



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:34 AM UTC

ENTRY-ADMIN-INFO INFOmissingINFO

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

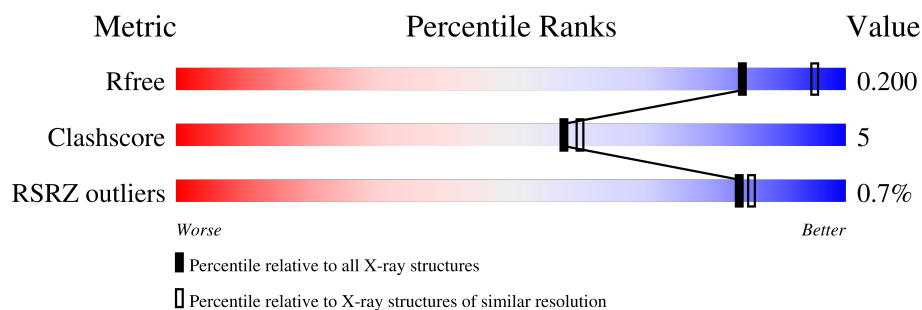
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	163	
1	B	163	
2	C	3	
2	D	3	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7683 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.

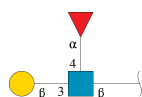
- Molecule 1 is a protein called Alpha-1,3/4-fucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	456	Total	C	N	O	S	0	0	0
			3569	2234	644	678	13			
1	B	456	Total	C	N	O	S	0	0	0
			3569	2234	644	678	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	172	ALA	ASP	engineered mutation	UNP B7GNN8
A	217	ALA	GLU	engineered mutation	UNP B7GNN8
B	172	ALA	ASP	engineered mutation	UNP B7GNN8
B	217	ALA	GLU	engineered mutation	UNP B7GNN8

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			36	20	1	15			
2	D	3	Total	C	N	O	0	0	0
			36	20	1	15			

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Na	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	218	Total	O	0	0
			218	218		
5	B	245	Total	O	0	0
			245	245		

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: Alpha-1,3/4-fucosidase

Chain A: 

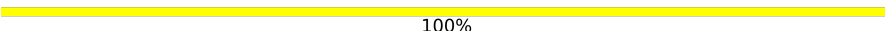


- Molecule 1: Alpha-1,3/4-fucosidase

Chain B: 



- Molecule 2: beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C: 



- Molecule 2: beta-D-galactopyranose-(1-3)-[alpha-L-fucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.59Å 105.97Å 120.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 32.05 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.10) 96.1 (32.05-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	(Not available) , (Not available) (Not available) , 0.200	Depositor DCC
R_{free} test set	3047 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	25.8	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 36.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7683	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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: FUC, EDO, NAG, NA, GAL

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	1.34	8/3656 (0.2%)	1.22	11/4974 (0.2%)
1	B	1.40	17/3656 (0.5%)	1.19	4/4974 (0.1%)
All	All	1.37	25/7312 (0.3%)	1.20	15/9948 (0.2%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	305	GLN	C-O	-6.72	1.16	1.24
1	B	38	GLY	C-O	-6.58	1.19	1.23
1	B	51	HIS	CG-CD2	6.31	1.42	1.35
1	B	321	LEU	N-CA	-6.22	1.39	1.46
1	B	36	HIS	CG-CD2	6.09	1.42	1.35
1	A	36	HIS	CG-CD2	6.07	1.42	1.35
1	A	414	HIS	ND1-CE1	6.03	1.38	1.32
1	B	151	PHE	C-O	5.79	1.30	1.24
1	B	130	VAL	N-CA	-5.71	1.39	1.46
1	B	309	LEU	CA-C	5.65	1.59	1.52
1	B	85	HIS	CG-CD2	5.45	1.41	1.35
1	B	372	HIS	CG-CD2	5.45	1.41	1.35
1	A	414	HIS	CG-CD2	5.44	1.41	1.35
1	B	293	HIS	CA-C	-5.16	1.46	1.52
1	B	312	SER	CA-C	5.12	1.59	1.52
1	B	372	HIS	CE1-NE2	5.10	1.37	1.32
1	B	279	PRO	C-O	5.09	1.29	1.23
1	B	227	SER	N-CA	5.08	1.52	1.46
1	B	36	HIS	ND1-CE1	5.07	1.37	1.32
1	B	220	HIS	CG-CD2	5.07	1.41	1.35
1	A	420	HIS	CG-CD2	5.06	1.41	1.35
1	B	289	GLY	N-CA	5.05	1.49	1.44
1	A	174	ALA	CA-C	5.04	1.59	1.52
1	A	460	HIS	CG-CD2	5.04	1.41	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	220	HIS	CG-CD2	5.03	1.41	1.35

