

Full wwPDB X-ray Structure Validation Report (i)

Nov 20, 2023 – 10:21 AM JST

PDB ID : 7D30

Title : Structure of sybody MR17-SR31 fusion in complex with the SARS-CoV-2 S

Receptor Binding domain (RBD)

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Deposited on : 2020-09-17

Resolution : 2.10 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 (1)) 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)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

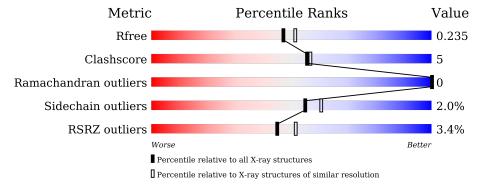
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},\ {\rm resolution\ range}({\rm \AA})) \end{array}$
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	298	71%	7% •	21%	_		
2	В	213	82%		12%	6%		
3	С	6	33% 67%					

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MAN	С	4	-	-	-	X
4	GOL	В	2112	-	-	X	-
5	ACT	A	1303	-	-	-	X
5	ACT	В	2109	-	-	-	X



2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 3891 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 sybody fusion of MR17-SR31 with a GS linker.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	234	Total 1821	C 1146	N 314	O 350	S 11	0	8	0

• Molecule 2 is a protein called Spike protein S1.

\mathbf{Mol}	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
2	В	201	Total 1616	C 1038	N 273	O 297	S 8	0	5	0	

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	327	ALA	-	expression tag	UNP P0DTC2
В	328	GLY	-	expression tag	UNP P0DTC2
В	329	SER	-	expression tag	UNP P0DTC2
В	532	GLY	-	expression tag	UNP P0DTC2
В	533	THR	-	expression tag	UNP P0DTC2
В	534	LEU	-	expression tag	UNP P0DTC2
В	535	GLU	-	expression tag	UNP P0DTC2
В	536	VAL	-	expression tag	UNP P0DTC2
В	537	LEU	-	expression tag	UNP P0DTC2
В	538	PHE	-	expression tag	UNP P0DTC2
В	539	GLN	-	expression tag	UNP P0DTC2

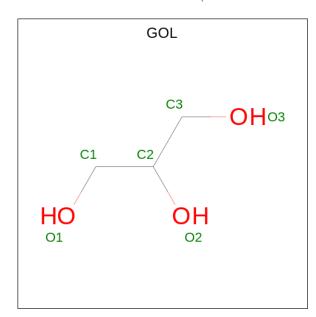
• Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranos e-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
3	С	6	Total 70	C 40	N 2	O 28	0	0	0

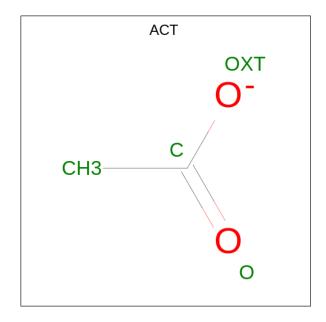
 \bullet Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $\mathrm{C_3H_8O_3}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0

 \bullet Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2).$

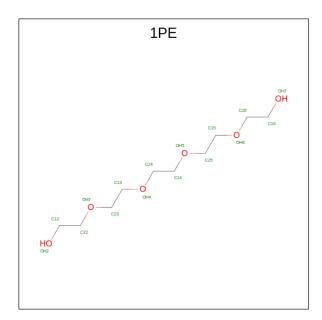




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0

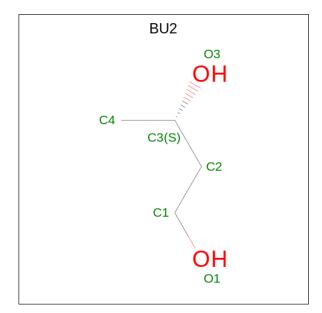


• Molecule 6 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 16 10 6	0	0
6	В	1	Total C O 16 10 6	0	0

 \bullet Molecule 7 is 1,3-BUTANEDIOL (three-letter code: BU2) (formula: $C_4H_{10}O_2)$ (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 6 4 2	0	0
7	A	1	Total C O 6 4 2	0	0
7	A	1	Total C O 6 4 2	0	0
7	В	1	Total C O 6 4 2	0	0
7	В	1	Total C O 6 4 2	0	0

• Molecule 8 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	12	Total Cd 12 12	0	0
8	В	5	Total Cd 5 5	0	0

• Molecule 9 is water.

