



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2024 – 06:27 PM EST

PDB ID : 5S59  
Title : Tubulin-Z1324080698-complex  
Authors : Muehlethaler, T.; Gioia, D.; Prota, A.E.; Sharpe, M.E.; Cavalli, A.; Steinmetz, M.O.  
Deposited on : 2020-11-08  
Resolution : 2.60 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

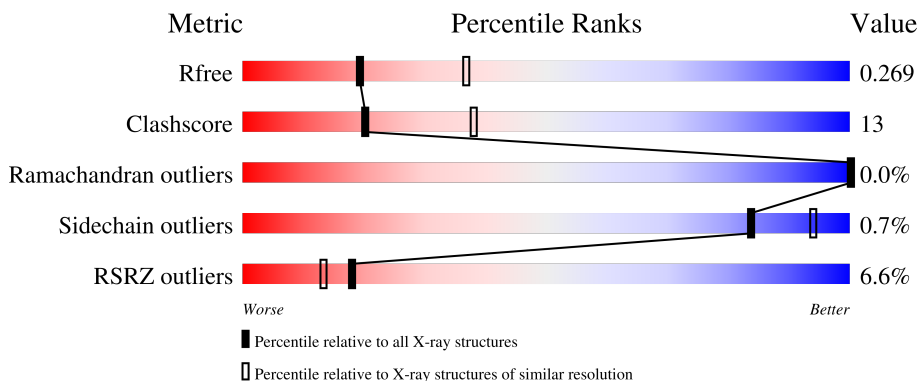
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

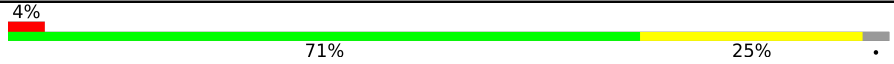
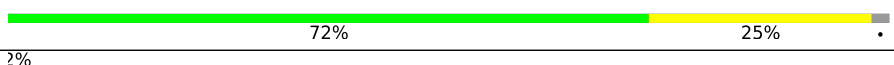
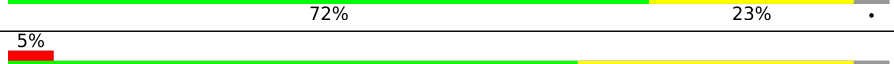
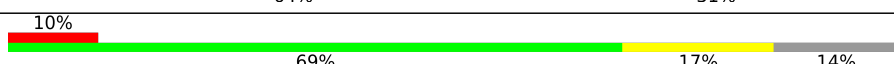

The reported resolution of this entry is 2.60 Å.

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.



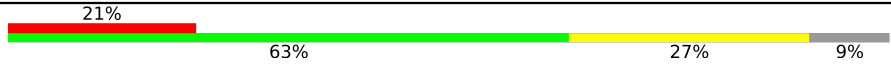
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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  $\geq 3$ , 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	 4% 71% 25% .
1	C	451	 72% 25% .
2	B	445	 2% 72% 23% .
2	D	445	 5% 64% 31% .
3	E	143	 10% 69% 17% 14%

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Mol	Chain	Length	Quality of chain										
4	F	384	 <p>A horizontal bar chart showing the quality distribution of chain F. The bar is divided into four segments: a red segment (21%), a green segment (63%), a yellow segment (27%), and a grey segment (9%).</p> <table border="1"><thead><tr><th>Quality Category</th><th>Percentage</th></tr></thead><tbody><tr><td>Red</td><td>21%</td></tr><tr><td>Green</td><td>63%</td></tr><tr><td>Yellow</td><td>27%</td></tr><tr><td>Grey</td><td>9%</td></tr></tbody></table>	Quality Category	Percentage	Red	21%	Green	63%	Yellow	27%	Grey	9%
Quality Category	Percentage												
Red	21%												
Green	63%												
Yellow	27%												
Grey	9%												

## 2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 17828 atoms, of which 24 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
			Total	C	N	O	S			
1	A	437	Total	C	N	O	S	0	0	0
			3416	2163	581	650	22			
1	C	440	Total	C	N	O	S	0	1	0
			3443	2178	585	657	23			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	425	Total	C	N	O	S	1	1	0
			3359	2109	577	646	27			
2	D	426	Total	C	N	O	S	5	0	0
			3343	2098	570	648	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
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
			Total	C	N	O	S			
4	F	349	Total	C	N	O	S	0	0	0
			2864	1836	492	522	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 (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
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 (three-letter code: MG) (formula: Mg).

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

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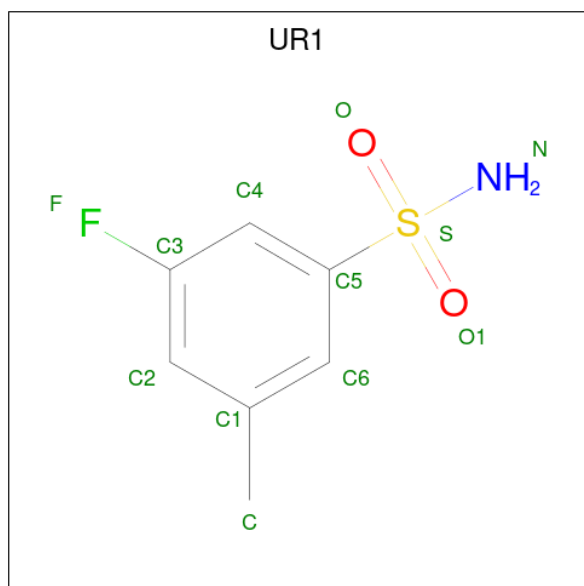
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

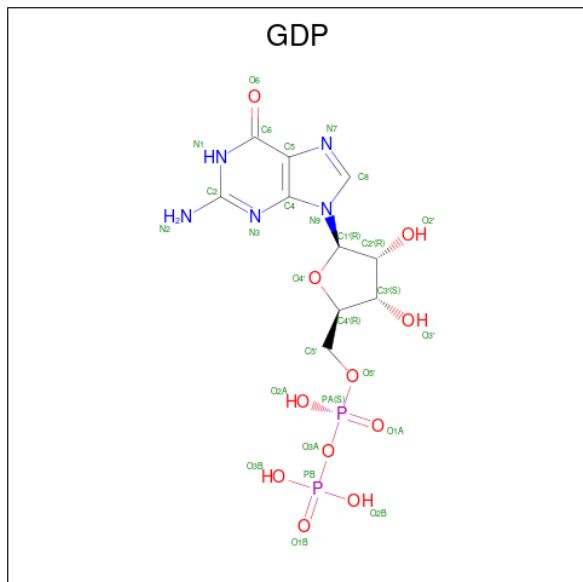
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		
7	E	1	Total	Ca	0	0
			1	1		

- Molecule 8 is 3-fluoro-5-methylbenzene-1-sulfonamide (three-letter code: UR1) (formula: C<sub>7</sub>H<sub>8</sub>FNO<sub>2</sub>S) (labeled as "Ligand of Interest" by depositor).



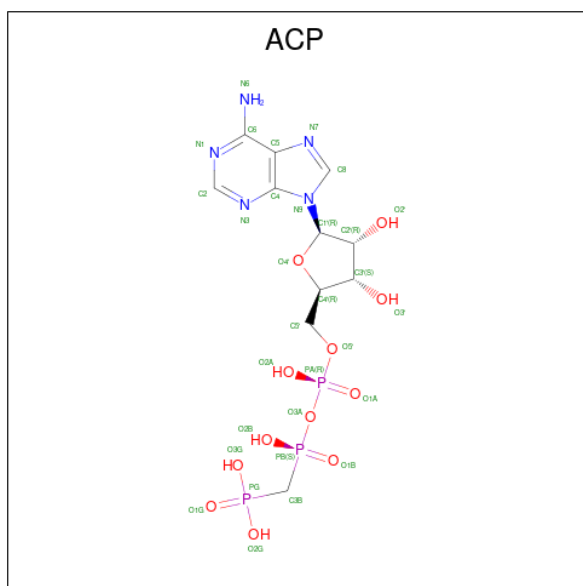
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	
8	A	1	Total	C	F	H	N	O	S	0	0
			20	7	1	8	1	2	1		
8	C	1	Total	C	F	H	N	O	S	0	0
			20	7	1	8	1	2	1		
8	D	1	Total	C	F	H	N	O	S	0	0
			20	7	1	8	1	2	1		

- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



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

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



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

- Molecule 12 is water.

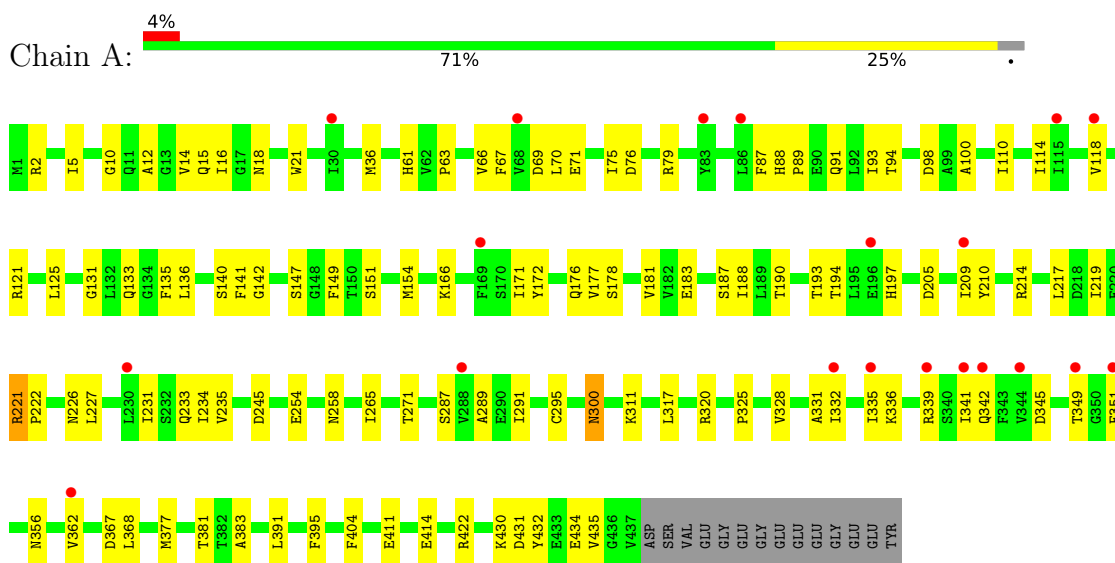
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	28	Total	O	0	0
			28	28		
12	B	38	Total	O	0	0
			38	38		
12	C	77	Total	O	0	0
			77	77		
12	D	9	Total	O	0	0
			9	9		
12	E	2	Total	O	0	0
			2	2		
12	F	3	Total	O	0	0
			3	3		



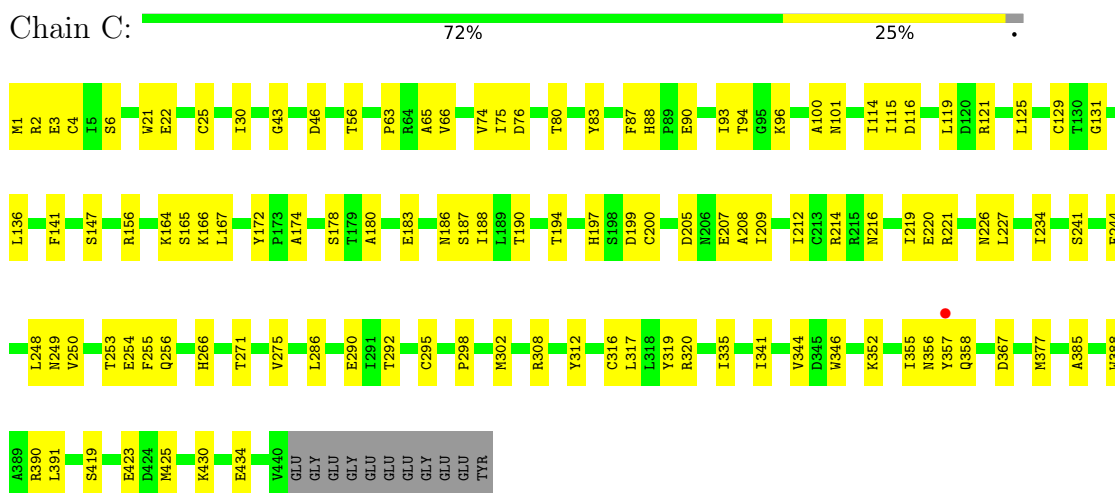
### 3 Residue-property plots [i](#)

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.

