



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:48 AM UTC

PDB ID : 4BSF / pdb_00004bsf
Title : Human H7N9 Influenza Virus Haemagglutinin in Complex with Avian Receptor Analogue 3'-SLN
Authors : Xiong, X.; Haire, L.F.; Martin, S.R.; Wharton, S.A.; Daniels, R.S.; Bennett, M.S.; McCauley, J.W.; Collins, P.J.; Walker, P.A.; Skehel, J.J.; Gamblin, S.J.
Deposited on : 2013-06-10
Resolution : 2.76 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

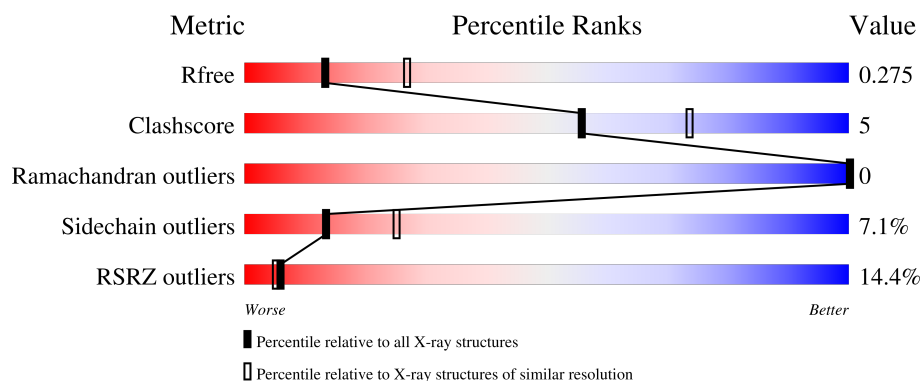
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	321	17% 81% 17% ..
2	B	177	10% 86% 8% ..
3	C	3	67% 33%
4	D	2	50% 50%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4078 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 HAEMAGGLUTININ HA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	1
			2413	1498	437	463	15			

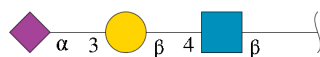
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	217	LEU	ILE	SEE REMARK 999	UNP M4YV75

- Molecule 2 is a protein called HAEMAGGLUTININ HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	170	Total	C	N	O	S	0	0	0
			1379	851	241	280	7			

- Molecule 3 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(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
			46	25	2	19			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

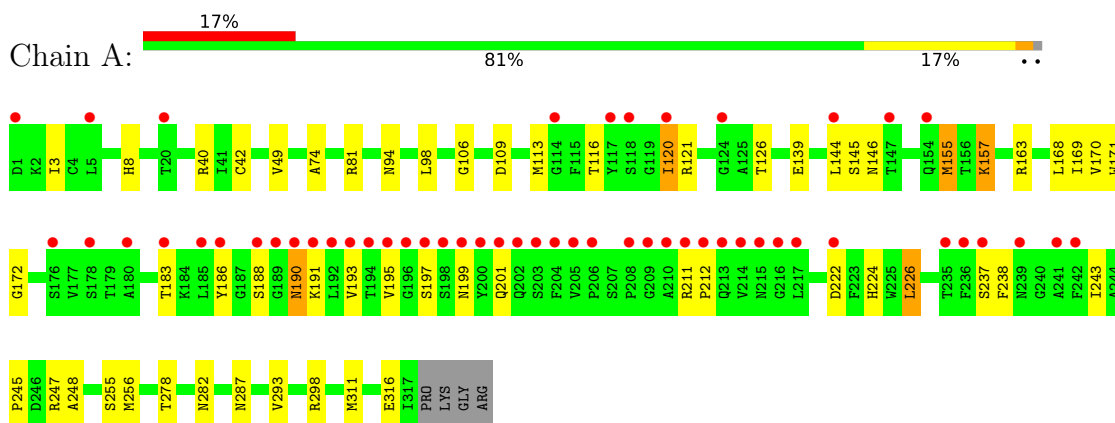
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	79	Total 79	O 79	0	0
7	B	26	Total 26	O 26	0	0

