



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:08 AM UTC

PDB ID : 6TJW / pdb_00006tjw
Title : Crystal structure of the haemagglutinin mutant (Gln226Leu, Del228) from an H10N7 seal influenza virus isolated in Germany
Authors : Zhang, J.; Xiong, X.; Purkiss, A.; Walker, P.; Gamblin, S.; Skehel, J.J.
Deposited on : 2019-11-27
Resolution : 2.31 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

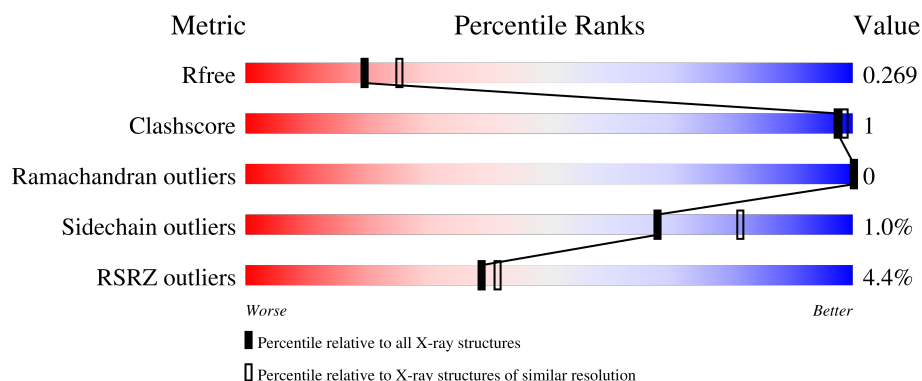
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	324	2% 94%
1	C	324	3% 94%
1	E	324	11% 96%
2	B	177	0% 96%
2	D	177	2% 93%

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Mol	Chain	Length	Quality of chain
2	F	177	3% 95%
3	G	2	50% 50%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12274 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 Hemagglutinin HA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	1	0
			2429	1508	438	467	16			
1	C	311	Total	C	N	O	S	0	2	0
			2397	1488	432	461	16			
1	E	319	Total	C	N	O	S	0	0	0
			2441	1515	442	468	16			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ASP	-	expression tag	UNP A0A0A7HR51
A	1	PRO	-	expression tag	UNP A0A0A7HR51
A	?	-	GLY	deletion	UNP A0A0A7HR51
C	0	ASP	-	expression tag	UNP A0A0A7HR51
C	1	PRO	-	expression tag	UNP A0A0A7HR51
C	?	-	GLY	deletion	UNP A0A0A7HR51
E	0	ASP	-	expression tag	UNP A0A0A7HR51
E	1	PRO	-	expression tag	UNP A0A0A7HR51
E	?	-	GLY	deletion	UNP A0A0A7HR51

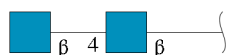
- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1386	857	241	280	8			
2	D	172	Total	C	N	O	S	0	0	0
			1386	857	241	280	8			
2	F	172	Total	C	N	O	S	0	0	0
			1386	857	241	280	8			

There are 3 discrepancies between the modelled and reference sequences:

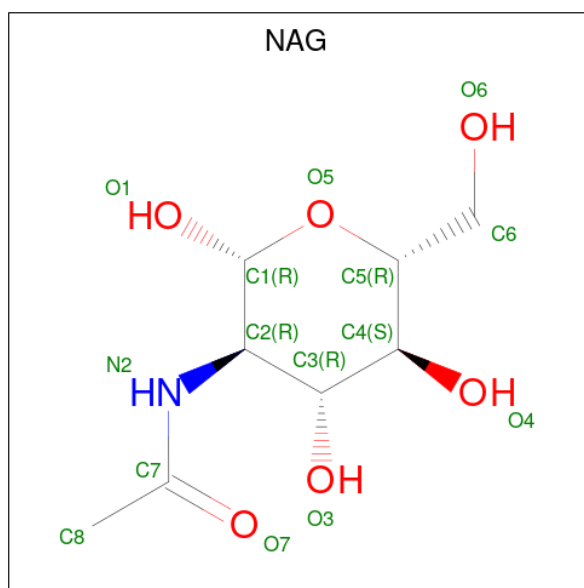
Chain	Residue	Modelled	Actual	Comment	Reference
B	177	LYS	-	expression tag	UNP A0A0A7HR51
D	177	LYS	-	expression tag	UNP A0A0A7HR51
F	177	LYS	-	expression tag	UNP A0A0A7HR51