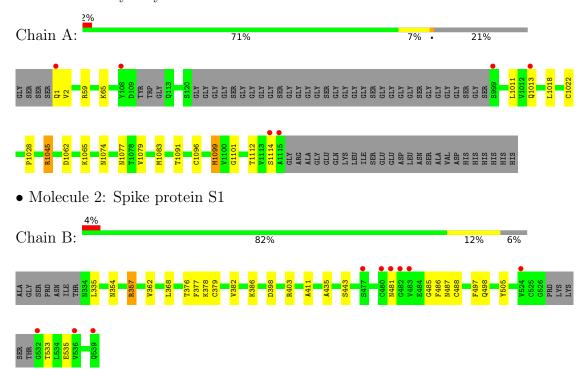
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	115	Total O 115 115	0	0
9	В	104	Total O 104 104	0	0



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: sybody fusion of MR17-SR31 with a GS linker



• Molecule 3: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants	73.38Å 73.38Å 478.36Å	Donositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.70 - 2.10	Depositor
Resolution (A)	49.70 - 2.10	EDS
% Data completeness	99.4 (49.70-2.10)	Depositor
(in resolution range)	99.6 (49.70-2.10)	EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.21 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D D.	0.195 , 0.236	Depositor
R, R_{free}	0.195 , 0.235	DCC
R_{free} test set	4617 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.655	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35, 57.8	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3891	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: BMA, ACT, BU2, GOL, NAG, 1PE, MAN, CD, FUC

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.42	0/1883	0.58	0/2547	
2	В	0.42	0/1674	0.53	0/2273	
All	All	0.42	0/3557	0.56	0/4820	

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	1821	0	1756	17	0
2	В	1616	0	1550	20	0
3	С	70	0	61	0	0
4	A	12	0	16	0	0
4	В	18	0	24	7	0
5	A	28	0	21	0	0
5	В	28	0	21	0	0
6	A	16	0	22	2	0
6	В	16	0	22	1	0
7	A	18	0	30	3	0
7	В	12	0	20	0	0



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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
8	A	12	0	0	0	0
8	В	5	0	0	0	0
9	A	115	0	0	3	0
9	В	104	0	0	2	0
All	All	3891	0	3543	37	0

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 5.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	$\text{overlap } (\text{\AA})$
2:B:487:ASN:H	4:B:2112:GOL:H12	1.13	1.14
2:B:487:ASN:N	4:B:2112:GOL:H12	1.98	0.74
2:B:378:LYS:HD3	4:B:2107:GOL:H2	1.73	0.70
1:A:1:GLN:NE2	9:A:1401:HOH:O	2.23	0.70
2:B:411:ALA:HB2	4:B:2107:GOL:H31	1.77	0.67
2:B:357[B]:ARG:NH1	9:B:2201:HOH:O	2.25	0.67
2:B:485:GLY:HA2	4:B:2112:GOL:H11	1.79	0.63
1:A:1:GLN:HE21	1:A:2:VAL:H	1.48	0.61
2:B:533:THR:HG22	2:B:535:GLU:H	1.66	0.60
1:A:1022:CYS:HB3	1:A:1079:VAL:HG13	1.83	0.60
2:B:498:GLN:NE2	9:B:2203:HOH:O	2.35	0.59
1:A:1074:ASN:O	7:A:1310:BU2:HC22	2.04	0.57
2:B:376[B]:THR:HG23	2:B:435:ALA:HB3	1.86	0.57
1:A:1062:ASP:OD1	1:A:1065:LYS:NZ	2.39	0.55
1:A:1091[A]:THR:HG23	1:A:1112:THR:HA	1.90	0.54
6:A:1305:1PE:H221	2:B:368:LEU:H	1.73	0.53
2:B:487:ASN:H	4:B:2112:GOL:C1	2.03	0.52
1:A:1:GLN:NE2	1:A:2:VAL:H	2.07	0.52
1:A:1013:GLN:NE2	9:A:1403:HOH:O	2.41	0.51
1:A:59:ARG:HD2	2:B:488:CYS:HB2	1.93	0.50
2:B:403[A]:ARG:HG2	2:B:505:TYR:HA	1.95	0.48
1:A:1091[B]:THR:HG23	1:A:1112:THR:HA	1.95	0.47
1:A:1022:CYS:HB3	1:A:1079:VAL:CG1	2.45	0.47
9:A:1423:HOH:O	2:B:379:CYS:HB2	2.15	0.46
2:B:378:LYS:HB3	2:B:378:LYS:HE3	1.50	0.46
1:A:1077:ASN:OD1	7:A:1310:BU2:HC21	2.16	0.45
2:B:335:LEU:HD23	2:B:362:VAL:HG23	1.99	0.44
2:B:354:ASN:O	2:B:398:ASP:HA	2.18	0.44
6:B:2102:1PE:H122	6:B:2102:1PE:H232	1.77	0.42