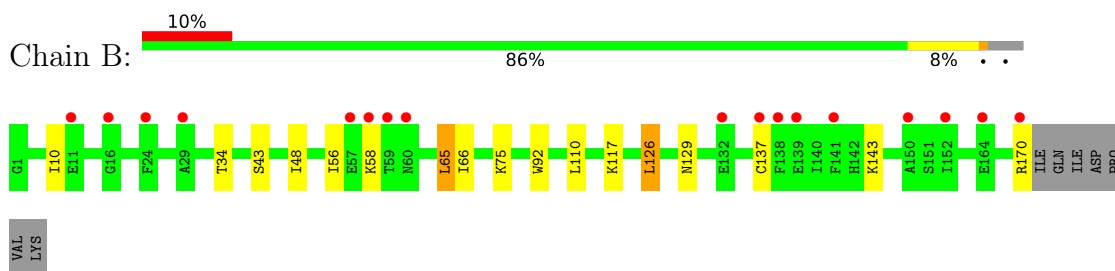
3 Residue-property plots

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.

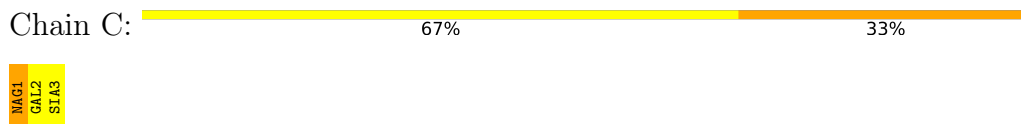
• Molecule 1: HAEMAGGLUTININ HA1



• Molecule 2: HAEMAGGLUTININ HA2



• Molecule 3: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 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	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	116.16Å 116.16Å 294.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.88 – 2.76 38.88 – 2.76	Depositor EDS
% Data completeness (in resolution range)	99.8 (38.88-2.76) 99.8 (38.88-2.76)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.223 , 0.276 0.226 , 0.275	Depositor DCC
R_{free} test set	1023 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.013 for $-1/3^*h+1/3^*k+1/3^*l,-k,8/3^*h+4/3^*k+1/3^*l$ 0.027 for $-2/3^*h-1/3^*k-1/3^*l,-1/3^*h-2/3^*k+1/3^*l,-4/3^*h+4/3^*k+1/3^*l$ 0.016 for $-h,1/3^*h-1/3^*k-1/3^*l,-4/3^*h-8/3^*k+1/3^*l$	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4078	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: SIA, GAL, SO4, NAG

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	0.55	1/2459 (0.0%)	0.77	0/3324
2	B	0.51	0/1403	0.76	0/1890
All	All	0.53	1/3862 (0.0%)	0.77	0/5214

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	316	GLU	C-N	-6.78	1.23	1.33

