



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:03 AM UTC

PDB ID : 1IEV / pdb_00001iev
Title : CRYSTAL STRUCTURE OF BARLEY BETA-D-GLUCAN GLUCOHYDROLASE ISOENZYME EXO1 IN COMPLEX WITH CYCLOHEXITOL
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Deposited on : 2001-04-11
Resolution : 2.80 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

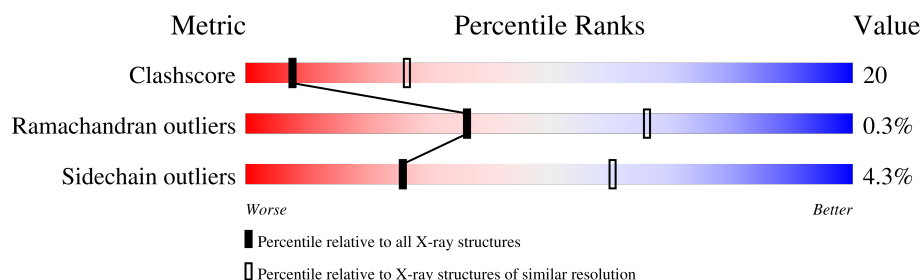
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	605	
2	B	6	

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	4	-	X	X	-
2	NAG	B	5	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4878 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.

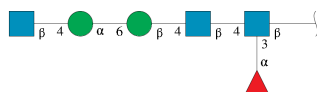
- Molecule 1 is a protein called BETA-D-GLUCAN GLUCOHYDROLASE ISOENZYME EXO1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	602	Total	C	N	O	S	0	0	0
			4566	2891	787	862	26			

There is a discrepancy between the modelled and reference sequences:

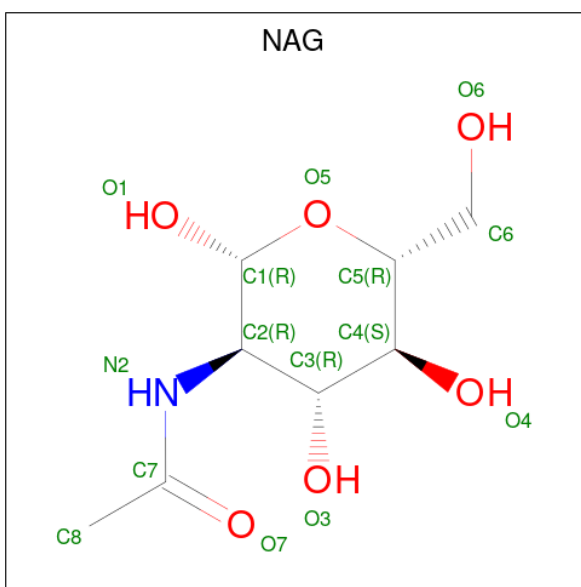
Chain	Residue	Modelled	Actual	Comment	Reference
A	320	LYS	ASN	SEE REMARK 999	GB 4566505

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



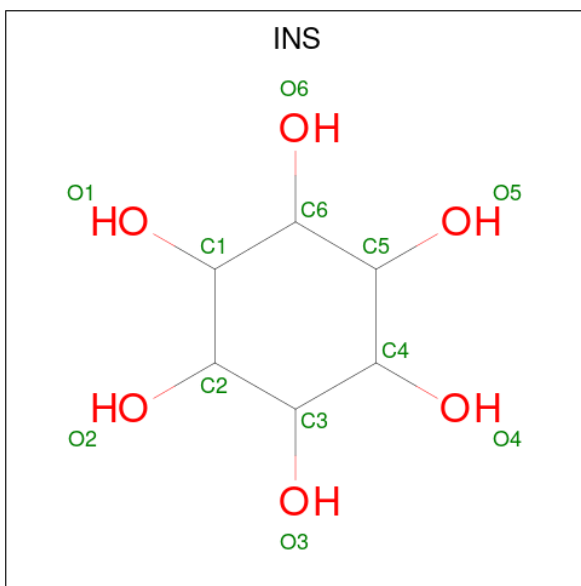
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	6	Total	C	N	O	0	0	0
			74	42	3	29			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is 1,2,3,4,5,6-HEXAHYDROXY-CYCLOHEXANE (CCD ID: INS) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is water.