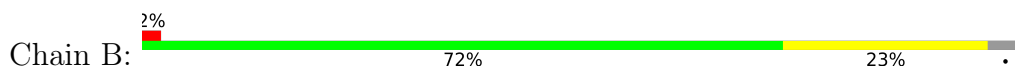
- Molecule 1: Tubulin alpha-1B chain



- Molecule 1: Tubulin alpha-1B chain

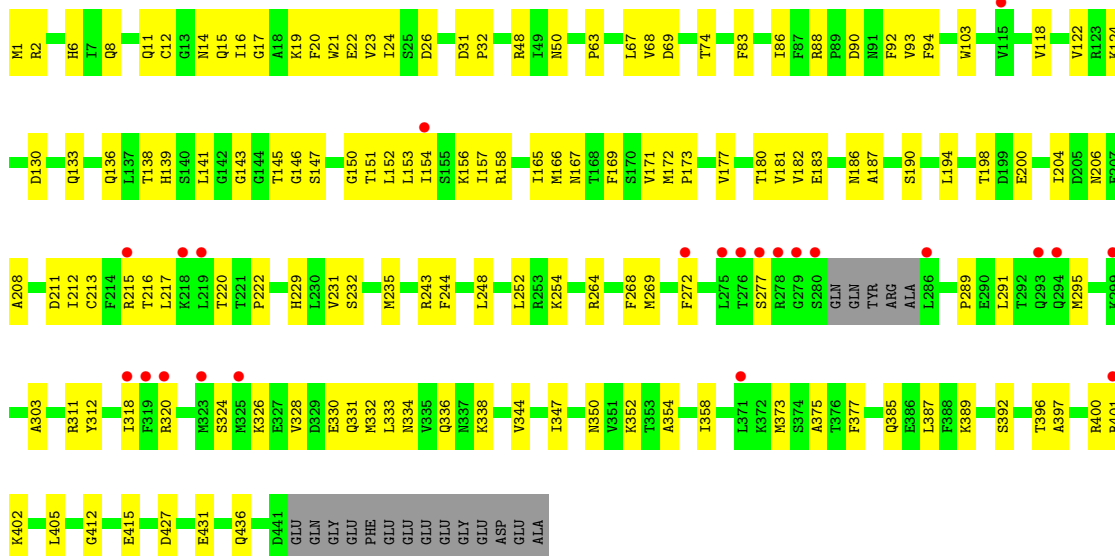


- Molecule 2: Tubulin beta-2B chain

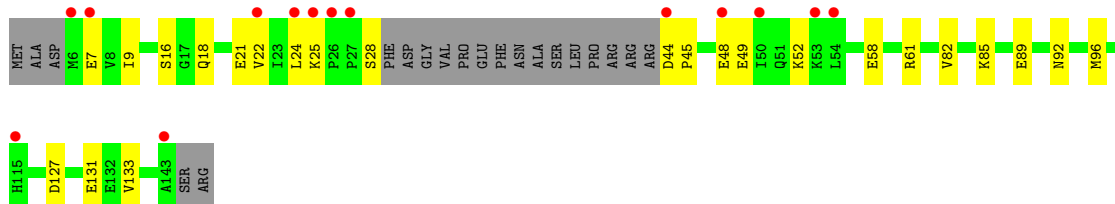




- Molecule 2: Tubulin beta-2B chain

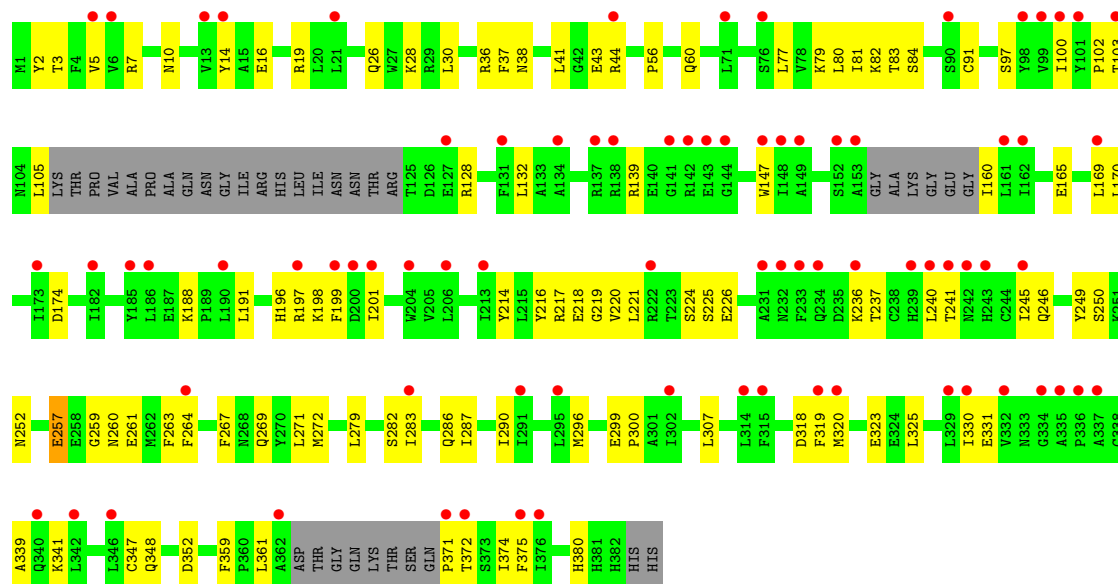


- Molecule 3: Stathmin-4



- 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, $\alpha$ , $\beta$ , $\gamma$	105.56Å 158.90Å 179.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.84 – 2.60 89.67 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (59.84-2.60) 99.3 (89.67-2.60)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.11 (at 2.62Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.220 , 0.268 0.220 , 0.269	Depositor DCC
$R_{free}$ test set	4548 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	76.6	Xtrriage
Anisotropy	0.434	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 60.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	17828	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	96.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GDP, CA, ACP, MES, GTP, UR1, MG

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	0.25	0/3494	0.42	0/4743
1	C	0.27	0/3521	0.42	0/4780
2	B	0.26	0/3433	0.41	0/4647
2	D	0.25	0/3416	0.41	0/4626
3	E	0.24	0/1022	0.35	0/1356
4	F	0.24	0/2931	0.39	0/3961
All	All	0.25	0/17817	0.41	0/24113

There are no bond length outliers.

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	3416	0	3330	94	0
1	C	3443	0	3352	78	0
2	B	3359	0	3235	78	0
2	D	3343	0	3222	101	0
3	E	1014	0	1029	22	0
4	F	2864	0	2828	87	0
5	A	32	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	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	12	8	0	0	0
8	C	12	8	0	0	0
8	D	12	8	0	0	0
9	B	28	0	12	0	0
9	D	28	0	12	2	0
10	B	12	0	12	1	0
11	F	31	0	14	3	0
12	A	28	0	0	4	0
12	B	38	0	0	1	0
12	C	77	0	0	2	0
12	D	9	0	0	2	0
12	E	2	0	0	0	0
12	F	3	0	0	0	0
All	All	17804	24	17070	435	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 13.