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	2413	0	2371	29	0
2	B	1379	0	1280	9	0
3	C	46	0	40	1	0
4	D	28	0	25	1	0
5	A	42	0	39	0	0
6	A	45	0	0	0	0
6	B	20	0	0	0	0
7	A	79	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	26	0	0	1	0
All	All	4078	0	3755	36	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 (36) 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:113:MET:HE2	1:A:248:ALA:HB2	1.78	0.64
1:A:282:ASN:HB3	2:B:56:ILE:HG23	1.85	0.59
2:B:129:ASN:ND2	7:B:2022:HOH:O	2.35	0.55
1:A:113:MET:HE3	1:A:245:PRO:HB2	1.89	0.54
1:A:183:THR:HG22	1:A:188:SER:HA	1.89	0.54
1:A:106:GLY:HA2	1:A:255:SER:HB3	1.90	0.53
1:A:139:GLU:OE1	1:A:247:ARG:HD3	2.09	0.53
1:A:121:ARG:NH1	1:A:145:SER:O	2.44	0.51
1:A:226:LEU:HD22	1:A:226:LEU:C	2.37	0.49
1:A:3:ILE:HG23	1:A:3:ILE:O	2.13	0.49
1:A:298:ARG:HG2	2:B:92:TRP:CE2	2.47	0.49
1:A:116:THR:O	1:A:157:LYS:NZ	2.46	0.49
1:A:293:VAL:HG11	2:B:65:LEU:HD13	1.97	0.47
1:A:172:GLY:O	1:A:243:ILE:N	2.38	0.47
2:B:129:ASN:HD22	2:B:129:ASN:N	2.14	0.46
1:A:49:VAL:HG23	1:A:74:ALA:HB2	1.97	0.46
2:B:110:LEU:C	2:B:110:LEU:HD23	2.41	0.46
1:A:171:TRP:CZ2	1:A:195:VAL:HG21	2.51	0.45
2:B:75:LYS:HE3	4:D:1:NAG:H81	1.99	0.45
1:A:120:ILE:HD12	1:A:155:MET:HE1	1.98	0.45
1:A:287:ASN:CG	1:A:287:ASN:O	2.60	0.44
3:C:1:NAG:O3	3:C:1:NAG:H82	2.17	0.44
1:A:222:ASP:HB3	1:A:224:HIS:CE1	2.53	0.43
1:A:170:VAL:O	1:A:245:PRO:HB3	2.18	0.43
1:A:121:ARG:NH1	1:A:146:ASN:O	2.51	0.43
1:A:139:GLU:OE1	1:A:139:GLU:HA	2.19	0.43
1:A:98:LEU:HD11	1:A:168:LEU:HD21	2.01	0.43
2:B:10:ILE:N	2:B:10:ILE:HD12	2.34	0.42
1:A:113:MET:HE1	1:A:169:ILE:HG23	2.02	0.41
1:A:211:ARG:HB3	1:A:212:PRO:HD2	2.00	0.41
1:A:193:VAL:HG22	1:A:238:PHE:CB	2.50	0.41
1:A:155:MET:O	1:A:237:SER:HA	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:126:LEU:N	2:B:126:LEU:HD13	2.34	0.41
1:A:190:ASN:OD1	1:A:190:ASN:N	2.50	0.41
1:A:8:HIS:CD2	1:A:311:MET:HE3	2.55	0.41
1:A:42:CYS:HB2	1:A:278:THR:HG21	2.02	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	315/321 (98%)	302 (96%)	13 (4%)	0	100	100
2	B	168/177 (95%)	159 (95%)	9 (5%)	0	100	100
All	All	483/498 (97%)	461 (95%)	22 (5%)	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	265/269 (98%)	247 (93%)	18 (7%)	14	27
2	B	145/152 (95%)	134 (92%)	11 (8%)	12	23
All	All	410/421 (97%)	381 (93%)	29 (7%)	13	25

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	81	ARG
1	A	94	ASN
1	A	109	ASP
1	A	120	ILE
1	A	126	THR
1	A	144	LEU
1	A	155	MET
1	A	157	LYS
1	A	163	ARG
1	A	186	TYR
1	A	190	ASN
1	A	191	LYS
1	A	197	SER
1	A	199	ASN
1	A	201	GLN
1	A	226	LEU
1	A	256	MET
2	B	34	THR
2	B	43	SER
2	B	48	ILE
2	B	58	LYS
2	B	65	LEU
2	B	66	ILE
2	B	117	LYS
2	B	126	LEU
2	B	137	CYS
2	B	143	LYS
2	B	170	ARG

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	146	ASN
1	A	199	ASN
1	A	201	GLN
1	A	224	HIS
1	A	287	ASN
2	B	129	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 ⓘ