- Molecule 3 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
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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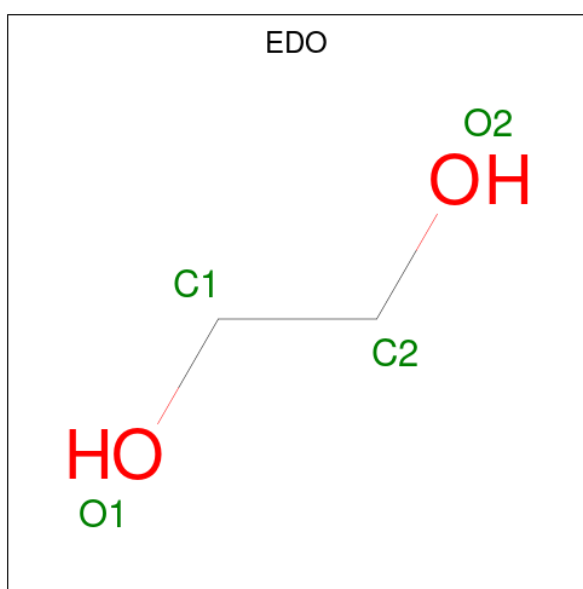
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	E	1	Total	C	O	0	0
			4	2	2		
6	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	190	Total	O	0	0
			190	190		

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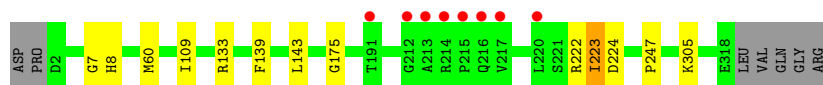
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	114	Total 114	O 114	0	0
7	C	160	Total 160	O 160	0	0
7	D	97	Total 97	O 97	0	0
7	E	80	Total 80	O 80	0	0
7	F	93	Total 93	O 93	0	0

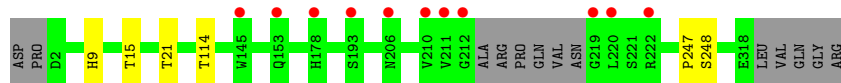
3 Residue-property plots [i](#)

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.

