



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:02 PM UTC

PDB ID : 5M8D / pdb_00005m8d
Title : Tubulin MTD265-R1 complex
Authors : Bohnacker, T.; Protá, A.E.; Steinmetz, M.O.; Wymann, M.P.
Deposited on : 2016-10-28
Resolution : 2.25 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

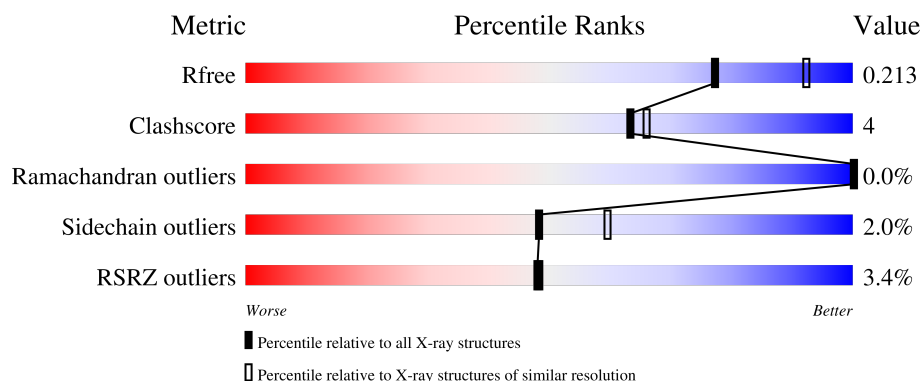
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	8% 86% 11%
1	C	451	87% 10%
2	B	445	4% 82% 13% 5%
2	D	445	3% 85% 10%
3	E	143	8% 82% 14%

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Mol	Chain	Length	Quality of chain
4	F	384	5% 78% 10% • 10%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 18103 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	438	Total	C	N	O	S	0	0	0
			3424	2167	582	653	22			
1	C	440	Total	C	N	O	S	0	0	0
			3437	2175	584	656	22			

- Molecule 2 is a protein called Tubulin beta-2B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	423	Total	C	N	O	S	0	0	0
			3331	2094	568	643	26			
2	D	427	Total	C	N	O	S	0	0	0
			3349	2101	572	650	26			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	123	Total	C	N	O	S	0	0	0
			1014	625	183	201	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	initiating methionine	UNP P63043
E	4	ALA	-	expression tag	UNP P63043

- Molecule 4 is a protein called Tubulin-Tyrosine Ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	344	Total	C	N	O	S	0	0	0
			2808	1800	483	511	14			

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: $C_{10}H_{16}N_5O_{14}P_3$).



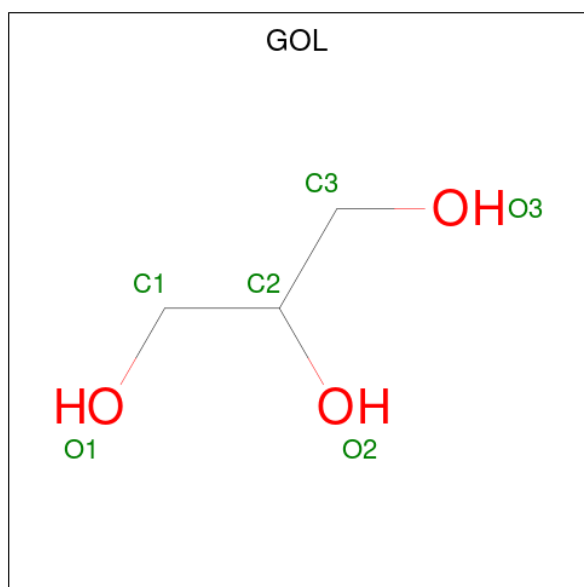
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

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

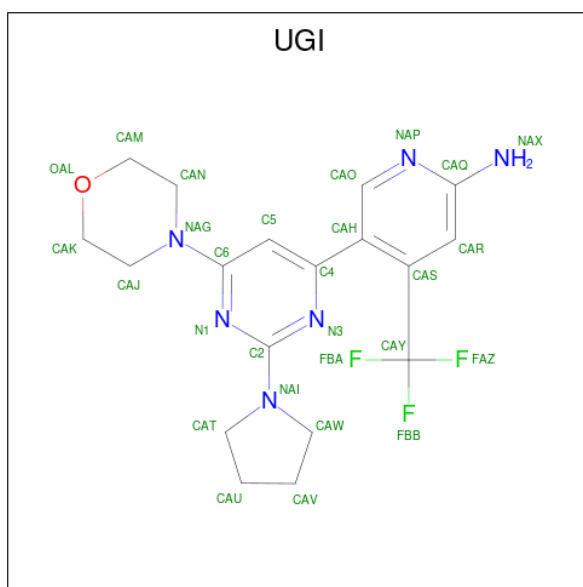
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total	Ca	0	0
			2	2		
7	B	2	Total	Ca	0	0
			2	2		
7	C	1	Total	Ca	0	0
			1	1		

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



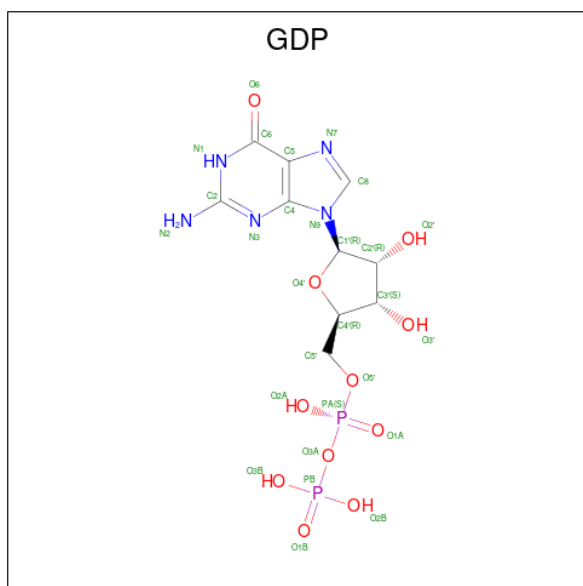
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 9 is 5-(6-morpholin-4-yl-2-pyrrolidin-1-yl-pyrimidin-4-yl)-4-(trifluoromethyl)pyridine-2-amine (CCD ID: UGI) (formula: C₁₈H₂₁F₃N₆O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	F	N	O	0	0
			28	18	3	6	1		

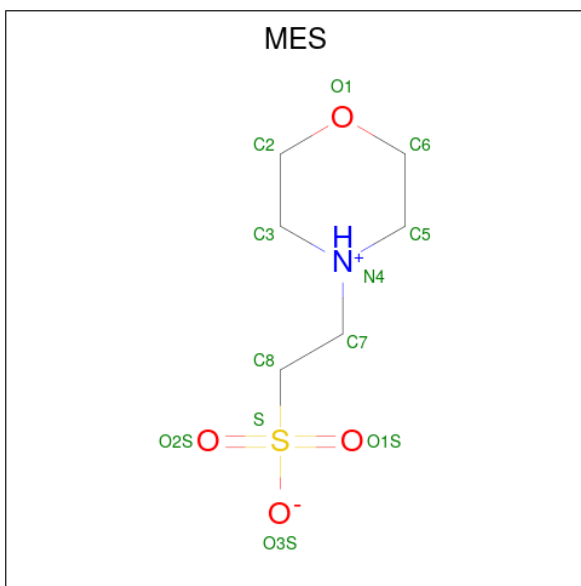
- Molecule 10 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



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

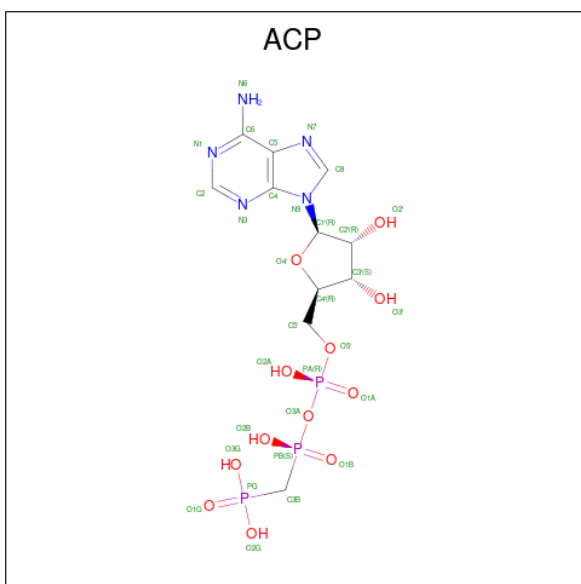
- Molecule 11 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES)

(formula: C₆H₁₃NO₄S).



