



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:08 AM UTC

PDB ID : 7CNO / pdb_00007cno
Title : Phomopsin A in complex with tubulin
Authors : Wu, C.Y.; Wang, Y.X.
Deposited on : 2020-08-02
Resolution : 2.50 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

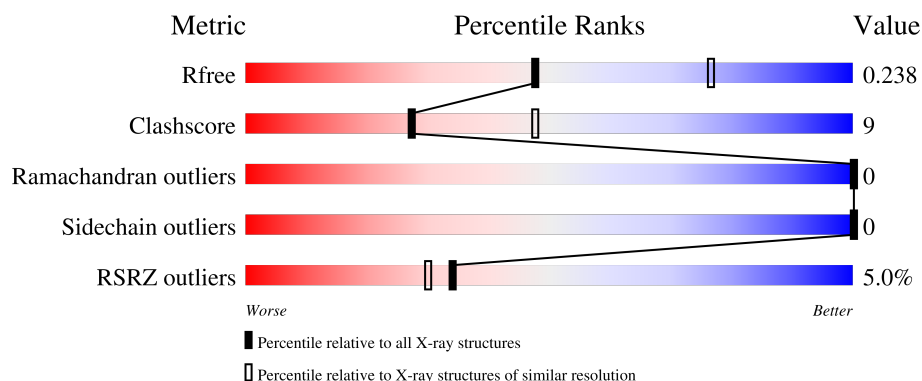
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	
1	C	451	
2	B	445	
2	D	445	
3	E	143	

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Mol	Chain	Length	Quality of chain
4	G	384	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	MES	B	504	-	-	X	-
9	GDP	D	501	-	-	X	-

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 18166 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	437	Total	C	N	O	S	0	5	0
			3439	2178	584	653	24			
1	C	440	Total	C	N	O	S	0	8	0
			3463	2193	584	662	24			

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	428	Total	C	N	O	S	0	4	0
			3383	2127	577	652	27			
2	D	422	Total	C	N	O	S	0	5	0
			3325	2090	563	645	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	122	Total	C	N	O	S	0	4	0
			1027	634	185	202	6			

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

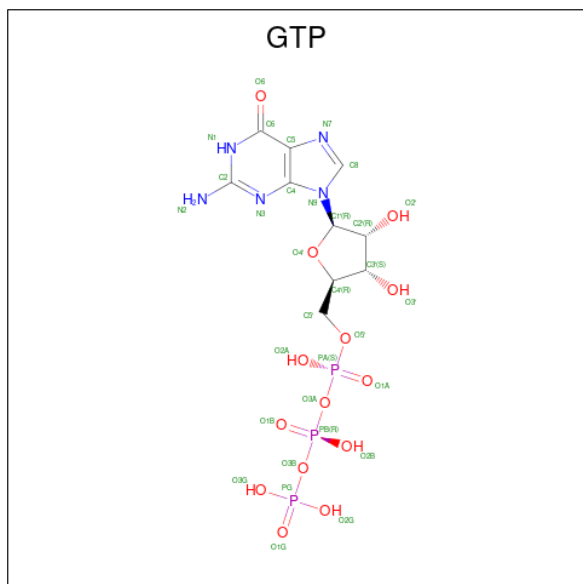
- Molecule 4 is a protein called Tubulin tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	338	Total	C	N	O	S	0	0	0
			2757	1770	469	504	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	379	HIS	-	expression tag	UNP E1BQ43
G	380	HIS	-	expression tag	UNP E1BQ43
G	381	HIS	-	expression tag	UNP E1BQ43
G	382	HIS	-	expression tag	UNP E1BQ43
G	383	HIS	-	expression tag	UNP E1BQ43
G	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	C	N	O	P	0	0
			32	10	5	14	3		
5	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- 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		

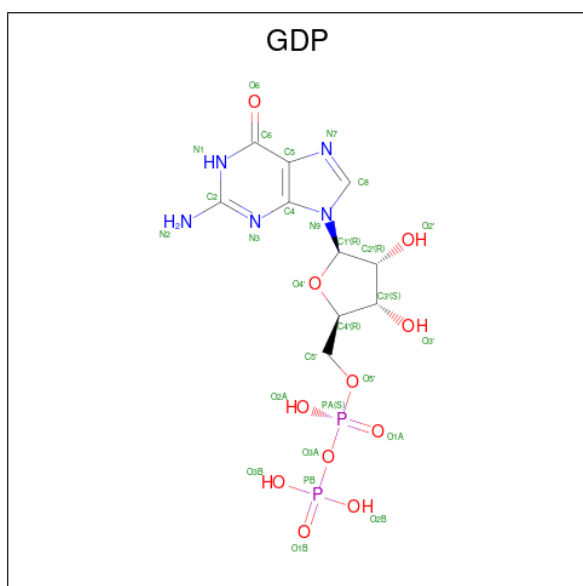
- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

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

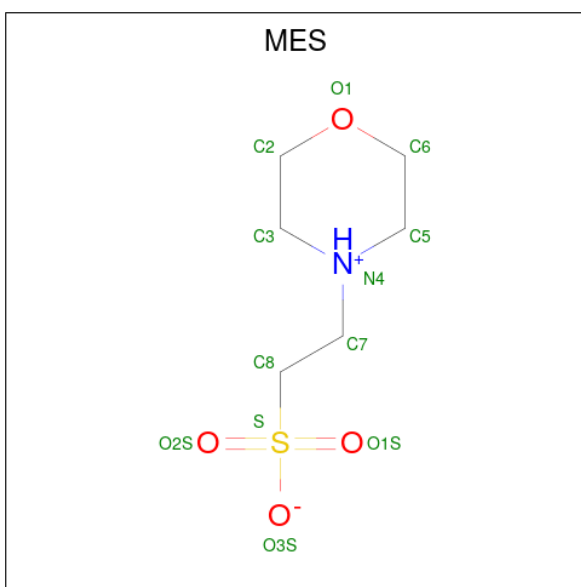
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0

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



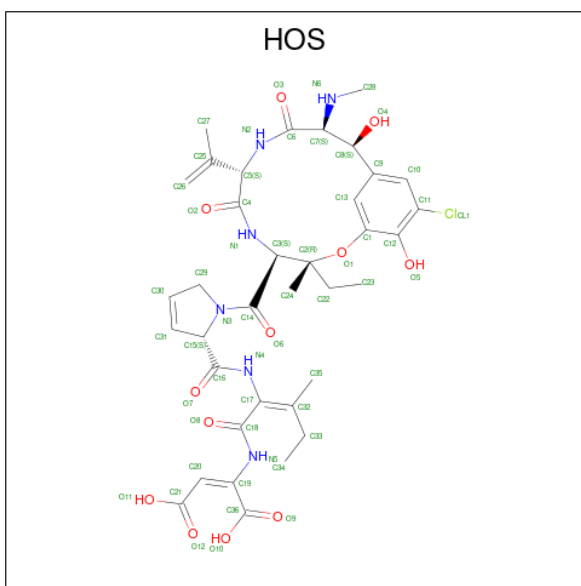
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C N O P 28 10 5 11 2	0	0
9	D	1	Total C N O P 28 10 5 11 2	0	0

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



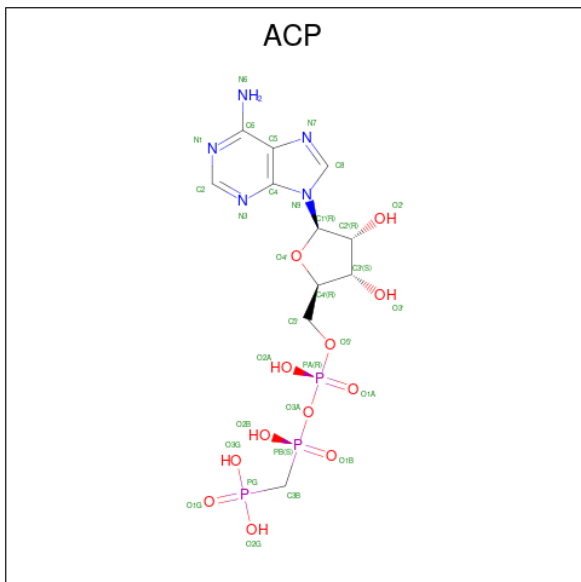
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	B	1	Total 12	C 6	N 1	O 4	S 1	0	0
10	B	1	Total 12	C 6	N 1	O 4	S 1	0	0

- Molecule 11 is Phomopsin A (CCD ID: HOS) (formula: $\text{C}_{36}\text{H}_{45}\text{ClN}_6\text{O}_{12}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	B	1	Total 55	C 36	Cl 1	N 6	O 12	0	0
11	D	1	Total 55	C 36	Cl 1	N 6	O 12	0	0

- Molecule 12 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: $\text{C}_{11}\text{H}_{18}\text{N}_5\text{O}_{12}\text{P}_3$).



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

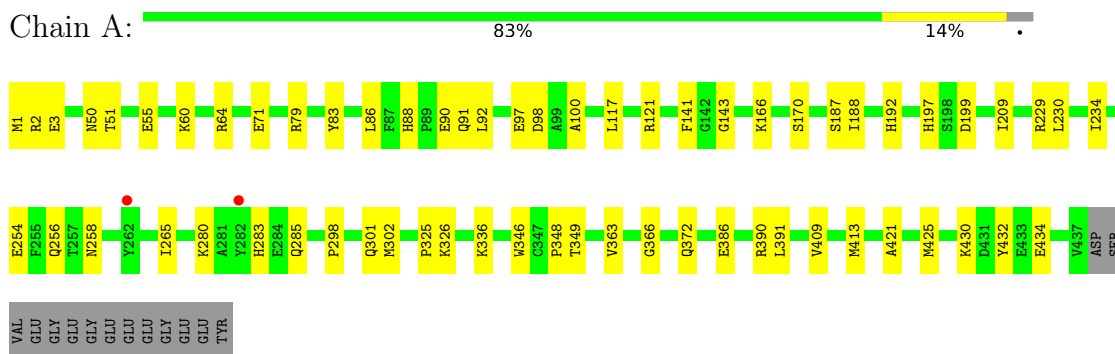
- Molecule 13 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	110	Total O 110 110	0	0
13	B	132	Total O 132 132	0	0
13	C	144	Total O 144 144	0	0
13	D	32	Total O 32 32	0	0
13	E	19	Total O 19 19	0	0
13	G	41	Total O 41 41	0	0

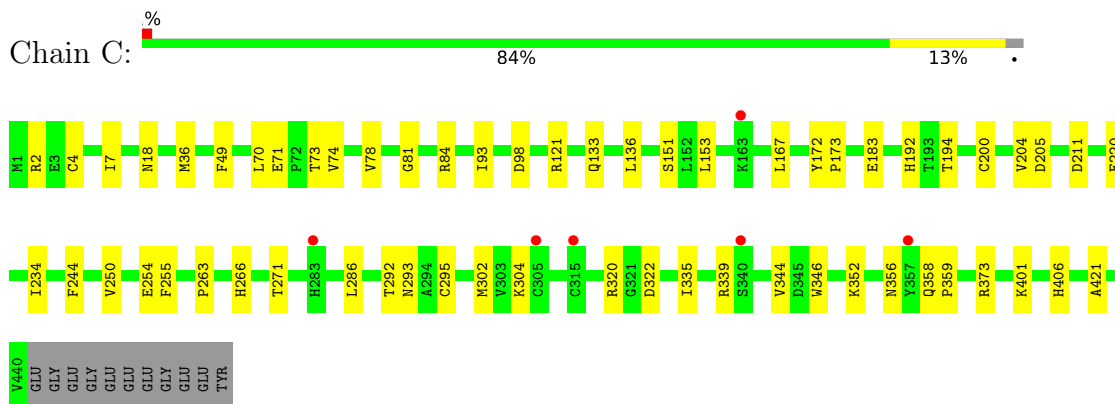
3 Residue-property plots

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.