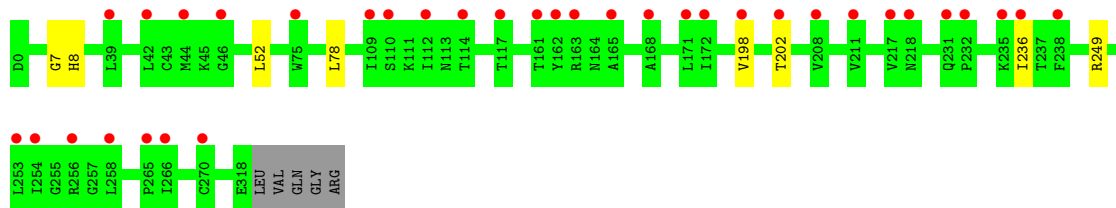
• Molecule 1: Hemagglutinin HA1



• Molecule 1: Hemagglutinin HA1



• Molecule 1: Hemagglutinin HA1



• Molecule 2: Hemagglutinin HA2

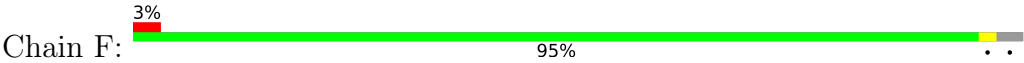


• Molecule 2: Hemagglutinin HA2





● Molecule 2: Hemagglutinin HA2



● Molecule 3: 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 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.29Å 210.46Å 82.75Å 90.00° 101.40° 90.00°	Depositor
Resolution (Å)	41.60 – 2.31 41.60 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.60-2.31) 99.7 (41.60-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.32Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.239 , 0.281 0.227 , 0.269	Depositor DCC
R_{free} test set	4952 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	35.4	Xtriage
Anisotropy	0.899	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 30.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12274	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, EDO, 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	0.51	0/2478	0.69	0/3357
1	C	0.50	0/2444	0.67	0/3307
1	E	0.55	0/2491	0.69	0/3375
2	B	0.50	0/1411	0.77	0/1903
2	D	0.53	0/1411	0.78	0/1903
2	F	0.52	0/1411	0.77	0/1903
All	All	0.52	0/11646	0.72	0/15748

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 [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	2429	0	2384	8	0
1	C	2397	0	2353	1	0
1	E	2441	0	2404	4	0
2	B	1386	0	1291	4	0
2	D	1386	0	1291	5	0
2	F	1386	0	1291	2	0
3	G	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	14	0	13	0	0
4	C	14	0	13	0	0
4	D	14	0	13	0	0
4	E	14	0	13	0	0
4	F	14	0	13	0	0
5	B	1	0	0	0	0
6	C	8	0	12	0	0
6	E	4	0	6	0	0
6	F	4	0	6	0	0
7	A	190	0	0	0	0
7	B	114	0	0	0	0
7	C	160	0	0	0	0
7	D	97	0	0	0	0
7	E	80	0	0	0	0
7	F	93	0	0	0	0
All	All	12274	0	11128	18	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 1.

All (18) 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:7:GLY:C	2:B:115:MET:HE1	2.20	0.66
1:A:60:MET:HE2	1:A:109:ILE:HD12	1.83	0.61
1:E:7:GLY:C	2:F:115:MET:HE1	2.28	0.59
2:D:44:ALA:HA	2:D:110:MET:HE1	1.87	0.55
1:A:175:GLY:HA3	1:A:223:ILE:HD11	1.88	0.54
2:D:74:ASP:HB2	2:D:77:ILE:HG22	1.90	0.53
1:A:8:HIS:HB3	2:B:115:MET:HE2	1.91	0.53
2:D:115:MET:HA	2:D:115:MET:HE3	1.94	0.50
1:E:8:HIS:HB3	2:F:115:MET:CE	2.44	0.47
1:E:52:LEU:HD21	1:E:78:LEU:HD11	1.95	0.47
1:A:143:LEU:HD23	1:A:247:PRO:HA	1.96	0.46
1:A:133:ARG:NH2	1:A:139:PHE:O	2.48	0.46
1:A:222:ARG:NH1	1:A:224:ASP:OD1	2.49	0.45
1:C:114:THR:HG21	1:C:247:PRO:O	2.17	0.44
2:D:76:GLN:HA	2:D:76:GLN:HE21	1.85	0.42
1:A:8:HIS:HB3	2:B:115:MET:CE	2.49	0.42
1:E:198:VAL:HG12	1:E:236:ILE:HD11	2.01	0.42
2:B:94:TYR:OH	2:D:99:LEU:HD22	2.20	0.41

