	N9-C8-N7	-3.90	108.41	113.94
5	C	501	GTP	C5-C4-N3	-3.90	122.19	128.39
9	B	501	GDP	C6-C5-N7	3.85	137.29	130.29
12	F	402	ACP	C2-N3-C4	3.77	121.03	111.83
12	F	402	ACP	N3-C4-N9	3.69	133.45	127.17
9	B	501	GDP	N9-C4-N3	3.53	133.02	125.95
9	D	501	GDP	C6-C5-N7	3.45	136.56	130.29
12	F	402	ACP	C3'-C2'-C1'	3.41	107.91	101.46
12	F	402	ACP	C5-C6-N6	3.35	131.59	123.29
5	C	501	GTP	N9-C8-N7	-3.34	107.21	113.40
12	F	402	ACP	C5-N7-C8	3.23	108.53	103.45
10	B	504	MES	C6-C5-N4	3.17	114.94	110.12
10	B	505	MES	C6-C5-N4	3.17	114.94	110.12
11	D	503	GZX	C24-C23-C21	-3.17	106.82	112.42
5	C	501	GTP	C8-N7-C5	2.92	109.47	104.26
5	A	501	GTP	C2-N1-C6	-2.92	119.81	125.11
10	B	505	MES	O2S-S-C8	2.90	111.12	106.73
9	D	501	GDP	C4-C5-N7	-2.88	106.11	110.67
12	F	402	ACP	C5'-C4'-C3'	-2.83	105.01	115.21
12	F	402	ACP	C4-C5-N7	-2.73	107.46	110.58
11	D	503	GZX	C05-S06-C07	2.70	94.76	89.73
12	F	402	ACP	PB-O3A-PA	-2.65	123.74	132.37
5	A	501	GTP	N9-C4-N3	2.64	131.24	125.95
9	B	501	GDP	O3'-C3'-C4'	-2.59	103.63	111.08
12	F	402	ACP	C6-C5-C4	2.59	120.71	117.18
5	A	501	GTP	O6-C6-C5	-2.58	119.72	126.53
10	B	504	MES	O2S-S-C8	-2.57	102.84	106.73
5	C	501	GTP	C6-C5-N7	2.54	134.91	130.29
5	A	501	GTP	N9-C8-N7	-2.53	108.71	113.40
9	B	501	GDP	O6-C6-C5	-2.49	119.97	126.53
5	C	501	GTP	C4-C5-N7	-2.42	106.83	110.67
9	B	501	GDP	C4-C5-N7	-2.35	106.95	110.67
5	A	501	GTP	C8-N7-C5	2.34	108.42	104.26
5	C	501	GTP	N9-C4-N3	2.33	130.61	125.95
5	A	501	GTP	C5-C6-N1	2.32	119.16	113.25
11	D	503	GZX	O31-C30-C27	-2.32	106.50	110.39
5	C	501	GTP	O3'-C3'-C4'	-2.31	104.44	111.08
5	C	501	GTP	O2B-PB-O3A	2.22	113.27	107.27
11	D	503	GZX	O31-C30-C32	2.20	113.75	108.50
5	C	501	GTP	O2A-PA-O3A	2.16	113.12	107.27
5	C	501	GTP	C5-C6-N1	2.16	118.75	113.25
5	C	501	GTP	C2-N1-C6	-2.15	121.21	125.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	501	GTP	N1-C2-N3	-2.15	119.39	123.32
5	A	501	GTP	O2A-PA-O3A	2.13	113.04	107.27
12	F	402	ACP	C2'-C3'-C4'	2.12	106.71	102.61
9	D	501	GDP	C8-N7-C5	2.10	108.00	104.26
12	F	402	ACP	C5-C4-N9	2.07	108.07	105.81
9	B	501	GDP	O4'-C1'-N9	-2.06	103.69	108.36
9	B	501	GDP	C6-C5-C4	-2.04	115.76	118.83

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	PB-O3B-PG-O3G
5	A	501	GTP	C5'-O5'-PA-O3A
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	C5'-O5'-PA-O3A
5	C	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	C5'-O5'-PA-O2A
9	B	501	GDP	C5'-O5'-PA-O3A
9	B	501	GDP	C5'-O5'-PA-O1A
9	B	501	GDP	C5'-O5'-PA-O2A
9	D	501	GDP	C5'-O5'-PA-O3A
9	D	501	GDP	C5'-O5'-PA-O1A
9	D	501	GDP	C5'-O5'-PA-O2A
10	B	504	MES	C8-C7-N4-C5
11	D	503	GZX	C15-C14-C16-C17
11	D	503	GZX	C16-C17-C18-C19
12	F	402	ACP	PB-O3A-PA-O1A
11	D	503	GZX	C30-C32-C33-O34
11	D	503	GZX	C30-C32-C33-N35
5	C	501	GTP	PB-O3B-PG-O3G
11	D	503	GZX	C19-C21-C23-C25
11	D	503	GZX	O13-C14-C16-C17
11	D	503	GZX	C02-C03-C04-N09
10	B	504	MES	N4-C7-C8-S
5	A	501	GTP	PB-O3B-PG-O1G
11	D	503	GZX	C12-C14-C16-C17
11	D	503	GZX	C17-C18-C19-C20
5	C	501	GTP	PB-O3A-PA-O2A
9	D	501	GDP	PB-O3A-PA-O2A
5	C	501	GTP	PB-O3B-PG-O1G

