



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:21 AM UTC

PDB ID : 1HWM / pdb_00001hwm
Title : EBULIN, ORTHORHOMBIC CRYSTAL FORM MODEL
Authors : Pascal, J.M.; Day, P.J.; Monzingo, A.F.; Ernst, S.R.; Robertus, J.D.
Deposited on : 2001-01-09
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) : 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

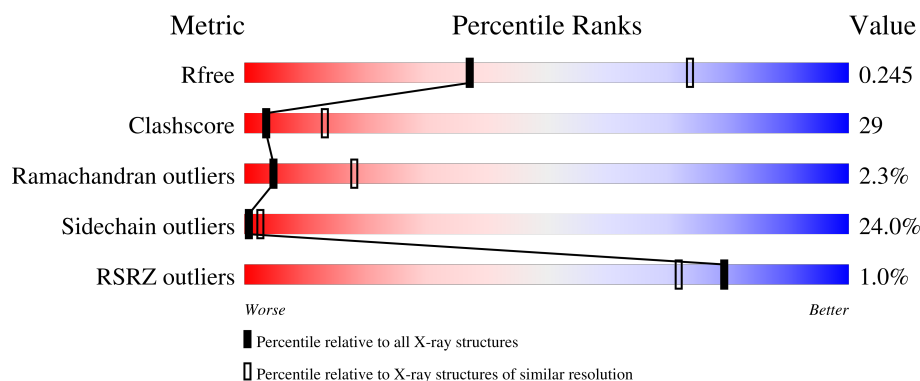
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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 $\leq 5\%$. 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	254	% 43% 45% 11% .
2	B	266	% 43% 39% 16% ..
3	C	5	40% 20% 40%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4154 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.

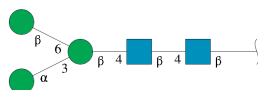
- Molecule 1 is a protein called EBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			1983	1253	340	385	5			

- Molecule 2 is a protein called EBULIN.

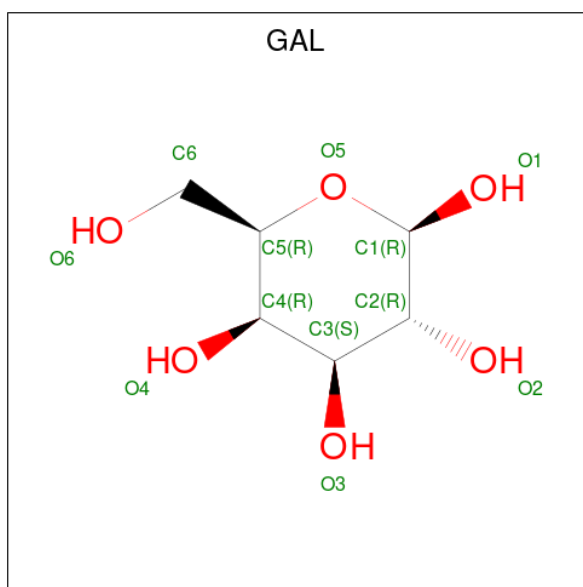
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	264	Total	C	N	O	S	0	0	0
			2042	1262	361	403	16			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is beta-D-galactopyranose (CCD ID: GAL) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			12	6	6		

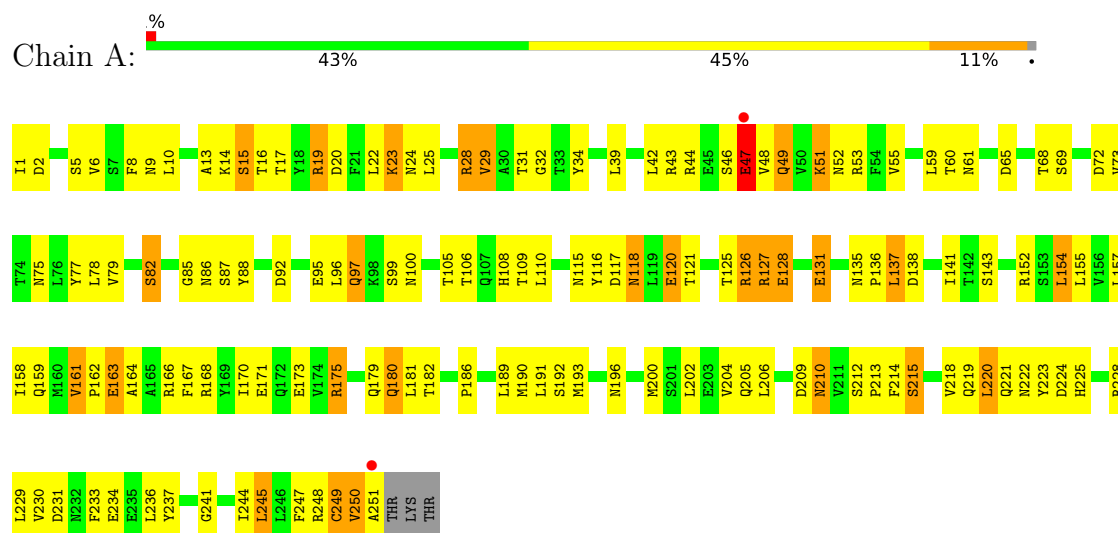
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	26	Total	O	0	0
			26	26		
5	B	30	Total	O	0	0
			30	30		

