Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 10:50 AM BST

PDB ID	:	1GQH
Title	:	Quercetin 2,3-dioxygenase in complex with the inhibitor kojic acid
Authors	:	Steiner, R.A.; Dijkstra, B.W.
Deposited on	:	2001-11-23
Resolution	:	2.15 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

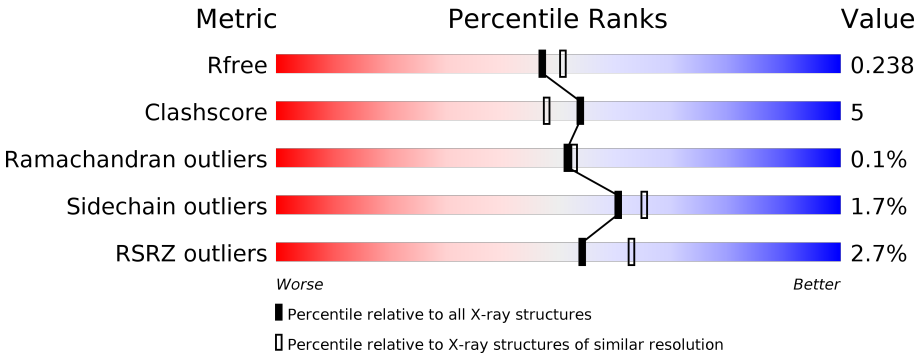
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 <=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	350	3% 83% 14%
1	B	350	2% 84% 10% 5%
1	C	350	3% 85% 10% 5%
1	D	350	3% 83% 12% 5%
2	E	3	33% 67%
3	F	4	25% 50% 25%

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Mol	Chain	Length	Quality of chain
3	G	4	100%
4	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
2	MAN	E	3	X	-	-	-
3	MAN	F	3	X	-	-	-
3	MAN	G	3	X	-	-	-

2 Entry composition

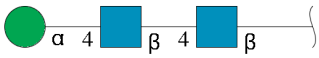
There are 8 unique types of molecules in this entry. The entry contains 11746 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 QUERCETIN 2,3-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	3	0
			2633	1671	428	529	5			
1	B	334	Total	C	N	O	S	0	0	0
			2581	1644	420	512	5			
1	C	333	Total	C	N	O	S	0	2	0
			2573	1636	419	513	5			
1	D	331	Total	C	N	O	S	0	0	0
			2561	1631	417	508	5			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	4	Total	C	N	O	0	0	0
			50	28	2	20			

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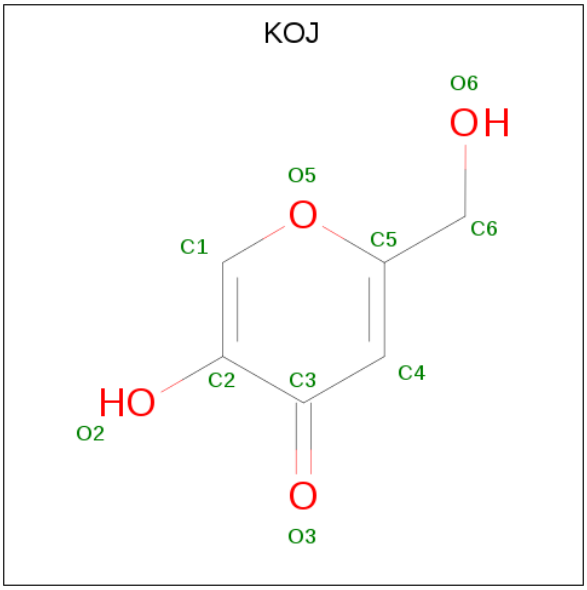
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	G	4	Total C N O 50 28 2 20	0	0	0

- Molecule 4 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
4	H	2	Total C N O 28 16 2 10	0	0	0

- Molecule 5 is 5-HYDROXY-2-(HYDROXYMETHYL)-4H-PYRAN-4-ONE (three-letter code: KOJ) (formula: $C_6H_6O_4$).

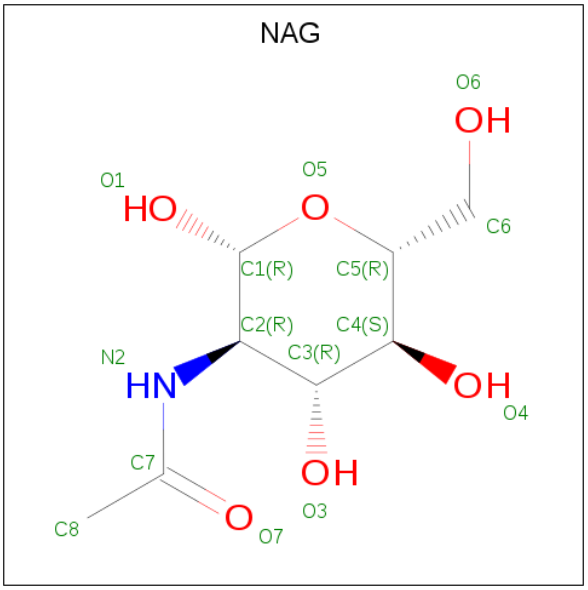


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 10 6 4	0	0
5	B	1	Total C O 10 6 4	0	0
5	C	1	Total C O 10 6 4	0	0
5	D	1	Total C O 10 6 4	0	0

- Molecule 6 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Cu 1 1	0	0
6	A	1	Total Cu 1 1	0	0
6	D	1	Total Cu 1 1	0	0
6	C	1	Total Cu 1 1	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N O 14 8 1 5	0	0
7	A	1	Total C N O 14 8 1 5	0	0
7	A	1	Total C N O 14 8 1 5	0	0
7	A	1	Total C N O 14 8 1 5	0	0
7	B	1	Total C N O 14 8 1 5	0	0
7	B	1	Total C N O 14 8 1 5	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is water.

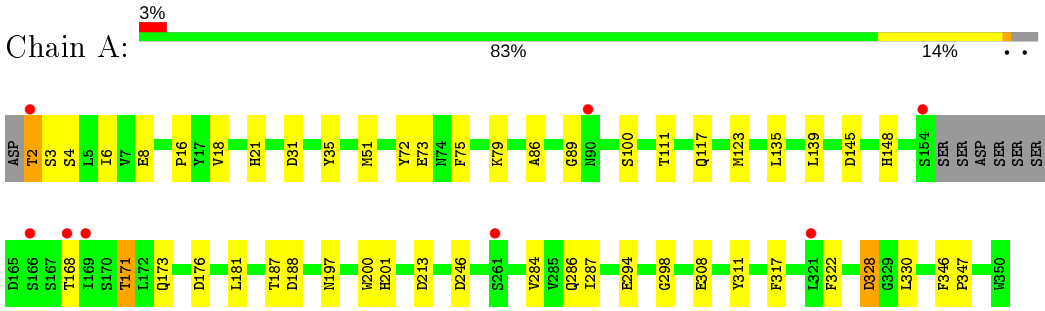
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	294	Total	O	0	0
			294	294		
8	B	251	Total	O	0	0
			251	251		
8	C	251	Total	O	0	0
			251	251		
8	D	223	Total	O	0	0
			223	223		

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.

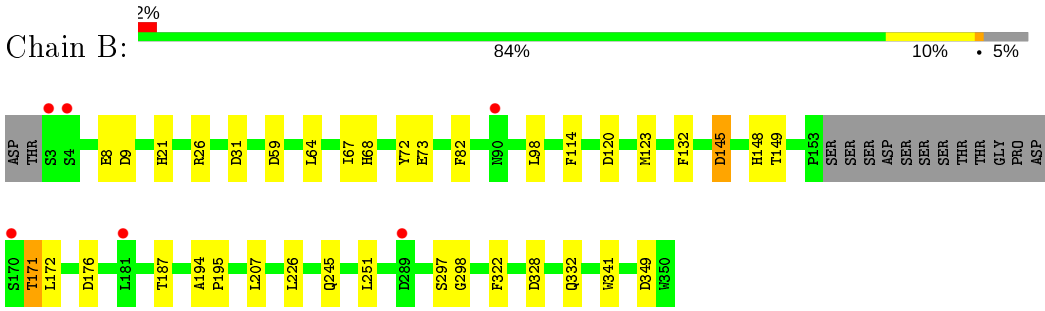
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE

Chain A:



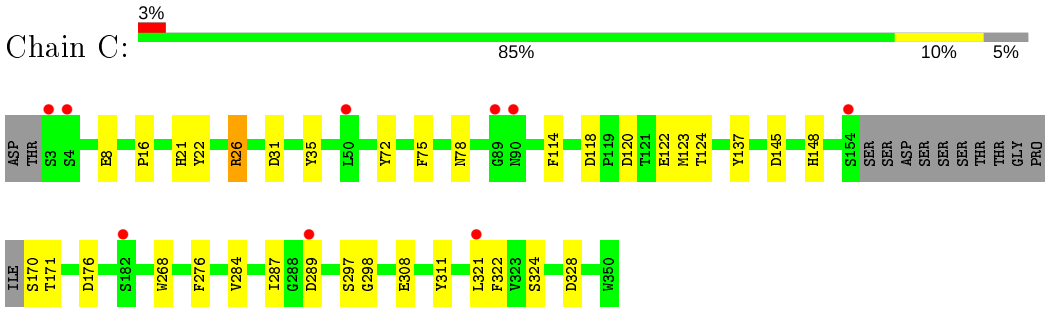
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE

Chain B:



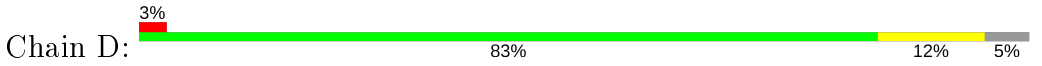
- Molecule 1: QUERCETIN 2,3-DIOXYGENASE

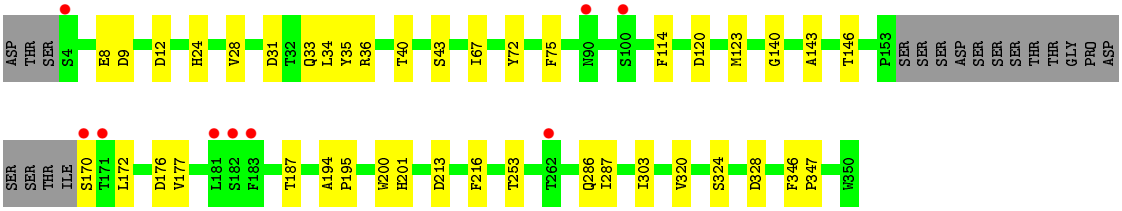
Chain C:



- Molecule 1: QUERCETIN 2,3-DIOXYGENASE

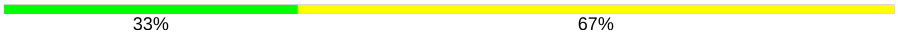
Chain D:





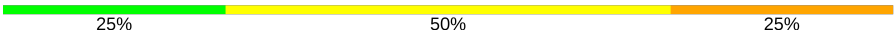
• Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:



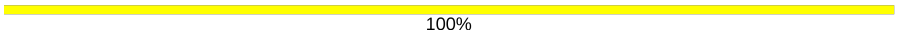
• Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:



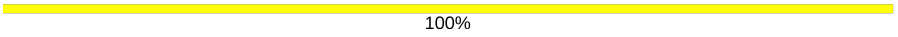
• Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



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

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	108.64Å 55.40Å 124.42Å 90.00° 98.26° 90.00°	Depositor
Resolution (Å)	49.39 – 2.15 37.95 – 2.15	Depositor EDS
% Data completeness (in resolution range)	89.2 (49.39-2.15) 89.2 (37.95-2.15)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.74 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.178 , 0.228 0.195 , 0.238	Depositor DCC
R_{free} test set	3587 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	20.8	Xtriage
Anisotropy	0.629	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 38.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11746	wwPDB-VP
Average B, all atoms (Å^2)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KOJ, NAG, CU, MAN

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	0.51	0/2728	0.79	6/3740 (0.2%)
1	B	0.49	0/2660	0.82	8/3647 (0.2%)
1	C	0.46	0/2662	0.79	7/3648 (0.2%)
1	D	0.48	0/2640	0.80	6/3619 (0.2%)
All	All	0.49	0/10690	0.80	27/14654 (0.2%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	176	ASP	CB-CG-OD2	7.39	124.96	118.30
1	D	31	ASP	CB-CG-OD2	7.23	124.81	118.30
1	D	120	ASP	CB-CG-OD2	7.01	124.61	118.30
1	C	176	ASP	CB-CG-OD2	6.80	124.42	118.30
1	B	145	ASP	CB-CG-OD2	6.38	124.04	118.30
1	A	176	ASP	CB-CG-OD2	6.29	123.96	118.30
1	C	31	ASP	CB-CG-OD2	6.12	123.80	118.30
1	C	120	ASP	CB-CG-OD2	5.91	123.62	118.30
1	D	328	ASP	CB-CG-OD2	5.89	123.60	118.30
1	B	31	ASP	CB-CG-OD2	5.89	123.60	118.30
1	C	145	ASP	CB-CG-OD2	5.81	123.53	118.30
1	A	31	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	213	ASP	CB-CG-OD2	5.54	123.29	118.30
1	C	289	ASP	CB-CG-OD2	5.50	123.25	118.30
1	B	349	ASP	CB-CG-OD2	5.34	123.11	118.30
1	A	188	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	59	ASP	CB-CG-OD2	5.30	123.07	118.30
1	D	213	ASP	CB-CG-OD2	5.18	122.97	118.30
1	A	246	ASP	CB-CG-OD2	5.18	122.96	118.30
1	C	118	ASP	CB-CG-OD2	5.11	122.90	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	120	ASP	CB-CG-OD2	5.08	122.88	118.30
1	B	328	ASP	CB-CG-OD2	5.08	122.87	118.30
1	B	9	ASP	CB-CG-OD2	5.06	122.86	118.30
1	D	12	ASP	CB-CG-OD2	5.04	122.84	118.30
1	A	145	ASP	CB-CG-OD2	5.03	122.83	118.30
1	B	176	ASP	CB-CG-OD2	5.01	122.81	118.30
1	C	328	ASP	CB-CG-OD2	5.01	122.81	118.30