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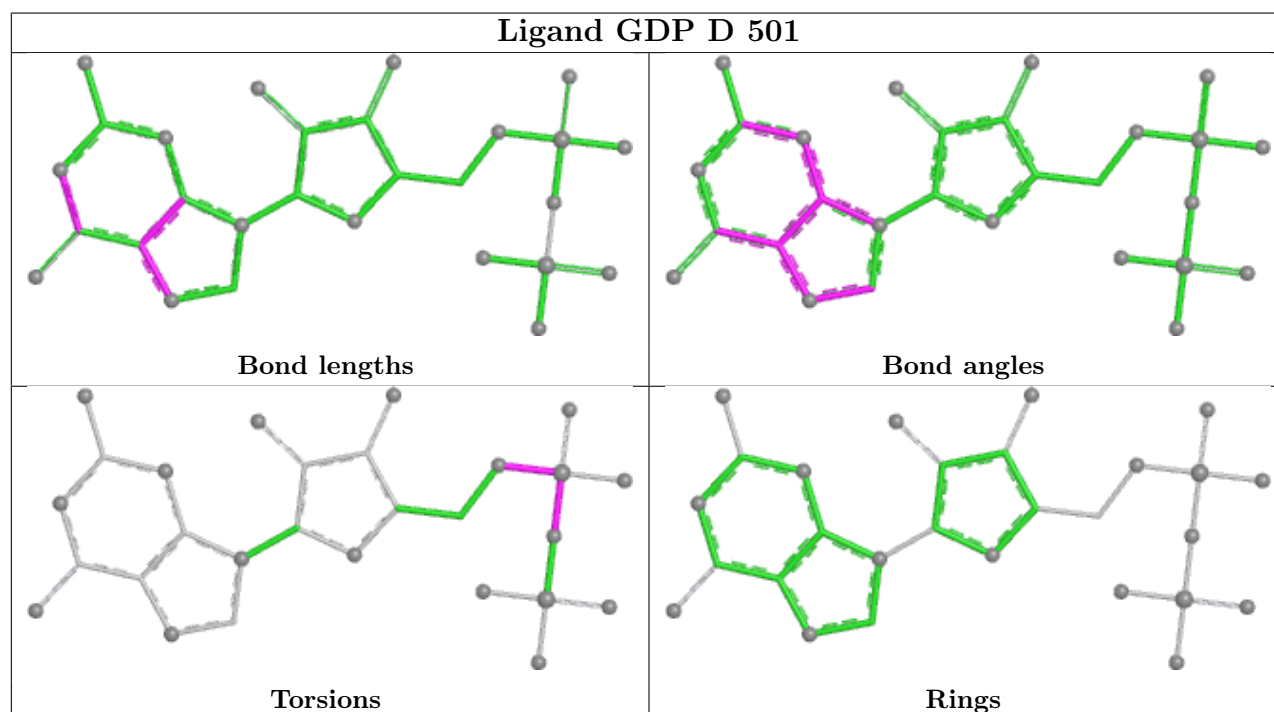
Mol	Chain	Res	Type	Atoms
5	C	501	GTP	C4'-C5'-O5'-PA
11	D	503	GZX	N35-C10-C11-C12

There are no ring outliers.

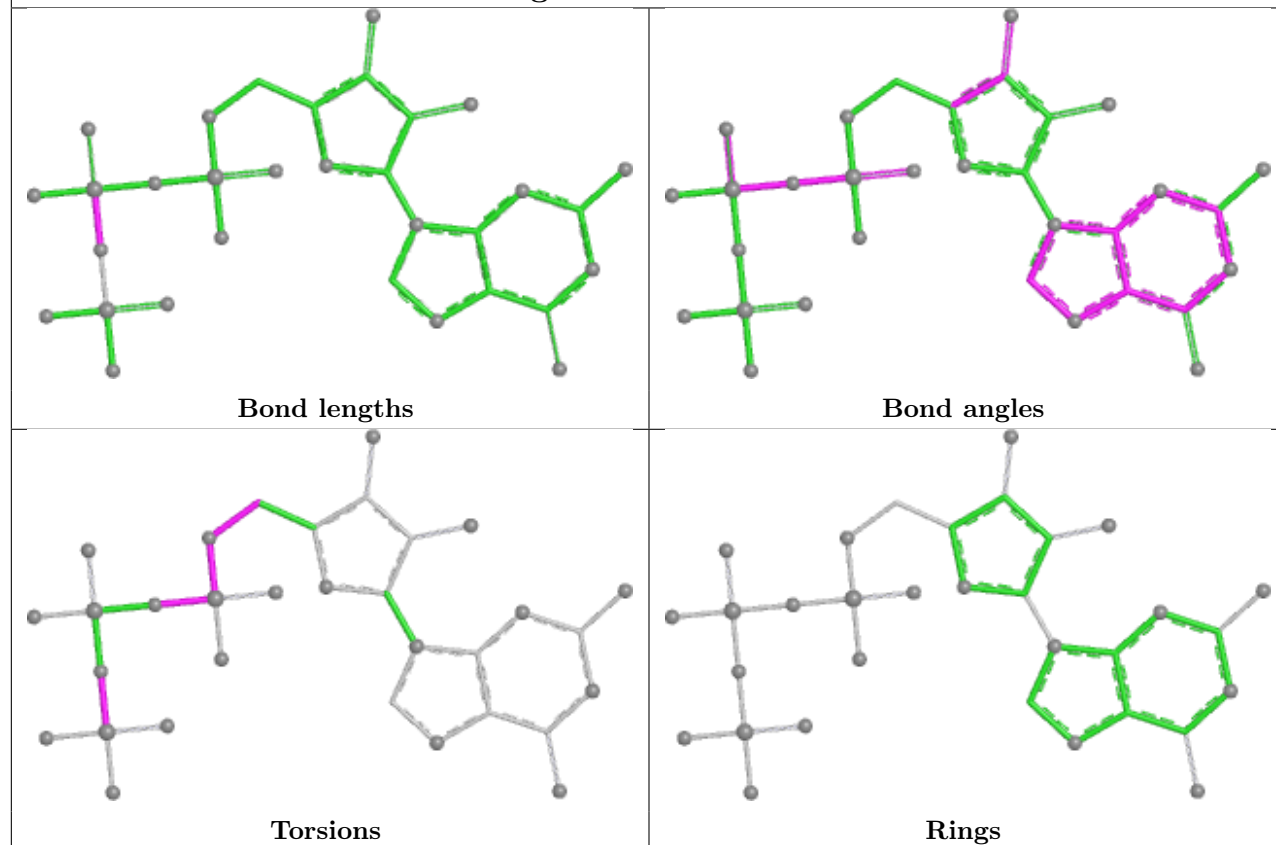
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	F	402	ACP	1	0
10	B	504	MES	4	0
11	D	503	GZX	2	0