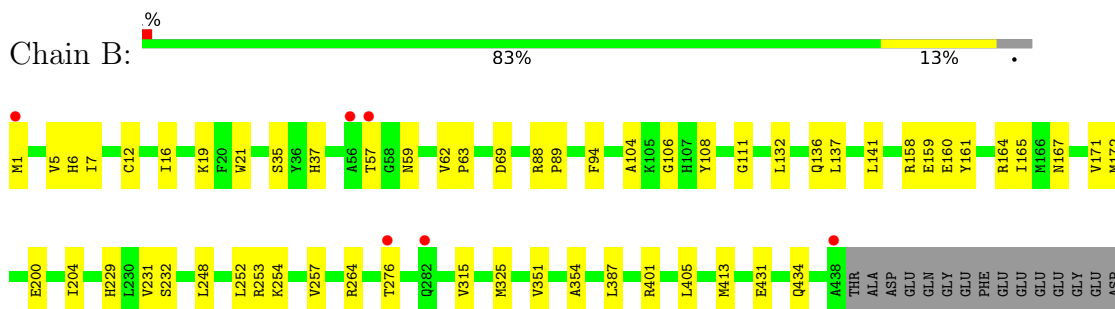
• Molecule 1: Tubulin alpha-1B chain



• Molecule 1: Tubulin alpha-1B chain



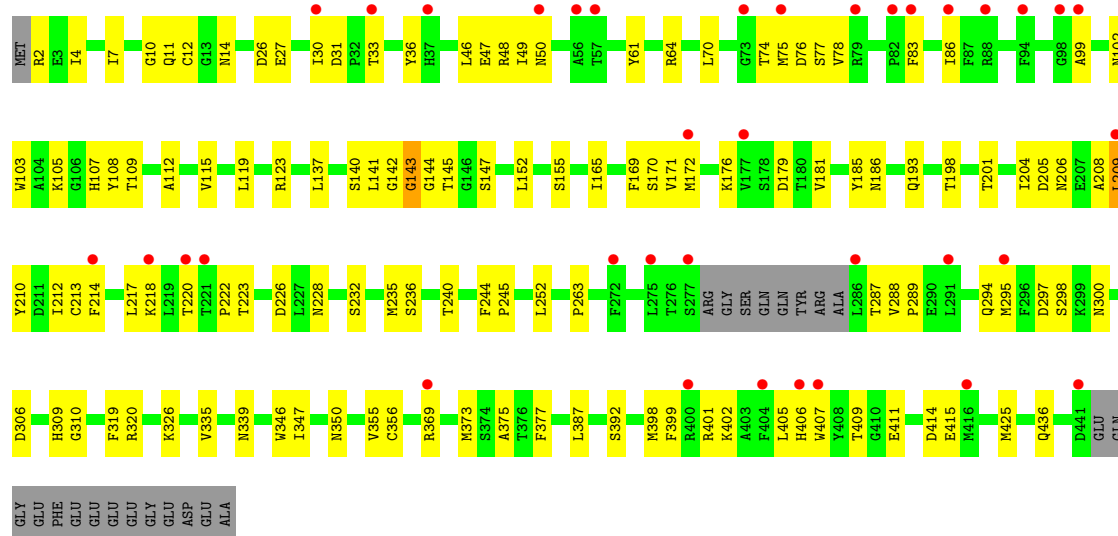
• Molecule 2: Tubulin beta chain



GLU
ALA

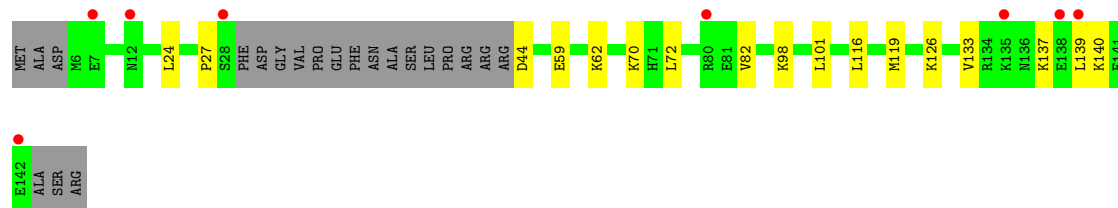
• Molecule 2: Tubulin beta chain

Chain D: 



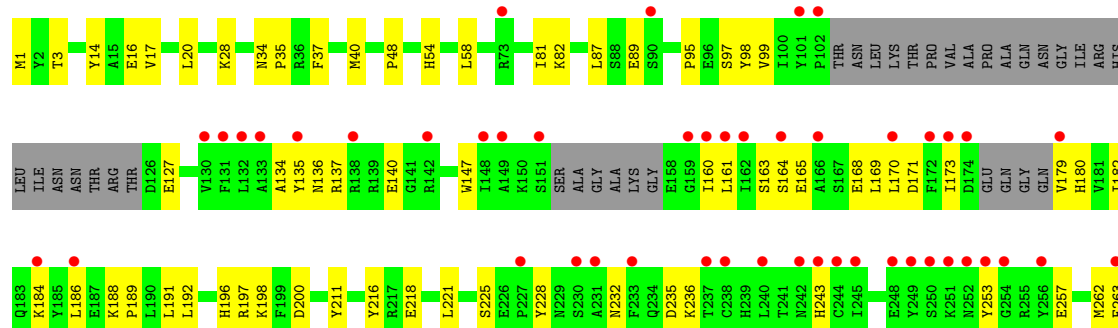
• Molecule 3: Stathmin-4

Chain E: 



• Molecule 4: Tubulin tyrosine ligase

Chain G: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.28Å 155.22Å 184.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.70 – 2.50 30.70 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.7 (30.70-2.50) 95.6 (30.70-2.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.187 , 0.239 0.189 , 0.238	Depositor DCC
R_{free} test set	5043 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	38.2	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18166	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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

5.1 Standard geometry

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

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	0.37	0/3532	0.56	0/4794
1	C	0.42	0/3562	0.61	0/4835
2	B	0.38	0/3467	0.58	0/4696
2	D	0.35	0/3412	0.63	3/4623 (0.1%)
3	E	0.34	0/1048	0.54	0/1392
4	G	0.33	0/2819	0.55	0/3810
All	All	0.37	0/17840	0.59	3/24150 (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	143	GLY	CA-C-N	-5.35	110.92	121.41
2	D	143	GLY	C-N-CA	-5.35	110.92	121.41
2	D	209	LEU	CA-CB-CG	5.34	135.00	116.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3439	0	3365	47	0
1	C	3463	0	3381	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3383	0	3264	46	0
2	D	3325	0	3200	108	0
3	E	1027	0	1041	18	0
4	G	2757	0	2708	62	0
5	A	32	0	12	1	0
5	C	32	0	12	1	0
6	A	1	0	0	0	0
6	B	2	0	0	0	0
6	C	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	1	0
9	D	28	0	12	9	0
10	B	24	0	25	7	0
11	B	55	0	43	0	0
11	D	55	0	42	12	0
12	G	31	0	14	6	0
13	A	110	0	0	4	0
13	B	132	0	0	0	0
13	C	144	0	0	3	0
13	D	32	0	0	1	0
13	E	19	0	0	2	0
13	G	41	0	0	2	0
All	All	18166	0	17131	317	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 9.

