



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 05:06 PM UTC

PDB ID : 6DF3 / pdb_00006df3
Title : Crystal structure of ternary complex of IL-24 with soluble receptors IL-22RA and IL-20RB
Authors : Lubkowski, J.; Wlodawer, A.
Deposited on : 2018-05-14
Resolution : 2.15 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)
Xtriage (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

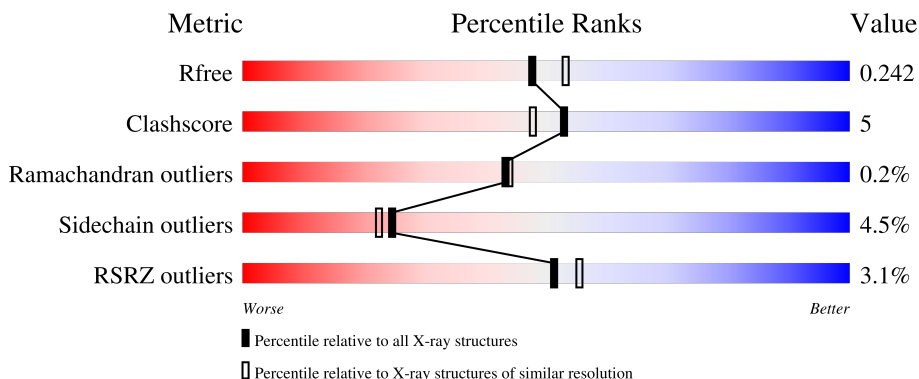
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	L	206	 3% 79% 15%
2	C	155	 2% 84% 16%
3	H	190	 4% 87% 11%
4	A	2	 50% 50%

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
6	GOL	C	302	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4529 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 Interleukin-22 receptor subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	199	1610	1024	277	299	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	229	GLY	-	expression tag	UNP Q8N6P7

- Molecule 2 is a protein called Interleukin-24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	155	1283	828	222	228	5	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	85	GLN	ASN	engineered mutation	UNP Q13007
C	99	GLN	ASN	engineered mutation	UNP Q13007
C	124	HIS	TYR	conflict	UNP Q13007
C	126	GLN	ASN	engineered mutation	UNP Q13007

- Molecule 3 is a protein called Interleukin-20 receptor subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	190	1502	962	247	284	9	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	134	GLN	ASN	engineered mutation	UNP Q6UXL0

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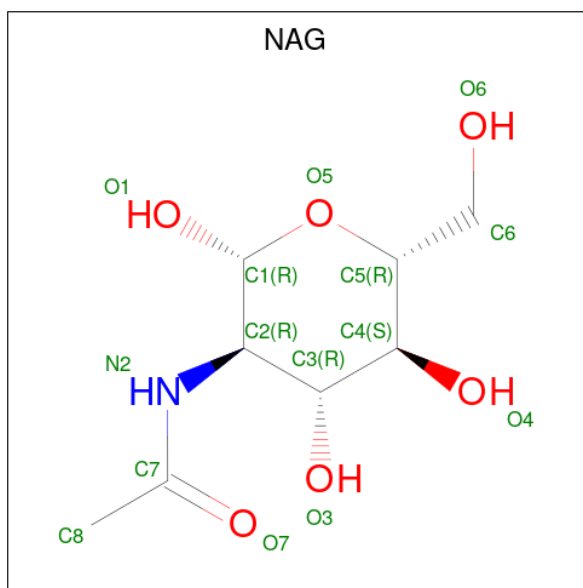
Chain	Residue	Modelled	Actual	Comment	Reference
H	206	GLU	GLN	conflict	UNP Q6UXL0

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	A	2	28	16	2	10	0	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	L	1	14	8	1	5	0	0

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	14	Total O 14 14	0	0
7	C	28	Total O 28 28	0	0
7	H	38	Total O 38 38	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	77.70Å 77.70Å 124.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.15 30.00 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.7 (30.00-2.15) 99.7 (30.00-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.16Å)	Xtrriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.182 , 0.225 (Not available) , 0.242	Depositor DCC
R_{free} test set	1978 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	53.1	Xtrriage
Anisotropy	0.006	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.048 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4529	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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: GOL, NAG

