



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:07 AM UTC

PDB ID : 5E2Z / pdb_00005e2z
Title : Crystal structure of H5 hemagglutinin Q226L mutant from the influenza virus
A/duck/Egypt/10185SS/2010 (H5N1) with LSTa
Authors : Zhu, X.; Wilson, I.A.
Deposited on : 2015-10-01
Resolution : 2.62 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 : 4-5-2 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

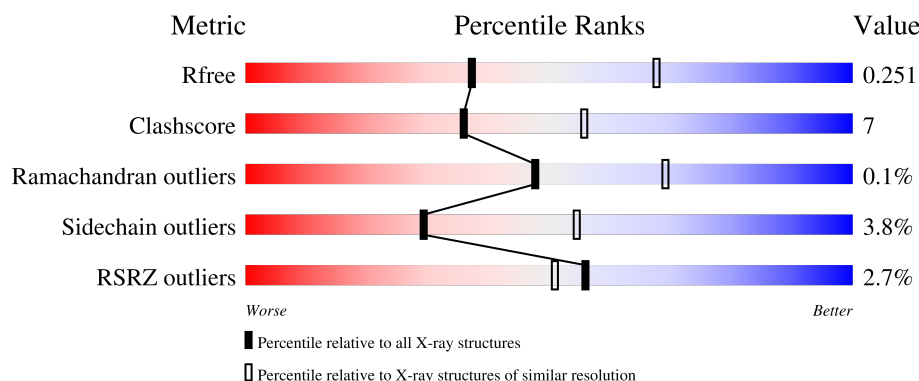
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	333	
1	C	333	
1	E	333	
2	B	180	
2	D	180	

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Mol	Chain	Length	Quality of chain
2	F	180	3% 79% 17%
3	G	3	33% 67%
3	K	3	33% 67%
4	H	2	50% 50%
4	L	2	100%
5	I	4	25% 25% 50%
6	J	3	67% 33%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12369 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	323	Total	C	N	O	S	0	0	0
			2558	1611	443	490	14			
1	A	323	Total	C	N	O	S	0	0	0
			2558	1611	443	490	14			
1	E	323	Total	C	N	O	S	0	0	0
			2558	1611	443	490	14			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	7	ALA	-	expression tag	UNP G8IPF0
C	8	ASP	-	expression tag	UNP G8IPF0
C	9	PRO	-	expression tag	UNP G8IPF0
C	10	GLY	-	expression tag	UNP G8IPF0
C	226	LEU	GLN	engineered mutation	UNP G8IPF0
A	7	ALA	-	expression tag	UNP G8IPF0
A	8	ASP	-	expression tag	UNP G8IPF0
A	9	PRO	-	expression tag	UNP G8IPF0
A	10	GLY	-	expression tag	UNP G8IPF0
A	226	LEU	GLN	engineered mutation	UNP G8IPF0
E	7	ALA	-	expression tag	UNP G8IPF0
E	8	ASP	-	expression tag	UNP G8IPF0
E	9	PRO	-	expression tag	UNP G8IPF0
E	10	GLY	-	expression tag	UNP G8IPF0
E	226	LEU	GLN	engineered mutation	UNP G8IPF0

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	175	Total	C	N	O	S	0	0	0
			1418	880	248	282	8			

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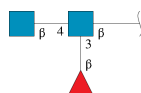
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	175	Total	C	N	O	S	0	0	0
			1418	880	248	282	8			
2	F	175	Total	C	N	O	S	0	0	0
			1418	880	248	282	8			

There are 18 discrepancies between the modelled and reference sequences:

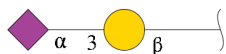
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	GLY	-	expression tag	UNP G8IPF0
D	176	ARG	-	expression tag	UNP G8IPF0
D	177	LEU	-	expression tag	UNP G8IPF0
D	178	VAL	-	expression tag	UNP G8IPF0
D	179	PRO	-	expression tag	UNP G8IPF0
D	180	ARG	-	expression tag	UNP G8IPF0
B	1	GLY	-	expression tag	UNP G8IPF0
B	176	ARG	-	expression tag	UNP G8IPF0
B	177	LEU	-	expression tag	UNP G8IPF0
B	178	VAL	-	expression tag	UNP G8IPF0
B	179	PRO	-	expression tag	UNP G8IPF0
B	180	ARG	-	expression tag	UNP G8IPF0
F	1	GLY	-	expression tag	UNP G8IPF0
F	176	ARG	-	expression tag	UNP G8IPF0
F	177	LEU	-	expression tag	UNP G8IPF0
F	178	VAL	-	expression tag	UNP G8IPF0
F	179	PRO	-	expression tag	UNP G8IPF0
F	180	ARG	-	expression tag	UNP G8IPF0

- Molecule 3 is an oligosaccharide called beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose.



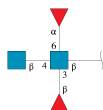
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	3	Total	C	N	O	0	0	0
			38	22	2	14			
3	K	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 4 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	H	2	Total	C	N	O	0	0	0
			31	17	1	13			
4	L	2	Total	C	N	O	0	0	0
			31	17	1	13			

- Molecule 5 is an oligosaccharide called beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	I	4	Total	C	N	O	0	0	0
			48	28	2	18			

- Molecule 6 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	J	3	Total	C	N	O	0	0	0
			46	25	2	19			

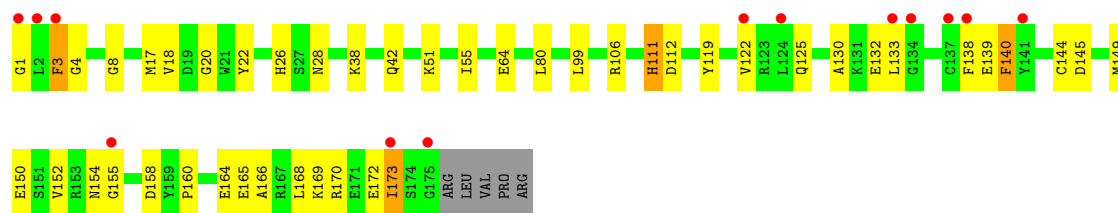
- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



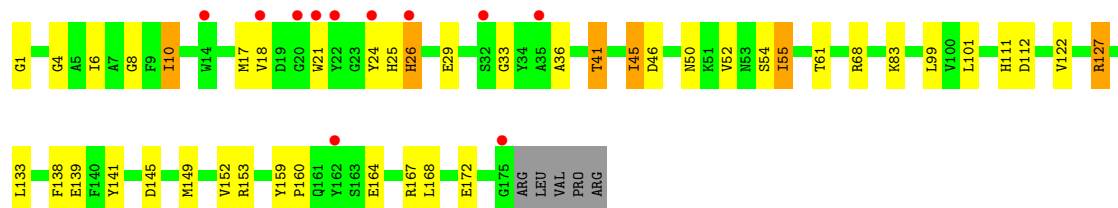
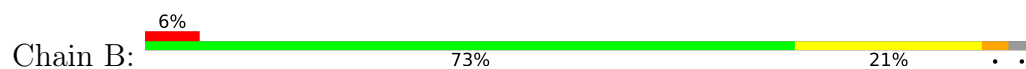
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is water.

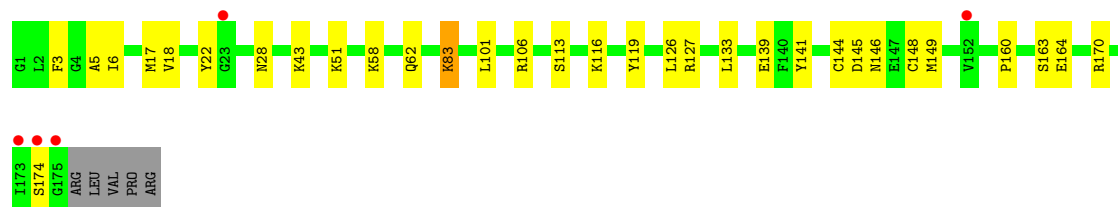
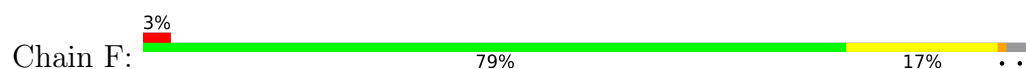
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	47	Total	O	0	0
			47	47		
8	D	7	Total	O	0	0
			7	7		
8	A	54	Total	O	0	0
			54	54		
8	B	8	Total	O	0	0
			8	8		
8	E	43	Total	O	0	0
			43	43		
8	F	8	Total	O	0	0
			8	8		



• Molecule 2: Hemagglutinin



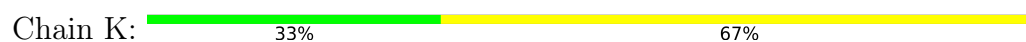
• Molecule 2: Hemagglutinin



• Molecule 3: beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose



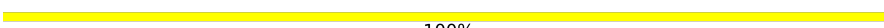
• Molecule 3: beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose



- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose

Chain L:  100%

GAL1
SIA2

- Molecule 5: beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  25% 25% 50%

MAG1
FUL2
MAG3
FUC4

- Molecule 6: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  67% 33%

MAG1
GAL2
SIA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.06Å 234.15Å 72.95Å 90.00° 115.49° 90.00°	Depositor
Resolution (Å)	50.00 – 2.62 50.00 – 2.62	Depositor EDS
% Data completeness (in resolution range)	86.8 (50.00-2.62) 86.8 (50.00-2.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.202 , 0.248 0.206 , 0.251	Depositor DCC
R_{free} test set	2919 reflections (4.43%)	wwPDB-VP
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12369	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GAL, NAG, FUC, FUL, SIA

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	0.73	1/2619 (0.0%)	0.98	1/3559 (0.0%)
1	C	0.71	0/2619	0.97	4/3559 (0.1%)
1	E	0.64	0/2619	0.92	2/3559 (0.1%)
2	B	0.54	0/1445	0.88	3/1942 (0.2%)
2	D	0.55	0/1445	0.87	2/1942 (0.1%)
2	F	0.53	0/1445	0.83	0/1942
All	All	0.64	1/12192 (0.0%)	0.92	12/16503 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	260	ILE	CA-CB	5.22	1.58	1.53

