



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:58 PM UTC

PDB ID : 4RUS / pdb_00004rus
Title : Carp Fischelectin, holo form
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Deposited on : 2014-11-21
Resolution : 1.70 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

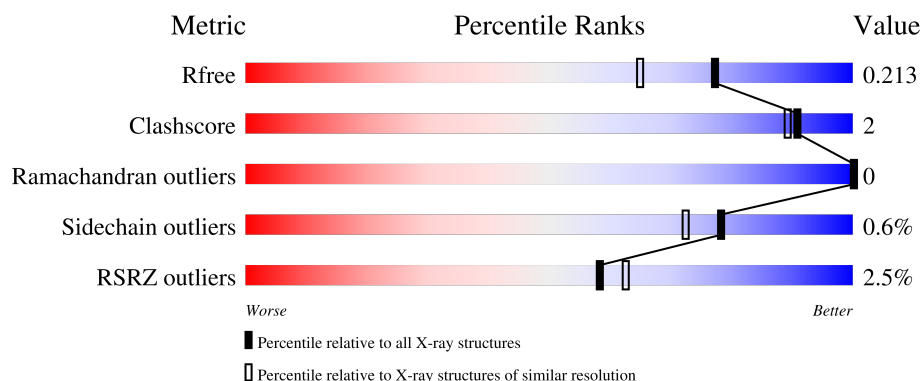
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	238	% 97% .
1	B	238	3% 96% ..
1	C	238	3% 96% ..
1	D	238	3% 97% .
1	E	238	2% 96% .

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Mol	Chain	Length	Quality of chain
1	F	238	
2	G	2	
2	H	2	
2	I	2	
2	J	2	
2	K	2	
2	L	2	

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
5	1PE	A	305	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11774 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 Fish-egg lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	0	0	0
			1778	1121	300	344	13			
1	B	235	Total	C	N	O	S	0	0	0
			1763	1111	298	341	13			
1	C	236	Total	C	N	O	S	0	0	0
			1771	1117	299	342	13			
1	D	237	Total	C	N	O	S	0	0	0
			1778	1121	300	344	13			
1	E	237	Total	C	N	O	S	0	0	0
			1778	1121	300	344	13			
1	F	237	Total	C	N	O	S	0	0	0
			1778	1121	300	344	13			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	119	LEU	ILE	conflict	UNP P68512
B	119	LEU	ILE	conflict	UNP P68512
C	119	LEU	ILE	conflict	UNP P68512
D	119	LEU	ILE	conflict	UNP P68512
E	119	LEU	ILE	conflict	UNP P68512
F	119	LEU	ILE	conflict	UNP P68512

