



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 21, 2021 – 03:07 PM EDT

PDB ID : 5S5E  
Title : Tubulin-Z1515654336-complex  
Authors : Muehlethaler, T.; Gioia, D.; Protá, A.E.; Sharpe, M.E.; Cavalli, A.; Steinmetz, M.O.  
Deposited on : 2020-11-08  
Resolution : 2.67 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.

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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	:	2.20
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)	:	2.20

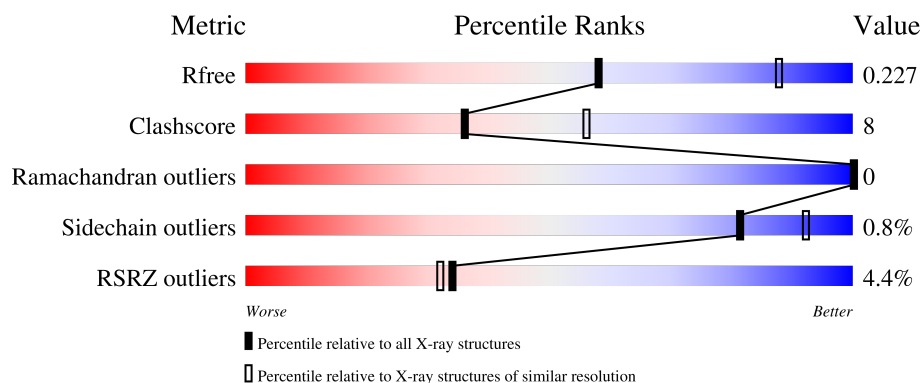
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.67 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	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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	<div> <div>2%</div> <div>79%</div> <div>17%</div> <div>..</div> </div>
1	C	451	<div> <div>81%</div> <div>16%</div> <div>.</div> </div>
2	B	445	<div> <div>3%</div> <div>77%</div> <div>19%</div> <div>.</div> </div>
2	D	445	<div> <div>2%</div> <div>75%</div> <div>20%</div> <div>.</div> </div>
3	E	143	<div> <div>7%</div> <div>81%</div> <div>5%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
4	F	384	<div><div></div><div>13%</div><div>77%</div><div>15%</div><div>8%</div></div>

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 17999 atoms, of which 14 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3424	2167	582	653	22			
1	C	440	Total	C	N	O	S	0	1	0
			3443	2178	585	657	23			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	425	Total	C	N	O	S	2	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
3	E	123	Total	C	N	O	S	0	0	0
			1014	625	183	201	5			

There are 2 discrepancies between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	352	Total	C	N	O	S	0	0	0
			2877	1843	495	525	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
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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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	2	Total	Ca	0	0
			2	2		
7	B	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		

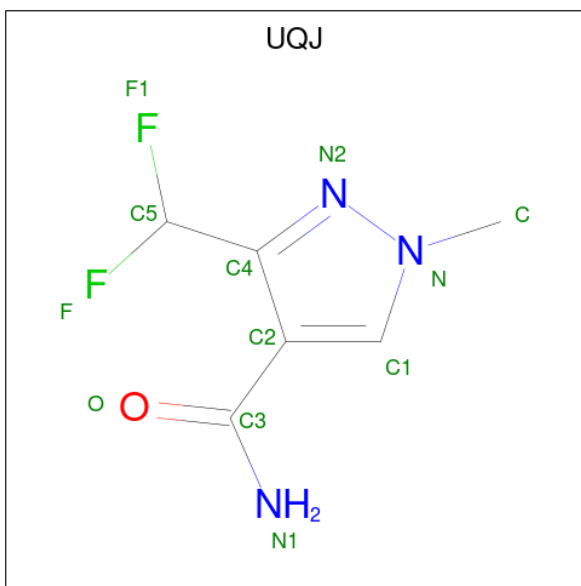
- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).





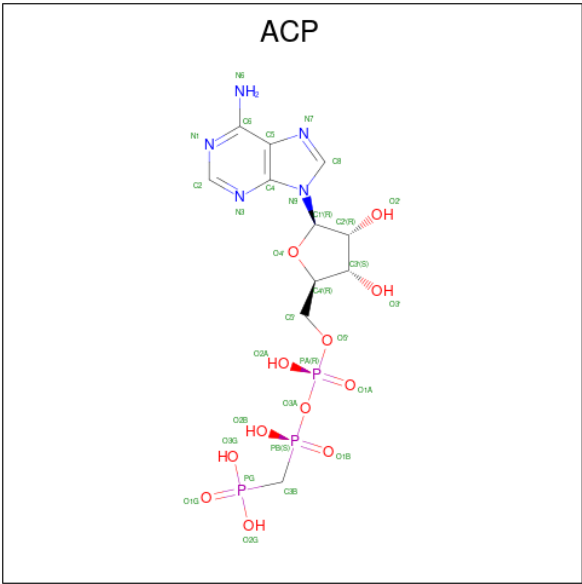
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 10 is 3-(difluoromethyl)-1-methyl-1H-pyrazole-4-carboxamide (three-letter code: UQJ) (formula:  $C_6H_7F_2N_3O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	B	1	Total	C	F	H	N	O	0
			19	6	2	7	3	1	
10	B	1	Total	C	F	H	N	O	0
			19	6	2	7	3	1	

- 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.

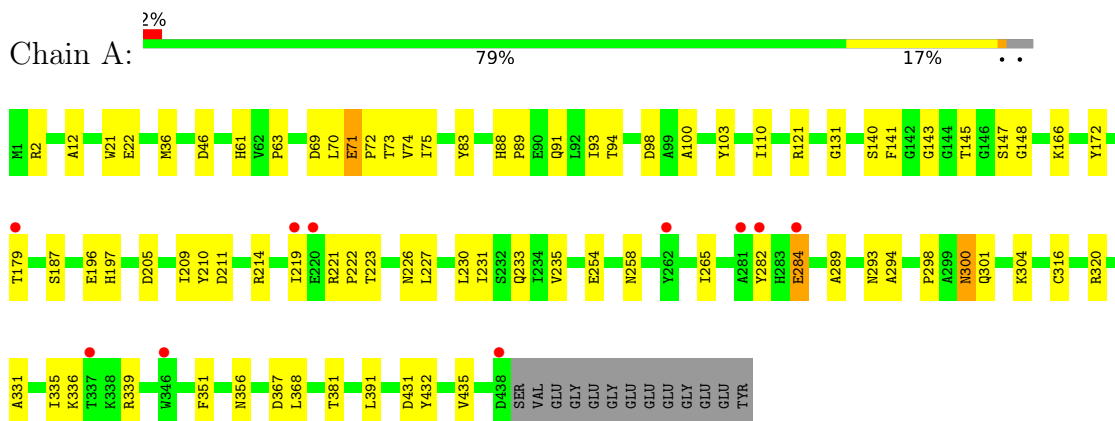
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	55	Total	O	0	0
			55	55		
12	B	67	Total	O	0	0
			67	67		
12	C	166	Total	O	0	0
			166	166		
12	D	27	Total	O	0	0
			27	27		
12	E	5	Total	O	0	0
			5	5		
12	F	9	Total	O	0	0
			9	9		



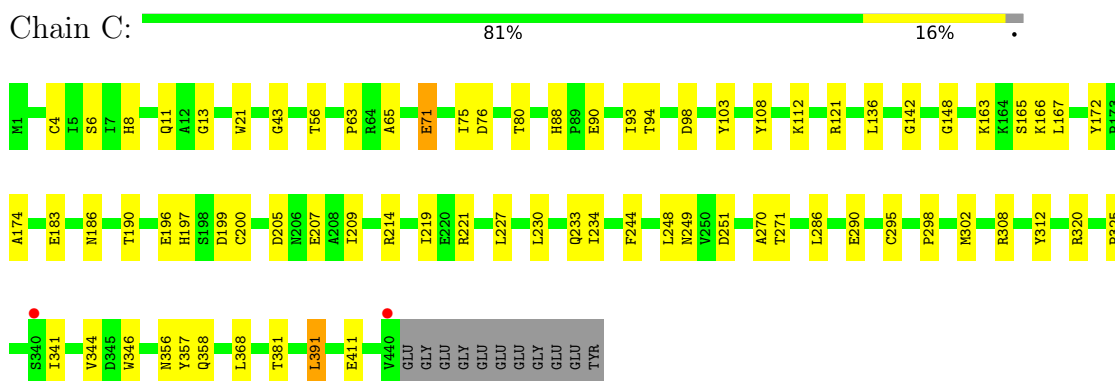
### 3 Residue-property plots [i](#)

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.

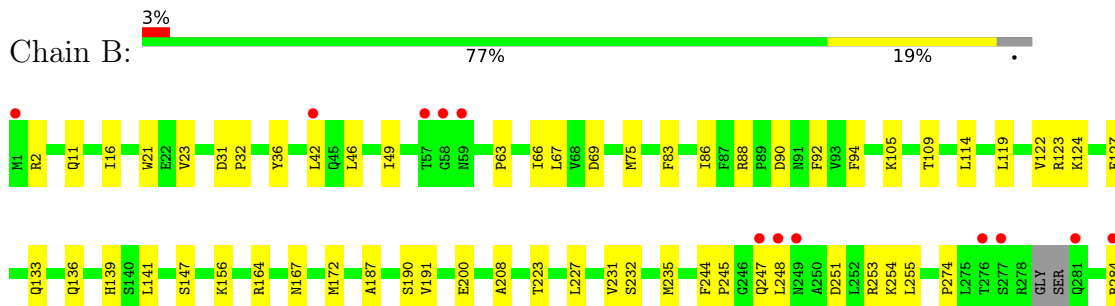
#### • Molecule 1: Tubulin alpha-1B chain

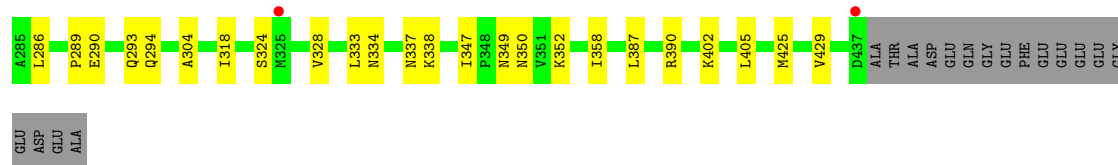


#### • Molecule 1: Tubulin alpha-1B chain

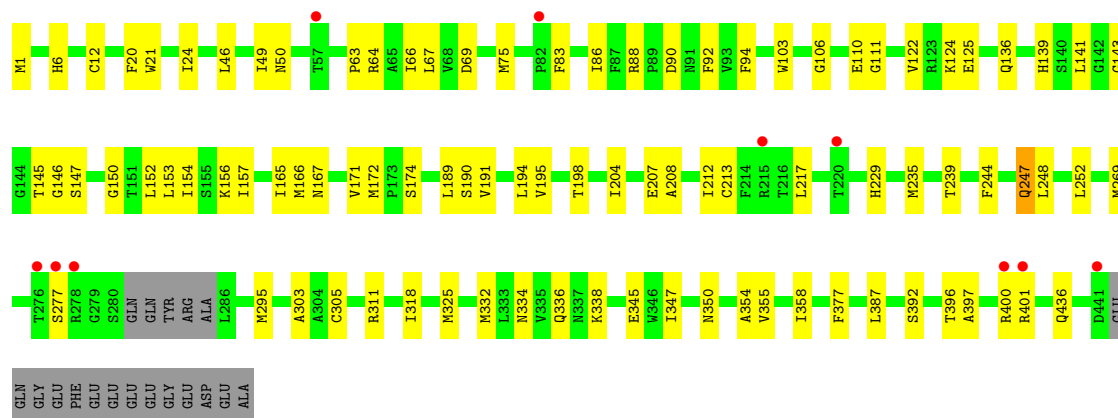
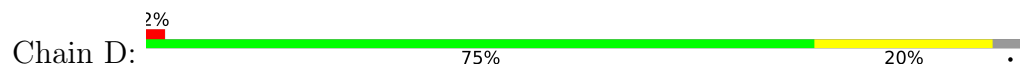


