



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 4, 2024 – 04:59 pm GMT

PDB ID : 5IYZ  
Title : Tubulin-MMAE complex  
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Deposited on : 2016-03-24  
Resolution : 1.80 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 : 1.8.4, CSD as541be (2020)  
Xtrriage (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

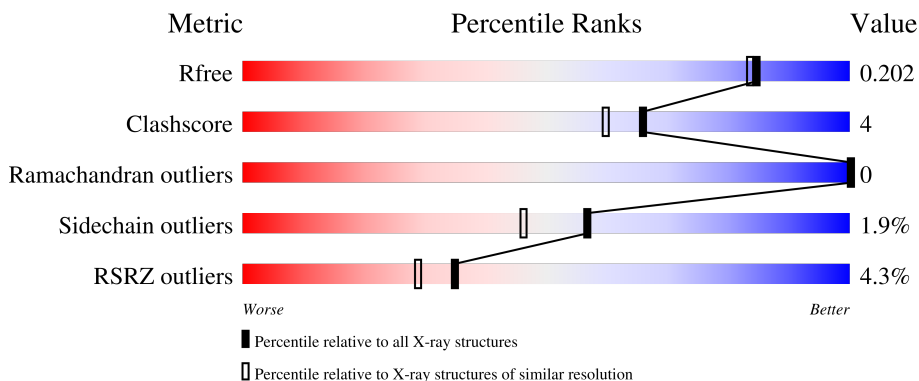
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	<p>91% 6% .</p>
1	C	451	<p>89% 8% .</p>
2	B	445	<p>87% 10% .</p>
2	D	445	<p>84% 10% 5% 3%</p>
3	E	143	<p>74% 12% 14% 3%</p>

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Mol	Chain	Length	Quality of chain
4	F	384	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a red segment on the left labeled '18%', a large green segment labeled '73%', a yellow segment labeled '13%', and a grey segment on the far right labeled '14%'. A small black dot is located between the yellow and grey segments.</p>

## 2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 19140 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
			Total	C	N	O	S			
1	A	437	Total	C	N	O	S	0	12	0
			3467	2206	582	654	25			
1	C	440	Total	C	N	O	S	0	11	0
			3482	2208	585	664	25			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	430	Total	C	N	O	S	3	14	0
			3447	2169	586	663	29			
2	D	424	Total	C	N	O	S	0	3	0
			3347	2101	570	648	28			

- 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	6	0
			1047	646	189	207	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

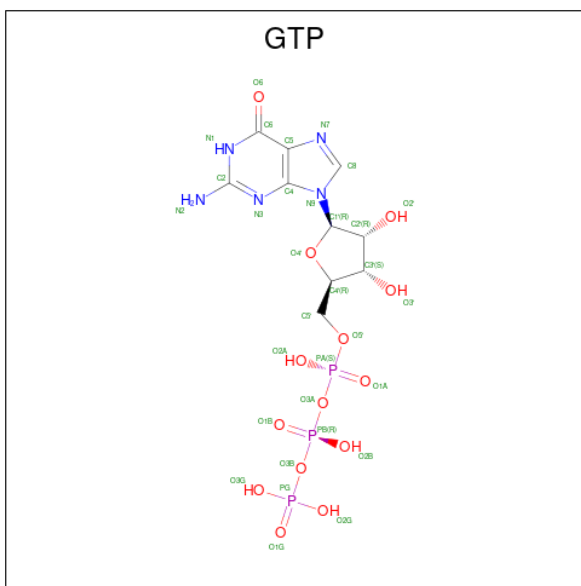
- Molecule 4 is a protein called TUBULIN-TYROSINE LIGASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	F	331	Total	C	N	O	S	0	3	0
			2725	1757	461	493	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
			Total	Mg		
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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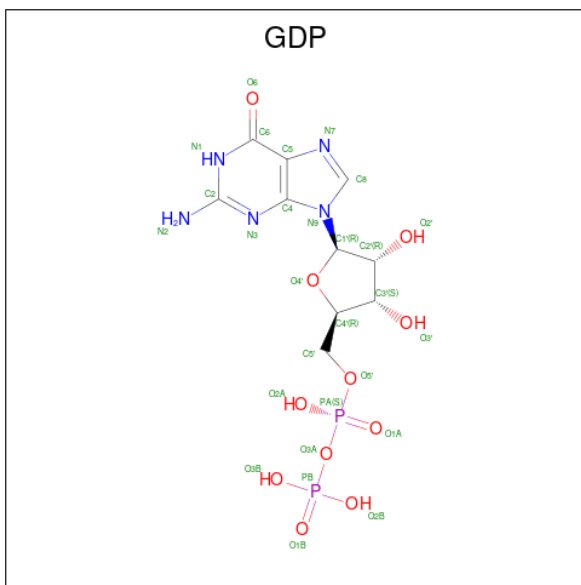
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

- 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	C	1	Total	Ca	0	0
			1	1		

- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



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

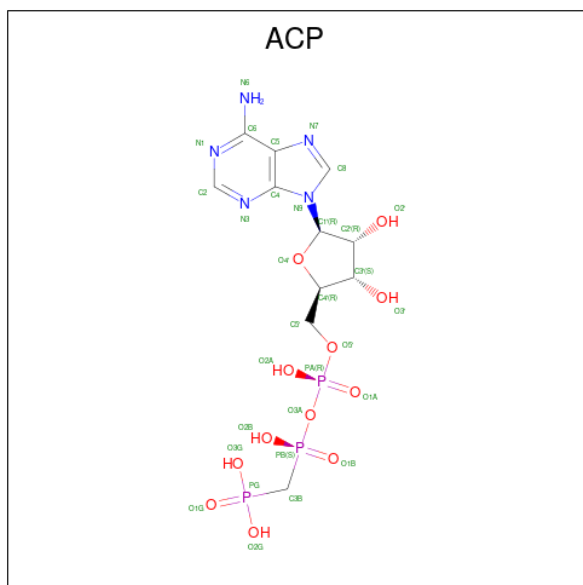
- Molecule 9 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	D	1	Total	C	N	O	0	0
			51	39	5	7		

- Molecule 11 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>).



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

- Molecule 12 is water.

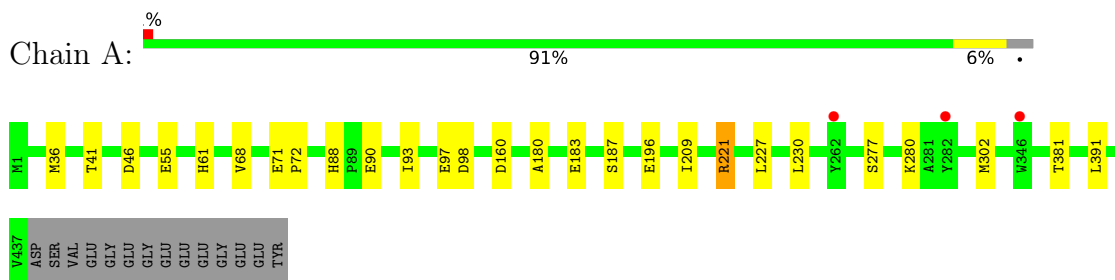
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	259	Total	O	0	0
			259	259		
12	B	314	Total	O	0	0
			314	314		
12	C	434	Total	O	0	0
			434	434		
12	D	178	Total	O	0	0
			178	178		
12	E	67	Total	O	0	0
			67	67		
12	F	101	Total	O	0	0
			101	101		



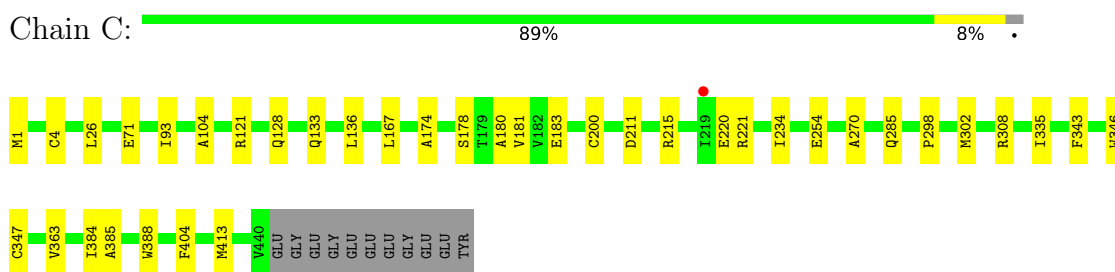
### 3 Residue-property plots [i](#)

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.