All (435) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:10:ASN:HB2	4:F:44:ARG:HH22	1.28	0.99
4:F:102:PRO:HG2	4:F:105:LEU:HD13	1.49	0.95
4:F:269:GLN:HA	4:F:272:MET:HE2	1.49	0.92
4:F:236:LYS:HB3	4:F:240:LEU:HD13	1.57	0.85
1:A:335:ILE:HG23	1:A:339:ARG:HG3	1.59	0.83
1:A:226:ASN:ND2	1:A:367:ASP:OD2	2.14	0.81
2:D:11:GLN:HA	2:D:74:THR:HG21	1.65	0.79
1:A:2:ARG:HB2	1:A:133:GLN:HE21	1.46	0.79
1:C:93:ILE:HG22	1:C:114:ILE:HD11	1.68	0.75
1:C:76:ASP:O	1:C:80:THR:HG22	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:PHE:HE1	3:E:24:LEU:HD11	1.53	0.73
2:D:136:GLN:HA	2:D:167:ASN:O	1.87	0.73
2:B:325:MET:HG3	2:B:355:VAL:HG21	1.71	0.73
1:A:210:TYR:CE1	1:A:222:PRO:HD2	2.25	0.71
1:C:178:SER:OG	2:D:352:LYS:NZ	2.23	0.71
1:A:381:THR:HG22	1:A:383:ALA:H	1.56	0.70
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.25	0.70
1:C:165:SER:HA	1:C:199:ASP:OD2	1.90	0.70
1:C:209:ILE:HG22	1:C:227:LEU:HD22	1.72	0.70
1:A:142:GLY:HA3	1:A:183:GLU:HG2	1.74	0.70
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.32	0.70
1:A:100:ALA:HA	2:B:254:LYS:HG3	1.74	0.69
1:A:345:ASP:HB3	3:E:28:SER:HB2	1.74	0.69
4:F:246:GLN:O	4:F:250:SER:HB3	1.92	0.69
4:F:269:GLN:HA	4:F:272:MET:CE	2.23	0.69
1:A:142:GLY:CA	1:A:183:GLU:HG2	2.24	0.68
4:F:188:LYS:HD3	4:F:323:GLU:OE2	1.93	0.68
2:D:180:THR:O	2:D:183:GLU:HG3	1.94	0.68
4:F:139:ARG:NH2	4:F:165:GLU:OE1	2.26	0.68
1:A:414:GLU:HB3	12:A:619:HOH:O	1.93	0.68
2:D:217:LEU:HA	2:D:277:SER:HB3	1.76	0.68
4:F:201:ILE:HG12	4:F:221:LEU:HG	1.76	0.68
3:E:48:GLU:HG2	3:E:52:LYS:HE3	1.76	0.67
2:B:286:LEU:HD12	2:B:290:GLU:OE1	1.95	0.66
4:F:128:ARG:NH2	4:F:174:ASP:OD1	2.28	0.66
2:B:163:ASP:O	2:B:253[B]:ARG:NH1	2.29	0.65
1:A:166:LYS:HE2	1:A:197:HIS:O	1.97	0.65
2:B:88:ARG:NH1	2:B:90:ASP:OD2	2.30	0.65
2:D:334:ASN:HD21	2:D:338:LYS:HE3	1.62	0.64
4:F:16:GLU:OE2	4:F:19:ARG:NH2	2.28	0.64
2:B:141:LEU:HD12	2:B:172:MET:SD	2.38	0.64
1:C:180:ALA:O	1:C:183:GLU:HG3	1.97	0.64
2:B:67:LEU:HD22	2:B:92:PHE:CE2	2.33	0.64
1:C:93:ILE:HD11	1:C:121:ARG:HG3	1.80	0.64
2:D:213:CYS:HA	2:D:217:LEU:HB2	1.78	0.64
2:B:69:ASP:O	2:B:94:PHE:HA	1.99	0.63
4:F:331:GLU:OE2	11:F:401:ACP:O3G	2.14	0.63
2:D:169:PHE:CD2	2:D:235:MET:HG2	2.33	0.63
2:B:46:LEU:HA	2:B:49:ILE:HB	1.81	0.63
2:D:141:LEU:HA	2:D:147:SER:HB3	1.80	0.63
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:236:LYS:HB3	4:F:240:LEU:CD1	2.29	0.63
1:C:226:ASN:ND2	1:C:367:ASP:OD2	2.33	0.62
1:C:312:TYR:CD1	1:C:341:ILE:HG23	2.34	0.62
1:C:430:LYS:HE2	1:C:434:GLU:OE2	1.99	0.62
2:D:152:LEU:O	2:D:156:LYS:HG2	2.00	0.62
1:A:328:VAL:O	1:A:332:ILE:HG13	2.00	0.62
2:B:244:PHE:CD1	2:B:358:ILE:HD12	2.35	0.62
4:F:371:PRO:HA	4:F:372:THR:O	1.99	0.62
1:C:320:ARG:HA	1:C:356:ASN:O	1.99	0.61
2:D:145:THR:HB	9:D:501:GDP:O2B	2.00	0.61
2:D:147:SER:HB2	2:D:190:SER:OG	2.00	0.61
2:D:83:PHE:O	2:D:86:ILE:HG22	2.01	0.61
2:D:264:ARG:NE	2:D:431:GLU:OE2	2.34	0.61
2:D:392:SER:O	2:D:396:THR:HG22	2.01	0.61
2:B:23:VAL:HG21	2:B:232:SER:HB3	1.83	0.61
1:C:209:ILE:HD11	1:C:302:MET:CE	2.31	0.60
2:B:231:VAL:O	2:B:235:MET:HG3	2.02	0.60
2:D:311:ARG:NH1	2:D:436:GLN:O	2.34	0.60
1:C:174:ALA:HB1	1:C:207:GLU:HB2	1.83	0.60
2:D:181:VAL:HG13	2:D:182:VAL:HG13	1.84	0.60
2:D:21:TRP:CZ3	2:D:63:PRO:HB3	2.37	0.59
4:F:14:TYR:HB3	4:F:41:LEU:HD13	1.84	0.59
1:A:15:GLN:NE2	5:A:501:GTP:O6	2.35	0.59
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.20	0.59
3:E:85:LYS:O	3:E:89:GLU:HG3	2.02	0.59
2:B:40:SER:OG	2:B:42:LEU:HD13	2.03	0.59
1:A:300:ASN:HB3	12:A:601:HOH:O	2.03	0.59
1:A:431:ASP:O	1:A:435:VAL:HG23	2.03	0.59
2:D:332:MET:O	2:D:336:GLN:HG3	2.03	0.59
2:B:83:PHE:O	2:B:86:ILE:HG22	2.03	0.58
1:A:430:LYS:HE2	1:A:434:GLU:OE2	2.03	0.58
4:F:10:ASN:CB	4:F:44:ARG:HH22	2.09	0.58
1:A:76:ASP:OD1	1:A:79:ARG:NH1	2.35	0.58
4:F:197:ARG:NH1	4:F:257:GLU:OE2	2.26	0.58
3:E:48:GLU:CG	3:E:52:LYS:HE3	2.33	0.58
4:F:245:ILE:HG23	4:F:249:TYR:HD2	1.69	0.58
1:A:21:TRP:CZ3	1:A:63:PRO:HB3	2.39	0.58
1:A:75:ILE:HD12	1:A:94:THR:HG22	1.84	0.57
2:D:165:ILE:HG21	2:D:252:LEU:HB3	1.84	0.57
4:F:371:PRO:HA	4:F:372:THR:C	2.24	0.57
1:A:181:VAL:H	2:B:258:ASN:ND2	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:LYS:NZ	2:D:130:ASP:OD1	2.37	0.57
1:C:271:THR:HG21	1:C:295:CYS:O	2.04	0.57
4:F:371:PRO:HA	4:F:372:THR:HB	1.86	0.57
1:C:166:LYS:HE2	1:C:197:HIS:O	2.04	0.57
2:D:204:ILE:HG21	2:D:231:VAL:HG22	1.86	0.56
2:D:347:ILE:HG22	2:D:350:ASN:HB3	1.87	0.56
2:D:1:MET:CE	2:D:50:ASN:HB2	2.35	0.56
2:B:172:MET:HG3	2:B:387:LEU:HD11	1.87	0.56
4:F:267:PHE:CE2	4:F:279:LEU:HD13	2.41	0.56
2:B:325:MET:HE2	2:B:355:VAL:HG11	1.87	0.56
1:C:292:THR:HG22	1:C:335:ILE:CD1	2.35	0.56
2:B:136:GLN:HA	2:B:167:ASN:O	2.05	0.56
4:F:371:PRO:CA	4:F:372:THR:HB	2.36	0.56
1:A:245:ASP:HB3	3:E:16:SER:OG	2.06	0.56
2:B:337:ASN:OD1	4:F:36:ARG:HD3	2.06	0.56
2:B:163:ASP:O	2:B:253[A]:ARG:NH2	2.30	0.56
4:F:217:ARG:NH2	4:F:374:ILE:HG22	2.21	0.56
1:A:209:ILE:HG22	1:A:227:LEU:HD22	1.87	0.55
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.41	0.55
1:A:271:THR:HG21	1:A:295:CYS:O	2.07	0.55
2:B:274:PRO:HB3	2:B:286:LEU:HD22	1.88	0.55
2:D:248:LEU:HD23	2:D:354:ALA:HB2	1.88	0.55
1:A:289:ALA:HA	1:A:331:ALA:CB	2.37	0.55
1:C:75:ILE:HD12	1:C:94:THR:HG22	1.88	0.55
2:B:187:ALA:O	2:B:191:VAL:HG23	2.06	0.55
1:C:186:ASN:O	1:C:190:THR:HG22	2.07	0.55
2:D:21:TRP:CE3	2:D:63:PRO:HB3	2.41	0.55
2:D:158:ARG:NH2	12:D:602:HOH:O	2.39	0.55
2:B:167:ASN:OD1	2:B:200:GLU:HB2	2.07	0.55
2:B:305:CYS:O	2:B:307:PRO:HD3	2.08	0.54
1:C:21:TRP:CZ3	1:C:63:PRO:HB3	2.42	0.54
1:A:93:ILE:HD11	1:A:121:ARG:HG3	1.90	0.54
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.88	0.54
1:A:217:LEU:HD21	1:A:368:LEU:CD2	2.37	0.54
1:C:241:SER:HA	1:C:249:ASN:OD1	2.08	0.54
2:D:150:GLY:O	2:D:154:ILE:HG13	2.07	0.54
2:D:427:ASP:O	2:D:431:GLU:HG3	2.07	0.54
1:C:254:GLU:HG2	1:C:352:LYS:HE2	1.90	0.54
2:D:200:GLU:HB2	2:D:268:PHE:CE2	2.43	0.54
2:D:220:THR:O	2:D:222:PRO:HD3	2.07	0.53
2:D:291:LEU:HG	2:D:375:ALA:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:279:LEU:HD12	4:F:283:ILE:HB	1.90	0.53
1:C:244:PHE:CD1	1:C:358:GLN:HG2	2.43	0.53
1:C:292:THR:HG22	1:C:335:ILE:HD12	1.90	0.53
1:A:98:ASP:HB2	5:A:501:GTP:O2G	2.08	0.53
1:C:1:MET:HE3	1:C:131:GLY:HA3	1.91	0.53
1:A:209:ILE:HG22	1:A:227:LEU:CD2	2.38	0.53
4:F:147:TRP:HB2	4:F:169:LEU:HD11	1.90	0.53
2:B:209:LEU:HD23	2:B:302:MET:HG2	1.90	0.53
2:D:69:ASP:O	2:D:94:PHE:HA	2.08	0.53
4:F:225:SER:HG	4:F:250:SER:HG	1.55	0.53
1:C:88:HIS:HE1	1:C:90:GLU:HG3	1.73	0.53
2:D:22:GLU:HG2	2:D:83:PHE:CD1	2.44	0.53
4:F:147:TRP:HB2	4:F:169:LEU:CD1	2.39	0.53
4:F:225:SER:OG	4:F:250:SER:OG	2.25	0.53
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.45	0.53
2:B:209:LEU:CD2	2:B:302:MET:HG2	2.39	0.53
2:D:141:LEU:HD12	2:D:172:MET:SD	2.49	0.53
1:C:312:TYR:CE1	1:C:341:ILE:HG23	2.45	0.52
2:D:11:GLN:O	2:D:15:GLN:HG2	2.08	0.52
1:C:74:VAL:HB	12:C:620:HOH:O	2.08	0.52
2:B:208:ALA:O	2:B:212:ILE:HG13	2.09	0.52
1:A:227:LEU:O	1:A:231:ILE:HG13	2.09	0.52
2:B:42:LEU:H	2:B:42:LEU:HD12	1.75	0.52
1:C:390:ARG:NH2	12:C:606:HOH:O	2.42	0.52
2:D:169:PHE:CE2	2:D:235:MET:HG2	2.44	0.52
4:F:3:THR:HA	4:F:28:LYS:O	2.10	0.52
1:A:188:ILE:HD12	1:A:395:PHE:HB2	1.92	0.52
1:A:325:PRO:HD3	3:E:18:GLN:NE2	2.24	0.52
2:B:349:ASN:O	2:B:352:LYS:HE2	2.09	0.52
3:E:44:ASP:HB3	3:E:45:PRO:HD2	1.90	0.52
2:D:154:ILE:HG23	2:D:166:MET:HG2	1.92	0.52
2:D:289:PRO:HG3	2:D:331:GLN:NE2	2.25	0.52
1:C:93:ILE:CD1	1:C:121:ARG:HG3	2.40	0.51
1:A:404:PHE:CD1	2:B:261:PRO:HA	2.45	0.51
2:B:2:ARG:HB2	2:B:133:GLN:CG	2.40	0.51
1:A:345:ASP:O	3:E:28:SER:N	2.40	0.51
2:B:213:CYS:HA	2:B:217:LEU:HB2	1.92	0.51
1:C:46:ASP:N	1:C:46:ASP:OD1	2.44	0.51
4:F:79:LYS:O	4:F:83:THR:OG1	2.25	0.51
1:A:176:GLN:HG3	4:F:56:PRO:HG3	1.92	0.51
2:D:312:TYR:O	2:D:344:VAL:HG22	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:226:GLU:HG3	4:F:237:THR:HG22	1.92	0.51
2:D:88:ARG:NH1	2:D:90:ASP:HB2	2.25	0.51
2:D:8:GLN:HB3	2:D:138:THR:OG1	2.11	0.51
1:A:356:ASN:HB2	12:A:607:HOH:O	2.11	0.50
4:F:77:LEU:O	4:F:81:ILE:HG13	2.11	0.50
1:A:181:VAL:H	2:B:258:ASN:HD22	1.57	0.50
1:C:234:ILE:HD12	1:C:234:ILE:H	1.76	0.50
3:E:127:ASP:O	3:E:131:GLU:HG2	2.11	0.50
4:F:7:ARG:NH2	4:F:43:GLU:OE1	2.43	0.50
2:B:295:MET:CG	2:B:377:PHE:HB2	2.42	0.50
4:F:259:GLY:O	4:F:261:GLU:HG3	2.12	0.50
1:A:320:ARG:HA	1:A:356:ASN:O	2.12	0.50
2:D:2:ARG:HB3	2:D:133:GLN:CG	2.41	0.50
2:B:345:GLU:OE1	2:B:345:GLU:N	2.35	0.50
2:B:390:ARG:NH1	12:B:601:HOH:O	2.30	0.50
1:C:250:VAL:HB	1:C:255:PHE:CE2	2.47	0.50
4:F:103:THR:HG23	4:F:128:ARG:NH2	2.27	0.50
2:B:103:TRP:CE3	2:B:189:LEU:HD13	2.47	0.50
4:F:102:PRO:HG2	4:F:105:LEU:CD1	2.32	0.50
1:A:70:LEU:HD13	1:A:110:ILE:HG21	1.94	0.50
2:B:88:ARG:HD3	2:B:91:ASN:OD1	2.12	0.50
1:C:298:PRO:HG2	1:C:308:ARG:NH2	2.27	0.50
1:C:419:SER:O	1:C:423:GLU:HG3	2.12	0.50
2:D:412:GLY:C	3:E:133:VAL:HG13	2.32	0.49
3:E:7:GLU:O	3:E:22:VAL:HA	2.12	0.49
4:F:132:LEU:HD21	4:F:170:LEU:HD11	1.94	0.49
4:F:267:PHE:CE2	4:F:271:LEU:HD11	2.47	0.49
1:C:244:PHE:CE1	1:C:358:GLN:HG2	2.47	0.49
2:B:318:ILE:N	2:B:318:ILE:HD12	2.27	0.49
1:A:114:ILE:HG12	1:A:114:ILE:O	2.13	0.49
2:B:6:HIS:CD2	2:B:21:TRP:HE1	2.30	0.49
2:B:31:ASP:HB2	2:B:32:PRO:CD	2.42	0.49
2:D:171:VAL:HA	2:D:204:ILE:O	2.12	0.49
1:A:10:GLY:O	1:A:14:VAL:HG23	2.12	0.49
2:D:153:LEU:O	2:D:157:ILE:HG13	2.11	0.49
2:D:211:ASP:O	2:D:215:ARG:HB2	2.11	0.49
1:C:209:ILE:HD11	1:C:302:MET:HE3	1.94	0.49
2:D:124:LYS:C	2:D:124:LYS:HD3	2.33	0.49
1:A:289:ALA:HA	1:A:331:ALA:HB2	1.95	0.49
3:E:45:PRO:HA	3:E:49:GLU:OE1	2.12	0.49
4:F:216:TYR:CE2	4:F:218:GLU:HB2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:SER:O	1:A:291:ILE:HG23	2.13	0.49
2:D:213:CYS:HA	2:D:217:LEU:HD12	1.95	0.49
2:B:181:VAL:HG21	2:B:404:PHE:CZ	2.48	0.48
4:F:287:ILE:HG23	4:F:319:PHE:CE2	2.48	0.48
2:B:274:PRO:HB3	2:B:286:LEU:CD2	2.44	0.48