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	L	1.23	5/1649 (0.3%)	1.17	1/2238 (0.0%)
2	C	1.34	3/1311 (0.2%)	1.22	3/1771 (0.2%)
3	H	1.25	6/1545 (0.4%)	1.13	4/2109 (0.2%)
All	All	1.27	14/4505 (0.3%)	1.17	8/6118 (0.1%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	126	ILE	C-O	-8.31	1.14	1.24
1	L	123	PRO	CA-C	-6.51	1.47	1.52
2	C	64	VAL	N-CA	6.43	1.54	1.46
1	L	123	PRO	C-O	-6.34	1.19	1.24
1	L	62	GLU	N-CA	5.86	1.52	1.45

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	182	VAL	N-CA-C	6.74	116.89	110.42
2	C	186	LEU	CA-CB-CG	6.11	137.69	116.30
3	H	89	CYS	N-CA-C	5.89	118.21	108.49
2	C	182	VAL	CA-C-O	-5.36	115.48	121.17
1	L	64	ASP	N-CA-C	5.16	117.13	108.73

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	L	1610	0	1581	20	0
2	C	1283	0	1289	14	0
3	H	1502	0	1456	10	0
4	A	28	0	25	1	0
5	L	14	0	13	0	0
6	C	12	0	16	7	0
7	C	28	0	0	0	0
7	H	38	0	0	4	0
7	L	14	0	0	1	0
All	All	4529	0	4380	43	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 5.

The worst 5 of 43 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)
3:H:146:THR:HG23	3:H:153:VAL:HG13	1.42	0.98
1:L:144:THR:HG22	1:L:146:ILE:H	1.47	0.78
2:C:201:GLN:OE1	6:C:302:GOL:O2	2.13	0.66
2:C:70:TRP:CD1	6:C:302:GOL:HO1	2.13	0.66
3:H:160:GLY:HA2	7:H:328:HOH:O	1.95	0.66

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	L	193/206 (94%)	186 (96%)	7 (4%)	0	100	100
2	C	153/155 (99%)	151 (99%)	2 (1%)	0	100	100
3	H	188/190 (99%)	171 (91%)	16 (8%)	1 (0%)	24	20
All	All	534/551 (97%)	508 (95%)	25 (5%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	175	GLY

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	L	180/184 (98%)	169 (94%)	11 (6%)	17	12
2	C	141/141 (100%)	137 (97%)	4 (3%)	38	40
3	H	166/166 (100%)	159 (96%)	7 (4%)	26	25
All	All	487/491 (99%)	465 (96%)	22 (4%)	24	22

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	181	ASP
3	H	121	THR
3	H	119	SER
3	H	153	VAL
1	L	109	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	123	ASN
3	H	71	GLN

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Mol	Chain	Res	Type
3	H	134	GLN
3	H	110	ASN
1	L	72	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](#)

2 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	A	1	1,4	14,14,15	0.71	0	17,19,21	2.46	6 (35%)
4	NAG	A	2	4	14,14,15	0.61	0	17,19,21	2.55	4 (23%)

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	A	1	1,4	-	5/6/23/26	0/1/1/1
4	NAG	A	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2	NAG	C1-O5-C5	9.33	124.69	112.19
4	A	1	NAG	O5-C1-C2	-4.93	103.67	111.29
4	A	1	NAG	C1-O5-C5	4.35	118.02	112.19
4	A	1	NAG	C8-C7-N2	3.95	122.68	116.12
4	A	1	NAG	O4-C4-C5	3.54	118.05	109.32

There are no chirality outliers.

All (5) torsion outliers are listed below:

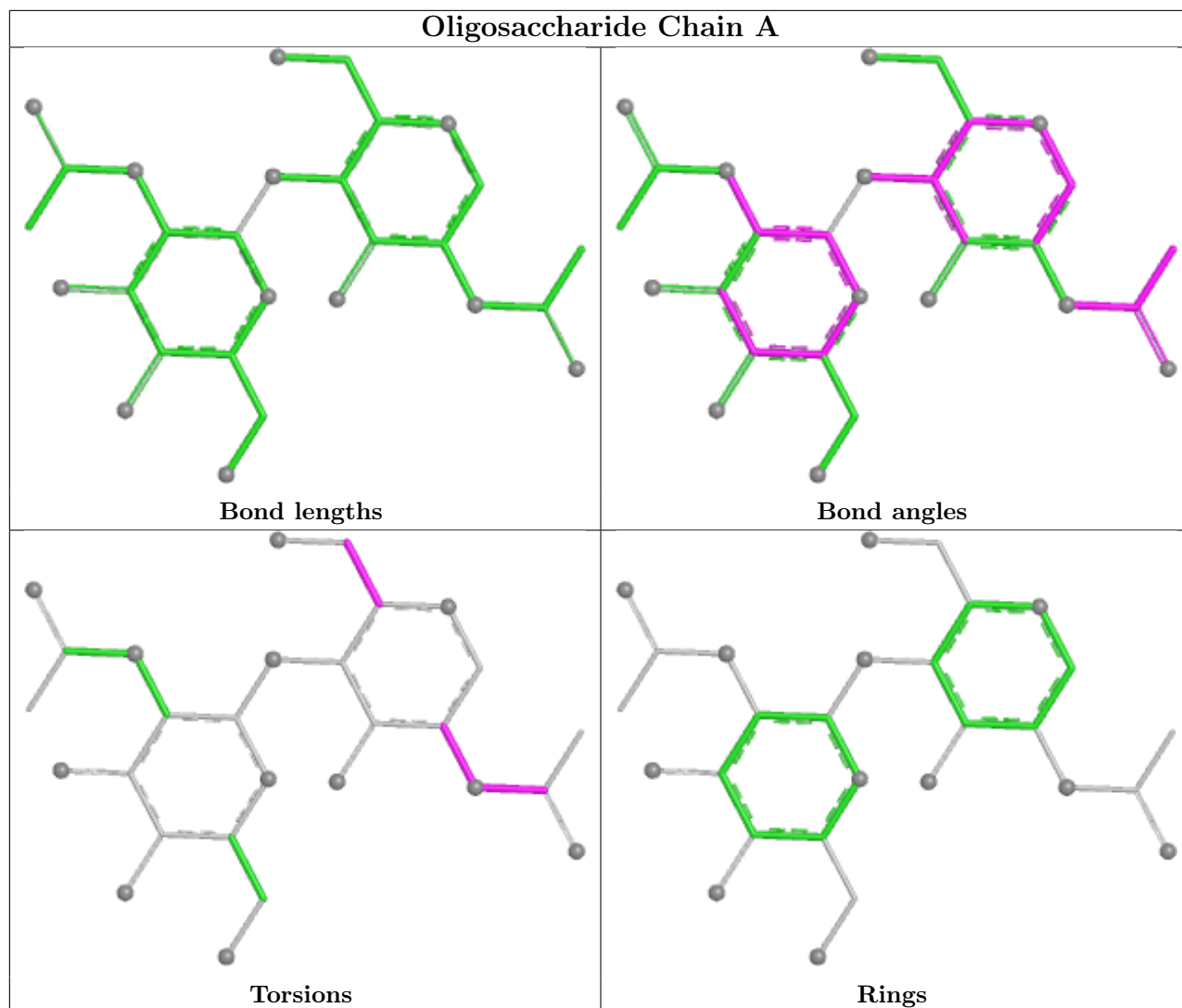
Mol	Chain	Res	Type	Atoms
4	A	1	NAG	C8-C7-N2-C2
4	A	1	NAG	O7-C7-N2-C2
4	A	1	NAG	O5-C5-C6-O6
4	A	1	NAG	C4-C5-C6-O6
4	A	1	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1	NAG	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 oligosaccharide.



5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
6	GOL	C	301	-	5,5,5	0.47	0	5,5,5	0.35	0
5	NAG	L	303	1	14,14,15	1.14	1 (7%)	17,19,21	2.62	8 (47%)
6	GOL	C	302	-	5,5,5	0.79	0	5,5,5	1.80	1 (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
6	GOL	C	301	-	-	1/4/4/4	-
5	NAG	L	303	1	-	4/6/23/26	0/1/1/1
6	GOL	C	302	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	303	NAG	O5-C5	2.93	1.49	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	303	NAG	C1-O5-C5	5.56	119.63	112.19
5	L	303	NAG	C8-C7-N2	4.37	123.36	116.12
5	L	303	NAG	O5-C5-C6	4.03	115.51	107.66
5	L	303	NAG	O5-C1-C2	-3.46	105.94	111.29
6	C	302	GOL	O3-C3-C2	-3.23	95.82	110.38

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	302	GOL	O1-C1-C2-C3
5	L	303	NAG	O5-C5-C6-O6
5	L	303	NAG	C4-C5-C6-O6
5	L	303	NAG	C8-C7-N2-C2
5	L	303	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	302	GOL	7	0

