



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:12 PM UTC

PDB ID : 8TUI / pdb_00008tui
Title : Crystal structure of Fab-Lirilumab bound to KIR2DL3
Authors : Lorig-Roach, N.; DuBois, R.M.
Deposited on : 2023-08-16
Resolution : 2.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)
Xtrriage (Phenix) : 2.0
EDS : 3.0
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

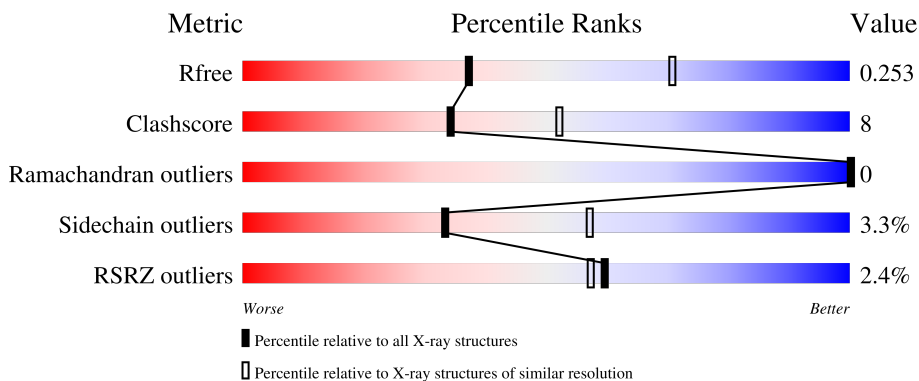
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	H	265	 3% 68% 17% 15%
2	L	214	 80% 18% ..
3	A	257	 2% 30% 8% 62%
4	B	7	 86% 14%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4176 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 Lirilumab Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	225	1673	1058	273	335	7	0	0	0

- Molecule 2 is a protein called Lirilumab Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	212	1640	1028	278	329	5	0	0	0

- Molecule 3 is a protein called Killer cell immunoglobulin-like receptor 2DL3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	98	773	493	137	139	4	0	0	0

There are 33 discrepancies between the modelled and reference sequences:

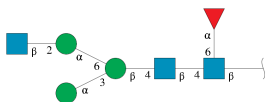
Chain	Residue	Modelled	Actual	Comment	Reference
A	225	ALA	-	expression tag	UNP P43628
A	226	ALA	-	expression tag	UNP P43628
A	227	ALA	-	expression tag	UNP P43628
A	228	GLU	-	expression tag	UNP P43628
A	229	GLN	-	expression tag	UNP P43628
A	230	LYS	-	expression tag	UNP P43628
A	231	LEU	-	expression tag	UNP P43628
A	232	ILE	-	expression tag	UNP P43628
A	233	SER	-	expression tag	UNP P43628
A	234	GLU	-	expression tag	UNP P43628
A	235	GLU	-	expression tag	UNP P43628
A	236	ASP	-	expression tag	UNP P43628
A	237	LEU	-	expression tag	UNP P43628
A	238	ASN	-	expression tag	UNP P43628

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Chain	Residue	Modelled	Actual	Comment	Reference
A	239	LEU	-	expression tag	UNP P43628
A	240	ASP	-	expression tag	UNP P43628
A	241	LEU	-	expression tag	UNP P43628
A	242	VAL	-	expression tag	UNP P43628
A	243	PRO	-	expression tag	UNP P43628
A	244	ARG	-	expression tag	UNP P43628
A	245	GLY	-	expression tag	UNP P43628
A	246	SER	-	expression tag	UNP P43628
A	247	SER	-	expression tag	UNP P43628
A	248	SER	-	expression tag	UNP P43628
A	249	HIS	-	expression tag	UNP P43628
A	250	HIS	-	expression tag	UNP P43628
A	251	HIS	-	expression tag	UNP P43628
A	252	HIS	-	expression tag	UNP P43628
A	253	HIS	-	expression tag	UNP P43628
A	254	HIS	-	expression tag	UNP P43628
A	255	SER	-	expression tag	UNP P43628
A	256	SER	-	expression tag	UNP P43628
A	257	GLY	-	expression tag	UNP P43628

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




Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	B	7	85	48	3	34	0	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	2	Total	O	0	0
			2	2		
5	L	3	Total	O	0	0
			3	3		