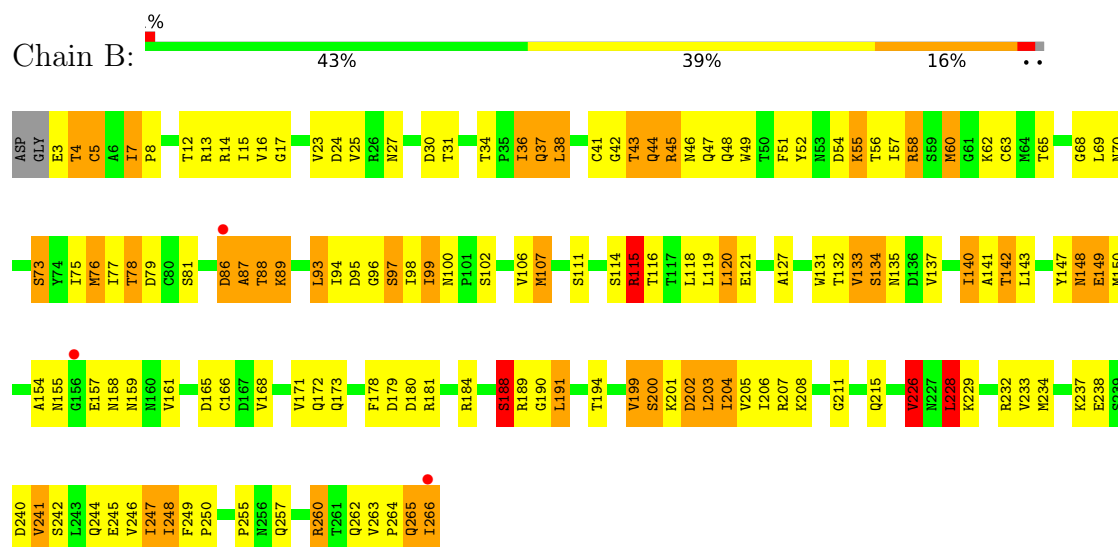
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

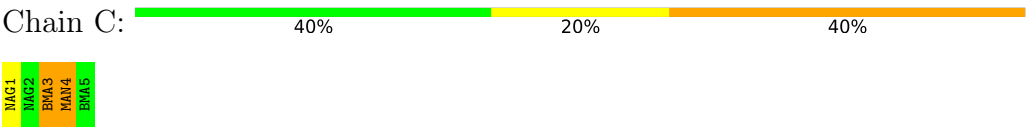
• Molecule 1: EBULIN



• Molecule 2: EBULIN



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.33Å 97.69Å 113.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 30.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.80) 83.0 (30.00-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.12 (at 2.79Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.194 , 0.285 0.203 , 0.245	Depositor DCC
R_{free} test set	1368 reflections (10.08%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 62.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4154	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, GAL, MAN, 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	0.31	0/2020	0.80	1/2746 (0.0%)
2	B	0.29	0/2079	0.83	3/2831 (0.1%)
All	All	0.30	0/4099	0.81	4/5577 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	87	ALA	N-CA-C	-5.43	106.43	113.16
1	A	34	TYR	N-CA-C	-5.21	101.22	109.76
2	B	142	THR	N-CA-C	5.20	116.71	108.96
2	B	226	VAL	N-CA-C	5.00	116.96	109.20

There are no chirality outliers.

There are no planarity outliers.

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	1983	0	1955	112	0
2	B	2042	0	1975	143	0
3	C	61	0	52	1	0
4	B	12	0	12	2	0
5	A	26	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	30	0	0	3	0
All	All	4154	0	3994	238	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 29.