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	GLY	CA-C-N	7.34	127.76	119.83
1	A	164	GLY	C-N-CA	7.34	127.76	119.83
1	A	319	SER	CB-CA-C	6.79	121.00	109.53
1	A	351	ARG	NE-CZ-NH1	6.47	127.97	121.50
1	B	324	ILE	CA-C-N	-6.35	113.84	120.38
1	B	324	ILE	C-N-CA	-6.35	113.84	120.38
1	B	353	ALA	N-CA-C	-6.27	104.55	111.82
1	B	14	LEU	N-CA-C	5.92	118.22	111.11
1	A	50	GLY	N-CA-C	-5.64	104.62	112.18
1	A	61	ASN	N-CA-C	5.48	117.02	110.44
1	A	305	GLN	N-CA-C	-5.18	105.64	111.28
1	A	18	ARG	CA-C-N	5.01	124.78	119.76
1	A	18	ARG	C-N-CA	5.01	124.78	119.76
1	A	190	ARG	N-CA-C	-5.01	105.89	111.36
1	A	399	GLN	N-CA-C	-5.01	102.44	108.25

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	3569	0	3429	31	0
1	B	3569	0	3430	30	0
2	C	36	0	33	0	0
2	D	36	0	34	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	6	0	0
4	B	4	0	6	0	0
5	A	218	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	245	0	0	3	0
All	All	7683	0	6938	63	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.

