



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:11 AM UTC

PDB ID : 6EPY / pdb_00006epy
Title : Structure of the PBP MelB (Atu4661) in complex with raffinose from A.fabrum C58
Authors : Morera, S.; Vigouroux, A.
Deposited on : 2017-10-12
Resolution : 2.04 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

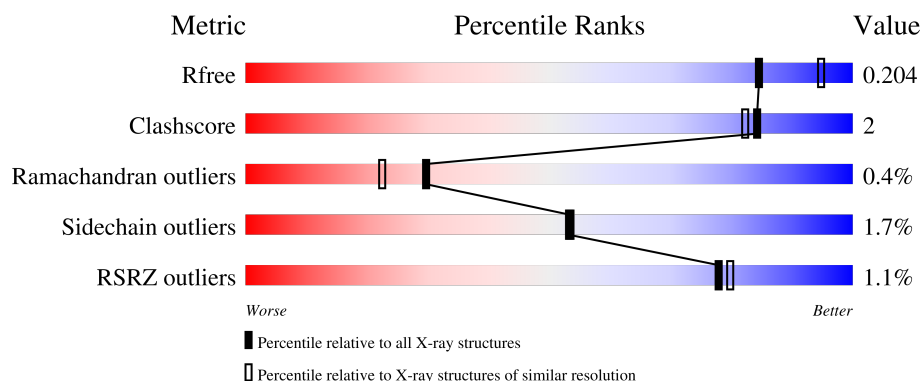
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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.



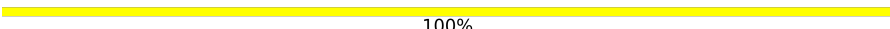
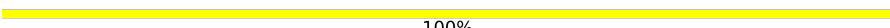
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	683	89% 8% .
1	B	683	91% 7% .
1	C	683	89% 8% .
1	D	683	88% 9% .
2	E	3	33% 67%

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

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
3	EDO	A	703	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 22571 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 Periplasmic alpha-galactoside-binding protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	669	Total	C	N	O	S	Se	0	2	0
			5291	3379	896	999	2	15			
1	B	669	Total	C	N	O	S	Se	0	1	0
			5285	3375	895	998	2	15			
1	C	669	Total	C	N	O	S	Se	0	1	0
			5285	3375	895	998	2	15			
1	D	665	Total	C	N	O	S	Se	0	0	0
			5254	3355	890	993	2	14			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	678	HIS	-	expression tag	UNP A0A083ZM57
A	679	HIS	-	expression tag	UNP A0A083ZM57
A	680	HIS	-	expression tag	UNP A0A083ZM57
A	681	HIS	-	expression tag	UNP A0A083ZM57
A	682	HIS	-	expression tag	UNP A0A083ZM57
A	683	HIS	-	expression tag	UNP A0A083ZM57
B	678	HIS	-	expression tag	UNP A0A083ZM57
B	679	HIS	-	expression tag	UNP A0A083ZM57
B	680	HIS	-	expression tag	UNP A0A083ZM57
B	681	HIS	-	expression tag	UNP A0A083ZM57
B	682	HIS	-	expression tag	UNP A0A083ZM57
B	683	HIS	-	expression tag	UNP A0A083ZM57
C	678	HIS	-	expression tag	UNP A0A083ZM57
C	679	HIS	-	expression tag	UNP A0A083ZM57
C	680	HIS	-	expression tag	UNP A0A083ZM57
C	681	HIS	-	expression tag	UNP A0A083ZM57
C	682	HIS	-	expression tag	UNP A0A083ZM57
C	683	HIS	-	expression tag	UNP A0A083ZM57
D	678	HIS	-	expression tag	UNP A0A083ZM57
D	679	HIS	-	expression tag	UNP A0A083ZM57
D	680	HIS	-	expression tag	UNP A0A083ZM57

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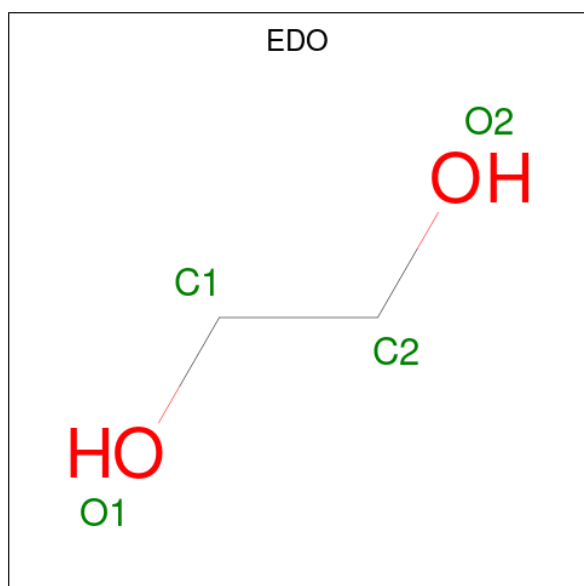
Chain	Residue	Modelled	Actual	Comment	Reference
D	681	HIS	-	expression tag	UNP A0A083ZM57
D	682	HIS	-	expression tag	UNP A0A083ZM57
D	683	HIS	-	expression tag	UNP A0A083ZM57

- Molecule 2 is an oligosaccharide called alpha-D-galactopyranose-(1-6)-alpha-D-glucopyranoside-(1-2)-beta-D-fructofuranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	3	Total	C	O	0	0	0
			34	18	16			
2	F	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 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	49	Total	Ca	0	0
			49	49		
4	B	36	Total	Ca	0	0
			36	36		
4	C	27	Total	Ca	0	0
			27	27		
4	D	13	Total	Ca	0	0
			13	13		

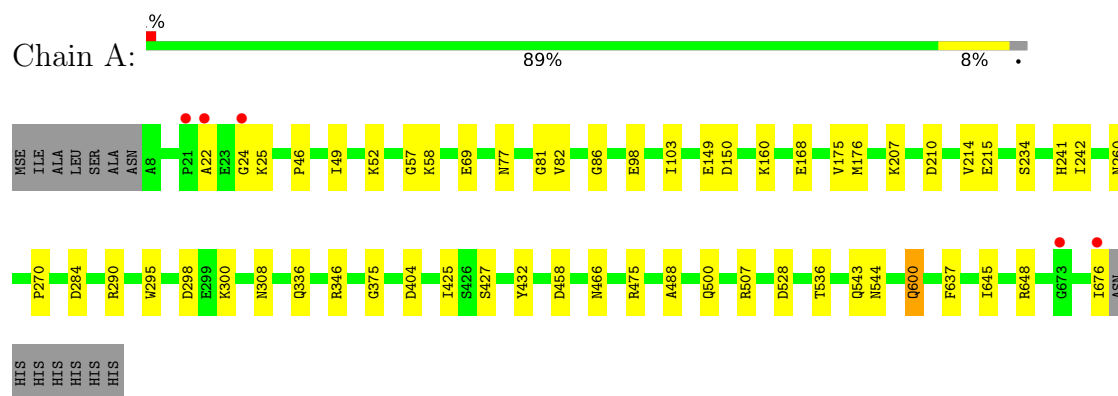
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	369	Total	O	0	0
			369	369		
5	B	333	Total	O	0	0
			333	333		
5	C	276	Total	O	0	0
			276	276		
5	D	201	Total	O	0	0
			201	201		

