wwPDB X-ray Structure Validation Summary Report (i)

Oct 27, 2026 – 03:15 pm GMT

PDB ID	:	33CN / pdb_000033cn
Title	:	Streptomyces sp. TLI_171 GH5_7 Mannanase, E337Q, mannan bound
Authors	:	Bloch, Y.
Deposited on	:	2026-08-10
Resolution	:	1.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

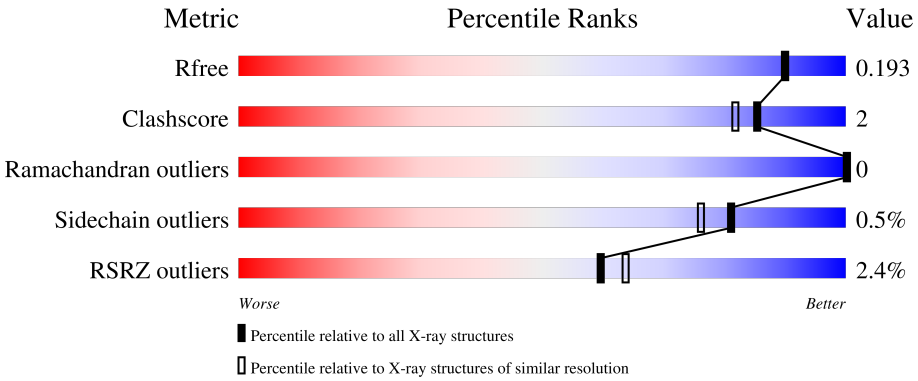
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	A	398	2% 89% 7% .
1	C	398	3% 91% . .
2	B	398	2% 90% 6% .
2	D	398	3% 90% 6% .
3	E	6	67% 33%

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Mol	Chain	Length	Quality of chain
3	F	6	50% 17% 33%
4	G	5	40% 60%
5	H	7	71% 14% 14%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 25763 atoms, of which 11916 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 GH5_7 Mannanase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	381	Total	C	H	N	O	S	0	19	0
			6028	1948	2922	560	586	12			
1	C	381	Total	C	H	N	O	S	0	14	0
			5968	1932	2892	554	578	12			

- Molecule 2 is a protein called GH5_7 Mannanase.

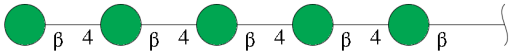
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	381	Total	C	H	N	O	S	0	21	0
			6042	1953	2930	561	587	11			
2	D	381	Total	C	H	N	O	S	0	20	0
			6028	1950	2924	558	585	11			

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose.



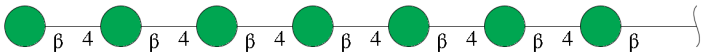
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	6	Total	C	H	O	0	0	0
			129	36	62	31			
3	F	6	Total	C	H	O	0	0	0
			129	36	62	31			

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	5	Total	C	H	O	0	0	0
			108	30	52	26			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-beta-D-mannopyranose -(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1 -4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	7	Total	C	H	O	0	0	0
			150	42	72	36			

- Molecule 6 is water.

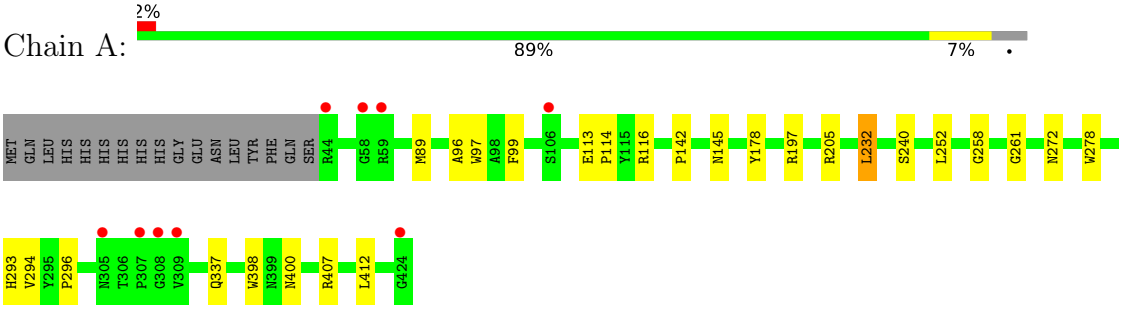
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	314	Total	O	0	0
			314	314		
6	B	310	Total	O	0	1
			310	310		
6	C	279	Total	O	0	0
			279	279		
6	D	278	Total	O	0	0
			278	278		

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.