5 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	15,15,15	0.51	0	21,21,21	1.70	5 (23%)
3	GAL	C	2	3	11,11,12	0.47	0	15,15,17	1.01	1 (6%)
3	SIA	C	3	3	20,20,21	0.64	0	21,28,31	1.21	3 (14%)
4	NAG	D	1	2,4	14,14,15	0.55	0	17,19,21	1.19	2 (11%)
4	NAG	D	2	4	14,14,15	0.65	0	17,19,21	1.09	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
3	NAG	C	1	3	-	6/6/26/26	0/1/1/1
3	GAL	C	2	3	-	1/2/19/22	0/1/1/1
3	SIA	C	3	3	-	2/18/34/38	0/1/1/1
4	NAG	D	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C1-C2-N2	-4.99	104.95	110.73
3	C	3	SIA	C4-C5-N5	-3.42	103.70	110.44
3	C	1	NAG	C8-C7-N2	2.66	120.53	116.12
3	C	1	NAG	C4-C3-C2	2.55	114.11	110.40
4	D	2	NAG	C4-C3-C2	2.50	114.68	111.02
3	C	1	NAG	C2-N2-C7	2.40	128.72	123.11
3	C	2	GAL	C2-C3-C4	2.35	115.00	110.86
3	C	1	NAG	C3-C4-C5	2.18	114.18	110.23
3	C	3	SIA	O6-C2-C1	2.15	111.78	107.72
3	C	3	SIA	O1B-C1-C2	2.14	118.27	112.71
4	D	1	NAG	O7-C7-N2	2.10	125.70	121.98
4	D	1	NAG	O5-C1-C2	-2.10	108.04	111.29
4	D	2	NAG	O7-C7-C8	-2.10	118.32	122.05

There are no chirality outliers.

All (11) torsion outliers are listed below:

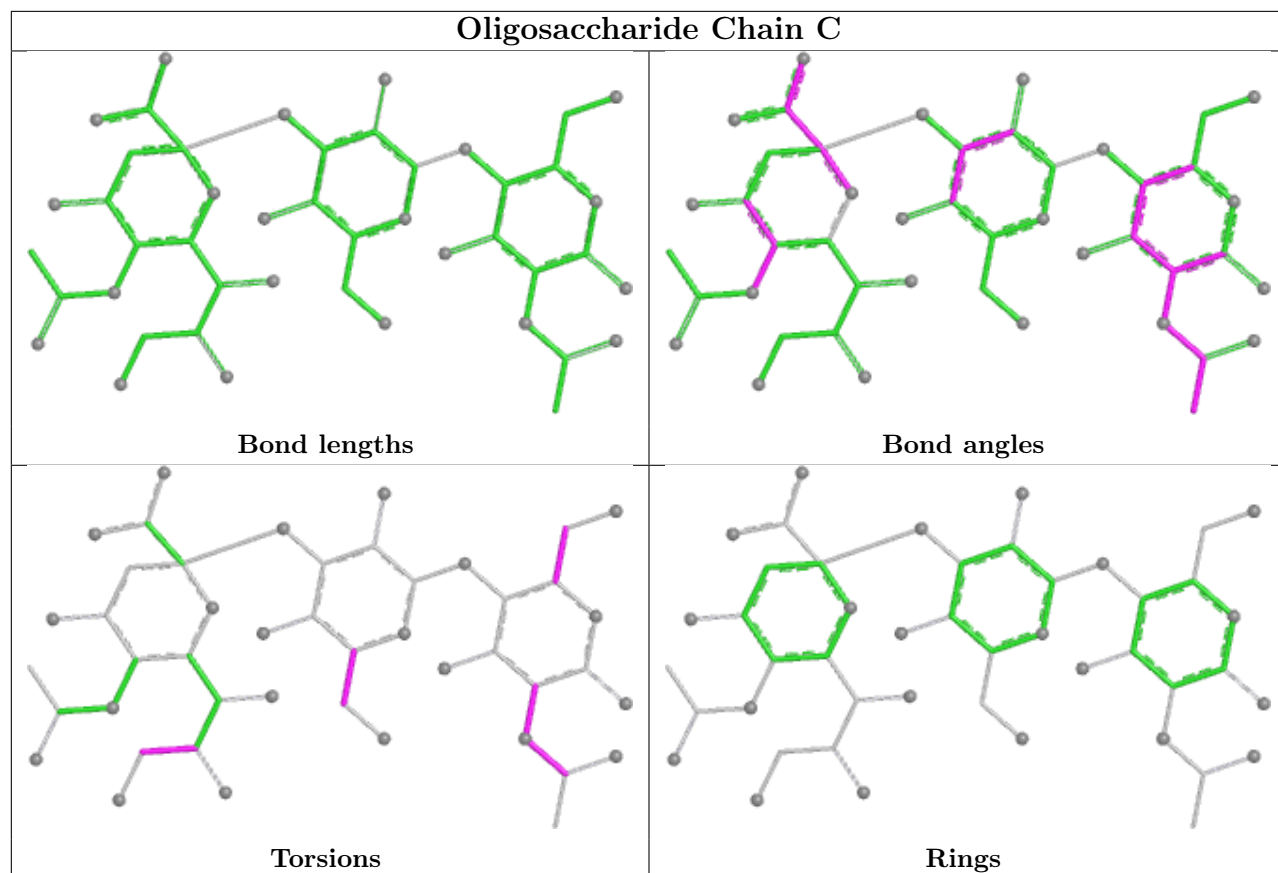
Mol	Chain	Res	Type	Atoms
3	C	3	SIA	C7-C8-C9-O9
3	C	3	SIA	O8-C8-C9-O9
3	C	1	NAG	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
3	C	1	NAG	C8-C7-N2-C2
3	C	1	NAG	O7-C7-N2-C2
3	C	1	NAG	C1-C2-N2-C7
3	C	2	GAL	C4-C5-C6-O6
3	C	1	NAG	C3-C2-N2-C7