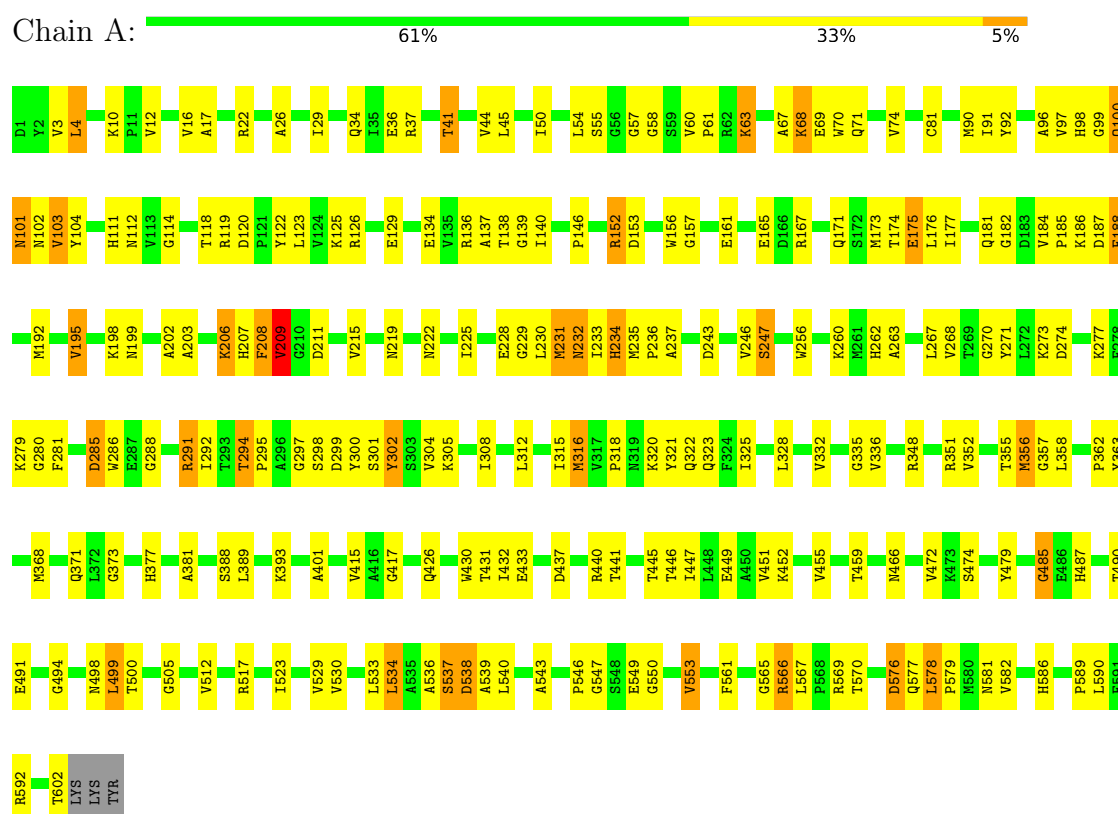
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	213	Total 213	O 213	0	0

3 Residue-property plots

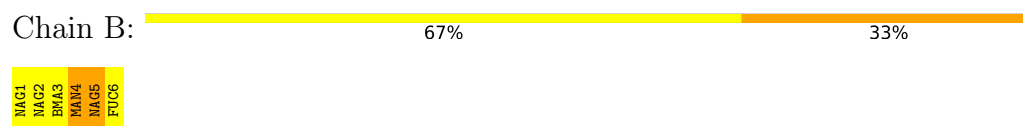
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: BETA-D-GLUCAN GLUCOHYDROLASE ISOENZYME EXO1



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



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	101.01Å 101.01Å 181.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (12.00-2.80)	Depositor
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.180 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4878	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, BMA, MAN, NAG, INS

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	1.12	10/4663 (0.2%)	1.38	51/6334 (0.8%)

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	3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	285	ASP	CG-OD1	8.59	1.41	1.25
1	A	316	MET	SD-CE	-8.02	1.59	1.79
1	A	356	MET	SD-CE	-6.28	1.63	1.79
1	A	530	VAL	CA-C	5.77	1.59	1.52
1	A	432	ILE	CA-CB	5.63	1.62	1.54
1	A	26	ALA	CA-CB	-5.60	1.44	1.53
1	A	209	VAL	N-CA	-5.58	1.39	1.46
1	A	17	ALA	CA-CB	-5.43	1.44	1.53
1	A	231	MET	SD-CE	-5.19	1.66	1.79
1	A	3	VAL	CA-CB	5.16	1.59	1.53

