



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:21 AM UTC

PDB ID : 6S0B / pdb_00006s0b
Title : Crystal Structure of Properdin in complex with the CTC domain of C3/C3b
Authors : van den Bos, R.M.; Pearce, N.M.; Gros, P.
Deposited on : 2019-06-14
Resolution : 2.31 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

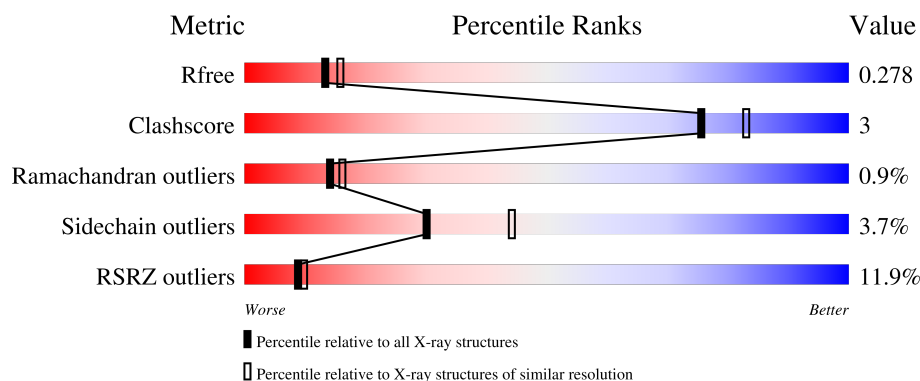
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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	225	
2	B	110	
3	C	149	
4	D	2	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3645 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 Properdin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1611	995	302	292	22			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	254	GLY	-	expression tag	UNP P27918
A	255	SER	-	expression tag	UNP P27918
A	470	ALA	-	expression tag	UNP P27918
A	471	ALA	-	expression tag	UNP P27918
A	472	ALA	-	expression tag	UNP P27918
A	473	HIS	-	expression tag	UNP P27918
A	474	HIS	-	expression tag	UNP P27918
A	475	HIS	-	expression tag	UNP P27918
A	476	HIS	-	expression tag	UNP P27918
A	477	HIS	-	expression tag	UNP P27918
A	478	HIS	-	expression tag	UNP P27918

- Molecule 2 is a protein called Properdin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	103	Total	C	N	O	S	0	4	0
			774	477	137	148	12			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	133	ALA	-	expression tag	UNP P27918
B	134	ALA	-	expression tag	UNP P27918
B	135	ALA	-	expression tag	UNP P27918

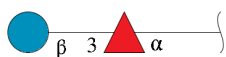
- Molecule 3 is a protein called Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	139	Total	C	N	O	S	0	0	0
			1067	673	175	210	9			

There are 2 discrepancies between the modelled and reference sequences:

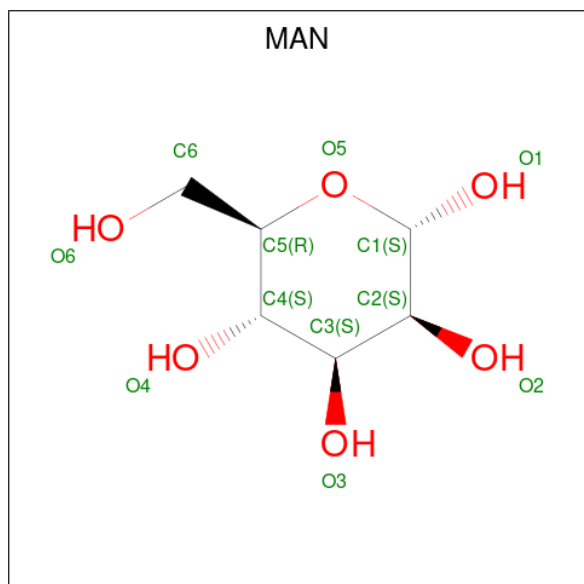
Chain	Residue	Modelled	Actual	Comment	Reference
C	1515	GLY	-	expression tag	UNP P01024
C	1516	SER	-	expression tag	UNP P01024

