



Full wwPDB X-ray Structure Validation Report i

Oct 15, 2023 – 11:48 PM EDT

PDB ID : 8FVD
Title : E coli. CTP synthase in complex with dF-dCTP (potassium malonate + 100 mM MgCl₂)
Authors : Holyoak, T.; McLeod, M.J.; Tran, N.
Deposited on : 2023-01-18
Resolution : 2.38 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
A user guide is available at
<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>
with specific help available everywhere you see the i symbol.

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

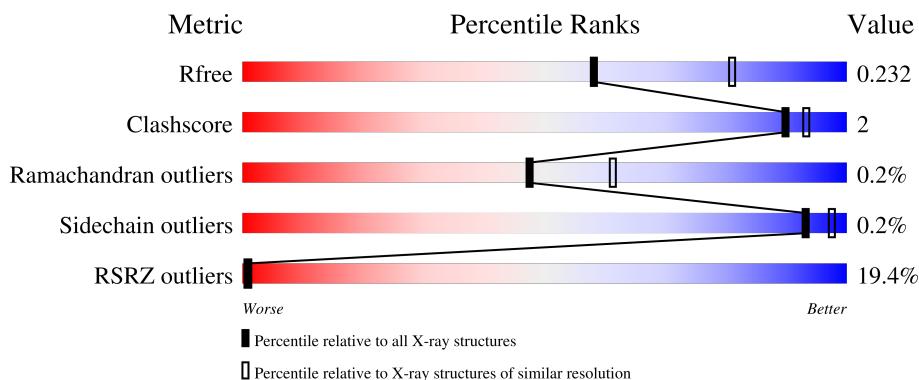
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

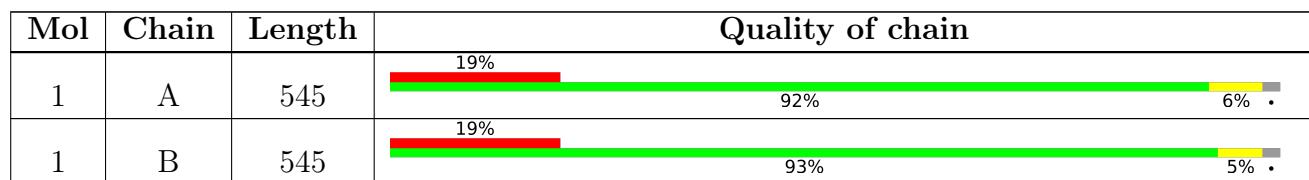
The reported resolution of this entry is 2.38 Å.

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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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.



2 Entry composition (i)

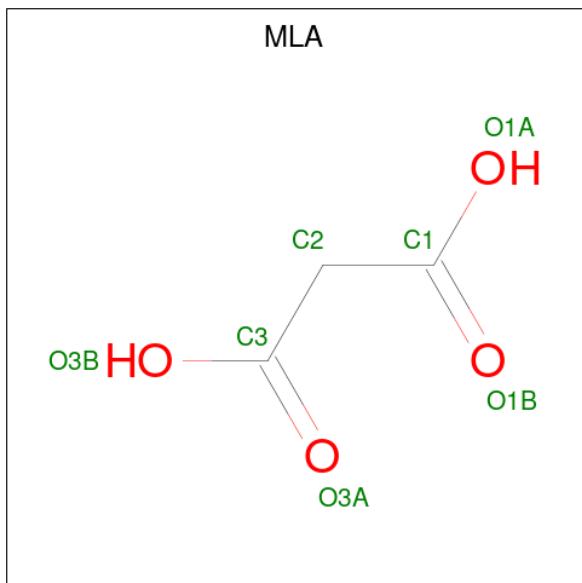
There are 5 unique types of molecules in this entry. The entry contains 8638 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called CTP synthase.

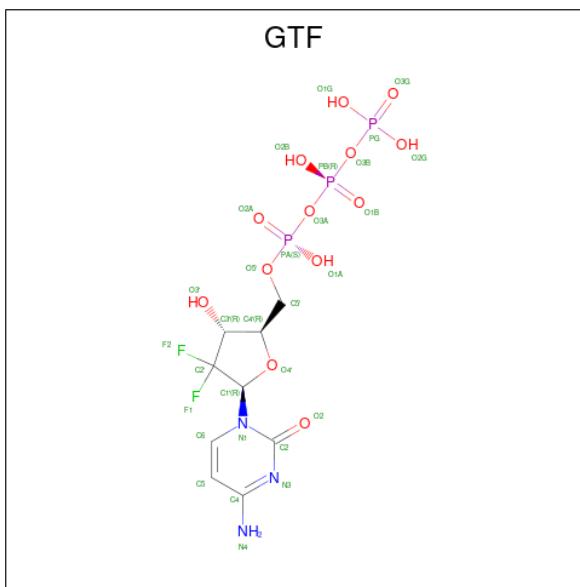
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	533	4187	2650	727	787	23	0	6	0
1	B	534	4195	2655	729	789	22	0	7	0