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	127	ARG	CB-CA-C	-6.40	109.20	116.63
1	A	61	LEU	N-CA-C	-6.09	101.92	110.50
2	B	33	GLY	N-CA-C	6.04	118.14	110.96
1	C	56	VAL	N-CA-C	5.65	116.44	108.36
1	E	218	ALA	N-CA-C	5.43	115.54	107.88
1	C	52	CYS	N-CA-C	5.31	117.34	109.69
2	B	141	TYR	N-CA-C	-5.30	106.40	112.92
2	D	3	PHE	N-CA-C	5.10	121.66	110.80
1	E	61	LEU	N-CA-C	-5.09	103.33	110.50
2	D	111	HIS	N-CA-C	-5.05	105.78	111.28
1	C	253	ALA	CA-C-N	5.01	124.92	119.76
1	C	253	ALA	C-N-CA	5.01	124.92	119.76

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	2558	0	2492	33	0
1	C	2558	0	2492	37	0
1	E	2558	0	2492	36	0
2	B	1418	0	1322	32	0
2	D	1418	0	1322	37	0
2	F	1418	0	1322	21	0
3	G	38	0	34	0	0
3	K	38	0	34	0	0
4	H	31	0	26	1	0
4	L	31	0	26	0	0
5	I	48	0	43	3	0
6	J	46	0	40	3	0
7	A	14	0	13	0	0
7	C	14	0	13	0	0
7	E	14	0	13	0	0
8	A	54	0	0	2	0
8	B	8	0	0	0	0
8	C	47	0	0	0	0
8	D	7	0	0	0	0
8	E	43	0	0	2	0
8	F	8	0	0	0	0
All	All	12369	0	11684	174	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 7.

All (174) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:26:HIS:HD2	2:B:149:MET:HE3	1.26	1.00
2:B:26:HIS:CD2	2:B:149:MET:HE3	2.04	0.91
1:C:206:THR:HG22	1:C:208:THR:H	1.38	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:268:MET:HE3	1:E:284:PRO:HA	1.59	0.84
1:E:206:THR:HG22	1:E:209:LEU:H	1.43	0.83
1:E:28:THR:HG22	1:E:30:MET:H	1.45	0.81
2:D:125:GLN:HE22	2:D:155:GLY:HA2	1.47	0.78
1:A:222:LYS:NZ	6:J:1:NAG:H82	2.04	0.73
1:C:268:MET:HE3	1:C:284:PRO:HA	1.70	0.72
1:E:174:GLU:HG3	1:E:259:LYS:HB3	1.72	0.72
2:B:17:MET:HE1	2:B:36:ALA:HA	1.70	0.71
1:E:20:ASN:OD1	1:E:322:ASN:ND2	2.25	0.70
2:D:140:PHE:H	2:D:140:PHE:HD1	1.37	0.69
1:E:307:LYS:HE2	2:F:62:GLN:HB3	1.73	0.69
1:A:206:THR:HG22	1:A:209:LEU:H	1.58	0.68
1:A:268:MET:HE3	1:A:284:PRO:HA	1.75	0.68
1:E:280:LYS:NZ	8:E:1101:HOH:O	2.26	0.67
1:E:21:ASN:ND2	8:E:1102:HOH:O	2.29	0.65
1:A:206:THR:HG22	1:A:208:THR:H	1.62	0.65
5:I:3:NAG:H5	5:I:4:FUC:H63	1.77	0.65
2:D:130:ALA:HA	2:D:140:PHE:HA	1.77	0.65
2:D:28:ASN:ND2	2:D:144:CYS:O	2.30	0.64
1:C:29:ILE:HD11	2:F:51:LYS:HE2	1.79	0.64
1:A:26:VAL:HG21	1:A:317:ALA:HB2	1.79	0.63
2:B:167:ARG:HD2	2:F:174:SER:HA	1.81	0.63
2:B:24:TYR:CZ	2:B:153:ARG:HG2	2.36	0.61
1:E:206:THR:HG22	1:E:208:THR:H	1.65	0.61
2:D:1:GLY:HA3	2:D:3:PHE:CZ	2.36	0.60
2:D:3:PHE:HD1	2:D:4:GLY:H	1.46	0.60
2:F:145:ASP:OD1	2:F:148:CYS:N	2.33	0.60
1:A:289:ASN:ND2	8:A:1103:HOH:O	2.35	0.60
2:F:164:GLU:H	2:F:164:GLU:CD	2.11	0.58
1:C:15:ILE:HD13	2:D:119:TYR:HA	1.86	0.58
1:A:222:LYS:HZ2	6:J:1:NAG:H82	1.67	0.58
2:B:6:ILE:HD13	2:B:112:ASP:HA	1.86	0.57
1:C:43:LEU:O	1:C:45:LYS:NZ	2.37	0.57
2:D:132:GLU:HG2	2:D:138:PHE:HE1	1.70	0.57
1:A:292:MET:HA	1:A:292:MET:HE2	1.86	0.57
2:D:64:GLU:O	2:B:83:LYS:NZ	2.33	0.56
2:D:168:LEU:O	2:D:172:GLU:HG3	2.06	0.56
2:B:168:LEU:O	2:B:172:GLU:HG3	2.06	0.54
1:C:206:THR:HB	1:C:209:LEU:HB3	1.89	0.54
2:D:150:GLU:O	2:D:154:ASN:ND2	2.40	0.54
2:D:133:LEU:HA	2:F:127:ARG:HH12	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:46:ASP:O	2:B:50:ASN:ND2	2.28	0.54
1:C:185:PRO:HG2	1:C:217:ILE:HG12	1.88	0.54
1:C:313:ARG:HH21	1:C:315:VAL:HG11	1.73	0.54
1:E:206:THR:HG22	1:E:209:LEU:N	2.20	0.53
2:D:3:PHE:HD1	2:D:4:GLY:N	2.06	0.53
2:D:3:PHE:HB2	2:D:112:ASP:OD1	2.08	0.53
1:A:58:PRO:HB3	1:A:86:TYR:CE1	2.44	0.53
1:C:15:ILE:HD11	2:D:122:VAL:HG21	1.90	0.53
2:F:17:MET:HE1	2:F:22:TYR:C	2.34	0.53
1:C:52:CYS:HB2	1:C:279:THR:HG22	1.91	0.52
2:D:106:ARG:NH2	2:F:106:ARG:HH21	2.06	0.52
2:B:21:TRP:H	2:B:41:THR:HG21	1.73	0.52
1:C:285:ILE:HD11	1:C:297:ILE:HG23	1.91	0.52
1:A:15:ILE:O	2:B:10:ILE:HD12	2.09	0.52
2:D:51:LYS:HG3	1:A:29:ILE:HD12	1.92	0.52
2:F:133:LEU:HD11	2:F:139:GLU:HB2	1.91	0.51
1:C:98:TYR:CD1	1:C:230:MET:HG3	2.46	0.51
1:A:206:THR:HB	1:A:209:LEU:HB3	1.91	0.51
1:E:206:THR:CG2	1:E:208:THR:H	2.23	0.51
2:D:51:LYS:HE2	1:A:29:ILE:HD11	1.91	0.51
2:B:149:MET:O	2:B:152:VAL:HG22	2.11	0.51
2:D:17:MET:HE1	2:D:22:TYR:C	2.36	0.50
2:D:169:LYS:O	2:D:173:ILE:HD12	2.11	0.50
1:E:43:LEU:O	1:E:45:LYS:NZ	2.44	0.50
1:C:164:ILE:O	1:C:246:GLU:HA	2.11	0.50
2:B:133:LEU:HD11	2:B:139:GLU:HB2	1.94	0.50
1:C:135:VAL:HG13	1:C:145:SER:HB3	1.94	0.49
2:B:41:THR:O	2:B:45:ILE:HG12	2.12	0.49
2:B:54:SER:OG	1:E:32:LYS:NZ	2.35	0.49
2:B:26:HIS:HD2	2:B:149:MET:CE	2.13	0.49
1:E:101:ASN:OD1	1:E:231:GLU:HG3	2.11	0.49
1:E:206:THR:HB	1:E:209:LEU:HB3	1.94	0.49
2:D:149:MET:O	2:D:152:VAL:HG22	2.13	0.49
1:C:134:GLY:HA3	1:C:153:TRP:HB3	1.93	0.49
1:E:32:LYS:N	1:E:32:LYS:HD2	2.28	0.49
1:E:268:MET:HG2	1:E:284:PRO:HG3	1.94	0.49
1:E:77:ASP:O	1:E:80:LEU:HD12	2.13	0.49
1:C:100:GLY:HA3	1:C:230:MET:O	2.12	0.48
1:C:216:LYS:NZ	1:E:210:ASN:O	2.42	0.48
2:D:158:ASP:OD1	2:D:160:PRO:HD2	2.14	0.48
2:D:125:GLN:NE2	2:D:155:GLY:HA2	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:TRP:HB2	2:B:41:THR:HG22	1.94	0.48
1:A:288:ILE:HD11	1:A:297:ILE:HD13	1.96	0.48
2:B:145:ASP:O	2:B:149:MET:HG2	2.14	0.47
1:A:14:CYS:HB2	2:B:25:HIS:HB3	1.97	0.47
2:D:38:LYS:O	2:D:42:GLN:N	2.43	0.47
2:B:127:ARG:NH2	2:F:133:LEU:O	2.47	0.47
1:E:44:GLU:HB2	1:E:292:MET:HG3	1.95	0.47
2:F:3:PHE:CE2	2:F:113:SER:HB2	2.50	0.47
1:E:56:VAL:HB	1:E:85:SER:HB3	1.96	0.47
2:D:164:GLU:CD	2:D:164:GLU:H	2.22	0.46
2:D:26:HIS:HB2	2:D:149:MET:HE3	1.97	0.46
1:A:29:ILE:HG13	1:A:30:MET:N	2.30	0.46
1:A:170:ASN:HB2	1:A:237:LEU:HD23	1.98	0.46
1:C:206:THR:CG2	1:C:207:SER:N	2.78	0.46
2:B:164:GLU:H	2:B:164:GLU:CD	2.24	0.46
1:A:61:LEU:H	1:A:61:LEU:HD22	1.81	0.46
2:B:52:VAL:O	2:B:55:ILE:HG22	2.16	0.46
2:F:28:ASN:ND2	2:F:146:ASN:OD1	2.30	0.46
1:A:31:GLU:OE1	1:A:321:ARG:NH2	2.43	0.45
1:C:320:LEU:HB3	2:D:111:HIS:CD2	2.52	0.45
2:B:159:TYR:HB3	2:B:160:PRO:HD3	1.98	0.45
1:C:38:HIS:C	1:C:318:THR:HG22	2.42	0.45
1:C:284:PRO:HD3	1:C:300:LEU:O	2.16	0.45
2:D:130:ALA:HB2	2:D:140:PHE:HB3	1.97	0.45
1:C:307:LYS:HA	1:C:307:LYS:HD3	1.76	0.45
1:A:61:LEU:HA	1:A:79:PHE:CZ	2.52	0.45
1:A:320:LEU:HB3	2:B:111:HIS:CD2	2.52	0.45
1:C:123:ILE:HG13	1:C:124:THR:HG22	1.99	0.45
2:B:1:GLY:HA3	2:B:112:ASP:OD2	2.17	0.45
1:A:166:ARG:HG3	8:A:1120:HOH:O	2.17	0.44
1:E:75:MET:HE2	1:E:140:PRO:O	2.17	0.44
1:A:14:CYS:O	2:B:24:TYR:HA	2.18	0.44
1:E:295:HIS:HD2	1:E:306:PRO:HB2	1.82	0.44
5:I:3:NAG:H5	5:I:4:FUC:C6	2.46	0.44
1:E:74:PRO:HG3	1:E:147:PHE:O	2.16	0.44
2:D:55:ILE:HG23	2:D:99:LEU:HD21	2.00	0.44
1:E:100:GLY:HA3	1:E:230:MET:O	2.18	0.44
1:E:135:VAL:HG22	1:E:146:SER:HA	2.00	0.44
1:E:216:LYS:O	1:E:220:ARG:NH2	2.51	0.44
2:F:141:TYR:CE2	2:F:170:ARG:HD3	2.52	0.44
2:F:160:PRO:HA	2:F:163:SER:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:61:LEU:HA	1:C:79:PHE:CZ	2.53	0.44
1:A:135:VAL:HG22	1:A:146:SER:HA	1.99	0.44
1:A:124:THR:HA	1:A:125:PRO:HD3	1.88	0.43
2:D:140:PHE:CE2	2:D:144:CYS:HB2	2.53	0.43
1:C:190:GLU:OE2	4:H:2:SIA:O9	2.31	0.43
1:C:21:ASN:OD1	1:C:21:ASN:N	2.49	0.43
1:A:323:SER:HA	1:A:324:PRO:HD3	1.90	0.43
2:D:164:GLU:HG2	2:D:165:GLU:N	2.33	0.43
1:E:55:ASP:HB3	1:E:55(A):GLY:H	1.68	0.43
1:C:29:ILE:HD12	2:F:51:LYS:HG3	2.01	0.43
1:A:50:LYS:HB3	1:A:50:LYS:HE2	1.75	0.43
2:D:4:GLY:O	2:D:8:GLY:HA3	2.19	0.43
2:B:29:GLU:H	2:B:29:GLU:CD	2.27	0.43
2:B:145:ASP:OD1	2:B:145:ASP:N	2.52	0.43
1:C:9:PRO:HA	2:D:139:GLU:OE2	2.19	0.43
1:C:125:PRO:HB2	1:C:125(B):ASN:OD1	2.18	0.43
2:B:4:GLY:O	2:B:8:GLY:HA3	2.19	0.43
1:A:222:LYS:HZ3	6:J:1:NAG:H82	1.80	0.42
1:C:132:ALA:HB1	1:C:152:VAL:HG11	2.01	0.42
1:A:91:ILE:HG13	1:A:271:GLU:OE2	2.19	0.42
2:B:55:ILE:HD11	2:B:99:LEU:HG	2.02	0.42
1:E:176:LEU:HD22	1:E:257:ALA:HB1	2.00	0.42
1:E:283:THR:HG22	1:E:301:THR:HG22	2.01	0.42
1:C:101:ASN:OD1	1:C:231:GLU:HG3	2.19	0.42
1:E:15:ILE:HD13	2:F:119:TYR:HA	2.01	0.42
5:I:2:FUL:H5	5:I:3:NAG:O3	2.19	0.42
1:A:222:LYS:HA	1:A:226:LEU:O	2.19	0.42
1:C:24:GLU:OE1	1:C:39:ALA:HB3	2.19	0.42
1:A:52:CYS:HB2	1:A:279:THR:HG22	2.01	0.42
1:E:28:THR:CG2	1:E:29:ILE:N	2.82	0.42
1:E:124:THR:HA	1:E:125:PRO:HD2	1.88	0.42
2:B:122:VAL:HG23	2:B:138:PHE:HE2	1.85	0.42
2:D:3:PHE:CD1	2:D:4:GLY:N	2.83	0.42
1:E:125:PRO:HG2	1:E:126:SER:HB2	2.02	0.42
1:C:55:ASP:O	1:C:278:ASN:OD1	2.37	0.41
1:C:124:THR:HA	1:C:125:PRO:HD2	1.92	0.41
2:B:68:ARG:NH2	2:F:83:LYS:HD3	2.34	0.41
1:C:25:GLN:HA	1:C:34:VAL:O	2.20	0.41
1:A:183:HIS:CD2	1:A:230:MET:HE2	2.55	0.41
1:E:314:LEU:HD23	1:E:314:LEU:HA	1.92	0.41
2:D:166:ALA:O	2:D:170:ARG:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:PRO:HD3	1:A:300:LEU:O	2.20	0.41
2:F:145:ASP:O	2:F:149:MET:HG2	2.20	0.41
2:F:5:ALA:HB2	2:F:116:LYS:HB2	2.02	0.40
1:C:11:ASP:HB2	2:D:140:PHE:CE1	2.57	0.40
2:F:58:LYS:HD3	2:F:58:LYS:HA	1.88	0.40
1:E:17:TYR:CZ	2:F:6:ILE:HG23	2.57	0.40
1:C:18:HIS:HB2	2:D:20:GLY:O	2.21	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	321/333 (96%)	309 (96%)	12 (4%)	0	100	100
1	C	321/333 (96%)	308 (96%)	13 (4%)	0	100	100
1	E	321/333 (96%)	309 (96%)	12 (4%)	0	100	100
2	B	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
2	D	173/180 (96%)	160 (92%)	12 (7%)	1 (1%)	21	39
2	F	173/180 (96%)	158 (91%)	15 (9%)	0	100	100
All	All	1482/1539 (96%)	1404 (95%)	77 (5%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	145	ASP