- Molecule 4 is an oligosaccharide called beta-D-glucopyranose-(1-3)-alpha-L-fucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	D	2	Total	C	O	0	0	0
			21	12	9			

- Molecule 5 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



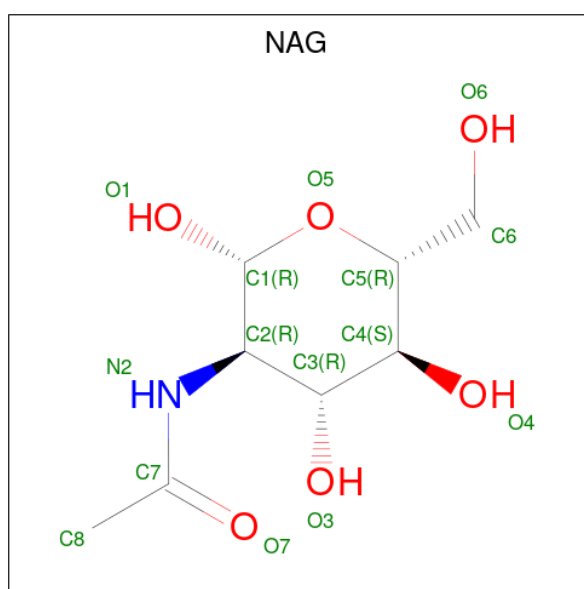
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		
5	A	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		
5	A	1	Total	C	O	0	0
			11	6	5		
5	A	1	Total	C	O	0	0
			11	6	5		
5	A	1	Total	C	O	0	0
			11	6	5		
5	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	33	Total	O	0	0
			33	33		
7	B	21	Total	O	0	0
			21	21		

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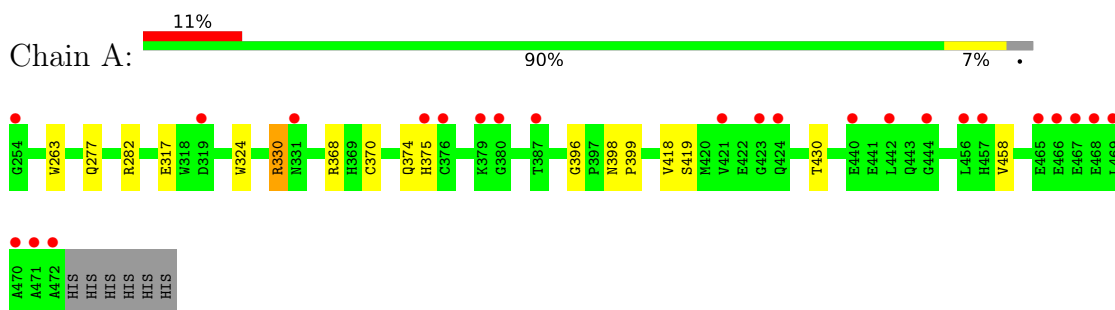
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	16	Total	O	0	0
			16	16		

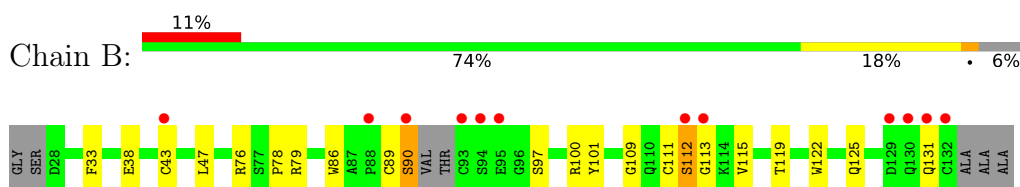
3 Residue-property plots [i](#)

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.

