



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:08 PM UTC

PDB ID : 5NN9 / pdb_00005nn9
Title : REFINED ATOMIC STRUCTURES OF N9 SUBTYPE INFLUENZA VIRUS
NEURAMINIDASE AND ESCAPE MUTANTS
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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 ⓘ 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

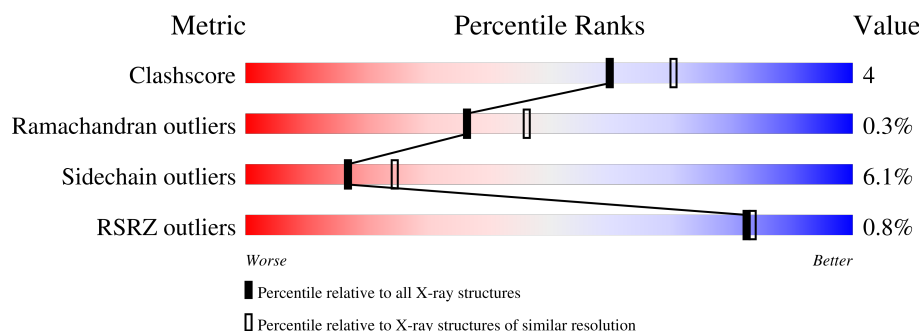
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 $\leq 5\%$. 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	388	% 69% 26% .
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	-	-	-

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.

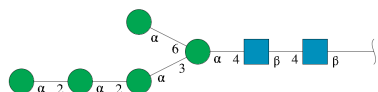
- Molecule 1 is a protein called NEURAMINIDASE N9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	0	0
			3070	1915	538	594	23			

There is a discrepancy between the modelled and reference sequences:

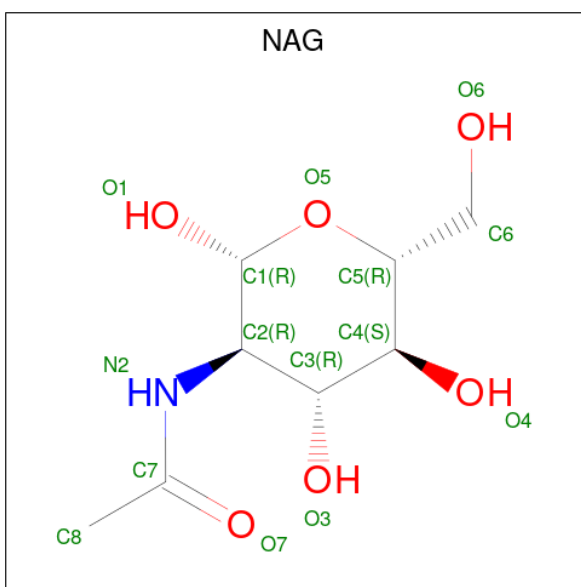
Chain	Residue	Modelled	Actual	Comment	Reference
A	369	ASP	ALA	conflict	UNP P03472

- 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
2	B	7	Total	C	N	O	0	0	0
			83	46	2	35			

