



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:46 AM UTC

PDB ID : 8CR5 / pdb_00008cr5
Title : Murine Interleukin-12 receptor beta 1 domain 1 in complex with murine Interleukin-12 beta.
Authors : Merceron, R.; Bloch, Y.; Felix, J.; Savvides, S.N.
Deposited on : 2023-03-07
Resolution : 2.15 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

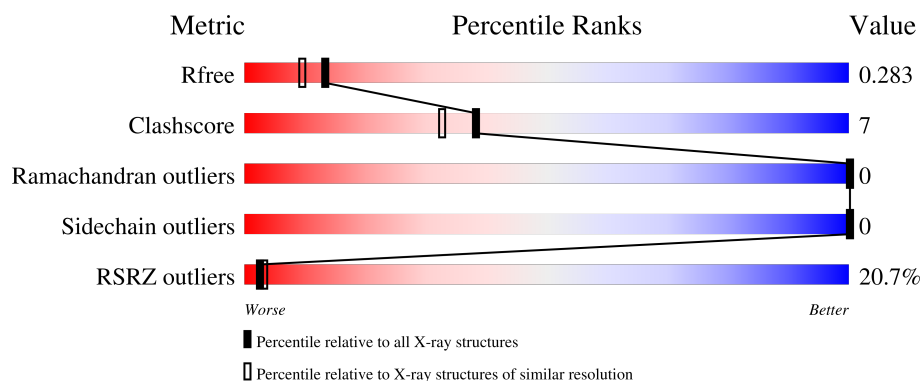
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	A	344	21% 70% 15% 15%
2	B	265	5% 39% • 57%
3	C	4	75% 25%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3363 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
			Total	C	N	O	S			
1	A	292	2267	1432	371	447	17	0	2	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197	SER	CYS	engineered mutation	UNP P43432
A	336	GLY	-	expression tag	UNP P43432
A	337	THR	-	expression tag	UNP P43432
A	338	LYS	-	expression tag	UNP P43432
A	339	HIS	-	expression tag	UNP P43432
A	340	HIS	-	expression tag	UNP P43432
A	341	HIS	-	expression tag	UNP P43432
A	342	HIS	-	expression tag	UNP P43432
A	343	HIS	-	expression tag	UNP P43432
A	344	HIS	-	expression tag	UNP P43432

- Molecule 2 is a protein called Interleukin-12 receptor subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	114	919	583	161	169	6	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	MET	-	initiating methionine	UNP Q60837
B	4	GLY	-	expression tag	UNP Q60837
B	5	VAL	-	expression tag	UNP Q60837
B	6	LYS	-	expression tag	UNP Q60837
B	7	VAL	-	expression tag	UNP Q60837
B	8	LEU	-	expression tag	UNP Q60837

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Chain	Residue	Modelled	Actual	Comment	Reference
B	9	PHE	-	expression tag	UNP Q60837
B	10	ALA	-	expression tag	UNP Q60837
B	11	LEU	-	expression tag	UNP Q60837
B	12	ILE	-	expression tag	UNP Q60837
B	13	CYS	-	expression tag	UNP Q60837
B	14	ILE	-	expression tag	UNP Q60837
B	15	ALA	-	expression tag	UNP Q60837
B	16	VAL	-	expression tag	UNP Q60837
B	17	ALA	-	expression tag	UNP Q60837
B	18	GLU	-	expression tag	UNP Q60837
B	19	ALA	-	expression tag	UNP Q60837
B	259	GLY	-	expression tag	UNP Q60837
B	260	THR	-	expression tag	UNP Q60837
B	261	LYS	-	expression tag	UNP Q60837
B	262	HIS	-	expression tag	UNP Q60837
B	263	HIS	-	expression tag	UNP Q60837
B	264	HIS	-	expression tag	UNP Q60837
B	265	HIS	-	expression tag	UNP Q60837
B	266	HIS	-	expression tag	UNP Q60837
B	267	HIS	-	expression tag	UNP Q60837

- Molecule 3 is an oligosaccharide called 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	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

