



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 10, 2021 – 10:22 AM EDT

PDB ID : 6XDJ
Title : Crystal Structure Analysis of MBP-SIN3
Authors : Seo, H.-S.; Dhe-Paganon, S.
Deposited on : 2020-06-10
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.20
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.20

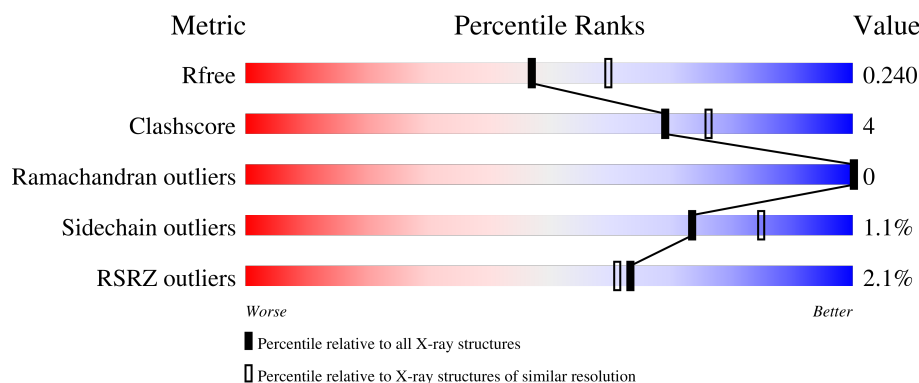
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	443	<div> <div></div> <div>91%9%</div> </div>
1	B	443	<div> <div></div> <div>90%9%</div> </div>
1	C	443	<div> <div>4%</div> <div>80%7%13%</div> </div>
1	D	443	<div> <div></div> <div>74%9%16%</div> </div>
2	E	3	<div> <div></div> <div>33%33%33%</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	3	 100%
2	H	3	 33%67%
3	F	2	 100%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13335 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 Maltodextrin-binding protein, Transcriptional regulatory protein SIN3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	0	0
			3410	2203	556	645	6			
1	B	438	Total	C	N	O	S	0	0	0
			3356	2175	545	629	7			
1	C	386	Total	C	N	O	S	0	0	0
			2908	1871	477	554	6			
1	D	371	Total	C	N	O	S	0	0	0
			2834	1827	462	539	6			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A4P1LXE0
A	83	ALA	ASP	conflict	UNP A0A4P1LXE0
A	84	ALA	LYS	conflict	UNP A0A4P1LXE0
A	173	ALA	GLU	conflict	UNP A0A4P1LXE0
A	174	ALA	ASN	conflict	UNP A0A4P1LXE0
A	240	ALA	LYS	conflict	UNP A0A4P1LXE0
A	360	ALA	-	linker	UNP A0A4P1LXE0
A	361	ALA	-	linker	UNP A0A4P1LXE0
A	362	LEU	-	linker	UNP A0A4P1LXE0
A	363	ALA	-	linker	UNP A0A4P1LXE0
A	364	ALA	-	linker	UNP A0A4P1LXE0
A	365	ALA	-	linker	UNP A0A4P1LXE0
A	366	GLN	-	linker	UNP A0A4P1LXE0
A	367	THR	-	linker	UNP A0A4P1LXE0
A	368	ASN	-	linker	UNP A0A4P1LXE0
A	369	ALA	-	linker	UNP A0A4P1LXE0
A	370	ALA	-	linker	UNP A0A4P1LXE0
A	371	ALA	-	linker	UNP A0A4P1LXE0
B	1	MET	-	initiating methionine	UNP A0A4P1LXE0
B	83	ALA	ASP	conflict	UNP A0A4P1LXE0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	84	ALA	LYS	conflict	UNP A0A4P1LXE0
B	173	ALA	GLU	conflict	UNP A0A4P1LXE0
B	174	ALA	ASN	conflict	UNP A0A4P1LXE0
B	240	ALA	LYS	conflict	UNP A0A4P1LXE0
B	360	ALA	-	linker	UNP A0A4P1LXE0
B	361	ALA	-	linker	UNP A0A4P1LXE0
B	362	LEU	-	linker	UNP A0A4P1LXE0
B	363	ALA	-	linker	UNP A0A4P1LXE0
B	364	ALA	-	linker	UNP A0A4P1LXE0
B	365	ALA	-	linker	UNP A0A4P1LXE0
B	366	GLN	-	linker	UNP A0A4P1LXE0
B	367	THR	-	linker	UNP A0A4P1LXE0
B	368	ASN	-	linker	UNP A0A4P1LXE0
B	369	ALA	-	linker	UNP A0A4P1LXE0
B	370	ALA	-	linker	UNP A0A4P1LXE0
B	371	ALA	-	linker	UNP A0A4P1LXE0
C	1	MET	-	initiating methionine	UNP A0A4P1LXE0
C	83	ALA	ASP	conflict	UNP A0A4P1LXE0
C	84	ALA	LYS	conflict	UNP A0A4P1LXE0
C	173	ALA	GLU	conflict	UNP A0A4P1LXE0
C	174	ALA	ASN	conflict	UNP A0A4P1LXE0
C	240	ALA	LYS	conflict	UNP A0A4P1LXE0
C	360	ALA	-	linker	UNP A0A4P1LXE0
C	361	ALA	-	linker	UNP A0A4P1LXE0
C	362	LEU	-	linker	UNP A0A4P1LXE0
C	363	ALA	-	linker	UNP A0A4P1LXE0
C	364	ALA	-	linker	UNP A0A4P1LXE0
C	365	ALA	-	linker	UNP A0A4P1LXE0
C	366	GLN	-	linker	UNP A0A4P1LXE0
C	367	THR	-	linker	UNP A0A4P1LXE0
C	368	ASN	-	linker	UNP A0A4P1LXE0
C	369	ALA	-	linker	UNP A0A4P1LXE0
C	370	ALA	-	linker	UNP A0A4P1LXE0
C	371	ALA	-	linker	UNP A0A4P1LXE0
D	1	MET	-	initiating methionine	UNP A0A4P1LXE0
D	83	ALA	ASP	conflict	UNP A0A4P1LXE0
D	84	ALA	LYS	conflict	UNP A0A4P1LXE0
D	173	ALA	GLU	conflict	UNP A0A4P1LXE0
D	174	ALA	ASN	conflict	UNP A0A4P1LXE0
D	240	ALA	LYS	conflict	UNP A0A4P1LXE0
D	360	ALA	-	linker	UNP A0A4P1LXE0
D	361	ALA	-	linker	UNP A0A4P1LXE0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	362	LEU	-	linker	UNP A0A4P1LXE0
D	363	ALA	-	linker	UNP A0A4P1LXE0
D	364	ALA	-	linker	UNP A0A4P1LXE0
D	365	ALA	-	linker	UNP A0A4P1LXE0
D	366	GLN	-	linker	UNP A0A4P1LXE0
D	367	THR	-	linker	UNP A0A4P1LXE0
D	368	ASN	-	linker	UNP A0A4P1LXE0
D	369	ALA	-	linker	UNP A0A4P1LXE0
D	370	ALA	-	linker	UNP A0A4P1LXE0
D	371	ALA	-	linker	UNP A0A4P1LXE0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	3	Total	C	O	0	0	0
			34	18	16			
2	G	3	Total	C	O	0	0	0
			34	18	16			
2	H	3	Total	C	O	0	0	0
			34	18	16			