All (238) 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:142:THR:HA	2:B:264:PRO:HD3	1.33	1.05
1:A:19:ARG:HG2	1:A:19:ARG:HH11	1.11	1.04
2:B:127:ALA:HB3	2:B:211:GLY:HA2	1.47	0.94
1:A:251:ALA:HA	2:B:5:CYS:HB2	1.51	0.92
2:B:38:LEU:HD13	2:B:118:LEU:HD21	1.48	0.92
1:A:161:VAL:HB	1:A:162:PRO:HD3	1.51	0.92
1:A:1:ILE:HD11	1:A:100:ASN:HD22	1.32	0.92
1:A:120:GLU:HG2	1:A:126:ARG:HA	1.50	0.90
1:A:250:VAL:HG21	2:B:3:GLU:HA	1.51	0.90
2:B:142:THR:HA	2:B:264:PRO:CD	2.03	0.88
2:B:234:MET:HE3	2:B:246:VAL:HG11	1.56	0.87
2:B:99:ILE:HG12	2:B:100:ASN:N	1.90	0.85
2:B:41:CYS:SG	2:B:137:VAL:HG21	2.17	0.85
2:B:141:ALA:O	2:B:264:PRO:HD2	1.79	0.82
2:B:265:GLN:O	2:B:266:ILE:HB	1.79	0.82
2:B:114:SER:O	2:B:115:ARG:HB2	1.81	0.81
1:A:24:ASN:O	1:A:28:ARG:HG2	1.81	0.80
1:A:115:ASN:HB2	1:A:118:ASN:HB2	1.64	0.79
2:B:24:ASP:HB3	2:B:47:GLN:HG2	1.64	0.77
1:A:39:LEU:HB2	1:A:245:LEU:HD22	1.67	0.77
1:A:19:ARG:HG2	1:A:19:ARG:NH1	1.86	0.76
1:A:228:ARG:HD3	2:B:266:ILE:HG12	1.67	0.76
2:B:37:GLN:HG2	2:B:38:LEU:N	2.01	0.75
2:B:140:ILE:HG22	2:B:142:THR:HG23	1.67	0.75
3:C:3:BMA:O4	3:C:4:MAN:H2	1.87	0.73
2:B:194:THR:HG21	2:B:207:ARG:HH11	1.53	0.73
2:B:16:VAL:HG22	2:B:137:VAL:HG23	1.71	0.72
1:A:1:ILE:HD13	1:A:100:ASN:HB3	1.69	0.72
2:B:203:LEU:HA	2:B:247:ILE:HG22	1.71	0.72
1:A:9:ASN:O	1:A:13:ALA:HB2	1.90	0.72
1:A:231:ASP:OD2	2:B:134:SER:HB2	1.89	0.72
2:B:65:THR:HA	2:B:87:ALA:O	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:ILE:CD1	1:A:100:ASN:HD22	2.02	0.72
1:A:250:VAL:CG2	2:B:3:GLU:HA	2.19	0.72
1:A:190:MET:HA	1:A:193:MET:HE3	1.73	0.71
1:A:224:ASP:O	1:A:225:HIS:HB2	1.90	0.71
1:A:158:ILE:O	1:A:162:PRO:HD2	1.91	0.70
1:A:95:GLU:OE1	1:A:99:SER:HB2	1.92	0.69
2:B:142:THR:HG22	2:B:263:VAL:HG12	1.73	0.69
2:B:23:VAL:HG22	2:B:118:LEU:HD11	1.75	0.68
2:B:226:VAL:HG13	2:B:233:VAL:HG12	1.74	0.68
1:A:31:THR:HG23	1:A:43:ARG:HH21	1.59	0.68
2:B:142:THR:CG2	2:B:263:VAL:HG12	2.25	0.66
2:B:132:THR:HB	2:B:179:ASP:HB3	1.75	0.66
1:A:135:ASN:HB2	1:A:136:PRO:HD3	1.78	0.65
2:B:202:ASP:HB2	2:B:248:ILE:HD11	1.78	0.65
2:B:260:ARG:HE	2:B:262:GLN:NE2	1.94	0.65
2:B:142:THR:HG22	2:B:263:VAL:HA	1.79	0.65
1:A:161:VAL:HB	1:A:162:PRO:CD	2.27	0.63
1:A:228:ARG:CZ	2:B:266:ILE:HG13	2.29	0.63
1:A:196:ASN:O	1:A:200:MET:HG3	1.99	0.62
2:B:194:THR:HG21	2:B:207:ARG:HD3	1.80	0.62
1:A:127:ARG:HG3	1:A:155:LEU:HD22	1.81	0.61
2:B:58:ARG:HB3	2:B:63:CYS:HA	1.81	0.61
2:B:98:ILE:HG21	2:B:107:MET:HE3	1.82	0.61
1:A:59:LEU:HD12	1:A:157:LEU:HD11	1.80	0.61
1:A:250:VAL:HB	2:B:4:THR:H	1.65	0.61
1:A:161:VAL:CB	1:A:162:PRO:HD3	2.30	0.61
1:A:206:LEU:HA	2:B:5:CYS:SG	2.41	0.61
1:A:247:PHE:CZ	1:A:250:VAL:HG22	2.36	0.60
2:B:44:GLN:H	2:B:44:GLN:NE2	1.99	0.60
1:A:247:PHE:HZ	1:A:250:VAL:HG22	1.65	0.60
1:A:61:ASN:ND2	1:A:65:ASP:HB2	2.16	0.60
2:B:24:ASP:CB	2:B:47:GLN:HG2	2.31	0.60
1:A:23:LYS:HE2	1:A:23:LYS:HA	1.83	0.60
2:B:16:VAL:CG2	2:B:137:VAL:HG23	2.31	0.60
2:B:194:THR:HG23	2:B:215:GLN:HG2	1.82	0.60
2:B:148:ASN:O	2:B:149:GLU:HB2	2.00	0.60
2:B:99:ILE:HB	2:B:106:VAL:HG12	1.83	0.60
1:A:126:ARG:HB2	1:A:128:GLU:HG2	1.84	0.59
1:A:206:LEU:HD23	2:B:5:CYS:SG	2.42	0.59
2:B:86:ASP:O	2:B:100:ASN:ND2	2.35	0.59
2:B:143:LEU:HD23	2:B:173:GLN:O	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:200:SER:O	2:B:201:LYS:HB2	2.02	0.58
1:A:212:SER:HB3	1:A:213:PRO:HD3	1.86	0.57
1:A:228:ARG:NH1	2:B:266:ILE:HG23	2.19	0.57
2:B:7:ILE:HD12	2:B:7:ILE:O	2.05	0.57
2:B:265:GLN:O	2:B:266:ILE:CB	2.52	0.57
2:B:114:SER:O	2:B:115:ARG:CB	2.51	0.56
