



Preliminary Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2022 – 08:24 pm GMT

Deposition ID : D_1292121133

This wwPDB validation report is NOT for manuscript review

This is a Preliminary Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB Deposition System during initial deposition but before annotation of the structure.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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)
Xtriage (Phenix)	:	1.13
EDS	:	2.26
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

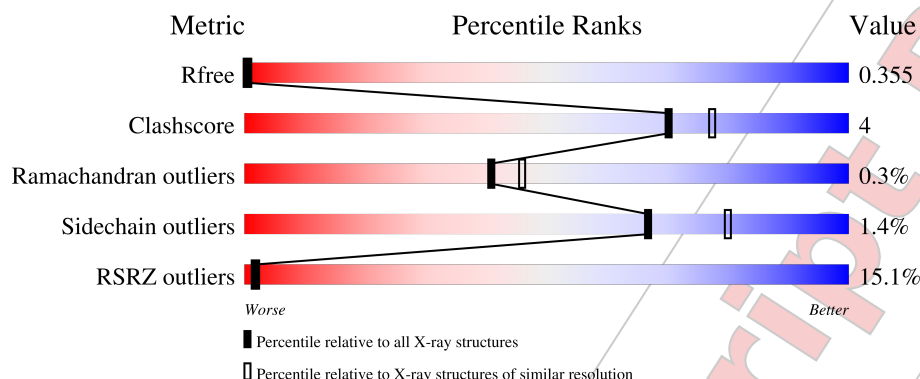
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	437	<div> <div>11%</div> <div>92%</div> <div>8%</div> </div>
2	B	426	<div> <div>23%</div> <div>87%</div> <div>13%</div> </div>
3	F	155	<div> <div>7%</div> <div>90%</div> <div>10%</div> </div>

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 8211 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	437	3419	2166	580	650	23	4	3	0

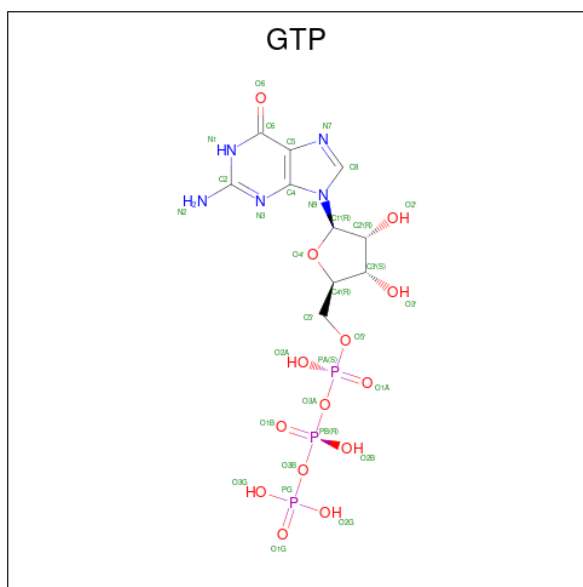
- Molecule 2 is a protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	426	3342	2100	569	646	27	0	2	0

- Molecule 3 is a protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	F	155	1154	727	198	226	3	0	0	0