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	F	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	200	Total	O	0	0
			200	200		

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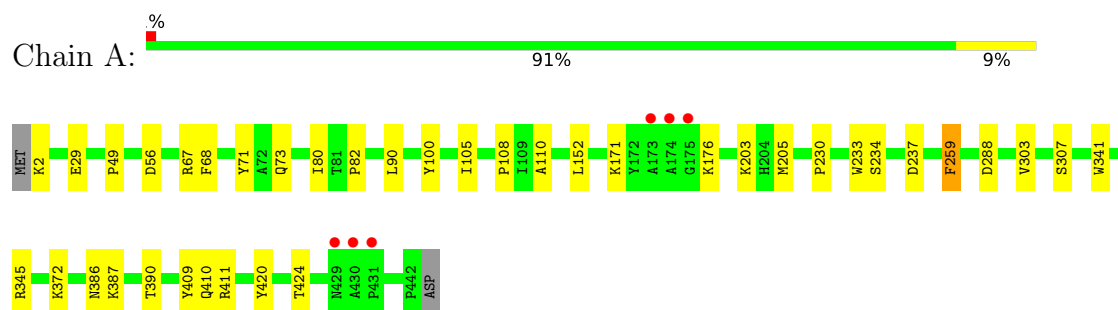
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	204	Total 204	O 204	0	0
4	C	119	Total 119	O 119	0	0
4	D	179	Total 179	O 179	0	0

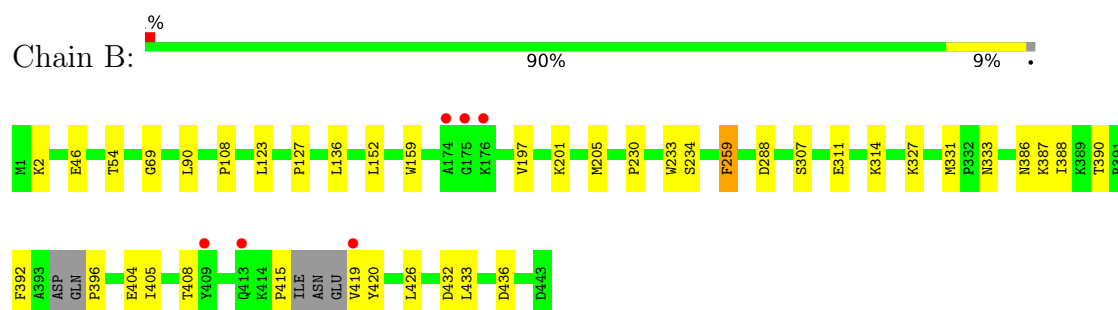
3 Residue-property plots [i](#)

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.

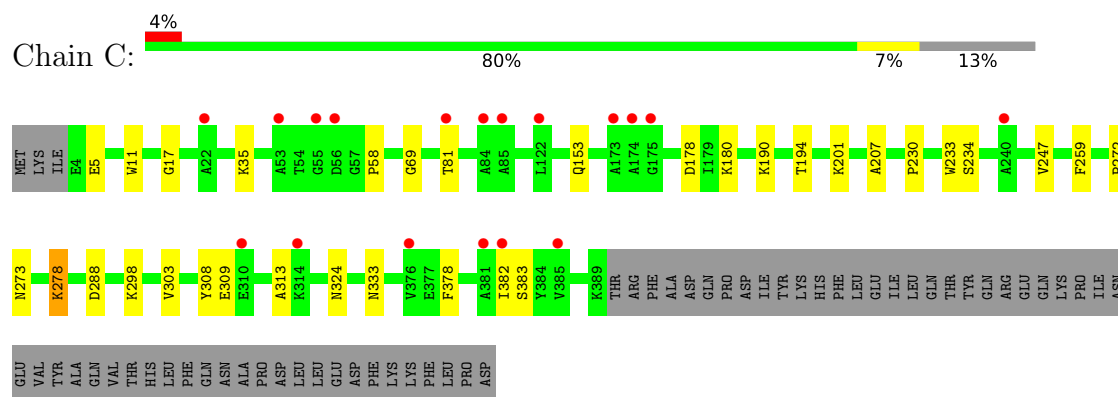
- Molecule 1: Maltodextrin-binding protein, Transcriptional regulatory protein SIN3



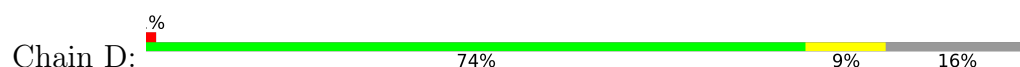
- Molecule 1: Maltodextrin-binding protein, Transcriptional regulatory protein SIN3



- Molecule 1: Maltodextrin-binding protein, Transcriptional regulatory protein SIN3



- Molecule 1: Maltodextrin-binding protein, Transcriptional regulatory protein SIN3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.73Å 144.86Å 97.09Å 90.00° 107.97° 90.00°	Depositor
Resolution (Å)	75.84 – 2.20 75.84 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.1 (75.84-2.20) 99.1 (75.84-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.206 , 0.240 0.206 , 0.240	Depositor DCC
R_{free} test set	5335 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13335	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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: BGC, GLC

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	0.28	0/3495	0.42	0/4755
1	B	0.29	0/3438	0.43	0/4676
1	C	0.27	0/2977	0.43	0/4053
1	D	0.28	0/2902	0.44	0/3947
All	All	0.28	0/12812	0.43	0/17431

There are no bond length outliers.