2:D:402:LYS:HE2	2:D:415:GLU:OE1	2.12	0.48
4:F:267:PHE:HE2	4:F:279:LEU:HD13	1.77	0.48
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.48	0.48
2:D:2:ARG:HB2	2:D:133:GLN:HE21	1.78	0.48
2:D:387:LEU:HD23	2:D:387:LEU:C	2.33	0.48
1:C:234:ILE:HD12	1:C:234:ILE:N	2.29	0.48
1:A:336:LYS:HD2	1:A:341:ILE:HD12	1.94	0.48
1:A:100:ALA:CB	2:B:253[B]:ARG:HG2	2.44	0.48
1:A:154:MET:HG3	1:A:194:THR:HG23	1.94	0.48
1:C:1:MET:HG3	1:C:2:ARG:H	1.78	0.48
1:C:167:LEU:HG	1:C:200:CYS:HB3	1.94	0.48
2:D:8:GLN:NE2	2:D:14:ASN:HA	2.28	0.48
2:D:318:ILE:N	2:D:318:ILE:HD12	2.28	0.48
2:B:205:ASP:OD1	2:B:207:GLU:N	2.42	0.48
1:C:172:TYR:HB3	1:C:205:ASP:HA	1.95	0.48
2:D:402:LYS:HB3	2:D:405:LEU:HD12	1.96	0.48
1:A:231:ILE:O	1:A:235:VAL:HG23	2.14	0.48
1:A:265:ILE:HG23	1:A:432:TYR:CZ	2.48	0.48
1:C:317:LEU:HD23	1:C:377:MET:HG3	1.96	0.48
4:F:5:VAL:HG12	4:F:30:LEU:HB2	1.95	0.48
1:A:362:VAL:HG22	12:A:609:HOH:O	2.14	0.47
2:B:199:ASP:O	2:B:266:HIS:HB2	2.14	0.47
1:C:216:ASN:HB3	1:C:275:VAL:O	2.14	0.47
4:F:100:ILE:CD1	4:F:128:ARG:HA	2.44	0.47
4:F:191:LEU:HD12	4:F:196:HIS:CE1	2.49	0.47
4:F:80:LEU:HD12	4:F:84:SER:OG	2.14	0.47
1:C:209:ILE:HD11	1:C:302:MET:SD	2.54	0.47
2:D:326:LYS:O	2:D:330:GLU:HG3	2.15	0.47
2:D:16:ILE:HG13	2:D:17:GLY:N	2.28	0.47
1:A:87:PHE:HA	1:A:91:GLN:OE1	2.15	0.47
1:A:254:GLU:HG2	1:A:258:ASN:ND2	2.30	0.47
2:B:208:ALA:HB2	2:B:304:ALA:HB2	1.97	0.47
2:D:48:ARG:HB2	2:D:243:ARG:O	2.14	0.47
2:D:143:GLY:HA3	9:D:501:GDP:O3A	2.15	0.47
2:D:244:PHE:CE1	2:D:358:ILE:HD12	2.50	0.47
1:A:66:VAL:HG23	1:A:125:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:ILE:HG23	1:A:339:ARG:CG	2.38	0.47
1:A:88:HIS:HB2	1:A:89:PRO:HD2	1.97	0.47
1:A:135:PHE:C	1:A:136:LEU:HD23	2.34	0.47
1:A:335:ILE:CG2	1:A:339:ARG:HG3	2.39	0.47
2:D:212:ILE:O	2:D:216:THR:HB	2.15	0.47
1:C:3:GLU:OE1	1:C:129:CYS:HB3	2.14	0.47
1:C:141:PHE:O	1:C:147:SER:HB3	2.14	0.47
1:A:2:ARG:HB3	1:A:131:GLY:O	2.15	0.46
1:A:147:SER:HB2	1:A:190:THR:HB	1.97	0.46
2:D:295:MET:CE	2:D:377:PHE:HB2	2.44	0.46
1:A:16:ILE:CD1	1:A:171:ILE:HD11	2.45	0.46
1:C:21:TRP:CH2	1:C:63:PRO:HB3	2.50	0.46
1:C:188:ILE:HG13	1:C:425:MET:HG3	1.97	0.46
2:D:295:MET:HE2	2:D:377:PHE:HB2	1.98	0.46
4:F:38:ASN:HB3	4:F:359:PHE:CE1	2.51	0.46
1:C:214:ARG:HG2	1:C:219:ILE:O	2.15	0.46
2:B:200:GLU:OE2	2:B:255:LEU:HG	2.16	0.46
4:F:245:ILE:HG23	4:F:249:TYR:CD2	2.48	0.46
1:A:311:LYS:HA	1:A:342:GLN:O	2.15	0.46
2:D:248:LEU:HD11	2:D:352:LYS:HB3	1.98	0.46
4:F:241:THR:OG1	11:F:401:ACP:O3'	2.14	0.46
1:C:208:ALA:O	1:C:212:ILE:HG13	2.15	0.46
1:C:286:LEU:HA	1:C:290:GLU:OE1	2.16	0.46
4:F:237:THR:HG21	4:F:250:SER:HA	1.97	0.46
2:B:67:LEU:N	2:B:67:LEU:HD12	2.30	0.46
2:B:199:ASP:OD1	10:B:504:MES:H62	2.16	0.46
1:A:177:VAL:HG12	1:A:221:ARG:HH12	1.81	0.46
2:B:114:LEU:O	2:B:114:LEU:HG	2.14	0.46
2:B:290:GLU:O	2:B:294:GLN:HG3	2.16	0.46
1:C:172:TYR:CE2	1:C:391:LEU:HD22	2.51	0.46
1:C:187:SER:HB3	1:C:391:LEU:HD21	1.97	0.46
4:F:219:GLY:HA3	4:F:264:PHE:CZ	2.51	0.46
1:A:12:ALA:HB3	1:A:140:SER:HB3	1.98	0.45
1:A:217:LEU:HD21	1:A:368:LEU:HD23	1.98	0.45
1:A:351:PHE:HE1	3:E:24:LEU:CD1	2.26	0.45
4:F:216:TYR:CZ	4:F:218:GLU:HB2	2.51	0.45
4:F:318:ASP:OD2	11:F:401:ACP:O2G	2.34	0.45
1:A:178:SER:OG	1:A:183:GLU:OE1	2.27	0.45
2:B:26:ASP:OD1	2:B:369:ARG:NH2	2.49	0.45
1:C:319:TYR:HB2	1:C:355:ILE:HG12	1.98	0.45
2:D:12:CYS:SG	2:D:171:VAL:HG21	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:177:VAL:HG11	2:D:206:ASN:ND2	2.31	0.45
2:D:248:LEU:CD1	2:D:352:LYS:HB3	2.47	0.45
2:D:397:ALA:HA	2:D:400:ARG:NH1	2.32	0.45
4:F:160:ILE:HD12	4:F:160:ILE:N	2.31	0.45
1:C:385:ALA:HA	1:C:388:TRP:CD1	2.50	0.45
2:D:67:LEU:N	2:D:67:LEU:HD12	2.31	0.45
2:D:385:GLN:O	2:D:389:LYS:HG3	2.16	0.45
4:F:37:PHE:O	4:F:60:GLN:HG2	2.16	0.45
2:B:255:LEU:CD1	2:B:259:MET:HG3	2.46	0.45
2:D:334:ASN:ND2	2:D:338:LYS:HE3	2.30	0.45
4:F:10:ASN:HB2	4:F:44:ARG:NH2	2.12	0.45
1:A:141:PHE:HB3	1:A:187:SER:OG	2.17	0.45
2:B:36:TYR:CD1	2:B:46:LEU:HD21	2.51	0.45
2:B:105:LYS:HA	2:B:109:THR:OG1	2.17	0.45
2:D:68:VAL:HA	2:D:93:VAL:O	2.17	0.45
2:D:23:VAL:HG21	2:D:232:SER:HB2	1.98	0.45
2:D:272:PHE:HE2	12:D:606:HOH:O	2.00	0.45
4:F:214:TYR:HB3	4:F:375:PHE:HB3	1.99	0.45
4:F:341:LYS:HG2	4:F:341:LYS:O	2.17	0.45
1:A:12:ALA:CB	1:A:140:SER:HB3	2.47	0.44
2:D:147:SER:O	2:D:151:THR:HG23	2.18	0.44
4:F:225:SER:HB2	4:F:252:ASN:O	2.17	0.44
4:F:240:LEU:HD12	4:F:240:LEU:N	2.33	0.44
1:A:411:GLU:O	3:E:61:ARG:NH1	2.40	0.44
2:B:5:VAL:HG23	2:B:132:LEU:CD1	2.46	0.44
2:B:66:ILE:HD12	2:B:122:VAL:HG22	1.99	0.44
1:A:176:GLN:CG	4:F:56:PRO:HB3	2.46	0.44
2:B:115:VAL:HG11	2:B:156:LYS:HE3	1.99	0.44
2:D:118:VAL:O	2:D:122:VAL:HG23	2.17	0.44
4:F:296:MET:SD	4:F:380:HIS:HB2	2.58	0.44
1:A:214:ARG:HG2	1:A:219:ILE:O	2.18	0.44
2:B:191:VAL:O	2:B:195:VAL:HG23	2.18	0.44
2:B:359:PRO:HB2	2:B:371:LEU:O	2.17	0.44
1:C:250:VAL:HG11	1:C:352:LYS:HE3	1.98	0.44
2:D:1:MET:HE3	2:D:50:ASN:HB2	1.98	0.44
4:F:220:VAL:HG12	4:F:263:PHE:CE1	2.52	0.44
1:C:1:MET:CE	1:C:131:GLY:HA3	2.47	0.44
1:C:43:GLY:HA2	1:C:56:THR:O	2.17	0.44
2:B:387:LEU:C	2:B:387:LEU:HD23	2.38	0.44
3:E:92:ASN:O	3:E:96:MET:HG2	2.16	0.44
2:D:295:MET:HB2	2:D:295:MET:HE3	1.72	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:320:ARG:O	2:D:373:MET:HA	2.18	0.44
1:A:345:ASP:HB3	3:E:28:SER:CB	2.45	0.44
1:C:63:PRO:HG2	1:C:87:PHE:CE1	2.52	0.44
2:D:173:PRO:HG3	2:D:187:ALA:HB2	2.00	0.44
1:A:395:PHE:CD1	1:A:422:ARG:HD3	2.53	0.43
1:C:194:THR:O	1:C:194:THR:HG22	2.18	0.43
1:A:75:ILE:HB	1:A:94:THR:CG2	2.48	0.43
1:A:136:LEU:HD23	1:A:136:LEU:N	2.33	0.43
2:B:269:MET:HE1	2:B:307:PRO:HG3	2.01	0.43
1:C:220:GLU:HB3	2:D:326:LYS:HD2	2.00	0.43
2:D:397:ALA:O	2:D:401:ARG:NH1	2.51	0.43
4:F:16:GLU:HB3	4:F:347:CYS:SG	2.58	0.43
4:F:19:ARG:HD2	4:F:19:ARG:C	2.39	0.43
1:C:119:LEU:HD11	1:C:156:ARG:HB3	2.00	0.43
2:D:20:PHE:CZ	2:D:24:ILE:HD13	2.53	0.43
2:D:220:THR:C	2:D:222:PRO:HD3	2.37	0.43
4:F:197:ARG:HB2	4:F:224:SER:O	2.18	0.43
4:F:217:ARG:HH22	4:F:374:ILE:HG22	1.82	0.43
2:B:276:THR:HG21	2:B:282:GLN:HA	2.00	0.43
1:C:6:SER:O	1:C:65:ALA:HA	2.18	0.43
4:F:225:SER:O	4:F:252:ASN:HB2	2.19	0.43
4:F:237:THR:O	4:F:246:GLN:NE2	2.50	0.43
4:F:299:GLU:HB3	4:F:300:PRO:HD3	2.00	0.43
2:D:103:TRP:HB2	2:D:186:ASN:OD1	2.19	0.43
4:F:287:ILE:HG23	4:F:319:PHE:CZ	2.54	0.43
1:A:75:ILE:HB	1:A:94:THR:HG21	2.01	0.43
2:B:42:LEU:HD12	2:B:42:LEU:N	2.34	0.43
4:F:26:GLN:OE1	4:F:361:LEU:HD22	2.19	0.43
1:A:176:GLN:HG3	4:F:56:PRO:CG	2.49	0.43
1:A:118:VAL:HG21	1:A:149:PHE:CZ	2.54	0.42
1:A:234:ILE:HD12	1:A:234:ILE:N	2.34	0.42
1:A:317:LEU:HD23	1:A:377:MET:HG3	2.01	0.42
4:F:286:GLN:O	4:F:290:ILE:HG13	2.19	0.42
1:A:188:ILE:HD12	1:A:395:PHE:CB	2.48	0.42
2:B:88:ARG:HH11	2:B:90:ASP:HB2	1.84	0.42
2:B:336:GLN:OE1	2:B:351:VAL:HB	2.18	0.42
2:D:324:SER:O	2:D:328:VAL:HG23	2.19	0.42
4:F:82:LYS:NZ	4:F:97:SER:O	2.52	0.42
4:F:307:LEU:HD12	4:F:307:LEU:HA	1.90	0.42
2:B:88:ARG:NH1	2:B:90:ASP:HB2	2.34	0.42
1:C:255:PHE:CE1	1:C:316:CYS:HB3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:208:ALA:O	2:D:212:ILE:HG13	2.18	0.42
3:E:58:GLU:HA	3:E:61:ARG:NH2	2.35	0.42
2:B:385:GLN:OE1	2:B:389:LYS:HE3	2.20	0.42
1:A:14:VAL:HG13	1:A:67:PHE:HD2	1.84	0.42
2:B:28:HIS:HB3	2:B:49:ILE:HD13	2.01	0.42
2:D:31:ASP:HB2	2:D:32:PRO:HD2	2.01	0.42
4:F:2:TYR:CE1	4:F:359:PHE:HB3	2.54	0.42
4:F:348:GLN:NE2	4:F:352:ASP:OD1	2.53	0.42
1:A:5:ILE:O	1:A:135:PHE:HA	2.20	0.42
3:E:9:ILE:HD11	3:E:21:GLU:OE1	2.20	0.42
4:F:320:MET:HG3	4:F:330:ILE:HD11	2.01	0.42
1:C:25:CYS:HB3	1:C:30:ILE:O	2.20	0.42
2:D:20:PHE:CE1	2:D:24:ILE:HG21	2.55	0.42
2:D:352:LYS:HA	2:D:352:LYS:HD3	1.84	0.42
4:F:282:SER:HB2	4:F:325:LEU:HD13	2.01	0.42
1:C:391:LEU:HD12	1:C:391:LEU:HA	1.94	0.41
1:A:336:LYS:HG3	3:E:24:LEU:HD13	2.00	0.41
2:D:2:ARG:CB	2:D:133:GLN:HE21	2.32	0.41
1:A:233:GLN:HG3	1:A:368:LEU:HD12	2.03	0.41
2:B:1:MET:HB2	2:B:130:ASP:HB3	2.02	0.41
2:D:22:GLU:HG2	2:D:83:PHE:HD1	1.85	0.41
1:C:22:GLU:HG3	1:C:83:TYR:OH	2.20	0.41
1:C:115:ILE:HG23	1:C:116:ASP:N	2.35	0.41
1:C:430:LYS:O	1:C:434:GLU:HG3	2.20	0.41
4:F:3:THR:HB	4:F:30:LEU:HD11	2.01	0.41
2:B:295:MET:HG2	2:B:377:PHE:HB2	2.01	0.41
1:C:253:THR:O	1:C:256:GLN:HB2	2.20	0.41
1:C:255:PHE:CD1	1:C:316:CYS:HB3	2.55	0.41
4:F:220:VAL:HG11	4:F:339:ALA:HB2	2.03	0.41
4:F:199:PHE:HA	4:F:241:THR:HG21	2.03	0.41
1:A:194:THR:HG22	1:A:194:THR:O	2.21	0.41
1:A:336:LYS:CD	1:A:341:ILE:HD12	2.51	0.41
1:C:101:ASN:ND2	1:C:180:ALA:HB2	2.36	0.41
1:C:248:LEU:HD12	1:C:357:TYR:OH	2.21	0.41
2:D:19:LYS:O	2:D:23:VAL:HG23	2.21	0.41
4:F:246:GLN:HB3	4:F:260:ASN:ND2	2.36	0.41
1:A:188:ILE:HD12	1:A:395:PHE:CD2	2.56	0.41
2:B:412:GLY:C	3:E:82:VAL:HG13	2.42	0.40
1:C:66:VAL:HG23	1:C:125:LEU:CD1	2.51	0.40
2:D:146:GLY:O	2:D:150:GLY:HA3	2.21	0.40
2:B:1:MET:HB3	2:B:3:GLU:OE2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:2:TYR:O	4:F:28:LYS:N	2.51	0.40
2:D:1:MET:HG3	2:D:50:ASN:HB2	2.03	0.40
2:D:194:LEU:HD22	2:D:198:THR:HG21	2.02	0.40
4:F:198:LYS:HG2	4:F:199:PHE:H	1.86	0.40
1:A:151:SER:HB2	1:A:193:THR:OG1	2.22	0.40
1:A:187:SER:HB3	1:A:391:LEU:HD21	2.04	0.40
2:B:31:ASP:HB2	2:B:32:PRO:HD2	2.02	0.40
2:D:67:LEU:HD22	2:D:92:PHE:CE2	2.57	0.40
1:A:69:ASP:O	1:A:94:THR:HA	2.21	0.40
1:A:349:THR:HB	3:E:25:LYS:HB3	2.02	0.40
2:B:70:LEU:HD12	2:B:99:ALA:HB2	2.04	0.40
2:B:287:THR:HB	2:B:289:PRO:HD2	2.03	0.40
1:C:100:ALA:HA	2:D:254:LYS:HG3	2.03	0.40
1:C:164:LYS:HB2	1:C:164:LYS:HE3	1.82	0.40
2:D:333:LEU:HD23	2:D:333:LEU:HA	1.97	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	435/451 (96%)	422 (97%)	13 (3%)	0	100	100
1	C	439/451 (97%)	428 (98%)	11 (2%)	0	100	100
2	B	422/445 (95%)	402 (95%)	19 (4%)	1 (0%)	47	71
2	D	422/445 (95%)	408 (97%)	14 (3%)	0	100	100
3	E	119/143 (83%)	117 (98%)	2 (2%)	0	100	100
4	F	341/384 (89%)	328 (96%)	13 (4%)	0	100	100
All	All	2178/2319 (94%)	2105 (97%)	72 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	250	ALA