- Molecule 2 is MALONIC ACID (three-letter code: MLA) (formula: $C_3H_4O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	7	3	4	0	0
2	B	1	7	3	4	0	0

- Molecule 3 is 2'-deoxy-2',2'-difluorocytidine 5'-(tetrahydrogen triphosphate) (three-letter code: GTF) (formula: $C_9H_{14}F_2N_3O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	P	0	0
			30	9	2	3	13	3		

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	B	1	Total	C	F	N	O	P	0	0
			30	9	2	3	13	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	B	1	Total	Mg					0	0
			1	1						

- Molecule 5 is water.

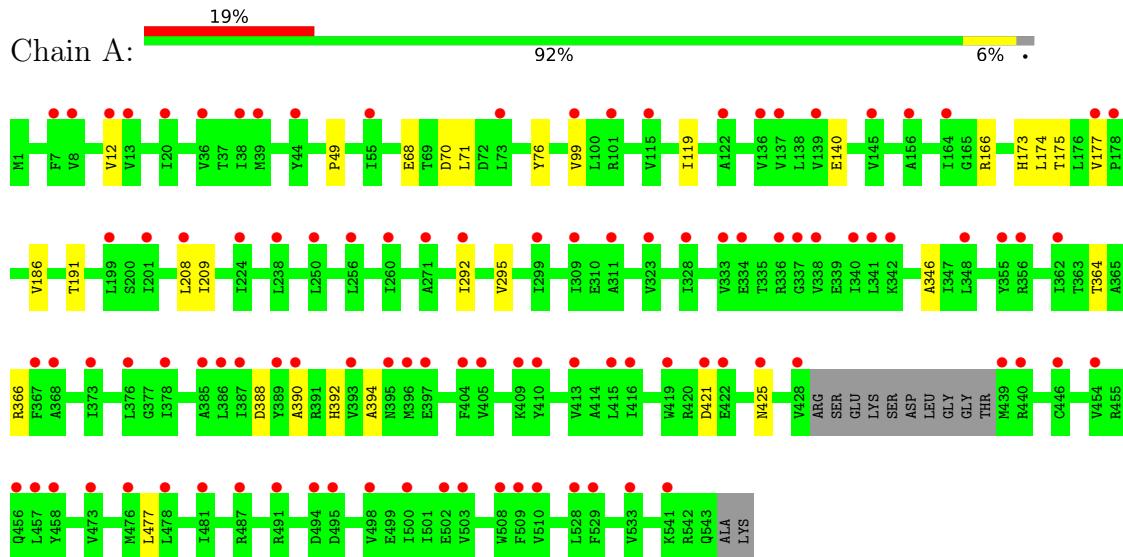
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	95	Total	O					0	0
			95	95						

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	B	85	Total	O					0	0
			85	85						

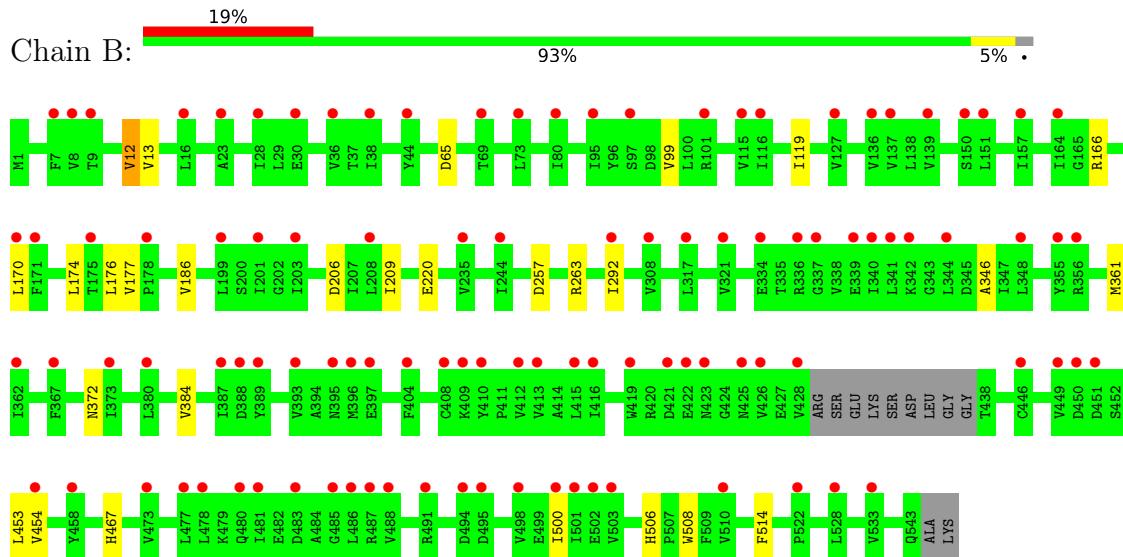
3 Residue-property plots [\(i\)](#)