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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	$\operatorname{distance}\ (ext{Å})$	overlap (Å)
1:A:1018:LEU:HB2	1:A:1083:MET:HE3	2.02	0.41
1:A:1011:LEU:HD11	1:A:1114:SER:OG	2.20	0.41
2:B:443[A]:SER:OG	2:B:497:PHE:HB3	2.20	0.41
1:A:1045:ARG:HH12	6:A:1305:1PE:H122	1.85	0.41
2:B:486:PHE:N	4:B:2112:GOL:H11	2.36	0.41
1:A:1099[A]:MET:HE3	1:A:1101:GLY:H	1.86	0.40
1:A:1028:PRO:HB3	7:A:1310:BU2:HC12	2.02	0.40
2:B:382:VAL:HG23	2:B:386:LYS:HD2	2.04	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	Perce	ntiles
1	A	$236/298 \ (79\%)$	232 (98%)	4 (2%)	0	100	100
2	В	$202/213 \ (95\%)$	194 (96%)	8 (4%)	0	100	100
All	All	438/511 (86%)	426 (97%)	12 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	189/218 (87%)	183 (97%)	6 (3%)	39 41



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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	В	176/183 (96%)	172 (98%)	4 (2%)	50 55
All	All	365/401 (91%)	355 (97%)	10 (3%)	55 48

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65[A]	LYS
1	A	65[B]	LYS
1	A	1045	ARG
1	A	1096	CYS
1	A	1099[A]	MET
1	A	1099[B]	MET
2	В	357[A]	ARG
2	В	357[B]	ARG
2	В	377	PHE
2	В	481	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1	GLN
1	A	1013	GLN
2	В	474	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)

6 monosaccharides 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		
IVIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	С	1	2,3	14,14,15	0.28	0	17,19,21	0.41	0
3	NAG	С	2	3	14,14,15	0.49	0	17,19,21	0.48	0
3	BMA	С	3	3	11,11,12	0.93	0	15,15,17	1.16	2 (13%)
3	MAN	С	4	3	11,11,12	0.65	0	15,15,17	0.96	2 (13%)
3	FUC	С	5	3	10,10,11	0.99	0	14,14,16	1.04	2 (14%)
3	FUC	С	6	3	10,10,11	1.35	1 (10%)	14,14,16	0.96	0

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	NAG	С	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	С	2	3	-	0/6/23/26	0/1/1/1
3	BMA	С	3	3	-	2/2/19/22	0/1/1/1
3	MAN	С	4	3	-	0/2/19/22	0/1/1/1
3	FUC	С	5	3	-	-	0/1/1/1
3	FUC	С	6	3	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(ext{\AA})$
3	С	6	FUC	C2-C3	3.42	1.57	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
3	С	3	BMA	C3-C4-C5	2.59	114.86	110.24
3	С	4	MAN	C1-O5-C5	2.32	115.33	112.19
3	С	5	FUC	C1-O5-C5	2.17	117.69	112.78
3	С	4	MAN	O2-C2-C3	-2.11	105.92	110.14
3	С	3	BMA	C2-C3-C4	2.06	114.46	110.89
3	С	5	FUC	O5-C5-C4	2.01	113.12	109.52

There are no chirality outliers.



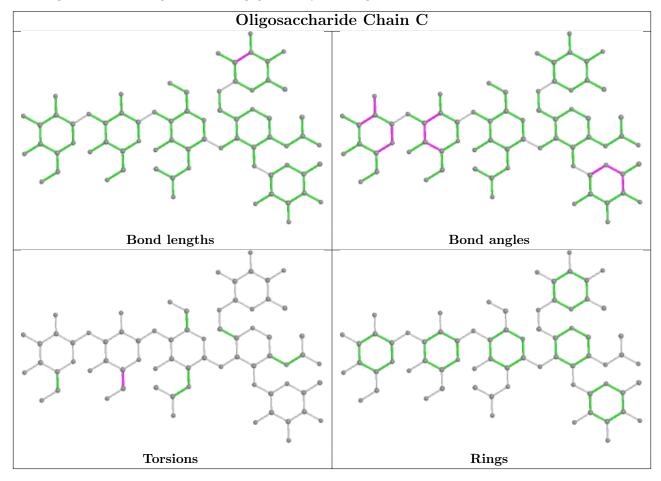
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	С	3	BMA	C4-C5-C6-O6
3	С	3	BMA	O5-C5-C6-O6

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 oligosaccharide.



