



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:03 PM UTC

PDB ID : 3C6E / pdb_00003c6e
Title : Crystal structure of the precursor membrane protein- envelope protein heterodimer from the dengue 2 virus at neutral pH
Authors : Li, L.
Deposited on : 2008-02-04
Resolution : 2.60 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

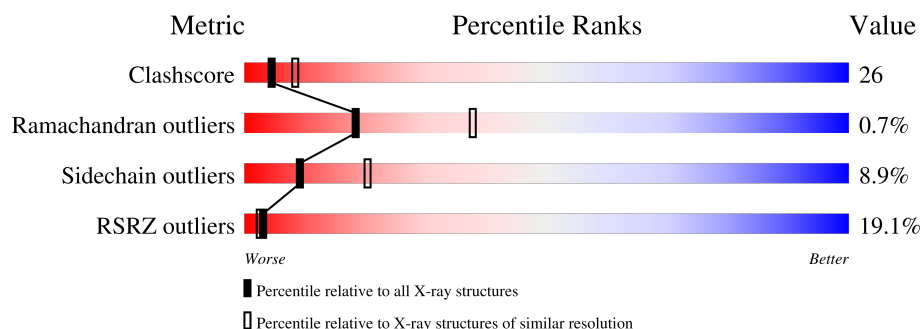
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	402	21% 55% 35% 6% ..
2	C	130	4% 36% 22% .. 38%
3	B	4	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
3	NAG	B	1	X	-	X	-
3	MAN	B	4	X	-	-	-
4	NDG	C	1396	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3811 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 Envelope protein E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3046	1926	524	569	27			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	expression tag	UNP O09234
A	-6	GLU	-	expression tag	UNP O09234
A	-5	ASN	-	expression tag	UNP O09234
A	-4	LEU	-	expression tag	UNP O09234
A	-3	TYR	-	expression tag	UNP O09234
A	-2	PHE	-	expression tag	UNP O09234
A	-1	GLN	-	expression tag	UNP O09234
A	0	GLY	-	expression tag	UNP O09234

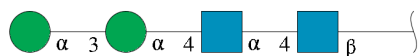
- Molecule 2 is a protein called prM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	81	Total	C	N	O	S	0	0	0
			640	396	106	128	10			

There are 3 discrepancies between the modelled and reference sequences:

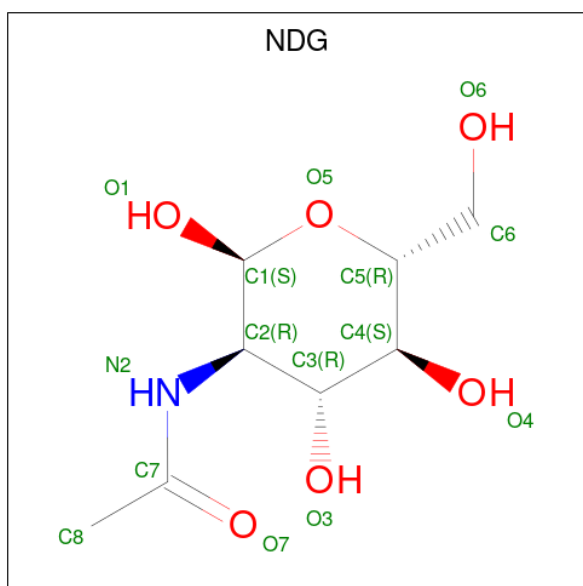
Chain	Residue	Modelled	Actual	Comment	Reference
C	87	SER	ARG	engineered mutation	UNP O09234
C	88	THR	ARG	engineered mutation	UNP O09234
C	91	SER	ARG	engineered mutation	UNP O09234

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



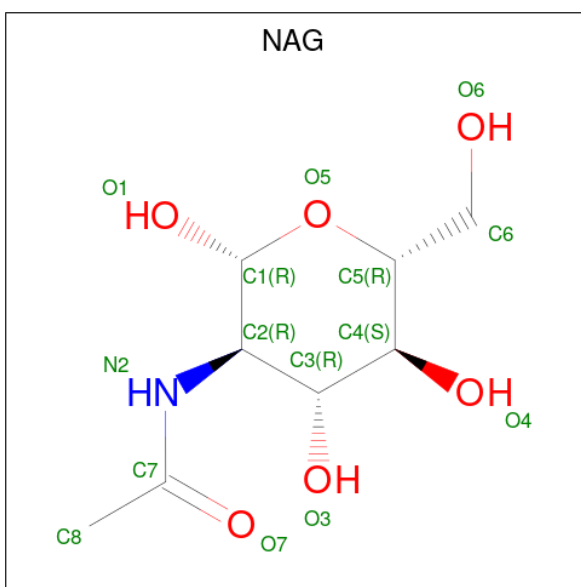
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 4 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (CCD ID: NDG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	N	O	0	0
			15	8	1	6		

- 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	C	1	Total	C	N	O	0	0
			15	8	1	6		