#### • Molecule 2: Tubulin beta-2B chain

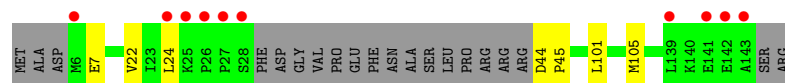
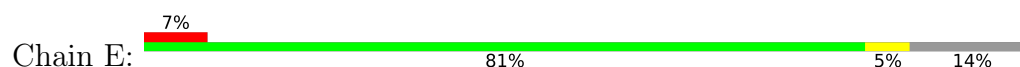




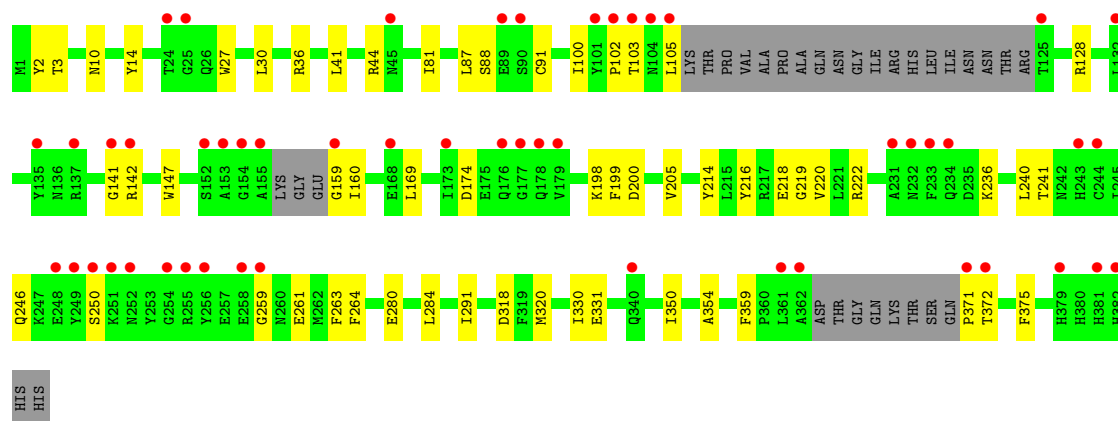
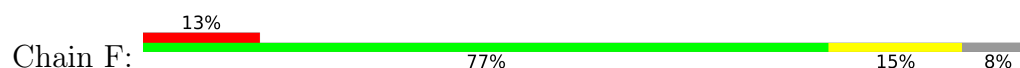
• Molecule 2: Tubulin beta-2B chain



• 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, $\alpha$ , $\beta$ , $\gamma$	105.41Å 159.50Å 179.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.76 – 2.67 29.76 – 2.67	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.76-2.67) 99.8 (29.76-2.67)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 2.68Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.186 , 0.227 0.186 , 0.227	Depositor DCC
$R_{free}$ test set	1997 reflections (2.31%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.1	Xtriage
Anisotropy	0.250	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 40.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	17999	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: CA, MG, MES, GTP, GDP, ACP, UQJ

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	0/3502	0.42	0/4754
1	C	0.26	0/3521	0.43	0/4780
2	B	0.26	0/3433	0.42	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	0/2944	0.40	0/3978
All	All	0.25	0/17838	0.41	0/24141

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	3424	0	3334	62	0
1	C	3443	0	3352	49	0
2	B	3359	0	3235	62	0
2	D	3343	0	3222	63	0
3	E	1014	0	1029	5	0
4	F	2877	0	2839	44	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	2	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
8	B	28	0	12	0	0
8	D	28	0	12	3	0
9	B	12	0	12	2	0
10	B	24	14	0	0	0
11	F	31	0	14	5	0
12	A	55	0	0	4	0
12	B	67	0	0	4	0
12	C	166	0	0	2	0
12	D	27	0	0	0	0
12	E	5	0	0	0	0
12	F	9	0	0	0	0
All	All	17985	14	17085	277	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 8.