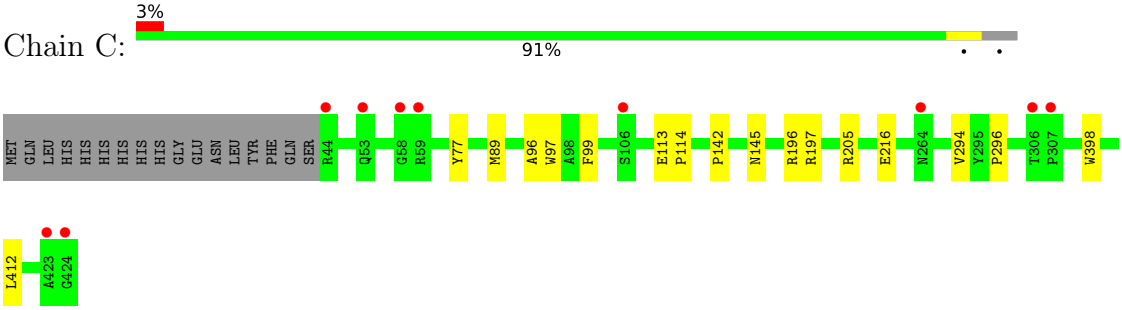
• Molecule 1: GH5_7 Mannanase

Chain A:



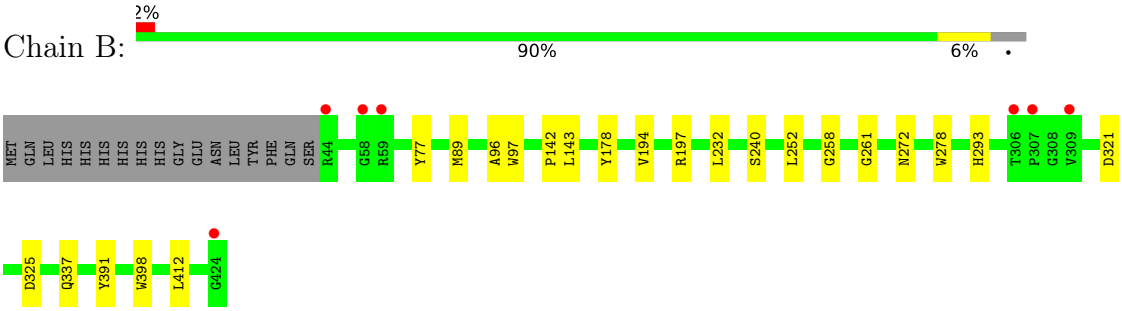
• Molecule 1: GH5_7 Mannanase

Chain C:



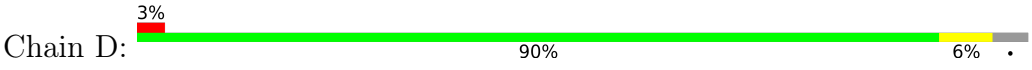
• Molecule 2: GH5_7 Mannanase

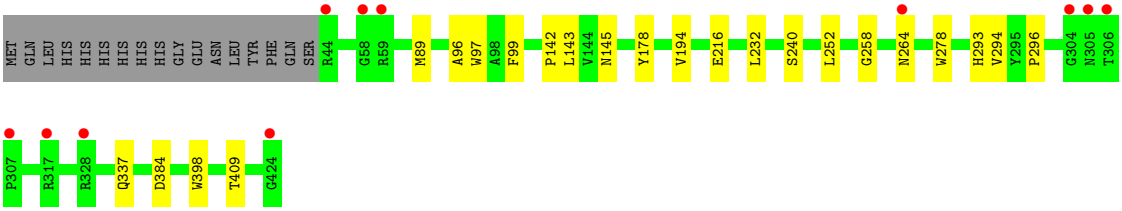
Chain B:



• Molecule 2: GH5_7 Mannanase

Chain D:

