



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:39 PM UTC

PDB ID : 8CR8 / pdb_00008cr8
Title : human Interleukin-23
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Deposited on : 2023-03-08
Resolution : 2.00 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
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

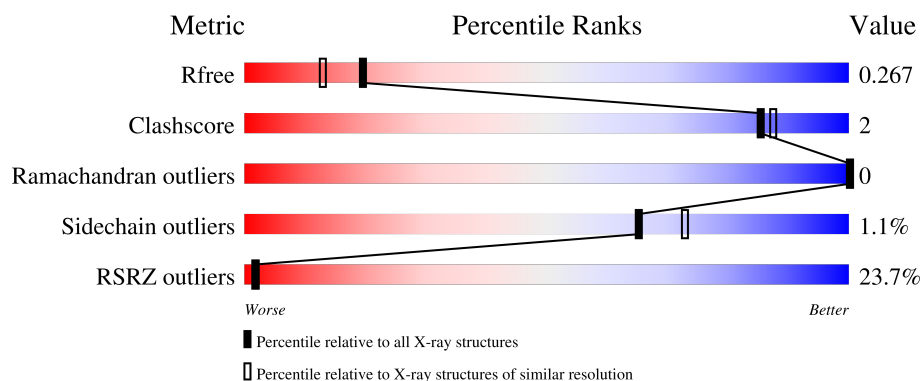
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	325	
2	B	196	
3	C	6	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3595 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-12 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	0	3	0
			2370	1504	379	475	12			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	MET	-	initiating methionine	UNP P29460
A	5	GLY	-	expression tag	UNP P29460
A	6	VAL	-	expression tag	UNP P29460
A	7	LYS	-	expression tag	UNP P29460
A	8	VAL	-	expression tag	UNP P29460
A	9	LEU	-	expression tag	UNP P29460
A	10	PHE	-	expression tag	UNP P29460
A	11	ALA	-	expression tag	UNP P29460
A	12	LEU	-	expression tag	UNP P29460
A	13	ILE	-	expression tag	UNP P29460
A	14	CYS	-	expression tag	UNP P29460
A	15	ILE	-	expression tag	UNP P29460
A	16	ALA	-	expression tag	UNP P29460
A	17	VAL	-	expression tag	UNP P29460
A	18	ALA	-	expression tag	UNP P29460
A	19	GLU	-	expression tag	UNP P29460
A	20	ALA	-	expression tag	UNP P29460
A	21	LEU	-	expression tag	UNP P29460
A	22	GLU	-	expression tag	UNP P29460
A	303	ASP	ASN	engineered mutation	UNP P29460

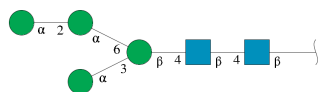
- Molecule 2 is a protein called Interleukin-23 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	138	Total	C	N	O	S	0	1	0
			1068	681	190	192	5			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP Q9NPF7
B	1	GLY	-	expression tag	UNP Q9NPF7
B	2	TRP	-	expression tag	UNP Q9NPF7
B	3	SER	-	expression tag	UNP Q9NPF7
B	4	CYS	-	expression tag	UNP Q9NPF7
B	5	ILE	-	expression tag	UNP Q9NPF7
B	6	ILE	-	expression tag	UNP Q9NPF7
B	7	LEU	-	expression tag	UNP Q9NPF7
B	8	PHE	-	expression tag	UNP Q9NPF7
B	9	LEU	-	expression tag	UNP Q9NPF7
B	10	VAL	-	expression tag	UNP Q9NPF7
B	11	ALA	-	expression tag	UNP Q9NPF7
B	12	THR	-	expression tag	UNP Q9NPF7
B	13	ALA	-	expression tag	UNP Q9NPF7
B	14	THR	-	expression tag	UNP Q9NPF7
B	15	GLY	-	expression tag	UNP Q9NPF7
B	16	VAL	-	expression tag	UNP Q9NPF7
B	17	HIS	-	expression tag	UNP Q9NPF7
B	18	SER	-	expression tag	UNP Q9NPF7
B	19	SER	-	expression tag	UNP Q9NPF7
B	20	ARG	-	expression tag	UNP Q9NPF7
B	21	ASN	-	expression tag	UNP Q9NPF7
B	190	HIS	-	expression tag	UNP Q9NPF7
B	191	HIS	-	expression tag	UNP Q9NPF7
B	192	HIS	-	expression tag	UNP Q9NPF7
B	193	HIS	-	expression tag	UNP Q9NPF7
B	194	HIS	-	expression tag	UNP Q9NPF7
B	195	HIS	-	expression tag	UNP Q9NPF7

