



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:40 PM UTC

PDB ID : 3PA2 / pdb_00003pa2
Title : Crystal Structure of P Domain from Norwalk Virus Strain Vietnam 026 in complex with HBGA type Ley
Authors : Hansman, G.S.; Biertumpfel, C.; Chen, L.; Georgiev, I.; McLellan, J.S.; Katayama, K.; Kwong, P.D.
Deposited on : 2010-10-18
Resolution : 1.48 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

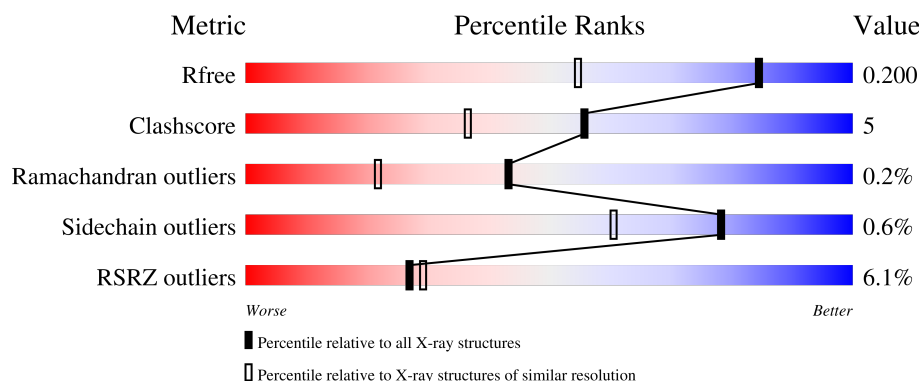
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

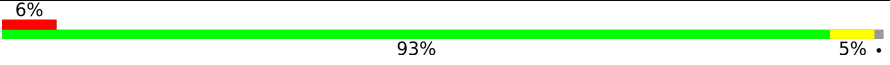
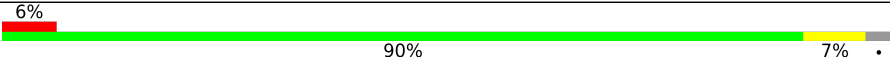
The reported resolution of this entry is 1.48 Å.

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	6779 (1.50-1.46)
Clashscore	190562	7025 (1.50-1.46)
Ramachandran outliers	187476	6917 (1.50-1.46)
Sidechain outliers	187428	6914 (1.50-1.46)
RSRZ outliers	180081	6781 (1.50-1.46)

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	319	
1	B	319	
2	C	4	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5778 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.

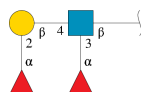
- Molecule 1 is a protein called Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	1	0
			2436	1552	416	459	9			
1	B	310	Total	C	N	O	S	0	6	0
			2434	1551	415	459	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	220	GLY	-	expression tag	UNP Q5F4T5
A	221	PRO	-	expression tag	UNP Q5F4T5
A	222	GLY	-	expression tag	UNP Q5F4T5
A	223	SER	-	expression tag	UNP Q5F4T5
B	220	GLY	-	expression tag	UNP Q5F4T5
B	221	PRO	-	expression tag	UNP Q5F4T5
B	222	GLY	-	expression tag	UNP Q5F4T5
B	223	SER	-	expression tag	UNP Q5F4T5

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	0	0	0
			46	26	1	19			

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



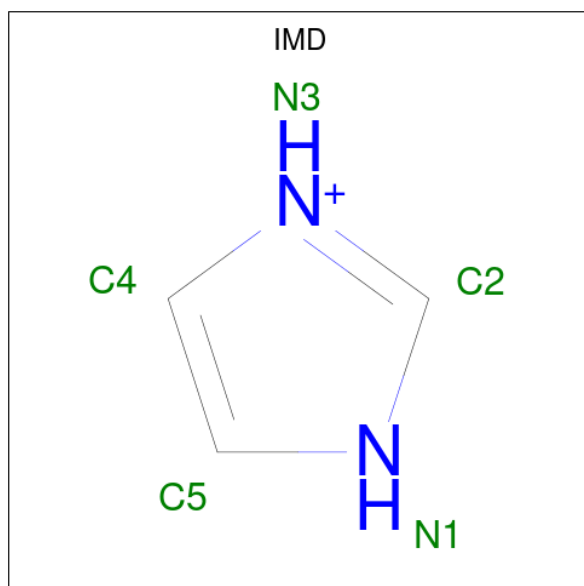
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			8	4	4		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is IMIDAZOLE (CCD ID: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			5	3	2		