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

- Molecule 12 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



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

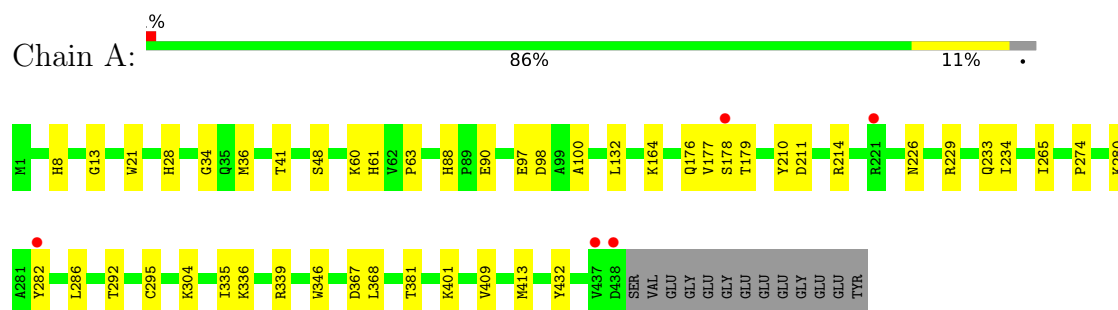
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	113	Total 113	O 113	0	0
13	B	95	Total 95	O 95	0	0
13	C	199	Total 199	O 199	0	0
13	D	69	Total 69	O 69	0	0
13	E	18	Total 18	O 18	0	0
13	F	39	Total 39	O 39	0	0

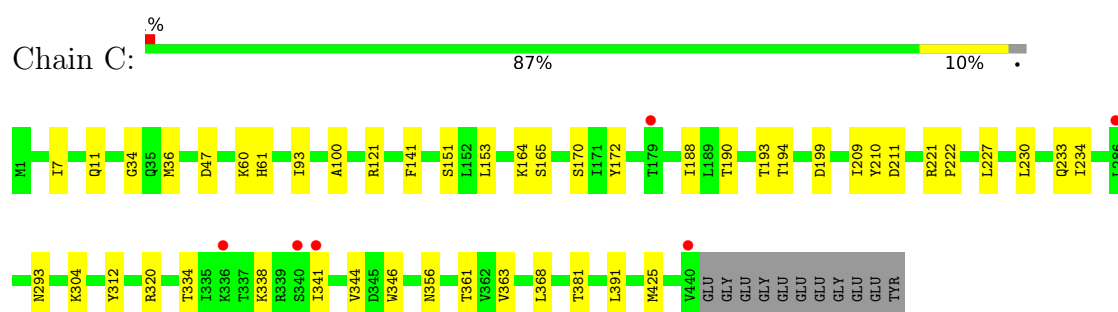
3 Residue-property plots [i](#)

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.

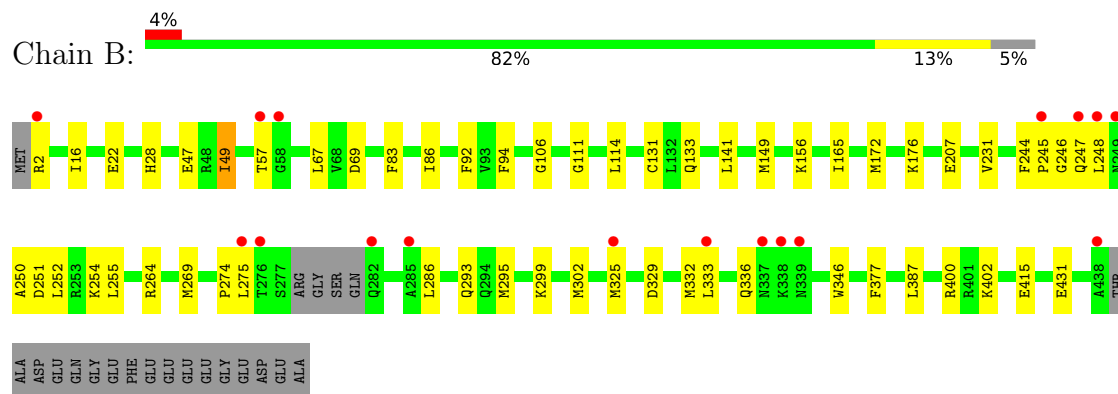
- Molecule 1: Tubulin alpha-1B chain



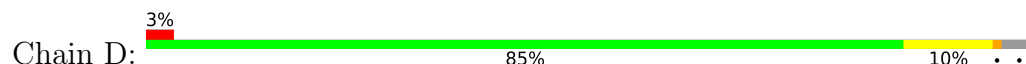
- Molecule 1: Tubulin alpha-1B chain

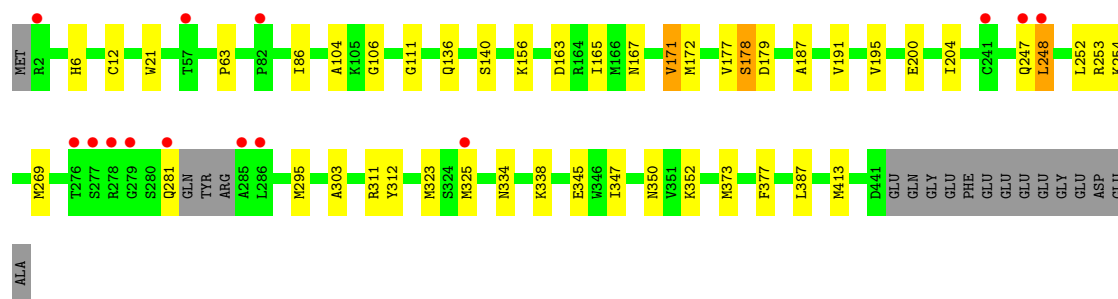


- Molecule 2: Tubulin beta-2B chain

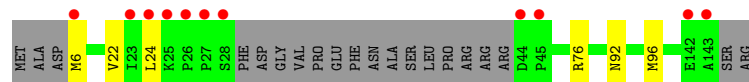
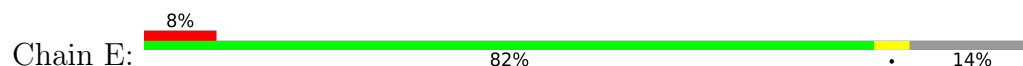


- Molecule 2: Tubulin beta-2B chain

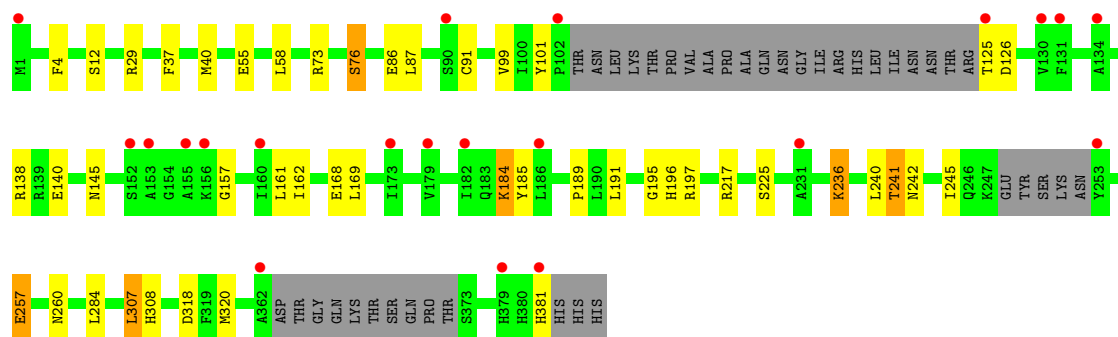
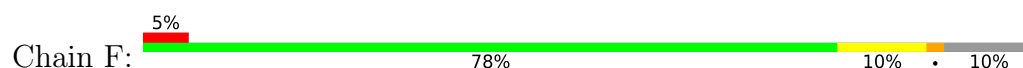




- Molecule 3: Stathmin-4



- 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	104.18Å 157.02Å 179.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	68.10 – 2.25 68.10 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.5 (68.10-2.25) 99.5 (68.10-2.25)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.25Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.170 , 0.210 0.175 , 0.213	Depositor DCC
R_{free} test set	6885 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	45.1	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.3	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	0.96	EDS
Total number of atoms	18103	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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: UGI, GDP, CA, MG, ACP, GTP, MES, GOL

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	0.31	0/3502	0.50	0/4754
1	C	0.40	0/3515	0.56	0/4772
2	B	0.34	0/3405	0.52	0/4612
2	D	0.30	1/3422 (0.0%)	0.48	0/4635
3	E	0.32	0/1022	0.44	0/1356
4	F	0.24	0/2872	0.45	0/3878
All	All	0.33	1/17738 (0.0%)	0.50	0/24007

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	171	VAL	C-N	5.21	1.44	1.33

There are no bond angle outliers.

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	3424	0	3335	25	0
1	C	3437	0	3348	25	0
2	B	3331	0	3208	37	0
2	D	3349	0	3223	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	1014	0	1029	4	0
4	F	2808	0	2776	25	0
5	A	32	0	12	1	0
5	C	32	0	12	0	0
6	A	1	0	0	0	0
6	B	1	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	2	0	0	0	0
7	B	2	0	0	0	0
7	C	1	0	0	0	0
8	A	6	0	8	0	0
9	B	28	0	0	1	0
10	B	28	0	12	0	0
10	D	28	0	12	1	0
11	B	12	0	12	0	0
12	F	31	0	14	4	0
13	A	113	0	0	1	0
13	B	95	0	0	2	0
13	C	199	0	0	1	0
13	D	69	0	0	2	0
13	E	18	0	0	0	0
13	F	39	0	0	0	0
All	All	18103	0	17001	138	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 4.