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	101	ASN	N-CA-C	11.19	126.03	112.38
1	A	590	LEU	N-CA-C	-9.93	99.89	112.90
1	A	206	LYS	N-CA-C	9.89	125.75	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	PHE	CA-C-N	8.56	137.38	121.97
1	A	208	PHE	C-N-CA	8.56	137.38	121.97
1	A	578	LEU	N-CA-C	8.49	121.79	110.08
1	A	188	PHE	N-CA-C	8.48	122.81	110.42
1	A	198	LYS	N-CA-C	7.77	121.86	112.38
1	A	209	VAL	N-CA-C	7.75	125.46	109.34
1	A	206	LYS	CA-C-N	7.63	136.12	121.54
1	A	206	LYS	C-N-CA	7.63	136.12	121.54
1	A	415	VAL	N-CA-C	-7.16	98.09	108.11
1	A	485	GLY	N-CA-C	6.98	119.53	110.45
1	A	112	ASN	N-CA-C	6.98	122.88	111.37
1	A	153	ASP	CA-C-N	-6.56	112.83	120.12
1	A	153	ASP	C-N-CA	-6.56	112.83	120.12
1	A	247	SER	N-CA-C	6.26	117.77	111.07
1	A	182	GLY	N-CA-C	-6.25	104.91	112.48
1	A	63	LYS	N-CA-C	-6.22	101.72	110.50
1	A	455	VAL	N-CA-C	6.16	117.17	110.21
1	A	103	VAL	N-CA-C	5.93	117.12	108.58
1	A	186	LYS	N-CA-C	-5.92	104.95	111.82
1	A	96	ALA	N-CA-C	-5.88	98.33	108.56
1	A	530	VAL	N-CA-C	5.80	119.33	113.47
1	A	291	ARG	N-CA-C	5.79	119.95	113.01
1	A	401	ALA	N-CA-C	-5.74	102.42	109.65
1	A	99	GLY	N-CA-C	-5.72	103.58	111.76
1	A	315	ILE	N-CA-C	5.69	116.06	107.80
1	A	69	GLU	N-CA-C	-5.68	105.17	111.36
1	A	175	GLU	N-CA-C	-5.65	106.23	113.01
1	A	537	SER	N-CA-C	5.61	119.24	110.32
1	A	381	ALA	N-CA-C	-5.60	105.08	111.07
1	A	536	ALA	N-CA-C	5.54	119.21	112.23
1	A	538	ASP	N-CA-C	-5.51	104.68	111.40
1	A	120	ASP	CA-C-N	-5.49	114.01	119.56
1	A	120	ASP	C-N-CA	-5.49	114.01	119.56
1	A	561	PHE	N-CA-C	-5.49	100.73	109.07
1	A	234	HIS	N-CA-C	5.48	119.68	112.89
1	A	202	ALA	N-CA-C	-5.46	102.19	110.28
1	A	301	SER	N-CA-C	-5.37	105.32	111.07
1	A	268	VAL	N-CA-C	5.36	116.02	110.82
1	A	553	VAL	CB-CA-C	-5.35	105.01	112.02
1	A	565	GLY	N-CA-C	5.34	118.07	111.93
1	A	499	LEU	N-CA-C	5.33	118.54	111.30
1	A	123	LEU	N-CA-C	-5.30	105.58	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	459	THR	N-CA-C	5.26	116.73	109.15
1	A	417	GLY	N-CA-C	5.21	118.55	111.72
1	A	195	VAL	N-CA-C	-5.17	101.19	108.27
1	A	576	ASP	N-CA-C	-5.14	106.96	113.18
1	A	550	GLY	N-CA-C	5.12	120.55	113.99
1	A	100	GLN	N-CA-C	-5.09	102.81	110.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	LYS	Mainchain
1	A	208	PHE	Mainchain
1	A	302	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	4566	0	4551	168	0
2	B	74	0	64	20	0
3	A	14	0	13	2	0
4	A	11	0	10	3	0
5	A	213	0	0	20	0
All	All	4878	0	4638	185	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 20.