All (63) 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:61:ASN:HB3	5:A:653:HOH:O	1.71	0.89
1:B:362:ARG:HH11	1:B:362:ARG:HG3	1.35	0.88
2:D:1:NAG:HO4	2:D:3:FUC:C1	1.84	0.86
1:B:232:ARG:HH22	1:B:254:THR:HG22	1.59	0.67
1:B:362:ARG:HG3	1:B:362:ARG:NH1	2.09	0.67
1:B:362:ARG:HH11	1:B:362:ARG:CG	2.09	0.66
1:A:82:THR:HA	1:A:131:TYR:HB3	1.79	0.65
1:B:232:ARG:NH2	1:B:254:THR:HG22	2.13	0.64
1:B:95:ARG:HH22	1:B:162:GLN:HE22	1.45	0.63
1:A:183:THR:CG2	1:A:185:TYR:HE2	2.14	0.61
1:A:406:ILE:C	1:A:406:ILE:HD12	2.27	0.59
1:B:233:LEU:HD21	1:B:255:VAL:HG12	1.83	0.58
1:A:183:THR:HG22	1:A:185:TYR:CE2	2.37	0.58
1:A:30:GLU:OE1	1:A:351:ARG:NH2	2.29	0.58
1:A:183:THR:CG2	1:A:185:TYR:CE2	2.87	0.58
1:B:35:LEU:HD11	1:B:79:VAL:HG21	1.84	0.58
1:B:95:ARG:HH22	1:B:162:GLN:NE2	2.02	0.57
1:A:204:ILE:HB	1:A:209:PRO:HD2	1.86	0.56
1:A:351:ARG:NH2	5:A:578:HOH:O	2.37	0.56
1:A:224:ASN:OD1	1:A:439:GLY:HA3	2.06	0.55
1:A:183:THR:HG21	1:A:185:TYR:HE2	1.71	0.54
1:A:215:GLY:O	1:A:258:GLN:HG3	2.08	0.53
2:D:1:NAG:C4	2:D:3:FUC:C1	2.84	0.52
1:B:35:LEU:CD1	1:B:79:VAL:HG21	2.39	0.52
1:B:42:MET:HE2	1:B:58:ASN:H	1.73	0.52
1:B:90:CYS:HB2	1:B:100:THR:HG22	1.93	0.51
1:B:353:ALA:O	1:B:357:VAL:HG22	2.10	0.51
1:B:42:MET:HE1	5:B:586:HOH:O	2.11	0.51
1:B:353:ALA:HB1	1:B:476:VAL:CG2	2.41	0.50
1:A:472:ARG:HG3	1:A:473:ALA:N	2.27	0.48
1:B:476:VAL:HG22	1:B:477:ARG:N	2.29	0.47
1:A:37:PHE:CD1	1:A:326:PRO:HB2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:ASN:ND2	1:B:182:LYS:HD3	2.31	0.46
1:B:421:LEU:HD11	1:B:459:LEU:HB3	1.97	0.46
1:B:95:ARG:NH2	5:B:603:HOH:O	2.49	0.45
1:A:67:TRP:O	1:A:71:LEU:HG	2.17	0.45
1:A:60:ARG:HG2	5:A:619:HOH:O	2.17	0.45
1:A:73:ALA:O	1:A:344:GLY:HA3	2.16	0.45
1:A:91:LEU:N	1:A:91:LEU:HD22	2.31	0.45
1:B:351:ARG:NH2	5:B:539:HOH:O	2.49	0.45
1:A:425:GLY:O	1:A:432:GLU:HA	2.17	0.45
1:B:29:MET:HE1	1:B:167:PHE:CE1	2.52	0.44
1:A:358:ARG:O	1:A:398:PRO:HD3	2.17	0.44
1:B:170:TRP:CZ2	1:B:206:VAL:HG21	2.54	0.43
1:B:34:PHE:HB3	1:B:323:ASN:HB2	2.01	0.43
1:B:472:ARG:HG2	1:B:473:ALA:N	2.34	0.43
1:A:401:THR:O	1:A:453:GLU:HA	2.19	0.43
1:B:428:PRO:C	1:B:430:GLY:H	2.27	0.42
1:B:112:ASP:OD1	1:B:112:ASP:C	2.63	0.42
1:B:131:TYR:CD2	1:B:131:TYR:C	2.98	0.42
1:A:334:GLU:N	1:A:335:PRO:CD	2.83	0.42
1:B:354:LEU:HD12	1:B:354:LEU:HA	1.84	0.42
1:A:90:CYS:HB2	1:A:100:THR:HG22	2.02	0.41
1:A:177:GLU:OE1	1:A:182:LYS:N	2.49	0.41
1:B:235:SER:HA	1:B:238:LEU:HG	2.03	0.41
1:A:159:LEU:HD23	1:A:159:LEU:HA	1.91	0.41
1:B:327:SER:HB2	1:B:328:PRO:HD2	2.01	0.41
1:A:42:MET:HE2	1:A:58:ASN:H	1.86	0.41
1:A:287:ARG:HD3	5:A:486:HOH:O	2.21	0.41
1:A:329:GLU:OE1	1:A:331:LEU:HD12	2.21	0.41
1:A:55:ALA:HA	1:A:105:PRO:HD3	2.02	0.40
1:A:46:GLU:O	1:A:47:TRP:HD1	2.03	0.40
1:A:34:PHE:HB3	1:A:323:ASN:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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](#)

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$
2	NAG	C	1	2	15,15,15	1.30	1 (6%)	21,21,21	1.87	5 (23%)
2	GAL	C	2	2	11,11,12	1.04	1 (9%)	15,15,17	1.27	1 (6%)
2	FUC	C	3	2	10,10,11	1.30	1 (10%)	14,14,16	1.20	1 (7%)
2	NAG	D	1	2	15,15,15	1.06	1 (6%)	21,21,21	1.99	5 (23%)
2	GAL	D	2	2	11,11,12	0.78	1 (9%)	15,15,17	1.75	2 (13%)
2	FUC	D	3	2	10,10,11	0.84	0	14,14,16	1.91	2 (14%)