5.6 Ligand geometry (i)

Of 43 ligands modelled in this entry, 17 are monoatomic - leaving 26 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	Во	ond leng	ths	В	ond ang	les
IVIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	В	2105	-	3,3,3	1.46	1 (33%)	3,3,3	1.51	0
6	1PE	В	2102	-	15,15,15	0.53	0	14,14,14	0.32	0
4	GOL	В	2112	-	5,5,5	0.90	0	5,5,5	1.28	1 (20%)
4	GOL	В	2107	-	5,5,5	0.88	0	5,5,5	0.76	0
7	BU2	A	1309	_	5,5,5	0.46	0	5,5,5	0.79	0
5	ACT	A	1304	-	3,3,3	1.43	1 (33%)	3,3,3	1.48	0
5	ACT	A	1302	8	3,3,3	1.47	1 (33%)	3,3,3	1.57	0
4	GOL	A	1308	-	5,5,5	1.05	0	5,5,5	0.64	0
7	BU2	В	2111	_	5,5,5	0.47	0	5,5,5	0.59	0
7	BU2	A	1311	-	5,5,5	0.46	0	5,5,5	0.85	0
5	ACT	В	2108	8	3,3,3	1.59	1 (33%)	3,3,3	1.22	0
5	ACT	A	1303	8	3,3,3	1.35	0	3,3,3	1.43	0
5	ACT	В	2104	8	3,3,3	1.43	1 (33%)	3,3,3	1.47	0
5	ACT	A	1307	8	3,3,3	1.62	1 (33%)	3,3,3	1.46	0
5	ACT	A	1313	-	3,3,3	1.22	0	3,3,3	1.58	0
5	ACT	A	1306	8	3,3,3	1.58	1 (33%)	3,3,3	1.24	0
5	ACT	В	2113	-	3,3,3	1.54	1 (33%)	3,3,3	1.47	0
5	ACT	В	2109	-	3,3,3	1.47	1 (33%)	3,3,3	1.48	0
5	ACT	В	2101	-	3,3,3	1.40	0	3,3,3	1.49	0
5	ACT	В	2103	-	3,3,3	1.23	0	3,3,3	1.62	1 (33%)
4	GOL	A	1301	-	5,5,5	0.59	0	5,5,5	1.04	0
4	GOL	В	2106	-	5,5,5	0.93	0	5,5,5	0.91	0
6	1PE	A	1305	-	15,15,15	0.53	0	14,14,14	0.30	0
7	BU2	В	2110	-	5,5,5	0.46	0	5,5,5	0.64	0
5	ACT	A	1312	_	3,3,3	1.52	1 (33%)	3,3,3	1.44	0
7	BU2	A	1310	-	5,5,5	0.48	0	5,5,5	0.30	0

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	1PE	В	2102	-	-	6/13/13/13	-
4	GOL	В	2106	-	-	0/4/4/4	-
7	BU2	A	1311	-	-	1/3/3/3	-
4	GOL	В	2112	-	-	2/4/4/4	-



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	1PE	A	1305	-	-	7/13/13/13	-
4	GOL	В	2107	-	-	2/4/4/4	-
7	BU2	A	1309	-	-	0/3/3/3	-
7	BU2	A	1310	_	-	0/3/3/3	-
7	BU2	В	2110	-	-	2/3/3/3	-
7	BU2	В	2111	-	-	0/3/3/3	-
4	GOL	A	1308	-	-	4/4/4/4	-
4	GOL	A	1301	-	-	2/4/4/4	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
5	A	1307	ACT	СН3-С	2.51	1.59	1.49
5	A	1306	ACT	СН3-С	2.44	1.59	1.49
5	В	2113	ACT	СН3-С	2.32	1.58	1.49
5	В	2108	ACT	СН3-С	2.30	1.58	1.49
5	A	1312	ACT	СН3-С	2.26	1.58	1.49
5	В	2109	ACT	СН3-С	2.23	1.58	1.49
5	A	1302	ACT	СН3-С	2.22	1.58	1.49
5	В	2105	ACT	СН3-С	2.17	1.58	1.49
5	A	1304	ACT	СН3-С	2.12	1.58	1.49
5	В	2104	ACT	СН3-С	2.02	1.57	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
4	В	2112	GOL	C3-C2-C1	-2.23	103.03	111.70
5	В	2103	ACT	O-C-CH3	-2.03	114.43	122.33

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1308	GOL	O1-C1-C2-O2
4	В	2112	GOL	O1-C1-C2-C3
7	A	1311	BU2	O1-C1-C2-C3
7	В	2110	BU2	O1-C1-C2-C3
6	В	2102	1PE	OH6-C15-C25-OH5
6	A	1305	1PE	OH4-C13-C23-OH3
6	В	2102	1PE	ОН4-С13-С23-ОН3