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	290/298 (97%)	276 (95%)	14 (5%)	23	45
1	C	290/298 (97%)	280 (97%)	10 (3%)	32	58
1	E	290/298 (97%)	282 (97%)	8 (3%)	38	64
2	B	149/154 (97%)	141 (95%)	8 (5%)	20	40
2	D	149/154 (97%)	145 (97%)	4 (3%)	39	65
2	F	149/154 (97%)	143 (96%)	6 (4%)	28	53
All	All	1317/1356 (97%)	1267 (96%)	50 (4%)	29	54

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	29	ILE
1	C	75	MET
1	C	124	THR
1	C	135	VAL
1	C	167	SER
1	C	174	GLU
1	C	206	THR
1	C	235	THR
1	C	297	ILE
1	C	315	VAL
2	D	18	VAL
2	D	80	LEU
2	D	140	PHE
2	D	173	ILE
1	A	29	ILE
1	A	35	THR
1	A	51	LEU
1	A	61	LEU
1	A	91	ILE
1	A	135	VAL
1	A	166	ARG
1	A	174	GLU

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Mol	Chain	Res	Type
1	A	192	THR
1	A	206	THR
1	A	213	LEU
1	A	283	THR
1	A	291	SER
1	A	292	MET
2	B	10	ILE
2	B	18	VAL
2	B	26	HIS
2	B	41	THR
2	B	45	ILE
2	B	55	ILE
2	B	61	THR
2	B	101	LEU
1	E	26	VAL
1	E	28	THR
1	E	29	ILE
1	E	80	LEU
1	E	135	VAL
1	E	174	GLU
1	E	206	THR
1	E	283	THR
2	F	18	VAL
2	F	43	LYS
2	F	83	LYS
2	F	101	LEU
2	F	126	LEU
2	F	144	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	159	ASN
1	C	197	ASN
1	C	210	ASN
1	C	256	ASN
2	D	25	HIS
2	D	125	GLN
1	A	150	ASN
1	A	159	ASN
1	A	256	ASN
2	B	25	HIS

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Mol	Chain	Res	Type
2	B	125	GLN
2	F	42	GLN
2	F	142	HIS