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	2633	0	2432	39	0
1	B	2581	0	2392	25	0
1	C	2573	0	2380	20	0
1	D	2561	0	2373	27	0
2	E	39	0	34	0	0
3	F	50	0	43	2	0
3	G	50	0	43	0	0
4	H	28	0	25	0	0
5	A	10	0	4	2	0
5	B	10	0	4	3	0
5	C	10	0	4	3	0
5	D	10	0	4	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	56	0	52	0	0
7	B	42	0	39	0	0
7	C	42	0	39	0	0
7	D	28	0	26	0	0
8	A	294	0	0	10	0
8	B	251	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	251	0	0	3	0
8	D	223	0	0	4	0
All	All	11746	0	9894	110	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 (110) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8[A]:GLU:OE2	1:A:148:HIS:HE1	1.44	0.99
1:A:8[A]:GLU:OE2	1:A:148:HIS:CE1	2.31	0.82
1:C:114:PHE:CE1	5:C:1351:KOJ:H4	2.15	0.81
1:B:245:GLN:HG2	8:B:2172:HOH:O	1.80	0.81
1:A:139:LEU:HD13	1:A:164:PRO:HG3	1.66	0.76
1:C:8:GLU:OE2	1:C:148:HIS:HE1	1.67	0.76
1:B:8:GLU:OE2	1:B:148:HIS:HE1	1.72	0.72
1:B:168:THR:O	1:B:172:LEU:HG	1.92	0.69
1:A:173:GLN:HG3	8:A:2143:HOH:O	1.92	0.69
1:A:8[B]:GLU:OE2	8:A:2006:HOH:O	2.10	0.68
1:B:332:GLN:NE2	8:B:2231:HOH:O	2.28	0.65
1:A:197:ASN:OD1	1:A:197:ASN:O	2.14	0.65
1:A:171:THR:HG23	8:A:2141:HOH:O	1.96	0.65
1:D:75:PHE:CD2	1:D:123:MET:HE1	2.32	0.64
1:A:171:THR:CG2	1:A:171:THR:O	2.47	0.63
1:D:33:GLN:NE2	1:D:35:TYR:OH	2.34	0.61
1:A:308:GLU:HB2	8:A:2248:HOH:O	2.00	0.61
8:B:2013:HOH:O	1:C:171:THR:HG23	2.00	0.60
1:A:117:GLN:HG3	8:C:2156:HOH:O	2.02	0.60
1:B:168:THR:HA	1:B:171:THR:HG23	1.84	0.59
1:B:114:PHE:CE1	5:B:1351:KOJ:H4	2.37	0.59
1:D:28:VAL:HG21	1:D:140:GLY:HA3	1.84	0.59
1:D:75:PHE:HD2	1:D:123:MET:HE1	1.69	0.58
1:D:28:VAL:CG2	1:D:140:GLY:HA3	2.32	0.58
1:A:86:ALA:HA	1:A:111:THR:O	2.05	0.56
1:C:26:ARG:NH1	8:C:2025:HOH:O	2.38	0.56
1:D:24:HIS:HE1	1:D:143:ALA:O	1.89	0.55
1:D:287:ILE:HD13	1:D:303:ILE:HG13	1.88	0.55
1:D:75:PHE:HD2	1:D:123:MET:CE	2.21	0.53
8:B:2013:HOH:O	1:C:171:THR:CG2	2.55	0.53
1:A:294:GLU:HG2	8:A:2240:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:35:TYR:HE2	5:C:1351:KOJ:H6C2	1.74	0.53
1:D:40:THR:H	1:D:43:SER:HB3	1.75	0.52
1:B:8:GLU:HG2	8:B:2002:HOH:O	2.08	0.52
1:A:73:GLU:OE2	5:A:1351:KOJ:O2	2.28	0.51
1:D:8:GLU:HG2	8:D:2005:HOH:O	2.10	0.51
1:A:16:PRO:HB3	1:A:287:ILE:HG21	1.92	0.51
1:D:146:THR:HG22	8:D:2112:HOH:O	2.10	0.51
1:B:82:PHE:CE2	1:B:123:MET:HG2	2.45	0.51
1:A:197:ASN:C	1:A:197:ASN:OD1	2.49	0.50
1:A:2:THR:OG1	1:A:3:SER:N	2.40	0.50
1:B:73:GLU:OE2	5:B:1351:KOJ:C1	2.60	0.50
1:C:114:PHE:HE1	5:C:1351:KOJ:H4	1.75	0.50
1:A:21:HIS:CG	1:A:298:GLY:HA3	2.47	0.49
1:C:26:ARG:HD2	8:C:2025:HOH:O	2.12	0.49
1:A:328:ASP:HB2	8:A:2264:HOH:O	2.11	0.49
1:A:4:SER:HB3	8:A:2003:HOH:O	2.12	0.49
1:C:26:ARG:HD3	1:C:137:TYR:OH	2.13	0.49
1:B:73:GLU:OE2	5:B:1351:KOJ:C2	2.60	0.49
1:D:67:ILE:HD11	8:D:2084:HOH:O	2.12	0.48
1:C:78[A]:ASN:ND2	1:C:124:THR:OG1	2.45	0.48
1:C:8:GLU:OE2	1:C:148:HIS:CE1	2.58	0.48
1:D:9:ASP:OD1	1:D:24:HIS:HD2	1.96	0.48
1:A:35:TYR:HD2	1:A:51:MET:CE	2.27	0.47
1:D:114:PHE:CE2	5:D:1351:KOJ:H4	2.50	0.47
1:A:171:THR:HG23	1:A:171:THR:O	2.14	0.46
1:D:172:LEU:HB2	1:D:177:VAL:HB	1.97	0.46
1:B:251:LEU:HD12	1:B:322:PHE:O	2.16	0.46
1:B:297:SER:HB2	8:B:2199:HOH:O	2.16	0.46
1:B:297:SER:HB3	8:B:2200:HOH:O	2.15	0.45
1:C:78[A]:ASN:HB2	1:C:122:GLU:HB3	1.99	0.45
1:C:21:HIS:CG	1:C:298:GLY:HA3	2.51	0.45
1:A:284:VAL:O	1:A:311:TYR:HA	2.16	0.45
1:D:216:PHE:CD1	1:D:216:PHE:N	2.85	0.45
1:B:21:HIS:CG	1:B:298:GLY:HA3	2.52	0.45
1:A:73:GLU:CD	5:A:1351:KOJ:O2	2.55	0.44
1:B:8:GLU:OE2	1:B:148:HIS:CE1	2.62	0.44
1:B:82:PHE:CD2	1:B:123:MET:HG2	2.53	0.44
1:D:253:THR:HA	1:D:320:VAL:O	2.17	0.44
1:D:346:PHE:HB2	1:D:347:PRO:HD2	1.99	0.44
1:D:187:THR:OG1	3:F:3:MAN:H62	2.18	0.44
1:A:317:PHE:HB3	1:C:22:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:268:TRP:O	1:C:308:GLU:HA	2.19	0.43
1:A:346:PHE:HB2	1:A:347:PRO:CD	2.48	0.43
1:B:98:LEU:N	1:B:98:LEU:HD12	2.33	0.43
1:D:75:PHE:CE2	1:D:123:MET:HE1	2.54	0.43
1:A:187:THR:HG23	8:A:2154:HOH:O	2.18	0.43
1:D:200:TRP:O	1:D:201:HIS:HB2	2.18	0.43
1:D:346:PHE:HB2	1:D:347:PRO:CD	2.49	0.42
1:A:75:PHE:HD2	1:A:123:MET:HE2	1.83	0.42
1:B:132:PHE:CB	8:B:2098:HOH:O	2.67	0.42
1:C:322:PHE:CZ	1:C:324:SER:HB2	2.54	0.42
1:A:8[A]:GLU:HG2	8:A:2007:HOH:O	2.18	0.42
1:C:16:PRO:HB3	1:C:287:ILE:HG21	2.02	0.42
1:B:145:ASP:OD2	1:B:149:THR:O	2.37	0.42
1:A:168:THR:O	1:A:171:THR:HB	2.19	0.42
1:B:226:LEU:HB2	1:B:341:TRP:CG	2.54	0.42
1:B:67:ILE:CG2	1:B:68:HIS:N	2.82	0.42
1:D:40:THR:OG1	1:D:43:SER:HB2	2.20	0.42
1:C:75:PHE:HD2	1:C:123:MET:CE	2.33	0.42
1:A:322:PHE:CZ	1:A:330:LEU:HB3	2.55	0.42
1:C:284:VAL:O	1:C:311:TYR:HA	2.20	0.42
1:D:286:GLN:HA	8:D:2178:HOH:O	2.19	0.42
1:A:75:PHE:CD2	1:A:123:MET:HE2	2.54	0.41
1:A:79:LYS:HA	1:A:100[B]:SER:OG	2.20	0.41
1:D:34:LEU:HD22	1:D:36:ARG:NH1	2.36	0.41
1:A:171:THR:HG22	1:A:171:THR:O	2.20	0.41
1:A:346:PHE:HB2	1:A:347:PRO:HD2	2.01	0.41
1:D:187:THR:HG21	3:F:3:MAN:H62	2.02	0.41
1:D:194:ALA:HA	1:D:195:PRO:C	2.40	0.41
1:B:132:PHE:HB3	8:B:2098:HOH:O	2.20	0.41
1:B:187:THR:HG22	8:B:2131:HOH:O	2.21	0.41
1:B:207:LEU:N	1:B:207:LEU:HD12	2.36	0.41
1:A:200:TRP:O	1:A:201:HIS:HB2	2.20	0.41
1:A:286:GLN:NE2	8:A:2233:HOH:O	2.54	0.41
1:C:276:PHE:HA	1:C:321:LEU:O	2.21	0.40
1:A:75:PHE:HD2	1:A:123:MET:CE	2.34	0.40
1:A:6:ILE:HA	1:A:18:VAL:O	2.21	0.40
1:B:194:ALA:HA	1:B:195:PRO:C	2.41	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	340/350 (97%)	329 (97%)	10 (3%)	1 (0%)	41	37
1	B	330/350 (94%)	319 (97%)	11 (3%)	0	100	100
1	C	331/350 (95%)	318 (96%)	13 (4%)	0	100	100
1	D	327/350 (93%)	320 (98%)	7 (2%)	0	100	100
All	All	1328/1400 (95%)	1286 (97%)	41 (3%)	1 (0%)	51	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	GLY

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	287/294 (98%)	281 (98%)	6 (2%)	53	57
1	B	278/294 (95%)	272 (98%)	6 (2%)	52	55
1	C	279/294 (95%)	275 (99%)	4 (1%)	67	72
1	D	276/294 (94%)	273 (99%)	3 (1%)	73	78
All	All	1120/1176 (95%)	1101 (98%)	19 (2%)	60	65

