



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 04:48 am BST

PDB ID : 5A3M
Title : Structure of Cea1A in complex with Chitobiose
Authors : Kock, M.; Brueckner, S.; Wozniak, N.; Veelders, M.; Schlereth, J.; Moesch, H.-U.; Essen, L.-O.
Deposited on : 2015-06-02
Resolution : 1.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
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) : 2.36.2

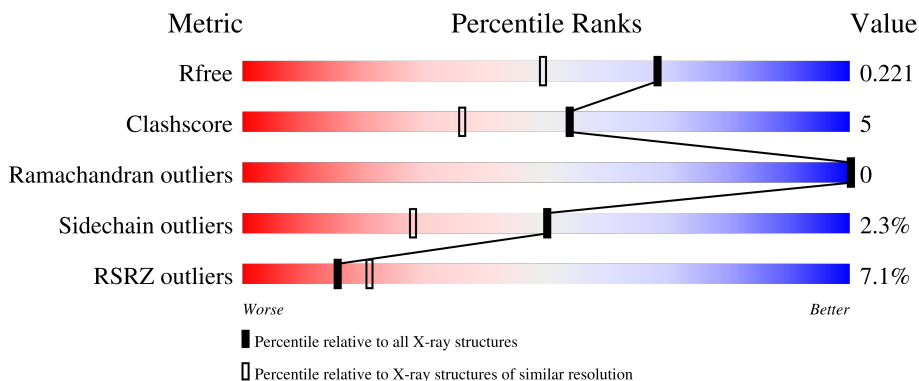
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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.





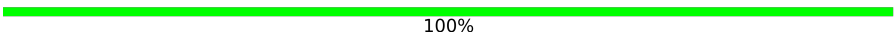
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	240	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 76%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 10%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 13%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 10px;">3% 76% 10% 13%</p>
1	B	240	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 80%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 13%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 10px;">2% 80% 6% • 13%</p>
1	C	240	<div style="display: flex; align-items: center;"> <div style="width: 10%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 77%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 10px;">10% 77% 5% • 16%</p>
1	D	240	<div style="display: flex; align-items: center;"> <div style="width: 10%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 75%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 10px;">10% 75% 8% 16%</p>
2	E	2	<div style="display: flex; align-items: center;"> <div style="width: 50%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 50%; height: 10px; background-color: yellow;"></div> </div> <p style="margin-left: 10px;">50% 50%</p>

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Mol	Chain	Length	Quality of chain
2	F	2	 50% 50%
2	G	2	 50% 50%
2	H	2	 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
4	PEG	A	1242	-	-	X	-
4	PEG	A	1243	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 8031 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 CEA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	209	Total 1714	C 1100	N 273	O 334	S 7	0	10	0
1	B	209	Total 1717	C 1099	N 277	O 334	S 7	0	11	0
1	C	201	Total 1646	C 1061	N 265	O 314	S 6	0	11	0
1	D	202	Total 1622	C 1041	N 259	O 316	S 6	0	5	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	2	Total 29	C 16	N 2	O 11	0	0	0
2	F	2	Total 58	C 32	N 4	O 22	0	2	0
2	G	2	Total 29	C 16	N 2	O 11	0	0	0
2	H	2	Total 29	C 16	N 2	O 11	0	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

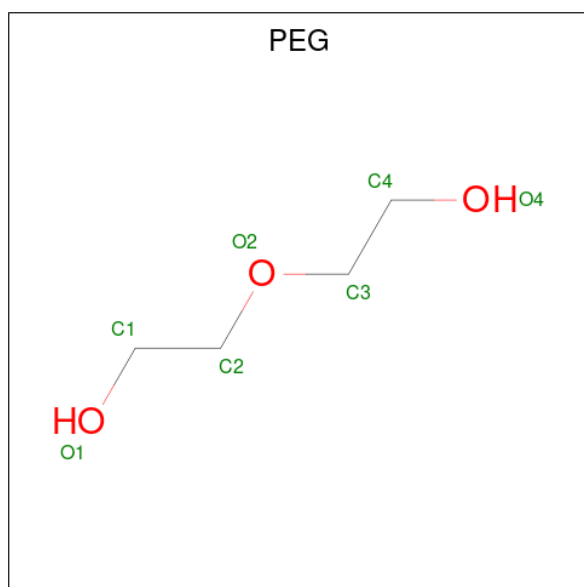
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Ca 1	0	0

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	B	1	Total C O 7 4 3	0	0

- Molecule 5 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Na 1 1	0	0
7	C	2	Total Na 2 2	0	0
7	D	1	Total Na 1 1	0	0

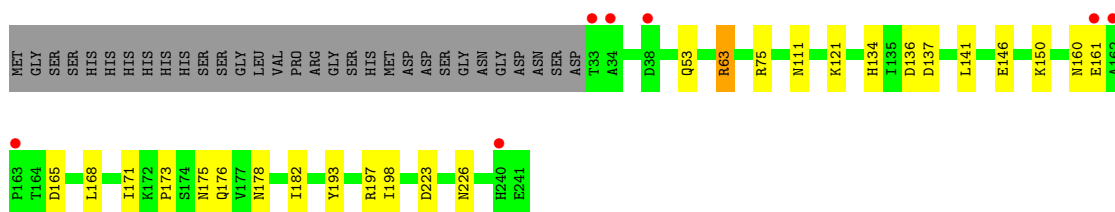
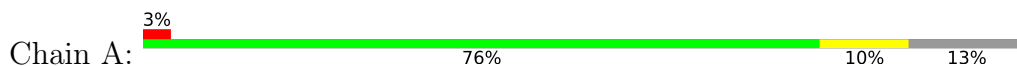
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	297	Total O 320 320	0	23
8	B	309	Total O 325 325	0	16
8	C	231	Total O 238 238	0	7
8	D	240	Total O 250 250	0	10

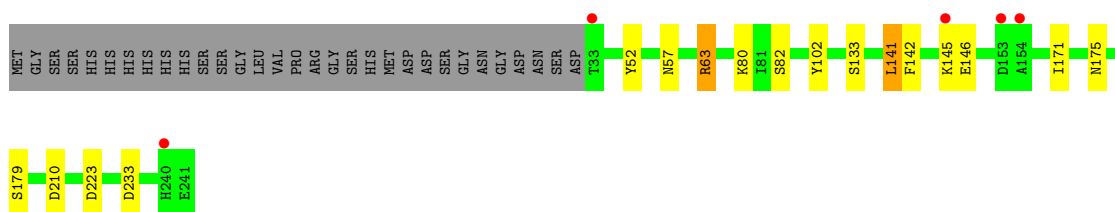
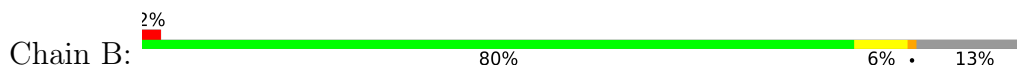
3 Residue-property plots

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.