There are no bond angle outliers.

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	3410	0	3346	24	0
1	B	3356	0	3297	26	0
1	C	2908	0	2837	18	0
1	D	2834	0	2796	26	0
2	E	34	0	30	2	0
2	G	34	0	30	0	0
2	H	34	0	30	2	0
3	F	23	0	21	0	0
4	A	200	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	204	0	0	4	0
4	C	119	0	0	1	0
4	D	179	0	0	5	0
All	All	13335	0	12387	93	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 4.

All (93) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:LYS:NZ	4:A:601:HOH:O	1.93	1.01
1:D:185:ASP:OD1	4:D:601:HOH:O	2.05	0.75
1:C:81:THR:H	1:C:278:LYS:HZ1	1.35	0.74
1:A:29:GLU:OE1	4:A:602:HOH:O	2.06	0.72
1:D:81:THR:OG1	4:D:602:HOH:O	2.08	0.72
1:A:80:ILE:HG22	1:A:82:PRO:HD3	1.76	0.68
1:C:178:ASP:OD2	4:C:601:HOH:O	2.12	0.67
1:A:237:ASP:OD2	4:A:603:HOH:O	2.13	0.66
1:B:54:THR:OG1	4:B:602:HOH:O	2.12	0.66
1:C:190:LYS:O	1:C:194:THR:HG23	1.99	0.63
1:A:2:LYS:N	1:A:56:ASP:OD1	2.33	0.61
1:D:80:ILE:HG22	1:D:82:PRO:HD3	1.83	0.60
1:A:288:ASP:OD1	1:A:307:SER:OG	2.19	0.60
1:A:171:LYS:NZ	4:A:608:HOH:O	2.34	0.60
1:C:178:ASP:OD1	1:C:180:LYS:HE2	2.01	0.59
1:B:152:LEU:HD11	1:B:205:MET:HE3	1.85	0.58
1:B:386:ASN:O	1:B:390:THR:HG23	2.03	0.58
1:B:90:LEU:HD23	1:B:108:PRO:HG2	1.87	0.57
1:D:11:TRP:O	1:D:62:PHE:HB2	2.05	0.57
1:D:127:PRO:HB3	1:D:132:GLU:HG3	1.85	0.56
1:B:123:LEU:HD11	1:B:136:LEU:HD21	1.88	0.55
1:D:123:LEU:HD21	1:D:127:PRO:HD3	1.88	0.55
1:D:67:ARG:HD3	2:H:3:GLC:O2	2.07	0.55
1:D:42:ASP:O	1:D:47:LYS:NZ	2.33	0.54
1:B:388:ILE:HG12	1:B:433:LEU:HD13	1.89	0.54
1:A:67:ARG:HD3	2:E:3:GLC:O2	2.08	0.53
1:D:292:GLU:HG2	1:D:296:LYS:HD2	1.88	0.53
1:D:194:THR:HG23	1:D:358:VAL:HG11	1.90	0.53
1:D:63:TRP:HB3	1:D:68:PHE:HE1	1.73	0.52
1:A:90:LEU:HD23	1:A:108:PRO:HG2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:GLY:HA2	1:C:298:LYS:HD3	1.91	0.52
1:C:153:GLN:NE2	1:C:207:ALA:O	2.38	0.52
1:D:275:GLU:OE1	4:D:603:HOH:O	2.19	0.51
1:B:288:ASP:OD1	1:B:307:SER:OG	2.27	0.51
1:A:410:GLN:NE2	4:A:610:HOH:O	2.44	0.49
1:B:230:PRO:HA	1:B:233:TRP:CE2	2.48	0.49
1:C:230:PRO:HA	1:C:233:TRP:CE2	2.47	0.49
1:D:122:LEU:HD11	1:D:145:LYS:HD2	1.94	0.49
1:D:69:GLY:HA3	1:D:333:ASN:O	2.13	0.48
1:B:392:PHE:O	1:B:396:PRO:HA	2.14	0.48
1:C:81:THR:N	1:C:278:LYS:HZ1	2.07	0.47
1:B:2:LYS:HA	1:B:2:LYS:HD2	1.68	0.47
1:B:259:PHE:HB3	1:B:331:MET:HG3	1.96	0.47
1:B:415:PRO:HB2	4:B:608:HOH:O	2.14	0.47
1:C:5:GLU:C	1:C:273:ASN:HD21	2.17	0.47
1:B:311:GLU:HA	1:B:314:LYS:HE2	1.97	0.46
1:A:49:PRO:HG3	1:A:71:TYR:CE1	2.50	0.46
1:D:62:PHE:HA	1:D:264:SER:O	2.14	0.46
1:A:345:ARG:NH1	2:E:3:GLC:H62	2.30	0.46
1:B:419:VAL:HG12	1:B:420:TYR:H	1.81	0.46
1:B:404:GLU:O	1:B:408:THR:HG23	2.16	0.46
1:D:234:SER:HB3	1:D:299:PRO:HD3	1.98	0.45
1:C:309:GLU:O	1:C:313:ALA:N	2.41	0.45
1:A:73:GLN:OE1	1:A:100:TYR:OH	2.19	0.45
1:A:409:TYR:OH	4:A:604:HOH:O	2.19	0.45
1:A:152:LEU:HD11	1:A:205:MET:HE3	1.99	0.45
1:A:411:ARG:HD2	1:B:46:GLU:OE2	2.16	0.45
1:A:387:LYS:O	1:A:390:THR:OG1	2.23	0.44
1:C:11:TRP:HB2	1:C:58:PRO:HG3	1.99	0.44
1:D:67:ARG:HD2	4:D:689:HOH:O	2.17	0.44
1:A:68:PHE:HB3	1:A:105:ILE:CD1	2.48	0.44
1:A:230:PRO:HA	1:A:233:TRP:CE2	2.52	0.44
1:D:49:PRO:HG3	1:D:71:TYR:CE1	2.52	0.44
1:D:160:PRO:HG3	1:D:258:PRO:HA	2.00	0.44
1:A:259:PHE:HD1	1:A:341:TRP:CH2	2.36	0.44
1:A:386:ASN:O	1:A:390:THR:HG23	2.18	0.43
1:A:110:ALA:HA	1:A:303:VAL:HA	2.01	0.43
1:B:432:ASP:OD2	1:B:432:ASP:N	2.50	0.43
1:D:342:TYR:CE1	2:H:3:GLC:H4	2.53	0.43
1:B:387:LYS:NZ	1:B:436:ASP:OD2	2.43	0.43
1:B:159:TRP:NE1	1:B:259:PHE:CE2	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:201:LYS:HA	1:C:201:LYS:HD3	1.89	0.43
1:D:230:PRO:HA	1:D:233:TRP:CE2	2.54	0.43
1:A:68:PHE:HB3	1:A:105:ILE:HD13	2.01	0.43
1:B:405:ILE:HD12	1:B:426:LEU:HD22	2.00	0.43
1:B:201:LYS:NZ	4:B:618:HOH:O	2.50	0.43
1:C:5:GLU:HA	1:C:272:PRO:HG2	2.01	0.42
1:C:35:LYS:HB3	1:C:35:LYS:HE2	1.82	0.42
1:C:247:VAL:HA	1:C:324:ASN:HD21	1.84	0.42
1:C:69:GLY:HA3	1:C:333:ASN:O	2.19	0.42
1:D:210:ASP:HB2	4:D:733:HOH:O	2.20	0.42
1:C:378:PHE:O	1:C:382:ILE:HG13	2.19	0.42
1:B:127:PRO:HG3	1:B:136:LEU:HD22	2.01	0.42
1:B:197:VAL:HG12	1:B:201:LYS:HE2	2.01	0.42
1:D:159:TRP:NE1	1:D:259:PHE:CE2	2.88	0.42
1:D:251:PHE:CZ	1:D:252:LYS:HE2	2.55	0.41
1:A:420:TYR:O	1:A:424:THR:HG23	2.20	0.41
1:D:357:THR:HG23	1:D:360:ALA:H	1.85	0.41
1:C:303:VAL:HG21	1:C:308:TYR:HB3	2.01	0.41
1:D:8:LEU:HD23	1:D:8:LEU:HA	1.95	0.41
1:B:69:GLY:HA3	1:B:333:ASN:O	2.21	0.41
1:B:159:TRP:CE2	1:B:259:PHE:CE2	3.09	0.41
1:B:327:LYS:NZ	4:B:612:HOH:O	2.47	0.41