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	72	TYR
1	A	135	LEU
1	A	171	THR
1	A	181	LEU
1	A	328	ASP
1	B	26	ARG
1	B	64	LEU
1	B	72	TYR
1	B	168	THR
1	B	169	ILE
1	B	171	THR
1	C	26	ARG
1	C	72	TYR
1	C	170	SER
1	C	297	SER
1	D	72	TYR
1	D	170	SER
1	D	324	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	117	GLN
1	A	148	HIS
1	A	173	GLN
1	A	332	GLN
1	A	336	ASN
1	B	83	GLN
1	B	148	HIS
1	B	286	GLN
1	B	332	GLN
1	C	83	GLN
1	C	148	HIS
1	D	24	HIS
1	D	33	GLN
1	D	83	GLN
1	D	332	GLN
1	D	336	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

13 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	1,2	14,14,15	0.54	0	17,19,21	1.32	2 (11%)
2	NAG	E	2	2	14,14,15	0.63	0	17,19,21	1.05	1 (5%)
2	MAN	E	3	2	11,11,12	0.79	0	15,15,17	0.91	0
3	NAG	F	1	1,3	14,14,15	0.75	0	17,19,21	1.04	0
3	NAG	F	2	3	14,14,15	0.78	1 (7%)	17,19,21	1.00	1 (5%)
3	MAN	F	3	3	11,11,12	0.62	0	15,15,17	1.22	1 (6%)
3	MAN	F	4	3	11,11,12	0.55	0	15,15,17	1.23	2 (13%)
3	NAG	G	1	1,3	14,14,15	0.70	0	17,19,21	1.01	1 (5%)
3	NAG	G	2	3	14,14,15	0.55	0	17,19,21	1.11	2 (11%)
3	MAN	G	3	3	11,11,12	0.76	1 (9%)	15,15,17	1.23	2 (13%)
3	MAN	G	4	3	11,11,12	0.66	0	15,15,17	1.41	3 (20%)
4	NAG	H	1	1,4	14,14,15	0.54	0	17,19,21	1.05	1 (5%)
4	NAG	H	2	4	14,14,15	0.60	0	17,19,21	1.33	2 (11%)

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	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	MAN	E	3	2	1/1/4/5	0/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	MAN	F	3	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	2/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	MAN	G	3	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	G	4	3	-	2/2/19/22	0/1/1/1
4	NAG	H	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	3	MAN	O5-C1	-2.09	1.40	1.43
3	F	2	NAG	O5-C1	-2.03	1.40	1.43

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	H	2	NAG	C1-O5-C5	4.23	117.93	112.19
3	G	4	MAN	O5-C5-C6	3.91	113.33	107.20
4	H	1	NAG	O5-C1-C2	-3.09	106.40	111.29
3	F	3	MAN	O5-C5-C6	3.04	111.96	107.20
2	E	2	NAG	O5-C1-C2	-2.91	106.70	111.29
3	F	2	NAG	O5-C1-C2	-2.75	106.95	111.29
3	F	4	MAN	O5-C5-C6	2.70	111.44	107.20
2	E	1	NAG	O5-C1-C2	-2.50	107.33	111.29
3	G	3	MAN	C1-C2-C3	2.39	112.60	109.67
2	E	1	NAG	C1-O5-C5	2.28	115.28	112.19
3	F	4	MAN	C3-C4-C5	-2.23	106.27	110.24
3	G	4	MAN	O3-C3-C2	2.13	114.07	109.99
3	G	3	MAN	C3-C4-C5	2.13	114.03	110.24
3	G	1	NAG	O5-C1-C2	-2.12	107.94	111.29
3	G	2	NAG	O5-C1-C2	-2.09	108.00	111.29
3	G	4	MAN	C1-C2-C3	-2.05	107.15	109.67
4	H	2	NAG	C6-C5-C4	-2.04	108.24	113.00
3	G	2	NAG	O5-C5-C6	2.02	110.36	107.20

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	F	3	MAN	C1
3	G	3	MAN	C1
2	E	3	MAN	C1

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	4	MAN	O5-C5-C6-O6
3	G	4	MAN	C4-C5-C6-O6
3	F	4	MAN	O5-C5-C6-O6
3	F	4	MAN	C4-C5-C6-O6
3	G	1	NAG	C8-C7-N2-C2
3	G	1	NAG	O7-C7-N2-C2

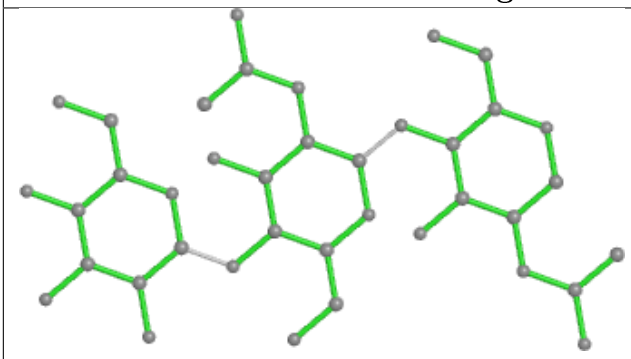
There are no ring outliers.

1 monomer is involved in 2 short contacts:

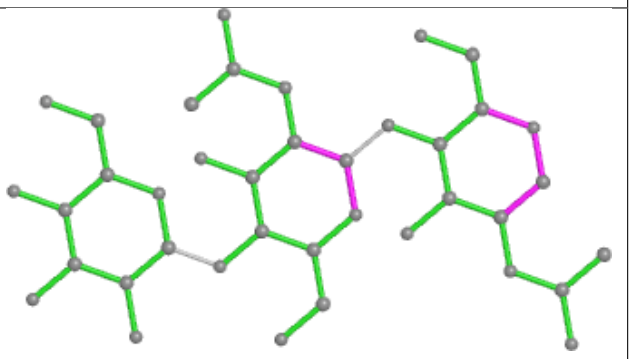
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	3	MAN	2	0

