



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:22 AM UTC

PDB ID : 3D4K / pdb_00003d4k
Title : Concanavalin A Complexed to a Synthetic Analog of the Trimannoside
Authors : Kadirvelraj, R.; Foley, B.L.; Dyekjaer, J.D.; Woods, R.J.
Deposited on : 2008-05-14
Resolution : 1.80 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)	:	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

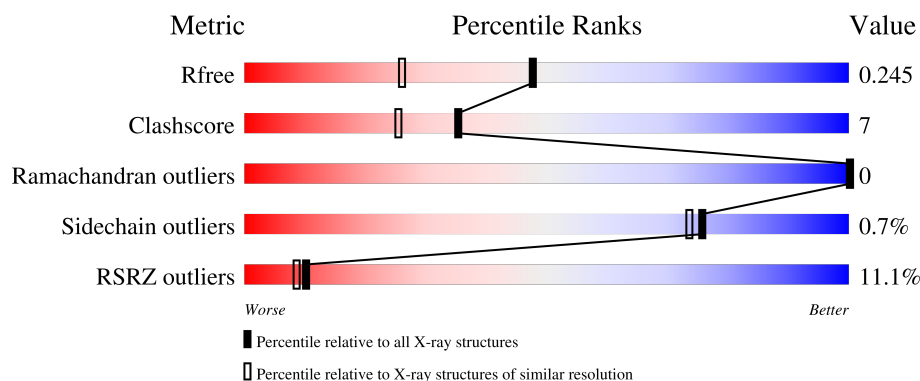
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 $\leq 5\%$. 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	237	13% 82% 16% .
1	B	237	9% 81% 17% .
1	C	237	13% 80% 18% .
1	D	237	10% 81% 16% .
2	E	3	67% 33%

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Mol	Chain	Length	Quality of chain
2	F	3	 67%33%
2	G	3	 67%33%
2	H	3	 67%33%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7988 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 Concanavalin-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			
1	B	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			
1	C	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			
1	D	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]methyl 2-deoxy-2-(2-hydroxyethyl)-alpha-D-mannopyranoside.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	3	Total	C	O	0	0	0
			37	21	16			
2	F	3	Total	C	O	0	0	0
			37	21	16			
2	G	3	Total	C	O	0	0	0
			37	21	16			
2	H	3	Total	C	O	0	0	0
			37	21	16			

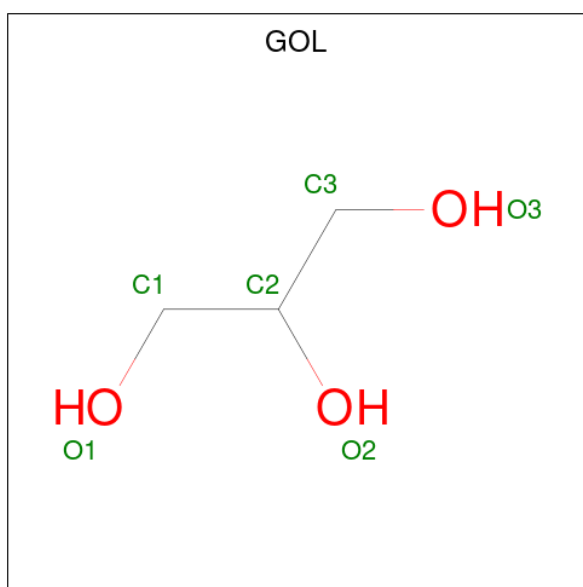
- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mn	0	0
			1	1		
3	B	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		
3	D	1	Total	Mn	0	0
			1	1		

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

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

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	D	1	Total 6	C 3	O 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	145	Total 145	O 145	0	0

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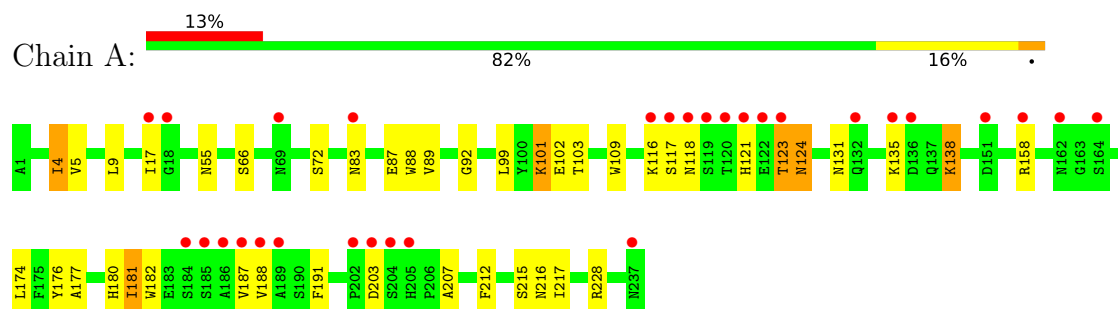
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	144	Total 144	O 144	0	0
6	C	134	Total 134	O 134	0	0
6	D	149	Total 149	O 149	0	0

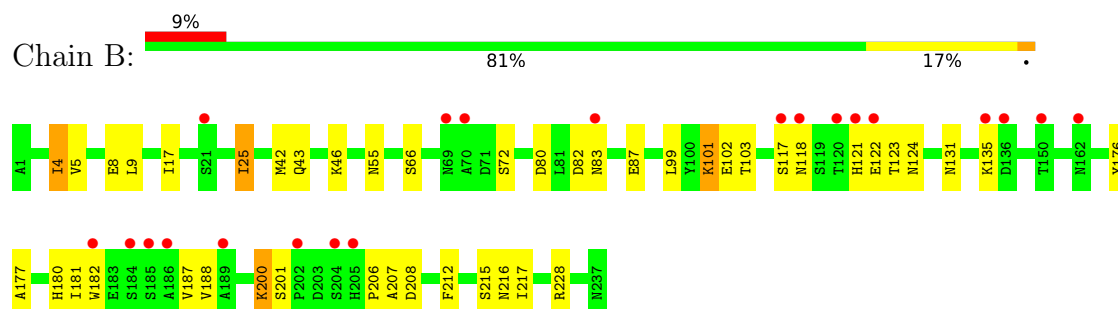
3 Residue-property plots [i](#)

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.