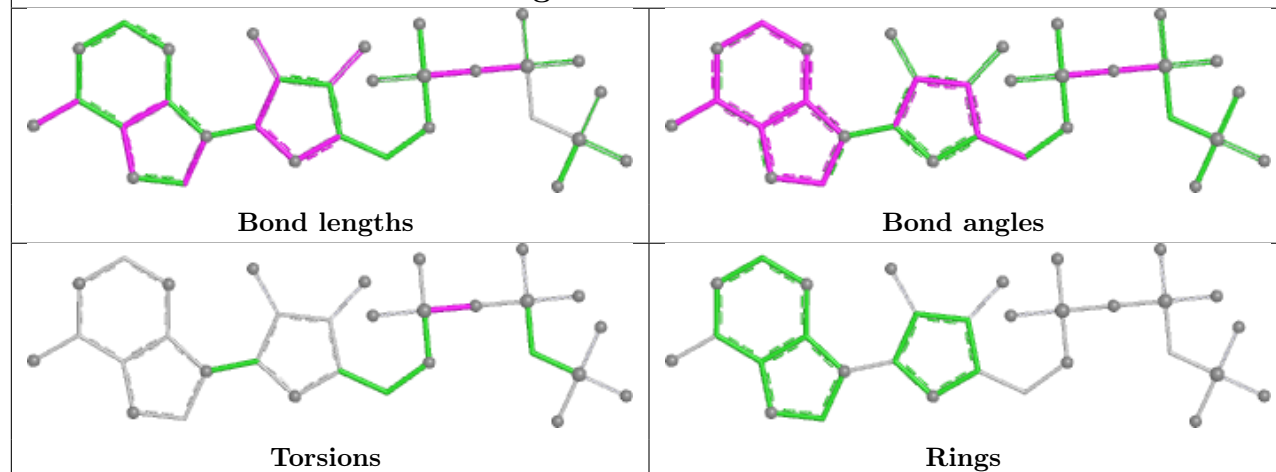
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

