



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 24, 2025 – 02:20 PM EDT

PDB ID : 9E7P / pdb_00009e7p
Title : Pfs230 D13D14 in complex with nanobody W2812
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Deposited on : 2024-11-03
Resolution : 3.22 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 Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

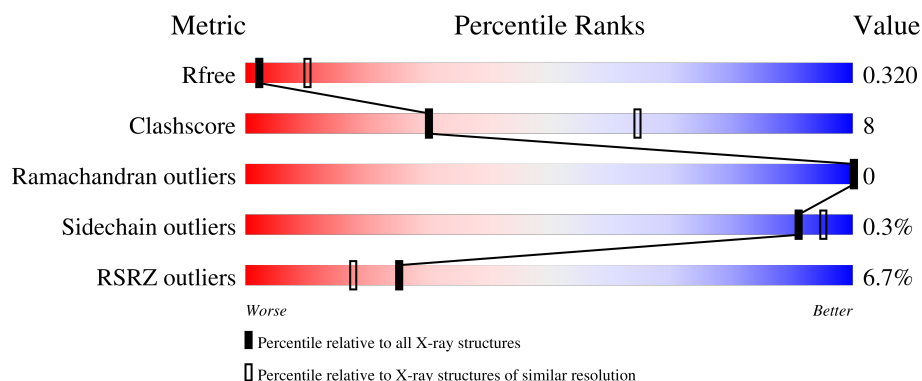
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.22 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}	164625	1638 (3.24-3.20)
Clashscore	180529	1778 (3.24-3.20)
Ramachandran outliers	177936	1751 (3.24-3.20)
Sidechain outliers	177891	1750 (3.24-3.20)
RSRZ outliers	164620	1639 (3.24-3.20)

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	133	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>21%</div> <div>6%</div> </div> </div>
2	B	288	<div> <div>7%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div></div> </div> </div>
3	C	3	<div> <div></div> <div> <div>67%</div> <div>33%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3147 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 Nanobody W2812.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	125	Total	C	N	O	S	0	0	0
			935	582	166	183	4			

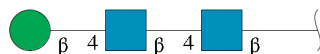
- Molecule 2 is a protein called Gametocyte surface protein P230.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	279	Total	C	N	O	S	0	0	0
			2160	1385	348	419	8			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	2824	GLY	-	expression tag	UNP P68874
B	2825	ALA	-	expression tag	UNP P68874
B	2826	SER	-	expression tag	UNP P68874

- Molecule 3 is an oligosaccharide called 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	3	Total	C	N	O		0	0	0
			39	22	2	15				

- Molecule 4 is CITRIC ACID (CCD ID: CIT) (formula: C₆H₈O₇).

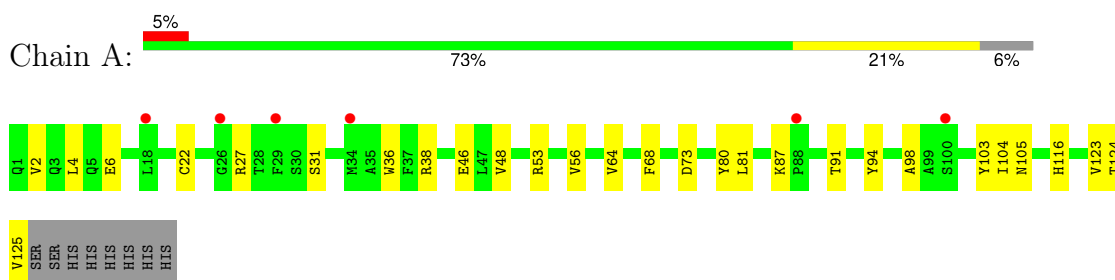


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		

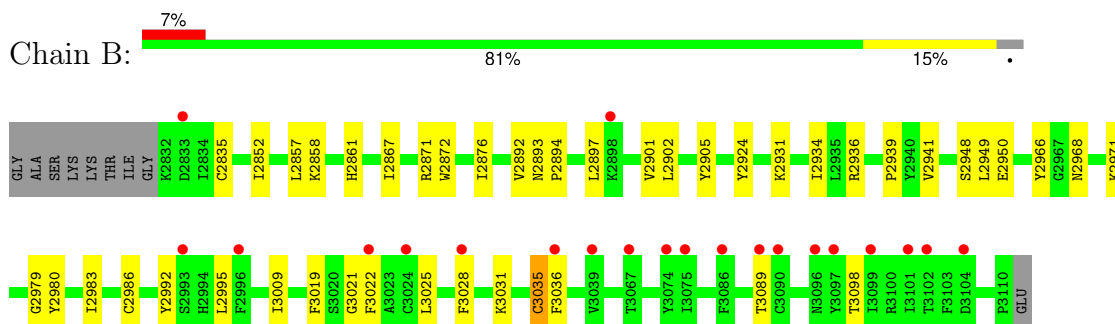
3 Residue-property plots [i](#)

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.

