



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 05:47 PM BST

PDB ID : 4ATF
Title : Crystal structure of inactivated mutant beta-agarase B in complex with agaro-octaose
Authors : Bernard, T.; Hehemann, J.H.; Correc, G.; Jam, M.; Michel, G.; Czjzek, M.
Deposited on : 2012-05-06
Resolution : 1.90 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 ⓘ 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 : 2.13.1
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) : 2.13.1

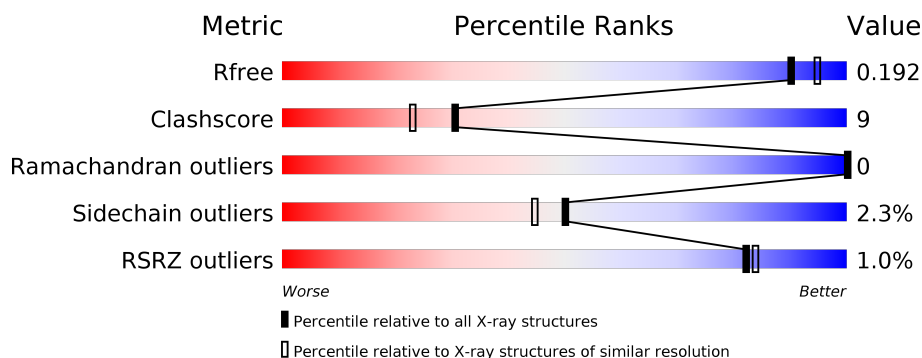
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 on 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	308	<div> <div>80%</div> <div>14%</div> <div>..</div> </div>
1	B	308	<div> <div>%</div> <div>82%</div> <div>12%</div> <div>.</div> </div>
1	C	308	<div> <div>2%</div> <div>82%</div> <div>11%</div> <div>...</div> </div>
1	D	308	<div> <div>%</div> <div>82%</div> <div>12%</div> <div>.</div> </div>
2	E	8	<div> <div>50%</div> <div>50%</div> </div>
2	F	8	<div> <div>63%</div> <div>38%</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	8	 63%38%
2	H	8	 50%50%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GAL	E	1	-	-	X	X
2	AAL	E	2	-	-	-	X
2	GAL	E	3	-	-	-	X
2	AAL	E	4	-	-	-	X
2	GAL	F	1	-	-	-	X
2	AAL	F	2	-	-	-	X
2	GAL	F	3	-	-	-	X
2	AAL	F	4	X	-	-	X
2	GAL	G	1	-	-	-	X
2	AAL	G	2	X	-	-	X
2	GAL	G	3	X	-	-	X
2	AAL	G	4	-	-	X	X
2	GAL	H	1	-	-	X	X
2	AAL	H	2	-	-	-	X
2	GAL	H	3	-	-	-	X
2	AAL	H	4	X	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11129 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 BETA-AGARASE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	9	0
			2482	1575	413	488	6			
1	B	296	Total	C	N	O	S	0	4	0
			2454	1557	407	484	6			
1	C	297	Total	C	N	O	S	0	2	0
			2443	1553	406	478	6			
1	D	297	Total	C	N	O	S	0	4	0
			2461	1561	412	482	6			

There are 32 discrepancies between the modelled and reference sequences:

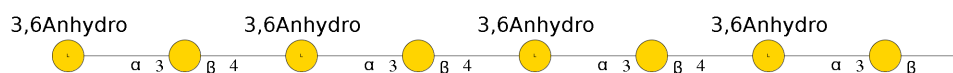
Chain	Residue	Modelled	Actual	Comment	Reference
A	47	HIS	-	expression tag	UNP Q9RGX8
A	48	HIS	-	expression tag	UNP Q9RGX8
A	49	HIS	-	expression tag	UNP Q9RGX8
A	50	HIS	-	expression tag	UNP Q9RGX8
A	51	HIS	-	expression tag	UNP Q9RGX8
A	52	HIS	-	expression tag	UNP Q9RGX8
A	189	ASP	GLU	engineered mutation	UNP Q9RGX8
A	354	LEU	-	expression tag	UNP Q9RGX8
B	47	HIS	-	expression tag	UNP Q9RGX8
B	48	HIS	-	expression tag	UNP Q9RGX8
B	49	HIS	-	expression tag	UNP Q9RGX8
B	50	HIS	-	expression tag	UNP Q9RGX8
B	51	HIS	-	expression tag	UNP Q9RGX8
B	52	HIS	-	expression tag	UNP Q9RGX8
B	189	ASP	GLU	engineered mutation	UNP Q9RGX8
B	354	LEU	-	expression tag	UNP Q9RGX8
C	47	HIS	-	expression tag	UNP Q9RGX8
C	48	HIS	-	expression tag	UNP Q9RGX8
C	49	HIS	-	expression tag	UNP Q9RGX8
C	50	HIS	-	expression tag	UNP Q9RGX8
C	51	HIS	-	expression tag	UNP Q9RGX8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	52	HIS	-	expression tag	UNP Q9RGX8
C	189	ASP	GLU	engineered mutation	UNP Q9RGX8
C	354	LEU	-	expression tag	UNP Q9RGX8
D	47	HIS	-	expression tag	UNP Q9RGX8
D	48	HIS	-	expression tag	UNP Q9RGX8
D	49	HIS	-	expression tag	UNP Q9RGX8
D	50	HIS	-	expression tag	UNP Q9RGX8
D	51	HIS	-	expression tag	UNP Q9RGX8
D	52	HIS	-	expression tag	UNP Q9RGX8
D	189	ASP	GLU	engineered mutation	UNP Q9RGX8
D	354	LEU	-	expression tag	UNP Q9RGX8