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

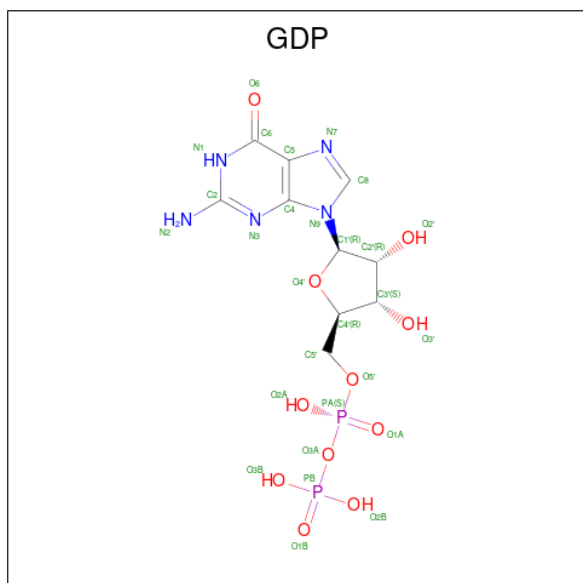


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	1	Total	Ca	0	0
			1	1		

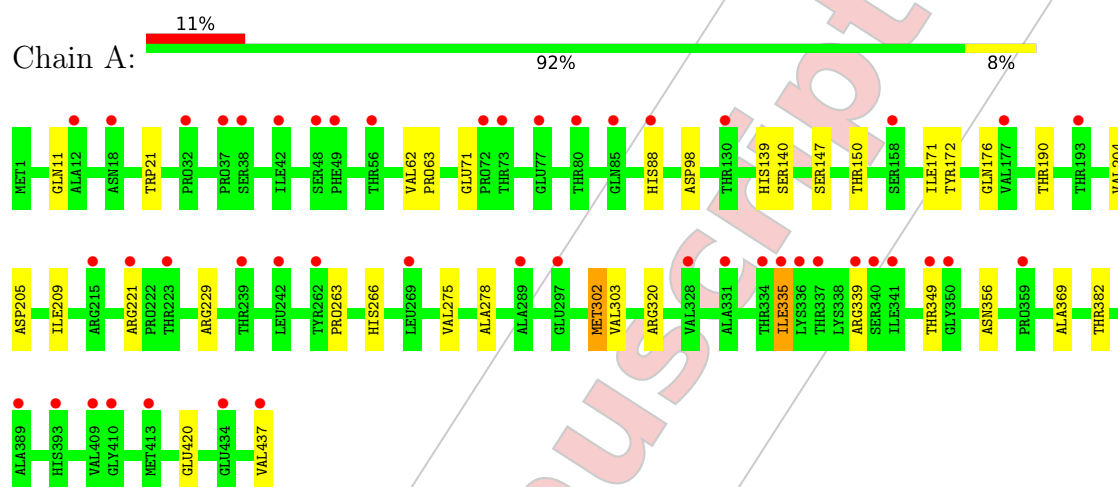
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	S	211	Total	O	0	0
			211	211		

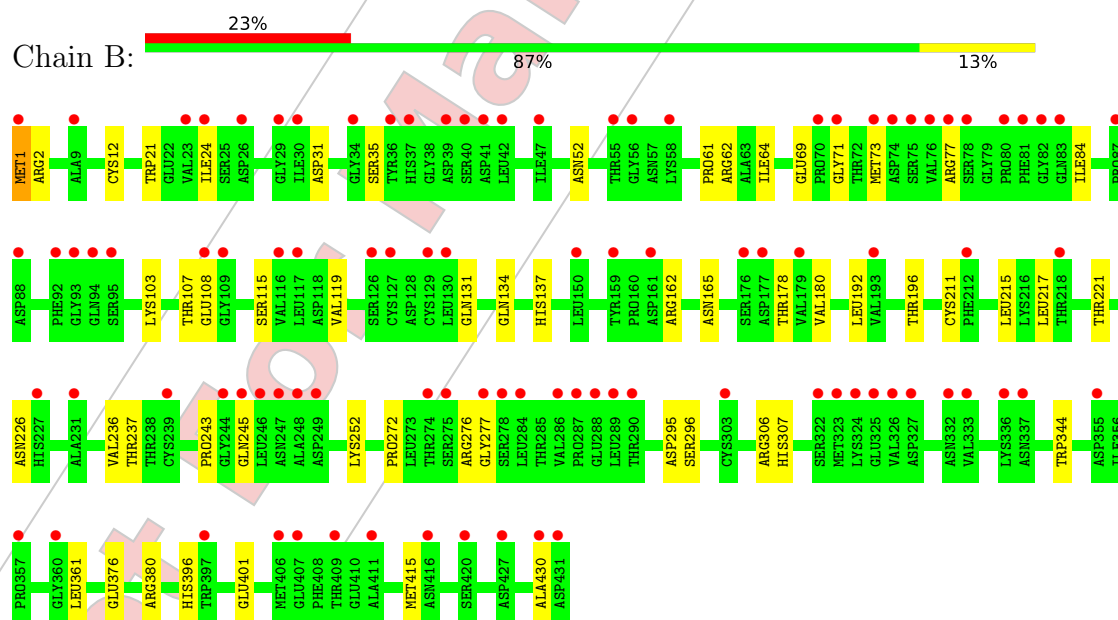
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

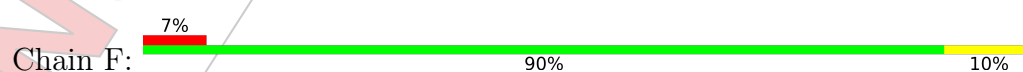
• Molecule 1:

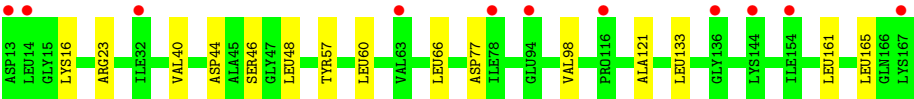


• Molecule 2:



• Molecule 3:





Not For Manuscript Review

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.53Å 92.58Å 83.99Å 90.00° 96.71° 90.00°	Depositor
Resolution (Å)	9.49 – 2.20 9.49 – 2.20	Depositor EDS
% Data completeness (in resolution range)	92.3 (9.49-2.20) 92.4 (9.49-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.74 (at 2.21Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.311 , 0.355 0.311 , 0.355	Depositor DCC
R_{free} test set	1815 reflections (3.46%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	8211	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.24	0/3506	0.46	0/4762
2	B	0.24	0/3421	0.46	0/4633
3	F	0.23	0/1170	0.40	0/1590
All	All	0.24	0/8097	0.45	0/10985