All (317) 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)
2:B:158:ARG:NE	10:B:504:MES:H62	1.69	1.07
2:D:11:GLN:HB3	9:D:501:GDP:O2A	1.62	0.99
11:D:502:HOS:H28B	11:D:502:HOS:HN2	1.26	0.98
2:B:158:ARG:HE	10:B:504:MES:H62	1.35	0.89
4:G:40:MET:SD	13:G:538:HOH:O	2.31	0.88
2:B:158:ARG:HH21	10:B:504:MES:H31	1.44	0.81
2:B:158:ARG:NH2	10:B:504:MES:H31	1.95	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ARG:HD2	1:A:363:VAL:HG21	1.63	0.80
2:D:287:THR:HB	2:D:289:PRO:HD2	1.64	0.78
1:C:234:ILE:HG21	1:C:302[B]:MET:SD	2.23	0.78
4:G:192:LEU:HD21	4:G:262:MET:HE1	1.64	0.78
4:G:280:GLU:O	4:G:285:LEU:HD13	1.83	0.76
12:G:401:ACP:O2G	12:G:401:ACP:O1B	2.05	0.75
2:D:47:GLU:HG2	2:D:245:PRO:HG3	1.69	0.74
12:G:401:ACP:O2A	12:G:401:ACP:O2B	2.05	0.73
2:D:102:ASN:HB3	2:D:105:LYS:HG3	1.70	0.73
1:C:293[A]:ASN:OD1	1:C:339:ARG:NH2	2.21	0.73
3:E:44:ASP:N	13:E:301:HOH:O	2.21	0.73
4:G:232:ASN:HB3	4:G:235:ASP:HB3	1.72	0.71
3:E:98:LYS:NZ	13:E:303:HOH:O	2.24	0.71
1:A:97:GLU:HG2	2:B:1:MET:HE3	1.73	0.70
1:C:322:ASP:OD2	1:C:373:ARG:NH1	2.25	0.70
4:G:1:MET:CE	4:G:28:LYS:HB2	2.22	0.70
1:A:79:ARG:HG2	1:A:92:LEU:HD12	1.72	0.69
1:C:244:PHE:HB2	1:C:356:ASN:HD21	1.56	0.69
2:D:208:ALA:O	2:D:212:ILE:HD12	1.93	0.69
2:D:143:GLY:HA3	9:D:501:GDP:O5'	1.94	0.68
2:D:222:PRO:O	11:D:502:HOS:H22A	1.93	0.68
2:D:11:GLN:CB	9:D:501:GDP:O2A	2.42	0.67
2:D:83:PHE:HD2	2:D:86:ILE:HD12	1.59	0.67
1:C:4[A]:CYS:SG	1:C:136:LEU:HD13	2.34	0.67
2:D:4:ILE:O	2:D:64:ARG:NH1	2.27	0.67
2:D:172:MET:SD	2:D:387:LEU:HD11	2.36	0.66
2:D:145:THR:N	9:D:501:GDP:O2B	2.23	0.66
2:B:160:GLU:HG2	2:B:161:TYR:CE1	2.30	0.66
2:D:222:PRO:HD2	11:D:502:HOS:O5	1.96	0.66
2:D:411:GLU:HA	3:E:137:LYS:HD2	1.77	0.66
1:A:230:LEU:O	1:A:234:ILE:HD12	1.97	0.65
1:C:220:GLU:HB2	2:D:326:LYS:HE2	1.77	0.65
2:D:142:GLY:O	2:D:186:ASN:ND2	2.28	0.65
2:D:48:ARG:NH1	2:D:244:PHE:O	2.29	0.65
2:D:220:THR:O	2:D:222:PRO:HD3	1.96	0.65
2:D:76:ASP:OD1	2:D:76:ASP:N	2.30	0.64
11:D:502:HOS:HN2	11:D:502:HOS:C28	2.04	0.64
1:C:2:ARG:HG2	1:C:2:ARG:HH11	1.64	0.63
2:D:295:MET:HE2	2:D:377:PHE:HB2	1.80	0.63
2:D:347:ILE:HG22	2:D:350:ASN:HB3	1.81	0.63
2:B:172:MET:HG2	2:B:387:LEU:HD21	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:HIS:CD2	1:A:90:GLU:HB2	2.34	0.62
2:D:144:GLY:N	9:D:501:GDP:O2B	2.33	0.62
2:B:158:ARG:CD	10:B:504:MES:H62	2.29	0.62
2:B:253:ARG:NH1	10:B:504:MES:O1S	2.29	0.61
4:G:1:MET:HE3	4:G:28:LYS:HB2	1.81	0.61
1:A:166:LYS:HE2	1:A:197:HIS:O	2.01	0.61
2:D:46:LEU:HA	2:D:49:ILE:HB	1.82	0.61
4:G:280:GLU:HA	4:G:284:LEU:HB2	1.83	0.61
4:G:14:TYR:HA	4:G:17:VAL:HB	1.83	0.60
1:C:211[A]:ASP:OD2	1:C:304:LYS:NZ	2.34	0.60
4:G:147:TRP:HB3	4:G:182:ILE:HD11	1.84	0.60
2:B:35:SER:HB2	2:B:37:HIS:HE1	1.66	0.59
2:D:74:THR:O	2:D:77:SER:HB2	2.02	0.59
2:D:36:TYR:CZ	2:D:46:LEU:HD21	2.38	0.59
4:G:163:SER:OG	4:G:165:GLU:N	2.34	0.59
2:B:6:HIS:CD2	2:B:21:TRP:HE1	2.20	0.59
11:D:502:HOS:H28B	11:D:502:HOS:N2	2.06	0.59
2:D:214:PHE:O	2:D:218:LYS:HA	2.03	0.58
1:A:326:LYS:NZ	13:A:608:HOH:O	2.37	0.58
2:D:228:ASN:ND2	9:D:501:GDP:O6	2.29	0.58
11:D:502:HOS:H28A	11:D:502:HOS:O4	2.04	0.58
1:A:346:TRP:H	1:A:346:TRP:CD1	2.22	0.57
1:C:7:ILE:HG21	1:C:153:LEU:HD21	1.86	0.57
2:D:26:ASP:OD1	2:D:369:ARG:HG3	2.06	0.56
4:G:192:LEU:HD21	4:G:262:MET:CE	2.32	0.56
1:C:250:VAL:HG22	1:C:255:PHE:CZ	2.39	0.56
2:D:218:LYS:HZ1	2:D:220:THR:HG22	1.70	0.56
4:G:189:PRO:HG2	4:G:191:LEU:HD21	1.88	0.56
4:G:263:PHE:HZ	4:G:341:LYS:HD3	1.70	0.56
1:A:280:LYS:HD3	1:A:283:HIS:HB2	1.85	0.56
2:D:103:TRP:HD1	2:D:147[A]:SER:OG	1.88	0.56
2:D:112:ALA:O	2:D:115:VAL:HG12	2.06	0.56
4:G:136:ASN:O	4:G:140:GLU:N	2.35	0.56
4:G:1:MET:HE2	4:G:28:LYS:HB2	1.86	0.55
3:E:59:GLU:OE2	3:E:62:LYS:HD3	2.06	0.55
4:G:197:ARG:HH22	4:G:257:GLU:CD	2.14	0.55
1:C:2:ARG:HB3	1:C:133:GLN:HB2	1.89	0.55
1:A:88:HIS:HB3	1:A:91:GLN:HG3	1.87	0.55
2:D:218:LYS:NZ	2:D:220:THR:HG22	2.21	0.55
2:B:136:GLN:HA	2:B:167:ASN:O	2.06	0.55
2:D:119:LEU:O	2:D:123:ARG:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:223:THR:HG21	11:D:502:HOS:O12	2.07	0.55
2:D:141:LEU:HD11	2:D:170:SER:HB3	1.88	0.55
1:A:254:GLU:HG2	1:A:258:ASN:ND2	2.22	0.54
2:D:306:ASP:HB3	2:D:309:HIS:CD2	2.42	0.54
2:D:193:GLN:HE22	3:E:126:LYS:NZ	2.05	0.54
4:G:98:TYR:HB2	4:G:182:ILE:HG23	1.88	0.54
4:G:160:ILE:O	4:G:161:LEU:HD22	2.07	0.54
1:A:188:ILE:HG13	1:A:425:MET:HG3	1.89	0.54
2:D:2:ARG:HH12	2:D:50:ASN:HB2	1.73	0.54
2:D:50:ASN:O	2:D:64:ARG:NH2	2.40	0.54
4:G:16:GLU:HG3	4:G:20:LEU:HD11	1.90	0.53
1:A:348:PRO:HG3	3:E:27:PRO:HG3	1.91	0.53
4:G:184:LYS:HG2	13:G:506:HOH:O	2.08	0.53
1:C:167:LEU:HG	1:C:200:CYS:HB3	1.91	0.53
2:D:7:ILE:O	2:D:137:LEU:HD12	2.08	0.53
1:A:430:LYS:O	1:A:434:GLU:HG3	2.09	0.53
2:D:193:GLN:HE22	3:E:126:LYS:HZ1	1.57	0.53
1:A:336:LYS:HG2	3:E:24:LEU:HD22	1.90	0.53
2:D:141:LEU:CD1	2:D:170:SER:HB3	2.39	0.53
2:B:12:CYS:HB2	9:B:501:GDP:C8	2.45	0.52
2:D:143:GLY:O	2:D:186:ASN:ND2	2.43	0.52
2:D:223:THR:OG1	2:D:226:ASP:CG	2.52	0.52
2:B:229:HIS:NE2	2:B:276:THR:HG23	2.25	0.52
1:C:292:THR:HG22	1:C:335:ILE:CD1	2.40	0.52
2:D:210:TYR:HE1	2:D:222:PRO:HG2	1.75	0.52
2:B:167:ASN:OD1	2:B:200:GLU:HG3	2.09	0.52
2:D:108:TYR:CG	3:E:133:VAL:HG21	2.45	0.52
2:D:240[B]:THR:HG21	2:D:320:ARG:HD2	1.92	0.52
1:A:192:HIS:CG	1:A:421:ALA:HA	2.45	0.52
2:D:223:THR:O	2:D:226:ASP:HB2	2.10	0.52
1:A:1:MET:N	13:A:610:HOH:O	2.41	0.51
1:A:285:GLN:HG3	1:A:372:GLN:NE2	2.26	0.51
4:G:98:TYR:HA	4:G:127:GLU:OE1	2.10	0.51
2:B:16[B]:ILE:HD13	2:B:231:VAL:HG11	1.91	0.51
2:D:205:ASP:O	2:D:209:LEU:HD22	2.11	0.51
1:A:3:GLU:HG2	1:A:64:ARG:CZ	2.40	0.51
2:B:108:TYR:CG	3:E:82:VAL:HG11	2.46	0.51
1:C:204:VAL:HG13	1:C:302[B]:MET:HE3	1.92	0.51
2:D:213:CYS:HA	2:D:217:LEU:HD12	1.93	0.51
4:G:211:TYR:CE1	4:G:299:GLU:HG3	2.45	0.51
1:C:93:ILE:HD11	1:C:121:ARG:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ASP:HB3	1:A:256:GLN:HG2	1.93	0.51
2:D:176:LYS:HB3	2:D:210:TYR:CD2	2.44	0.51
4:G:186:LEU:HD23	12:G:401:ACP:N1	2.26	0.51
1:C:263:PRO:O	1:C:266:HIS:HD2	1.93	0.50
1:A:143:GLY:HA3	5:A:501:GTP:O3A	2.11	0.50
2:D:176:LYS:HB3	2:D:210:TYR:CE2	2.47	0.50
2:D:206:ASN:HA	2:D:209:LEU:HD23	1.93	0.50
3:E:116:LEU:HD23	3:E:119:MET:HE3	1.94	0.50
2:D:405:LEU:O	2:D:409:THR:HG22	2.12	0.50
2:D:206:ASN:ND2	9:D:501:GDP:O2'	2.45	0.50
4:G:225:SER:OG	4:G:253:TYR:HA	2.12	0.50
2:D:171:VAL:HA	2:D:204:ILE:O	2.12	0.50
2:D:155[B]:SER:OG	3:E:126:LYS:HD3	2.12	0.49
2:B:7:ILE:O	2:B:137:LEU:HA	2.12	0.49
2:D:179:ASP:OD2	11:D:502:HOS:H28	2.12	0.49
2:D:402:LYS:C	2:D:405:LEU:HD23	2.37	0.49
4:G:320:MET:HG2	4:G:330:ILE:HG21	1.94	0.49
1:A:209:ILE:HG23	1:A:230:LEU:HD23	1.94	0.49
1:C:204:VAL:HG22	1:C:302[B]:MET:CE	2.43	0.49
2:D:109:THR:HG21	2:D:411:GLU:HB3	1.95	0.49
1:C:293[A]:ASN:ND2	13:C:602:HOH:O	2.32	0.49
2:D:83:PHE:CD2	2:D:86:ILE:HD12	2.43	0.49
2:D:141:LEU:HD22	2:D:172:MET:HE2	1.95	0.49
4:G:135:TYR:HD2	4:G:136:ASN:OD1	1.96	0.49
1:A:71:GLU:HG2	1:A:98:ASP:HB3	1.94	0.48
1:C:71:GLU:HG2	1:C:98:ASP:HB3	1.94	0.48
2:D:402:LYS:HE3	2:D:415:GLU:OE1	2.12	0.48
4:G:163:SER:OG	4:G:164:SER:N	2.46	0.48
1:C:254:GLU:HG2	1:C:352:LYS:HE2	1.96	0.48
1:A:83:TYR:CD2	1:A:86:LEU:HD22	2.49	0.48
2:D:70:LEU:HG	2:D:145:THR:HG23	1.95	0.48
1:C:98:ASP:HB2	5:C:501:GTP:O2G	2.13	0.48
2:D:30:ILE:HD12	2:D:61:TYR:HB2	1.96	0.48
2:D:210:TYR:CE1	2:D:222:PRO:HG2	2.48	0.48
4:G:82:LYS:HE2	4:G:89:GLU:HG2	1.96	0.48
4:G:95:PRO:O	4:G:97:SER:OG	2.31	0.48
2:B:35:SER:HB2	2:B:37:HIS:CE1	2.46	0.48
2:D:297:ASP:OD1	2:D:298:SER:N	2.47	0.48
4:G:221:LEU:HD22	4:G:262:MET:HE3	1.94	0.48
4:G:268:ASN:HA	4:G:271:LEU:HD12	1.96	0.48
2:D:74:THR:O	2:D:78:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:198:LYS:NZ	12:G:401:ACP:N3	2.62	0.47
1:C:320:ARG:HA	1:C:356:ASN:O	2.13	0.47
2:D:11:GLN:N	9:D:501:GDP:O3B	2.39	0.47
4:G:197:ARG:NH2	4:G:257:GLU:OE2	2.46	0.47
4:G:211:TYR:CD1	4:G:299:GLU:HG3	2.49	0.47
2:D:306:ASP:CG	2:D:309:HIS:HD2	2.22	0.47
2:B:248:LEU:HD23	2:B:354:ALA:HB2	1.97	0.47
2:D:27:GLU:OE1	2:D:236:SER:OG	2.23	0.47
1:A:2:ARG:O	1:A:51:THR:HG23	2.15	0.47
1:A:325:PRO:HD2	13:A:608:HOH:O	2.14	0.47
1:C:250:VAL:CG2	1:C:255:PHE:CZ	2.97	0.47
1:C:406:HIS:CD2	2:D:263:PRO:HD3	2.49	0.47
2:D:10:GLY:O	2:D:14:ASN:ND2	2.36	0.47
2:D:70:LEU:HD12	2:D:99:ALA:HB2	1.97	0.47
2:D:185:TYR:OH	2:D:399:PHE:HA	2.15	0.47
2:B:159:GLU:HB2	3:E:72:LEU:HD13	1.96	0.47
2:D:294:GLN:HE21	2:D:300:ASN:HD21	1.63	0.47
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.50	0.47
1:A:117:LEU:O	1:A:121:ARG:HG2	2.14	0.46
2:D:107:HIS:O	2:D:152:LEU:HD13	2.16	0.46
2:B:165:ILE:HG21	2:B:252:LEU:HB3	1.96	0.46
2:B:253:ARG:O	2:B:257:VAL:HG23	2.16	0.46
1:C:36:MET:HE1	1:C:49:PHE:CE2	2.51	0.46
4:G:168:GLU:O	4:G:171:ASP:HB3	2.14	0.46
2:D:143:GLY:CA	9:D:501:GDP:H5'	2.45	0.46
1:A:409:VAL:HA	1:A:413:MET:O	2.15	0.46
2:D:181:VAL:O	2:D:398:MET:SD	2.74	0.46
2:B:158:ARG:HG3	10:B:504:MES:C6	2.46	0.46
2:D:402:LYS:HG3	2:D:405:LEU:HG	1.98	0.46
1:A:363:VAL:HG23	1:A:366:GLY:HA3	1.98	0.46
2:D:288:VAL:HB	2:D:289:PRO:HD3	1.97	0.46
1:A:97:GLU:OE1	2:B:164[A]:ARG:NH1	2.46	0.46
1:A:298:PRO:HA	1:A:301:GLN:CD	2.41	0.46
2:D:165:ILE:HG21	2:D:252:LEU:HB3	1.98	0.46
1:A:326:LYS:CE	13:A:608:HOH:O	2.63	0.46
1:C:271:THR:HG21	1:C:295:CYS:O	2.15	0.46
2:B:106:GLY:O	2:B:111:GLY:HA3	2.16	0.45
2:D:12:CYS:CB	2:D:140:SER:HB3	2.46	0.45
1:C:74:VAL:HB	13:C:619:HOH:O	2.15	0.45
1:C:266:HIS:HE1	13:C:611:HOH:O	1.98	0.45
2:D:295:MET:HE3	2:D:375:ALA:HB1	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:165:GLU:HB3	4:G:168:GLU:H	1.81	0.45
1:A:390[B]:ARG:HD2	4:G:54:HIS:CD2	2.51	0.45
1:C:286:LEU:H	1:C:286:LEU:HD12	1.82	0.45
4:G:200:ASP:OD2	12:G:401:ACP:O3'	2.33	0.45
2:B:19:LYS:HB3	2:B:19:LYS:HE3	1.76	0.45
2:D:310:GLY:HA2	2:D:436:GLN:OE1	2.15	0.45
2:D:141:LEU:CD2	2:D:172:MET:HE2	2.46	0.45
2:B:5:VAL:HG23	2:B:132:LEU:HD11	1.97	0.45
2:D:223:THR:CG2	11:D:502:HOS:O12	2.64	0.45
1:A:209:ILE:HD11	1:A:302:MET:SD	2.56	0.44
2:B:161:TYR:HB3	2:B:164[B]:ARG:HG2	1.98	0.44
1:C:71:GLU:OE2	1:C:73:THR:HG23	2.16	0.44
1:C:339:ARG:HD3	1:C:339:ARG:HA	1.80	0.44
1:C:151[B]:SER:HA	1:C:194:THR:HG22	2.00	0.44
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.52	0.44
2:D:169:PHE:CE2	2:D:235:MET:HG2	2.53	0.44
11:D:502:HOS:C21	11:D:502:HOS:O8	2.66	0.44
2:D:12:CYS:SG	2:D:140:SER:HB3	2.57	0.44
2:D:335:VAL:O	2:D:339:ASN:HB2	2.17	0.44
4:G:243:HIS:O	4:G:243:HIS:ND1	2.51	0.44
2:B:62:VAL:HG11	2:B:88:ARG:HB3	2.00	0.43
1:C:172:TYR:HB3	1:C:205:ASP:HA	2.00	0.43
11:D:502:HOS:H34B	11:D:502:HOS:H35	1.85	0.43
1:C:151[A]:SER:HA	1:C:194:THR:HG22	2.00	0.43
4:G:134:ALA:HA	4:G:137:ARG:HE	1.83	0.43
1:A:187:SER:HB3	1:A:391:LEU:HD21	2.00	0.43
1:A:336:LYS:HZ1	1:A:349:THR:HG21	1.84	0.43
2:D:414:ASP:OD1	2:D:415:GLU:N	2.51	0.43
4:G:179:VAL:C	4:G:180:HIS:HD1	2.26	0.43
1:A:336:LYS:HD2	1:A:336:LYS:O	2.19	0.43
2:B:88:ARG:HA	2:B:89:PRO:HD3	1.90	0.43
2:B:405:LEU:HD23	2:B:405:LEU:HA	1.87	0.43
1:A:83:TYR:HD2	1:A:86:LEU:HD22	1.84	0.43
2:B:104:ALA:HB2	2:B:413:MET:SD	2.58	0.43
2:B:171:VAL:HA	2:B:204:ILE:O	2.19	0.43
1:C:18:ASN:HD21	1:C:78:VAL:HG22	1.84	0.43
2:D:326:LYS:HB3	2:D:326:LYS:HE3	1.79	0.43
1:C:401:LYS:HG3	2:D:346:TRP:CE3	2.53	0.43
2:D:401:ARG:HE	2:D:401:ARG:HB2	1.57	0.43
4:G:170:LEU:O	4:G:173:ILE:HG12	2.18	0.43
1:A:100:ALA:HA	2:B:254:LYS:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:GLU:O	1:A:390[A]:ARG:HD3	2.19	0.43
1:A:1:MET:HE2	1:A:50:ASN:HB3	2.01	0.43
2:B:57:THR:C	2:B:59:ASN:H	2.27	0.43
1:C:70:LEU:HA	1:C:70:LEU:HD23	1.76	0.43
2:B:264:ARG:HE	2:B:431[A]:GLU:CD	2.26	0.42
2:D:75:MET:HG3	13:D:609:HOH:O	2.17	0.42
4:G:16:GLU:O	4:G:20:LEU:HD12	2.19	0.42
4:G:81:ILE:HA	4:G:87:LEU:HD12	2.00	0.42
2:D:49:ILE:HD12	2:D:49:ILE:HA	1.83	0.42
3:E:140:LYS:HE2	3:E:140:LYS:HA	2.00	0.42
1:C:204:VAL:HG22	1:C:302[B]:MET:HE3	2.01	0.42
2:D:7:ILE:O	2:D:137:LEU:HA	2.19	0.42
2:D:108:TYR:CD1	3:E:133:VAL:HG21	2.55	0.42
2:D:228:ASN:O	2:D:232:SER:HB2	2.19	0.42
4:G:81:ILE:HG12	4:G:87:LEU:HD13	2.01	0.42
4:G:330:ILE:O	4:G:331:GLU:HB3	2.19	0.42
2:B:69:ASP:O	2:B:94:PHE:HA	2.19	0.42
4:G:275:LEU:HD23	4:G:275:LEU:HA	1.77	0.42
1:C:173:PRO:HB3	1:C:183:GLU:OE2	2.19	0.42
1:C:2:ARG:HG2	1:C:2:ARG:NH1	2.32	0.42
1:C:358:GLN:HA	1:C:359:PRO:HD3	1.93	0.41
2:B:19:LYS:HE3	2:B:232:SER:HB3	2.02	0.41
2:D:36:TYR:CE2	2:D:46:LEU:HD21	2.55	0.41
2:D:319:PHE:HB2	2:D:355:VAL:HG22	2.03	0.41
1:A:283:HIS:HD2	1:A:285:GLN:NE2	2.18	0.41
2:B:315:VAL:HB	2:B:351:VAL:HG22	2.02	0.41
2:B:431[B]:GLU:O	2:B:434:GLN:HB2	2.21	0.41
1:C:81:GLY:O	1:C:84:ARG:HG2	2.21	0.41
2:D:31:ASP:OD2	2:D:33:THR:OG1	2.38	0.41
4:G:40:MET:HE1	4:G:48:PRO:HD2	2.01	0.41
4:G:160:ILE:C	4:G:161:LEU:HD22	2.46	0.41
2:B:401:ARG:HA	2:B:401:ARG:HD2	1.97	0.41
3:E:101:LEU:HD23	3:E:101:LEU:HA	1.80	0.41
4:G:196:HIS:O	4:G:228:TYR:N	2.51	0.41
1:A:55:GLU:HA	1:A:60:LYS:O	2.21	0.41
2:B:325:MET:HE2	2:B:325:MET:HB3	1.92	0.41
4:G:99:VAL:N	4:G:127:GLU:OE1	2.47	0.41
1:A:98:ASP:OD1	1:A:98:ASP:C	2.64	0.41
2:B:5:VAL:HG23	2:B:132:LEU:CD1	2.51	0.41
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.56	0.41
3:E:139:LEU:HD23	3:E:139:LEU:HA	1.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:170:LEU:HD23	4:G:173:ILE:HD13	2.02	0.41
4:G:282:SER:HB2	4:G:325:LEU:HD13	2.01	0.41
4:G:331:GLU:OE1	12:G:401:ACP:O1B	2.38	0.41
2:B:141:LEU:HD12	2:B:172:MET:SD	2.61	0.41
1:C:192:HIS:CG	1:C:421:ALA:HA	2.56	0.41
2:D:392:SER:HB2	2:D:425:MET:HE3	2.02	0.41
4:G:37:PHE:O	4:G:58:LEU:HD13	2.21	0.41
1:A:141:PHE:CE1	1:A:170:SER:HB3	2.56	0.40
2:D:373:MET:HE3	2:D:373:MET:HB3	1.96	0.40
2:D:102:ASN:ND2	2:D:407:TRP:HB3	2.36	0.40
2:D:198:THR:HG21	2:D:201:THR:OG1	2.20	0.40
4:G:169:LEU:O	4:G:173:ILE:HG23	2.21	0.40
2:D:320:ARG:HA	2:D:356:CYS:O	2.21	0.40
4:G:3:THR:OG1	4:G:37:PHE:HA	2.22	0.40
4:G:34:ASN:OD1	4:G:35:PRO:HD2	2.22	0.40
4:G:147:TRP:CB	4:G:182:ILE:HD11	2.49	0.40
4:G:188:LYS:HB3	4:G:188:LYS:HE2	1.81	0.40
4:G:216:TYR:CE2	4:G:218:GLU:HB2	2.57	0.40
1:A:209:ILE:HG23	1:A:209:ILE:HD12	1.83	0.40
2:D:406:HIS:CD2	2:D:407:TRP:HD1	2.39	0.40
11:D:502:HOS:C10	11:D:502:HOS:O3	2.69	0.40
3:E:70:LYS:HA	3:E:70:LYS:HD3	1.91	0.40
4:G:160:ILE:O	4:G:236:LYS:HE2	2.21	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	440/451 (98%)	428 (97%)	12 (3%)	0	100	100
1	C	445/451 (99%)	434 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	430/445 (97%)	412 (96%)	18 (4%)	0	100	100
2	D	422/445 (95%)	403 (96%)	19 (4%)	0	100	100
3	E	122/143 (85%)	121 (99%)	1 (1%)	0	100	100
4	G	328/384 (85%)	314 (96%)	14 (4%)	0	100	100
All	All	2187/2319 (94%)	2112 (97%)	75 (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	373/379 (98%)	373 (100%)	0	100	100
1	C	377/379 (100%)	377 (100%)	0	100	100
2	B	371/383 (97%)	371 (100%)	0	100	100
2	D	367/383 (96%)	367 (100%)	0	100	100
3	E	113/127 (89%)	113 (100%)	0	100	100
4	G	301/342 (88%)	301 (100%)	0	100	100
All	All	1902/1993 (95%)	1902 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	85	GLN
1	A	101	ASN
1	A	176	GLN
1	A	283	HIS
1	A	300	ASN
1	A	301	GLN