All (185) 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)
2:B:4:MAN:C4	2:B:4:MAN:C5	1.92	1.45
2:B:5:NAG:C5	2:B:5:NAG:O5	1.70	1.37
2:B:4:MAN:C5	2:B:4:MAN:C3	2.05	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:MAN:C5	2:B:4:MAN:H3	1.75	1.09
2:B:4:MAN:H3	2:B:4:MAN:H5	1.30	1.07
2:B:4:MAN:H2	2:B:5:NAG:O5	1.64	0.95
2:B:4:MAN:C2	2:B:5:NAG:C1	2.44	0.95
1:A:181:GLN:NE2	1:A:203:ALA:H	1.65	0.94
1:A:487:HIS:CE1	2:B:5:NAG:C1	2.50	0.94
1:A:156:TRP:HE1	1:A:219:ASN:HD22	1.14	0.91
1:A:41:THR:HG22	1:A:44:VAL:H	1.33	0.90
1:A:181:GLN:HE21	1:A:203:ALA:H	0.91	0.89
1:A:487:HIS:ND1	2:B:4:MAN:O4	2.06	0.89
1:A:181:GLN:HE21	1:A:203:ALA:N	1.71	0.88
1:A:487:HIS:ND1	2:B:5:NAG:C1	2.37	0.87
2:B:4:MAN:C4	2:B:5:NAG:C1	2.53	0.87
1:A:316:MET:HE1	4:A:617:INS:H2	1.56	0.86
1:A:125:LYS:O	1:A:129:GLU:HG3	1.81	0.80
1:A:199:ASN:HD22	1:A:368:MET:HE2	1.47	0.79
1:A:207:HIS:HB2	1:A:211:ASP:OD2	1.82	0.79
1:A:566:ARG:HH11	1:A:566:ARG:HG3	1.49	0.78
1:A:579:PRO:HA	5:A:790:HOH:O	1.82	0.77
1:A:487:HIS:HD1	2:B:5:NAG:C1	2.00	0.74
1:A:566:ARG:HG3	1:A:566:ARG:NH1	2.02	0.73
1:A:122:TYR:CE2	1:A:126:ARG:HD2	2.24	0.72
1:A:231:MET:HE1	1:A:271:TYR:CZ	2.23	0.72
1:A:577:GLN:O	1:A:586:HIS:HE1	1.71	0.72
2:B:4:MAN:C3	2:B:4:MAN:H5	1.92	0.72
1:A:500:THR:HG22	1:A:529:VAL:HG21	1.71	0.72
2:B:4:MAN:O2	2:B:5:NAG:N2	2.23	0.72
1:A:188:PHE:HZ	1:A:192:MET:O	1.73	0.71
1:A:199:ASN:HD22	1:A:368:MET:CE	2.02	0.71
1:A:286:TRP:HB2	1:A:316:MET:HE2	1.72	0.71
1:A:91:ILE:HD12	1:A:356:MET:HE1	1.71	0.71
1:A:58:GLY:H	1:A:102:ASN:ND2	1.89	0.70
1:A:91:ILE:CD1	1:A:356:MET:HE1	2.21	0.70
1:A:231:MET:HE1	1:A:271:TYR:OH	1.91	0.70
3:A:610:NAG:H81	5:A:827:HOH:O	1.90	0.70
2:B:4:MAN:H2	2:B:5:NAG:C1	2.17	0.69
1:A:320:LYS:HB3	5:A:830:HOH:O	1.91	0.69
2:B:4:MAN:HO4	2:B:5:NAG:C1	2.03	0.68
1:A:167:ARG:O	1:A:171:GLN:HG3	1.93	0.68
1:A:316:MET:SD	5:A:869:HOH:O	2.52	0.68
1:A:97:VAL:H	1:A:101:ASN:HD21	1.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:HIS:H	1:A:101:ASN:HD22	1.43	0.67
1:A:98:HIS:H	1:A:101:ASN:ND2	1.93	0.66
1:A:4:LEU:HD13	1:A:10:LYS:HG3	1.78	0.65
1:A:286:TRP:CB	1:A:316:MET:HE2	2.28	0.64
1:A:312:LEU:HD12	1:A:312:LEU:H	1.61	0.64
1:A:181:GLN:HE22	1:A:247:SER:H	1.46	0.64
1:A:335:GLY:HA2	5:A:832:HOH:O	1.99	0.63
1:A:286:TRP:HB2	1:A:316:MET:CE	2.30	0.62
1:A:209:VAL:HG21	1:A:235:MET:HE2	1.80	0.62
1:A:300:TYR:CE2	1:A:323:GLN:HG2	2.37	0.60
1:A:602:THR:HG21	5:A:864:HOH:O	2.02	0.60
1:A:222:ASN:HB2	3:A:610:NAG:H82	1.83	0.60
1:A:589:PRO:HG3	1:A:592:ARG:HG2	1.84	0.60
1:A:263:ALA:HB2	1:A:292:ILE:HD13	1.84	0.59
1:A:312:LEU:HD12	1:A:312:LEU:N	2.17	0.59
1:A:322:GLN:HB2	5:A:836:HOH:O	2.02	0.58
1:A:114:GLY:O	1:A:388:SER:HB2	2.02	0.58
1:A:68:LYS:HG3	5:A:852:HOH:O	2.03	0.58
1:A:185:PRO:HB2	1:A:187:ASP:OD1	2.04	0.58
2:B:4:MAN:O2	2:B:5:NAG:C1	2.51	0.57
1:A:490:THR:HG22	1:A:491:GLU:HG3	1.86	0.57
1:A:209:VAL:HG21	1:A:235:MET:CE	2.34	0.56
2:B:4:MAN:C3	2:B:5:NAG:C1	2.83	0.56
1:A:207:HIS:HB2	1:A:211:ASP:CG	2.31	0.56
1:A:92:TYR:O	1:A:140:ILE:HG23	2.06	0.56
1:A:262:HIS:HE1	1:A:285:ASP:H	1.52	0.55
1:A:445:THR:HA	1:A:449:GLU:OE1	2.05	0.55
2:B:4:MAN:C2	2:B:5:NAG:O5	2.47	0.55
1:A:234:HIS:HE1	5:A:872:HOH:O	1.90	0.55
1:A:70:TRP:CB	1:A:138:THR:HB	2.37	0.54
1:A:295:PRO:O	1:A:298:SER:HB3	2.07	0.54
1:A:70:TRP:HB3	1:A:138:THR:HB	1.88	0.54
1:A:228:GLU:O	1:A:232:ASN:HB3	2.06	0.54
1:A:316:MET:HE1	4:A:617:INS:C2	2.36	0.54
1:A:500:THR:HG22	1:A:529:VAL:CG2	2.37	0.54
1:A:447:ILE:O	1:A:451:VAL:HG23	2.09	0.53
1:A:485:GLY:HA3	1:A:523:ILE:O	2.09	0.53
1:A:270:GLY:O	1:A:274:ASP:HB2	2.09	0.53
1:A:305:LYS:HD2	1:A:336:VAL:HG11	1.90	0.53
1:A:137:ALA:HB2	1:A:371:GLN:HB2	1.91	0.53
1:A:152:ARG:HD3	5:A:871:HOH:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:THR:HA	1:A:295:PRO:C	2.34	0.52
1:A:570:THR:HG23	1:A:589:PRO:HB3	1.91	0.52
1:A:60:VAL:HB	1:A:61:PRO:HD2	1.91	0.52
1:A:389:LEU:HD11	1:A:553:VAL:HA	1.91	0.52
1:A:231:MET:O	1:A:236:PRO:HD3	2.10	0.52
1:A:546:PRO:HA	5:A:764:HOH:O	2.10	0.52
1:A:91:ILE:HD12	1:A:356:MET:CE	2.37	0.51
1:A:566:ARG:HH11	1:A:566:ARG:CG	2.19	0.51