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

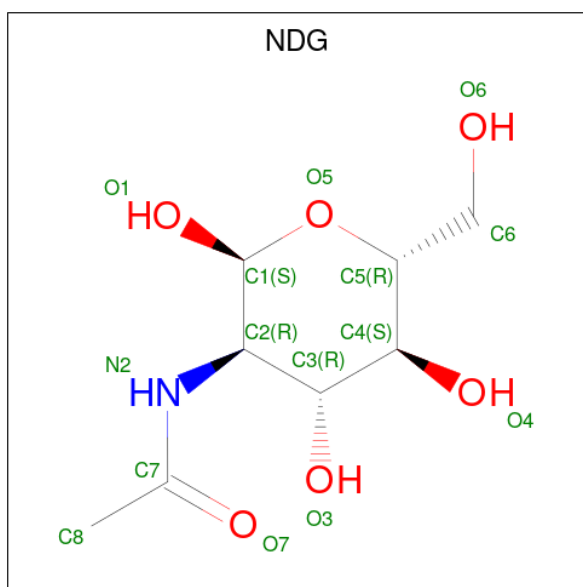


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

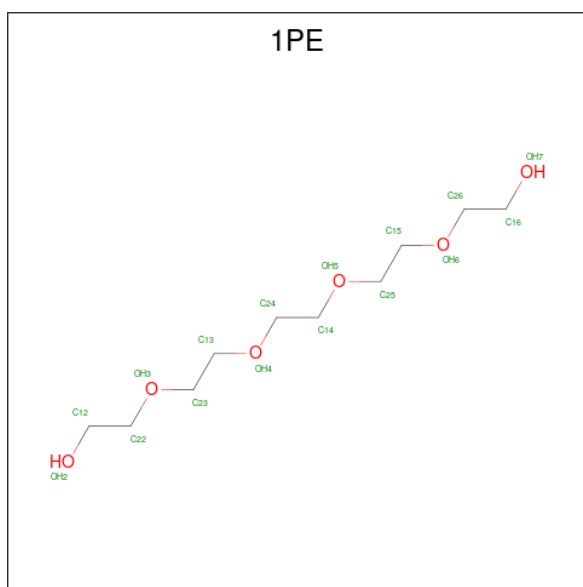
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		
3	B	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		
3	D	1	Total	Ca	0	0
			1	1		
3	E	1	Total	Ca	0	0
			1	1		
3	F	1	Total	Ca	0	0
			1	1		

- Molecule 4 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (CCD ID: NDG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			15	8	1	6		
4	B	1	Total	C	N	O	0	0
			15	8	1	6		
4	B	1	Total	C	N	O	0	0
			15	8	1	6		
4	D	1	Total	C	N	O	0	0
			15	8	1	6		
4	F	1	Total	C	N	O	0	0
			15	8	1	6		
4	F	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 5 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			16	10	6		
5	E	1	Total	C	O	0	0
			16	10	6		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Mg	0	0
			2	2		
6	C	1	Total	Mg	0	0
			1	1		
6	E	1	Total	Mg	0	0
			1	1		

- 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
			15	8	1	6		
7	C	1	Total	C	N	O	0	0
			15	8	1	6		
7	E	1	Total	C	N	O	0	0
			15	8	1	6		

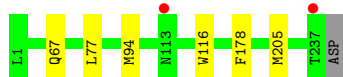
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	178	Total	O	0	0
			178	178		
8	B	125	Total	O	0	0
			125	125		
8	C	116	Total	O	0	0
			116	116		
8	D	137	Total	O	0	0
			137	137		
8	E	125	Total	O	0	0
			125	125		
8	F	102	Total	O	0	0
			102	102		

3 Residue-property plots [i](#)

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: Fish-egg lectin



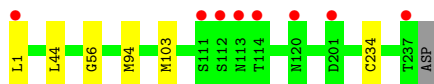
- Molecule 1: Fish-egg lectin



- Molecule 1: Fish-egg lectin



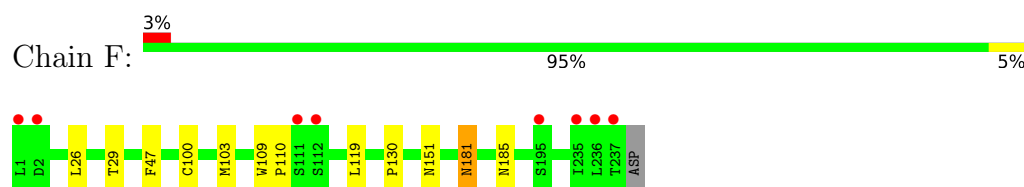
- Molecule 1: Fish-egg lectin



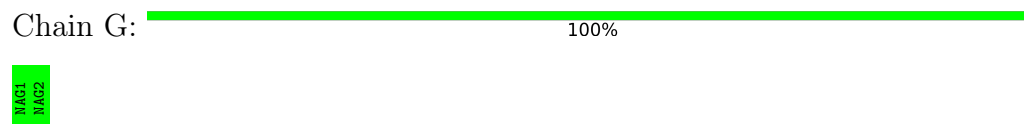
- Molecule 1: Fish-egg lectin



- Molecule 1: Fish-egg lectin



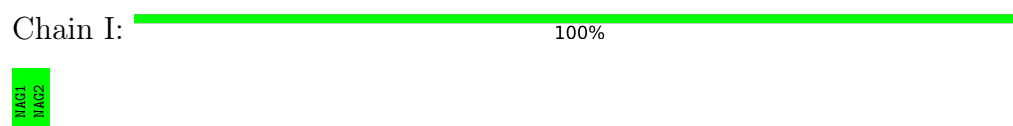
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