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: CTP synthase



- Molecule 1: CTP synthase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	161.07Å 110.01Å 129.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.93 – 2.38 100.93 – 2.38	Depositor EDS
% Data completeness (in resolution range)	80.7 (100.93-2.38) 80.7 (100.93-2.38)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	0.92 (at 2.40Å)	Xtriage
Refinement program	REFMAC 1.20.1_4487	Depositor
R , R_{free}	0.209 , 0.232 0.214 , 0.232	Depositor DCC
R_{free} test set	3762 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	67.7	Xtriage
Anisotropy	0.177	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.5	EDS
L-test for twinning ²	$< L > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8638	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, GTF, MLA

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	0/4282	0.48	0/5800
1	B	0.24	0/4293	0.47	0/5814
All	All	0.24	0/8575	0.48	0/11614

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	4187	0	4213	14	0
1	B	4195	0	4223	16	0
2	A	7	0	2	0	0
2	B	7	0	2	0	0
3	A	30	0	10	0	0
3	B	30	0	10	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	95	0	0	0	0
5	B	85	0	0	0	0
All	All	8638	0	8460	30	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 2.

All (30) 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:B:174:LEU:HG	1:B:209:ILE:HB	1.85	0.59
1:A:174:LEU:HG	1:A:209:ILE:HB	1.86	0.57
1:B:177:VAL:HG12	1:B:186:VAL:HB	1.88	0.55
1:A:292:ILE:HG12	1:A:346:ALA:HB3	1.87	0.54
1:A:421:ASP:OD1	1:A:425:ASN:N	2.38	0.54
1:A:177:VAL:HG12	1:A:186:VAL:HB	1.89	0.54
1:A:76:TYR:OH	1:A:140:GLU:OE1	2.26	0.52
1:B:292:ILE:HG12	1:B:346:ALA:HB3	1.91	0.51
1:A:295:VAL:HG21	1:A:364:THR:HG21	1.91	0.51
1:B:186:VAL:HG23	1:B:220:GLU:HG2	1.93	0.50
1:B:99:VAL:HG21	1:B:119:ILE:HD13	1.94	0.48
1:B:166:ARG:NH2	1:B:206:ASP:OD2	2.48	0.47
1:B:12:VAL:HG12	1:B:13:VAL:HG13	1.98	0.45
1:A:70:ASP:OD1	1:A:71:LEU:N	2.49	0.45
1:A:175:THR:HG21	1:A:191:THR:HG23	1.97	0.45
1:A:366:ARG:HD2	1:A:392:HIS:CE1	2.53	0.44
1:B:65:ASP:N	1:B:65:ASP:OD1	2.50	0.43
1:B:453:LEU:HD21	1:B:508:TRP:CD1	2.52	0.43
1:B:12:VAL:HG11	1:B:176:LEU:HB3	2.00	0.43
1:A:421:ASP:HA	1:A:477:LEU:HD21	2.01	0.43
1:B:170:LEU:HD21	1:B:263:ARG:HG2	2.00	0.42
1:B:372:ASN:HA	1:B:506:HIS:CD2	2.55	0.42
1:A:99:VAL:HG21	1:A:119:ILE:HD13	2.02	0.42
1:B:361:MET:HB2	1:B:384:VAL:HG11	2.02	0.41
1:A:390:ALA:HA	1:A:394:ALA:HB3	2.02	0.41
1:B:257:ASP:OD1	1:B:257:ASP:N	2.54	0.41
1:B:454:VAL:HG11	1:B:500:ILE:HG21	2.02	0.41
1:A:173:HIS:HB3	1:A:208:LEU:HD23	2.02	0.40
1:A:49:PRO:HD2	1:A:68:GLU:O	2.22	0.40
1:B:467:HIS:CE1	1:B:514:PHE:HB3	2.56	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	535/545 (98%)	519 (97%)	15 (3%)	1 (0%)	47 61
1	B	537/545 (98%)	522 (97%)	14 (3%)	1 (0%)	47 61
All	All	1072/1090 (98%)	1041 (97%)	29 (3%)	2 (0%)	47 61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	12	VAL
1	A	12	VAL

5.3.2 Protein sidechains [\(i\)](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	458/461 (99%)	456 (100%)	2 (0%)	91 96
1	B	459/461 (100%)	459 (100%)	0	100 100
All	All	917/922 (100%)	915 (100%)	2 (0%)	93 97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ARG
1	A	388	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are

no such sidechains identified.