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
2	NAG	C	1	2	-	4/6/26/26	0/1/1/1
2	GAL	C	2	2	-	0/2/19/22	0/1/1/1
2	FUC	C	3	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	2	-	4/6/26/26	0/1/1/1
2	GAL	D	2	2	-	2/2/19/22	0/1/1/1
2	FUC	D	3	2	-	-	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	NAG	C1-C2	3.49	1.57	1.52
2	C	3	FUC	C2-C3	3.09	1.57	1.52
2	D	1	NAG	C1-C2	2.80	1.56	1.52
2	C	2	GAL	O5-C1	-2.13	1.40	1.43
2	D	2	GAL	O5-C1	-2.13	1.40	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3	FUC	C1-O5-C5	6.14	127.44	112.97
2	D	1	NAG	O1-C1-C2	5.38	120.39	109.22
2	C	1	NAG	O1-C1-C2	4.67	118.93	109.22
2	D	2	GAL	C1-O5-C5	-4.03	106.78	112.19
2	D	2	GAL	C1-C2-C3	-3.69	104.27	109.64
2	D	1	NAG	C1-C2-N2	3.65	114.96	110.73
2	C	2	GAL	O2-C2-C1	-3.45	101.33	109.22
2	D	1	NAG	C1-C2-C3	-3.38	105.94	110.54
2	D	1	NAG	O6-C6-C5	-3.30	100.11	111.33
2	C	1	NAG	O6-C6-C5	-3.24	100.29	111.33
2	C	1	NAG	O3-C3-C2	3.21	115.97	109.58
2	C	1	NAG	C1-C2-C3	-2.52	107.11	110.54
2	C	1	NAG	C2-N2-C7	2.52	129.00	123.11
2	D	1	NAG	O7-C7-C8	-2.48	117.64	122.05
2	C	3	FUC	O5-C5-C4	2.39	113.86	109.55
2	D	3	FUC	O3-C3-C2	-2.04	105.90	110.05

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C3-C2-N2-C7
2	D	2	GAL	C4-C5-C6-O6

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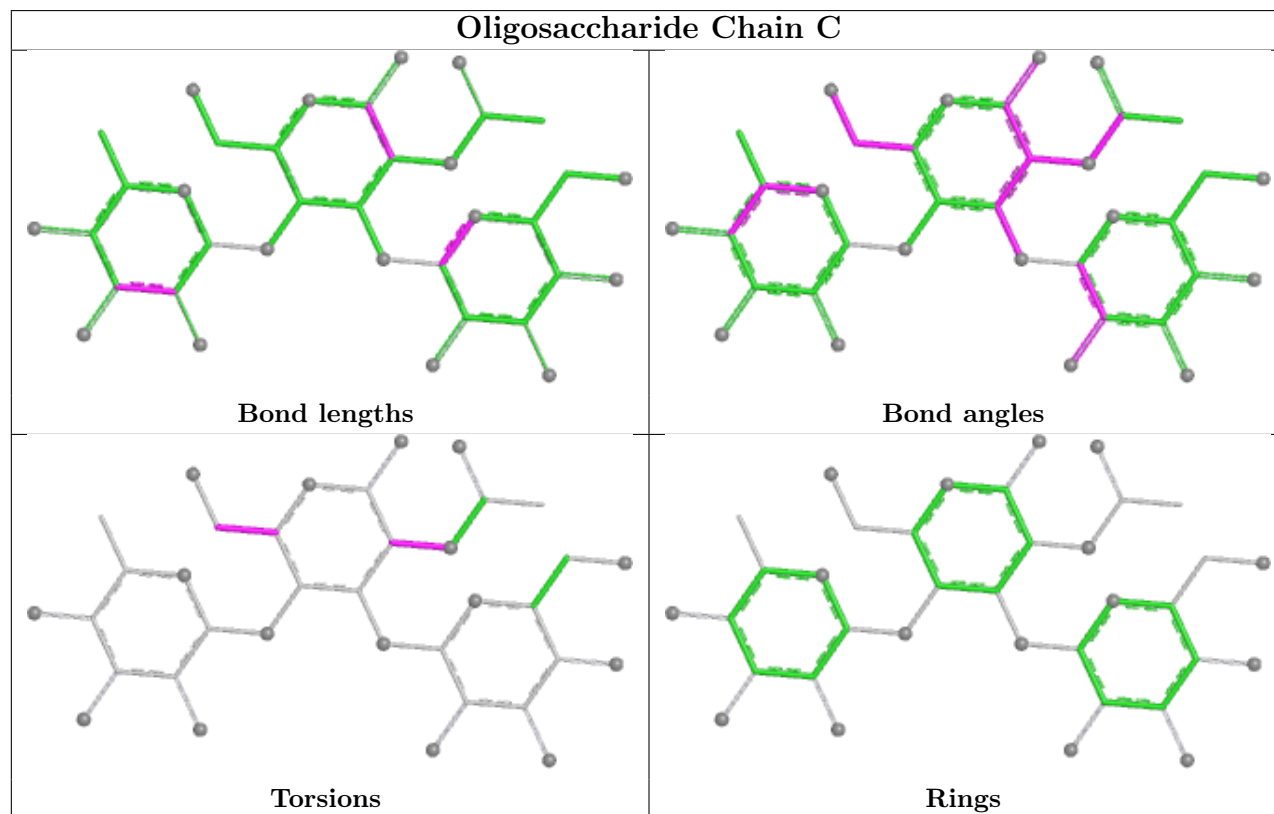
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C1-C2-N2-C7
2	C	1	NAG	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
2	D	1	NAG	C3-C2-N2-C7
2	D	2	GAL	O5-C5-C6-O6
2	C	1	NAG	C1-C2-N2-C7