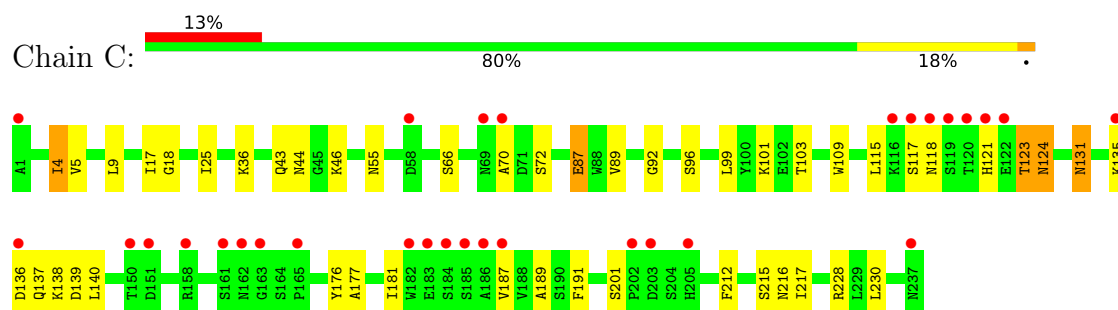
• Molecule 1: Concanavalin-A



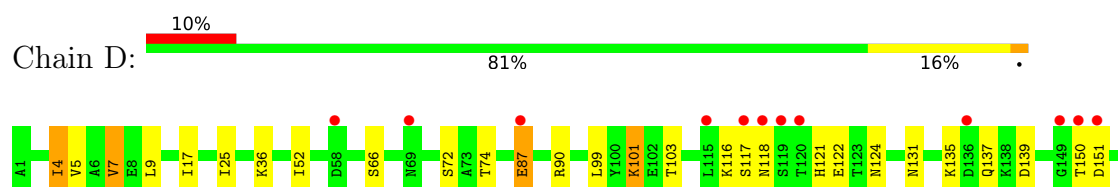
• Molecule 1: Concanavalin-A

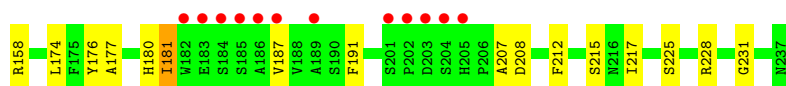


• Molecule 1: Concanavalin-A



• Molecule 1: Concanavalin-A





- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]methyl 2-deoxy-2-(2-hydroxyethyl)-alpha-D-mannopyranoside

Chain E: 67% 33%



- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]methyl 2-deoxy-2-(2-hydroxyethyl)-alpha-D-mannopyranoside

Chain F: 67% 33%



- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]methyl 2-deoxy-2-(2-hydroxyethyl)-alpha-D-mannopyranoside

Chain G: 67% 33%



- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]methyl 2-deoxy-2-(2-hydroxyethyl)-alpha-D-mannopyranoside

Chain H: 67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	60.02Å 63.55Å 126.22Å 90.00° 86.91° 90.00°	Depositor
Resolution (Å)	30.00 – 1.80 30.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (30.00-1.80) 99.0 (30.00-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 1.80Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.205 , 0.238 0.212 , 0.245	Depositor DCC
R_{free} test set	8749 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å ²)	19.1	Xtriage
Anisotropy	0.528	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7988	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.16% 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: CA, MAN, MN, GOL, H1M

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	0.35	0/1851	0.99	15/2522 (0.6%)
1	B	0.34	0/1851	1.00	14/2522 (0.6%)
1	C	0.35	0/1851	0.99	16/2522 (0.6%)
1	D	0.36	0/1851	0.99	16/2522 (0.6%)
All	All	0.35	0/7404	0.99	61/10088 (0.6%)

There are no bond length outliers.

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	PHE	N-CA-C	-7.12	97.63	109.24
1	D	212	PHE	N-CA-C	-6.98	97.86	109.24
1	C	217	ILE	N-CA-C	6.97	118.57	110.62
1	B	212	PHE	N-CA-C	-6.88	98.02	109.24
1	C	212	PHE	N-CA-C	-6.88	98.03	109.24
1	C	4	ILE	N-CA-C	6.85	118.35	108.48
1	A	217	ILE	N-CA-C	6.78	118.35	110.62
1	A	4	ILE	N-CA-C	6.76	118.21	108.48
1	D	5	VAL	N-CA-C	-6.74	98.42	108.12
1	C	5	VAL	N-CA-C	-6.64	98.56	108.12
1	C	216	ASN	N-CA-C	-6.58	101.39	110.35
1	A	181	ILE	N-CA-C	6.56	117.34	110.72
1	B	4	ILE	N-CA-C	6.41	118.02	108.46
1	D	103	THR	N-CA-C	-6.33	101.12	110.48
1	D	176	TYR	N-CA-C	6.26	117.77	111.07
1	C	99	LEU	N-CA-C	-6.21	104.59	111.36
1	A	216	ASN	N-CA-C	-6.17	101.96	110.35
1	B	217	ILE	N-CA-C	6.14	117.62	110.62
1	D	4	ILE	N-CA-C	6.07	117.50	108.46
1	D	131	ASN	N-CA-C	-6.05	105.85	113.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	LEU	N-CA-C	-6.00	104.82	111.36
1	D	9	LEU	N-CA-C	-6.00	96.93	107.73
1	C	123	THR	N-CA-C	5.99	119.30	109.72
1	D	99	LEU	N-CA-C	-5.90	104.93	111.36
1	B	177	ALA	N-CA-C	5.85	117.02	109.65
1	B	103	THR	N-CA-C	-5.80	101.04	110.20
1	C	101	LYS	N-CA-C	5.79	117.02	108.86
1	B	5	VAL	N-CA-C	-5.75	99.84	108.12
1	B	131	ASN	N-CA-C	-5.68	106.33	113.72
1	C	176	TYR	N-CA-C	5.67	117.46	111.28
1	D	181	ILE	N-CA-C	5.62	118.12	111.09
1	A	5	VAL	N-CA-C	-5.53	99.58	107.77
1	B	9	LEU	N-CA-C	-5.53	97.77	107.73
1	A	176	TYR	N-CA-C	5.52	116.98	111.07
1	C	18	GLY	N-CA-C	5.46	122.30	115.21
1	D	25	ILE	N-CA-C	-5.44	100.62	108.89
1	C	131	ASN	N-CA-C	-5.43	106.66	113.72
1	C	124	ASN	N-CA-C	-5.42	100.87	109.59
1	C	9	LEU	N-CA-C	-5.41	98.00	107.73
1	B	99	LEU	N-CA-C	-5.41	105.47	111.36
1	D	90	ARG	N-CA-C	-5.38	101.00	109.50
1	D	7	VAL	N-CA-C	-5.37	99.91	107.75
1	D	101	LYS	N-CA-C	5.37	116.81	109.18
1	C	177	ALA	N-CA-C	5.37	116.59	109.93
1	D	158	ARG	N-CA-C	5.36	118.08	110.10
1	A	101	LYS	N-CA-C	5.36	116.78	109.18
1	B	216	ASN	N-CA-C	-5.34	103.08	110.35
1	B	176	TYR	N-CA-C	5.34	117.51	111.11
1	A	123	THR	N-CA-C	5.32	118.23	109.72
1	A	9	LEU	N-CA-C	-5.29	98.20	107.73
1	A	177	ALA	N-CA-C	5.29	116.49	109.93
1	A	138	LYS	N-CA-C	5.22	118.75	112.38
1	C	103	THR	N-CA-C	-5.22	101.96	110.20
1	B	181	ILE	N-CA-C	5.19	117.58	111.09
1	D	177	ALA	N-CA-C	5.14	116.12	109.65
1	A	103	THR	N-CA-C	-5.14	102.09	110.20
1	B	101	LYS	N-CA-C	5.13	116.09	108.86
1	A	124	ASN	N-CA-C	-5.09	101.39	109.59
1	D	217	ILE	N-CA-C	5.05	118.13	111.17
1	B	25	ILE	N-CA-C	-5.03	101.11	108.85
1	C	25	ILE	N-CA-C	-5.01	101.27	108.48

There are no chirality outliers.