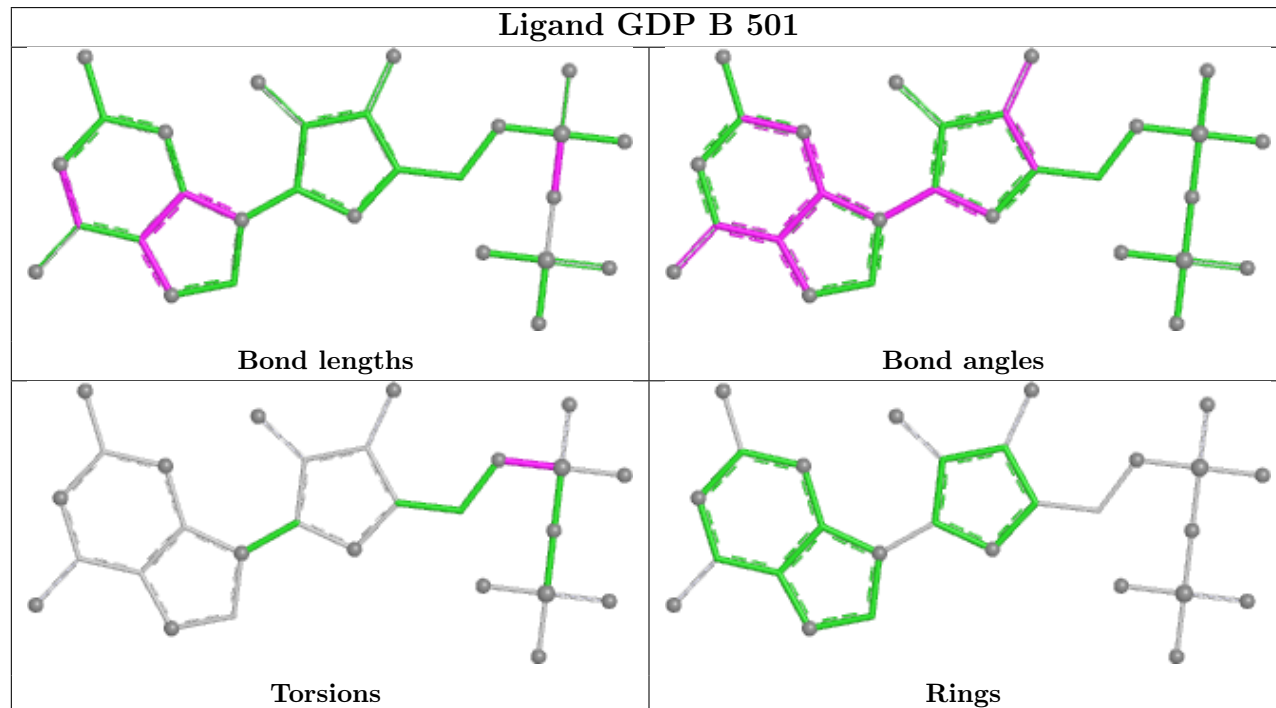
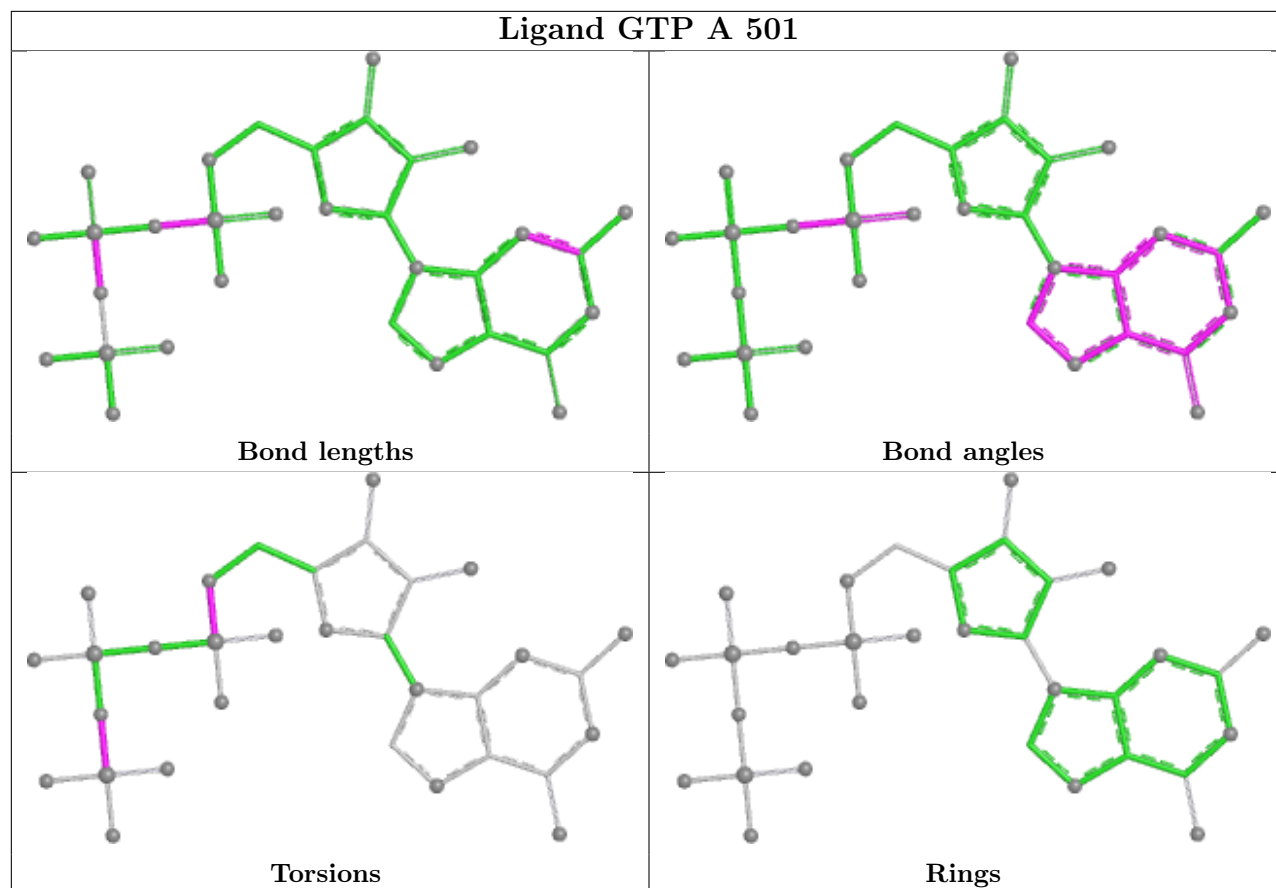