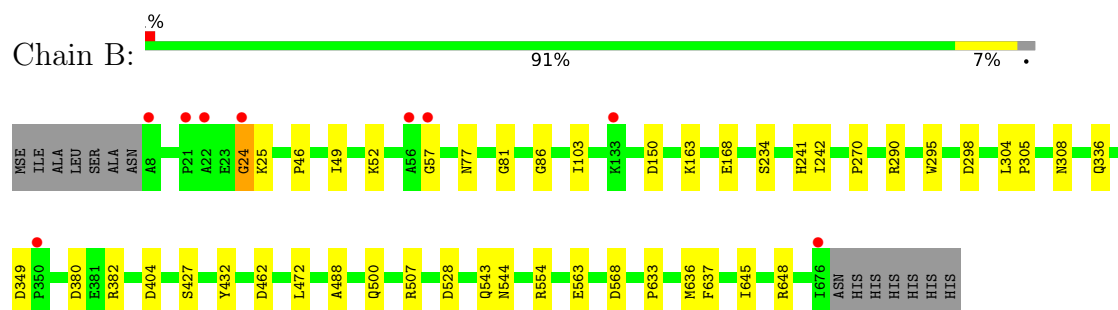
3 Residue-property plots

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.

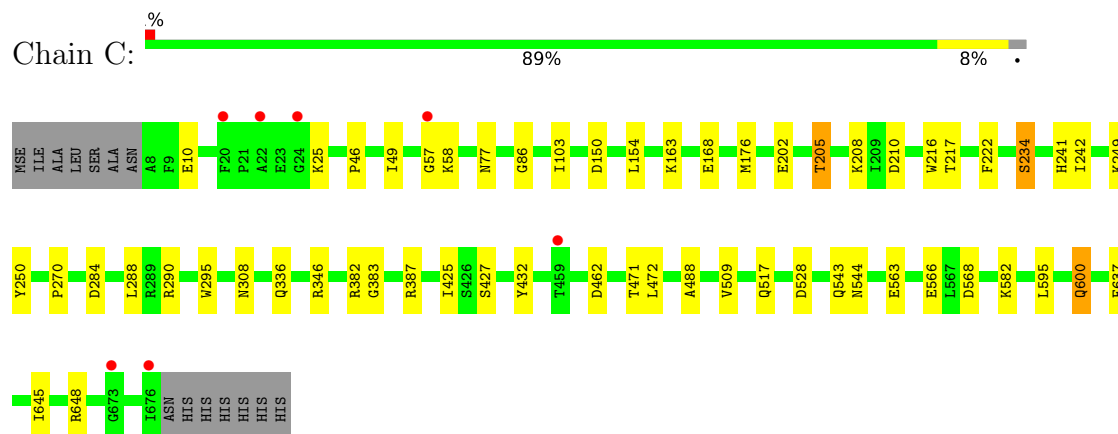
- Molecule 1: Periplasmic alpha-galactoside-binding protein



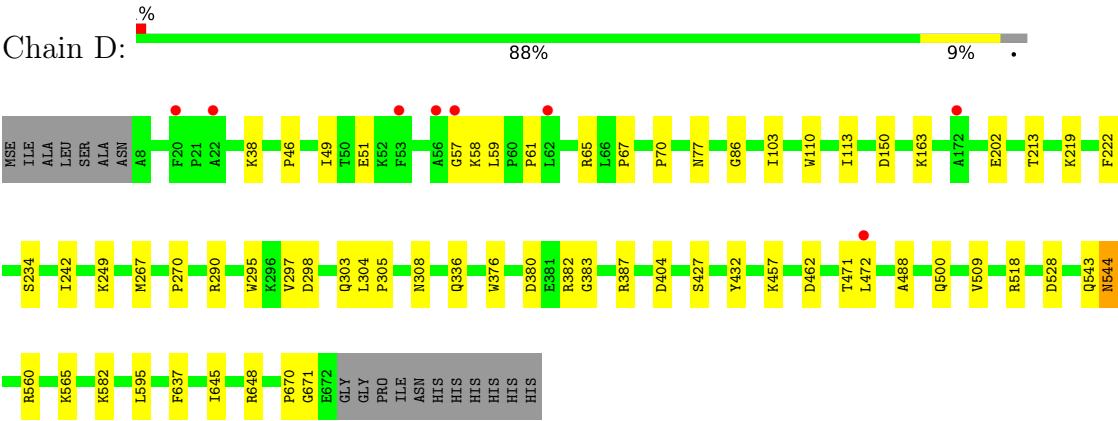
- Molecule 1: Periplasmic alpha-galactoside-binding protein



- Molecule 1: Periplasmic alpha-galactoside-binding protein



● Molecule 1: Periplasmic alpha-galactoside-binding protein



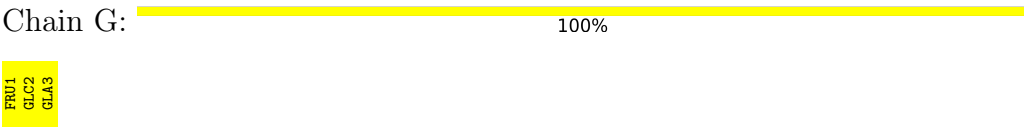
● Molecule 2: alpha-D-galactopyranose-(1-6)-alpha-D-glucopyranose-(1-2)-beta-D-fructofuranose



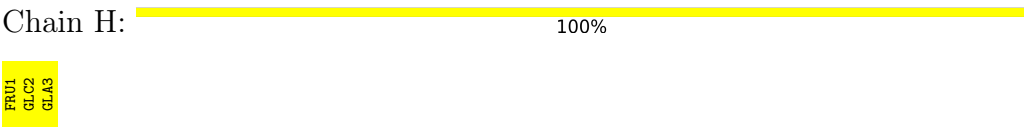
● Molecule 2: alpha-D-galactopyranose-(1-6)-alpha-D-glucopyranose-(1-2)-beta-D-fructofuranose



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● Molecule 2: alpha-D-galactopyranose-(1-6)-alpha-D-glucopyranose-(1-2)-beta-D-fructofuranose



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	354.30Å 74.27Å 108.22Å 90.00° 105.50° 90.00°	Depositor
Resolution (Å)	45.14 – 2.04 45.14 – 2.04	Depositor EDS
% Data completeness (in resolution range)	98.9 (45.14-2.04) 99.2 (45.14-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.05Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.174 , 0.200 0.177 , 0.204	Depositor DCC
R_{free} test set	8544 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.9	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for -h-2*1,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	22571	wwPDB-VP
Average B, all atoms (Å ²)	44.0	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 59.27 % 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 1.8080e-05. 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: GLA, GLC, EDO, FRU, CA