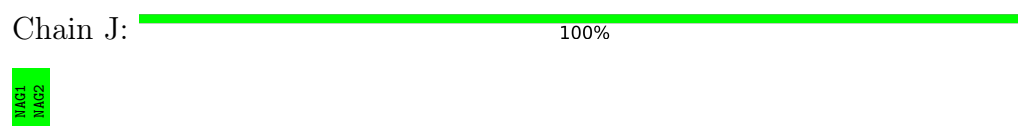
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



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



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





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	204.41Å 120.81Å 69.27Å 90.00° 91.42° 90.00°	Depositor
Resolution (Å)	29.67 – 1.70 29.67 – 1.70	Depositor EDS
% Data completeness (in resolution range)	93.1 (29.67-1.70) 93.1 (29.67-1.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.195 , 0.214 0.194 , 0.213	Depositor DCC
R_{free} test set	8614 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å ²)	15.4	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 30.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.011 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.012 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.017 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.016 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11774	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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: NAG, CA, NDG, 1PE, MG

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	0.50	0/1813	0.70	0/2462
1	B	0.49	0/1798	0.69	0/2441
1	C	0.46	0/1806	0.69	0/2452
1	D	0.49	0/1813	0.69	0/2462
1	E	0.47	0/1813	0.70	0/2462
1	F	0.46	0/1813	0.68	0/2462
All	All	0.48	0/10856	0.69	0/14741

There are no bond length outliers.

There are no bond angle outliers.

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	1778	0	1734	4	0
1	B	1763	0	1716	3	0
1	C	1771	0	1727	6	0
1	D	1778	0	1734	3	0
1	E	1778	0	1734	6	0
1	F	1778	0	1734	11	0
2	G	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	28	0	25	1	0
2	I	28	0	25	0	0
2	J	28	0	25	0	0
2	K	28	0	25	0	0
2	L	28	0	25	3	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
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	15	0	12	0	0
4	B	30	0	24	0	0
4	D	15	0	12	0	0
4	F	30	0	24	0	0
5	A	16	0	22	9	0
5	E	16	0	22	1	0
6	A	2	0	0	0	0
6	C	1	0	0	0	0
6	E	1	0	0	0	0
7	C	30	0	30	0	0
7	E	15	0	15	0	0
8	A	178	0	0	2	0
8	B	125	0	0	0	0
8	C	116	0	0	0	0
8	D	137	0	0	0	0
8	E	125	0	0	0	0
8	F	102	0	0	0	0
All	All	11774	0	10690	37	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:VAL:HG11	2:L:2:NAG:O6	1.47	1.12
1:A:77:LEU:H	5:A:305:1PE:H121	1.40	0.86
1:C:5:VAL:HG11	2:L:2:NAG:HO6	1.55	0.69
5:A:305:1PE:H122	5:A:305:1PE:H131	1.76	0.66
1:F:181:ASN:C	1:F:181:ASN:HD22	2.04	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:LEU:N	5:A:305:1PE:H121	2.12	0.61
1:F:103:MET:HE2	1:F:151:ASN:HD21	1.66	0.60
1:F:181:ASN:HD21	1:F:185:ASN:H	1.51	0.59
1:F:181:ASN:ND2	1:F:185:ASN:H	2.01	0.58
1:F:103:MET:HE2	1:F:151:ASN:ND2	2.22	0.54
1:D:1:LEU:HD22	1:D:234:CYS:HB3	1.92	0.52
5:A:305:1PE:H122	8:A:419:HOH:O	2.09	0.52
1:E:12:GLN:HE22	1:E:47:PHE:H	1.58	0.50
1:E:12:GLN:NE2	1:E:47:PHE:H	2.09	0.49
5:A:305:1PE:H131	8:A:419:HOH:O	2.12	0.48
1:F:181:ASN:C	1:F:181:ASN:ND2	2.73	0.46
5:A:305:1PE:H131	5:A:305:1PE:C12	2.44	0.46
1:F:26:LEU:HA	2:L:1:NAG:H82	1.98	0.46
5:A:305:1PE:H141	5:A:305:1PE:H132	1.70	0.45
1:C:109:TRP:HA	1:C:110:PRO:C	2.40	0.45
5:A:305:1PE:H261	5:A:305:1PE:H252	1.75	0.45
1:C:196:LYS:NZ	1:C:200:THR:HG22	2.33	0.43
1:B:26:LEU:HA	2:H:1:NAG:H82	2.00	0.43
1:A:178:PHE:CE2	1:A:205:MET:HE1	2.53	0.43
1:E:67:GLN:CD	1:E:72:VAL:HG21	2.44	0.42
1:E:103:MET:CE	1:F:130:PRO:HB3	2.49	0.42
1:C:130:PRO:HB3	1:D:103:MET:CE	2.49	0.42
1:E:77:LEU:O	5:E:305:1PE:H121	2.19	0.41
1:B:109:TRP:HA	1:B:110:PRO:C	2.45	0.41
1:F:29:THR:HG23	1:F:47:PHE:CD2	2.56	0.41
1:B:100:CYS:SG	1:B:119:LEU:HD11	2.61	0.41
1:E:29:THR:HG23	1:E:47:PHE:CD2	2.56	0.41
1:F:109:TRP:HA	1:F:110:PRO:C	2.45	0.41
1:D:44:LEU:HD13	1:D:56:GLY:HA3	2.03	0.41
1:F:100:CYS:SG	1:F:119:LEU:HD11	2.61	0.40
1:C:21:VAL:HB	1:C:47:PHE:CD2	2.56	0.40
1:A:116:TRP:CD1	5:A:305:1PE:H222	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries