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 ⓘ

17 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	G	1	3,1	14,14,15	0.68	1 (7%)	17,19,21	1.00	0
3	FUL	G	2	3	10,10,11	1.59	2 (20%)	14,14,16	1.41	3 (21%)
3	NAG	G	3	3	14,14,15	0.46	0	17,19,21	0.44	0
4	GAL	H	1	4	11,11,12	1.81	3 (27%)	15,15,17	0.96	1 (6%)
4	SIA	H	2	4	20,20,21	0.83	0	21,28,31	0.90	1 (4%)
5	NAG	I	1	1,5	14,14,15	0.50	0	17,19,21	0.63	0
5	FUL	I	2	5	10,10,11	1.36	1 (10%)	14,14,16	1.25	2 (14%)
5	NAG	I	3	5	14,14,15	0.57	0	17,19,21	0.47	0
5	FUC	I	4	5	10,10,11	1.50	2 (20%)	14,14,16	1.73	4 (28%)
6	NAG	J	1	6	15,15,15	0.59	1 (6%)	21,21,21	0.78	0
6	GAL	J	2	6	11,11,12	1.31	2 (18%)	15,15,17	1.72	2 (13%)
6	SIA	J	3	6	20,20,21	0.86	0	21,28,31	1.15	2 (9%)
3	NAG	K	1	3,1	14,14,15	0.68	1 (7%)	17,19,21	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FUL	K	2	3	10,10,11	1.20	1 (10%)	14,14,16	0.77	0
3	NAG	K	3	3	14,14,15	0.33	0	17,19,21	0.40	0
4	GAL	L	1	4	11,11,12	1.80	5 (45%)	15,15,17	1.16	1 (6%)
4	SIA	L	2	4	20,20,21	0.77	0	21,28,31	1.27	2 (9%)

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	NAG	G	1	3,1	-	1/6/23/26	0/1/1/1
3	FUL	G	2	3	-	-	0/1/1/1
3	NAG	G	3	3	-	2/6/23/26	0/1/1/1
4	GAL	H	1	4	-	0/2/19/22	0/1/1/1
4	SIA	H	2	4	-	2/18/34/38	0/1/1/1
5	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	FUL	I	2	5	-	-	0/1/1/1
5	NAG	I	3	5	-	0/6/23/26	0/1/1/1
5	FUC	I	4	5	-	-	0/1/1/1
6	NAG	J	1	6	-	0/6/26/26	0/1/1/1
6	GAL	J	2	6	-	0/2/19/22	0/1/1/1
6	SIA	J	3	6	-	0/18/34/38	0/1/1/1
3	NAG	K	1	3,1	-	2/6/23/26	0/1/1/1
3	FUL	K	2	3	-	-	0/1/1/1
3	NAG	K	3	3	-	2/6/23/26	0/1/1/1
4	GAL	L	1	4	-	0/2/19/22	0/1/1/1
4	SIA	L	2	4	-	0/18/34/38	0/1/1/1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1	GAL	C4-C3	3.50	1.61	1.52
5	I	4	FUC	C1-C2	3.17	1.59	1.52
3	G	2	FUL	O5-C5	3.02	1.49	1.43
5	I	4	FUC	O5-C5	2.79	1.49	1.43
4	H	1	GAL	C2-C3	2.74	1.56	1.52
5	I	2	FUL	C4-C3	2.73	1.59	1.52
3	G	2	FUL	C1-C2	2.72	1.58	1.52
4	L	1	GAL	O3-C3	2.72	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	1	GAL	C4-C5	2.66	1.58	1.53
6	J	2	GAL	C1-C2	2.38	1.57	1.52
4	H	1	GAL	O3-C3	2.27	1.48	1.43
4	L	1	GAL	O5-C5	2.26	1.47	1.43
3	K	2	FUL	O5-C5	2.22	1.48	1.43
4	L	1	GAL	C2-C3	2.22	1.55	1.52
3	G	1	NAG	O5-C1	-2.20	1.40	1.43
3	K	1	NAG	O5-C1	-2.11	1.40	1.43
6	J	1	NAG	O5-C1	2.10	1.48	1.42
4	L	1	GAL	C1-C2	2.03	1.57	1.52
6	J	2	GAL	C2-C3	2.02	1.55	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	2	GAL	C1-C2-C3	4.30	115.91	109.64
6	J	2	GAL	C1-O5-C5	3.98	117.52	112.19
5	I	4	FUC	C1-O5-C5	3.74	121.79	112.97
5	I	4	FUC	C1-C2-C3	2.96	113.95	109.64
4	L	2	SIA	O1B-C1-C2	2.93	120.34	112.71
5	I	2	FUL	C1-C2-C3	-2.93	105.38	109.64
3	G	2	FUL	C2-C3-C4	-2.85	105.85	110.86
6	J	3	SIA	O1B-C1-C2	2.79	119.95	112.71
4	H	2	SIA	O1B-C1-C2	2.58	119.43	112.71
5	I	2	FUL	O2-C2-C1	2.55	115.05	109.22
4	L	2	SIA	O1A-C1-C2	-2.55	117.35	122.85
4	H	1	GAL	C1-C2-C3	2.51	113.30	109.64
5	I	4	FUC	O5-C1-C2	2.42	116.55	110.79
6	J	3	SIA	O1A-C1-C2	-2.40	117.67	122.85
4	L	1	GAL	C1-O5-C5	2.31	115.28	112.19
3	G	2	FUL	O2-C2-C1	2.27	114.42	109.22
5	I	4	FUC	O5-C5-C4	2.20	113.51	109.55
3	G	2	FUL	C3-C4-C5	-2.15	106.55	109.81

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	K	3	NAG	C4-C5-C6-O6
3	K	3	NAG	O5-C5-C6-O6
3	G	3	NAG	C4-C5-C6-O6
5	I	1	NAG	O5-C5-C6-O6

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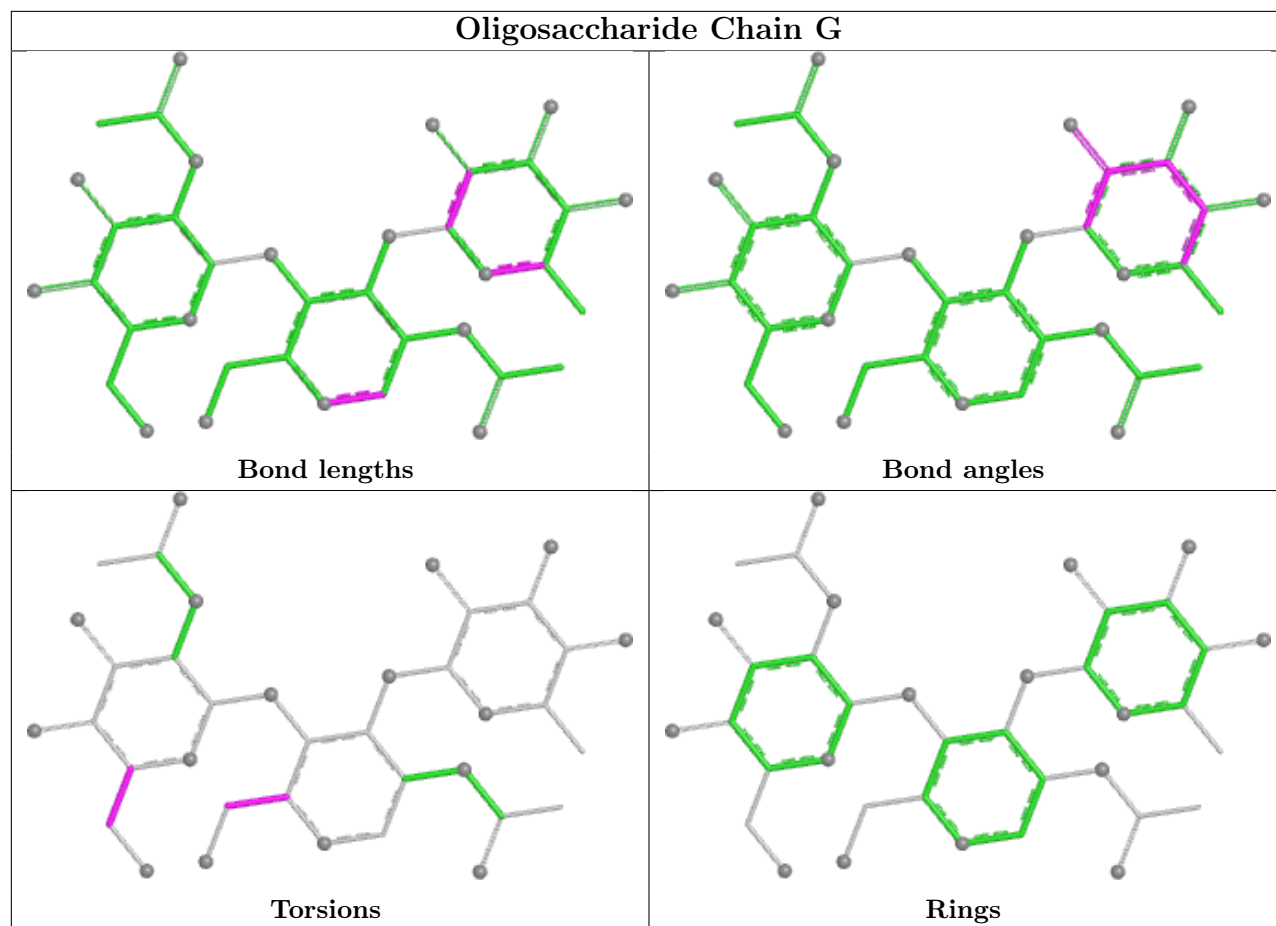
Mol	Chain	Res	Type	Atoms
5	I	1	NAG	C4-C5-C6-O6
3	G	3	NAG	O5-C5-C6-O6
3	K	1	NAG	C4-C5-C6-O6
3	K	1	NAG	O5-C5-C6-O6
4	H	2	SIA	C6-C7-C8-O8
4	H	2	SIA	C6-C7-C8-C9
3	G	1	NAG	C4-C5-C6-O6