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Mol	Chain	Res	Type	Atoms
6	В	2102	1PE	OH5-C14-C24-OH4
4	В	2107	GOL	O2-C2-C3-O3
6	A	1305	1PE	OH2-C12-C22-OH3
6	A	1305	1PE	ОН7-С16-С26-ОН6
4	A	1301	GOL	O1-C1-C2-C3
4	A	1308	GOL	O1-C1-C2-C3
4	A	1308	GOL	C1-C2-C3-O3
4	В	2107	GOL	C1-C2-C3-O3
4	A	1308	GOL	O2-C2-C3-O3
4	В	2112	GOL	O1-C1-C2-O2
6	В	2102	1PE	ОН7-С16-С26-ОН6
6	В	2102	1PE	C12-C22-OH3-C23
6	A	1305	1PE	C24-C14-OH5-C25
6	В	2102	1PE	C24-C14-OH5-C25
6	A	1305	1PE	OH6-C15-C25-OH5
6	A	1305	1PE	C14-C24-OH4-C13
6	A	1305	1PE	C12-C22-OH3-C23
7	В	2110	BU2	C1-C2-C3-O3
4	A	1301	GOL	O1-C1-C2-O2

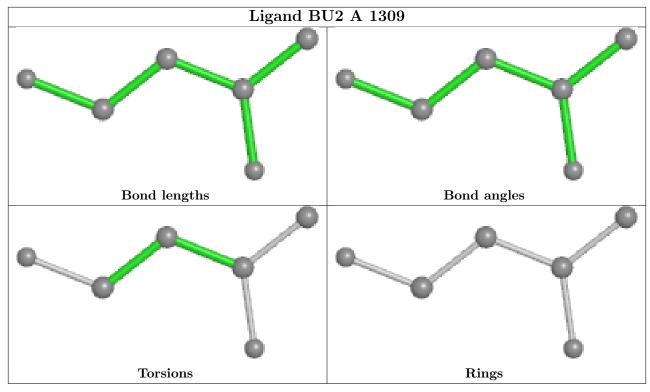
There are no ring outliers.

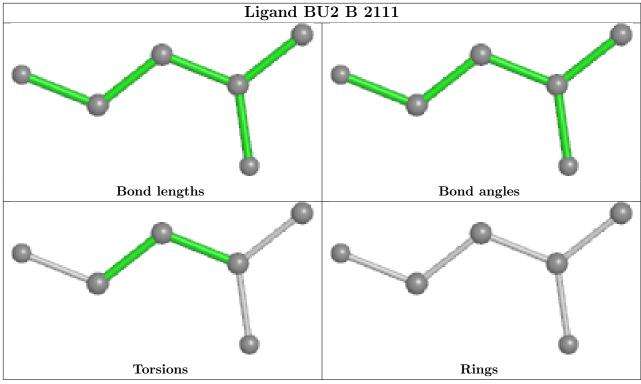
5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	В	2102	1PE	1	0
4	В	2112	GOL	5	0
4	В	2107	GOL	2	0
6	A	1305	1PE	2	0
7	A	1310	BU2	3	0

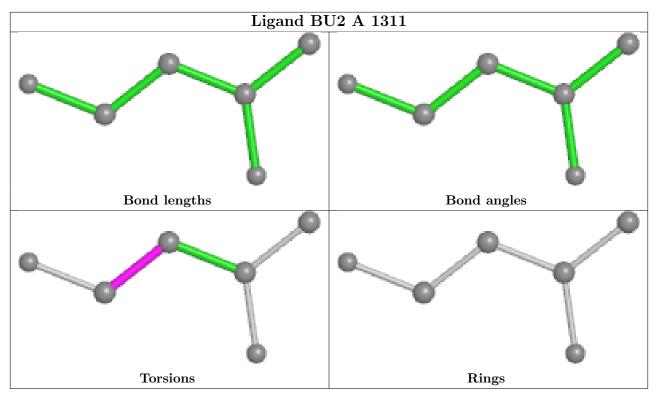
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