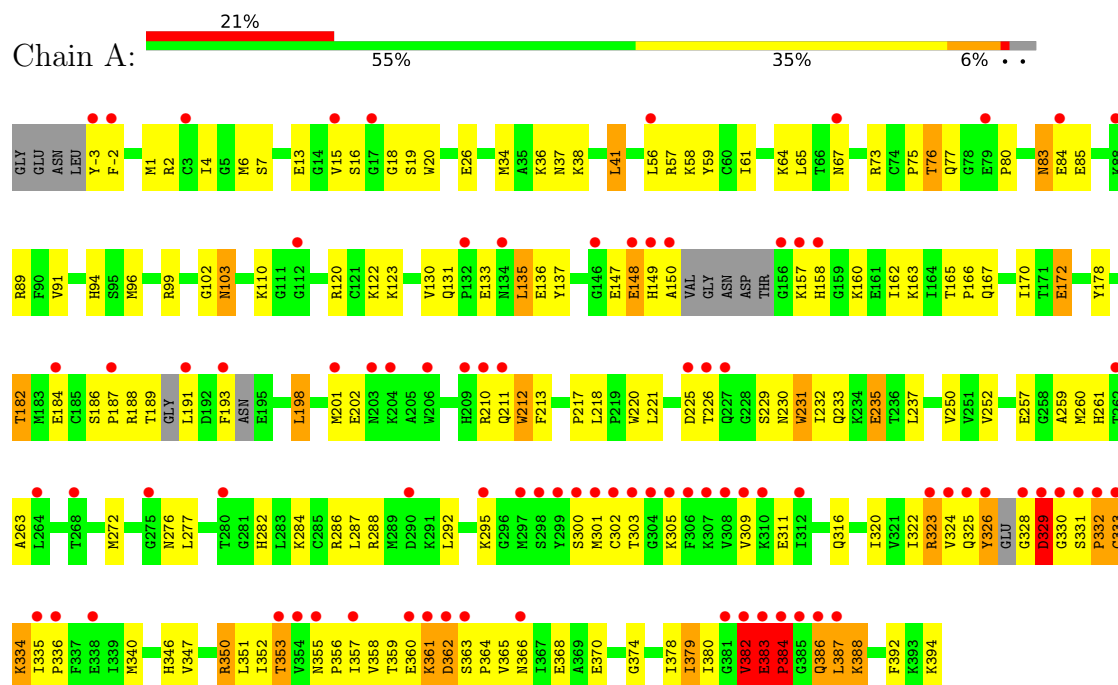
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	38	Total	O	0	0
			38	38		
6	C	7	Total	O	0	0
			7	7		

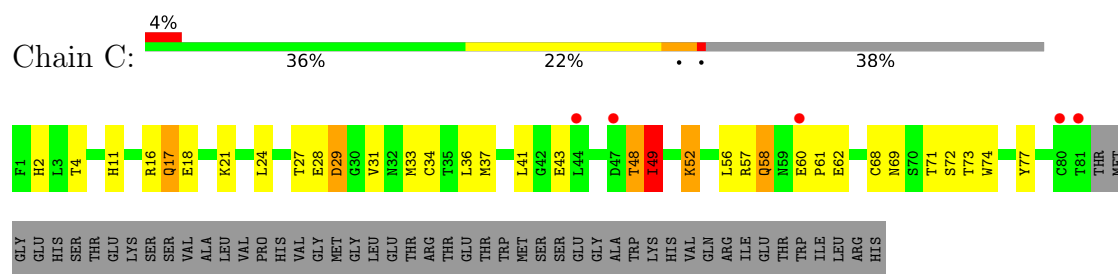
3 Residue-property plots [i](#)

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.

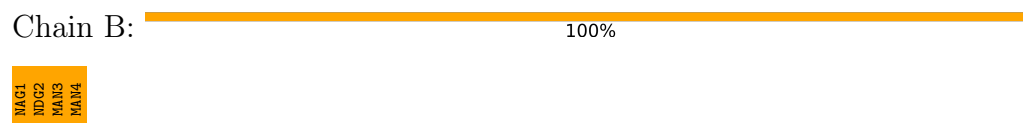
- Molecule 1: Envelope protein E



- Molecule 2: prM



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.10Å 108.37Å 108.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.60) 99.7 (50.00-2.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.07 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.250 , 0.293 0.251 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	57.4	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -h,l,k	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3811	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: MAN, NDG, 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	0.71	2/3106 (0.1%)	1.10	26/4186 (0.6%)
2	C	0.87	2/652 (0.3%)	0.94	2/883 (0.2%)
All	All	0.74	4/3758 (0.1%)	1.07	28/5069 (0.6%)

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
2	C	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	334	LYS	C-N	-27.36	1.02	1.33
2	C	48	THR	C-N	-14.25	1.12	1.33
1	A	335	ILE	C-N	-12.19	1.05	1.33
2	C	49	ILE	C-N	-11.85	1.17	1.33

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	334	LYS	O-C-N	-13.90	106.94	122.79
1	A	352	ILE	N-CA-C	-11.39	102.01	111.81
1	A	384	PRO	N-CA-C	-10.77	90.28	112.47
1	A	383	GLU	N-CA-C	10.54	133.10	109.81
1	A	332	PRO	N-CA-C	-10.35	91.14	112.47
1	A	334	LYS	CA-C-N	9.60	139.88	122.13
1	A	334	LYS	C-N-CA	9.60	139.88	122.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	TRP	N-CA-C	-8.29	102.76	113.12
1	A	330	GLY	N-CA-C	8.01	122.45	110.75
2	C	48	THR	O-C-N	-7.79	114.23	123.03
1	A	333	CYS	N-CA-C	7.33	120.55	109.41
1	A	353	THR	N-CA-C	-7.03	98.58	109.76
1	A	329	ASP	N-CA-C	6.86	125.41	110.80
1	A	148	GLU	N-CA-C	6.81	120.69	110.14
1	A	387	LEU	N-CA-C	6.48	120.16	108.17
1	A	305	LYS	N-CA-C	6.25	119.38	109.50
1	A	382	VAL	N-CA-C	6.11	116.28	108.82
1	A	386	GLN	N-CA-C	-6.04	101.24	110.30
2	C	52	LYS	N-CA-C	5.88	119.40	109.76
1	A	91	VAL	N-CA-C	-5.58	100.36	108.17
1	A	335	ILE	O-C-N	-5.56	114.76	121.10
1	A	379	ILE	N-CA-C	5.56	115.65	107.15
1	A	361	LYS	N-CA-C	-5.44	101.11	109.76
1	A	135	LEU	N-CA-C	-5.33	101.01	109.96
1	A	335	ILE	CA-C-N	5.18	126.32	119.84
1	A	335	ILE	C-N-CA	5.18	126.32	119.84
1	A	77	GLN	N-CA-C	5.10	118.33	112.57
1	A	231	TRP	N-CA-C	5.03	117.33	110.24