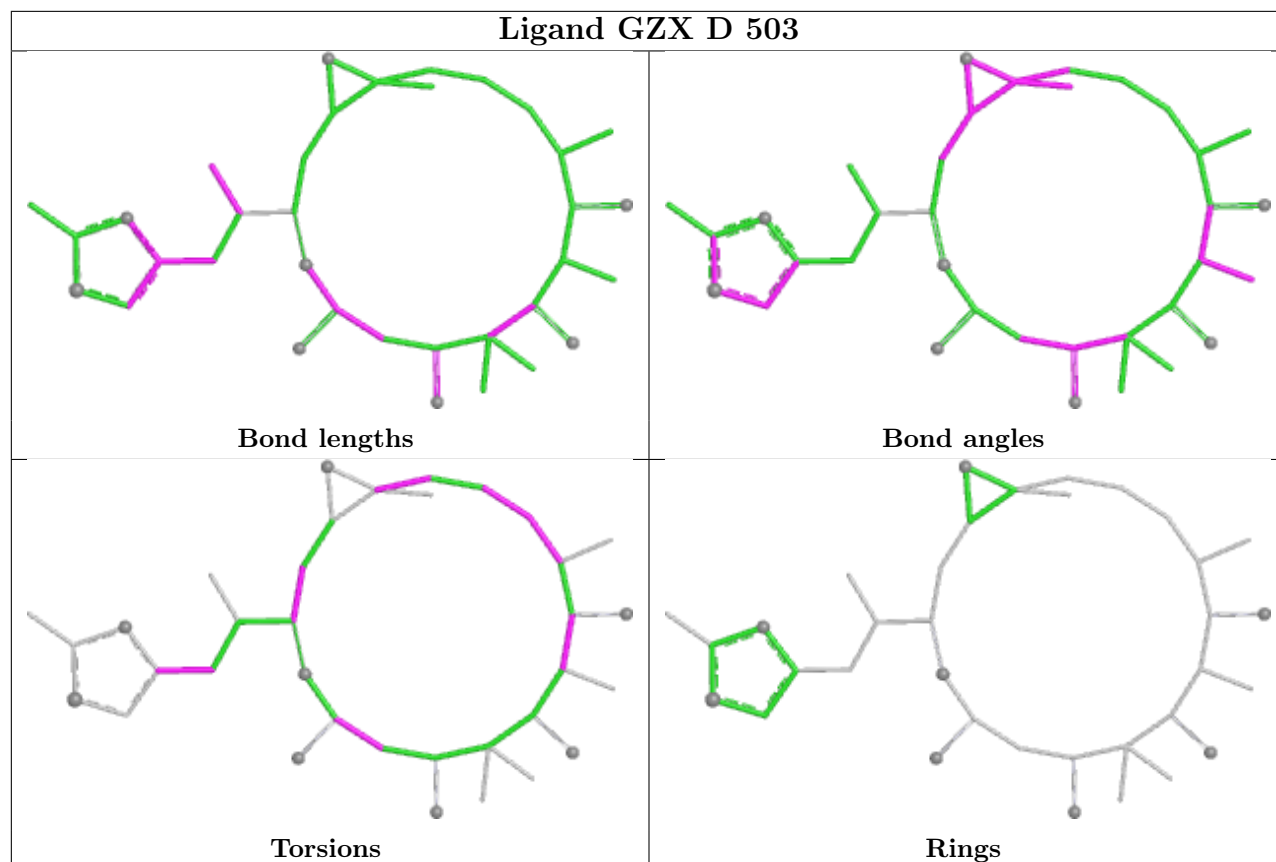
Ligand GTP C 501



Ligand ACP F 402







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	442/451 (98%)	-0.34	4 (0%)	81 78	18, 36, 64, 126	6 (1%)
1	C	440/451 (97%)	-0.60	6 (1%)	73 69	19, 29, 53, 92	11 (2%)
2	B	423/445 (95%)	-0.34	4 (0%)	81 78	18, 37, 66, 111	7 (1%)
2	D	430/445 (96%)	0.12	17 (3%)	42 38	24, 48, 83, 128	7 (1%)
3	E	123/143 (86%)	0.39	6 (4%)	35 31	21, 51, 88, 124	3 (2%)
4	F	351/384 (91%)	0.73	63 (17%)	3 3	24, 59, 134, 157	6 (1%)
All	All	2209/2319 (95%)	-0.09	100 (4%)	38 34	18, 40, 90, 157	40 (1%)

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	283	ALA	7.6
1	A	440	VAL	6.5
3	E	143	ALA	5.7
4	F	169	LEU	5.7
4	F	105	LEU	4.9
4	F	182	ILE	4.1
4	F	170	LEU	4.1
4	F	372	THR	4.0
2	D	96	GLY	3.9
1	A	450	GLU	3.9
2	D	55	THR	3.9
4	F	173	ILE	3.8
4	F	125	THR	3.7
4	F	161	LEU	3.7
4	F	181	VAL	3.6
4	F	158	GLU	3.6
3	E	28	SER	3.6
2	B	55	THR	3.5
4	F	249	TYR	3.4