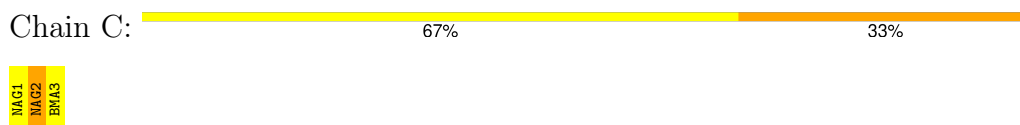
- Molecule 1: Nanobody W2812



- Molecule 2: Gametocyte surface protein P230



- Molecule 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 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	134.65Å 134.65Å 75.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.60 – 3.22 47.60 – 3.22	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.60-3.22) 99.9 (47.60-3.22)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 3.25Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, R_{free}	0.286 , 0.320 0.286 , 0.320	Depositor DCC
R_{free} test set	1058 reflections (9.01%)	wwPDB-VP
Wilson B-factor (Å ²)	114.0	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 74.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3147	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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: BMA, NAG, CIT

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	0/957	0.29	0/1305
2	B	0.14	0/2218	0.35	0/3037
All	All	0.14	0/3175	0.33	0/4342

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	935	0	867	24	0
2	B	2160	0	1941	29	0
3	C	39	0	34	1	0
4	A	13	0	5	2	0
All	All	3147	0	2847	50	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.

All (50) 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:56:VAL:HA	3:C:2:NAG:H83	1.68	0.73
1:A:38:ARG:HB2	1:A:46:GLU:HG2	1.70	0.73
2:B:2941:VAL:H	2:B:2979:GLY:HA3	1.55	0.70
2:B:2992:TYR:HD2	2:B:2995:LEU:HD12	1.60	0.66
2:B:2983:ILE:HG23	2:B:3019:PHE:HB3	1.76	0.65
2:B:2871:ARG:HD2	2:B:2980:TYR:HD2	1.63	0.63
2:B:2901:VAL:HG12	2:B:2949:LEU:HD21	1.85	0.57
2:B:2924:TYR:HB2	2:B:2931:LYS:HG2	1.86	0.57
2:B:2892:VAL:HB	2:B:2897:LEU:HD21	1.88	0.55
2:B:2871:ARG:HD2	2:B:2980:TYR:CD2	2.43	0.52
1:A:53:ARG:HB2	1:A:104:ILE:HG22	1.91	0.51
2:B:2858:LYS:HZ3	2:B:2968:ASN:HB3	1.75	0.51
1:A:105:ASN:O	2:B:2966:TYR:N	2.42	0.51
1:A:73:ASP:HB2	1:A:80:TYR:HE2	1.76	0.50
2:B:2905:TYR:CD1	2:B:2948:SER:HB3	2.47	0.49
2:B:2893:ASN:HB3	2:B:2950:GLU:HB2	1.95	0.49
2:B:2861:HIS:O	2:B:2968:ASN:HB2	2.13	0.49
2:B:2950:GLU:HG2	2:B:2971:LYS:HG2	1.94	0.48
2:B:2894:PRO:HD3	2:B:2902:LEU:HG	1.96	0.48
1:A:38:ARG:HG2	1:A:94:TYR:CE1	2.49	0.47
1:A:31:SER:HA	1:A:53:ARG:NH1	2.29	0.47
1:A:31:SER:HA	1:A:53:ARG:HH11	1.80	0.46
2:B:2852:ILE:HA	2:B:2968:ASN:OD1	2.15	0.46
1:A:91:THR:HG23	1:A:124:THR:HG22	1.98	0.46
1:A:116:HIS:CE1	4:A:201:CIT:H42	2.50	0.45
2:B:2876:ILE:HG13	2:B:2934:ILE:HG23	1.99	0.45
1:A:2:VAL:HG23	1:A:27:ARG:HB2	1.99	0.45
2:B:2835:CYS:SG	2:B:2867:ILE:HD11	2.57	0.45
1:A:103:TYR:CD2	2:B:2857:LEU:HB3	2.53	0.44
1:A:36:TRP:CG	1:A:81:LEU:HD22	2.52	0.44
2:B:2872:TRP:O	2:B:2936:ARG:NH1	2.51	0.44
1:A:4:LEU:HD12	1:A:22:CYS:SG	2.59	0.43
1:A:87:LYS:O	1:A:125:VAL:HG21	2.18	0.43
2:B:2858:LYS:HZ2	2:B:2858:LYS:HB2	1.83	0.43
2:B:3031:LYS:HB3	2:B:3089:THR:HB	2.01	0.43
1:A:64:VAL:HB	1:A:68:PHE:CG	2.54	0.43
2:B:3025:LEU:HB2	2:B:3028:PHE:CD1	2.53	0.43
2:B:2986:CYS:O	2:B:3022:PHE:HA	2.19	0.43
1:A:4:LEU:HD21	1:A:98:ALA:HB3	2.00	0.42
1:A:103:TYR:CD1	2:B:2857:LEU:HD23	2.53	0.42
2:B:3021:GLY:HA2	2:B:3036:PHE:CE2	2.54	0.42
1:A:6:GLU:N	1:A:6:GLU:OE1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3035:CYS:O	2:B:3036:PHE:HB2	2.20	0.42
2:B:2939:PRO:HB2	2:B:2983:ILE:HG12	2.02	0.42
2:B:3009:ILE:HG12	2:B:3098:THR:HB	2.01	0.42
1:A:22:CYS:HB2	1:A:36:TRP:CH2	2.55	0.41
1:A:38:ARG:HG3	1:A:48:VAL:HG11	2.02	0.41
1:A:91:THR:HG23	1:A:124:THR:HA	2.03	0.41
1:A:116:HIS:NE2	4:A:201:CIT:H42	2.35	0.41
1:A:91:THR:HA	1:A:123:VAL:O	2.21	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	123/133 (92%)	117 (95%)	6 (5%)	0	100	100
2	B	277/288 (96%)	261 (94%)	16 (6%)	0	100	100
All	All	400/421 (95%)	378 (94%)	22 (6%)	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	95/110 (86%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	230/272 (85%)	229 (100%)	1 (0%)	89	93
All	All	325/382 (85%)	324 (100%)	1 (0%)	91	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	3035	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	82	GLN
1	A	113	ASN
1	A	122	GLN
2	B	2910	ASN
2	B	2975	HIS
2	B	3005	ASN
2	B	3065	GLN
2	B	3096	ASN