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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
3	GTF	A	602	4	25,31,31	3.80	13 (52%)	35,50,50	1.56	6 (17%)
2	MLA	A	601	-	6,6,6	1.64	1 (16%)	7,7,7	1.22	1 (14%)
2	MLA	B	703	-	6,6,6	1.65	1 (16%)	7,7,7	1.20	1 (14%)
3	GTF	B	701	4	25,31,31	3.81	13 (52%)	35,50,50	1.64	7 (20%)

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
3	GTF	A	602	4	-	1/22/42/42	0/2/2/2
2	MLA	A	601	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MLA	B	703	-	-	2/4/4/4	-
3	GTF	B	701	4	-	5/22/42/42	0/2/2/2

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	GTF	O4'-C4'	-8.24	1.26	1.45
3	B	701	GTF	O4'-C4'	-8.21	1.26	1.45
3	B	701	GTF	O4'-C1'	6.62	1.53	1.42
3	A	602	GTF	O4'-C1'	6.60	1.53	1.42
3	B	701	GTF	C6-C5	6.55	1.50	1.35
3	A	602	GTF	C6-C5	6.50	1.50	1.35
3	B	701	GTF	C2-N3	6.35	1.49	1.36
3	A	602	GTF	C2-N3	6.27	1.49	1.36
3	B	701	GTF	C4-N4	5.79	1.47	1.33
3	A	602	GTF	C4-N4	5.77	1.47	1.33
3	B	701	GTF	C4-N3	5.35	1.45	1.34
3	A	602	GTF	C4-N3	5.30	1.45	1.34
3	A	602	GTF	C4'-C3'	5.20	1.64	1.53
3	B	701	GTF	C4'-C3'	5.12	1.63	1.53
3	B	701	GTF	C2-N1	4.52	1.49	1.40
3	A	602	GTF	C2-N1	4.41	1.49	1.40
3	A	602	GTF	C1'-N1	-4.35	1.34	1.47
3	B	701	GTF	C1'-N1	-4.27	1.35	1.47
3	B	701	GTF	C6-N1	3.23	1.45	1.38
3	A	602	GTF	C6-N1	3.21	1.45	1.38
3	B	701	GTF	C5-C4	3.03	1.49	1.42
3	A	602	GTF	C5-C4	2.95	1.49	1.42
3	B	701	GTF	O2-C2	-2.89	1.18	1.23
3	A	602	GTF	O2-C2	-2.89	1.18	1.23
3	B	701	GTF	O3'-C3'	2.58	1.47	1.42
3	A	602	GTF	O3'-C3'	2.52	1.47	1.42
2	B	703	MLA	C2-C3	2.31	1.54	1.51
2	A	601	MLA	C2-C3	2.26	1.54	1.51

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	701	GTF	F2-C2'-F1	4.72	110.60	105.20
3	A	602	GTF	F2-C2'-F1	4.59	110.44	105.20
3	A	602	GTF	C4'-O4'-C1'	-4.10	102.08	109.45
3	B	701	GTF	C4'-O4'-C1'	-3.95	102.36	109.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	GTF	PB-O3B-PG	-3.61	120.44	132.83
3	B	701	GTF	PB-O3B-PG	-3.59	120.52	132.83
3	B	701	GTF	C5'-C4'-C3'	-3.06	109.53	114.66
3	B	701	GTF	O4'-C1'-N1	2.68	110.67	108.44
3	A	602	GTF	PB-O3A-PA	-2.53	124.15	132.83
3	B	701	GTF	PB-O3A-PA	-2.43	124.50	132.83
3	A	602	GTF	C5'-C4'-C3'	-2.40	110.65	114.66
3	B	701	GTF	O4'-C4'-C3'	2.22	106.85	104.42
2	A	601	MLA	O1B-C1-C2	-2.22	115.59	122.08
2	B	703	MLA	O1B-C1-C2	-2.09	115.97	122.08
3	A	602	GTF	O4'-C4'-C3'	2.02	106.63	104.42

There are no chirality outliers.