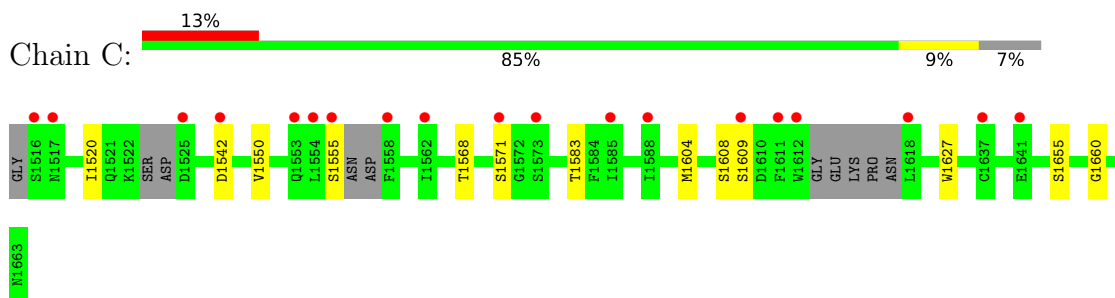
- Molecule 1: Properdin



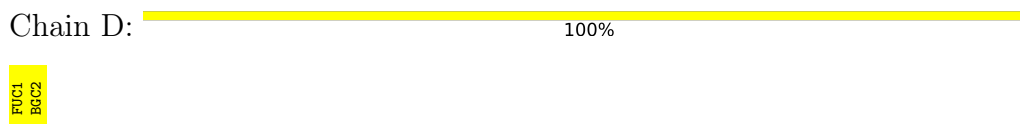
- Molecule 2: Properdin



- Molecule 3: Complement C3



- Molecule 4: beta-D-glucopyranose-(1-3)-alpha-L-fucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.47Å 71.50Å 134.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.96 – 2.31 48.96 – 2.31	Depositor EDS
% Data completeness (in resolution range)	67.9 (48.96-2.31) 68.6 (48.96-2.31)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.61 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.230 , 0.277 0.233 , 0.278	Depositor DCC
R_{free} test set	1069 reflections (3.43%)	wwPDB-VP
Wilson B-factor (Å ²)	47.2	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3645	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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: NAG, BGC, MAN, 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	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.02	0/1664	1.32	0/2279
2	B	1.01	0/792	1.30	0/1076
3	C	1.00	0/1086	1.39	0/1467
All	All	1.01	0/3542	1.34	0/4822

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	1611	0	1452	8	0
2	B	774	0	685	10	0
3	C	1067	0	958	4	0
4	D	21	0	19	0	0
5	A	77	0	70	0	0
5	B	11	0	10	0	0
6	A	14	0	13	0	0
7	A	33	0	0	0	0
7	B	21	0	0	0	0
7	C	16	0	0	0	0
All	All	3645	0	3207	20	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 3.

All (20) 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:374:GLN:HE21	1:A:375:HIS:CE1	2.05	0.74
1:A:370:CYS:HA	1:A:430:THR:O	2.06	0.55
3:C:1604:MET:HA	3:C:1627:TRP:O	2.10	0.51
1:A:330:ARG:NH2	3:C:1660:GLY:O	2.45	0.50
2:B:76:ARG:HD2	2:B:79:ARG:NH2	2.28	0.49
2:B:89:CYS:O	2:B:90:SER:OG	2.27	0.49
2:B:97:SER:HA	2:B:125:GLN:O	2.14	0.47
1:A:324:TRP:CZ3	1:A:368:ARG:HG2	2.50	0.46
1:A:263:TRP:CZ3	1:A:282:ARG:HG2	2.52	0.45
2:B:101:TYR:HB3	2:B:122:TRP:CZ3	2.53	0.43
1:A:418:VAL:HG22	1:A:419:SER:O	2.19	0.43
2:B:115[B]:VAL:CG1	2:B:119:THR:HB	2.49	0.43
3:C:1568:THR:CG2	3:C:1571:SER:HB3	2.49	0.43
2:B:78:PRO:HG2	2:B:109:GLY:C	2.44	0.43
2:B:33:PHE:CG	2:B:43:CYS:HB3	2.53	0.42
1:A:277:GLN:NE2	2:B:47:LEU:O	2.53	0.42
2:B:111:CYS:O	2:B:113[A]:GLY:N	2.53	0.41
2:B:86:TRP:CE2	2:B:100:ARG:HD3	2.55	0.41
3:C:1568:THR:HG21	3:C:1571:SER:HB3	2.03	0.41
1:A:398:ASN:N	1:A:399:PRO:HD3	2.37	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	217/225 (96%)	211 (97%)	5 (2%)	1 (0%)	24 30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	103/110 (94%)	95 (92%)	5 (5%)	3 (3%)	3	2
3	C	131/149 (88%)	125 (95%)	5 (4%)	1 (1%)	16	19
All	All	451/484 (93%)	431 (96%)	15 (3%)	5 (1%)	14	12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	112[A]	SER
2	B	112[B]	SER
2	B	131	GLN
3	C	1520	ILE
1	A	396	GLY