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



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

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

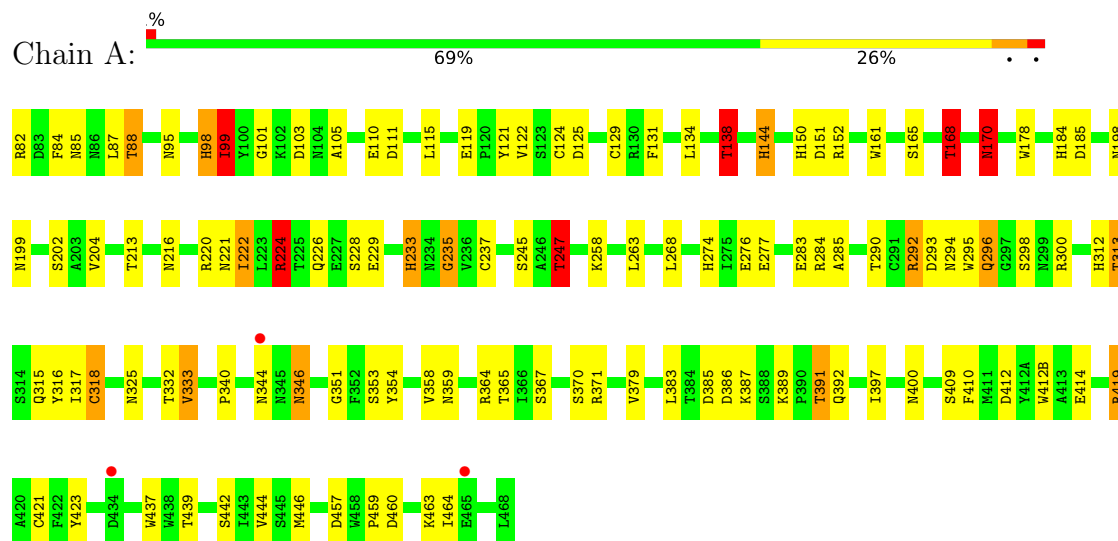
- Molecule 5 is water.

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

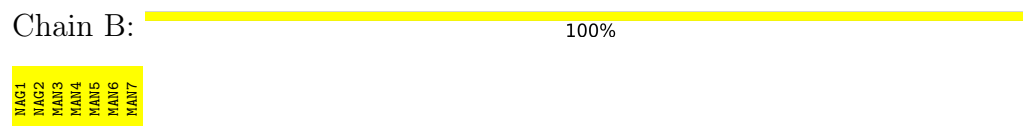
3 Residue-property plots

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: NEURAMINIDASE N9



• 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



4 Data and refinement statistics

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) 53.2 (6.00-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.160 , (Not available) 0.176 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	13.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 54.4	EDS
L-test for twinning ¹	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	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 4.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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: 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	1.18	11/3153 (0.3%)	2.11	132/4294 (3.1%)

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

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	457	ASP	C-N	7.37	1.44	1.33
1	A	150	HIS	CD2-NE2	-6.71	1.30	1.37
1	A	233	HIS	CD2-NE2	-6.58	1.30	1.37
1	A	144	HIS	CD2-NE2	-6.32	1.30	1.37
1	A	161	TRP	CA-C	6.14	1.58	1.52
1	A	274	HIS	CD2-NE2	-6.03	1.31	1.37
1	A	161	TRP	CA-CB	5.92	1.61	1.53
1	A	184	HIS	CD2-NE2	-5.65	1.31	1.37
1	A	312	HIS	CD2-NE2	-5.63	1.31	1.37
1	A	98	HIS	CD2-NE2	-5.34	1.31	1.37
1	A	125	ASP	CA-CB	-5.28	1.45	1.53