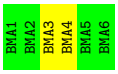




• Molecule 3: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose

Chain E:

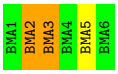




• Molecule 3: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose

Chain F:





• Molecule 4: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose

Chain G:

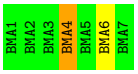




• Molecule 5: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	95.90Å 106.40Å 158.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	63.43 – 1.70 63.43 – 1.70	Depositor EDS
% Data completeness (in resolution range)	90.5 (63.43-1.70) 90.5 (63.43-1.70)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.75 (at 1.60Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.172 , 0.194 0.172 , 0.193	Depositor DCC
R_{free} test set	8801 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	18.3	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 34.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	25763	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, CSS

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	0.20	0/3251	0.46	0/4424
1	C	0.18	0/3208	0.44	0/4367
2	B	0.20	0/3273	0.45	0/4455
2	D	0.19	0/3271	0.44	0/4453
All	All	0.19	0/13003	0.45	0/17699

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

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	3106	2922	2861	16	0
1	C	3076	2892	2833	11	0
2	B	3112	2930	2858	14	0
2	D	3104	2924	2845	13	0
3	E	67	62	57	0	0
3	F	67	62	57	2	0
4	G	56	52	48	0	0
5	H	78	72	66	1	0
6	A	314	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	310	0	0	1	0
6	C	279	0	0	1	0
6	D	278	0	0	0	0
All	All	13847	11916	11625	54	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 2.

The worst 5 of 54 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:D:240:SER:HA	2:D:252[B]:LEU:HD21	1.84	0.59
2:B:391:TYR:CE1	2:D:264:ASN:HB3	2.45	0.52
1:C:96:ALA:O	1:C:142:PRO:HD2	2.09	0.52
2:D:89:MET:HG2	2:D:398:TRP:CE3	2.47	0.50
1:A:113[A]:GLU:HB2	1:A:114:PRO:HD2	1.95	0.48

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	397/398 (100%)	383 (96%)	14 (4%)	0	100	100
1	C	392/398 (98%)	377 (96%)	15 (4%)	0	100	100
2	B	400/398 (100%)	385 (96%)	15 (4%)	0	100	100
2	D	399/398 (100%)	380 (95%)	19 (5%)	0	100	100
All	All	1588/1592 (100%)	1525 (96%)	63 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	310/309 (100%)	308 (99%)	2 (1%)	78	72
1	C	306/309 (99%)	305 (100%)	1 (0%)	86	83
2	B	313/310 (101%)	312 (100%)	1 (0%)	86	83
2	D	313/310 (101%)	311 (99%)	2 (1%)	78	72
All	All	1242/1238 (100%)	1236 (100%)	6 (0%)	81	76

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	97	TRP
2	D	97	TRP
2	D	409	THR
1	A	232	LEU
1	A	97	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	305	ASN
2	D	134	GLN
2	D	305	ASN
2	D	155	GLN
2	B	130	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	CSS	A	207	1	4,6,7	0.74	0	1,6,8	0.96	0
1	CSS	C	207	1	4,6,7	0.65	0	1,6,8	0.70	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
1	CSS	A	207	1	-	0/1/5/7	-
1	CSS	C	207	1	-	0/1/5/7	-

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.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

