Full wwPDB X-ray Structure Validation Report (i)

Sep 28, 2024 – 06:44 AM EDT

PDB ID	:	4NN9
Title	:	REFINED ATOMIC STRUCTURES OF N9 SUBTYPE INFLUENZA VIRUS NEURAMINIDASE AND ESCAPE MUTANTS
Authors	:	Tulip, W.R.; Varghese, J.N.; Baker, A.T.; Vandonkelaar, A.; Laver, W.G.; Webster, R.G.; Colman, P.M.
Deposited on	:	1991-03-28
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

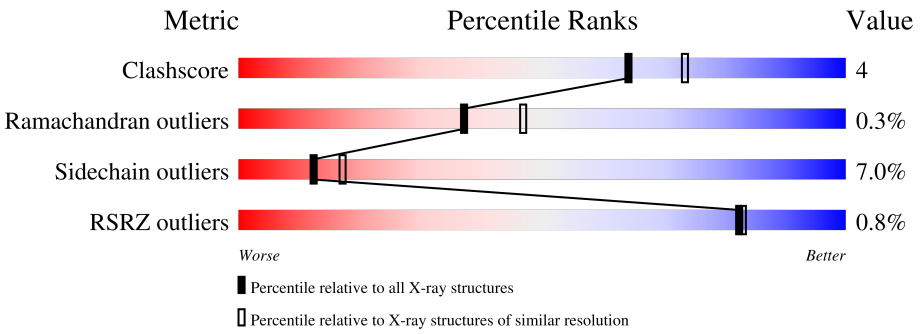
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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 <=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	388	% 76% 21% • •
2	B	7	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MAN	B	3	X	-	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3271 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.

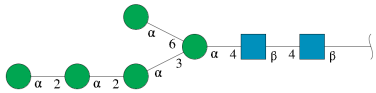
- Molecule 1 is a protein called NEURAMINIDASE N9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	388	3070	1914	541	592	23	0	0	0

There is a discrepancy between the modelled and reference sequences:

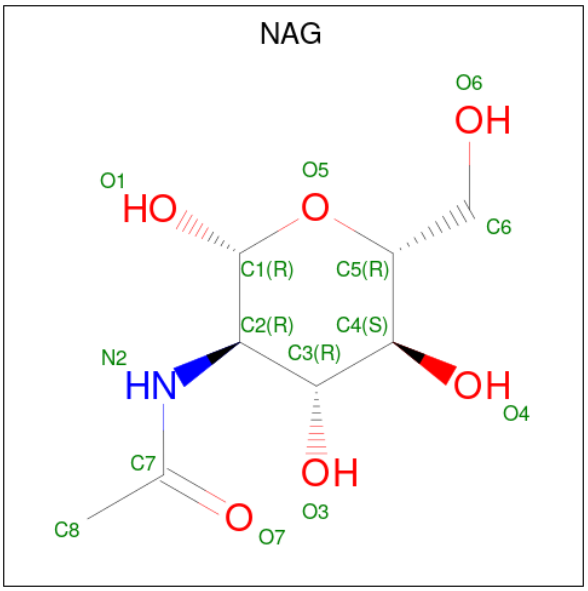
Chain	Residue	Modelled	Actual	Comment	Reference
A	368	ARG	ILE	conflict	UNP P03472

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	7	83	46	2	35	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ca 1 1	0	0

- Molecule 5 is water.

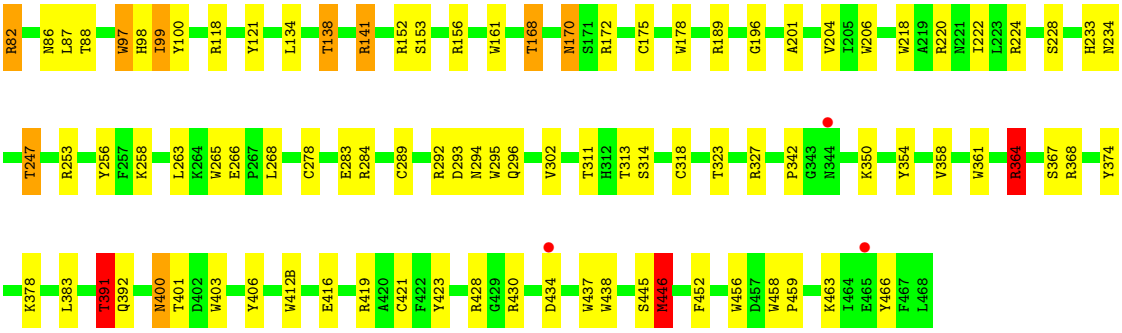
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	89	Total O 89 89	0	0

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.