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	166/191 (87%)	163 (98%)	3 (2%)	51	69
2	B	80/89 (90%)	76 (95%)	4 (5%)	22	32
3	C	110/136 (81%)	103 (94%)	7 (6%)	16	22
All	All	356/416 (86%)	342 (96%)	14 (4%)	30	42

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	317	GLU
1	A	330	ARG
1	A	458	VAL
2	B	38	GLU
2	B	90	SER
2	B	112[A]	SER
2	B	112[B]	SER
3	C	1542	ASP
3	C	1550	VAL

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Mol	Chain	Res	Type
3	C	1555	SER
3	C	1583	THR
3	C	1608	SER
3	C	1609	SER
3	C	1655	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	277	GLN
1	A	365	GLN
1	A	374	GLN
1	A	457	HIS
2	B	98	GLN
2	B	125	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 ⓘ

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	FUC	D	1	4,1	10,10,11	0.58	0	14,14,16	1.12	1 (7%)
4	BGC	D	2	4	11,11,12	0.81	0	15,15,17	1.09	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
4	FUC	D	1	4,1	-	-	0/1/1/1
4	BGC	D	2	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	2	BGC	O6-C6-C5	-2.06	104.33	111.33
4	D	1	FUC	O5-C5-C6	2.04	111.82	107.40

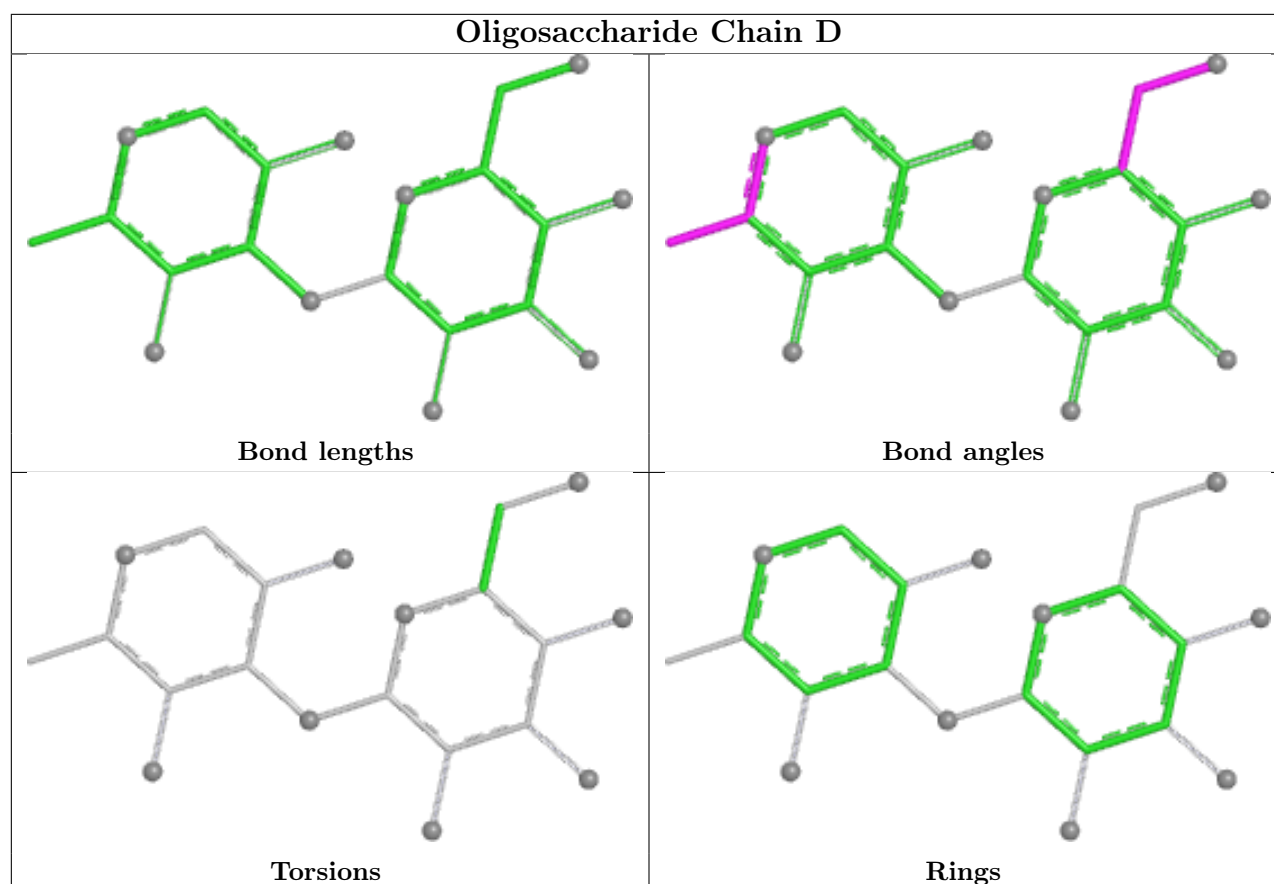
There are no chirality outliers.