All (277) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:ARG:HG3	2:D:325:MET:HG2	1.42	0.99
2:D:1:MET:HG3	2:D:50:ASN:HB2	1.56	0.88
1:A:335:ILE:HG23	1:A:339:ARG:HG3	1.62	0.81
1:C:209:ILE:HD11	1:C:302:MET:HE3	1.62	0.81
4:F:102:PRO:HG2	4:F:105:LEU:HD13	1.65	0.78
4:F:318:ASP:OD2	11:F:401:ACP:O2G	2.01	0.77
1:A:71:GLU:OE2	1:A:73:THR:OG1	2.03	0.76
4:F:241:THR:OG1	11:F:401:ACP:O3'	2.03	0.74
4:F:236:LYS:HB3	4:F:240:LEU:HD13	1.68	0.73
2:D:347:ILE:HG22	2:D:350:ASN:HB3	1.69	0.72
2:B:11:GLN:OE1	12:B:601:HOH:O	2.07	0.72
2:D:217:LEU:HA	2:D:277:SER:HB3	1.72	0.72
2:D:136:GLN:HA	2:D:167:ASN:O	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:83:PHE:O	2:B:86:ILE:HG22	1.91	0.71
1:C:270:ALA:O	1:C:302:MET:HG2	1.91	0.70
2:D:334:ASN:HD21	2:D:338:LYS:HE3	1.57	0.68
2:B:253[A]:ARG:NH1	9:B:504:MES:O2S	2.27	0.67
1:C:76:ASP:O	1:C:80:THR:HG22	1.95	0.67
4:F:331:GLU:OE2	11:F:401:ACP:O3G	2.12	0.66
2:D:21:TRP:CZ3	2:D:63:PRO:HB3	2.30	0.66
4:F:10:ASN:HB2	4:F:44:ARG:HH22	1.60	0.66
2:D:1:MET:HG3	2:D:50:ASN:CB	2.25	0.65
1:C:209:ILE:HG22	1:C:227:LEU:HD22	1.78	0.65
1:A:293:ASN:OD1	1:A:339:ARG:NH2	2.24	0.64
1:C:248:LEU:HD12	1:C:357:TYR:OH	1.97	0.64
2:D:295:MET:HE2	2:D:377:PHE:HB2	1.79	0.64
1:A:179:THR:HA	2:B:352:LYS:HD2	1.78	0.64
1:C:93:ILE:HD11	1:C:121:ARG:HG3	1.79	0.64
2:B:67:LEU:HD22	2:B:92:PHE:CE2	2.33	0.64
2:B:123:ARG:O	2:B:127:GLU:HG3	1.98	0.63
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.80	0.63
4:F:371:PRO:HA	4:F:372:THR:O	1.99	0.63
1:C:209:ILE:HD11	1:C:302:MET:CE	2.28	0.62
2:B:69:ASP:O	2:B:94:PHE:HA	2.00	0.62
1:C:230:LEU:O	1:C:234:ILE:HD12	1.99	0.62
2:D:171:VAL:HA	2:D:204:ILE:O	2.00	0.62
2:B:75:MET:HE3	2:B:92:PHE:HD2	1.64	0.61
2:B:274:PRO:HB3	2:B:286:LEU:HD22	1.83	0.61
1:A:166:LYS:HE2	1:A:197:HIS:O	2.01	0.60
4:F:200:ASP:OD1	4:F:222:ARG:HB2	2.00	0.60
1:A:336:LYS:HG3	3:E:24:LEU:HD13	1.83	0.60
4:F:87:LEU:O	4:F:91:CYS:HB2	2.02	0.60
2:D:248:LEU:HD23	2:D:354:ALA:HB2	1.82	0.60
2:B:141:LEU:HD12	2:B:172:MET:SD	2.41	0.60
2:D:165:ILE:HG21	2:D:252:LEU:HB3	1.84	0.60
2:B:36:TYR:CD1	2:B:46:LEU:HD21	2.37	0.60
1:A:351:PHE:HE1	3:E:24:LEU:HD11	1.66	0.59
2:D:152:LEU:O	2:D:156:LYS:HG2	2.01	0.59
1:C:271:THR:HG21	1:C:295:CYS:O	2.03	0.59
4:F:320:MET:HG3	4:F:330:ILE:HD11	1.85	0.59
1:A:21:TRP:CZ3	1:A:63:PRO:HB3	2.38	0.59
2:D:397:ALA:O	2:D:401:ARG:NH1	2.35	0.58
2:D:83:PHE:O	2:D:86:ILE:HG22	2.04	0.58
1:A:98:ASP:HB2	5:A:501:GTP:O2G	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:23:VAL:HG21	2:B:232:SER:HB3	1.86	0.58
4:F:350:ILE:O	4:F:354:ALA:HB3	2.03	0.58
2:B:136:GLN:HA	2:B:167:ASN:O	2.04	0.57
4:F:159:GLY:C	4:F:160:ILE:HD12	2.25	0.57
1:A:100:ALA:HA	2:B:254:LYS:HG3	1.86	0.57
1:C:320:ARG:HA	1:C:356:ASN:O	2.04	0.57
1:A:211:ASP:OD2	1:A:304:LYS:NZ	2.32	0.57
2:D:213:CYS:HA	2:D:217:LEU:HB2	1.87	0.57
4:F:371:PRO:HA	4:F:372:THR:C	2.24	0.57
4:F:371:PRO:CA	4:F:372:THR:HB	2.35	0.56
2:B:208:ALA:HB2	2:B:304:ALA:HB2	1.86	0.56
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.41	0.56
2:B:244:PHE:HB3	2:B:245:PRO:HD2	1.88	0.56
4:F:371:PRO:HA	4:F:372:THR:HB	1.87	0.55
2:B:75:MET:HE3	2:B:92:PHE:CD2	2.42	0.55
1:A:103:TYR:OH	12:A:601:HOH:O	2.18	0.55
2:B:402:LYS:HB3	2:B:405:LEU:HD12	1.88	0.55
1:A:233:GLN:HG3	1:A:368:LEU:CD1	2.37	0.54
1:A:294:ALA:O	1:A:300:ASN:ND2	2.40	0.54
2:B:147:SER:HG	2:B:190:SER:HG	1.55	0.54
1:A:22:GLU:HG3	1:A:83:TYR:HE2	1.73	0.54
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.43	0.54
2:D:147:SER:HB2	2:D:190:SER:OG	2.08	0.54
4:F:10:ASN:CB	4:F:44:ARG:HH22	2.20	0.53
1:A:254:GLU:HG2	1:A:258:ASN:ND2	2.23	0.53
2:B:223:THR:O	2:B:227:LEU:HD13	2.09	0.53
4:F:216:TYR:CE2	4:F:218:GLU:HB2	2.43	0.53
1:C:172:TYR:HB3	1:C:205:ASP:HA	1.91	0.53
2:B:231:VAL:O	2:B:235:MET:HG3	2.08	0.53
1:C:244:PHE:CD1	1:C:358:GLN:HG2	2.44	0.53
4:F:246:GLN:O	4:F:250:SER:HB3	2.07	0.53
2:B:274:PRO:HB3	2:B:286:LEU:CD2	2.39	0.53
2:D:244:PHE:CE1	2:D:358:ILE:HD12	2.43	0.53
2:B:289:PRO:O	2:B:293:GLN:HG3	2.09	0.53
1:C:75:ILE:HD12	1:C:94:THR:HG22	1.90	0.53
1:C:214:ARG:HG2	1:C:219:ILE:O	2.09	0.53
2:D:67:LEU:HD22	2:D:92:PHE:CE2	2.44	0.53
4:F:205:VAL:HG21	4:F:291:ILE:HD13	1.91	0.53
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.91	0.53
1:C:11:GLN:HE22	2:D:247:GLN:NE2	2.07	0.52
2:D:1:MET:CG	2:D:50:ASN:HB2	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:42:LEU:H	2:B:42:LEU:HD12	1.73	0.52
2:D:21:TRP:CE3	2:D:63:PRO:HB3	2.44	0.52
4:F:14:TYR:HB3	4:F:41:LEU:HD13	1.91	0.52
2:B:337:ASN:OD1	4:F:36:ARG:HD3	2.10	0.51
1:A:74:VAL:HB	12:A:604:HOH:O	2.10	0.51
2:B:164:ARG:HD2	12:B:650:HOH:O	2.09	0.51
1:C:172:TYR:CE2	1:C:391:LEU:HD22	2.45	0.51
2:B:16:ILE:HD13	2:B:231:VAL:HG11	1.91	0.51
1:A:210:TYR:CE1	1:A:222:PRO:HD2	2.45	0.51
1:A:22:GLU:HG3	1:A:83:TYR:CE2	2.46	0.51
2:B:244:PHE:CE1	2:B:358:ILE:HD12	2.46	0.51
1:C:142:GLY:HA3	1:C:183:GLU:HG2	1.93	0.51
1:A:284:GLU:CD	1:A:284:GLU:H	2.14	0.51
2:B:324:SER:O	2:B:328:VAL:HG23	2.11	0.51
2:D:145:THR:HB	8:D:501:GDP:O2B	2.11	0.51
2:D:67:LEU:N	2:D:67:LEU:HD12	2.26	0.51
1:C:136:LEU:HD23	1:C:167:LEU:HB2	1.93	0.51
2:B:251:ASP:OD1	2:B:254:LYS:HB2	2.10	0.50
2:B:290:GLU:O	2:B:294:GLN:HG3	2.10	0.50
2:B:318:ILE:N	2:B:318:ILE:HD12	2.26	0.50
1:C:165:SER:HA	1:C:199:ASP:OD2	2.11	0.50
2:D:172:MET:HG3	2:D:387:LEU:HD11	1.92	0.50
1:A:69:ASP:O	1:A:94:THR:HA	2.10	0.50
1:A:179:THR:HG21	2:B:248:LEU:CB	2.42	0.50
2:D:103:TRP:CE3	2:D:189:LEU:HD13	2.47	0.50
1:A:70:LEU:HD22	1:A:110:ILE:CG2	2.42	0.50
1:C:21:TRP:CZ3	1:C:63:PRO:HB3	2.47	0.50
2:D:69:ASP:O	2:D:94:PHE:HA	2.12	0.50
4:F:81:ILE:O	4:F:88:SER:HB3	2.12	0.50
1:A:226:ASN:ND2	1:A:367:ASP:OD2	2.42	0.49
2:B:31:ASP:HB2	2:B:32:PRO:CD	2.42	0.49
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.30	0.49
1:A:265:ILE:HG23	1:A:432:TYR:CZ	2.47	0.49
2:D:318:ILE:N	2:D:318:ILE:HD12	2.27	0.49
2:D:392:SER:O	2:D:396:THR:HG22	2.13	0.49
1:C:196:GLU:HG2	12:C:642:HOH:O	2.12	0.49
2:D:174:SER:OG	2:D:207:GLU:OE1	2.29	0.48
4:F:214:TYR:HB3	4:F:375:PHE:HB3	1.95	0.48
1:A:300:ASN:HB3	12:A:602:HOH:O	2.12	0.48
2:D:12:CYS:HB2	8:D:501:GDP:C8	2.48	0.48
4:F:147:TRP:HB2	4:F:169:LEU:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:298:PRO:HG2	1:C:308:ARG:NH2	2.29	0.48
2:D:64:ARG:HG3	2:D:125:GLU:OE1	2.14	0.48
2:D:143:GLY:HA3	8:D:501:GDP:O3A	2.14	0.48
4:F:2:TYR:CE1	4:F:359:PHE:HB3	2.49	0.48
1:A:88:HIS:CD2	1:A:91:GLN:HG3	2.49	0.48
2:D:66:ILE:HD12	2:D:122:VAL:HG22	1.96	0.47
2:D:146:GLY:O	2:D:150:GLY:HA3	2.13	0.47
2:D:208:ALA:O	2:D:212:ILE:HG13	2.13	0.47
1:A:12:ALA:HB3	1:A:140:SER:HB3	1.96	0.47
1:C:142:GLY:CA	1:C:183:GLU:HG2	2.45	0.47
4:F:128:ARG:NH2	4:F:174:ASP:OD1	2.48	0.47
2:B:88:ARG:NH1	2:B:90:ASP:HB2	2.29	0.47
2:B:164:ARG:O	9:B:504:MES:H31	2.15	0.47
1:C:8:HIS:HB3	1:C:13:GLY:O	2.14	0.47
4:F:320:MET:CG	4:F:330:ILE:HD11	2.45	0.47
2:B:2:ARG:HB2	2:B:133:GLN:CG	2.44	0.47
1:A:93:ILE:HD11	1:A:121:ARG:HG3	1.97	0.47
2:D:141:LEU:HA	2:D:147:SER:HB3	1.97	0.46
2:D:191:VAL:O	2:D:195:VAL:HG23	2.15	0.46
1:C:88:HIS:HE1	1:C:90:GLU:HG3	1.79	0.46
4:F:103:THR:HG23	4:F:128:ARG:NH2	2.30	0.46
1:A:209:ILE:HG23	1:A:230:LEU:HD23	1.97	0.46
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.50	0.46
2:B:124:LYS:HD3	2:B:124:LYS:C	2.36	0.46
1:A:187:SER:HB3	1:A:391:LEU:HD21	1.97	0.46
2:B:114:LEU:O	2:B:114:LEU:HG	2.15	0.46
2:B:187:ALA:O	2:B:191:VAL:HG23	2.15	0.46
2:B:347:ILE:HG22	2:B:350:ASN:HB3	1.98	0.46
2:B:105:LYS:HA	2:B:109:THR:OG1	2.16	0.46
2:B:334:ASN:O	2:B:338:LYS:HG3	2.15	0.46
1:A:103:TYR:CD2	1:A:148:GLY:HA2	2.51	0.46
1:A:143:GLY:HA3	5:A:501:GTP:O3A	2.16	0.46
1:A:75:ILE:HD12	1:A:94:THR:HG22	1.97	0.45
4:F:141:GLY:O	4:F:142:ARG:HB2	2.16	0.45
1:A:196:GLU:OE1	1:A:196:GLU:HA	2.16	0.45
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.56	0.45
2:D:153:LEU:O	2:D:157:ILE:HG13	2.15	0.45
1:A:298:PRO:HA	1:A:301:GLN:CD	2.37	0.45
4:F:198:LYS:HZ1	11:F:401:ACP:C2	2.30	0.45
1:C:43:GLY:HA2	1:C:56:THR:O	2.17	0.45
1:A:12:ALA:CB	1:A:140:SER:HB3	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:HIS:HB2	1:A:89:PRO:HD2	1.98	0.45
1:C:167:LEU:HG	1:C:200:CYS:HB3	1.99	0.45
1:C:108:TYR:O	1:C:112:LYS:HG2	2.17	0.45
1:A:71:GLU:HG2	1:A:72:PRO:N	2.32	0.45
1:A:320:ARG:HD2	12:A:630:HOH:O	2.17	0.45
1:A:231:ILE:O	1:A:235:VAL:HG23	2.18	0.44
2:B:88:ARG:HH11	2:B:90:ASP:HB2	1.83	0.44
4:F:280:GLU:OE1	4:F:284:LEU:HD23	2.17	0.44
1:A:21:TRP:CH2	1:A:63:PRO:HB3	2.52	0.44
4:F:220:VAL:HG12	4:F:263:PHE:CE1	2.52	0.44
1:A:233:GLN:HG3	1:A:368:LEU:HD12	2.00	0.44
2:B:390:ARG:NH1	12:B:604:HOH:O	2.39	0.44
1:A:100:ALA:CB	2:B:253[B]:ARG:HG2	2.48	0.44
2:B:200:GLU:OE2	2:B:255:LEU:HG	2.18	0.44
1:A:227:LEU:O	1:A:231:ILE:HG13	2.18	0.44
1:C:391:LEU:HD12	1:C:391:LEU:HA	1.82	0.44
3:E:44:ASP:HB3	3:E:45:PRO:HD2	2.00	0.44
4:F:2:TYR:HB2	4:F:27:TRP:CD2	2.52	0.44
4:F:205:VAL:CG2	4:F:291:ILE:HD13	2.47	0.44
2:D:235:MET:O	2:D:239:THR:HG23	2.18	0.44
2:D:110:GLU:H	2:D:110:GLU:HG2	1.65	0.44
1:A:141:PHE:O	1:A:147:SER:HB3	2.18	0.43
2:D:75:MET:HE3	2:D:92:PHE:HD2	1.83	0.43
2:D:124:LYS:C	2:D:124:LYS:HD3	2.37	0.43
1:A:335:ILE:CG2	1:A:339:ARG:HG3	2.40	0.43
1:C:209:ILE:HG23	1:C:230:LEU:HD23	2.01	0.43
2:D:325:MET:HE2	2:D:355:VAL:HG21	2.00	0.43
2:B:66:ILE:HD12	2:B:122:VAL:HG22	2.00	0.43
1:A:46:ASP:OD1	1:A:46:ASP:N	2.51	0.43
1:A:431:ASP:O	1:A:435:VAL:HG23	2.18	0.43
2:D:141:LEU:HD12	2:D:172:MET:SD	2.58	0.43
2:D:311:ARG:NH1	2:D:436:GLN:O	2.51	0.43
2:B:349:ASN:O	2:B:352:LYS:HE2	2.18	0.43
2:D:397:ALA:HA	2:D:400:ARG:NH1	2.34	0.43
2:B:425:MET:O	2:B:429:VAL:HG23	2.19	0.43
1:C:233:GLN:HG3	1:C:368:LEU:CD1	2.49	0.43
2:D:347:ILE:CG2	2:D:350:ASN:HB3	2.44	0.43
2:D:387:LEU:HD23	2:D:387:LEU:C	2.39	0.43
2:D:332:MET:O	2:D:336:GLN:HG3	2.18	0.43
1:A:187:SER:CB	1:A:391:LEU:HD21	2.49	0.42
1:A:214:ARG:HG2	1:A:219:ILE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:172:MET:HG3	2:B:387:LEU:HD11	2.01	0.42
2:B:402:LYS:CB	2:B:405:LEU:HD12	2.49	0.42
1:C:186:ASN:O	1:C:190:THR:HG22	2.20	0.42
1:A:103:TYR:CE2	1:A:148:GLY:HA2	2.55	0.42
2:B:46:LEU:HA	2:B:49:ILE:HB	2.00	0.42
2:D:106:GLY:O	2:D:111:GLY:HA3	2.19	0.42
2:B:286:LEU:HD12	2:B:290:GLU:OE1	2.19	0.42
2:D:154:ILE:HG23	2:D:166:MET:HG2	2.00	0.42
4:F:236:LYS:HB3	4:F:240:LEU:CD1	2.45	0.42
4:F:259:GLY:O	4:F:261:GLU:HG3	2.20	0.42
1:C:71:GLU:HB3	1:C:98:ASP:HB3	2.01	0.42
1:C:103:TYR:CE2	1:C:148:GLY:HA2	2.55	0.42
1:C:325:PRO:HD2	12:C:681:HOH:O	2.19	0.42
1:C:21:TRP:CH2	1:C:63:PRO:HB3	2.54	0.42
2:D:303:ALA:O	2:D:305:CYS:N	2.53	0.42
1:C:174:ALA:CB	1:C:207:GLU:HB2	2.50	0.42
2:D:1:MET:HE3	2:D:1:MET:HB3	1.90	0.42
2:D:88:ARG:NH1	2:D:90:ASP:HB2	2.35	0.42
4:F:219:GLY:HA3	4:F:264:PHE:CZ	2.55	0.42
1:C:6:SER:O	1:C:65:ALA:HA	2.20	0.41
1:C:166:LYS:HE2	1:C:197:HIS:O	2.19	0.41
2:D:345:GLU:H	2:D:345:GLU:HG2	1.71	0.41
1:C:286:LEU:HA	1:C:290:GLU:OE1	2.19	0.41
2:B:2:ARG:HB2	2:B:133:GLN:HG3	2.02	0.41
1:A:223:THR:O	1:A:227:LEU:HG	2.20	0.41
2:B:42:LEU:HD12	2:B:42:LEU:N	2.34	0.41
2:B:119:LEU:HD11	2:B:156:LYS:HB3	2.01	0.41
2:B:284:ARG:NH2	2:B:290:GLU:OE2	2.54	0.41
1:C:411:GLU:OE1	1:C:411:GLU:HA	2.21	0.41
2:D:66:ILE:CD1	2:D:122:VAL:HG22	2.50	0.41
4:F:147:TRP:HB2	4:F:169:LEU:CD1	2.51	0.41
4:F:198:LYS:HG2	4:F:199:PHE:H	1.86	0.41
1:A:335:ILE:HG23	1:A:339:ARG:CG	2.42	0.41
2:D:20:PHE:CZ	2:D:24:ILE:HD13	2.56	0.41
4:F:100:ILE:CD1	4:F:128:ARG:HA	2.50	0.41
11:F:401:ACP:O3G	11:F:401:ACP:O1B	2.39	0.41
1:A:2:ARG:HB3	1:A:131:GLY:O	2.21	0.41
1:A:70:LEU:HD12	1:A:145:THR:OG1	2.21	0.41
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.56	0.41
1:A:289:ALA:HA	1:A:331:ALA:CB	2.50	0.41
1:A:320:ARG:HA	1:A:356:ASN:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:ILE:CD1	1:C:121:ARG:HG3	2.49	0.41
2:D:75:MET:HE3	2:D:92:PHE:CD2	2.56	0.41
1:A:141:PHE:HB3	1:A:187:SER:OG	2.21	0.41
2:B:67:LEU:N	2:B:67:LEU:HD12	2.36	0.41
1:C:88:HIS:CE1	1:C:90:GLU:HG3	2.55	0.41
1:C:249:ASN:OD1	1:C:356:ASN:ND2	2.50	0.41
2:D:194:LEU:HD22	2:D:198:THR:HG21	2.03	0.41
3:E:101:LEU:O	3:E:105:MET:HG2	2.21	0.41
4:F:3:THR:HB	4:F:30:LEU:HD11	2.03	0.41
4:F:216:TYR:CZ	4:F:218:GLU:HB2	2.55	0.41
4:F:240:LEU:HD12	4:F:240:LEU:N	2.36	0.41
4:F:371:PRO:HA	4:F:372:THR:CB	2.49	0.41
2:B:247:GLN:OE1	2:B:247:GLN:N	2.38	0.40
2:B:333:LEU:O	2:B:337:ASN:ND2	2.54	0.40
1:C:312:TYR:CD2	1:C:341:ILE:HG23	2.57	0.40
12:B:625:HOH:O	1:C:163:LYS:HD2	2.21	0.40
2:D:46:LEU:HA	2:D:49:ILE:HB	2.04	0.40
3:E:7:GLU:O	3:E:22:VAL:HA	2.20	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	436/451 (97%)	424 (97%)	12 (3%)	0	100	100
1	C	439/451 (97%)	430 (98%)	9 (2%)	0	100	100
2	B	422/445 (95%)	410 (97%)	12 (3%)	0	100	100
2	D	422/445 (95%)	412 (98%)	10 (2%)	0	100	100
3	E	119/143 (83%)	118 (99%)	1 (1%)	0	100	100
4	F	344/384 (90%)	330 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2182/2319 (94%)	2124 (97%)	58 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	369/379 (97%)	362 (98%)	7 (2%)	57	80
1	C	372/379 (98%)	368 (99%)	4 (1%)	73	89
2	B	368/383 (96%)	367 (100%)	1 (0%)	92	97
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%)	315 (100%)	0	100	100
All	All	1902/1993 (95%)	1887 (99%)	15 (1%)	81	92

