



Preliminary Full wwPDB X-ray Structure Validation Report ⓘ

Feb 16, 2022 – 01:27 pm GMT

Deposition ID : D_1292121161

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

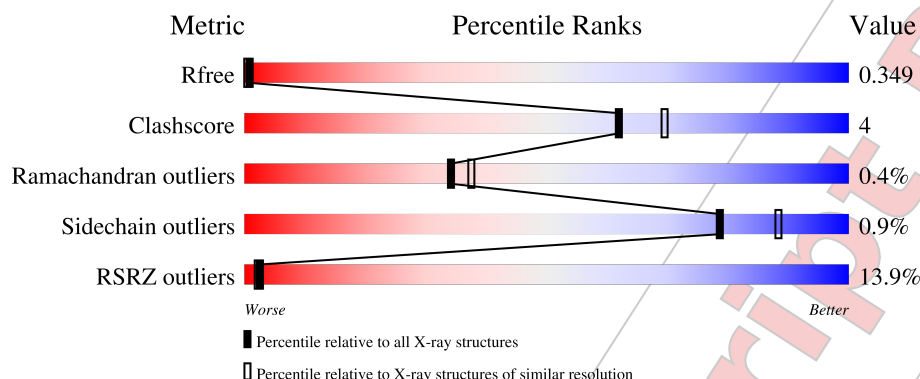
1 Overall quality at a glance i

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>8%</div> <div>89%</div> <div>10%</div> </div>
2	B	426	<div> <div>22%</div> <div>84%</div> <div>15%</div> </div>
3	F	155	<div> <div>8%</div> <div>91%</div> <div>9%</div> </div>

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 8217 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	3416	2164	579	649	24	4	3	0

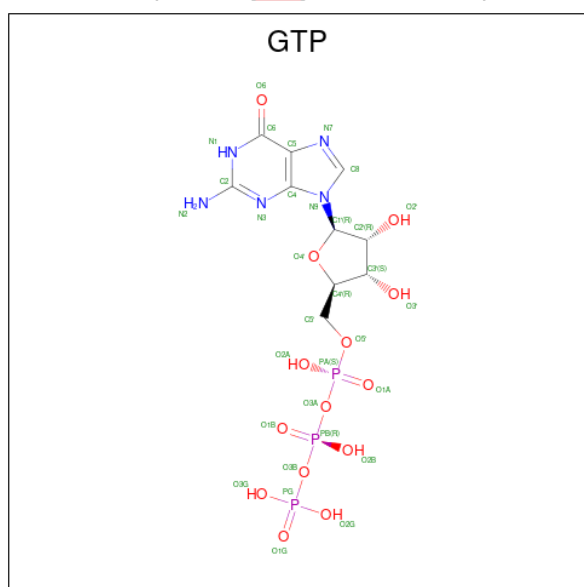
- Molecule 2 is a protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	426	3339	2097	569	646	27	0	1	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: $C_{10}H_{16}N_5O_{14}P_3$).

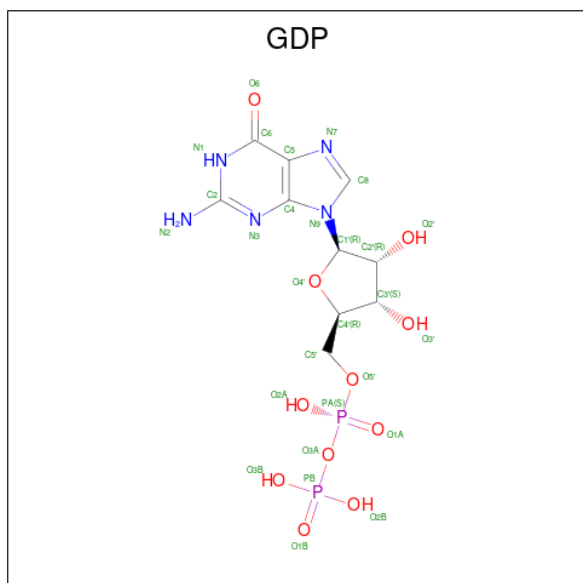


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- 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		