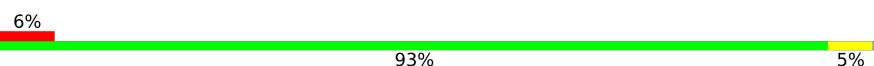
- Molecule 5 is water.

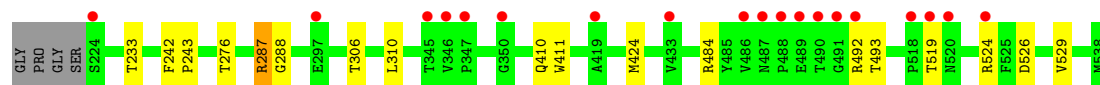
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	413	Total 413	O 413	0	0
5	B	352	Total 352	O 352	0	0

3 Residue-property plots [i](#)

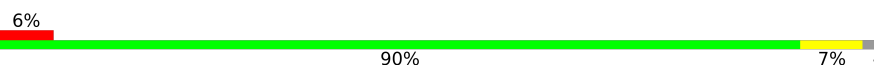
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

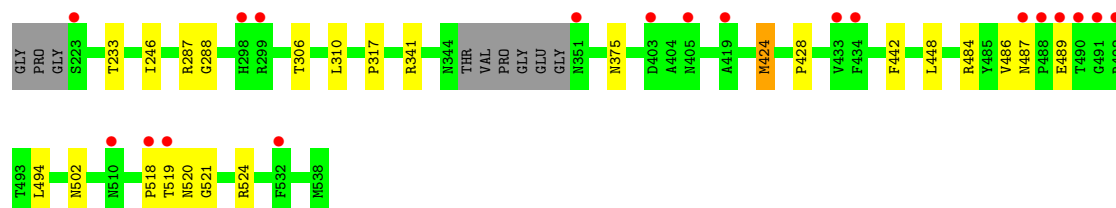
- Molecule 1: Capsid protein

Chain A: 



- Molecule 1: Capsid protein

Chain B: 



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

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.27Å 79.13Å 69.07Å 90.00° 100.27° 90.00°	Depositor
Resolution (Å)	29.08 – 1.48 29.08 – 1.48	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.08-1.48) 99.7 (29.08-1.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 1.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.185 , 0.204 0.181 , 0.200	Depositor DCC
R_{free} test set	5772 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	13.2	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5778	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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: IMD, GAL, EDO, NAG, 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	0.46	0/2510	0.71	0/3439
1	B	0.46	0/2507	0.72	0/3434
All	All	0.46	0/5017	0.72	0/6873