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	49	ILE	Mainchain

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	3046	0	3045	157	0
2	C	640	0	609	32	0
3	B	50	0	39	12	0
4	C	15	0	12	10	0
5	C	15	0	15	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	38	0	0	4	0
6	C	7	0	0	0	0
All	All	3811	0	3720	196	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 26.

All (196) 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:188:ARG:HD3	1:A:284:LYS:HD2	1.24	1.11
2:C:2:HIS:NE2	3:B:4:MAN:O2	1.96	0.98
1:A:198:LEU:HD22	1:A:277:LEU:HD13	1.46	0.97
2:C:2:HIS:HE2	3:B:4:MAN:HO2	1.12	0.91
1:A:75:PRO:O	1:A:76:THR:HB	1.72	0.87
4:C:1396:NDG:O3	5:C:1397:NAG:H1	1.76	0.86
1:A:147:GLU:HB3	1:A:157:LYS:HE3	1.58	0.83
1:A:188:ARG:CD	1:A:284:LYS:HD2	2.08	0.83
1:A:-2:PHE:CD2	1:A:1:MET:HE3	2.14	0.82
1:A:170:ILE:HG12	1:A:184:GLU:HB2	1.64	0.80
1:A:83:ASN:HD22	1:A:83:ASN:N	1.82	0.77
1:A:-3:TYR:CE1	1:A:1:MET:HE1	2.21	0.76
1:A:56:LEU:HD22	1:A:213:PHE:HE2	1.49	0.76
1:A:73:ARG:HG3	1:A:80:PRO:HB3	1.66	0.76
1:A:303:THR:HA	1:A:382:VAL:HG21	1.67	0.75
1:A:309:VAL:HG11	1:A:323:ARG:HH21	1.52	0.75
1:A:388:LYS:H	1:A:388:LYS:HD2	1.51	0.74
1:A:351:LEU:HB3	1:A:353:THR:O	1.88	0.74
1:A:347:VAL:HG23	6:A:1436:HOH:O	1.88	0.73
1:A:99:ARG:HE	1:A:103:ASN:ND2	1.86	0.73
1:A:148:GLU:OE2	1:A:364:PRO:HB2	1.90	0.72
1:A:41:LEU:HD21	1:A:292:LEU:HD11	1.71	0.71
1:A:83:ASN:ND2	1:A:83:ASN:H	1.89	0.70
1:A:166:PRO:HB3	1:A:187:PRO:HG2	1.75	0.69
1:A:149:HIS:O	1:A:150:ALA:CB	2.41	0.68
1:A:218:LEU:HD11	1:A:260:MET:HE1	1.73	0.68
1:A:67:ASN:OD1	3:B:1:NAG:O5	2.10	0.67
1:A:148:GLU:CD	1:A:364:PRO:HB2	2.21	0.66
1:A:59:TYR:CD1	1:A:220:TRP:HB3	2.30	0.66
1:A:148:GLU:CD	1:A:364:PRO:O	2.39	0.66
1:A:178:TYR:CE1	1:A:295:LYS:HB3	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:ASN:N	1:A:83:ASN:ND2	2.42	0.66
1:A:-3:TYR:CD1	1:A:1:MET:HE1	2.32	0.65
1:A:56:LEU:HD23	1:A:57:ARG:HB2	1.79	0.65
2:C:69:ASN:OD1	4:C:1396:NDG:O1	2.15	0.64
1:A:333:CYS:O	1:A:357:ILE:HG23	1.98	0.64
1:A:56:LEU:HD23	1:A:56:LEU:C	2.23	0.63
1:A:38:LYS:HE2	1:A:292:LEU:O	1.98	0.63
1:A:388:LYS:H	1:A:388:LYS:CD	2.12	0.63
1:A:165:THR:HG23	1:A:166:PRO:HD2	1.80	0.63
2:C:57:ARG:HH11	2:C:57:ARG:HG3	1.64	0.62
1:A:360:GLU:HB2	1:A:363:SER:HB3	1.82	0.62
1:A:123:LYS:HE3	1:A:202:GLU:OE1	2.01	0.61
1:A:188:ARG:HD3	1:A:284:LYS:CD	2.17	0.61
1:A:302:CYS:SG	1:A:334:LYS:O	2.58	0.60
4:C:1396:NDG:H4	5:C:1397:NAG:H5	1.81	0.60
1:A:182:THR:HG23	1:A:288:ARG:HB3	1.82	0.60
1:A:147:GLU:CB	1:A:157:LYS:HE3	2.30	0.60
1:A:326:TYR:C	1:A:328:GLY:N	2.60	0.60
1:A:334:LYS:HA	1:A:357:ILE:HG12	1.83	0.59
2:C:69:ASN:HD21	4:C:1396:NDG:C1	2.15	0.59
4:C:1396:NDG:C4	5:C:1397:NAG:H5	2.32	0.59
1:A:64:LYS:HB2	1:A:122:LYS:HE3	1.84	0.59
2:C:69:ASN:ND2	4:C:1396:NDG:C1	2.66	0.58
1:A:309:VAL:HB	1:A:323:ARG:HB3	1.85	0.58
1:A:201:MET:HE1	1:A:257:GLU:HG3	1.86	0.58
1:A:131:GLN:HB2	6:A:1414:HOH:O	2.03	0.57
1:A:131:GLN:O	1:A:133:GLU:O	2.23	0.57
1:A:301:MET:O	1:A:302:CYS:C	2.47	0.57
1:A:165:THR:CG2	1:A:166:PRO:HD2	2.35	0.57