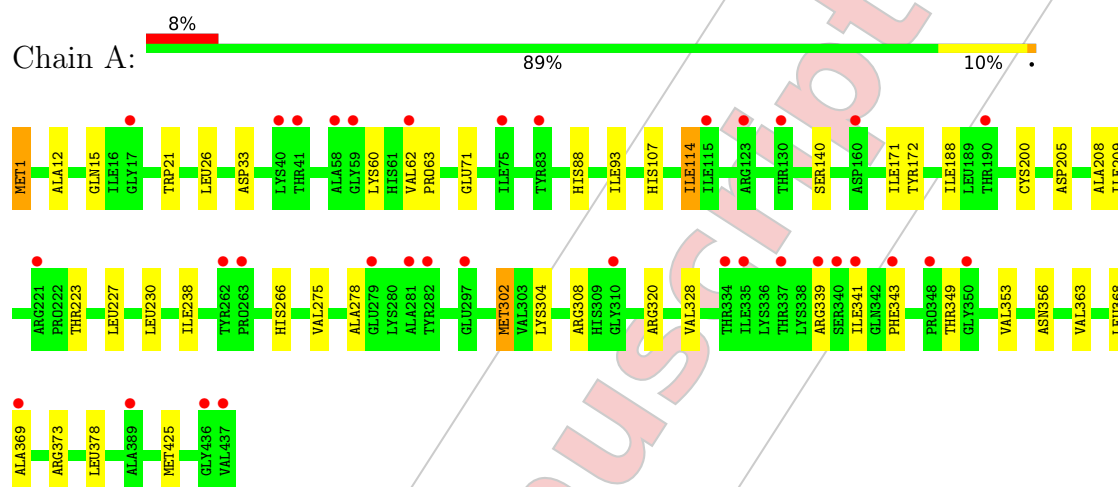
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	S	223	Total	O	0	0
			223	223		

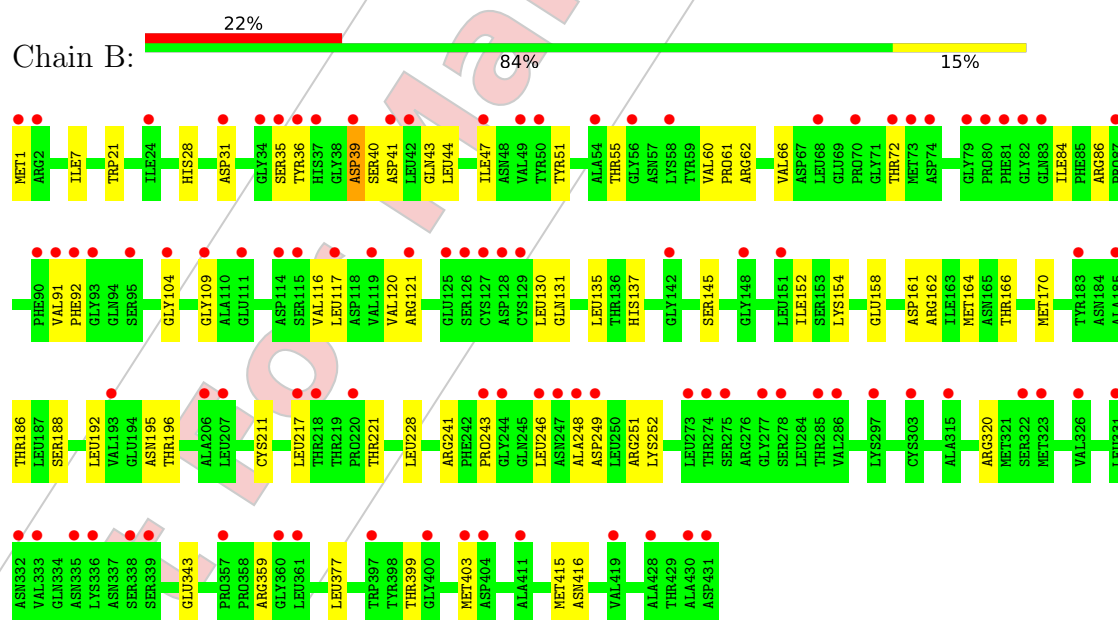
3 Residue-property plots

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.