- Molecule 2 is an oligosaccharide called 3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	8	Total	C	O	0	0	0
			85	48	37			
2	F	8	Total	C	O	0	0	0
			85	48	37			
2	G	8	Total	C	O	0	0	0
			85	48	37			
2	H	8	Total	C	O	0	0	0
			85	48	37			

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

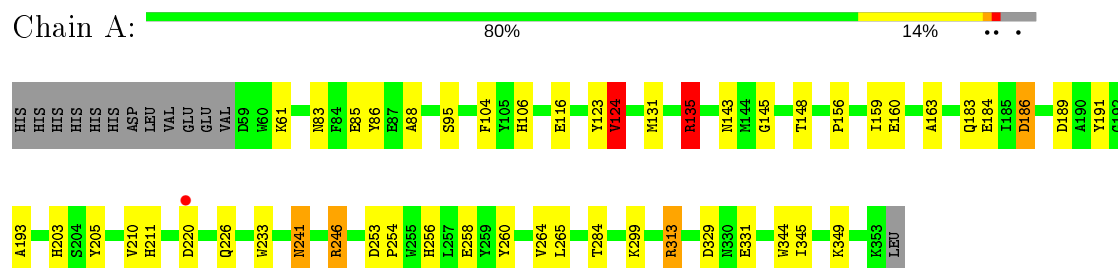
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	243	Total 243	O 243	0	0
4	B	250	Total 250	O 250	0	0
4	C	225	Total 225	O 225	0	0
4	D	227	Total 227	O 227	0	0

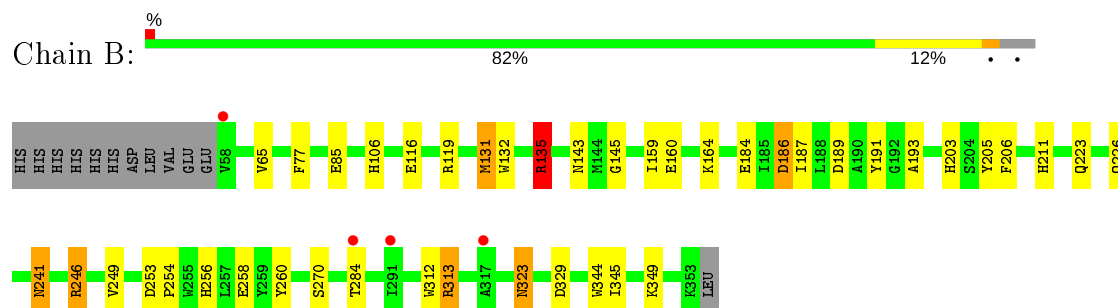
3 Residue-property plots

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.

