



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:39 PM UTC

PDB ID : 7KBL / pdb_00007kbl
Title : Biotin Carboxylase domain of Thermophilic 2-Oxoglutarate Carboxylase bound to Bicarbonate
Authors : Buhrman, G.K.; Rose, R.B.; Enriquez, P.; Truong, V.
Deposited on : 2020-10-02
Resolution : 2.30 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

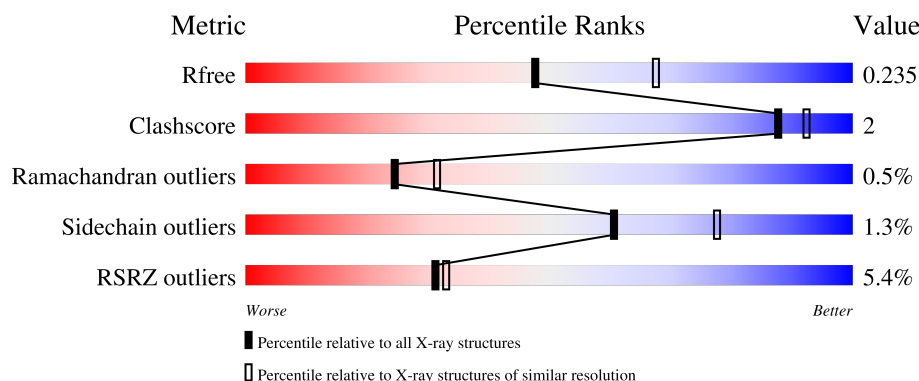
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	481	9% 87% 5% 8%
1	B	481	% 88% 6% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14087 atoms, of which 6782 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.

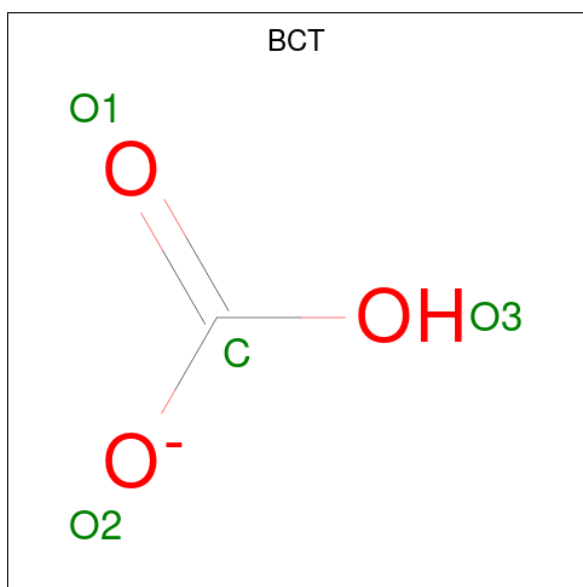
- Molecule 1 is a protein called 2-oxoglutarate carboxylase small subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	443	Total	C	H	N	O	S	0	0	0
			6559	2145	3195	576	628	15			
1	B	451	Total	C	H	N	O	S	0	0	0
			7162	2282	3585	614	665	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	initiating methionine	UNP D3DJ42
A	-7	LYS	-	expression tag	UNP D3DJ42
A	-6	HIS	-	expression tag	UNP D3DJ42
A	-5	HIS	-	expression tag	UNP D3DJ42
A	-4	HIS	-	expression tag	UNP D3DJ42
A	-3	HIS	-	expression tag	UNP D3DJ42
A	-2	HIS	-	expression tag	UNP D3DJ42
A	-1	HIS	-	expression tag	UNP D3DJ42
A	0	ALA	-	expression tag	UNP D3DJ42
B	-8	MET	-	initiating methionine	UNP D3DJ42
B	-7	LYS	-	expression tag	UNP D3DJ42
B	-6	HIS	-	expression tag	UNP D3DJ42
B	-5	HIS	-	expression tag	UNP D3DJ42
B	-4	HIS	-	expression tag	UNP D3DJ42
B	-3	HIS	-	expression tag	UNP D3DJ42
B	-2	HIS	-	expression tag	UNP D3DJ42
B	-1	HIS	-	expression tag	UNP D3DJ42
B	0	ALA	-	expression tag	UNP D3DJ42

- Molecule 2 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3) (labeled as "Ligand of Interest" by depositor).

