



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:01 PM UTC

PDB ID : 8CEM / pdb_00008cem
Title : Structure of bovine native C3, re-refinement
Authors : Andersen, G.R.; Fredslund, F.
Deposited on : 2023-02-02
Resolution : 3.00 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:

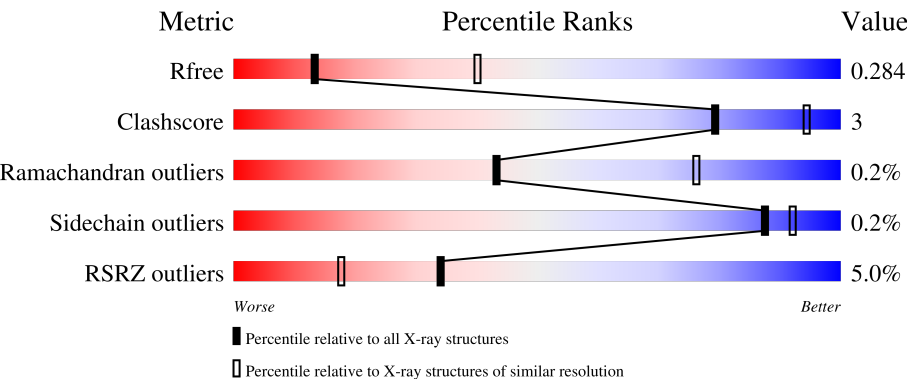
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 <=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	E	643	9% 90% 10%
1	F	643	3% 93% 6%
2	A	992	5% 89% 9%
2	B	992	4% 91% 8%
3	C	3	100%

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Mol	Chain	Length	Quality of chain
3	D	3	33% 67%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 25695 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.

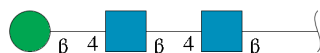
- Molecule 1 is a protein called Complement C3 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	640	Total	C	N	O	S	0	0	0
			5012	3185	861	953	13			
1	F	639	Total	C	N	O	S	0	0	0
			5005	3180	860	952	13			

- Molecule 2 is a protein called Complement C3 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	975	Total	C	N	O	S	0	0	0
			7804	4938	1331	1492	43			
2	B	974	Total	C	N	O	S	0	0	0
			7796	4932	1330	1491	43			

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

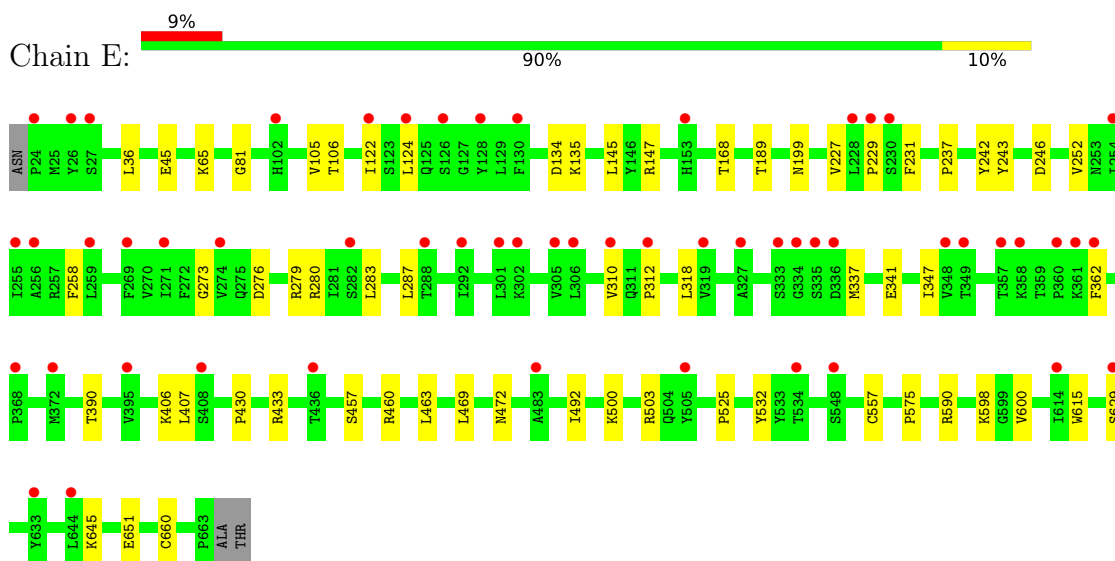


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

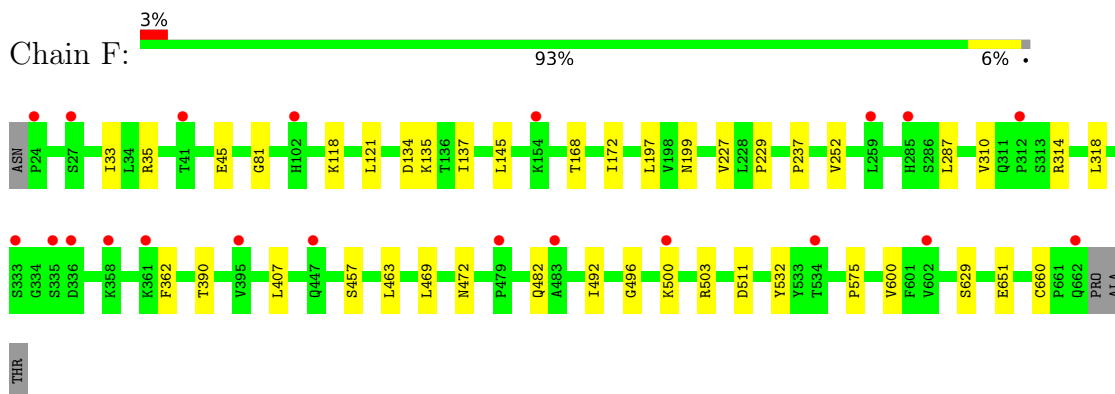
3 Residue-property plots

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.