All (132) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	ASP	N-CA-C	10.94	126.45	112.89
1	A	216	ASN	OD1-CG-ND2	-10.67	111.93	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	ASN	OD1-CG-ND2	-9.76	112.84	122.60
1	A	99	ILE	N-CA-CB	9.17	122.42	110.13
1	A	385	ASP	CA-CB-CG	9.16	121.76	112.60
1	A	88	THR	N-CA-CB	-9.09	96.26	110.44
1	A	95	ASN	OD1-CG-ND2	-9.06	113.54	122.60
1	A	247	THR	N-CA-CB	-9.02	96.52	111.49
1	A	105	ALA	N-CA-C	8.95	121.85	111.11
1	A	161	TRP	O-C-N	-8.81	116.07	121.71
1	A	131	PHE	CA-CB-CG	8.75	122.55	113.80
1	A	99	ILE	CB-CA-C	-8.62	97.53	111.59
1	A	457	ASP	CA-C-N	-8.49	112.72	123.16
1	A	457	ASP	C-N-CA	-8.49	112.72	123.16
1	A	379	VAL	N-CA-C	-8.47	99.76	108.15
1	A	185	ASP	CA-CB-CG	8.25	120.85	112.60
1	A	170	ASN	OD1-CG-ND2	-8.10	114.50	122.60
1	A	226	GLN	N-CA-C	7.88	119.95	111.36
1	A	392	GLN	OE1-CD-NE2	-7.67	114.93	122.60
1	A	170	ASN	CB-CG-ND2	7.62	127.84	116.40
1	A	103	ASP	CA-CB-CG	7.62	120.22	112.60
1	A	285	ALA	N-CA-C	7.55	121.91	112.24
1	A	437	TRP	CG-CD2-CE3	7.50	141.40	133.90
1	A	359	ASN	OD1-CG-ND2	-7.49	115.11	122.60
1	A	220	ARG	N-CA-C	7.43	121.64	112.58
1	A	229	GLU	N-CA-C	7.38	120.92	110.23
1	A	233	HIS	CB-CG-CD2	-7.29	121.72	131.20
1	A	216	ASN	CB-CG-ND2	7.14	127.11	116.40
1	A	84	PHE	CA-CB-CG	7.12	120.92	113.80
1	A	391	THR	N-CA-CB	-7.10	100.80	110.67
1	A	463	LYS	CG-CD-CE	-7.06	95.06	111.30
1	A	379	VAL	CA-C-O	-6.88	116.20	120.88
1	A	125	ASP	O-C-N	-6.85	116.21	121.14
1	A	138	THR	CB-CA-C	-6.75	98.06	110.62
1	A	392	GLN	CG-CD-NE2	6.75	126.53	116.40
1	A	247	THR	CA-CB-OG1	-6.75	99.48	109.60
1	A	296	GLN	O-C-N	-6.75	115.58	121.85
1	A	386	ASP	CA-CB-CG	6.66	119.26	112.60
1	A	412(B)	TRP	CG-CD2-CE3	6.65	140.55	133.90
1	A	332	THR	N-CA-C	-6.65	105.30	113.41
1	A	325	ASN	CB-CG-ND2	6.54	126.20	116.40
1	A	101	GLY	O-C-N	-6.53	117.50	123.57
1	A	247	THR	CB-CA-C	6.51	121.53	110.85
1	A	150	HIS	CB-CG-CD2	-6.49	122.76	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	235	GLY	CA-C-O	-6.46	113.94	119.56
1	A	410	PHE	CA-CB-CG	6.46	120.26	113.80
1	A	274	HIS	CB-CG-CD2	-6.44	122.82	131.20
1	A	318	CYS	N-CA-C	6.42	119.10	111.33
1	A	400	ASN	OD1-CG-ND2	-6.33	116.27	122.60
1	A	359	ASN	CA-CB-CG	6.31	118.91	112.60
1	A	85	ASN	OD1-CG-ND2	-6.20	116.40	122.60
1	A	296	GLN	N-CA-C	6.19	121.88	113.21
1	A	460	ASP	CA-CB-CG	6.19	118.79	112.60
1	A	290	THR	N-CA-C	-6.14	99.19	109.07
1	A	295	TRP	CG-CD2-CE3	6.12	140.01	133.90
1	A	397	ILE	N-CA-CB	-6.11	104.69	111.41
1	A	412	ASP	CA-CB-CG	6.06	118.66	112.60
1	A	459	PRO	O-C-N	-6.06	115.77	123.04
1	A	353	SER	O-C-N	-6.05	116.91	123.26
1	A	346	ASN	N-CA-C	6.04	119.97	111.52
1	A	400	ASN	CB-CG-ND2	5.99	125.39	116.40
1	A	277	GLU	N-CA-C	5.96	123.48	110.80
1	A	457	ASP	CA-CB-CG	5.93	118.53	112.60
1	A	144	HIS	CB-CG-CD2	-5.91	123.52	131.20
1	A	359	ASN	CB-CG-ND2	5.91	125.26	116.40