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	2436	0	2360	19	0
1	B	2434	0	2354	24	0
2	C	46	0	42	1	0
3	A	64	0	96	10	0
3	B	28	0	42	1	0
4	A	5	0	5	1	0
5	A	413	0	0	4	0
5	B	352	0	0	5	0
All	All	5778	0	4899	47	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 (47) 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:B:233:THR:HB	1:B:519[B]:THR:O	1.66	0.94
1:B:306:THR:HG22	1:B:375:ASN:HD21	1.47	0.77
1:A:287[A]:ARG:HD2	5:A:618:HOH:O	1.90	0.71
1:A:287[B]:ARG:HH12	3:A:18:EDO:H21	1.58	0.69
1:A:287[B]:ARG:NH1	3:A:18:EDO:H21	2.08	0.68
1:B:306:THR:HG22	1:B:375:ASN:ND2	2.12	0.64
1:A:233:THR:HB	1:A:519:THR:O	1.97	0.63
3:A:6:EDO:H12	5:A:560:HOH:O	1.97	0.63
1:A:410:GLN:HG2	3:A:6:EDO:H21	1.85	0.59
1:A:276:THR:O	4:A:24:IMD:H4	2.04	0.58
1:B:233:THR:HB	1:B:520[B]:ASN:HA	1.83	0.58
3:A:18:EDO:H22	5:B:78:HOH:O	2.04	0.58
1:A:484:ARG:HH21	1:A:524:ARG:HH21	1.52	0.57
1:B:487:ASN:HD21	1:B:520[A]:ASN:HD21	1.52	0.57
1:B:233:THR:CG2	1:B:520[B]:ASN:HA	2.35	0.57
1:A:484:ARG:HH11	1:A:526:ASP:HB2	1.71	0.56
1:A:492:ARG:HD2	1:A:493:THR:H	1.70	0.55
1:B:518[B]:PRO:HB2	1:B:520[B]:ASN:OD1	2.06	0.55
1:B:287[B]:ARG:HD3	1:B:310:LEU:O	2.09	0.53
1:B:487:ASN:C	1:B:487:ASN:HD22	2.17	0.52
1:B:233:THR:CB	1:B:520[B]:ASN:HA	2.40	0.52
3:A:16:EDO:H21	1:B:287[A]:ARG:HH22	1.74	0.52
1:A:484:ARG:NH1	1:A:526:ASP:HB2	2.24	0.51
1:B:424:MET:HE3	5:B:124:HOH:O	2.11	0.50
1:B:484:ARG:HH22	1:B:524:ARG:HH21	1.60	0.50
1:B:494:LEU:HD13	1:B:518[A]:PRO:HD2	1.94	0.50
1:B:428:PRO:HG2	1:B:502:ASN:OD1	2.13	0.48
1:A:492:ARG:CD	1:A:493:THR:H	2.27	0.48
3:A:16:EDO:H21	1:B:287[A]:ARG:NH2	2.28	0.47
1:B:233:THR:HG21	1:B:520[B]:ASN:HA	1.97	0.47
1:A:288:GLY:HA3	1:A:306:THR:O	2.16	0.46
1:A:484:ARG:HH21	1:A:524:ARG:NH2	2.15	0.45
3:A:16:EDO:H21	5:B:177:HOH:O	2.17	0.44
1:B:486:VAL:O	1:B:521[A]:GLY:HA2	2.17	0.44
1:B:489:GLU:HG3	1:B:520[A]:ASN:ND2	2.33	0.44
1:B:341:ARG:NH1	3:B:7:EDO:H12	2.33	0.44
1:B:317:PRO:HB3	5:B:639:HOH:O	2.17	0.43
5:B:728:HOH:O	2:C:1:NAG:H81	2.18	0.43
1:A:310:LEU:HD22	3:A:539:EDO:H21	2.00	0.43
1:B:246:ILE:HD12	1:B:442:PHE:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:487:ASN:HD21	1:B:520[A]:ASN:ND2	2.14	0.43
1:A:424:MET:HB2	5:A:804:HOH:O	2.19	0.42
1:A:411:TRP:CD1	3:A:6:EDO:H22	2.56	0.41
1:A:242:PHE:CD2	1:A:243:PRO:HD2	2.56	0.41
1:A:242:PHE:CG	1:A:243:PRO:HD2	2.56	0.41
1:B:288:GLY:HA3	1:B:306:THR:O	2.20	0.41
1:A:287[A]:ARG:HD3	5:A:767:HOH: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	314/319 (98%)	305 (97%)	8 (2%)	1 (0%)	36	17
1	B	312/319 (98%)	303 (97%)	9 (3%)	0	100	100
All	All	626/638 (98%)	608 (97%)	17 (3%)	1 (0%)	43	22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	529	VAL

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	269/272 (99%)	267 (99%)	2 (1%)	76	56
1	B	268/272 (98%)	266 (99%)	2 (1%)	76	56
All	All	537/544 (99%)	533 (99%)	4 (1%)	78	56

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

Mol	Chain	Res	Type
1	A	287[A]	ARG
1	A	287[B]	ARG
1	B	424	MET
1	B	448	LEU

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	263	ASN
1	A	425	ASN
1	B	293	GLN
1	B	304	ASN
1	B	333	GLN
1	B	375	ASN
1	B	377	GLN
1	B	384	GLN
1	B	487	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 ⓘ