There are no torsion outliers.

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](#)

9 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	NAG	A	506	1	14,14,15	0.37	0	17,19,21	0.70	0
5	MAN	A	502	1	11,11,12	0.45	0	15,15,17	1.45	2 (13%)
5	MAN	B	200	2	11,11,12	0.32	0	15,15,17	1.49	2 (13%)
5	MAN	A	507	1	11,11,12	0.25	0	15,15,17	1.98	2 (13%)
5	MAN	A	501	1	11,11,12	0.39	0	15,15,17	1.69	3 (20%)
5	MAN	A	504	1	11,11,12	0.49	0	15,15,17	1.31	1 (6%)
5	MAN	A	505	1	11,11,12	0.43	0	15,15,17	1.93	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MAN	A	508	1	11,11,12	0.79	0	15,15,17	1.77	2 (13%)
5	MAN	A	503	1	11,11,12	0.43	0	15,15,17	1.26	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
6	NAG	A	506	1	-	3/6/23/26	0/1/1/1
5	MAN	A	502	1	-	0/2/19/22	0/1/1/1
5	MAN	B	200	2	-	0/2/19/22	0/1/1/1
5	MAN	A	507	1	-	2/2/19/22	0/1/1/1
5	MAN	A	501	1	-	0/2/19/22	0/1/1/1
5	MAN	A	504	1	-	0/2/19/22	0/1/1/1
5	MAN	A	505	1	-	0/2/19/22	0/1/1/1
5	MAN	A	508	1	-	1/2/19/22	0/1/1/1
5	MAN	A	503	1	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	507	MAN	C1-O5-C5	5.78	119.94	112.19
5	A	508	MAN	C1-O5-C5	4.95	118.82	112.19
5	A	505	MAN	C3-C4-C5	4.78	118.90	110.23
5	A	501	MAN	C1-O5-C5	4.39	118.06	112.19
5	A	502	MAN	C1-O5-C5	3.78	117.25	112.19
5	B	200	MAN	C1-O5-C5	3.41	116.76	112.19
5	A	504	MAN	C1-O5-C5	3.33	116.65	112.19
5	A	508	MAN	C3-C4-C5	3.29	116.20	110.23
5	A	505	MAN	C1-O5-C5	2.97	116.16	112.19
5	B	200	MAN	C3-C4-C5	2.91	115.50	110.23
5	A	502	MAN	O5-C5-C6	2.74	113.00	107.66
5	A	507	MAN	O5-C5-C6	-2.68	102.44	107.66
5	A	503	MAN	C3-C4-C5	2.48	114.73	110.23
5	A	505	MAN	O5-C5-C4	2.26	116.33	110.83
5	A	505	MAN	O4-C4-C3	-2.16	105.28	110.38
5	A	501	MAN	C1-C2-C3	2.05	112.62	109.64
5	A	501	MAN	O4-C4-C3	-2.04	105.56	110.38
5	A	505	MAN	C1-C2-C3	-2.02	106.71	109.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	506	NAG	O5-C5-C6-O6
6	A	506	NAG	C4-C5-C6-O6
5	A	507	MAN	C4-C5-C6-O6
5	A	507	MAN	O5-C5-C6-O6
5	A	508	MAN	O5-C5-C6-O6
6	A	506	NAG	C1-C2-N2-C7