of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	235/238 (99%)	233 (99%)	2 (1%)	0	100	100
1	B	233/238 (98%)	231 (99%)	2 (1%)	0	100	100
1	C	234/238 (98%)	231 (99%)	3 (1%)	0	100	100
1	D	235/238 (99%)	234 (100%)	1 (0%)	0	100	100
1	E	235/238 (99%)	234 (100%)	1 (0%)	0	100	100
1	F	235/238 (99%)	233 (99%)	2 (1%)	0	100	100
All	All	1407/1428 (98%)	1396 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	200/201 (100%)	198 (99%)	2 (1%)	68	58
1	B	198/201 (98%)	197 (100%)	1 (0%)	81	76
1	C	199/201 (99%)	199 (100%)	0	100	100
1	D	200/201 (100%)	199 (100%)	1 (0%)	81	76
1	E	200/201 (100%)	198 (99%)	2 (1%)	68	58
1	F	200/201 (100%)	199 (100%)	1 (0%)	81	76
All	All	1197/1206 (99%)	1190 (99%)	7 (1%)	78	72

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	A	94	MET
1	B	235	ILE

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Mol	Chain	Res	Type
1	D	94	MET
1	E	1	LEU
1	E	5	VAL
1	F	181	ASN

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	67	GLN
1	A	188	GLN
1	B	35	ASN
1	B	161	ASN
1	B	185	ASN
1	C	25	ASN
1	C	67	GLN
1	D	54	GLN
1	D	161	ASN
1	D	185	ASN
1	E	12	GLN
1	E	46	HIS
1	E	188	GLN
1	F	9	ASN
1	F	139	ASN
1	F	161	ASN
1	F	181	ASN
1	F	185	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 ⓘ

12 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	G	1	2,1	14,14,15	0.56	0	17,19,21	0.73	0
2	NAG	G	2	2	14,14,15	0.56	0	17,19,21	0.97	0
2	NAG	H	1	2,1	14,14,15	0.59	0	17,19,21	0.63	0
2	NAG	H	2	2	14,14,15	0.56	0	17,19,21	0.69	0
2	NAG	I	1	2,1	14,14,15	0.50	0	17,19,21	0.69	0
2	NAG	I	2	2	14,14,15	0.54	0	17,19,21	0.85	0
2	NAG	J	1	2,1	14,14,15	0.59	0	17,19,21	0.84	0
2	NAG	J	2	2	14,14,15	0.56	0	17,19,21	0.86	0
2	NAG	K	1	2,1	14,14,15	0.58	0	17,19,21	0.84	0
2	NAG	K	2	2	14,14,15	0.56	0	17,19,21	0.73	0
2	NAG	L	1	2,1	14,14,15	0.43	0	17,19,21	0.99	0
2	NAG	L	2	2	14,14,15	0.55	0	17,19,21	0.81	1 (5%)

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	G	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	3/6/23/26	0/1/1/1
2	NAG	H	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	NAG	I	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1
2	NAG	J	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	J	2	2	-	1/6/23/26	0/1/1/1
2	NAG	K	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	K	2	2	-	0/6/23/26	0/1/1/1
2	NAG	L	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	L	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	2	NAG	O6-C6-C5	-2.16	103.99	111.33

There are no chirality outliers.