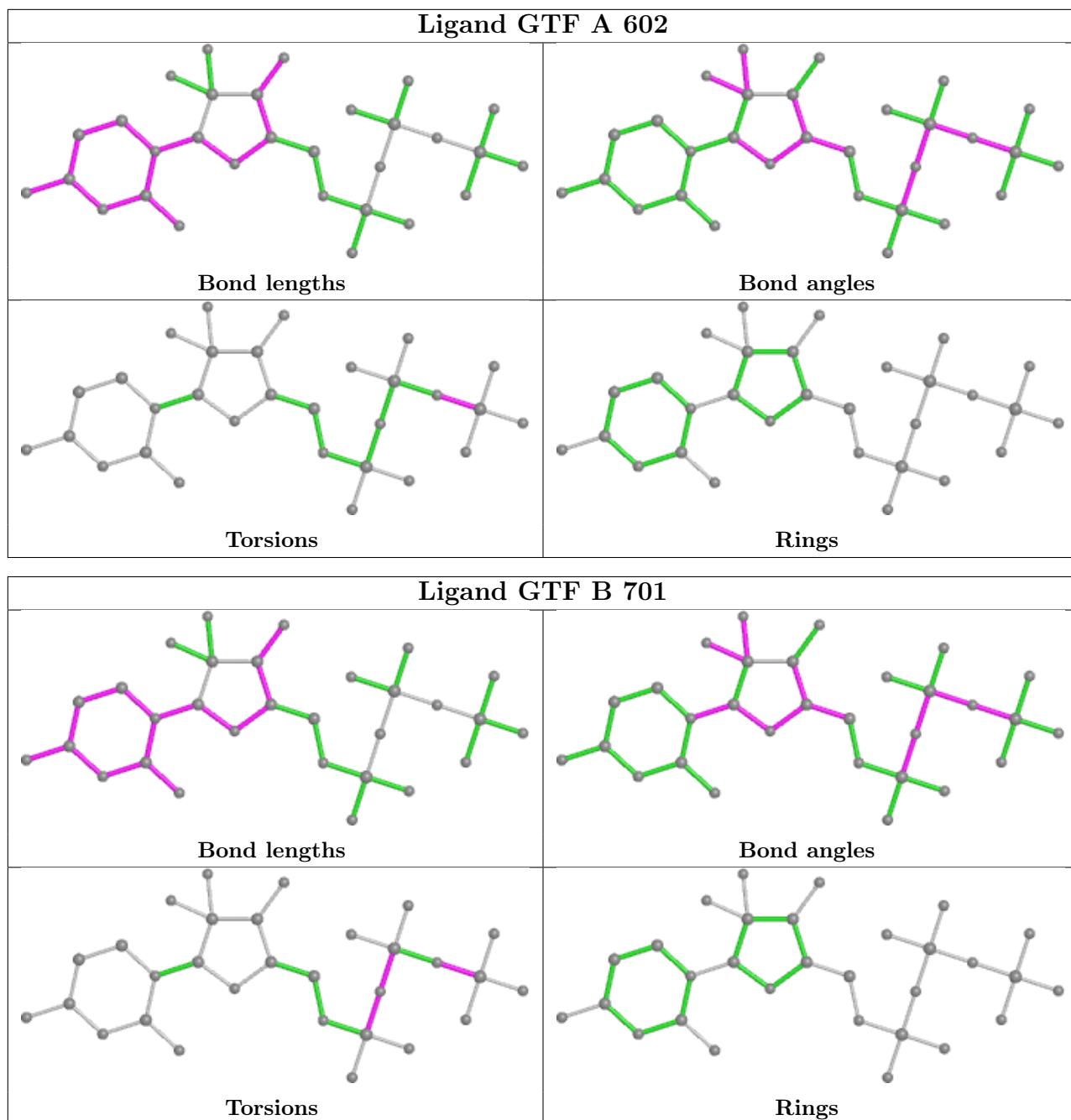
All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	701	GTF	PB-O3B-PG-O1G
3	B	701	GTF	PB-O3B-PG-O2G
2	A	601	MLA	C1-C2-C3-O3B
2	A	601	MLA	C1-C2-C3-O3A
3	B	701	GTF	PA-O3A-PB-O2B
3	B	701	GTF	PB-O3A-PA-O2A
2	B	703	MLA	C1-C2-C3-O3A
2	B	703	MLA	C1-C2-C3-O3B
3	A	602	GTF	PB-O3B-PG-O1G
3	B	701	GTF	PB-O3A-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

6 Fit of model and data [\(i\)](#)

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	533/545 (97%)	1.29	102 (19%) 1 1	47, 77, 119, 139	0
1	B	534/545 (97%)	1.33	105 (19%) 1 1	46, 75, 114, 140	0
All	All	1067/1090 (97%)	1.31	207 (19%) 1 1	46, 76, 118, 140	0