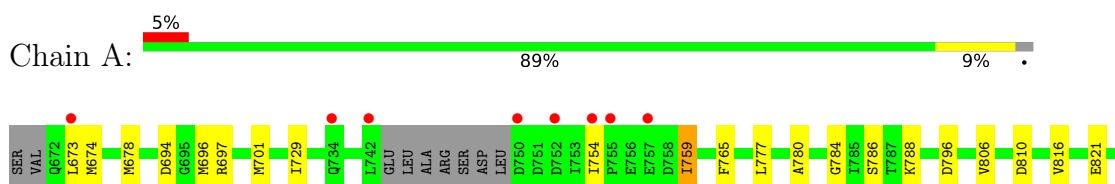
• Molecule 1: Complement C3 beta chain

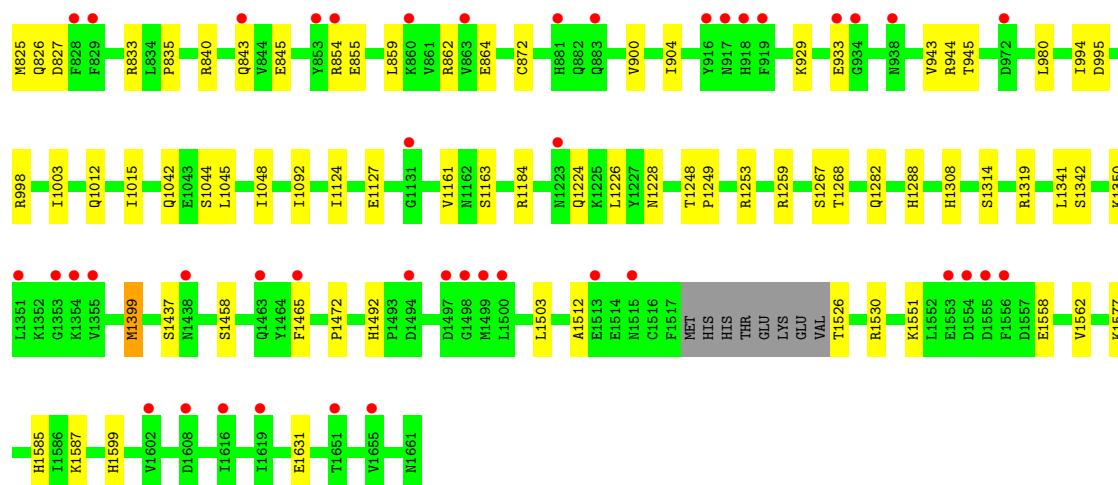


• Molecule 1: Complement C3 beta chain

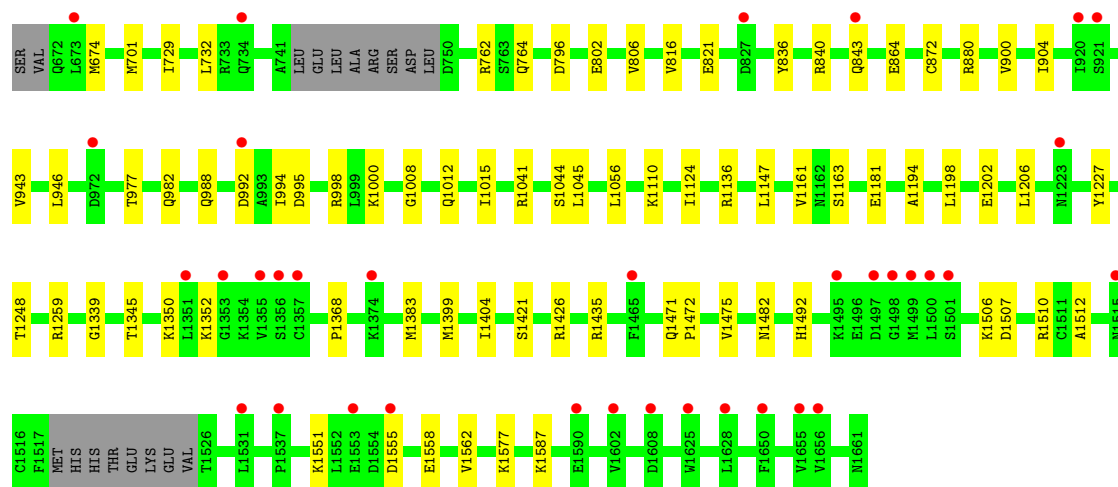


• Molecule 2: Complement C3 alpha chain





• Molecule 2: Complement C3 alpha chain



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



• Molecule 3: 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 2	Depositor
Cell constants a, b, c, α , β , γ	254.25Å 246.86Å 113.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.85 – 3.00 37.85 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.2 (37.85-3.00) 97.2 (37.85-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.259 , 0.284 0.259 , 0.284	Depositor DCC
R_{free} test set	1392 reflections (0.97%)	wwPDB-VP
Wilson B-factor (Å ²)	68.4	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 62.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.008 for k,h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	25695	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.36% 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: BMA, 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	E	0.24	0/5113	0.50	0/6945
1	F	0.23	0/5105	0.49	0/6933
2	A	0.31	0/7953	0.65	4/10749 (0.0%)
2	B	0.31	0/7945	0.64	4/10738 (0.0%)
All	All	0.28	0/26116	0.59	8/35365 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1248	THR	N-CA-C	6.32	123.78	109.81
2	A	1248	THR	N-CA-C	6.16	123.42	109.81
2	A	826	GLN	CA-C-N	5.72	132.47	121.54
2	A	826	GLN	C-N-CA	5.72	132.47	121.54
2	B	1506	LYS	CA-C-N	5.20	131.47	121.54
2	B	1506	LYS	C-N-CA	5.20	131.47	121.54
2	B	1352	LYS	CA-CB-CG	5.18	124.47	114.10
2	A	1249	PRO	N-CA-C	5.18	117.02	110.70

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	E	5012	0	5071	35	0
1	F	5005	0	5064	23	0
2	A	7804	0	7756	52	0
2	B	7796	0	7745	41	0
3	C	39	0	34	0	0
3	D	39	0	34	0	0
All	All	25695	0	25704	140	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 3.