1	A	115	LEU	N-CA-C	5.86	118.76	110.50
1	A	412(B)	TRP	CB-CG-CD1	-5.83	118.16	126.90
1	A	313	THR	OG1-CB-CG2	5.81	120.92	109.30
1	A	221	ASN	OD1-CG-ND2	-5.81	116.79	122.60
1	A	317	ILE	N-CA-C	-5.80	99.95	108.54
1	A	178	TRP	CB-CG-CD1	-5.78	118.23	126.90
1	A	247	THR	CA-CB-CG2	5.77	120.31	110.50
1	A	419	ARG	O-C-N	-5.75	115.94	123.02
1	A	444	VAL	N-CA-C	-5.75	99.89	108.46
1	A	152	ARG	NE-CZ-NH2	-5.74	114.03	119.20
1	A	161	TRP	CA-C-N	5.74	125.67	119.76
1	A	161	TRP	C-N-CA	5.74	125.67	119.76
1	A	199	ASN	CA-CB-CG	5.74	118.34	112.60
1	A	122	VAL	O-C-N	-5.72	116.69	123.04
1	A	110	GLU	N-CA-C	-5.71	105.57	112.54
1	A	224	ARG	CA-CB-CG	5.70	125.49	114.10
1	A	439	THR	O-C-N	-5.69	115.61	123.12
1	A	98	HIS	CA-CB-CG	5.67	119.47	113.80
1	A	389	LYS	CA-C-N	5.67	125.60	119.76
1	A	389	LYS	C-N-CA	5.67	125.60	119.76
1	A	298	SER	N-CA-CB	-5.63	101.62	110.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	98	HIS	O-C-N	-5.61	116.34	123.24
1	A	198	ASN	CB-CG-ND2	5.60	124.81	116.40
1	A	165	SER	CA-C-O	-5.60	115.09	120.97
1	A	119	GLU	CA-C-N	5.58	125.78	120.31
1	A	119	GLU	C-N-CA	5.58	125.78	120.31
1	A	178	TRP	CG-CD2-CE3	5.55	139.45	133.90
1	A	170	ASN	N-CA-CB	-5.55	101.83	110.98
1	A	125	ASP	CA-C-N	5.47	125.30	119.28
1	A	125	ASP	C-N-CA	5.47	125.30	119.28
1	A	138	THR	N-CA-CB	5.46	120.02	111.56
1	A	168	THR	N-CA-CB	-5.45	101.75	110.63
1	A	346	ASN	OD1-CG-ND2	-5.43	117.17	122.60
1	A	442	SER	CA-CB-OG	5.42	121.95	111.10
1	A	437	TRP	CB-CG-CD1	-5.39	118.81	126.90
1	A	111	ASP	N-CA-CB	-5.38	105.33	111.79
1	A	237	CYS	CA-C-N	5.38	125.14	119.76
1	A	237	CYS	C-N-CA	5.38	125.14	119.76
1	A	213	THR	CA-CB-OG1	-5.37	101.54	109.60
1	A	354	TYR	N-CA-C	-5.35	98.66	108.02
1	A	293	ASP	CA-CB-CG	5.34	117.94	112.60
1	A	295	TRP	CE2-CD2-CG	-5.34	100.79	107.20
1	A	178	TRP	CE2-CD2-CG	-5.34	100.79	107.20
1	A	397	ILE	CB-CG1-CD1	5.33	125.00	113.80
1	A	344	ASN	OD1-CG-ND2	-5.29	117.31	122.60
1	A	184	HIS	CB-CG-CD2	-5.28	124.33	131.20
1	A	82	ARG	CA-CB-CG	5.28	124.66	114.10
1	A	105	ALA	O-C-N	-5.27	116.61	122.09
1	A	221	ASN	CB-CG-ND2	5.27	124.31	116.40
1	A	414	GLU	O-C-N	-5.25	116.81	123.01
1	A	421	CYS	CA-CB-SG	5.24	126.44	114.40
1	A	178	TRP	N-CA-C	5.23	119.62	112.88
1	A	459	PRO	CA-C-O	-5.22	115.26	122.15
1	A	88	THR	N-CA-C	5.22	119.70	113.23
1	A	98	HIS	CB-CG-CD2	-5.21	124.43	131.20
1	A	245	SER	N-CA-C	5.21	117.43	110.35
1	A	351	GLY	O-C-N	-5.20	115.94	122.70
1	A	144	HIS	N-CA-C	-5.20	106.97	113.15
1	A	88	THR	CB-CA-C	5.18	120.08	109.55
1	A	292	ARG	NE-CZ-NH2	5.17	123.85	119.20
1	A	295	TRP	N-CA-CB	-5.15	102.39	109.91
1	A	412(B)	TRP	CE2-CD2-CG	-5.15	101.02	107.20
1	A	98	HIS	CA-C-O	-5.12	115.11	121.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	TRP	CB-CG-CD1	-5.12	119.23	126.90
1	A	300	ARG	CA-C-N	5.11	125.01	119.85
1	A	300	ARG	C-N-CA	5.11	125.01	119.85
1	A	437	TRP	CE2-CD2-CG	-5.07	101.12	107.20