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	L	199/206 (96%)	0.33	6 (3%) 52 56	46, 73, 128, 158	0
2	C	155/155 (100%)	-0.09	3 (1%) 66 70	39, 59, 91, 108	0
3	H	190/190 (100%)	0.41	8 (4%) 40 45	41, 79, 149, 173	0
All	All	544/551 (98%)	0.24	17 (3%) 51 55	39, 71, 130, 173	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	101	ALA	5.8
1	L	24	LEU	4.6
3	H	203	VAL	3.6
3	H	58	ILE	3.0
3	H	188	ILE	3.0

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

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

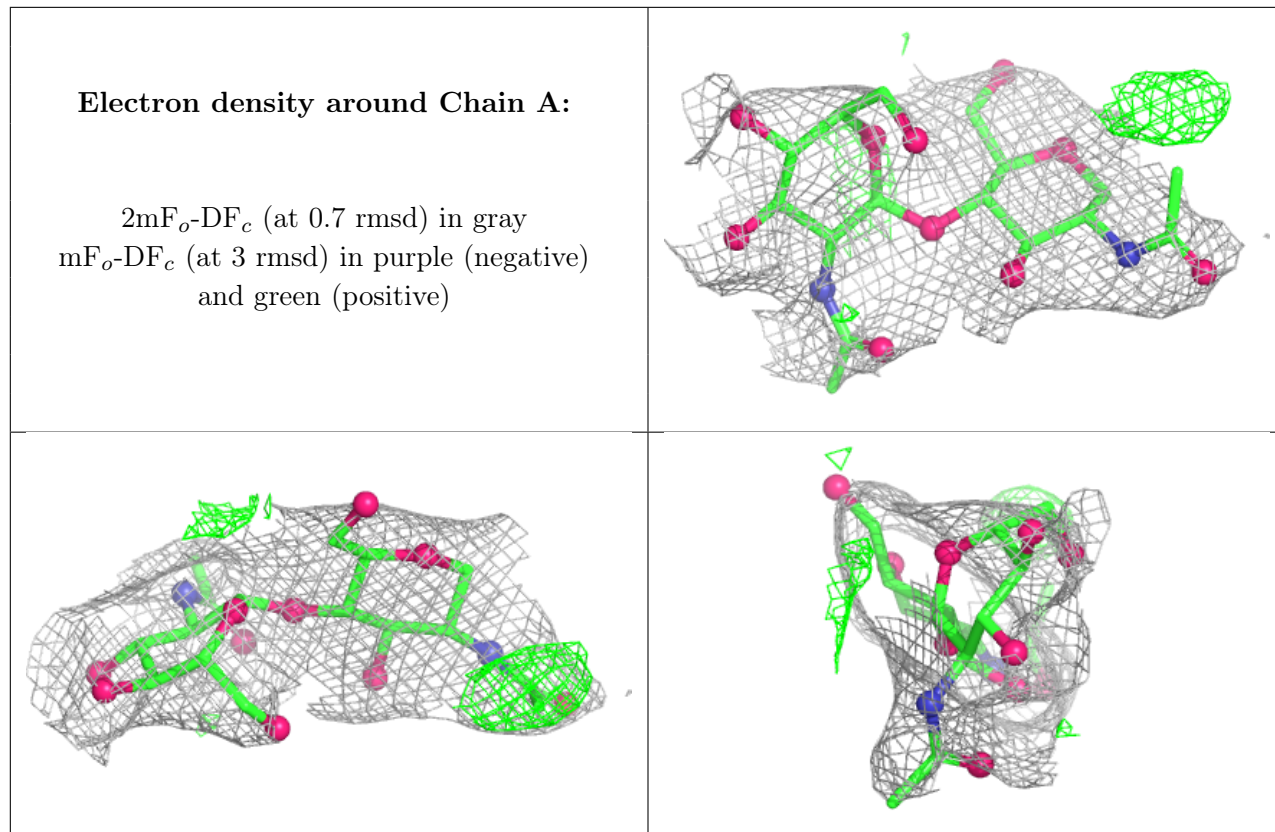
6.3 Carbohydrates [i](#)

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	A	1	14/15	-	-	96,106,117,120	0
4	NAG	A	2	14/15	-	-	118,134,143,147	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. 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, 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
5	NAG	L	303	14/15	0.71	0.12	99,111,122,125	0
6	GOL	C	301	6/6	0.92	0.08	78,87,91,91	0
6	GOL	C	302	6/6	0.95	0.15	36,39,41,49	6

6.5 Other polymers [i](#)

There are no such residues in this entry.