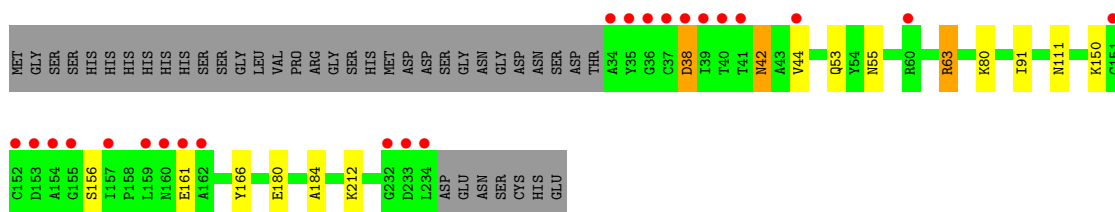
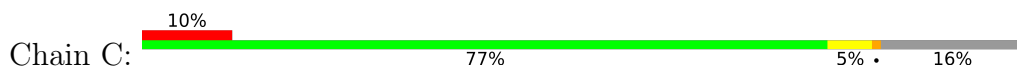
- Molecule 1: CEA1



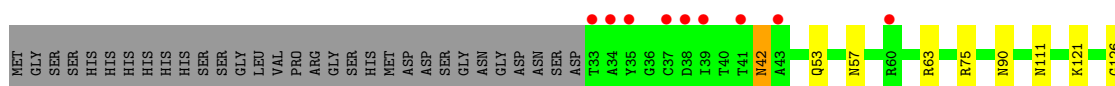
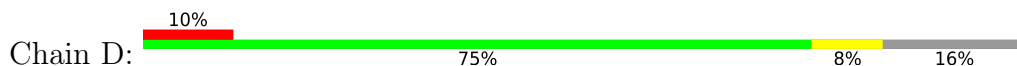
- Molecule 1: CEA1

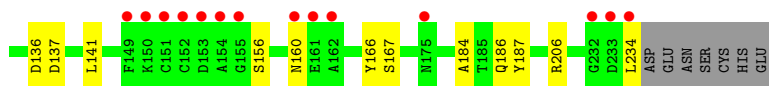


- Molecule 1: CEA1



- Molecule 1: CEA1





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

Chain E: 50% 50%



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

Chain F: 50% 50%



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

Chain G: 50% 50%



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

Chain H: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	101.70Å 105.35Å 106.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 1.75 19.98 – 1.75	Depositor EDS
% Data completeness (in resolution range)	92.2 (19.99-1.75) 92.3 (19.98-1.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.183 , 0.211 0.191 , 0.221	Depositor DCC
R_{free} test set	1619 reflections (1.52%)	wwPDB-VP
Wilson B-factor (Å ²)	12.3	Xtriage
Anisotropy	0.161	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 61.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.038 for -h,l,k 0.027 for -l,-k,-h 0.046 for k,h,-l 0.027 for k,l,h 0.027 for l,h,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8031	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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: CIT, CA, NAG, PEG, NA, GOL

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	0.65	0/1775	0.85	3/2411 (0.1%)
1	B	0.67	0/1783	0.85	2/2419 (0.1%)
1	C	0.63	1/1714 (0.1%)	0.79	1/2326 (0.0%)
1	D	0.61	0/1669	0.78	0/2269
All	All	0.64	1/6941 (0.0%)	0.82	6/9425 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	180	GLU	CG-CD	-5.05	1.44	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	180	GLU	OE1-CD-OE2	6.16	130.69	123.30
1	A	223	ASP	CB-CG-OD2	-5.58	113.28	118.30
1	A	146	GLU	N-CA-CB	-5.37	100.93	110.60
1	B	223	ASP	CB-CG-OD2	-5.32	113.51	118.30
1	B	80	LYS	CD-CE-NZ	5.16	123.56	111.70
1	A	197	ARG	NE-CZ-NH1	5.15	122.87	120.30

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	1714	0	1656	21	0
1	B	1717	0	1673	20	0
1	C	1646	0	1626	12	0
1	D	1622	0	1568	15	0
2	E	29	0	25	0	0
2	F	58	0	50	3	0
2	G	29	0	25	0	0
2	H	29	0	25	0	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	14	0	20	8	0
4	B	7	0	10	3	0
5	B	13	0	5	1	0
6	B	6	0	8	3	0
6	D	6	0	8	2	0
7	B	1	0	0	0	0
7	C	2	0	0	0	0
7	D	1	0	0	0	0
8	A	320	0	0	9	0
8	B	325	0	0	3	0
8	C	238	0	0	4	0
8	D	250	0	0	3	0
All	All	8031	0	6699	72	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 5.