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(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)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 4 is TERBIUM(III) ION (CCD ID: TB) (formula: Tb).

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

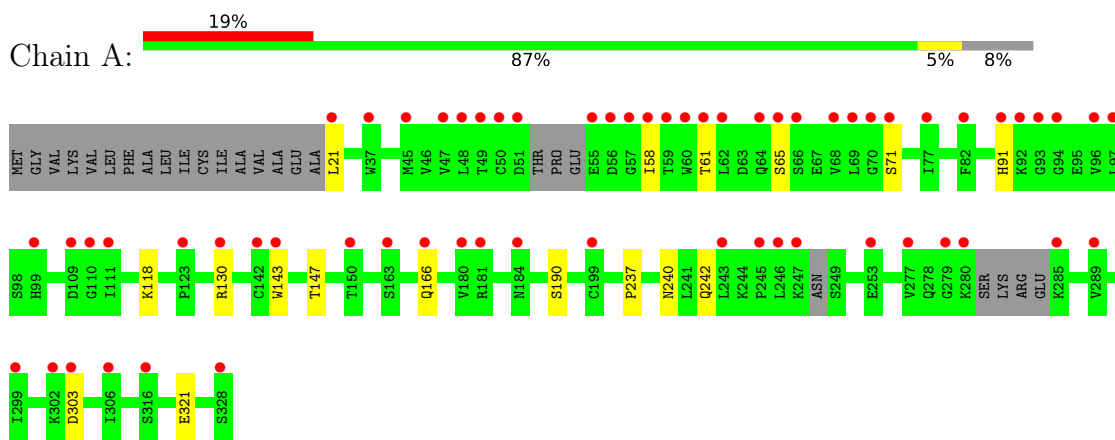
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	73	Total 73	O 73	0	0
5	B	11	Total 11	O 11	0	0

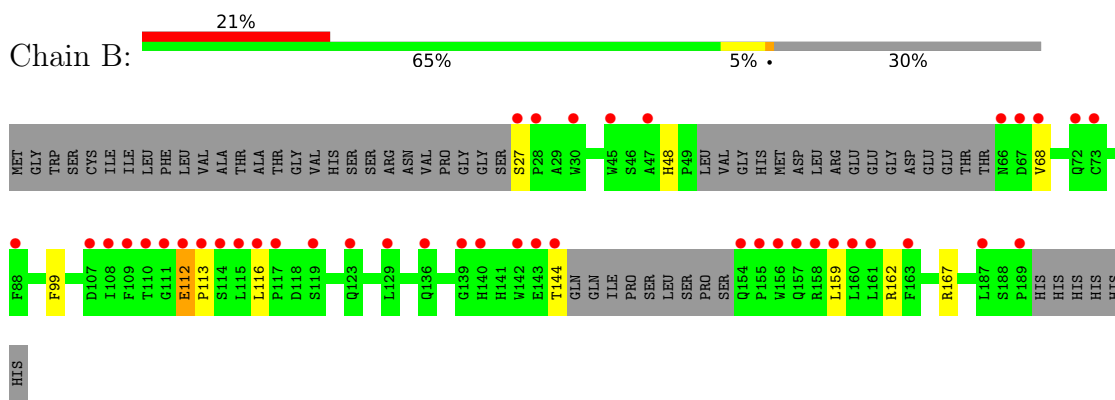
3 Residue-property plots [i](#)

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: Interleukin-12 subunit beta