1:A:303:THR:HG23	1:A:303:THR:O	2.05	0.57
2:C:2:HIS:CE1	3:B:4:MAN:O2	2.58	0.57
1:A:334:LYS:HE2	1:A:355:ASN:OD1	2.05	0.56
1:A:166:PRO:HB3	1:A:187:PRO:CG	2.36	0.56
2:C:4:THR:HG23	2:C:11:HIS:HB3	1.87	0.56
2:C:52:LYS:HD3	2:C:72:SER:OG	2.06	0.56
1:A:383:GLU:O	1:A:383:GLU:HG2	2.06	0.56
1:A:160:LYS:HE3	6:A:1418:HOH:O	2.06	0.55
1:A:186:SER:C	1:A:188:ARG:H	2.14	0.55
1:A:201:MET:CE	1:A:257:GLU:HG3	2.37	0.55
2:C:16:ARG:O	2:C:16:ARG:HD3	2.06	0.55
1:A:13:GLU:HG3	1:A:34:MET:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:LEU:HD22	1:A:213:PHE:CE2	2.37	0.54
1:A:7:SER:HB3	1:A:316:GLN:HE22	1.73	0.53
1:A:167:GLN:O	1:A:167:GLN:HG2	2.07	0.53
1:A:326:TYR:O	1:A:328:GLY:N	2.41	0.53
1:A:37:ASN:O	1:A:38:LYS:HD2	2.09	0.53
1:A:325:GLN:OE1	1:A:362:ASP:HA	2.08	0.53
1:A:386:GLN:O	1:A:388:LYS:HD2	2.10	0.52
1:A:147:GLU:OE1	1:A:157:LYS:NZ	2.42	0.52
2:C:31:VAL:HG21	5:C:1397:NAG:O3	2.10	0.52
2:C:60:GLU:HG3	2:C:61:PRO:HD2	1.92	0.52
2:C:49:ILE:O	2:C:49:ILE:HG13	2.10	0.52
4:C:1396:NDG:O4	5:C:1397:NAG:H5	2.10	0.52
1:A:148:GLU:OE2	1:A:323:ARG:NH1	2.43	0.52
1:A:201:MET:HE1	1:A:257:GLU:HA	1.92	0.52
1:A:323:ARG:HG3	1:A:366:ASN:OD1	2.10	0.52
1:A:130:VAL:O	1:A:193:PHE:HB3	2.10	0.52
1:A:61:ILE:HD13	1:A:201:MET:HE3	1.92	0.51
1:A:210:ARG:C	1:A:212:TRP:H	2.18	0.51
2:C:2:HIS:CE1	3:B:4:MAN:HO2	2.28	0.51
2:C:31:VAL:O	4:C:1396:NDG:H3	2.10	0.51
1:A:18:GLY:O	1:A:288:ARG:NH2	2.43	0.51
1:A:382:VAL:O	1:A:384:PRO:HD2	2.11	0.51
1:A:357:ILE:HG22	1:A:358:VAL:N	2.26	0.51
2:C:34:CYS:HA	2:C:68:CYS:HA	1.92	0.51
3:B:1:NAG:O3	3:B:2:NDG:C1	2.59	0.51
2:C:49:ILE:HD11	2:C:77:TYR:CZ	2.46	0.51
1:A:-3:TYR:HE2	1:A:366:ASN:HD21	1.59	0.51
2:C:18:GLU:O	2:C:21:LYS:HG2	2.11	0.51
1:A:67:ASN:HD22	3:B:1:NAG:C7	2.24	0.51
1:A:272:MET:HB2	1:A:276:ASN:O	2.10	0.50
3:B:1:NAG:H62	3:B:2:NDG:C7	2.41	0.50
1:A:340:MET:CE	1:A:379:ILE:HG13	2.41	0.50
1:A:2:ARG:HG3	1:A:2:ARG:HH11	1.76	0.50
1:A:237:LEU:O	1:A:252:VAL:HG23	2.13	0.49
1:A:301:MET:HE3	1:A:336:PRO:HG3	1.94	0.49
1:A:261:HIS:C	1:A:263:ALA:H	2.19	0.49
1:A:172:GLU:OE2	1:A:182:THR:HB	2.13	0.49
1:A:26:GLU:OE2	1:A:282:HIS:CD2	2.66	0.48
2:C:57:ARG:HG3	2:C:57:ARG:NH1	2.26	0.48
1:A:149:HIS:O	1:A:150:ALA:HB2	2.13	0.48
1:A:382:VAL:O	1:A:384:PRO:CD	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:GLU:OE1	1:A:364:PRO:HB2	2.14	0.48
1:A:235:GLU:H	1:A:235:GLU:CD	2.19	0.48
1:A:89:ARG:HG2	1:A:229:SER:HB3	1.94	0.48
1:A:15:VAL:HG22	1:A:15:VAL:O	2.14	0.48
1:A:187:PRO:O	1:A:188:ARG:C	2.56	0.48
1:A:357:ILE:CG2	1:A:358:VAL:N	2.76	0.48
2:C:57:ARG:C	2:C:58:GLN:HG2	2.38	0.48
1:A:20:TRP:NE1	1:A:288:ARG:NH1	2.62	0.48
1:A:41:LEU:CD2	1:A:292:LEU:HD11	2.43	0.48
1:A:96:MET:HE3	1:A:110:LYS:HB3	1.96	0.47
1:A:324:VAL:HG11	1:A:380:ILE:HD13	1.95	0.47
1:A:2:ARG:O	1:A:6:MET:HG3	2.14	0.47
1:A:67:ASN:ND2	3:B:1:NAG:C7	2.77	0.47
1:A:172:GLU:OE2	1:A:172:GLU:HA	2.14	0.47
2:C:24:LEU:HD23	2:C:33:MET:HA	1.97	0.47
1:A:165:THR:HG22	1:A:167:GLN:H	1.79	0.47
1:A:301:MET:HG3	1:A:336:PRO:HG3	1.96	0.47
1:A:75:PRO:O	1:A:76:THR:CB	2.52	0.46