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	439/443 (99%)	433 (99%)	6 (1%)	0	100	100
1	B	432/443 (98%)	423 (98%)	9 (2%)	0	100	100
1	C	384/443 (87%)	378 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	367/443 (83%)	358 (98%)	9 (2%)	0	100	100
All	All	1622/1772 (92%)	1592 (98%)	30 (2%)	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	345/355 (97%)	341 (99%)	4 (1%)	71	83
1	B	336/355 (95%)	334 (99%)	2 (1%)	86	93
1	C	286/355 (81%)	281 (98%)	5 (2%)	60	74
1	D	284/355 (80%)	281 (99%)	3 (1%)	73	85
All	All	1251/1420 (88%)	1237 (99%)	14 (1%)	73	85

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	203	LYS
1	A	234	SER
1	A	259	PHE
1	A	372	LYS
1	B	234	SER
1	B	259	PHE
1	C	234	SER
1	C	259	PHE
1	C	278	LYS
1	C	288	ASP
1	C	383	SER
1	D	128	LYS
1	D	171	LYS
1	D	259	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such

sidechains are listed below:

Mol	Chain	Res	Type
1	C	235	ASN
1	C	273	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 ⓘ

11 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	BGC	E	1	2	12,12,12	0.44	0	17,17,17	1.02	1 (5%)
2	GLC	E	2	2	11,11,12	0.29	0	15,15,17	0.87	0
2	GLC	E	3	2	11,11,12	0.27	0	15,15,17	0.90	1 (6%)
3	GLC	F	1	3	12,12,12	0.48	0	17,17,17	0.73	0
3	GLC	F	2	3	11,11,12	0.46	0	15,15,17	0.96	0
2	BGC	G	1	2	12,12,12	0.43	0	17,17,17	0.97	0
2	GLC	G	2	2	11,11,12	0.29	0	15,15,17	0.85	0
2	GLC	G	3	2	11,11,12	0.22	0	15,15,17	0.83	0
2	BGC	H	1	2	12,12,12	0.41	0	17,17,17	0.99	1 (5%)
2	GLC	H	2	2	11,11,12	0.29	0	15,15,17	0.77	0
2	GLC	H	3	2	11,11,12	0.18	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	BGC	E	1	2	-	1/2/22/22	0/1/1/1
2	GLC	E	2	2	-	0/2/19/22	0/1/1/1
2	GLC	E	3	2	-	0/2/19/22	0/1/1/1
3	GLC	F	1	3	-	0/2/22/22	0/1/1/1
3	GLC	F	2	3	-	0/2/19/22	0/1/1/1
2	BGC	G	1	2	-	0/2/22/22	0/1/1/1
2	GLC	G	2	2	-	0/2/19/22	0/1/1/1
2	GLC	G	3	2	-	0/2/19/22	0/1/1/1
2	BGC	H	1	2	-	1/2/22/22	0/1/1/1
2	GLC	H	2	2	-	0/2/19/22	0/1/1/1
2	GLC	H	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	BGC	O5-C1-C2	-2.58	105.68	110.28
2	E	3	GLC	C1-O5-C5	2.33	115.34	112.19
2	H	1	BGC	O5-C1-C2	-2.13	106.49	110.28

There are no chirality outliers.