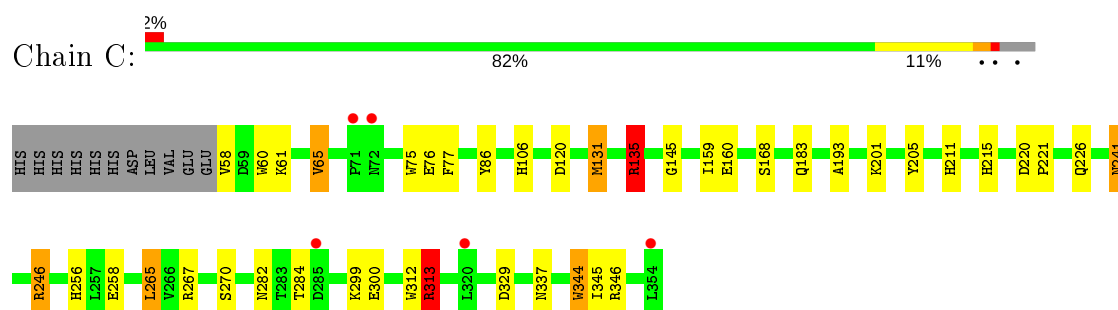
• Molecule 1: BETA-AGARASE B



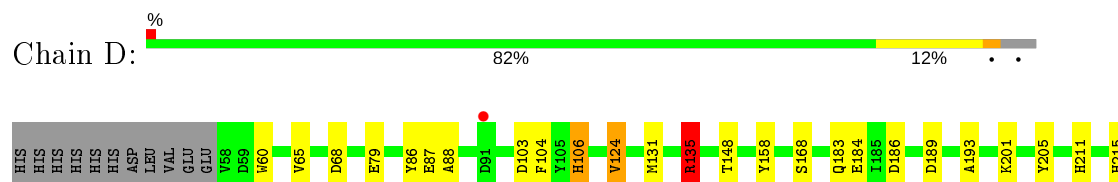
• Molecule 1: BETA-AGARASE B

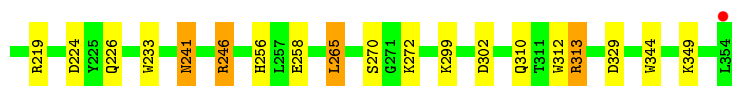


• Molecule 1: BETA-AGARASE B



• Molecule 1: BETA-AGARASE B





● Molecule 2: 3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose

Chain E: 50% 50%



● Molecule 2: 3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose

Chain F: 63% 38%



● Molecule 2: 3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose

Chain G: 63% 38%



● Molecule 2: 3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose

Chain H: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.19 Å 106.23 Å 96.98 Å 90.00° 93.22° 90.00°	Depositor
Resolution (Å)	65.35 – 1.90 20.03 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.3 (65.35-1.90) 97.2 (20.03-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 1.90 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.134 , 0.190 0.138 , 0.192	Depositor DCC
R_{free} test set	5657 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	14.2	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11129	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 72.88 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0333e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: AAL, GAL, NA

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	1.28	8/2557 (0.3%)	1.28	12/3484 (0.3%)
1	B	1.28	7/2528 (0.3%)	1.20	15/3442 (0.4%)
1	C	1.28	10/2517 (0.4%)	1.30	14/3428 (0.4%)
1	D	1.24	4/2537 (0.2%)	1.34	17/3454 (0.5%)
All	All	1.27	29/10139 (0.3%)	1.28	58/13808 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	131	MET	CB-CG	-8.12	1.25	1.51
1	C	86	TYR	CD1-CE1	7.11	1.50	1.39
1	B	77	PHE	CE2-CZ	6.82	1.50	1.37
1	B	131	MET	CB-CG	-6.67	1.30	1.51
1	C	313	ARG	CD-NE	-6.48	1.35	1.46

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	313	ARG	NE-CZ-NH1	-34.86	102.87	120.30
1	D	313	ARG	NE-CZ-NH1	-31.08	104.76	120.30
1	A	313	ARG	NE-CZ-NH1	-28.68	105.96	120.30
1	B	313	ARG	NE-CZ-NH2	-23.66	108.47	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	246	ARG	NE-CZ-NH2	-22.65	108.98	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	313	ARG	Sidechain

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	2482	0	2303	53	0
1	B	2454	0	2276	30	0
1	C	2443	0	2281	40	0
1	D	2461	0	2284	43	0
2	E	85	0	66	21	0
2	F	85	0	67	7	0
2	G	85	0	67	21	0
2	H	85	0	66	29	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	243	0	0	8	0
4	B	250	0	0	5	0
4	C	225	0	0	6	0
4	D	227	0	0	6	0
All	All	11129	0	9410	180	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 9.

The worst 5 of 180 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:C:215:HIS:NE2	2:G:4:AAL:H4	1.50	1.24
1:A:205:TYR:CE2	2:E:1:GAL:H3	1.75	1.20
1:D:189:ASP:OD2	2:H:4:AAL:H3	1.45	1.17
4:C:2123:HOH:O	2:G:4:AAL:H62	0.96	1.12
2:H:4:AAL:H5	2:H:5:GAL:H2	1.37	1.05

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	302/308 (98%)	298 (99%)	4 (1%)	0	100	100
1	B	298/308 (97%)	293 (98%)	5 (2%)	0	100	100
1	C	297/308 (96%)	294 (99%)	3 (1%)	0	100	100
1	D	299/308 (97%)	293 (98%)	6 (2%)	0	100	100
All	All	1196/1232 (97%)	1178 (98%)	18 (2%)	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	269/273 (98%)	263 (98%)	6 (2%)	52	47
1	B	265/273 (97%)	260 (98%)	5 (2%)	57	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	264/273 (97%)	258 (98%)	6 (2%)	50	45
1	D	266/273 (97%)	258 (97%)	8 (3%)	41	33
All	All	1064/1092 (97%)	1039 (98%)	25 (2%)	50	45

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	60	TRP
1	C	135	ARG
1	D	265	LEU
1	C	106	HIS
1	C	201	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	241	ASN
1	B	323	ASN
1	D	241	ASN
1	B	310	GLN
1	C	183	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 ⓘ