24 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	BMA	E	1	3	12,12,12	0.31	0	17,17,17	0.65	0
3	BMA	E	2	3	11,11,12	0.42	0	15,15,17	1.04	0
3	BMA	E	3	3	11,11,12	0.63	0	15,15,17	1.23	2 (13%)
3	BMA	E	4	3	11,11,12	0.48	0	15,15,17	1.10	1 (6%)
3	BMA	E	5	3	11,11,12	0.54	0	15,15,17	0.85	0
3	BMA	E	6	3	11,11,12	0.43	0	15,15,17	0.68	0
3	BMA	F	1	3	12,12,12	0.38	0	17,17,17	0.53	0
3	BMA	F	2	3	11,11,12	0.58	0	15,15,17	1.04	1 (6%)
3	BMA	F	3	3	11,11,12	0.40	0	15,15,17	1.09	1 (6%)
3	BMA	F	4	3	11,11,12	0.61	0	15,15,17	0.72	0
3	BMA	F	5	3	11,11,12	0.32	0	15,15,17	0.92	1 (6%)
3	BMA	F	6	3	11,11,12	0.26	0	15,15,17	0.63	0
4	BMA	G	1	4	12,12,12	0.66	0	17,17,17	0.78	0
4	BMA	G	2	4	11,11,12	0.44	0	15,15,17	0.95	1 (6%)
4	BMA	G	3	4	11,11,12	0.54	0	15,15,17	1.25	2 (13%)
4	BMA	G	4	4	11,11,12	0.75	1 (9%)	15,15,17	0.78	0
4	BMA	G	5	4	11,11,12	0.34	0	15,15,17	0.51	0
5	BMA	H	1	5	12,12,12	0.28	0	17,17,17	0.66	0
5	BMA	H	2	5	11,11,12	0.62	0	15,15,17	0.78	0
5	BMA	H	3	5	11,11,12	0.41	0	15,15,17	1.00	0
5	BMA	H	4	5	11,11,12	0.36	0	15,15,17	1.11	1 (6%)
5	BMA	H	5	5	11,11,12	0.47	0	15,15,17	0.68	0
5	BMA	H	6	5	11,11,12	0.33	0	15,15,17	0.91	1 (6%)
5	BMA	H	7	5	11,11,12	0.26	0	15,15,17	0.52	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	BMA	E	1	3	-	0/2/22/22	0/1/1/1
3	BMA	E	2	3	-	0/2/19/22	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	BMA	E	4	3	-	0/2/19/22	1/1/1/1
3	BMA	E	5	3	-	0/2/19/22	0/1/1/1
3	BMA	E	6	3	-	0/2/19/22	0/1/1/1
3	BMA	F	1	3	-	0/2/22/22	0/1/1/1
3	BMA	F	2	3	-	0/2/19/22	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	1/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	F	4	3	-	0/2/19/22	0/1/1/1
3	BMA	F	5	3	-	0/2/19/22	0/1/1/1
3	BMA	F	6	3	-	0/2/19/22	0/1/1/1
4	BMA	G	1	4	-	0/2/22/22	0/1/1/1
4	BMA	G	2	4	-	0/2/19/22	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	1/1/1/1
4	BMA	G	4	4	-	0/2/19/22	0/1/1/1
4	BMA	G	5	4	-	0/2/19/22	0/1/1/1
5	BMA	H	1	5	-	2/2/22/22	0/1/1/1
5	BMA	H	2	5	-	0/2/19/22	0/1/1/1
5	BMA	H	3	5	-	0/2/19/22	0/1/1/1
5	BMA	H	4	5	-	0/2/19/22	1/1/1/1
5	BMA	H	5	5	-	0/2/19/22	0/1/1/1
5	BMA	H	6	5	-	0/2/19/22	0/1/1/1
5	BMA	H	7	5	-	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)
4	G	4	BMA	C2-C3	-2.18	1.49	1.52

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	4	BMA	C1-O5-C5	3.86	117.42	112.19
5	H	4	BMA	C1-O5-C5	3.32	116.69	112.19
4	G	3	BMA	C1-O5-C5	3.25	116.60	112.19
3	E	3	BMA	C1-C2-C3	2.83	113.15	109.67
3	F	3	BMA	C1-O5-C5	2.60	115.71	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	1	BMA	C4-C5-C6-O6
5	H	1	BMA	O5-C5-C6-O6

All (4) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	3	BMA	C1-C2-C3-C4-C5-O5