1:A:190:MET:O	1:A:193:MET:HG2	2.04	0.56
2:B:93:LEU:HB2	2:B:95:ASP:OD1	2.06	0.56
1:A:117:ASP:O	1:A:121:THR:HG23	2.05	0.56
2:B:76:MET:HG2	2:B:77:ILE:N	2.20	0.55
1:A:23:LYS:HE3	5:A:319:HOH:O	2.07	0.55
1:A:192:SER:OG	1:A:220:LEU:HA	2.06	0.55
2:B:157:GLU:HB2	2:B:159:ASN:HD22	1.70	0.55
1:A:49:GLN:OE1	1:A:52:ASN:HB2	2.06	0.55
1:A:228:ARG:HD3	2:B:266:ILE:CG1	2.34	0.55
2:B:159:ASN:O	2:B:205:VAL:HB	2.05	0.55
1:A:228:ARG:NH1	2:B:266:ILE:HG13	2.21	0.54
1:A:186:PRO:HB2	1:A:191:LEU:HD21	1.89	0.54
1:A:61:ASN:CG	1:A:65:ASP:HB2	2.32	0.54
2:B:150:MET:HE2	2:B:165:ASP:N	2.23	0.54
2:B:127:ALA:HB3	2:B:211:GLY:CA	2.30	0.54
1:A:209:ASP:O	1:A:210:ASN:HB2	2.06	0.54
1:A:61:ASN:HB2	1:A:138:ASP:OD1	2.08	0.53
1:A:25:LEU:O	1:A:29:VAL:HG13	2.08	0.53
2:B:241:VAL:HG22	2:B:242:SER:N	2.22	0.53
1:A:1:ILE:N	1:A:1:ILE:HD12	2.24	0.53
1:A:250:VAL:HB	2:B:4:THR:N	2.23	0.53
2:B:161:VAL:HG21	2:B:204:ILE:HG22	1.91	0.52
2:B:37:GLN:HG3	2:B:115:ARG:HA	1.92	0.52
2:B:41:CYS:SG	2:B:137:VAL:CG2	2.96	0.52
2:B:44:GLN:O	2:B:48:GLN:NE2	2.42	0.52
1:A:189:LEU:O	1:A:192:SER:HB3	2.08	0.52
1:A:206:LEU:HD23	1:A:249:CYS:SG	2.51	0.51
2:B:38:LEU:CD1	2:B:118:LEU:HD21	2.32	0.51
2:B:34:THR:O	2:B:76:MET:HB2	2.11	0.51
2:B:137:VAL:O	2:B:137:VAL:HG22	2.11	0.51
1:A:82:SER:HB2	1:A:87:SER:HB3	1.93	0.51
2:B:14:ARG:NH2	2:B:42:GLY:O	2.44	0.50
2:B:25:VAL:HG11	2:B:77:ILE:HD13	1.93	0.50
1:A:171:GLU:O	1:A:175:ARG:HB2	2.11	0.50
1:A:167:PHE:HB2	1:A:170:ILE:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:199:VAL:O	2:B:202:ASP:HB2	2.12	0.49
1:A:131:GLU:CD	1:A:131:GLU:H	2.21	0.49
1:A:234:GLU:HG3	2:B:181:ARG:NH1	2.27	0.49
2:B:30:ASP:HB3	2:B:60:MET:HE3	1.94	0.49
2:B:31:THR:HG23	5:B:317:HOH:O	2.12	0.49
2:B:203:LEU:HD23	2:B:247:ILE:HG23	1.95	0.49
1:A:48:VAL:HG11	1:A:53:ARG:HA	1.95	0.49
2:B:43:THR:O	2:B:44:GLN:C	2.56	0.49
2:B:140:ILE:HG22	2:B:142:THR:CG2	2.38	0.49
1:A:248:ARG:HG3	1:A:248:ARG:HH11	1.78	0.48
1:A:224:ASP:O	1:A:225:HIS:CB	2.60	0.48
2:B:12:THR:C	2:B:13:ARG:HG2	2.37	0.48
2:B:95:ASP:HB2	2:B:228:LEU:HD21	1.94	0.48
2:B:25:VAL:HG11	2:B:77:ILE:CD1	2.43	0.48
1:A:85:GLY:O	1:A:105:THR:HB	2.14	0.48
2:B:13:ARG:HA	2:B:135:ASN:OD1	2.14	0.48
1:A:19:ARG:NH1	1:A:19:ARG:CG	2.66	0.48
1:A:22:LEU:HD11	1:A:164:ALA:HB1	1.95	0.48
2:B:157:GLU:O	2:B:158:ASN:C	2.56	0.48
1:A:79:VAL:HG21	1:A:97:GLN:CD	2.39	0.48
2:B:107:MET:HG2	2:B:131:TRP:CE2	2.48	0.48
1:A:43:ARG:HB3	1:A:47:GLU:CG	2.45	0.47
1:A:215:SER:HB3	2:B:8:PRO:HB2	1.96	0.47
2:B:37:GLN:CG	2:B:38:LEU:N	2.73	0.47
2:B:51:PHE:N	2:B:51:PHE:CD1	2.82	0.47
1:A:180:GLN:NE2	1:A:182:THR:OG1	2.46	0.47
2:B:14:ARG:NH2	2:B:48:GLN:OE1	2.48	0.47
2:B:36:ILE:HD11	2:B:77:ILE:HG23	1.97	0.47
2:B:56:THR:HG22	2:B:89:LYS:HE2	1.97	0.47
2:B:180:ASP:O	2:B:181:ARG:HB2	2.15	0.47
2:B:263:VAL:HG23	2:B:263:VAL:O	2.15	0.47
1:A:237:TYR:O	1:A:241:GLY:N	2.47	0.46
2:B:255:PRO:C	2:B:257:GLN:H	2.23	0.46
2:B:78:THR:OG1	2:B:79:ASP:N	2.49	0.46
2:B:44:GLN:HB2	2:B:46:ASN:OD1	2.15	0.46
2:B:94:ILE:C	2:B:96:GLY:H	2.23	0.46
2:B:42:GLY:HA3	2:B:44:GLN:OE1	2.16	0.46
2:B:17:GLY:O	2:B:180:ASP:HB3	2.16	0.46
1:A:10:LEU:HD13	1:A:138:ASP:HB2	1.97	0.46
1:A:233:PHE:O	1:A:234:GLU:C	2.58	0.45
2:B:54:ASP:O	2:B:55:LYS:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:68:GLY:HA3	2:B:73:SER:OG	2.16	0.45
2:B:25:VAL:HG12	2:B:34:THR:CG2	2.46	0.45
2:B:36:ILE:HG22	2:B:118:LEU:HB2	1.98	0.45
1:A:204:VAL:HG11	1:A:245:LEU:HD21	1.97	0.45
1:A:75:ASN:OD1	1:A:77:TYR:HB2	2.17	0.45
1:A:213:PRO:HB3	5:B:321:HOH:O	2.17	0.45