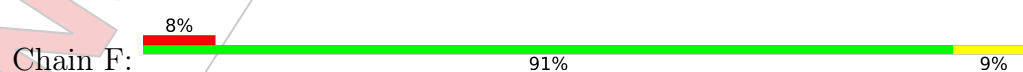
• Molecule 1:

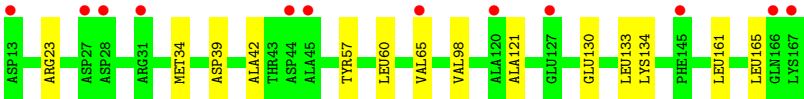


• Molecule 2:



• 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)	91.9 (9.49-2.20) 92.0 (9.49-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.66 (at 2.21Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.305 , 0.349 0.305 , 0.349	Depositor DCC
R_{free} test set	1818 reflections (3.48%)	wwPDB-VP
Wilson B-factor (Å ²)	33.3	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.39$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	8217	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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: XXX, MG, CA, GTP, GDP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.24	0/3503	0.46	0/4758
2	B	0.24	0/3415	0.45	0/4625
3	F	0.23	0/1170	0.40	0/1590
All	All	0.24	0/8088	0.45	0/10973

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3416	0	3325	27	0
2	B	3339	0	3213	35	0
3	F	1154	0	1156	7	0
4	A	32	0	12	1	0
5	A	1	0	0	0	0
6	B	28	0	12	0	0
7	B	23	0	1	0	0
8	C	1	0	0	0	0
9	S	223	0	0	9	0
All	All	8217	0	7719	69	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 (69) 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:308:ARG:HH11	1:A:339:ARG:HH22	1.42	0.68
2:B:145:SER:HG	2:B:188:SER:HG	1.37	0.68
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.74	0.67
2:B:121:ARG:NH2	2:B:158:GLU:OE1	2.33	0.62
2:B:31:ASP:OD1	2:B:35:SER:N	2.34	0.60
2:B:195:ASN:ND2	9:S:203:HOH:O	2.34	0.59
2:B:130:LEU:O	2:B:162:ARG:NH1	2.33	0.59
1:A:308:ARG:NH2	9:S:146:HOH:O	2.36	0.58
2:B:51:TYR:O	2:B:62:ARG:NH2	2.37	0.58
3:F:121:ALA:HB1	3:F:161:LEU:HD21	1.84	0.58
2:B:117:LEU:HD11	2:B:154:LYS:HB3	1.85	0.58
1:A:209:ILE:HG23	1:A:230:LEU:HD23	1.86	0.57
2:B:211:CYS:HB3	2:B:217:LEU:HD12	1.87	0.56
2:B:416:ASN:ND2	9:S:77:HOH:O	2.38	0.56
3:F:133:LEU:HD11	3:F:165:LEU:HD23	1.88	0.56
2:B:61:PRO:HD3	2:B:84:ILE:HG13	1.88	0.55
2:B:161:ASP:O	2:B:251:ARG:NH2	2.41	0.53
1:A:15:GLN:NE2	4:A:501:GTP:O6	2.41	0.53
1:A:140:SER:HA	1:A:171:ILE:HB	1.91	0.53
3:F:39:ASP:HB3	3:F:42:ALA:HB2	1.92	0.52
1:A:302[B]:MET:SD	9:S:83:HOH:O	2.59	0.52
1:A:1:MET:N	9:S:68:HOH:O	2.42	0.50
1:A:33:ASP:O	1:A:60:LYS:NZ	2.42	0.50
1:A:373:ARG:NH2	9:S:183:HOH:O	2.44	0.50
1:A:26:LEU:HD12	1:A:363:VAL:HG12	1.94	0.49
2:B:44:LEU:HA	2:B:47:ILE:HB	1.94	0.48
1:A:343:PHE:HB2	1:A:349:THR:HG23	1.94	0.48