### 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	368/379 (97%)	364 (99%)	4 (1%)	73 88
1	C	372/379 (98%)	370 (100%)	2 (0%)	88 96
2	B	368/383 (96%)	366 (100%)	2 (0%)	88 96
2	D	368/383 (96%)	365 (99%)	3 (1%)	81 92
3	E	110/127 (87%)	110 (100%)	0	100 100
4	F	315/342 (92%)	313 (99%)	2 (1%)	86 95
All	All	1901/1993 (95%)	1888 (99%)	13 (1%)	84 94

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	71	GLU
1	A	221	ARG
1	A	300	ASN
2	B	139	HIS
2	B	302	MET
1	C	221	ARG
1	C	266	HIS
2	D	26	ASP
2	D	139	HIS
2	D	229	HIS
4	F	91	CYS
4	F	257	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	133	GLN
2	B	258	ASN
3	E	18	GLN
4	F	180	HIS

### 5.3.3 RNA [i](#)

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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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	B	501	6	24,30,30	0.96	1 (4%)	30,47,47	1.20	4 (13%)
5	GTP	A	501	6	26,34,34	1.15	2 (7%)	32,54,54	1.50	5 (15%)
10	MES	B	504	-	12,12,12	2.26	1 (8%)	14,16,16	1.99	6 (42%)
11	ACP	F	401	6	27,33,33	1.40	5 (18%)	32,52,52	1.52	4 (12%)
8	UR1	C	504	-	12,12,12	0.46	0	18,18,18	1.08	1 (5%)
8	UR1	A	504	-	12,12,12	0.53	0	18,18,18	1.19	2 (11%)
9	GDP	D	501	6	24,30,30	0.94	1 (4%)	30,47,47	1.19	3 (10%)
8	UR1	D	503	-	12,12,12	0.52	0	18,18,18	1.30	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GTP	C	501	6	26,34,34	1.13	2 (7%)	32,54,54	1.44	6 (18%)

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	B	501	6	-	3/12/32/32	0/3/3/3
5	GTP	A	501	6	-	6/18/38/38	0/3/3/3
10	MES	B	504	-	-	4/6/14/14	0/1/1/1
11	ACP	F	401	6	-	9/15/38/38	0/3/3/3
8	UR1	C	504	-	-	4/6/6/6	0/1/1/1
8	UR1	A	504	-	-	4/6/6/6	0/1/1/1
9	GDP	D	501	6	-	2/12/32/32	0/3/3/3
8	UR1	D	503	-	-	4/6/6/6	0/1/1/1
5	GTP	C	501	6	-	8/18/38/38	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	504	MES	C8-S	-7.54	1.66	1.77
5	C	501	GTP	C5-C6	-3.95	1.39	1.47
5	A	501	GTP	C5-C6	-3.95	1.39	1.47
11	F	401	ACP	PG-O3G	2.94	1.61	1.54
11	F	401	ACP	PG-O2G	2.92	1.61	1.54
11	F	401	ACP	PB-O3A	2.77	1.61	1.58
11	F	401	ACP	C5-C4	2.53	1.47	1.40
9	B	501	GDP	C6-N1	-2.49	1.34	1.37
9	D	501	GDP	C6-N1	-2.33	1.34	1.37
11	F	401	ACP	PB-O2B	2.27	1.61	1.56
5	A	501	GTP	C2-N3	2.16	1.38	1.33
5	C	501	GTP	C2-N3	2.16	1.38	1.33

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	401	ACP	PB-O3A-PA	-4.30	118.93	132.56
10	B	504	MES	C5-N4-C3	3.80	117.38	108.83
11	F	401	ACP	C3'-C2'-C1'	3.60	106.40	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	501	GTP	PB-O3B-PG	-3.47	120.93	132.83
5	C	501	GTP	PA-O3A-PB	-3.26	121.62	132.83
5	A	501	GTP	C5-C6-N1	3.20	119.60	113.95
9	D	501	GDP	PA-O3A-PB	-3.19	121.89	132.83
5	C	501	GTP	C8-N7-C5	3.18	109.05	102.99
11	F	401	ACP	N3-C2-N1	-3.12	123.80	128.68
5	A	501	GTP	C8-N7-C5	3.11	108.91	102.99
5	C	501	GTP	C5-C6-N1	3.07	119.37	113.95
5	A	501	GTP	PA-O3A-PB	-3.00	122.54	132.83
10	B	504	MES	C6-C5-N4	-2.92	105.67	110.10
5	A	501	GTP	C2-N1-C6	-2.89	119.78	125.10
9	B	501	GDP	PA-O3A-PB	-2.88	122.94	132.83
5	C	501	GTP	C2-N1-C6	-2.83	119.89	125.10
11	F	401	ACP	C4-C5-N7	-2.71	106.58	109.40
10	B	504	MES	O2S-S-C8	2.52	109.95	106.92
8	C	504	UR1	C5-S-N	-2.48	104.88	108.38
5	C	501	GTP	PB-O3B-PG	-2.44	124.44	132.83
9	B	501	GDP	C8-N7-C5	2.42	107.61	102.99
8	D	503	UR1	C5-S-N	-2.41	104.97	108.38
9	B	501	GDP	C5-C6-N1	2.33	118.07	113.95
10	B	504	MES	O1S-S-C8	2.33	109.72	106.92
9	D	501	GDP	C8-N7-C5	2.33	107.43	102.99
9	D	501	GDP	C5-C6-N1	2.26	117.94	113.95
10	B	504	MES	C7-N4-C5	2.21	116.89	111.23
8	A	504	UR1	O-S-N	-2.18	104.14	107.36
10	B	504	MES	O3S-S-C8	2.17	109.28	105.77
8	D	503	UR1	O1-S-C5	2.16	109.76	107.35
8	A	504	UR1	O1-S-C5	2.14	109.74	107.35
8	D	503	UR1	O-S-C5	2.09	109.69	107.35
5	C	501	GTP	O6-C6-C5	-2.06	120.34	124.37
9	B	501	GDP	O3B-PB-O3A	2.04	111.48	104.64

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	C5'-O5'-PA-O1A
9	B	501	GDP	C5'-O5'-PA-O1A
9	B	501	GDP	C5'-O5'-PA-O2A
9	D	501	GDP	C5'-O5'-PA-O3A
9	D	501	GDP	C5'-O5'-PA-O2A

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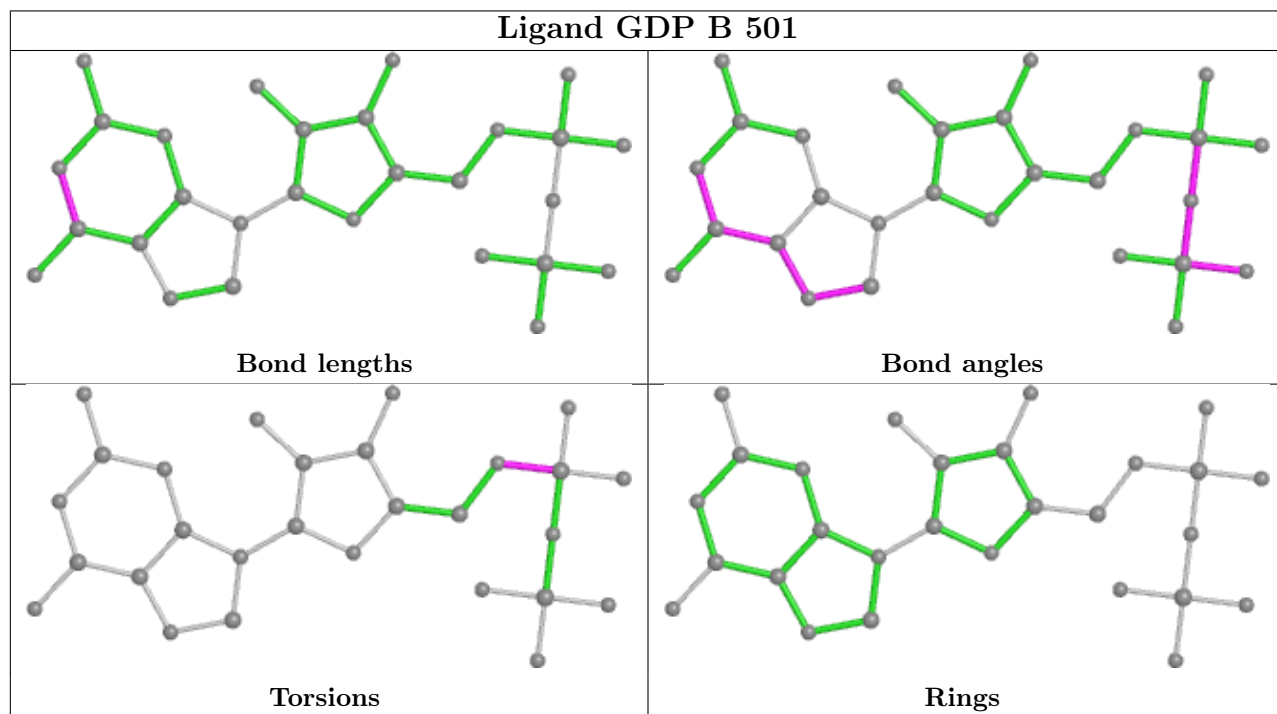
Mol	Chain	Res	Type	Atoms
10	B	504	MES	C8-C7-N4-C5
11	F	401	ACP	PB-C3B-PG-O1G
11	F	401	ACP	PG-C3B-PB-O1B
11	F	401	ACP	PG-C3B-PB-O2B
11	F	401	ACP	PG-C3B-PB-O3A
11	F	401	ACP	C5'-O5'-PA-O2A
11	F	401	ACP	C5'-O5'-PA-O3A
10	B	504	MES	C7-C8-S-O3S
8	A	504	UR1	C4-C5-S-N
8	A	504	UR1	C4-C5-S-O1
8	A	504	UR1	C6-C5-S-N
8	A	504	UR1	C6-C5-S-O1
8	D	503	UR1	C6-C5-S-N
8	D	503	UR1	C4-C5-S-N
11	F	401	ACP	PB-O3A-PA-O1A
8	D	503	UR1	C4-C5-S-O1
8	D	503	UR1	C6-C5-S-O1
5	C	501	GTP	C5'-O5'-PA-O3A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	C5'-O5'-PA-O2A
10	B	504	MES	C7-C8-S-O1S
10	B	504	MES	C7-C8-S-O2S
5	C	501	GTP	C3'-C4'-C5'-O5'
11	F	401	ACP	PB-C3B-PG-O2G
11	F	401	ACP	PB-C3B-PG-O3G
8	C	504	UR1	C6-C5-S-N
8	C	504	UR1	C6-C5-S-O1
5	C	501	GTP	PB-O3A-PA-O2A
8	C	504	UR1	C4-C5-S-O1
5	A	501	GTP	PB-O3B-PG-O1G
8	C	504	UR1	C4-C5-S-N
5	C	501	GTP	O4'-C4'-C5'-O5'
5	C	501	GTP	PB-O3B-PG-O1G
5	A	501	GTP	PB-O3B-PG-O2G
5	A	501	GTP	PB-O3B-PG-O3G
5	C	501	GTP	PB-O3B-PG-O3G
5	A	501	GTP	C5'-O5'-PA-O3A
9	B	501	GDP	C5'-O5'-PA-O3A

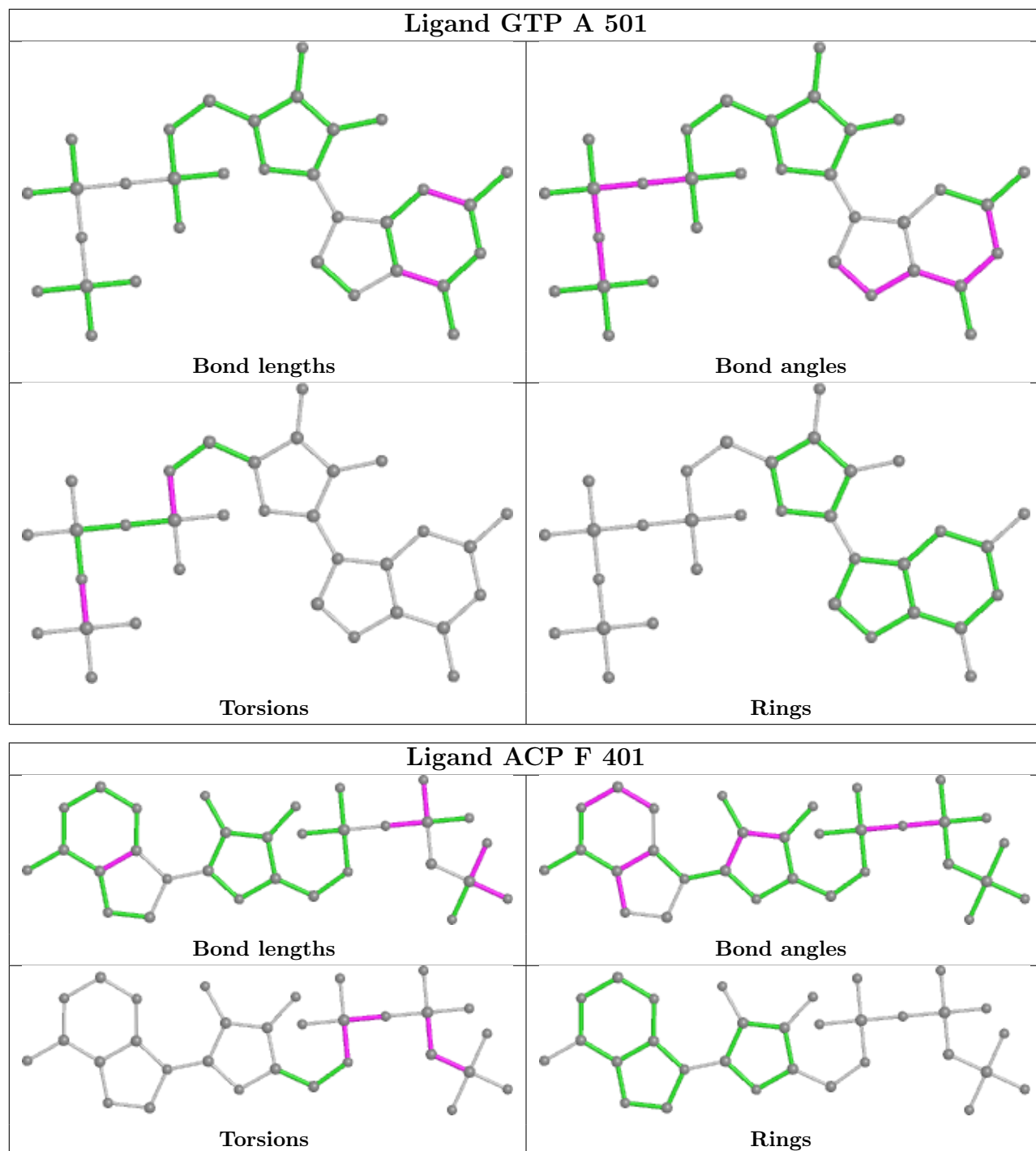
There are no ring outliers.