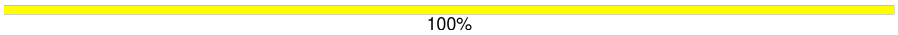
• Molecule 1: NEURAMINIDASE N9

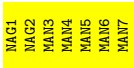
Chain A:



• Molecule 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4 3 2	Depositor
Cell constants a, b, c, α, β, γ	185.10Å 185.10Å 185.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.30 6.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-2.30) 56.4 (6.00-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$	-	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.163 , (Not available) 0.176 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	14.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 59.0	EDS
L-test for twinning[1]	$< \|L\| > = 0.37$, $< L^2 > = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3271	wwPDB-VP
Average B, all atoms (Å^2)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.93% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG, CA, MAN

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	0.94	0/3153	1.85	97/4293 (2.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (97) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	419	ARG	NE-CZ-NH1	13.74	127.17	120.30
1	A	364	ARG	NE-CZ-NH1	13.48	127.04	120.30
1	A	220	ARG	NE-CZ-NH2	-12.96	113.82	120.30
1	A	220	ARG	NE-CZ-NH1	10.80	125.70	120.30
1	A	438	TRP	CG-CD2-CE3	10.14	143.03	133.90
1	A	364	ARG	NE-CZ-NH2	-9.99	115.31	120.30
1	A	406	TYR	CB-CG-CD2	-9.54	115.28	121.00
1	A	403	TRP	CD1-CG-CD2	9.34	113.77	106.30
1	A	438	TRP	CE2-CD2-CG	-9.25	99.90	107.30
1	A	97	TRP	CD1-CG-CD2	8.94	113.45	106.30
1	A	361	TRP	CG-CD2-CE3	8.87	141.88	133.90
1	A	361	TRP	CE2-CD2-CG	-8.61	100.41	107.30
1	A	438	TRP	CD1-CG-CD2	8.40	113.02	106.30
1	A	403	TRP	CE2-CD2-CG	-8.34	100.63	107.30
1	A	265	TRP	CG-CD2-CE3	8.22	141.30	133.90
1	A	419	ARG	NE-CZ-NH2	-8.17	116.22	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	284	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	A	121	TYR	CB-CG-CD2	-8.06	116.17	121.00
1	A	206	TRP	CD1-CG-CD2	7.94	112.65	106.30
1	A	178	TRP	CD1-CG-CD2	7.82	112.56	106.30
1	A	361	TRP	CD1-CG-CD2	7.72	112.48	106.30
1	A	374	TYR	CG-CD1-CE1	-7.72	115.12	121.30
1	A	421	CYS	CA-CB-SG	7.67	127.81	114.00
1	A	265	TRP	CD1-CG-CD2	7.58	112.37	106.30
1	A	97	TRP	CE2-CD2-CG	-7.58	101.24	107.30
1	A	446	MET	CG-SD-CE	-7.54	88.14	100.20
1	A	218	TRP	CE2-CD2-CG	-7.47	101.32	107.30
1	A	218	TRP	CD1-CG-CD2	7.39	112.21	106.30
1	A	284	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	A	437	TRP	CD1-CG-CD2	7.29	112.14	106.30
1	A	265	TRP	CE2-CD2-CG	-7.27	101.48	107.30
1	A	437	TRP	CE2-CD2-CG	-7.17	101.56	107.30
1	A	438	TRP	CB-CG-CD1	-7.00	117.90	127.00
1	A	458	TRP	CD1-CG-CD2	6.86	111.78	106.30
1	A	161	TRP	CE2-CD2-CG	-6.83	101.83	107.30
1	A	456	TRP	CD1-CG-CD2	6.79	111.73	106.30
1	A	295	TRP	CE2-CD2-CG	-6.79	101.87	107.30