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	GLU
1	A	221	ARG
1	A	282	TYR
1	A	284	GLU
1	A	300	ASN
1	A	316	CYS
1	A	381	THR
2	B	139	HIS
1	C	71	GLU
1	C	251	ASP
1	C	381	THR
1	C	391	LEU
2	D	139	HIS
2	D	229	HIS

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Mol	Chain	Res	Type
2	D	247	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	HIS
2	B	15	GLN
2	B	294	GLN
1	C	11	GLN
1	C	300	ASN
2	D	294	GLN
4	F	229	ASN
4	F	333	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 17 ligands modelled in this entry, 9 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
11	ACP	F	401	6	27,33,33	1.40	5 (18%)	32,52,52	1.47	4 (12%)
8	GDP	D	501	6	24,30,30	1.17	2 (8%)	31,47,47	1.89	7 (22%)
5	GTP	A	501	6	26,34,34	1.00	1 (3%)	33,54,54	1.71	7 (21%)
10	UQJ	B	505	-	8,12,12	1.76	2 (25%)	4,17,17	0.91	0
10	UQJ	B	506	-	8,12,12	1.75	2 (25%)	4,17,17	0.72	0
8	GDP	B	501	6	24,30,30	1.16	2 (8%)	31,47,47	1.90	7 (22%)
9	MES	B	504	-	12,12,12	2.27	1 (8%)	14,16,16	1.97	6 (42%)
5	GTP	C	501	6	26,34,34	0.98	1 (3%)	33,54,54	1.69	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
11	ACP	F	401	6	-	12/15/38/38	0/3/3/3
8	GDP	D	501	6	-	3/12/32/32	0/3/3/3
5	GTP	A	501	6	-	6/18/38/38	0/3/3/3
10	UQJ	B	505	-	-	0/1/8/8	0/1/1/1
10	UQJ	B	506	-	-	0/1/8/8	0/1/1/1
8	GDP	B	501	6	-	3/12/32/32	0/3/3/3
9	MES	B	504	-	-	4/6/14/14	0/1/1/1
5	GTP	C	501	6	-	9/18/38/38	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	504	MES	C8-S	-7.61	1.66	1.77
10	B	506	UQJ	C2-C4	4.09	1.43	1.38
8	D	501	GDP	C6-C5	4.07	1.48	1.41
8	B	501	GDP	C6-C5	3.91	1.48	1.41
10	B	505	UQJ	C2-C4	3.67	1.42	1.38
5	C	501	GTP	C6-N1	3.32	1.38	1.33
5	A	501	GTP	C6-N1	3.14	1.38	1.33
11	F	401	ACP	PG-O3G	2.96	1.61	1.54
10	B	505	UQJ	C2-C3	-2.95	1.46	1.50
11	F	401	ACP	PG-O2G	2.93	1.61	1.54
11	F	401	ACP	PB-O3A	2.80	1.61	1.58
11	F	401	ACP	C5-C4	2.54	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	501	GDP	C5-C4	2.39	1.47	1.40
8	B	501	GDP	C5-C4	2.36	1.47	1.40
10	B	506	UQJ	C2-C3	-2.26	1.47	1.50
11	F	401	ACP	PB-O2B	2.24	1.61	1.56

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	501	GTP	N3-C2-N1	-5.33	120.11	127.22
5	C	501	GTP	N3-C2-N1	-5.19	120.30	127.22
8	D	501	GDP	C2-N3-C4	4.80	120.84	115.36
8	B	501	GDP	C2-N3-C4	4.77	120.80	115.36
5	A	501	GTP	C2-N3-C4	4.32	120.30	115.36
11	F	401	ACP	PA-O3A-PB	-4.23	119.14	132.56
8	B	501	GDP	C6-C5-C4	-4.22	116.77	120.80
5	C	501	GTP	C2-N3-C4	4.09	120.03	115.36
8	B	501	GDP	C6-N1-C2	4.09	122.43	115.93
8	D	501	GDP	C6-N1-C2	4.06	122.39	115.93
8	D	501	GDP	C5-C6-N1	-4.03	117.92	123.43
8	D	501	GDP	C6-C5-C4	-3.88	117.09	120.80
8	B	501	GDP	C5-C6-N1	-3.88	118.13	123.43
9	B	504	MES	C5-N4-C3	3.71	117.18	108.83
11	F	401	ACP	C3'-C2'-C1'	3.47	106.20	100.98
8	B	501	GDP	N3-C2-N1	-3.45	122.63	127.22
8	D	501	GDP	N3-C2-N1	-3.33	122.78	127.22
5	C	501	GTP	C5-C6-N1	-3.15	119.12	123.43
9	B	504	MES	C6-C5-N4	-3.10	105.41	110.10
11	F	401	ACP	N3-C2-N1	-3.04	123.93	128.68
5	C	501	GTP	PA-O3A-PB	-2.96	122.67	132.83
5	A	501	GTP	C5-C6-N1	-2.95	119.40	123.43
5	A	501	GTP	PA-O3A-PB	-2.83	123.10	132.83
8	D	501	GDP	C4-C5-N7	-2.74	106.54	109.40
8	D	501	GDP	PA-O3A-PB	-2.73	123.46	132.83
8	B	501	GDP	PA-O3A-PB	-2.70	123.58	132.83
11	F	401	ACP	C4-C5-N7	-2.63	106.65	109.40
5	C	501	GTP	C6-N1-C2	2.59	120.04	115.93
5	A	501	GTP	C6-N1-C2	2.56	120.00	115.93
9	B	504	MES	O1S-S-C8	2.54	109.98	106.92
8	B	501	GDP	C4-C5-N7	-2.53	106.77	109.40
5	A	501	GTP	PB-O3B-PG	-2.50	124.26	132.83
5	C	501	GTP	PB-O3B-PG	-2.37	124.69	132.83
9	B	504	MES	O3S-S-C8	2.25	109.40	105.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	504	MES	C7-N4-C5	2.18	116.82	111.23
9	B	504	MES	O2S-S-C8	2.12	109.46	106.92
5	A	501	GTP	N2-C2-N1	2.01	120.38	117.25

There are no chirality outliers.