All (140) 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:E:135:LYS:HB2	1:E:600:VAL:HG11	1.63	0.81
2:B:1041:ARG:O	2:B:1045:LEU:HD23	1.96	0.65
1:F:135:LYS:HB2	1:F:600:VAL:HG11	1.82	0.60
2:A:854:ARG:HH11	2:A:859:LEU:HD21	1.67	0.60
2:A:994:ILE:HG23	2:A:1044:SER:HB3	1.85	0.59
1:F:227:VAL:HG12	1:F:229:PRO:HD3	1.85	0.58
1:F:310:VAL:HG21	1:F:318:LEU:HD21	1.85	0.58
1:F:575:PRO:HB3	2:B:796:ASP:HA	1.84	0.58
1:E:575:PRO:HB3	2:A:796:ASP:HA	1.84	0.58
1:E:310:VAL:HG21	1:E:318:LEU:HD21	1.86	0.58
1:E:457:SER:HB3	1:E:472:ASN:HB2	1.85	0.57
2:B:1136:ARG:HG2	2:B:1181:GLU:HB3	1.84	0.57
2:B:994:ILE:HG23	2:B:1044:SER:HB3	1.86	0.57
2:A:1512:ALA:HB1	2:A:1587:LYS:HE2	1.87	0.57
2:B:843:GLN:HG3	2:B:900:VAL:HG22	1.86	0.56
2:A:862:ARG:NH2	2:A:864:GLU:OE2	2.36	0.56
1:E:341:GLU:HB2	2:A:759:ILE:HG13	1.88	0.56
2:A:843:GLN:HG3	2:A:900:VAL:HG22	1.88	0.55
1:E:645:LYS:NZ	1:E:651:GLU:OE1	2.40	0.55
2:A:980:LEU:HB3	2:A:1342:SER:HB2	1.90	0.54
2:B:992:ASP:HB2	2:B:998:ARG:HB3	1.89	0.54
1:E:65:LYS:HE2	1:E:106:THR:HG21	1.89	0.54
2:A:1472:PRO:HB3	2:A:1492:HIS:HB2	1.89	0.54
2:A:777:LEU:HD22	2:A:786:SER:HB3	1.89	0.53
2:A:1267:SER:OG	2:A:1268:THR:N	2.41	0.53
2:A:1526:THR:O	2:A:1530:ARG:NH1	2.41	0.53
2:A:1551:LYS:HB2	2:A:1558:GLU:HB2	1.89	0.53
1:E:36:LEU:HB2	1:E:124:LEU:HG	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:872:CYS:HB3	2:B:900:VAL:HB	1.89	0.53
1:F:137:ILE:HG22	1:F:600:VAL:HG13	1.90	0.53
1:E:227:VAL:HG12	1:E:229:PRO:HD3	1.91	0.53
2:B:1350:LYS:HE2	2:B:1555:ASP:HB2	1.90	0.53
2:B:1471:GLN:NE2	2:B:1555:ASP:OD1	2.42	0.53
1:E:430:PRO:HD2	1:E:433:ARG:HD2	1.91	0.52
2:B:1472:PRO:HB3	2:B:1492:HIS:HB2	1.90	0.52
2:B:762:ARG:NH1	2:B:764:GLN:O	2.43	0.52
2:B:943:VAL:HG21	2:B:1259:ARG:HB2	1.91	0.52
2:B:1124:ILE:HG23	2:B:1399:MET:HG3	1.92	0.52
1:F:457:SER:HB3	1:F:472:ASN:HB2	1.91	0.51
1:F:81:GLY:O	1:F:503:ARG:NH1	2.44	0.51
2:A:845:GLU:HB2	2:A:1503:LEU:HD21	1.93	0.51
1:E:287:LEU:HD21	2:A:674:MET:HE2	1.93	0.51
2:B:1551:LYS:HB2	2:B:1558:GLU:HB2	1.93	0.50
1:F:362:PHE:HB2	1:F:629:SER:HB3	1.94	0.50
2:A:943:VAL:HG21	2:A:1259:ARG:HB2	1.93	0.50
1:F:168:THR:HB	1:F:199:ASN:HD22	1.76	0.50
2:A:777:LEU:HD21	2:A:788:LYS:HB2	1.94	0.49
1:E:81:GLY:O	1:E:503:ARG:NH1	2.45	0.49
2:A:1562:VAL:HG13	2:A:1577:LYS:HA	1.93	0.49
2:B:1421:SER:O	2:B:1426:ARG:NH2	2.42	0.49
1:F:237:PRO:HA	1:F:252:VAL:HA	1.95	0.49
2:B:1000:LYS:HA	2:B:1015:ILE:HD11	1.94	0.49
2:B:1202:GLU:HA	2:B:1206:LEU:HD12	1.95	0.49
2:A:929:LYS:NZ	2:A:1437:SER:O	2.46	0.49
2:A:1124:ILE:HG23	2:A:1399:MET:HG3	1.94	0.48
2:B:946:LEU:O	2:B:1339:GLY:N	2.46	0.48
1:E:105:VAL:HG13	1:E:122:ILE:HD13	1.94	0.48
2:A:945:THR:HG21	2:A:1253:ARG:HG2	1.95	0.48
2:B:995:ASP:HB3	2:B:998:ARG:HB2	1.95	0.48
1:E:237:PRO:HA	1:E:252:VAL:HA	1.97	0.47
1:F:197:LEU:HD11	2:B:1008:GLY:HA2	1.96	0.47
1:E:590:ARG:NH2	2:A:810:ASP:OD1	2.47	0.47
1:F:35:ARG:HH22	1:F:496:GLY:HA3	1.80	0.47
2:A:1042:GLN:HA	2:A:1045:LEU:HD12	1.95	0.47
2:B:1147:LEU:HD23	2:B:1194:ALA:HB1	1.96	0.47
1:F:134:ASP:HB3	1:F:145:LEU:HB2	1.97	0.47
1:F:172:ILE:HD13	2:B:1056:LEU:HD12	1.97	0.46
2:A:696:MET:HA	2:A:729:ILE:HD11	1.96	0.46
1:F:390:THR:HG23	1:F:407:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:390:THR:HG23	1:E:407:LEU:HD22	1.96	0.46
2:A:806:VAL:HG22	2:A:816:VAL:HG22	1.98	0.45
2:A:1127:GLU:OE2	2:A:1184:ARG:NH2	2.49	0.45