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 ⓘ

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	2892	26	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	0	1
All	All	3271	0	2988	26	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 (26) 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:87:LEU:H	1:A:233:HIS:HD2	1.46	0.63
1:A:235:GLY:HA3	1:A:258:LYS:HE3	1.86	0.57
1:A:292:ARG:HH21	1:A:294:ASN:ND2	2.02	0.57
1:A:318:CYS:SG	1:A:383:LEU:O	2.63	0.56
1:A:333:VAL:HG12	1:A:387:LYS:HG2	1.87	0.56
1:A:168:THR:H	1:A:170:ASN:ND2	2.03	0.55
1:A:87:LEU:H	1:A:233:HIS:CD2	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:HIS:CE1	1:A:419:ARG:HH21	2.29	0.50
1:A:292:ARG:HE	1:A:294:ASN:HD22	1.61	0.49
1:A:168:THR:H	1:A:170:ASN:HD21	1.61	0.48
1:A:296:GLN:O	1:A:340:PRO:HB2	2.13	0.48
1:A:367:SER:HB3	1:A:370:SER:O	2.13	0.48
1:A:284:ARG:HG2	1:A:284:ARG:HH11	1.80	0.47
1:A:315:GLN:HG2	1:A:316:TYR:H	1.81	0.46
1:A:258:LYS:HB2	1:A:263:LEU:HD11	1.98	0.45
1:A:247:THR:HA	1:A:346:ASN:ND2	2.31	0.45
1:A:138:THR:HG23	1:A:144:HIS:HB2	1.97	0.45
1:A:292:ARG:HH21	1:A:294:ASN:HD21	1.65	0.44
1:A:99:ILE:H	1:A:99:ILE:HG13	1.68	0.44
1:A:121:TYR:CG	1:A:228:SER:HA	2.53	0.43
1:A:222:ILE:O	1:A:224:ARG:HG3	2.19	0.43
1:A:138:THR:CG2	1:A:144:HIS:HB2	2.48	0.42
1:A:124:CYS:HA	1:A:129:CYS:HA	2.02	0.42
1:A:168:THR:HB	1:A:170:ASN:ND2	2.34	0.42
1:A:365:THR:HG21	1:A:371:ARG:HA	2.03	0.40
1:A:168:THR:HG22	1:A:170:ASN:H	1.85	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]	1.02	1.18

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%)	356 (92%)	29 (8%)	1 (0%)	36	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	ILE

5.3.2 Protein sidechains ⓘ

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	342/342 (100%)	321 (94%)	21 (6%)	17	24