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
2	NAG	C	1	2	15,15,15	0.56	0	21,21,21	1.16	1 (4%)
2	GAL	C	2	2	11,11,12	0.55	0	15,15,17	0.88	1 (6%)
2	FUC	C	3	2	10,10,11	0.66	0	14,14,16	0.57	0
2	FUC	C	4	2	10,10,11	0.68	0	14,14,16	0.76	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
2	NAG	C	1	2	-	2/6/26/26	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
2	FUC	C	4	2	-	-	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(°)
2	C	1	NAG	O5-C1-C2	2.72	112.25	109.52
2	C	2	GAL	C1-C2-C3	2.10	112.71	109.64

There are no chirality outliers.

All (2) torsion outliers are listed below:

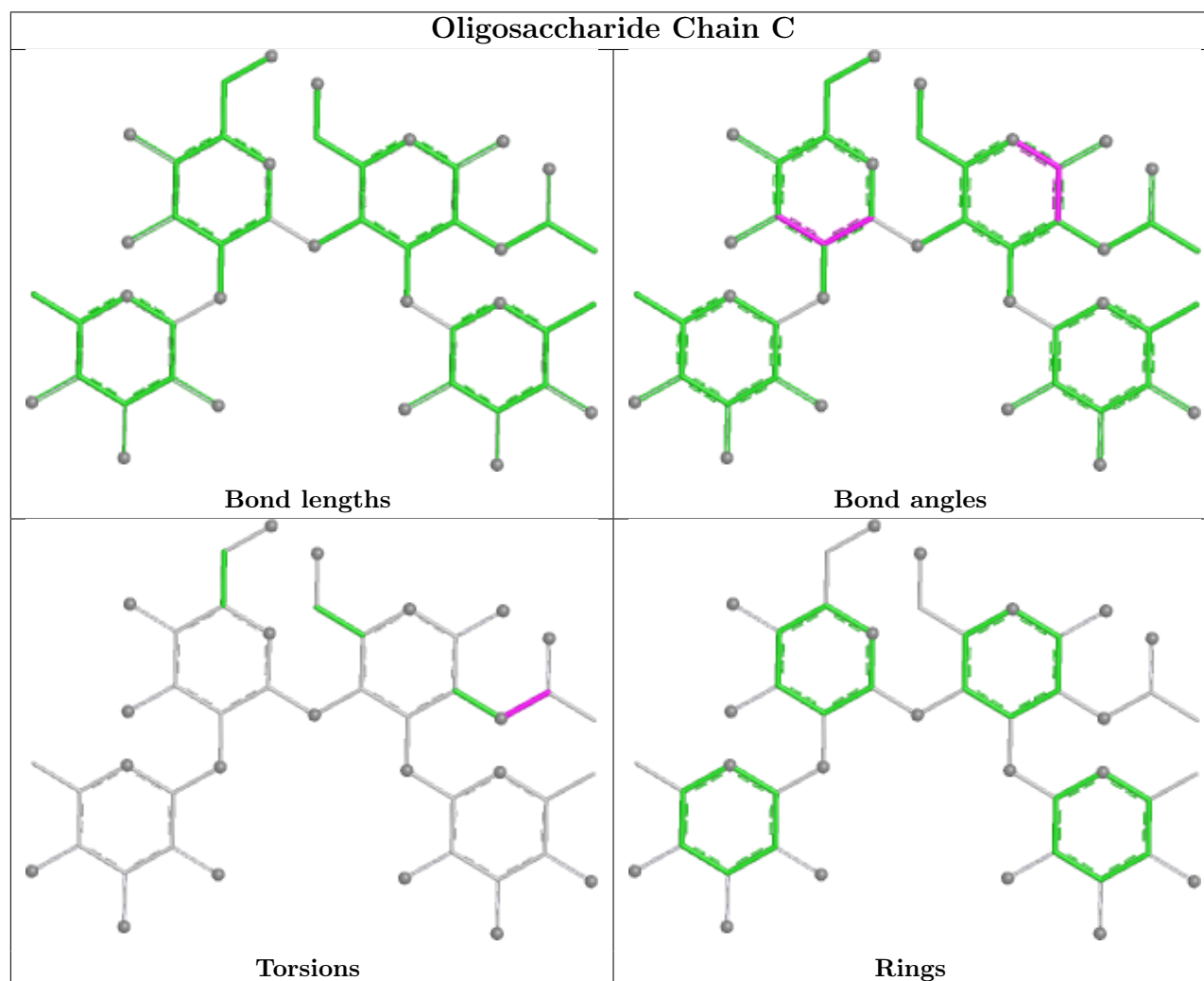
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	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](#)