All (37) torsion outliers are listed below:

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

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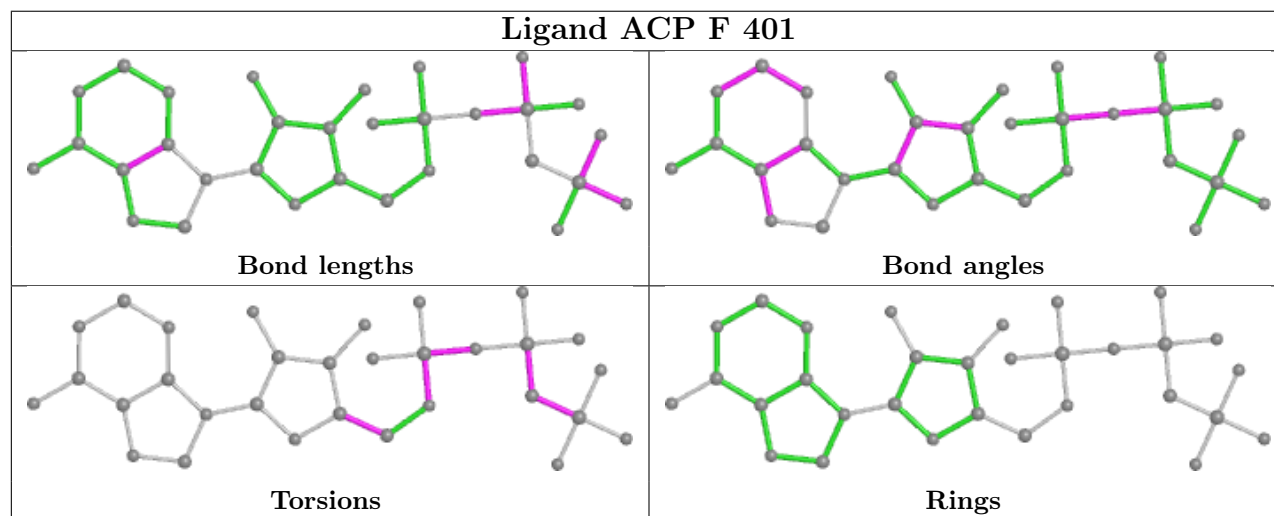
Mol	Chain	Res	Type	Atoms
5	C	501	GTP	C5'-O5'-PA-O3A
8	B	501	GDP	C5'-O5'-PA-O3A
5	C	501	GTP	PB-O3A-PA-O1A

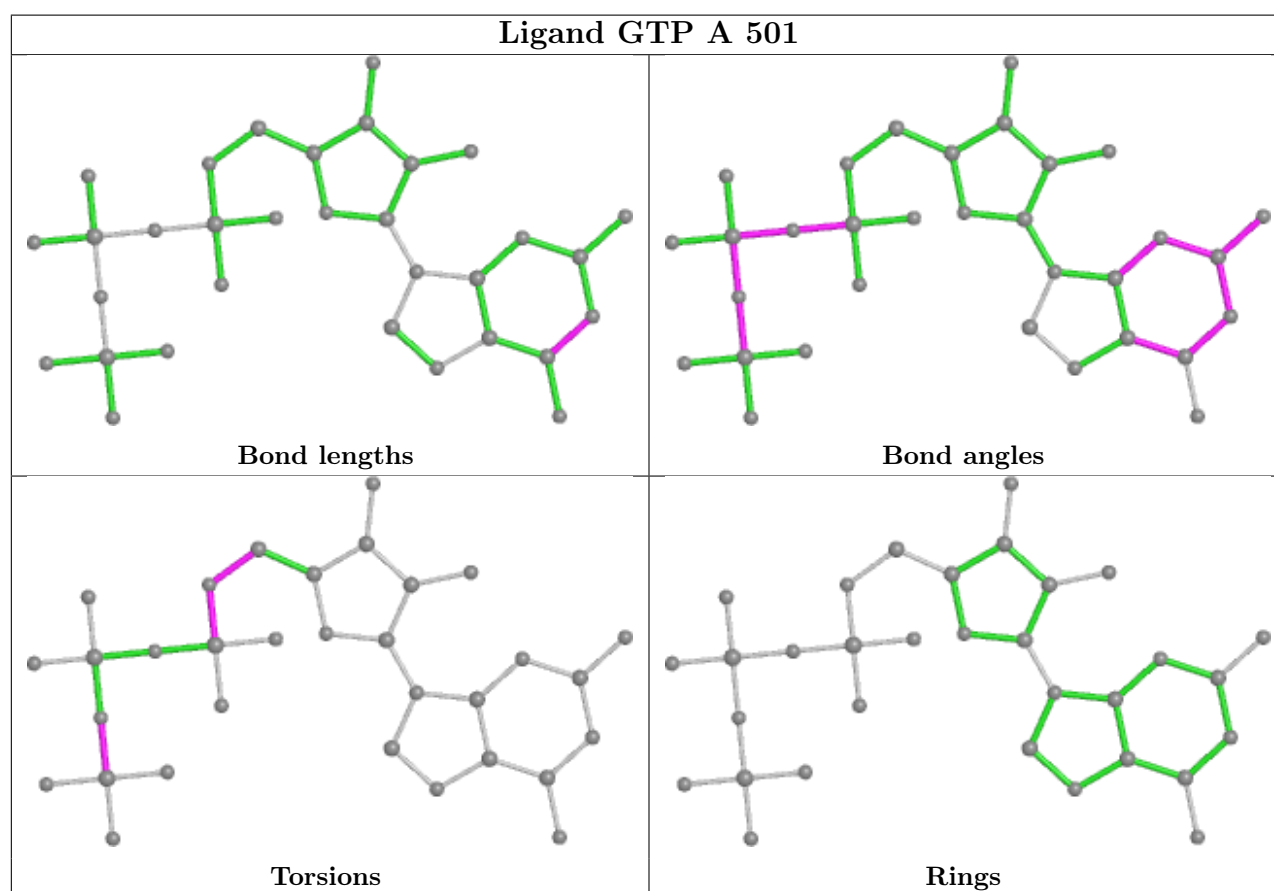
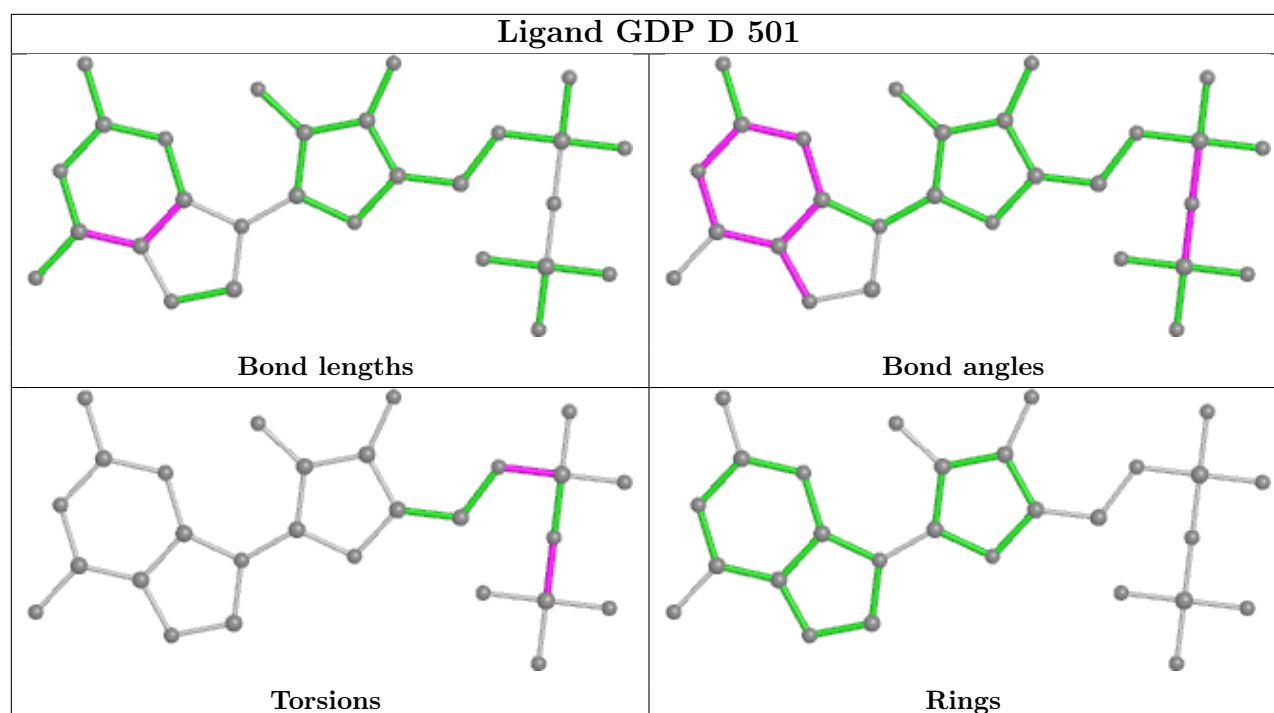
There are no ring outliers.