4 monomers are involved in 8 short contacts:

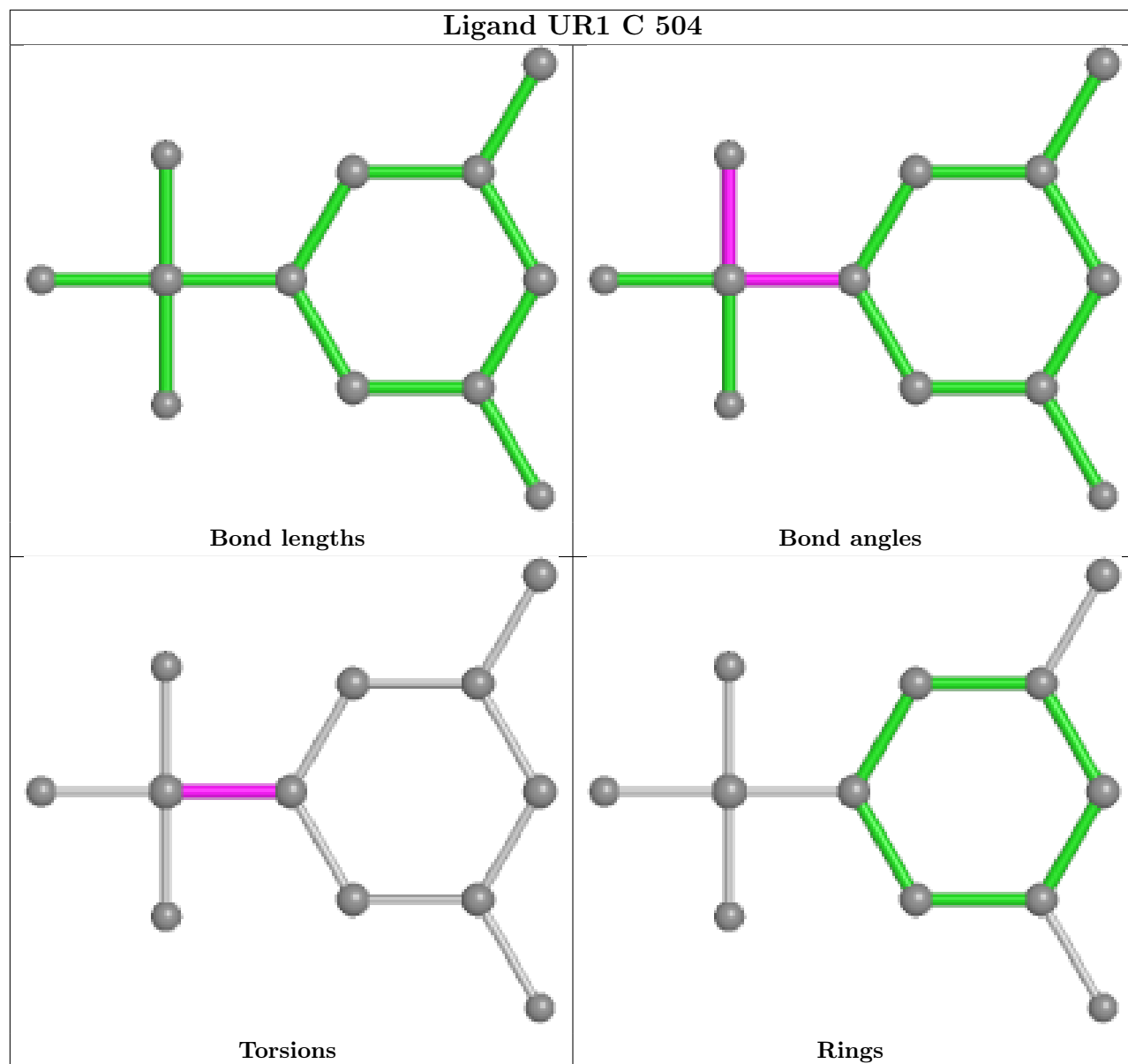
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	501	GTP	2	0
10	B	504	MES	1	0
11	F	401	ACP	3	0
9	D	501	GDP	2	0

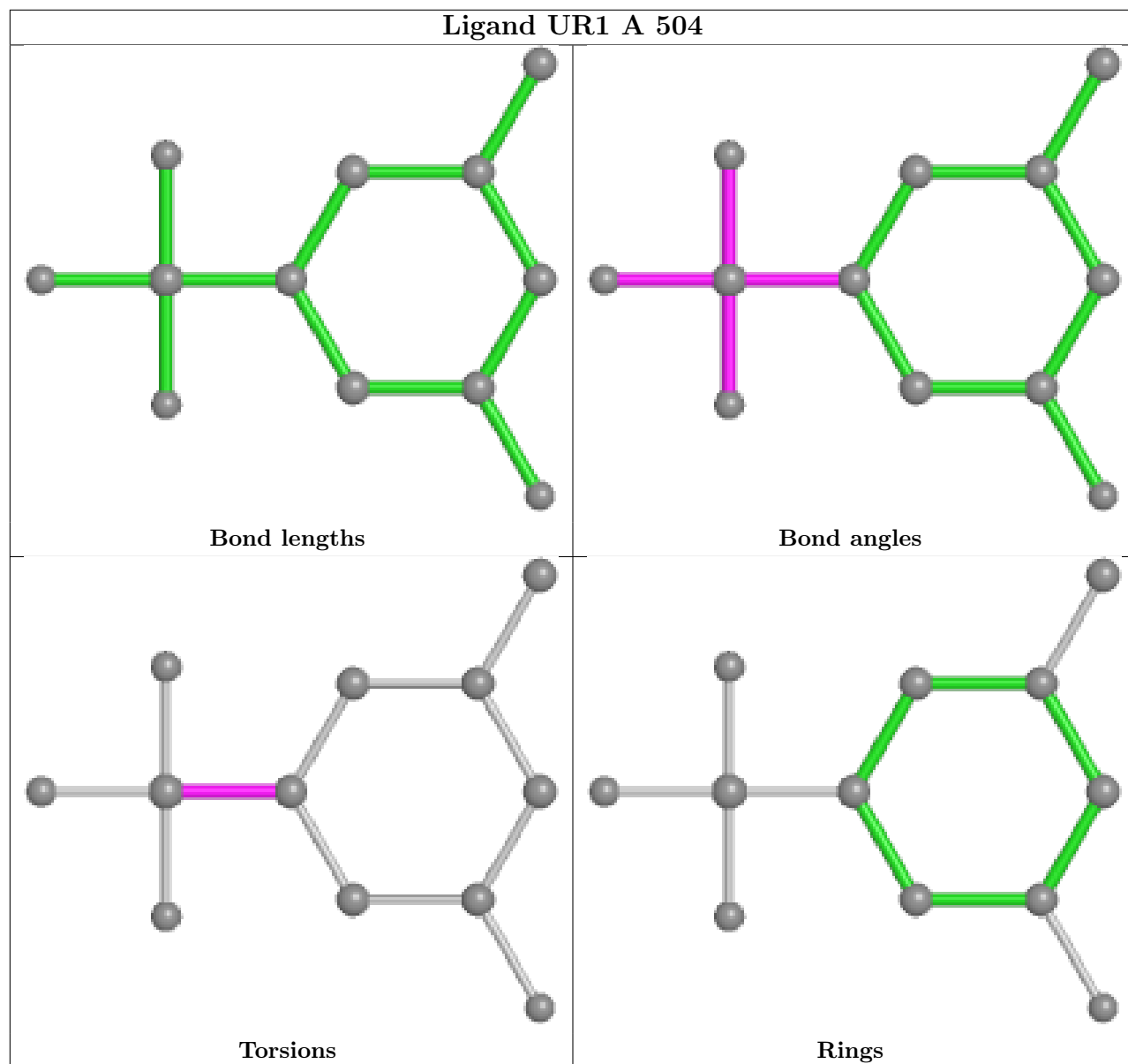
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