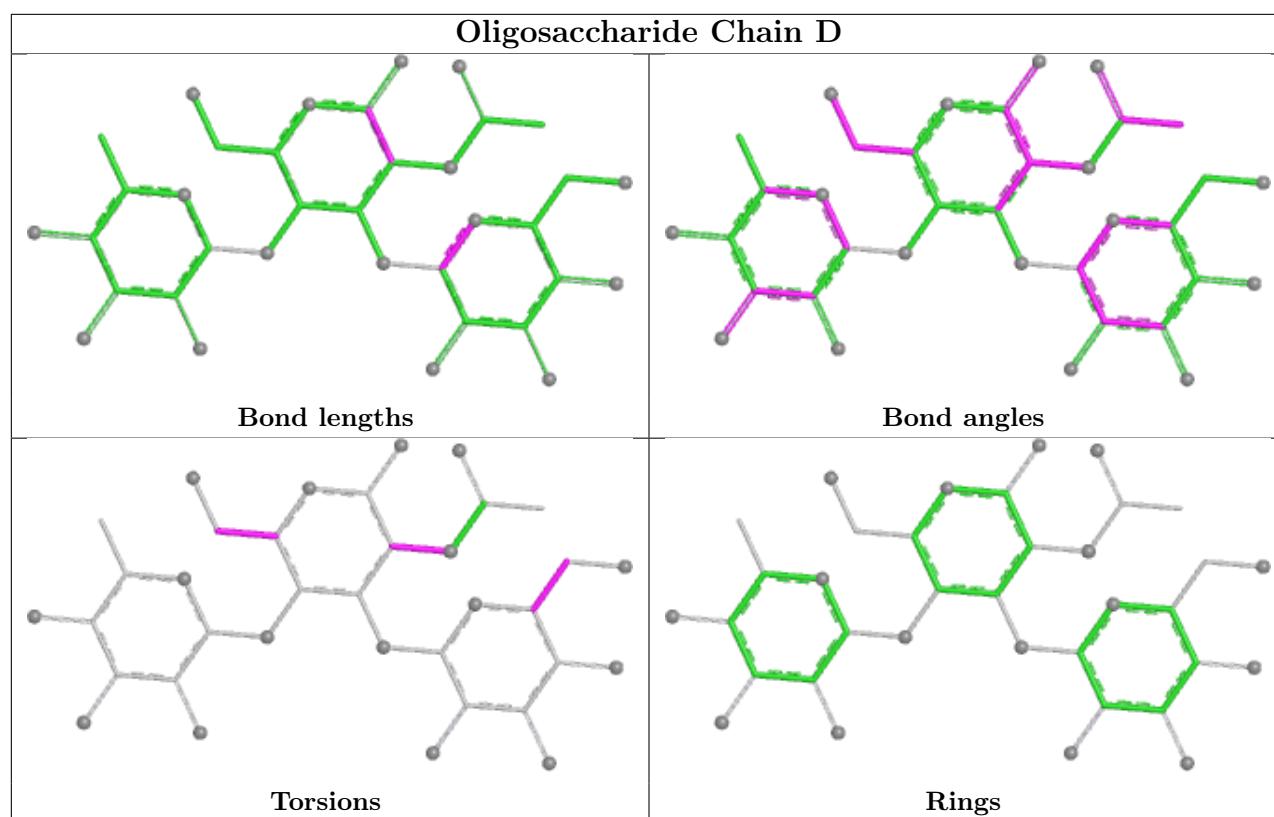
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	NAG	2	0
2	D	3	FUC	2	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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	EDO	A	505	-	3,3,3	0.36	0	2,2,2	0.35	0
4	EDO	B	505	-	3,3,3	0.22	0	2,2,2	0.60	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	EDO	A	505	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	505	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	505	EDO	O1-C1-C2-O2
4	B	505	EDO	O1-C1-C2-O2