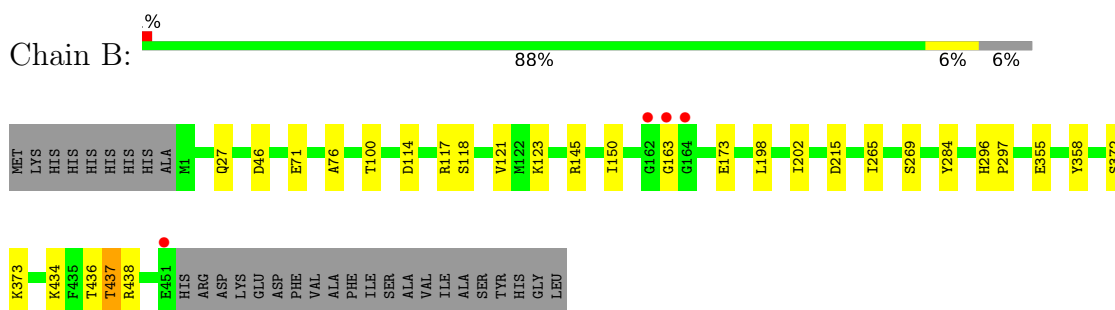


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			5	1	1	3		
2	B	1	Total	C	H	O	0	0
			5	1	1	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	157	Total	O	0	0
			157	157		
3	B	199	Total	O	0	0
			199	199		

- Molecule 1: 2-oxoglutarate carboxylase small subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.50Å 125.15Å 125.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.75 – 2.30 29.75 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.75-2.30) 99.7 (29.75-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 2.31Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.181 , 0.234 0.183 , 0.235	Depositor DCC
R_{free} test set	1998 reflections (3.66%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.783	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 32.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.010 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14087	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% 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: BCT

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	0.58	0/3433	0.68	0/4659
1	B	0.58	0/3649	0.70	3/4927 (0.1%)
All	All	0.58	0/7082	0.69	3/9586 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	437	THR	N-CA-C	-6.80	101.10	110.35
1	B	437	THR	CA-C-N	-5.41	118.37	126.86
1	B	437	THR	C-N-CA	-5.41	118.37	126.86

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	3364	3195	3197	15	0
1	B	3577	3585	3577	14	0
2	A	4	1	1	0	0
2	B	4	1	1	0	0
3	A	157	0	0	3	0
3	B	199	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7305	6782	6776	28	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 (28) 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:437:THR:O	1:B:438:ARG:CB	2.44	0.64
1:A:40:ARG:HD3	1:B:358:TYR:CD1	2.40	0.56
1:B:438:ARG:HA	3:B:733:HOH:O	2.06	0.55
1:B:76:ALA:HA	1:B:100:THR:O	2.11	0.51
1:A:204:ASN:H	1:A:438:ARG:HH12	1.59	0.50
1:B:114:ASP:O	1:B:117:ARG:O	2.31	0.48
1:A:234:ASN:ND2	3:A:610:HOH:O	2.48	0.46
1:A:209:GLU:O	1:A:225:GLU:HA	2.18	0.44
1:A:339:ASN:O	1:A:416:THR:HA	2.17	0.44
1:B:434:LYS:NZ	3:B:623:HOH:O	2.51	0.43
1:B:71:GLU:OE1	3:B:601:HOH:O	2.21	0.43
1:B:436:THR:C	1:B:437:THR:O	2.57	0.43
1:A:382:ASP:OD1	1:A:382:ASP:C	2.61	0.43
1:A:133:SER:OG	1:A:135:GLY:O	2.36	0.43
1:B:121:VAL:HG11	1:B:265:ILE:HG21	2.01	0.42
1:B:202:ILE:HD12	1:B:284:TYR:CE2	2.54	0.42
1:A:296:HIS:CG	1:A:297:PRO:HD3	2.54	0.42
1:A:278:ASP:OD1	1:A:278:ASP:C	2.62	0.42
1:A:27:GLN:NE2	3:A:603:HOH:O	2.39	0.42
1:B:150:ILE:HD11	1:B:198:LEU:HD21	2.01	0.42
1:A:40:ARG:HD2	3:A:720:HOH:O	2.19	0.42
1:A:180:TYR:CD1	1:A:180:TYR:C	2.97	0.41
1:B:27:GLN:HA	1:B:46:ASP:OD2	2.20	0.41
1:A:297:PRO:O	1:A:301:MET:HG2	2.21	0.41
1:A:443:HIS:O	1:A:446:VAL:HG22	2.21	0.41
1:B:215:ASP:OD1	1:B:215:ASP:C	2.63	0.41
1:B:296:HIS:N	1:B:297:PRO:CD	2.84	0.41
1:A:155:LEU:O	1:A:198:LEU:HA	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	439/481 (91%)	428 (98%)	10 (2%)	1 (0%)	43	55
1	B	449/481 (93%)	435 (97%)	11 (2%)	3 (1%)	18	23
All	All	888/962 (92%)	863 (97%)	21 (2%)	4 (0%)	24	31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	118	SER
1	A	269	SER
1	B	163	GLY
1	B	269	SER