1:A:222:ASN:HB3	1:A:224:ASP:OD1	2.17	0.45
2:B:17:GLY:HA3	2:B:131:TRP:CE3	2.52	0.45
2:B:37:GLN:HG3	2:B:115:ARG:CA	2.46	0.45
2:B:25:VAL:HG12	2:B:34:THR:HG21	1.99	0.45
2:B:133:VAL:O	2:B:133:VAL:CG2	2.65	0.45
2:B:184:ARG:HB3	2:B:191:LEU:O	2.17	0.45
1:A:92:ASP:N	1:A:92:ASP:OD1	2.47	0.45
1:A:234:GLU:OE1	1:A:234:GLU:HA	2.17	0.44
2:B:36:ILE:HD13	2:B:76:MET:HA	1.99	0.44
2:B:178:PHE:HB3	2:B:180:ASP:OD1	2.17	0.44
1:A:32:GLY:O	1:A:43:ARG:HD3	2.16	0.44
2:B:226:VAL:HG11	5:B:355:HOH:O	2.16	0.44
2:B:41:CYS:CB	2:B:137:VAL:HG21	2.47	0.44
2:B:260:ARG:HE	2:B:262:GLN:HE21	1.63	0.44
1:A:60:THR:HA	1:A:65:ASP:O	2.18	0.44
1:A:72:ASP:HB3	1:A:75:ASN:OD1	2.18	0.44
2:B:17:GLY:C	2:B:180:ASP:HB3	2.42	0.44
2:B:159:ASN:HA	2:B:206:ILE:HB	1.99	0.44
2:B:166:CYS:HA	2:B:173:GLN:HE22	1.83	0.43
2:B:188:SER:C	2:B:190:GLY:H	2.26	0.43
1:A:234:GLU:HG3	2:B:181:ARG:HH12	1.83	0.43
2:B:234:MET:HE2	2:B:234:MET:HB3	1.89	0.43
1:A:88:TYR:HB3	1:A:110:LEU:HD21	2.00	0.43
2:B:203:LEU:HD22	2:B:204:ILE:H	1.83	0.43
1:A:47:GLU:HG3	1:A:48:VAL:N	2.30	0.43
1:A:86:ASN:OD1	1:A:108:HIS:CE1	2.71	0.43
2:B:52:TYR:HB2	2:B:54:ASP:OD1	2.18	0.43
1:A:214:PHE:O	2:B:13:ARG:NH2	2.49	0.43
2:B:120:LEU:HD23	2:B:120:LEU:HA	1.87	0.43
2:B:88:THR:CG2	2:B:89:LYS:HE3	2.49	0.43
2:B:155:ASN:HA	2:B:172:GLN:HE21	1.83	0.42
2:B:27:ASN:HA	4:B:280:GAL:O1	2.19	0.42
2:B:203:LEU:HD23	2:B:247:ILE:CG2	2.49	0.42
1:A:42:LEU:HD21	1:A:244:ILE:HG21	2.01	0.42
1:A:218:VAL:O	1:A:229:LEU:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:27:ASN:HA	4:B:280:GAL:C1	2.49	0.42
1:A:127:ARG:HG2	1:A:159:GLN:NE2	2.34	0.42
1:A:155:LEU:O	1:A:159:GLN:HG3	2.20	0.42
2:B:44:GLN:H	2:B:44:GLN:CD	2.27	0.42
2:B:93:LEU:HG	2:B:97:SER:O	2.19	0.42
2:B:181:ARG:HA	2:B:181:ARG:HD3	1.63	0.42
2:B:161:VAL:CG2	2:B:204:ILE:HG22	2.49	0.42
2:B:240:ASP:CB	2:B:244:GLN:HA	2.49	0.42
1:A:15:SER:OG	1:A:175:ARG:HG2	2.19	0.42
2:B:94:ILE:C	2:B:96:GLY:N	2.76	0.42
2:B:107:MET:HG2	2:B:131:TRP:CZ2	2.54	0.42
1:A:244:ILE:HG22	1:A:245:LEU:N	2.35	0.42
1:A:77:TYR:HD1	1:A:166:ARG:HH12	1.66	0.41
2:B:154:ALA:O	2:B:172:GLN:HG2	2.20	0.41
1:A:43:ARG:HB2	1:A:48:VAL:CG2	2.50	0.41
1:A:49:GLN:HE22	1:A:51:LYS:HG2	1.85	0.41
1:A:251:ALA:HA	2:B:5:CYS:CB	2.35	0.41
1:A:168:ARG:HB2	1:A:241:GLY:O	2.19	0.41
1:A:8:PHE:HB3	1:A:59:LEU:CD2	2.51	0.41
1:A:161:VAL:CB	1:A:162:PRO:CD	2.92	0.41
2:B:226:VAL:HG13	2:B:233:VAL:CG1	2.48	0.41
1:A:19:ARG:HH12	1:A:20:ASP:CG	2.29	0.41
2:B:60:MET:HE2	2:B:60:MET:HB2	1.78	0.41
1:A:106:THR:O	1:A:108:HIS:CE1	2.73	0.41
1:A:229:LEU:N	1:A:229:LEU:HD12	2.35	0.41
2:B:249:PHE:CG	2:B:250:PRO:HD2	2.55	0.41
1:A:1:ILE:HD12	1:A:1:ILE:H3	1.86	0.41
1:A:1:ILE:HG22	1:A:2:ASP:N	2.36	0.41
1:A:159:GLN:HA	1:A:163:GLU:HB2	2.03	0.41
2:B:45:ARG:NH1	2:B:60:MET:HG2	2.36	0.41
2:B:157:GLU:HB2	2:B:159:ASN:ND2	2.36	0.41
1:A:233:PHE:O	1:A:236:LEU:N	2.55	0.40
1:A:6:VAL:HG23	1:A:6:VAL:O	2.21	0.40
1:A:120:GLU:OE2	1:A:127:ARG:HB2	2.22	0.40
1:A:137:LEU:O	1:A:141:ILE:HD12	2.21	0.40
1:A:16:THR:OG1	1:A:17:THR:N	2.54	0.40
1:A:154:LEU:O	1:A:158:ILE:HG13	2.22	0.40
2:B:7:ILE:H	2:B:7:ILE:HG13	1.48	0.40
2:B:49:TRP:HB3	2:B:57:ILE:HG22	2.03	0.40
2:B:133:VAL:O	2:B:133:VAL:HG22	2.21	0.40
1:A:223:TYR:H	1:A:223:TYR:HD1	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:27:ASN:OD1	2:B:27:ASN:N	2.55	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	249/254 (98%)	222 (89%)	22 (9%)	5 (2%)	6	21
2	B	262/266 (98%)	230 (88%)	25 (10%)	7 (3%)	4	15
All	All	511/520 (98%)	452 (88%)	47 (9%)	12 (2%)	5	18