1:A:62:VAL:HG11	1:A:88:HIS:CD2	2.49	0.48
2:B:152:ILE:HG23	2:B:164:MET:HG2	1.96	0.48
2:B:399:THR:HA	2:B:403:MET:O	2.13	0.48
1:A:328:VAL:HG11	1:A:353:VAL:HG11	1.96	0.48
1:A:188:ILE:HG23	1:A:425:MET:HG3	1.96	0.48
2:B:135:LEU:HB3	2:B:166:THR:HG22	1.96	0.47
2:B:72:THR:HB	2:B:92:PHE:HE2	1.79	0.47
1:A:21:TRP:CZ3	1:A:63:PRO:HB3	2.49	0.47
1:A:275:VAL:HG13	1:A:368:LEU:HD21	1.96	0.47
2:B:192:LEU:O	2:B:196:THR:OG1	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:104:GLY:O	2:B:109:GLY:HA3	2.16	0.46
2:B:66:VAL:HA	2:B:91:VAL:O	2.17	0.45
2:B:186:THR:HG23	2:B:415:MET:HE1	1.98	0.45
3:F:130:GLU:O	3:F:134:LYS:HG3	2.17	0.44
2:B:28:HIS:CE1	2:B:241:ARG:HB3	2.52	0.44
2:B:7:ILE:O	2:B:135:LEU:HA	2.17	0.44
2:B:116:VAL:O	2:B:120:VAL:HG23	2.18	0.43
2:B:343:GLU:OE1	2:B:343:GLU:N	2.46	0.43
2:B:249:ASP:HB3	2:B:252:LYS:HB2	2.00	0.43
1:A:93:ILE:HG22	1:A:114:ILE:HD11	2.00	0.43
1:A:208:ALA:HA	1:A:304:LYS:HE3	2.01	0.42
2:B:36:TYR:OH	2:B:40:SER:O	2.38	0.42
1:A:238:ILE:HG12	1:A:378:LEU:HD21	2.02	0.42
1:A:12:ALA:HB3	1:A:140:SER:HB3	2.00	0.42
1:A:320:ARG:HA	1:A:356:ASN:O	2.19	0.42
2:B:228:LEU:O	9:S:206:HOH:O	2.22	0.42
2:B:359:ARG:NH1	9:S:36:HOH:O	2.44	0.42
2:B:21:TRP:CZ3	2:B:61:PRO:HB3	2.54	0.42
2:B:41:ASP:C	2:B:43:GLN:H	2.23	0.42
3:F:60:LEU:HD11	3:F:98:VAL:HG21	2.02	0.41
1:A:278:ALA:HA	1:A:369:ALA:HB2	2.01	0.41
1:A:339:ARG:HB2	1:A:341:ILE:HG12	2.02	0.41
2:B:170:MET:HG3	2:B:377:LEU:HD11	2.01	0.41
2:B:28:HIS:NE2	2:B:241:ARG:HB3	2.36	0.41
1:A:107:HIS:O	9:S:218:HOH:O	2.22	0.41
2:B:39:ASP:OD1	2:B:39:ASP:N	2.53	0.41
2:B:60:VAL:HG11	2:B:86:ARG:HG3	2.03	0.41
3:F:23:ARG:NH1	3:F:57:TYR:OH	2.54	0.41
3:F:34:MET:HE1	3:F:65:VAL:HG12	2.02	0.40
2:B:1:MET:HA	2:B:131:GLN:HB3	2.03	0.40
1:A:200:CYS:HA	1:A:266:HIS:HB2	2.02	0.40
1:A:223:THR:O	1:A:227:LEU:HG	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	438/437 (100%)	425 (97%)	12 (3%)	1 (0%)	47	55
2	B	423/426 (99%)	406 (96%)	14 (3%)	3 (1%)	22	22
3	F	153/155 (99%)	149 (97%)	4 (3%)	0	100	100
All	All	1014/1018 (100%)	980 (97%)	30 (3%)	4 (0%)	34	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	243	PRO
2	B	55	THR
2	B	248	ALA
1	A	114	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%)	364 (99%)	4 (1%)	73	85
2	B	366/368 (100%)	361 (99%)	5 (1%)	67	80
3	F	120/120 (100%)	120 (100%)	0	100	100
All	All	854/856 (100%)	845 (99%)	9 (1%)	78	85