24 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	$\# Z > 2$
3	EDO	A	539	-	3,3,3	0.34	0	2,2,2	0.41	0
3	EDO	A	19	-	3,3,3	0.46	0	2,2,2	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	16	-	3,3,3	0.39	0	2,2,2	0.41	0
4	IMD	A	24	-	5,5,5	0.53	0	5,5,5	0.52	0
3	EDO	A	541	-	3,3,3	0.50	0	2,2,2	0.26	0
3	EDO	A	6	-	3,3,3	0.41	0	2,2,2	0.37	0
3	EDO	B	1	-	3,3,3	0.33	0	2,2,2	0.47	0
3	EDO	A	23[B]	-	3,3,3	0.45	0	2,2,2	0.82	0
3	EDO	A	8	-	3,3,3	0.48	0	2,2,2	0.44	0
3	EDO	A	20	-	3,3,3	0.43	0	2,2,2	0.53	0
3	EDO	A	21	-	3,3,3	0.44	0	2,2,2	0.29	0
3	EDO	B	10	-	3,3,3	0.40	0	2,2,2	0.66	0
3	EDO	A	540	-	3,3,3	0.47	0	2,2,2	0.59	0
3	EDO	B	11	-	3,3,3	0.48	0	2,2,2	0.20	0
3	EDO	A	23[A]	-	3,3,3	0.44	0	2,2,2	0.59	0
3	EDO	A	22	-	3,3,3	0.43	0	2,2,2	0.43	0
3	EDO	B	15	-	3,3,3	0.42	0	2,2,2	0.48	0
3	EDO	A	13	-	3,3,3	0.46	0	2,2,2	0.32	0
3	EDO	B	7	-	3,3,3	0.43	0	2,2,2	0.19	0
3	EDO	A	18	-	3,3,3	0.39	0	2,2,2	0.30	0
3	EDO	A	5	-	3,3,3	0.44	0	2,2,2	0.38	0
3	EDO	B	14	-	3,3,3	0.44	0	2,2,2	0.36	0
3	EDO	B	12	-	3,3,3	0.47	0	2,2,2	0.26	0
3	EDO	A	17	-	3,3,3	0.44	0	2,2,2	0.31	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
3	EDO	A	539	-	-	0/1/1/1	-
3	EDO	A	19	-	-	1/1/1/1	-
3	EDO	A	16	-	-	0/1/1/1	-
4	IMD	A	24	-	-	-	0/1/1/1
3	EDO	A	541	-	-	0/1/1/1	-
3	EDO	A	6	-	-	1/1/1/1	-
3	EDO	B	1	-	-	0/1/1/1	-
3	EDO	A	23[B]	-	-	1/1/1/1	-
3	EDO	A	8	-	-	0/1/1/1	-
3	EDO	A	20	-	-	0/1/1/1	-
3	EDO	A	21	-	-	0/1/1/1	-
3	EDO	B	10	-	-	1/1/1/1	-
3	EDO	A	540	-	-	0/1/1/1	-
3	EDO	B	11	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	23[A]	-	-	1/1/1/1	-
3	EDO	A	22	-	-	0/1/1/1	-
3	EDO	B	15	-	-	0/1/1/1	-
3	EDO	A	13	-	-	0/1/1/1	-
3	EDO	B	7	-	-	0/1/1/1	-
3	EDO	A	18	-	-	0/1/1/1	-
3	EDO	A	5	-	-	0/1/1/1	-
3	EDO	B	14	-	-	0/1/1/1	-
3	EDO	B	12	-	-	1/1/1/1	-
3	EDO	A	17	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	19	EDO	O1-C1-C2-O2
3	A	6	EDO	O1-C1-C2-O2
3	A	23[A]	EDO	O1-C1-C2-O2
3	A	23[B]	EDO	O1-C1-C2-O2
3	B	10	EDO	O1-C1-C2-O2
3	B	12	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	539	EDO	1	0
3	A	16	EDO	3	0
4	A	24	IMD	1	0
3	A	6	EDO	3	0
3	B	7	EDO	1	0
3	A	18	EDO	3	0