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	3419	0	3329	19	0
2	B	3342	0	3217	30	0
3	F	1154	0	1156	9	0
4	A	32	0	12	0	0
5	A	1	0	0	0	0
6	B	28	0	12	2	0
7	B	23	0	1	0	0
8	C	1	0	0	0	0
9	S	211	0	0	8	0
All	All	8211	0	7727	56	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 (56) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.75	0.69
1:A:229:ARG:NH2	9:S:205:HOH:O	2.31	0.62
1:A:98:ASP:OD2	2:B:252:LYS:NZ	2.28	0.61
2:B:52:ASN:OD1	2:B:62:ARG:NH2	2.36	0.58
1:A:221:ARG:NH2	9:S:119:HOH:O	2.37	0.57
2:B:103:LYS:NZ	2:B:401:GLU:OE2	2.38	0.55
2:B:31:ASP:OD1	2:B:35:SER:N	2.41	0.54
1:A:11:GLN:NE2	9:S:83:HOH:O	2.40	0.54
3:F:23:ARG:NH2	9:S:73:HOH:O	2.39	0.53
2:B:245:GLN:NE2	9:S:188:HOH:O	2.35	0.51
1:A:147:SER:HB2	1:A:190:THR:HB	1.92	0.51
2:B:115:SER:O	9:S:155:HOH:O	2.20	0.51
2:B:211:CYS:HB3	2:B:217:LEU:HD12	1.94	0.50
3:F:121:ALA:HB1	3:F:161:LEU:HD21	1.93	0.50
1:A:263:PRO:O	1:A:266:HIS:ND1	2.41	0.50
2:B:344:TRP:HB3	2:B:430:ALA:HB2	1.94	0.49
2:B:69:GLU:HG2	2:B:71:GLY:H	1.78	0.49
2:B:307:HIS:ND1	2:B:376:GLU:OE2	2.40	0.49
1:A:139:HIS:CD2	1:A:150:THR:HG21	2.48	0.48
2:B:12:CYS:HB2	6:B:501:GDP:C8	2.49	0.48
2:B:1:MET:HE1	2:B:162:ARG:HH12	1.79	0.47
2:B:178:THR:HG22	2:B:180:VAL:HG22	1.97	0.47
2:B:61:PRO:HD3	2:B:84:ILE:HG13	1.97	0.46
3:F:44:ASP:OD2	3:F:48:LEU:HB2	2.16	0.46
2:B:134:GLN:HA	2:B:165:ASN:O	2.15	0.45
2:B:73:MET:HG2	2:B:77:ARG:HE	1.80	0.45
2:B:226:ASN:OD1	6:B:501:GDP:N1	2.37	0.45
1:A:320:ARG:HA	1:A:356:ASN:O	2.17	0.45
2:B:211:CYS:HA	2:B:215:LEU:HB2	1.98	0.45
2:B:192:LEU:O	2:B:196:THR:OG1	2.34	0.45
2:B:21:TRP:CZ3	2:B:61:PRO:HB3	2.51	0.45
3:F:16:LYS:HA	3:F:16:LYS:HD3	1.79	0.45
1:A:275:VAL:N	9:S:45:HOH:O	2.39	0.44
3:F:133:LEU:HD11	3:F:165:LEU:HD23	2.00	0.44
1:A:382:THR:HB	1:A:437:VAL:HB	2.00	0.44
2:B:396:HIS:NE2	3:F:57:TYR:OH	2.40	0.44
1:A:171:ILE:HD13	1:A:204:VAL:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:380:ARG:NH1	9:S:141:HOH:O	2.31	0.43
2:B:107:THR:OG1	2:B:108:GLU:N	2.50	0.43
2:B:1:MET:HE1	2:B:162:ARG:NH1	2.34	0.43
3:F:40:VAL:HG13	3:F:66:LEU:HD22	2.01	0.42
3:F:60:LEU:HD11	3:F:98:VAL:HG21	2.00	0.42
1:A:205:ASP:HB2	1:A:303:VAL:HA	2.01	0.42
2:B:236:VAL:HG23	2:B:237:THR:HG23	1.99	0.42
1:A:278:ALA:HA	1:A:369:ALA:HB2	2.02	0.42
2:B:1:MET:HG3	2:B:131:GLN:HB3	2.00	0.42
1:A:140:SER:HA	1:A:171:ILE:HB	2.02	0.42
2:B:272:PRO:HD2	2:B:361:LEU:HD13	2.02	0.41
2:B:295:ASP:OD1	2:B:296:SER:N	2.54	0.41
2:B:21:TRP:CE3	2:B:24:ILE:HD11	2.55	0.41
3:F:46:SER:O	3:F:77:ASP:HB2	2.21	0.41
1:A:21:TRP:CZ3	1:A:63:PRO:HB3	2.56	0.41
1:A:62:VAL:HG11	1:A:88:HIS:CD2	2.55	0.41
2:B:64:ILE:HD13	2:B:119:VAL:HG13	2.03	0.41
1:A:209:ILE:HD11	1:A:302[B]:MET:HG3	2.02	0.41
1:A:335:ILE:HG23	1:A:339:ARG:HD3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	438/437 (100%)	422 (96%)	15 (3%)	1 (0%)	47	55
2	B	424/426 (100%)	412 (97%)	10 (2%)	2 (0%)	29	31
3	F	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
All	All	1015/1018 (100%)	984 (97%)	28 (3%)	3 (0%)	41	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	243	PRO
2	B	277	GLY
1	A	335	ILE