All (138) 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)
1:A:97:GLU:OE1	2:B:2:ARG:NH1	2.16	0.78
1:A:229:ARG:NH2	13:A:601:HOH:O	2.19	0.74
2:D:295:MET:HE2	2:D:377:PHE:HB2	1.71	0.73
1:C:211:ASP:OD2	1:C:304:LYS:NZ	2.27	0.67
4:F:195:GLY:HA3	4:F:197:ARG:HD3	1.80	0.64
2:D:12:CYS:HB2	10:D:501:GDP:C8	2.34	0.62
2:D:281:GLN:NE2	13:D:602:HOH:O	2.30	0.62
1:A:210:TYR:CE2	1:A:214:ARG:HD2	2.35	0.61
2:D:311:ARG:NH2	2:D:345:GLU:OE1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:6:MET:HE3	3:E:22:VAL:HG21	1.81	0.60
2:B:274:PRO:HB3	2:B:286:LEU:HD22	1.82	0.60
2:B:295:MET:HE2	2:B:377:PHE:HB2	1.83	0.60
2:B:2:ARG:HB3	2:B:133:GLN:HG3	1.82	0.60
4:F:241:THR:OG1	12:F:402:ACP:O2'	2.19	0.60
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.83	0.60
4:F:162:ILE:H	4:F:236:LYS:NZ	2.00	0.59
1:A:132:LEU:O	1:A:164:LYS:NZ	2.34	0.59
2:D:167:ASN:ND2	13:D:604:HOH:O	2.36	0.58
2:B:250:ALA:HB1	2:B:255:LEU:HD21	1.86	0.58
2:B:299:LYS:NZ	13:B:602:HOH:O	2.30	0.57
12:F:402:ACP:O3G	12:F:402:ACP:O1A	2.22	0.56
2:B:83:PHE:O	2:B:86:ILE:HG12	2.06	0.56
4:F:225:SER:OG	4:F:260:ASN:ND2	2.35	0.56
2:B:172:MET:HG3	2:B:387:LEU:HD11	1.89	0.55
4:F:161:LEU:HD23	4:F:169:LEU:HD23	1.89	0.55
2:B:329:ASP:O	2:B:333:LEU:HG	2.07	0.55
1:C:312:TYR:CD1	1:C:341:ILE:HG23	2.43	0.54
2:B:16:ILE:HD13	2:B:231:VAL:HG11	1.89	0.53
2:B:69:ASP:O	2:B:94:PHE:HA	2.09	0.53
2:D:347:ILE:HG22	2:D:350:ASN:HB3	1.91	0.53
1:C:7:ILE:HG21	1:C:153:LEU:HD21	1.89	0.53
2:B:47:GLU:HB3	2:B:245:PRO:HG3	1.90	0.53
1:A:226:ASN:ND2	1:A:367:ASP:OD2	2.43	0.53
4:F:241:THR:HG1	12:F:402:ACP:HO2'	1.57	0.52
4:F:101:TYR:HD1	4:F:126:ASP:HB2	1.74	0.52
2:B:251:ASP:O	2:B:255:LEU:HG	2.10	0.52
2:B:2:ARG:HB3	2:B:133:GLN:CG	2.40	0.51
1:C:93:ILE:HD11	1:C:121:ARG:HG3	1.92	0.51
1:C:47:ASP:OD2	13:C:601:HOH:O	2.19	0.51
1:A:100:ALA:HA	2:B:254:LYS:HG3	1.93	0.51
4:F:191:LEU:HD12	4:F:196:HIS:CE1	2.46	0.51
1:C:320:ARG:HA	1:C:356:ASN:O	2.11	0.50
2:B:156:LYS:HD3	3:E:76:ARG:CZ	2.41	0.50
2:B:244:PHE:O	2:B:246:GLY:N	2.44	0.50
2:D:334:ASN:HD21	2:D:338:LYS:NZ	2.09	0.49
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.47	0.49
1:A:336:LYS:HG2	3:E:24:LEU:HD23	1.93	0.49
2:B:165:ILE:HG21	2:B:252:LEU:HB3	1.94	0.49
1:C:334:THR:HG23	1:C:338:LYS:HE2	1.94	0.49
4:F:189:PRO:HG2	4:F:191:LEU:HD21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:106:GLY:O	2:B:111:GLY:HA3	2.12	0.49
1:A:401:LYS:HG3	2:B:346:TRP:CE3	2.48	0.49
2:D:178:SER:CB	2:D:179:ASP:HA	2.43	0.49
1:A:88:HIS:CE1	1:A:90:GLU:HG3	2.48	0.48
1:C:151:SER:HB3	1:C:193:THR:HG21	1.93	0.48
4:F:162:ILE:H	4:F:236:LYS:HZ2	1.59	0.48
4:F:184:LYS:NZ	4:F:185:TYR:O	2.47	0.48
1:C:188:ILE:HG13	1:C:425:MET:HG3	1.94	0.48
2:B:176:LYS:HD3	2:B:207:GLU:HG3	1.97	0.47
1:C:230:LEU:O	1:C:234:ILE:HD12	2.15	0.47
2:B:332:MET:O	2:B:336:GLN:HG3	2.15	0.47
1:C:11:GLN:HE22	2:D:247:GLN:HE22	1.63	0.47
4:F:318:ASP:OD2	12:F:402:ACP:O3G	2.32	0.47
2:B:264:ARG:NE	2:B:431:GLU:OE2	2.39	0.47
2:D:323:MET:HB3	2:D:373:MET:HE1	1.97	0.47
4:F:101:TYR:CD1	4:F:126:ASP:HB2	2.50	0.46
2:B:244:PHE:C	2:B:246:GLY:H	2.23	0.46
2:D:136:GLN:HA	2:D:167:ASN:O	2.16	0.46
1:A:274:PRO:HB3	1:A:286:LEU:HD12	1.96	0.46
1:C:190:THR:O	1:C:194:THR:HG23	2.15	0.46
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.34	0.46
2:D:248:LEU:HD11	2:D:352:LYS:HB3	1.97	0.46
2:D:163:ASP:O	2:D:253:ARG:NH2	2.49	0.46
2:B:67:LEU:HD22	2:B:92:PHE:CE2	2.51	0.46
1:C:221:ARG:HG3	2:D:325:MET:HB3	1.97	0.45
1:A:21:TRP:CZ3	1:A:63:PRO:HB3	2.52	0.45
2:B:402:LYS:HD3	2:B:415:GLU:OE2	2.17	0.45
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.52	0.45
2:D:172:MET:HG3	2:D:387:LEU:HD11	1.98	0.44
1:C:209:ILE:HG22	1:C:227:LEU:HD22	1.98	0.44
1:A:34:GLY:HA3	1:A:60:LYS:HG3	2.00	0.44
2:D:156:LYS:HA	2:D:156:LYS:HD2	1.85	0.44
2:B:286:LEU:HD12	2:B:286:LEU:HA	1.85	0.44
1:A:177:VAL:O	1:A:178:SER:C	2.60	0.44
1:A:211:ASP:OD2	1:A:304:LYS:NZ	2.31	0.44
1:C:341:ILE:H	1:C:341:ILE:HD12	1.82	0.44
1:A:28:HIS:O	1:A:36:MET:HE3	2.18	0.43
1:A:335:ILE:HG23	1:A:339:ARG:HG3	1.99	0.43
2:B:2:ARG:HA	2:B:131:CYS:O	2.18	0.43
2:B:141:LEU:HD12	2:B:172:MET:SD	2.57	0.43
2:B:293:GLN:NE2	13:B:601:HOH:O	2.28	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:92:ASN:O	3:E:96:MET:HG2	2.18	0.43
4:F:73:ARG:HB2	4:F:76:SER:OG	2.18	0.43
4:F:242:ASN:HD22	4:F:245:ILE:HD12	1.83	0.43
2:B:255:LEU:HD22	9:B:501:UGI:CAO	2.48	0.43
2:D:171:VAL:HA	2:D:204:ILE:O	2.19	0.43
4:F:101:TYR:N	4:F:126:ASP:OD2	2.31	0.43
2:D:187:ALA:O	2:D:191:VAL:HG23	2.18	0.43
1:A:346:TRP:CD1	1:A:346:TRP:H	2.35	0.43
2:D:21:TRP:CZ3	2:D:63:PRO:HB3	2.54	0.43
1:A:280:LYS:HE2	1:A:282:TYR:O	2.18	0.42
2:D:165:ILE:HG21	2:D:252:LEU:HB3	2.01	0.42
4:F:307:LEU:HD22	4:F:308:HIS:CE1	2.53	0.42
2:B:22:GLU:HG2	2:B:83:PHE:CD1	2.54	0.42
1:C:36:MET:HB3	1:C:61:HIS:CE1	2.54	0.42
4:F:138:ARG:HB3	4:F:145:ASN:CG	2.44	0.42
1:A:292:THR:O	1:A:295:CYS:HB2	2.18	0.42
2:D:106:GLY:O	2:D:111:GLY:HA3	2.19	0.42
4:F:55:GLU:HB3	4:F:58:LEU:HD12	2.00	0.42
2:B:28:HIS:HB3	2:B:49:ILE:HD12	2.02	0.42
1:C:100:ALA:HA	2:D:254:LYS:HG3	2.02	0.42
2:B:269:MET:HE2	2:B:269:MET:HB3	1.80	0.42
1:C:172:TYR:CE2	1:C:391:LEU:HD22	2.55	0.42
1:C:210:TYR:CZ	1:C:222:PRO:HD2	2.55	0.42
1:C:165:SER:HA	1:C:199:ASP:OD2	2.19	0.42
2:B:114:LEU:HD23	2:B:149:MET:HE1	2.02	0.41
4:F:37:PHE:CZ	4:F:40:MET:HE3	2.55	0.41
2:D:312:TYR:CE1	2:D:377:PHE:HZ	2.37	0.41
2:D:104:ALA:HB2	2:D:413:MET:SD	2.60	0.41
2:D:269:MET:HE3	2:D:269:MET:HB2	1.75	0.41
2:D:12:CYS:HB3	2:D:140:SER:HB3	2.02	0.41
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.56	0.41
4:F:197:ARG:NH1	4:F:257:GLU:OE2	2.49	0.41
1:A:8:HIS:HB3	1:A:13:GLY:O	2.20	0.41
1:C:233:GLN:HG3	1:C:368:LEU:CD1	2.51	0.41
2:D:191:VAL:O	2:D:195:VAL:HG23	2.20	0.41
4:F:4:PHE:CZ	4:F:29:ARG:HB2	2.56	0.41
1:A:233:GLN:HG3	1:A:368:LEU:HD12	2.04	0.40
2:B:402:LYS:NZ	2:B:415:GLU:OE1	2.54	0.40
4:F:284:LEU:HD12	4:F:284:LEU:HA	1.97	0.40
2:B:325:MET:HE3	2:B:325:MET:HB3	1.78	0.40
1:C:141:PHE:CE1	1:C:170:SER:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:VAL:HA	1:A:413:MET:O	2.21	0.40
1:C:34:GLY:HA3	1:C:60:LYS:HG3	2.02	0.40
4:F:87:LEU:O	4:F:91:CYS:HB2	2.21	0.40
1:C:164:LYS:HB2	1:C:164:LYS:HE2	1.83	0.40
1:A:98:ASP:HB2	5:A:501:GTP:O1G	2.22	0.40
4:F:157:GLY:HA2	4:F:245:ILE:HD11	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	436/451 (97%)	428 (98%)	8 (2%)	0	100	100
1	C	438/451 (97%)	427 (98%)	11 (2%)	0	100	100
2	B	419/445 (94%)	410 (98%)	8 (2%)	1 (0%)	43	50
2	D	423/445 (95%)	417 (99%)	6 (1%)	0	100	100
3	E	119/143 (83%)	119 (100%)	0	0	100	100
4	F	336/384 (88%)	325 (97%)	11 (3%)	0	100	100
All	All	2171/2319 (94%)	2126 (98%)	44 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	247	GLN