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	THR
1	A	99	ILE
1	A	134	LEU
1	A	138	THR
1	A	168	THR
1	A	170	ASN
1	A	202	SER
1	A	204	VAL
1	A	224	ARG
1	A	247	THR
1	A	268	LEU
1	A	276	GLU
1	A	283	GLU
1	A	313	THR
1	A	333	VAL
1	A	358	VAL
1	A	364	ARG
1	A	391	THR
1	A	409	SER
1	A	446	MET
1	A	464	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	ASN
1	A	98	HIS
1	A	150	HIS
1	A	170	ASN
1	A	221	ASN
1	A	233	HIS
1	A	234	ASN
1	A	294	ASN
1	A	325	ASN
1	A	344	ASN
1	A	346	ASN
1	A	381	ASN
1	A	392	GLN
1	A	395	GLN
1	A	400	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 ⓘ

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	1.22	2 (14%)	17,19,21	1.46	2 (11%)
2	NAG	B	2	2	14,14,15	0.58	0	17,19,21	1.14	2 (11%)
2	MAN	B	3	2	11,11,12	0.77	0	15,15,17	1.52	2 (13%)
2	MAN	B	4	2	11,11,12	0.64	0	15,15,17	1.50	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	B	5	2	11,11,12	0.92	0	15,15,17	1.10	1 (6%)
2	MAN	B	6	2	11,11,12	0.96	1 (9%)	15,15,17	1.75	1 (6%)
2	MAN	B	7	2	11,11,12	0.61	0	15,15,17	1.11	1 (6%)

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	-	0/2/19/22	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
2	MAN	B	7	2	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	O4-C4	2.23	1.48	1.43
2	B	6	MAN	O5-C5	2.10	1.47	1.43
2	B	1	NAG	C4-C3	2.04	1.57	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6	MAN	C1-O5-C5	5.99	120.22	112.19
2	B	3	MAN	C1-O5-C5	4.06	117.63	112.19
2	B	1	NAG	C1-C2-N2	4.05	116.81	110.43
2	B	4	MAN	O2-C2-C1	-3.35	101.54	109.22
2	B	4	MAN	C1-O5-C5	3.02	116.24	112.19
2	B	3	MAN	C6-C5-C4	2.42	118.95	113.02
2	B	5	MAN	C1-C2-C3	2.29	112.98	109.64
2	B	2	NAG	C3-C4-C5	2.27	114.35	110.23
2	B	2	NAG	O4-C4-C5	-2.17	103.99	109.32
2	B	1	NAG	O5-C1-C2	-2.14	107.97	111.29
2	B	7	MAN	C6-C5-C4	-2.03	108.03	113.02