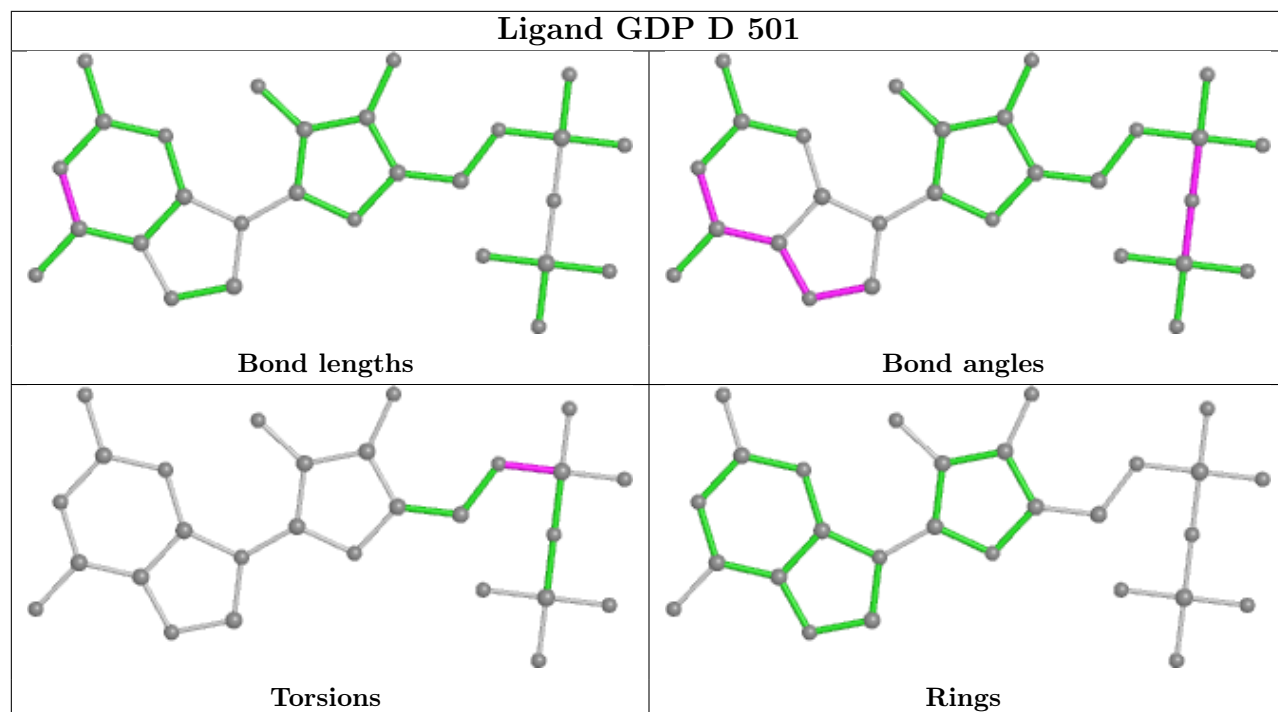


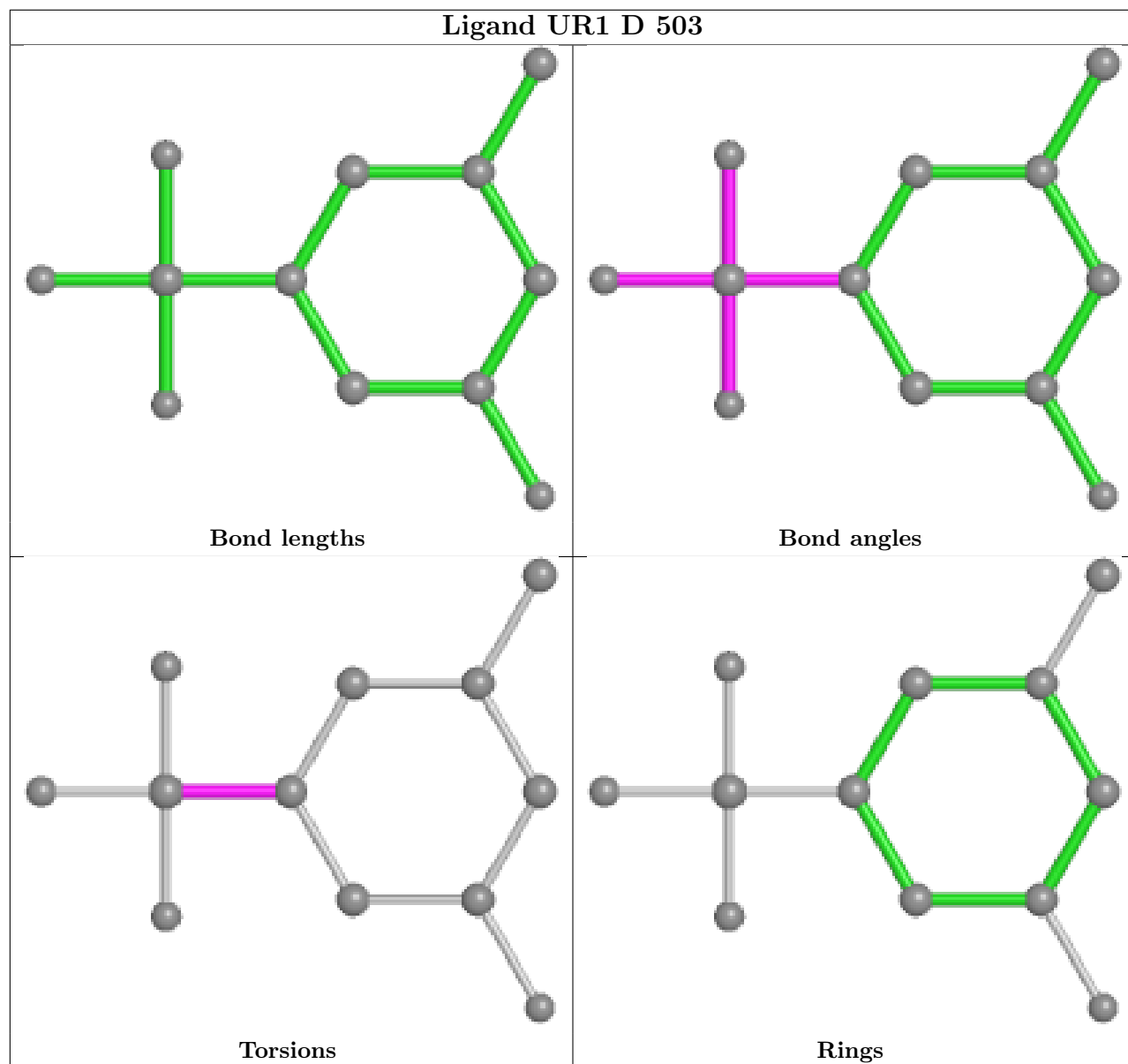


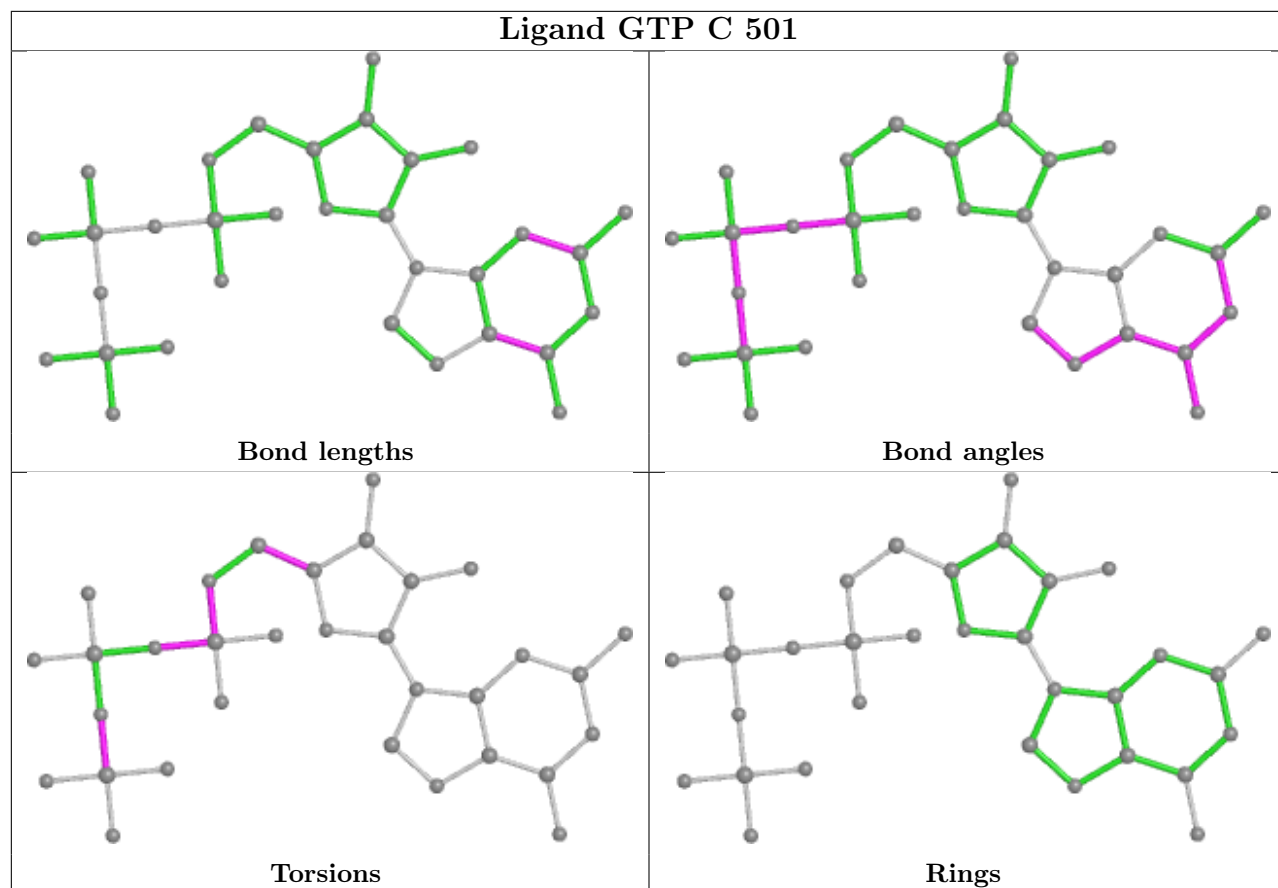












## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	437/451 (96%)	0.45	20 (4%) 32 26	66, 87, 123, 200	0
1	C	440/451 (97%)	0.37	1 (0%) 95 95	59, 74, 105, 134	0
2	B	425/445 (95%)	0.41	9 (2%) 63 58	62, 84, 128, 163	2 (0%)
2	D	426/445 (95%)	0.35	23 (5%) 25 20	71, 97, 134, 174	4 (0%)
3	E	123/143 (86%)	0.65	14 (11%) 5 3	77, 100, 140, 182	0
4	F	349/384 (90%)	1.03	79 (22%) 0 0	82, 122, 178, 208	0
All	All	2200/2319 (94%)	0.51	146 (6%) 18 13	59, 91, 146, 208	6 (0%)

All (146) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	276	THR	7.4
4	F	240	LEU	6.6
4	F	142	ARG	6.2
2	D	277	SER	5.5
3	E	6	MET	5.4
3	E	24	LEU	5.0
4	F	143	GLU	4.8
2	D	279	GLY	4.8
4	F	330	ILE	4.6
4	F	334	GLY	4.5
4	F	131	PHE	4.3
2	D	278	ARG	4.3
3	E	25	LYS	4.1
4	F	138	ARG	4.1
3	E	27	PRO	4.1
4	F	169	LEU	4.0
4	F	152	SER	4.0
1	A	86	LEU	4.0
4	F	329	LEU	3.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
4	F	99	VAL	3.8
4	F	173	ILE	3.6
4	F	314	LEU	3.6
4	F	186	LEU	3.5
4	F	371	PRO	3.5
4	F	233	PHE	3.4
2	D	280	SER	3.4
4	F	71	LEU	3.3
4	F	206	LEU	3.3
1	A	118	VAL	3.2
3	E	115	HIS	3.2
4	F	149	ALA	3.1
2	D	371	LEU	3.1
4	F	231	ALA	3.1
4	F	182	ILE	3.1
4	F	147	TRP	3.1
4	F	315	PHE	3.1
2	D	293	GLN	3.0
4	F	234	GLN	3.0
4	F	320	MET	3.0
1	A	196	GLU	3.0
4	F	375	PHE	2.9
3	E	50	ILE	2.9
3	E	26	PRO	2.8
1	A	332	ILE	2.8
4	F	90	SER	2.8
4	F	201	ILE	2.8
2	D	219	LEU	2.8
1	A	339	ARG	2.8
2	D	275	LEU	2.7
4	F	232	ASN	2.7
4	F	100	ILE	2.7
2	D	115	VAL	2.7
4	F	291	ILE	2.7
4	F	137	ARG	2.6
4	F	362	ALA	2.6
3	E	44	ASP	2.6
4	F	161	LEU	2.6
4	F	319	PHE	2.6
4	F	101	TYR	2.6
2	D	154	ILE	2.6
2	B	360	PRO	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
4	F	241	THR	2.5
4	F	245	ILE	2.5
4	F	204	TRP	2.5
2	D	318	ILE	2.5
4	F	148	ILE	2.5
4	F	14	TYR	2.5
4	F	185	TYR	2.5
4	F	340	GLN	2.5
1	A	30	ILE	2.5
4	F	372	THR	2.5
1	A	344	VAL	2.5
2	D	215	ARG	2.5
2	D	286	LEU	2.4
4	F	295	LEU	2.4
1	A	288	VAL	2.4
2	D	401	ARG	2.4
1	A	362	VAL	2.4
4	F	243	HIS	2.4
4	F	242	ASN	2.4
1	A	349	THR	2.4
3	E	54	LEU	2.4
2	D	320	ARG	2.4
4	F	342	LEU	2.3
4	F	346	LEU	2.3
2	B	59	ASN	2.3
4	F	213	ILE	2.3
2	D	319	PHE	2.3
4	F	98	TYR	2.3
1	A	341	ILE	2.3
2	B	437	ASP	2.3
4	F	332	VAL	2.3
4	F	222	ARG	2.3
2	D	294	GLN	2.3
4	F	76	SER	2.3
4	F	44	ARG	2.3
2	B	281	GLN	2.2
4	F	134	ALA	2.2
2	D	299	LYS	2.2
4	F	21	LEU	2.2
4	F	239	HIS	2.2
4	F	144	GLY	2.2
4	F	127	GLU	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	342	GLN	2.2
1	A	230	LEU	2.2
4	F	141	GLY	2.2
4	F	302	ILE	2.2
2	D	323	MET	2.2
3	E	143	ALA	2.2
3	E	7	GLU	2.2
4	F	236	LYS	2.2
1	A	115	ILE	2.2
4	F	197	ARG	2.2
2	D	325	MET	2.2
4	F	153	ALA	2.2
1	A	68	VAL	2.2
4	F	336	PRO	2.2
3	E	22	VAL	2.1
4	F	6	VAL	2.1
4	F	335	ALA	2.1
4	F	103	THR	2.1
3	E	48	GLU	2.1
2	B	308	ARG	2.1
2	B	277	SER	2.1
1	A	83	TYR	2.1
4	F	5	VAL	2.1
1	A	209	ILE	2.1
4	F	13	VAL	2.1
1	C	357	TYR	2.1
2	B	318	ILE	2.1
4	F	337	ALA	2.1
4	F	283	ILE	2.1
2	B	373	MET	2.1
1	A	169	PHE	2.1
4	F	264	PHE	2.1
4	F	376	ILE	2.1
2	D	218	LYS	2.1
2	B	340	SER	2.1
4	F	200	ASP	2.1
3	E	53	LYS	2.0
4	F	190	LEU	2.0
2	D	272	PHE	2.0
4	F	162	ILE	2.0
1	A	351	PHE	2.0
1	A	335	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
4	F	199	PHE	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

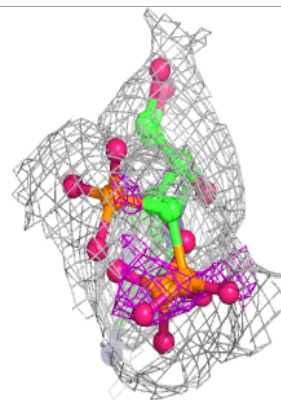
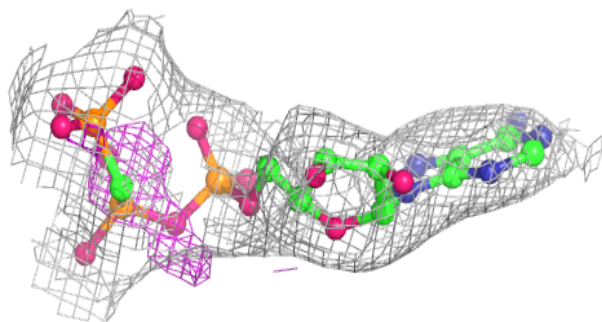
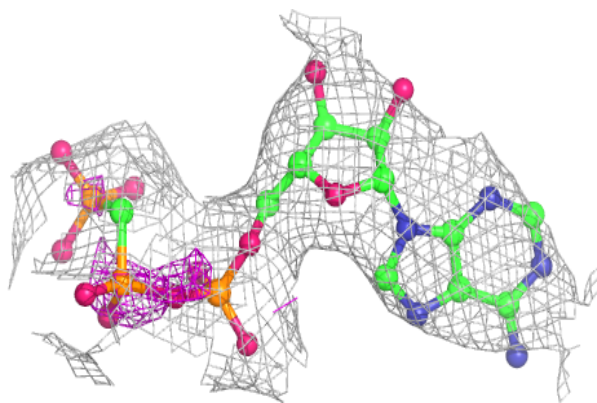
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
7	CA	E	201	1/1	0.72	0.15	108,108,108,108	0
7	CA	B	503	1/1	0.73	0.17	131,131,131,131	0
11	ACP	F	401	31/31	0.88	0.22	118,128,139,141	0
6	MG	D	502	1/1	0.90	0.18	91,91,91,91	0
8	UR1	D	503	12/12	0.93	0.22	76,80,96,96	20
7	CA	A	503	1/1	0.93	0.11	126,126,126,126	0
9	GDP	D	501	28/28	0.94	0.17	87,90,99,100	0
10	MES	B	504	12/12	0.94	0.16	92,102,114,120	0
6	MG	B	502	1/1	0.94	0.15	75,75,75,75	0
8	UR1	C	504	12/12	0.95	0.21	61,73,86,88	20
8	UR1	A	504	12/12	0.96	0.30	72,80,96,96	20
7	CA	C	503	1/1	0.96	0.17	96,96,96,96	0
6	MG	A	502	1/1	0.97	0.17	74,74,74,74	0
6	MG	F	402	1/1	0.97	0.14	124,124,124,124	0
5	GTP	A	501	32/32	0.97	0.16	64,69,74,78	0
6	MG	C	502	1/1	0.97	0.17	68,68,68,68	0
9	GDP	B	501	28/28	0.98	0.19	57,68,73,78	0
5	GTP	C	501	32/32	0.98	0.20	58,65,76,80	0

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

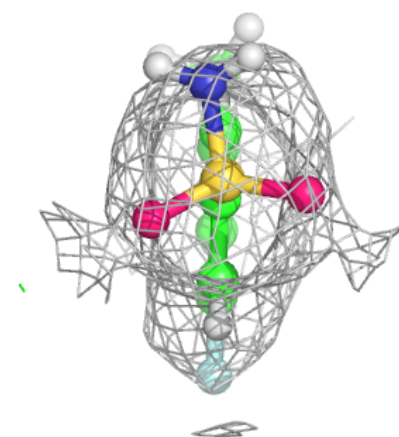
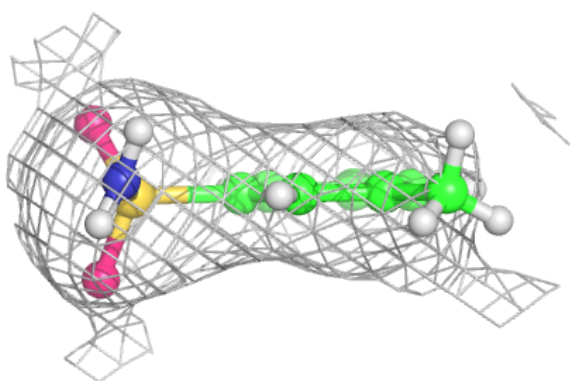
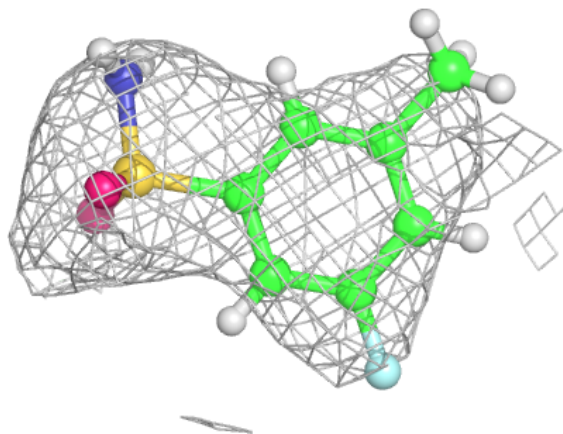
**Electron density around ACP F 401:**