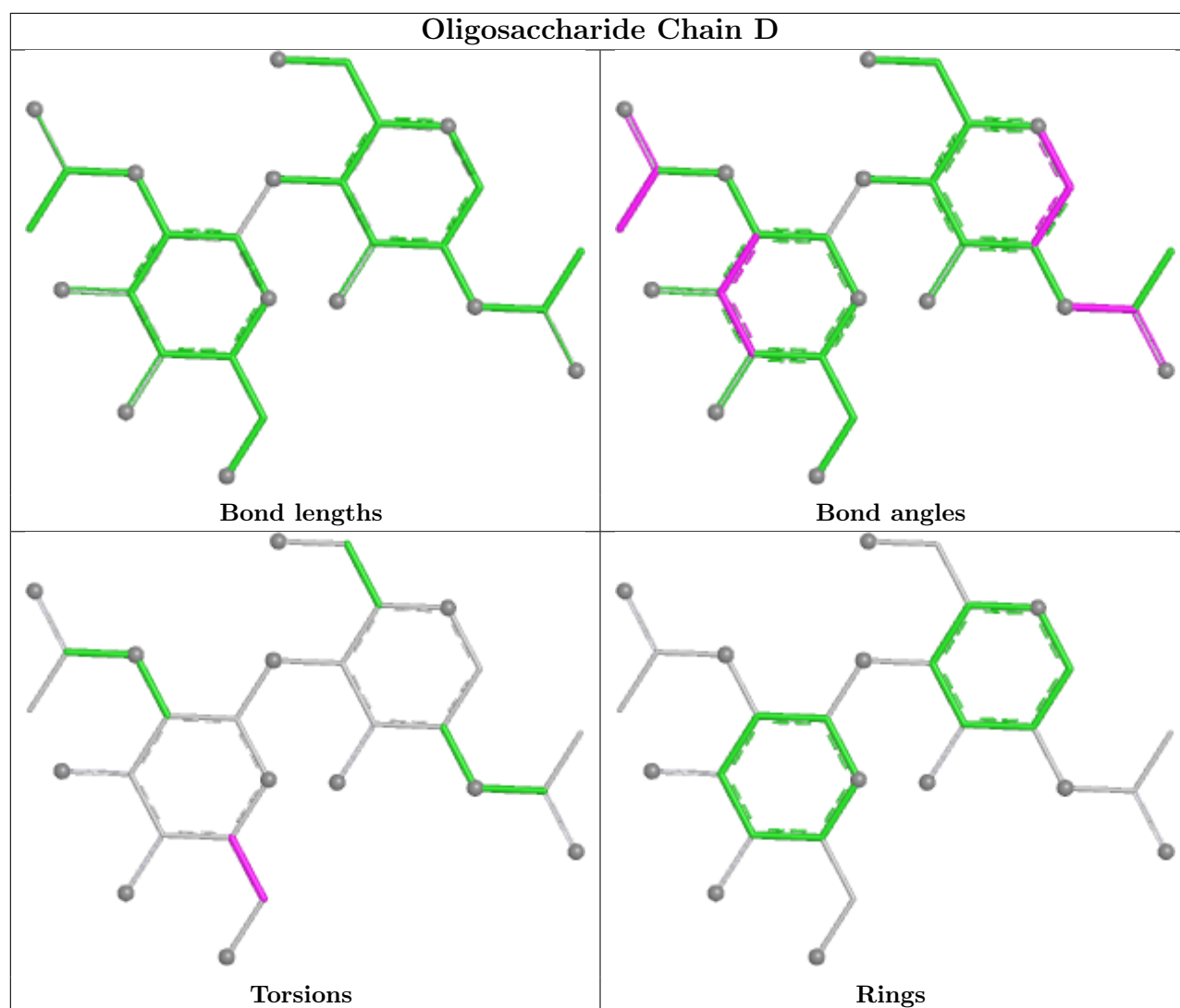
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	1	0
4	D	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](#)