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 ⓘ

3 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	3,2	14,14,15	0.70	0	17,19,21	1.34	2 (11%)
3	NAG	C	2	3	14,14,15	0.78	0	17,19,21	1.93	4 (23%)
3	BMA	C	3	3	11,11,12	0.81	0	15,15,17	2.31	5 (33%)

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

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	3	BMA	C1-O5-C5	7.11	121.72	112.19
3	C	2	NAG	C1-C2-N2	4.67	117.79	110.43
3	C	1	NAG	C4-C3-C2	3.75	116.51	111.02
3	C	2	NAG	C2-N2-C7	3.57	127.69	122.90
3	C	3	BMA	C3-C4-C5	2.65	115.04	110.23
3	C	2	NAG	O5-C1-C2	-2.59	107.28	111.29
3	C	3	BMA	O4-C4-C3	-2.16	105.29	110.38
3	C	3	BMA	O3-C3-C2	-2.16	105.66	110.05
3	C	2	NAG	O4-C4-C3	-2.11	105.41	110.38
3	C	1	NAG	O4-C4-C5	2.09	114.47	109.32
3	C	3	BMA	C2-C3-C4	2.05	114.46	110.86

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1	NAG	C4-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6

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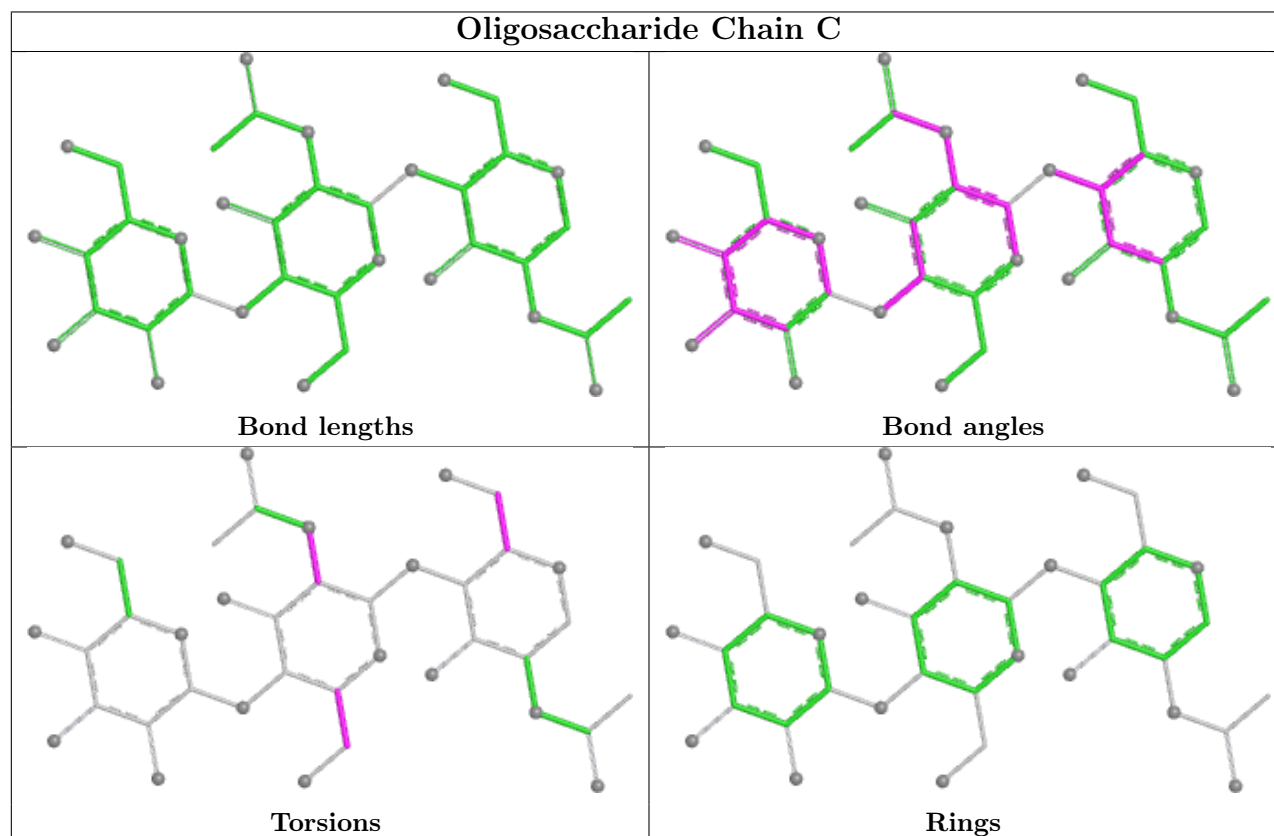
Mol	Chain	Res	Type	Atoms
3	C	2	NAG	C3-C2-N2-C7
3	C	2	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	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](#)

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	CIT	A	201	-	12,12,12	1.33	1 (8%)	17,17,17	1.44	2 (11%)