1:A:133:GLU:HA	1:A:166:PRO:HG2	1.98	0.46
1:A:379:ILE:HG21	1:A:386:GLN:NE2	2.30	0.46
2:C:69:ASN:OD1	2:C:69:ASN:C	2.59	0.46
2:C:69:ASN:CG	4:C:1396:NDG:O1	2.59	0.46
1:A:149:HIS:O	1:A:150:ALA:HB3	2.14	0.46
1:A:350:ARG:HD2	1:A:370:GLU:OE1	2.15	0.46
1:A:59:TYR:CE1	1:A:220:TRP:HB3	2.50	0.46
1:A:232:ILE:O	1:A:233:GLN:HG2	2.16	0.46
1:A:374:GLY:O	1:A:392:PHE:HA	2.16	0.45
1:A:67:ASN:HD22	3:B:1:NAG:C8	2.29	0.45
1:A:210:ARG:O	1:A:211:GLN:HB2	2.17	0.45
1:A:99:ARG:HE	1:A:103:ASN:HD22	1.62	0.44
1:A:259:ALA:O	1:A:263:ALA:HB2	2.17	0.44
5:C:1397:NAG:O1	5:C:1397:NAG:H83	2.17	0.44
1:A:-2:PHE:HZ	1:A:4:ILE:HD12	1.82	0.44
1:A:133:GLU:HB2	6:A:1416:HOH:O	2.17	0.44
1:A:133:GLU:HA	1:A:166:PRO:CG	2.48	0.44
1:A:359:THR:HG22	1:A:360:GLU:HG3	1.99	0.44
2:C:69:ASN:ND2	4:C:1396:NDG:O1	2.51	0.44
2:C:29:ASP:OD1	2:C:29:ASP:N	2.51	0.44
1:A:232:ILE:O	1:A:233:GLN:CG	2.66	0.43
1:A:260:MET:O	1:A:263:ALA:HB3	2.18	0.43
1:A:363:SER:O	1:A:365:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:GLY:HA3	2:C:62:GLU:HB3	2.01	0.43
1:A:56:LEU:CD2	1:A:57:ARG:HB2	2.47	0.43
1:A:64:LYS:HG2	1:A:65:LEU:N	2.33	0.43
1:A:188:ARG:O	1:A:189:THR:C	2.61	0.43
1:A:323:ARG:HD3	1:A:364:PRO:HB3	1.99	0.43
1:A:16:SER:HB3	1:A:19:SER:HB3	2.01	0.43
1:A:165:THR:C	1:A:167:GLN:H	2.26	0.43
1:A:165:THR:C	1:A:167:GLN:N	2.76	0.43
1:A:355:ASN:N	1:A:356:PRO:CD	2.82	0.43
1:A:303:THR:O	1:A:329:ASP:HB3	2.19	0.43
2:C:17:GLN:N	2:C:17:GLN:CD	2.76	0.43
1:A:217:PRO:O	1:A:218:LEU:HD23	2.20	0.42
1:A:73:ARG:NE	1:A:80:PRO:HA	2.35	0.42
1:A:392:PHE:CE2	1:A:394:LYS:HB2	2.54	0.42
2:C:73:THR:HG22	2:C:74:TRP:O	2.18	0.42
1:A:162:ILE:O	1:A:162:ILE:HG13	2.18	0.42
1:A:322:ILE:HD11	1:A:378:ILE:HD13	2.02	0.42
1:A:16:SER:HB3	1:A:19:SER:CB	2.49	0.42
1:A:85:GLU:OE1	1:A:94:HIS:NE2	2.47	0.42
1:A:102:GLY:HA2	2:C:60:GLU:O	2.20	0.42
1:A:225:ASP:CG	1:A:226:THR:N	2.77	0.42
1:A:58:LYS:O	1:A:220:TRP:HA	2.19	0.42
1:A:218:LEU:HD11	1:A:260:MET:CE	2.45	0.42
1:A:221:LEU:HG	1:A:231:TRP:CE3	2.55	0.42
2:C:16:ARG:HG3	2:C:43:GLU:OE2	2.20	0.42
1:A:221:LEU:HD13	1:A:225:ASP:OD2	2.20	0.41
3:B:2:NDG:C4	3:B:3:MAN:C1	2.86	0.41
1:A:136:GLU:OE2	1:A:163:LYS:HD3	2.20	0.41
1:A:137:TYR:N	1:A:137:TYR:CD1	2.87	0.41
1:A:135:LEU:HD23	1:A:135:LEU:HA	1.84	0.41
1:A:257:GLU:HG2	1:A:261:HIS:CD2	2.56	0.41
3:B:1:NAG:O3	3:B:2:NDG:O5	2.38	0.41
1:A:76:THR:O	1:A:76:THR:HG23	2.20	0.41
1:A:221:LEU:HD21	1:A:230:ASN:C	2.46	0.41
1:A:233:GLN:HA	1:A:235:GLU:OE2	2.21	0.41
1:A:320:ILE:O	1:A:368:GLU:HA	2.20	0.41
2:C:27:THR:O	2:C:28:GLU:C	2.63	0.41
1:A:83:ASN:HD22	1:A:83:ASN:H	1.49	0.40
1:A:361:LYS:O	1:A:362:ASP:HB2	2.21	0.40
2:C:49:ILE:HD11	2:C:77:TYR:OH	2.20	0.40
1:A:148:GLU:OE1	1:A:364:PRO:O	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:GLU:H	1:A:311:GLU:HG2	1.73	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	380/402 (94%)	345 (91%)	32 (8%)	3 (1%)	16	34
2	C	79/130 (61%)	70 (89%)	9 (11%)	0	100	100
All	All	459/532 (86%)	415 (90%)	41 (9%)	3 (1%)	18	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	329	ASP
1	A	383	GLU
1	A	384	PRO