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Mol	Chain	Res	Type
1	A	309	HIS
1	A	329	ASN
1	A	358	GLN
1	A	372	GLN
1	A	393	HIS
2	B	37	HIS
2	B	282	GLN
2	B	385	GLN
2	B	433	GLN
2	B	436	GLN
1	C	11	GLN
1	C	266	HIS
1	C	283	HIS
1	C	356	ASN
1	C	406	HIS
2	D	15	GLN
2	D	50	ASN
2	D	193	GLN
2	D	247	GLN
2	D	294	GLN
2	D	309	HIS
4	G	26	GLN
4	G	234	GLN

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 18 ligands modelled in this entry, 9 are monoatomic - leaving 9 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	-	29,30,30	2.28	13 (44%)	45,47,47	1.89	11 (24%)
10	MES	B	505	-	12,12,12	2.16	1 (8%)	15,16,16	2.35	5 (33%)
11	HOS	B	507	-	49,57,57	3.08	23 (46%)	52,83,83	1.63	13 (25%)
9	GDP	B	501	6	29,30,30	1.06	2 (6%)	45,47,47	1.78	7 (15%)
11	HOS	D	502	-	49,57,57	1.78	12 (24%)	52,83,83	3.00	15 (28%)
12	ACP	G	401	-	31,33,33	1.64	6 (19%)	47,52,52	2.07	11 (23%)
5	GTP	C	501	6	33,34,34	1.08	4 (12%)	50,54,54	1.59	10 (20%)
5	GTP	A	501	6	33,34,34	1.19	4 (12%)	50,54,54	1.62	9 (18%)
10	MES	B	504	-	12,12,12	0.57	0	15,16,16	1.44	2 (13%)

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	-	-	4/16/32/32	0/3/3/3
10	MES	B	505	-	-	1/6/14/14	0/1/1/1
11	HOS	B	507	-	-	17/82/92/92	0/2/3/3
9	GDP	B	501	6	-	5/16/32/32	0/3/3/3
11	HOS	D	502	-	-	27/82/92/92	0/2/3/3
12	ACP	G	401	-	-	6/19/38/38	0/3/3/3
5	GTP	C	501	6	-	7/22/38/38	0/3/3/3
5	GTP	A	501	6	-	7/22/38/38	0/3/3/3
10	MES	B	504	-	-	3/6/14/14	0/1/1/1

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B	507	HOS	C16-N4	8.12	1.51	1.36
10	B	505	MES	C8-S	-7.09	1.67	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B	507	HOS	C17-C18	6.21	1.58	1.47
11	B	507	HOS	C14-N3	5.90	1.47	1.34
11	B	507	HOS	C29-C30	-5.63	1.41	1.49
11	B	507	HOS	C18-N5	5.49	1.48	1.37
11	B	507	HOS	C26-C25	5.27	1.54	1.34
11	B	507	HOS	C4-N1	5.04	1.44	1.34
9	D	501	GDP	C4-N9	-4.89	1.25	1.38
11	B	507	HOS	C6-N2	4.81	1.44	1.34
9	D	501	GDP	C6-N1	-4.74	1.30	1.38
11	B	507	HOS	C31-C30	4.72	1.53	1.33
11	D	502	HOS	C12-C11	4.35	1.46	1.39
9	D	501	GDP	C5-N7	-4.31	1.30	1.39
11	B	507	HOS	C17-N4	4.10	1.50	1.41
11	B	507	HOS	C27-C25	-4.00	1.32	1.48
11	D	502	HOS	C1-C12	3.95	1.45	1.40
12	G	401	ACP	C5-N7	-3.68	1.32	1.39
11	D	502	HOS	O8-C18	-3.65	1.16	1.23
11	B	507	HOS	C9-C8	3.48	1.57	1.51
11	B	507	HOS	C5-N2	-3.40	1.40	1.45
11	D	502	HOS	C3-C14	-3.36	1.48	1.53
5	A	501	GTP	PA-O3A	3.33	1.63	1.59
12	G	401	ACP	C8-N9	-3.31	1.31	1.37
9	D	501	GDP	C8-N9	-3.20	1.30	1.37
11	B	507	HOS	C19-N5	3.07	1.48	1.41
9	D	501	GDP	PB-O3B	-3.01	1.43	1.54
11	B	507	HOS	O1-C1	2.99	1.46	1.39
9	D	501	GDP	PA-O3A	-2.91	1.56	1.59
12	G	401	ACP	C4-N9	-2.83	1.31	1.37
11	D	502	HOS	C5-C4	-2.74	1.48	1.54
11	D	502	HOS	O11-C21	-2.73	1.23	1.30
11	B	507	HOS	C20-C21	2.72	1.54	1.47
12	G	401	ACP	C5-C4	2.71	1.43	1.39
11	B	507	HOS	C15-C31	-2.70	1.40	1.49
9	B	501	GDP	C5-C4	2.62	1.45	1.38
5	A	501	GTP	PB-O3A	2.61	1.62	1.59
9	B	501	GDP	C6-N1	-2.59	1.34	1.38
11	B	507	HOS	O3-C6	-2.58	1.18	1.23
11	B	507	HOS	O7-C16	-2.54	1.18	1.23
5	C	501	GTP	PA-O3A	2.51	1.62	1.59
11	D	502	HOS	C6-N2	-2.49	1.28	1.34
11	D	502	HOS	O3-C6	-2.48	1.18	1.23
11	D	502	HOS	O6-C14	-2.44	1.18	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	G	401	ACP	PG-O2G	2.41	1.60	1.55
5	A	501	GTP	C2-N3	2.40	1.39	1.33
11	D	502	HOS	C9-C8	-2.40	1.48	1.51
11	B	507	HOS	C35-C32	2.40	1.54	1.50
9	D	501	GDP	PA-O2A	-2.37	1.44	1.55
9	D	501	GDP	C4-N3	-2.33	1.28	1.34
11	D	502	HOS	O1-C1	-2.32	1.33	1.39
9	D	501	GDP	O4'-C4'	-2.26	1.40	1.45
11	B	507	HOS	C1-C12	-2.25	1.37	1.40
9	D	501	GDP	PB-O2B	-2.24	1.46	1.54
11	B	507	HOS	O8-C18	-2.22	1.19	1.23
11	D	502	HOS	C3-N1	-2.21	1.42	1.45
5	C	501	GTP	C2-N3	2.15	1.38	1.33
12	G	401	ACP	PB-O1B	-2.15	1.46	1.51
5	C	501	GTP	PB-O3A	2.14	1.61	1.59
5	C	501	GTP	PB-O3B	2.08	1.61	1.59
11	B	507	HOS	O2-C4	-2.06	1.19	1.23
9	D	501	GDP	C2'-C1'	-2.05	1.47	1.53
9	D	501	GDP	C2-N1	-2.05	1.32	1.37
5	A	501	GTP	PB-O3B	2.02	1.61	1.59
9	D	501	GDP	O4'-C1'	-2.01	1.37	1.42