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	71	GLU
1	A	302[A]	MET
1	A	302[B]	MET
2	B	39	ASP

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Mol	Chain	Res	Type
2	B	137	HIS
2	B	221	THR
2	B	246	LEU
2	B	320	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	342	GLN
2	B	8	GLN
2	B	37	HIS
2	B	134	GLN
2	B	245	GLN
3	F	166	GLN

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
4	GTP	A	501	5	26,34,34	0.98	1 (3%)	33,54,54	1.81	7 (21%)
6	GDP	B	501	-	24,30,30	1.20	2 (8%)	31,47,47	1.97	8 (25%)

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
4	GTP	A	501	5	-	8/18/38/38	0/3/3/3
6	GDP	B	501	-	-	3/12/32/32	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	4.26	1.48	1.41
4	A	501	GTP	C6-N1	3.16	1.38	1.33
6	B	501	GDP	C5-C4	2.44	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	-5.31	120.14	127.22
6	B	501	GDP	C2-N3-C4	4.91	120.96	115.36
4	A	501	GTP	C2-N3-C4	4.20	120.15	115.36
6	B	501	GDP	C2-N1-C6	4.06	122.39	115.93
6	B	501	GDP	C5-C6-N1	-4.05	117.90	123.43
6	B	501	GDP	C4-C5-C6	-3.71	117.26	120.80
4	A	501	GTP	PB-O3B-PG	-3.30	121.50	132.83
4	A	501	GTP	PA-O3A-PB	-3.29	121.52	132.83
6	B	501	GDP	N3-C2-N1	-3.29	122.84	127.22
6	B	501	GDP	PA-O3A-PB	-3.15	122.02	132.83
6	B	501	GDP	C3'-C2'-C1'	3.01	105.50	100.98
4	A	501	GTP	C5-C6-N1	-2.87	119.51	123.43
6	B	501	GDP	C4-C5-N7	-2.67	106.62	109.40
4	A	501	GTP	C2-N1-C6	2.54	119.96	115.93
4	A	501	GTP	C3'-C2'-C1'	2.51	104.76	100.98

There are no chirality outliers.

All (11) torsion outliers are listed below:

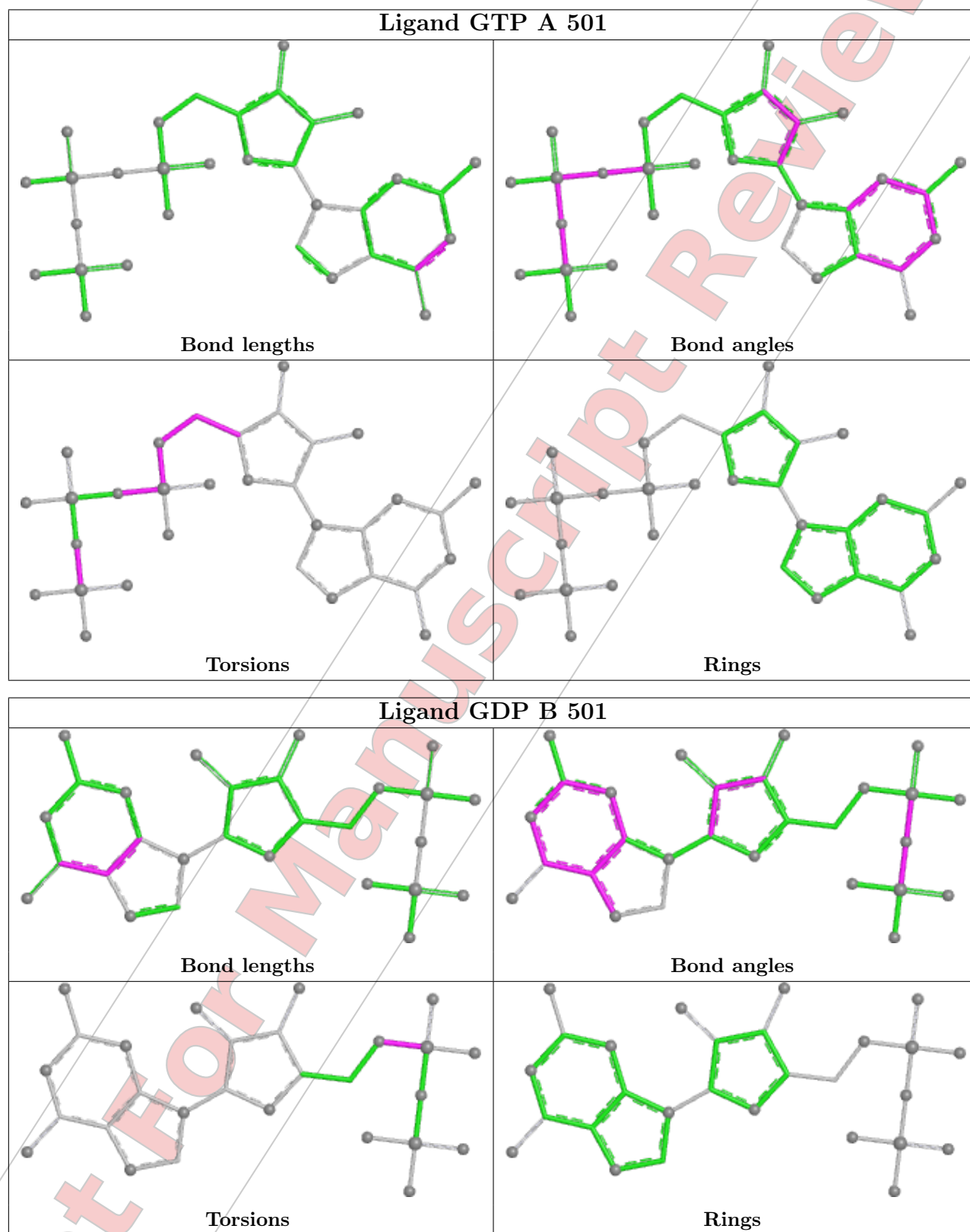
Mol	Chain	Res	Type	Atoms
4	A	501	GTP	PB-O3B-PG-O2G
4	A	501	GTP	C5'-O5'-PA-O1A
4	A	501	GTP	C5'-O5'-PA-O2A
6	B	501	GDP	C5'-O5'-PA-O1A
6	B	501	GDP	C5'-O5'-PA-O2A
4	A	501	GTP	C5'-O5'-PA-O3A
4	A	501	GTP	C3'-C4'-C5'-O5'
4	A	501	GTP	PB-O3A-PA-O1A
4	A	501	GTP	O4'-C4'-C5'-O5'
4	A	501	GTP	C4'-C5'-O5'-PA
6	B	501	GDP	C5'-O5'-PA-O3A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	GTP	1	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	278:SER	C	284:LEU	N	12.96