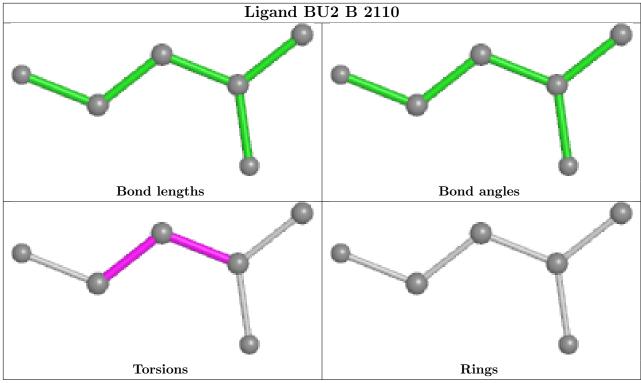




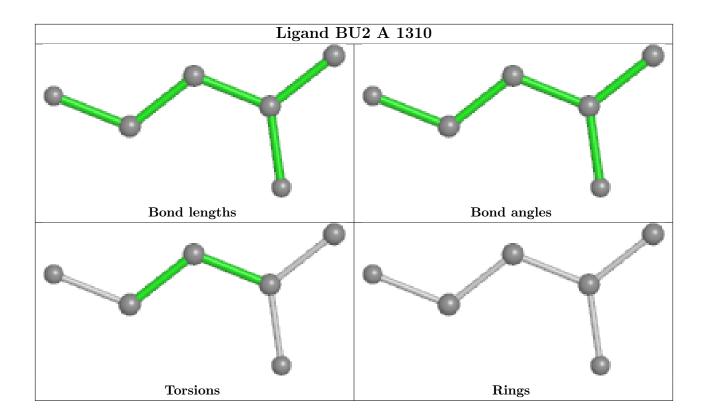












5.7 Other polymers (i)

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, 95^{th} 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	$234/298 \ (78\%)$	0.11	6 (2%) 56 61	35, 45, 68, 91	0
2	В	201/213 (94%)	0.22	9 (4%) 33 38	33, 45, 79, 98	0
All	All	435/511 (85%)	0.16	15 (3%) 45 51	33, 45, 73, 98	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	483	VAL	3.8
2	В	481	ASN	3.6
2	В	482	GLY	3.5
1	A	999	SER	3.5
2	В	532	GLY	3.3
1	A	1114	SER	3.2
1	A	1	GLN	2.8
2	В	524	VAL	2.8
2	В	539	GLN	2.7
1	A	1115	ALA	2.4
2	В	477	SER	2.4
1	A	1013	GLN	2.2
2	В	480	CYS	2.2
2	В	536	VAL	2.2
1	A	108	TYR	2.2

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

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

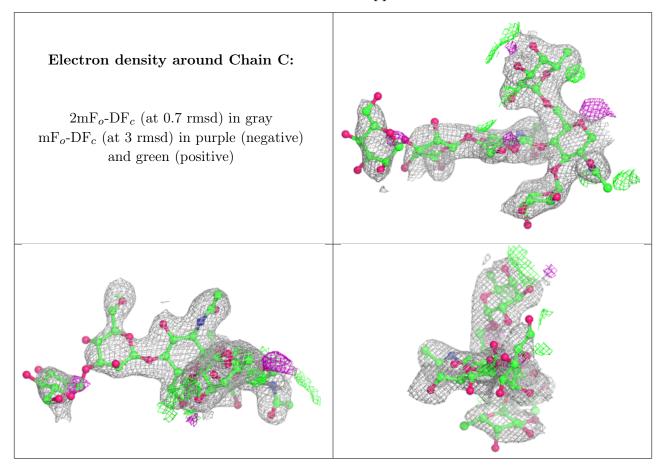


6.3 Carbohydrates (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
3	BMA	С	3	11/12	0.64	0.33	77,94,102,110	0
3	MAN	С	4	11/12	0.75	0.47	104,111,115,119	0
3	FUC	С	5	10/11	0.83	0.24	80,85,89,94	0
3	NAG	С	2	14/15	0.88	0.15	55,68,78,81	0
3	FUC	С	6	10/11	0.91	0.10	42,49,53,60	0
3	NAG	С	1	14/15	0.92	0.17	60,70,85,89	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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, 95^{th} 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.