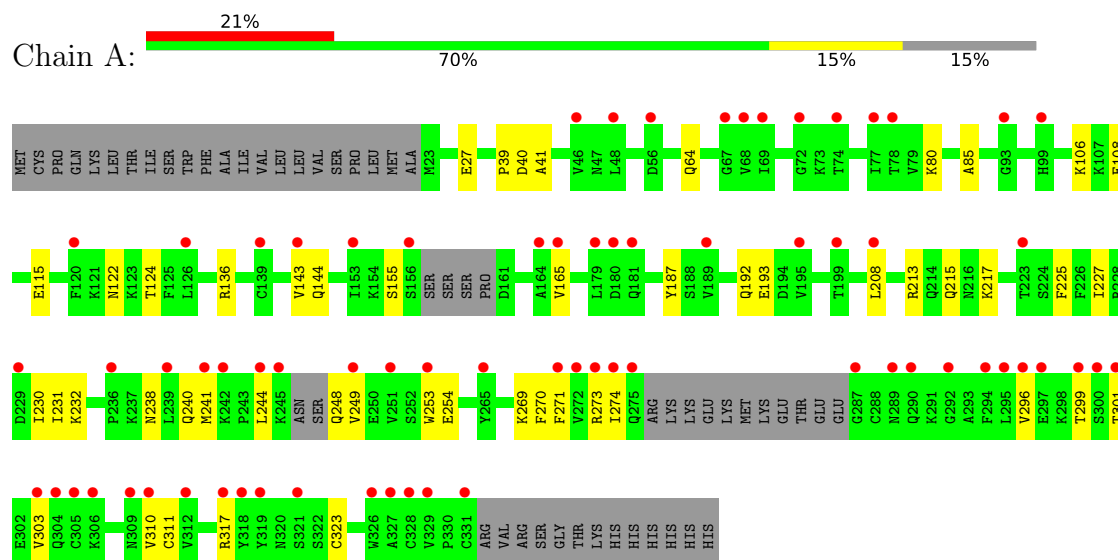
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	73	Total	O	0	0
			73	73		
5	B	40	Total	O	0	0
			40	40		

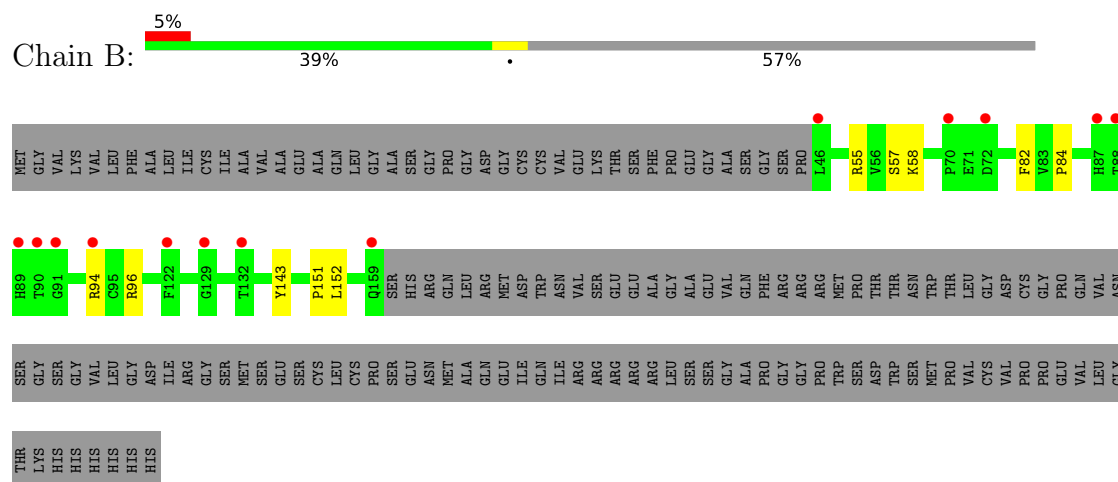
3 Residue-property plots [i](#)