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

Chain B:  86% 14%

MAG3
MAG2
MAN3
MAN4
MAG5
MAN6
FUC7

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.38Å 84.27Å 62.27Å 90.00° 115.86° 90.00°	Depositor
Resolution (Å)	46.66 – 2.75 46.66 – 2.75	Depositor EDS
% Data completeness (in resolution range)	95.3 (46.66-2.75) 95.3 (46.66-2.75)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.77Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.211 , 0.254 0.210 , 0.253	Depositor DCC
R_{free} test set	570 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å ²)	60.9	Xtrriage
Anisotropy	0.275	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.042 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4176	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.65% 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: NAG, FUC, BMA, MAN

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	H	0.69	0/1715	0.94	0/2338
2	L	0.49	0/1676	0.69	2/2277 (0.1%)
3	A	0.51	0/796	0.64	1/1080 (0.1%)
All	All	0.59	0/4187	0.79	3/5695 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	186	TYR	N-CA-C	-6.05	102.55	110.53
2	L	186	TYR	CA-C-O	-5.21	115.83	121.87
3	A	87	PRO	N-CA-C	-5.12	107.18	113.84

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	H	1673	0	1625	31	0
2	L	1640	0	1597	23	0
3	A	773	0	751	13	0
4	B	85	0	73	0	0
5	H	2	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	3	0	0	1	0
All	All	4176	0	4046	62	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 8.

The worst 5 of 62 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:H:43:GLN:HB3	5:H:301:HOH:O	1.87	0.74
1:H:43:GLN:CB	5:H:301:HOH:O	2.37	0.73
1:H:37:VAL:HG21	5:L:303:HOH:O	1.89	0.72
3:A:7:LYS:HG3	3:A:94:SER:HA	1.70	0.72
2:L:181:LEU:HD22	2:L:185:ASP:HB3	1.76	0.67

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	H	223/265 (84%)	212 (95%)	11 (5%)	0	100	100
2	L	210/214 (98%)	201 (96%)	9 (4%)	0	100	100
3	A	96/257 (37%)	89 (93%)	7 (7%)	0	100	100
All	All	529/736 (72%)	502 (95%)	27 (5%)	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	H	187/215 (87%)	180 (96%)	7 (4%)	30	54
2	L	185/187 (99%)	179 (97%)	6 (3%)	34	58
3	A	86/222 (39%)	84 (98%)	2 (2%)	44	66
All	All	458/624 (73%)	443 (97%)	15 (3%)	33	57

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	4	LEU
3	A	17	LEU
2	L	33	LEU
3	A	61	LYS
2	L	203	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	39	GLN
2	L	38	GLN
2	L	90	GLN
3	A	13	HIS
3	A	85	HIS

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

7 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		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	1	3,4	14,14,15	0.41	0	17,19,21	0.67	0
4	NAG	B	2	4	14,14,15	0.38	0	17,19,21	0.82	1 (5%)
4	BMA	B	3	4	11,11,12	0.30	0	15,15,17	0.46	0
4	MAN	B	4	4	11,11,12	0.39	0	15,15,17	0.60	0
4	NAG	B	5	4	14,14,15	0.39	0	17,19,21	0.28	0
4	MAN	B	6	4	11,11,12	0.26	0	15,15,17	0.47	0
4	FUC	B	7	4	10,10,11	0.31	0	14,14,16	0.44	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
4	NAG	B	1	3,4	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	1/6/23/26	0/1/1/1
4	BMA	B	3	4	-	0/2/19/22	0/1/1/1
4	MAN	B	4	4	-	0/2/19/22	0/1/1/1
4	NAG	B	5	4	-	2/6/23/26	0/1/1/1
4	MAN	B	6	4	-	0/2/19/22	0/1/1/1
4	FUC	B	7	4	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2	NAG	C2-N2-C7	3.12	127.08	122.90

There are no chirality outliers.