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	325/401 (81%)	322 (99%)	3 (1%)	70	84
1	B	373/401 (93%)	367 (98%)	6 (2%)	55	73
All	All	698/802 (87%)	689 (99%)	9 (1%)	61	77

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

Mol	Chain	Res	Type
1	A	64	ARG
1	A	351	ILE

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Mol	Chain	Res	Type
1	A	355	GLU
1	B	123	LYS
1	B	145	ARG
1	B	173	GLU
1	B	355	GLU
1	B	372	SER
1	B	373	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	27	GLN
1	B	105	HIS
1	B	207	HIS
1	B	330	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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	$\# Z > 2$
2	BCT	A	501	-	3,3,3	1.28	0	2,3,3	4.12	2 (100%)
2	BCT	B	501	-	3,3,3	1.15	0	2,3,3	4.06	2 (100%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	BCT	O2-C-O1	5.01	132.49	119.68
2	B	501	BCT	O2-C-O1	4.92	132.27	119.68
2	A	501	BCT	O3-C-O1	-2.97	112.08	119.68
2	B	501	BCT	O3-C-O1	-2.96	112.10	119.68

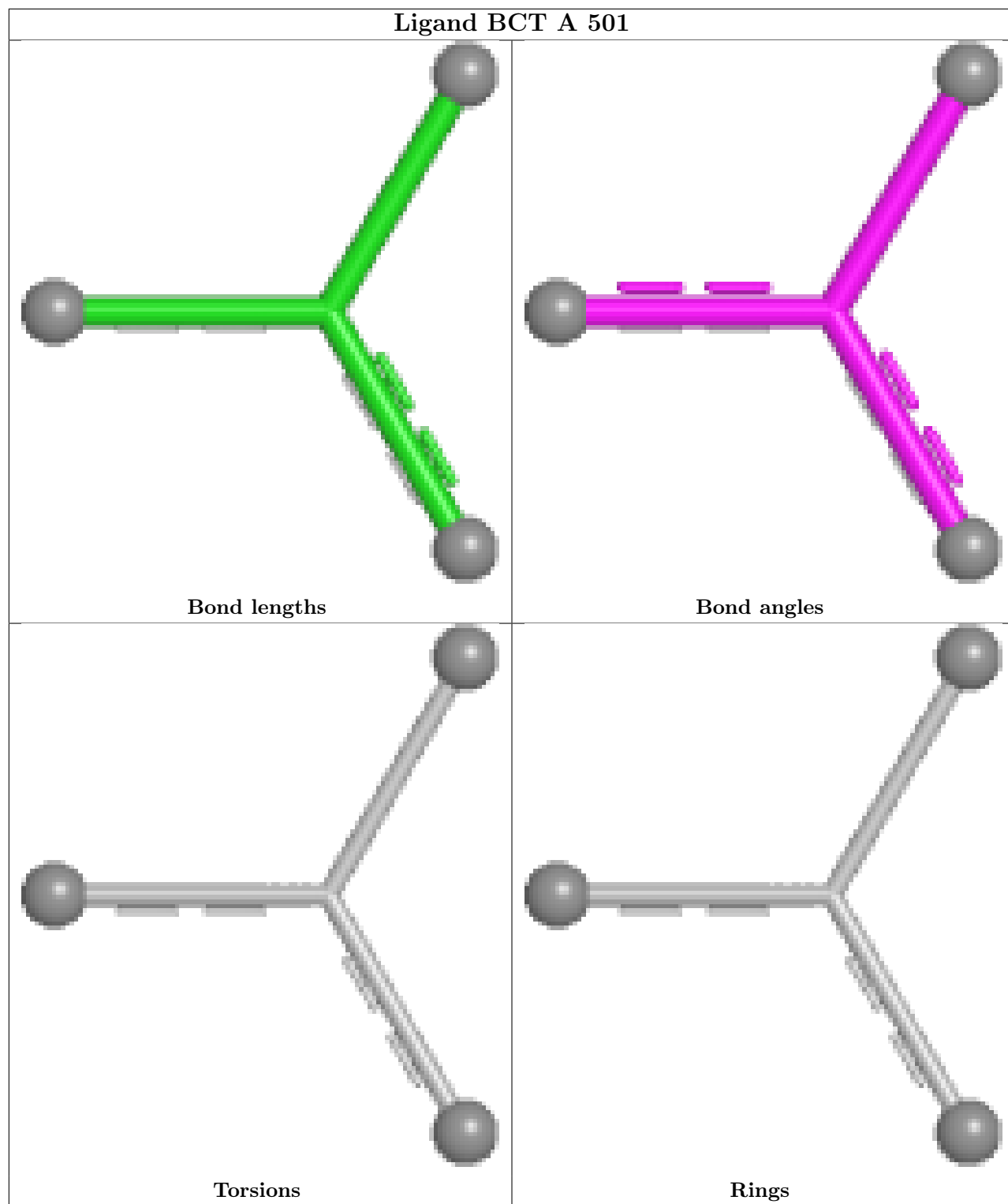
There are no chirality outliers.