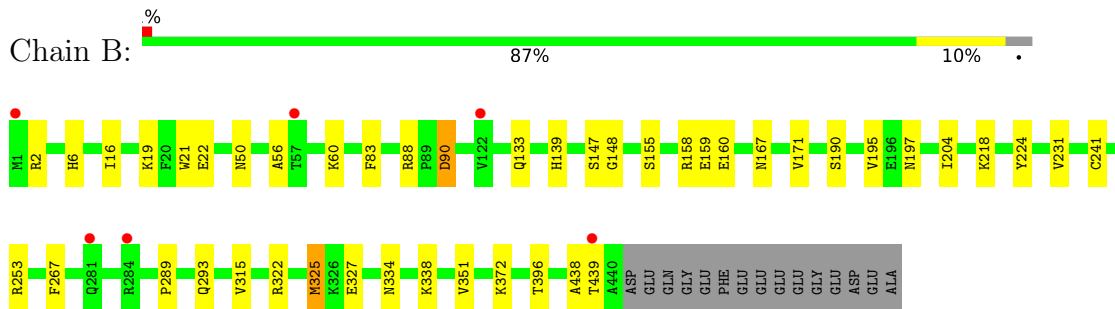
- Molecule 1: Tubulin alpha-1B chain



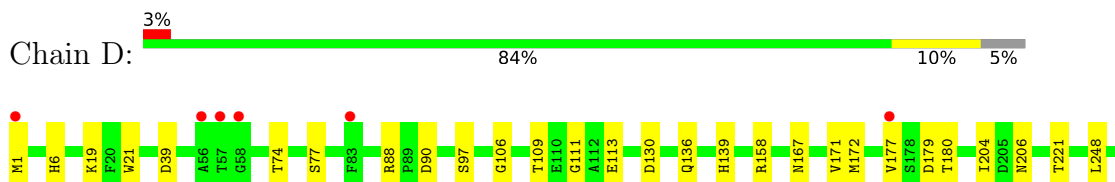
- Molecule 1: Tubulin alpha-1B chain

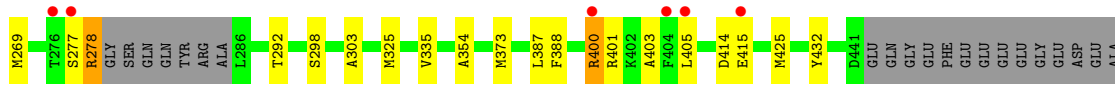


- Molecule 2: Tubulin beta-2B chain

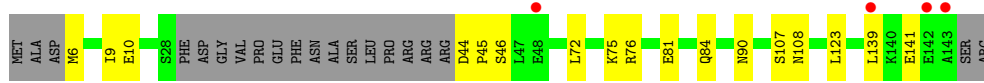
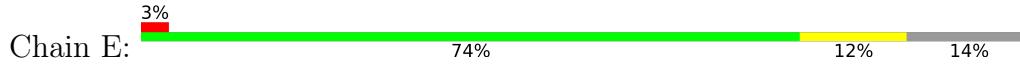


- Molecule 2: Tubulin beta-2B chain

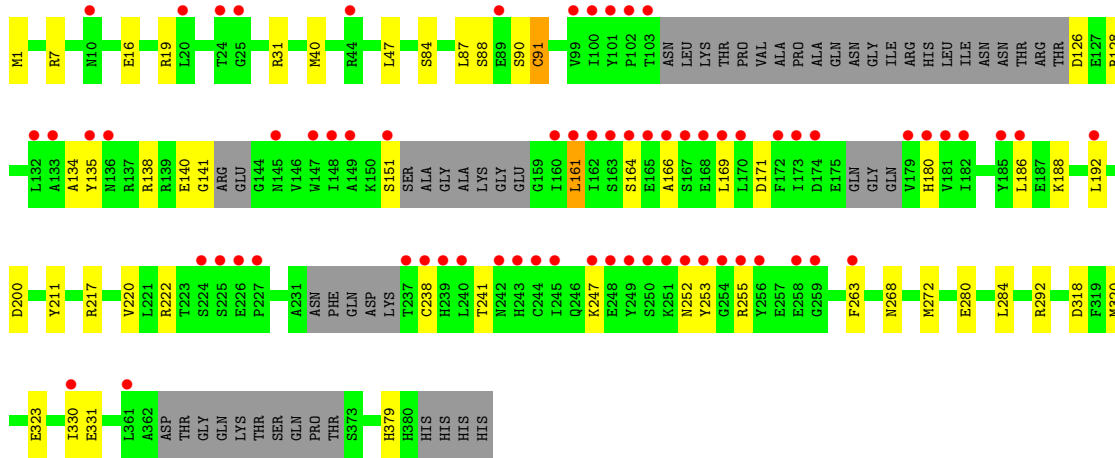
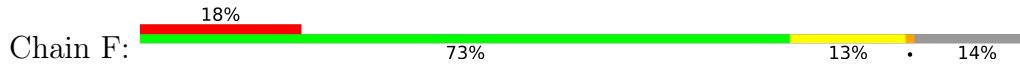




• Molecule 3: Stathmin-4



• 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, $\alpha$ , $\beta$ , $\gamma$	104.51Å 156.61Å 182.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.96 – 1.80 71.96 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (71.96-1.80) 99.9 (71.96-1.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.00 (at 1.80Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.167 , 0.202 0.168 , 0.202	Depositor DCC
$R_{free}$ test set	13782 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.2	Xtrriage
Anisotropy	0.162	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 52.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	19140	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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: 4Q5, MES, GDP, GTP, ACP, CA, 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	0.41	0/3582	0.54	0/4864
1	C	0.55	0/3590	0.60	0/4877
2	B	0.49	0/3559	0.55	0/4817
2	D	0.37	0/3426	0.50	0/4640
3	E	0.43	0/1071	0.46	0/1423
4	F	0.32	0/2794	0.49	0/3772
All	All	0.44	0/18022	0.54	0/24393