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	0.86	0/5432	1.12	13/7367 (0.2%)
1	B	0.86	0/5423	1.12	12/7355 (0.2%)
1	C	0.83	1/5423 (0.0%)	1.12	11/7355 (0.1%)
1	D	0.81	1/5391 (0.0%)	1.16	14/7312 (0.2%)
All	All	0.84	2/21669 (0.0%)	1.13	50/29389 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	222	PHE	CA-C	5.91	1.57	1.53
1	C	222	PHE	CA-C	5.34	1.57	1.53

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	57	GLY	CA-C-N	6.45	133.85	121.54
1	D	57	GLY	C-N-CA	6.45	133.85	121.54
1	B	86	GLY	N-CA-C	5.87	118.01	112.08
1	C	528	ASP	CA-CB-CG	5.87	118.47	112.60
1	A	528	ASP	CA-CB-CG	5.84	118.44	112.60

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	5291	0	5114	28	0
1	B	5285	0	5107	19	0
1	C	5285	0	5107	25	0
1	D	5254	0	5075	26	0
2	E	34	0	30	0	0
2	F	34	0	30	1	0
2	G	34	0	30	0	0
2	H	34	0	30	0	0
3	A	8	0	11	5	0
3	C	4	0	6	0	0
3	D	4	0	6	0	0
4	A	49	0	0	0	0
4	B	36	0	0	0	0
4	C	27	0	0	0	0
4	D	13	0	0	0	0
5	A	369	0	0	0	0
5	B	333	0	0	1	0
5	C	276	0	0	0	0
5	D	201	0	0	1	0
All	All	22571	0	20546	96	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 96 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:D:59:LEU:O	1:D:61:PRO:HD3	1.77	0.85
1:D:267:MSE:O	1:D:671:GLY:HA2	1.76	0.85
1:A:507:ARG:HD2	1:C:509:VAL:HG11	1.63	0.79
1:C:425:ILE:H	1:C:600:GLN:HE22	1.29	0.79
1:A:425:ILE:H	1:A:600:GLN:HE22	1.31	0.78

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	A	669/683 (98%)	644 (96%)	21 (3%)	4 (1%)	21	13
1	B	668/683 (98%)	639 (96%)	27 (4%)	2 (0%)	36	30
1	C	668/683 (98%)	645 (97%)	21 (3%)	2 (0%)	36	30
1	D	663/683 (97%)	629 (95%)	32 (5%)	2 (0%)	36	30
All	All	2668/2732 (98%)	2557 (96%)	101 (4%)	10 (0%)	30	22

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	58	LYS
1	A	22	ALA
1	A	58	LYS
1	C	58	LYS
1	B	24	GLY

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	558/553 (101%)	550 (99%)	8 (1%)	59	60
1	B	557/553 (101%)	553 (99%)	4 (1%)	76	80
1	C	557/553 (101%)	544 (98%)	13 (2%)	44	42
1	D	554/553 (100%)	542 (98%)	12 (2%)	45	44
All	All	2226/2212 (101%)	2189 (98%)	37 (2%)	53	53

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	163	LYS
1	D	518	ARG
1	D	213	THR
1	D	249	LYS
1	C	10	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	27	ASN
1	D	516	ASN
1	C	336	GLN
1	D	336	GLN
1	D	598	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 ⓘ

12 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	FRU	E	1	2	11,12,12	1.83	1 (9%)	10,18,18	0.73	0
2	GLC	E	2	2	11,11,12	0.87	0	15,15,17	0.93	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLA	E	3	2	11,11,12	1.28	1 (9%)	15,15,17	1.44	2 (13%)
2	FRU	F	1	2	11,12,12	1.86	1 (9%)	10,18,18	0.84	0
2	GLC	F	2	2	11,11,12	1.41	1 (9%)	15,15,17	1.05	2 (13%)
2	GLA	F	3	2	11,11,12	1.34	1 (9%)	15,15,17	1.06	1 (6%)
2	FRU	G	1	2	11,12,12	2.33	1 (9%)	10,18,18	0.87	0
2	GLC	G	2	2	11,11,12	1.15	1 (9%)	15,15,17	1.08	1 (6%)
2	GLA	G	3	2	11,11,12	1.23	1 (9%)	15,15,17	1.03	1 (6%)
2	FRU	H	1	2	11,12,12	2.07	1 (9%)	10,18,18	0.66	0
2	GLC	H	2	2	11,11,12	1.34	2 (18%)	15,15,17	1.07	1 (6%)
2	GLA	H	3	2	11,11,12	1.26	1 (9%)	15,15,17	0.94	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	FRU	E	1	2	-	1/5/24/24	0/1/1/1
2	GLC	E	2	2	-	2/2/19/22	0/1/1/1
2	GLA	E	3	2	-	0/2/19/22	0/1/1/1
2	FRU	F	1	2	-	4/5/24/24	0/1/1/1
2	GLC	F	2	2	-	2/2/19/22	0/1/1/1
2	GLA	F	3	2	-	0/2/19/22	0/1/1/1
2	FRU	G	1	2	-	4/5/24/24	0/1/1/1
2	GLC	G	2	2	-	2/2/19/22	0/1/1/1
2	GLA	G	3	2	-	0/2/19/22	0/1/1/1
2	FRU	H	1	2	-	4/5/24/24	0/1/1/1
2	GLC	H	2	2	-	2/2/19/22	0/1/1/1
2	GLA	H	3	2	-	0/2/19/22	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1	FRU	O2-C2	7.34	1.53	1.40
2	H	1	FRU	O2-C2	6.48	1.52	1.40
2	F	1	FRU	O2-C2	5.78	1.50	1.40
2	E	1	FRU	O2-C2	5.44	1.50	1.40
2	F	2	GLC	O5-C1	3.28	1.49	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	3	GLA	C1-O5-C5	4.45	118.15	112.19
2	H	2	GLC	C1-O5-C5	2.87	116.03	112.19
2	G	2	GLC	C1-O5-C5	2.86	116.01	112.19
2	F	3	GLA	C1-O5-C5	2.51	115.55	112.19
2	F	2	GLC	C1-O5-C5	2.40	115.40	112.19