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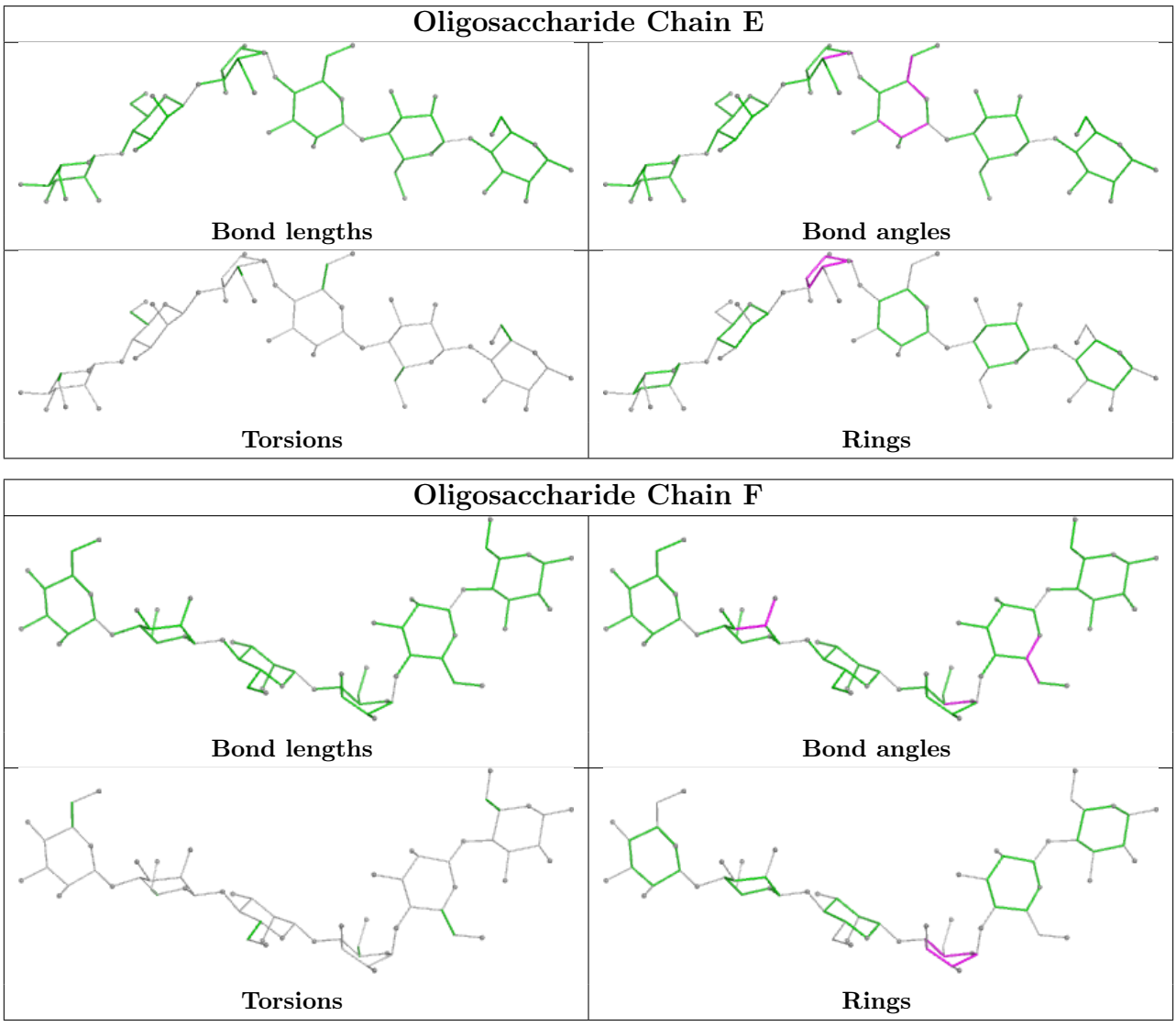
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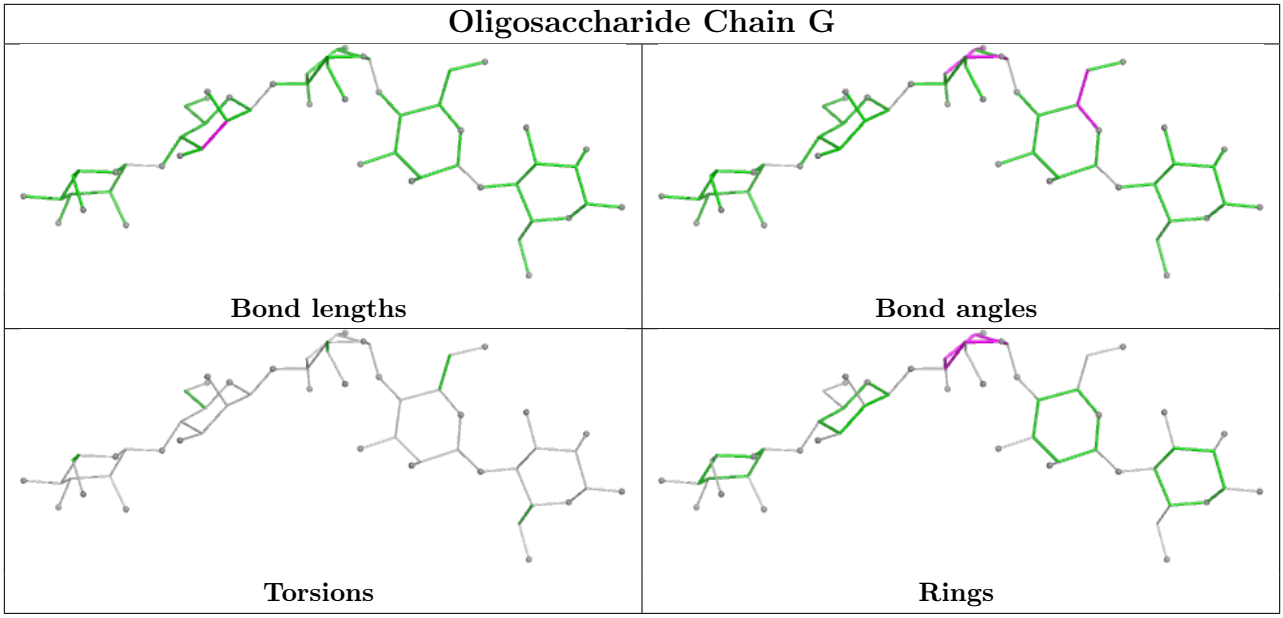
Mol	Chain	Res	Type	Atoms
5	H	4	BMA	C1-C2-C3-C4-C5-O5
3	E	4	BMA	C1-C2-C3-C4-C5-O5
4	G	3	BMA	C1-C2-C3-C4-C5-O5