There are no planarity outliers.

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	1809	0	1755	29	0
1	B	1809	0	1755	25	0
1	C	1809	0	1755	30	0
1	D	1809	0	1755	26	0
2	E	37	0	36	0	0
2	F	37	0	36	0	0
2	G	37	0	36	0	0
2	H	37	0	36	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	6	0	8	2	0
5	B	6	0	8	2	0
5	C	6	0	8	0	0
5	D	6	0	8	3	0
6	A	145	0	0	3	0
6	B	144	0	0	4	0
6	C	134	0	0	5	0
6	D	149	0	0	5	0
All	All	7988	0	7196	108	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 7.

All (108) 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:B:118:ASN:HA	1:B:187:VAL:HG23	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4:ILE:HD13	1:D:215:SER:HB3	1.66	0.76
1:D:74:THR:HG23	6:D:487:HOH:O	1.88	0.73
1:D:116:LYS:HD2	1:D:121:HIS:C	2.14	0.72
1:D:118:ASN:HA	1:D:187:VAL:HG23	1.72	0.71
1:A:135:LYS:HD3	1:A:135:LYS:H	1.57	0.68
1:C:43:GLN:HE21	1:C:46:LYS:HD3	1.59	0.66
1:C:118:ASN:HA	1:C:187:VAL:HG23	1.77	0.66
1:A:17:ILE:HD13	1:A:228:ARG:HD2	1.79	0.64
1:C:135:LYS:HD3	1:C:136:ASP:H	1.64	0.63
1:A:118:ASN:HA	1:A:187:VAL:HG23	1.82	0.62
1:A:124:ASN:HB3	5:A:900:GOL:H12	1.82	0.60
1:D:116:LYS:HD2	1:D:121:HIS:O	2.02	0.60
1:C:118:ASN:HA	1:C:187:VAL:CG2	2.32	0.60
1:D:87:GLU:HG2	6:D:400:HOH:O	2.02	0.58
1:A:116:LYS:HG3	1:A:123:THR:OG1	2.04	0.58
1:C:17:ILE:HD13	1:C:228:ARG:HD2	1.84	0.57
1:C:55:ASN:HB3	6:C:734:HOH:O	2.03	0.57
1:B:17:ILE:HD13	1:B:228:ARG:HD2	1.86	0.57
1:B:66:SER:HB3	1:B:72:SER:CB	2.36	0.56
1:A:87:GLU:HG3	1:A:182:TRP:O	2.05	0.56
1:C:43:GLN:NE2	1:C:46:LYS:HD3	2.21	0.55
1:B:4:ILE:HD13	1:B:215:SER:HB3	1.89	0.55
1:D:135:LYS:H	1:D:135:LYS:HD3	1.72	0.54
1:B:123:THR:HG22	6:B:465:HOH:O	2.06	0.54
1:C:66:SER:HB3	1:C:72:SER:HB3	1.89	0.54
1:B:55:ASN:HB3	6:B:801:HOH:O	2.07	0.53
1:A:135:LYS:HD3	1:A:135:LYS:N	2.24	0.53
1:B:124:ASN:HB3	5:B:900:GOL:H12	1.90	0.53
1:D:180:HIS:HB3	5:D:900:GOL:H11	1.90	0.53
1:D:17:ILE:HD13	1:D:228:ARG:HD2	1.92	0.52
1:B:42:MET:HE3	6:B:586:HOH:O	2.08	0.52
1:C:87:GLU:HG2	6:C:583:HOH:O	2.09	0.52
1:A:180:HIS:HB3	5:A:900:GOL:H2	1.92	0.52
1:A:4:ILE:HD13	1:A:215:SER:HB3	1.91	0.51
1:A:117:SER:O	1:A:121:HIS:HA	2.10	0.51
1:D:150:THR:HG22	1:D:151:ASP:OD2	2.10	0.51
1:C:181:ILE:HD11	1:C:191:PHE:CD2	2.46	0.51
1:C:117:SER:O	1:C:121:HIS:HA	2.11	0.51
1:D:135:LYS:HD3	1:D:135:LYS:N	2.25	0.51
1:B:187:VAL:HG12	1:B:188:VAL:HG23	1.93	0.50
1:A:118:ASN:HA	1:A:187:VAL:CG2	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:87:GLU:H	1:D:87:GLU:CD	2.20	0.50
1:B:180:HIS:HB3	5:B:900:GOL:H2	1.95	0.49
1:C:43:GLN:HE22	1:C:46:LYS:NZ	2.10	0.48
1:D:36:LYS:HD2	6:D:395:HOH:O	2.14	0.48
1:D:118:ASN:HA	1:D:187:VAL:CG2	2.43	0.48
1:A:92:GLY:HA2	1:A:109:TRP:CH2	2.48	0.48
1:D:66:SER:HB3	1:D:72:SER:HB3	1.95	0.48
1:C:4:ILE:HD13	1:C:215:SER:HB3	1.95	0.48
1:B:118:ASN:HA	1:B:187:VAL:CG2	2.39	0.47
1:D:124:ASN:HB3	5:D:900:GOL:H32	1.96	0.47
1:C:189:ALA:CB	6:C:459:HOH:O	2.61	0.47
1:A:187:VAL:HG12	1:A:188:VAL:HG23	1.97	0.47
1:A:102:GLU:HG2	1:A:207:ALA:O	2.15	0.47
1:C:66:SER:HB3	1:C:72:SER:CB	2.44	0.46
1:A:131:ASN:HB3	1:D:122:GLU:HB3	1.97	0.46
1:D:66:SER:HB3	1:D:72:SER:CB	2.46	0.46
1:B:200:LYS:HB3	1:B:200:LYS:NZ	2.31	0.45
1:C:92:GLY:HA2	1:C:109:TRP:CH2	2.52	0.45
1:A:135:LYS:H	1:A:135:LYS:CD	2.27	0.45
1:D:181:ILE:HD11	1:D:191:PHE:CD2	2.51	0.45
1:B:80:ASP:OD1	1:B:82:ASP:HB2	2.17	0.44
1:D:137:GLN:HG3	1:D:139:ASP:OD1	2.18	0.44
1:A:203:ASP:HB3	6:A:691:HOH:O	2.16	0.44
1:A:89:VAL:HB	1:A:215:SER:O	2.17	0.44
1:C:36:LYS:HE3	6:C:641:HOH:O	2.17	0.44
1:A:55:ASN:HB3	6:A:666:HOH:O	2.16	0.44
1:B:207:ALA:HB1	1:B:208:ASP:CG	2.43	0.44
1:C:70:ALA:HB2	6:C:745:HOH:O	2.18	0.44
1:B:135:LYS:N	1:B:135:LYS:HD3	2.33	0.43
1:C:135:LYS:HD3	1:C:135:LYS:N	2.33	0.43
1:A:87:GLU:HG2	1:A:180:HIS:CD2	2.53	0.43
1:C:135:LYS:HD3	1:C:136:ASP:N	2.30	0.43
1:C:87:GLU:HG2	1:C:87:GLU:H	1.59	0.43
1:C:115:LEU:HD23	1:C:189:ALA:HB2	2.00	0.43
1:A:66:SER:HB3	1:A:72:SER:HB3	2.00	0.43
1:C:89:VAL:HB	1:C:215:SER:O	2.19	0.43
1:B:43:GLN:HE21	1:B:46:LYS:HG3	1.83	0.43
1:A:158:ARG:HD2	6:A:786:HOH:O	2.19	0.43
1:B:117:SER:O	1:B:121:HIS:HA	2.19	0.42
1:A:174:LEU:HD12	1:A:174:LEU:N	2.34	0.42
1:B:102:GLU:HG2	1:B:207:ALA:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:ASN:HD21	1:C:201:SER:HB3	1.84	0.42
1:C:137:GLN:HG2	1:C:140:LEU:HD12	2.01	0.42
1:B:87:GLU:HG3	1:B:182:TRP:O	2.18	0.42
1:B:207:ALA:HA	1:B:208:ASP:HA	1.87	0.42
1:B:8:GLU:O	1:B:25:ILE:HA	2.19	0.42
1:B:122:GLU:HB3	1:C:131:ASN:HB3	2.00	0.42
1:A:181:ILE:HD11	1:A:191:PHE:CD2	2.55	0.42
1:D:7:VAL:HG21	1:D:52:ILE:HG12	2.01	0.42
1:D:174:LEU:N	1:D:174:LEU:HD12	2.34	0.42
1:D:207:ALA:HA	1:D:208:ASP:HA	1.90	0.42
1:A:88:TRP:HH2	1:D:137:GLN:NE2	2.17	0.42
1:A:138:LYS:HE3	6:D:766:HOH:O	2.19	0.41
1:B:66:SER:HB3	1:B:72:SER:HB3	2.01	0.41
1:C:137:GLN:HG3	1:C:139:ASP:OD1	2.20	0.41
1:A:87:GLU:HG2	1:A:180:HIS:NE2	2.34	0.41
5:D:900:GOL:H31	6:D:509:HOH:O	2.19	0.41
1:D:117:SER:O	1:D:121:HIS:HA	2.21	0.41
1:A:83:ASN:O	1:A:83:ASN:CG	2.64	0.41
6:B:714:HOH:O	1:C:138:LYS:HE3	2.21	0.41
1:C:96:SER:OG	1:C:230:LEU:HA	2.21	0.41
1:B:201:SER:HB3	1:B:206:PRO:HB3	2.02	0.41
1:C:123:THR:HG22	1:C:124:ASN:N	2.36	0.41
1:A:66:SER:HB3	1:A:72:SER:CB	2.50	0.40
1:B:83:ASN:N	1:B:83:ASN:ND2	2.70	0.40
1:D:225:SER:OG	1:D:231:GLY:HA2	2.22	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	235/237 (99%)	220 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	235/237 (99%)	223 (95%)	12 (5%)	0	100	100
1	C	235/237 (99%)	219 (93%)	16 (7%)	0	100	100
1	D	235/237 (99%)	222 (94%)	13 (6%)	0	100	100
All	All	940/948 (99%)	884 (94%)	56 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	203/203 (100%)	202 (100%)	1 (0%)	81	80
1	B	203/203 (100%)	201 (99%)	2 (1%)	68	64
1	C	203/203 (100%)	202 (100%)	1 (0%)	81	80
1	D	203/203 (100%)	201 (99%)	2 (1%)	68	64
All	All	812/812 (100%)	806 (99%)	6 (1%)	76	73