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

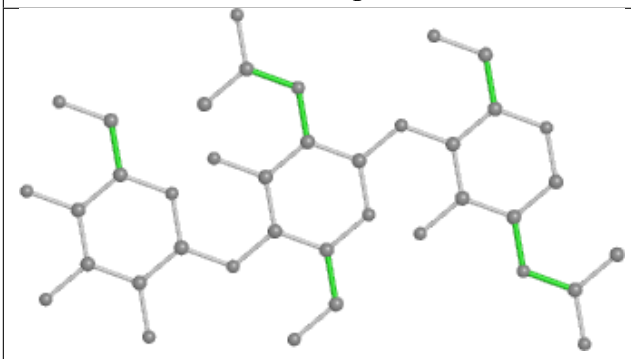
Oligosaccharide Chain E



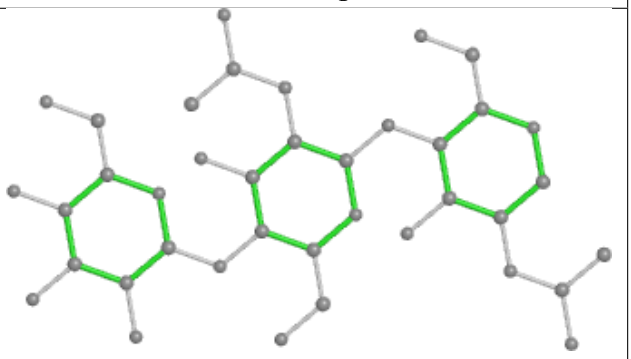
Bond lengths



Bond angles

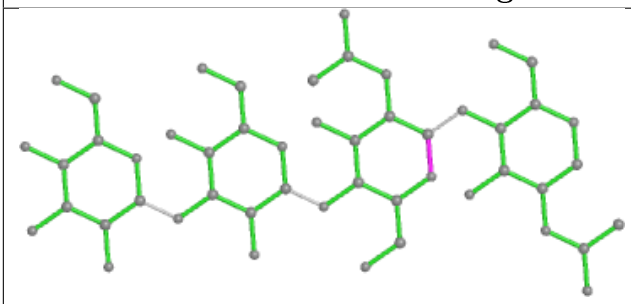


Torsions

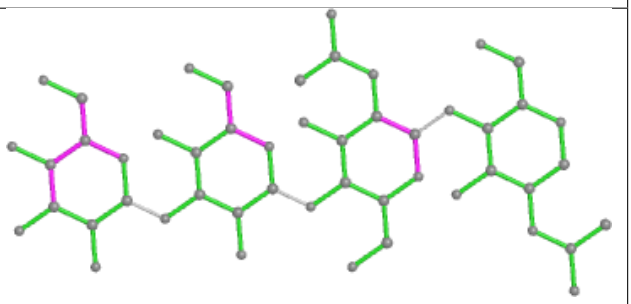


Rings

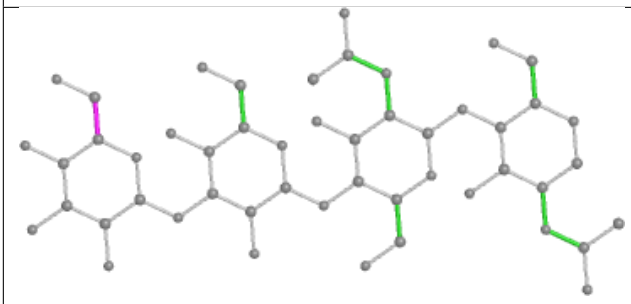
Oligosaccharide Chain F



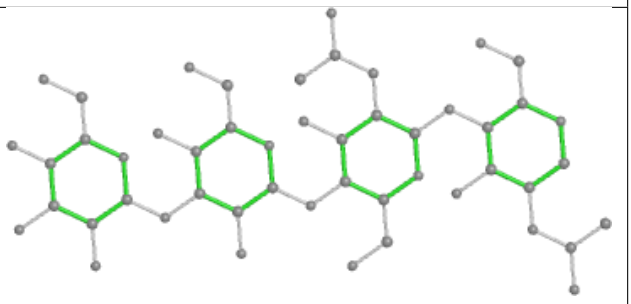
Bond lengths



Bond angles

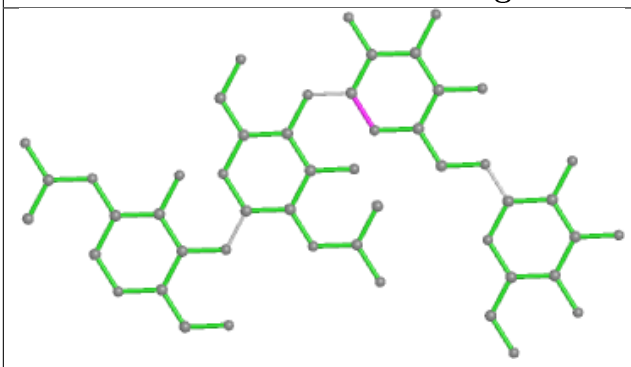


Torsions

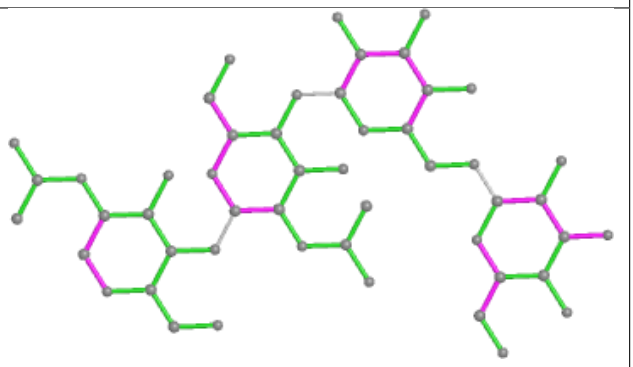


Rings

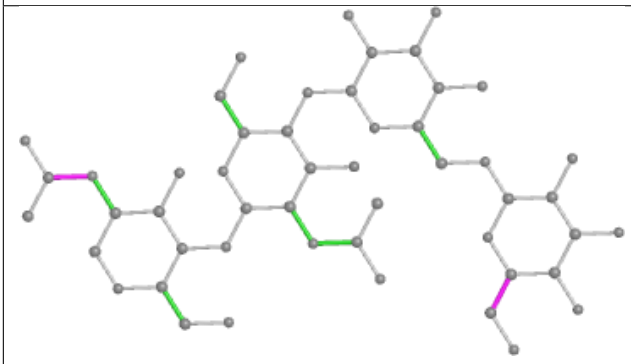
Oligosaccharide Chain G



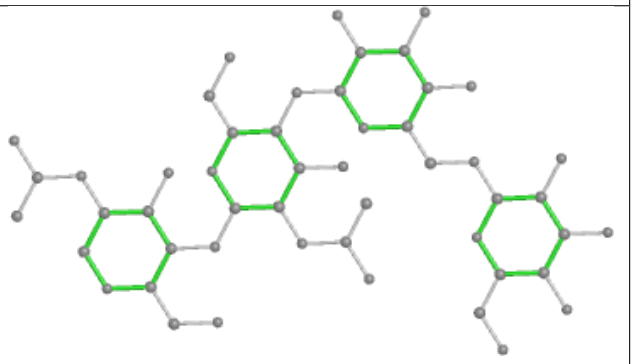
Bond lengths



Bond angles

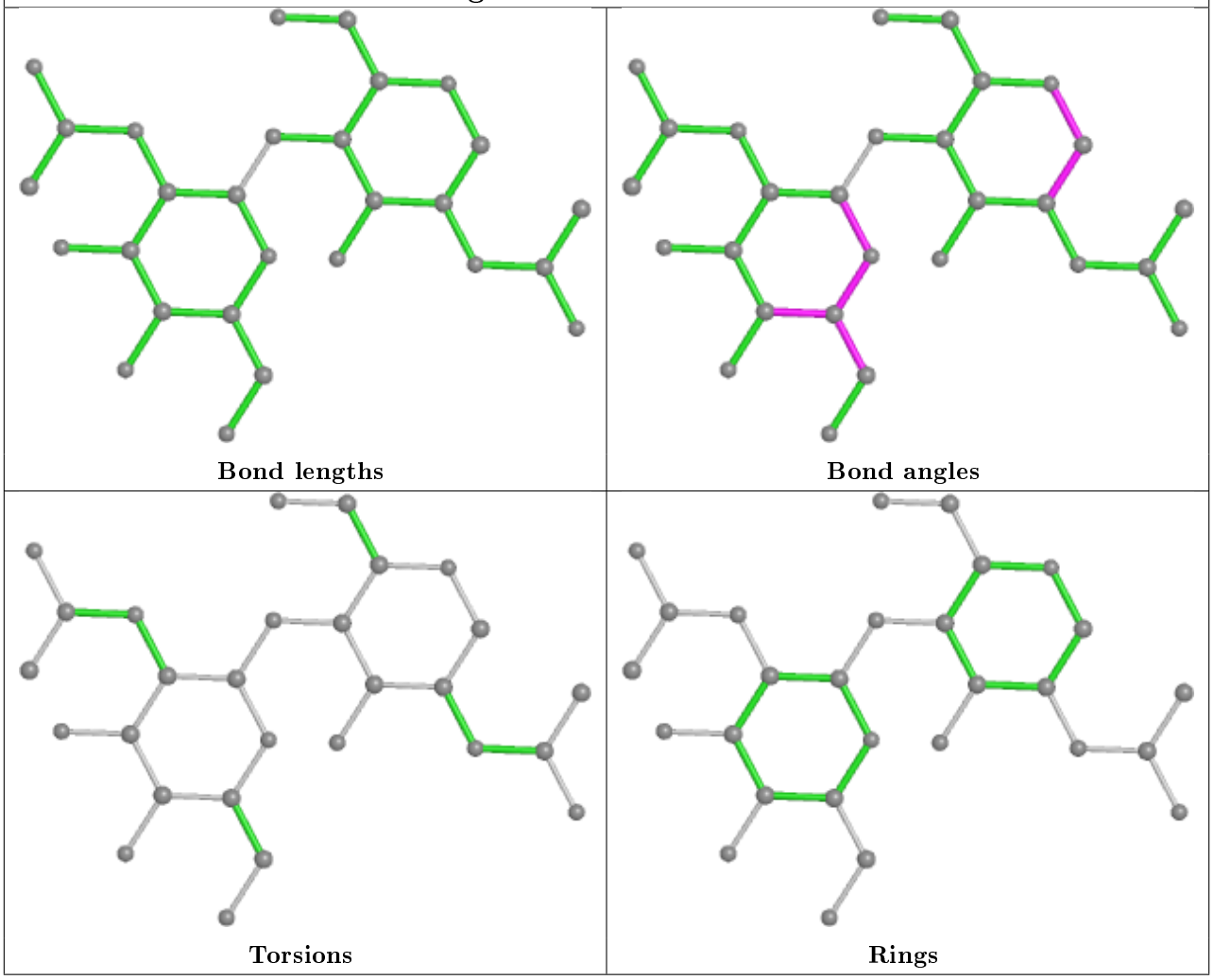


Torsions



Rings

Oligosaccharide Chain H



5.6 Ligand geometry

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 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	$\#\|Z\| > 2$
7	NAG	D	1356	1	14,14,15	0.61	0	17,19,21	1.13	3 (17%)
7	NAG	B	1356	1	14,14,15	0.67	0	17,19,21	1.63	5 (29%)
7	NAG	D	1353	1	14,14,15	0.51	0	17,19,21	1.24	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	NAG	B	1353	1	14,14,15	0.64	0	17,19,21	0.97	1 (5%)
5	KOJ	D	1351	6	8,10,10	3.79	4 (50%)	6,13,13	1.06	0
7	NAG	B	1357	1	14,14,15	0.65	0	17,19,21	1.03	0
7	NAG	A	1357	1	14,14,15	0.65	0	17,19,21	1.51	4 (23%)
7	NAG	C	1354	1	14,14,15	0.66	0	17,19,21	1.43	3 (17%)
5	KOJ	B	1351	6	8,10,10	3.40	3 (37%)	6,13,13	1.91	1 (16%)
7	NAG	C	1358	1	14,14,15	0.64	0	17,19,21	1.99	5 (29%)
7	NAG	A	1358	1	14,14,15	0.49	0	17,19,21	1.36	3 (17%)
7	NAG	A	1353	1	14,14,15	0.73	0	17,19,21	1.22	2 (11%)
5	KOJ	C	1351	6	8,10,10	3.53	4 (50%)	6,13,13	1.56	1 (16%)
5	KOJ	A	1351	6	8,10,10	3.60	4 (50%)	6,13,13	1.46	1 (16%)
7	NAG	C	1357	1	14,14,15	0.76	0	17,19,21	1.20	1 (5%)
7	NAG	A	1356	1	14,14,15	0.61	0	17,19,21	1.30	2 (11%)

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
7	NAG	D	1356	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1356	1	-	2/6/23/26	0/1/1/1
7	NAG	D	1353	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1353	1	-	2/6/23/26	0/1/1/1
5	KOJ	D	1351	6	-	0/1/2/2	0/1/1/1
7	NAG	B	1357	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1357	1	-	0/6/23/26	0/1/1/1
7	NAG	C	1354	1	-	0/6/23/26	0/1/1/1
5	KOJ	B	1351	6	-	1/1/2/2	0/1/1/1
7	NAG	C	1358	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1358	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1353	1	-	2/6/23/26	0/1/1/1
5	KOJ	C	1351	6	-	0/1/2/2	0/1/1/1
5	KOJ	A	1351	6	-	0/1/2/2	0/1/1/1
7	NAG	C	1357	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1356	1	-	0/6/23/26	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	1351	KOJ	O5-C5	-8.01	1.24	1.35
5	A	1351	KOJ	O5-C5	-7.61	1.25	1.35
5	B	1351	KOJ	O5-C5	-7.01	1.25	1.35
5	C	1351	KOJ	O5-C5	-6.82	1.26	1.35
5	D	1351	KOJ	O3-C3	5.84	1.33	1.23
5	C	1351	KOJ	O3-C3	5.84	1.33	1.23
5	B	1351	KOJ	O3-C3	5.33	1.32	1.23
5	A	1351	KOJ	O3-C3	5.30	1.32	1.23
5	B	1351	KOJ	C4-C5	2.62	1.40	1.35
5	C	1351	KOJ	C4-C5	2.52	1.40	1.35
5	C	1351	KOJ	C6-C5	-2.31	1.48	1.50
5	A	1351	KOJ	C6-C5	-2.28	1.48	1.50
5	D	1351	KOJ	C4-C5	2.22	1.39	1.35
5	D	1351	KOJ	C6-C5	-2.13	1.48	1.50