All (72) 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:B:52:TYR:OH	5:B:1242:CIT:O4	1.88	0.90
4:A:1243:PEG:H31	8:A:2462:HOH:O	1.72	0.90
1:B:141[A]:LEU:HD22	1:B:142:PHE:N	1.95	0.80
1:C:91:ILE:HD11	8:C:2546:HOH:O	1.82	0.78
1:D:42:ASN:H	1:D:42:ASN:HD22	1.32	0.76
1:C:42:ASN:HD22	1:C:42:ASN:H	1.34	0.75
4:A:1243:PEG:H22	8:A:2612:HOH:O	1.89	0.72
1:C:63[A]:ARG:NH1	8:C:2401:HOH:O	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:175:ASN:OD1	8:B:2401:HOH:O	2.08	0.70
1:A:63[A]:ARG:HG3	1:A:171:ILE:HG21	1.74	0.69
1:A:63[B]:ARG:HG3	1:A:171:ILE:HD13	1.74	0.69
1:B:63[B]:ARG:HG3	1:B:63[B]:ARG:HH11	1.58	0.69
1:C:53:GLN:HE22	1:C:55:ASN:HD22	1.42	0.65
1:A:226:ASN:HB3	4:A:1242:PEG:C4	2.27	0.64
1:B:233:ASP:H	6:B:1243:GOL:C3	2.10	0.63
1:C:42:ASN:HD21	1:C:156:SER:H	1.47	0.62
2:F:1[B]:NAG:H61	2:F:2[B]:NAG:C1	2.29	0.62
1:D:42:ASN:HD21	1:D:156:SER:H	1.48	0.62
1:D:160:ASN:ND2	8:D:2401:HOH:O	2.34	0.61
1:C:161:GLU:N	1:C:161:GLU:OE1	2.33	0.61
1:A:134:HIS:HE1	8:A:2618:HOH:O	1.82	0.60
1:B:63[B]:ARG:HG2	1:B:171:ILE:HG21	1.82	0.60
1:C:38:ASP:OD1	1:C:38:ASP:N	2.32	0.59
1:B:233:ASP:H	6:B:1243:GOL:H32	1.70	0.57
1:B:102:TYR:HB3	4:B:1244:PEG:H21	1.88	0.55
1:A:173:PRO:HB2	1:A:176:GLN:HG2	1.88	0.55
1:A:134:HIS:HD2	1:A:178:ASN:O	1.90	0.54
1:D:90:ASN:O	6:D:1235:GOL:H11	2.08	0.54
1:A:160:ASN:HA	8:A:2559[B]:HOH:O	2.08	0.52
1:A:226:ASN:HB3	4:A:1242:PEG:H42	1.92	0.51
1:A:226:ASN:HB3	4:A:1242:PEG:H41	1.92	0.50
1:A:75:ARG:CZ	4:A:1243:PEG:H11	2.42	0.49
1:B:145[A]:LYS:HZ2	1:B:146:GLU:H	1.61	0.48
1:B:63[C]:ARG:HG3	1:B:171:ILE:HG21	1.95	0.47
1:A:141[A]:LEU:HD23	1:A:141[A]:LEU:C	2.35	0.47
1:A:141[B]:LEU:HD12	1:A:168:LEU:HD12	1.97	0.46
1:A:161:GLU:N	8:A:2559[B]:HOH:O	2.48	0.46
1:D:57:ASN:HB3	8:D:2537:HOH:O	2.14	0.46
1:D:42:ASN:H	1:D:42:ASN:ND2	2.09	0.46
1:B:233:ASP:H	6:B:1243:GOL:H31	1.80	0.46
1:B:57:ASN:HB3	8:B:2607:HOH:O	2.17	0.45
1:B:63[B]:ARG:HG3	1:B:63[B]:ARG:NH1	2.28	0.45
1:D:75:ARG:HD3	8:D:2559:HOH:O	2.15	0.45
1:B:82:SER:O	4:B:1244:PEG:C1	2.65	0.45
8:B:2432:HOH:O	2:F:1[A]:NAG:H61	2.17	0.45
1:B:175:ASN:HB2	2:F:1[B]:NAG:H82	1.98	0.44
4:A:1242:PEG:H42	8:A:2482:HOH:O	2.17	0.44
1:D:166:TYR:CE1	1:D:184:ALA:CB	3.00	0.44
1:A:150:LYS:NZ	8:A:2608[B]:HOH:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:53:GLN:HE22	1:D:75:ARG:NH2	2.16	0.43
1:B:141[A]:LEU:CD2	1:B:142:PHE:N	2.76	0.43
1:D:126:GLY:HA2	1:D:187:TYR:CE2	2.54	0.43
1:B:133:SER:O	1:B:210:ASP:HB3	2.18	0.43
1:B:102:TYR:HA	4:B:1244:PEG:H32	2.00	0.43
1:D:136:ASP:HA	1:D:137:ASP:HA	1.87	0.43
1:A:141[B]:LEU:HD23	1:A:198:ILE:HG13	2.01	0.42
1:A:175:ASN:ND2	8:A:2405:HOH:O	2.43	0.42
1:A:182:ILE:HG22	1:C:184:ALA:HA	2.01	0.42
1:B:179:SER:OG	1:D:186[A]:GLN:HG3	2.20	0.42
1:C:212[A]:LYS:CE	8:C:2434:HOH:O	2.67	0.42
1:A:121:LYS:HD2	1:A:193:TYR:CZ	2.55	0.42
4:A:1243:PEG:C3	8:A:2462:HOH:O	2.49	0.42
1:C:166:TYR:CE1	1:C:184:ALA:CB	3.04	0.41
1:D:53:GLN:HE22	1:D:75:ARG:HH21	1.69	0.41
1:C:212[A]:LYS:HE3	8:C:2434:HOH:O	2.20	0.41
1:D:141:LEU:O	1:D:167:SER:HA	2.21	0.41
1:C:212[B]:LYS:HE2	1:C:212[B]:LYS:HB2	1.58	0.40
1:D:206:ARG:NH1	6:D:1235:GOL:O1	2.43	0.40
1:A:136:ASP:HA	1:A:137:ASP:HA	1.85	0.40
1:A:53:GLN:HE22	1:A:75:ARG:HH11	1.70	0.40

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	217/240 (90%)	214 (99%)	3 (1%)	0	100	100
1	B	219/240 (91%)	215 (98%)	4 (2%)	0	100	100
1	C	210/240 (88%)	205 (98%)	5 (2%)	0	100	100
1	D	205/240 (85%)	202 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	851/960 (89%)	836 (98%)	15 (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	191/207 (92%)	188 (98%)	3 (2%)	62	45
1	B	192/207 (93%)	187 (97%)	5 (3%)	46	23
1	C	184/207 (89%)	176 (96%)	8 (4%)	29	9
1	D	179/207 (86%)	174 (97%)	5 (3%)	43	20
All	All	746/828 (90%)	725 (97%)	21 (3%)	50	20

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63[A]	ARG
1	A	63[B]	ARG
1	A	111	ASN
1	B	63[A]	ARG
1	B	63[B]	ARG
1	B	63[C]	ARG
1	B	141[A]	LEU
1	B	141[B]	LEU
1	C	38	ASP
1	C	42	ASN
1	C	44	VAL
1	C	63[A]	ARG
1	C	63[B]	ARG
1	C	80	LYS
1	C	111	ASN
1	C	150	LYS
1	D	42	ASN

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Mol	Chain	Res	Type
1	D	63	ARG
1	D	111	ASN
1	D	121	LYS
1	D	234	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	GLN
1	A	55	ASN
1	A	57	ASN
1	A	111	ASN
1	A	134	HIS
1	A	175	ASN
1	B	53	GLN
1	B	55	ASN
1	B	175	ASN
1	C	42	ASN
1	C	55	ASN
1	C	111	ASN
1	D	42	ASN
1	D	53	GLN
1	D	111	ASN
1	D	160	ASN
1	D	176	GLN
1	D	226	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

10 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	NAG	E	1	2	15,15,15	0.49	0	21,21,21	0.61	0
2	NAG	E	2	3,2	14,14,15	0.62	0	17,19,21	1.17	1 (5%)
2	NAG	F	1[A]	2	15,15,15	0.46	0	21,21,21	2.12	6 (28%)
2	NAG	F	1[B]	2	15,15,15	0.54	0	21,21,21	1.74	7 (33%)
2	NAG	F	2[A]	3,2	14,14,15	0.39	0	17,19,21	0.62	0
2	NAG	F	2[B]	3,2	14,14,15	0.43	0	17,19,21	0.61	0
2	NAG	G	1	2	15,15,15	0.70	0	21,21,21	1.20	2 (9%)
2	NAG	G	2	3,2	14,14,15	0.56	0	17,19,21	0.81	0
2	NAG	H	1	2	15,15,15	0.49	0	21,21,21	1.04	0
2	NAG	H	2	3,2	14,14,15	0.45	0	17,19,21	1.09	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	NAG	E	1	2	-	0/6/26/26	0/1/1/1
2	NAG	E	2	3,2	-	0/6/23/26	0/1/1/1
2	NAG	F	1[A]	2	-	4/6/26/26	0/1/1/1
2	NAG	F	1[B]	2	-	4/6/26/26	0/1/1/1
2	NAG	F	2[A]	3,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2[B]	3,2	-	0/6/23/26	0/1/1/1
2	NAG	G	1	2	-	0/6/26/26	0/1/1/1
2	NAG	G	2	3,2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	2	-	0/6/26/26	0/1/1/1
2	NAG	H	2	3,2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1[A]	NAG	O5-C5-C4	5.03	118.83	109.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1[A]	NAG	O5-C1-C2	-4.83	104.66	109.52
2	F	1[A]	NAG	C6-C5-C4	-3.60	104.57	113.00
2	F	1[B]	NAG	C4-C3-C2	-3.56	105.13	110.34
2	F	1[A]	NAG	C1-C2-C3	-3.50	105.78	110.54
2	G	1	NAG	O5-C1-C2	3.40	112.93	109.52
2	F	1[B]	NAG	C1-C2-C3	-3.17	106.22	110.54
2	F	1[B]	NAG	O5-C5-C4	3.01	115.16	109.69
2	F	1[B]	NAG	C3-C2-N2	2.82	115.94	110.62
2	G	1	NAG	O4-C4-C3	-2.74	104.02	110.35
2	E	2	NAG	C1-O5-C5	-2.23	109.17	112.19
2	F	1[A]	NAG	C3-C4-C5	2.17	114.11	110.24
2	F	1[B]	NAG	C6-C5-C4	-2.17	107.93	113.00
2	F	1[B]	NAG	O3-C3-C2	2.11	113.91	109.66
2	F	1[B]	NAG	C1-O5-C5	2.08	117.59	113.66
2	F	1[A]	NAG	C3-C2-N2	2.07	114.52	110.62