- Molecule 2: Interleukin-23 subunit alpha



- Molecule 3: alpha-D-mannopyranose-(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)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.75Å 59.84Å 69.99Å 90.00° 98.06° 90.00°	Depositor
Resolution (Å)	69.30 – 2.00 69.30 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.3 (69.30-2.00) 94.3 (69.30-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.235 , 0.256 0.242 , 0.267	Depositor DCC
R_{free} test set	2014 reflections (5.35%)	wwPDB-VP
Wilson B-factor (Å ²)	47.0	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3595	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, NAG, TB, BMA

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	0.12	0/2430	0.28	0/3305
2	B	0.12	0/1095	0.25	0/1490
All	All	0.12	0/3525	0.27	0/4795

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

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	2370	0	2220	10	0
2	B	1068	0	1038	5	0
3	C	72	0	61	1	0
4	A	1	0	0	0	0
5	A	73	0	0	1	0
5	B	11	0	0	0	0
All	All	3595	0	3319	15	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 (15) 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:A:240:ASN:OD1	1:A:242:GLN:NE2	2.33	0.62
1:A:61:THR:OG1	1:A:65:SER:O	2.16	0.61
2:B:48:HIS:CD2	2:B:167:ARG:HG2	2.44	0.52
2:B:116:LEU:HD12	2:B:116:LEU:H	1.75	0.51
2:B:159:LEU:HD12	2:B:162:ARG:HD2	1.93	0.50
1:A:58:ILE:HA	1:A:91:HIS:O	2.10	0.50
1:A:21:LEU:N	3:C:3:BMA:HO2	2.10	0.49
1:A:143[A]:TRP:CD1	1:A:190:SER:HB3	2.47	0.48
1:A:166:GLN:NE2	5:A:507:HOH:O	2.46	0.48
1:A:58:ILE:O	1:A:71:SER:HA	2.16	0.46
1:A:130:ARG:HB3	1:A:143[B]:TRP:CE2	2.52	0.45
2:B:112:GLU:HA	2:B:113:PRO:C	2.42	0.45
2:B:68:VAL:HG13	2:B:99:PHE:CE1	2.54	0.42
1:A:237:PRO:HG3	1:A:321:GLU:HB2	2.00	0.42
1:A:118:LYS:HD2	1:A:147:THR:HG23	2.02	0.41

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	295/325 (91%)	287 (97%)	8 (3%)	0	100	100
2	B	133/196 (68%)	126 (95%)	7 (5%)	0	100	100
All	All	428/521 (82%)	413 (96%)	15 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	261/291 (90%)	260 (100%)	1 (0%)	84	89
2	B	114/167 (68%)	111 (97%)	3 (3%)	40	44
All	All	375/458 (82%)	371 (99%)	4 (1%)	65	73

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	303	ASP
2	B	27	SER
2	B	112	GLU
2	B	144	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	166	GLN
1	A	216	HIS
1	A	240	ASN
1	A	242	GLN
1	A	278	GLN
1	A	311	GLN
2	B	48	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates

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		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	NAG	C	1	1,3	14,14,15	0.39	0	17,19,21	0.40	0
3	NAG	C	2	3	14,14,15	0.25	0	17,19,21	0.50	0
3	BMA	C	3	3	11,11,12	0.58	0	15,15,17	0.86	0
3	MAN	C	4	3	11,11,12	1.05	1 (9%)	15,15,17	1.83	2 (13%)
3	MAN	C	5	3	11,11,12	1.07	1 (9%)	15,15,17	1.03	2 (13%)
3	MAN	C	6	3	11,11,12	0.91	1 (9%)	15,15,17	0.75	1 (6%)

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	6	MAN	O5-C1	-2.42	1.39	1.43
3	C	4	MAN	O5-C5	2.14	1.47	1.43
3	C	5	MAN	C1-C2	2.09	1.57	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4	MAN	C1-O5-C5	5.92	120.12	112.19
3	C	4	MAN	C1-C2-C3	3.18	114.28	109.64
3	C	5	MAN	O2-C2-C3	-2.37	105.23	110.15
3	C	5	MAN	C1-O5-C5	2.19	115.12	112.19
3	C	6	MAN	O2-C2-C3	-2.10	105.81	110.15

There are no chirality outliers.

There are no torsion outliers.