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	3467	0	3426	17	0
1	C	3482	0	3416	22	0
2	B	3447	0	3364	34	0
2	D	3347	0	3229	31	0
3	E	1047	0	1067	10	0
4	F	2725	0	2712	31	0
5	A	32	0	12	0	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	C	1	0	0	0	0
8	B	28	0	12	0	0
8	D	28	0	12	0	0
9	B	12	0	12	4	0
10	B	51	0	0	0	0
10	D	51	0	0	0	0
11	F	31	0	14	3	0
12	A	259	0	0	2	0
12	B	314	0	0	10	0
12	C	434	0	0	5	0
12	D	178	0	0	8	0
12	E	67	0	0	3	0
12	F	101	0	0	3	0
All	All	19140	0	17288	140	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (140) 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:320:MET:HG2	4:F:330:ILE:HD11	1.60	0.83
1:C:128:GLN:NE2	12:C:601:HOH:O	2.11	0.83
4:F:40:MET:SD	12:F:595:HOH:O	2.40	0.78
4:F:200:ASP:OD2	4:F:241:THR:OG1	2.05	0.74
3:E:6:MET:N	12:E:202:HOH:O	2.21	0.74
4:F:241:THR:OG1	11:F:402:ACP:O3'	2.07	0.71
4:F:217:ARG:NH1	12:F:501:HOH:O	2.22	0.70
4:F:272:MET:SD	12:F:542:HOH:O	2.48	0.70
4:F:252:ASN:HB3	4:F:255:ARG:HD3	1.74	0.69
2:B:56:ALA:HB3	2:B:60:LYS:HB2	1.75	0.68
2:B:438:ALA:O	12:B:601:HOH:O	2.11	0.67
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.78	0.65
1:A:88:HIS:CE1	1:A:90:GLU:HB2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.37	0.64
2:D:180:THR:OG1	12:D:601:HOH:O	2.14	0.64
2:D:158:ARG:HG2	3:E:123:LEU:HD11	1.80	0.64
2:B:88:ARG:NH1	12:B:609:HOH:O	2.30	0.64
1:A:209[A]:ILE:HD11	1:A:302[A]:MET:SD	2.38	0.63
3:E:108[B]:ASN:ND2	12:E:204:HOH:O	2.31	0.62
4:F:280:GLU:HA	4:F:284:LEU:HB2	1.81	0.62
4:F:88:SER:OG	4:F:90:SER:O	2.19	0.61
1:A:97:GLU:OE2	2:B:2:ARG:NH1	2.33	0.60
2:D:432:TYR:OH	12:D:602:HOH:O	2.14	0.60
4:F:318:ASP:OD2	11:F:402:ACP:O3G	2.19	0.59
4:F:16:GLU:OE2	4:F:19:ARG:NH2	2.35	0.59
4:F:134:ALA:O	4:F:138:ARG:HG2	2.01	0.59
1:C:133:GLN:NE2	12:C:608:HOH:O	2.35	0.58
2:B:147[A]:SER:HG	2:B:190:SER:HG	1.52	0.58
1:C:1:MET:O	12:C:602:HOH:O	2.18	0.57
2:B:241[B]:CYS:SG	12:B:779:HOH:O	2.57	0.57
2:D:248:LEU:HD23	2:D:354:ALA:HB2	1.87	0.55
3:E:90[B]:ASN:OD1	12:E:201:HOH:O	2.17	0.55
2:D:414:ASP:OD1	2:D:415:GLU:N	2.40	0.55
2:D:39:ASP:OD1	2:D:39:ASP:N	2.39	0.54
2:B:147[A]:SER:OG	2:B:190:SER:OG	2.24	0.54
1:C:181[B]:VAL:HG12	12:D:615:HOH:O	2.07	0.54
4:F:135:TYR:CE2	4:F:166:ALA:HB2	2.43	0.53
2:D:278:ARG:H	2:D:278:ARG:HD2	1.72	0.53
1:A:68[B]:VAL:HG12	1:A:93:ILE:HB	1.90	0.53
1:C:180:ALA:O	1:C:183:GLU:HG3	2.09	0.53
2:D:177:VAL:HG21	2:D:206:ASN:HB3	1.90	0.52
4:F:7:ARG:HD3	4:F:40:MET:HE3	1.90	0.52
4:F:126:ASP:OD1	4:F:128:ARG:HB2	2.09	0.52
1:A:71:GLU:HB2	1:A:98:ASP:HB3	1.92	0.51
2:B:327:GLU:OE2	12:B:604:HOH:O	2.19	0.51
2:D:97:SER:OG	12:D:603:HOH:O	2.19	0.51
2:D:278:ARG:H	2:D:278:ARG:CD	2.21	0.51
1:A:71:GLU:HG2	1:A:72:PRO:HD2	1.91	0.51
2:B:88:ARG:NH1	2:B:90:ASP:HB2	2.25	0.51
2:B:224:TYR:OH	12:B:602:HOH:O	2.18	0.51
2:D:167:ASN:ND2	12:D:613:HOH:O	2.42	0.51
2:B:159:GLU:OE1	12:B:603:HOH:O	2.19	0.51
1:A:88:HIS:ND1	1:A:90:GLU:OE1	2.44	0.51
4:F:40:MET:HE2	4:F:47:LEU:HG	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:401:ARG:HE	2:D:403:ALA:HB2	1.75	0.50
1:A:277:SER:HB3	1:A:280:LYS:HG3	1.92	0.50
2:B:197:ASN:HD21	3:E:75:LYS:NZ	2.09	0.50
2:B:6:HIS:CD2	2:B:21:TRP:HE1	2.30	0.49
2:B:155[B]:SER:OG	3:E:76:ARG:NH2	2.44	0.49
1:C:181[B]:VAL:HG11	1:C:404:PHE:CZ	2.48	0.49
1:C:211:ASP:O	1:C:215:ARG:HD2	2.11	0.49
1:C:221:ARG:HG3	2:D:325:MET:HG2	1.94	0.49
2:D:373:MET:HE1	12:D:755:HOH:O	2.13	0.49
1:A:88:HIS:HE1	1:A:90:GLU:HB2	1.78	0.49
2:B:253[B]:ARG:NH1	9:B:503:MES:O3S	2.41	0.49
1:C:343:PHE:HD2	1:C:347[A]:CYS:SG	2.36	0.49
3:E:9:ILE:HG13	3:E:10:GLU:HG3	1.95	0.48
1:C:234:ILE:HG21	1:C:302:MET:SD	2.53	0.48
4:F:135:TYR:CZ	4:F:166:ALA:HB2	2.48	0.48
1:A:187:SER:HB3	1:A:391:LEU:HD21	1.95	0.48
1:C:26:LEU:HD12	1:C:363[B]:VAL:HG12	1.96	0.48
4:F:151:SER:HG	4:F:180:HIS:CD2	2.32	0.47
2:B:50[B]:ASN:H	2:B:50[B]:ASN:ND2	2.13	0.47
4:F:161:LEU:HD23	4:F:169:LEU:HD23	1.96	0.47
4:F:247:LYS:HG3	4:F:253:TYR:CE2	2.49	0.47
4:F:140:GLU:HA	4:F:141:GLY:HA2	1.57	0.47
2:D:400:ARG:HG2	2:D:401:ARG:N	2.29	0.47
2:B:22:GLU:HG2	2:B:83:PHE:CD1	2.50	0.46
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.50	0.46
1:C:167:LEU:HG	1:C:200:CYS:HB3	1.96	0.46
1:C:298:PRO:HG2	1:C:308:ARG:NH2	2.30	0.46
1:C:285:GLN:NE2	12:C:623:HOH:O	2.48	0.46
3:E:44:ASP:HB3	3:E:45:PRO:HD3	1.98	0.46
2:D:1:MET:HE2	12:D:776:HOH:O	2.15	0.45
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.34	0.45
2:D:106:GLY:O	2:D:111:GLY:HA3	2.17	0.45
2:B:2:ARG:HB3	2:B:133:GLN:HG2	1.98	0.45
2:B:289:PRO:O	2:B:293:GLN:HG2	2.17	0.45
1:A:180:ALA:O	1:A:183:GLU:HG3	2.17	0.45
2:D:171:VAL:HA	2:D:204:ILE:O	2.17	0.45
4:F:220[A]:VAL:HG12	4:F:263:PHE:CE1	2.52	0.45
4:F:292:ARG:NH1	4:F:379:HIS:O	2.50	0.45
2:B:253[B]:ARG:NH2	9:B:503:MES:O2S	2.44	0.44
4:F:268:ASN:O	4:F:272:MET:HG3	2.17	0.44
2:B:16[B]:ILE:HD13	2:B:231:VAL:HG11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:503:MES:H51	9:B:503:MES:H82	1.59	0.44
1:C:174:ALA:O	1:C:178:SER:HB3	2.18	0.44
2:D:292:THR:HG22	2:D:335:VAL:HG21	2.00	0.44
2:B:218:LYS:NZ	12:B:624:HOH:O	2.51	0.43
2:D:1:MET:HG3	2:D:130:ASP:OD2	2.18	0.43
2:D:109:THR:O	2:D:113:GLU:HG3	2.17	0.43
2:D:388:PHE:HD1	2:D:425:MET:HE3	1.83	0.43
2:D:278:ARG:HD2	2:D:278:ARG:N	2.34	0.43
3:E:72:LEU:O	3:E:76:ARG:HG2	2.18	0.43
4:F:188:LYS:HD3	4:F:323:GLU:OE1	2.18	0.43
2:D:19:LYS:HA	2:D:19:LYS:HD3	1.86	0.43
4:F:151:SER:HG	4:F:180:HIS:CE1	2.31	0.43
1:A:196:GLU:OE1	12:A:601:HOH:O	2.21	0.43
4:F:186:LEU:HD13	4:F:320:MET:HE2	2.01	0.43
1:A:209[A]:ILE:HG23	1:A:230:LEU:HD23	1.99	0.43
2:D:74:THR:O	2:D:77:SER:HB2	2.19	0.43
2:B:315:VAL:HB	2:B:351:VAL:HG22	2.00	0.43
1:C:254:GLU:OE1	12:C:603:HOH:O	2.22	0.43
4:F:84:SER:O	4:F:88:SER:N	2.51	0.43
4:F:87:LEU:O	4:F:91:CYS:HB2	2.19	0.42
4:F:200:ASP:OD1	4:F:222:ARG:NE	2.32	0.42
2:D:88:ARG:NH1	2:D:90:ASP:HB2	2.34	0.42
1:C:93:ILE:HD11	1:C:121:ARG:HG3	2.00	0.42
1:C:104:ALA:HB2	1:C:413:MET:SD	2.60	0.42
2:D:136:GLN:HA	2:D:167:ASN:O	2.19	0.42
2:B:158:ARG:CZ	9:B:503:MES:H21	2.49	0.42
2:B:167:ASN:ND2	12:B:628:HOH:O	2.52	0.41
2:B:334:ASN:HD21	2:B:338:LYS:NZ	2.17	0.41
1:C:385:ALA:HA	1:C:388:TRP:CD1	2.55	0.41
1:A:209[A]:ILE:HG22	1:A:227:LEU:HD22	2.02	0.41
2:B:396:THR:HG23	12:B:631:HOH:O	2.20	0.41
2:B:438:ALA:C	2:B:439:THR:N	2.74	0.41
1:C:346:TRP:CZ3	1:C:347[B]:CYS:SG	3.14	0.41
1:C:270:ALA:HB3	1:C:302:MET:HE2	2.02	0.41
4:F:331:GLU:OE2	11:F:402:ACP:O2B	2.38	0.41
2:B:19:LYS:HA	2:B:19:LYS:HD3	1.94	0.41
2:B:160:GLU:HG3	12:B:758:HOH:O	2.20	0.41
2:B:171:VAL:HA	2:B:204:ILE:O	2.21	0.41
2:B:195[B]:VAL:HG12	2:B:267:PHE:CE2	2.56	0.41
2:D:74:THR:OG1	12:D:604:HOH:O	2.21	0.41
2:D:172:MET:HG3	2:D:387:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:ARG:HG3	2:B:325:MET:HB3	2.02	0.40
2:B:147[B]:SER:OG	2:B:148:GLY:N	2.55	0.40
3:E:81:GLU:HA	3:E:84[B]:GLN:HG2	2.03	0.40
1:A:160:ASP:OD2	12:A:602:HOH:O	2.22	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	447/451 (99%)	439 (98%)	8 (2%)	0	100	100
1	C	449/451 (100%)	437 (97%)	12 (3%)	0	100	100
2	B	440/445 (99%)	435 (99%)	5 (1%)	0	100	100
2	D	423/445 (95%)	417 (99%)	6 (1%)	0	100	100
3	E	125/143 (87%)	125 (100%)	0	0	100	100
4	F	320/384 (83%)	314 (98%)	6 (2%)	0	100	100
All	All	2204/2319 (95%)	2167 (98%)	37 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	380/379 (100%)	375 (99%)	5 (1%)	69	62
1	C	382/379 (101%)	378 (99%)	4 (1%)	76	71
2	B	385/383 (100%)	380 (99%)	5 (1%)	69	62
2	D	370/383 (97%)	362 (98%)	8 (2%)	52	39
3	E	116/127 (91%)	112 (97%)	4 (3%)	37	22
4	F	301/342 (88%)	292 (97%)	9 (3%)	41	27
All	All	1934/1993 (97%)	1899 (98%)	35 (2%)	57	48