All (2) torsion outliers are listed below:

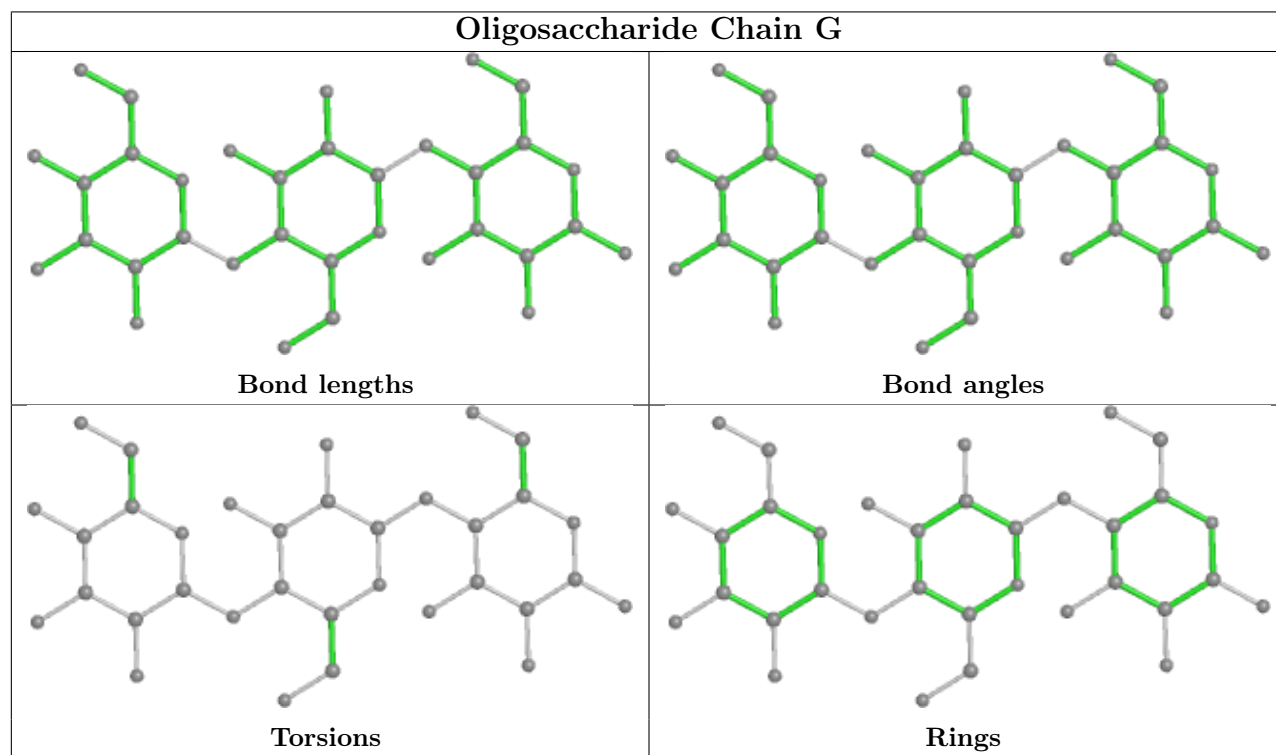
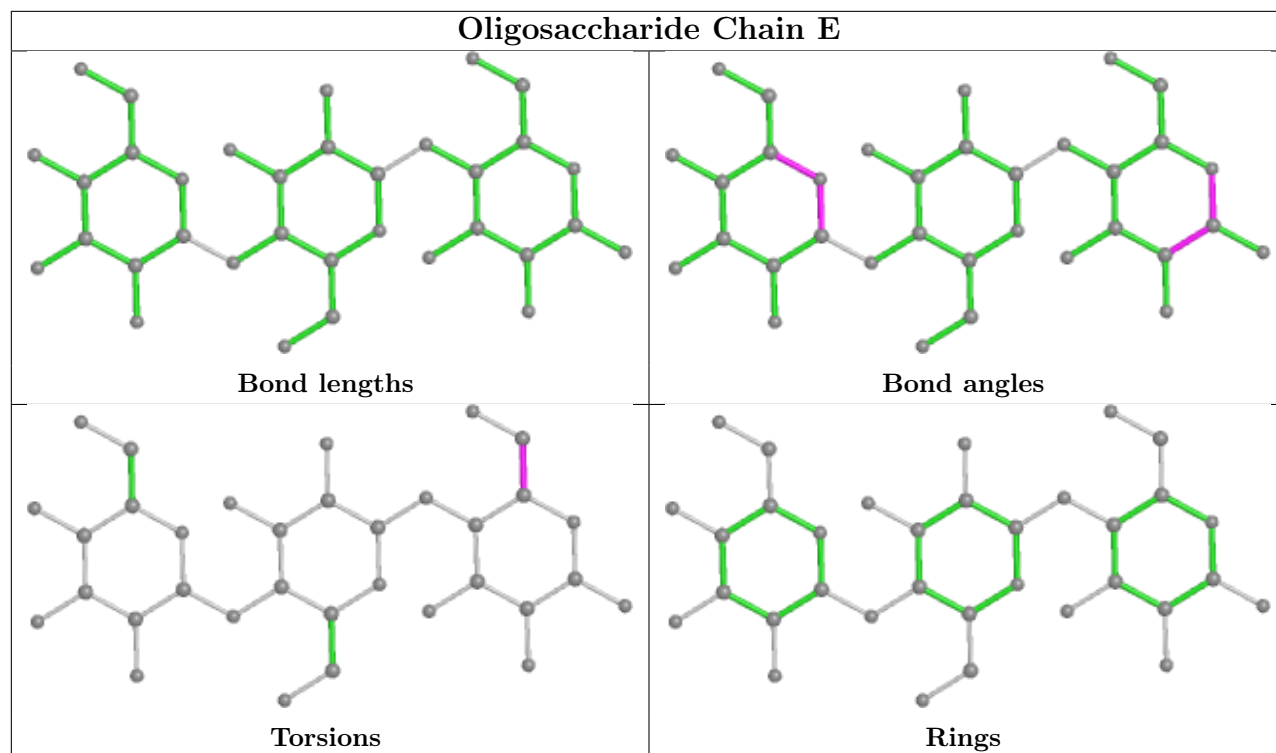
Mol	Chain	Res	Type	Atoms
2	E	1	BGC	C4-C5-C6-O6
2	H	1	BGC	C4-C5-C6-O6

There are no ring outliers.