1:F:463:LEU:HD11	1:F:469:LEU:HD13	1.98	0.45
1:E:598:LYS:HE3	2:A:821:GLU:OE2	2.15	0.45
1:E:463:LEU:HD11	1:E:469:LEU:HD13	1.99	0.45
2:A:1599:HIS:ND1	2:A:1631:GLU:OE2	2.49	0.45
2:B:701:MET:SD	2:B:701:MET:N	2.89	0.45
1:F:492:ILE:HD12	1:F:500:LYS:HB3	1.98	0.45
1:E:600:VAL:HG22	2:A:765:PHE:CD1	2.51	0.45
2:A:1226:LEU:HD13	2:A:1267:SER:HB3	2.00	0.44
1:F:314:ARG:HD2	1:F:314:ARG:HA	1.73	0.44
2:A:1161:VAL:HG12	2:A:1163:SER:H	1.82	0.44
1:E:45:GLU:OE1	1:E:532:TYR:OH	2.31	0.44
2:A:1048:ILE:HB	2:A:1092:ILE:HG13	2.00	0.44
1:F:45:GLU:OE1	1:F:532:TYR:OH	2.31	0.44
2:A:678:MET:HE2	2:A:678:MET:HB3	1.92	0.44
2:A:780:ALA:HB1	2:A:784:GLY:HA2	1.99	0.44
2:A:995:ASP:HB3	2:A:998:ARG:HB2	2.00	0.44
2:B:806:VAL:HG22	2:B:816:VAL:HG22	1.99	0.44
2:B:1161:VAL:HG12	2:B:1163:SER:H	1.83	0.44
2:A:1224:GLN:O	2:A:1228:ASN:ND2	2.51	0.44
2:B:864:GLU:OE2	2:B:880:ARG:HD3	2.18	0.44
2:A:673:LEU:HD12	2:A:674:MET:HG3	1.98	0.44
2:A:1282:GLN:HG3	2:A:1288:HIS:HD2	1.82	0.44
1:E:147:ARG:HG2	1:E:189:THR:HA	2.00	0.44
1:E:134:ASP:HB3	1:E:145:LEU:HB2	2.00	0.43
2:A:1003:ILE:HG12	2:A:1268:THR:HG22	1.98	0.43
2:A:840:ARG:HD3	2:A:904:ILE:HG13	2.00	0.43
2:B:982:GLN:OE1	2:B:988:GLN:HB2	2.18	0.43
1:E:337:MET:HE1	2:A:754:ILE:HD12	2.01	0.43
2:A:835:PRO:HB3	2:A:1465:PHE:HZ	1.84	0.43
2:B:802:GLU:HG3	2:B:821:GLU:HG2	2.00	0.43
2:B:729:ILE:HA	2:B:732:LEU:HB3	2.01	0.43
2:A:694:ASP:HA	2:A:697:ARG:HG3	2.00	0.42
1:F:33:ILE:HG12	1:F:121:LEU:HD23	2.01	0.42
1:E:273:GLY:HA2	1:E:283:LEU:HG	2.01	0.42
2:A:777:LEU:HD23	2:A:777:LEU:HA	1.85	0.42
2:A:944:ARG:HB2	2:A:1341:LEU:HB3	2.01	0.42
1:E:231:PHE:HA	1:E:258:PHE:HA	2.01	0.42
1:E:406:LYS:HD2	1:E:460:ARG:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:701:MET:HE2	2:A:1458:SER:H	1.85	0.42
2:B:836:TYR:OH	2:B:1435:ARG:O	2.36	0.42
1:F:118:LYS:NZ	1:F:651:GLU:OE1	2.52	0.42
1:F:287:LEU:HD21	2:B:674:MET:HE2	2.02	0.42
2:B:1404:ILE:HG23	2:B:1475:VAL:HG22	2.00	0.42
2:A:1308:HIS:HB3	2:A:1319:ARG:HD3	2.01	0.42
2:B:1562:VAL:HG13	2:B:1577:LYS:HA	2.02	0.41
1:E:279:ARG:NH1	1:E:280:ARG:O	2.53	0.41
2:B:977:THR:HA	2:B:1345:THR:HA	2.02	0.41
2:B:1368:PRO:HA	2:B:1383:MET:HG2	2.01	0.41
1:E:242:TYR:HD2	1:E:347:ILE:HG23	1.85	0.41
1:E:525:PRO:HB3	1:E:615:TRP:HB3	2.02	0.41
2:A:872:CYS:HB3	2:A:900:VAL:HB	2.02	0.41
1:E:492:ILE:HD12	1:E:500:LYS:HB3	2.02	0.41
2:A:1003:ILE:HB	2:A:1015:ILE:HD12	2.02	0.41
1:E:243:TYR:HB2	1:E:246:ASP:HB2	2.03	0.41
2:A:825:MET:HE3	2:A:827:ASP:HA	2.02	0.41
2:B:1147:LEU:HD11	2:B:1198:LEU:HD11	2.02	0.41
2:A:833:ARG:HA	2:A:833:ARG:HD2	1.91	0.41
2:B:1507:ASP:HA	2:B:1510:ARG:HB3	2.02	0.41
1:E:276:ASP:HB3	1:E:279:ARG:HB3	2.03	0.41
1:E:310:VAL:HG12	1:E:312:PRO:HD2	2.03	0.41
1:E:362:PHE:HB2	1:E:629:SER:HB3	2.03	0.41
1:F:482:GLN:NE2	1:F:511:ASP:OD1	2.51	0.41
1:E:168:THR:HB	1:E:199:ASN:HD22	1.86	0.40
2:A:933:GLU:OE1	2:A:1585:HIS:NE2	2.47	0.40
2:B:840:ARG:HD3	2:B:904:ILE:HG13	2.02	0.40
2:B:1110:LYS:HA	2:B:1110:LYS:HD3	1.90	0.40
2:B:1227:TYR:CE2	2:B:1482:ASN:HB2	2.57	0.40
2:B:1512:ALA:HB1	2:B:1587:LYS:HE2	2.03	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	E	638/643 (99%)	615 (96%)	23 (4%)	0	100	100
1	F	637/643 (99%)	617 (97%)	20 (3%)	0	100	100
2	A	969/992 (98%)	925 (96%)	39 (4%)	5 (0%)	24	60
2	B	968/992 (98%)	933 (96%)	35 (4%)	0	100	100
All	All	3212/3270 (98%)	3090 (96%)	117 (4%)	5 (0%)	43	76