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	316/324 (98%)	309 (98%)	7 (2%)	0	100	100
1	C	309/324 (95%)	301 (97%)	8 (3%)	0	100	100
1	E	317/324 (98%)	307 (97%)	10 (3%)	0	100	100
2	B	170/177 (96%)	164 (96%)	6 (4%)	0	100	100
2	D	170/177 (96%)	165 (97%)	5 (3%)	0	100	100
2	F	170/177 (96%)	165 (97%)	5 (3%)	0	100	100
All	All	1452/1503 (97%)	1411 (97%)	41 (3%)	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	269/275 (98%)	267 (99%)	2 (1%)	76	86
1	C	266/275 (97%)	262 (98%)	4 (2%)	57	73
1	E	271/275 (98%)	269 (99%)	2 (1%)	76	86
2	B	146/151 (97%)	146 (100%)	0	100	100
2	D	146/151 (97%)	144 (99%)	2 (1%)	59	75
2	F	146/151 (97%)	144 (99%)	2 (1%)	59	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1244/1278 (97%)	1232 (99%)	12 (1%)	68 81

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	ILE
1	A	305	LYS
1	C	9	HIS
1	C	15	THR
1	C	21	THR
1	C	248	SER
2	D	76	GLN
2	D	125	GLN
1	E	202	THR
1	E	249	ARG
2	F	125	GLN
2	F	171	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	HIS
1	A	113	ASN
1	A	137	ASN
1	A	150	ASN
1	A	157	GLN
1	A	206	ASN
1	A	216	GLN
1	A	268	ASN
1	A	297	GLN
2	B	105	GLN
1	C	9	HIS
2	D	12	ASN
2	D	47	GLN
2	D	75	HIS
2	D	76	GLN
2	D	79	ASN
2	D	95	GLN
2	D	155	ASN
2	D	161	GLN
1	E	49	HIS

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Mol	Chain	Res	Type
1	E	186	ASN
1	E	216	GLN
1	E	226	HIS
1	E	231	GLN
2	F	12	ASN
2	F	159	HIS
2	F	161	GLN
2	F	172	ASN

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](#)

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	G	1	2,3,5	14,14,15	0.41	0	17,19,21	0.96	1 (5%)
3	NAG	G	2	3	14,14,15	0.38	0	17,19,21	0.74	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	NAG	G	1	2,3,5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	1	NAG	C1-O5-C5	2.21	115.15	112.19