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-12 receptor subunit beta-1



- Molecule 3: 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	29.22Å 165.09Å 51.87Å 90.00° 90.44° 90.00°	Depositor
Resolution (Å)	49.48 – 2.15 49.48 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.48-2.15) 99.4 (49.48-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.241 , 0.282 0.242 , 0.283	Depositor DCC
R_{free} test set	1325 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.755	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.063 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3363	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.75% 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: BMA, NAG, 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	A	0.19	0/2319	0.40	0/3156
2	B	0.15	0/949	0.34	0/1294
All	All	0.18	0/3268	0.38	0/4450

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	2267	0	2084	36	0
2	B	919	0	853	9	0
3	C	50	0	43	0	0
4	B	14	0	13	0	0
5	A	73	0	0	6	0
5	B	40	0	0	1	0
All	All	3363	0	2993	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 7.

All (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)
1:A:215:GLN:OE1	5:A:401:HOH:O	2.11	0.69
1:A:165:VAL:HG12	1:A:193:GLU:HA	1.78	0.65
1:A:108:GLU:OE1	5:A:402:HOH:O	2.14	0.65
1:A:269:LYS:HE2	1:A:317:ARG:HA	1.80	0.62
1:A:238:ASN:ND2	1:A:254:GLU:OE2	2.32	0.62
2:B:94:ARG:HH21	2:B:96:ARG:HH21	1.51	0.58
1:A:136:ARG:HG3	1:A:192:GLN:HE22	1.69	0.58
1:A:249:VAL:N	1:A:303:VAL:O	2.35	0.57
2:B:55:ARG:O	5:B:401:HOH:O	2.18	0.57
2:B:151:PRO:HB2	2:B:152:LEU:HD22	1.89	0.54
1:A:40:ASP:O	5:A:403:HOH:O	2.19	0.53
1:A:27:GLU:OE2	1:A:213[B]:ARG:NH2	2.42	0.51
2:B:94:ARG:HE	2:B:96:ARG:NH2	2.09	0.51
1:A:232:LYS:HG3	1:A:323:CYS:O	2.12	0.50
1:A:270:PHE:C	1:A:271:PHE:HD1	2.19	0.49
1:A:238:ASN:HB3	1:A:240:GLN:HE22	1.76	0.49
1:A:238:ASN:O	1:A:253:TRP:HA	2.13	0.49
1:A:273:ARG:O	1:A:311:CYS:N	2.33	0.49
1:A:115:GLU:O	5:A:405:HOH:O	2.20	0.48
1:A:64:GLN:NE2	1:A:85:ALA:O	2.45	0.48
1:A:144:GLN:NE2	5:A:417:HOH:O	2.34	0.48
1:A:165:VAL:HG21	1:A:208:LEU:HD21	1.96	0.47
1:A:136:ARG:HG3	1:A:192:GLN:NE2	2.29	0.47
1:A:269:LYS:CE	1:A:317:ARG:HA	2.44	0.46
1:A:227:ILE:O	1:A:231:ILE:HG12	2.16	0.46
1:A:39:PRO:HD3	2:B:143:TYR:CZ	2.52	0.44
1:A:106:LYS:HE2	1:A:217:LYS:HE3	1.99	0.44
1:A:155:SER:HB3	1:A:165:VAL:HG22	1.98	0.44
2:B:94:ARG:HE	2:B:96:ARG:HH22	1.64	0.44
1:A:244:LEU:N	1:A:248:GLN:O	2.51	0.43
1:A:122:ASN:ND2	1:A:124:THR:OG1	2.51	0.43
2:B:55:ARG:HG2	2:B:57:SER:O	2.19	0.43
1:A:115:GLU:OE2	2:B:58:LYS:HB3	2.19	0.43
1:A:225:PHE:CE2	1:A:230:ILE:HD13	2.53	0.43
1:A:143:VAL:HG22	1:A:187:TYR:HE1	1.83	0.42
1:A:296:VAL:HG11	1:A:301:THR:OG1	2.20	0.42
1:A:241:MET:HE3	1:A:241:MET:HB2	1.91	0.42
1:A:208:LEU:HD12	1:A:225:PHE:HE1	1.84	0.42
1:A:41:ALA:O	1:A:80:LYS:NZ	2.51	0.41
1:A:253:TRP:CE2	1:A:299:THR:HA	2.56	0.41
2:B:82:PHE:CE1	2:B:84:PRO:HG3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:ILE:HA	1:A:310:VAL:HA	2.02	0.40
1:A:64:GLN:OE1	5:A:406:HOH:O	2.22	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	Percentiles	
1	A	286/344 (83%)	273 (96%)	13 (4%)	0	100	100
2	B	112/265 (42%)	110 (98%)	2 (2%)	0	100	100
All	All	398/609 (65%)	383 (96%)	15 (4%)	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	244/315 (78%)	244 (100%)	0	100	100
2	B	102/230 (44%)	102 (100%)	0	100	100
All	All	346/545 (64%)	346 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	ASN
1	A	144	GLN
1	A	152	ASN
1	A	192	GLN