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	CIT	A	201	-	-	5/16/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	201	CIT	C3-C6	2.85	1.56	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	201	CIT	O5-C6-C3	-3.31	115.68	122.09
4	A	201	CIT	O6-C6-C3	2.80	118.51	113.14

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	201	CIT	C2-C3-C6-O5
4	A	201	CIT	C2-C3-C6-O6
4	A	201	CIT	O7-C3-C6-O5
4	A	201	CIT	O7-C3-C6-O6
4	A	201	CIT	O7-C3-C4-C5

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	201	CIT	2	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

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	125/133 (93%)	0.34	6 (4%) 36 25	79, 114, 141, 154	0
2	B	279/288 (96%)	0.63	21 (7%) 22 15	72, 106, 157, 161	0
All	All	404/421 (95%)	0.54	27 (6%) 25 18	72, 109, 156, 161	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	3086	PHE	4.8
2	B	3036	PHE	3.5
2	B	3074	TYR	3.3
2	B	3090	CYS	3.3
2	B	3075	ILE	3.1
1	A	100	SER	2.8
1	A	26	GLY	2.7
2	B	3024	CYS	2.5
2	B	3099	ILE	2.4
2	B	2898	LYS	2.4
2	B	2996	PHE	2.4
2	B	3101	ILE	2.4
2	B	3104	ASP	2.4
2	B	3089	THR	2.3
2	B	2993	SER	2.3
1	A	34	MET	2.3
2	B	3028	PHE	2.3
2	B	3097	TYR	2.3
2	B	3067	THR	2.3
1	A	29	PHE	2.2
1	A	88	PRO	2.2
2	B	2833	ASP	2.2
2	B	3102	THR	2.1
2	B	3022	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	18	LEU	2.0
2	B	3096	ASN	2.0
2	B	3039	VAL	2.0