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	46	ASP
1	A	55	GLU
1	A	221	ARG
1	A	381	THR
2	B	90	ASP
2	B	139	HIS
2	B	322	ARG
2	B	325	MET
2	B	372	LYS
1	C	71	GLU
1	C	220	GLU
1	C	335	ILE
1	C	384	ILE
2	D	139	HIS
2	D	179	ASP
2	D	221	THR
2	D	277	SER
2	D	278	ARG
2	D	298	SER
2	D	400	ARG
2	D	405	LEU
3	E	46	SER
3	E	107	SER
3	E	139	LEU
3	E	141	GLU
4	F	1	MET
4	F	31	ARG
4	F	91	CYS
4	F	161	LEU

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Mol	Chain	Res	Type
4	F	164	SER
4	F	171	ASP
4	F	192	LEU
4	F	211	TYR
4	F	238	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	334	ASN

### 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 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	GDP	B	501	6	24,30,30	1.11	2 (8%)	30,47,47	1.38	4 (13%)
9	MES	B	503	-	12,12,12	2.30	1 (8%)	14,16,16	2.52	7 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
10	4Q5	D	503	-	52,52,52	1.29	2 (3%)	55,72,72	1.94	10 (18%)
5	GTP	C	501	6	26,34,34	0.86	0	32,54,54	1.33	5 (15%)
11	ACP	F	402	6	27,33,33	1.44	4 (14%)	32,52,52	1.40	4 (12%)
10	4Q5	B	504	-	52,52,52	1.47	5 (9%)	55,72,72	1.76	9 (16%)
5	GTP	A	501	6	26,34,34	0.94	1 (3%)	32,54,54	1.33	3 (9%)
8	GDP	D	501	6	24,30,30	0.88	1 (4%)	30,47,47	1.16	3 (10%)

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
8	GDP	B	501	6	-	5/12/32/32	0/3/3/3
9	MES	B	503	-	-	2/6/14/14	0/1/1/1
10	4Q5	D	503	-	-	2/76/86/86	0/2/2/2
5	GTP	C	501	6	-	5/18/38/38	0/3/3/3
11	ACP	F	402	6	-	4/15/38/38	0/3/3/3
10	4Q5	B	504	-	-	1/76/86/86	0/2/2/2
5	GTP	A	501	6	-	6/18/38/38	0/3/3/3
8	GDP	D	501	6	-	4/12/32/32	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	D	503	4Q5	CBN-CBM	-7.94	1.40	1.51
9	B	503	MES	C8-S	-7.69	1.66	1.77
10	B	504	4Q5	CBN-CBM	-6.35	1.42	1.51
10	B	504	4Q5	CBH-CBD	4.17	1.58	1.52
8	B	501	GDP	O4'-C1'	3.66	1.46	1.41
11	F	402	ACP	PG-O3G	3.24	1.62	1.54
11	F	402	ACP	PB-O3A	3.04	1.61	1.58
11	F	402	ACP	PG-O2G	3.02	1.61	1.54
10	D	503	4Q5	CBE-CBD	2.59	1.58	1.53
11	F	402	ACP	C5-C4	2.44	1.47	1.40
10	B	504	4Q5	OBO-CBH	2.19	1.48	1.42
8	B	501	GDP	C6-N1	-2.16	1.34	1.37
10	B	504	4Q5	OBA-CAW	2.15	1.49	1.43
8	D	501	GDP	C6-N1	-2.13	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	501	GTP	C6-N1	-2.10	1.34	1.37
10	B	504	4Q5	CBF-CBG	2.09	1.59	1.51

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	504	4Q5	CAW-CAX-CAY	-6.25	102.76	112.42
9	B	503	MES	C5-N4-C3	6.14	122.64	108.83
10	D	503	4Q5	CBF-CBE-CBD	-5.99	94.09	104.16
10	D	503	4Q5	CBG-NAZ-CBD	-5.74	102.72	111.74
10	B	504	4Q5	CBG-NAZ-CBD	-5.25	103.48	111.74
10	B	504	4Q5	CBE-CBF-CBG	-5.18	90.28	104.98
10	D	503	4Q5	CAW-CAX-CAY	-4.97	104.75	112.42
10	D	503	4Q5	CBE-CBF-CBG	-4.74	91.52	104.98
10	D	503	4Q5	CBG-NAZ-CAY	4.21	138.58	126.04
5	A	501	GTP	O3G-PG-O2G	3.61	121.44	107.64
10	B	504	4Q5	CBF-CBE-CBD	-3.57	98.16	104.16
11	F	402	ACP	PB-O3A-PA	-3.55	121.31	132.56
10	D	503	4Q5	CAQ-NAG-CAR	3.44	126.23	119.46
10	D	503	4Q5	OBO-CBH-CBI	3.38	113.83	105.83
10	B	504	4Q5	CBG-NAZ-CAY	3.37	136.08	126.04
11	F	402	ACP	C3'-C2'-C1'	3.24	105.85	100.98
8	B	501	GDP	O6-C6-C5	-3.20	118.11	124.37
11	F	402	ACP	N3-C2-N1	-3.16	123.74	128.68
9	B	503	MES	C2-C3-N4	3.10	114.81	110.10
9	B	503	MES	O1S-S-C8	2.91	110.42	106.92
9	B	503	MES	O3S-S-C8	2.68	110.11	105.77
9	B	503	MES	C7-N4-C5	2.68	118.08	111.23
10	D	503	4Q5	OBC-CAY-CAX	-2.65	117.41	122.20
8	D	501	GDP	C8-N7-C5	2.65	108.04	102.99
8	B	501	GDP	C5-C6-N1	2.64	118.62	113.95
5	C	501	GTP	C5-C6-N1	2.62	118.58	113.95
5	C	501	GTP	O6-C6-C5	-2.55	119.40	124.37
8	B	501	GDP	C8-N7-C5	2.54	107.82	102.99
10	D	503	4Q5	CBS-CBL-CBM	-2.49	110.31	112.67
5	C	501	GTP	C8-N7-C5	2.47	107.69	102.99
9	B	503	MES	C7-N4-C3	2.47	117.54	111.23
11	F	402	ACP	C4-C5-N7	-2.45	106.85	109.40
8	D	501	GDP	PA-O3A-PB	-2.30	124.94	132.83
5	A	501	GTP	O6-C6-C5	-2.22	120.03	124.37
8	B	501	GDP	O6-C6-N1	2.21	123.26	120.65
5	A	501	GTP	C8-N7-C5	2.17	107.12	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	503	MES	O1-C2-C3	2.16	116.54	111.80
5	C	501	GTP	O3G-PG-O2G	2.15	115.87	107.64
5	C	501	GTP	O3'-C3'-C4'	-2.14	104.86	111.05
10	B	504	4Q5	CBQ-CBI-CBH	-2.14	108.08	112.92
10	B	504	4Q5	CAF-CAE-NAD	-2.13	103.02	108.03
8	D	501	GDP	C5-C6-N1	2.09	117.64	113.95
10	B	504	4Q5	CAV-CAS-CAT	-2.08	106.50	111.78
10	D	503	4Q5	CAV-CAS-CAT	-2.04	106.61	111.78
10	B	504	4Q5	CAQ-NAG-CAR	2.03	123.45	119.46

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	PB-O3B-PG-O2G
5	A	501	GTP	PB-O3B-PG-O3G
5	A	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	PB-O3B-PG-O3G
5	C	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	C5'-O5'-PA-O2A
8	B	501	GDP	C5'-O5'-PA-O1A
8	D	501	GDP	C5'-O5'-PA-O1A
9	B	503	MES	C8-C7-N4-C5
11	F	402	ACP	PG-C3B-PB-O1B
11	F	402	ACP	PG-C3B-PB-O2B
11	F	402	ACP	PG-C3B-PB-O3A
9	B	503	MES	N4-C7-C8-S
10	B	504	4Q5	CBS-CBL-CBM-CBN
10	D	503	4Q5	CBS-CBL-CBM-CBN
5	A	501	GTP	C5'-O5'-PA-O2A
8	B	501	GDP	C5'-O5'-PA-O2A
8	D	501	GDP	C5'-O5'-PA-O2A
5	A	501	GTP	C5'-O5'-PA-O3A
5	C	501	GTP	C5'-O5'-PA-O3A
8	B	501	GDP	C5'-O5'-PA-O3A
8	D	501	GDP	C5'-O5'-PA-O3A
5	C	501	GTP	C4'-C5'-O5'-PA
8	B	501	GDP	PB-O3A-PA-O1A
8	B	501	GDP	PB-O3A-PA-O2A
8	D	501	GDP	PB-O3A-PA-O2A
11	F	402	ACP	C5'-O5'-PA-O1A
5	A	501	GTP	PB-O3B-PG-O1G