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%)	0.78	34 (7%) 13 11	20, 34, 54, 74	0
2	B	426/426 (100%)	1.32	95 (22%) 0 0	24, 45, 71, 83	0
3	F	155/155 (100%)	0.79	12 (7%) 13 12	25, 36, 52, 65	0
All	All	1018/1018 (100%)	1.01	141 (13%) 2 2	20, 38, 65, 83	0

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	437	VAL	10.5
2	B	73	MET	6.4
2	B	244	GLY	5.9
2	B	326	VAL	5.7
2	B	275	SER	5.5
2	B	80	PRO	5.5
1	A	41	THR	5.1
2	B	248	ALA	5.0
2	B	115	SER	5.0
2	B	93	GLY	4.8
2	B	79	GLY	4.7
2	B	218	THR	4.6
2	B	128	ASP	4.6
2	B	127	CYS	4.6
2	B	114	ASP	4.5
1	A	389	ALA	4.5
2	B	54	ALA	4.4
2	B	246	LEU	4.3
2	B	431	ASP	4.3
2	B	126	SER	4.3
2	B	111	GLU	4.2
2	B	39	ASP	4.2
2	B	95	SER	4.1

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Mol	Chain	Res	Type	RSRZ
2	B	36	TYR	4.0
1	A	334	THR	4.0
3	F	13	ASP	3.9
1	A	436	GLY	3.8
1	A	62	VAL	3.8
2	B	322	SER	3.8
2	B	34	GLY	3.7
2	B	360	GLY	3.7
1	A	339	ARG	3.7
2	B	243	PRO	3.7
1	A	348	PRO	3.6
2	B	109	GLY	3.5
2	B	404	ASP	3.5
2	B	82	GLY	3.4
2	B	331	LEU	3.4
2	B	332	ASN	3.3
2	B	247	ASN	3.2
2	B	403	MET	3.2
2	B	129	CYS	3.2
1	A	340	SER	3.2
2	B	35	SER	3.2
2	B	361	LEU	3.2
3	F	31	ARG	3.2
2	B	193	VAL	3.1
1	A	337	THR	3.1
1	A	221	ARG	3.1
1	A	350	GLY	3.1
2	B	411	ALA	3.1
3	F	166	GLN	3.1
2	B	58	LYS	3.0
2	B	400	GLY	3.0
2	B	336	LYS	3.0
2	B	220	PRO	3.0
1	A	281	ALA	3.0
2	B	24	ILE	3.0
2	B	31	ASP	2.9
2	B	207	LEU	2.9
3	F	45	ALA	2.9
2	B	206	ALA	2.8
2	B	217	LEU	2.8
2	B	56	GLY	2.8
2	B	273	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	117	LEU	2.8
2	B	2	ARG	2.8
1	A	75	ILE	2.8
1	A	335	ILE	2.8
2	B	397	TRP	2.8
2	B	92	PHE	2.8
2	B	286	VAL	2.8
2	B	249	ASP	2.7
2	B	315	ALA	2.7
1	A	369	ALA	2.7
2	B	68	LEU	2.7
2	B	81	PHE	2.7
3	F	65	VAL	2.6
1	A	262	TYR	2.6
1	A	40	LYS	2.6
1	A	279	GLU	2.6
1	A	58	ALA	2.6
2	B	37	HIS	2.6
2	B	285	THR	2.6
2	B	70	PRO	2.6
2	B	87	PRO	2.5
3	F	145	PHE	2.5
2	B	339	SER	2.5
2	B	119	VAL	2.5
2	B	428	ALA	2.5
2	B	430	ALA	2.5
3	F	28	ASP	2.4
1	A	123	ARG	2.4
1	A	59	GLY	2.4
2	B	72	THR	2.4
2	B	91	VAL	2.4
2	B	74	ASP	2.3
2	B	274	THR	2.3
2	B	419	VAL	2.3
2	B	104	GLY	2.3
2	B	142	GLY	2.3
2	B	83	GLN	2.3
2	B	121	ARG	2.3
1	A	130	THR	2.3
2	B	1	MET	2.3
2	B	148	GLY	2.3
3	F	44	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	341	ILE	2.3
3	F	167	LYS	2.3
1	A	297	GLU	2.2
2	B	42	LEU	2.2
2	B	50	TYR	2.2
2	B	125	GLU	2.2
1	A	160	ASP	2.2
1	A	343	PHE	2.2
2	B	277	GLY	2.2
1	A	190	THR	2.2
1	A	263	PRO	2.2
1	A	310	GLY	2.2
3	F	120	ALA	2.1
2	B	335	ASN	2.1
1	A	17	GLY	2.1
3	F	27	ASP	2.1
1	A	83	TYR	2.1
1	A	282	TYR	2.1
2	B	303	CYS	2.1
2	B	47	ILE	2.0
2	B	151	LEU	2.0
2	B	297	LYS	2.0
2	B	323	MET	2.0
2	B	333	VAL	2.0
1	A	115	ILE	2.0
3	F	127	GLU	2.0
2	B	185	ALA	2.0
2	B	338	SER	2.0
2	B	357	PRO	2.0
2	B	49	VAL	2.0
2	B	90	PHE	2.0
2	B	183	TYR	2.0
2	B	41	ASP	2.0
2	B	278	SER	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](#)