16 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	SO4	A	1330	-	4,4,4	0.45	0	6,6,6	0.13	0
6	SO4	A	1331	-	4,4,4	0.45	0	6,6,6	0.16	0
6	SO4	B	1176	-	4,4,4	0.42	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	1318	1	14,14,15	0.46	0	17,19,21	1.30	1 (5%)
5	NAG	A	1319	1	14,14,15	0.52	0	17,19,21	1.16	2 (11%)
6	SO4	A	1324	-	4,4,4	0.45	0	6,6,6	0.11	0
6	SO4	A	1325	-	4,4,4	0.50	0	6,6,6	0.32	0
6	SO4	B	1173	-	4,4,4	0.46	0	6,6,6	0.18	0
5	NAG	A	1317	1	14,14,15	0.67	0	17,19,21	1.22	1 (5%)
6	SO4	A	1326	-	4,4,4	0.45	0	6,6,6	0.08	0
6	SO4	B	1174	-	4,4,4	0.44	0	6,6,6	0.09	0
6	SO4	A	1327	-	4,4,4	0.46	0	6,6,6	0.29	0
6	SO4	A	1328	-	4,4,4	0.47	0	6,6,6	0.23	0
6	SO4	B	1175	-	4,4,4	0.47	0	6,6,6	0.33	0
6	SO4	A	1329	-	4,4,4	0.44	0	6,6,6	0.15	0
6	SO4	A	1323	-	4,4,4	0.47	0	6,6,6	0.12	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
5	NAG	A	1317	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1318	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1319	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1317	NAG	C4-C3-C2	3.49	116.13	111.02
5	A	1319	NAG	C1-O5-C5	2.79	115.93	112.19
5	A	1318	NAG	O5-C1-C2	-2.75	107.04	111.29
5	A	1319	NAG	C1-C2-N2	2.58	114.51	110.43