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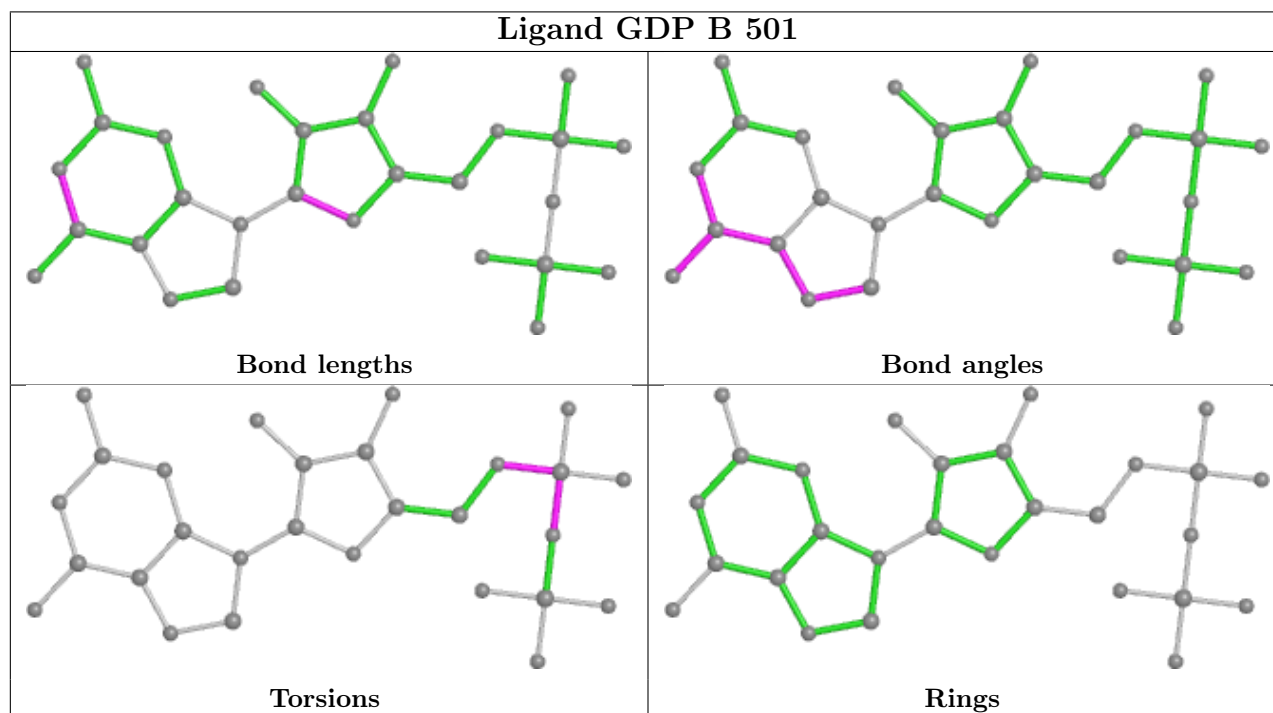
Mol	Chain	Res	Type	Atoms
10	D	503	4Q5	CAX-CAW-OBA-CBB

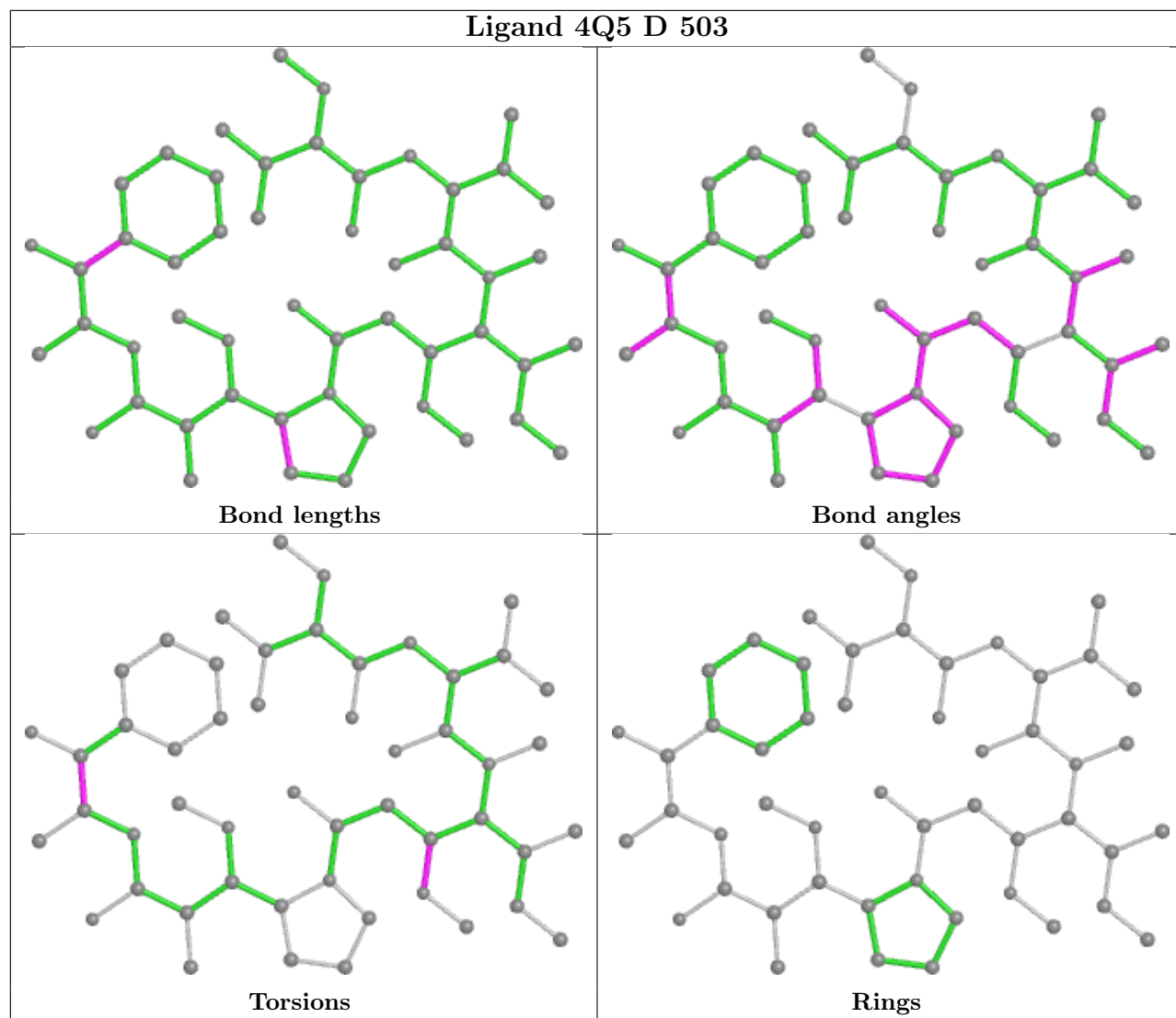
There are no ring outliers.

2 monomers are involved in 7 short contacts:

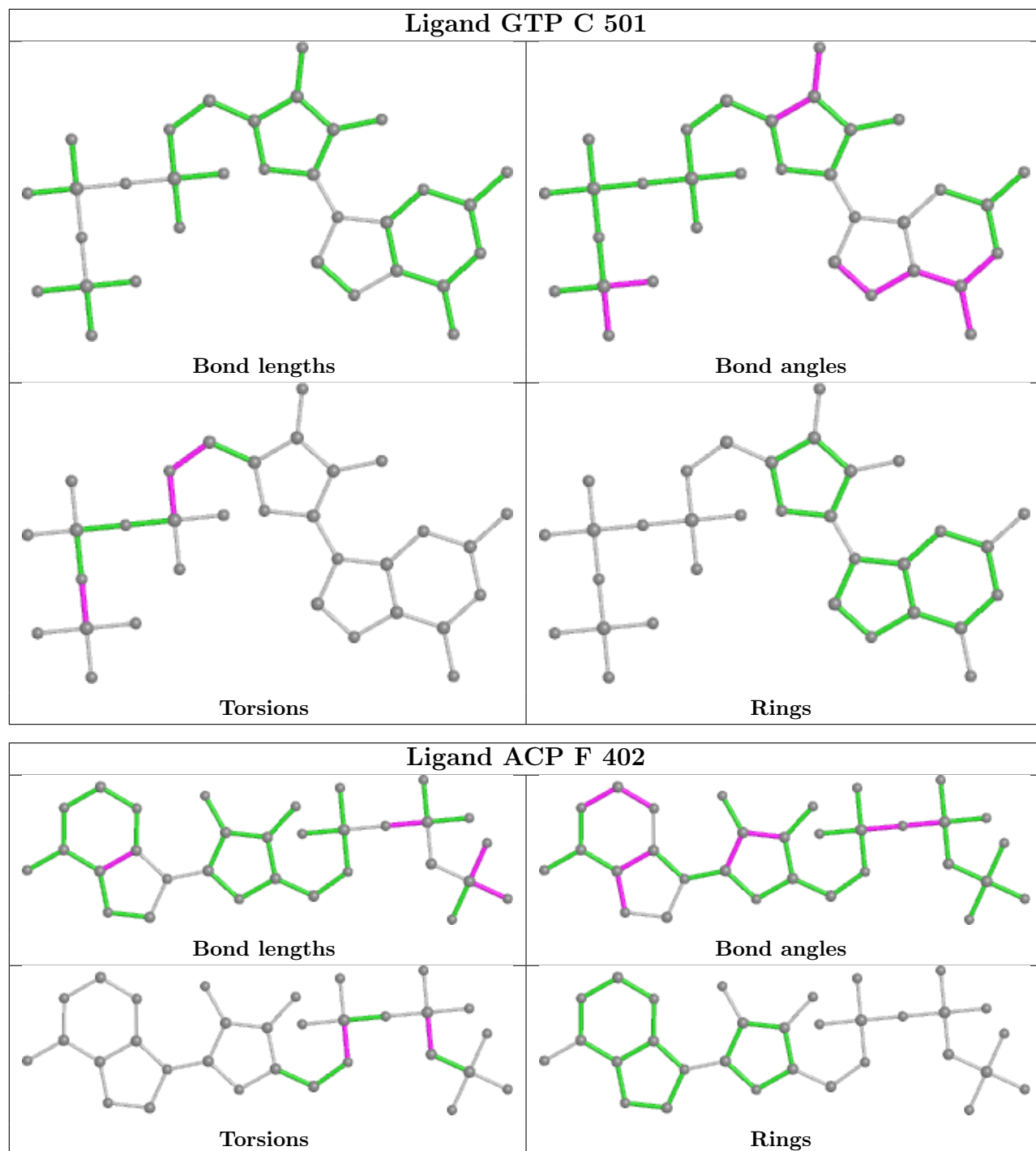
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	503	MES	4	0
11	F	402	ACP	3	0