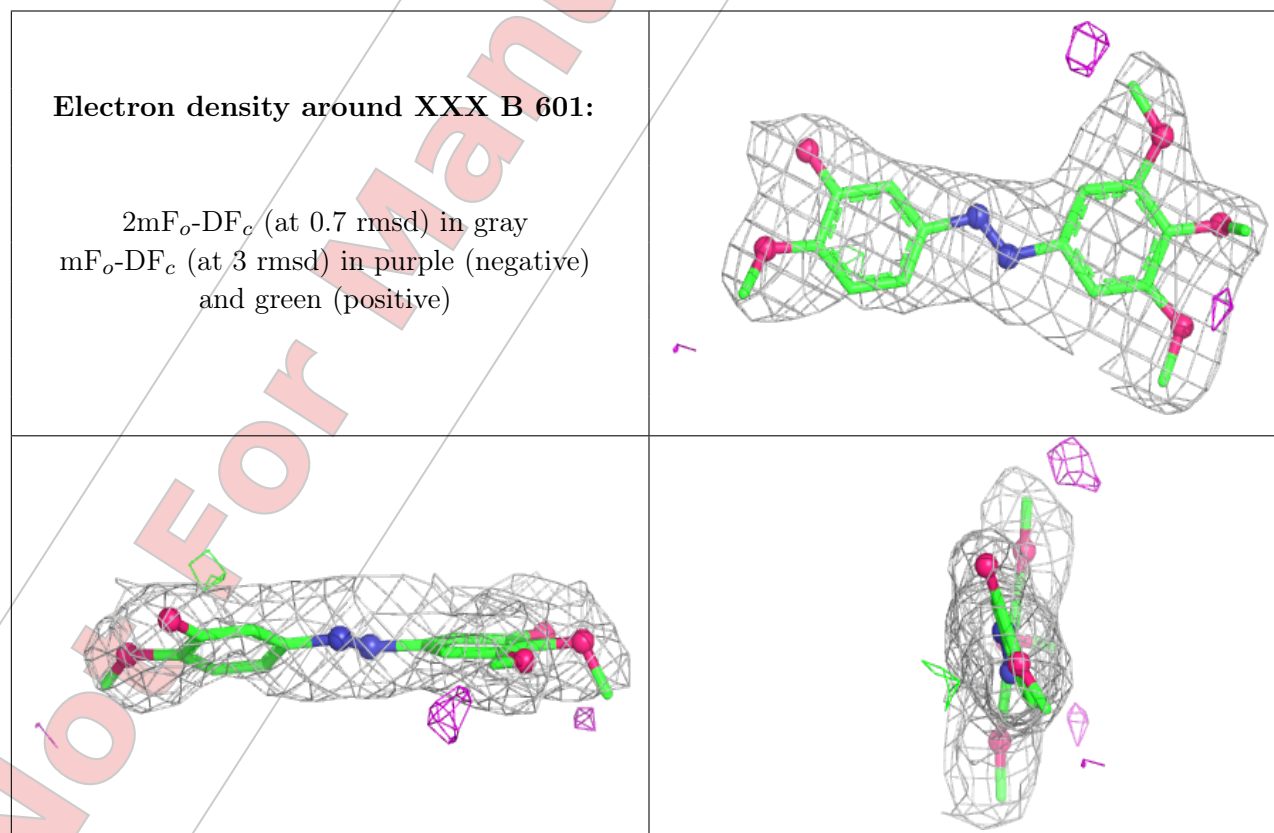
There are no monosaccharides in this entry.