There are no chirality outliers.

All (8) torsion outliers are listed below:

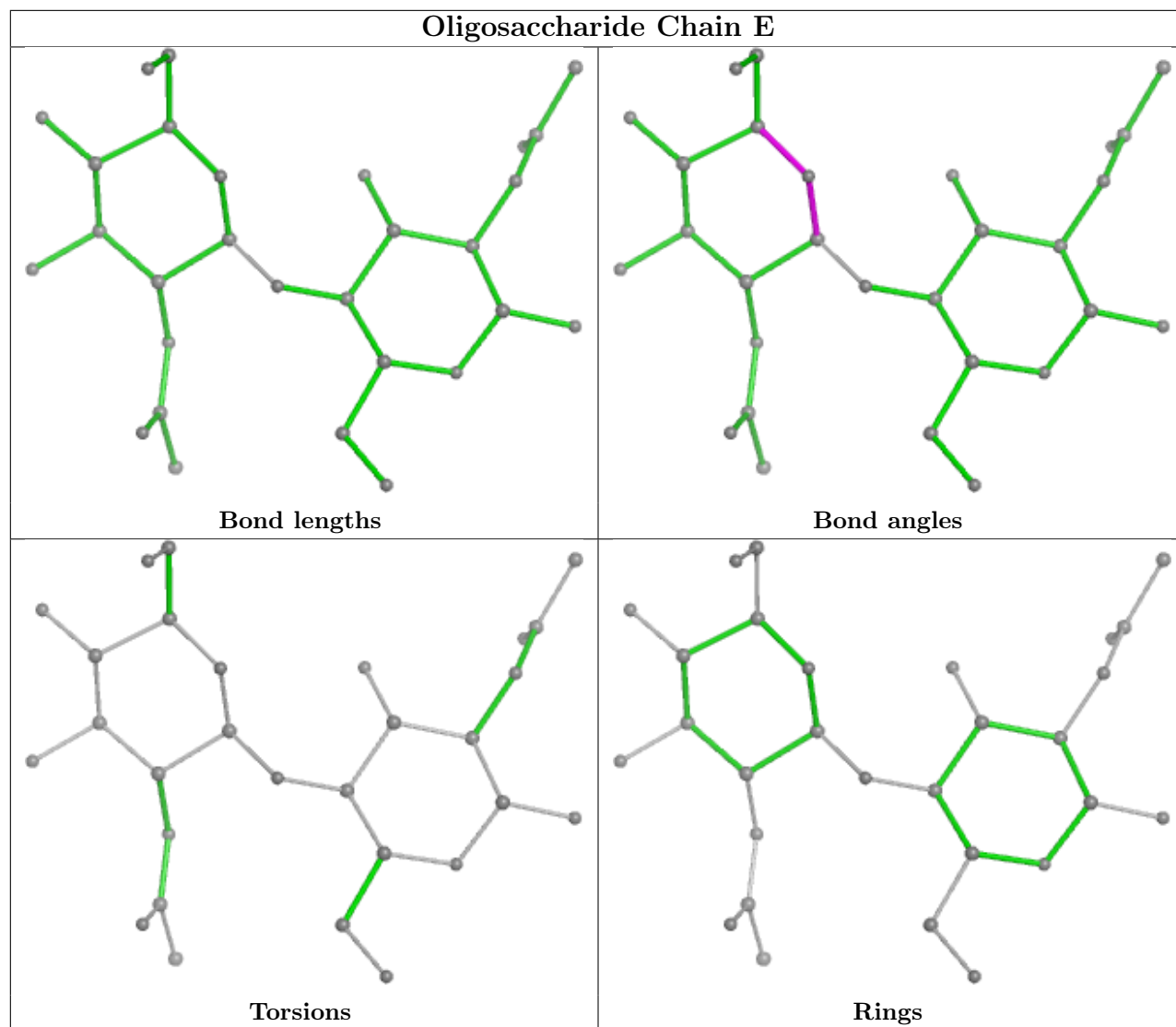
Mol	Chain	Res	Type	Atoms
2	F	1[B]	NAG	C1-C2-N2-C7
2	F	1[A]	NAG	C4-C5-C6-O6
2	F	1[A]	NAG	O5-C5-C6-O6
2	F	1[B]	NAG	C4-C5-C6-O6
2	F	1[A]	NAG	C3-C2-N2-C7
2	F	1[B]	NAG	O5-C5-C6-O6
2	F	1[B]	NAG	C3-C2-N2-C7
2	F	1[A]	NAG	C1-C2-N2-C7