1	A	178	TRP	CE2-CD2-CG	-6.78	101.88	107.30
1	A	141	ARG	NE-CZ-NH1	6.67	123.63	120.30
1	A	156	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	A	428	ARG	NE-CZ-NH1	6.62	123.61	120.30
1	A	247	THR	N-CA-CB	-6.62	97.72	110.30
1	A	412(B)	TRP	CE2-CD2-CG	-6.57	102.04	107.30
1	A	456	TRP	CE2-CD2-CG	-6.50	102.10	107.30
1	A	82	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	A	161	TRP	CB-CG-CD1	-6.48	118.57	127.00
1	A	295	TRP	CD1-CG-CD2	6.47	111.48	106.30
1	A	412(B)	TRP	CG-CD2-CE3	6.43	139.69	133.90
1	A	406	TYR	CB-CG-CD1	6.40	124.84	121.00
1	A	161	TRP	CD1-CG-CD2	6.39	111.42	106.30
1	A	175	CYS	CA-CB-SG	6.36	125.45	114.00
1	A	161	TRP	CG-CD2-CE3	6.16	139.44	133.90
1	A	178	TRP	CG-CD1-NE1	-6.07	104.03	110.10
1	A	253	ARG	NE-CZ-NH1	6.07	123.33	120.30
1	A	100	TYR	CB-CG-CD1	-5.96	117.43	121.00
1	A	266	GLU	CA-CB-CG	5.94	126.46	113.40
1	A	293	ASP	O-C-N	-5.90	113.26	122.70
1	A	218	TRP	CG-CD2-CE3	5.89	139.20	133.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	138	THR	CA-CB-CG2	-5.80	104.28	112.40
1	A	121	TYR	CA-CB-CG	5.77	124.37	113.40
1	A	99	ILE	CB-CA-C	-5.77	100.06	111.60
1	A	189	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	403	TRP	CG-CD1-NE1	-5.69	104.41	110.10
1	A	368	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	A	354	TYR	CB-CG-CD2	-5.65	117.61	121.00
1	A	463	LYS	CG-CD-CE	-5.62	95.06	111.90
1	A	327	ARG	NE-CZ-NH2	-5.61	117.49	120.30
1	A	437	TRP	CG-CD2-CE3	5.61	138.95	133.90
1	A	152	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	A	296	GLN	CA-C-N	5.54	127.29	116.20
1	A	438	TRP	CG-CD1-NE1	-5.54	104.56	110.10
1	A	97	TRP	CG-CD1-NE1	-5.54	104.56	110.10
1	A	358	VAL	CG1-CB-CG2	-5.54	102.05	110.90
1	A	265	TRP	NE1-CE2-CZ2	-5.53	124.31	130.40
1	A	374	TYR	CZ-CE2-CD2	-5.53	114.83	119.80
1	A	403	TRP	CB-CG-CD1	-5.50	119.86	127.00
1	A	265	TRP	CB-CG-CD1	-5.46	119.91	127.00
1	A	206	TRP	CE2-CD2-CG	-5.43	102.95	107.30
1	A	138	THR	CB-CA-C	-5.42	96.96	111.60
1	A	138	THR	N-CA-CB	5.41	120.57	110.30
1	A	459	PRO	CA-C-N	5.35	128.97	117.20
1	A	88	THR	N-CA-CB	-5.32	100.20	110.30
1	A	327	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	A	256	TYR	CB-CG-CD2	-5.27	117.84	121.00
1	A	391	THR	N-CA-CB	-5.25	100.32	110.30
1	A	437	TRP	CB-CG-CD1	-5.23	120.20	127.00
1	A	97	TRP	CB-CG-CD1	-5.22	120.22	127.00
1	A	97	TRP	CG-CD2-CE3	5.22	138.60	133.90
1	A	206	TRP	CG-CD1-NE1	-5.19	104.91	110.10
1	A	361	TRP	CB-CG-CD1	-5.17	120.28	127.00
1	A	438	TRP	NE1-CE2-CZ2	-5.13	124.75	130.40
1	A	265	TRP	CG-CD1-NE1	-5.12	104.98	110.10
1	A	88	THR	CA-CB-CG2	5.07	119.50	112.40
1	A	361	TRP	CG-CD1-NE1	-5.07	105.03	110.10
1	A	293	ASP	CA-C-N	5.06	128.33	117.20
1	A	247	THR	CA-CB-CG2	5.02	119.43	112.40
1	A	172	ARG	NE-CZ-NH1	5.01	122.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	423	TYR	Sidechain