All (207) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	478	LEU	5.6
1	A	410	TYR	4.4
1	A	528	LEU	4.0
1	A	44[A]	TYR	3.8
1	B	44[A]	TYR	3.8
1	B	397	GLU	3.8
1	A	487	ARG	3.7
1	A	533	VAL	3.7
1	B	478	LEU	3.7
1	A	491	ARG	3.7
1	A	494	ASP	3.6
1	A	446[A]	CYS	3.6
1	A	405	VAL	3.6
1	B	415	LEU	3.6
1	B	409	LYS	3.5
1	B	426	VAL	3.5
1	A	502	GLU	3.5
1	A	373	ILE	3.5
1	A	508	TRP	3.5
1	B	446[A]	CYS	3.4
1	B	419	TRP	3.4
1	A	333	VAL	3.4
1	A	362	ILE	3.4
1	B	340	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	502	GLU	3.4
1	B	487	ARG	3.4
1	A	393	VAL	3.3
1	B	498	VAL	3.3
1	A	476	MET	3.3
1	B	451	ASP	3.3
1	A	368	ALA	3.3
1	B	342	LYS	3.3
1	A	355	TYR	3.2
1	A	481	ILE	3.2
1	B	36	VAL	3.2
1	B	101	ARG	3.2
1	A	498	VAL	3.2
1	A	386	LEU	3.2
1	B	413	VAL	3.2
1	B	341	LEU	3.2
1	B	416	ILE	3.2
1	B	495	ASP	3.1
1	A	428	VAL	3.1
1	B	292	ILE	3.1
1	A	336	ARG	3.0
1	A	395	ASN	3.0
1	B	450	ASP	3.0
1	B	449	VAL	3.0
1	B	423	ASN	3.0
1	B	136	VAL	3.0
1	B	500	ILE	3.0
1	A	409	LYS	3.0
1	A	334	GLU	2.9
1	A	337	GLY	2.9
1	B	410	TYR	2.9
1	B	367	PHE	2.9
1	B	421	ASP	2.9
1	B	528	LEU	2.9
1	B	488	VAL	2.8
1	A	341	LEU	2.8
1	B	317	LEU	2.8
1	A	422	GLU	2.8
1	A	292	ILE	2.8
1	A	413	VAL	2.8
1	B	533	VAL	2.8
1	A	367	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	503	VAL	2.7
1	B	425	ASN	2.7
1	B	408	CYS	2.7
1	B	494	ASP	2.7
1	B	422	GLU	2.7
1	B	336	ARG	2.7
1	A	404	PHE	2.7
1	A	20	ILE	2.7
1	B	396	MET	2.7
1	B	373	ILE	2.7
1	A	36	VAL	2.7
1	B	454	VAL	2.7
1	A	397	GLU	2.7
1	A	376	LEU	2.7
1	B	393	VAL	2.7
1	B	501	ILE	2.6
1	A	101	ARG	2.6
1	A	390	ALA	2.6
1	B	80	ILE	2.6
1	A	454	VAL	2.6
1	B	30[A]	GLU	2.6
1	B	481	ILE	2.6
1	B	208	LEU	2.6
1	A	309	ILE	2.6
1	B	73	LEU	2.6
1	A	396	MET	2.6
1	A	356	ARG	2.5
1	A	419	TRP	2.5
1	B	201	ILE	2.5
1	A	8	VAL	2.5
1	A	137	VAL	2.5
1	A	199	LEU	2.5
1	B	235	VAL	2.5
1	B	38	ILE	2.5
1	A	529	PHE	2.5
1	B	244	ILE	2.5
1	B	356	ARG	2.4
1	B	510	VAL	2.4
1	B	485	GLY	2.4
1	A	55	ILE	2.4
1	A	456	GLN	2.4
1	B	16	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	509	PHE	2.4
1	B	355	TYR	2.4
1	B	388	ASP	2.4
1	A	342	LYS	2.4
1	B	7	PHE	2.4
1	B	334	GLU	2.4
1	A	338	VAL	2.4
1	A	38	ILE	2.4
1	A	340	ILE	2.4
1	A	425	ASN	2.4
1	A	385	ALA	2.4
1	A	495	ASP	2.4
1	B	473	VAL	2.4
1	B	150[A]	SER	2.4
1	A	328	ILE	2.4
1	B	389	TYR	2.4
1	A	136	VAL	2.4
1	B	380	LEU	2.3
1	A	473	VAL	2.3
1	B	203	ILE	2.3
1	A	238	LEU	2.3
1	A	12	VAL	2.3
1	A	457	LEU	2.3
1	B	491	ARG	2.3
1	B	137	VAL	2.3
1	B	404	PHE	2.3
1	A	458	TYR	2.3
1	B	344	LEU	2.3
1	B	486	LEU	2.3
1	B	97[A]	SER	2.3
1	B	157	ILE	2.3
1	A	7	PHE	2.3
1	A	139	VAL	2.2
1	A	156	ALA	2.2
1	A	387	ILE	2.2
1	B	28	ILE	2.2
1	B	387	ILE	2.2
1	A	39[A]	MET	2.2
1	B	483	ASP	2.2
1	A	271	ALA	2.2
1	A	208	LEU	2.2
1	B	170	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	421	ASP	2.2
1	A	250	LEU	2.2
1	A	178	PRO	2.2
1	B	308	VAL	2.2
1	B	95	ILE	2.2
1	A	122	ALA	2.2
1	B	9	THR	2.2
1	B	23	ALA	2.2
1	A	201	ILE	2.2
1	A	378	ILE	2.2
1	B	362	ILE	2.2
1	A	348	LEU	2.2
1	B	337	GLY	2.2
1	B	412	VAL	2.1
1	B	69	THR	2.1
1	A	99	VAL	2.1
1	B	348	LEU	2.1
1	B	395	ASN	2.1
1	B	522	PRO	2.1
1	A	510	VAL	2.1
1	B	458	TYR	2.1
1	A	224	ILE	2.1
1	A	299	ILE	2.1
1	A	416	ILE	2.1
1	A	73	LEU	2.1
1	A	415	LEU	2.1
1	A	145	VAL	2.1
1	B	8	VAL	2.1
1	B	428	VAL	2.1
1	A	260	ILE	2.1
1	A	256	LEU	2.1
1	B	477	LEU	2.1
1	B	480	GLN	2.1
1	B	339	GLU	2.1
1	A	323	VAL	2.1
1	B	127	VAL	2.1
1	B	139	VAL	2.1
1	B	503	VAL	2.1
1	B	178	PRO	2.1
1	B	151	LEU	2.1
1	B	171	PHE	2.1
1	A	164	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	440	ARG	2.0
1	B	116	ILE	2.0
1	A	541	LYS	2.0
1	B	175	THR	2.0
1	A	311	ALA	2.0
1	A	115	VAL	2.0
1	B	115	VAL	2.0
1	A	439	MET	2.0
1	A	13	VAL	2.0
1	A	177	VAL	2.0
1	B	321	VAL	2.0
1	A	389	TYR	2.0
1	A	500	ILE	2.0
1	B	164	ILE	2.0
1	B	199	LEU	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.