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 ⓘ

4 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	3,1	14,14,15	0.56	0	17,19,21	0.45	0
3	NAG	C	2	3	14,14,15	0.22	0	17,19,21	0.42	0
3	BMA	C	3	3	11,11,12	0.45	0	15,15,17	0.71	0
3	MAN	C	4	3	11,11,12	0.74	0	15,15,17	0.91	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	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	C	3	3	-	2/2/19/22	0/1/1/1
3	MAN	C	4	3	-	2/2/19/22	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(°)
3	C	4	MAN	O2-C2-C3	-2.15	105.70	110.15

There are no chirality outliers.

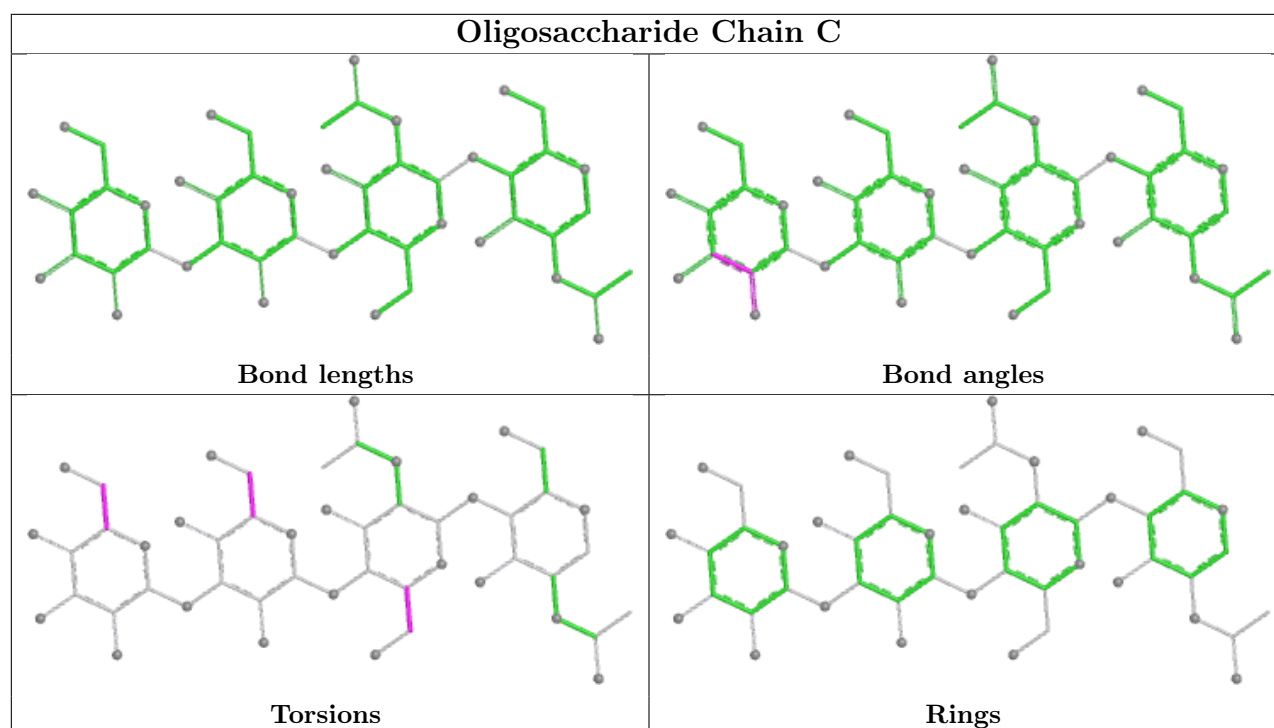
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	4	MAN	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
3	C	4	MAN	C4-C5-C6-O6
3	C	3	BMA	C4-C5-C6-O6
3	C	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](#)