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	3070	0	2895	23	0
2	B	83	0	70	0	0
3	A	28	0	26	0	0
4	A	1	0	0	0	0
5	A	89	0	0	1	1
All	All	3271	0	2991	23	1

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 4.

All (23) 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:466:TYR:OH	5:A:484:HOH:O	1.86	0.93
1:A:292:ARG:HH21	1:A:294:ASN:ND2	1.94	0.66
1:A:292:ARG:HE	1:A:294:ASN:HD22	1.50	0.57
1:A:302:VAL:O	1:A:314:SER:HA	2.05	0.56
1:A:278:CYS:HB3	1:A:289:CYS:HB3	1.88	0.56
1:A:87:LEU:H	1:A:233:HIS:HD2	1.54	0.55
1:A:392:GLN:NE2	1:A:452:PHE:HE2	2.06	0.53
1:A:367:SER:HB2	1:A:400:ASN:HD21	1.74	0.53
1:A:196:GLY:HA3	1:A:201:ALA:HA	1.89	0.53
1:A:168:THR:H	1:A:170:ASN:ND2	2.07	0.52
1:A:168:THR:HB	1:A:170:ASN:ND2	2.25	0.51
1:A:323:THR:HG22	1:A:364:ARG:HB3	1.93	0.49
1:A:98:HIS:O	1:A:446:MET:HG3	2.12	0.48
1:A:258:LYS:HB2	1:A:263:LEU:HD11	1.94	0.48
1:A:228:SER:HB3	1:A:350:LYS:HE2	1.97	0.47
1:A:318:CYS:SG	1:A:383:LEU:O	2.73	0.47
1:A:292:ARG:HH21	1:A:294:ASN:HD21	1.61	0.45
1:A:86:ASN:OD1	1:A:234:ASN:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:THR:HG22	1:A:170:ASN:N	2.34	0.42
1:A:168:THR:HG22	1:A:170:ASN:H	1.83	0.42
1:A:378:LYS:HD3	1:A:391:THR:HG22	2.02	0.41
1:A:430:ARG:HG2	1:A:434:ASP:HA	2.03	0.41
1:A:97:TRP:HB3	1:A:446:MET:HG2	2.02	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:557:HOH:O	5:A:557:HOH:O[48_555]	2.11	0.09

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	386/388 (100%)	359 (93%)	26 (7%)	1 (0%)	37 47

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	ILE

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	341/341 (100%)	317 (93%)	24 (7%)	12 17

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	99	ILE
1	A	118	ARG
1	A	134	LEU
1	A	138	THR
1	A	141	ARG
1	A	153	SER
1	A	168	THR
1	A	170	ASN
1	A	204	VAL
1	A	224	ARG
1	A	247	THR
1	A	268	LEU
1	A	283	GLU
1	A	311	THR
1	A	313	THR
1	A	342	PRO
1	A	364	ARG
1	A	391	THR
1	A	400	ASN
1	A	401	THR
1	A	416	GLU
1	A	445	SER
1	A	446	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	HIS
1	A	170	ASN
1	A	233	HIS
1	A	294	ASN
1	A	346	ASN
1	A	392	GLN
1	A	400	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)