All (4) torsion outliers are listed below:

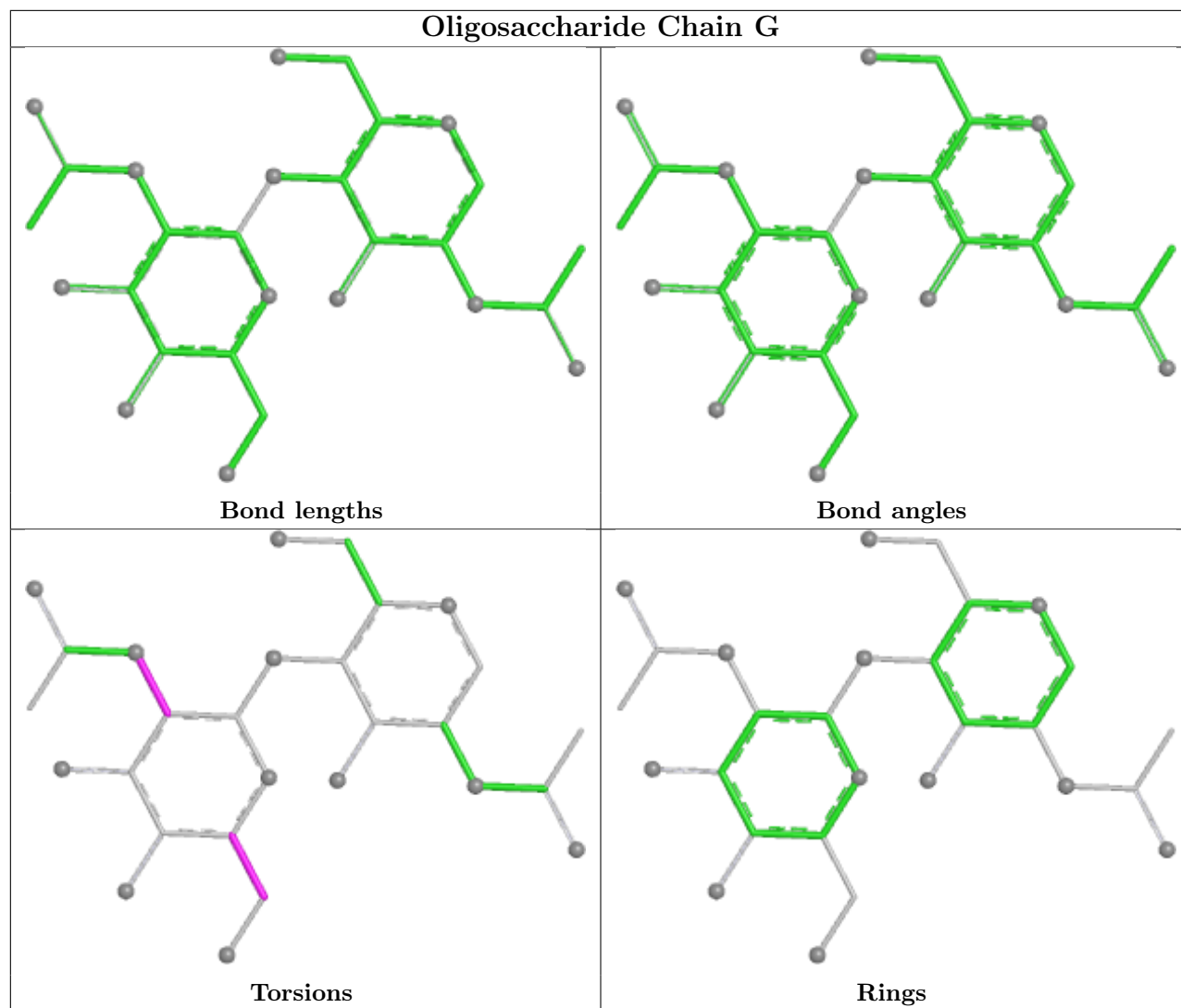
Mol	Chain	Res	Type	Atoms
2	G	2	NAG	C4-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6
2	G	2	NAG	C1-C2-N2-C7
2	J	2	NAG	C1-C2-N2-C7