32 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	GAL	E	1	2	12,12,12	0.67	0	17,17,17	1.35	2 (11%)
2	AAL	E	2	2	11,11,12	0.89	0	15,16,18	2.95	7 (46%)
2	GAL	E	3	2	11,11,12	1.13	1 (9%)	15,15,17	2.19	6 (40%)
2	AAL	E	4	2	11,11,12	0.99	0	15,16,18	2.74	5 (33%)
2	GAL	E	5	2	11,11,12	0.88	0	15,15,17	2.14	5 (33%)
2	AAL	E	6	2	11,11,12	1.83	2 (18%)	15,16,18	1.71	3 (20%)
2	GAL	E	7	2	11,11,12	1.03	0	15,15,17	2.01	4 (26%)
2	AAL	E	8	2	11,11,12	1.59	2 (18%)	15,16,18	1.83	4 (26%)
2	GAL	F	1	2	12,12,12	0.58	0	17,17,17	2.50	8 (47%)
2	AAL	F	2	2	11,11,12	0.86	0	15,16,18	2.61	8 (53%)
2	GAL	F	3	2	11,11,12	1.01	1 (9%)	15,15,17	2.07	5 (33%)
2	AAL	F	4	2	11,11,12	1.18	1 (9%)	15,16,18	2.65	7 (46%)
2	GAL	F	5	2	11,11,12	1.21	3 (27%)	15,15,17	1.53	2 (13%)
2	AAL	F	6	2	11,11,12	1.75	3 (27%)	15,16,18	1.92	6 (40%)
2	GAL	F	7	2	11,11,12	1.21	2 (18%)	15,15,17	1.64	4 (26%)
2	AAL	F	8	2	11,11,12	1.33	2 (18%)	15,16,18	2.35	6 (40%)
2	GAL	G	1	2	12,12,12	0.57	0	17,17,17	1.33	1 (5%)
2	AAL	G	2	2	11,11,12	1.21	1 (9%)	15,16,18	2.40	4 (26%)
2	GAL	G	3	2	11,11,12	0.96	1 (9%)	15,15,17	2.90	7 (46%)
2	AAL	G	4	2	11,11,12	1.43	2 (18%)	15,16,18	4.36	8 (53%)
2	GAL	G	5	2	11,11,12	0.59	0	15,15,17	1.83	3 (20%)
2	AAL	G	6	2	11,11,12	1.59	3 (27%)	15,16,18	1.48	2 (13%)
2	GAL	G	7	2	11,11,12	1.26	0	15,15,17	1.40	2 (13%)
2	AAL	G	8	2	11,11,12	1.44	2 (18%)	15,16,18	1.49	3 (20%)
2	GAL	H	1	2	12,12,12	0.80	0	17,17,17	1.64	3 (17%)
2	AAL	H	2	2	11,11,12	0.78	0	15,16,18	2.88	7 (46%)
2	GAL	H	3	2	11,11,12	0.64	0	15,15,17	3.78	5 (33%)
2	AAL	H	4	2	11,11,12	1.89	3 (27%)	15,16,18	4.09	9 (60%)
2	GAL	H	5	2	11,11,12	0.82	0	15,15,17	1.39	2 (13%)
2	AAL	H	6	2	11,11,12	1.42	2 (18%)	15,16,18	1.65	4 (26%)
2	GAL	H	7	2	11,11,12	1.30	3 (27%)	15,15,17	1.51	1 (6%)
2	AAL	H	8	2	11,11,12	1.46	2 (18%)	15,16,18	1.69	4 (26%)

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	GAL	E	1	2	-	0/2/22/22	0/1/1/1
2	AAL	E	2	2	-	-	0/3/2/2
2	GAL	E	3	2	-	2/2/19/22	0/1/1/1
2	AAL	E	4	2	-	-	0/3/2/2
2	GAL	E	5	2	-	0/2/19/22	0/1/1/1
2	AAL	E	6	2	-	-	0/3/2/2
2	GAL	E	7	2	-	0/2/19/22	0/1/1/1
2	AAL	E	8	2	-	-	0/3/2/2
2	GAL	F	1	2	-	2/2/22/22	0/1/1/1
2	AAL	F	2	2	-	-	0/3/2/2
2	GAL	F	3	2	-	1/2/19/22	0/1/1/1
2	AAL	F	4	2	1/1/4/5	-	0/3/2/2
2	GAL	F	5	2	-	0/2/19/22	0/1/1/1
2	AAL	F	6	2	-	-	0/3/2/2
2	GAL	F	7	2	-	0/2/19/22	0/1/1/1
2	AAL	F	8	2	-	-	0/3/2/2
2	GAL	G	1	2	-	2/2/22/22	0/1/1/1
2	AAL	G	2	2	1/1/4/5	-	0/3/2/2
2	GAL	G	3	2	1/1/4/5	1/2/19/22	0/1/1/1
2	AAL	G	4	2	-	-	0/3/2/2
2	GAL	G	5	2	-	0/2/19/22	0/1/1/1
2	AAL	G	6	2	-	-	0/3/2/2
2	GAL	G	7	2	-	0/2/19/22	0/1/1/1
2	AAL	G	8	2	-	-	0/3/2/2
2	GAL	H	1	2	-	2/2/22/22	0/1/1/1
2	AAL	H	2	2	-	-	0/3/2/2
2	GAL	H	3	2	-	1/2/19/22	0/1/1/1
2	AAL	H	4	2	1/1/4/5	-	0/3/2/2
2	GAL	H	5	2	-	0/2/19/22	0/1/1/1
2	AAL	H	6	2	-	-	0/3/2/2
2	GAL	H	7	2	-	0/2/19/22	0/1/1/1
2	AAL	H	8	2	-	-	0/3/2/2