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1319	NAG	O5-C5-C6-O6
5	A	1319	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	317/321 (98%)	0.69	53 (16%) 4 4	24, 51, 115, 147	0
2	B	170/177 (96%)	0.65	17 (10%) 12 12	20, 75, 123, 139	0
All	All	487/498 (97%)	0.68	70 (14%) 6 5	20, 59, 122, 147	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	196	GLY	7.6
1	A	192	LEU	5.9
1	A	205	VAL	5.5
1	A	194	THR	5.1
1	A	195	VAL	5.0
1	A	214	VAL	4.8
1	A	204	PHE	4.6
1	A	198	SER	4.6
1	A	215	ASN	4.6
1	A	201	GLN	4.5
1	A	213	GLN	4.5
1	A	217	LEU	4.3
1	A	189	GLY	4.1
1	A	197	SER	4.1
1	A	216	GLY	3.9
1	A	191	LYS	3.8
1	A	193	VAL	3.8
1	A	200	TYR	3.6
1	A	203	SER	3.6
1	A	237	SER	3.6
1	A	1	ASP	3.5
1	A	212	PRO	3.5
1	A	235	THR	3.2
1	A	186	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	239	ASN	3.0
2	B	58	LYS	3.0
1	A	188	SER	3.0
1	A	190	ASN	3.0
1	A	183	THR	3.0
2	B	132	GLU	2.9
1	A	210	ALA	2.9
1	A	199	ASN	2.8
1	A	185	LEU	2.8
1	A	202	GLN	2.7
1	A	180	ALA	2.6
2	B	138	PHE	2.5
1	A	222	ASP	2.4
1	A	5	LEU	2.4
2	B	16	GLY	2.4
1	A	118	SER	2.3
1	A	241	ALA	2.3
1	A	120	ILE	2.3
1	A	20	THR	2.3
1	A	147	THR	2.3
2	B	139	GLU	2.3
1	A	154	GLN	2.3
1	A	114	GLY	2.3
1	A	209	GLY	2.3
2	B	141	PHE	2.3
1	A	211	ARG	2.2
2	B	24	PHE	2.2
2	B	57	GLU	2.2
1	A	178	SER	2.2
2	B	11	GLU	2.1
2	B	164	GLU	2.1
2	B	60	ASN	2.1
1	A	117	TYR	2.1
1	A	176	SER	2.1
1	A	242	PHE	2.1
1	A	206	PRO	2.1
2	B	59	THR	2.1
1	A	208	PRO	2.1
1	A	124	GLY	2.1
1	A	236	PHE	2.1
1	A	144	LEU	2.1
2	B	137	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	29	ALA	2.0
2	B	150	ALA	2.0
2	B	152	ILE	2.0
2	B	170	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

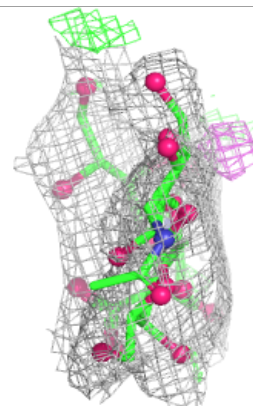
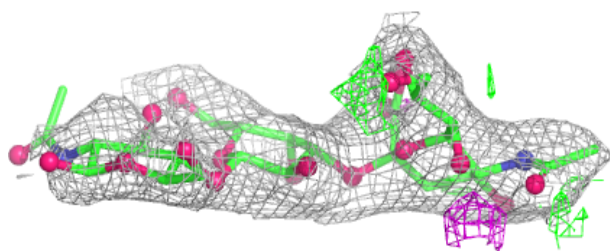
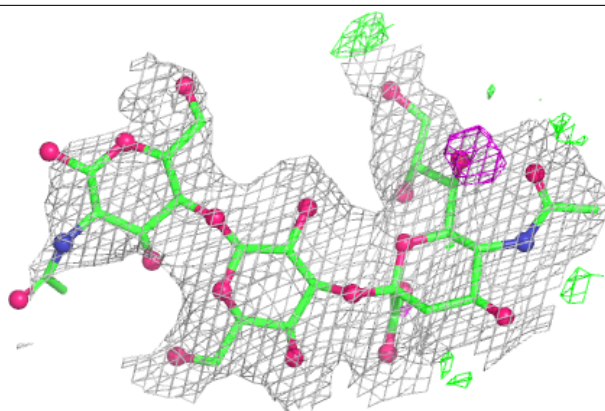
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	C	1	15/15	0.63	0.17	96,106,111,112	0
4	NAG	D	2	14/15	0.75	0.14	61,69,76,76	0
3	GAL	C	2	11/12	0.79	0.12	68,79,84,86	0
3	SIA	C	3	20/21	0.85	0.13	53,55,63,64	0
4	NAG	D	1	14/15	0.87	0.11	42,52,56,63	0