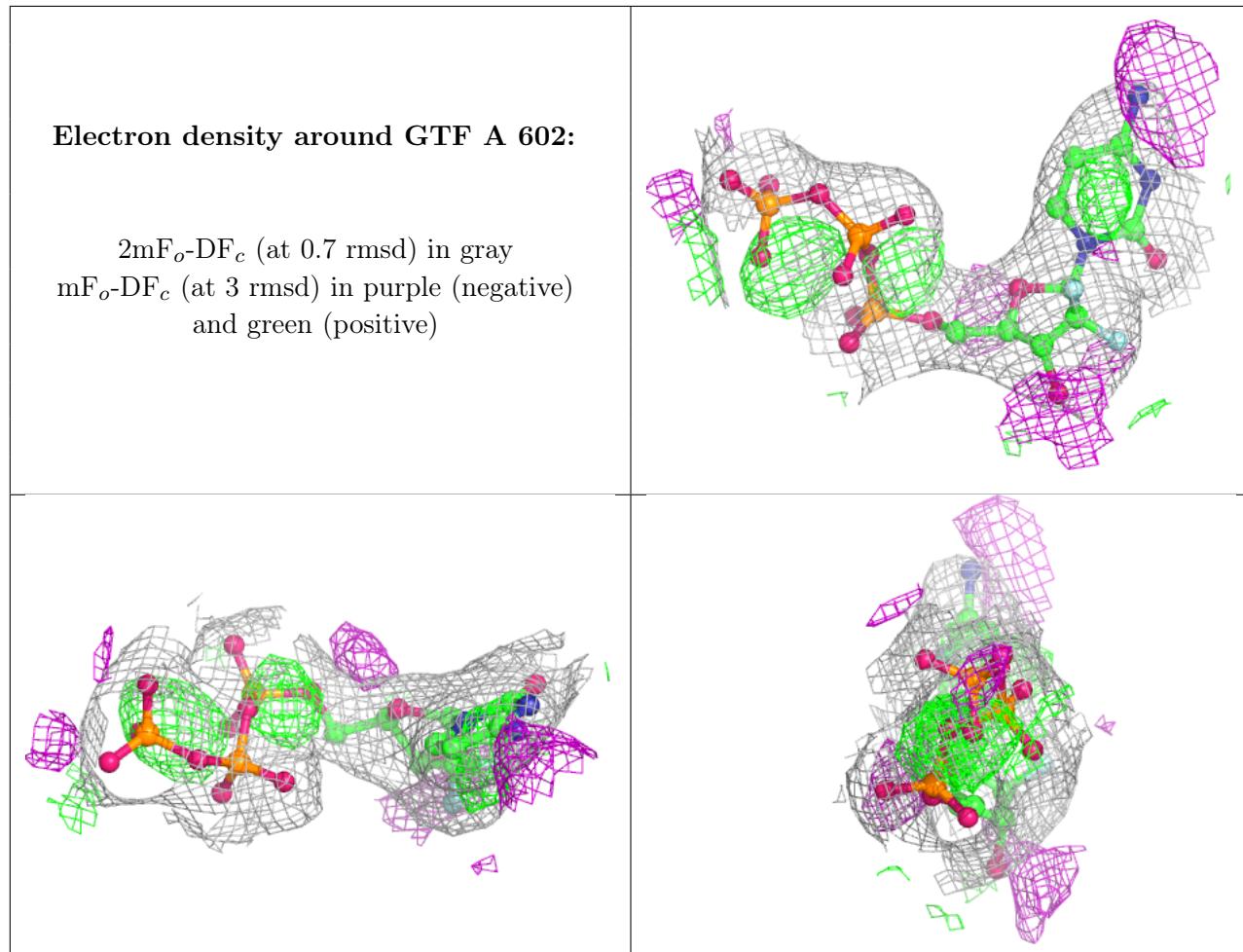
6.4 Ligands [\(i\)](#)