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

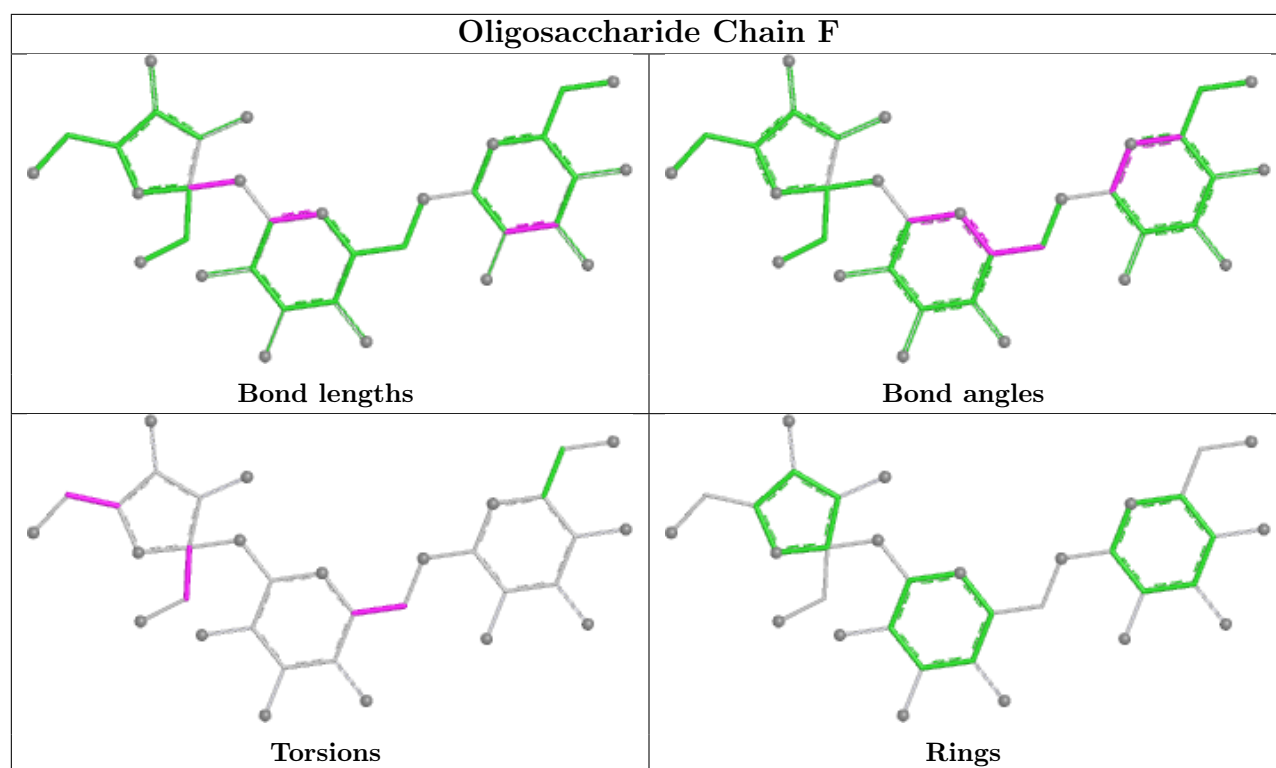
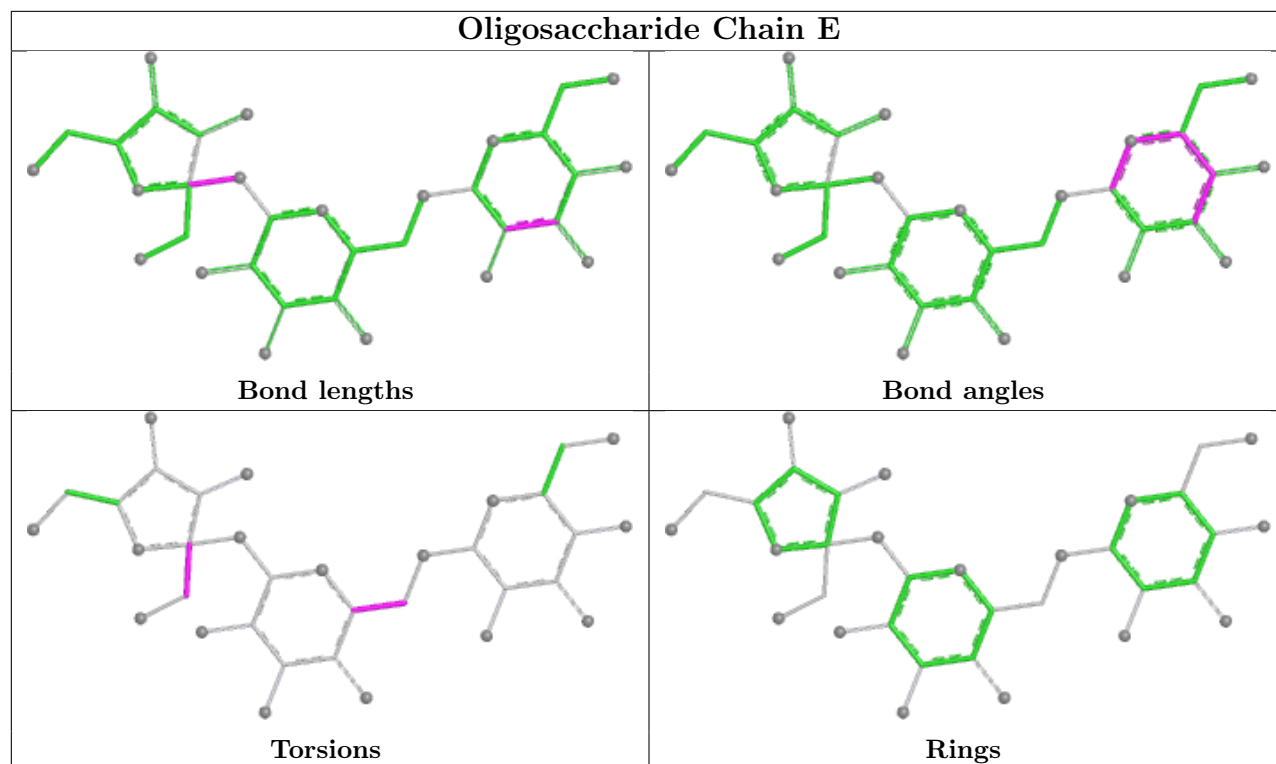
Mol	Chain	Res	Type	Atoms
2	F	1	FRU	O1-C1-C2-C3
2	F	1	FRU	O1-C1-C2-O2
2	F	1	FRU	O1-C1-C2-O5
2	G	1	FRU	O1-C1-C2-C3
2	G	1	FRU	O1-C1-C2-O2