1:A:98:HIS:CD2	1:A:111:HIS:CE1	2.99	0.51
1:A:534:LEU:HD13	1:A:540:LEU:HD13	1.93	0.51
1:A:45:LEU:HD23	1:A:50:ILE:HB	1.92	0.50
1:A:173:MET:C	1:A:175:GLU:H	2.20	0.50
1:A:225:ILE:HD11	1:A:229:GLY:HA3	1.93	0.50
1:A:316:MET:CE	4:A:617:INS:H2	2.36	0.50
1:A:286:TRP:HE3	1:A:316:MET:CE	2.25	0.49
1:A:523:ILE:HD13	1:A:543:ALA:HB3	1.94	0.49
1:A:104:TYR:HB2	5:A:793:HOH:O	2.11	0.49
1:A:472:VAL:HG21	1:A:512:VAL:HA	1.93	0.49
1:A:237:ALA:HB3	5:A:823:HOH:O	2.13	0.49
1:A:134:GLU:CD	1:A:373:GLY:H	2.21	0.49
1:A:352:VAL:O	1:A:356:MET:HG2	2.13	0.48
1:A:426:GLN:HG2	1:A:547:GLY:O	2.13	0.48
1:A:134:GLU:OE2	1:A:377:HIS:HD2	1.97	0.48
1:A:437:ASP:HB3	1:A:441:THR:HG21	1.94	0.48
1:A:98:HIS:NE2	1:A:430:TRP:O	2.44	0.48
1:A:281:PHE:CD2	1:A:352:VAL:HG21	2.49	0.48
1:A:452:LYS:HE3	5:A:907:HOH:O	2.12	0.48
1:A:177:ILE:HD13	1:A:246:VAL:HB	1.96	0.48
1:A:256:TRP:CE3	1:A:267:LEU:HD11	2.49	0.48
1:A:362:PRO:HG2	1:A:363:TYR:CD1	2.49	0.47
1:A:152:ARG:HD2	1:A:233:ILE:HG21	1.95	0.47
1:A:286:TRP:CA	1:A:316:MET:HE2	2.45	0.47
1:A:231:MET:HE3	1:A:231:MET:HB3	1.69	0.47
1:A:273:LYS:O	1:A:277:LYS:HA	2.14	0.47
1:A:297:GLY:HA2	5:A:736:HOH:O	2.15	0.47
1:A:74:VAL:HG11	1:A:139:GLY:O	2.15	0.47
1:A:304:VAL:O	1:A:308:ILE:HG12	2.15	0.47
1:A:262:HIS:CE1	1:A:288:GLY:HA3	2.50	0.47
1:A:260:LYS:HE3	1:A:291:ARG:O	2.15	0.46
1:A:247:SER:O	1:A:280:GLY:HA3	2.16	0.46
1:A:499:LEU:O	1:A:529:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:ARG:HD3	1:A:140:ILE:O	2.15	0.46
1:A:479:TYR:C	1:A:479:TYR:CD1	2.94	0.45
1:A:165:GLU:CD	1:A:581:ASN:HD22	2.24	0.45
1:A:156:TRP:HE1	1:A:219:ASN:ND2	1.96	0.45
1:A:352:VAL:HG12	1:A:356:MET:CE	2.46	0.45
1:A:188:PHE:CZ	1:A:192:MET:O	2.61	0.45
1:A:321:TYR:O	1:A:325:ILE:HG13	2.17	0.45
1:A:184:VAL:HB	1:A:188:PHE:CG	2.52	0.45
1:A:34:GLN:OE1	1:A:316:MET:HG3	2.17	0.44
1:A:589:PRO:CG	1:A:592:ARG:HG2	2.47	0.44
1:A:393:LYS:NZ	1:A:537:SER:O	2.39	0.44
1:A:549:GLU:HB3	5:A:766:HOH:O	2.17	0.44
1:A:567:LEU:HB3	1:A:569:ARG:O	2.17	0.44
2:B:4:MAN:O2	2:B:5:NAG:C2	2.66	0.44
1:A:67:ALA:O	1:A:71:GLN:HG3	2.17	0.44
1:A:90:MET:C	1:A:90:MET:SD	3.01	0.44
1:A:100:GLN:HG3	1:A:103:VAL:CG2	2.48	0.44
1:A:431:THR:O	1:A:433:GLU:N	2.50	0.44
1:A:498:ASN:O	1:A:500:THR:HG23	2.18	0.44
1:A:118:THR:O	1:A:119:ARG:C	2.61	0.43
1:A:300:TYR:CD2	1:A:323:GLN:HG2	2.52	0.43
1:A:348:ARG:HG2	1:A:348:ARG:NH1	2.33	0.43
1:A:29:ILE:HG21	1:A:325:ILE:HG23	2.00	0.43
1:A:362:PRO:HG2	1:A:363:TYR:CE1	2.53	0.43
1:A:122:TYR:CZ	1:A:126:ARG:HD2	2.54	0.43
1:A:97:VAL:N	1:A:101:ASN:HD21	2.13	0.43
1:A:299:ASP:O	1:A:302:TYR:HB3	2.19	0.43
1:A:328:LEU:O	1:A:332:VAL:HG23	2.19	0.43
1:A:57:GLY:HA2	1:A:102:ASN:HD21	1.83	0.42
1:A:195:VAL:HB	1:A:356:MET:HA	2.00	0.42
1:A:305:LYS:HD2	1:A:336:VAL:CG1	2.48	0.42
1:A:4:LEU:CD2	1:A:10:LYS:HE2	2.49	0.42
1:A:174:THR:C	1:A:176:LEU:N	2.77	0.42
1:A:348:ARG:HG2	1:A:348:ARG:HH11	1.84	0.42
1:A:81:CYS:SG	1:A:90:MET:HB3	2.59	0.42
1:A:146:PRO:HB3	1:A:176:LEU:HD23	2.02	0.42
1:A:22:ARG:HG2	5:A:858:HOH:O	2.19	0.42
1:A:173:MET:C	1:A:175:GLU:N	2.76	0.42
1:A:100:GLN:HA	1:A:100:GLN:OE1	2.20	0.42
1:A:279:LYS:NZ	5:A:825:HOH:O	2.50	0.41
1:A:393:LYS:O	1:A:539:ALA:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:ARG:HH22	1:A:446:THR:HG23	1.86	0.41
1:A:517:ARG:HA	1:A:538:ASP:OD1	2.21	0.41
1:A:586:HIS:O	1:A:586:HIS:CG	2.72	0.41
1:A:161:GLU:HB3	5:A:743:HOH:O	2.20	0.41
1:A:235:MET:O	1:A:236:PRO:C	2.64	0.41
1:A:234:HIS:CD2	5:A:761:HOH:O	2.73	0.41
1:A:533:LEU:HD23	1:A:533:LEU:HA	1.92	0.41
1:A:312:LEU:H	1:A:312:LEU:CD1	2.32	0.41
1:A:146:PRO:HB3	1:A:176:LEU:CD2	2.51	0.40
1:A:578:LEU:HA	1:A:579:PRO:C	2.45	0.40
1:A:157:GLY:HA2	1:A:494:GLY:C	2.46	0.40
1:A:12:VAL:O	1:A:16:VAL:HG23	2.21	0.40
1:A:36:GLU:O	1:A:37:ARG:C	2.64	0.40
1:A:174:THR:C	1:A:176:LEU:H	2.28	0.40
1:A:300:TYR:HE2	1:A:323:GLN:HG2	1.83	0.40
1:A:351:ARG:HH11	1:A:351:ARG:HD2	1.77	0.40
1:A:355:THR:C	1:A:357:GLY:H	2.29	0.40
1:A:393:LYS:NZ	1:A:534:LEU:O	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	600/605 (99%)	564 (94%)	34 (6%)	2 (0%)	36 66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	VAL
1	A	505	GLY