5	A	1351	KOJ	C4-C5	2.07	1.39	1.35

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	1351	KOJ	O6-C6-C5	4.30	121.57	112.10
7	C	1358	NAG	C2-N2-C7	-4.09	117.08	122.90
7	C	1358	NAG	C1-O5-C5	-3.85	106.98	112.19
7	C	1354	NAG	O5-C5-C6	3.69	113.00	107.20
7	B	1356	NAG	O5-C1-C2	-3.61	105.59	111.29
7	C	1358	NAG	O5-C5-C6	3.54	112.76	107.20
5	C	1351	KOJ	O6-C6-C5	3.19	119.13	112.10
7	A	1357	NAG	C1-O5-C5	3.14	116.45	112.19
7	C	1358	NAG	C4-C3-C2	3.12	115.59	111.02
7	A	1356	NAG	C1-O5-C5	3.11	116.40	112.19
7	A	1353	NAG	C2-N2-C7	-3.07	118.53	122.90
7	C	1358	NAG	O5-C1-C2	-3.05	106.47	111.29
5	A	1351	KOJ	O6-C6-C5	2.99	118.69	112.10
7	B	1356	NAG	C1-O5-C5	2.91	116.13	112.19
7	C	1357	NAG	O5-C1-C2	-2.83	106.82	111.29
7	B	1356	NAG	C2-N2-C7	-2.68	119.08	122.90
7	A	1358	NAG	O5-C5-C6	2.63	111.32	107.20
7	A	1357	NAG	C3-C4-C5	2.57	114.83	110.24
7	A	1353	NAG	O5-C5-C6	2.51	111.13	107.20
7	C	1354	NAG	C3-C4-C5	-2.50	105.78	110.24
7	D	1353	NAG	C1-O5-C5	2.46	115.53	112.19
7	B	1353	NAG	O5-C1-C2	-2.42	107.47	111.29
7	D	1356	NAG	O5-C1-C2	-2.39	107.51	111.29
7	A	1358	NAG	C2-N2-C7	2.37	126.28	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	1356	NAG	C2-N2-C7	-2.28	119.65	122.90
7	D	1356	NAG	C2-N2-C7	-2.25	119.70	122.90
7	D	1356	NAG	C1-O5-C5	2.22	115.20	112.19
7	A	1357	NAG	O5-C1-C2	-2.19	107.83	111.29
7	A	1358	NAG	O7-C7-C8	-2.15	118.07	122.06
7	B	1356	NAG	C1-C2-N2	2.07	114.02	110.49
7	C	1354	NAG	O5-C5-C4	-2.06	105.82	110.83
7	B	1356	NAG	C4-C3-C2	-2.04	108.03	111.02
7	A	1357	NAG	C6-C5-C4	-2.03	108.25	113.00
7	D	1353	NAG	O5-C1-C2	-2.02	108.09	111.29

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	1358	NAG	O5-C5-C6-O6
7	C	1358	NAG	C4-C5-C6-O6
7	B	1353	NAG	C4-C5-C6-O6
7	A	1353	NAG	O5-C5-C6-O6
7	D	1353	NAG	O5-C5-C6-O6
7	A	1353	NAG	C4-C5-C6-O6
7	A	1358	NAG	O5-C5-C6-O6
7	D	1353	NAG	C4-C5-C6-O6
7	B	1357	NAG	O5-C5-C6-O6
7	B	1357	NAG	C4-C5-C6-O6
7	B	1353	NAG	O5-C5-C6-O6
7	A	1358	NAG	C4-C5-C6-O6
7	B	1356	NAG	C4-C5-C6-O6
7	B	1356	NAG	O5-C5-C6-O6
5	B	1351	KOJ	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1351	KOJ	1	0
5	B	1351	KOJ	3	0
5	C	1351	KOJ	3	0
5	A	1351	KOJ	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	341/350 (97%)	-0.12	10 (2%) 51 61	6, 11, 17, 25	0
1	B	334/350 (95%)	-0.19	8 (2%) 59 67	6, 11, 16, 26	0
1	C	333/350 (95%)	-0.08	9 (2%) 54 63	7, 11, 16, 24	0
1	D	331/350 (94%)	-0.07	9 (2%) 54 63	7, 11, 16, 24	0
All	All	1339/1400 (95%)	-0.12	36 (2%) 54 63	6, 11, 16, 26	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	154	SER	4.6
1	B	3	SER	4.5
1	D	181	LEU	3.9
1	A	90	ASN	3.8
1	D	182	SER	3.4
1	B	170	SER	3.1
1	C	4	SER	2.9
1	A	169	ILE	2.8
1	B	181	LEU	2.8
1	A	154	SER	2.7
1	D	170	SER	2.6
1	A	168	THR	2.6
1	B	168	THR	2.5
1	D	90	ASN	2.5
1	C	89	GLY	2.4
1	C	90	ASN	2.4
1	D	262	THR	2.4
1	D	171	THR	2.4
1	B	169	ILE	2.3
1	A	321	LEU	2.2
1	A	163	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	4	SER	2.2
1	B	4	SER	2.2
1	D	183	PHE	2.2
1	B	289	ASP	2.1
1	C	289	ASP	2.1
1	C	182	SER	2.1
1	D	100	SER	2.1
1	A	164	PRO	2.1
1	C	50	LEU	2.1
1	C	321	LEU	2.1
1	A	261	SER	2.1
1	C	3	SER	2.1
1	A	2	THR	2.0
1	A	166	SER	2.0
1	B	90	ASN	2.0