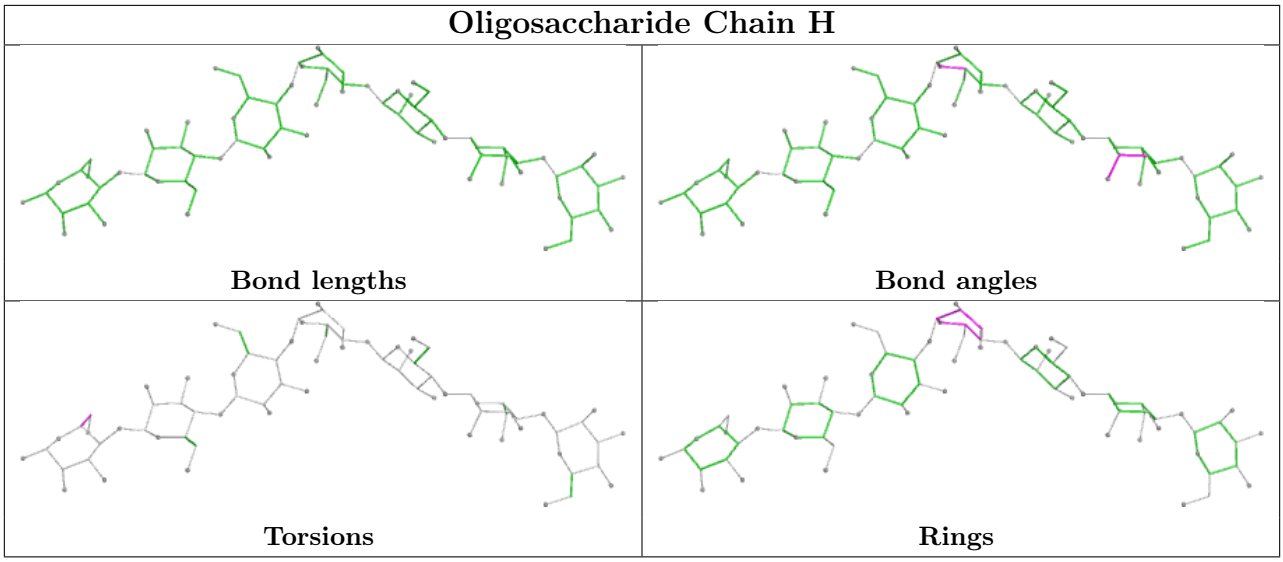
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	3	BMA	1	0
5	H	4	BMA	1	0
3	F	2	BMA	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)