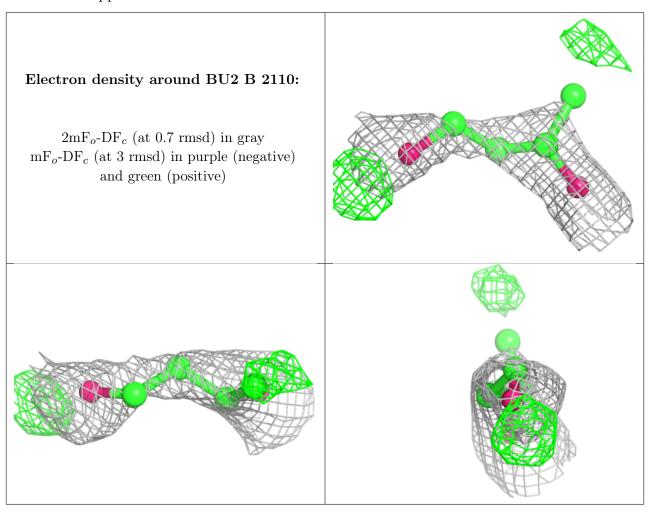
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\AA^2)$	Q < 0.9
8	CD	В	2116	1/1	0.03	0.16	141,141,141,141	1
8	CD	В	2114	1/1	0.31	0.08	112,112,112,112	1
7	BU2	В	2110	6/6	0.38	0.30	69,78,81,83	0
5	ACT	A	1306	4/4	0.50	0.36	64,91,96,99	0
8	CD	В	2117	1/1	0.53	0.15	127,127,127,127	1
8	CD	A	1317	1/1	0.57	0.17	150,150,150,150	1
7	BU2	A	1309	6/6	0.58	0.22	61,68,73,78	0
5	ACT	A	1304	4/4	0.58	0.28	71,81,85,87	0
5	ACT	A	1303	4/4	0.63	0.49	84,94,94,114	0
8	CD	A	1318	1/1	0.63	0.22	129,129,129,129	1
8	CD	A	1321	1/1	0.63	0.11	135,135,135,135	1
5	ACT	A	1312	4/4	0.65	0.25	51,67,68,73	0
4	GOL	A	1308	6/6	0.66	0.22	58,67,73,83	0
5	ACT	В	2108	4/4	0.66	0.16	60,75,86,86	0
5	ACT	В	2101	4/4	0.67	0.30	69,71,74,78	0
5	ACT	В	2113	4/4	0.69	0.22	54,63,74,76	0
7	BU2	В	2111	6/6	0.71	0.36	72,79,81,81	0
6	1PE	A	1305	16/16	0.73	0.20	65,78,86,89	0
8	CD	A	1315	1/1	0.73	0.30	129,129,129,129	1
7	BU2	A	1310	6/6	0.74	0.33	53,67,74,80	0
5	ACT	A	1307	4/4	0.75	0.20	48,64,84,92	0
5	ACT	В	2105	4/4	0.76	0.26	74,76,83,84	0
4	GOL	В	2106	6/6	0.76	0.19	60,69,73,81	0
4	GOL	В	2107	6/6	0.76	0.28	43,64,72,76	0
7	BU2	A	1311	6/6	0.78	0.31	68,70,75,76	0
5	ACT	В	2109	4/4	0.78	0.44	68,79,82,93	0
5	ACT	В	2103	4/4	0.80	0.22	73,75,76,76	0
8	CD	A	1320	1/1	0.83	0.17	143,143,143,143	1
8	CD	В	2118	1/1	0.83	0.09	94,94,94,94	1
4	GOL	В	2112	6/6	0.85	0.29	53,72,79,91	0
5	ACT	A	1313	4/4	0.86	0.18	72,81,84,85	0
8	CD	A	1322	1/1	0.86	0.05	106,106,106,106	1
8	CD	A	1319	1/1	0.87	0.12	102,102,102,102	1
8	CD	A	1314	1/1	0.90	0.06	69,69,69,69	1
6	1PE	В	2102	16/16	0.90	0.19	47,70,83,88	0
4	GOL	A	1301	6/6	0.92	0.16	49,55,62,64	0
5	ACT	A	1302	4/4	0.93	0.18	85,87,87,95	0
8	CD	A	1316	1/1	0.93	0.13	107,107,107,107	1
5	ACT	В	2104	4/4	0.93	0.16	84,92,94,95	0
8	CD	В	2115	1/1	0.98	0.06	67,67,67,67	1
8	CD	A	1324	1/1	0.98	0.20	39,39,39,39 Continued on mos	1



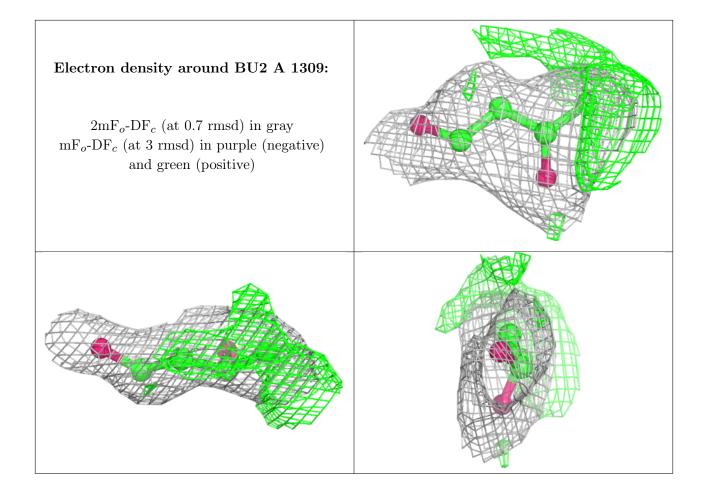
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
8	CD	A	1325	1/1	0.98	0.13	65,65,65,65	1
8	CD	A	1323	1/1	0.98	0.21	123,123,123,123	1