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	368/368 (100%)	362 (98%)	6 (2%)	62	76
2	B	366/368 (100%)	359 (98%)	7 (2%)	57	71
3	F	120/120 (100%)	120 (100%)	0	100	100
All	All	854/856 (100%)	841 (98%)	13 (2%)	67	78

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

Mol	Chain	Res	Type
1	A	71	GLU
1	A	176	GLN
1	A	302[A]	MET
1	A	302[B]	MET
1	A	349	THR
1	A	420	GLU
2	B	1	MET
2	B	2	ARG
2	B	137	HIS
2	B	221	THR
2	B	276	ARG
2	B	306	ARG
2	B	415	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	37	HIS
2	B	165	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 5 ligands modelled in this entry, 2 are monoatomic and 1 could not be matched to an existing wwPDB Chemical Component Dictionary definition at this stage - leaving 2 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
6	GDP	B	501	-	24,30,30	1.17	2 (8%)	31,47,47	1.95	8 (25%)
4	GTP	A	501	5	26,34,34	0.98	1 (3%)	33,54,54	1.77	7 (21%)

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
6	GDP	B	501	-	-	3/12/32/32	0/3/3/3
4	GTP	A	501	5	-	7/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	501	GDP	C5-C6	4.16	1.48	1.41
4	A	501	GTP	C6-N1	3.12	1.38	1.33
6	B	501	GDP	C5-C4	2.45	1.47	1.40

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	GTP	N3-C2-N1	-5.33	120.11	127.22
6	B	501	GDP	C2-N3-C4	4.87	120.92	115.36
4	A	501	GTP	C2-N3-C4	4.24	120.20	115.36
6	B	501	GDP	C2-N1-C6	4.03	122.34	115.93
6	B	501	GDP	C5-C6-N1	-3.94	118.05	123.43
6	B	501	GDP	C4-C5-C6	-3.83	117.14	120.80
6	B	501	GDP	N3-C2-N1	-3.28	122.85	127.22
4	A	501	GTP	PB-O3B-PG	-3.18	121.92	132.83
6	B	501	GDP	PA-O3A-PB	-2.99	122.56	132.83
4	A	501	GTP	C5-C6-N1	-2.88	119.49	123.43
4	A	501	GTP	PA-O3A-PB	-2.74	123.41	132.83
6	B	501	GDP	C3'-C2'-C1'	2.74	105.10	100.98
6	B	501	GDP	C4-C5-N7	-2.63	106.65	109.40
4	A	501	GTP	C2-N1-C6	2.55	119.99	115.93
4	A	501	GTP	C3'-C2'-C1'	2.17	104.24	100.98

There are no chirality outliers.

All (10) torsion outliers are listed below:

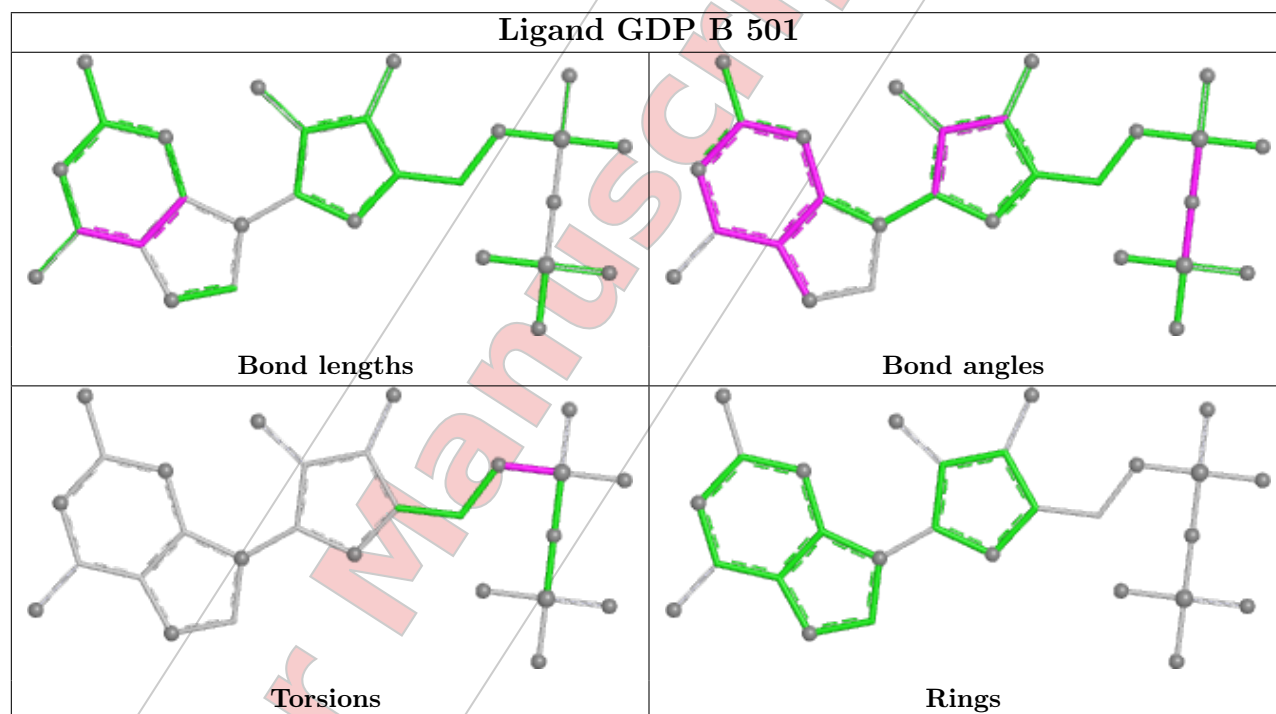
Mol	Chain	Res	Type	Atoms
4	A	501	GTP	C5'-O5'-PA-O1A
4	A	501	GTP	C5'-O5'-PA-O2A
6	B	501	GDP	C5'-O5'-PA-O1A
6	B	501	GDP	C5'-O5'-PA-O2A
4	A	501	GTP	PB-O3B-PG-O1G
4	A	501	GTP	C5'-O5'-PA-O3A
4	A	501	GTP	C4'-C5'-O5'-PA
4	A	501	GTP	PB-O3B-PG-O2G
4	A	501	GTP	PB-O3B-PG-O3G
6	B	501	GDP	C5'-O5'-PA-O3A

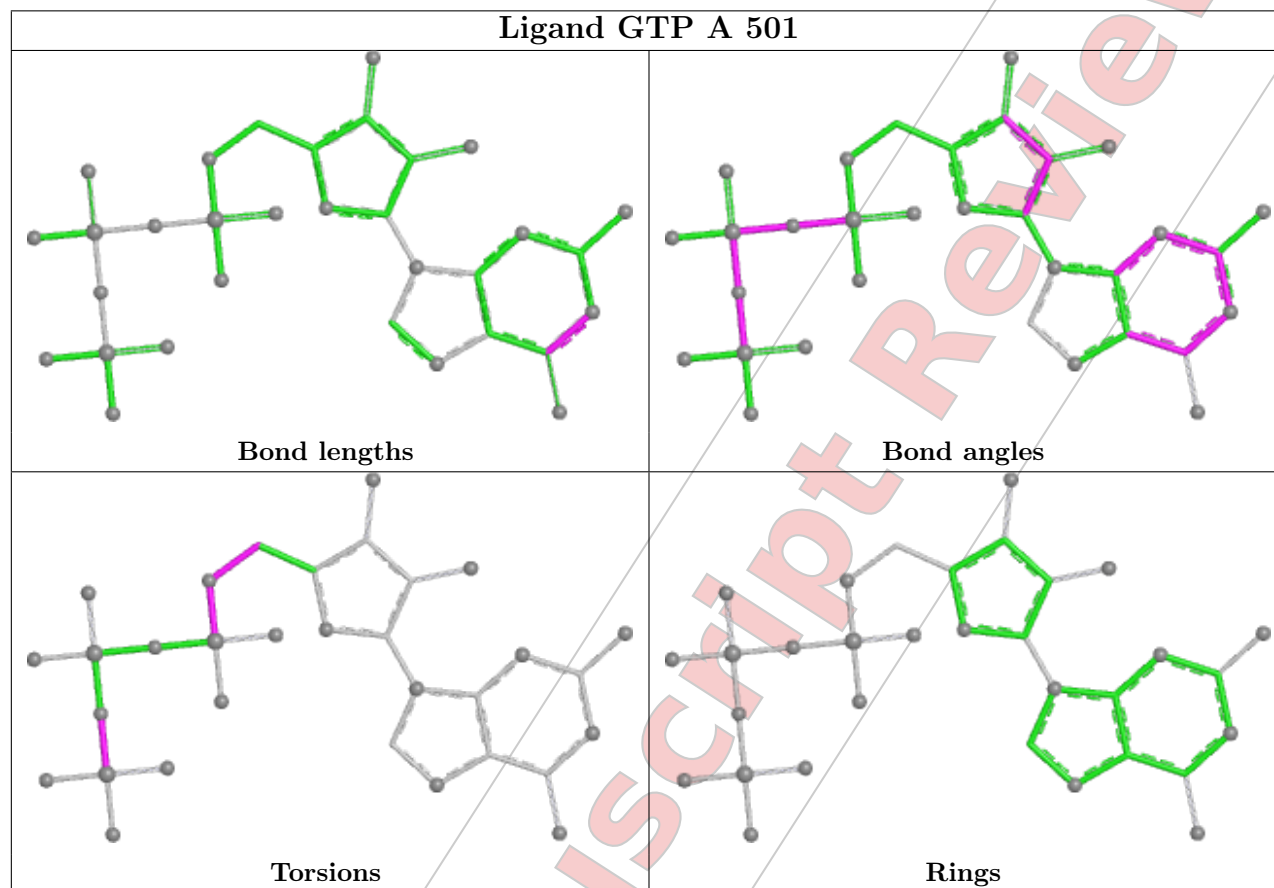
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	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](#)