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Mol	Chain	Res	Type	RSRZ
4	F	166	ALA	3.4
2	D	95	SER	3.2
4	F	225	SER	3.2
2	D	439	ASP	3.2
4	F	159	GLY	3.1
4	F	103	THR	3.1
2	D	178	THR	3.0
4	F	381	HIS	3.0
4	F	172	PHE	3.0
4	F	100	ILE	3.0
4	F	255[A]	ARG	3.0
2	D	217	LEU	3.0
4	F	238	CYS	3.0
4	F	101	TYR	2.9
4	F	132	LEU	2.9
4	F	251	LYS	2.8
4	F	233	PHE	2.8
1	A	262	TYR	2.8
4	F	130	VAL	2.8
2	B	57	ASN	2.8
4	F	144	GLY	2.7
2	D	281	TYR	2.7
4	F	134	ALA	2.7
4	F	253	TYR	2.7
4	F	90	SER	2.7
4	F	244	CYS	2.7
4	F	136	ASN	2.6
4	F	142	ARG	2.6
1	C	340	SER	2.6
1	C	46	ASP	2.6
1	C	1	MET	2.6
2	D	277	GLY	2.6
4	F	31	ARG	2.6
4	F	129	GLU	2.6
4	F	176	GLN	2.6
2	B	274	THR	2.6
1	C	440	VAL	2.5
4	F	133	ALA	2.5
4	F	231	ALA	2.5
2	D	218	THR	2.5
2	D	414	MET	2.5
3	E	48	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	439	SER	2.5
4	F	167	SER	2.5
2	D	69	GLU	2.5
4	F	135	TYR	2.4
4	F	168	GLU	2.4
4	F	177	GLY	2.4
3	E	139	LEU	2.4
4	F	98	TYR	2.4
2	D	80	PRO	2.4
4	F	235	ASP	2.4
4	F	131	PHE	2.4
4	F	179	VAL	2.3
4	F	305	LYS	2.3
1	C	285	GLN	2.3
4	F	245	ILE	2.3
4	F	149	ALA	2.3
2	B	218	THR	2.3
4	F	178	GLN	2.3
4	F	152	SER	2.3
4	F	180	HIS	2.3
3	E	45	PRO	2.3
4	F	163	SER	2.2
2	D	412	ASP	2.2
4	F	252	ASN	2.2
2	D	94	GLN	2.2
4	F	175	GLU	2.1
4	F	254	GLY	2.1
4	F	89	GLU	2.1
4	F	160	ILE	2.1
3	E	7	GLU	2.1
4	F	228	TYR	2.1
2	D	92	PHE	2.0
4	F	232	ASN	2.0
4	F	247	LYS	2.0
4	F	362	ALA	2.0
4	F	229	ASN	2.0
2	D	72	THR	2.0
4	F	126	ASP	2.0
1	C	357	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

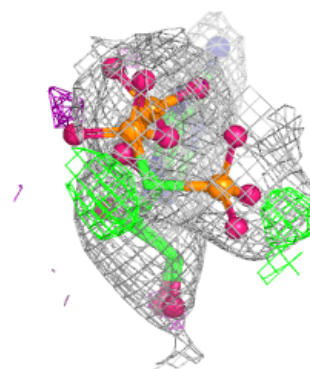
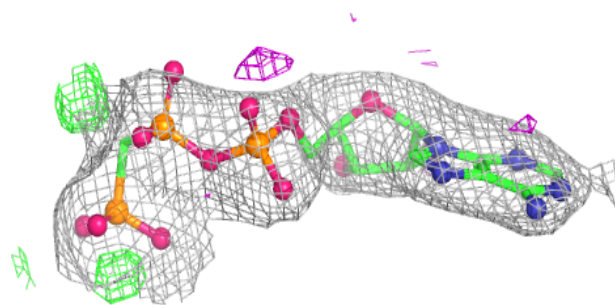
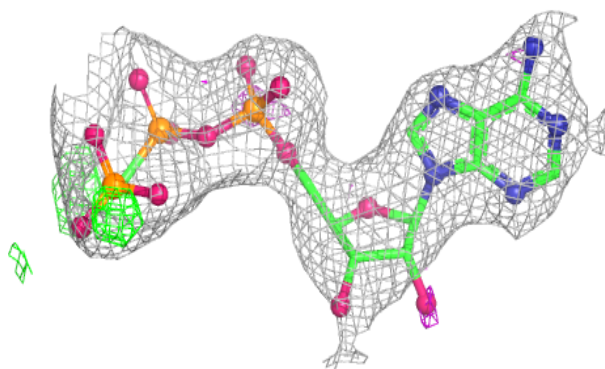
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	CA	E	201	1/1	0.27	0.26	71,71,71,71	0
6	MG	B	506	1/1	0.77	0.19	54,54,54,54	0
6	MG	F	401	1/1	0.83	0.12	78,78,78,78	0
6	MG	D	502	1/1	0.86	0.18	55,55,55,55	0
12	ACP	F	402	31/31	0.86	0.13	55,82,111,123	0
7	CA	B	503	1/1	0.89	0.16	82,82,82,82	0
11	GZX	D	503	35/35	0.90	0.11	47,58,69,78	0
6	MG	B	502	1/1	0.94	0.10	35,35,35,35	0
8	CL	A	504	1/1	0.94	0.12	75,75,75,75	0
10	MES	B	505	12/12	0.95	0.09	55,57,63,68	0
10	MES	B	504	12/12	0.96	0.08	33,43,54,54	0
9	GDP	D	501	28/28	0.96	0.07	35,43,53,54	0
7	CA	A	503	1/1	0.97	0.05	54,54,54,54	0
7	CA	C	503	1/1	0.98	0.03	41,41,41,41	0
6	MG	C	502	1/1	0.99	0.04	25,25,25,25	0
5	GTP	A	501	32/32	0.99	0.04	19,27,34,37	0
9	GDP	B	501	28/28	0.99	0.04	20,26,37,39	0
5	GTP	C	501	32/32	0.99	0.04	17,24,27,29	0
6	MG	A	502	1/1	1.00	0.03	27,27,27,27	0