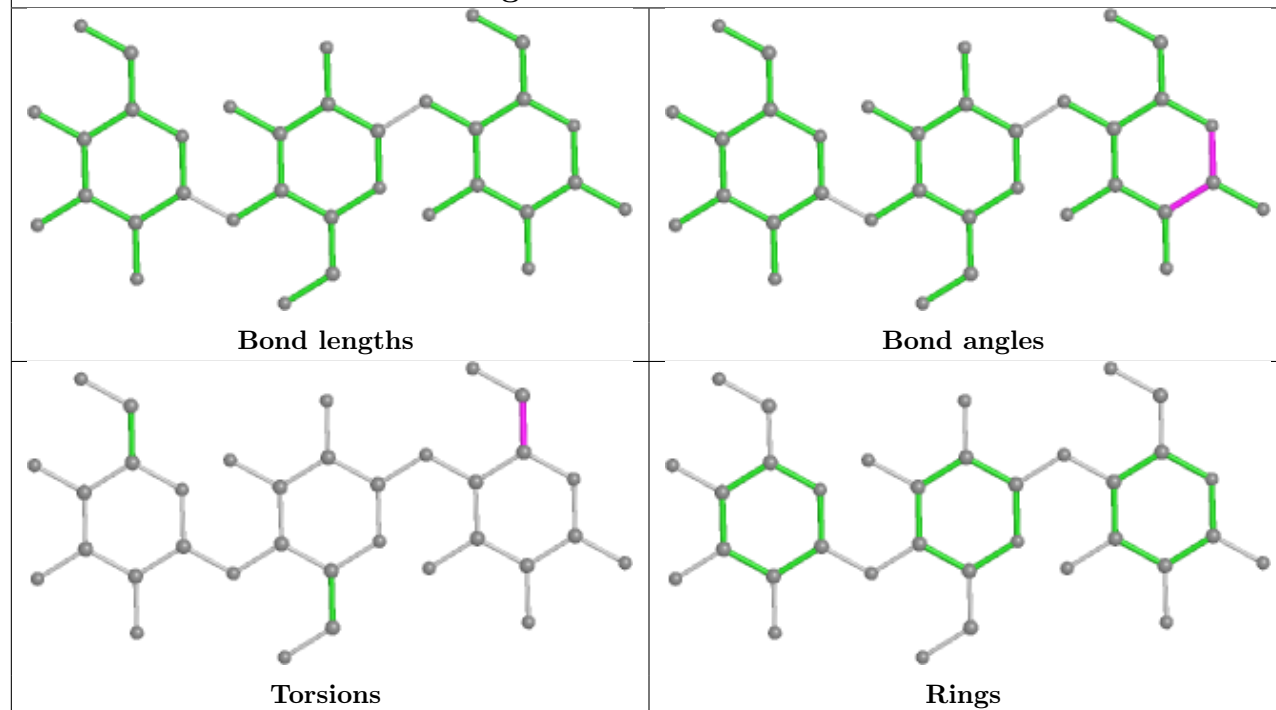
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	3	GLC	2	0
2	H	3	GLC	2	0

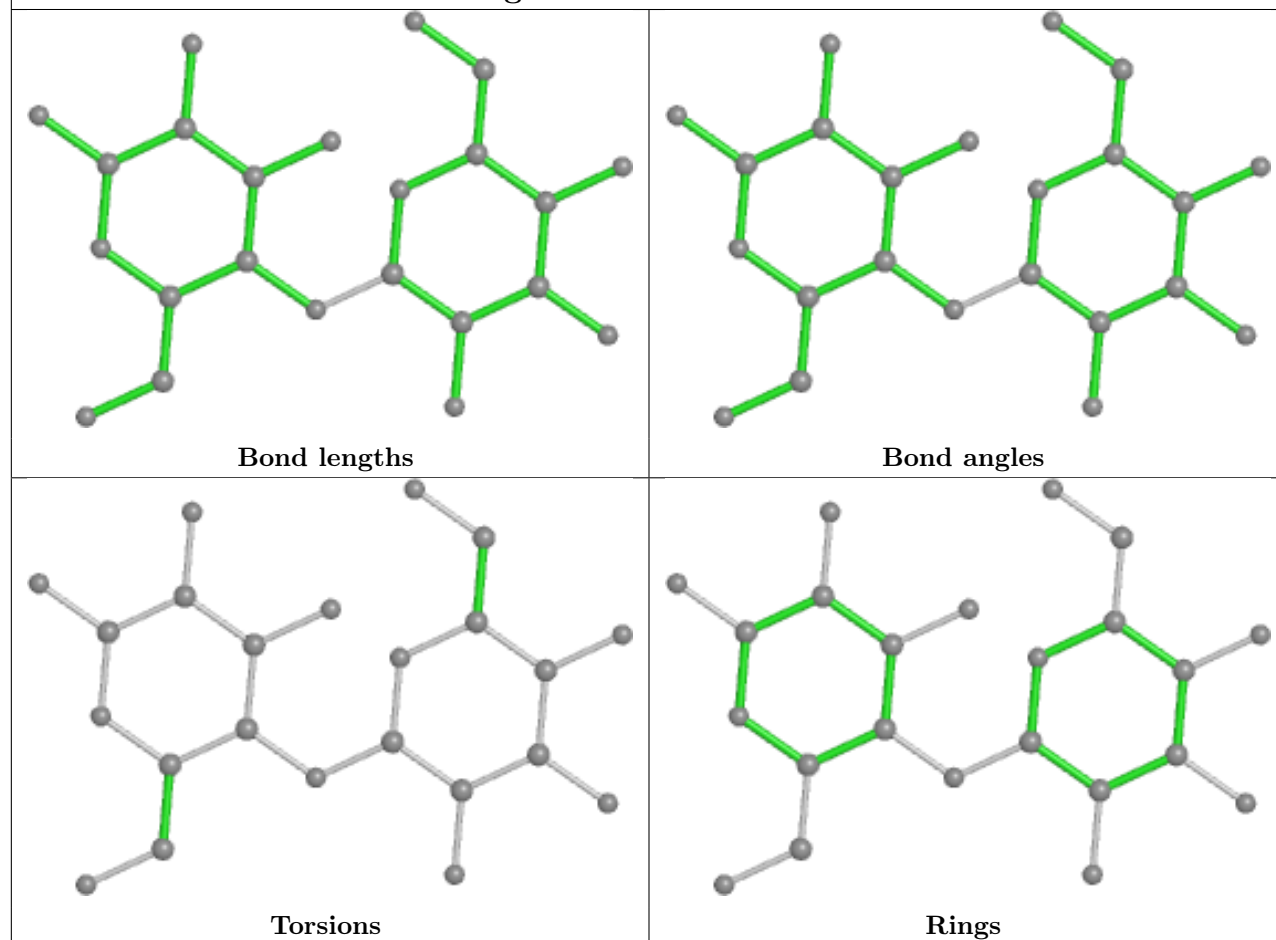
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



Oligosaccharide Chain H



Oligosaccharide Chain F



5.6 Ligand geometry

There are no ligands in this entry.