4 monomers are involved in 12 short contacts:

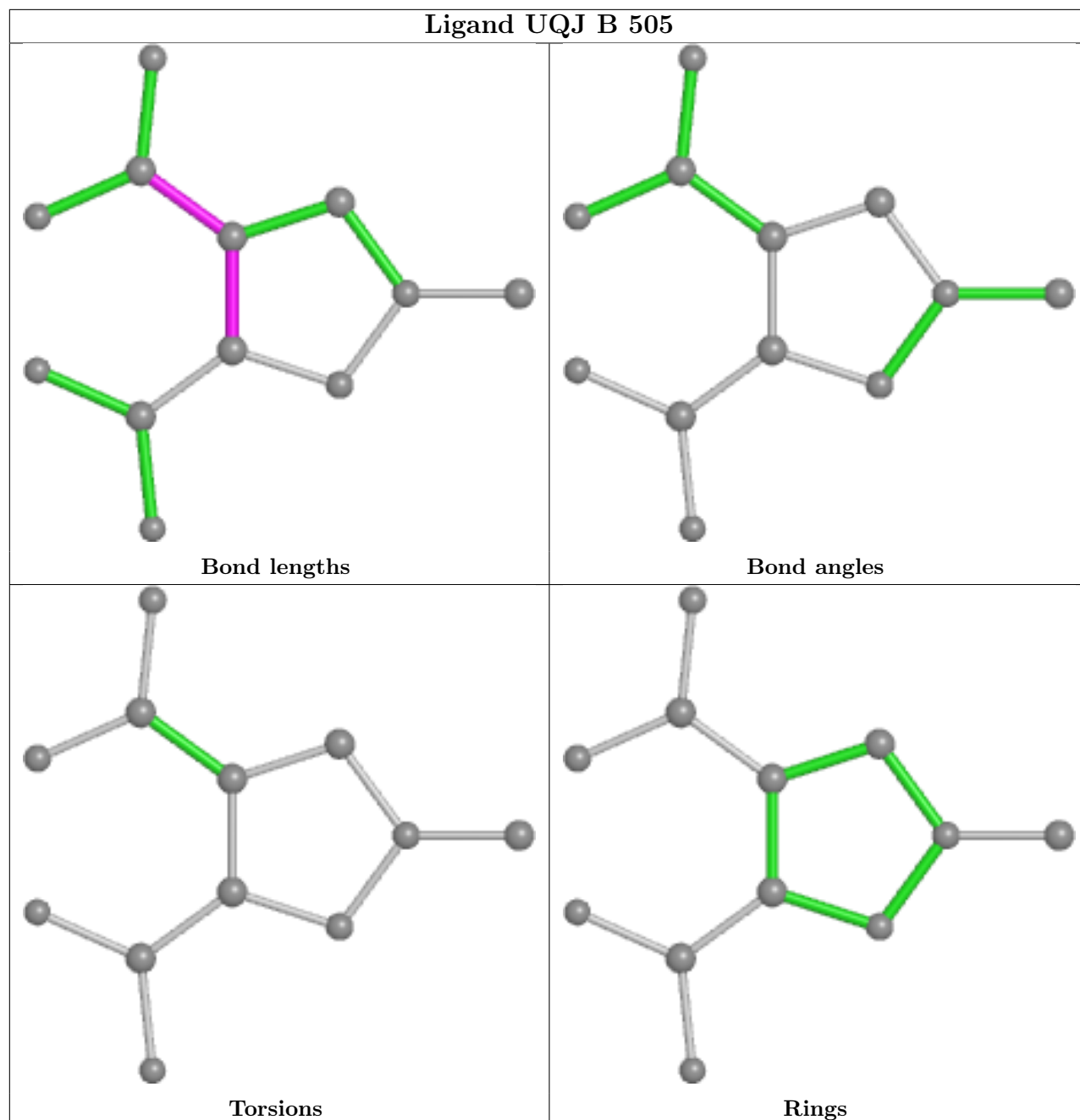
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	F	401	ACP	5	0
8	D	501	GDP	3	0
5	A	501	GTP	2	0
9	B	504	MES	2	0

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

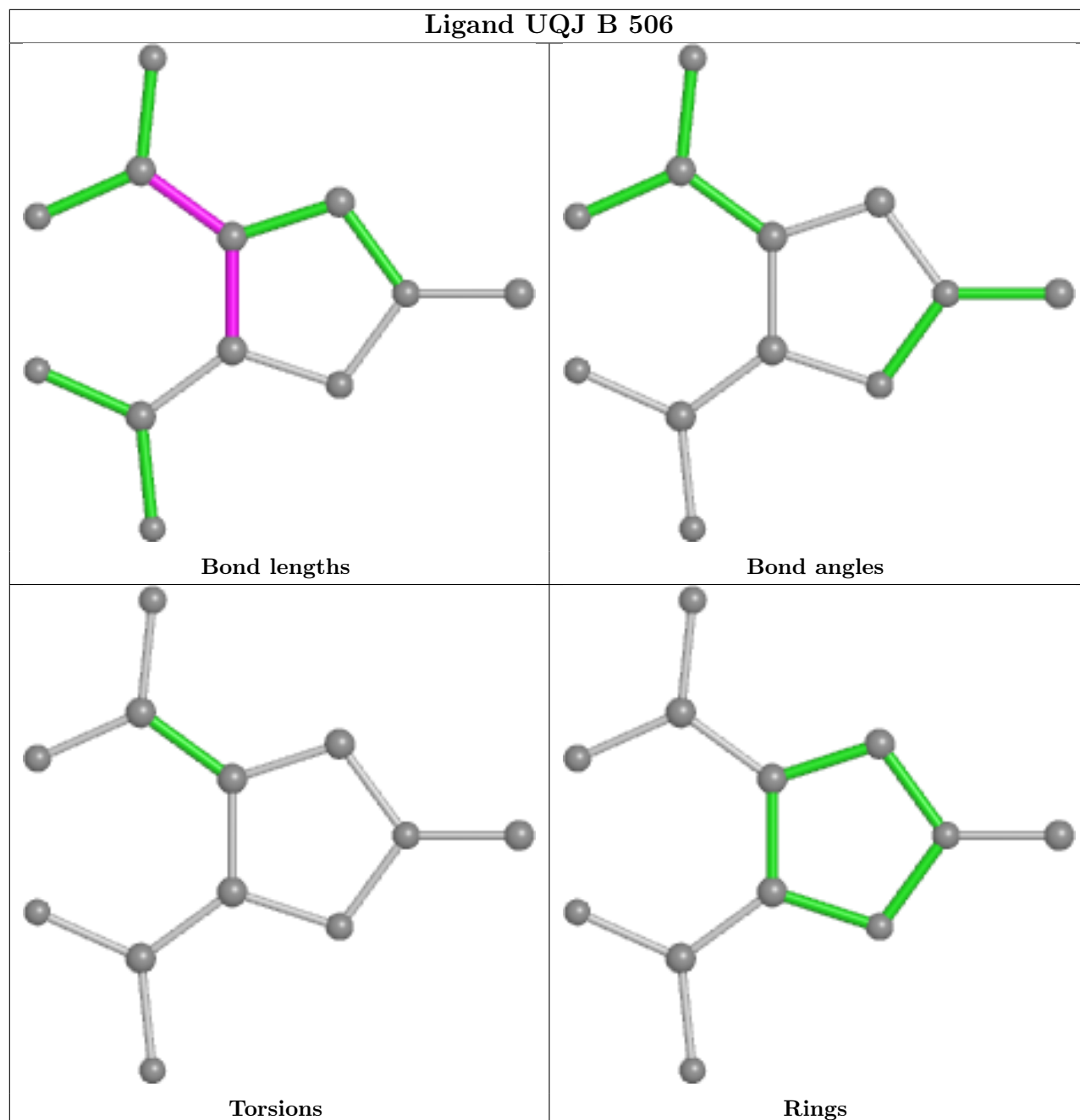


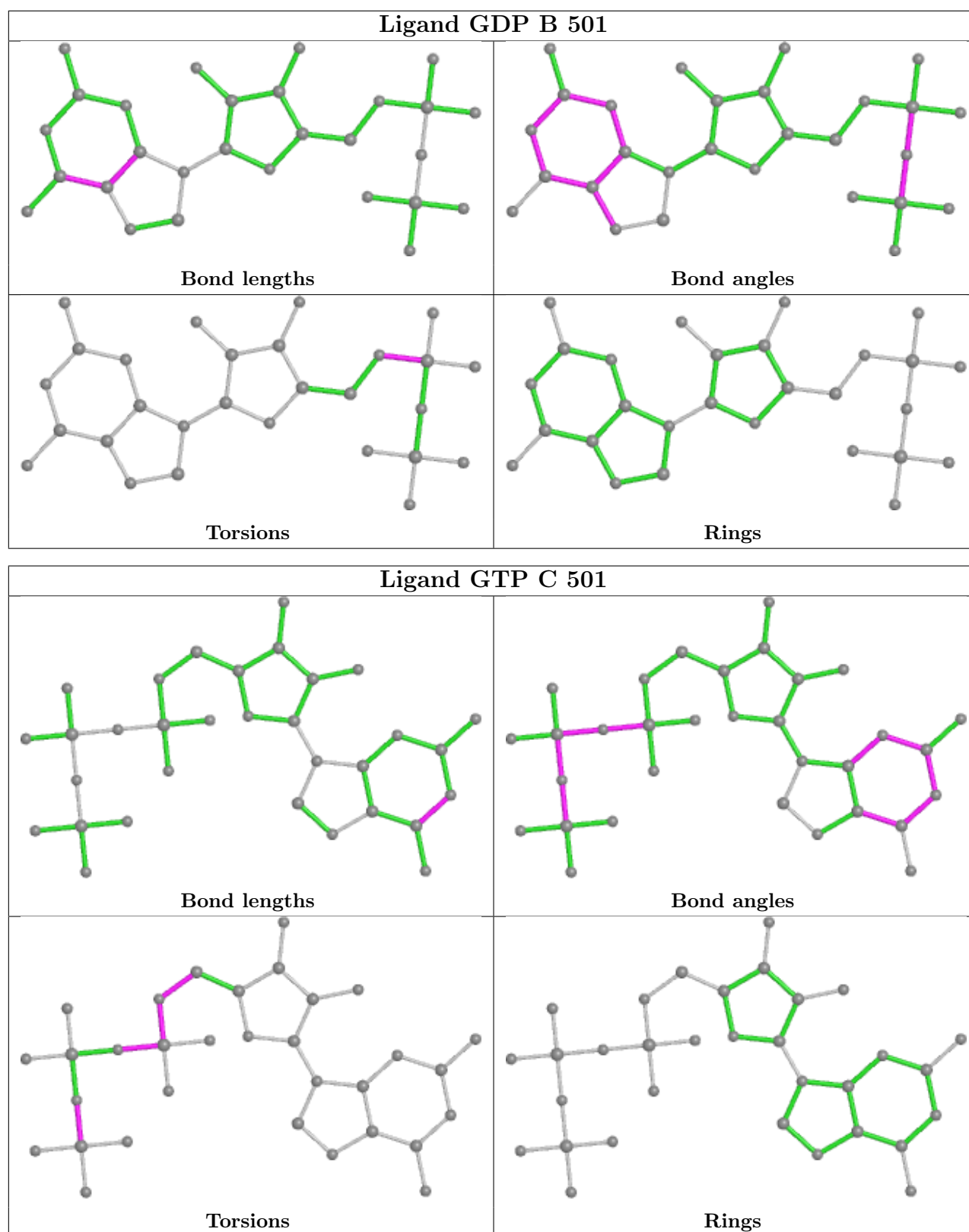


## Ligand UQJ B 505



## Ligand UQJ B 506





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	438/451 (97%)	-0.09	10 (2%) 60 60	42, 60, 97, 165	0
1	C	440/451 (97%)	-0.27	2 (0%) 91 92	35, 48, 73, 127	0
2	B	425/445 (95%)	0.05	14 (3%) 46 45	35, 59, 110, 164	2 (0%)
2	D	426/445 (95%)	-0.00	10 (2%) 60 60	42, 67, 100, 142	4 (0%)
3	E	123/143 (86%)	0.33	10 (8%) 12 10	48, 73, 125, 156	0
4	F	352/384 (91%)	0.49	51 (14%) 2 1	55, 87, 160, 196	0
All	All	2204/2319 (95%)	0.03	97 (4%) 34 32	35, 63, 121, 196	6 (0%)