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	485/488 (99%)	464 (96%)	21 (4%)	26 60

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

Mol	Chain	Res	Type
1	A	4	LEU
1	A	41	THR
1	A	54	LEU
1	A	55	SER
1	A	63	LYS
1	A	68	LYS
1	A	152	ARG
1	A	209	VAL
1	A	215	VAL
1	A	230	LEU
1	A	232	ASN
1	A	243	ASP
1	A	294	THR
1	A	318	PRO
1	A	358	LEU
1	A	466	ASN
1	A	474	SER
1	A	534	LEU
1	A	566	ARG
1	A	576	ASP
1	A	582	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	102	ASN
1	A	171	GLN
1	A	181	GLN

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Mol	Chain	Res	Type
1	A	199	ASN
1	A	219	ASN
1	A	234	HIS
1	A	262	HIS
1	A	323	GLN
1	A	375	GLN
1	A	377	HIS
1	A	551	GLN
1	A	581	ASN
1	A	586	HIS

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 ⓘ

6 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	2.35	4 (28%)	17,19,21	2.34	4 (23%)
2	NAG	B	2	2	14,14,15	1.89	5 (35%)	17,19,21	1.59	2 (11%)
2	BMA	B	3	2	11,11,12	3.09	6 (54%)	15,15,17	1.83	5 (33%)
2	MAN	B	4	2	11,11,12	6.69	8 (72%)	15,15,17	9.78	13 (86%)
2	NAG	B	5	2	14,14,15	6.37	7 (50%)	17,19,21	6.02	11 (64%)
2	FUC	B	6	2	10,10,11	1.80	3 (30%)	14,14,16	1.37	2 (14%)

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	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
2	MAN	B	4	2	-	0/2/19/22	0/1/1/1
2	NAG	B	5	2	-	0/6/23/26	0/1/1/1
2	FUC	B	6	2	-	-	0/1/1/1

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	4	MAN	C4-C5	18.73	1.92	1.53
2	B	5	NAG	O5-C5	13.97	1.70	1.43
2	B	5	NAG	C1-C2	11.09	1.67	1.52
2	B	5	NAG	O5-C1	11.08	1.62	1.43
2	B	5	NAG	C3-C2	9.68	1.72	1.52
2	B	1	NAG	C3-C2	6.52	1.66	1.52
2	B	3	BMA	C2-C3	6.46	1.62	1.52
2	B	4	MAN	O4-C4	5.66	1.57	1.43
2	B	4	MAN	C1-C2	5.20	1.64	1.52
2	B	4	MAN	C6-C5	4.91	1.68	1.51
2	B	4	MAN	O5-C1	4.90	1.51	1.43
2	B	3	BMA	C4-C3	4.70	1.64	1.52
2	B	2	NAG	C8-C7	3.66	1.58	1.50
2	B	5	NAG	C6-C5	3.64	1.64	1.51
2	B	4	MAN	O5-C5	3.62	1.50	1.43
2	B	2	NAG	C4-C5	3.40	1.60	1.53
2	B	6	FUC	C4-C3	3.31	1.60	1.52
2	B	5	NAG	O3-C3	3.12	1.50	1.43
2	B	4	MAN	O3-C3	3.09	1.50	1.43
2	B	2	NAG	C1-C2	3.09	1.56	1.52
2	B	1	NAG	C8-C7	2.99	1.56	1.50
2	B	4	MAN	C4-C3	2.96	1.60	1.52
2	B	3	BMA	O5-C5	-2.95	1.37	1.43
2	B	3	BMA	C6-C5	-2.89	1.42	1.51
2	B	3	BMA	O2-C2	2.88	1.49	1.43
2	B	1	NAG	O5-C5	2.80	1.48	1.43
2	B	3	BMA	C1-C2	2.63	1.58	1.52
2	B	6	FUC	C2-C3	2.41	1.56	1.52
2	B	5	NAG	O4-C4	2.39	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	O4-C4	-2.34	1.37	1.43
2	B	2	NAG	O5-C5	2.30	1.47	1.43
2	B	2	NAG	O4-C4	2.12	1.48	1.43
2	B	6	FUC	C1-C2	2.03	1.57	1.52