5.3.2 Protein sidechains [i](#)

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	369/379 (97%)	363 (98%)	6 (2%)	55	66
1	C	371/379 (98%)	367 (99%)	4 (1%)	65	75
2	B	366/383 (96%)	360 (98%)	6 (2%)	55	66
2	D	368/383 (96%)	363 (99%)	5 (1%)	59	70
3	E	110/127 (87%)	110 (100%)	0	100	100
4	F	306/342 (90%)	290 (95%)	16 (5%)	21	22
All	All	1890/1993 (95%)	1853 (98%)	37 (2%)	48	59

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	48	SER
1	A	176	GLN
1	A	179	THR
1	A	234	ILE
1	A	381	THR
2	B	49	ILE
2	B	57	THR
2	B	248	LEU
2	B	275	LEU
2	B	302	MET
2	B	400	ARG
1	C	293	ASN
1	C	361	THR
1	C	363	VAL
1	C	381	THR
2	D	86	ILE
2	D	177	VAL
2	D	178	SER
2	D	200	GLU
2	D	248	LEU
4	F	12	SER
4	F	76	SER
4	F	86	GLU
4	F	99	VAL
4	F	125	THR

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Mol	Chain	Res	Type
4	F	140	GLU
4	F	168	GLU
4	F	184	LYS
4	F	217	ARG
4	F	236	LYS
4	F	240	LEU
4	F	241	THR
4	F	257	GLU
4	F	307	LEU
4	F	320	MET
4	F	381	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	176	GLN
1	A	258	ASN
1	A	393	HIS
2	B	15	GLN
2	B	331	GLN
2	B	349	ASN
1	C	393	HIS
2	D	96	GLN
2	D	107	HIS
2	D	167	ASN
2	D	247	GLN
2	D	331	GLN
2	D	334	ASN
2	D	339	ASN
3	E	84	GLN
3	E	136	ASN
4	F	229	ASN
4	F	381	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 10 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
5	GTP	A	501	6	33,34,34	0.97	1 (3%)	50,54,54	1.47	8 (16%)
10	GDP	B	502	6	29,30,30	1.18	3 (10%)	45,47,47	1.76	9 (20%)
12	ACP	F	402	6	31,33,33	1.95	10 (32%)	47,52,52	1.83	11 (23%)
8	GOL	A	505	-	5,5,5	0.35	0	5,5,5	0.48	0
9	UGI	B	501	-	31,31,31	1.40	5 (16%)	42,45,45	1.96	12 (28%)
10	GDP	D	501	6	29,30,30	1.14	2 (6%)	45,47,47	1.81	7 (15%)
11	MES	B	506	-	12,12,12	1.98	1 (8%)	15,16,16	1.77	3 (20%)
5	GTP	C	501	6	33,34,34	0.97	2 (6%)	50,54,54	1.56	10 (20%)

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
5	GTP	A	501	6	-	5/22/38/38	0/3/3/3
10	GDP	B	502	6	-	5/16/32/32	0/3/3/3
12	ACP	F	402	6	-	5/19/38/38	0/3/3/3
8	GOL	A	505	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	UGI	B	501	-	-	4/18/33/33	0/4/4/4
10	GDP	D	501	6	-	5/16/32/32	0/3/3/3
11	MES	B	506	-	-	3/6/14/14	0/1/1/1
5	GTP	C	501	6	-	7/22/38/38	0/3/3/3

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B	506	MES	C8-S	-6.49	1.68	1.77
12	F	402	ACP	C5-C4	4.64	1.47	1.39
12	F	402	ACP	PB-O1B	4.12	1.61	1.51
9	B	501	UGI	CAY-CAS	-4.10	1.41	1.50
12	F	402	ACP	PB-O3A	3.91	1.62	1.58
9	B	501	UGI	CAH-C4	-3.70	1.39	1.48
5	C	501	GTP	PA-O3A	3.22	1.63	1.59
12	F	402	ACP	PA-O3A	3.17	1.62	1.59
12	F	402	ACP	PG-O2G	2.95	1.61	1.55
12	F	402	ACP	PB-O2B	-2.92	1.49	1.56
10	D	501	GDP	C5-C4	2.87	1.46	1.38
12	F	402	ACP	PG-O3G	2.87	1.61	1.55
5	A	501	GTP	PA-O3A	2.80	1.62	1.59
10	B	502	GDP	C6-N1	-2.71	1.33	1.38
12	F	402	ACP	C5-C6	2.64	1.48	1.41
10	B	502	GDP	C5-C4	2.63	1.45	1.38
10	D	501	GDP	C6-N1	-2.51	1.34	1.38
12	F	402	ACP	C8-N7	2.41	1.36	1.31
9	B	501	UGI	CAO-NAP	2.39	1.39	1.34
12	F	402	ACP	C5-N7	-2.31	1.34	1.39
9	B	501	UGI	FBB-CAY	-2.27	1.24	1.33
9	B	501	UGI	FBA-CAY	-2.24	1.25	1.33
10	B	502	GDP	PA-O3A	2.16	1.61	1.59
5	C	501	GTP	PB-O3B	2.00	1.61	1.59

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	501	UGI	C4-N3-C2	6.35	120.63	115.88
12	F	402	ACP	C5-C4-N3	-6.04	118.40	126.72
10	D	501	GDP	C5-C4-N3	-5.73	119.27	128.39
10	B	502	GDP	C5-C4-N3	-5.67	119.37	128.39
11	B	506	MES	C5-N4-C3	5.39	120.44	108.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	D	501	GDP	C2-N3-C4	5.01	120.94	112.30
12	F	402	ACP	N3-C4-N9	4.89	135.49	127.17
10	B	502	GDP	C2-N3-C4	4.85	120.66	112.30
9	B	501	UGI	CAO-CAH-C4	-4.72	113.98	121.24
9	B	501	UGI	CAN-NAG-CAJ	4.56	121.83	111.57
5	C	501	GTP	C2-N3-C4	4.40	119.88	112.30
5	C	501	GTP	C5-C4-N3	-4.31	121.54	128.39
10	D	501	GDP	N9-C4-N3	4.13	134.20	125.95
10	B	502	GDP	N9-C4-N3	3.97	133.88	125.95
5	A	501	GTP	C2-N3-C4	3.85	118.93	112.30
12	F	402	ACP	C2-N3-C4	3.82	121.16	111.83
5	A	501	GTP	C5-C4-N3	-3.64	122.59	128.39
10	B	502	GDP	C6-C5-N7	3.64	136.91	130.29
10	D	501	GDP	C6-C5-N7	3.44	136.54	130.29
12	F	402	ACP	N3-C2-N1	-3.24	123.67	128.58
12	F	402	ACP	C4-C5-N7	-3.22	106.91	110.58
5	C	501	GTP	N9-C8-N7	-3.10	107.66	113.40
9	B	501	UGI	C5-C4-N3	-2.96	118.91	122.34
10	D	501	GDP	O4'-C1'-N9	-2.85	101.89	108.36
5	A	501	GTP	N9-C8-N7	-2.80	108.21	113.40
5	C	501	GTP	C8-N7-C5	2.80	109.25	104.26
12	F	402	ACP	C4-N9-C8	2.71	108.58	105.74
5	A	501	GTP	O2B-PB-O3A	2.66	114.47	107.27
5	C	501	GTP	C2-N1-C6	-2.58	120.43	125.11
9	B	501	UGI	N3-C2-N1	-2.54	121.76	126.27
9	B	501	UGI	FBA-CAY-CAS	-2.51	108.19	112.65
9	B	501	UGI	C4-CAH-CAS	2.51	126.60	123.07
5	C	501	GTP	N9-C4-N3	2.51	130.97	125.95
5	C	501	GTP	O2A-PA-O3A	2.50	114.02	107.27
9	B	501	UGI	C2-N1-C6	2.48	119.91	115.02
12	F	402	ACP	C5-N7-C8	2.48	107.35	103.45
10	D	501	GDP	C4-C5-N7	-2.47	106.76	110.67
9	B	501	UGI	CAR-CAS-CAH	-2.46	116.96	119.85
10	B	502	GDP	C4-C5-N7	-2.45	106.78	110.67
11	B	506	MES	O3S-S-C8	2.45	110.80	106.00
5	A	501	GTP	C8-N7-C5	2.41	108.56	104.26
5	A	501	GTP	O2G-PG-O3B	2.34	112.49	104.64
11	B	506	MES	C7-N4-C3	2.32	117.42	111.24
10	B	502	GDP	O3'-C3'-C4'	-2.26	104.58	111.08
9	B	501	UGI	N3-C2-NAI	2.26	120.34	117.12
12	F	402	ACP	C3'-C2'-C1'	2.26	105.73	101.46
12	F	402	ACP	C2'-C1'-N9	-2.25	107.72	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	501	GTP	C5-C6-N1	2.21	118.88	113.25
9	B	501	UGI	CAM-CAN-NAG	2.20	114.08	109.93
12	F	402	ACP	PB-O3A-PA	-2.18	125.24	132.37
5	A	501	GTP	O2A-PA-O3A	2.18	113.16	107.27
10	B	502	GDP	C5-C6-N1	2.17	118.79	113.25
9	B	501	UGI	OAL-CAK-CAJ	-2.17	107.10	111.77
10	D	501	GDP	O6-C6-C5	-2.15	120.86	126.53
10	B	502	GDP	O2A-PA-O3A	2.14	113.04	107.27
5	C	501	GTP	C4-C5-N7	-2.09	107.36	110.67
10	B	502	GDP	O6-C6-C5	-2.07	121.06	126.53
5	C	501	GTP	O6-C6-C5	-2.05	121.12	126.53
12	F	402	ACP	N9-C8-N7	-2.03	111.05	113.94
5	A	501	GTP	O4'-C1'-N9	-2.02	103.77	108.36