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LYS
1	B	101	LYS
1	B	200	LYS
1	C	87	GLU
1	D	87	GLU
1	D	101	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	HIS
1	A	132	GLN

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Mol	Chain	Res	Type
1	A	205	HIS
1	A	237	ASN
1	B	43	GLN
1	B	51	HIS
1	B	69	ASN
1	B	83	ASN
1	B	166	GLN
1	B	205	HIS
1	C	41	ASN
1	C	43	GLN
1	C	121	HIS
1	C	132	GLN
1	C	205	HIS
1	C	237	ASN
1	D	43	GLN
1	D	166	GLN
1	D	205	HIS
1	D	237	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 ⓘ

12 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	H1M	E	1	2	15,15,15	0.71	0	17,20,20	1.06	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	E	2	2	11,11,12	0.44	0	15,15,17	0.71	0
2	MAN	E	3	2	11,11,12	0.49	0	15,15,17	0.69	0
2	H1M	F	1	2	15,15,15	0.77	0	17,20,20	1.10	2 (11%)
2	MAN	F	2	2	11,11,12	0.54	0	15,15,17	0.71	0
2	MAN	F	3	2	11,11,12	0.45	0	15,15,17	0.68	0
2	H1M	G	1	2	15,15,15	0.80	0	17,20,20	1.02	1 (5%)
2	MAN	G	2	2	11,11,12	0.48	0	15,15,17	0.71	0
2	MAN	G	3	2	11,11,12	0.52	0	15,15,17	0.67	0
2	H1M	H	1	2	15,15,15	0.81	1 (6%)	17,20,20	1.11	1 (5%)
2	MAN	H	2	2	11,11,12	0.53	0	15,15,17	0.68	0
2	MAN	H	3	2	11,11,12	0.48	0	15,15,17	0.71	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
2	H1M	E	1	2	-	0/7/27/27	0/1/1/1
2	MAN	E	2	2	-	2/2/19/22	0/1/1/1
2	MAN	E	3	2	-	0/2/19/22	0/1/1/1
2	H1M	F	1	2	-	0/7/27/27	0/1/1/1
2	MAN	F	2	2	-	0/2/19/22	0/1/1/1
2	MAN	F	3	2	-	0/2/19/22	0/1/1/1
2	H1M	G	1	2	-	0/7/27/27	0/1/1/1
2	MAN	G	2	2	-	0/2/19/22	0/1/1/1
2	MAN	G	3	2	-	0/2/19/22	0/1/1/1
2	H1M	H	1	2	-	0/7/27/27	0/1/1/1
2	MAN	H	2	2	-	0/2/19/22	0/1/1/1
2	MAN	H	3	2	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1	H1M	C1-C2	2.02	1.55	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	H1M	C9-O1-C1	2.95	117.74	113.26
2	E	1	H1M	C9-O1-C1	2.89	117.65	113.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	H1M	C9-O1-C1	2.87	117.63	113.26
2	G	1	H1M	C9-O1-C1	2.74	117.42	113.26
2	F	1	H1M	O5-C1-C2	-2.06	109.64	112.23
2	E	1	H1M	O5-C1-C2	-2.00	109.71	112.23

There are no chirality outliers.