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	339/348 (97%)	311 (92%)	28 (8%)	10	23
2	C	75/118 (64%)	66 (88%)	9 (12%)	5	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	414/466 (89%)	377 (91%)	37 (9%)	9 20

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	LYS
1	A	41	LEU
1	A	76	THR
1	A	83	ASN
1	A	84	GLU
1	A	103	ASN
1	A	120	ARG
1	A	158	HIS
1	A	172	GLU
1	A	182	THR
1	A	191	LEU
1	A	198	LEU
1	A	235	GLU
1	A	250	VAL
1	A	286	ARG
1	A	287	LEU
1	A	300	SER
1	A	323	ARG
1	A	326	TYR
1	A	329	ASP
1	A	331	SER
1	A	332	PRO
1	A	346	HIS
1	A	350	ARG
1	A	362	ASP
1	A	382	VAL
1	A	387	LEU
1	A	388	LYS
2	C	17	GLN
2	C	29	ASP
2	C	36	LEU
2	C	37	MET
2	C	41	LEU
2	C	48	THR
2	C	56	LEU
2	C	58	GLN
2	C	71	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	GLN
1	A	37	ASN
1	A	83	ASN
1	A	103	ASN
1	A	131	GLN
1	A	200	GLN
1	A	203	ASN
1	A	248	GLN
1	A	261	HIS
1	A	316	GLN
1	A	366	ASN
2	C	7	ASN
2	C	17	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	B	1	3,1	14,14,15	0.54	0	17,19,21	4.74	2 (11%)
3	NDG	B	2	3	14,14,15	1.91	1 (7%)	17,19,21	1.79	4 (23%)
3	MAN	B	3	3	11,11,12	0.85	1 (9%)	15,15,17	0.86	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MAN	B	4	3	11,11,12	1.10	1 (9%)	15,15,17	2.68	4 (26%)

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	B	1	3,1	1/1/5/7	5/6/23/26	0/1/1/1
3	NDG	B	2	3	-	4/6/23/26	0/1/1/1
3	MAN	B	3	3	-	2/2/19/22	0/1/1/1
3	MAN	B	4	3	1/1/4/5	1/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2	NDG	C2-N2	-6.68	1.35	1.46
3	B	4	MAN	C6-C5	-2.47	1.43	1.51
3	B	3	MAN	O3-C3	2.18	1.48	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1	NAG	O4-C4-C5	17.56	152.57	109.32
3	B	1	NAG	O4-C4-C3	-8.17	91.13	110.38
3	B	4	MAN	C6-C5-C4	8.07	132.82	113.02
3	B	2	NDG	C2-N2-C7	4.93	129.51	122.90
3	B	4	MAN	O5-C5-C6	4.13	115.70	107.66
3	B	4	MAN	O6-C6-C5	3.76	124.14	111.33
3	B	2	NDG	C1-C2-N2	3.70	116.27	110.43
3	B	4	MAN	C1-O5-C5	2.99	116.19	112.19
3	B	2	NDG	O7-C7-N2	2.79	126.90	121.98
3	B	3	MAN	O3-C3-C4	2.72	116.79	110.38
3	B	2	NDG	C8-C7-N2	-2.11	112.62	116.12

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	1	NAG	C1
3	B	4	MAN	C5

All (12) torsion outliers are listed below:

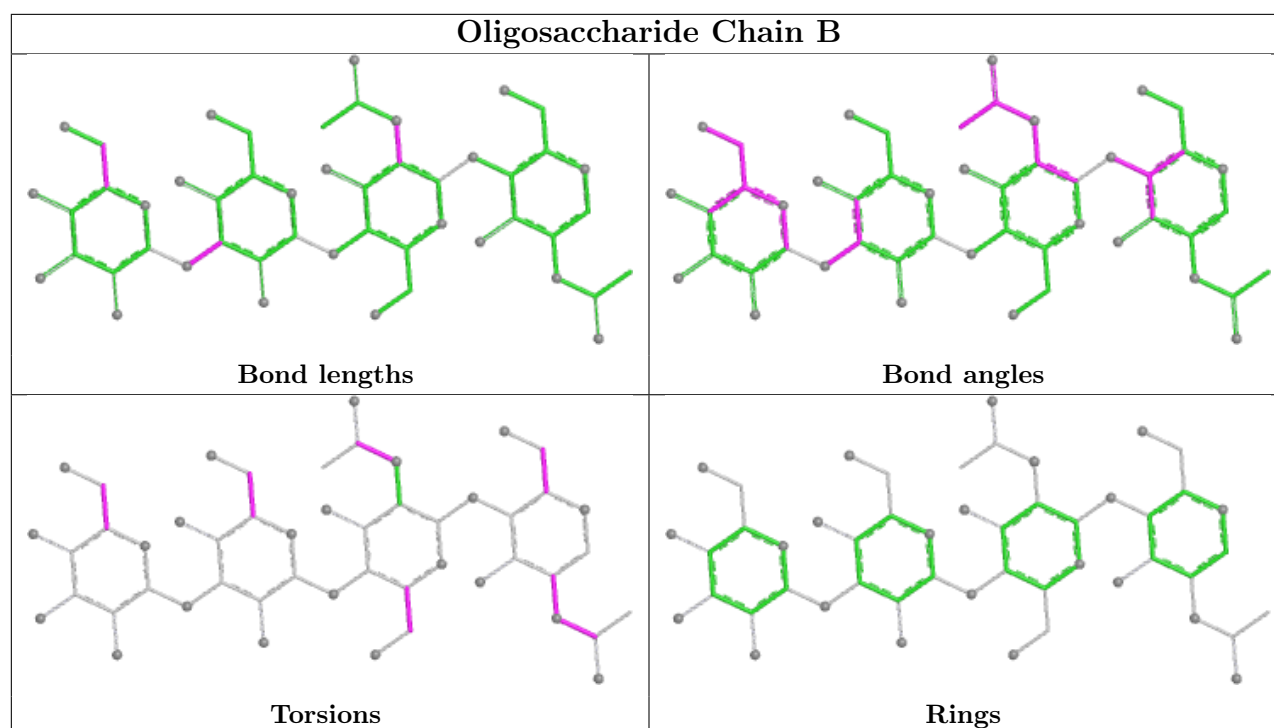
Mol	Chain	Res	Type	Atoms
3	B	1	NAG	C1-C2-N2-C7
3	B	1	NAG	C8-C7-N2-C2
3	B	1	NAG	O7-C7-N2-C2
3	B	2	NDG	C8-C7-N2-C2
3	B	2	NDG	O7-C7-N2-C2
3	B	4	MAN	O5-C5-C6-O6
3	B	3	MAN	O5-C5-C6-O6
3	B	3	MAN	C4-C5-C6-O6
3	B	2	NDG	O5-C5-C6-O6
3	B	1	NAG	C4-C5-C6-O6
3	B	1	NAG	O5-C5-C6-O6
3	B	2	NDG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	4	MAN	4	0
3	B	2	NDG	4	0
3	B	3	MAN	1	0
3	B	1	NAG	7	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](#)

2 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	$\# Z > 2$
5	NAG	C	1397	-	15,15,15	0.46	0	21,21,21	0.64	0
4	NDG	C	1396	-	15,15,15	0.40	0	21,21,21	0.78	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	C	1397	-	-	5/6/26/26	0/1/1/1
4	NDG	C	1396	-	-	3/6/26/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1396	NDG	C1-C2-N2-C7
5	C	1397	NAG	C1-C2-N2-C7
5	C	1397	NAG	C8-C7-N2-C2
5	C	1397	NAG	O7-C7-N2-C2
4	C	1396	NDG	C4-C5-C6-O6
4	C	1396	NDG	O5-C5-C6-O6
5	C	1397	NAG	O5-C5-C6-O6
5	C	1397	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1397	NAG	6	0
4	C	1396	NDG	10	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	C	2
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	49:ILE	C	50:THR	N	1.17
1	C	48:THR	C	49:ILE	N	1.12
1	A	335:ILE	C	336:PRO	N	1.05
1	A	334:LYS	C	335:ILE	N	1.02

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	390/402 (97%)	1.15	85 (21%) 2 2	27, 62, 105, 141	0
2	C	81/130 (62%)	0.56	5 (6%) 26 21	23, 51, 79, 95	0
All	All	471/532 (88%)	1.05	90 (19%) 3 2	23, 59, 104, 141	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	149	HIS	5.9
1	A	332	PRO	5.0
1	A	331	SER	4.8
1	A	385	GLY	4.8
1	A	191	LEU	4.5
1	A	384	PRO	4.5
1	A	-3	TYR	4.5
1	A	330	GLY	4.4
1	A	148	GLU	4.3
1	A	146	GLY	4.2
1	A	156	GLY	4.2
1	A	309	VAL	4.2
1	A	150	ALA	4.0
1	A	329	ASP	4.0
1	A	362	ASP	4.0
1	A	366	ASN	3.8
1	A	360	GLU	3.7
1	A	300	SER	3.7
1	A	333	CYS	3.6
1	A	184	GLU	3.6
1	A	268	THR	3.6
1	A	301	MET	3.5
1	A	304	GLY	3.5
1	A	306	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	-2	PHE	3.4
1	A	206	TRP	3.3
1	A	323	ARG	3.3
1	A	67	ASN	3.3
1	A	204	LYS	3.2
1	A	17	GLY	3.2
1	A	355	ASN	3.2
1	A	299	TYR	3.2
1	A	326	TYR	3.2
1	A	302	CYS	3.2
1	A	387	LEU	3.1
1	A	209	HIS	3.1
2	C	80	CYS	3.1
1	A	298	SER	3.1
1	A	134	ASN	3.1
1	A	310	LYS	3.1
1	A	305	LYS	2.9
1	A	354	VAL	2.9
1	A	211	GLN	2.8
1	A	193	PHE	2.8
1	A	312	ILE	2.8
2	C	44	LEU	2.8
1	A	15	VAL	2.8
1	A	297	MET	2.8
1	A	79	GLU	2.8
1	A	383	GLU	2.8
1	A	328	GLY	2.7
1	A	307	LYS	2.7
2	C	81	THR	2.7
1	A	363	SER	2.7
1	A	336	PRO	2.6
1	A	210	ARG	2.6
1	A	158	HIS	2.6
1	A	187	PRO	2.5
1	A	262	THR	2.5
1	A	381	GLY	2.5
1	A	275	GLY	2.4
1	A	386	GLN	2.4
1	A	226	THR	2.4
1	A	112	GLY	2.4
2	C	47	ASP	2.4
1	A	3	CYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	203	ASN	2.4
1	A	325	GLN	2.4
1	A	295	LYS	2.3
1	A	56	LEU	2.3
1	A	335	ILE	2.3
1	A	353	THR	2.3
1	A	88	LYS	2.3
1	A	132	PRO	2.3
1	A	225	ASP	2.3
1	A	264	LEU	2.3
1	A	324	VAL	2.3
1	A	308	VAL	2.2
1	A	157	LYS	2.2
1	A	361	LYS	2.2
1	A	303	THR	2.2
1	A	227	GLN	2.2
2	C	60	GLU	2.1
1	A	84	GLU	2.1
1	A	338	GLU	2.1
1	A	357	ILE	2.1
1	A	290	ASP	2.0
1	A	201	MET	2.0
1	A	280	THR	2.0
1	A	382	VAL	2.0