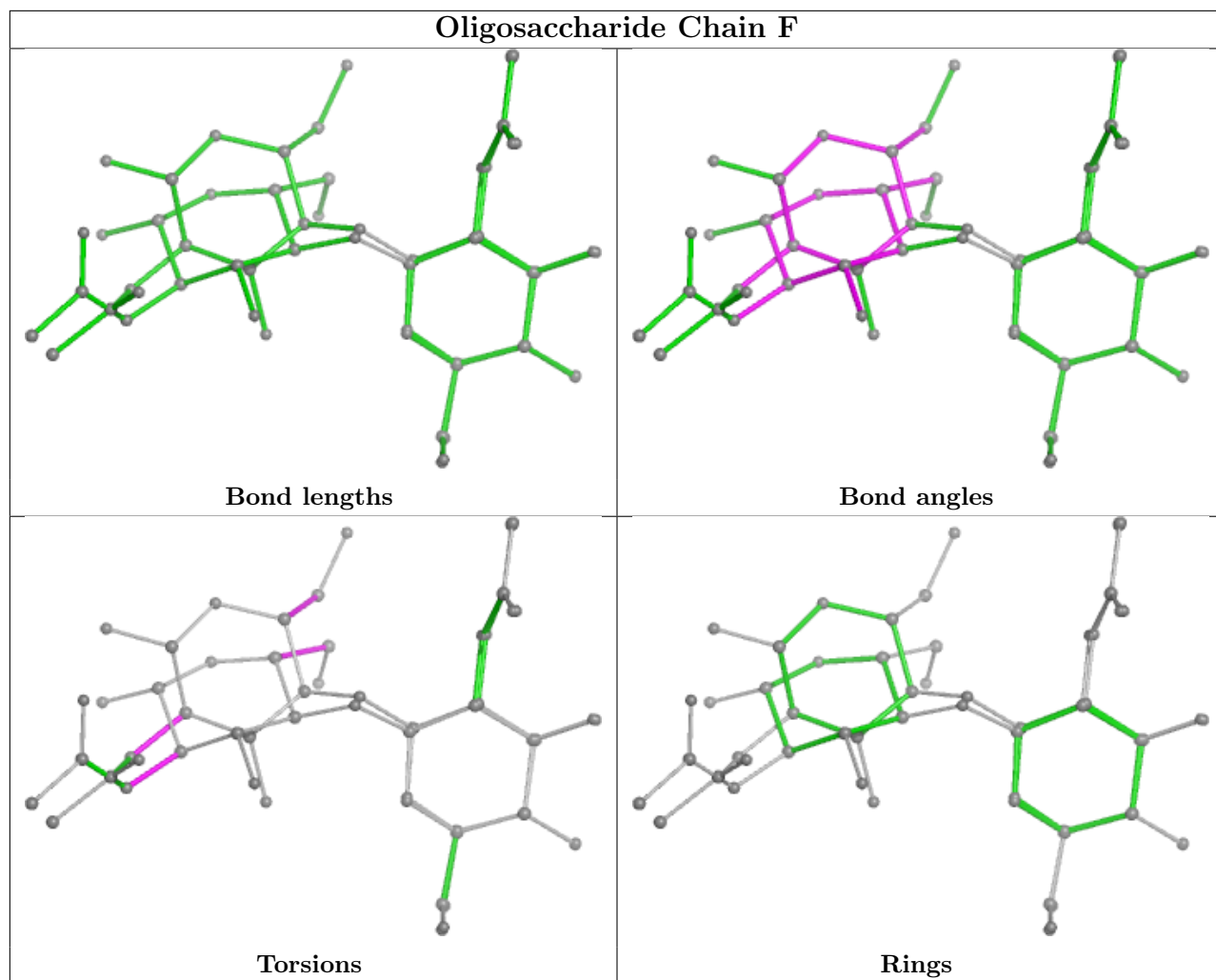
There are no ring outliers.

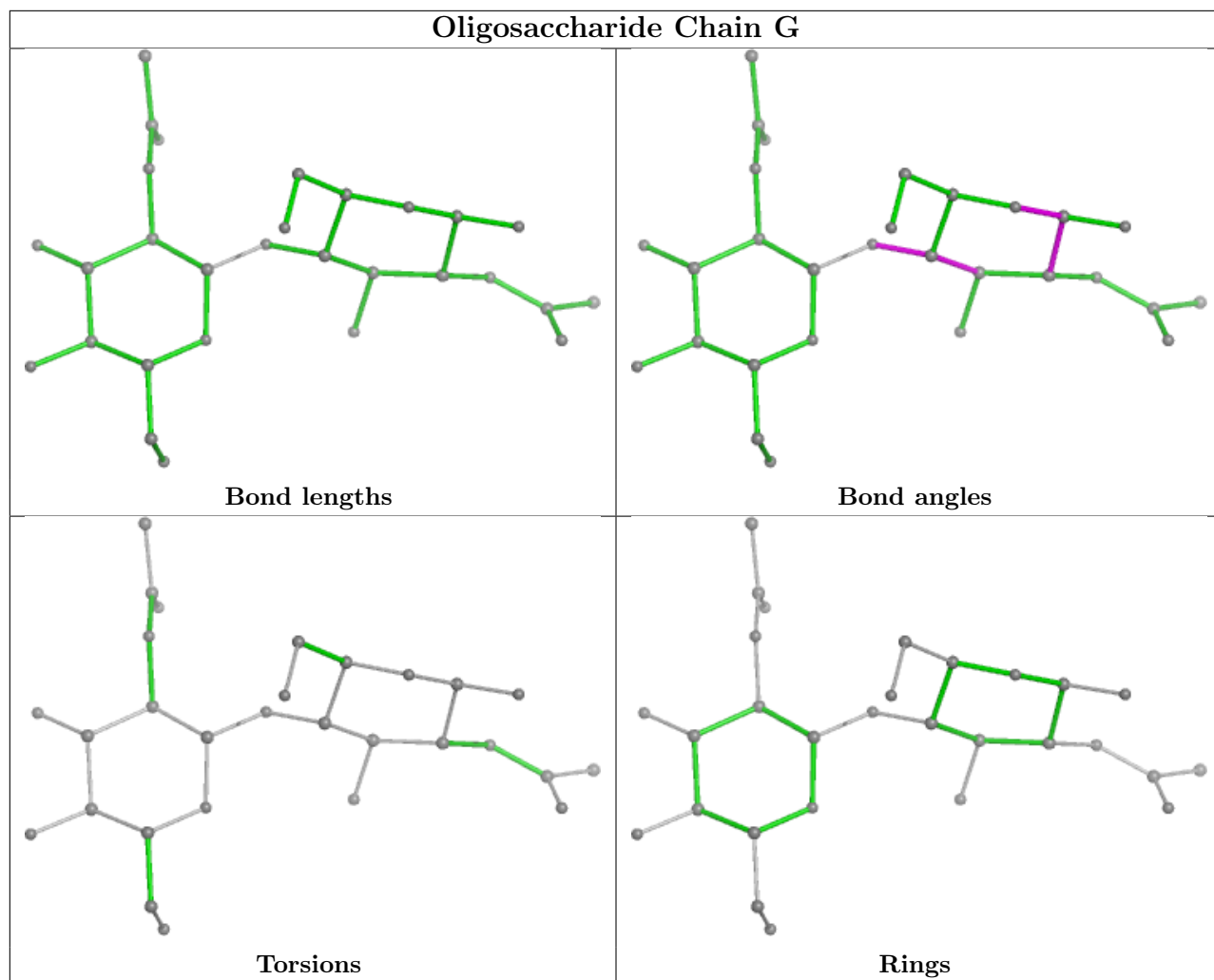
3 monomers are involved in 3 short contacts:

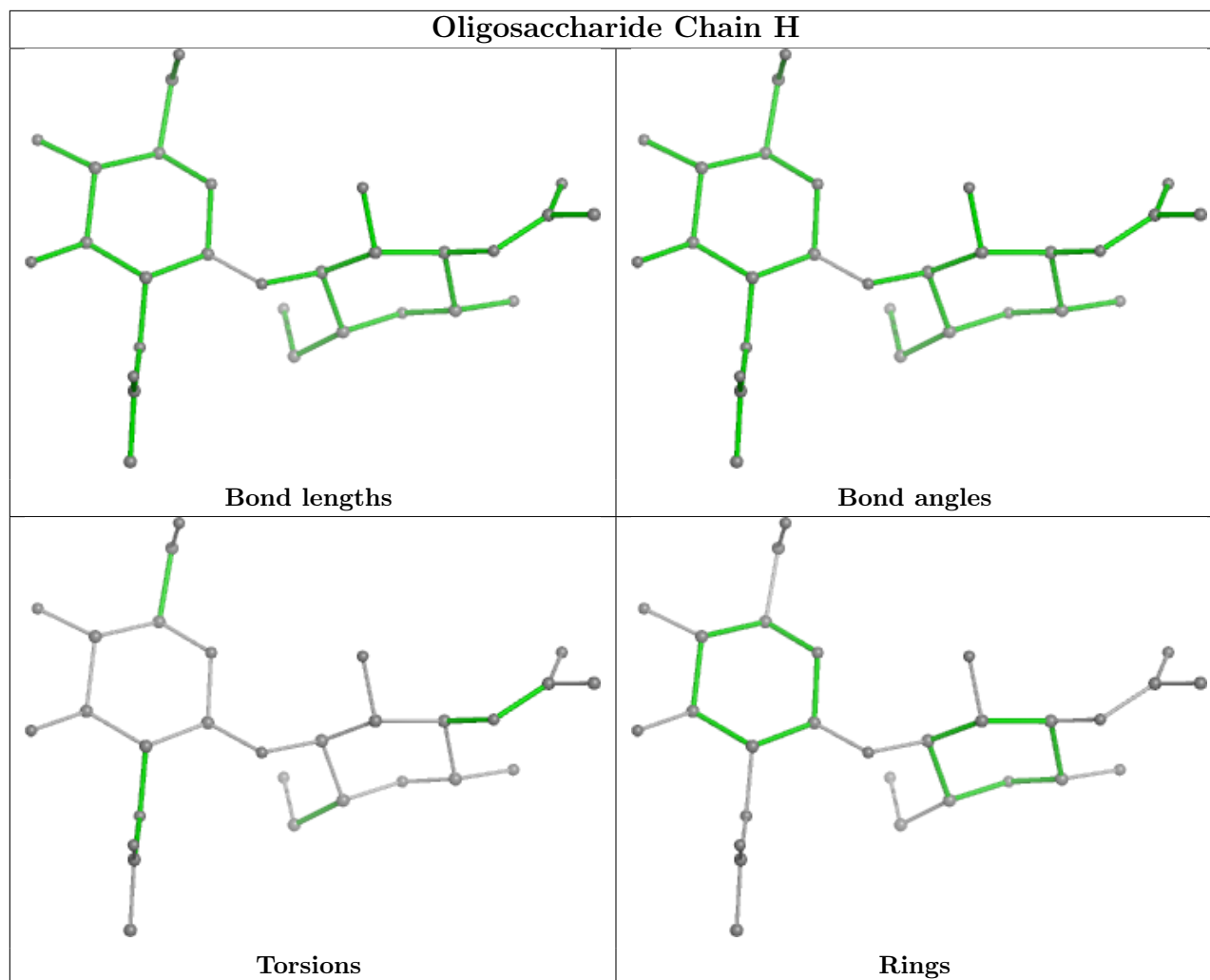
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1[A]	NAG	1	0
2	F	2[B]	NAG	1	0
2	F	1[B]	NAG	2	0

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









5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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$
4	PEG	A	1243	-	6,6,6	0.47	0	5,5,5	1.21	1 (20%)
6	GOL	B	1243	-	5,5,5	0.41	0	5,5,5	0.64	0
6	GOL	D	1235	-	5,5,5	0.10	0	5,5,5	0.47	0
5	CIT	B	1242	-	12,12,12	1.56	1 (8%)	17,17,17	4.64	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PEG	A	1242	-	6,6,6	0.62	0	5,5,5	0.88	0
4	PEG	B	1244	-	6,6,6	0.44	0	5,5,5	0.67	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
4	PEG	A	1243	-	-	2/4/4/4	-
6	GOL	B	1243	-	-	3/4/4/4	-
6	GOL	D	1235	-	-	2/4/4/4	-
5	CIT	B	1242	-	-	3/16/16/16	-
4	PEG	A	1242	-	-	2/4/4/4	-
4	PEG	B	1244	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1242	CIT	C4-C3	-3.43	1.49	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1242	CIT	O7-C3-C6	-11.53	92.67	108.86
5	B	1242	CIT	C2-C3-C6	-10.98	86.52	110.11
5	B	1242	CIT	O6-C6-C3	5.51	122.61	113.05
5	B	1242	CIT	O7-C3-C2	4.95	120.98	109.40
5	B	1242	CIT	C4-C3-C2	4.82	121.74	109.16
5	B	1242	CIT	O7-C3-C4	2.38	114.96	109.40
4	A	1243	PEG	C3-O2-C2	2.07	122.27	113.29
5	B	1242	CIT	O5-C6-C3	-2.04	119.37	122.25

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1242	CIT	C1-C2-C3-O7
6	B	1243	GOL	O1-C1-C2-C3
4	B	1244	PEG	O2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
6	D	1235	GOL	C1-C2-C3-O3
6	B	1243	GOL	O1-C1-C2-O2
6	D	1235	GOL	O2-C2-C3-O3
4	A	1242	PEG	C4-C3-O2-C2
4	A	1243	PEG	C1-C2-O2-C3
4	B	1244	PEG	C4-C3-O2-C2
4	A	1243	PEG	C4-C3-O2-C2
6	B	1243	GOL	O2-C2-C3-O3
4	A	1242	PEG	O1-C1-C2-O2
5	B	1242	CIT	C3-C4-C5-O4
5	B	1242	CIT	C3-C4-C5-O3

There are no ring outliers.

6 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1243	PEG	4	0
6	B	1243	GOL	3	0
6	D	1235	GOL	2	0
5	B	1242	CIT	1	0
4	A	1242	PEG	4	0
4	B	1244	PEG	3	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	209/240 (87%)	0.15	7 (3%) 46 53	6, 10, 25, 50	0
1	B	209/240 (87%)	0.04	5 (2%) 59 65	6, 10, 22, 40	0
1	C	201/240 (83%)	0.55	23 (11%) 5 7	7, 12, 50, 72	0
1	D	202/240 (84%)	0.54	23 (11%) 5 7	7, 12, 47, 62	0
All	All	821/960 (85%)	0.32	58 (7%) 16 21	6, 11, 39, 72	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	234	LEU	8.7
1	D	33	THR	7.6
1	A	33	THR	7.5
1	C	233	ASP	7.4
1	D	234	LEU	7.4
1	C	152	CYS	7.3
1	A	162	ALA	7.3
1	D	233	ASP	6.8
1	C	39	ILE	6.7
1	D	154	ALA	6.1
1	C	153	ASP	6.0
1	C	154	ALA	5.9
1	D	160	ASN	5.9
1	C	151	CYS	5.8
1	D	161	GLU	5.7
1	D	153	ASP	5.6
1	D	39	ILE	5.6
1	D	38	ASP	5.5
1	C	38	ASP	5.5
1	D	152	CYS	5.3
1	C	160	ASN	4.8