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



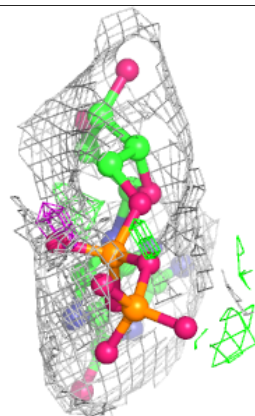
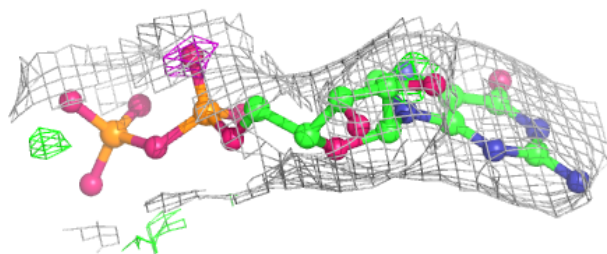
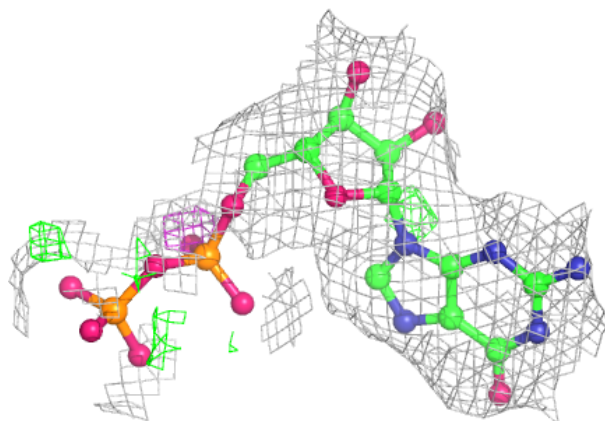
**Electron density around UR1 D 503:**

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



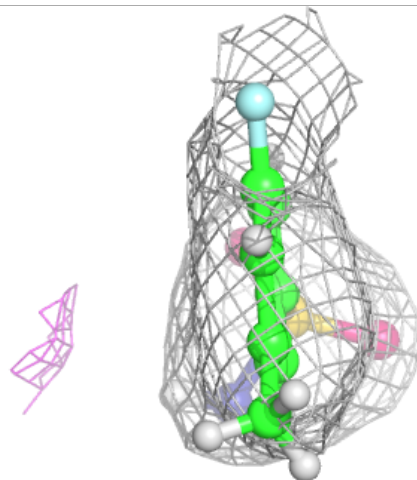
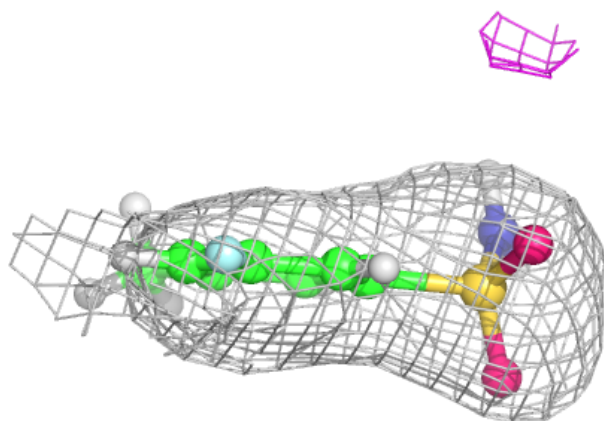
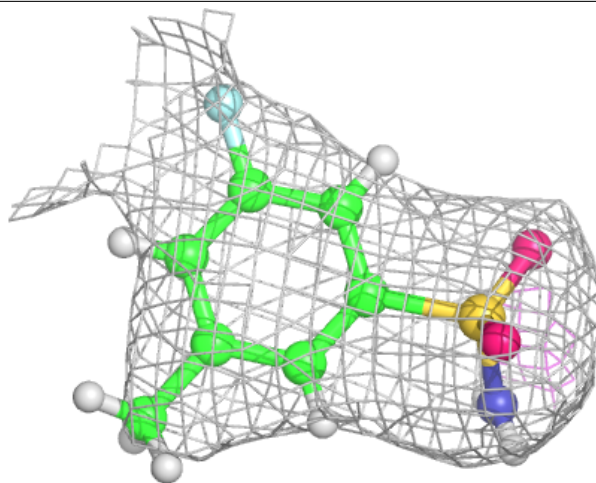
**Electron density around GDP D 501:**

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



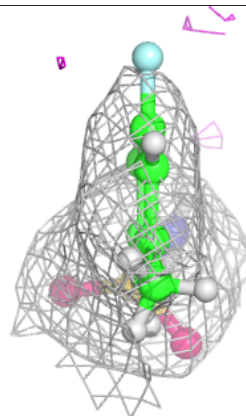
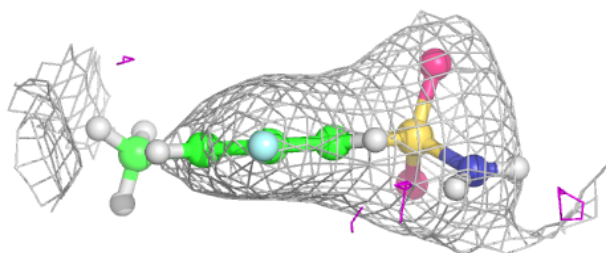
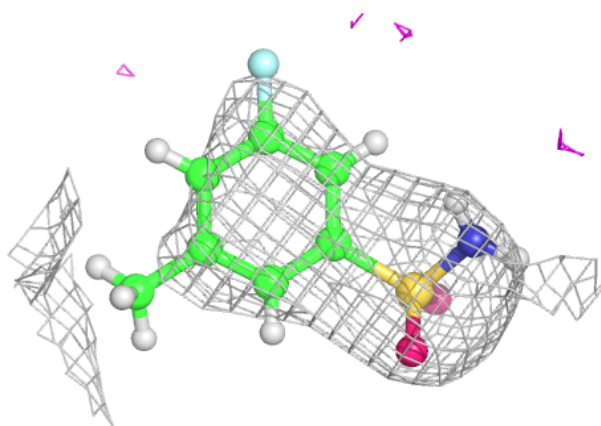
**Electron density around UR1 C 504:**

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

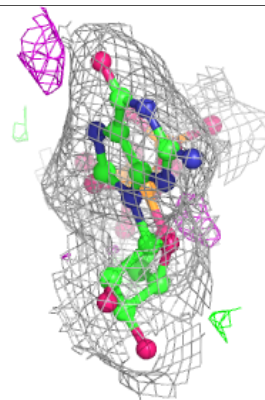
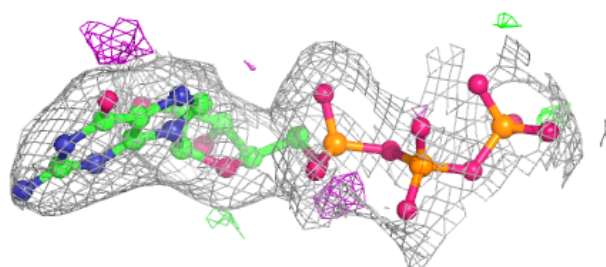
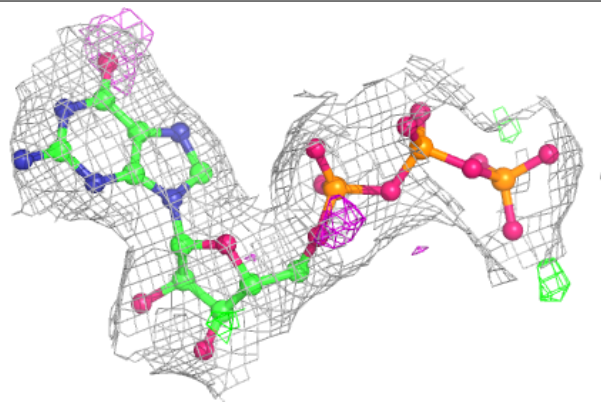


**Electron density around UR1 A 504:**

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

**Electron density around GTP A 501:**

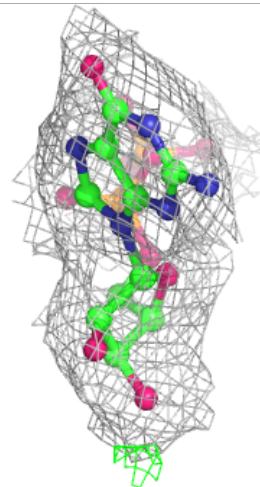
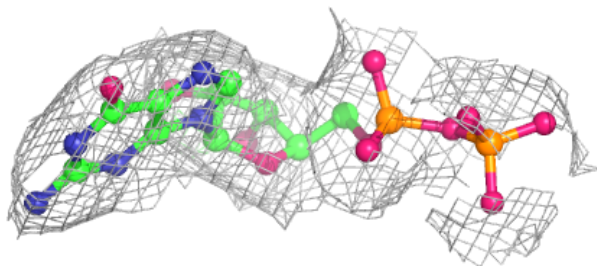
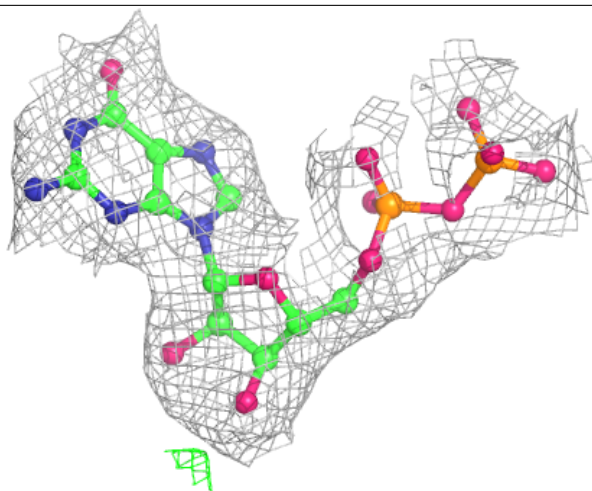
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



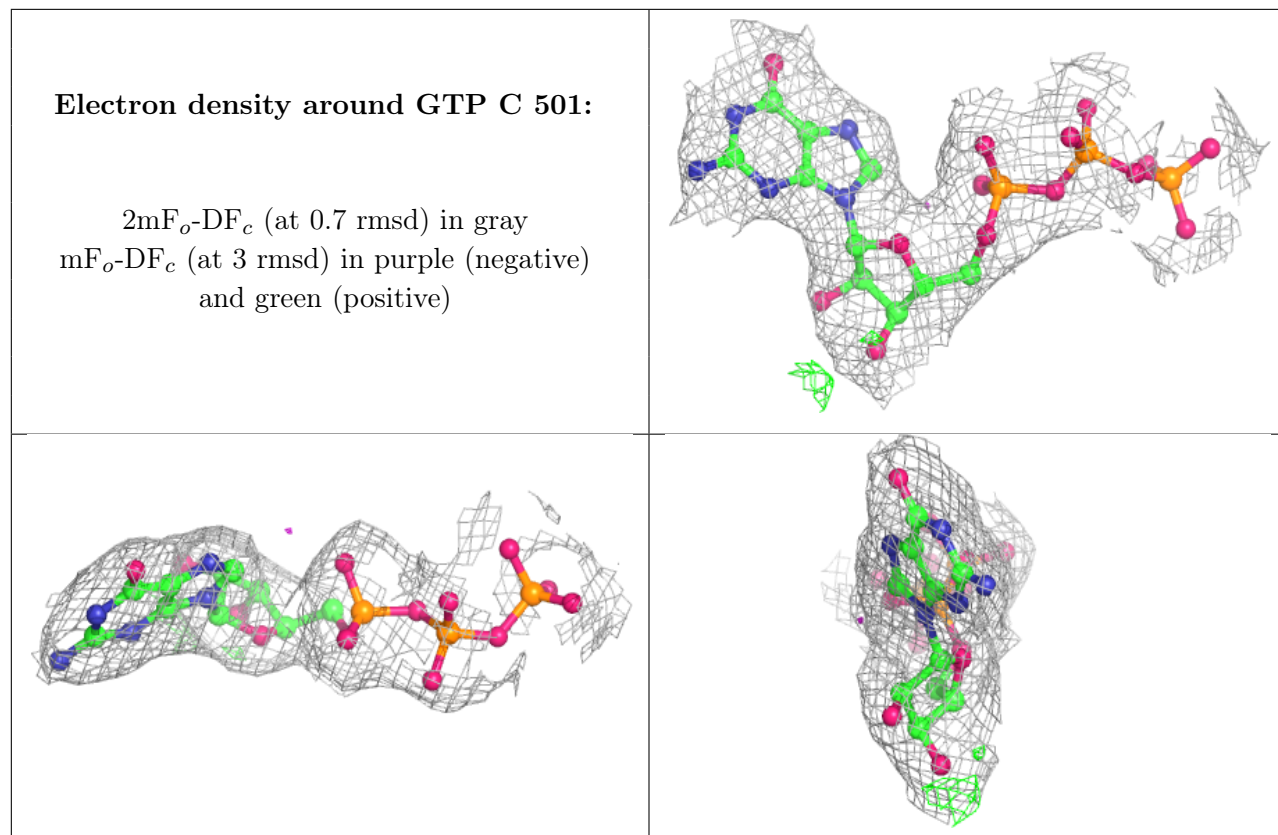


**Electron density around GDP B 501:**

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







## 6.5 Other polymers [i](#)

There are no such residues in this entry.