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	PB-O3B-PG-O2G
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
10	B	502	GDP	C5'-O5'-PA-O3A
10	B	502	GDP	C5'-O5'-PA-O1A
10	B	502	GDP	C5'-O5'-PA-O2A
10	D	501	GDP	C5'-O5'-PA-O3A
10	D	501	GDP	C5'-O5'-PA-O1A
10	D	501	GDP	C5'-O5'-PA-O2A
12	F	402	ACP	PG-C3B-PB-O1B
12	F	402	ACP	PG-C3B-PB-O2B
12	F	402	ACP	PG-C3B-PB-O3A
8	A	505	GOL	O1-C1-C2-O2
11	B	506	MES	C7-C8-S-O3S
8	A	505	GOL	O1-C1-C2-C3
11	B	506	MES	C7-C8-S-O1S
11	B	506	MES	C7-C8-S-O2S
12	F	402	ACP	C5'-O5'-PA-O1A
9	B	501	UGI	N3-C4-CAH-CAO
5	C	501	GTP	PB-O3B-PG-O1G

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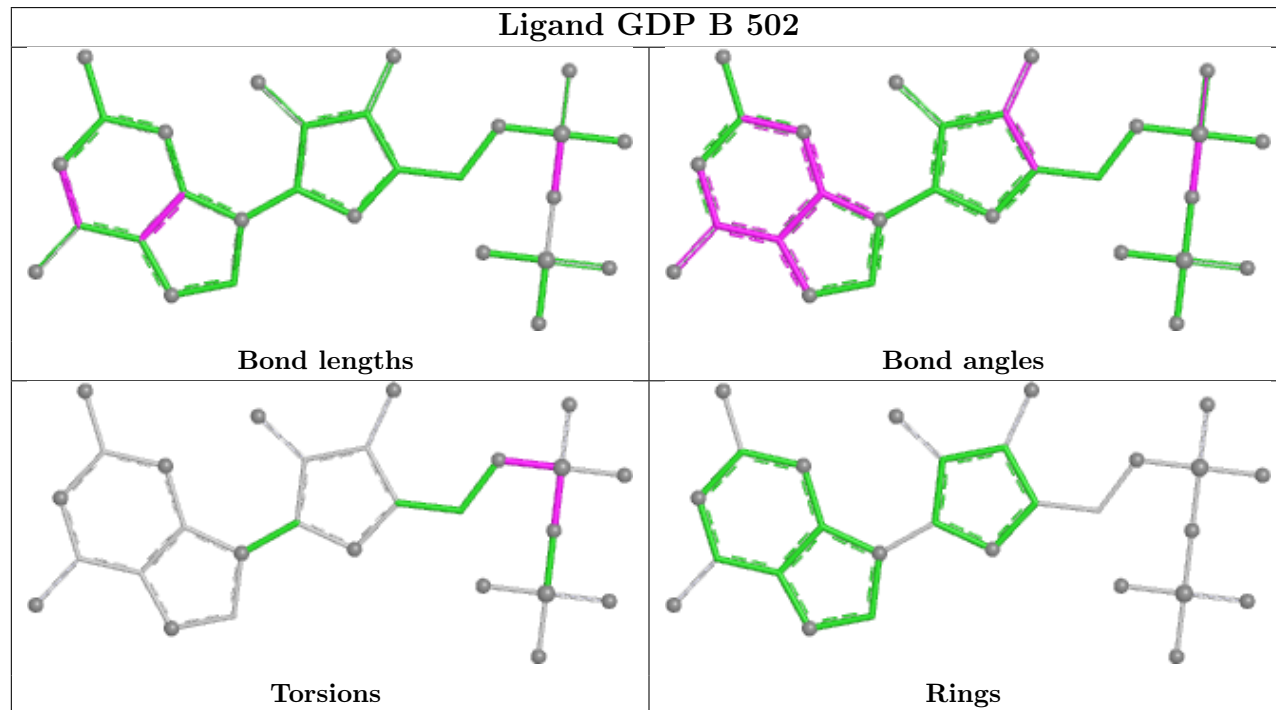
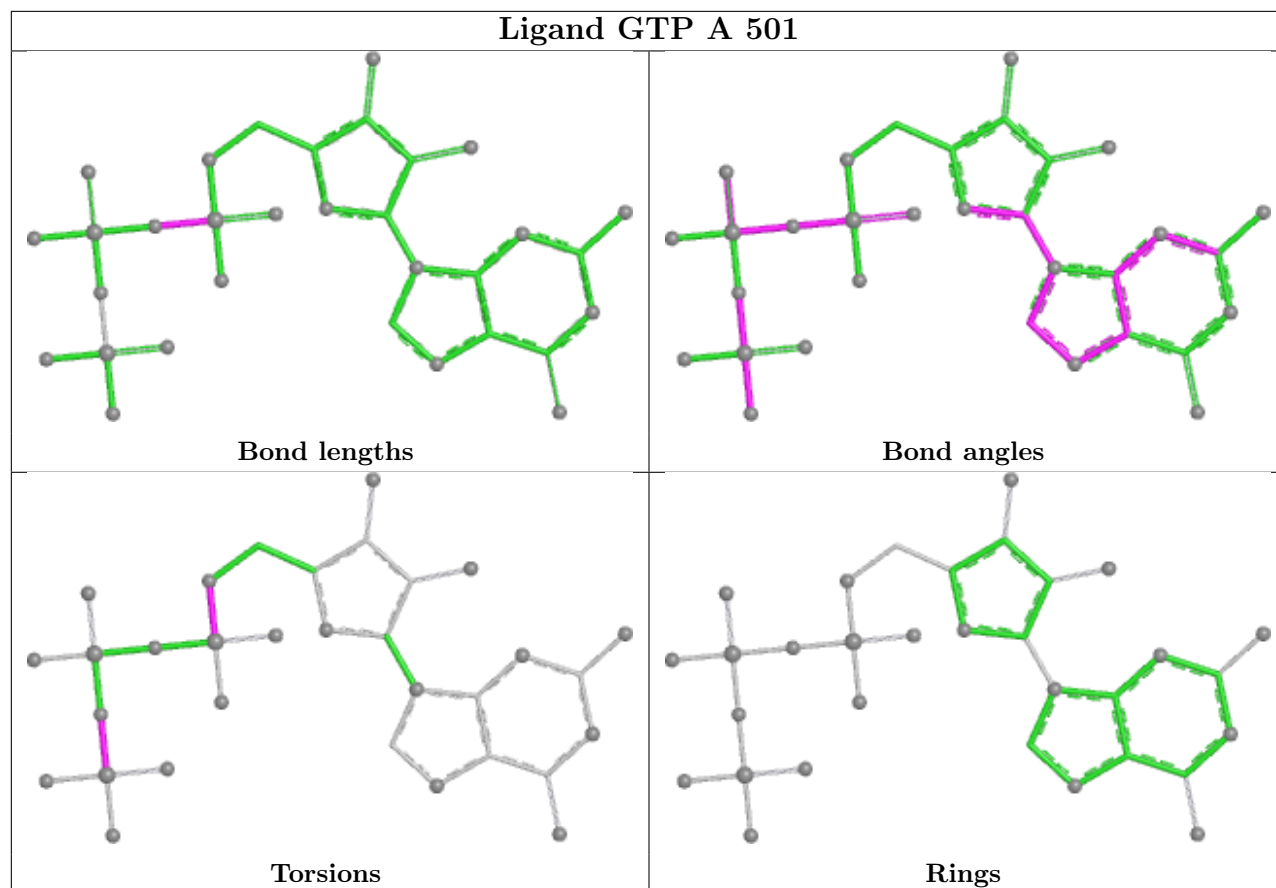
Mol	Chain	Res	Type	Atoms
9	B	501	UGI	C5-C4-CAH-CAO
9	B	501	UGI	C5-C4-CAH-CAS
10	D	501	GDP	PB-O3A-PA-O2A
9	B	501	UGI	N3-C4-CAH-CAS
5	A	501	GTP	PB-O3B-PG-O3G
5	C	501	GTP	PB-O3B-PG-O3G
12	F	402	ACP	PB-O3A-PA-O2A
5	C	501	GTP	PB-O3A-PA-O2A
10	B	502	GDP	PB-O3A-PA-O1A
10	B	502	GDP	PB-O3A-PA-O2A
10	D	501	GDP	PB-O3A-PA-O1A
5	C	501	GTP	PB-O3A-PA-O1A

There are no ring outliers.