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	1350	LYS
2	A	759	ILE
2	A	1314	SER
2	A	855	GLU
2	A	1399	MET

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	E	564/566 (100%)	562 (100%)	2 (0%)	84	90
1	F	563/566 (100%)	562 (100%)	1 (0%)	87	92
2	A	861/877 (98%)	860 (100%)	1 (0%)	88	93
2	B	860/877 (98%)	859 (100%)	1 (0%)	88	93
All	All	2848/2886 (99%)	2843 (100%)	5 (0%)	87	92

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	557	CYS
1	E	660	CYS
2	A	1012	GLN

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Mol	Chain	Res	Type
1	F	660	CYS
2	B	1012	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	71	ASN
1	E	73	ASN
1	E	215	GLN
1	E	578	GLN
1	E	604	ASN
2	A	672	GLN
2	A	1025	HIS
2	A	1042	GLN
2	A	1090	ASN
2	A	1178	HIS
2	A	1224	GLN
2	A	1288	HIS
2	A	1308	HIS
2	A	1395	GLN
2	A	1471	GLN
2	A	1505	HIS
2	A	1515	ASN
2	A	1653	ASN
1	F	71	ASN
1	F	75	GLN
1	F	215	GLN
1	F	385	HIS
1	F	445	ASN
1	F	455	HIS
1	F	474	HIS
1	F	572	HIS
2	B	683	GLN
2	B	764	GLN
2	B	969	GLN
2	B	988	GLN
2	B	1032	GLN
2	B	1090	ASN
2	B	1118	GLN
2	B	1151	HIS
2	B	1177	ASN
2	B	1282	GLN

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Mol	Chain	Res	Type
2	B	1308	HIS
2	B	1377	GLN
2	B	1434	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 ⓘ

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$
3	NAG	C	1	2,3	14,14,15	0.35	0	17,19,21	0.95	1 (5%)
3	NAG	C	2	3	14,14,15	0.35	0	17,19,21	0.85	1 (5%)
3	BMA	C	3	3	11,11,12	1.14	1 (9%)	15,15,17	0.95	1 (6%)
3	NAG	D	1	2,3	14,14,15	0.38	0	17,19,21	0.93	0
3	NAG	D	2	3	14,14,15	0.71	1 (7%)	17,19,21	0.65	0
3	BMA	D	3	3	11,11,12	1.11	1 (9%)	15,15,17	1.03	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	1	2,3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	NAG	D	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	3	BMA	C2-C3	2.31	1.56	1.52
3	D	3	BMA	C2-C3	2.20	1.55	1.52
3	D	2	NAG	O5-C1	2.13	1.47	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3	BMA	C1-O5-C5	2.99	116.19	112.19
3	C	2	NAG	C1-O5-C5	2.95	116.14	112.19
3	C	1	NAG	O4-C4-C5	-2.66	102.78	109.32
3	C	3	BMA	C1-O5-C5	2.60	115.67	112.19

There are no chirality outliers.