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	502	HOS	C17-C18-N5	11.15	132.97	115.82
11	D	502	HOS	C31-C15-C16	-9.16	95.35	109.98
11	D	502	HOS	O8-C18-C17	-9.13	108.66	120.87
12	G	401	ACP	C5-C4-N3	-5.66	118.92	126.72
10	B	505	MES	C5-N4-C3	5.60	120.91	108.84
9	B	501	GDP	C5-C4-N3	-5.58	119.51	128.39
11	B	507	HOS	C14-C3-N1	-5.42	100.83	107.40
11	D	502	HOS	O10-C36-C19	5.29	125.68	114.27
12	G	401	ACP	PB-O3A-PA	-5.20	115.39	132.37
9	B	501	GDP	C2-N3-C4	5.11	121.11	112.30
12	G	401	ACP	N3-C4-N9	4.81	135.35	127.17
5	A	501	GTP	C5-C4-N3	-4.79	120.77	128.39
11	D	502	HOS	C20-C19-C36	-4.74	107.91	119.93
9	D	501	GDP	C5-C4-N3	-4.64	121.00	128.39
5	C	501	GTP	C2-N3-C4	4.45	119.97	112.30
5	A	501	GTP	C2-N3-C4	4.44	119.95	112.30
5	C	501	GTP	C5-C4-N3	-4.34	121.48	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	504	MES	O1S-S-C8	-4.27	100.27	106.73
9	B	501	GDP	N9-C4-N3	4.07	134.08	125.95
9	D	501	GDP	C6-C5-N7	4.07	137.69	130.29
12	G	401	ACP	N3-C2-N1	-3.88	122.70	128.58
11	D	502	HOS	O7-C16-C15	-3.86	115.48	120.96
9	B	501	GDP	C6-C5-N7	3.78	137.17	130.29
9	D	501	GDP	C4-C5-N7	-3.77	104.70	110.67
12	G	401	ACP	C2-N3-C4	3.75	120.98	111.83
11	D	502	HOS	C36-C19-N5	3.68	122.89	115.47
12	G	401	ACP	C4-N9-C8	3.54	109.45	105.74
9	D	501	GDP	O3B-PB-O2B	3.48	120.86	107.80
10	B	505	MES	C7-N4-C3	3.44	120.39	111.24
5	C	501	GTP	O2A-PA-O3A	3.36	116.35	107.27
11	D	502	HOS	O9-C36-C19	-3.32	114.28	121.01
10	B	505	MES	O1S-S-C8	3.31	111.73	106.73
9	D	501	GDP	C2-N3-C4	3.30	117.98	112.30
12	G	401	ACP	C4-C5-N7	-3.27	106.84	110.58
11	B	507	HOS	C10-C11-CL1	3.17	123.64	118.45
11	D	502	HOS	C19-C20-C21	3.16	133.08	123.97
5	A	501	GTP	N9-C8-N7	-3.12	107.62	113.40
5	A	501	GTP	C2-N1-C6	-3.04	119.59	125.11
5	C	501	GTP	N9-C8-N7	-3.02	107.80	113.40
9	D	501	GDP	O2'-C2'-C1'	-2.99	99.80	110.10
11	B	507	HOS	C24-C2-C22	-2.97	106.08	111.42
9	D	501	GDP	N2-C2-N3	-2.94	113.94	119.67
5	C	501	GTP	O3'-C3'-C4'	-2.92	102.69	111.08
9	D	501	GDP	O2B-PB-O3A	-2.86	95.03	104.64
11	B	507	HOS	C8-C7-C6	-2.80	103.96	112.87
12	G	401	ACP	C5-N7-C8	2.77	107.81	103.45
5	A	501	GTP	N9-C4-N3	2.77	131.49	125.95
9	D	501	GDP	O4'-C1'-N9	-2.71	102.22	108.36
10	B	505	MES	O2S-S-C8	2.70	110.81	106.73
5	A	501	GTP	C8-N7-C5	2.69	109.06	104.26
11	B	507	HOS	C12-C11-CL1	-2.68	115.50	118.81
5	C	501	GTP	N9-C4-N3	2.67	131.30	125.95
5	C	501	GTP	C2-N1-C6	-2.66	120.28	125.11
12	G	401	ACP	N9-C8-N7	-2.65	110.17	113.94
9	B	501	GDP	C4-C5-N7	-2.60	106.55	110.67
5	A	501	GTP	O2B-PB-O3A	2.59	114.26	107.27
11	D	502	HOS	O8-C18-N5	-2.58	118.26	122.88
5	A	501	GTP	C5-C6-N1	2.57	119.79	113.25
11	D	502	HOS	C29-C30-C31	-2.56	109.28	112.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	501	GTP	C5-C6-N1	2.56	119.76	113.25
11	B	507	HOS	C36-C19-N5	2.56	120.62	115.47
9	B	501	GDP	O6-C6-C5	-2.51	119.90	126.53
11	B	507	HOS	O10-C36-C19	2.45	119.54	114.27
11	B	507	HOS	O6-C14-C3	2.43	123.68	119.91
10	B	505	MES	C6-C5-N4	-2.42	106.44	110.12
11	D	502	HOS	O7-C16-N4	-2.38	118.70	122.61
12	G	401	ACP	C2-N1-C6	2.33	122.56	118.73
11	B	507	HOS	C4-C5-N2	-2.32	101.44	108.50
11	B	507	HOS	O11-C21-C20	2.30	120.24	113.40
5	C	501	GTP	C8-N7-C5	2.30	108.36	104.26
11	B	507	HOS	C13-C9-C8	2.29	123.41	119.55
5	A	501	GTP	O6-C6-C5	-2.24	120.63	126.53
11	B	507	HOS	O1-C1-C13	2.23	128.53	122.77
9	D	501	GDP	O2A-PA-O5'	2.21	117.57	107.57
12	G	401	ACP	O2B-PB-C3B	2.20	115.82	106.73
10	B	504	MES	O2S-S-C8	-2.18	103.43	106.73
11	D	502	HOS	C19-N5-C18	2.16	134.24	125.85
9	B	501	GDP	C5-C6-N1	2.12	118.65	113.25
5	C	501	GTP	O6-C6-C5	-2.10	120.98	126.53
11	D	502	HOS	C13-C9-C8	2.08	123.05	119.55
11	D	502	HOS	O12-C21-C20	-2.07	117.68	124.02
9	D	501	GDP	C5-C4-N9	2.01	109.26	105.66
11	B	507	HOS	O8-C18-C17	2.00	123.55	120.87

There are no chirality outliers.

All (77) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
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	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	C7-C8-S-O2S
10	B	505	MES	C8-C7-N4-C3

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Mol	Chain	Res	Type	Atoms
11	B	507	HOS	C3-C2-C22-C23
11	B	507	HOS	N4-C17-C18-O8
11	B	507	HOS	N4-C17-C18-N5
11	B	507	HOS	C35-C32-C33-C34
11	B	507	HOS	C36-C19-N5-C18
11	B	507	HOS	N5-C19-C36-O10
11	B	507	HOS	C20-C19-C36-O9
11	B	507	HOS	C20-C19-C36-O10
11	B	507	HOS	C19-C20-C21-O12
11	D	502	HOS	N6-C7-C8-C9
11	D	502	HOS	C6-C7-C8-C9
11	D	502	HOS	N6-C7-C8-O4
11	D	502	HOS	C6-C7-C8-O4
11	D	502	HOS	O2-C4-C5-C25
11	D	502	HOS	N1-C4-C5-C25
11	D	502	HOS	N3-C15-C16-O7
11	D	502	HOS	C18-C17-N4-C16
11	D	502	HOS	N5-C19-C36-O9
11	D	502	HOS	N5-C19-C36-O10
12	G	401	ACP	C5'-O5'-PA-O1A
12	G	401	ACP	C5'-O5'-PA-O2A
12	G	401	ACP	C5'-O5'-PA-O3A
10	B	504	MES	C7-C8-S-O3S
11	D	502	HOS	N1-C4-C5-N2
11	B	507	HOS	C19-C20-C21-O11
11	D	502	HOS	C19-C20-C21-O11
11	D	502	HOS	C19-C20-C21-O12
11	D	502	HOS	N3-C15-C16-N4
11	B	507	HOS	N5-C19-C36-O9
11	B	507	HOS	C20-C19-N5-C18
11	D	502	HOS	C20-C19-N5-C18
11	D	502	HOS	C35-C32-C33-C34
10	B	504	MES	C7-C8-S-O1S
5	A	501	GTP	PB-O3B-PG-O1G
11	D	502	HOS	C3-C2-C22-C23
11	D	502	HOS	C20-C19-C36-O9
11	D	502	HOS	C20-C19-C36-O10
11	B	507	HOS	C8-C7-N6-C28
11	D	502	HOS	C4-C5-N2-C6
11	D	502	HOS	C17-C32-C33-C34
9	B	501	GDP	C5'-O5'-PA-O2A
11	B	507	HOS	O1-C2-C22-C23

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Mol	Chain	Res	Type	Atoms
11	D	502	HOS	O1-C2-C22-C23
12	G	401	ACP	PG-C3B-PB-O2B
11	B	507	HOS	C6-C7-N6-C28
5	C	501	GTP	PB-O3B-PG-O1G
11	B	507	HOS	C24-C2-C22-C23
12	G	401	ACP	PB-O3A-PA-O2A
12	G	401	ACP	O4'-C4'-C5'-O5'
5	A	501	GTP	PB-O3B-PG-O2G
5	A	501	GTP	PB-O3B-PG-O3G
5	C	501	GTP	PB-O3B-PG-O2G
5	C	501	GTP	PB-O3B-PG-O3G
11	B	507	HOS	C12-C1-O1-C2
9	D	501	GDP	C4'-C5'-O5'-PA
5	A	501	GTP	PB-O3A-PA-O2A
5	C	501	GTP	PB-O3A-PA-O2A
9	B	501	GDP	PB-O3A-PA-O2A
11	D	502	HOS	C24-C2-C22-C23
11	D	502	HOS	O2-C4-C5-N2
11	D	502	HOS	C8-C7-N6-C28
11	D	502	HOS	C32-C17-N4-C16
11	D	502	HOS	C36-C19-N5-C18
9	B	501	GDP	PB-O3A-PA-O1A