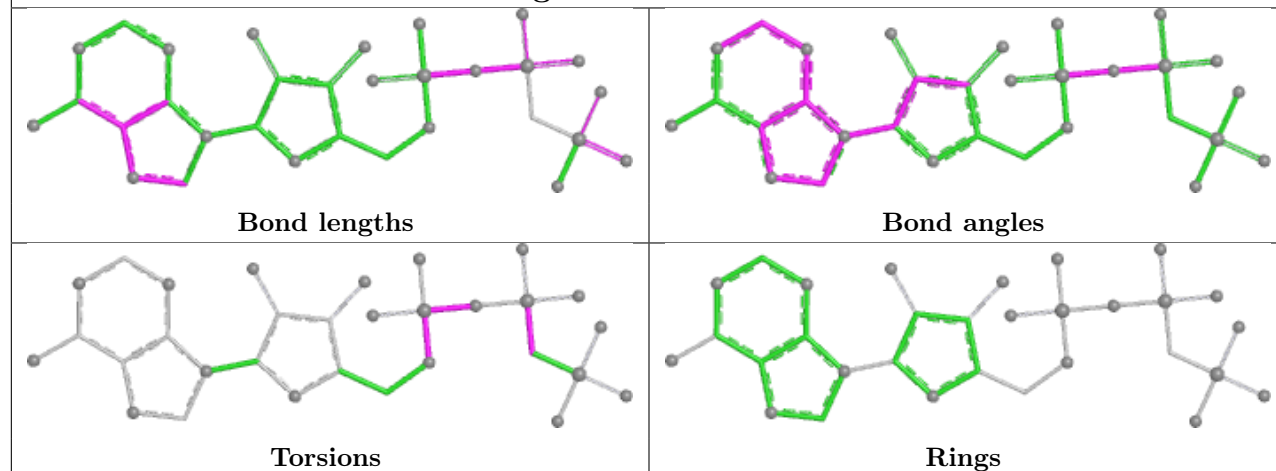
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	501	GTP	1	0
12	F	402	ACP	4	0
9	B	501	UGI	1	0
10	D	501	GDP	1	0

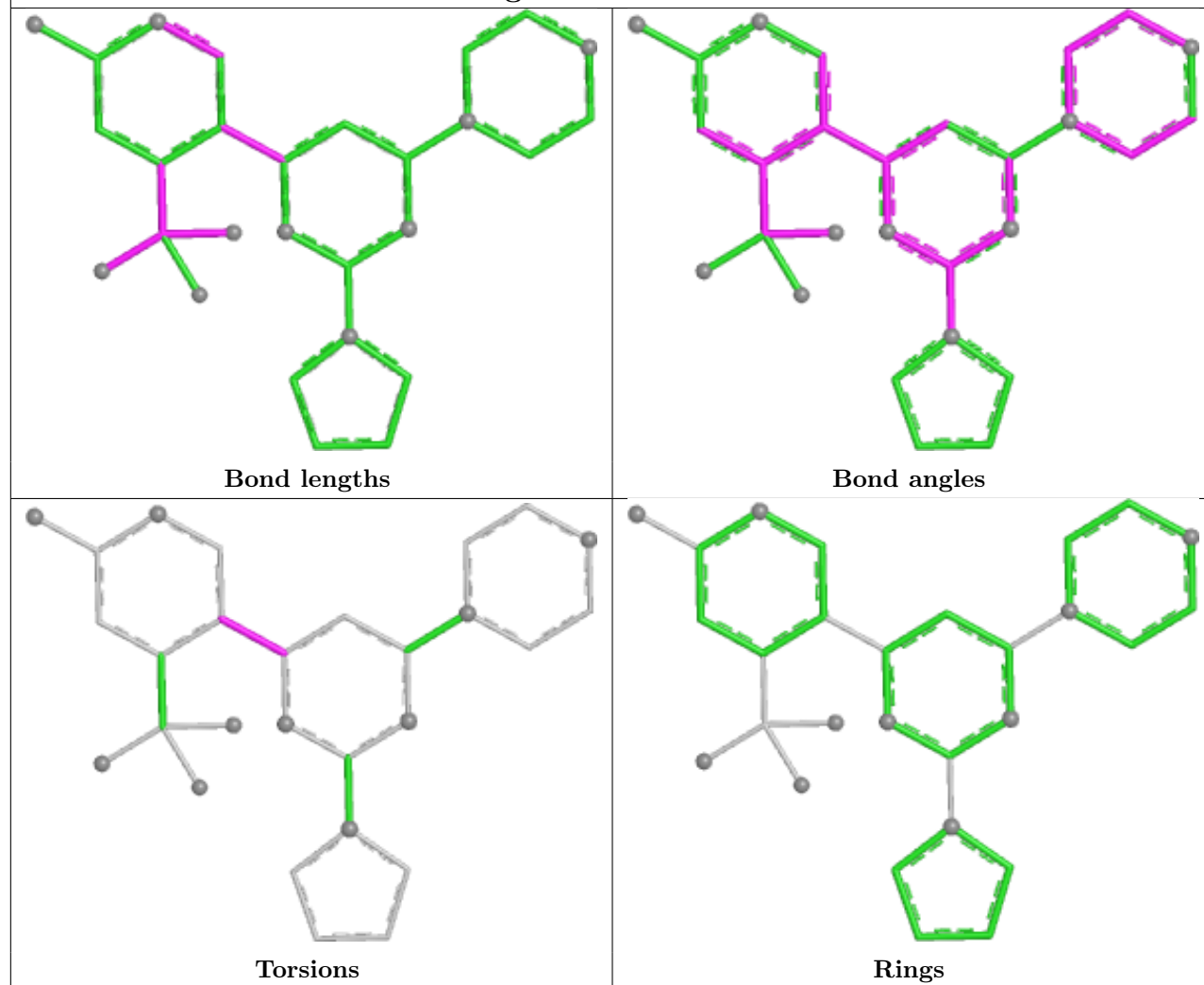
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