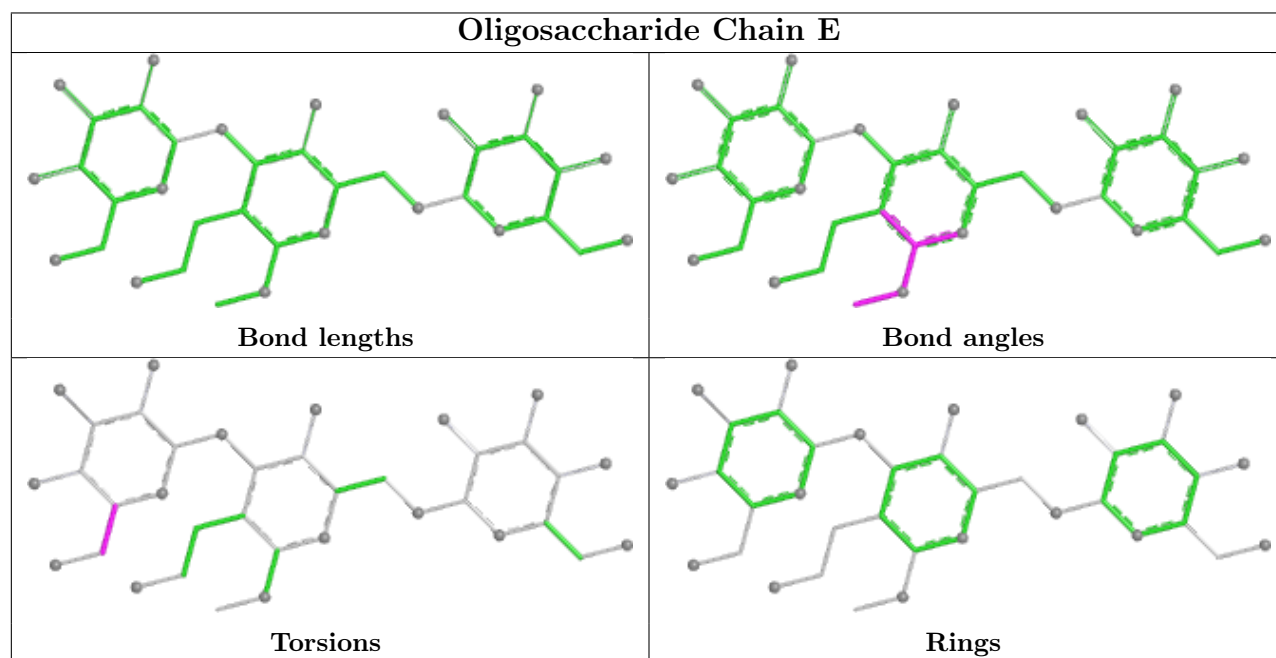
All (2) torsion outliers are listed below:

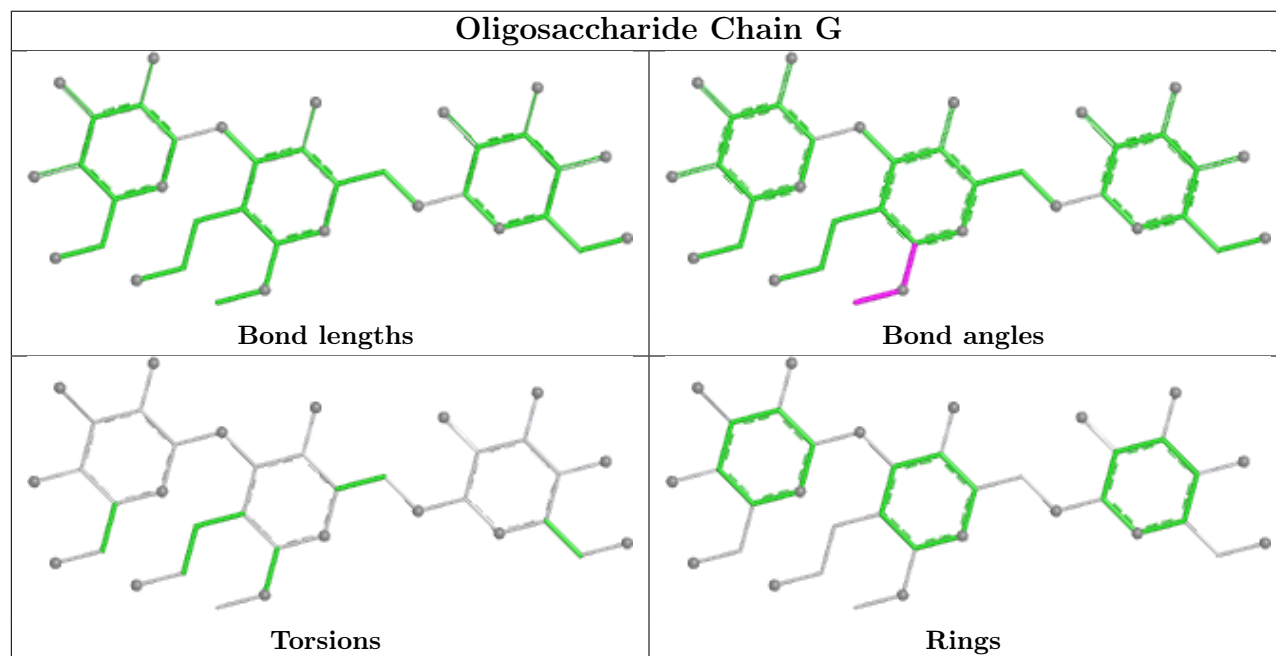
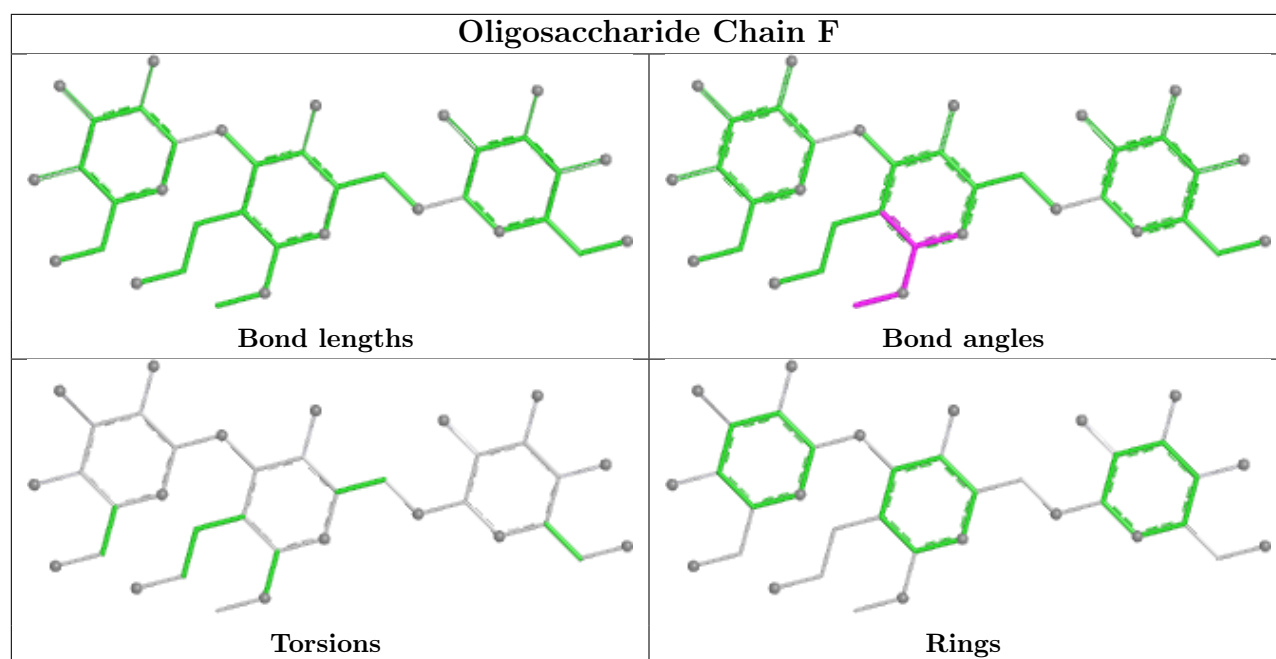
Mol	Chain	Res	Type	Atoms
2	E	2	MAN	C4-C5-C6-O6
2	E	2	MAN	O5-C5-C6-O6