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	4	AAL	C4-C3	-3.74	1.44	1.52
2	E	6	AAL	O5-C1	3.69	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	8	AAL	O5-C1	3.55	1.49	1.43
2	F	6	AAL	O5-C1	3.37	1.49	1.43
2	H	4	AAL	C1-C2	3.32	1.59	1.52

The worst 5 of 147 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	3	GAL	C2-C3-C4	-12.52	89.22	110.89
2	G	4	AAL	C1-C2-C3	7.93	118.76	109.17
2	H	4	AAL	O2-C2-C1	7.90	125.31	109.15
2	H	4	AAL	C2-C3-C4	-7.77	94.60	113.85
2	G	4	AAL	O3-C3-C4	-7.77	89.69	103.59

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	G	2	AAL	C1
2	F	4	AAL	C1
2	G	3	GAL	C1
2	H	4	AAL	C1

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	1	GAL	O5-C5-C6-O6
2	H	1	GAL	O5-C5-C6-O6
2	H	1	GAL	C4-C5-C6-O6
2	E	3	GAL	O5-C5-C6-O6
2	F	1	GAL	C4-C5-C6-O6

There are no ring outliers.

14 monomers are involved in 78 short contacts:

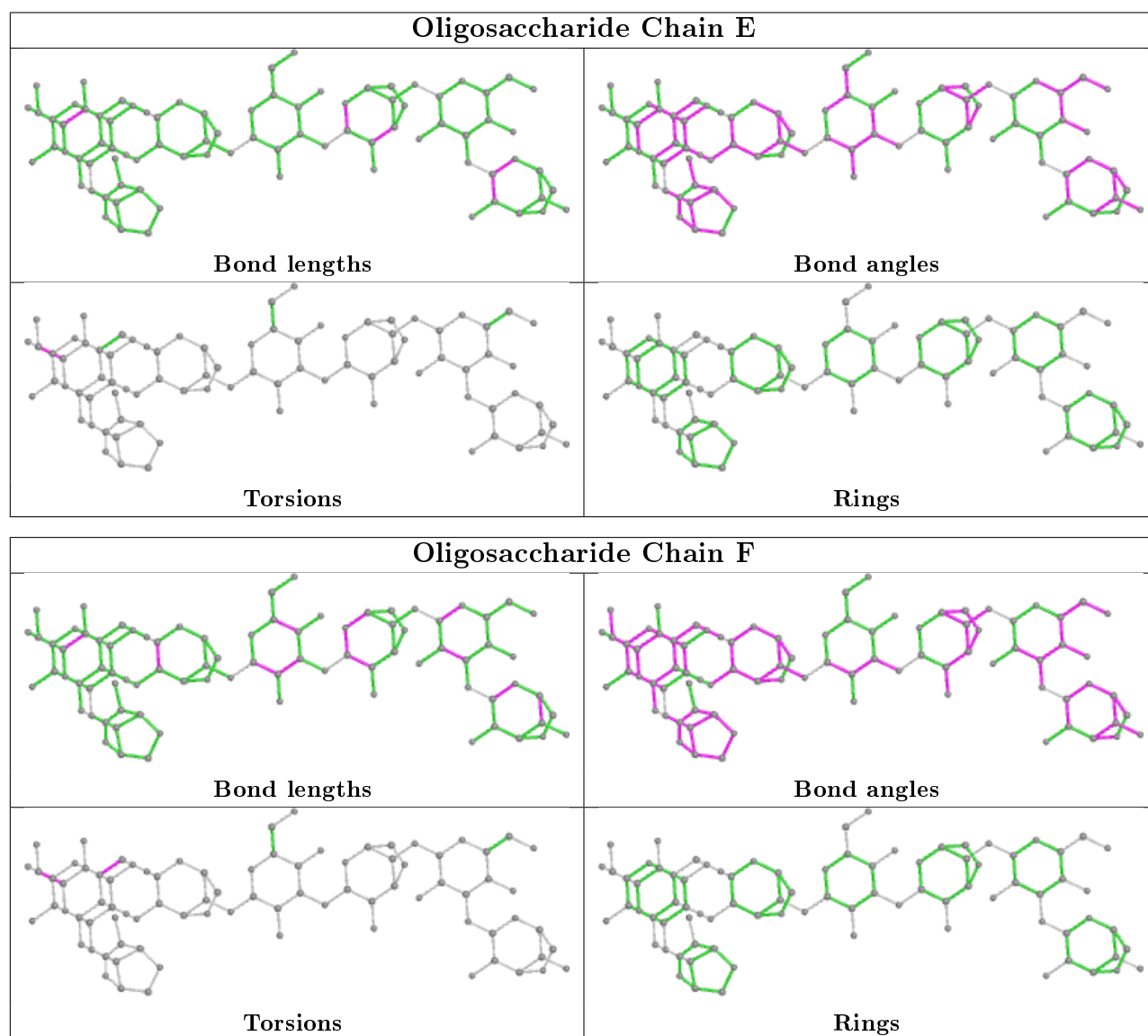
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	2	AAL	1	0
2	E	5	GAL	1	0
2	G	5	GAL	3	0
2	H	2	AAL	1	0
2	F	4	AAL	4	0
2	G	4	AAL	19	0
2	F	1	GAL	2	0