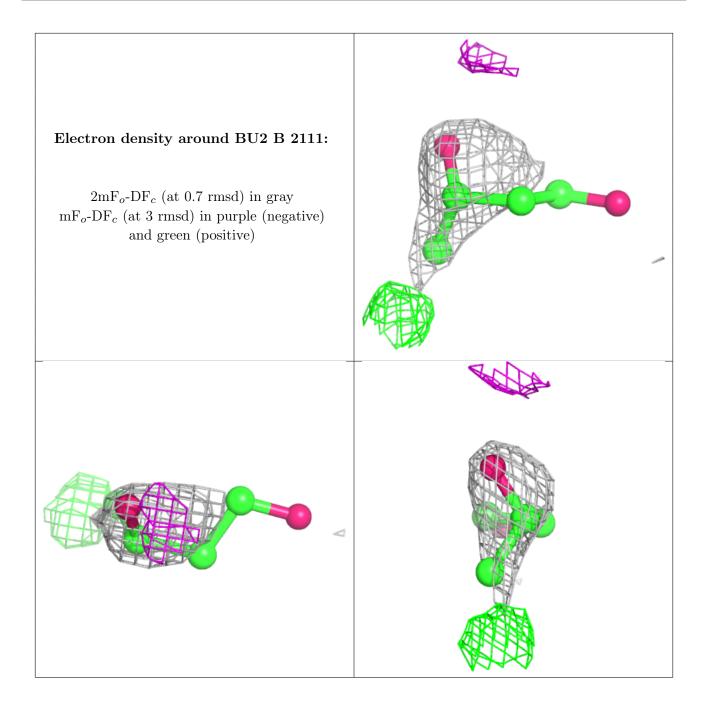
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



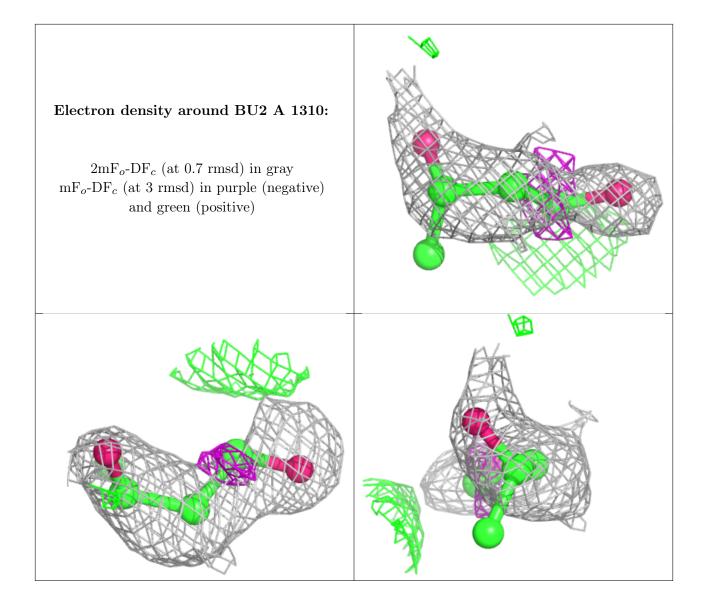




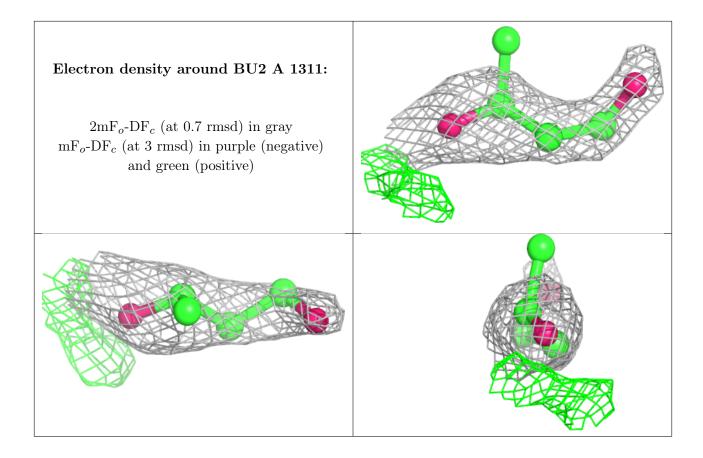












6.5 Other polymers (i)

There are no such residues in this entry.