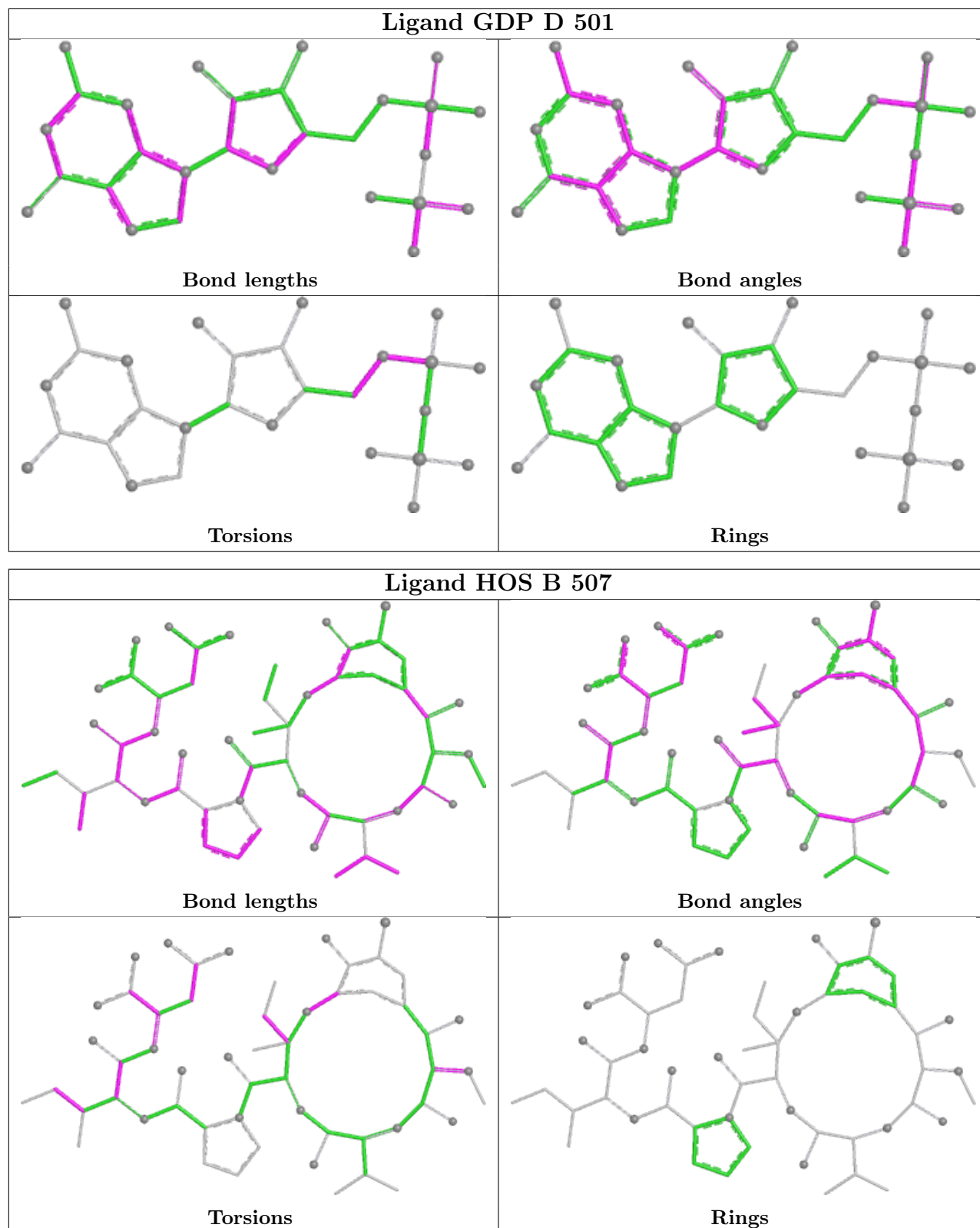
There are no ring outliers.

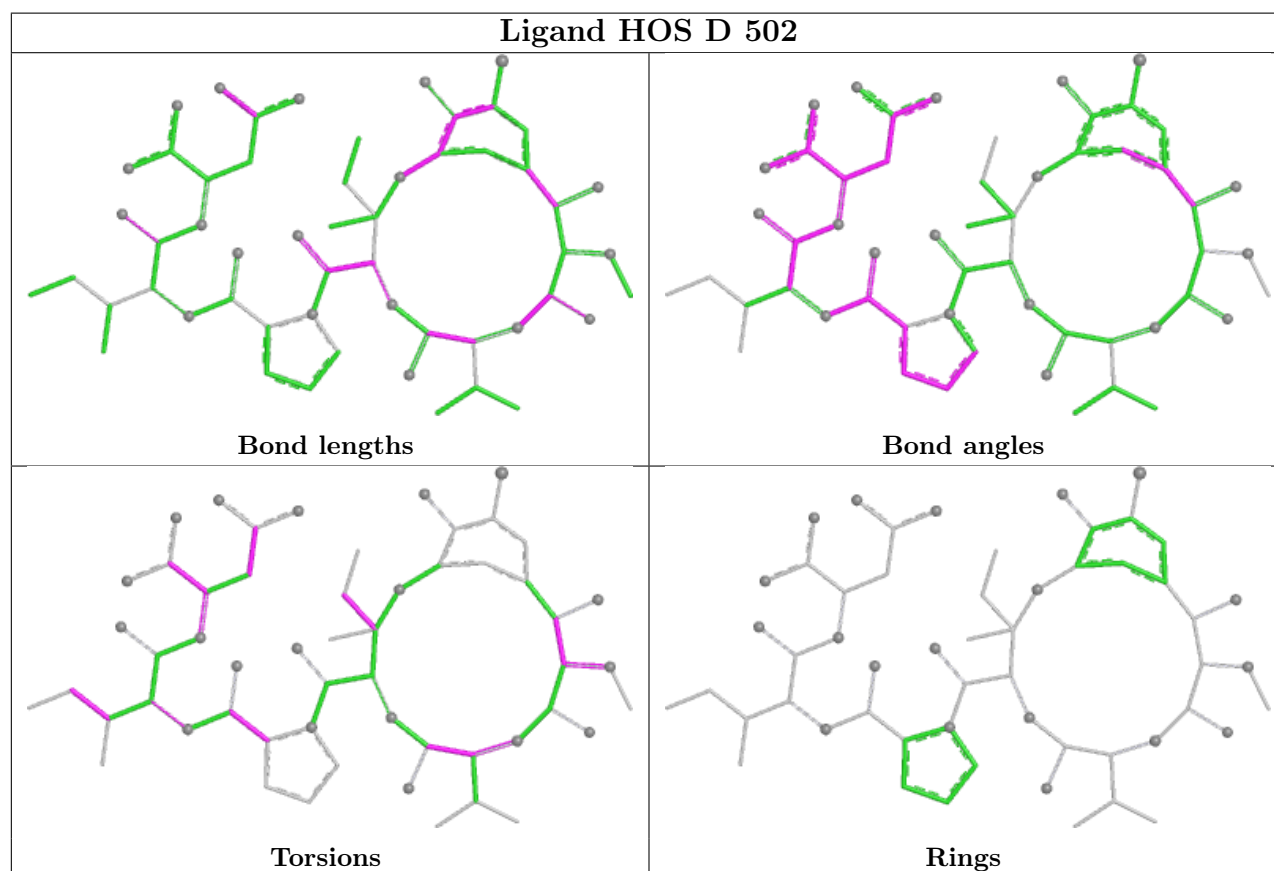
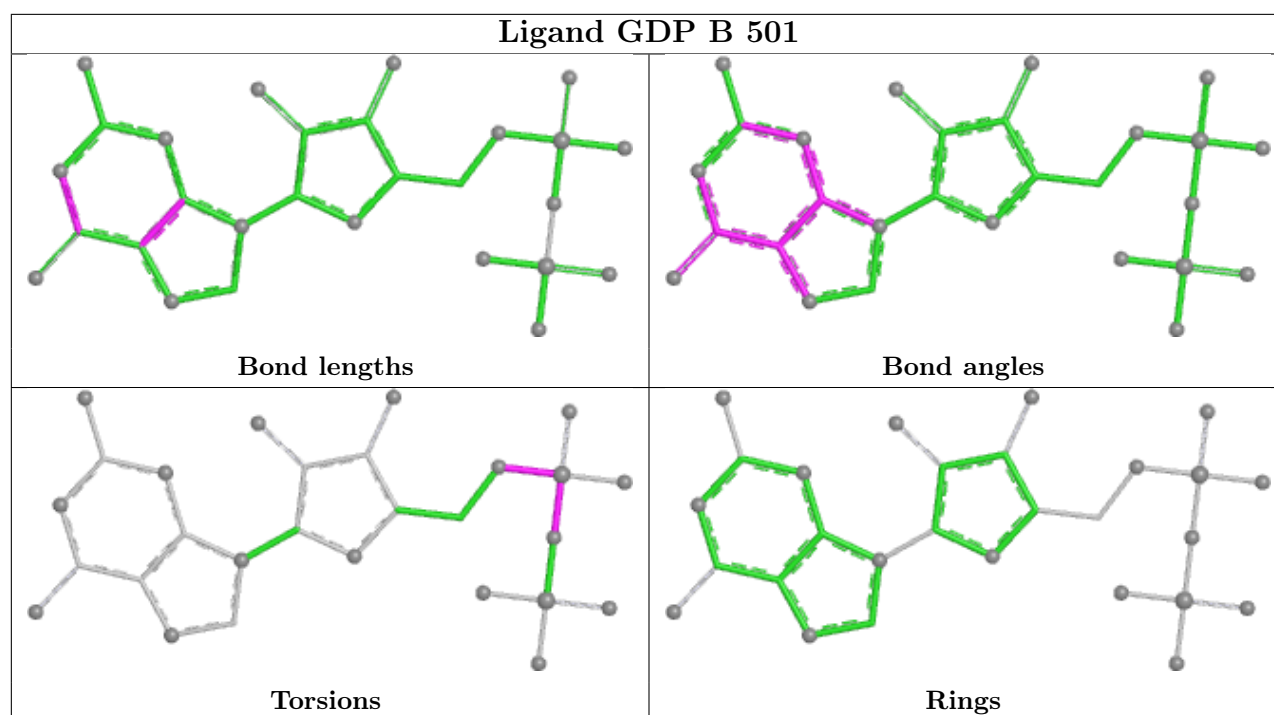
7 monomers are involved in 37 short contacts:

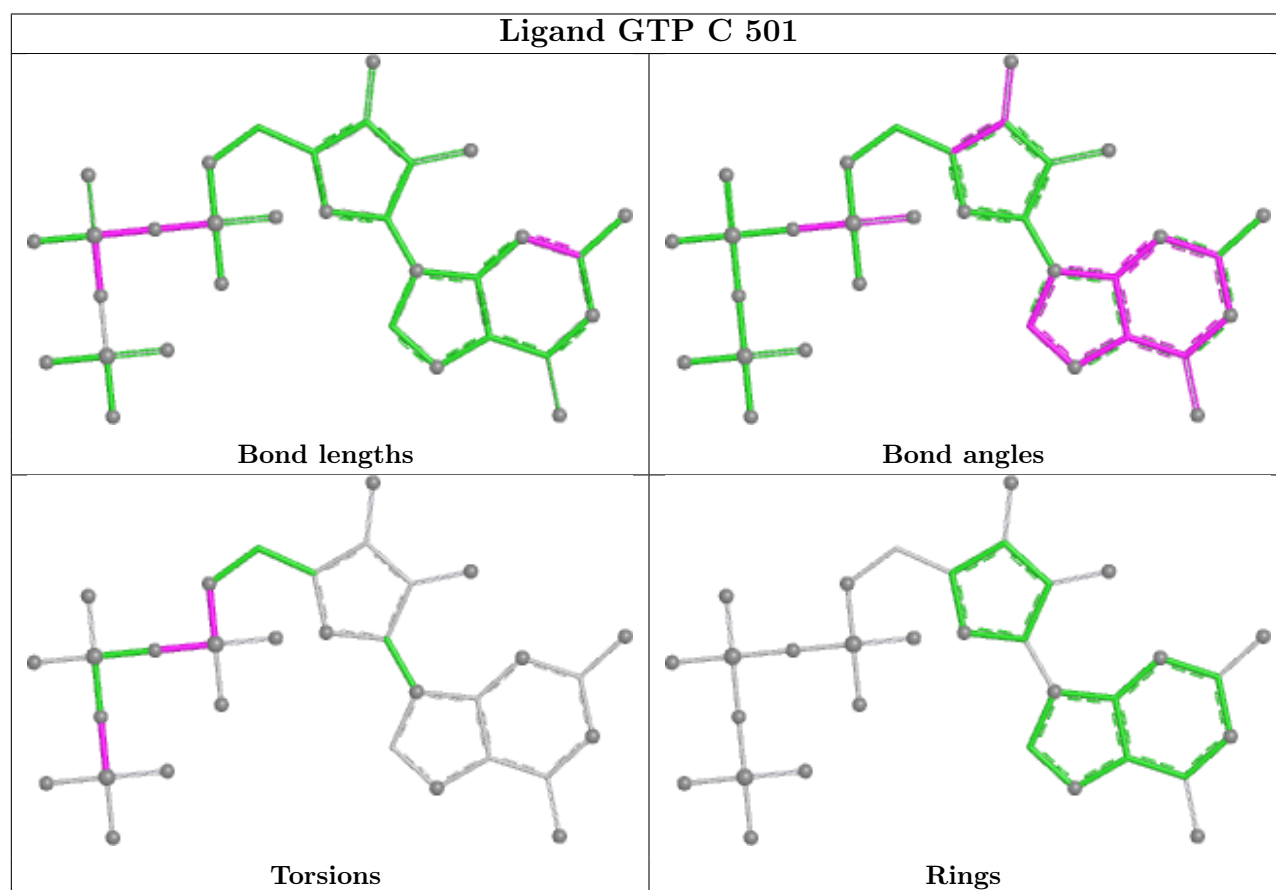
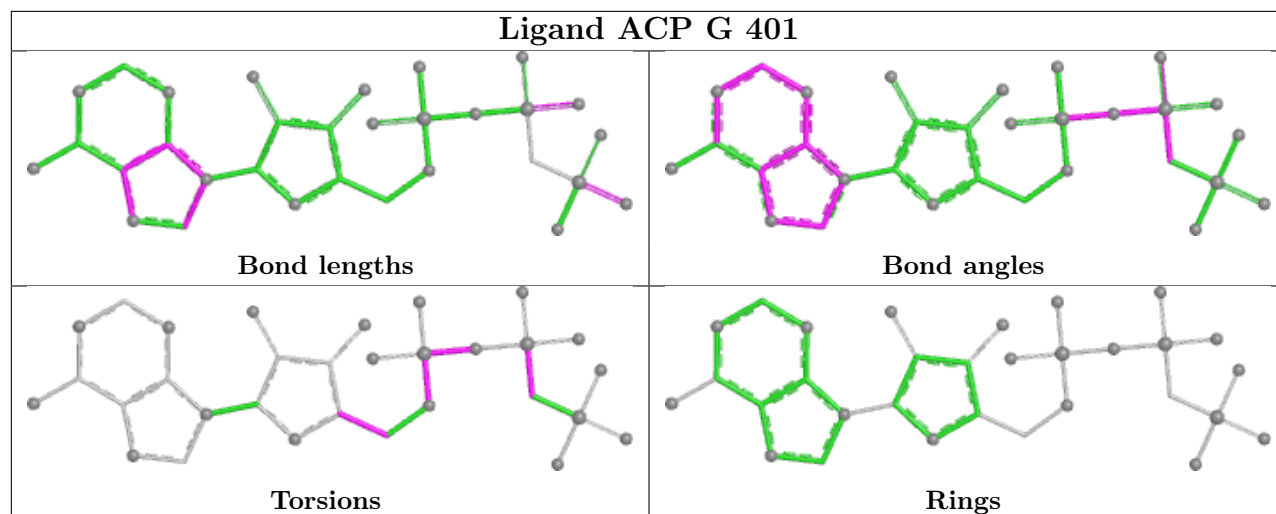
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	D	501	GDP	9	0
9	B	501	GDP	1	0
11	D	502	HOS	12	0
12	G	401	ACP	6	0
5	C	501	GTP	1	0
5	A	501	GTP	1	0
10	B	504	MES	7	0