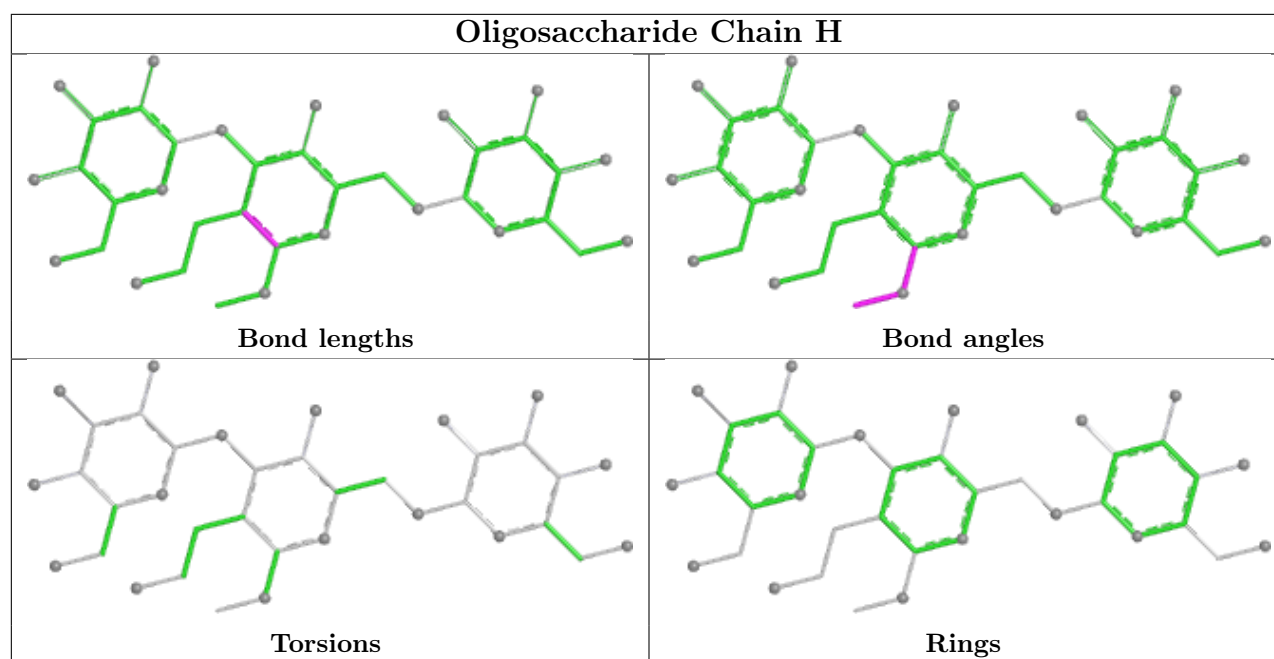
There are no ring outliers.

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.







5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	$\# Z > 2$
5	GOL	A	900	-	5,5,5	0.34	0	5,5,5	0.31	0
5	GOL	B	900	-	5,5,5	0.37	0	5,5,5	0.32	0
5	GOL	D	900	-	5,5,5	0.38	0	5,5,5	0.33	0
5	GOL	C	900	-	5,5,5	0.45	0	5,5,5	0.25	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	GOL	A	900	-	-	0/4/4/4	-
5	GOL	B	900	-	-	0/4/4/4	-
5	GOL	D	900	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	C	900	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	900	GOL	2	0
5	B	900	GOL	2	0
5	D	900	GOL	3	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

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	237/237 (100%)	0.56	30 (12%) 8 6	12, 21, 42, 53	0
1	B	237/237 (100%)	0.45	21 (8%) 15 13	12, 21, 40, 46	0
1	C	237/237 (100%)	0.57	30 (12%) 8 6	12, 22, 42, 53	0
1	D	237/237 (100%)	0.49	24 (10%) 12 11	11, 21, 42, 51	0
All	All	948/948 (100%)	0.52	105 (11%) 10 8	11, 21, 42, 53	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	186	ALA	4.7
1	B	205	HIS	4.3
1	D	186	ALA	4.2
1	A	203	ASP	4.1
1	A	185	SER	4.1
1	D	119	SER	4.0
1	A	119	SER	4.0
1	A	205	HIS	4.0
1	D	205	HIS	3.9
1	C	117	SER	3.8
1	C	205	HIS	3.8
1	A	136	ASP	3.8
1	D	120	THR	3.8
1	C	186	ALA	3.7
1	D	185	SER	3.7
1	A	186	ALA	3.6
1	C	118	ASN	3.6
1	C	136	ASP	3.5
1	D	118	ASN	3.5
1	D	189	ALA	3.5
1	C	203	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	184	SER	3.4
1	B	69	ASN	3.4
1	B	120	THR	3.4
1	D	150	THR	3.3
1	A	69	ASN	3.3
1	D	117	SER	3.3
1	D	203	ASP	3.2
1	C	119	SER	3.2
1	A	17	ILE	3.1
1	A	202	PRO	3.1
1	D	58	ASP	3.0
1	C	187	VAL	3.0
1	A	184	SER	2.9
1	B	185	SER	2.9
1	B	135	LYS	2.9
1	D	136	ASP	2.9
1	C	163	GLY	2.9
1	A	117	SER	2.9
1	A	123	THR	2.9
1	B	202	PRO	2.9
1	A	83	ASN	2.9
1	A	187	VAL	2.9
1	B	83	ASN	2.8
1	B	118	ASN	2.8
1	A	189	ALA	2.8
1	B	21	SER	2.8
1	B	150	THR	2.8
1	A	135	LYS	2.8
1	A	120	THR	2.7
1	B	122	GLU	2.7
1	C	151	ASP	2.6
1	B	204	SER	2.6
1	C	69	ASN	2.6
1	C	150	THR	2.6
1	C	184	SER	2.6
1	A	118	ASN	2.5
1	B	189	ALA	2.5
1	B	184	SER	2.5
1	D	151	ASP	2.5
1	C	116	LYS	2.5
1	D	187	VAL	2.5
1	C	58	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	162	ASN	2.5
1	B	182	TRP	2.5
1	B	70	ALA	2.5
1	C	237	ASN	2.4
1	A	151	ASP	2.4
1	C	202	PRO	2.4
1	D	69	ASN	2.4
1	D	149	GLY	2.4
1	C	70	ALA	2.4
1	D	182	TRP	2.4
1	C	122	GLU	2.4
1	C	162	ASN	2.4
1	A	121	HIS	2.4
1	B	117	SER	2.4
1	A	116	LYS	2.4
1	A	122	GLU	2.3
1	A	204	SER	2.3
1	D	204	SER	2.3
1	C	183	GLU	2.3
1	D	183	GLU	2.3
1	D	87	GLU	2.2
1	C	121	HIS	2.2
1	A	18	GLY	2.2
1	C	185	SER	2.2
1	C	182	TRP	2.2
1	A	164	SER	2.2
1	C	165	PRO	2.2
1	C	135	LYS	2.2
1	A	158	ARG	2.2
1	A	162	ASN	2.2
1	A	132	GLN	2.2
1	A	237	ASN	2.1
1	D	115	LEU	2.1
1	B	136	ASP	2.1
1	D	202	PRO	2.1
1	C	1	ALA	2.1
1	C	158	ARG	2.1
1	D	201	SER	2.0
1	C	120	THR	2.0
1	C	161	SER	2.0
1	B	121	HIS	2.0
1	A	188	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