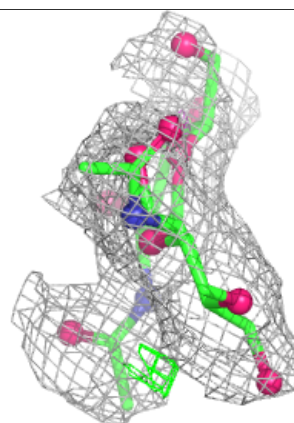
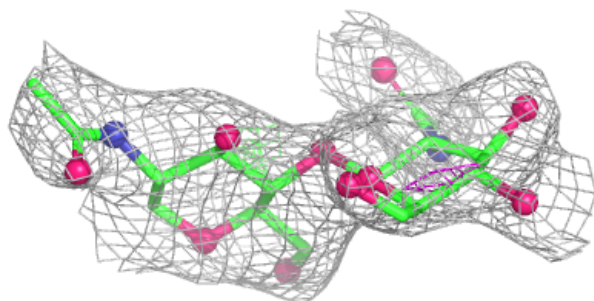
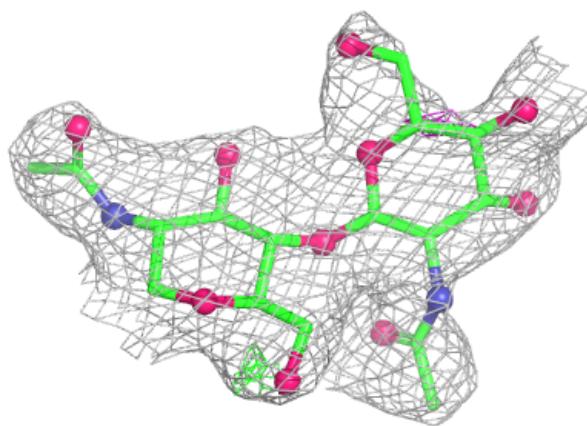
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

**Electron density around Chain D:**

$2mF_o-DF_c$ (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($\text{\AA}^2$)	Q<0.9
5	NAG	A	1319	14/15	0.46	0.17	87,98,101,106	0
6	SO4	A	1331	5/5	0.55	0.16	128,132,134,134	0
5	NAG	A	1317	14/15	0.62	0.16	70,82,84,84	0
6	SO4	A	1324	5/5	0.64	0.12	112,115,119,119	0
5	NAG	A	1318	14/15	0.68	0.14	62,75,82,85	0
6	SO4	A	1323	5/5	0.69	0.24	95,99,103,104	0
6	SO4	B	1174	5/5	0.70	0.14	123,128,130,132	0
6	SO4	A	1329	5/5	0.71	0.13	116,121,127,129	0
6	SO4	A	1330	5/5	0.71	0.22	92,92,94,97	0
6	SO4	A	1325	5/5	0.72	0.20	85,88,95,98	0
6	SO4	A	1326	5/5	0.73	0.14	121,123,126,127	0
6	SO4	A	1327	5/5	0.76	0.26	89,93,100,107	0
6	SO4	A	1328	5/5	0.81	0.16	85,89,92,94	0
6	SO4	B	1175	5/5	0.81	0.28	76,85,88,88	0
6	SO4	B	1176	5/5	0.82	0.28	90,90,91,92	4
6	SO4	B	1173	5/5	0.85	0.14	79,79,85,86	0

6.5 Other polymers

There are no such residues in this entry.