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 ⓘ

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	441/443 (99%)	0.06	6 (1%) 75 73	36, 46, 68, 92	0
1	B	438/443 (98%)	0.12	6 (1%) 75 73	34, 47, 72, 95	0
1	C	386/443 (87%)	0.30	18 (4%) 31 30	37, 56, 83, 95	0
1	D	371/443 (83%)	0.08	5 (1%) 77 75	34, 48, 68, 88	0
All	All	1636/1772 (92%)	0.14	35 (2%) 63 61	34, 49, 77, 95	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	175	GLY	5.5
1	C	385	VAL	5.5
1	A	174	ALA	5.2
1	D	174	ALA	5.1
1	A	431	PRO	4.7
1	C	240	ALA	4.3
1	C	175	GLY	3.8
1	C	55	GLY	3.8
1	A	175	GLY	3.5
1	B	174	ALA	3.4
1	C	173	ALA	3.4
1	A	429	ASN	3.3
1	D	240	ALA	3.3
1	C	122	LEU	3.1
1	B	413	GLN	2.9
1	B	409	TYR	2.9
1	A	173	ALA	2.8
1	C	53	ALA	2.7
1	D	142	ALA	2.7
1	A	430	ALA	2.7
1	C	314	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	419	VAL	2.7
1	C	381	ALA	2.6
1	C	310	GLU	2.6
1	C	56	ASP	2.5
1	D	61	ILE	2.5
1	D	326	GLN	2.4
1	B	176	LYS	2.4
1	C	81	THR	2.3
1	C	174	ALA	2.2
1	C	85	ALA	2.1
1	C	376	VAL	2.1
1	C	382	ILE	2.0
1	C	22	ALA	2.0
1	C	84	ALA	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](#)

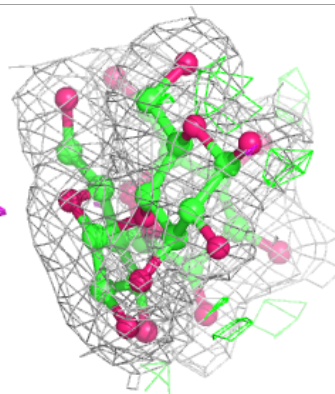
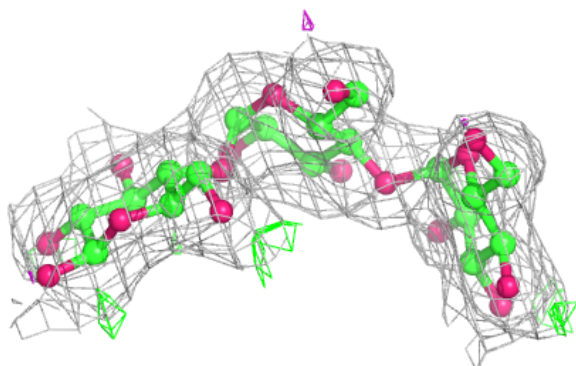
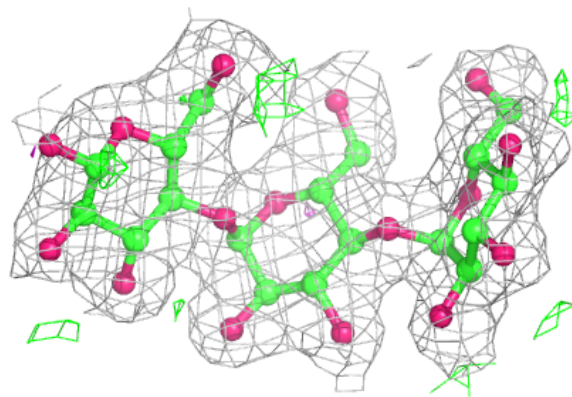
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLC	E	3	11/12	0.88	0.14	41,45,48,50	0
2	BGC	G	1	12/12	0.88	0.14	40,44,50,52	0
2	BGC	E	1	12/12	0.89	0.14	36,40,45,61	0
2	GLC	G	3	11/12	0.90	0.16	50,53,56,57	0
2	BGC	H	1	12/12	0.93	0.19	33,40,48,62	0
2	GLC	H	3	11/12	0.93	0.12	38,46,51,51	0
2	GLC	G	2	11/12	0.95	0.11	37,38,44,45	0
2	GLC	E	2	11/12	0.95	0.12	34,35,39,41	0
3	GLC	F	1	12/12	0.95	0.15	34,43,49,54	0
3	GLC	F	2	11/12	0.96	0.16	33,34,40,40	0
2	GLC	H	2	11/12	0.97	0.14	33,41,45,45	0

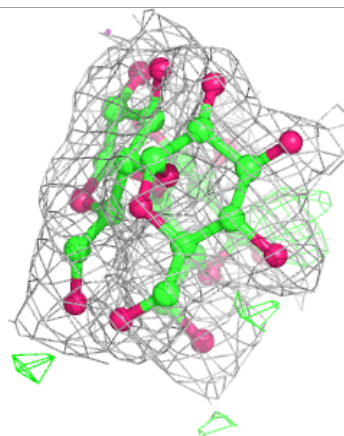
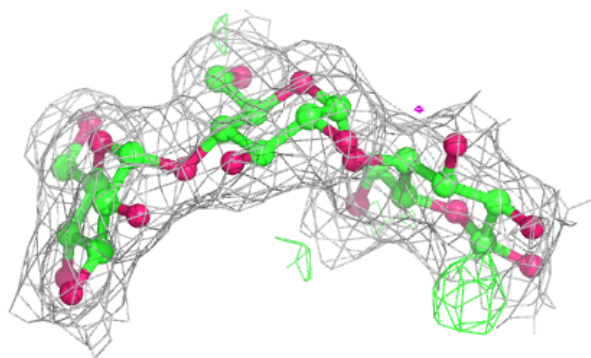
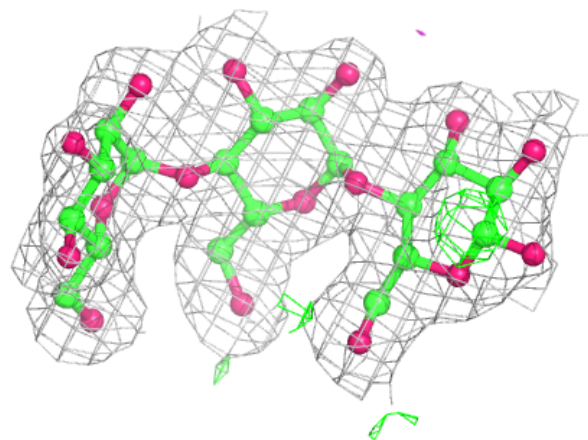
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