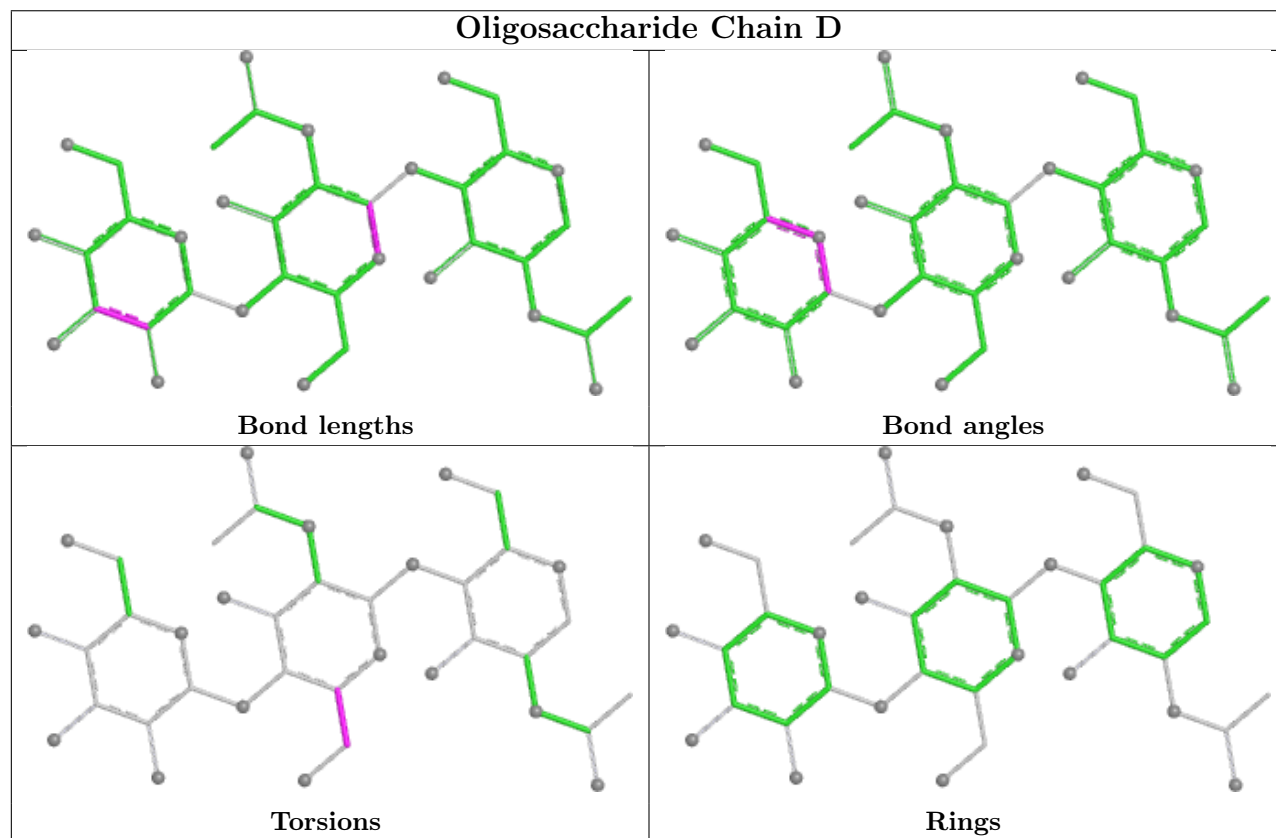
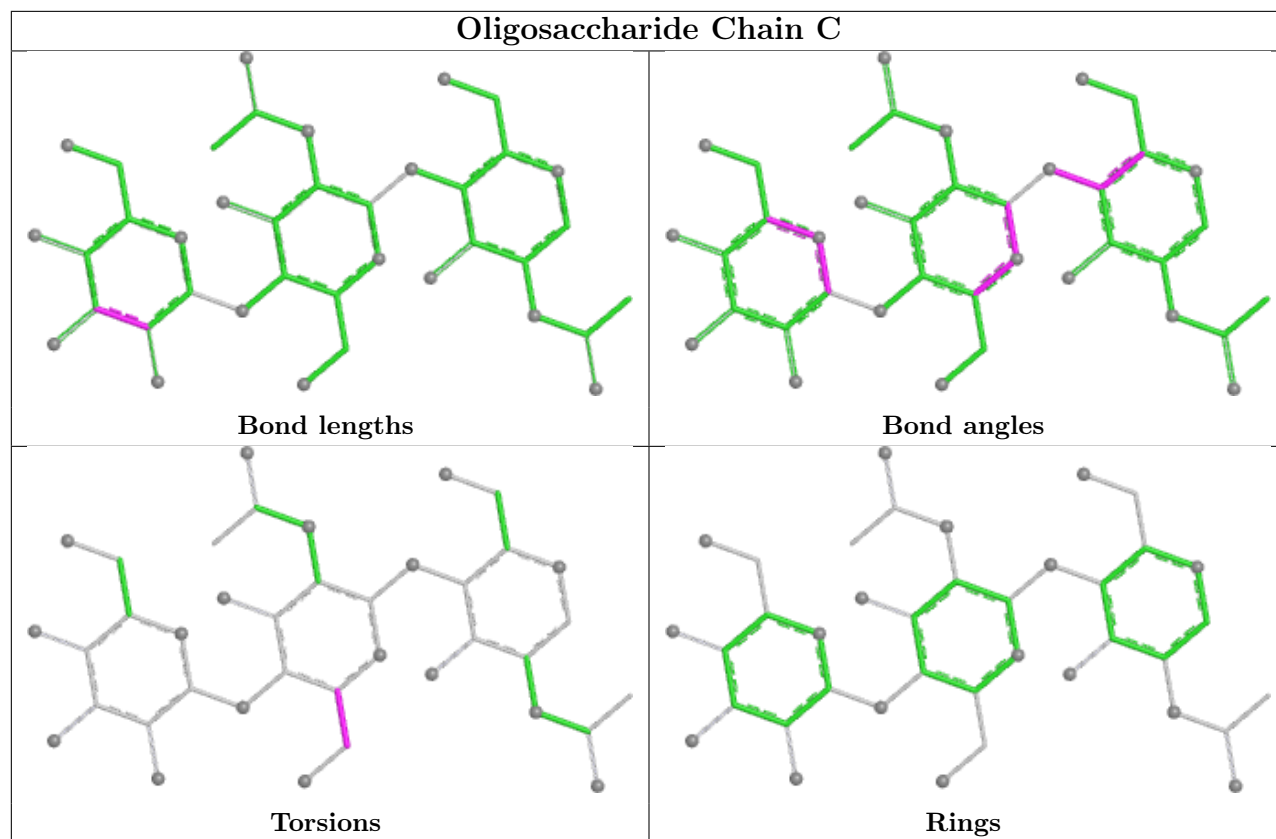
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	2	NAG	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](#)