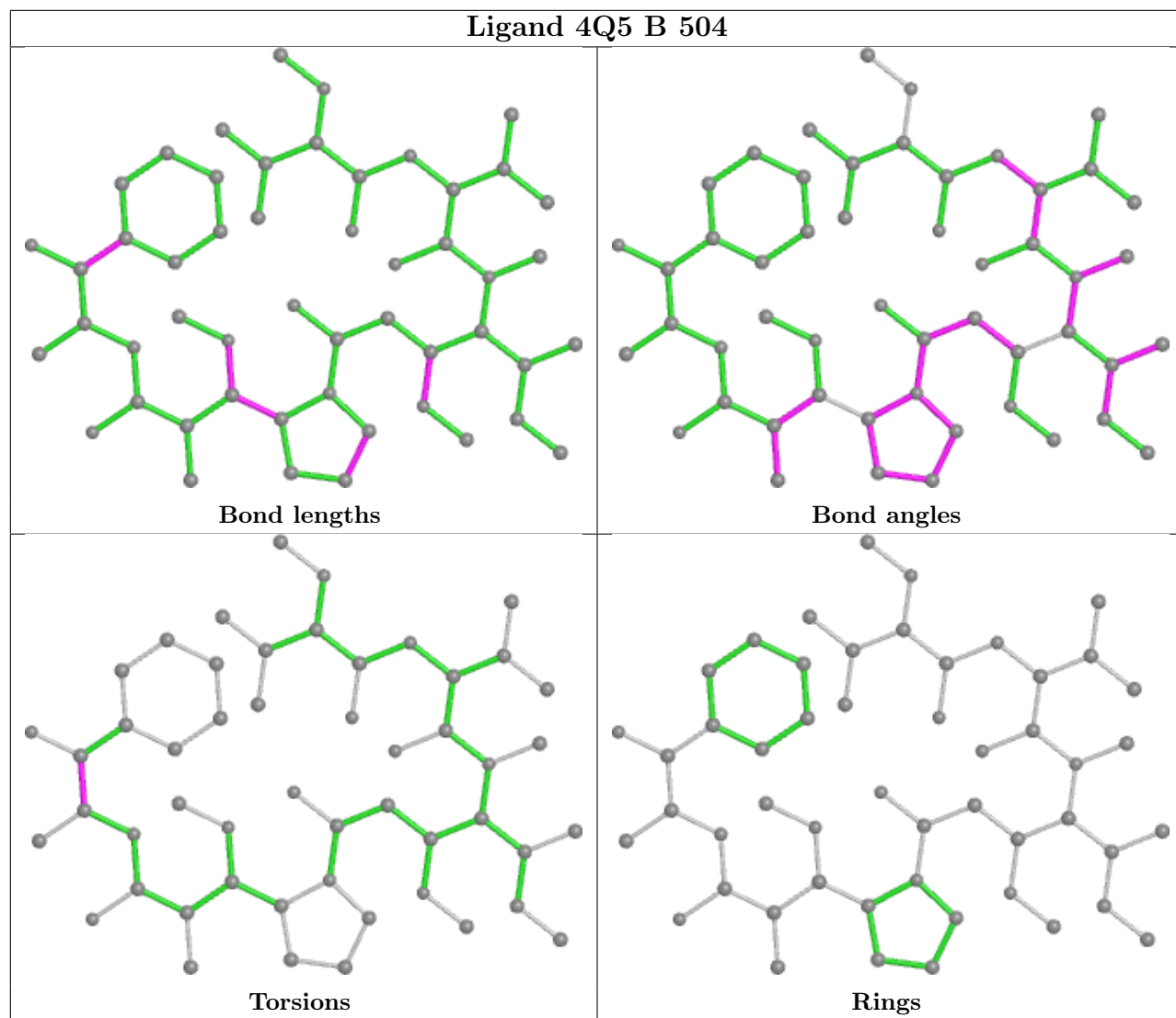
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

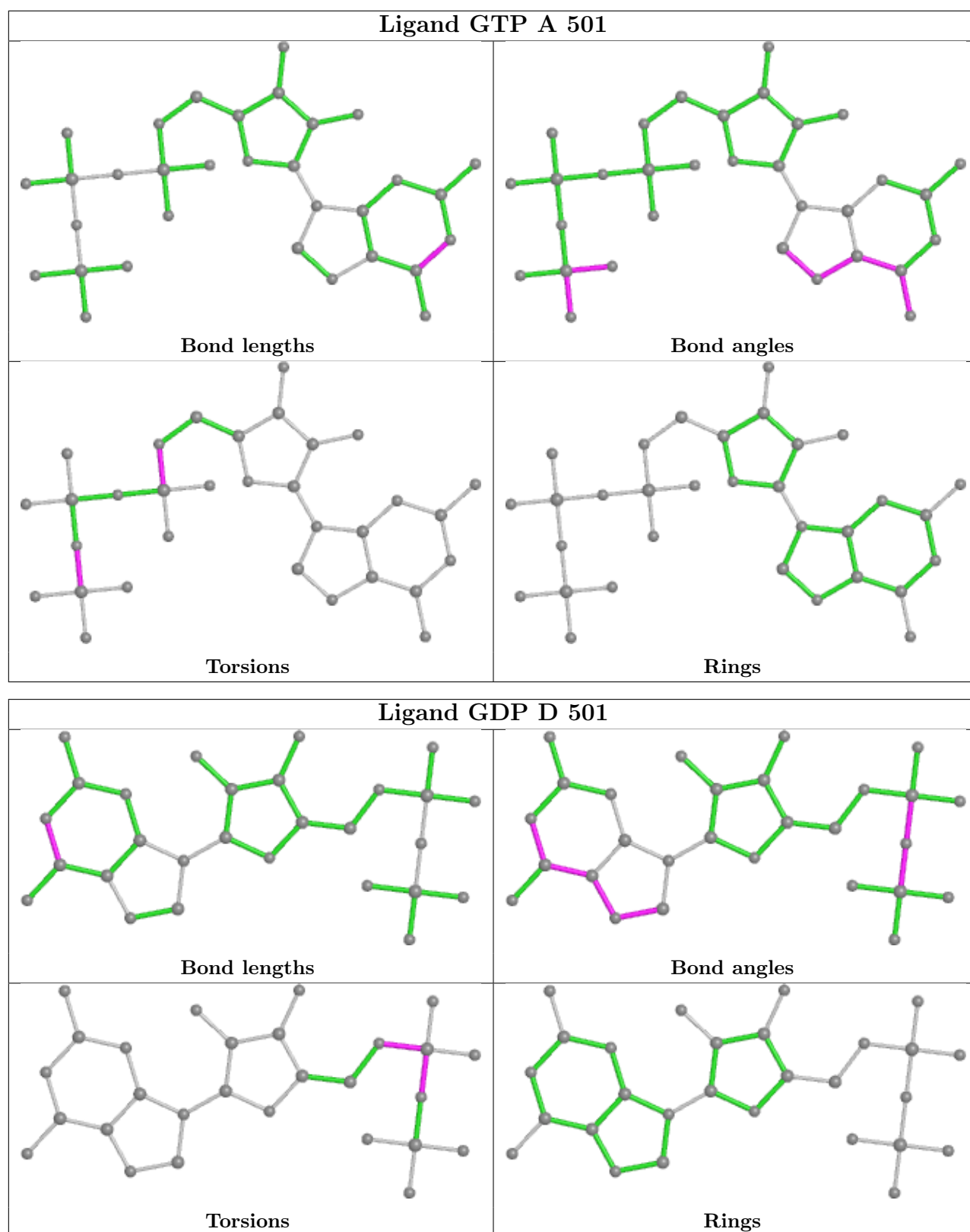












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	438:ALA	C	439:THR	N	2.74

## 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%)	-0.20	3 (0%) 87 86	32, 49, 83, 104	0
1	C	440/451 (97%)	-0.12	1 (0%) 95 93	26, 37, 61, 103	0
2	B	430/445 (96%)	-0.07	6 (1%) 75 72	27, 41, 79, 132	2 (0%)
2	D	424/445 (95%)	0.00	12 (2%) 53 47	33, 54, 86, 121	3 (0%)
3	E	123/143 (86%)	0.08	4 (3%) 46 40	34, 61, 96, 132	0
4	F	331/384 (86%)	0.80	68 (20%) 1 0	39, 69, 125, 156	0
All	All	2185/2319 (94%)	0.05	94 (4%) 35 29	26, 49, 95, 156	5 (0%)