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	147	TYR
1	A	161	VAL
1	A	181	LEU
2	B	4	THR
2	B	86	ASP
2	B	188	SER
2	B	189	ARG
1	A	47	GLU
2	B	115	ARG
2	B	228	LEU
1	A	210	ASN
1	A	250	VAL

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	220/223 (99%)	173 (79%)	47 (21%)	1	4
2	B	230/231 (100%)	169 (74%)	61 (26%)	0	2
All	All	450/454 (99%)	342 (76%)	108 (24%)	1	2

All (108) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	14	LYS
1	A	15	SER
1	A	19	ARG
1	A	23	LYS
1	A	28	ARG
1	A	29	VAL
1	A	44	ARG
1	A	46	SER
1	A	47	GLU
1	A	49	GLN
1	A	51	LYS
1	A	55	VAL
1	A	68	THR
1	A	69	SER
1	A	73	VAL
1	A	78	LEU
1	A	82	SER
1	A	96	LEU
1	A	97	GLN
1	A	109	THR
1	A	116	TYR
1	A	118	ASN
1	A	120	GLU
1	A	125	THR
1	A	126	ARG
1	A	127	ARG

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Mol	Chain	Res	Type
1	A	128	GLU
1	A	131	GLU
1	A	137	LEU
1	A	143	SER
1	A	152	ARG
1	A	154	LEU
1	A	163	GLU
1	A	173	GLU
1	A	175	ARG
1	A	179	GLN
1	A	180	GLN
1	A	202	LEU
1	A	205	GLN
1	A	215	SER
1	A	219	GLN
1	A	220	LEU
1	A	221	GLN
1	A	230	VAL
1	A	245	LEU
1	A	249	CYS
2	B	5	CYS
2	B	7	ILE
2	B	15	ILE
2	B	36	ILE
2	B	37	GLN
2	B	38	LEU
2	B	43	THR
2	B	44	GLN
2	B	45	ARG
2	B	55	LYS
2	B	58	ARG
2	B	60	MET
2	B	62	LYS
2	B	69	LEU
2	B	70	ASN
2	B	73	SER
2	B	75	ILE
2	B	76	MET
2	B	78	THR
2	B	81	SER
2	B	88	THR
2	B	89	LYS