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, 95^{th} 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	380/398 (95%)	-0.35	9 (2%)	59	64	8, 18, 32, 74	13 (3%)
1	C	380/398 (95%)	-0.17	10 (2%)	57	61	9, 22, 36, 85	9 (2%)
2	B	381/398 (95%)	-0.40	7 (1%)	67	72	8, 18, 31, 75	14 (3%)
2	D	381/398 (95%)	-0.12	11 (2%)	53	58	10, 22, 38, 78	14 (3%)
All	All	1522/1592 (95%)	-0.26	37 (2%)	59	64	8, 20, 35, 85	50 (3%)

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	424	GLY	5.9
1	C	424	GLY	5.2
2	B	424	GLY	4.8
2	D	307	PRO	4.3
2	D	424	GLY	4.2

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

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, 95^{th} 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
1	CSS	A	207	7/8	0.93	0.08	15,18,33,39	0
1	CSS	C	207	7/8	0.95	0.07	18,22,35,43	0

6.3 Carbohydrates (i)

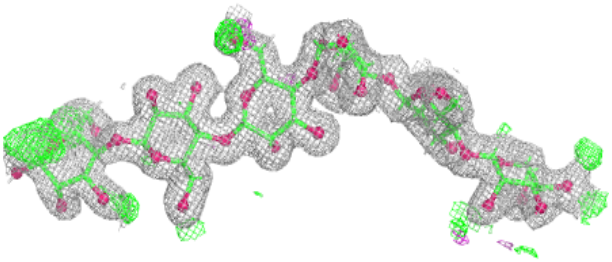
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

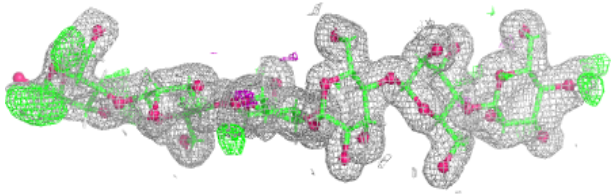
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	BMA	H	1	12/12	0.72	0.19	26,32,37,41	22
3	BMA	E	1	12/12	0.79	0.17	19,25,33,40	22
5	BMA	H	7	11/12	0.82	0.12	26,32,37,39	17
3	BMA	F	6	11/12	0.90	0.11	25,32,38,41	0
4	BMA	G	5	11/12	0.93	0.07	17,25,30,32	0
3	BMA	E	6	11/12	0.93	0.08	16,24,29,33	0
4	BMA	G	1	12/12	0.93	0.08	17,21,25,27	0
4	BMA	G	2	11/12	0.94	0.07	14,20,25,32	0
5	BMA	H	2	11/12	0.94	0.07	19,23,27,29	0
5	BMA	H	3	11/12	0.94	0.08	19,23,27,32	0
5	BMA	H	6	11/12	0.94	0.07	17,22,26,27	0
3	BMA	E	3	11/12	0.94	0.07	13,18,21,27	0
3	BMA	F	2	11/12	0.95	0.07	15,19,22,26	0
4	BMA	G	3	11/12	0.95	0.07	16,19,23,24	0
3	BMA	F	5	11/12	0.96	0.06	16,20,24,25	0
5	BMA	H	5	11/12	0.96	0.06	17,19,22,23	0
3	BMA	E	4	11/12	0.97	0.05	12,15,19,20	0
3	BMA	E	5	11/12	0.97	0.05	14,16,18,22	0
5	BMA	H	4	11/12	0.97	0.05	17,20,24,27	0
4	BMA	G	4	11/12	0.97	0.05	16,18,21,22	0
3	BMA	E	2	11/12	0.97	0.05	15,18,20,22	0
3	BMA	F	1	12/12	0.97	0.05	14,17,21,24	0
3	BMA	F	3	11/12	0.98	0.04	14,17,21,22	0
3	BMA	F	4	11/12	0.98	0.05	15,17,20,21	0