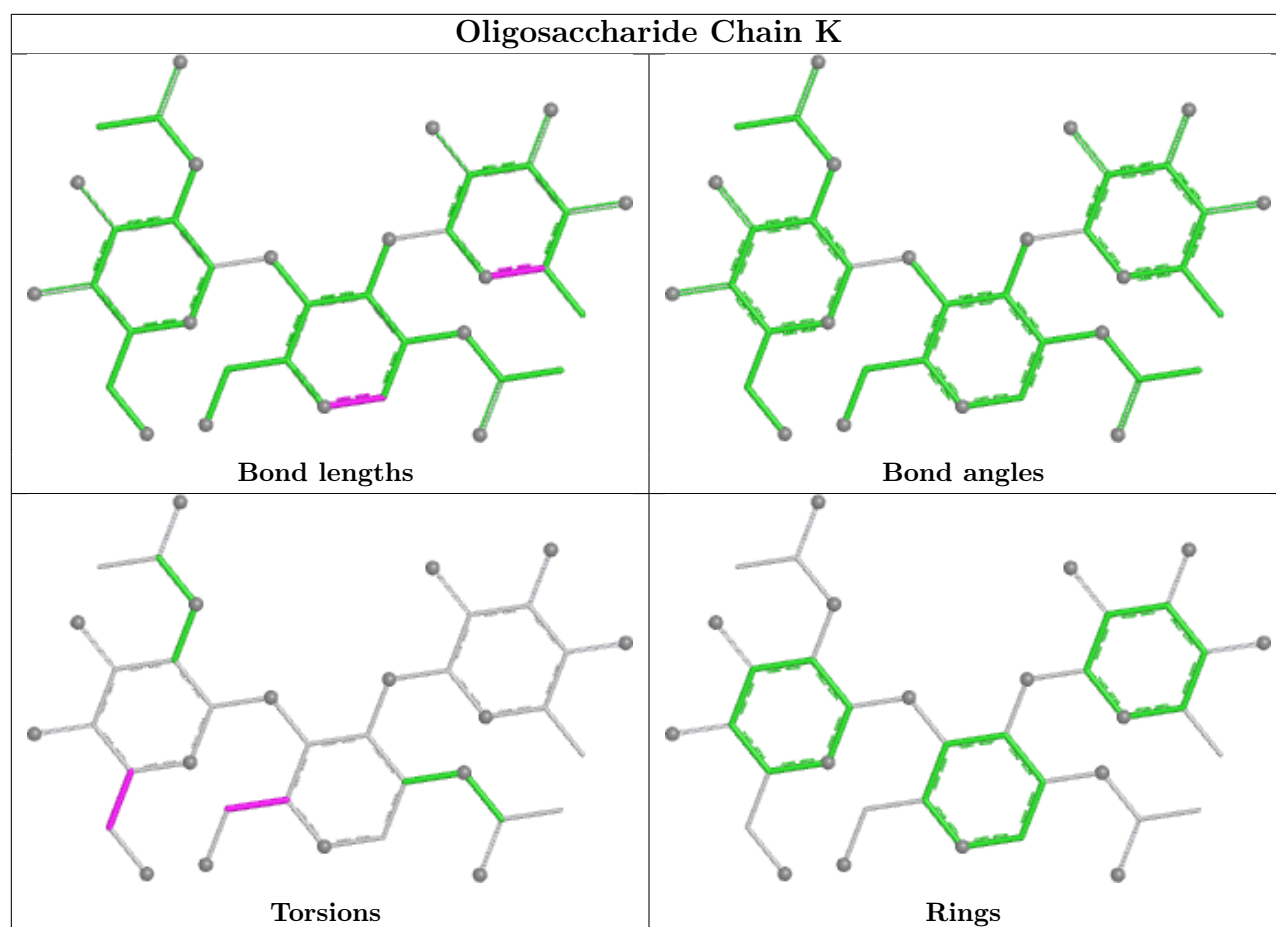
There are no ring outliers.

5 monomers are involved in 7 short contacts:

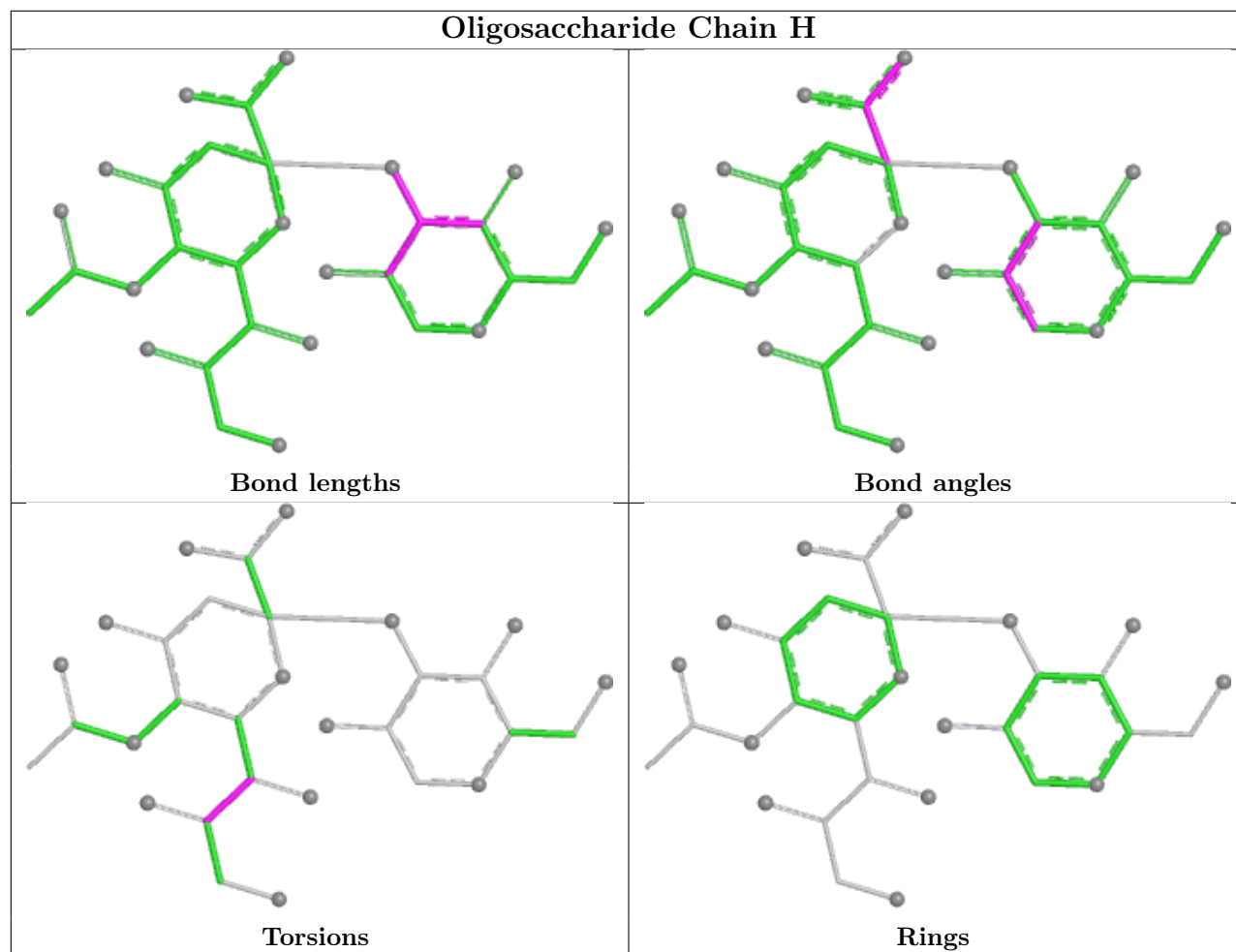
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	2	SIA	1	0
5	I	2	FUL	1	0
6	J	1	NAG	3	0
5	I	3	NAG	3	0
5	I	4	FUC	2	0

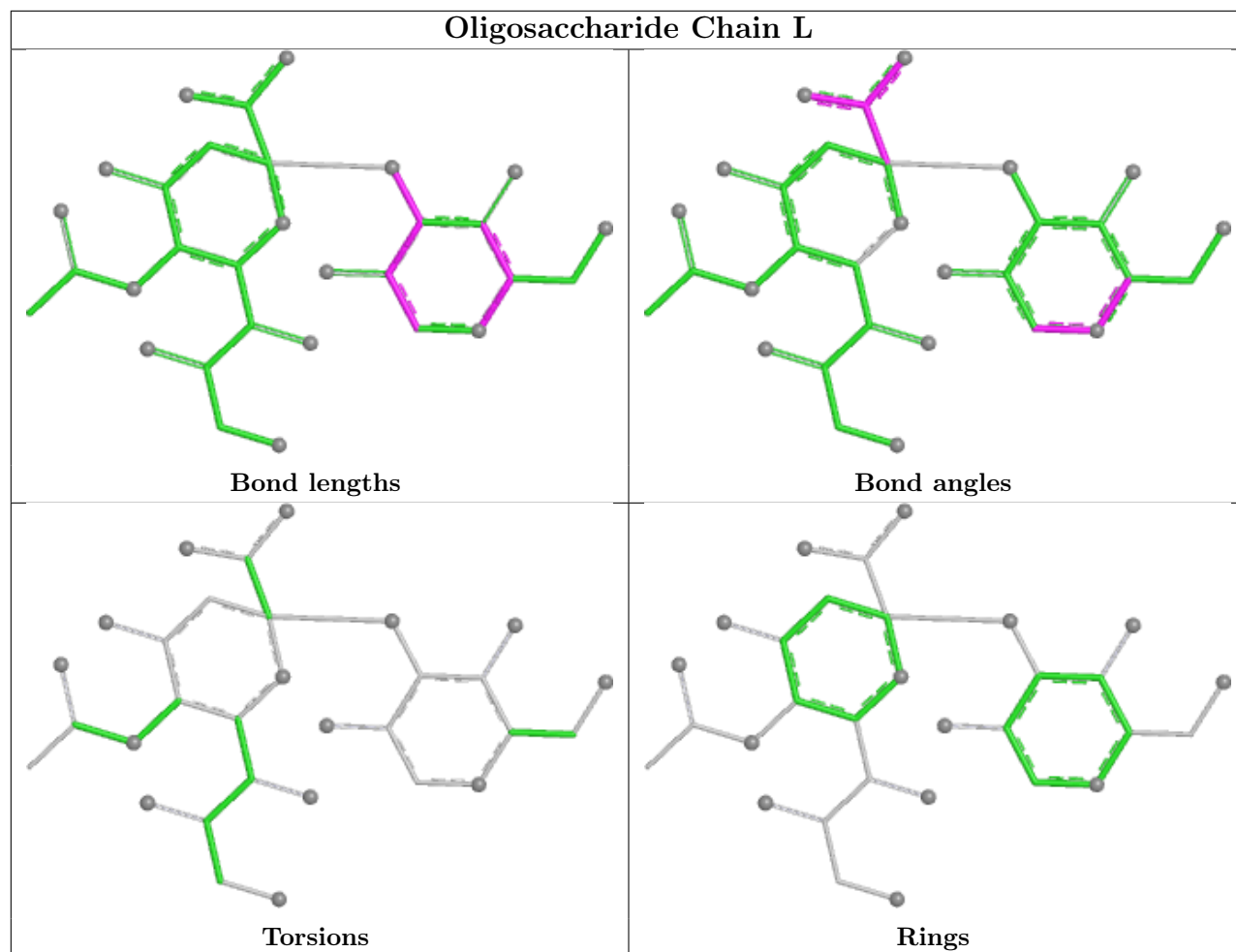
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