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Mol	Chain	Res	Type
2	B	93	LEU
2	B	97	SER
2	B	99	ILE
2	B	102	SER
2	B	107	MET
2	B	111	SER
2	B	115	ARG
2	B	116	THR
2	B	119	LEU
2	B	120	LEU
2	B	121	GLU
2	B	133	VAL
2	B	134	SER
2	B	140	ILE
2	B	148	ASN
2	B	149	GLU
2	B	168	VAL
2	B	171	VAL
2	B	188	SER
2	B	191	LEU
2	B	199	VAL
2	B	200	SER
2	B	202	ASP
2	B	203	LEU
2	B	204	ILE
2	B	208	LYS
2	B	226	VAL
2	B	228	LEU
2	B	229	LYS
2	B	232	ARG
2	B	237	LYS
2	B	238	GLU
2	B	241	VAL
2	B	245	GLU
2	B	247	ILE
2	B	248	ILE
2	B	260	ARG
2	B	265	GLN
2	B	266	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	100	ASN
1	A	159	GLN
1	A	180	GLN
2	B	44	GLN
2	B	153	GLN
2	B	172	GLN
2	B	173	GLN
2	B	262	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 ⓘ

5 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	C	1	2,3	14,14,15	0.50	0	17,19,21	0.65	1 (5%)
3	NAG	C	2	3	14,14,15	0.63	0	17,19,21	0.55	0
3	BMA	C	3	3	11,11,12	0.79	0	15,15,17	1.33	2 (13%)
3	MAN	C	4	3	11,11,12	0.72	0	15,15,17	0.89	1 (6%)
3	BMA	C	5	3	11,11,12	0.59	0	15,15,17	0.55	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
3	NAG	C	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	0/2/19/22	1/1/1/1
3	BMA	C	5	3	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	3	BMA	C3-C4-C5	-3.64	103.63	110.23
3	C	4	MAN	C1-O5-C5	3.01	116.22	112.19
3	C	3	BMA	C2-C3-C4	-2.07	107.21	110.86
3	C	1	NAG	C2-N2-C7	-2.03	120.18	122.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	5	BMA	O5-C5-C6-O6
3	C	5	BMA	C4-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6

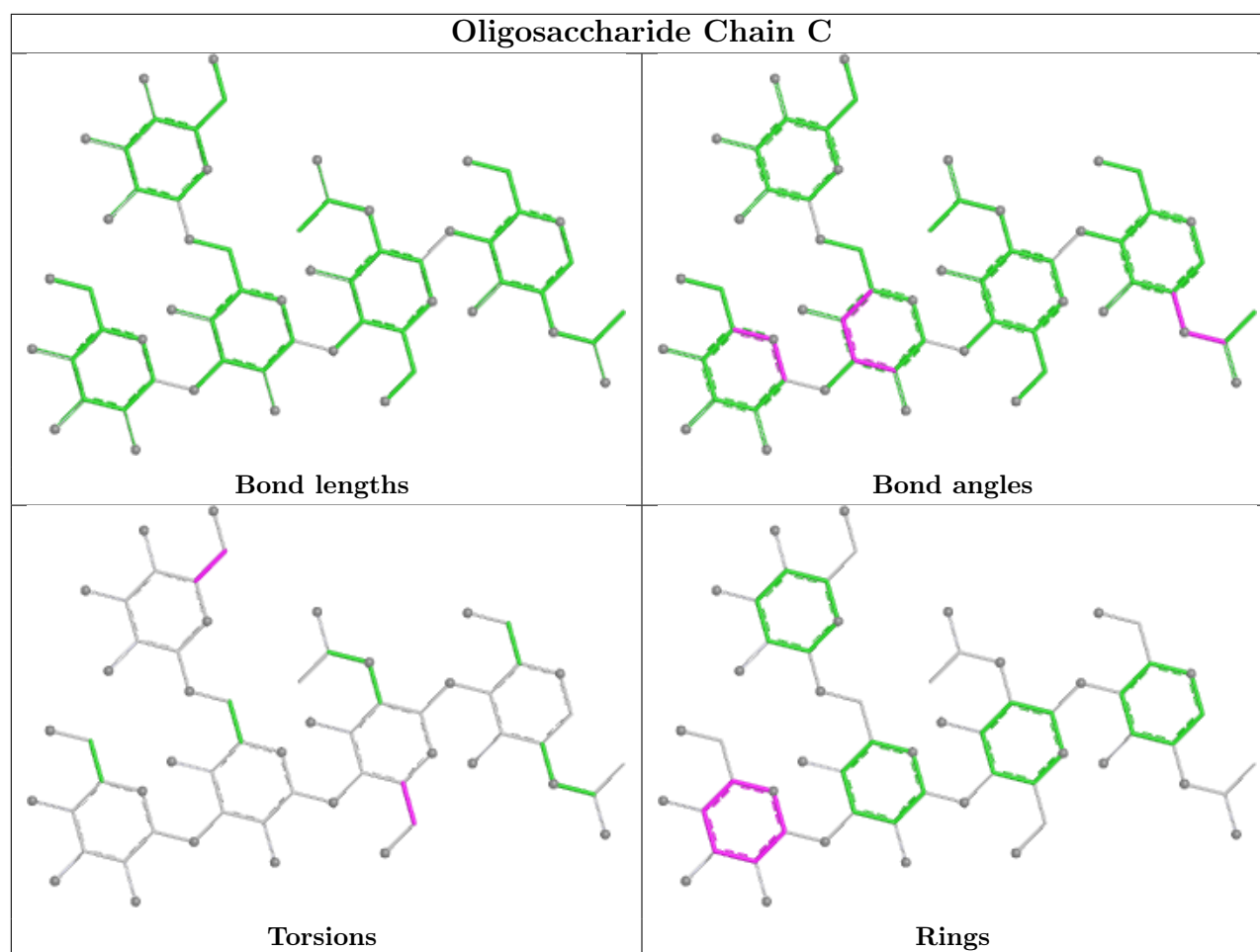
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	4	MAN	C1-C2-C3-C4-C5-O5