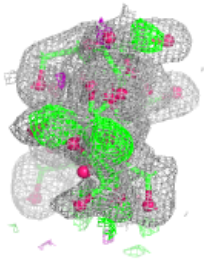
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

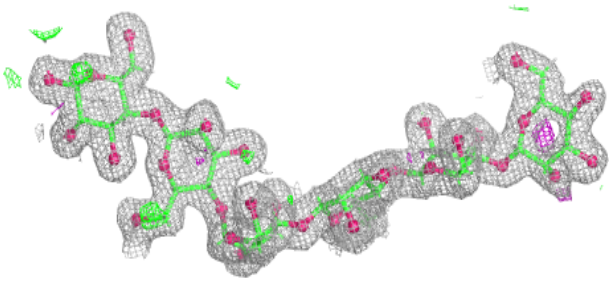


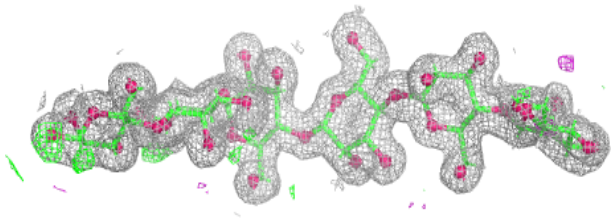


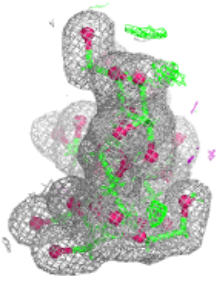


Electron density around Chain F:

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

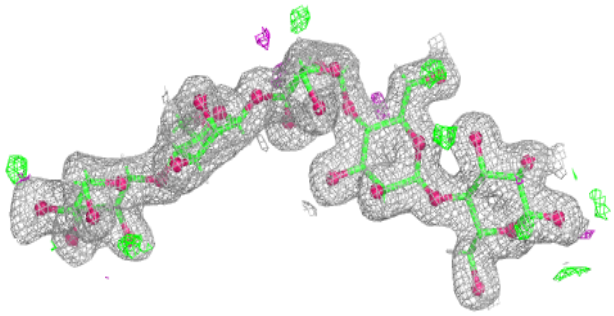


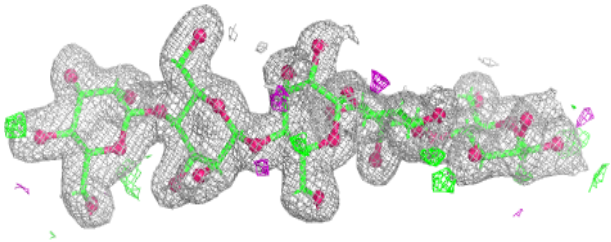


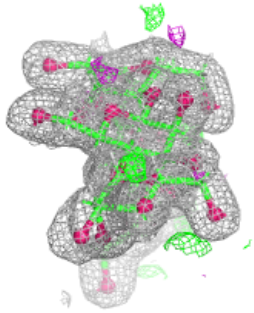


Electron density around Chain G:

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

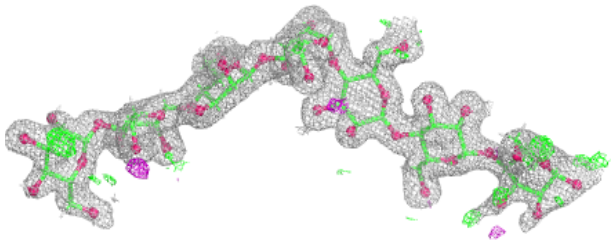


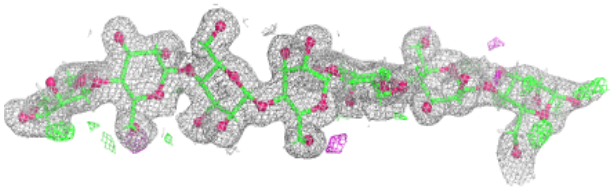


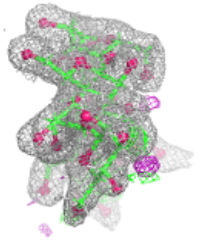


Electron density around Chain H:

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







6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.