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.

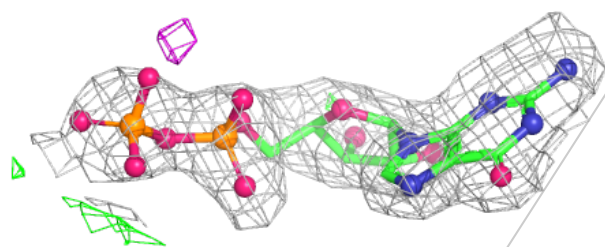
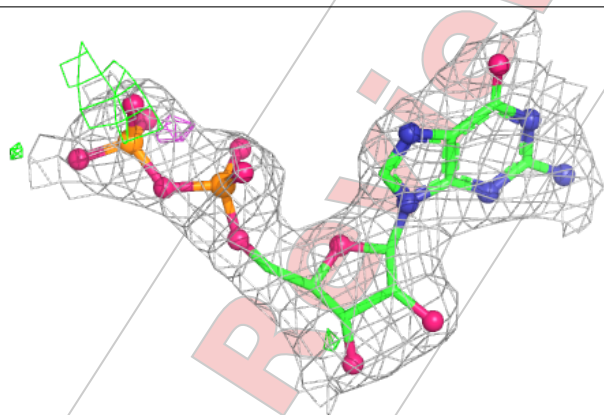
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	XXX	B	601	23/?	0.77	0.21	29,41,53,56	0
6	GDP	B	501	28/?	0.90	0.16	34,39,45,47	0
4	GTP	A	501	32/?	0.90	0.16	19,24,28,31	0
8	CA	C	1	1/?	0.93	0.10	42,42,42,42	0
5	MG	A	502	1/?	0.98	0.18	2,2,2,2	0

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.



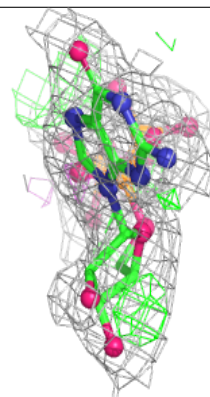
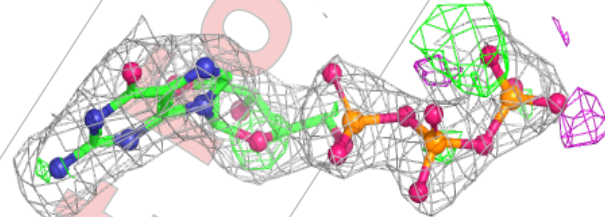
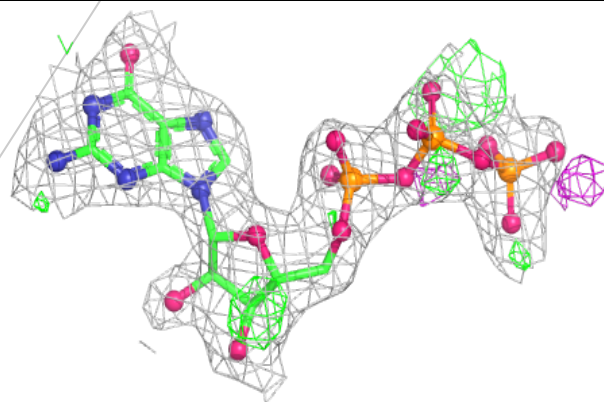
Electron density around GDP B 501:

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



Electron density around GTP 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 ⓘ

There are no such residues in this entry.

Not For Manuscript Review