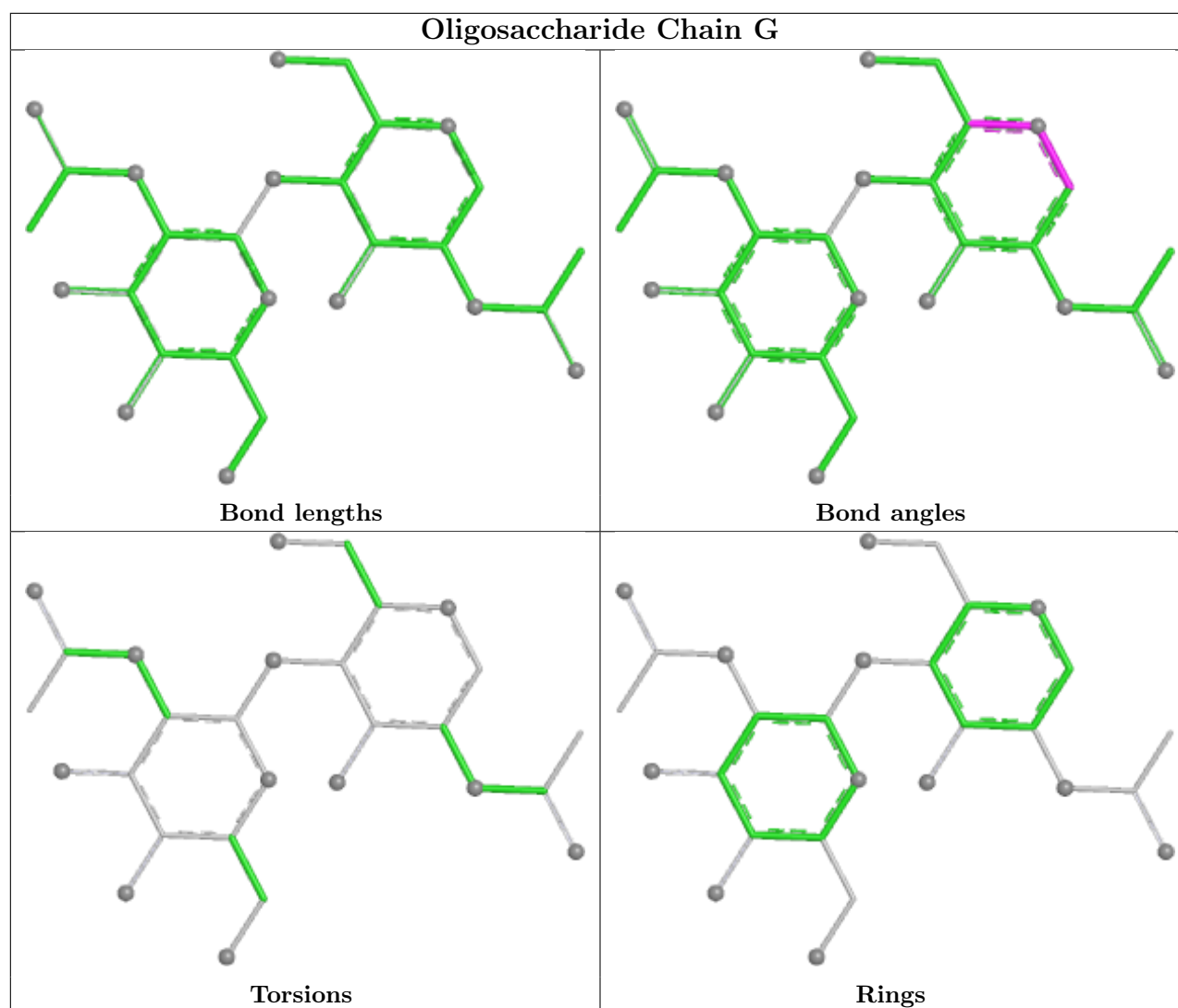
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	NAG	E	401	1	14,14,15	0.50	0	17,19,21	0.74	0
4	NAG	D	201	2	14,14,15	0.40	0	17,19,21	1.05	1 (5%)
6	EDO	E	402	-	3,3,3	0.39	0	2,2,2	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	F	202	-	3,3,3	0.42	0	2,2,2	0.39	0
6	EDO	C	402	-	3,3,3	0.49	0	2,2,2	0.19	0
6	EDO	C	403	-	3,3,3	0.41	0	2,2,2	0.40	0
4	NAG	C	401	1	14,14,15	0.38	0	17,19,21	1.17	2 (11%)
4	NAG	F	201	2	14,14,15	0.50	0	17,19,21	1.00	1 (5%)
4	NAG	A	401	1	14,14,15	0.46	0	17,19,21	0.75	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	NAG	E	401	1	-	0/6/23/26	0/1/1/1
4	NAG	D	201	2	-	2/6/23/26	0/1/1/1
6	EDO	E	402	-	-	0/1/1/1	-
6	EDO	F	202	-	-	1/1/1/1	-
6	EDO	C	402	-	-	1/1/1/1	-
6	EDO	C	403	-	-	0/1/1/1	-
4	NAG	C	401	1	-	2/6/23/26	0/1/1/1
4	NAG	F	201	2	-	0/6/23/26	0/1/1/1
4	NAG	A	401	1	-	1/6/23/26	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(°)
4	D	201	NAG	C1-O5-C5	3.02	116.23	112.19
4	F	201	NAG	C1-O5-C5	2.92	116.10	112.19
4	C	401	NAG	C2-N2-C7	2.74	126.57	122.90
4	C	401	NAG	C8-C7-N2	2.50	120.27	116.12