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	278:SER	C	284:LEU	N	12.23

6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	437/437 (100%)	0.91	47 (10%) 5 5	20, 29, 45, 65	0
2	B	426/426 (100%)	1.36	96 (22%) 0 0	23, 37, 59, 68	0
3	F	155/155 (100%)	0.84	11 (7%) 16 14	21, 30, 43, 56	0
All	All	1018/1018 (100%)	1.09	154 (15%) 2 2	20, 32, 55, 68	0

All (154) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	THR	7.2
2	B	73	MET	6.8
2	B	244	GLY	6.6
1	A	437	VAL	6.4
2	B	1	MET	6.3
2	B	409	THR	5.7
2	B	332	ASN	5.7
2	B	82	GLY	5.4
2	B	93	GLY	5.4
1	A	339	ARG	5.4
2	B	431	ASP	5.4
3	F	167	LYS	5.2
2	B	80	PRO	4.8
2	B	177	ASP	4.7
2	B	71	GLY	4.6
1	A	37	PRO	4.5
2	B	218	THR	4.5
2	B	360	GLY	4.4
2	B	245	GLN	4.3
2	B	55	THR	4.3
2	B	333	VAL	4.3
2	B	246	LEU	4.3
2	B	326	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
2	B	83	GLN	4.2
3	F	154	ILE	4.2
1	A	340	SER	4.0
2	B	39	ASP	3.9
1	A	335	ILE	3.8
2	B	36	TYR	3.8
2	B	42	LEU	3.7
2	B	95	SER	3.7
1	A	350	GLY	3.7
2	B	41	ASP	3.6
1	A	410	GLY	3.6
2	B	287	PRO	3.6
2	B	212	PHE	3.6
2	B	416	ASN	3.5
2	B	70	PRO	3.5
2	B	56	GLY	3.4
1	A	85	GLN	3.4
2	B	92	PHE	3.4
1	A	341	ILE	3.4
2	B	179	VAL	3.3
3	F	32	ILE	3.3
2	B	286	VAL	3.3
2	B	322	SER	3.3
2	B	397	TRP	3.3
1	A	269	LEU	3.3
2	B	420	SER	3.2
2	B	81	PHE	3.2
2	B	34	GLY	3.2
2	B	87	PRO	3.2
2	B	58	LYS	3.1
2	B	117	LEU	3.1
2	B	127	CYS	3.1
2	B	289	LEU	3.1
2	B	227	HIS	3.1
2	B	231	ALA	3.1
2	B	274	THR	3.0
2	B	357	PRO	3.0
1	A	38	SER	3.0
2	B	325	GLU	3.0
2	B	411	ALA	3.0
1	A	88	HIS	3.0
3	F	63	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
2	B	88	ASP	3.0
2	B	126	SER	2.9
1	A	80	THR	2.9
2	B	288	GLU	2.9
2	B	47	ILE	2.9
2	B	278	SER	2.8
1	A	389	ALA	2.8
2	B	303	CYS	2.8
2	B	324	LYS	2.8
2	B	248	ALA	2.8
1	A	359	PRO	2.8
1	A	289	ALA	2.8
2	B	336	LYS	2.8
2	B	284	LEU	2.7
2	B	290	THR	2.7
1	A	72	PRO	2.7
2	B	193	VAL	2.7
2	B	24	ILE	2.7
1	A	393	HIS	2.7
1	A	242	LEU	2.7
2	B	427	ASP	2.6
1	A	215	ARG	2.6
2	B	430	ALA	2.6
2	B	327	ASP	2.6
2	B	323	MET	2.6
1	A	262	TYR	2.6
3	F	78	ILE	2.6
2	B	129	CYS	2.5
2	B	247	ASN	2.5
1	A	239	THR	2.5
2	B	277	GLY	2.5
2	B	76	VAL	2.5
3	F	144	LYS	2.5
1	A	331	ALA	2.5
2	B	77	ARG	2.4
2	B	9	ALA	2.4
1	A	32	PRO	2.4
2	B	29	GLY	2.4
2	B	37	HIS	2.4
2	B	407	GLU	2.4
1	A	42	ILE	2.4
1	A	221	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	337	THR	2.4
1	A	349	THR	2.4
2	B	30	ILE	2.4
2	B	337	ASN	2.4
2	B	249	ASP	2.4
2	B	75	SER	2.4
1	A	223	THR	2.3
1	A	177	VAL	2.3
1	A	130	THR	2.3
2	B	74	ASP	2.3
1	A	77	GLU	2.3
1	A	409	VAL	2.3
2	B	130	LEU	2.3
2	B	161	ASP	2.3
3	F	13	ASP	2.3
1	A	18	ASN	2.2
1	A	49	PHE	2.2
3	F	116	PRO	2.2
2	B	275	SER	2.2
2	B	150	LEU	2.2
3	F	136	GLY	2.2
2	B	26	ASP	2.2
2	B	406	MET	2.2
3	F	94	GLU	2.2
2	B	40	SER	2.2
2	B	116	VAL	2.2
2	B	109	GLY	2.2
1	A	158	SER	2.2
2	B	355	ASP	2.2
3	F	14	LEU	2.2
2	B	108	GLU	2.1
1	A	328	VAL	2.1
2	B	23	VAL	2.1
2	B	78	SER	2.1
2	B	176	SER	2.1
1	A	413	MET	2.1
2	B	239	CYS	2.1
1	A	336	LYS	2.1
1	A	297	GLU	2.1
2	B	159	TYR	2.1
2	B	94	GLN	2.1
1	A	73	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	434	GLU	2.0
1	A	56	THR	2.0
1	A	12	ALA	2.0
1	A	48	SER	2.0
1	A	193	THR	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](#)