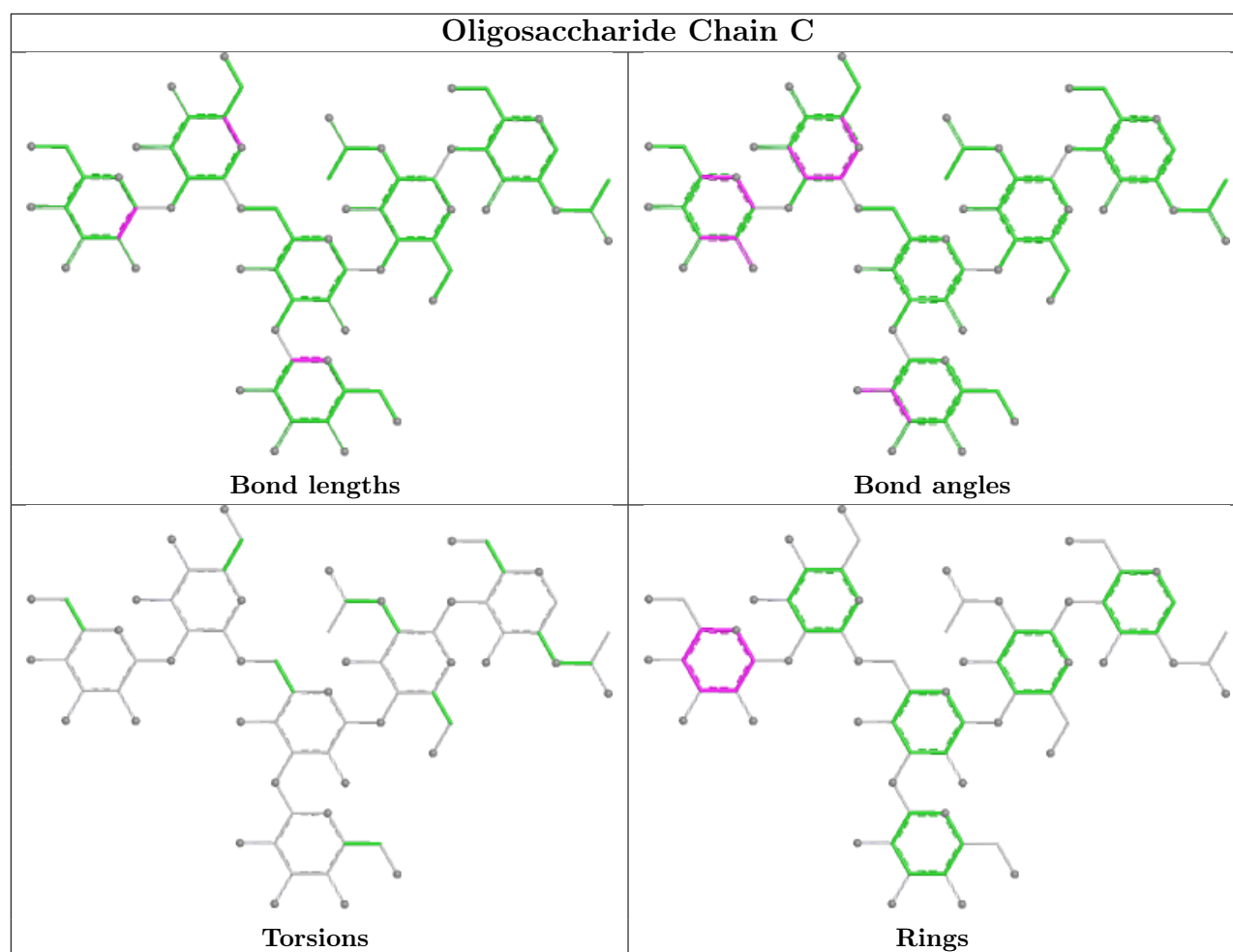
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	5	MAN	C1-C2-C3-C4-C5-O5

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	3	BMA	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	300/325 (92%)	1.12	62 (20%)	2 2	21, 58, 118, 154	3 (1%)
2	B	138/196 (70%)	1.37	42 (30%)	1 1	25, 61, 116, 144	1 (0%)
All	All	438/521 (84%)	1.20	104 (23%)	2 2	21, 60, 116, 154	4 (0%)