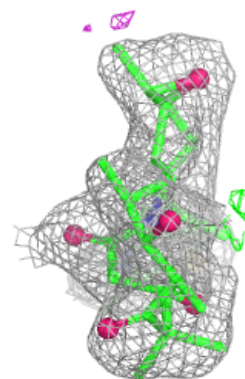
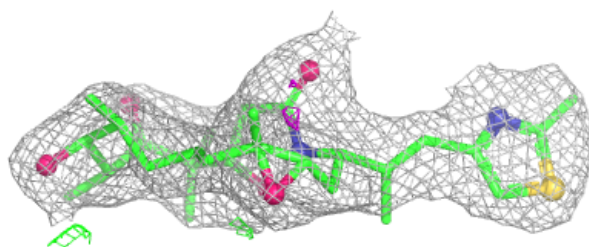
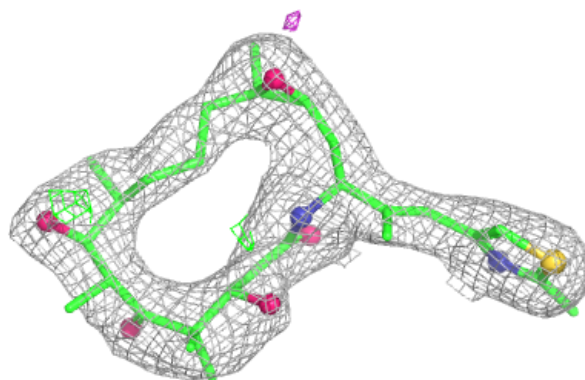
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ACP F 402:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

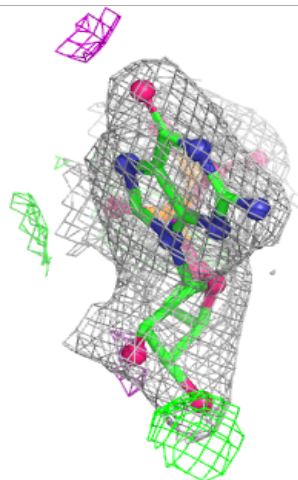
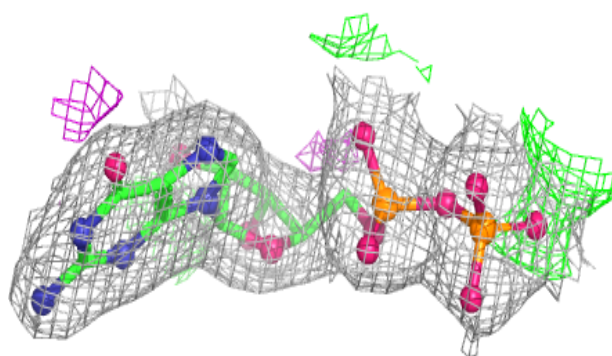
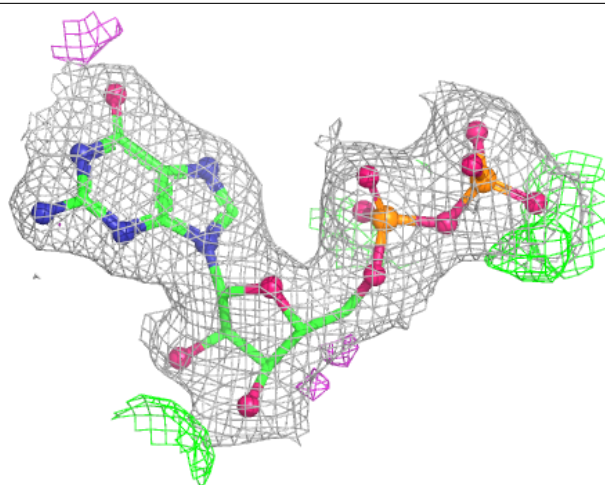
**Electron density around GZX D 503:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



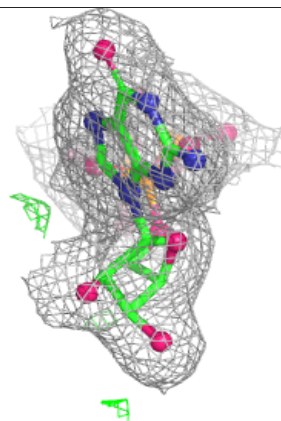
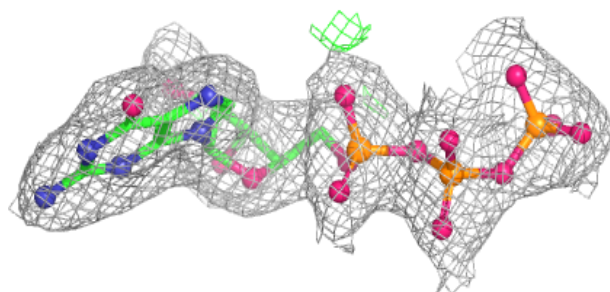
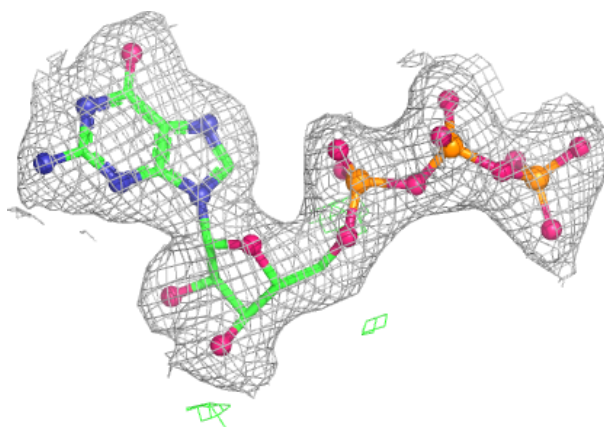
Electron density around GDP D 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