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 [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	A	155/163 (95%)	-0.54	0 100 100	18, 26, 42, 62	0
1	B	155/163 (95%)	-0.56	0 100 100	18, 25, 41, 54	0
All	All	310/326 (95%)	-0.55	0 84 100	18, 25, 42, 62	0

There are no RSRZ outliers to report.

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](#)

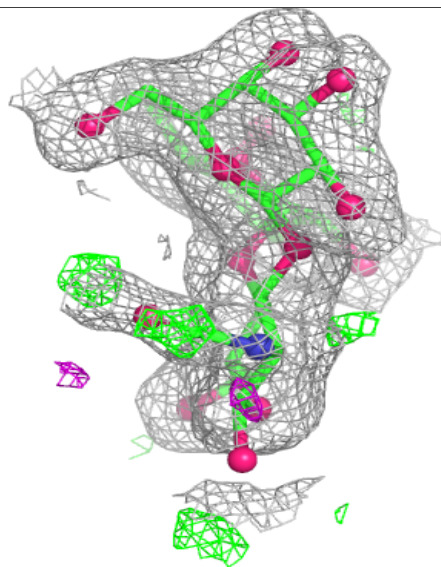
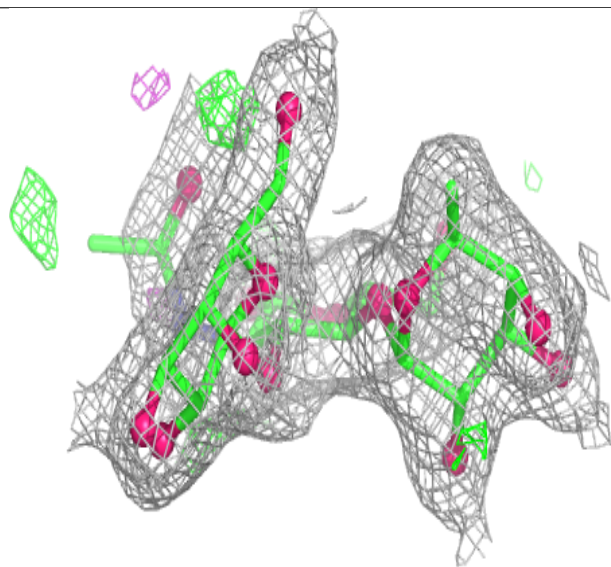
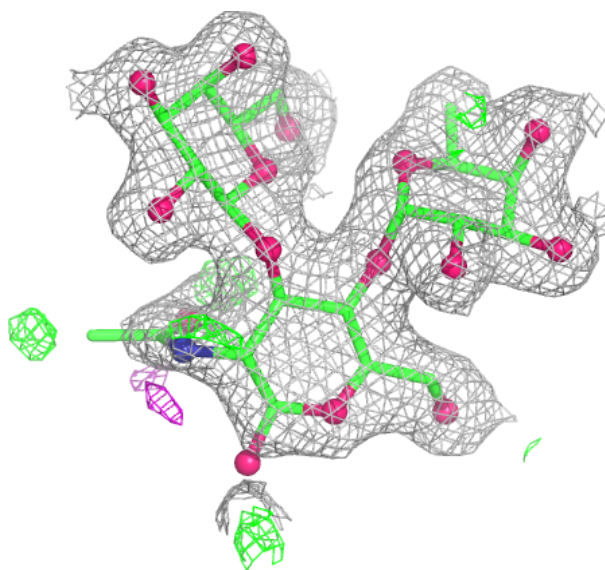
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