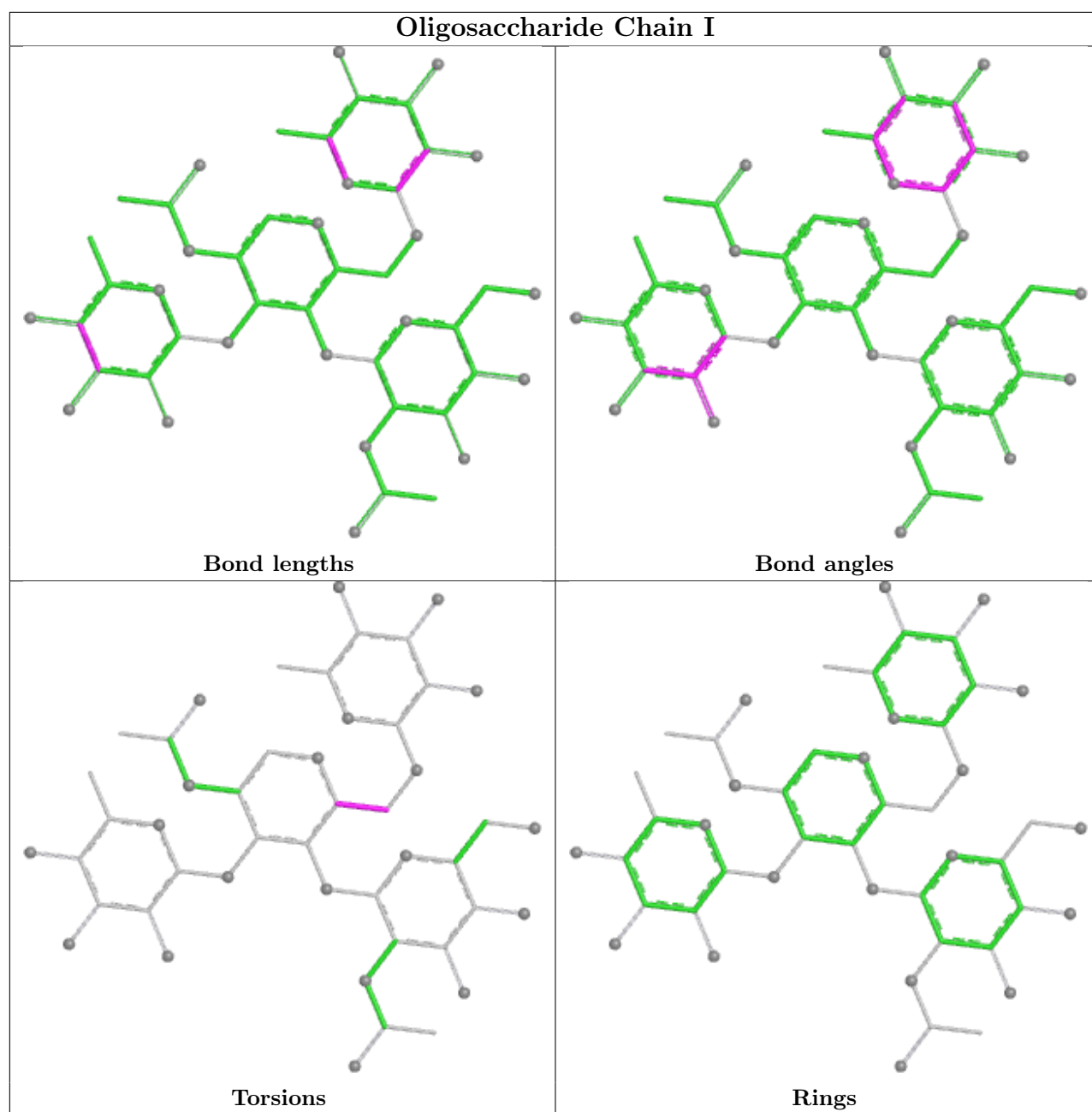


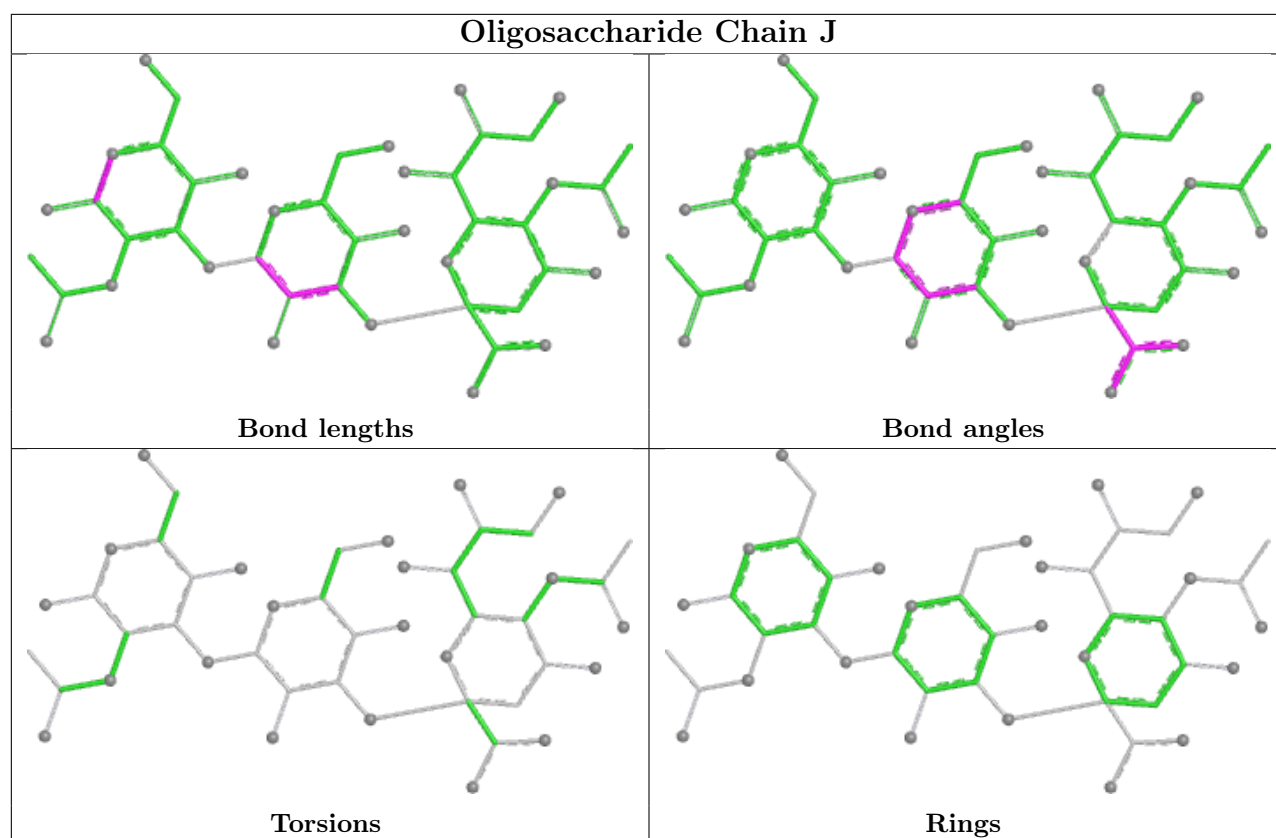


Oligosaccharide Chain H









5.6 Ligand geometry [i](#)

3 ligands 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	$\# Z > 2$
7	NAG	A	1001	1	14,14,15	0.79	1 (7%)	17,19,21	0.51	0
7	NAG	C	1001	1	14,14,15	0.40	0	17,19,21	0.49	0
7	NAG	E	1001	1	14,14,15	0.52	0	17,19,21	0.57	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
7	NAG	A	1001	1	-	1/6/23/26	0/1/1/1
7	NAG	C	1001	1	-	2/6/23/26	0/1/1/1
7	NAG	E	1001	1	-	3/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1001	NAG	O5-C1	2.03	1.47	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	E	1001	NAG	C4-C5-C6-O6
7	C	1001	NAG	C4-C5-C6-O6
7	E	1001	NAG	O5-C5-C6-O6
7	C	1001	NAG	O5-C5-C6-O6
7	A	1001	NAG	C3-C2-N2-C7
7	E	1001	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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, 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	323/333 (96%)	-0.28	5 (1%)	72 68	18, 40, 92, 124	0
1	C	323/333 (96%)	-0.31	5 (1%)	72 68	22, 42, 77, 128	0
1	E	323/333 (96%)	-0.13	1 (0%)	90 88	27, 51, 76, 119	0
2	B	175/180 (97%)	0.64	11 (6%)	26 21	24, 87, 110, 115	0
2	D	175/180 (97%)	0.62	13 (7%)	20 17	26, 89, 130, 134	0
2	F	175/180 (97%)	0.31	5 (2%)	53 48	23, 77, 106, 122	0
All	All	1494/1539 (97%)	0.03	40 (2%)	56 51	18, 52, 110, 134	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	138	PHE	4.6
1	C	14	CYS	4.4
2	B	35	ALA	4.3
2	B	21	TRP	3.8
2	B	162	TYR	3.3
2	B	22	TYR	3.2
2	D	137	CYS	3.2
2	D	1	GLY	3.1
2	B	24	TYR	3.0
1	C	13	ILE	2.9
1	A	324	PRO	2.9
2	F	23	GLY	2.9
2	B	14	TRP	2.8
1	A	13	ILE	2.8
2	D	175	GLY	2.8
2	F	175	GLY	2.7
2	B	26	HIS	2.7
1	C	324	PRO	2.7
2	F	173	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	20	GLY	2.7
2	D	173	ILE	2.6
2	D	133	LEU	2.6
1	C	9	PRO	2.5
2	D	134	GLY	2.5
2	B	175	GLY	2.5
1	C	10	GLY	2.4
2	B	18	VAL	2.4
1	A	19	ALA	2.3
2	D	141	TYR	2.3
2	D	124	LEU	2.3
1	E	8	ASP	2.3
2	B	32	SER	2.3
1	A	16	GLY	2.2
2	D	2	LEU	2.2
2	F	174	SER	2.2
2	D	3	PHE	2.2
1	A	12	GLN	2.1
2	D	155	GLY	2.1
2	D	122	VAL	2.1
2	F	152	VAL	2.1

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.