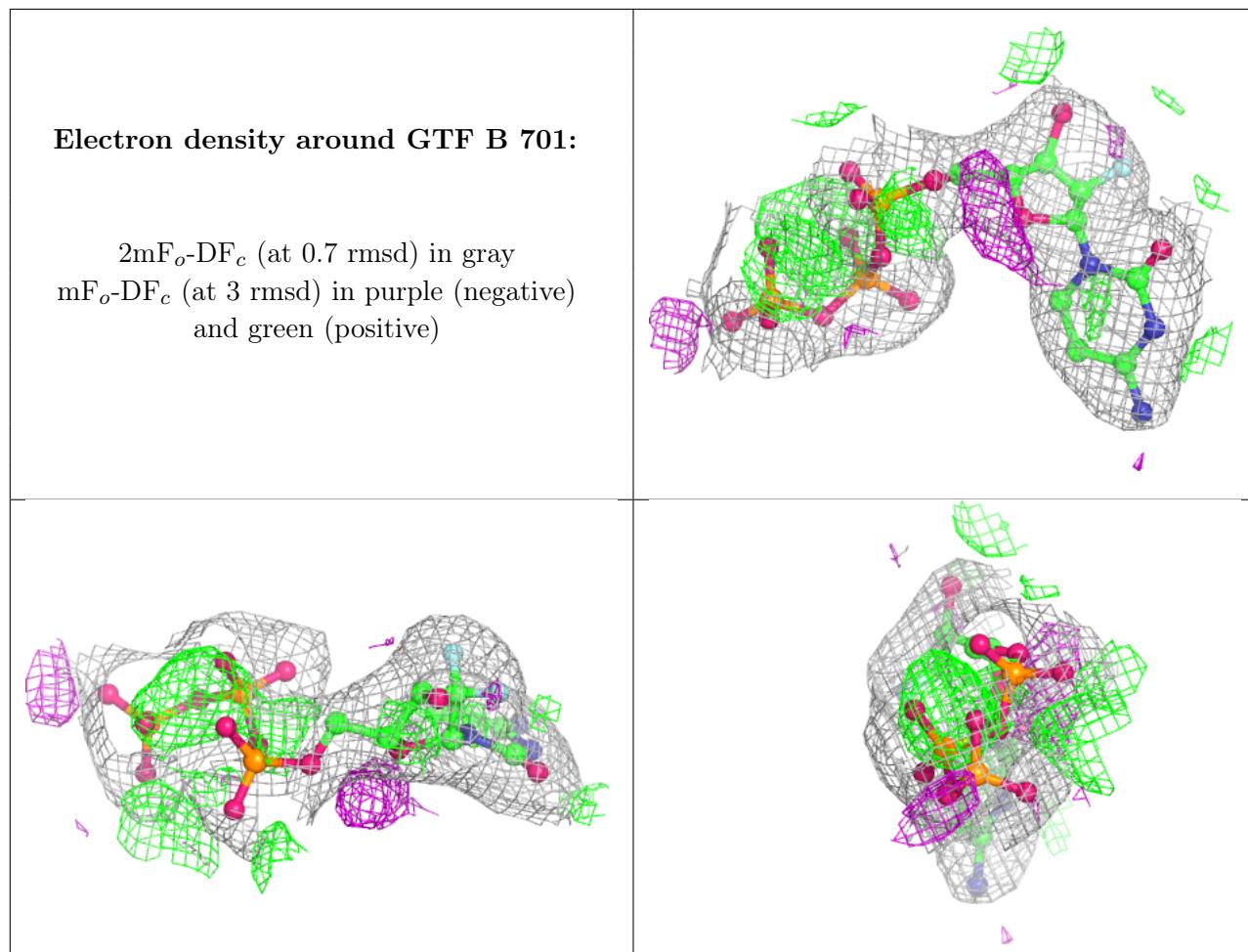
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MLA	A	601	7/7	0.84	0.20	66,73,93,95	0
2	MLA	B	703	7/7	0.85	0.20	63,69,88,89	0
4	MG	A	603	1/1	0.89	0.25	62,62,62,62	0
4	MG	B	702	1/1	0.95	0.22	66,66,66,66	0
3	GTF	A	602	30/30	0.96	0.23	41,57,65,67	0
3	GTF	B	701	30/30	0.96	0.24	44,56,64,65	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.





6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.