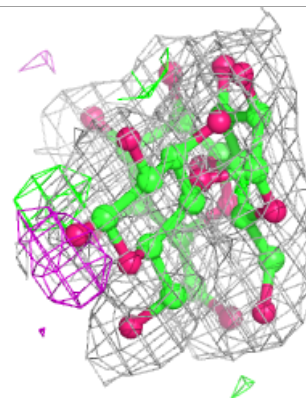
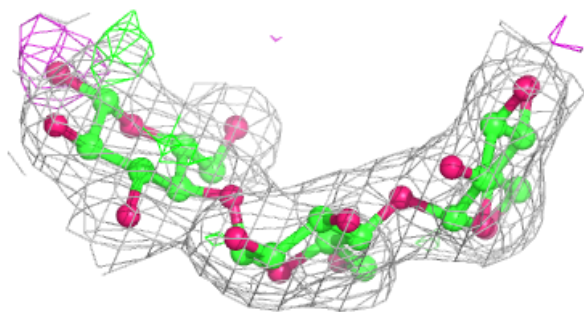
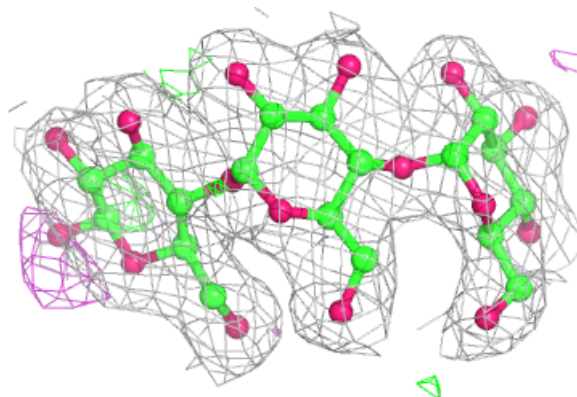
**Electron density around Chain G:**

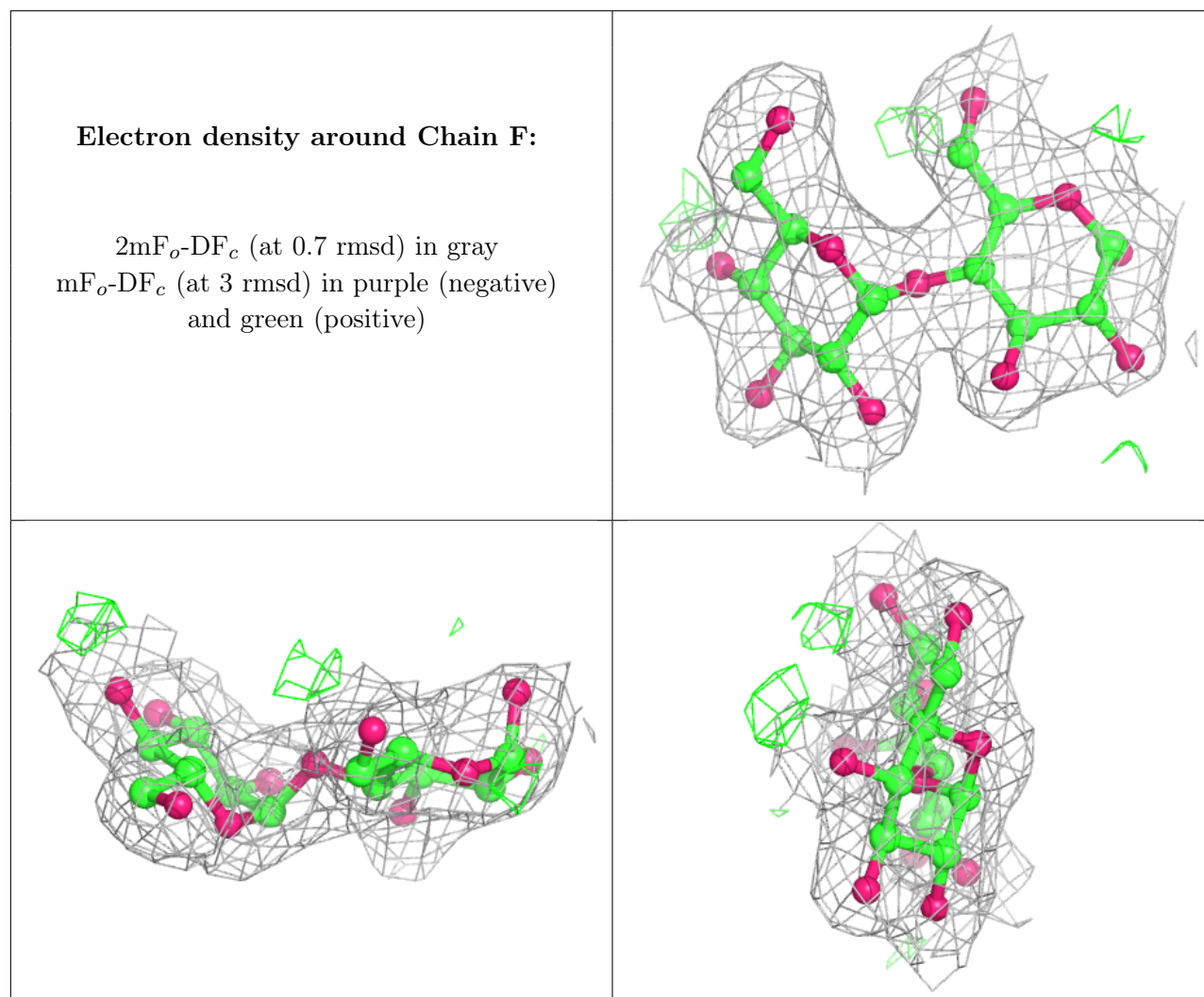
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

$2mF_o-DF_c$ (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.