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	315/319 (98%)	0.17	19 (6%) 27 30	6, 15, 36, 97	1 (0%)
1	B	310/319 (97%)	0.21	19 (6%) 27 29	7, 16, 39, 101	6 (1%)
All	All	625/638 (97%)	0.19	38 (6%) 27 29	6, 16, 38, 101	7 (1%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	490	THR	5.8
1	A	488	PRO	5.7
1	B	223	SER	5.5
1	A	491	GLY	5.3
1	B	434	PHE	4.7
1	B	298	HIS	4.5
1	B	490	THR	4.3
1	B	488	PRO	4.3
1	B	519[A]	THR	4.3
1	A	346	VAL	4.1
1	A	492	ARG	4.0
1	A	520	ASN	3.8
1	A	224	SER	3.8
1	A	519	THR	3.7
1	B	491	GLY	3.5
1	A	489	GLU	3.4
1	B	433	VAL	3.4
1	B	403	ASP	3.2
1	B	299	ARG	3.2
1	A	487	ASN	3.1
1	B	419	ALA	3.1
1	B	492	ARG	3.1
1	A	486	VAL	3.0
1	B	489	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	405	ASN	2.9
1	A	433	VAL	2.7
1	A	297	GLU	2.7
1	B	518[A]	PRO	2.7
1	A	518	PRO	2.7
1	B	351	ASN	2.6
1	A	347	PRO	2.6
1	B	510	ASN	2.4
1	A	419	ALA	2.4
1	A	345	THR	2.4
1	B	532	PHE	2.4
1	B	487	ASN	2.3
1	A	524	ARG	2.2
1	A	350	GLY	2.2

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

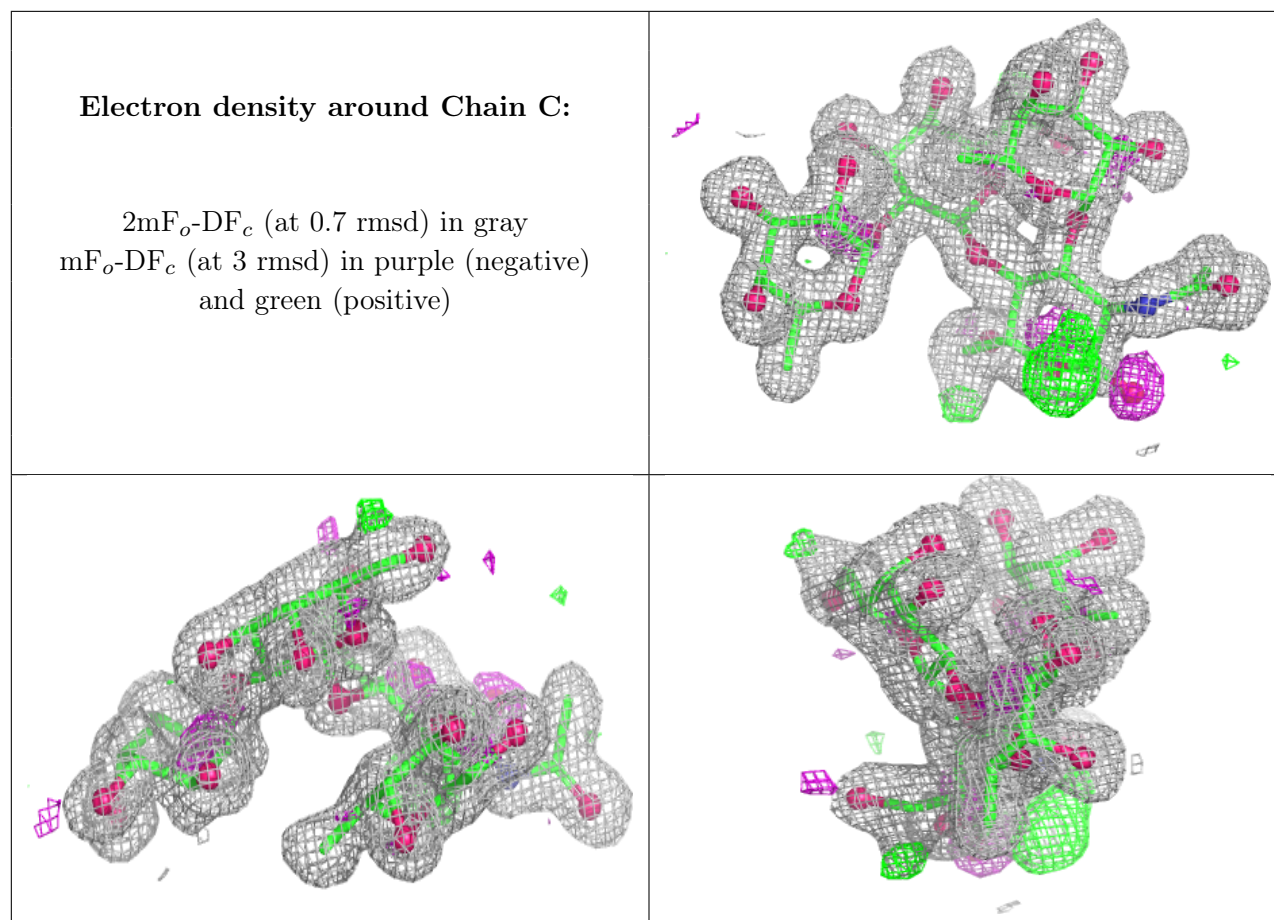
There are no non-standard protein/DNA/RNA residues in this entry.