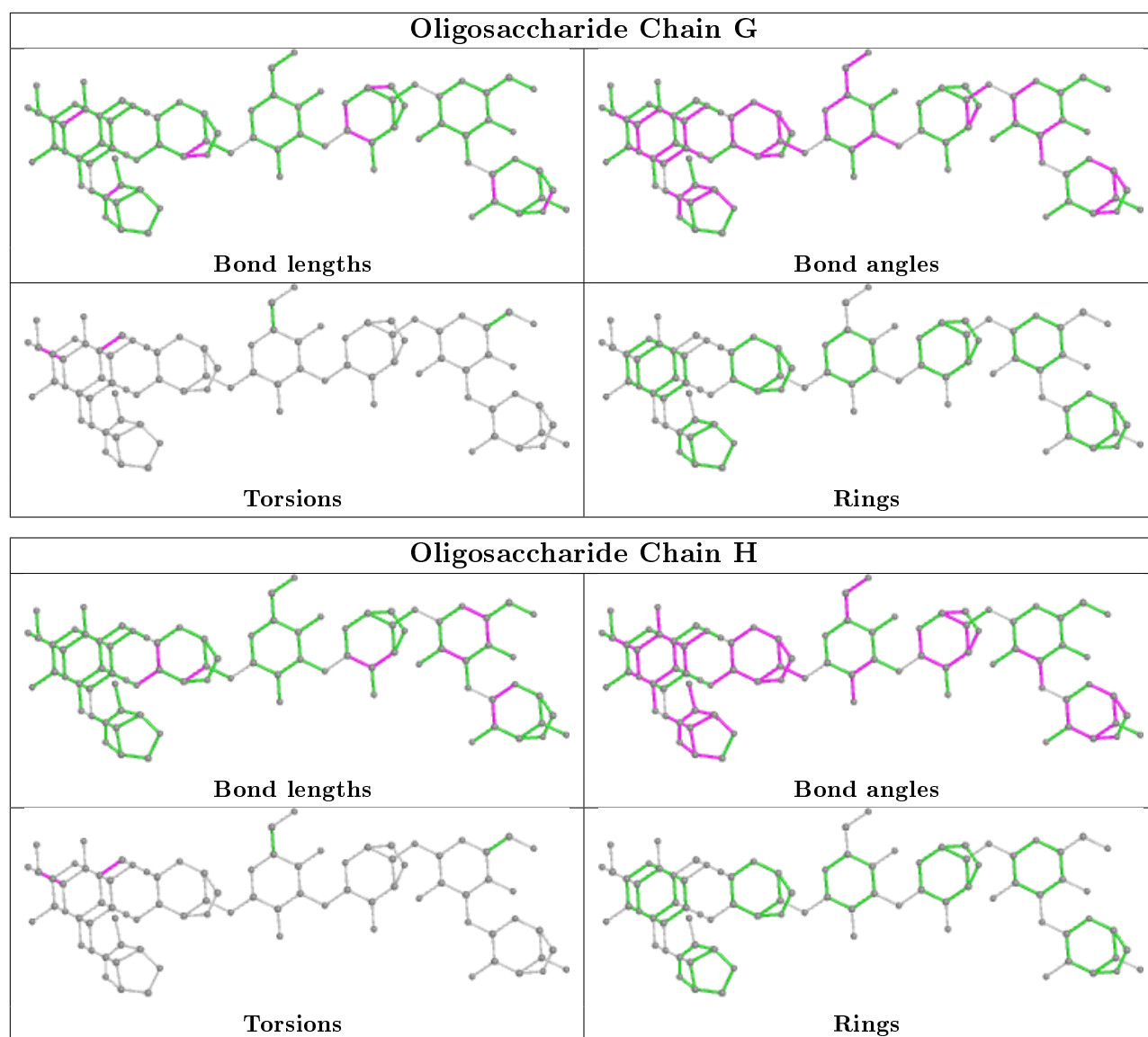
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1	GAL	14	0
2	F	5	GAL	3	0
2	E	4	AAL	3	0
2	G	1	GAL	2	0
2	H	4	AAL	14	0
2	H	5	GAL	4	0
2	E	1	GAL	16	0

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 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 [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	295/308 (95%)	-0.63	1 (0%) 94 94	9, 16, 28, 31	26 (8%)
1	B	296/308 (96%)	-0.54	4 (1%) 75 77	9, 16, 30, 43	16 (5%)
1	C	297/308 (96%)	-0.57	5 (1%) 70 72	9, 16, 28, 36	24 (8%)
1	D	297/308 (96%)	-0.55	2 (0%) 87 88	8, 16, 28, 34	20 (6%)
All	All	1185/1232 (96%)	-0.57	12 (1%) 82 84	8, 16, 29, 43	86 (7%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	291	ILE	4.1
1	B	58	VAL	3.4
1	C	72	ASN	3.4
1	D	354	LEU	3.1
1	B	284	THR	3.0