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	161	LEU	7.6
4	F	173	ILE	7.3
4	F	169	LEU	7.1
4	F	249	TYR	6.2
2	D	57	THR	6.0
4	F	170	LEU	5.3
4	F	251	LYS	5.3
4	F	244	CYS	5.1
4	F	245	ILE	5.0
4	F	186	LEU	4.8
4	F	172	PHE	4.8
4	F	151	SER	4.6
4	F	100	ILE	4.5
4	F	248	GLU	4.4
4	F	166	ALA	4.3
4	F	182	ILE	4.2
2	D	277	SER	4.2
4	F	250	SER	4.2
4	F	20	LEU	4.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	262	TYR	4.0
4	F	133	ALA	3.8
2	B	281	GLN	3.7
2	D	276	THR	3.7
4	F	148	ILE	3.7
2	D	177	VAL	3.6
4	F	165	GLU	3.5
4	F	160	ILE	3.5
4	F	253	TYR	3.5
4	F	240	LEU	3.5
4	F	252	ASN	3.5
4	F	162	ILE	3.4
4	F	239	HIS	3.4
2	B	439	THR	3.3
4	F	225	SER	3.3
4	F	247	LYS	3.3
4	F	180	HIS	3.2
2	D	56	ALA	3.2
2	D	1	MET	3.1
4	F	259	GLY	3.1
4	F	167	SER	3.1
4	F	181	VAL	3.1
2	D	405	LEU	3.1
4	F	101	TYR	3.1
4	F	255	ARG	3.0
2	B	1	MET	3.0
4	F	256	TYR	3.0
4	F	238	CYS	3.0
3	E	142	GLU	2.9
4	F	145	ASN	2.9
4	F	132	LEU	2.9
1	A	282	TYR	2.8
4	F	136	ASN	2.8
4	F	163	SER	2.8
4	F	227	PRO	2.7
4	F	361	LEU	2.7
3	E	48	GLU	2.7
2	D	58	GLY	2.7
4	F	10	ASN	2.7
2	B	57	THR	2.6
4	F	258	GLU	2.6
4	F	243	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
4	F	192	LEU	2.6
2	D	415	GLU	2.6
2	D	83	PHE	2.5
4	F	102	PRO	2.5
4	F	168	GLU	2.5
4	F	254	GLY	2.4
4	F	149	ALA	2.4
1	A	346	TRP	2.4
4	F	224	SER	2.4
4	F	263	PHE	2.4
4	F	99	VAL	2.3
4	F	164	SER	2.3
4	F	179	VAL	2.3
2	D	400	ARG	2.3
4	F	44	ARG	2.3
4	F	237	THR	2.3
4	F	226	GLU	2.3
4	F	103	THR	2.3
4	F	89	GLU	2.2
4	F	147	TRP	2.2
4	F	174	ASP	2.2
3	E	143	ALA	2.2
2	B	122	VAL	2.2
4	F	330	ILE	2.2
4	F	135	TYR	2.2
4	F	185	TYR	2.2
2	D	404	PHE	2.1
4	F	25	GLY	2.1
1	C	219	ILE	2.1
3	E	139	LEU	2.1
4	F	24	THR	2.1
4	F	242	ASN	2.0
2	B	284	ARG	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

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.

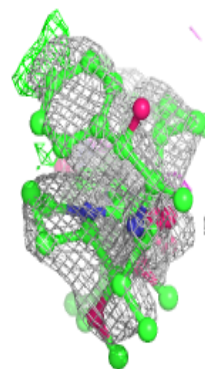
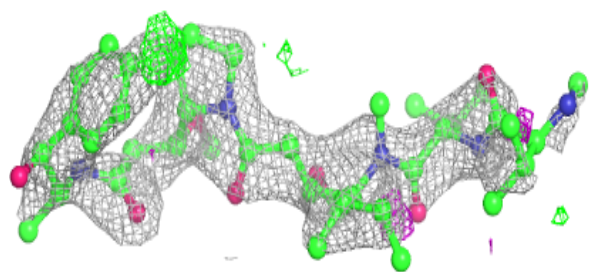
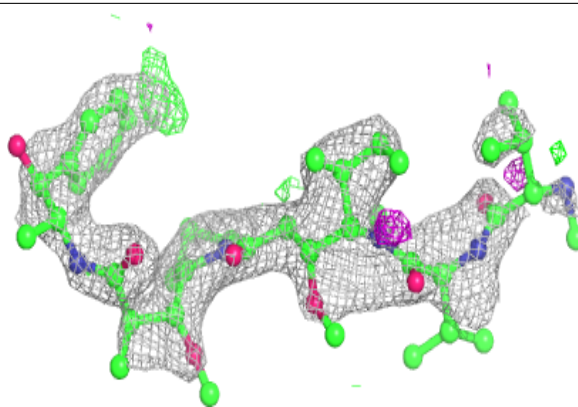
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	MG	B	502	1/1	0.81	0.12	63,63,63,63	0
6	MG	D	502	1/1	0.81	0.13	64,64,64,64	0
10	4Q5	D	503	51/51	0.82	0.34	73,106,125,133	0
6	MG	F	401	1/1	0.86	0.11	78,78,78,78	0
9	MES	B	503	12/12	0.88	0.18	55,86,118,124	0
11	ACP	F	402	31/31	0.91	0.12	61,70,108,130	0
7	CA	C	503	1/1	0.93	0.31	86,86,86,86	0
7	CA	A	503	1/1	0.93	0.05	67,67,67,67	0
6	MG	A	502	1/1	0.96	0.15	37,37,37,37	0
10	4Q5	B	504	51/51	0.97	0.09	26,32,39,42	0
8	GDP	D	501	28/28	0.97	0.09	42,47,57,60	0
6	MG	C	502	1/1	0.97	0.14	32,32,32,32	0
8	GDP	B	501	28/28	0.99	0.12	25,28,30,31	0
5	GTP	C	501	32/32	0.99	0.12	25,30,32,33	0
5	GTP	A	501	32/32	0.99	0.09	30,33,38,39	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.

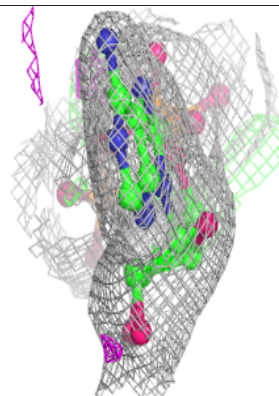
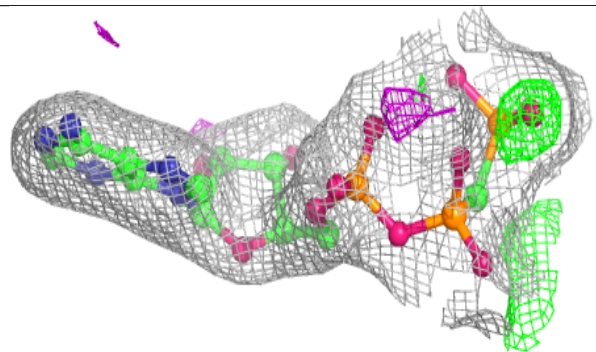
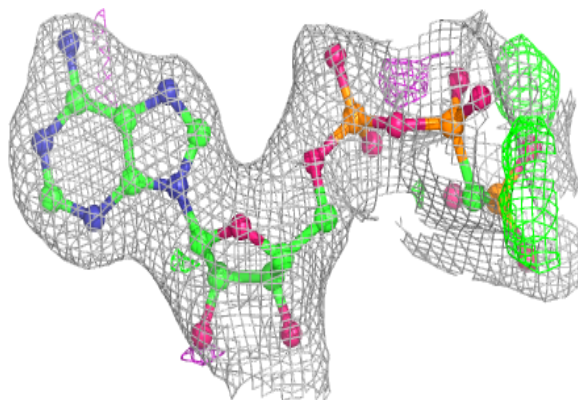


**Electron density around 4Q5 D 503:**

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

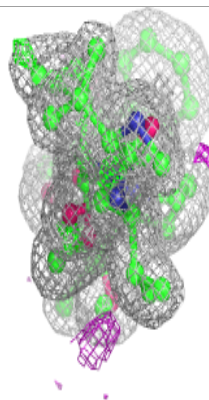
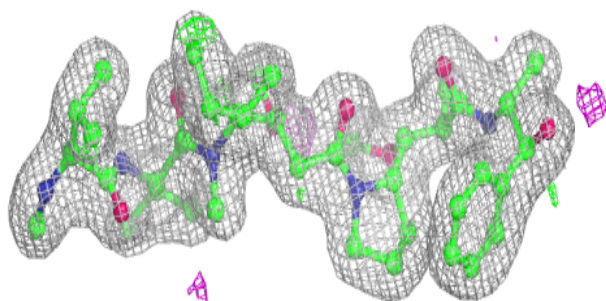
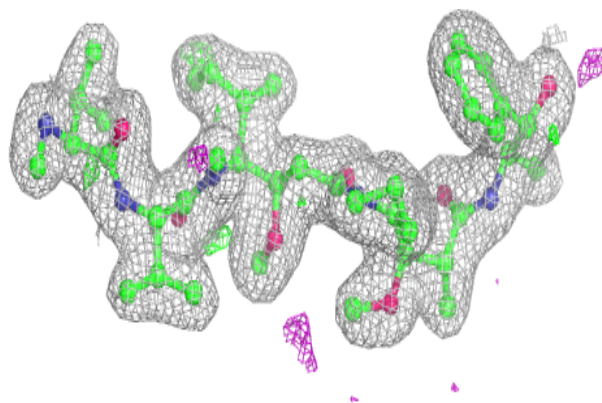
**Electron density around ACP F 402:**