7 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	B	1	1,2	14,14,15	1.54	3 (21%)	17,19,21	1.31	3 (17%)
2	NAG	B	2	2	14,14,15	0.68	0	17,19,21	1.44	3 (17%)
2	MAN	B	3	2	11,11,12	0.76	0	15,15,17	0.77	1 (6%)
2	MAN	B	4	2	11,11,12	0.68	0	15,15,17	1.47	2 (13%)
2	MAN	B	5	2	11,11,12	0.50	0	15,15,17	0.95	1 (6%)
2	MAN	B	6	2	11,11,12	1.13	3 (27%)	15,15,17	1.48	1 (6%)
2	MAN	B	7	2	11,11,12	1.10	1 (9%)	15,15,17	1.90	5 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	MAN	B	3	2	1/1/4/5	2/2/19/22	0/1/1/1
2	MAN	B	4	2	-	2/2/19/22	0/1/1/1
2	MAN	B	5	2	-	0/2/19/22	0/1/1/1
2	MAN	B	6	2	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	B	7	2	-	2/2/19/22	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	C3-C2	4.38	1.61	1.52
2	B	1	NAG	C1-C2	2.72	1.56	1.52
2	B	7	MAN	C2-C3	2.41	1.56	1.52
2	B	6	MAN	C2-C3	2.09	1.55	1.52
2	B	1	NAG	O4-C4	2.06	1.48	1.43
2	B	6	MAN	O5-C5	2.05	1.47	1.43
2	B	6	MAN	C4-C3	2.00	1.57	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	6	MAN	C1-O5-C5	4.50	118.21	112.19
2	B	4	MAN	O2-C2-C1	-3.13	102.05	109.22
2	B	2	NAG	O3-C3-C2	3.09	115.83	109.40
2	B	4	MAN	C1-O5-C5	3.08	116.32	112.19
2	B	7	MAN	C1-C2-C3	2.99	114.00	109.64
2	B	7	MAN	O3-C3-C4	-2.94	103.45	110.38
2	B	5	MAN	C1-O5-C5	2.79	115.93	112.19
2	B	7	MAN	C2-C3-C4	2.57	115.37	110.86
2	B	7	MAN	C1-O5-C5	2.39	115.39	112.19
2	B	2	NAG	C8-C7-N2	2.33	119.98	116.12
2	B	1	NAG	C2-N2-C7	2.20	125.84	122.90
2	B	1	NAG	O5-C1-C2	-2.12	108.01	111.29
2	B	2	NAG	C3-C4-C5	2.10	114.04	110.23
2	B	1	NAG	O3-C3-C2	2.08	113.73	109.40
2	B	7	MAN	O4-C4-C3	-2.08	105.47	110.38
2	B	3	MAN	C1-O5-C5	2.02	114.89	112.19

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	3	MAN	C1

All (9) torsion outliers are listed below:

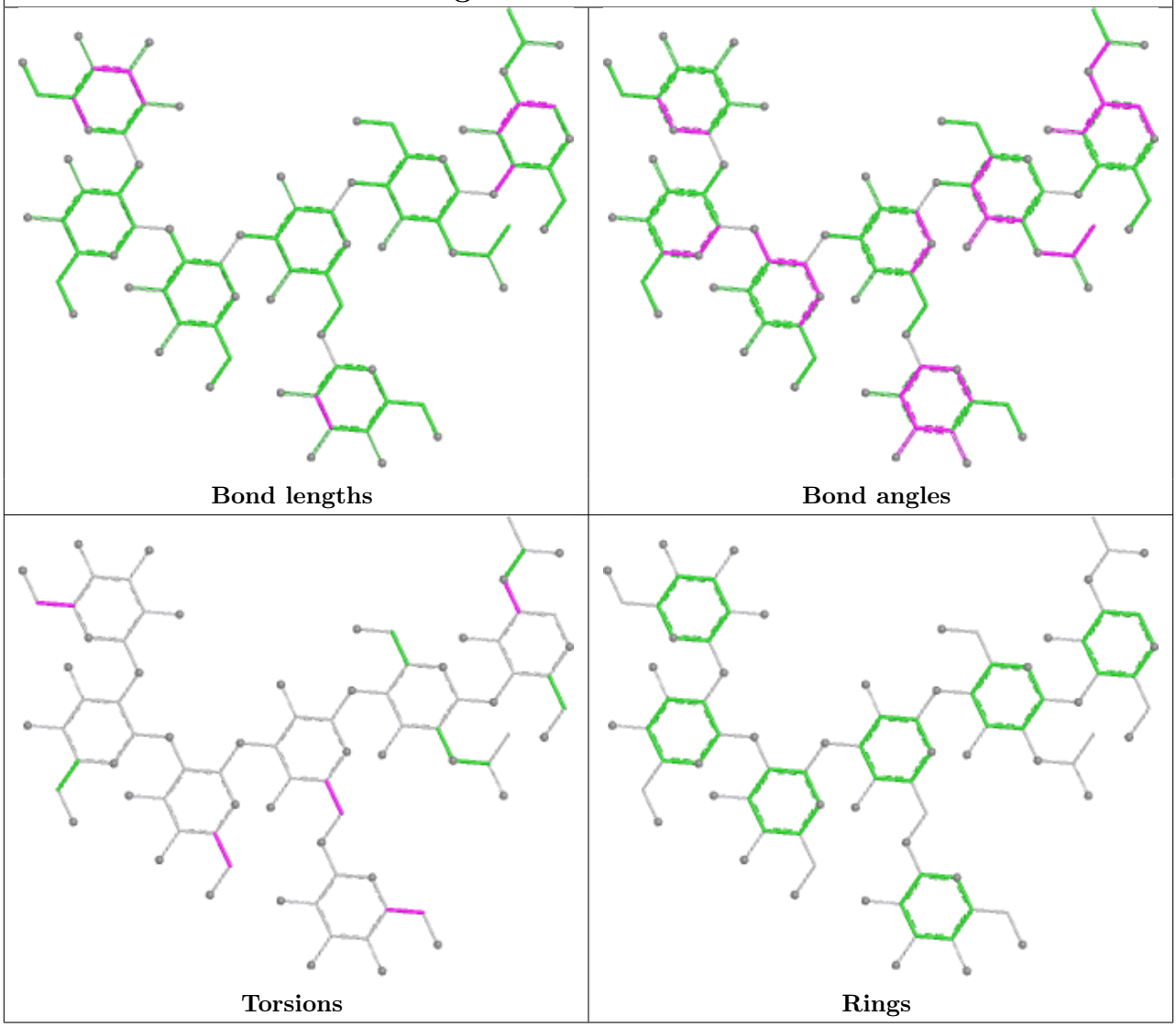
Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C1-C2-N2-C7
2	B	7	MAN	O5-C5-C6-O6
2	B	4	MAN	O5-C5-C6-O6
2	B	7	MAN	C4-C5-C6-O6
2	B	4	MAN	C4-C5-C6-O6
2	B	3	MAN	C4-C5-C6-O6
2	B	6	MAN	C4-C5-C6-O6
2	B	6	MAN	O5-C5-C6-O6
2	B	3	MAN	O5-C5-C6-O6

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.

Oligosaccharide Chain B



5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is 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	$\#\|Z\| > 2$
3	NAG	A	476(A)	1	14,14,15	0.58	0	17,19,21	1.42	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	A	477(A)	1	14,14,15	0.85	0	17,19,21	1.24	1 (5%)

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	A	476(A)	1	-	2/6/23/26	0/1/1/1
3	NAG	A	477(A)	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	477(A)	NAG	C1-C2-N2	-2.48	106.53	110.43
3	A	476(A)	NAG	C8-C7-N2	2.32	119.97	116.12
3	A	476(A)	NAG	O3-C3-C2	2.29	114.16	109.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	476(A)	NAG	O5-C5-C6-O6
3	A	476(A)	NAG	C4-C5-C6-O6
3	A	477(A)	NAG	C4-C5-C6-O6
3	A	477(A)	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 (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	388/388 (100%)	-0.94	3 (0%) 82 83	4, 12, 24, 40	10 (2%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	465	GLU	3.4
1	A	344	ASN	2.9
1	A	434	ASP	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.