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4	MAN	C3-C4-C5	-22.00	70.34	110.23
2	B	5	NAG	C1-O5-C5	14.65	131.82	112.19
2	B	4	MAN	O4-C4-C5	14.55	145.16	109.32
2	B	4	MAN	C2-C3-C4	-13.61	86.92	110.86
2	B	4	MAN	C1-C2-C3	-11.76	92.52	109.64
2	B	5	NAG	O5-C1-C2	-11.63	93.30	111.29
2	B	4	MAN	O2-C2-C1	-10.78	84.55	109.22
2	B	5	NAG	C2-N2-C7	-9.81	109.75	122.90
2	B	4	MAN	O4-C4-C3	-9.53	87.91	110.38
2	B	4	MAN	O2-C2-C3	8.10	126.93	110.15
2	B	1	NAG	O5-C1-C2	-7.95	98.98	111.29
2	B	4	MAN	O5-C5-C6	-7.38	93.30	107.66
2	B	4	MAN	O3-C3-C4	5.86	124.18	110.38
2	B	5	NAG	O3-C3-C2	5.64	121.12	109.40
2	B	5	NAG	C1-C2-N2	5.62	119.29	110.43
2	B	5	NAG	O5-C5-C6	5.08	117.54	107.66
2	B	5	NAG	C6-C5-C4	-4.53	101.89	113.02
2	B	5	NAG	O4-C4-C3	4.47	120.92	110.38
2	B	5	NAG	C3-C4-C5	-4.26	102.51	110.23
2	B	4	MAN	O5-C1-C2	3.83	119.93	110.79
2	B	2	NAG	C4-C3-C2	-3.68	105.63	111.02
2	B	4	MAN	O3-C3-C2	3.52	117.25	110.05
2	B	4	MAN	C6-C5-C4	3.42	121.41	113.02
2	B	3	BMA	C1-O5-C5	-3.38	107.66	112.19
2	B	2	NAG	C6-C5-C4	-3.25	105.04	113.02
2	B	1	NAG	O3-C3-C4	-2.96	103.41	110.38
2	B	3	BMA	C3-C4-C5	-2.95	104.89	110.23
2	B	5	NAG	O3-C3-C4	-2.79	103.81	110.38
2	B	4	MAN	C1-O5-C5	-2.78	108.46	112.19
2	B	3	BMA	O2-C2-C1	2.72	115.45	109.22
2	B	3	BMA	O4-C4-C3	2.53	116.35	110.38
2	B	5	NAG	O6-C6-C5	2.38	119.43	111.33
2	B	6	FUC	O4-C4-C3	2.34	115.90	110.38
2	B	1	NAG	O4-C4-C3	-2.34	104.87	110.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	6	FUC	O5-C5-C6	-2.24	102.54	107.40
2	B	1	NAG	C1-O5-C5	2.12	115.03	112.19
2	B	3	BMA	O6-C6-C5	-2.09	104.20	111.33

There are no chirality outliers.

All (2) torsion outliers are listed below:

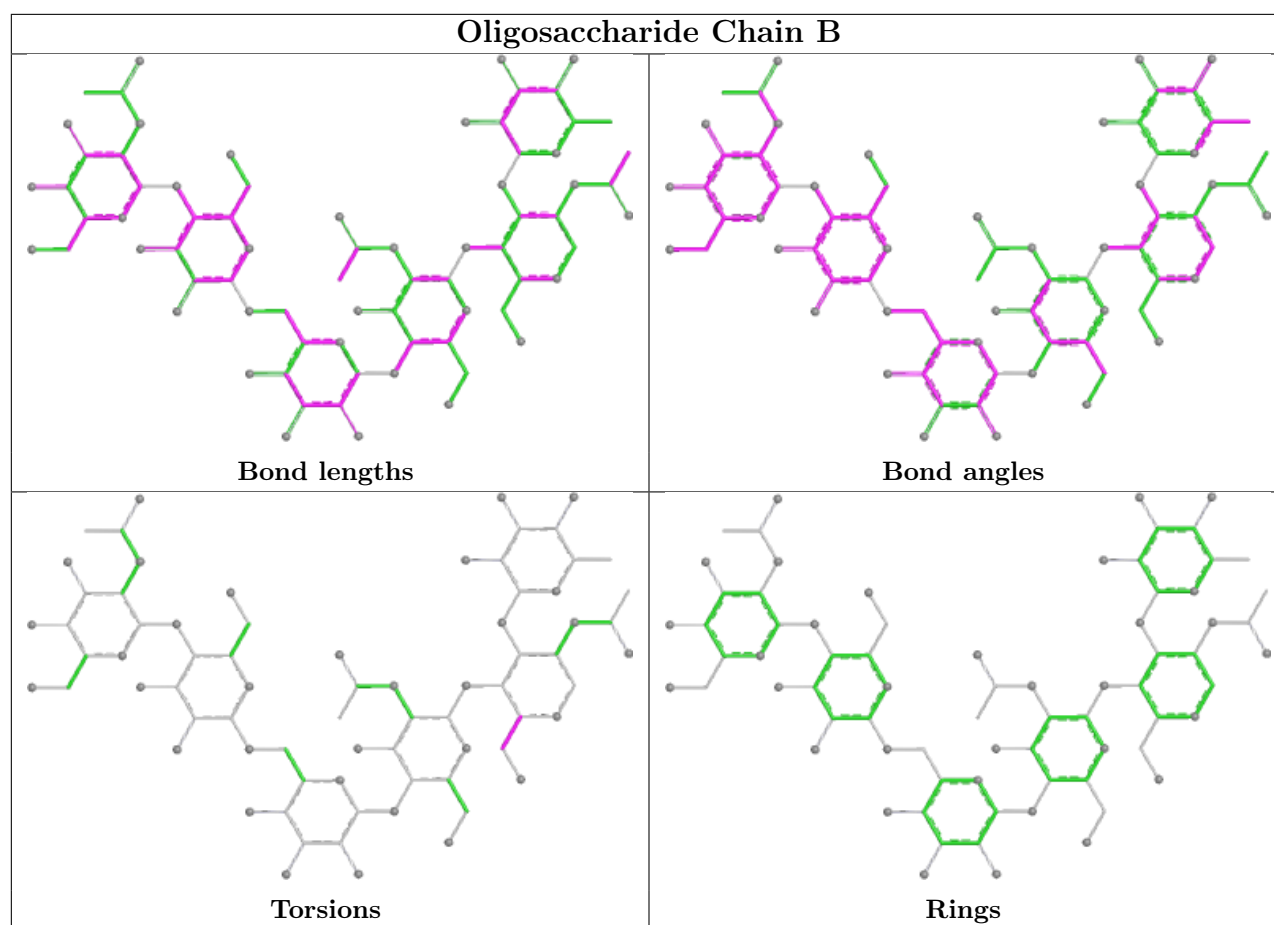
Mol	Chain	Res	Type	Atoms
2	B	1	NAG	O5-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4	MAN	16	0
2	B	5	NAG	14	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	$\# Z > 2$
4	INS	A	617	1	11,11,12	2.70	5 (45%)	16,16,18	4.52	11 (68%)
3	NAG	A	610	1	14,14,15	2.46	4 (28%)	17,19,21	3.34	11 (64%)

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	INS	A	617	1	-	-	0/1/1/1
3	NAG	A	610	1	-	0/6/23/26	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	610	NAG	O5-C1	-6.06	1.33	1.43
4	A	617	INS	C1-C6	5.71	1.63	1.52
3	A	610	NAG	C4-C5	4.86	1.63	1.53
4	A	617	INS	C6-C5	3.86	1.58	1.52
3	A	610	NAG	O4-C4	3.62	1.51	1.43
4	A	617	INS	C2-C3	3.15	1.57	1.52
4	A	617	INS	O5-C5	3.01	1.50	1.43
4	A	617	INS	O3-C3	2.32	1.48	1.43
3	A	610	NAG	C1-C2	-2.07	1.49	1.52

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	617	INS	C6-C1-C2	-10.46	99.35	111.50
4	A	617	INS	C1-C2-C3	7.84	121.97	110.67
3	A	610	NAG	O5-C5-C6	-6.77	94.48	107.66
4	A	617	INS	O2-C2-C1	-6.68	93.25	109.86
3	A	610	NAG	O4-C4-C3	5.92	124.34	110.38
4	A	617	INS	O5-C5-C6	5.42	121.11	110.05
3	A	610	NAG	C3-C4-C5	-5.17	100.86	110.23
3	A	610	NAG	O5-C1-C2	4.29	117.92	111.29
4	A	617	INS	C1-C6-C5	4.19	116.71	110.67
3	A	610	NAG	C2-N2-C7	-3.91	117.66	122.90
4	A	617	INS	C5-C4-C3	3.54	117.05	110.83
4	A	617	INS	O4-C4-C5	-3.50	102.12	110.38
4	A	617	INS	O2-C2-C3	3.24	116.85	110.15
4	A	617	INS	O4-C4-C3	-3.01	103.28	110.38
3	A	610	NAG	O6-C6-C5	-2.98	101.19	111.33
3	A	610	NAG	O5-C5-C4	2.86	117.80	110.83
3	A	610	NAG	O4-C4-C5	2.62	115.79	109.32
3	A	610	NAG	O3-C3-C2	2.61	114.81	109.40
4	A	617	INS	O3-C3-C4	-2.38	104.78	110.38
3	A	610	NAG	C6-C5-C4	-2.26	107.48	113.02
4	A	617	INS	C6-C5-C4	-2.11	107.14	110.86
3	A	610	NAG	C8-C7-N2	2.06	119.54	116.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	617	INS	3	0
3	A	610	NAG	2	0

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.