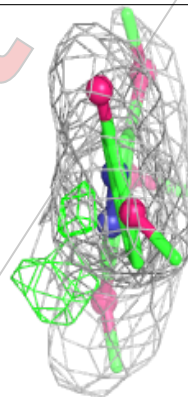
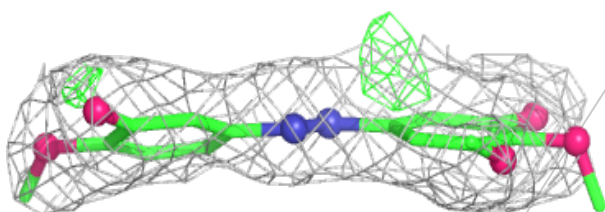
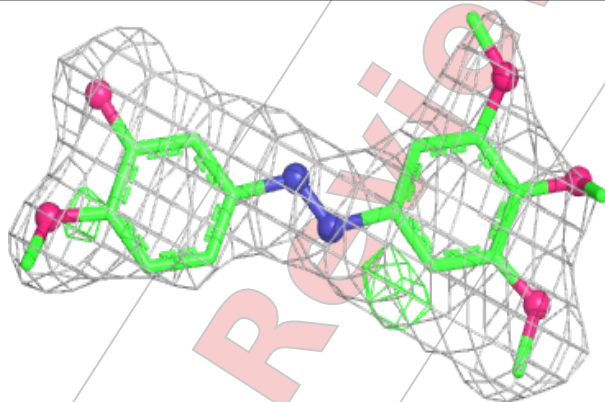
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	XXX	B	601	23/?	0.84	0.20	28,35,48,52	0
5	MG	A	502	1/?	0.89	0.34	31,31,31,31	0
8	CA	C	1	1/?	0.91	0.06	38,38,38,38	0
4	GTP	A	501	32/?	0.92	0.16	19,22,25,26	0
6	GDP	B	501	28/?	0.92	0.16	26,33,37,40	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.