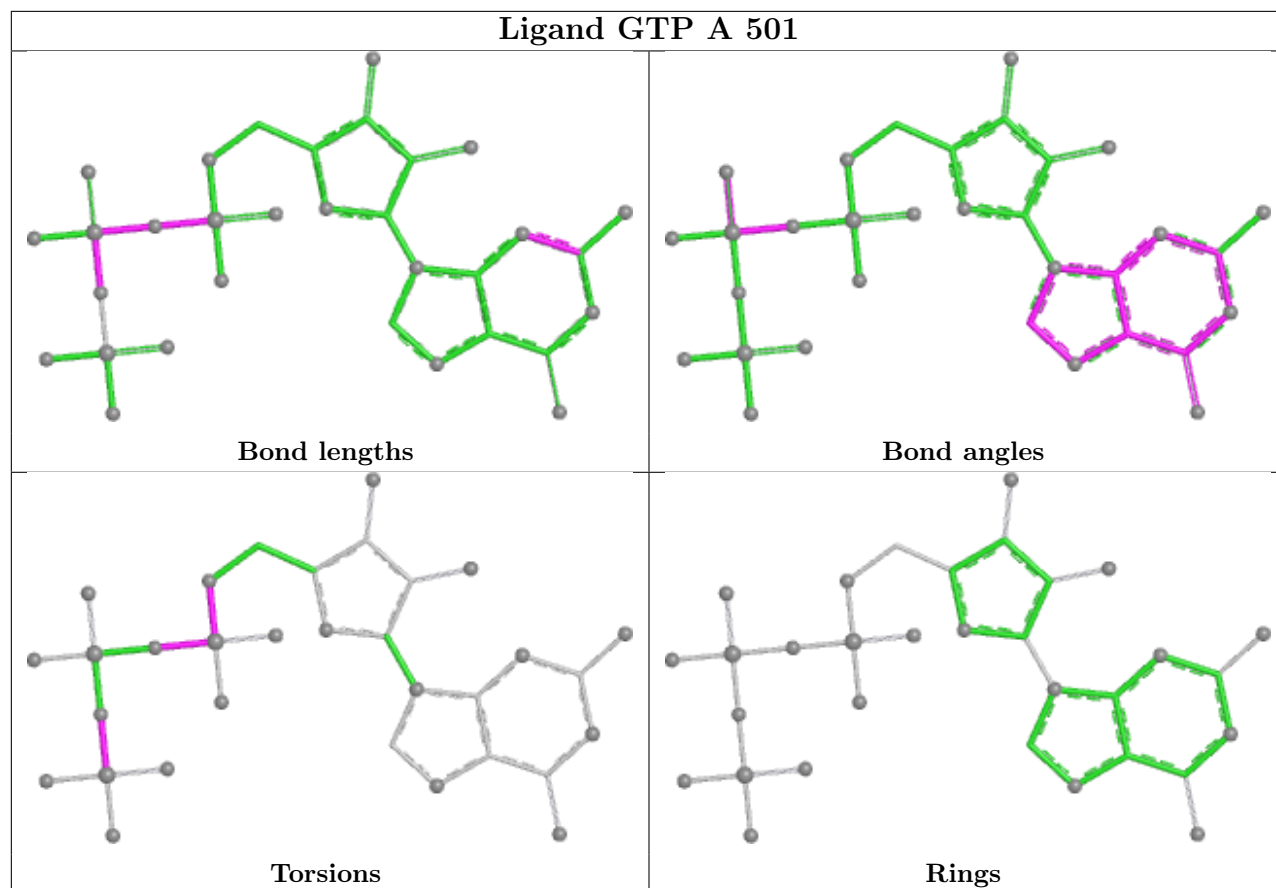
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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









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	437/451 (96%)	-0.28	2 (0%) 87 85	15, 39, 69, 92	5 (1%)
1	C	440/451 (97%)	-0.38	6 (1%) 73 70	18, 33, 60, 172	7 (1%)
2	B	428/445 (96%)	-0.39	6 (1%) 73 70	14, 33, 67, 111	5 (1%)
2	D	422/445 (94%)	0.55	36 (8%) 16 14	28, 63, 99, 136	7 (1%)
3	E	122/143 (85%)	0.41	8 (6%) 24 21	23, 56, 97, 129	4 (3%)
4	G	338/384 (88%)	0.65	51 (15%) 5 4	27, 63, 130, 158	0
All	All	2187/2319 (94%)	0.02	109 (4%) 34 30	14, 44, 99, 172	28 (1%)

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	315	CYS	9.8
1	C	340	SER	5.6
2	B	1	MET	5.3
4	G	362	ALA	5.0
4	G	237	THR	4.9
2	D	82	PRO	4.5
4	G	243	HIS	4.4
2	D	404	PHE	4.4
2	D	286	LEU	4.3
4	G	249	TYR	4.1
2	D	57	THR	4.0
2	D	221	THR	3.7
4	G	245	ILE	3.7
4	G	161	LEU	3.5
4	G	166	ALA	3.5
4	G	173	ILE	3.4
2	D	50	ASN	3.3
2	D	272	PHE	3.3
2	D	56	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
4	G	244	CYS	3.1
4	G	90	SER	3.1
2	D	369	ARG	3.1
2	D	83	PHE	3.0
2	D	86	ILE	3.0
4	G	160	ILE	3.0
1	C	163	LYS	3.0
4	G	231	ALA	2.9
2	D	441	ASP	2.9
1	A	262	TYR	2.8
2	D	220	THR	2.8
4	G	227	PRO	2.8
4	G	238	CYS	2.8
4	G	254	GLY	2.7
3	E	138	GLU	2.7
4	G	253	TYR	2.7
4	G	133	ALA	2.7
2	D	416	MET	2.7
2	B	282	GLN	2.7
4	G	159	GLY	2.6
2	D	214	PHE	2.6
3	E	139	LEU	2.6
1	C	305	CYS	2.6
2	B	276	THR	2.6
4	G	240	LEU	2.6
4	G	251	LYS	2.6
2	D	75	MET	2.6
2	D	295	MET	2.6
4	G	130	VAL	2.6
4	G	135	TYR	2.6
2	D	98	GLY	2.5
4	G	131	PHE	2.5
2	D	99	ALA	2.5
2	D	407	TRP	2.5
4	G	256	TYR	2.4
4	G	170	LEU	2.4
4	G	73	ARG	2.4
3	E	135	LYS	2.4
1	C	283	HIS	2.4
3	E	80	ARG	2.4
4	G	179	VAL	2.4
4	G	142	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
2	D	94	PHE	2.4
2	B	57	THR	2.3
4	G	138	ARG	2.3
1	C	357	TYR	2.3
3	E	142	GLU	2.3
4	G	379	HIS	2.3
4	G	233	PHE	2.3
3	E	12[A]	ASN	2.3
2	D	400	ARG	2.3
2	D	73	GLY	2.3
3	E	28	SER	2.3
2	D	406	HIS	2.3
1	A	282	TYR	2.3
4	G	102	PRO	2.3
4	G	372	THR	2.3
2	D	79	ARG	2.3
4	G	101	TYR	2.2
4	G	250	SER	2.2
2	D	275	LEU	2.2
2	D	177	VAL	2.2
2	D	37	HIS	2.2
4	G	252	ASN	2.2
4	G	151	SER	2.2
2	D	172	MET	2.1
2	D	291	LEU	2.1
4	G	186	LEU	2.1
3	E	7	GLU	2.1
4	G	164	SER	2.1
4	G	263	PHE	2.1
4	G	149	ALA	2.1
4	G	242	ASN	2.1
4	G	162	ILE	2.1
2	D	218	LYS	2.1
2	B	438	ALA	2.1
4	G	174	ASP	2.1
4	G	230	SER	2.1
4	G	132	LEU	2.1
4	G	184	LYS	2.1
4	G	380	HIS	2.1
4	G	172	PHE	2.0
2	B	56	ALA	2.0
2	D	209	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
2	D	30	ILE	2.0
2	D	33	THR	2.0
2	D	277	SER	2.0
2	D	88	ARG	2.0
4	G	248	GLU	2.0
4	G	148	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.

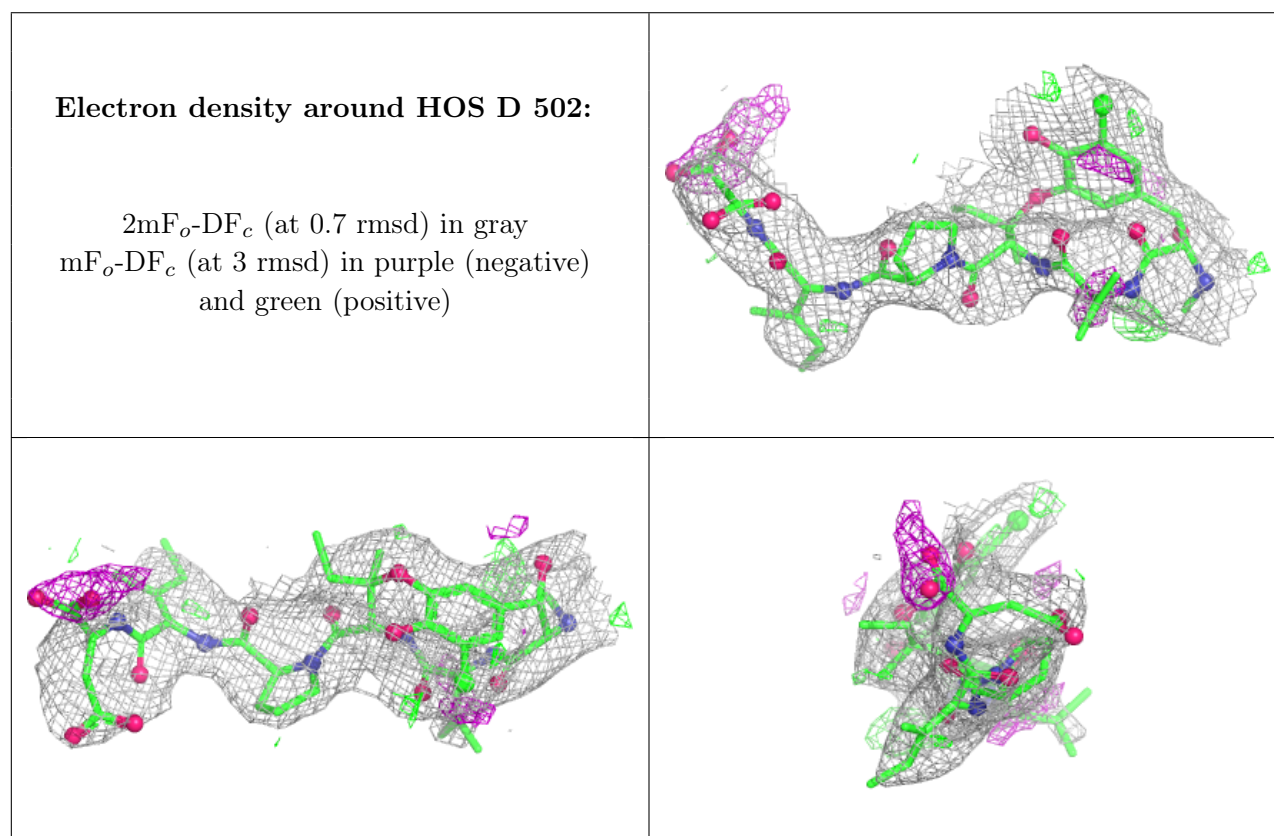
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
11	HOS	D	502	55/55	0.76	0.16	53,73,99,125	0
7	CA	B	503	1/1	0.79	0.13	74,74,74,74	0
12	ACP	G	401	31/31	0.79	0.12	68,95,122,124	0
7	CA	E	201	1/1	0.82	0.11	75,75,75,75	0
9	GDP	D	501	28/28	0.83	0.15	44,57,72,88	0
6	MG	A	502	1/1	0.86	0.08	32,32,32,32	0
6	MG	B	506	1/1	0.87	0.32	58,58,58,58	0
10	MES	B	504	12/12	0.87	0.14	32,57,71,81	0
6	MG	B	502	1/1	0.90	0.10	42,42,42,42	0
8	CL	A	504	1/1	0.94	0.07	60,60,60,60	0
10	MES	B	505	12/12	0.94	0.10	45,52,62,72	0
6	MG	C	502	1/1	0.95	0.07	33,33,33,33	0
11	HOS	B	507	55/55	0.95	0.09	20,32,71,82	0
5	GTP	A	501	32/32	0.98	0.05	21,27,34,35	0
9	GDP	B	501	28/28	0.98	0.05	14,22,28,36	0
7	CA	C	503	1/1	0.98	0.03	45,45,45,45	0
7	CA	A	503	1/1	0.98	0.04	64,64,64,64	0