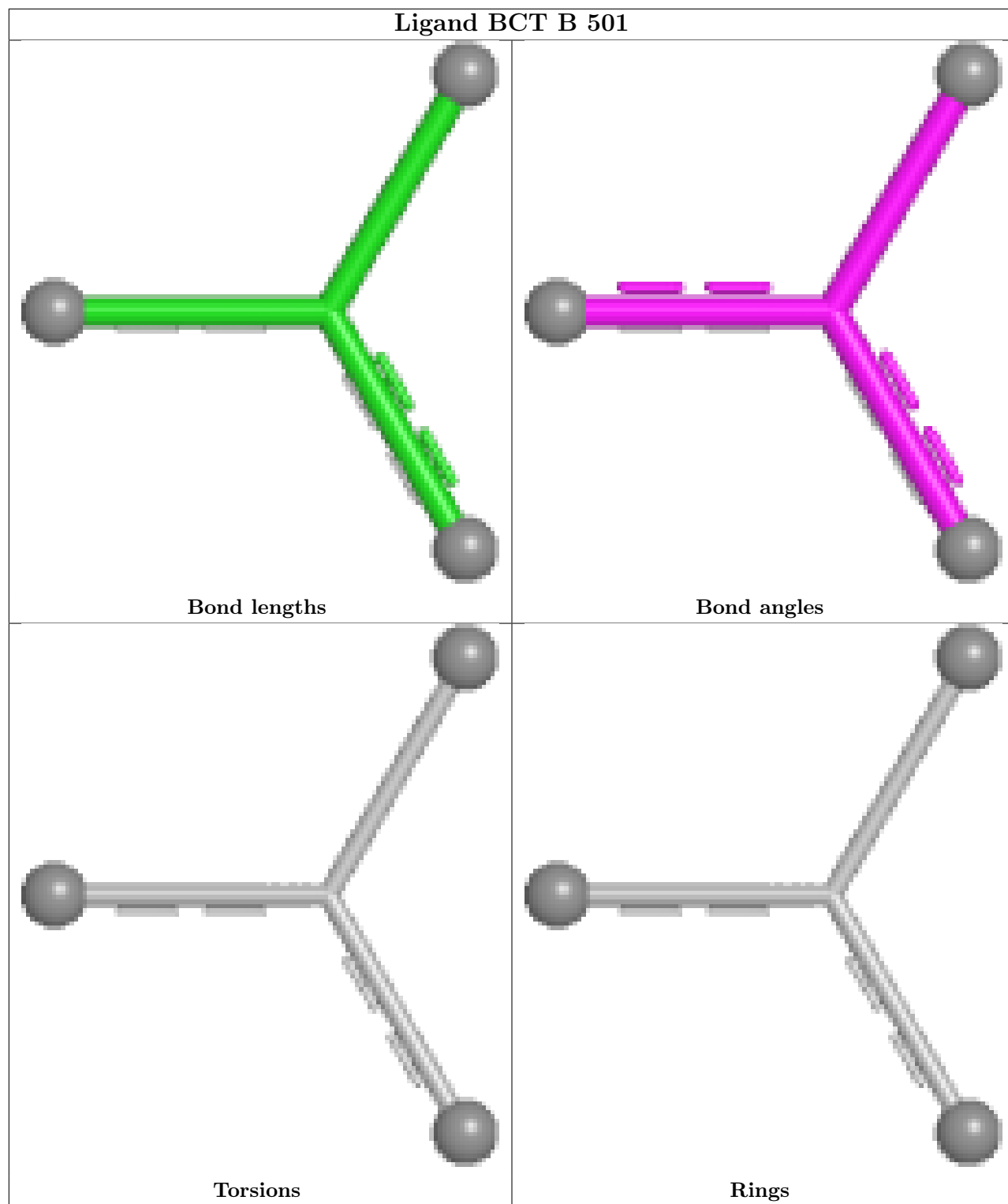
There are no torsion outliers.

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 ⓘ

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, 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	443/481 (92%)	0.17	44 (9%) 13 14	26, 41, 90, 103	0
1	B	451/481 (93%)	-0.18	4 (0%) 81 82	26, 39, 64, 102	0
All	All	894/962 (92%)	-0.01	48 (5%) 31 33	26, 39, 86, 103	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	170	CYS	6.8
1	A	159	SER	6.0
1	B	163	GLY	5.7
1	A	0	ALA	4.5
1	A	171	ARG	4.3
1	A	187	ALA	4.2
1	A	169	ILE	4.0
1	A	146	ILE	3.8
1	A	140	VAL	3.8
1	A	191	PHE	3.6
1	A	152	TYR	3.6
1	A	194	GLY	3.6
1	A	177	VAL	3.4
1	A	190	ALA	3.3
1	A	135	GLY	3.2
1	A	188	VAL	3.1
1	A	196	LEU	3.1
1	A	180	TYR	3.0
1	A	183	ALA	3.0
1	A	450	ALA	3.0
1	A	448	ASP	3.0
1	B	451	GLU	3.0
1	A	182	ASN	3.0
1	A	155	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	203	GLU	2.9
1	A	181	GLU	2.8
1	A	184	TYR	2.7
1	A	186	GLU	2.7
1	A	134	ASP	2.6
1	A	150	ILE	2.6
1	B	162	GLY	2.6
1	A	147	ALA	2.6
1	A	178	ARG	2.6
1	A	145	ARG	2.6
1	A	156	LEU	2.5
1	A	154	VAL	2.5
1	A	141	GLU	2.5
1	A	202	ILE	2.4
1	A	446	VAL	2.3
1	A	136	ILE	2.3
1	A	193	ARG	2.2
1	A	204	ASN	2.2
1	A	449	TYR	2.1
1	A	137	LEU	2.1
1	A	201	TYR	2.1
1	B	164	GLY	2.1
1	A	138	LYS	2.0
1	A	168	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