There are no ligands in this entry.

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	E	640/643 (99%)	0.73	55 (8%)	16 8	68, 146, 198, 230	0
1	F	639/643 (99%)	0.44	21 (3%)	49 28	61, 129, 165, 205	0
2	A	975/992 (98%)	0.27	51 (5%)	33 17	35, 80, 168, 214	0
2	B	974/992 (98%)	0.24	35 (3%)	46 26	28, 76, 192, 248	0
All	All	3228/3270 (98%)	0.39	162 (5%)	34 18	28, 110, 187, 248	0

All (162) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1353	GLY	5.7
2	A	1354	LYS	5.1
2	B	1500	LEU	5.1
1	E	256	ALA	5.0
2	A	1498	GLY	5.0
2	A	1555	ASP	4.7
2	A	1223	ASN	4.5
1	E	288	THR	4.4
2	A	1556	PHE	4.3
2	B	827	ASP	4.2
2	A	1500	LEU	4.1
1	E	362	PHE	4.1
2	A	752	ASP	4.1
1	E	336	ASP	4.0
1	E	305	VAL	3.9
2	B	1497	ASP	3.9
2	A	673	LEU	3.9
1	E	27	SER	3.9
1	E	255	ILE	3.9
1	E	358	LYS	3.9
2	A	919	PHE	3.9

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Mol	Chain	Res	Type	RSRZ
2	B	1628	LEU	3.8
2	B	1465	PHE	3.7
1	E	349	THR	3.6
2	A	853	TYR	3.6
1	E	306	LEU	3.6
2	A	750	ASP	3.6
2	B	1555	ASP	3.6
2	A	1655	VAL	3.5
1	E	335	SER	3.5
2	A	1497	ASP	3.5
1	E	312	PRO	3.5
2	A	1465	PHE	3.4
1	E	372	MET	3.4
2	A	917	ASN	3.4
2	B	920	ILE	3.3
2	A	755	PRO	3.3
1	F	312	PRO	3.2
1	E	301	LEU	3.2
2	A	1515	ASN	3.2
2	A	860	LYS	3.2
2	B	1495	LYS	3.1
2	B	972	ASP	3.1
1	F	361	LYS	3.1
1	F	483	ALA	3.0
2	B	1351	LEU	3.0
2	A	933	GLU	3.0
2	A	1499	MET	3.0
2	A	1616	ILE	3.0
2	A	972	ASP	3.0
1	E	153	HIS	3.0
1	F	395	VAL	3.0
2	B	1355	VAL	3.0
2	A	1353	GLY	3.0
2	B	1499	MET	3.0
1	E	310	VAL	3.0
1	E	269	PHE	3.0
1	F	534	THR	3.0
2	B	921	SER	2.9
1	E	395	VAL	2.9
1	F	24	PRO	2.9
2	A	757	GLU	2.9
1	E	360	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	F	335	SER	2.9
2	A	754	ILE	2.8
1	E	282	SER	2.8
1	E	102	HIS	2.8
1	E	24	PRO	2.8
2	B	1655	VAL	2.8
1	E	126	SER	2.8
1	E	228	LEU	2.8
1	E	629	SER	2.8
2	B	1501	SER	2.8
1	F	358	LYS	2.7
1	F	662	GLN	2.7
1	F	41	THR	2.7
2	A	881	HIS	2.7
2	B	1223	ASN	2.7
2	A	934	GLY	2.7
1	E	361	LYS	2.7
1	F	102	HIS	2.7
1	F	285	HIS	2.7
1	E	254	ILE	2.7
1	F	259	LEU	2.7
2	A	1351	LEU	2.7
1	E	259	LEU	2.6
1	F	27	SER	2.6
1	E	327	ALA	2.6
2	A	742	LEU	2.6
1	E	334	GLY	2.6
2	A	916	TYR	2.6
2	A	1355	VAL	2.6
1	F	336	ASP	2.6
1	E	505	TYR	2.5
2	A	1131	GLY	2.5
2	B	1515	ASN	2.5
1	E	333	SER	2.5
2	B	1498	GLY	2.5
2	B	1553	GLU	2.5
1	F	479	PRO	2.5
1	E	124	LEU	2.5
2	B	1656	VAL	2.5
1	E	229	PRO	2.5
1	E	26	TYR	2.5
1	E	408	SER	2.4