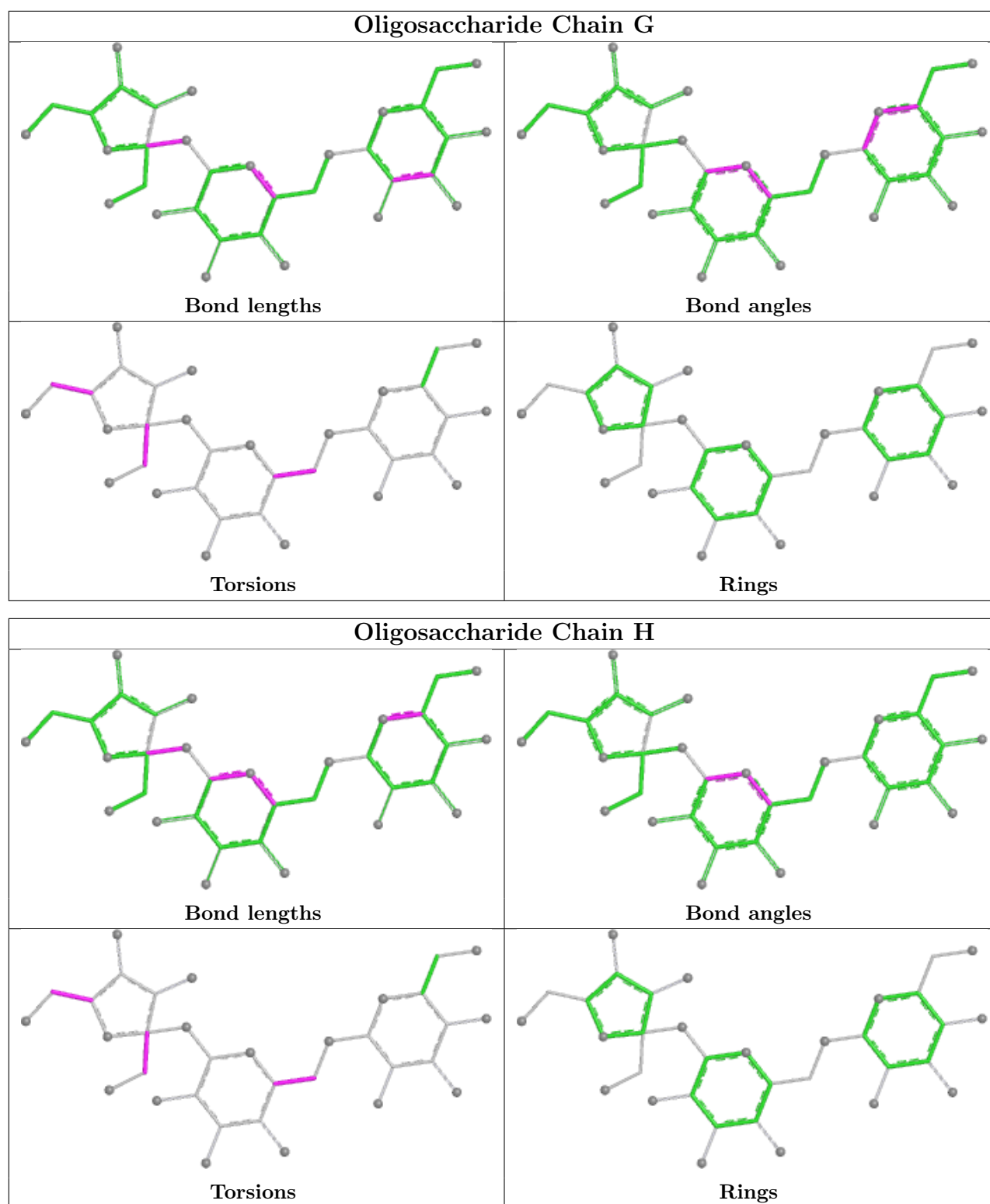
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	FRU	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](#)

Of 129 ligands modelled in this entry, 125 are monoatomic - leaving 4 for Mogul analysis.

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	EDO	D	702	-	3,3,3	0.49	0	2,2,2	0.40	0
3	EDO	A	702	4	3,3,3	0.53	0	2,2,2	0.30	0
3	EDO	A	703	-	3,3,3	0.80	0	2,2,2	0.79	0
3	EDO	C	702	-	3,3,3	0.52	0	2,2,2	0.34	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	EDO	D	702	-	-	1/1/1/1	-
3	EDO	A	702	4	-	0/1/1/1	-
3	EDO	A	703	-	-	0/1/1/1	-
3	EDO	C	702	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	702	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	EDO	1	0
3	A	703	EDO	4	0

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	655/683 (95%)	-0.27	5 (0%) 82 84	22, 35, 62, 90	1 (0%)
1	B	655/683 (95%)	-0.19	9 (1%) 73 75	25, 37, 65, 89	0
1	C	655/683 (95%)	-0.12	7 (1%) 78 80	26, 41, 77, 98	0
1	D	651/683 (95%)	0.15	8 (1%) 76 78	30, 50, 85, 120	0
All	All	2616/2732 (95%)	-0.11	29 (1%) 78 80	22, 41, 75, 120	1 (0%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	676	ILE	4.6
1	A	24	GLY	4.5
1	C	459	THR	3.2
1	B	56	ALA	3.1
1	B	24	GLY	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.

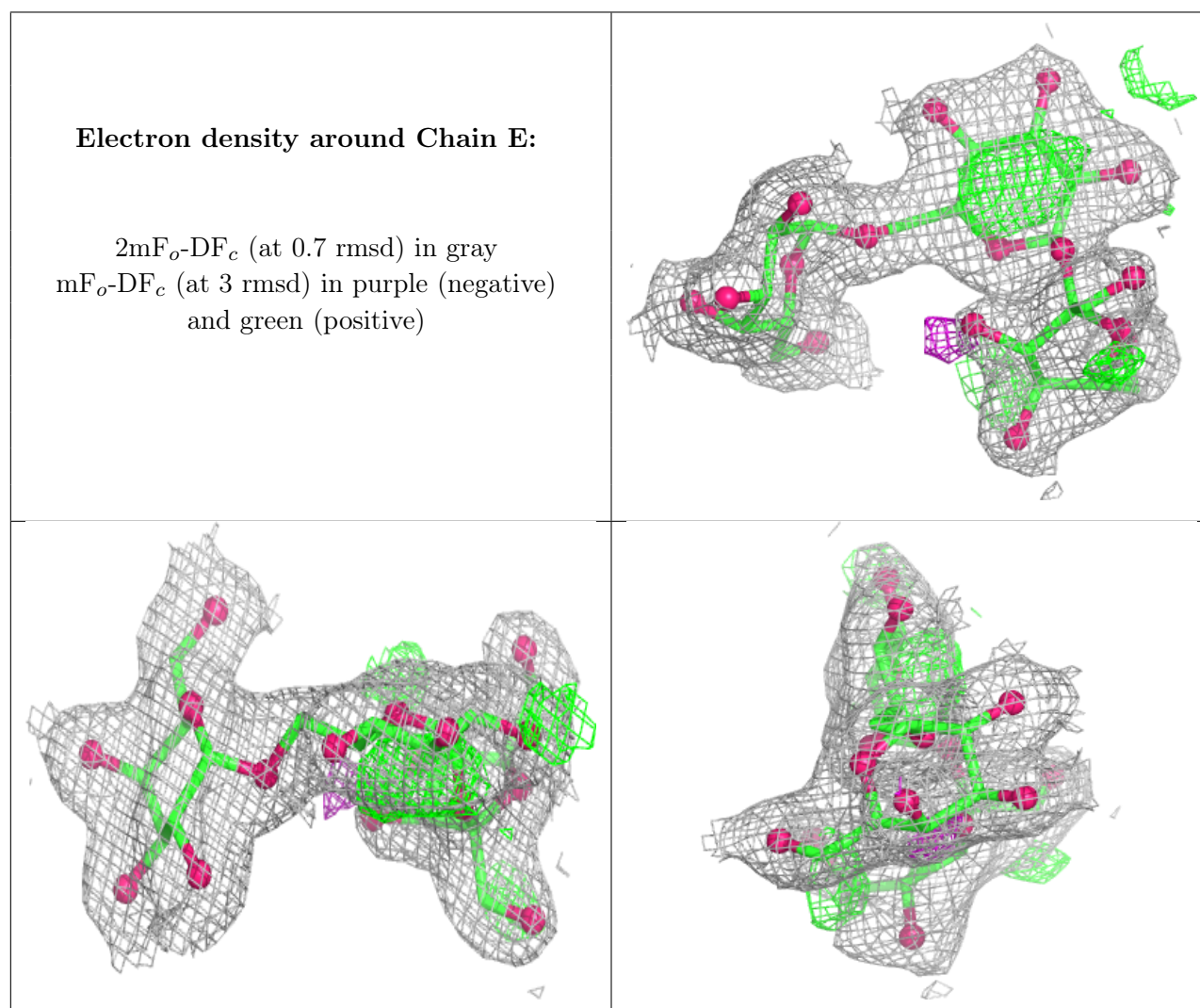
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FRU	H	1	12/12	0.86	0.13	48,55,61,63	0
2	FRU	E	1	12/12	0.87	0.13	44,49,50,52	0