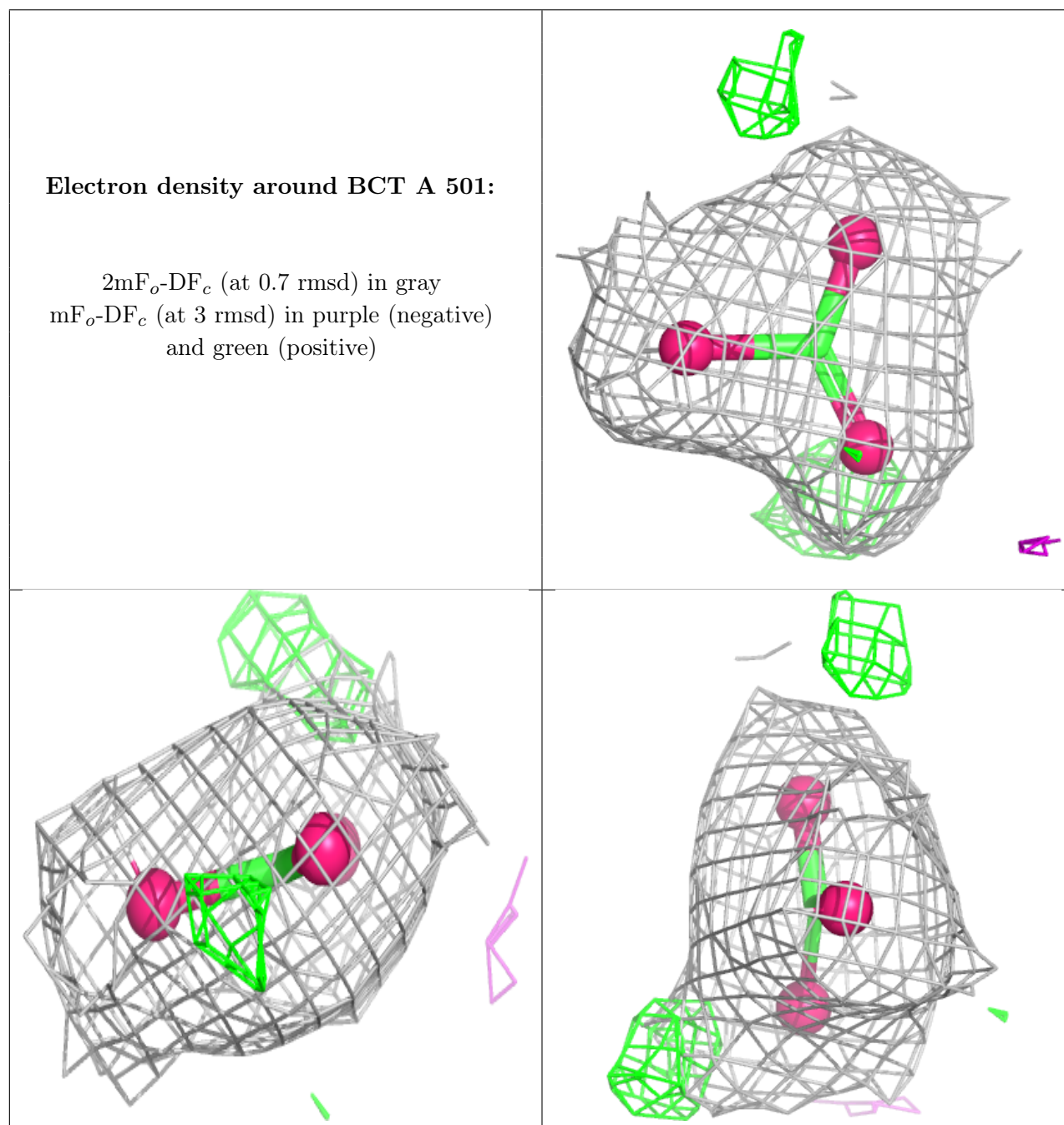
There are no oligosaccharides in this entry.