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	201	NAG	O5-C5-C6-O6
4	D	201	NAG	C4-C5-C6-O6
4	C	401	NAG	C8-C7-N2-C2
4	C	401	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
6	F	202	EDO	O1-C1-C2-O2
6	C	402	EDO	O1-C1-C2-O2
4	A	401	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	317/324 (97%)	0.16	8 (2%) 58 61	23, 45, 73, 144	1 (0%)
1	C	311/324 (95%)	0.21	11 (3%) 47 50	18, 46, 85, 108	2 (0%)
1	E	319/324 (98%)	0.96	35 (10%) 10 12	34, 74, 101, 119	0
2	B	172/177 (97%)	0.09	2 (1%) 76 78	27, 44, 60, 78	0
2	D	172/177 (97%)	0.19	3 (1%) 69 71	30, 48, 68, 86	0
2	F	172/177 (97%)	0.30	6 (3%) 47 50	31, 48, 83, 98	0
All	All	1463/1503 (97%)	0.35	65 (4%) 39 41	18, 49, 90, 144	3 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	215	PRO	5.7
1	A	213	ALA	5.2
1	A	220	LEU	4.5
1	A	217	VAL	4.4
1	C	220	LEU	3.8
1	E	253	LEU	3.8
2	F	73	ILE	3.8
1	E	270	CYS	3.5
1	C	210	VAL	3.4
1	E	117	THR	3.4
1	C	212	GLY	3.3
2	F	58	LYS	3.3
1	E	165	ALA	3.3
1	E	109	ILE	3.3
1	A	214	ARG	3.3
1	E	110	SER	3.3
1	E	162	TYR	3.2
2	D	74	ASP	3.2
1	E	112	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	216	GLN	3.0
1	C	219	GLY	3.0
1	E	171	LEU	3.0
1	E	266	ILE	3.0
2	F	59	THR	2.9
1	E	238	PHE	2.9
1	C	211	VAL	2.9
1	E	211	VAL	2.9
1	E	217	VAL	2.8
1	E	172	ILE	2.8
1	E	39	LEU	2.7
1	E	75	TRP	2.6
1	E	236	ILE	2.6
1	E	42	LEU	2.6
1	E	168	ALA	2.5
1	A	191	THR	2.5
1	E	114	THR	2.5
1	E	163	ARG	2.5
1	E	231	GLN	2.5
1	C	153	GLN	2.4
2	B	73	ILE	2.4
1	E	256	ARG	2.4
2	F	66	ILE	2.4
1	E	46	GLY	2.4
1	E	258	LEU	2.3
1	E	218	ASN	2.3
2	F	61	THR	2.3
1	E	232	PRO	2.3
1	C	222	ARG	2.2
1	E	254	ILE	2.2
2	F	60	ASN	2.2
1	E	265	PRO	2.2
1	A	212	GLY	2.2
1	E	44	MET	2.2
1	C	206	ASN	2.1
2	B	74	ASP	2.1
1	C	193	SER	2.1
1	E	208	VAL	2.1
1	C	145	TRP	2.1
1	E	161	THR	2.0
1	E	198	VAL	2.0
1	E	235	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	E	202	THR	2.0
1	C	178	HIS	2.0
2	D	75	HIS	2.0
2	D	73	ILE	2.0