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	3	BMA	1	0
3	C	4	MAN	1	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](#)

1 ligand is 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	GAL	B	280	-	12,12,12	0.35	0	17,17,17	0.39	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
4	GAL	B	280	-	-	1/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	280	GAL	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	280	GAL	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	251/254 (98%)	-0.09	2 (0%) 82 75	2, 18, 39, 70	0
2	B	264/266 (99%)	-0.08	3 (1%) 78 70	2, 19, 43, 76	0
All	All	515/520 (99%)	-0.08	5 (0%) 79 72	2, 18, 41, 76	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	251	ALA	2.8
2	B	156	GLY	2.6
1	A	47	GLU	2.5
2	B	86	ASP	2.4
2	B	266	ILE	2.3

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

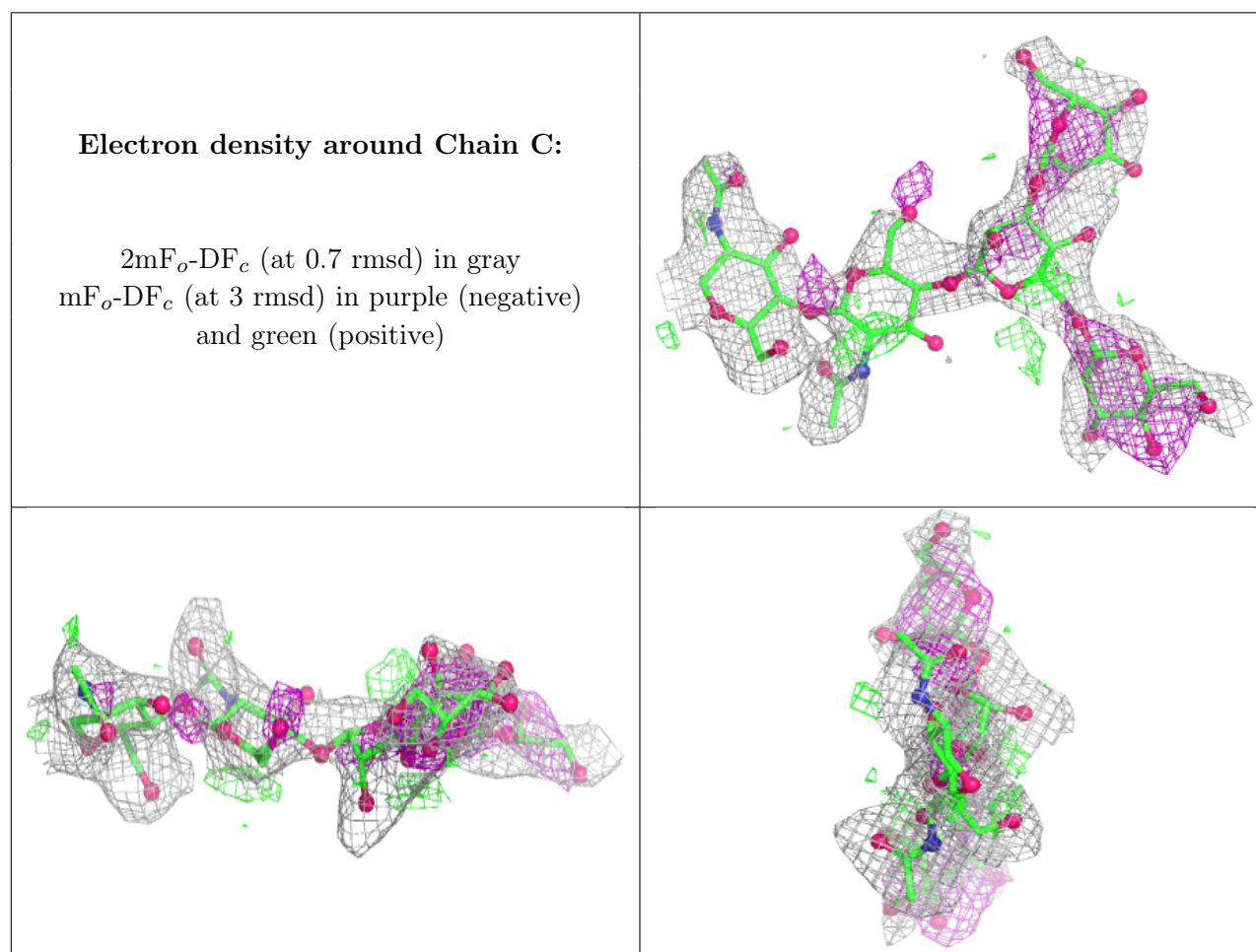
There are no non-standard protein/DNA/RNA residues in this entry.

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	BMA	C	3	11/12	0.60	0.14	19,19,19,19	0
3	NAG	C	2	14/15	0.64	0.16	19,19,19,19	0
3	MAN	C	4	11/12	0.69	0.14	19,19,19,19	0
3	BMA	C	5	11/12	0.70	0.14	19,19,19,19	0
3	NAG	C	1	14/15	0.76	0.13	19,19,19,19	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
4	GAL	B	280	12/12	0.70	0.20	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.