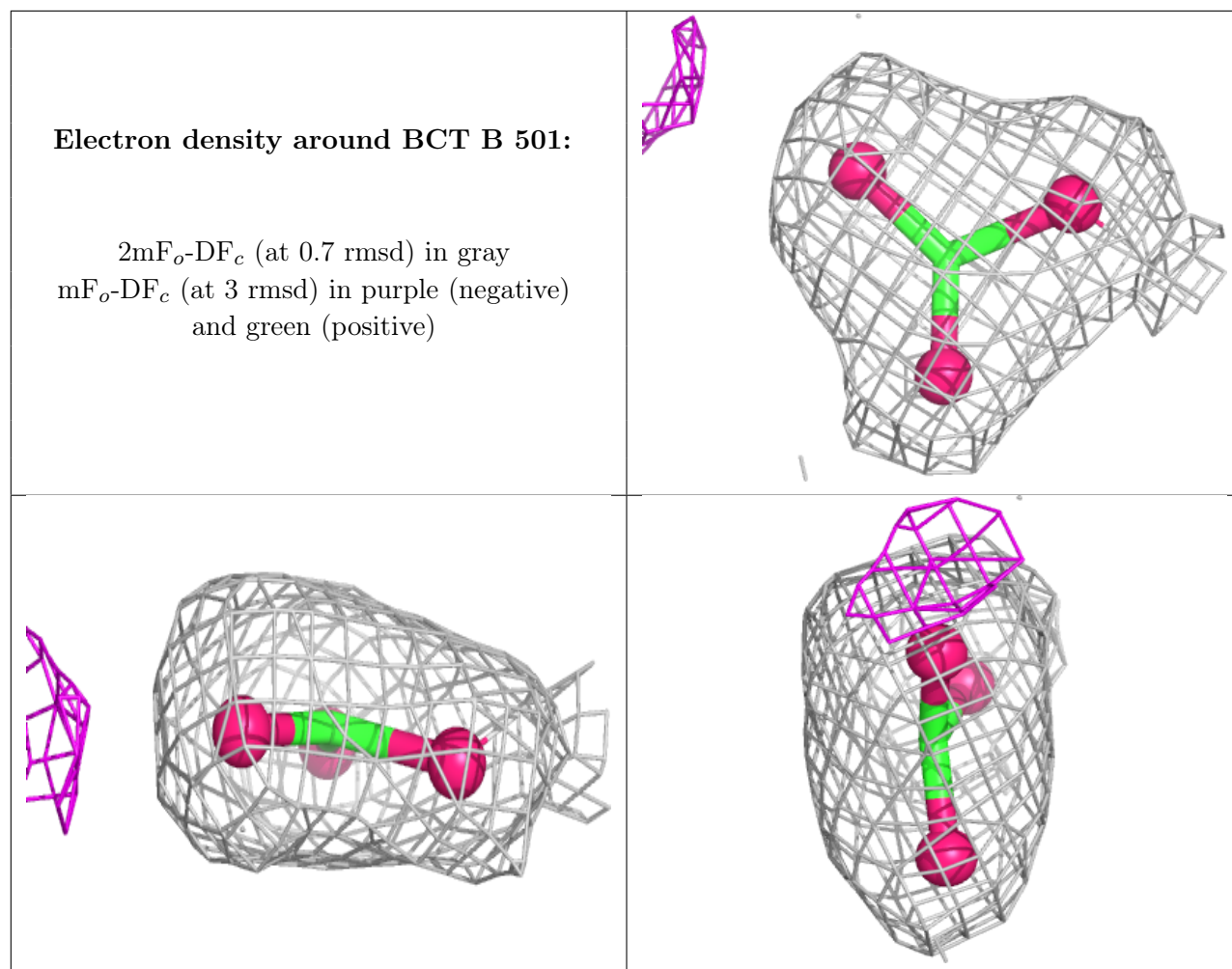
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
2	BCT	A	501	4/4	0.93	0.10	27,31,34,45	0
2	BCT	B	501	4/4	0.97	0.06	26,31,34,34	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.