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	GAL	E	1	12/12	0.14	1.00	37,39,40,41	12
2	GAL	H	1	12/12	0.25	1.01	36,38,40,40	12

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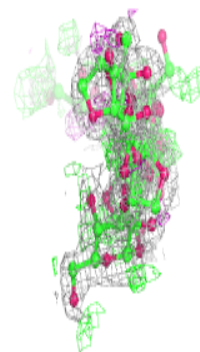
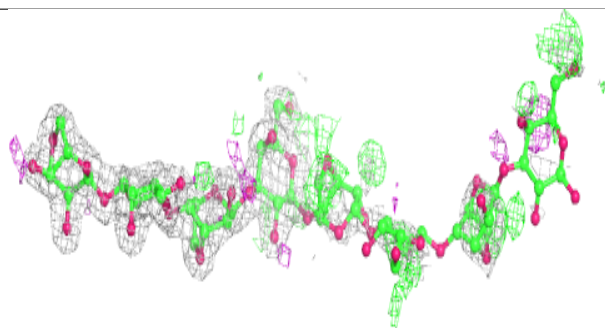
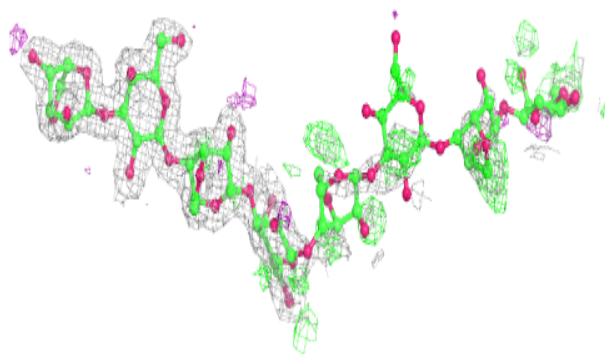
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	AAL	G	2	10/11	0.32	0.51	29,30,31,31	10
2	GAL	G	1	12/12	0.34	0.49	33,36,37,37	12
2	AAL	E	2	10/11	0.40	0.53	23,29,30,34	10
2	GAL	F	1	12/12	0.43	0.66	30,32,33,33	12
2	AAL	F	2	10/11	0.44	0.53	25,28,30,32	10
2	GAL	H	3	11/12	0.48	0.55	18,27,29,30	11
2	GAL	G	3	11/12	0.52	0.48	16,24,26,26	11
2	AAL	F	4	10/11	0.56	0.59	20,30,30,31	10
2	AAL	H	2	10/11	0.57	0.55	33,33,34,34	10
2	GAL	E	3	11/12	0.60	0.47	33,34,35,38	11
2	AAL	E	4	10/11	0.65	0.50	30,32,34,36	10
2	GAL	F	3	11/12	0.66	0.53	24,29,30,34	11
2	AAL	G	4	10/11	0.78	0.43	6,13,17,19	10
2	AAL	H	4	10/11	0.81	0.41	2,13,15,16	10
2	AAL	E	8	10/11	0.94	0.17	22,26,28,29	0
2	GAL	F	5	11/12	0.95	0.08	19,23,29,31	0
2	GAL	E	5	11/12	0.96	0.10	22,27,31,40	0
2	GAL	E	7	11/12	0.97	0.10	19,22,25,34	0
2	AAL	F	8	10/11	0.97	0.16	19,22,24,31	0
2	GAL	G	5	11/12	0.97	0.06	16,17,21,26	0
2	GAL	H	5	11/12	0.97	0.07	12,15,20,23	0
2	GAL	H	7	11/12	0.97	0.07	12,13,18,24	0
2	AAL	E	6	10/11	0.98	0.08	15,18,21,23	0
2	AAL	H	8	10/11	0.98	0.08	13,16,19,21	0
2	GAL	G	7	11/12	0.98	0.09	14,15,20,25	0
2	AAL	G	6	10/11	0.98	0.06	13,15,18,19	0
2	AAL	G	8	10/11	0.98	0.08	15,16,18,18	0
2	GAL	F	7	11/12	0.98	0.09	14,16,20,30	0
2	AAL	F	6	10/11	0.98	0.05	12,16,18,20	0
2	AAL	H	6	10/11	0.98	0.06	9,12,14,17	0