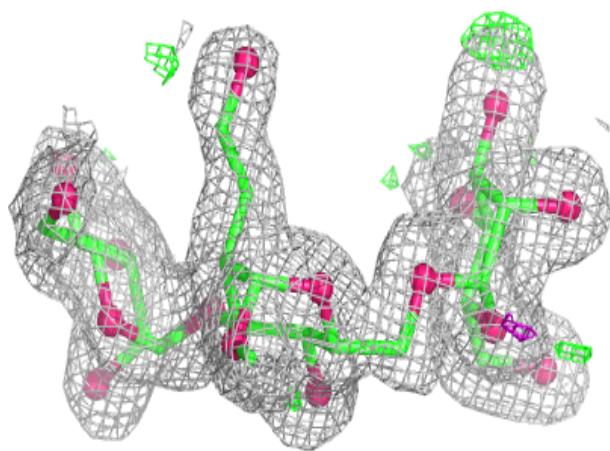
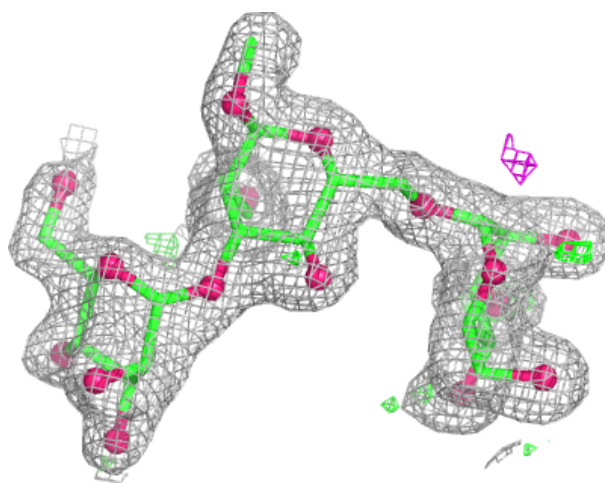
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	E	2	11/12	0.81	0.13	38,39,40,42	0
2	MAN	F	2	11/12	0.81	0.13	28,30,33,37	0
2	H1M	G	1	15/15	0.83	0.13	29,37,41,42	0
2	MAN	G	2	11/12	0.84	0.12	36,38,41,43	0
2	MAN	H	2	11/12	0.87	0.11	29,30,32,34	0
2	H1M	E	1	15/15	0.88	0.11	28,36,38,38	0
2	H1M	F	1	15/15	0.89	0.11	22,28,30,31	0
2	H1M	H	1	15/15	0.91	0.09	21,28,30,31	0
2	MAN	G	3	11/12	0.91	0.09	23,25,26,26	0
2	MAN	E	3	11/12	0.92	0.08	18,24,25,26	0
2	MAN	F	3	11/12	0.96	0.06	18,20,21,22	0
2	MAN	H	3	11/12	0.96	0.06	17,19,19,20	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.

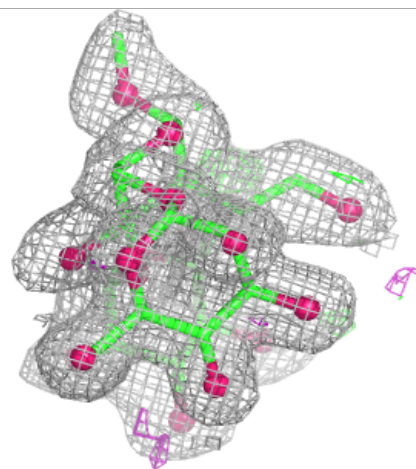
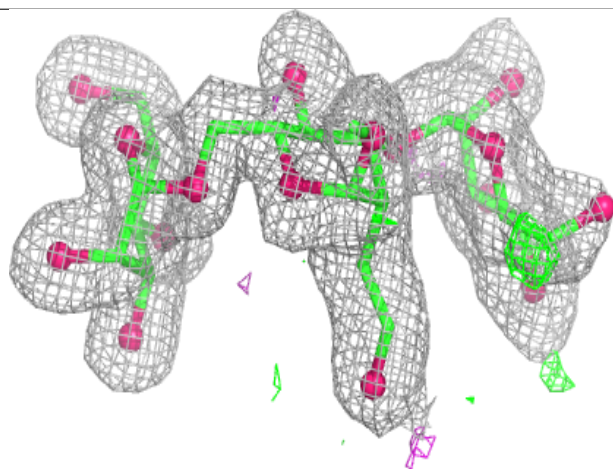
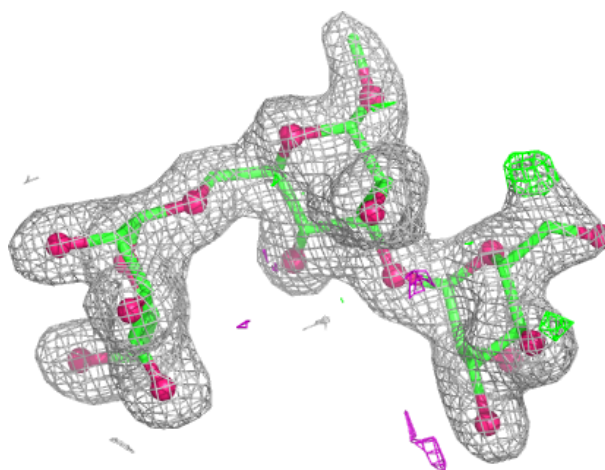
Electron density around Chain E:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