1 ligand is 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	301	2	14,14,15	0.33	0	17,19,21	0.48	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	301	2	-	0/6/23/26	0/1/1/1

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

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	292/344 (84%)	1.41	71 (24%) 2 2	19, 63, 151, 220	2 (0%)
2	B	114/265 (43%)	0.82	13 (11%) 10 11	28, 43, 111, 134	0
All	All	406/609 (66%)	1.24	84 (20%) 2 3	19, 57, 139, 220	2 (0%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	310	VAL	5.3
1	A	195	VAL	4.2
2	B	88	THR	3.9
1	A	180	ASP	3.9
1	A	179	LEU	3.6
1	A	275	GLN	3.6
1	A	289	ASN	3.5
2	B	87	HIS	3.5
1	A	244	LEU	3.4
1	A	296	VAL	3.4
2	B	91	GLY	3.4
1	A	48	LEU	3.3
1	A	319	TYR	3.3
1	A	295	LEU	3.3
1	A	303	VAL	3.3
1	A	251	VAL	3.2
1	A	306	LYS	3.2
1	A	272	VAL	3.1
1	A	239	LEU	3.1
1	A	305	CYS	3.1
1	A	274	ILE	3.1
1	A	236	PRO	3.1
1	A	99	HIS	3.1
1	A	327	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	329	VAL	3.0
1	A	153	ILE	3.0
1	A	301	THR	2.9
1	A	290	GLN	2.9
2	B	70	PRO	2.9
1	A	326	TRP	2.9
1	A	46	VAL	2.8
1	A	139	CYS	2.8
2	B	89	HIS	2.8
1	A	294	PHE	2.8
1	A	164	ALA	2.8
1	A	253	TRP	2.7
1	A	271	PHE	2.7
1	A	312	VAL	2.7
2	B	72	ASP	2.7
1	A	78	THR	2.6
1	A	299	THR	2.6
1	A	208	LEU	2.6
1	A	318	TYR	2.6
1	A	292	GLY	2.6
1	A	273	ARG	2.6
1	A	56	ASP	2.5
1	A	229	ASP	2.5
1	A	241	MET	2.5
1	A	68	VAL	2.5
1	A	242	LYS	2.5
1	A	304	GLN	2.5
1	A	120	PHE	2.5
1	A	165	VAL	2.4
2	B	46	LEU	2.4
1	A	156	SER	2.4
1	A	328	CYS	2.4
1	A	321	SER	2.4
1	A	287	GLY	2.3
1	A	265	TYR	2.3
1	A	126	LEU	2.3
1	A	223	THR	2.3
1	A	69	ILE	2.3
1	A	331	CYS	2.2
2	B	94	ARG	2.2
2	B	132	THR	2.2
1	A	143	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	93	GLY	2.2
1	A	245	LYS	2.2
2	B	129	GLY	2.1
2	B	159	GLN	2.1
2	B	90	THR	2.1
1	A	77	ILE	2.1
1	A	317	ARG	2.1
2	B	122	PHE	2.1
1	A	300	SER	2.1
1	A	309	ASN	2.1
1	A	181	GLN	2.1
1	A	189	VAL	2.1
1	A	297	GLU	2.0
1	A	74	THR	2.0
1	A	199	THR	2.0
1	A	67	GLY	2.0
1	A	249	VAL	2.0
1	A	72	GLY	2.0