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	177	GLY	7.3
4	F	105	LEU	6.8
4	F	251	LYS	6.4
4	F	372	THR	6.0
4	F	104	ASN	5.7
4	F	103	THR	5.4
4	F	234	GLN	5.2
2	B	281	GLN	5.1
4	F	371	PRO	5.0
2	B	277	SER	5.0
3	E	27	PRO	5.0
4	F	248	GLU	4.9
4	F	232	ASN	4.5
4	F	176	GLN	4.5
2	B	276	THR	4.4
1	A	438	ASP	4.3
4	F	231	ALA	4.2
4	F	362	ALA	4.1
3	E	28	SER	4.0

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Mol	Chain	Res	Type	RSRZ
2	B	249	ASN	3.9
4	F	89	GLU	3.9
1	A	281	ALA	3.8
3	E	142	GLU	3.7
4	F	249	TYR	3.6
4	F	179	VAL	3.6
2	B	59	ASN	3.6
2	B	247	GLN	3.6
2	D	276	THR	3.5
1	C	440	VAL	3.5
4	F	243	HIS	3.4
4	F	137	ARG	3.4
4	F	142	ARG	3.4
2	B	284	ARG	3.4
4	F	382	HIS	3.4
4	F	154	GLY	3.3
3	E	143	ALA	3.3
3	E	26	PRO	3.3
3	E	25	LYS	3.3
4	F	244	CYS	3.3
4	F	152	SER	3.3
4	F	173	ILE	3.2
2	B	1	MET	3.2
2	B	437	ASP	3.2
4	F	381	HIS	3.1
4	F	250	SER	3.1
1	A	337	THR	3.1
4	F	102	PRO	3.0
4	F	168	GLU	2.9
4	F	153	ALA	2.9
2	B	248	LEU	2.9
4	F	178	GLN	2.9
2	B	57	THR	2.9
4	F	379	HIS	2.8
4	F	259	GLY	2.8
2	D	278	ARG	2.8
3	E	24	LEU	2.7
1	A	282	TYR	2.7
4	F	255	ARG	2.7
4	F	159	GLY	2.6
2	D	220	THR	2.6
4	F	101	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	262	TYR	2.6
2	D	215	ARG	2.6
3	E	139	LEU	2.5
4	F	125	THR	2.5
2	B	325	MET	2.5
2	D	82	PRO	2.5
2	D	401	ARG	2.5
1	A	219	ILE	2.4
4	F	45	ASN	2.4
4	F	90	SER	2.3
1	A	346	TRP	2.3
4	F	252	ASN	2.3
1	C	340	SER	2.3
4	F	233	PHE	2.3
4	F	258	GLU	2.3
4	F	361	LEU	2.3
4	F	340	GLN	2.3
4	F	135	TYR	2.2
2	D	277	SER	2.2
4	F	155	ALA	2.2
1	A	179	THR	2.2
2	D	441	ASP	2.2
4	F	141	GLY	2.2
2	D	57	THR	2.2
2	B	58	GLY	2.1
2	D	400	ARG	2.1
4	F	254	GLY	2.1
4	F	256	TYR	2.1
4	F	25	GLY	2.1
4	F	24	THR	2.1
4	F	132	LEU	2.1
3	E	141	GLU	2.1
1	A	284	GLU	2.1
2	B	42	LEU	2.1
1	A	220	GLU	2.1
3	E	6	MET	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

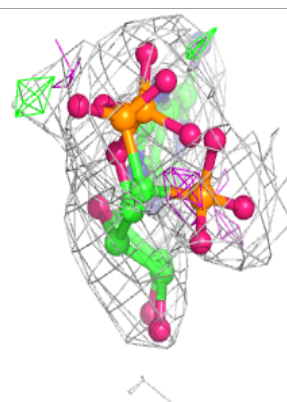
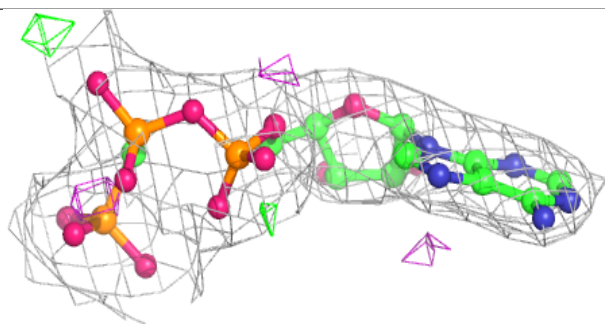
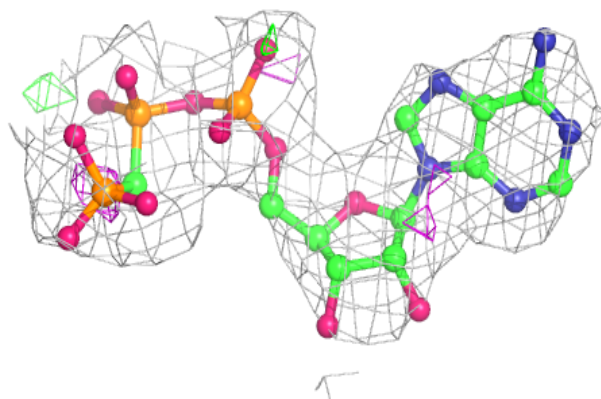
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
7	CA	A	503	1/1	0.85	0.05	83,83,83,83	0
7	CA	A	504	1/1	0.87	0.14	86,86,86,86	0
11	ACP	F	401	31/31	0.87	0.21	88,95,109,115	0
6	MG	D	502	1/1	0.89	0.09	64,64,64,64	0
9	MES	B	504	12/12	0.92	0.18	74,80,94,100	0
7	CA	B	503	1/1	0.92	0.06	98,98,98,98	0
10	UQJ	B	506	12/12	0.93	0.18	39,46,50,57	19
10	UQJ	B	505	12/12	0.93	0.17	48,56,71,71	0
6	MG	C	502	1/1	0.96	0.11	39,39,39,39	0
8	GDP	D	501	28/28	0.96	0.15	53,60,69,75	0
6	MG	A	502	1/1	0.97	0.14	44,44,44,44	0
6	MG	F	402	1/1	0.98	0.17	79,79,79,79	0
6	MG	B	502	1/1	0.98	0.09	40,40,40,40	0
5	GTP	C	501	32/32	0.98	0.14	32,38,44,46	0
5	GTP	A	501	32/32	0.98	0.13	38,42,47,50	0
7	CA	C	503	1/1	0.98	0.04	64,64,64,64	0
8	GDP	B	501	28/28	0.99	0.14	33,40,46,50	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.

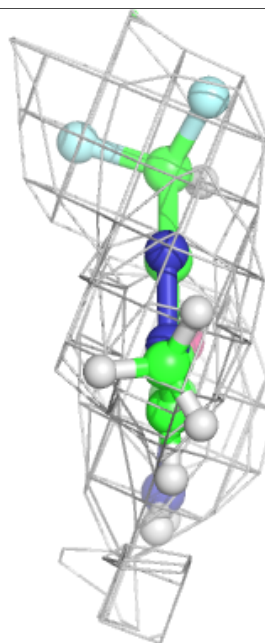
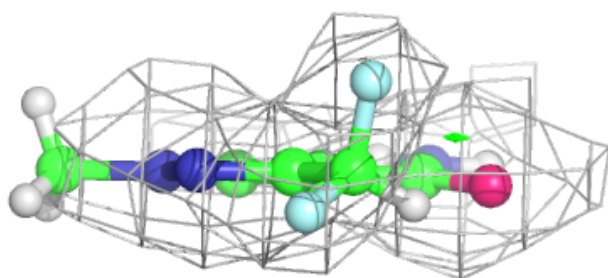
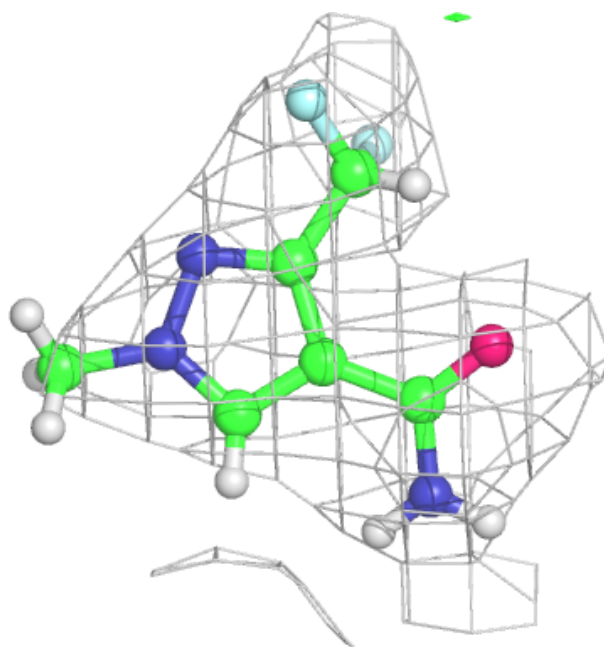
**Electron density around ACP F 401:**