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	3	MAN	C1

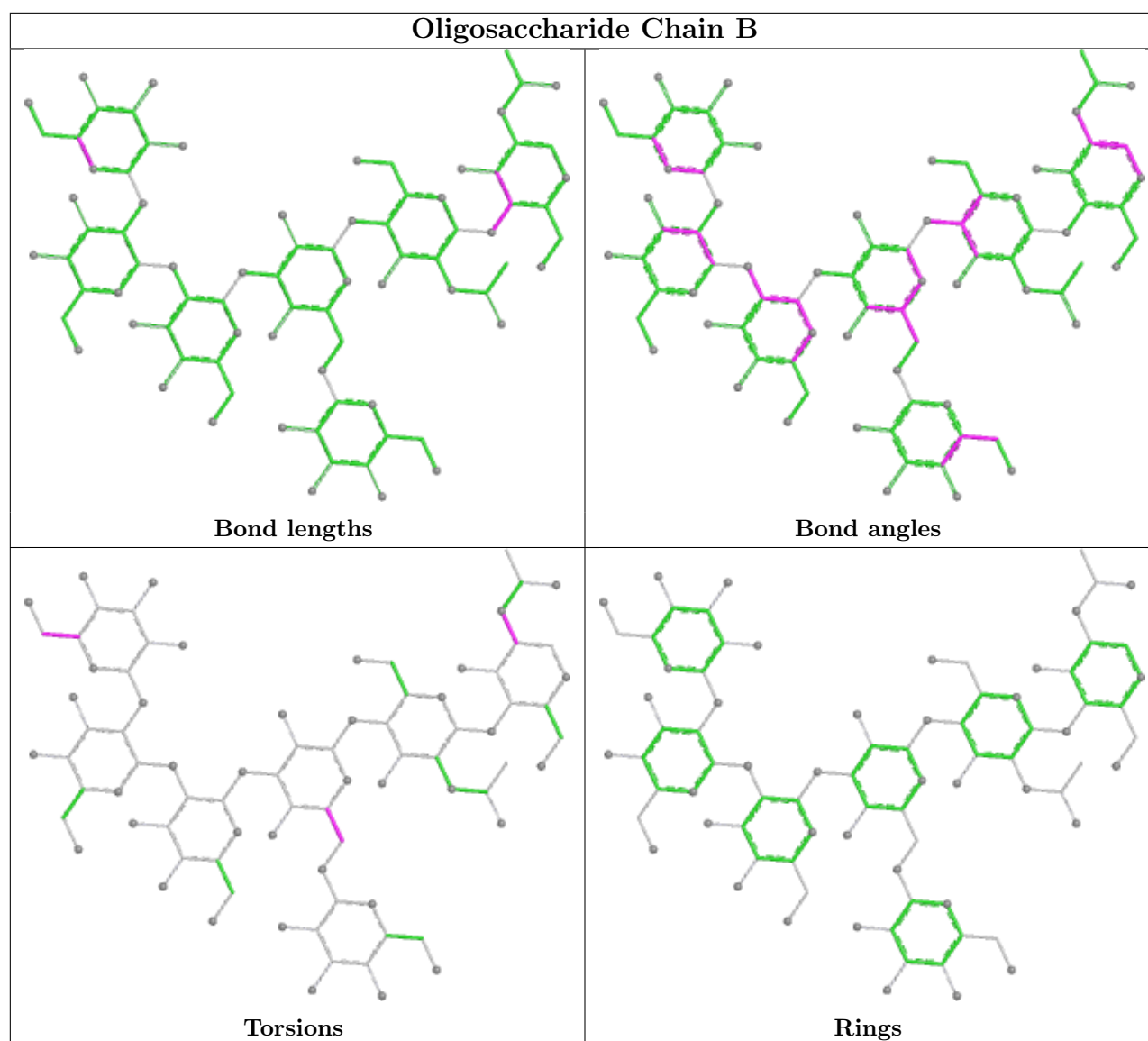
All (5) torsion outliers are listed below:

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



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	477(A)	1	14,14,15	0.87	0	17,19,21	1.39	3 (17%)

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	0.62	0	17,19,21	1.71	3 (17%)

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

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	476(A)	NAG	C8-C7-N2	3.71	122.28	116.12
3	A	476(A)	NAG	C1-O5-C5	3.70	117.14	112.19
3	A	477(A)	NAG	O4-C4-C3	-2.51	104.46	110.38
3	A	477(A)	NAG	C1-C2-N2	-2.49	106.51	110.43
3	A	476(A)	NAG	O4-C4-C3	-2.15	105.30	110.38
3	A	477(A)	NAG	O5-C1-C2	-2.09	108.05	111.29

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	477(A)	NAG	O5-C5-C6-O6
3	A	476(A)	NAG	O5-C5-C6-O6
3	A	477(A)	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 [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%)	-0.85	3 (0%) 82 83	3, 11, 23, 42	10 (2%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	465	GLU	3.8
1	A	344	ASN	3.3
1	A	434	ASP	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.