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

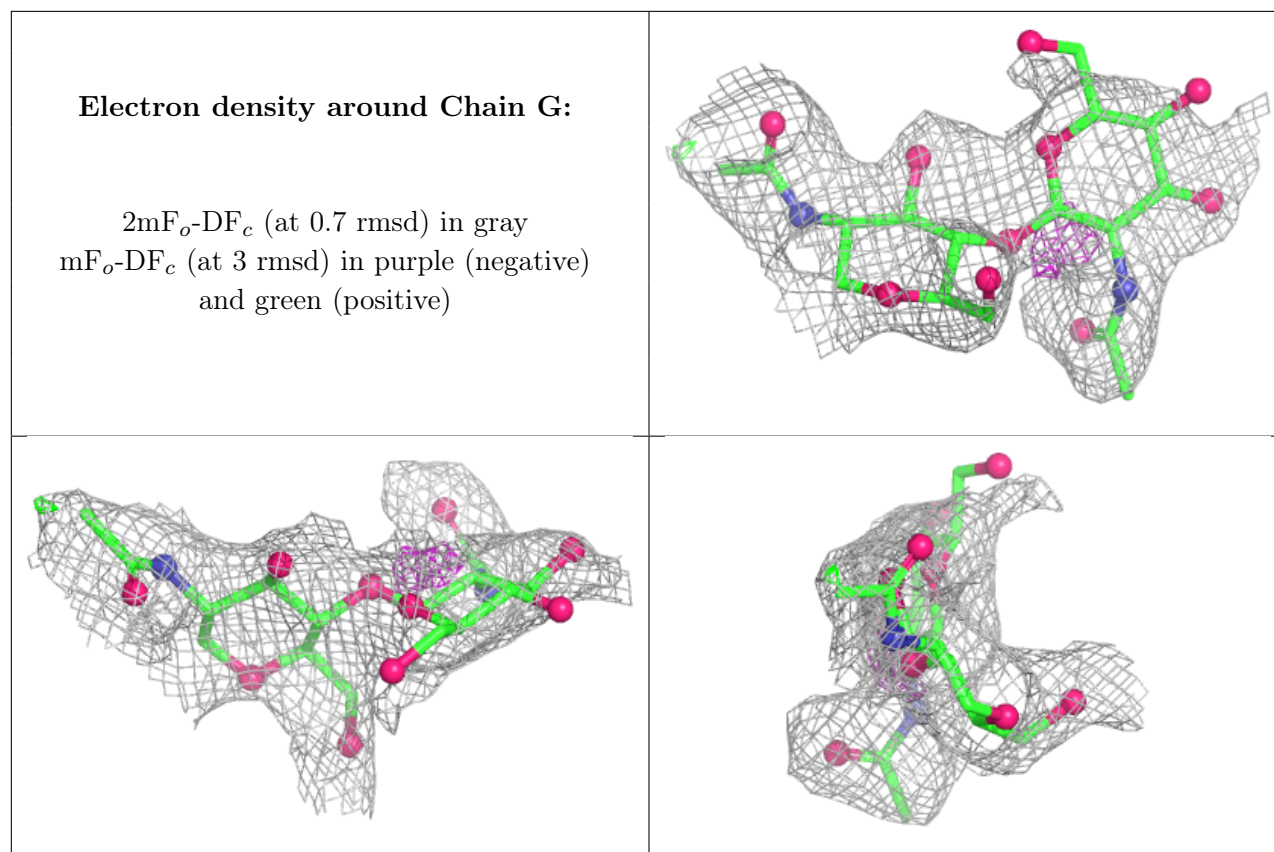
There are no non-standard protein/DNA/RNA residues in this entry.

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	G	2	14/15	0.80	0.15	86,96,99,99	0
3	NAG	G	1	14/15	0.81	0.13	74,80,85,91	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
4	NAG	A	401	14/15	0.50	0.20	81,86,89,92	0
4	NAG	C	401	14/15	0.73	0.16	81,88,91,92	0
4	NAG	E	401	14/15	0.76	0.16	84,88,93,93	0
4	NAG	F	201	14/15	0.81	0.14	74,78,82,83	0
4	NAG	D	201	14/15	0.83	0.12	70,73,75,76	0
6	EDO	F	202	4/4	0.86	0.21	64,67,68,70	0
6	EDO	C	402	4/4	0.88	0.18	57,58,59,59	0
5	CA	B	203	1/1	0.91	0.10	83,83,83,83	0
6	EDO	E	402	4/4	0.96	0.11	51,52,53,55	0
6	EDO	C	403	4/4	0.97	0.10	45,46,47,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.