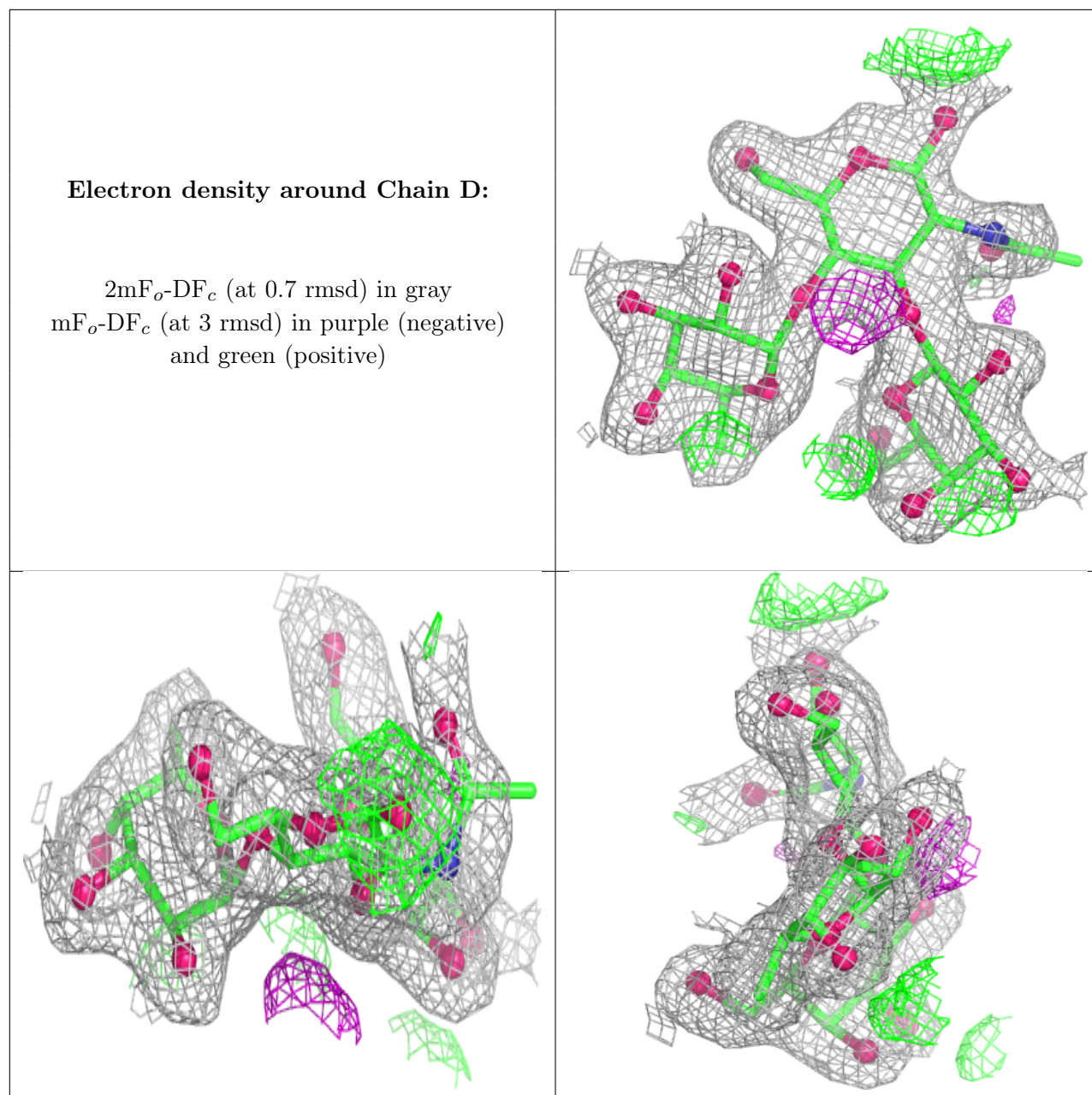
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	C	1	15/15	0.90	0.11	25,33,58,60	0
2	NAG	D	1	15/15	0.91	0.10	27,37,52,58	0
2	FUC	C	3	10/11	0.94	0.07	20,25,28,29	0
2	GAL	D	2	11/12	0.96	0.06	26,29,33,36	0
2	GAL	C	2	11/12	0.98	0.04	22,25,28,29	0
2	FUC	D	3	10/11	0.98	0.04	21,24,25,27	0

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.

Electron density around Chain C:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands ⓘ

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	EDO	A	505	4/4	0.96	0.09	33,36,40,42	0
4	EDO	B	505	4/4	0.96	0.07	31,32,33,36	0
3	NA	A	501	1/1	0.98	0.06	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NA	B	501	1/1	0.99	0.03	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.