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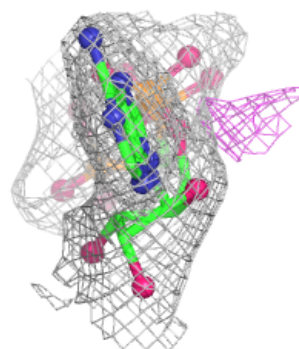
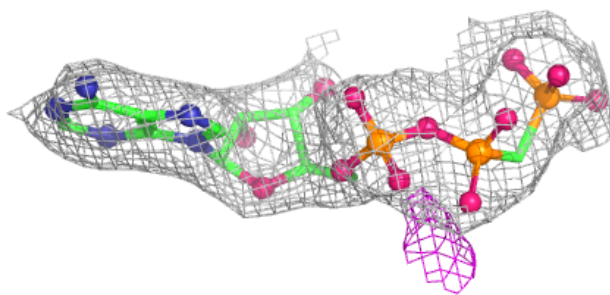
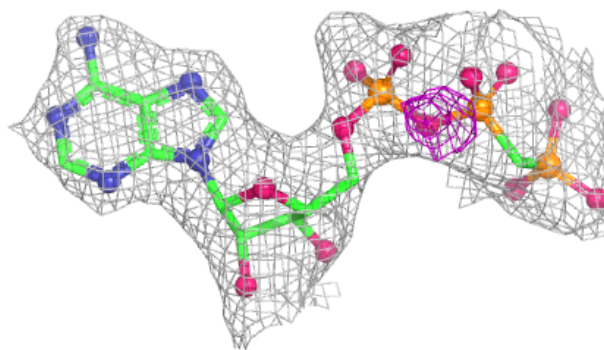
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	GTP	C	501	32/32	0.99	0.04	18,24,29,31	0

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.

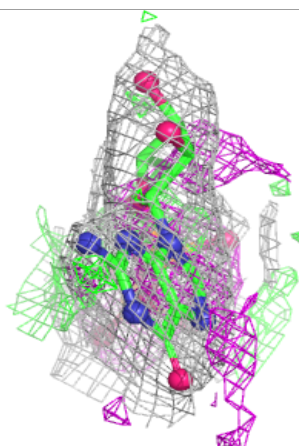
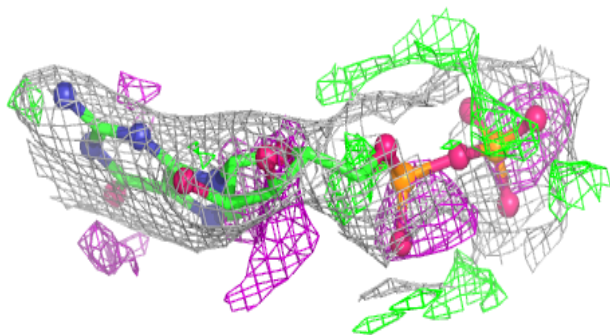
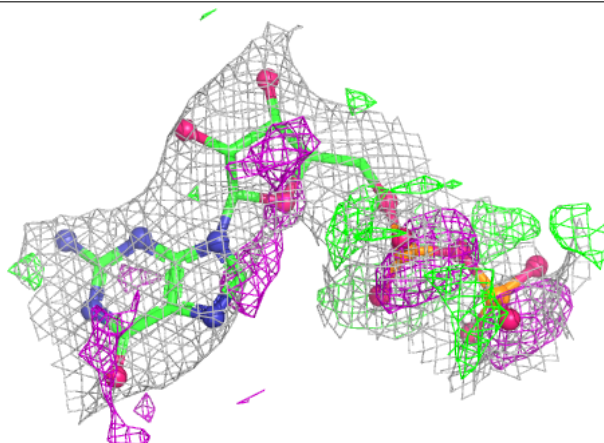


Electron density around ACP G 401:

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

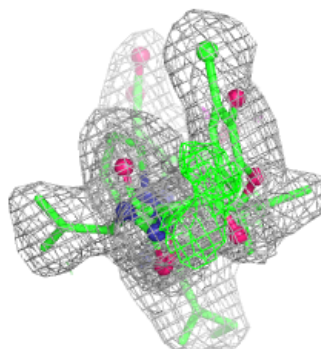
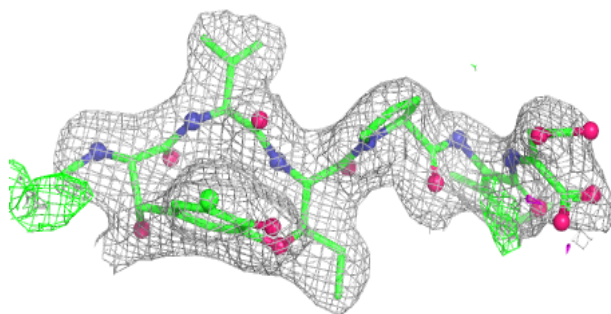
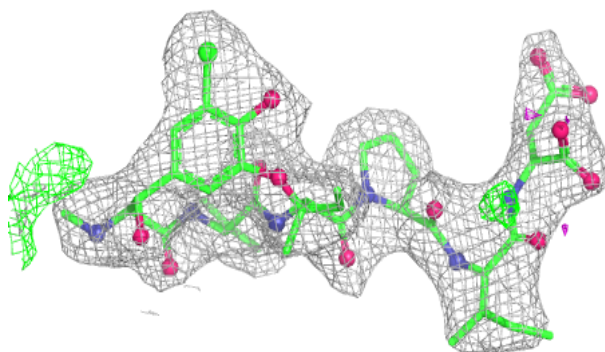
**Electron density around GDP D 501:**

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

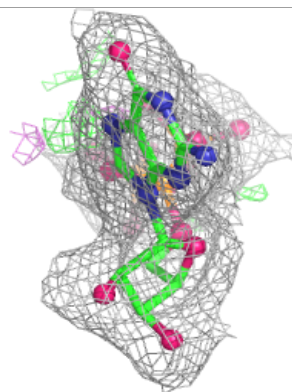
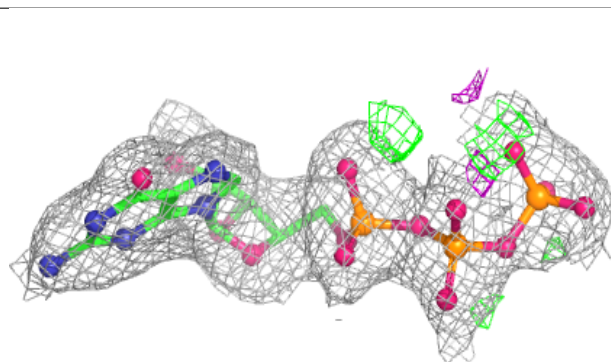
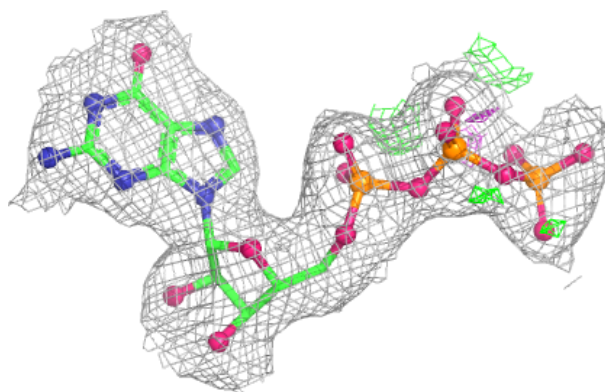


Electron density around HOS B 507:

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

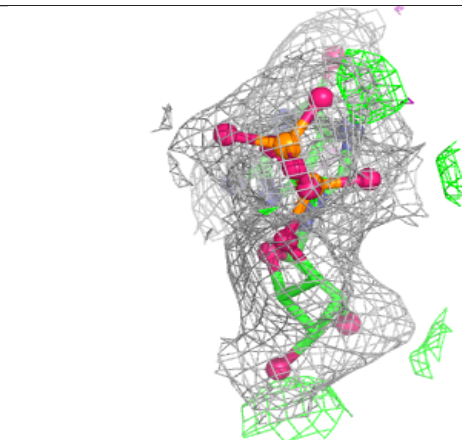
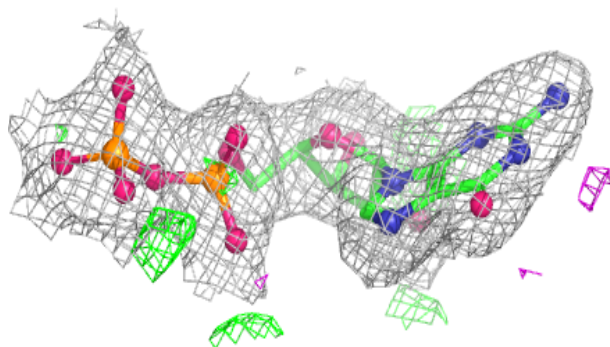
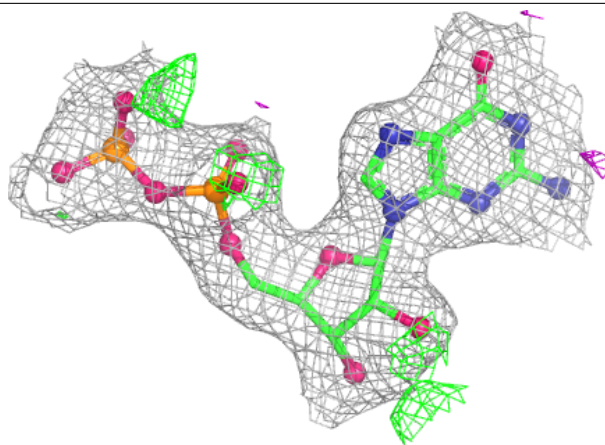
**Electron density around GTP A 501:**

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

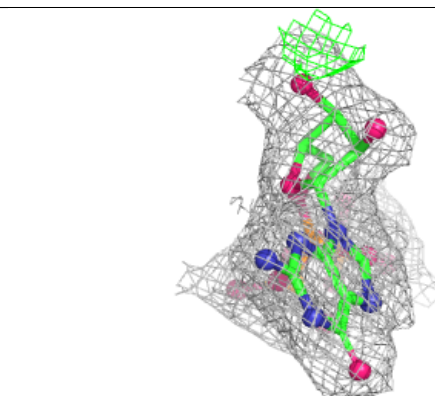
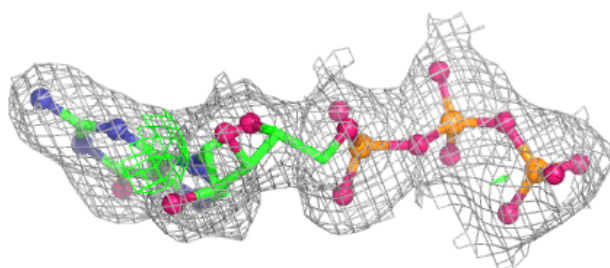
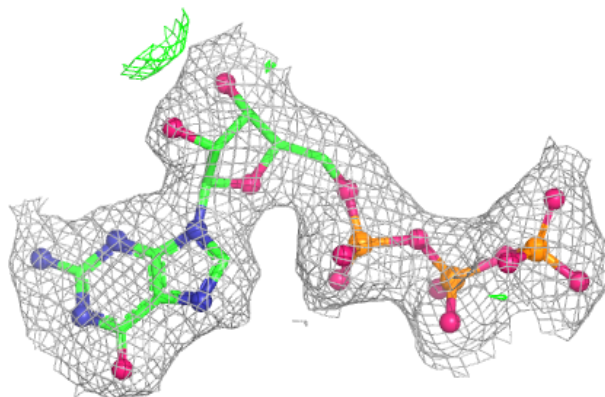


Electron density around GDP B 501:

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

**Electron density around GTP C 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.