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	159	LEU	6.1
1	A	91	HIS	5.6
1	A	97	LEU	5.2
2	B	116	LEU	5.0
2	B	45	TRP	4.9
1	A	50	CYS	4.8
1	A	57	GLY	4.7
1	A	96	VAL	4.6
1	A	59	THR	4.5
1	A	58	ILE	4.5
1	A	328	SER	4.2
2	B	119	SER	4.2
2	B	160	LEU	4.1
2	B	112	GLU	4.0
2	B	144	THR	3.9
1	A	246	LEU	3.7
1	A	77	ILE	3.5
2	B	113	PRO	3.5
1	A	99	HIS	3.5
2	B	156	TRP	3.4
2	B	88	PHE	3.4
2	B	189	PRO	3.4
1	A	109	ASP	3.3
2	B	155	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	247	LYS	3.2
1	A	143[A]	TRP	3.2
1	A	199	CYS	3.2
1	A	111	ILE	3.2
1	A	51	ASP	3.2
1	A	181	ARG	3.1
2	B	68	VAL	3.0
2	B	129	LEU	3.0
2	B	142	TRP	3.0
2	B	187	LEU	3.0
1	A	49	THR	3.0
1	A	37	TRP	3.0
1	A	60	TRP	3.0
2	B	111	GLY	2.9
1	A	280	LYS	2.9
1	A	69	LEU	2.9
2	B	67	ASP	2.8
1	A	66	SER	2.8
1	A	82	PHE	2.8
1	A	253	GLU	2.8
1	A	302	LYS	2.8
2	B	28	PRO	2.8
1	A	45	MET	2.7
1	A	70	GLY	2.7
2	B	107	ASP	2.7
2	B	154	GLN	2.6
2	B	143	GLU	2.6
1	A	21	LEU	2.6
2	B	158	ARG	2.6
2	B	140	HIS	2.6
1	A	123	PRO	2.6
2	B	136[A]	GLN	2.5
1	A	93	GLY	2.5
1	A	92	LYS	2.5
1	A	303	ASP	2.5
2	B	110	THR	2.5
2	B	115	LEU	2.5
1	A	279	GLY	2.5
1	A	130	ARG	2.5
1	A	68	VAL	2.4
2	B	161	LEU	2.4
1	A	94	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	110	GLY	2.4
2	B	139	GLY	2.4
1	A	166	GLN	2.4
1	A	180	VAL	2.4
1	A	289	VAL	2.4
2	B	123	GLN	2.4
2	B	66	ASN	2.3
1	A	316	SER	2.3
1	A	61	THR	2.3
1	A	48	LEU	2.3
1	A	71	SER	2.3
1	A	277	VAL	2.3
1	A	285	LYS	2.3
1	A	306	ILE	2.2
2	B	108	ILE	2.2
1	A	245	PRO	2.2
1	A	62	LEU	2.2
1	A	55	GLU	2.2
1	A	56	ASP	2.2
2	B	47	ALA	2.2
2	B	114	SER	2.2
1	A	150	THR	2.2
2	B	163	PHE	2.2
2	B	73	CYS	2.2
1	A	163	SER	2.2
2	B	117	PRO	2.1
1	A	299	ILE	2.1
1	A	64	GLN	2.1
1	A	142	CYS	2.1
1	A	184	ASN	2.1
2	B	157	GLN	2.1
2	B	109	PHE	2.1
2	B	30	TRP	2.1
2	B	27	SER	2.1
1	A	47	VAL	2.0
1	A	65	SER	2.0
1	A	243	LEU	2.0
2	B	72	GLN	2.0