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
2	NAG	C	1	15/15	0.87	0.11	16,21,30,39	0
2	GAL	C	2	11/12	0.92	0.08	16,20,23,27	0
2	FUC	C	3	10/11	0.94	0.07	14,16,16,18	0
2	FUC	C	4	10/11	0.96	0.06	14,17,19,21	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
3	EDO	A	20	4/4	0.71	0.20	40,40,44,47	0
3	EDO	A	16	4/4	0.81	0.15	33,33,34,36	0
3	EDO	A	19	4/4	0.82	0.15	31,34,37,37	0
3	EDO	A	8	4/4	0.84	0.16	24,27,27,29	0
3	EDO	A	13	4/4	0.85	0.17	25,26,28,29	0
3	EDO	A	18	4/4	0.85	0.16	31,34,35,37	0
3	EDO	B	15	4/4	0.87	0.24	25,27,28,31	0
3	EDO	A	5	4/4	0.89	0.10	25,27,30,32	0
4	IMD	A	24	5/5	0.89	0.12	14,18,25,27	0
3	EDO	A	17	4/4	0.90	0.11	27,29,31,32	0
3	EDO	B	12	4/4	0.91	0.10	27,30,31,32	0
3	EDO	B	14	4/4	0.91	0.09	30,31,33,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	A	6	4/4	0.91	0.10	27,28,30,35	0
3	EDO	B	10	4/4	0.91	0.10	19,22,26,34	0
3	EDO	A	540	4/4	0.93	0.10	16,21,26,28	0
3	EDO	A	21	4/4	0.93	0.10	14,22,23,27	0
3	EDO	A	23[A]	4/4	0.93	0.08	15,16,17,18	4
3	EDO	A	23[B]	4/4	0.93	0.08	14,17,18,18	4
3	EDO	B	7	4/4	0.93	0.11	23,25,26,26	0
3	EDO	A	539	4/4	0.95	0.09	12,12,16,19	0
3	EDO	B	1	4/4	0.95	0.07	11,11,11,13	0
3	EDO	A	22	4/4	0.96	0.12	13,15,19,22	0
3	EDO	A	541	4/4	0.96	0.08	13,14,15,16	0
3	EDO	B	11	4/4	0.97	0.06	13,14,15,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.