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

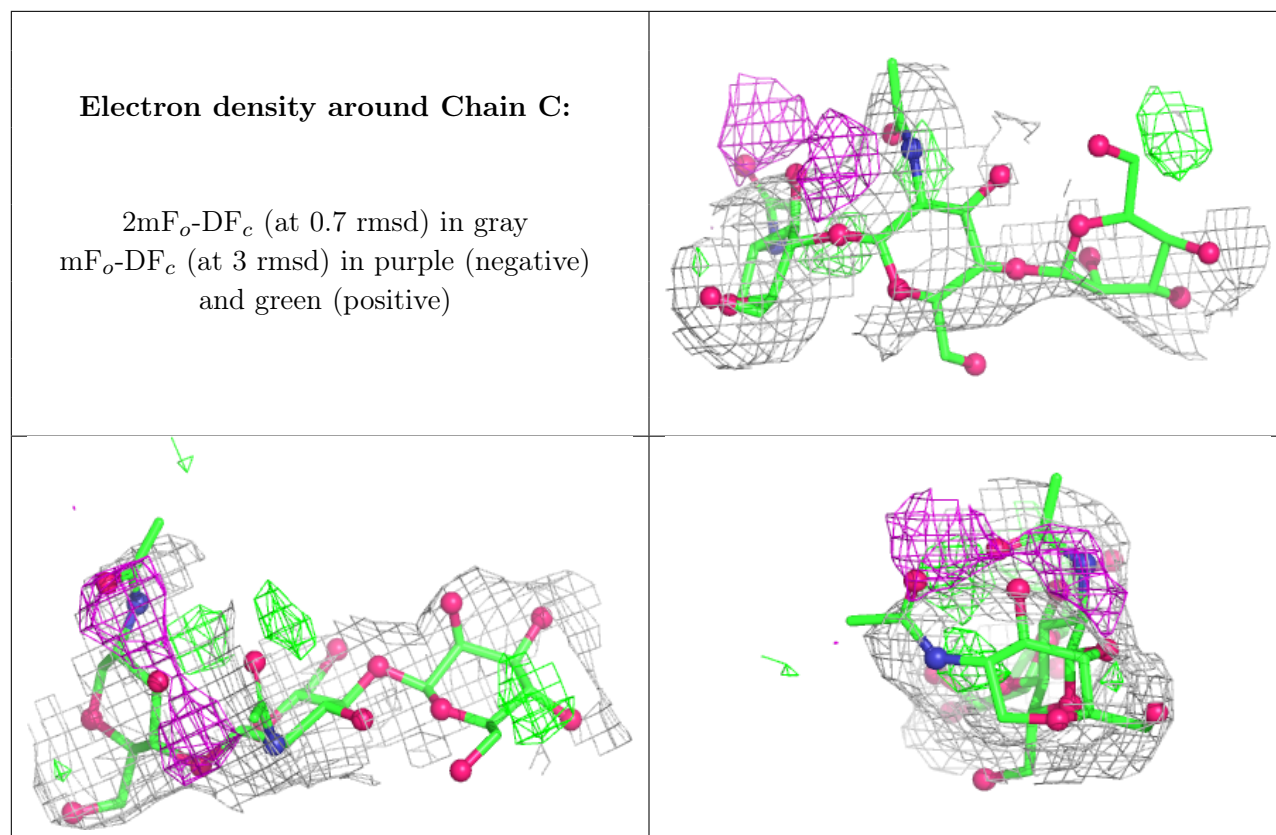
There are no non-standard protein/DNA/RNA residues in this entry.

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
3	BMA	C	3	11/12	0.11	0.18	138,151,161,162	0
3	NAG	C	2	14/15	0.59	0.17	109,139,155,158	0
3	NAG	C	1	14/15	0.74	0.22	95,109,121,128	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(\AA^2)	Q<0.9
4	CIT	A	201	13/13	0.77	0.15	108,112,119,120	0

6.5 Other polymers [i](#)

There are no such residues in this entry.