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 [i](#)

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	219/225 (97%)	0.71	24 (10%)	10	12	27, 51, 83, 119	0
2	B	103/110 (93%)	0.56	12 (11%)	9	10	15, 40, 91, 130	4 (3%)
3	C	139/149 (93%)	0.87	19 (13%)	6	7	30, 56, 86, 106	0
All	All	461/484 (95%)	0.73	55 (11%)	9	10	15, 49, 86, 130	4 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	470	ALA	7.2
2	B	113[A]	GLY	5.5
1	A	471	ALA	5.4
3	C	1612	TRP	5.0
1	A	469	LEU	4.4
2	B	93	CYS	4.3
2	B	90	SER	4.3
1	A	472	ALA	4.0
2	B	130	GLN	3.9
3	C	1558	PHE	3.8
1	A	468	GLU	3.8
3	C	1618	LEU	3.7
2	B	129	ASP	3.6
2	B	132	CYS	3.6
2	B	94	SER	3.5
1	A	465	GLU	3.5
2	B	112[A]	SER	3.2
3	C	1553	GLN	3.2
1	A	254	GLY	3.1
1	A	467	GLU	3.1
3	C	1554	LEU	3.1
3	C	1525	ASP	3.0
1	A	331	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
3	C	1555	SER	2.9
1	A	456	LEU	2.9
2	B	88	PRO	2.8
1	A	440	GLU	2.8
1	A	376	CYS	2.7
1	A	457	HIS	2.6
2	B	95	GLU	2.6
3	C	1611	PHE	2.5
3	C	1516	SER	2.5
3	C	1637	CYS	2.4
3	C	1571	SER	2.4
2	B	43	CYS	2.4
3	C	1542	ASP	2.3
3	C	1609	SER	2.3
3	C	1562	ILE	2.3
1	A	319	ASP	2.2
1	A	444	GLY	2.2
2	B	131	GLN	2.2
3	C	1517	ASN	2.2
1	A	380	GLY	2.2
1	A	466	GLU	2.2
1	A	421	VAL	2.2
3	C	1641	GLU	2.2
1	A	423	GLY	2.1
1	A	387	THR	2.1
1	A	442	LEU	2.1
1	A	375	HIS	2.1
1	A	424	GLN	2.1
3	C	1585	ILE	2.1
3	C	1573	SER	2.0
3	C	1588	ILE	2.0
1	A	379	LYS	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.