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

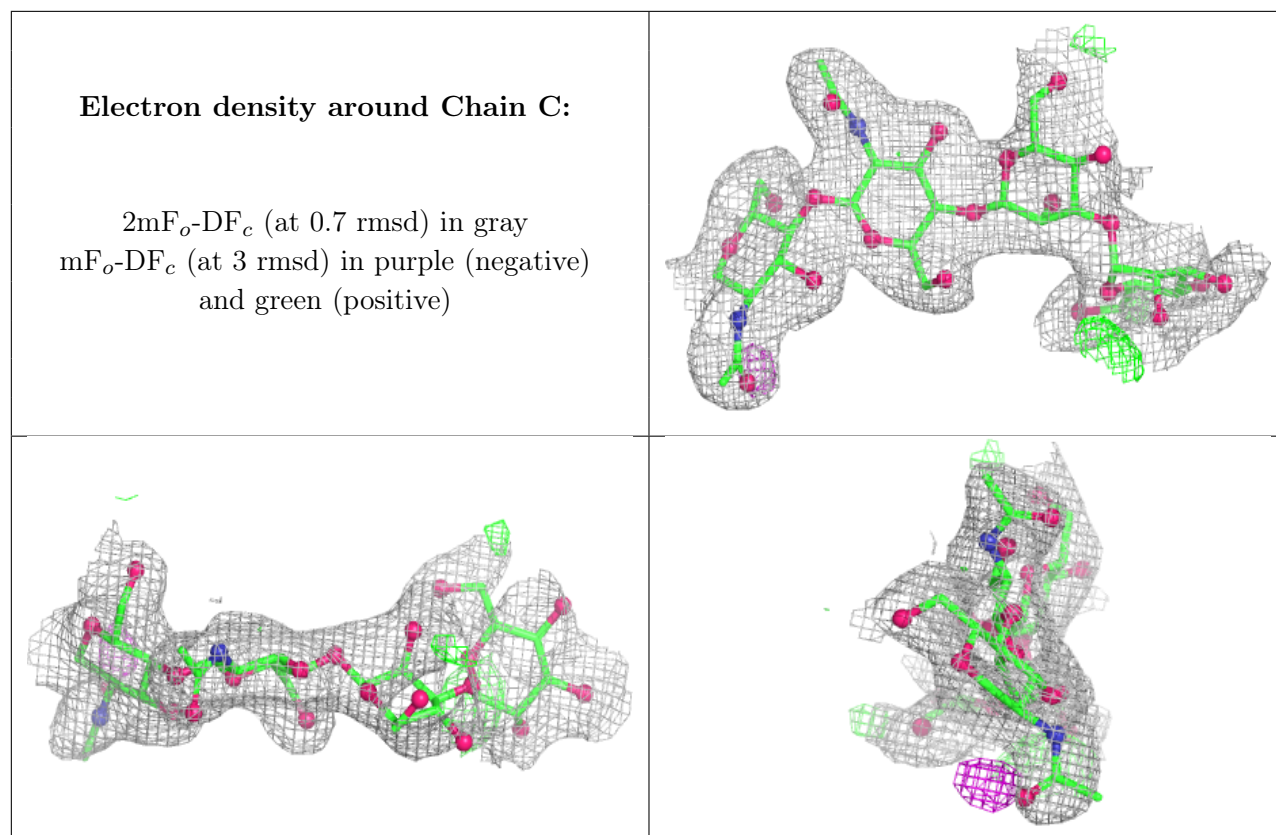
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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
3	MAN	C	4	11/12	0.49	0.15	64,93,100,103	0
3	BMA	C	3	11/12	0.81	0.11	56,74,86,90	0
3	NAG	C	1	14/15	0.89	0.12	36,42,57,60	0
3	NAG	C	2	14/15	0.91	0.10	39,49,58,63	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	NAG	B	301	14/15	0.91	0.09	29,35,42,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.