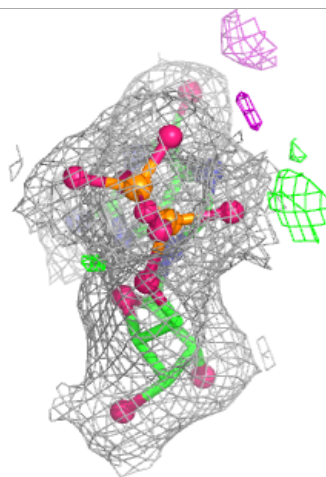
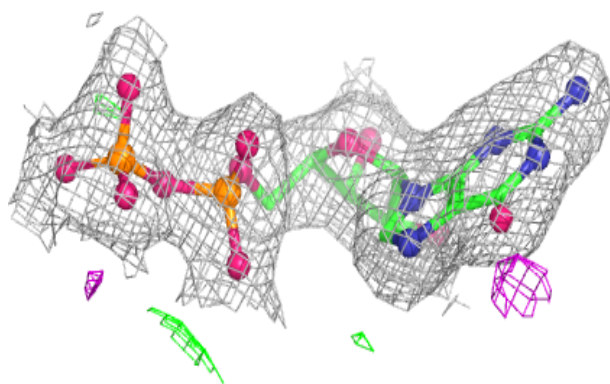
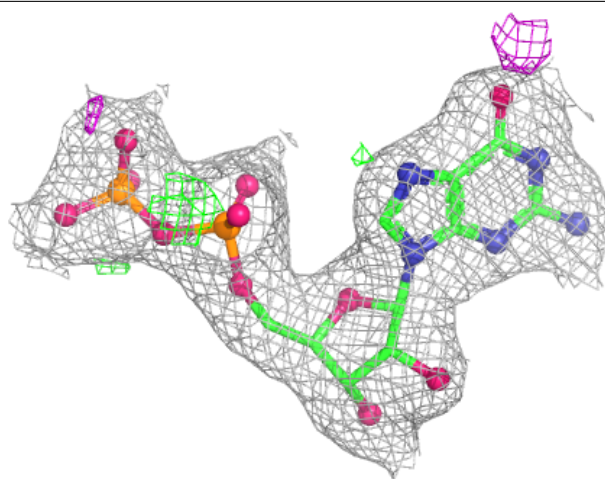
Electron density around GTP A 501:

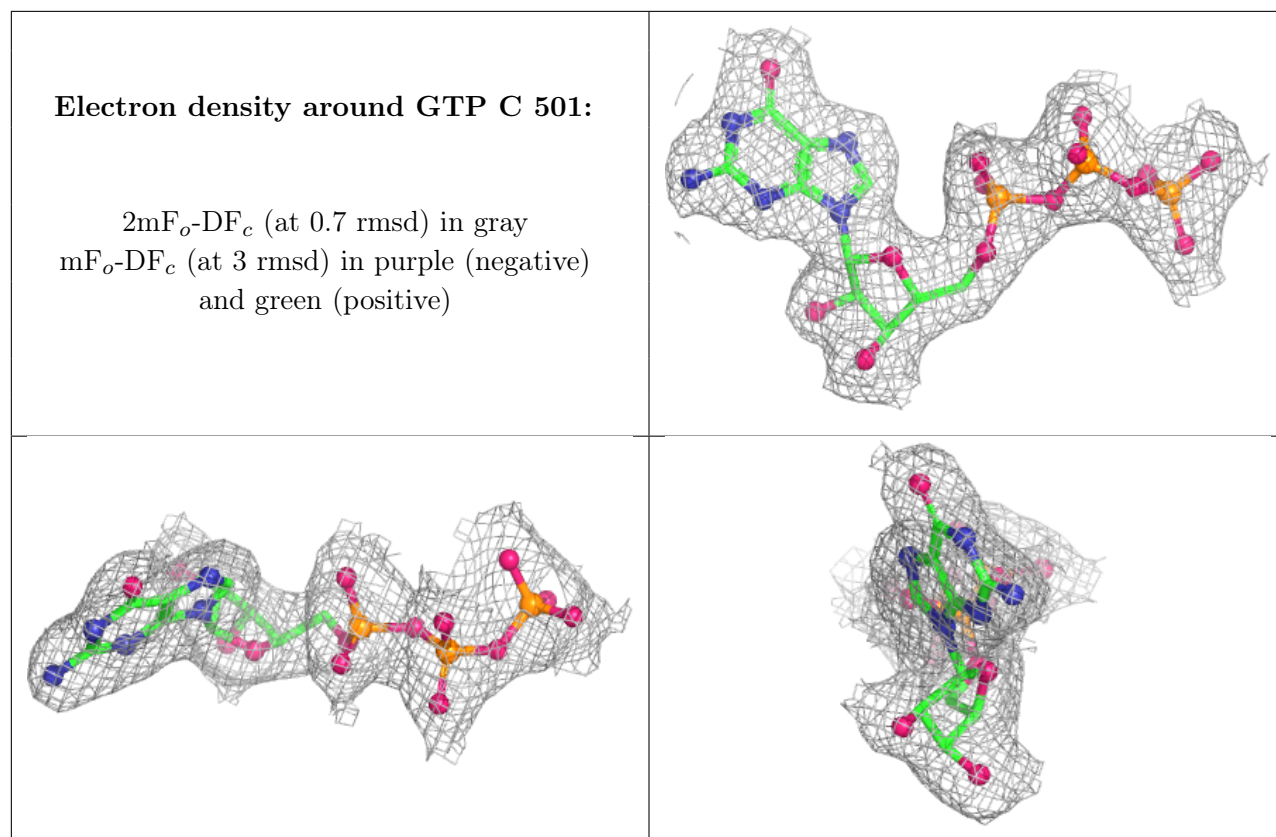
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GDP B 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.