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

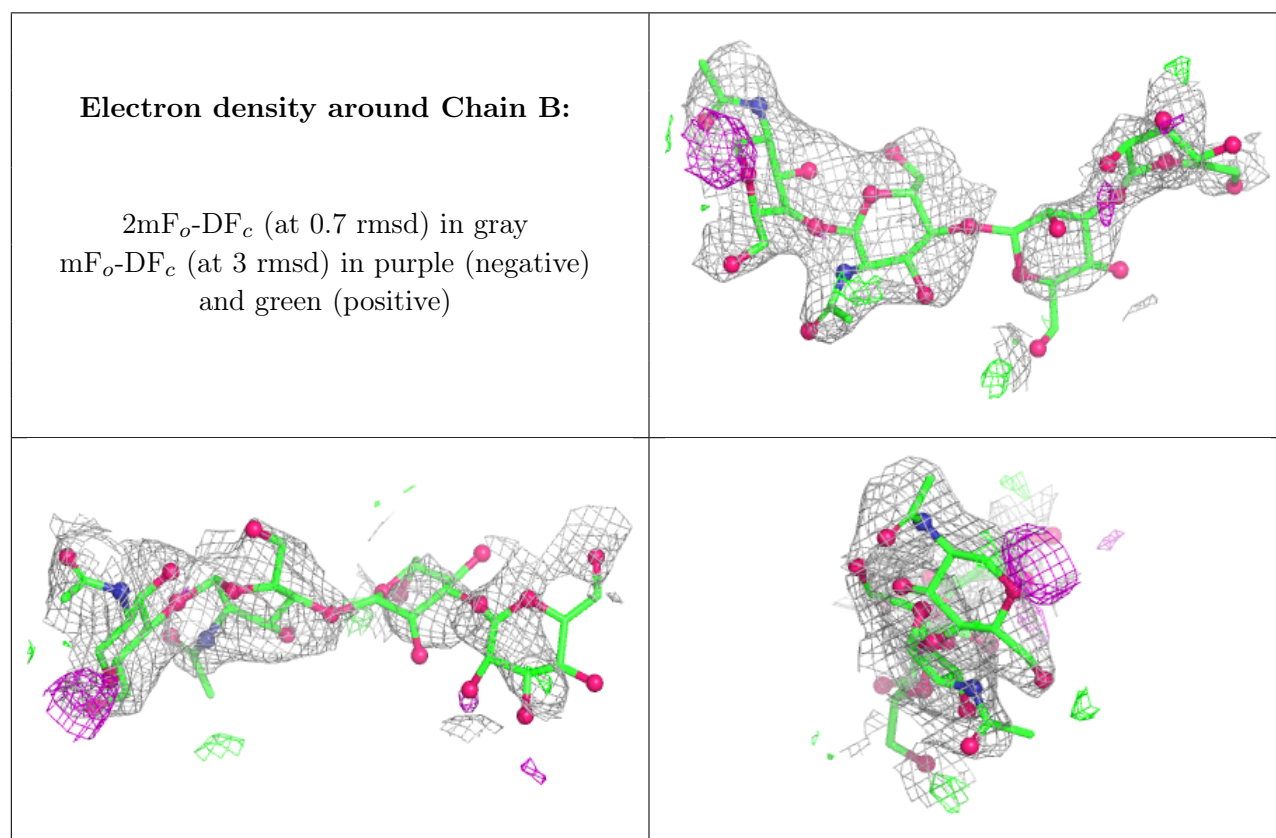
There are no non-standard protein/DNA/RNA residues in this entry.

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
3	NAG	B	1	14/15	-	-	88,89,90,90	0
3	NDG	B	2	14/15	-	-	103,107,120,144	0
3	MAN	B	3	11/12	-	-	169,184,191,193	0
3	MAN	B	4	11/12	-	-	171,172,175,177	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
5	NAG	C	1397	15/15	0.65	0.21	88,90,92,93	0
4	NDG	C	1396	15/15	0.80	0.14	58,63,65,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.