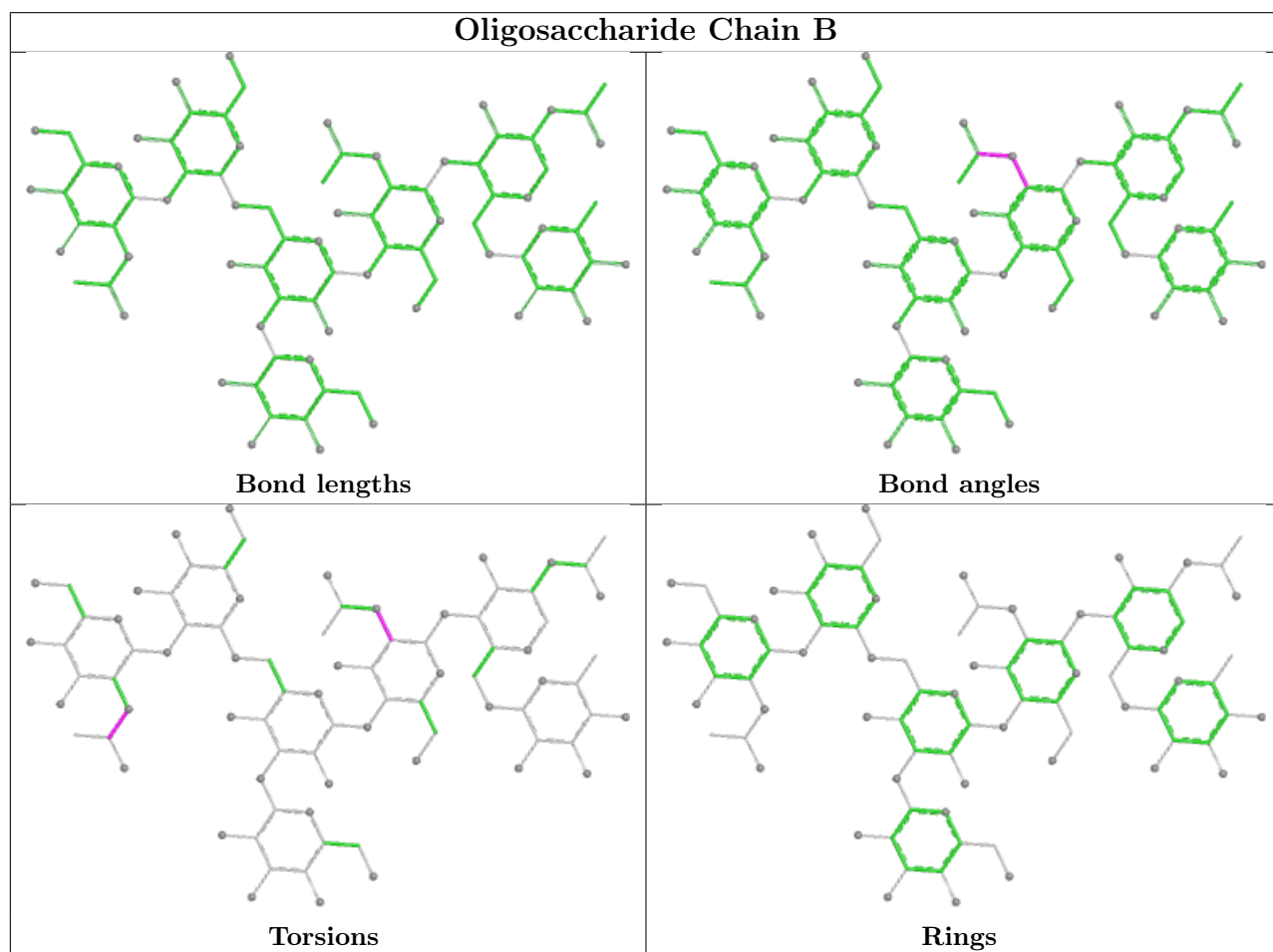
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	5	NAG	C8-C7-N2-C2
4	B	5	NAG	O7-C7-N2-C2
4	B	2	NAG	C3-C2-N2-C7

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](#)

There are no ligands in this entry.

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 [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	H	225/265 (84%)	0.32	8 (3%) 46 44	40, 65, 106, 133	0
2	L	212/214 (99%)	0.13	1 (0%) 87 87	30, 62, 93, 108	0
3	A	98/257 (38%)	0.29	4 (4%) 41 39	44, 68, 114, 148	0
All	All	535/736 (72%)	0.24	13 (2%) 59 57	30, 64, 98, 148	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	106	TYR	3.7
3	A	67	GLY	3.5
1	H	107	ASP	2.9
1	H	199	LEU	2.8
3	A	88	TYR	2.8

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, 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.