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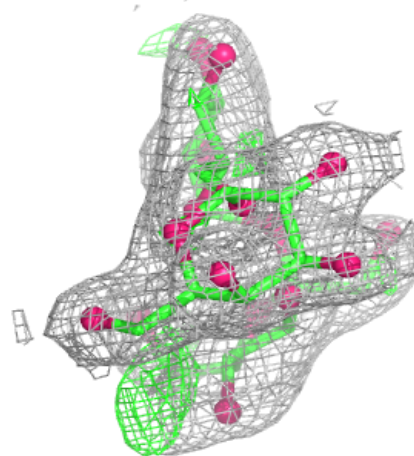
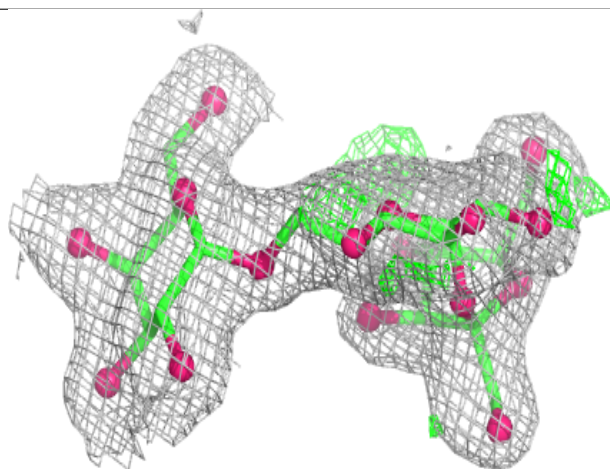
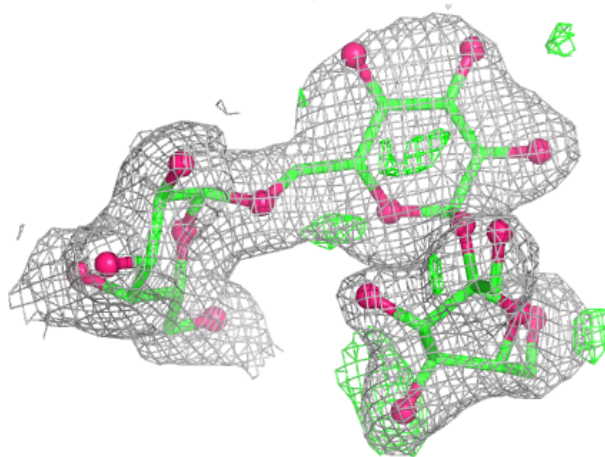
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FRU	G	1	12/12	0.88	0.12	41,45,47,47	0
2	FRU	F	1	12/12	0.88	0.13	44,52,54,56	0
2	GLC	F	2	11/12	0.92	0.11	34,42,54,57	0
2	GLC	E	2	11/12	0.93	0.09	28,40,48,51	0
2	GLC	G	2	11/12	0.94	0.08	31,40,49,52	0
2	GLC	H	2	11/12	0.94	0.08	36,52,55,56	0
2	GLA	F	3	11/12	0.97	0.06	26,27,29,32	0
2	GLA	H	3	11/12	0.97	0.05	28,31,33,33	0
2	GLA	G	3	11/12	0.98	0.05	22,27,30,31	0
2	GLA	E	3	11/12	0.98	0.04	23,25,27,29	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.



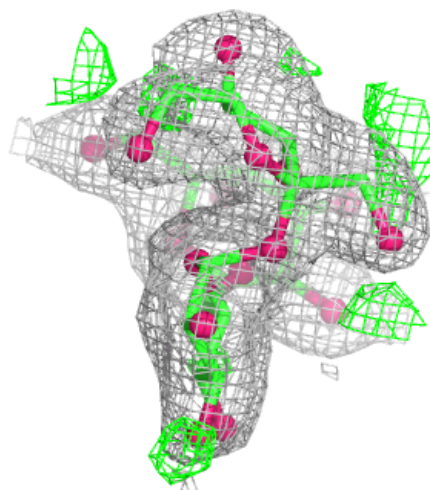
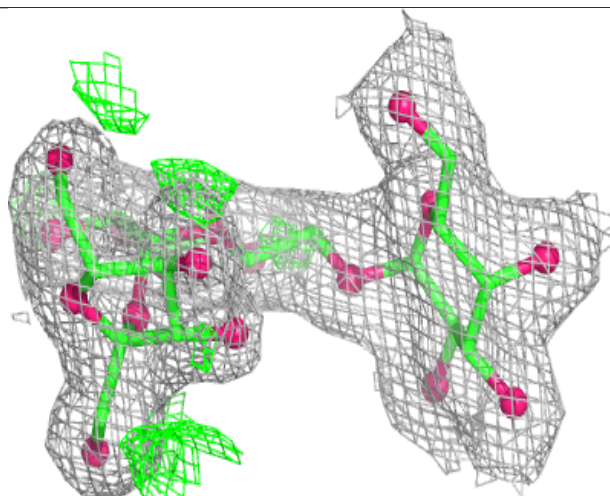
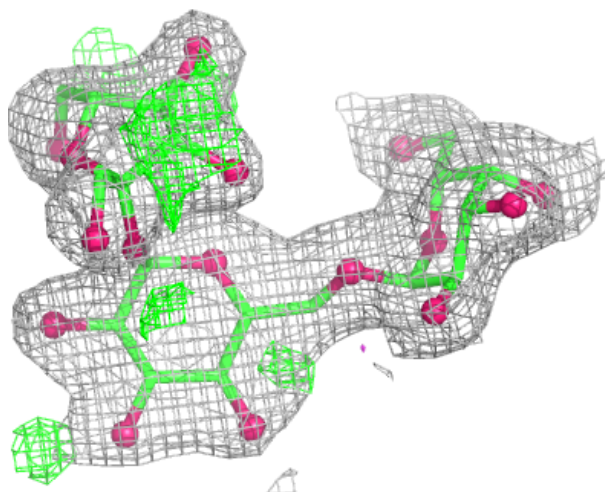
Electron density around Chain F:

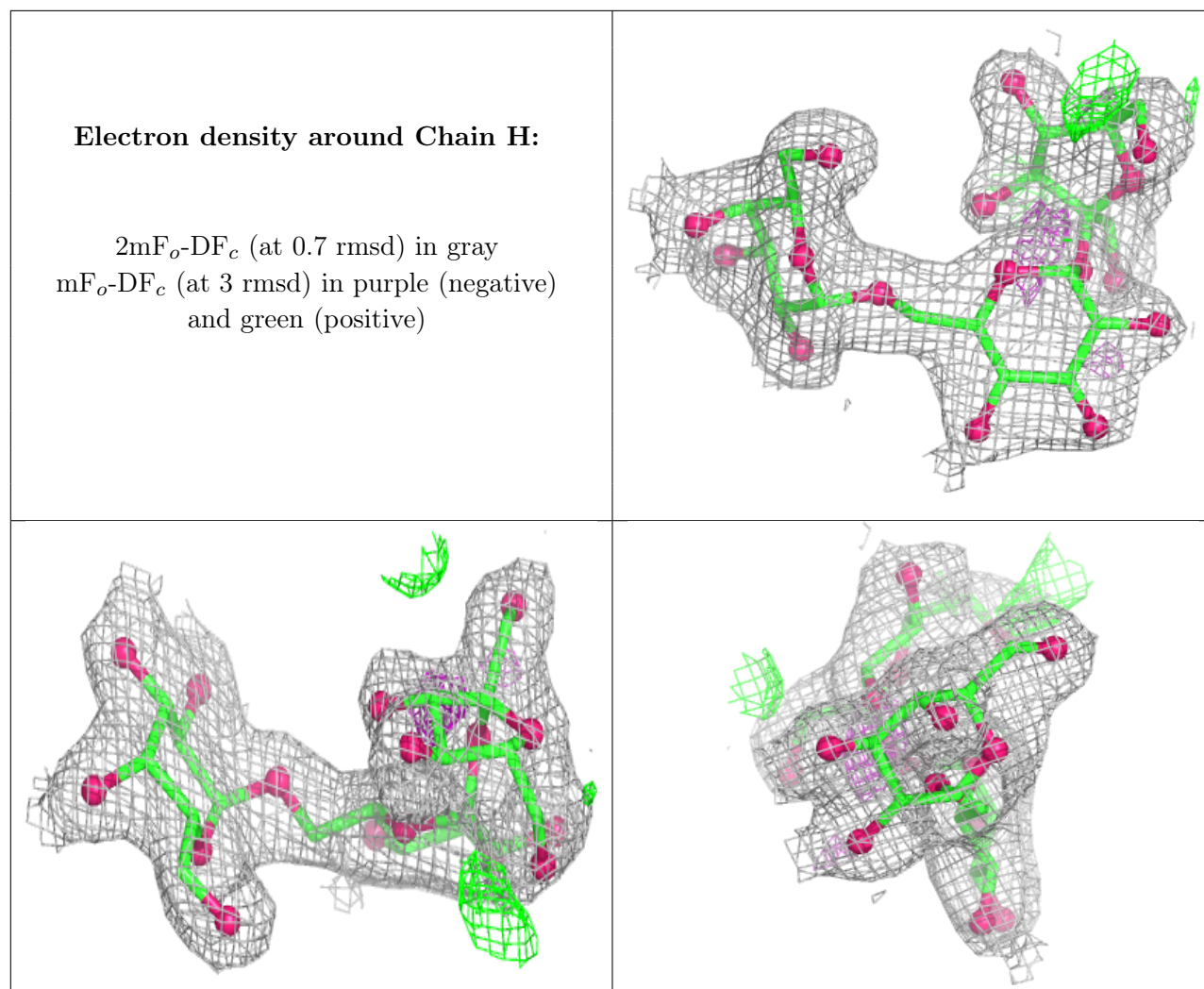
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.4 Ligands ⓘ