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Mol	Chain	Res	Type	RSRZ
2	A	1513	GLU	2.4
2	B	992	ASP	2.4
2	A	1608	ASP	2.4
2	A	1463	GLN	2.4
1	E	230	SER	2.4
1	E	633	TYR	2.3
2	B	1608	ASP	2.3
1	E	534	THR	2.3
2	A	829	PHE	2.3
2	B	1531	LEU	2.3
1	E	348	VAL	2.3
1	E	357	THR	2.3
1	E	271	ILE	2.3
2	A	1494	ASP	2.3
1	F	602	VAL	2.3
1	E	436	THR	2.3
2	A	918	HIS	2.3
2	B	734	GLN	2.3
2	B	1374	LYS	2.3
2	A	1554	ASP	2.3
1	E	130	PHE	2.2
2	A	734	GLN	2.2
2	A	883	GLN	2.2
1	F	154	LYS	2.2
2	A	1438	ASN	2.2
1	E	122	ILE	2.2
2	A	1553	GLU	2.2
2	B	1650	PHE	2.2
2	B	1356	SER	2.2
1	F	500	LYS	2.2
2	A	828	PHE	2.2
1	E	274	VAL	2.1
1	E	614	ILE	2.1
2	A	863	VAL	2.1
2	A	1651	THR	2.1
2	B	673	LEU	2.1
2	B	1357	CYS	2.1
2	B	1625	TRP	2.1
1	E	644	LEU	2.1
1	E	319	VAL	2.1
2	B	1602	VAL	2.1
2	A	1619	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	368	PRO	2.1
1	E	302	LYS	2.0
1	F	333	SER	2.0
1	E	292	ILE	2.0
2	A	938	ASN	2.0
1	E	128	TYR	2.0
2	B	843	GLN	2.0
2	B	1590	GLU	2.0
1	E	548	SER	2.0
1	E	483	ALA	2.0
1	F	447	GLN	2.0
2	A	843	GLN	2.0
2	B	1537	PRO	2.0
2	A	854	ARG	2.0
2	A	1602	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

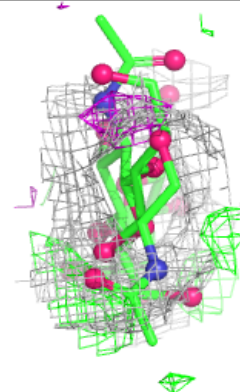
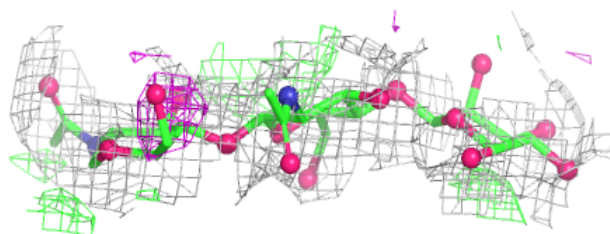
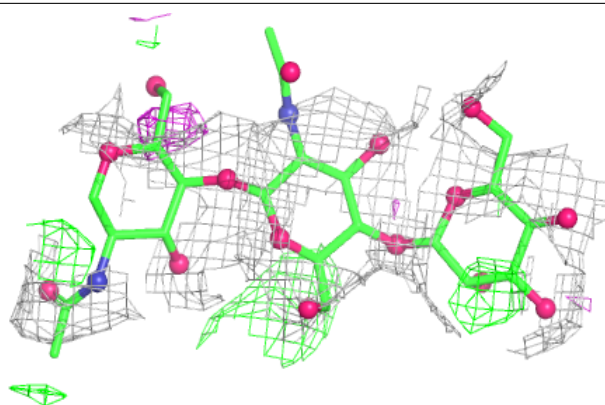
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	C	1	14/15	-	-	87,123,149,149	0
3	NAG	C	2	14/15	-	-	135,157,175,179	0
3	BMA	C	3	11/12	-	-	127,149,168,170	0
3	NAG	D	1	14/15	-	-	86,105,122,134	0
3	NAG	D	2	14/15	-	-	99,131,153,153	0
3	BMA	D	3	11/12	-	-	103,137,148,152	0

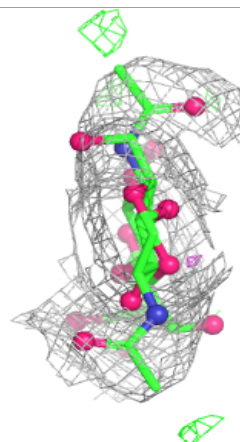
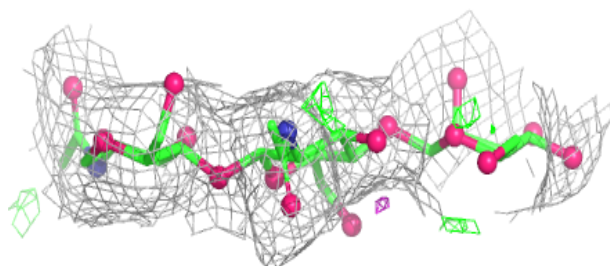
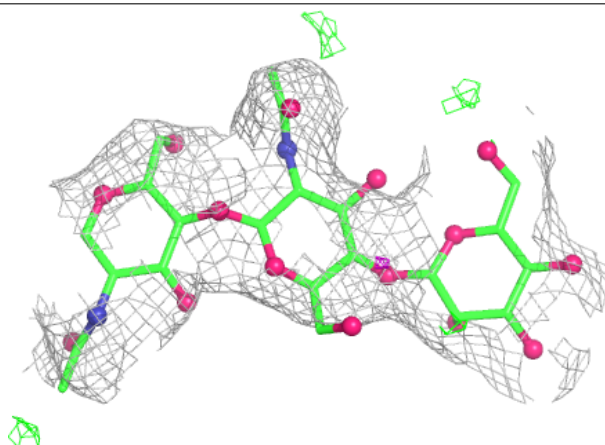
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

**Electron density around Chain D:**

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



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.