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



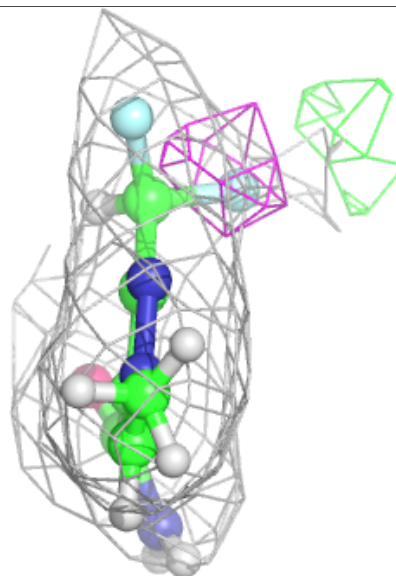
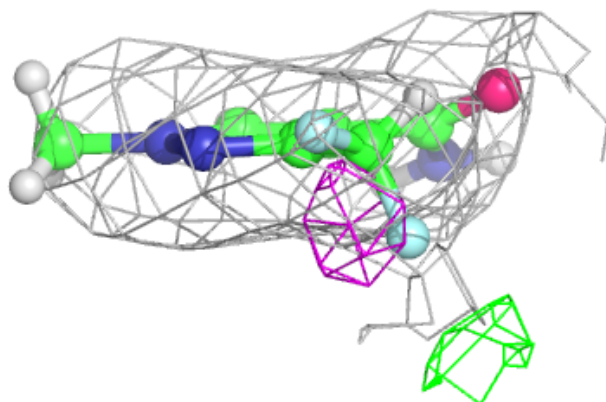
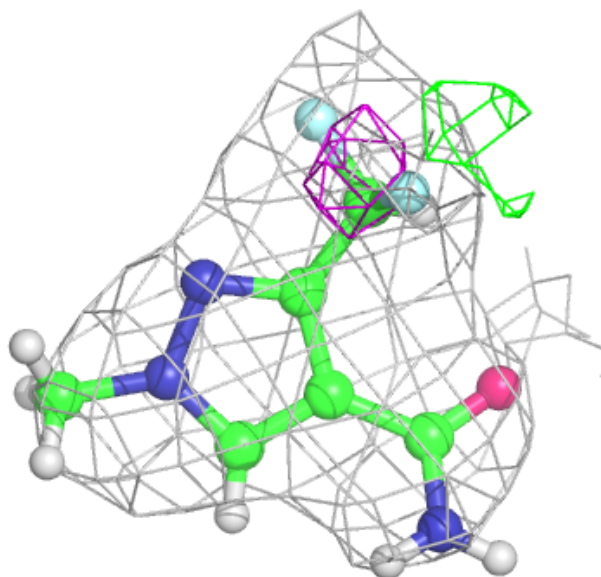
**Electron density around UQJ B 506:**

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and green (positive)



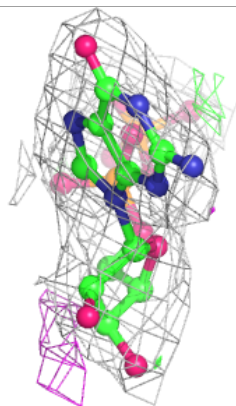
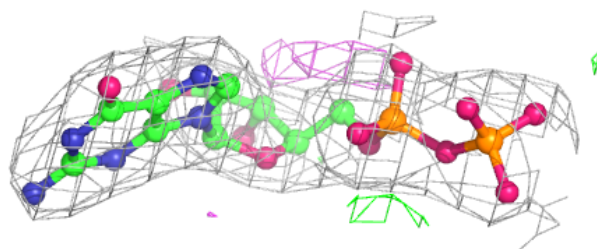
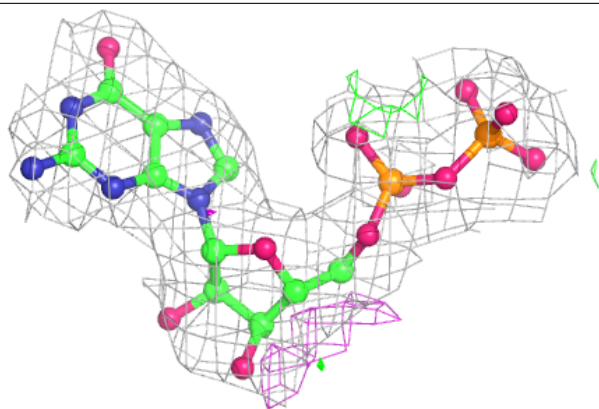
**Electron density around UQJ B 505:**

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

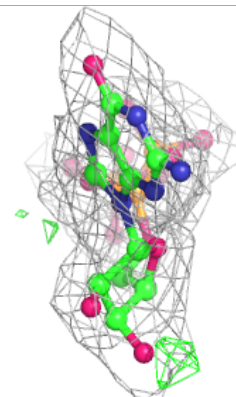
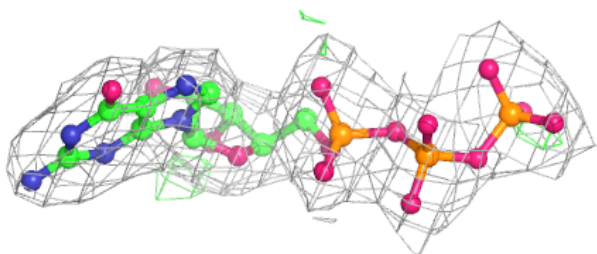
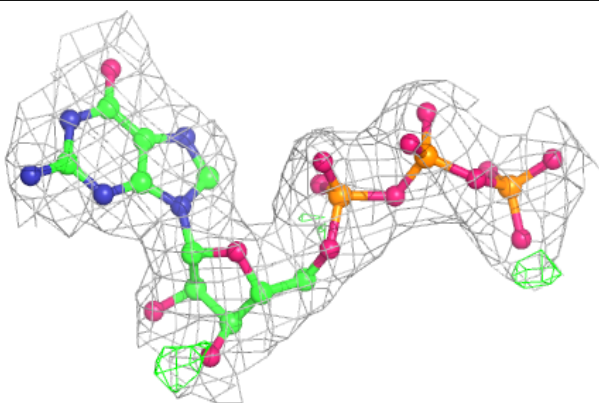


**Electron density around GDP D 501:**

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

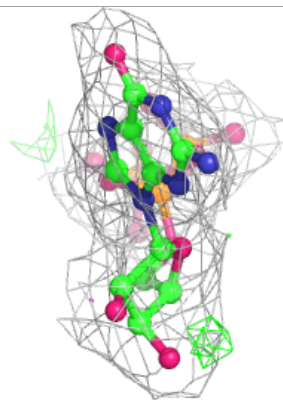
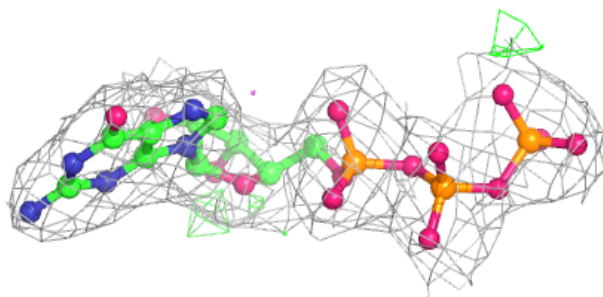
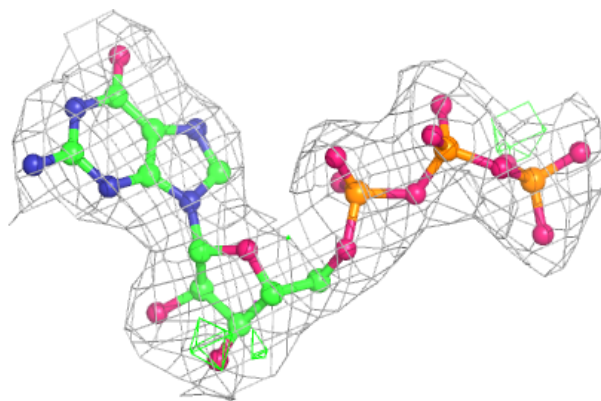
**Electron density around GTP C 501:**

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

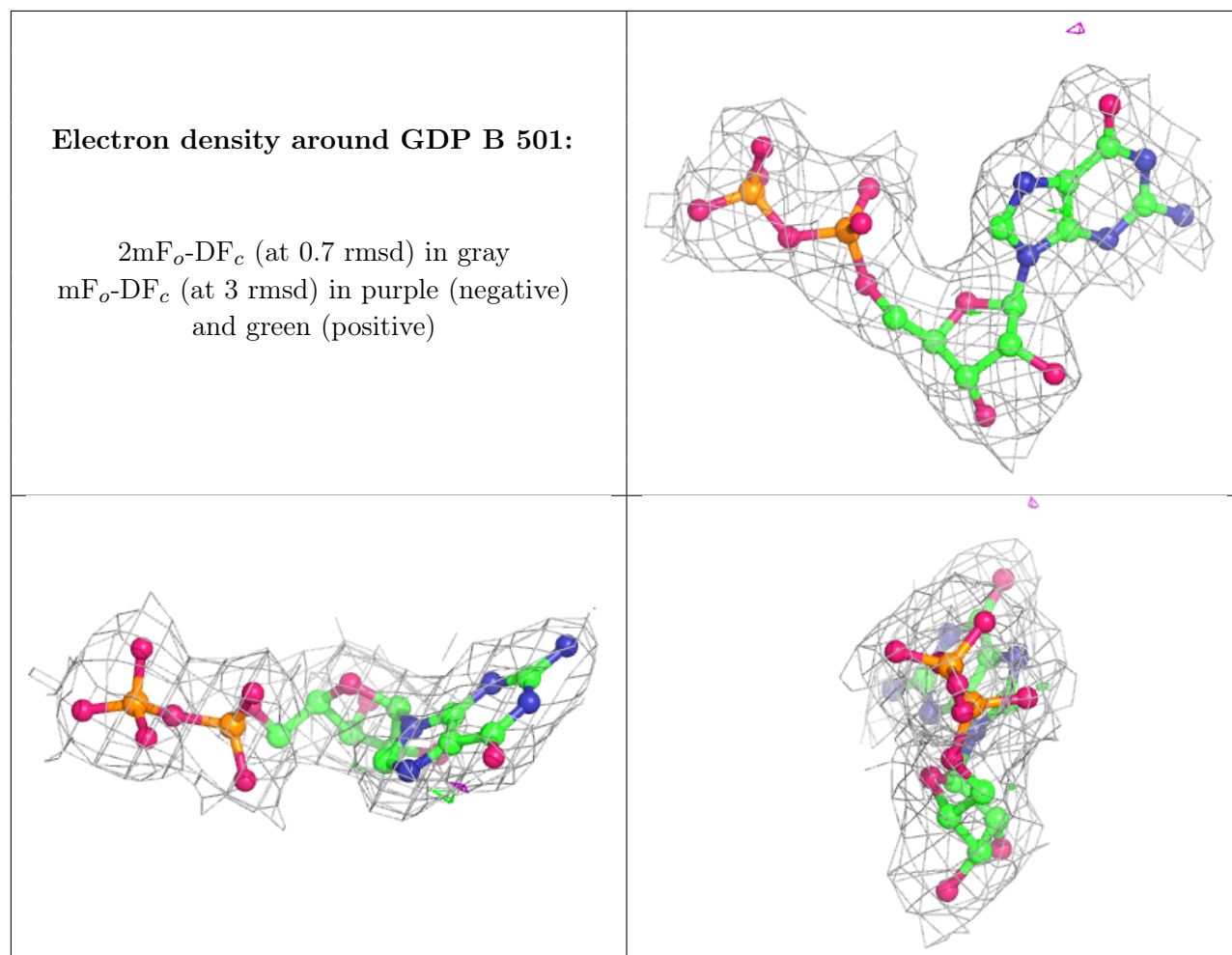


**Electron density around GTP A 501:**

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







## 6.5 Other polymers [i](#)

There are no such residues in this entry.