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

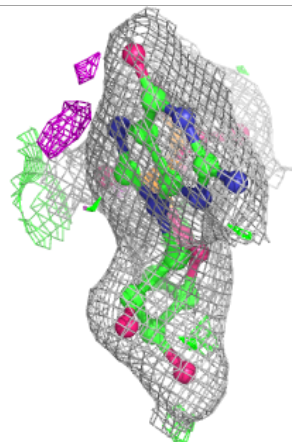
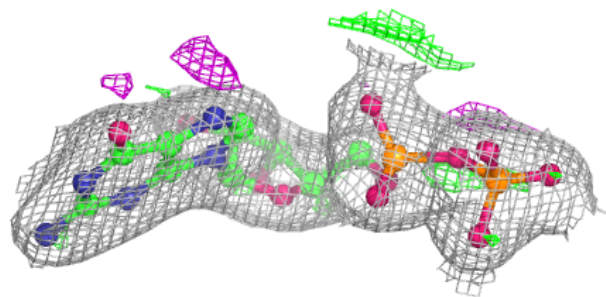
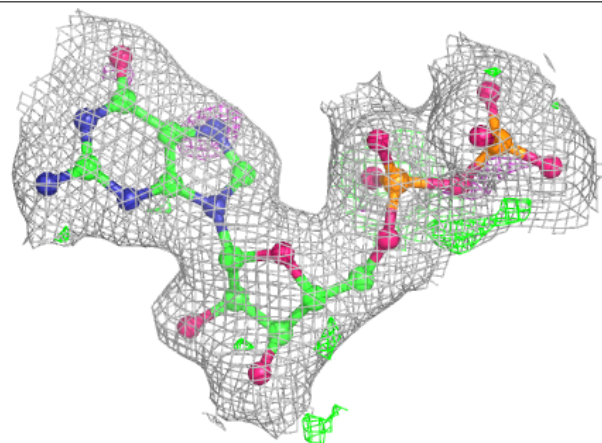


**Electron density around 4Q5 B 504:**

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

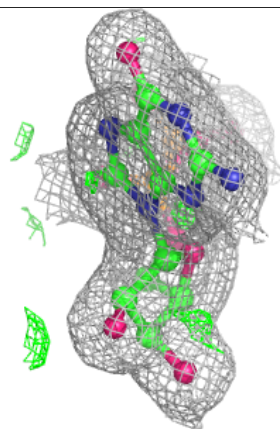
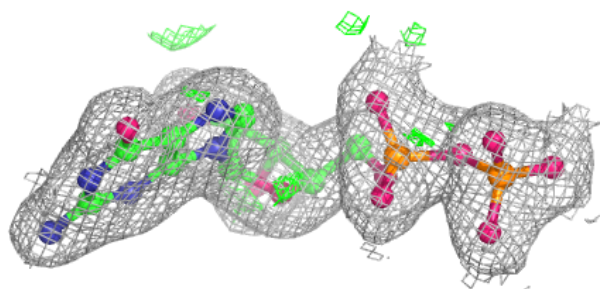
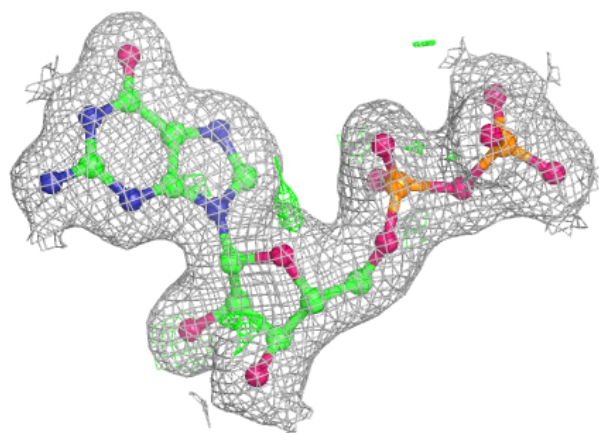
**Electron density around GDP D 501:**

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

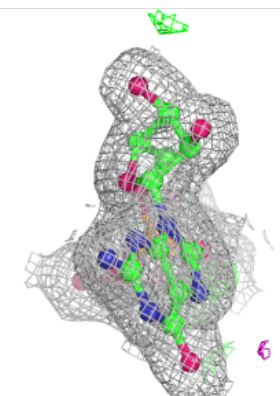
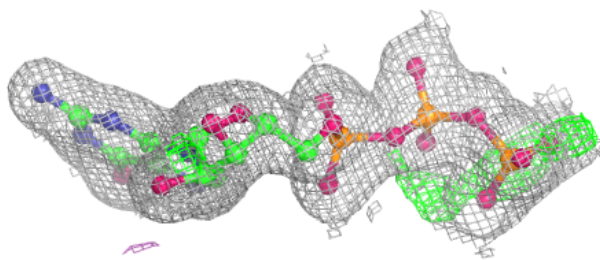
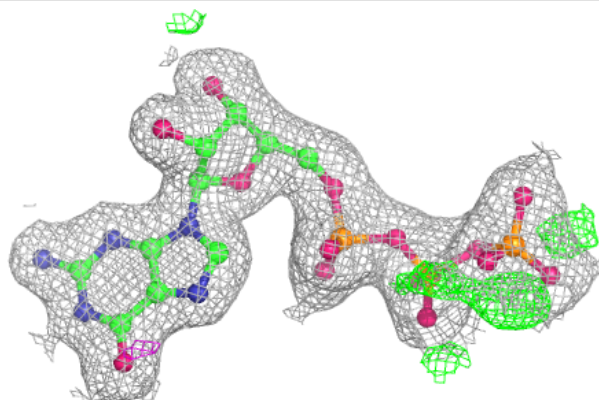


**Electron density around GDP B 501:**

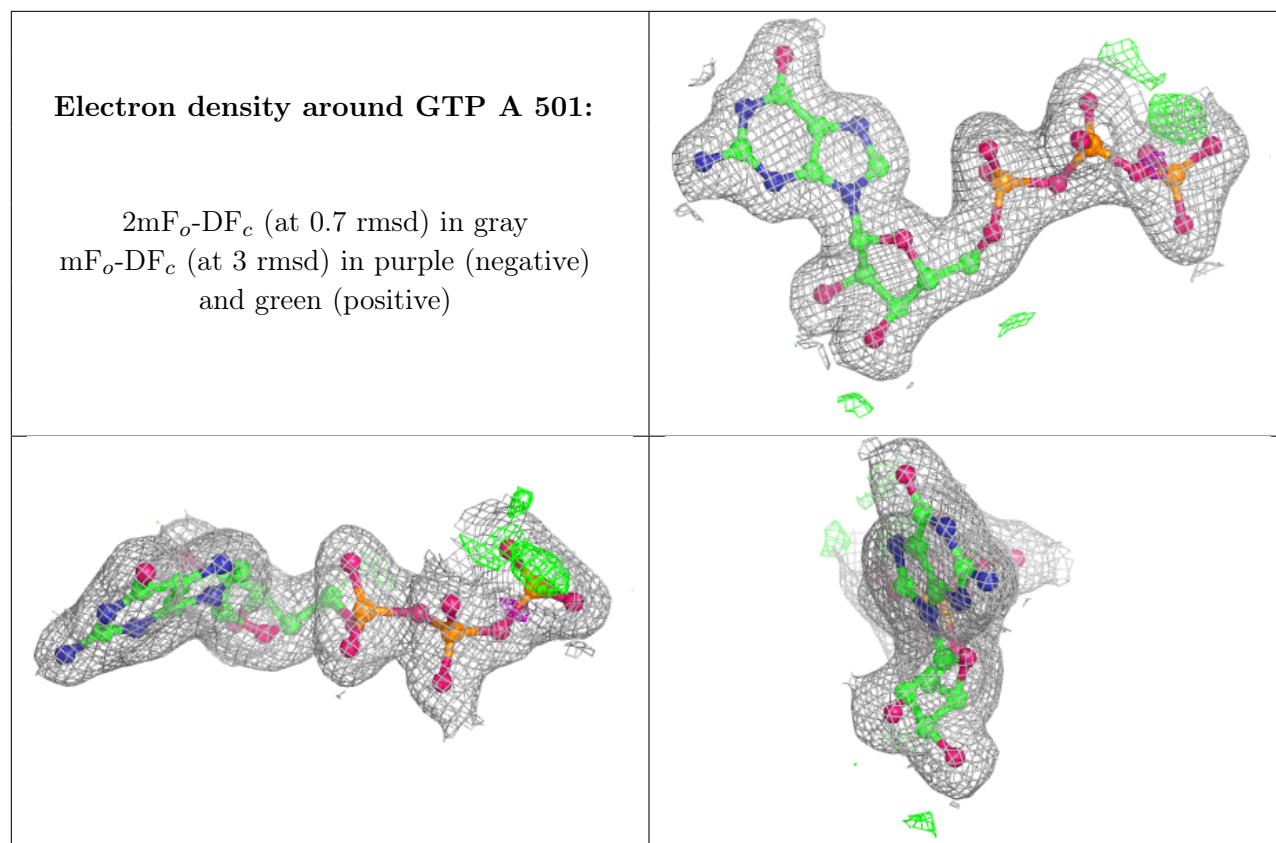
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**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.