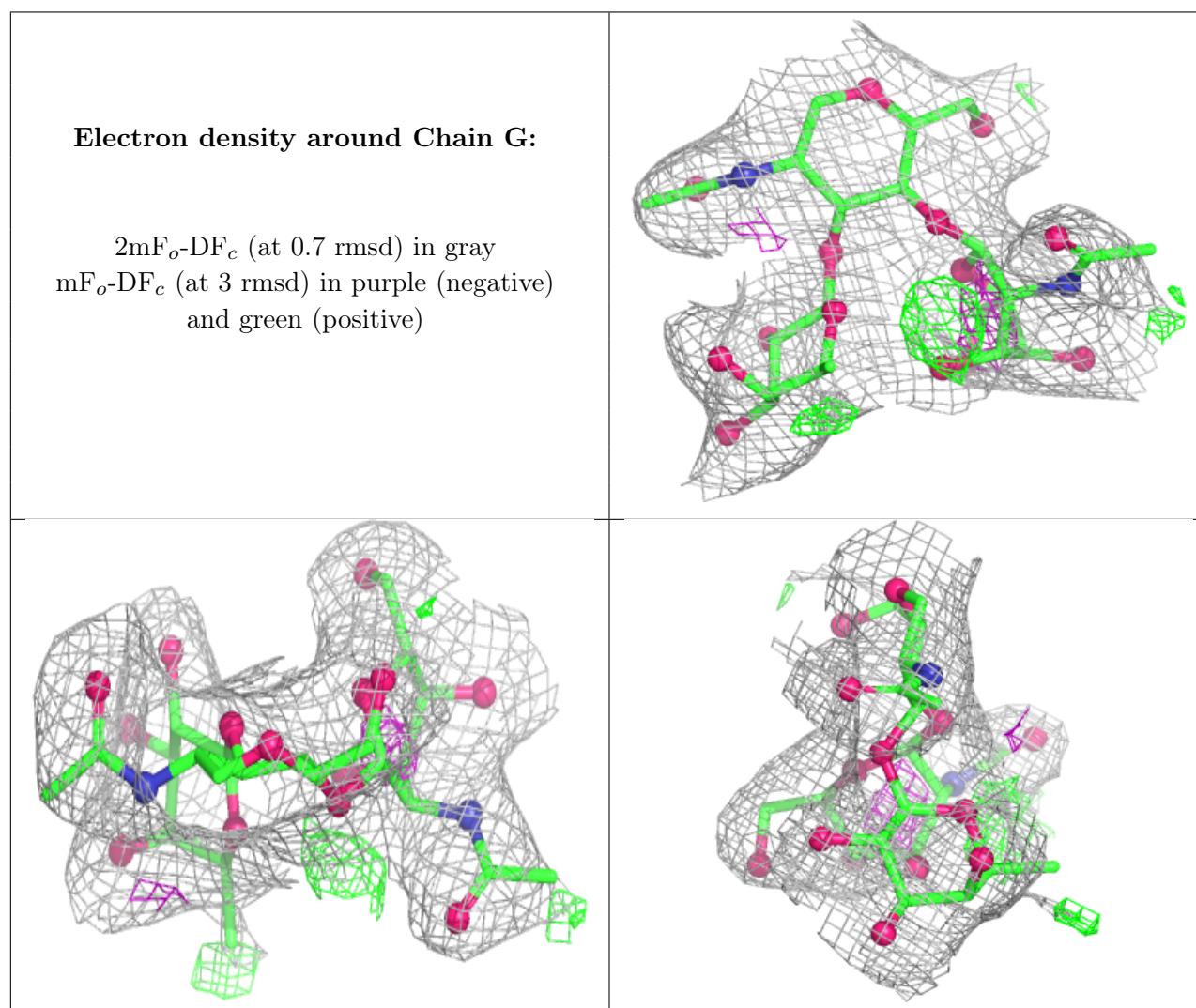
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	FUL	I	2	10/11	0.61	0.13	78,85,87,90	0
3	NAG	G	3	14/15	0.66	0.15	74,81,87,87	0
4	GAL	L	1	11/12	0.67	0.13	60,74,83,85	0
4	GAL	H	1	11/12	0.68	0.14	76,80,87,90	0
3	NAG	K	3	14/15	0.69	0.14	89,97,103,107	0
6	NAG	J	1	15/15	0.69	0.16	85,94,101,104	0
5	NAG	I	3	14/15	0.70	0.16	78,86,93,94	0

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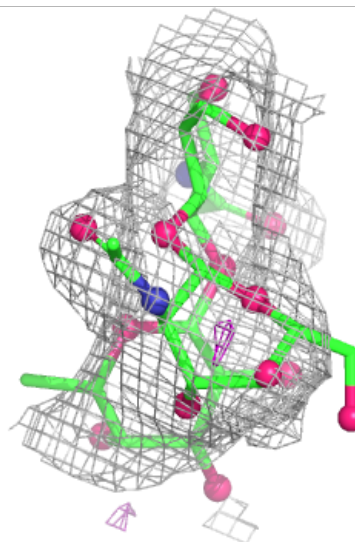
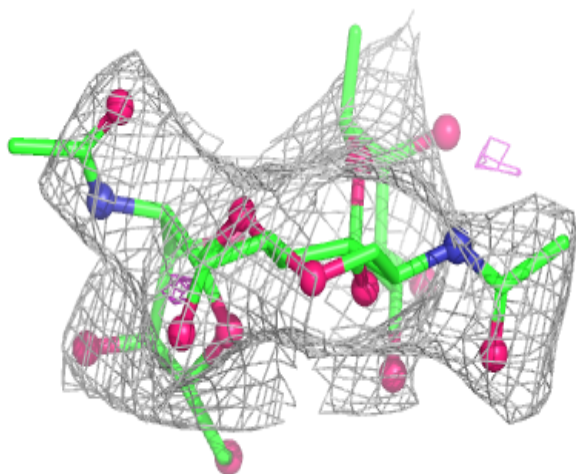
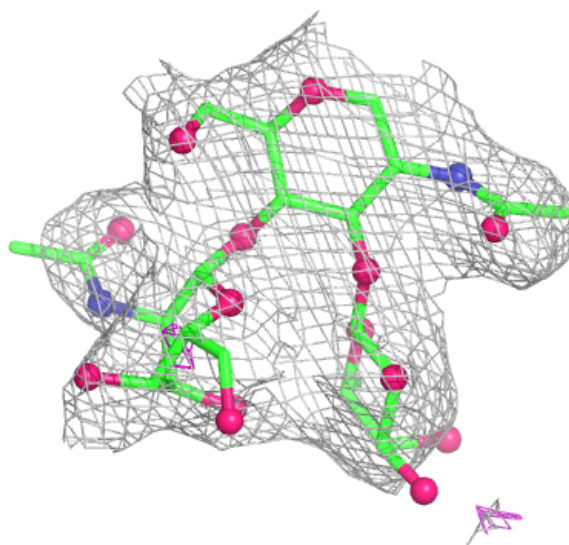
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FUL	K	2	10/11	0.72	0.14	90,96,103,108	0
3	FUL	G	2	10/11	0.79	0.13	72,77,83,86	0
4	SIA	H	2	20/21	0.83	0.12	50,68,78,79	0
5	FUC	I	4	10/11	0.84	0.12	59,69,78,81	0
5	NAG	I	1	14/15	0.85	0.10	52,69,76,81	0
4	SIA	L	2	20/21	0.88	0.10	42,57,68,70	0
6	GAL	J	2	11/12	0.88	0.09	51,58,70,73	0
3	NAG	K	1	14/15	0.89	0.09	52,72,84,87	0
3	NAG	G	1	14/15	0.92	0.08	50,61,71,75	0
6	SIA	J	3	20/21	0.97	0.06	25,36,42,45	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.