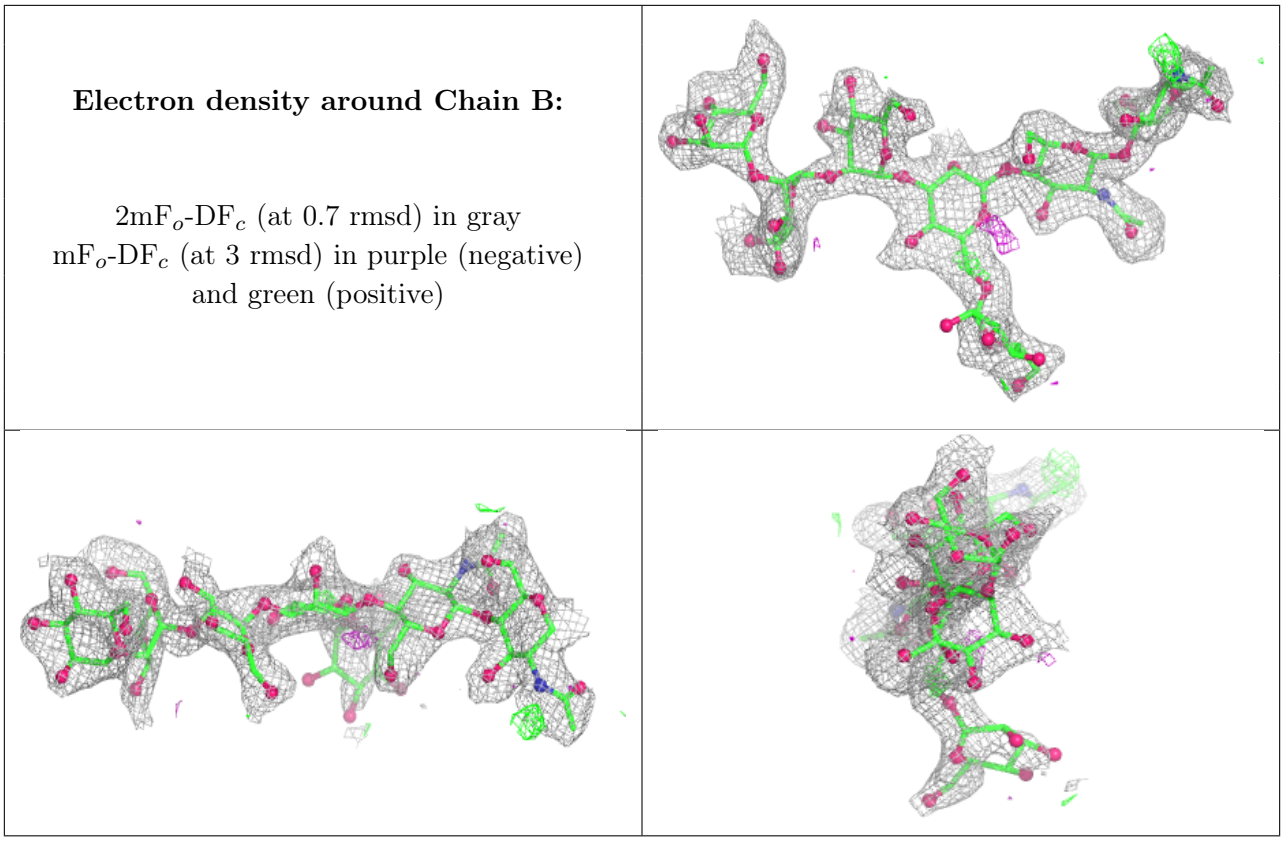
6.3 Carbohydrates (i)

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(Å^2)	Q<0.9
2	MAN	B	7	11/12	0.82	0.15	38,43,48,49	0
2	MAN	B	5	11/12	0.90	0.08	25,26,27,28	0
2	MAN	B	4	11/12	0.90	0.08	22,24,26,28	0
2	MAN	B	3	11/12	0.91	0.08	20,22,26,32	0
2	MAN	B	6	11/12	0.91	0.06	28,29,30,32	0
2	NAG	B	1	14/15	0.91	0.08	17,18,26,30	0
2	NAG	B	2	14/15	0.92	0.06	18,20,24,26	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. 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(Å^2)	Q<0.9
3	NAG	A	476(A)	14/15	0.84	0.09	36,41,45,46	0
3	NAG	A	477(A)	14/15	0.86	0.10	30,35,36,39	0
4	CA	A	18	1/1	0.98	0.23	2,2,2,2	0

6.5 Other polymers (i)

There are no such residues in this entry.