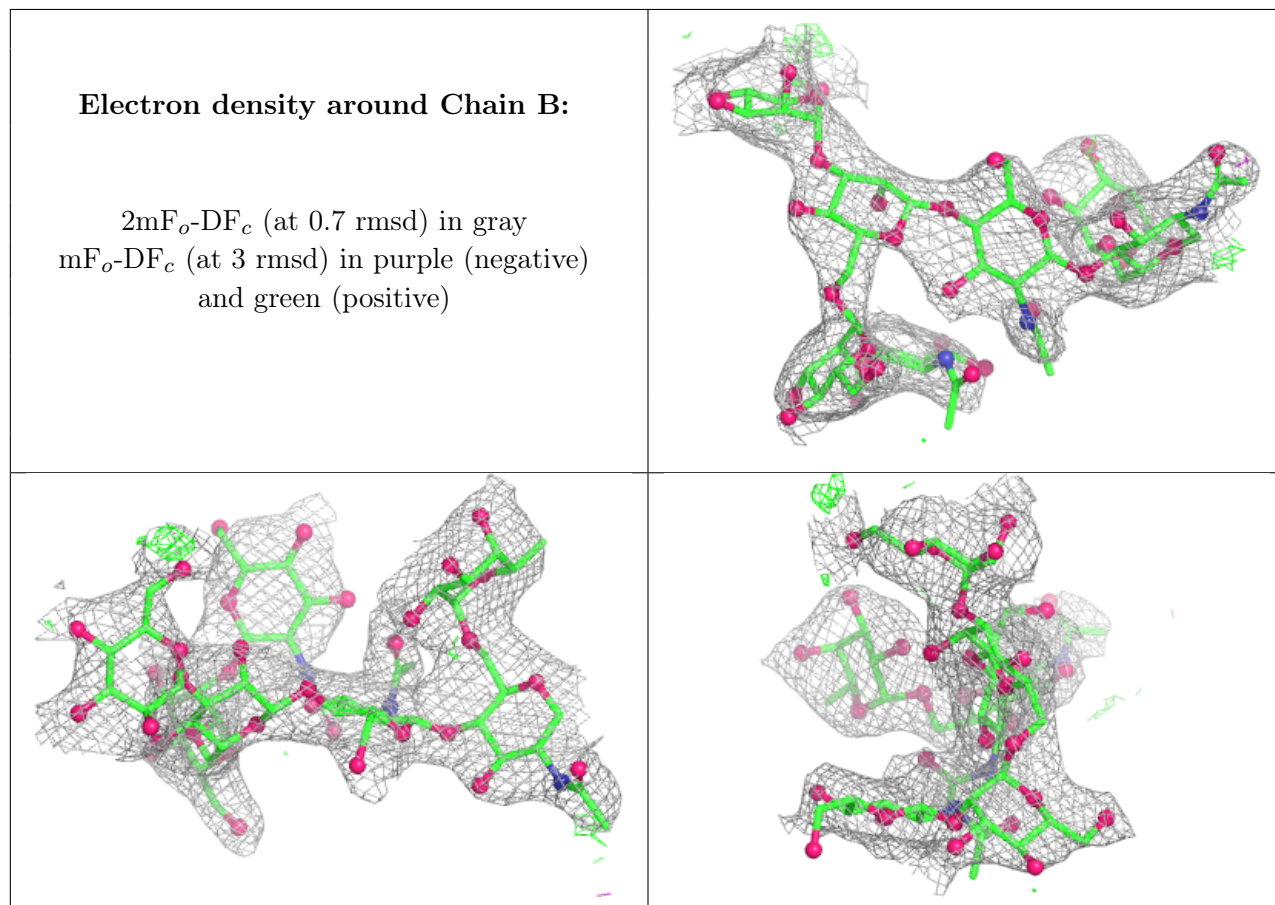
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	B	1	14/15	-	-	58,76,83,91	0
4	NAG	B	2	14/15	-	-	72,91,97,99	0
4	BMA	B	3	11/12	-	-	94,100,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MAN	B	4	11/12	-	-	99,111,122,123	0
4	NAG	B	5	14/15	-	-	107,110,118,122	0
4	MAN	B	6	11/12	-	-	94,101,112,113	0
4	FUC	B	7	10/11	-	-	62,68,75,82	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.