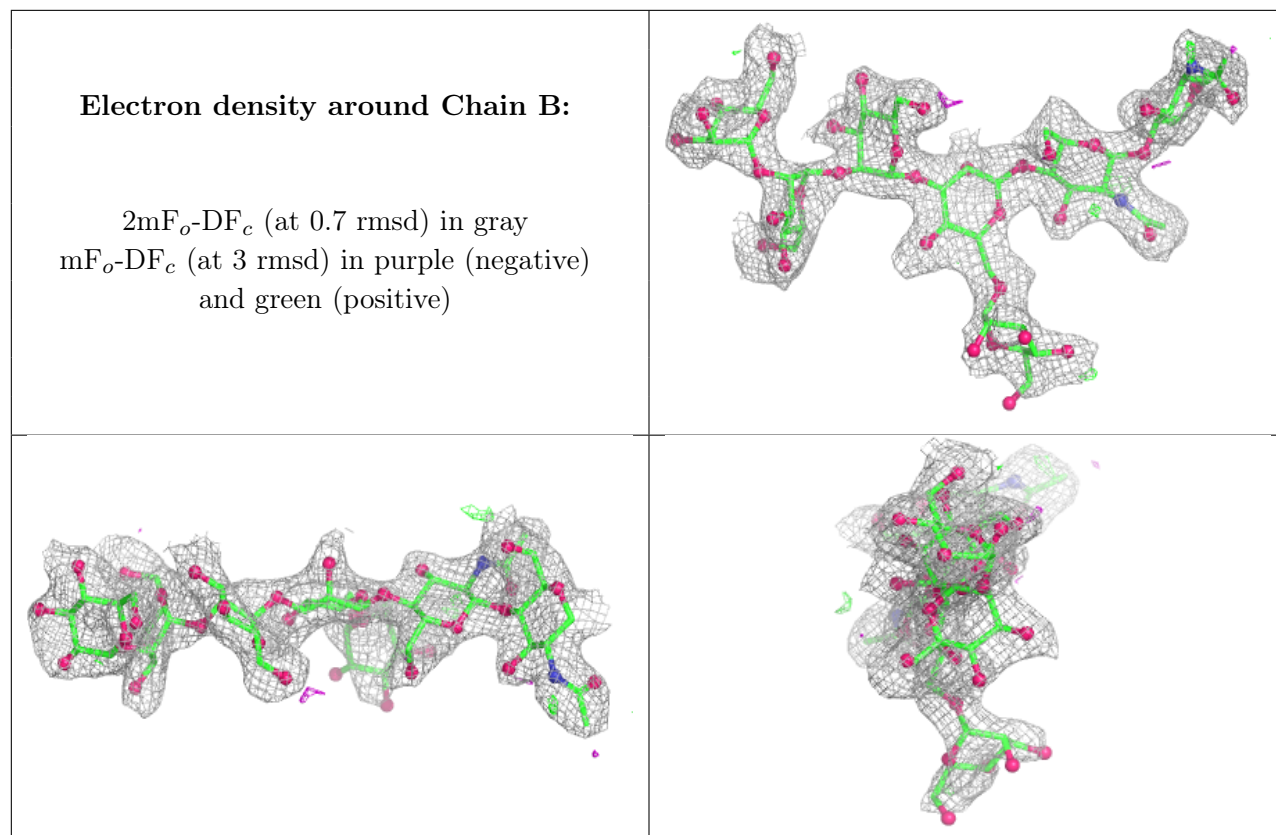
6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
2	MAN	B	7	11/12	0.83	0.14	39,43,46,48	0
2	NAG	B	2	14/15	0.88	0.08	13,17,23,27	0
2	MAN	B	4	11/12	0.91	0.06	21,22,23,27	0
2	NAG	B	1	14/15	0.92	0.06	15,16,21,24	0
2	MAN	B	6	11/12	0.93	0.07	21,24,26,28	0
2	MAN	B	3	11/12	0.93	0.07	22,23,27,32	0
2	MAN	B	5	11/12	0.94	0.05	21,22,23,24	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($\text{\AA}^2$)	Q<0.9
3	NAG	A	476(A)	14/15	0.82	0.08	36,39,43,44	0
3	NAG	A	477(A)	14/15	0.88	0.09	30,34,37,37	0
4	CA	A	18	1/1	0.95	0.23	2,2,2,2	0

6.5 Other polymers [i](#)

There are no such residues in this entry.