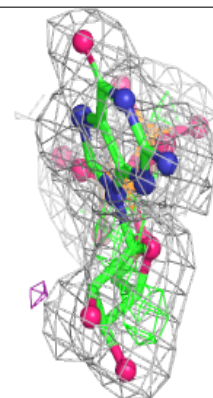
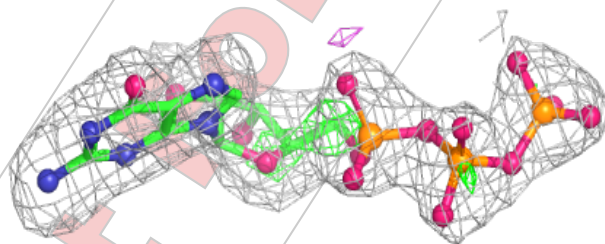
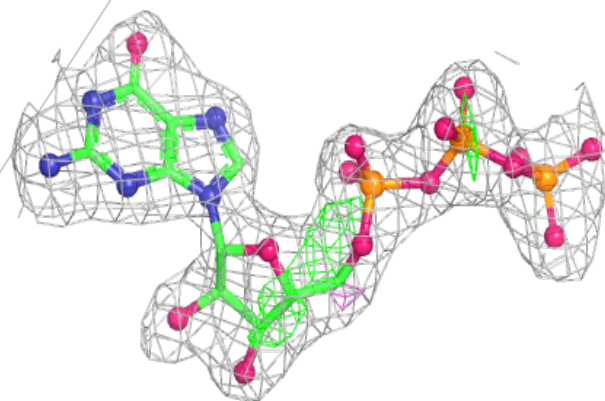
Electron density around XXX B 601:

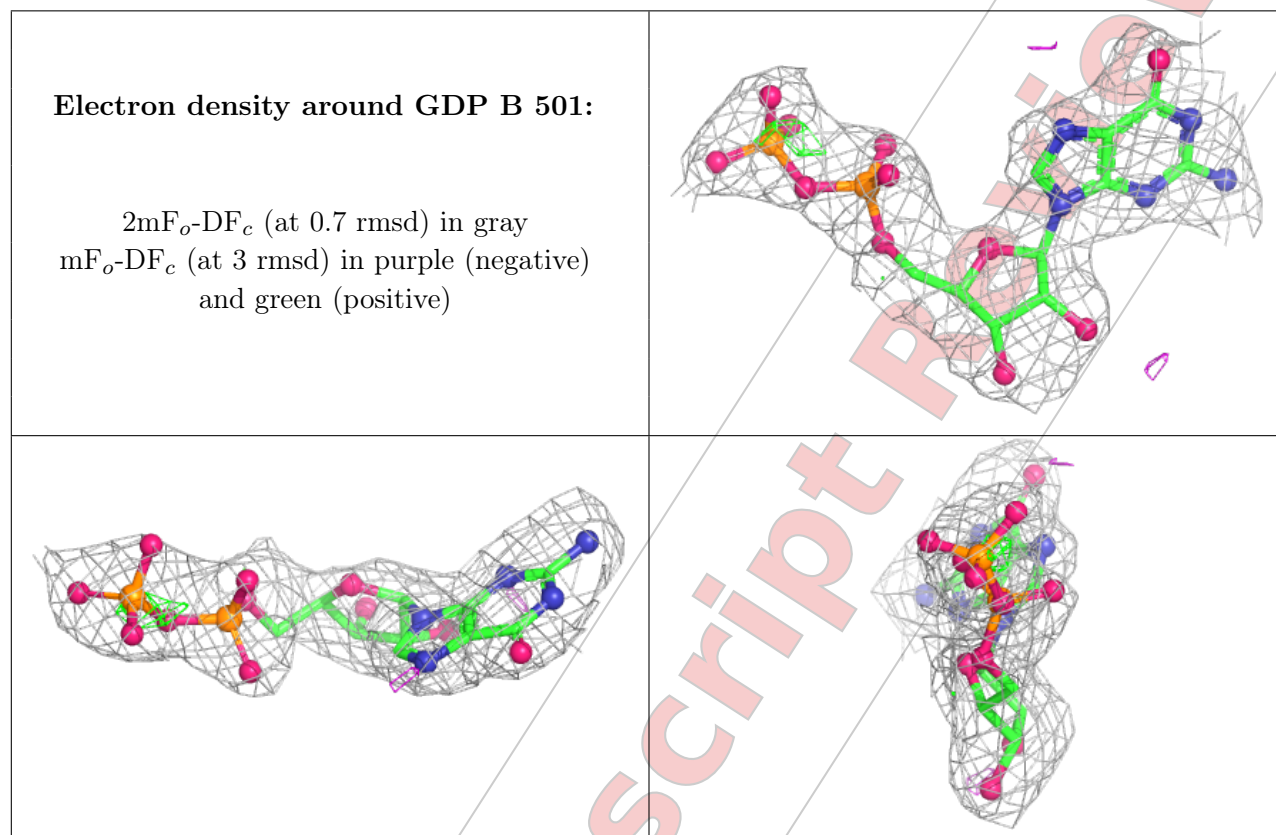
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
 and green (positive)



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.