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

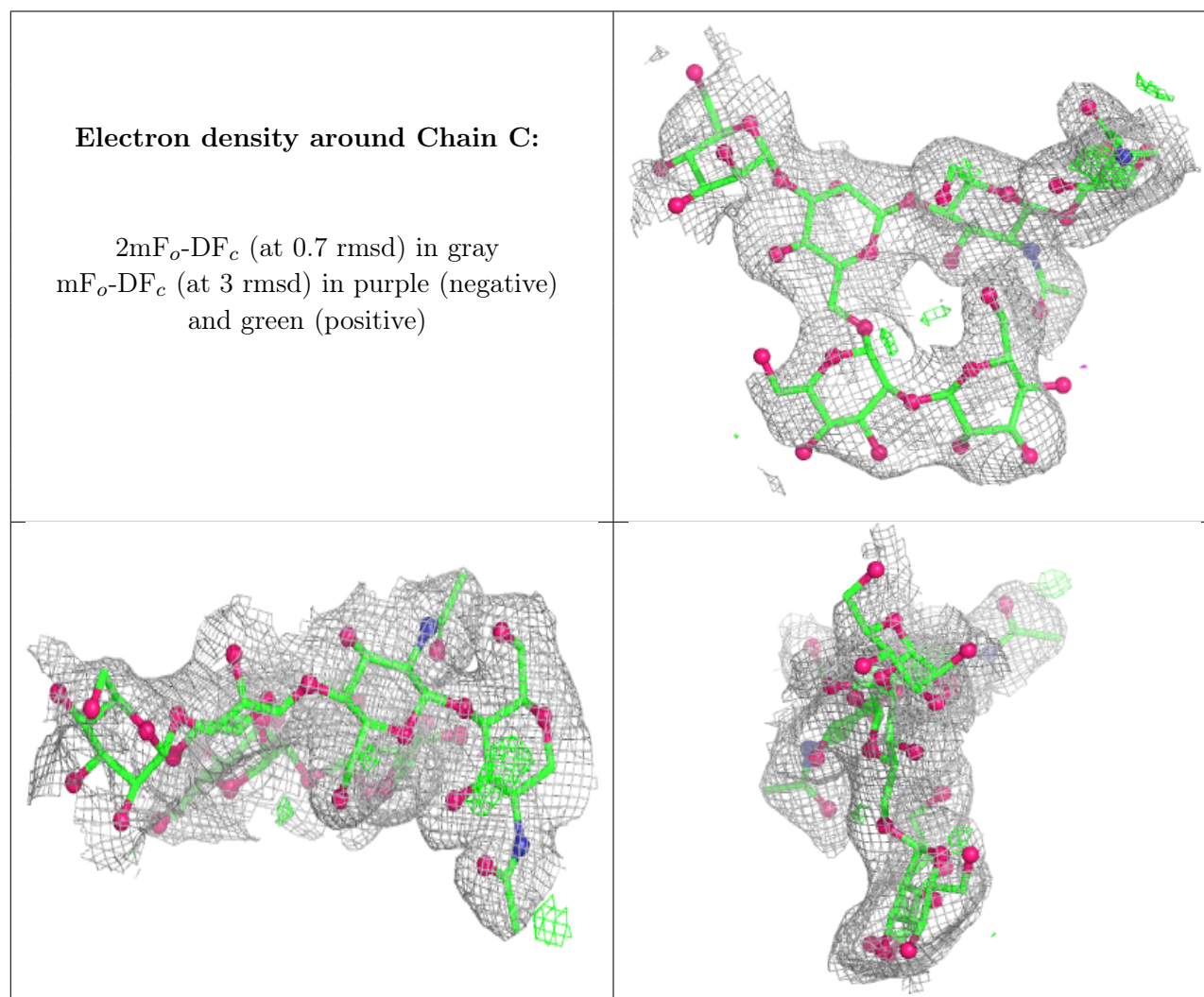
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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
3	MAN	C	5	11/12	0.58	0.18	99,100,103,103	0
3	MAN	C	4	11/12	0.64	0.13	109,111,116,117	0
3	MAN	C	6	11/12	0.67	0.13	113,117,119,119	0
3	NAG	C	1	14/15	0.90	0.12	48,49,51,52	0
3	BMA	C	3	11/12	0.91	0.10	69,72,76,77	0
3	NAG	C	2	14/15	0.91	0.11	51,54,55,56	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, 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
4	TB	A	401	1/1	0.97	0.06	71,71,71,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.