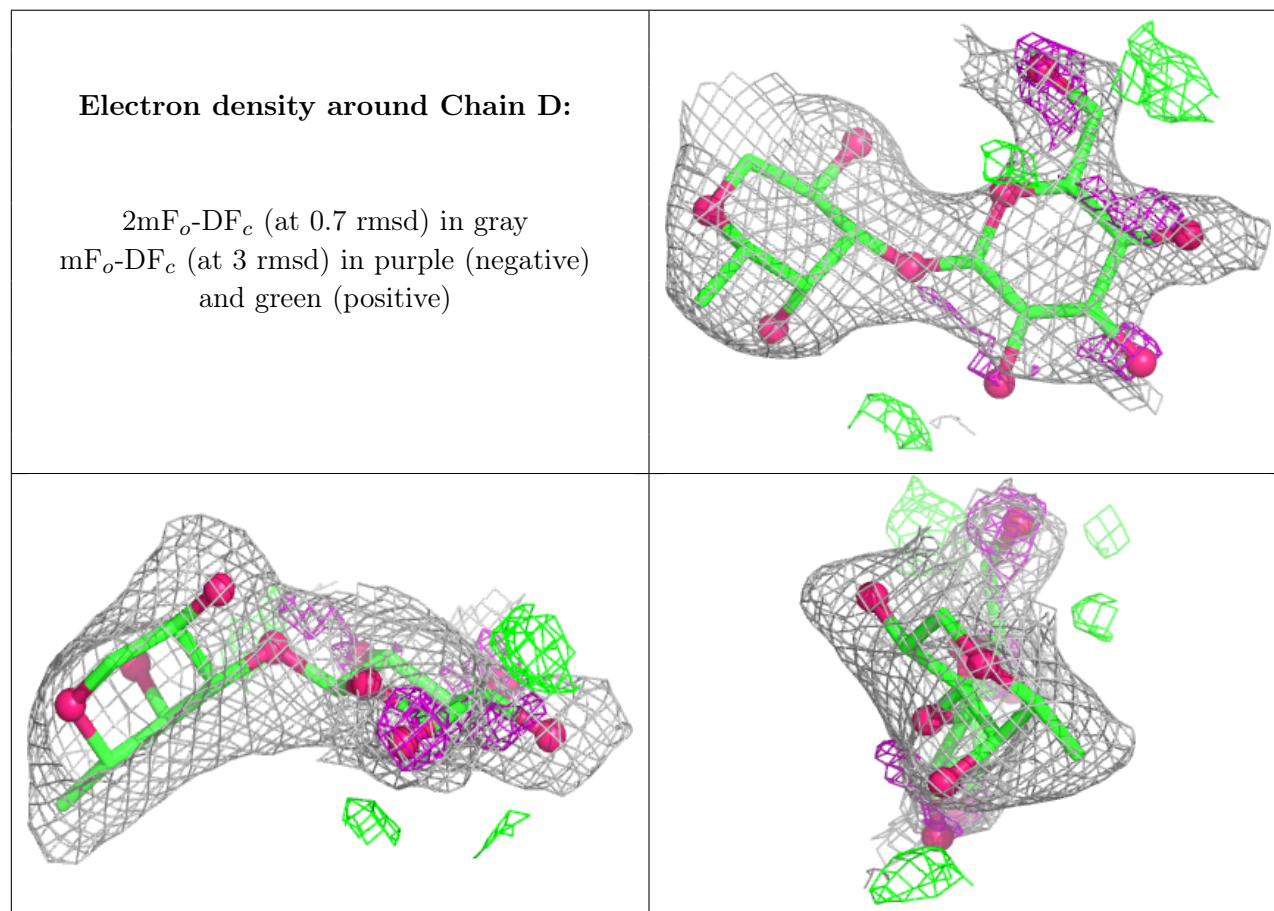
6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
4	BGC	D	2	11/12	0.87	0.12	29,36,40,41	0
4	FUC	D	1	10/11	0.94	0.08	37,39,40,42	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(Å ²)	Q<0.9
5	MAN	A	508	11/12	0.71	0.17	79,81,84,86	0
5	MAN	A	505	11/12	0.83	0.12	76,79,83,88	0
5	MAN	B	200	11/12	0.86	0.11	52,59,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NAG	A	506	14/15	0.87	0.10	63,67,76,78	0
5	MAN	A	507	11/12	0.88	0.11	75,80,84,84	0
5	MAN	A	504	11/12	0.89	0.09	40,44,47,48	0
5	MAN	A	501	11/12	0.89	0.10	46,51,53,53	0
5	MAN	A	502	11/12	0.90	0.09	45,49,53,53	0
5	MAN	A	503	11/12	0.91	0.09	37,41,45,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.