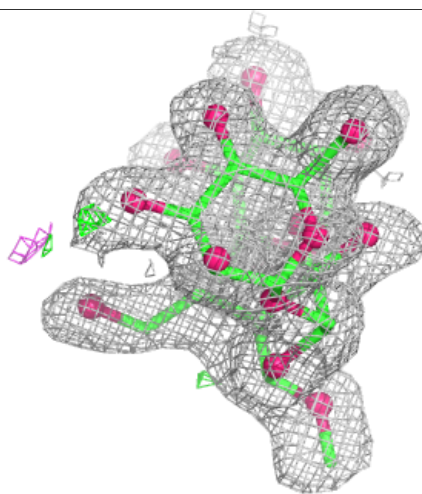
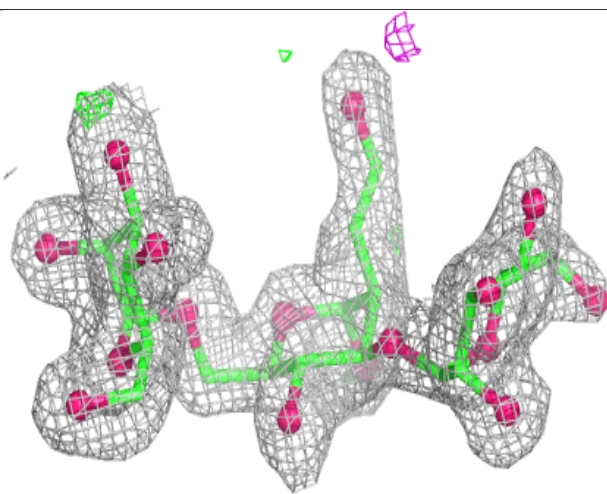
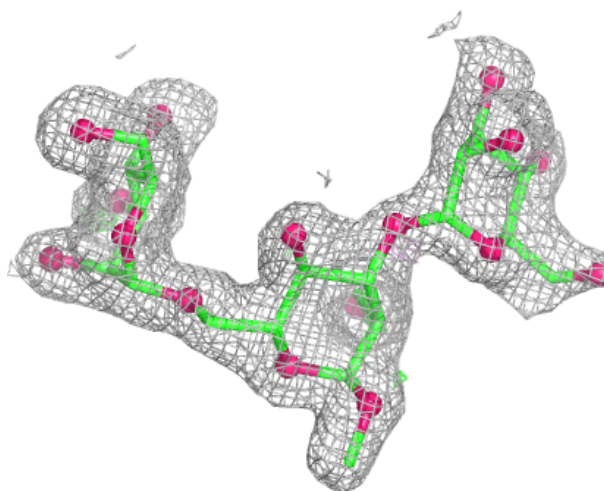
Electron density around Chain F:

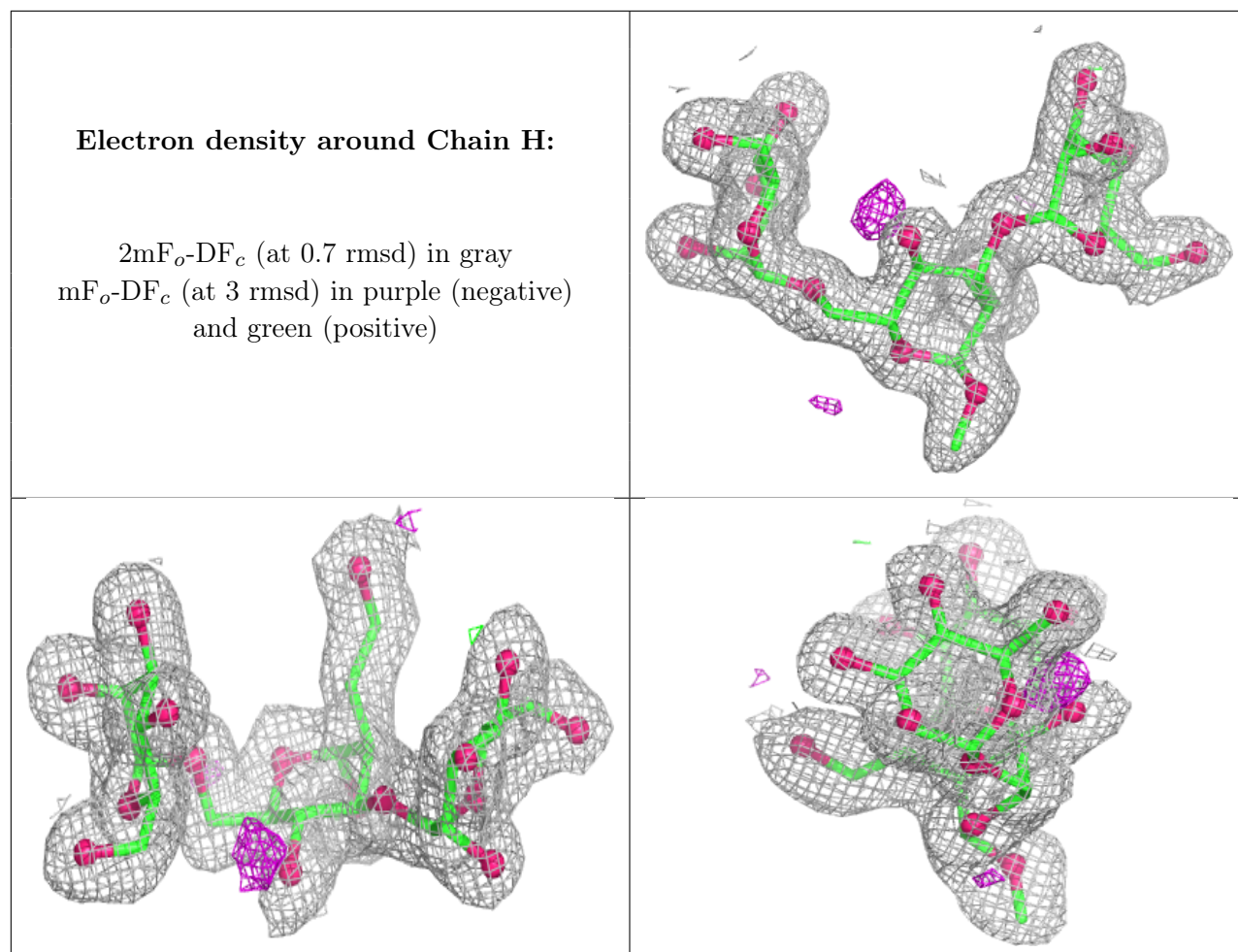
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





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
5	GOL	D	900	6/6	0.81	0.14	29,32,34,37	0
5	GOL	B	900	6/6	0.86	0.11	26,29,32,32	0
5	GOL	A	900	6/6	0.87	0.12	29,32,34,34	0
5	GOL	C	900	6/6	0.88	0.10	25,31,32,35	0
4	CA	C	239	1/1	0.98	0.04	20,20,20,20	0
3	MN	A	238	1/1	0.98	0.03	18,18,18,18	0
3	MN	C	238	1/1	0.98	0.03	17,17,17,17	0
4	CA	A	239	1/1	0.98	0.05	20,20,20,20	0
4	CA	B	239	1/1	0.98	0.04	18,18,18,18	0
3	MN	B	238	1/1	0.99	0.03	18,18,18,18	0
4	CA	D	239	1/1	0.99	0.03	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MN	D	238	1/1	0.99	0.02	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.