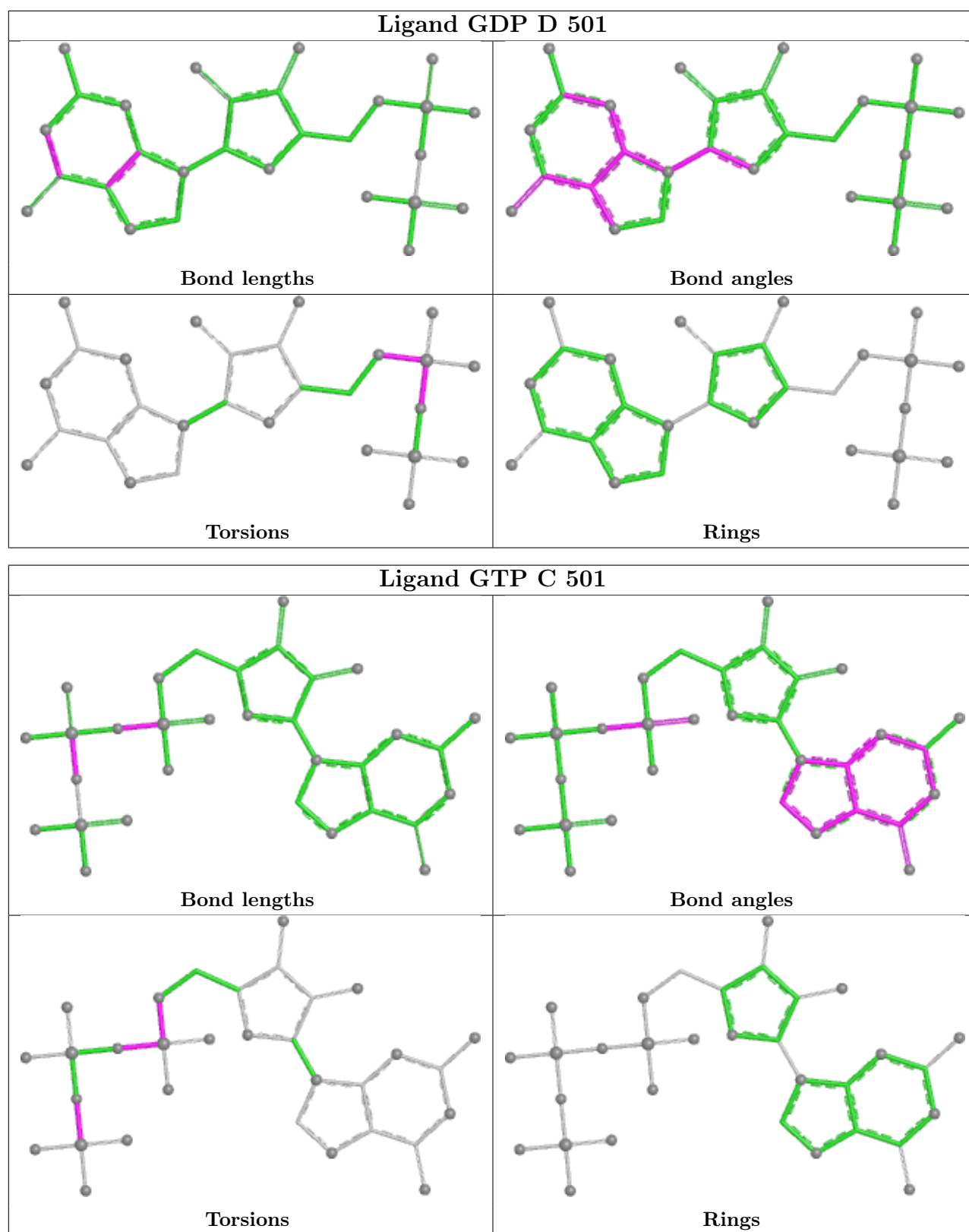


Ligand ACP F 402



Ligand UGI B 501





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	438/451 (97%)	-0.22	5 (1%)	78	79	36, 55, 89, 155	0
1	C	440/451 (97%)	-0.41	6 (1%)	73	74	30, 43, 73, 105	0
2	B	423/445 (95%)	-0.06	17 (4%)	42	42	30, 53, 89, 125	2 (0%)
2	D	427/445 (95%)	0.05	14 (3%)	49	49	37, 62, 98, 129	4 (0%)
3	E	123/143 (86%)	0.33	11 (8%)	15	14	41, 69, 112, 138	0
4	F	344/384 (89%)	0.37	21 (6%)	27	25	43, 81, 147, 165	0
All	All	2195/2319 (94%)	-0.05	74 (3%)	48	48	30, 58, 110, 165	6 (0%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	285	ALA	5.1
3	E	143	ALA	5.0
1	C	440	VAL	4.2
4	F	155	ALA	3.9
2	B	248	LEU	3.8
2	D	325	MET	3.7
1	A	282	TYR	3.7
2	B	245	PRO	3.4
2	B	438	ALA	3.3
2	B	338	LYS	3.3
4	F	362	ALA	3.2
4	F	381	HIS	3.1
2	D	276	THR	3.1
3	E	26	PRO	3.1
4	F	179	VAL	3.0
2	B	57	THR	3.0
2	D	279	GLY	2.9
1	A	437	VAL	2.9
4	F	102	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
4	F	231	ALA	2.8
2	B	276	THR	2.8
1	C	340	SER	2.7
4	F	130	VAL	2.7
2	B	337	ASN	2.7
2	D	278	ARG	2.7
2	B	333	LEU	2.6
1	A	438	ASP	2.6
2	D	281	GLN	2.6
4	F	182	ILE	2.6
4	F	253	TYR	2.6
4	F	134	ALA	2.5
3	E	28	SER	2.5
4	F	125	THR	2.5
4	F	379	HIS	2.5
1	C	179	THR	2.5
2	B	247	GLN	2.5
2	D	247	GLN	2.5
2	D	57	THR	2.4
2	D	277	SER	2.4
2	D	286	LEU	2.4
2	B	282	GLN	2.4
4	F	131	PHE	2.4
4	F	156	LYS	2.4
4	F	1	MET	2.4
4	F	173	ILE	2.4
2	B	325	MET	2.3
3	E	24	LEU	2.3
3	E	44	ASP	2.3
3	E	6	MET	2.3
2	B	2	ARG	2.3
4	F	186	LEU	2.3
2	B	249	ASN	2.3
4	F	153	ALA	2.3
1	C	336	LYS	2.3
2	D	241	CYS	2.2
1	A	178	SER	2.2
4	F	90	SER	2.2
4	F	152	SER	2.2
1	A	221	ARG	2.2
1	C	286	LEU	2.2
2	D	248	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
4	F	160	ILE	2.1
3	E	27	PRO	2.1
2	B	275	LEU	2.1
2	D	2	ARG	2.1
3	E	25	LYS	2.1
2	B	58	GLY	2.1
3	E	142	GLU	2.1
1	C	341	ILE	2.1
2	B	339	ASN	2.1
2	D	82	PRO	2.1
3	E	45	PRO	2.1
2	B	285	ALA	2.0
3	E	23	ILE	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(Å ²)	Q<0.9
7	CA	B	504	1/1	0.86	0.17	118,118,118,118	0
6	MG	F	401	1/1	0.89	0.11	78,78,78,78	0
7	CA	B	505	1/1	0.90	0.18	92,92,92,92	0
8	GOL	A	505	6/6	0.91	0.12	73,77,90,92	0
9	UGI	B	501	28/28	0.91	0.14	41,56,73,85	28
7	CA	A	504	1/1	0.92	0.13	102,102,102,102	0
12	ACP	F	402	31/31	0.92	0.09	82,98,121,125	0
11	MES	B	506	12/12	0.94	0.09	48,53,69,71	0
6	MG	D	502	1/1	0.94	0.07	55,55,55,55	0
10	GDP	D	501	28/28	0.96	0.08	45,55,64,65	0

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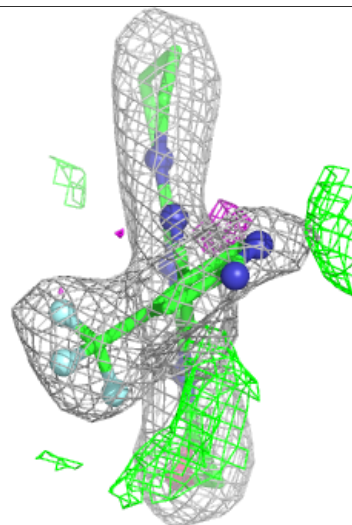
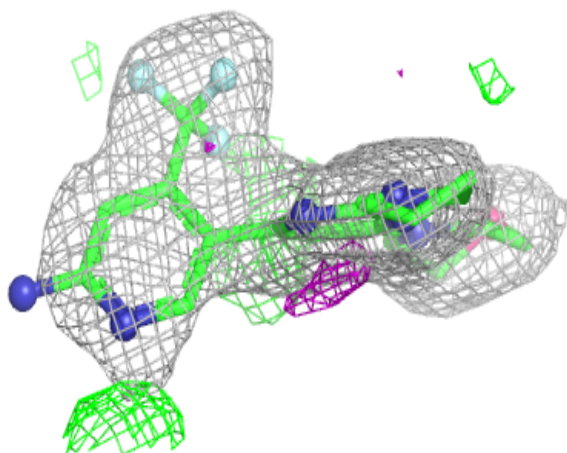
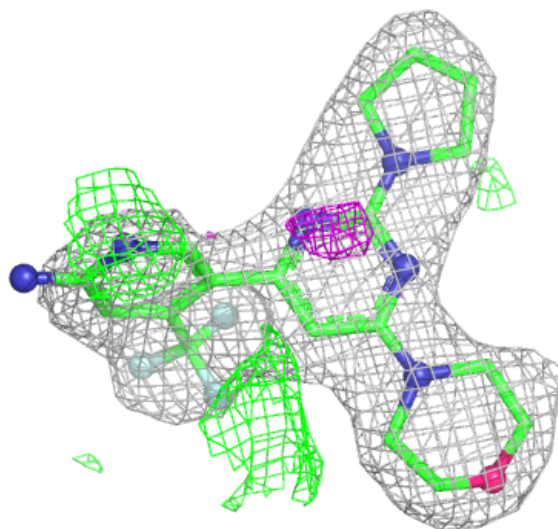
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	GTP	A	501	32/32	0.98	0.05	29,38,43,55	0
7	CA	A	503	1/1	0.98	0.04	71,71,71,71	0
10	GDP	B	502	28/28	0.99	0.04	27,37,41,44	0
7	CA	C	503	1/1	0.99	0.03	63,63,63,63	0
5	GTP	C	501	32/32	0.99	0.04	27,32,38,46	0
6	MG	B	503	1/1	0.99	0.07	33,33,33,33	0
6	MG	C	502	1/1	1.00	0.05	36,36,36,36	0
6	MG	A	502	1/1	1.00	0.02	37,37,37,37	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.

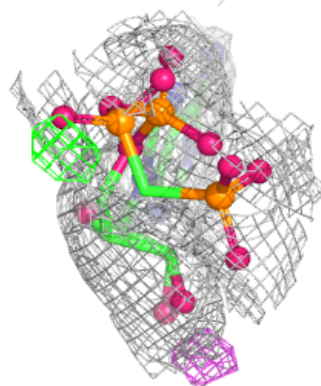
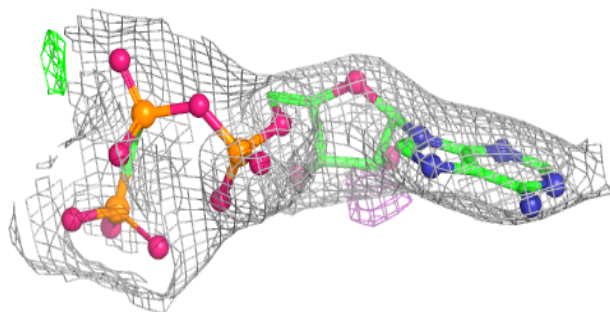
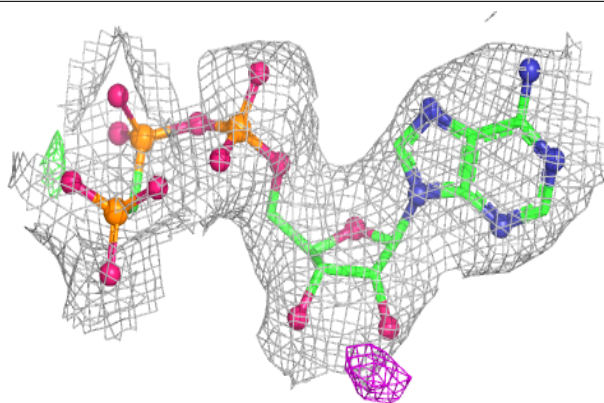
Electron density around UGI B 501:

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



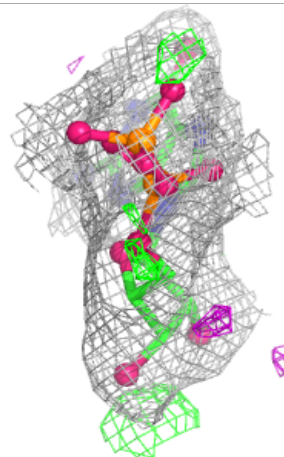
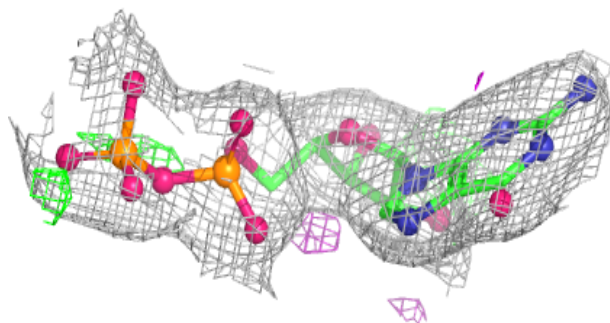
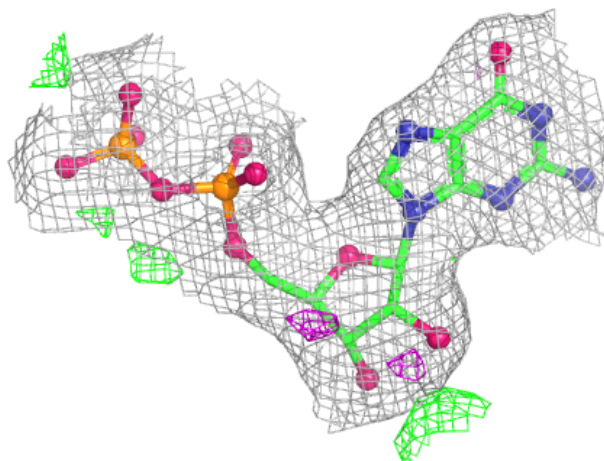
Electron density around ACP F 402:

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



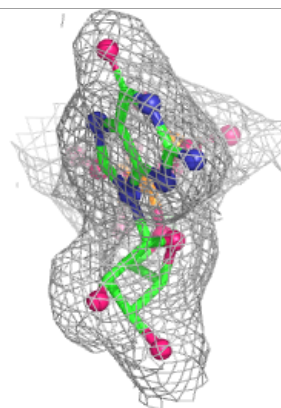
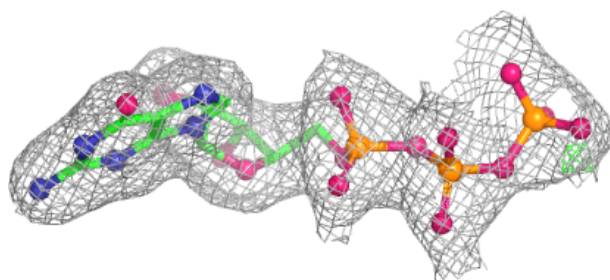
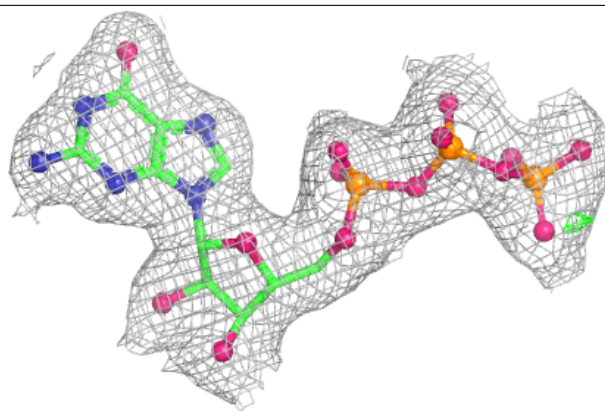
Electron density around GDP D 501:

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

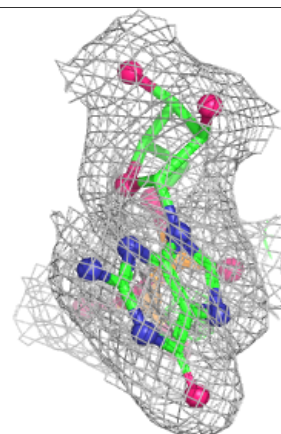
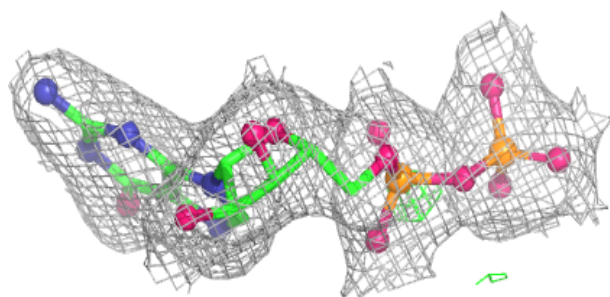
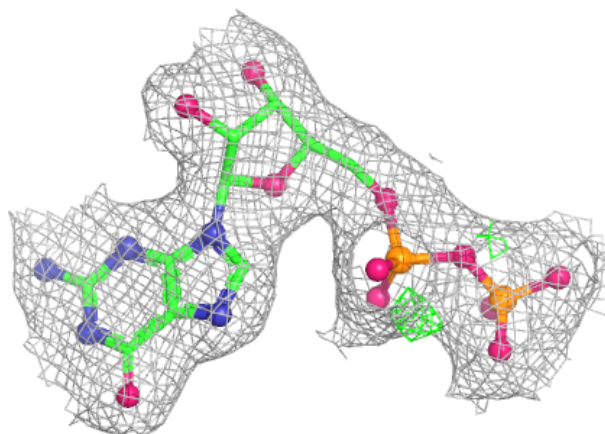


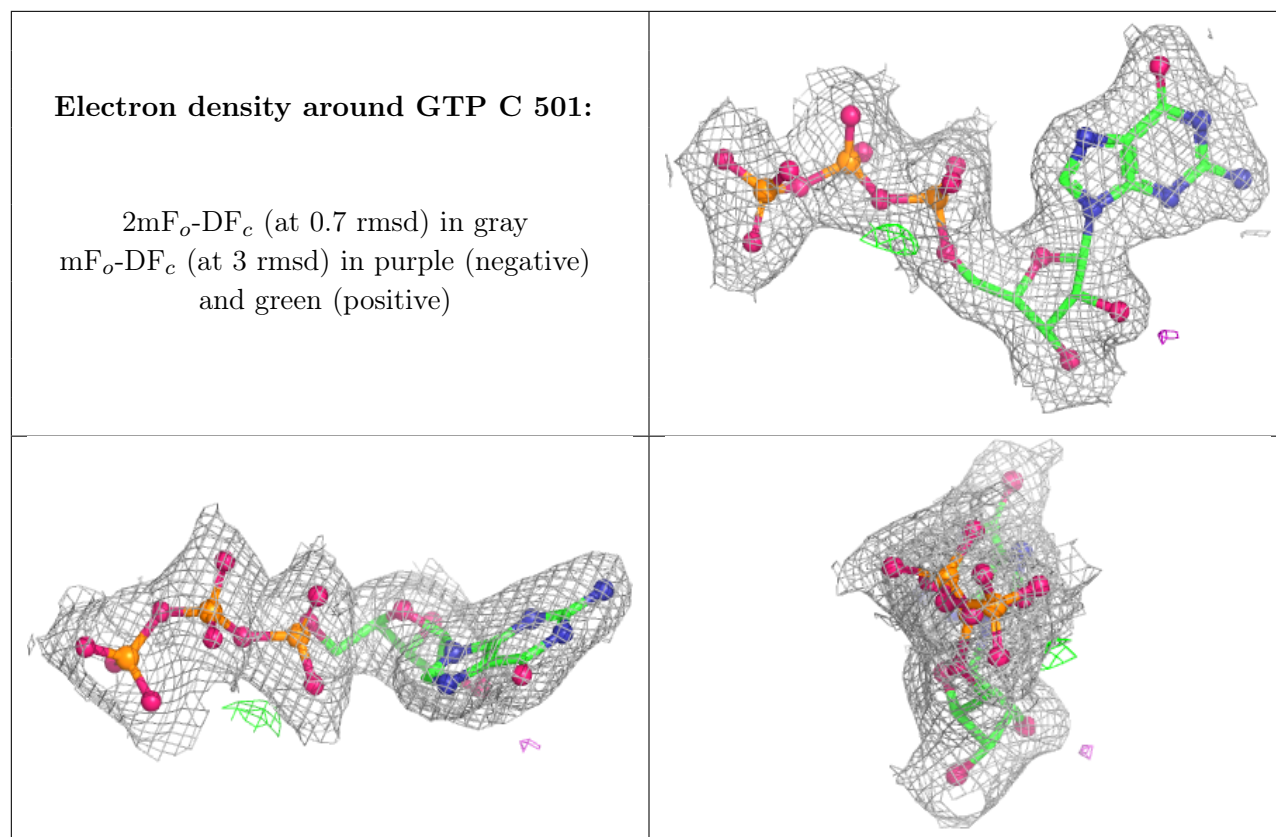
Electron density around GTP A 501:

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

**Electron density around GDP B 502:**

$2mF_o-DF_c$ (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.