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

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

6.3 Carbohydrates (i)

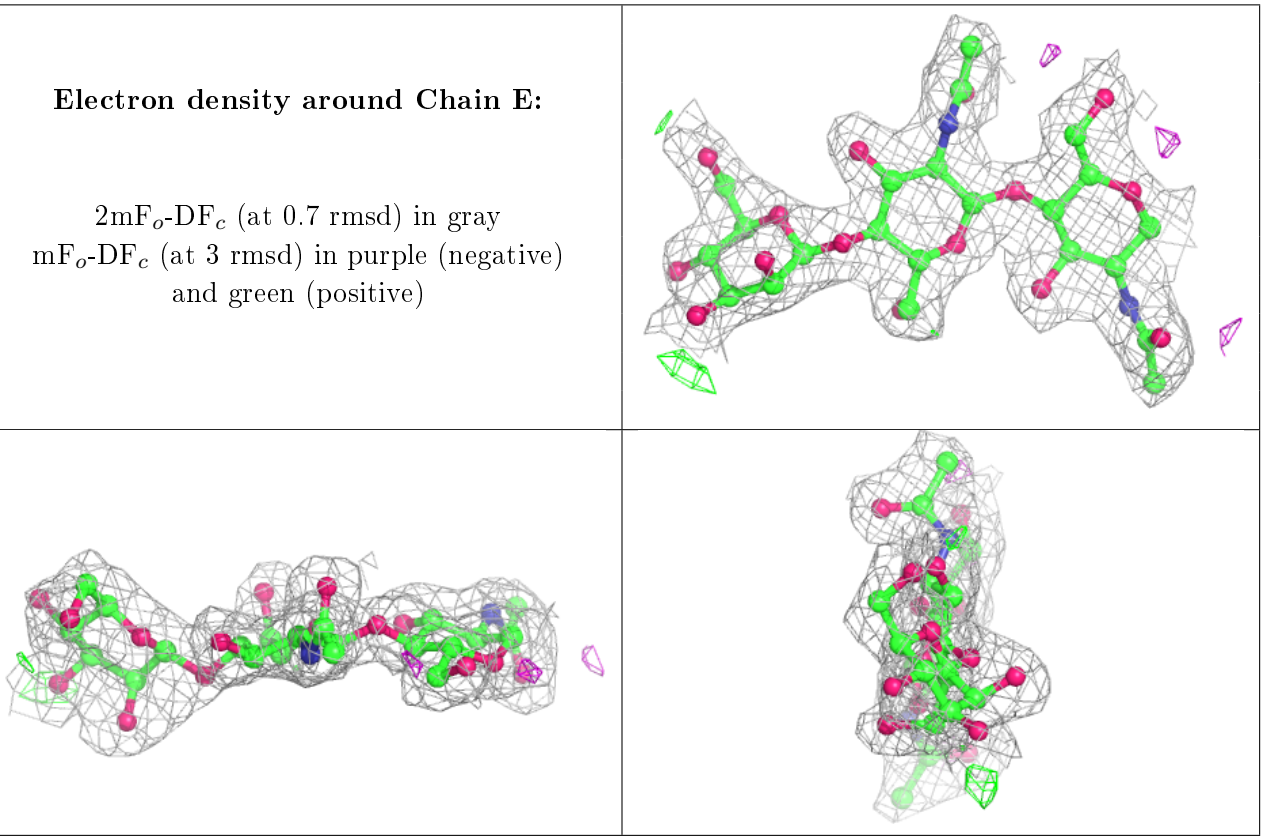
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MAN	G	4	11/12	0.72	0.27	41,42,44,44	0
3	MAN	F	4	11/12	0.84	0.24	46,48,50,50	0
3	MAN	F	3	11/12	0.86	0.24	43,45,47,50	0
4	NAG	H	2	14/15	0.87	0.13	24,30,34,35	0
2	NAG	E	2	14/15	0.89	0.13	26,30,35,35	0
3	MAN	G	3	11/12	0.89	0.19	37,40,42,43	0
3	NAG	F	2	14/15	0.90	0.13	27,35,38,41	0
2	MAN	E	3	11/12	0.91	0.13	37,40,41,43	0
3	NAG	F	1	14/15	0.94	0.12	24,29,31,31	0
3	NAG	G	2	14/15	0.94	0.12	25,30,34,34	0
2	NAG	E	1	14/15	0.95	0.09	22,26,27,29	0
4	NAG	H	1	14/15	0.96	0.10	22,26,29,30	0
3	NAG	G	1	14/15	0.96	0.08	23,26,32,33	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.

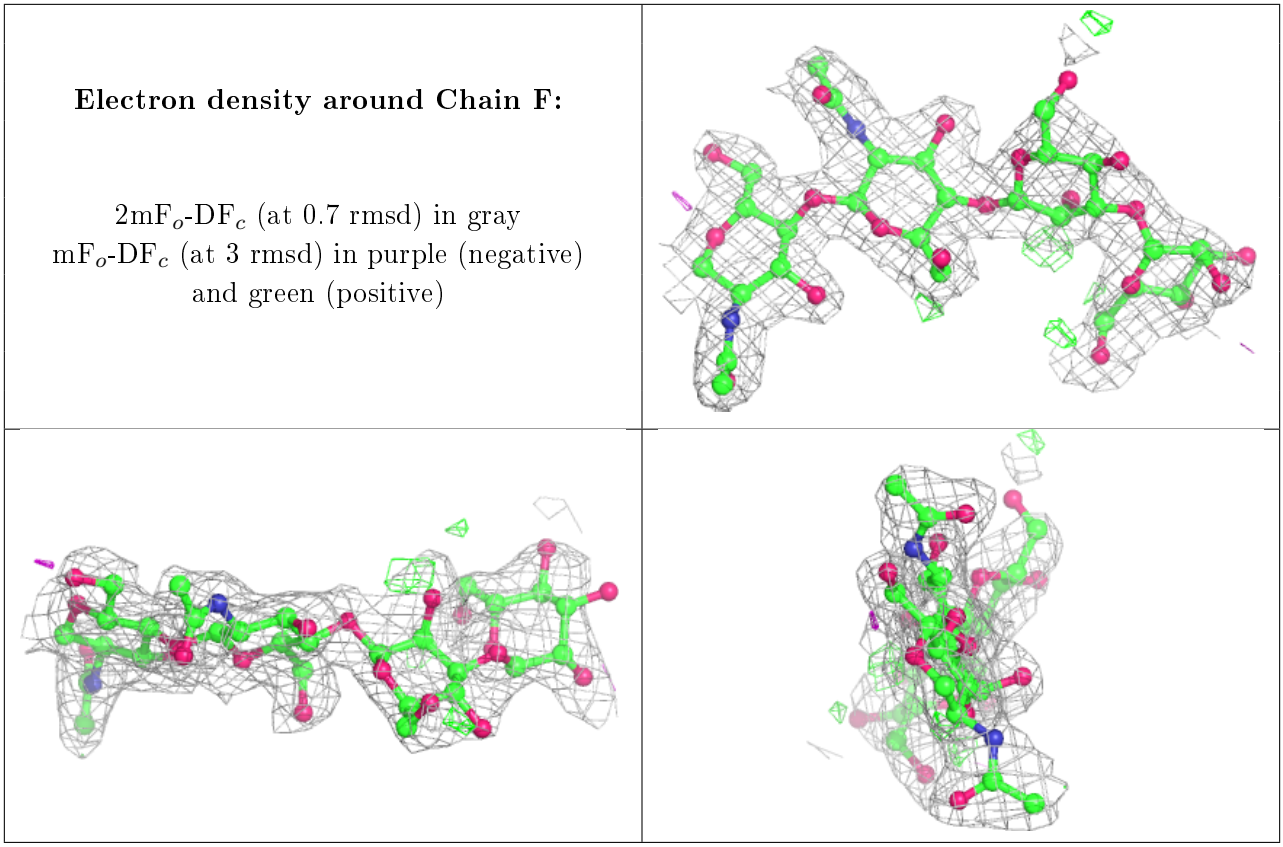
Electron density around Chain E:

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



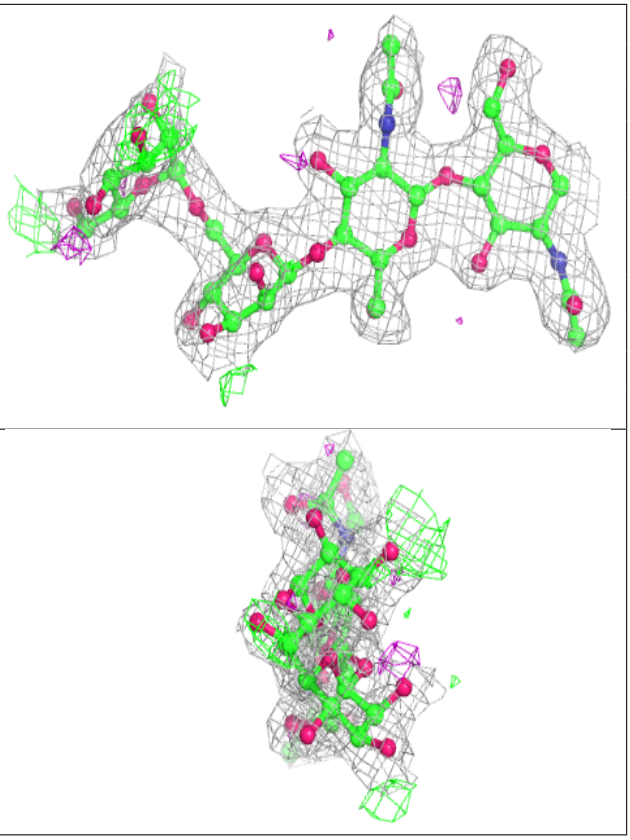
Electron density around Chain F:

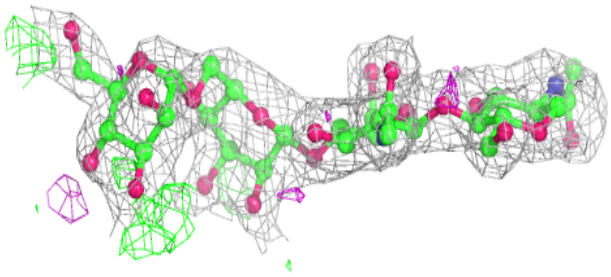
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around Chain G:

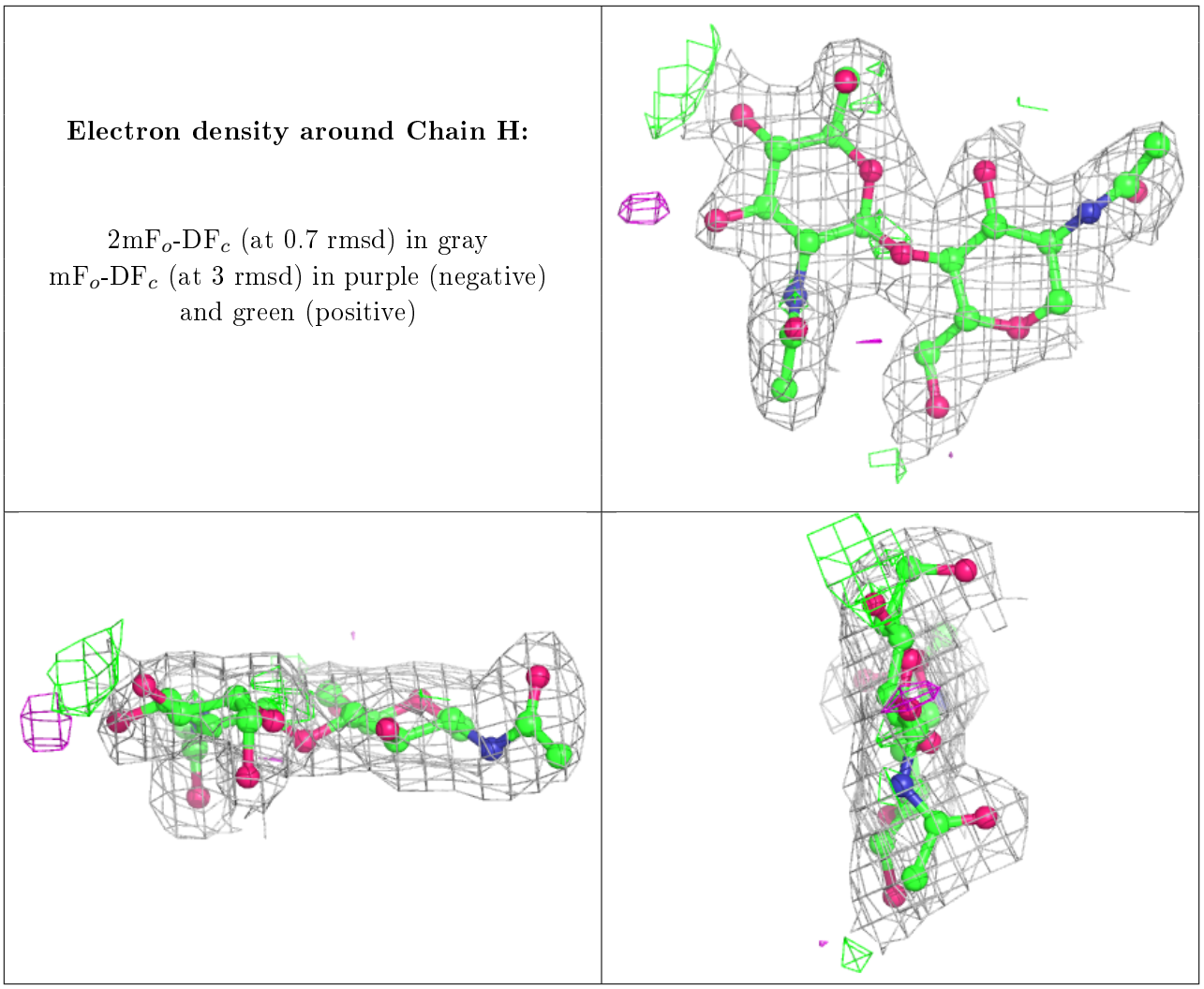
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	NAG	C	1358	14/15	0.78	0.21	36,43,45,46	0
7	NAG	A	1358	14/15	0.80	0.31	31,37,40,40	0
7	NAG	B	1356	14/15	0.83	0.28	29,35,40,41	0
7	NAG	A	1357	14/15	0.83	0.19	30,34,37,38	0
7	NAG	D	1353	14/15	0.89	0.16	31,36,39,39	0
7	NAG	C	1354	14/15	0.90	0.15	30,35,40,40	0
7	NAG	B	1357	14/15	0.90	0.16	33,39,41,41	0
7	NAG	A	1356	14/15	0.90	0.14	25,31,37,38	0
7	NAG	C	1357	14/15	0.91	0.16	31,35,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	NAG	B	1353	14/15	0.91	0.13	25,29,32,34	0
5	KOJ	A	1351	10/10	0.93	0.13	21,24,26,27	0
7	NAG	A	1353	14/15	0.93	0.13	24,27,30,34	0
5	KOJ	C	1351	10/10	0.93	0.16	30,30,32,32	0
7	NAG	D	1356	14/15	0.94	0.15	30,34,41,42	0
5	KOJ	D	1351	10/10	0.95	0.15	25,28,32,34	0
5	KOJ	B	1351	10/10	0.95	0.18	29,30,31,32	0
6	CU	C	1352	1/1	0.99	0.02	13,13,13,13	0
6	CU	D	1352	1/1	1.00	0.01	12,12,12,12	0
6	CU	B	1352	1/1	1.00	0.03	14,14,14,14	0
6	CU	A	1352	1/1	1.00	0.04	12,12,12,12	0

6.5 Other polymers (i)

There are no such residues in this entry.