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
4	CA	A	731	1/1	0.43	0.27	204,204,204,204	1
3	EDO	A	702	4/4	0.61	0.15	54,55,56,57	0
4	CA	D	714	1/1	0.64	0.12	109,109,109,109	0
3	EDO	C	702	4/4	0.70	0.14	67,67,68,68	0
4	CA	C	727	1/1	0.73	0.12	110,110,110,110	0
3	EDO	D	702	4/4	0.79	0.12	71,72,75,75	0
4	CA	A	750	1/1	0.79	0.18	86,86,86,86	0
4	CA	A	751	1/1	0.81	0.12	91,91,91,91	0
4	CA	D	709	1/1	0.82	0.11	105,105,105,105	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	B	718	1/1	0.83	0.19	82,82,82,82	0
4	CA	D	713	1/1	0.84	0.14	86,86,86,86	0
4	CA	A	726	1/1	0.84	0.17	79,79,79,79	0
4	CA	A	732	1/1	0.85	0.10	85,85,85,85	0
4	CA	D	708	1/1	0.86	0.09	104,104,104,104	0
4	CA	A	729	1/1	0.86	0.17	81,81,81,81	0
4	CA	A	730	1/1	0.87	0.12	87,87,87,87	0
4	CA	B	725	1/1	0.87	0.10	77,77,77,77	0
4	CA	D	711	1/1	0.87	0.15	89,89,89,89	0
4	CA	D	712	1/1	0.87	0.21	85,85,85,85	0
4	CA	C	712	1/1	0.87	0.22	74,74,74,74	0
4	CA	A	733	1/1	0.87	0.10	94,94,94,94	0
4	CA	B	737	1/1	0.88	0.19	75,75,75,75	0
4	CA	B	723	1/1	0.88	0.14	74,74,74,74	0
4	CA	B	721	1/1	0.88	0.09	68,68,68,68	0
4	CA	A	752	1/1	0.89	0.14	94,94,94,94	0
4	CA	A	728	1/1	0.90	0.11	87,87,87,87	0
4	CA	C	707	1/1	0.90	0.17	88,88,88,88	0
4	CA	A	721	1/1	0.90	0.10	81,81,81,81	0
4	CA	A	718	1/1	0.90	0.08	78,78,78,78	0
4	CA	B	711	1/1	0.90	0.09	82,82,82,82	0
4	CA	A	710	1/1	0.91	0.07	72,72,72,72	0
4	CA	A	723	1/1	0.91	0.16	72,72,72,72	0
4	CA	C	722	1/1	0.91	0.11	86,86,86,86	0
3	EDO	A	703	4/4	0.91	0.15	33,38,39,40	0
4	CA	C	728	1/1	0.91	0.21	67,67,67,67	0
4	CA	D	704	1/1	0.91	0.07	58,58,58,58	0
4	CA	A	734	1/1	0.92	0.21	68,68,68,68	0
4	CA	C	715	1/1	0.92	0.13	79,79,79,79	0
4	CA	A	717	1/1	0.92	0.11	78,78,78,78	0
4	CA	B	719	1/1	0.92	0.09	81,81,81,81	0
4	CA	B	710	1/1	0.92	0.08	80,80,80,80	0
4	CA	C	711	1/1	0.92	0.09	94,94,94,94	0
4	CA	B	715	1/1	0.93	0.12	58,58,58,58	0
4	CA	C	724	1/1	0.93	0.13	71,71,71,71	0
4	CA	C	725	1/1	0.93	0.17	73,73,73,73	0
4	CA	B	717	1/1	0.93	0.28	65,65,65,65	0
4	CA	A	744	1/1	0.93	0.15	62,62,62,62	0
4	CA	A	741	1/1	0.93	0.29	64,64,64,64	0
4	CA	C	718	1/1	0.94	0.29	56,56,56,56	0
4	CA	B	716	1/1	0.94	0.08	84,84,84,84	0
4	CA	B	726	1/1	0.94	0.23	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	B	728	1/1	0.94	0.25	63,63,63,63	0
4	CA	B	732	1/1	0.94	0.17	62,62,62,62	0
4	CA	B	736	1/1	0.94	0.19	71,71,71,71	0
4	CA	A	722	1/1	0.94	0.13	67,67,67,67	0
4	CA	A	749	1/1	0.94	0.23	65,65,65,65	0
4	CA	C	710	1/1	0.94	0.07	85,85,85,85	0
4	CA	A	727	1/1	0.94	0.12	76,76,76,76	0
4	CA	B	712	1/1	0.94	0.08	69,69,69,69	0
4	CA	C	714	1/1	0.94	0.24	59,59,59,59	0
4	CA	A	743	1/1	0.94	0.17	69,69,69,69	0
4	CA	C	713	1/1	0.95	0.12	50,50,50,50	0
4	CA	B	720	1/1	0.95	0.16	63,63,63,63	0
4	CA	C	729	1/1	0.95	0.25	64,64,64,64	0
4	CA	A	713	1/1	0.95	0.15	70,70,70,70	0
4	CA	C	708	1/1	0.95	0.10	57,57,57,57	0
4	CA	C	719	1/1	0.95	0.23	59,59,59,59	0
4	CA	D	710	1/1	0.95	0.11	65,65,65,65	0
4	CA	A	719	1/1	0.95	0.14	50,50,50,50	0
4	CA	B	735	1/1	0.95	0.23	68,68,68,68	0
4	CA	A	720	1/1	0.95	0.11	75,75,75,75	0
4	CA	C	726	1/1	0.95	0.12	62,62,62,62	0
4	CA	A	708	1/1	0.96	0.10	58,58,58,58	0
4	CA	B	724	1/1	0.96	0.12	61,61,61,61	0
4	CA	A	724	1/1	0.96	0.11	48,48,48,48	0
4	CA	B	702	1/1	0.96	0.06	60,60,60,60	0
4	CA	A	725	1/1	0.96	0.17	60,60,60,60	0
4	CA	B	729	1/1	0.96	0.26	61,61,61,61	0
4	CA	B	730	1/1	0.96	0.13	70,70,70,70	0
4	CA	A	736	1/1	0.96	0.21	67,67,67,67	0
4	CA	C	716	1/1	0.96	0.24	52,52,52,52	0
4	CA	A	740	1/1	0.96	0.17	68,68,68,68	0
4	CA	B	714	1/1	0.96	0.16	61,61,61,61	0
4	CA	B	722	1/1	0.96	0.10	69,69,69,69	0
4	CA	C	704	1/1	0.96	0.05	47,47,47,47	0
4	CA	D	715	1/1	0.96	0.20	74,74,74,74	0
4	CA	B	707	1/1	0.97	0.08	52,52,52,52	0
4	CA	C	709	1/1	0.97	0.09	49,49,49,49	0
4	CA	B	708	1/1	0.97	0.12	51,51,51,51	0
4	CA	A	746	1/1	0.97	0.17	60,60,60,60	0
4	CA	B	731	1/1	0.97	0.18	56,56,56,56	0
4	CA	A	714	1/1	0.97	0.19	63,63,63,63	0
4	CA	D	706	1/1	0.97	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	B	733	1/1	0.97	0.27	61,61,61,61	0
4	CA	A	737	1/1	0.97	0.24	63,63,63,63	0
4	CA	A	738	1/1	0.97	0.09	47,47,47,47	0
4	CA	A	739	1/1	0.97	0.20	55,55,55,55	0
4	CA	A	745	1/1	0.97	0.20	56,56,56,56	0
4	CA	C	721	1/1	0.97	0.22	54,54,54,54	0
4	CA	C	705	1/1	0.97	0.06	53,53,53,53	0
4	CA	B	703	1/1	0.97	0.04	52,52,52,52	0
4	CA	B	734	1/1	0.98	0.22	60,60,60,60	0
4	CA	D	703	1/1	0.98	0.06	57,57,57,57	0
4	CA	A	747	1/1	0.98	0.26	56,56,56,56	0
4	CA	D	705	1/1	0.98	0.05	57,57,57,57	0
4	CA	C	720	1/1	0.98	0.17	62,62,62,62	0
4	CA	A	706	1/1	0.98	0.03	52,52,52,52	0
4	CA	B	705	1/1	0.98	0.06	45,45,45,45	0
4	CA	C	723	1/1	0.98	0.26	63,63,63,63	0
4	CA	A	716	1/1	0.98	0.07	52,52,52,52	0
4	CA	A	735	1/1	0.98	0.16	44,44,44,44	0
4	CA	B	709	1/1	0.98	0.11	42,42,42,42	0
4	CA	A	742	1/1	0.98	0.15	60,60,60,60	0
4	CA	C	717	1/1	0.98	0.28	51,51,51,51	0
4	CA	C	703	1/1	0.99	0.05	41,41,41,41	0
4	CA	B	727	1/1	0.99	0.20	50,50,50,50	0
4	CA	A	712	1/1	0.99	0.10	41,41,41,41	0
4	CA	C	706	1/1	0.99	0.08	49,49,49,49	0
4	CA	A	705	1/1	0.99	0.04	33,33,33,33	0
4	CA	D	707	1/1	0.99	0.14	48,48,48,48	0
4	CA	A	709	1/1	0.99	0.07	47,47,47,47	0
4	CA	A	715	1/1	0.99	0.06	40,40,40,40	0
4	CA	A	707	1/1	0.99	0.03	38,38,38,38	0
4	CA	A	711	1/1	0.99	0.08	41,41,41,41	0
4	CA	B	713	1/1	0.99	0.10	62,62,62,62	0
4	CA	B	704	1/1	0.99	0.03	39,39,39,39	0
4	CA	A	748	1/1	0.99	0.30	50,50,50,50	0
4	CA	B	706	1/1	0.99	0.02	36,36,36,36	0
4	CA	A	704	1/1	1.00	0.01	41,41,41,41	0

6.5 Other polymers

There are no such residues in this entry.