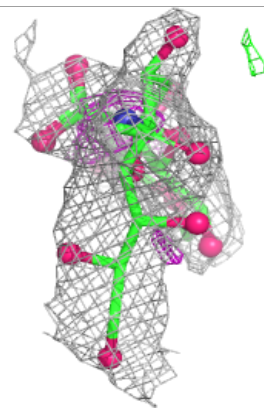
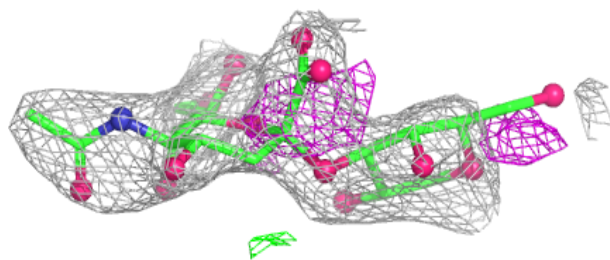
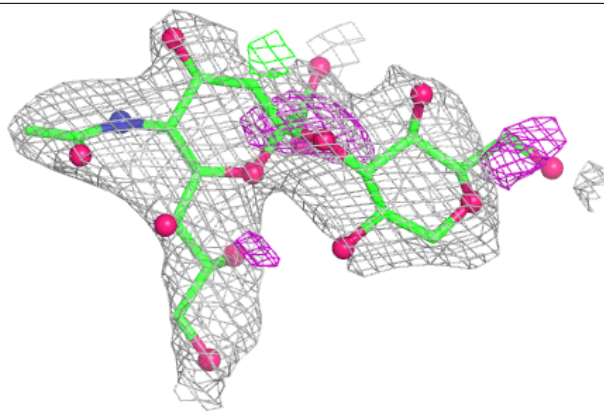
Electron density around Chain K:

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



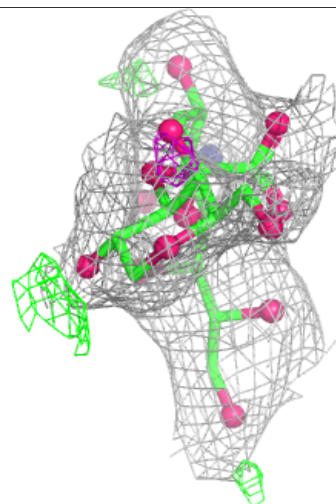
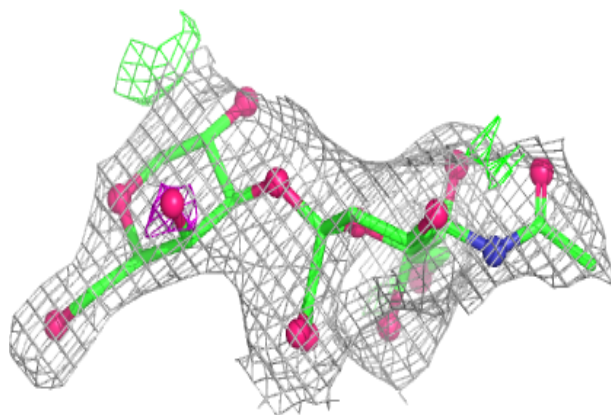
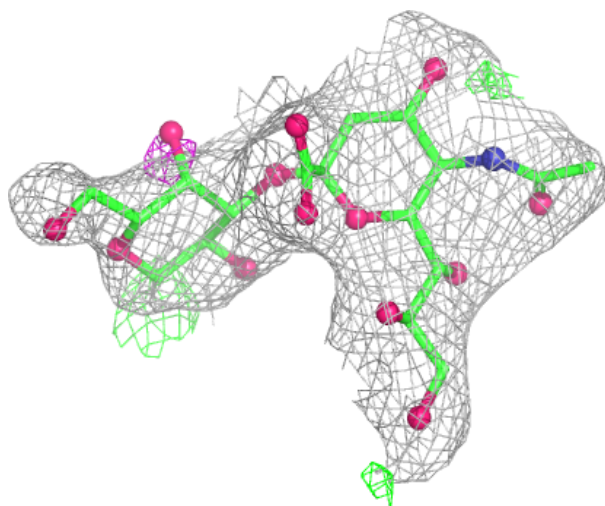
Electron density around Chain H:

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



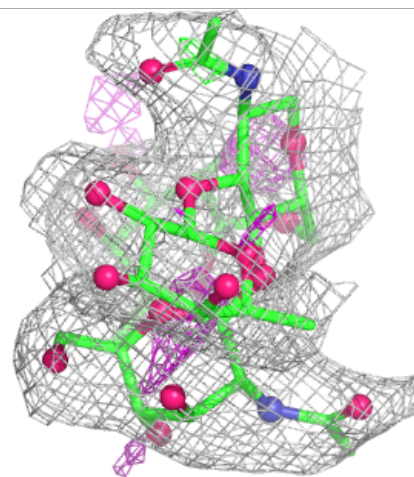
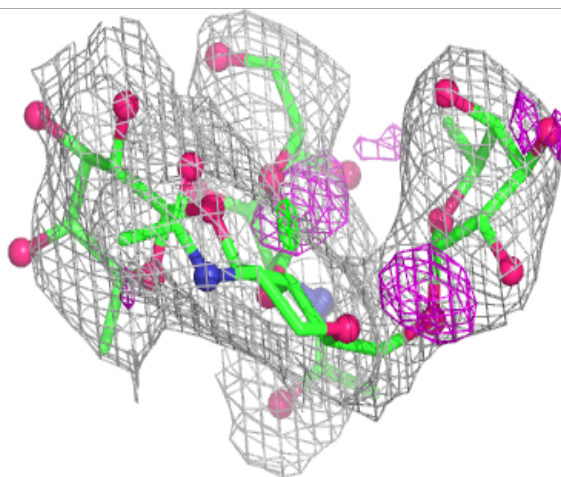
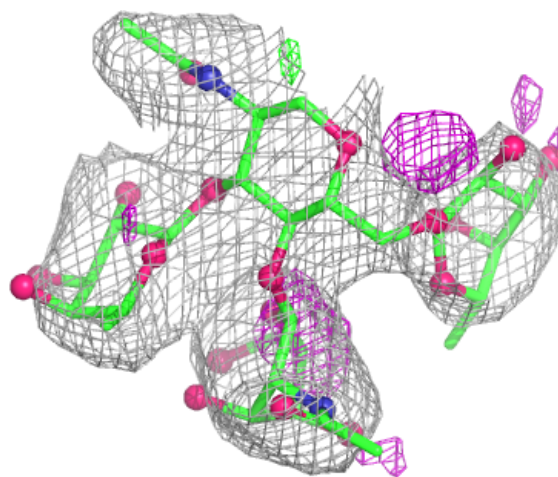
Electron density around Chain L:

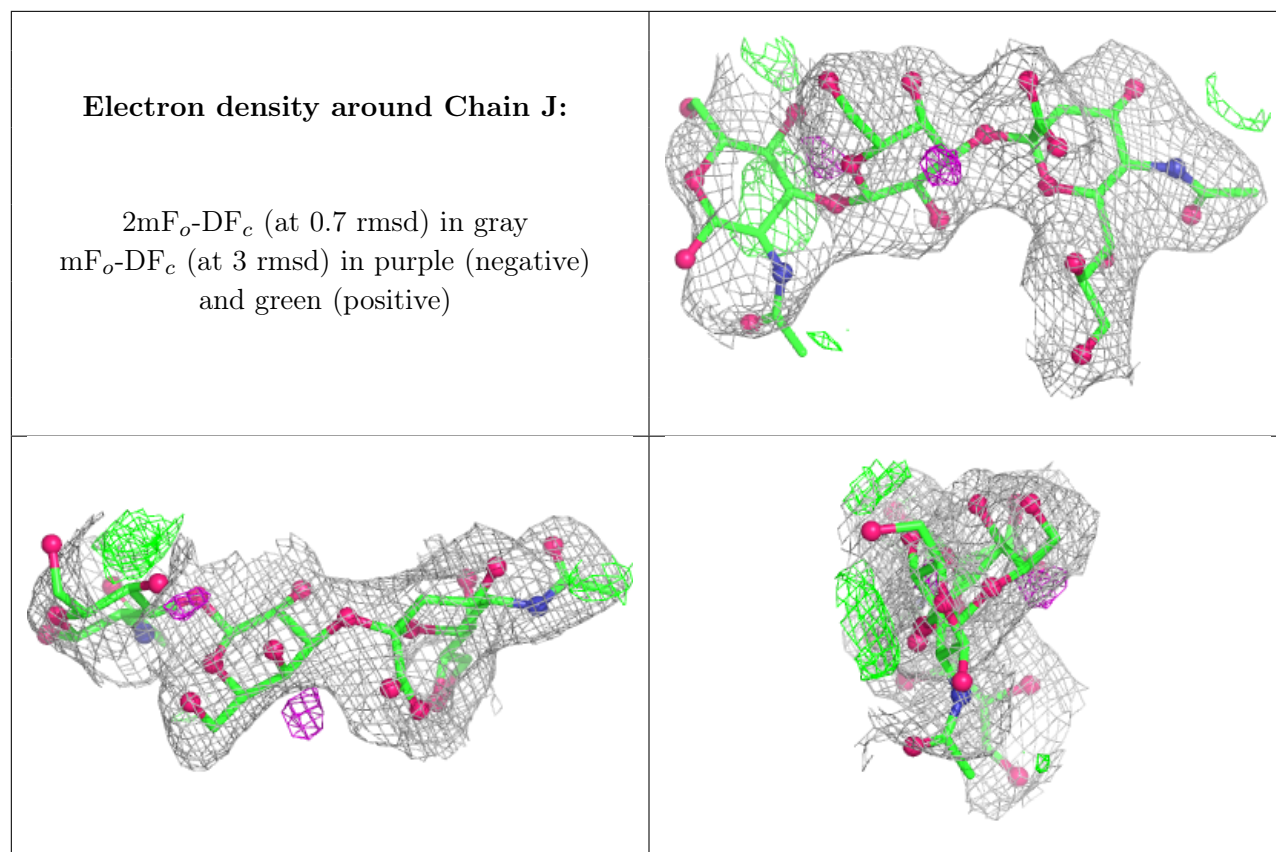
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain I:

$2mF_o-DF_c$ (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($\text{\AA}^2$)	Q<0.9
7	NAG	E	1001	14/15	0.70	0.11	95,101,103,105	0
7	NAG	A	1001	14/15	0.72	0.12	90,103,107,107	0
7	NAG	C	1001	14/15	0.82	0.11	83,90,92,94	0

6.5 Other polymers [i](#)

There are no such residues in this entry.