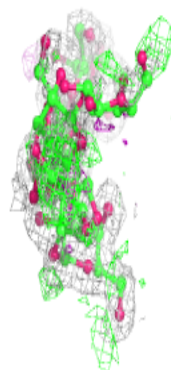
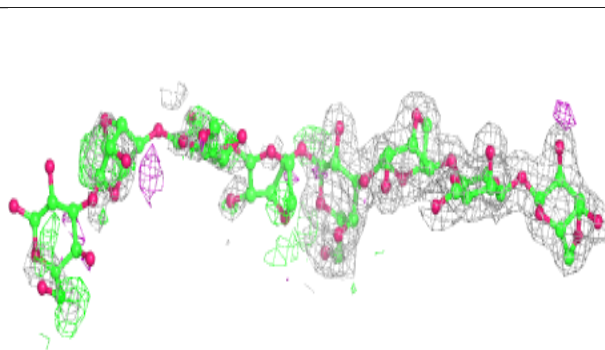
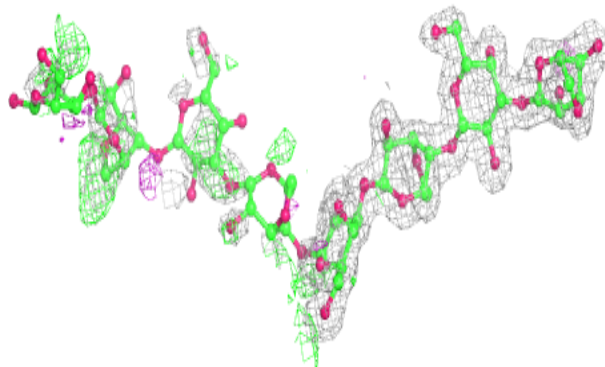
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

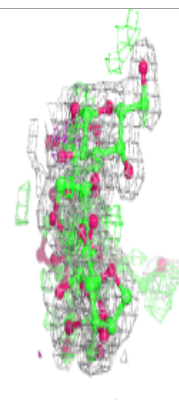
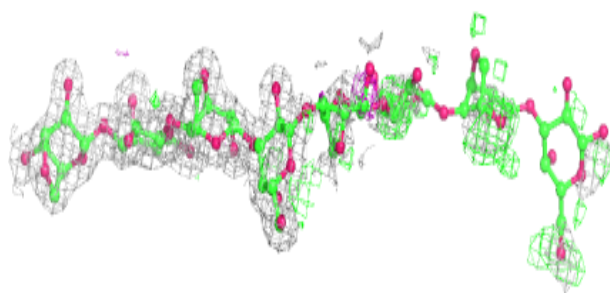
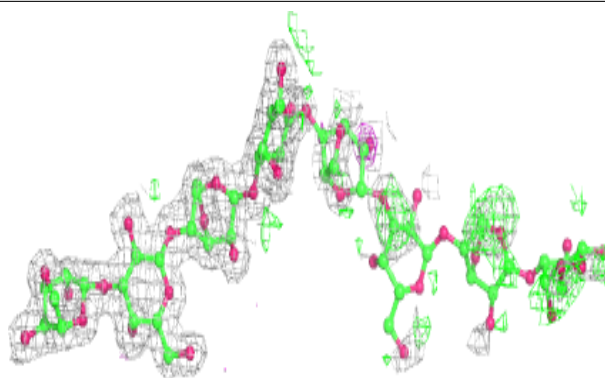
**Electron density around Chain F:**

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

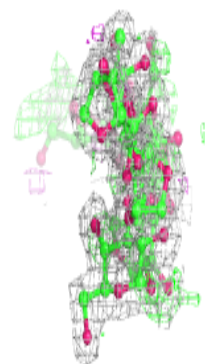
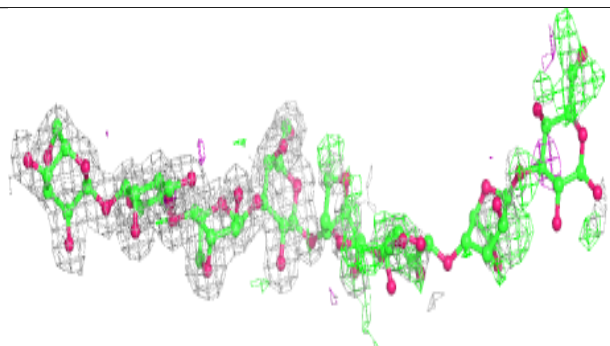
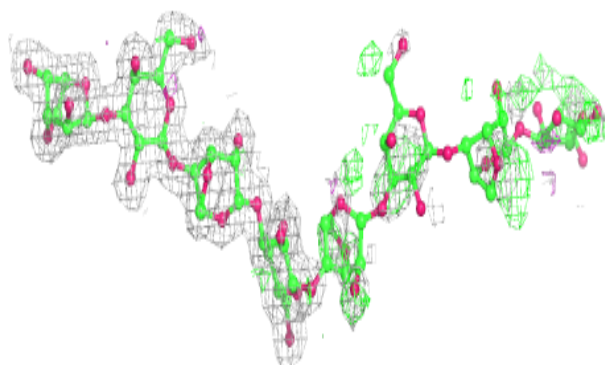


Electron density around Chain G:

$2mF_o-DF_c$ (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 [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(\AA^2)	Q<0.9
3	NA	C	500	1/1	0.99	0.05	22,22,22,22	0
3	NA	D	500	1/1	0.99	0.06	13,13,13,13	0
3	NA	B	500	1/1	1.00	0.03	14,14,14,14	0
3	NA	A	500	1/1	1.00	0.04	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.