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Mol	Chain	Res	Type	RSRZ
1	C	232	GLY	4.6
1	C	41	THR	4.6
1	C	40	THR	4.5
1	B	33	THR	4.5
1	D	34	ALA	4.5
1	C	36	GLY	4.4
1	C	34	ALA	4.4
1	C	60	ARG	3.8
1	D	35	TYR	3.8
1	D	150	LYS	3.5
1	C	161	GLU	3.4
1	C	35	TYR	3.4
1	A	161	GLU	3.3
1	D	155	GLY	3.3
1	C	37	CYS	3.3
1	A	163	PRO	3.2
1	D	162	ALA	3.1
1	A	240	HIS	3.1
1	B	240	HIS	3.0
1	D	41	THR	2.9
1	C	44	VAL	2.8
1	D	151	CYS	2.8
1	B	154	ALA	2.7
1	D	232	GLY	2.6
1	C	162	ALA	2.6
1	D	37	CYS	2.5
1	C	157	ILE	2.5
1	C	159	LEU	2.5
1	D	43	ALA	2.4
1	D	175	ASN	2.4
1	A	34	ALA	2.2
1	B	145[A]	LYS	2.2
1	B	153	ASP	2.1
1	D	149	PHE	2.1
1	C	155	GLY	2.1
1	D	60	ARG	2.1
1	A	38	ASP	2.0

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

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

6.3 Carbohydrates

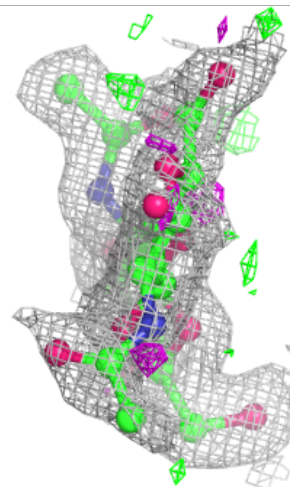
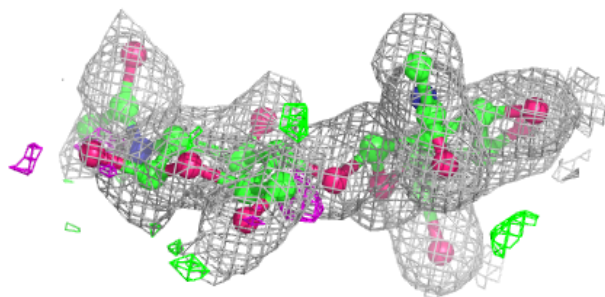
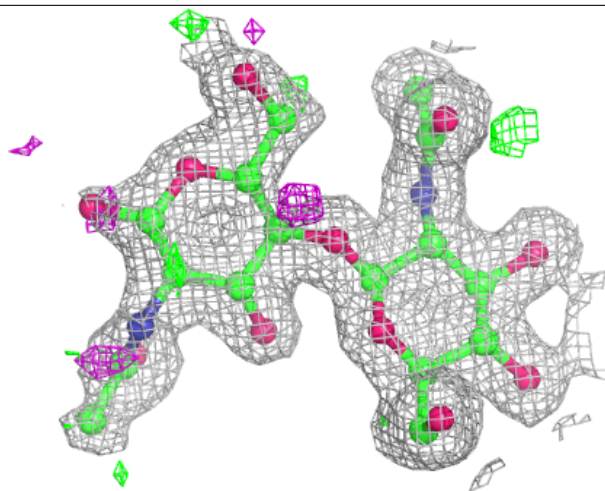
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	G	1	15/15	0.78	0.32	17,35,49,50	0
2	NAG	F	1[B]	15/15	0.79	0.32	13,18,24,26	15
2	NAG	F	1[A]	15/15	0.79	0.32	13,19,22,22	15
2	NAG	H	1	15/15	0.81	0.30	19,34,44,49	0
2	NAG	E	1	15/15	0.85	0.23	15,31,38,41	0
2	NAG	G	2	14/15	0.96	0.08	8,10,12,13	0
2	NAG	E	2	14/15	0.97	0.08	9,10,11,12	0
2	NAG	H	2	14/15	0.97	0.08	10,11,13,14	0
2	NAG	F	2[A]	14/15	0.98	0.07	8,9,10,11	14
2	NAG	F	2[B]	14/15	0.98	0.07	8,9,9,10	14

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.

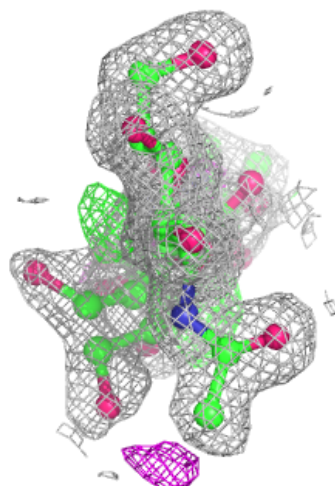
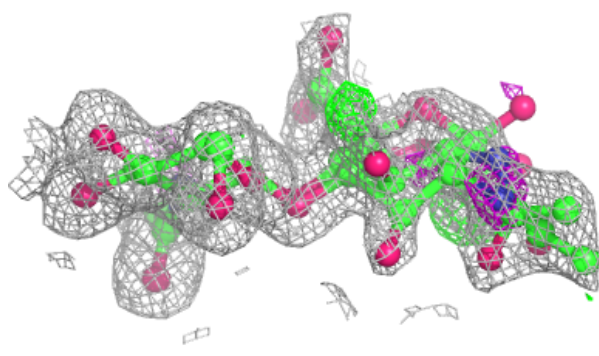
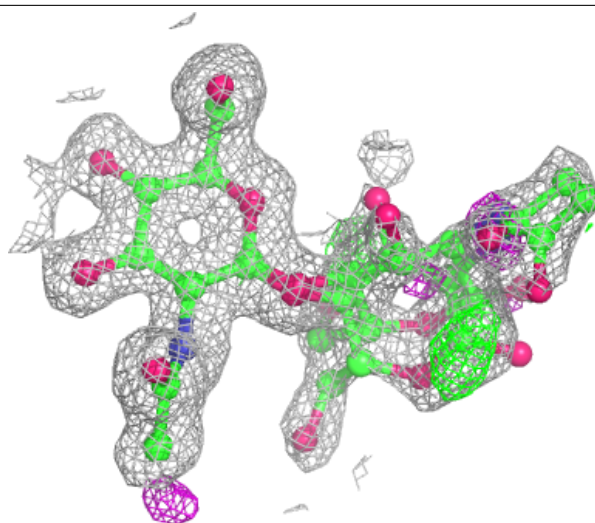
Electron density around Chain E:

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



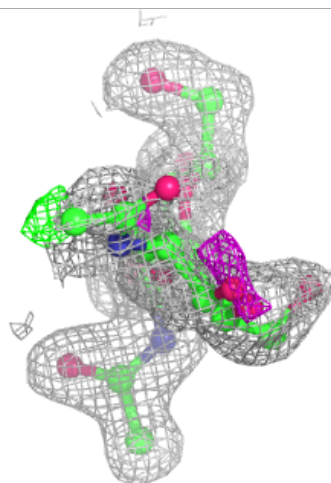
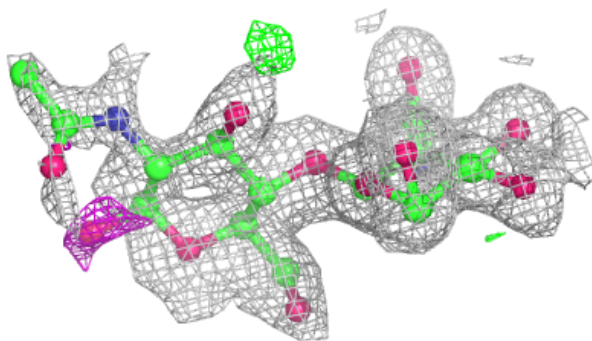
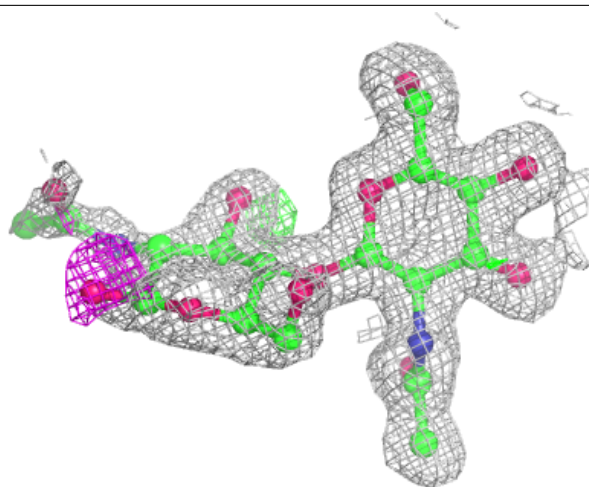
Electron density around Chain F:

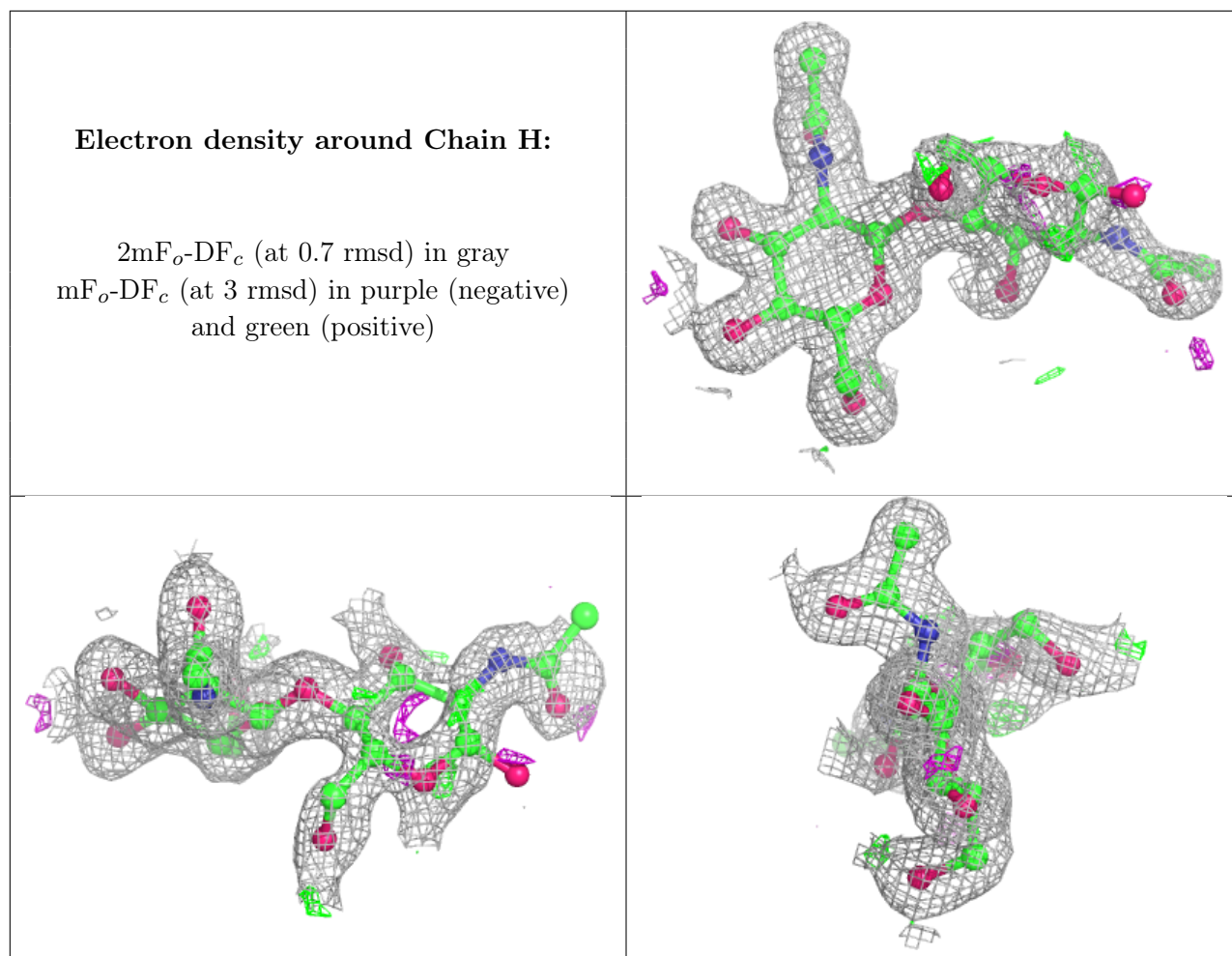
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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
5	CIT	B	1242	13/13	0.76	0.24	29,38,43,46	0
4	PEG	A	1242	7/7	0.81	0.23	26,28,30,32	0
6	GOL	B	1243	6/6	0.83	0.17	26,29,30,37	0
4	PEG	A	1243	7/7	0.88	0.17	21,24,29,31	0
6	GOL	D	1235	6/6	0.89	0.18	26,30,31,34	0
4	PEG	B	1244	7/7	0.90	0.18	24,26,28,28	0
7	NA	B	1245	1/1	0.97	0.15	10,10,10,10	0
3	CA	D	500	1/1	0.99	0.03	8,8,8,8	0
3	CA	A	500	1/1	0.99	0.05	7,7,7,7	0
7	NA	C	1236	1/1	0.99	0.14	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CA	C	500	1/1	1.00	0.04	8,8,8,8	0
7	NA	C	1235	1/1	1.00	0.19	2,2,2,2	0
3	CA	B	500	1/1	1.00	0.04	7,7,7,7	0
7	NA	D	1236	1/1	1.00	0.14	2,2,2,2	0

6.5 Other polymers [i](#)

There are no such residues in this entry.