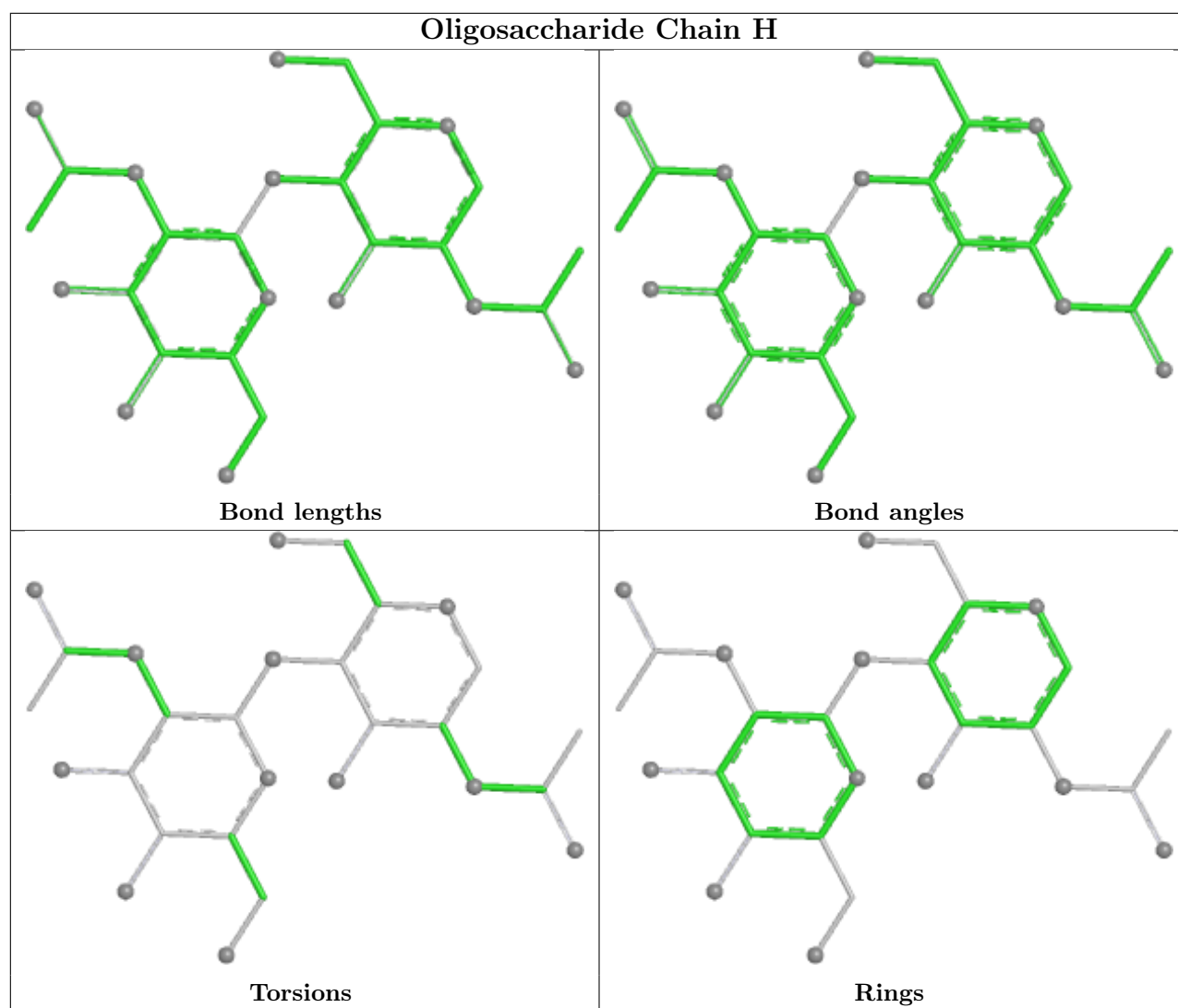
There are no ring outliers.

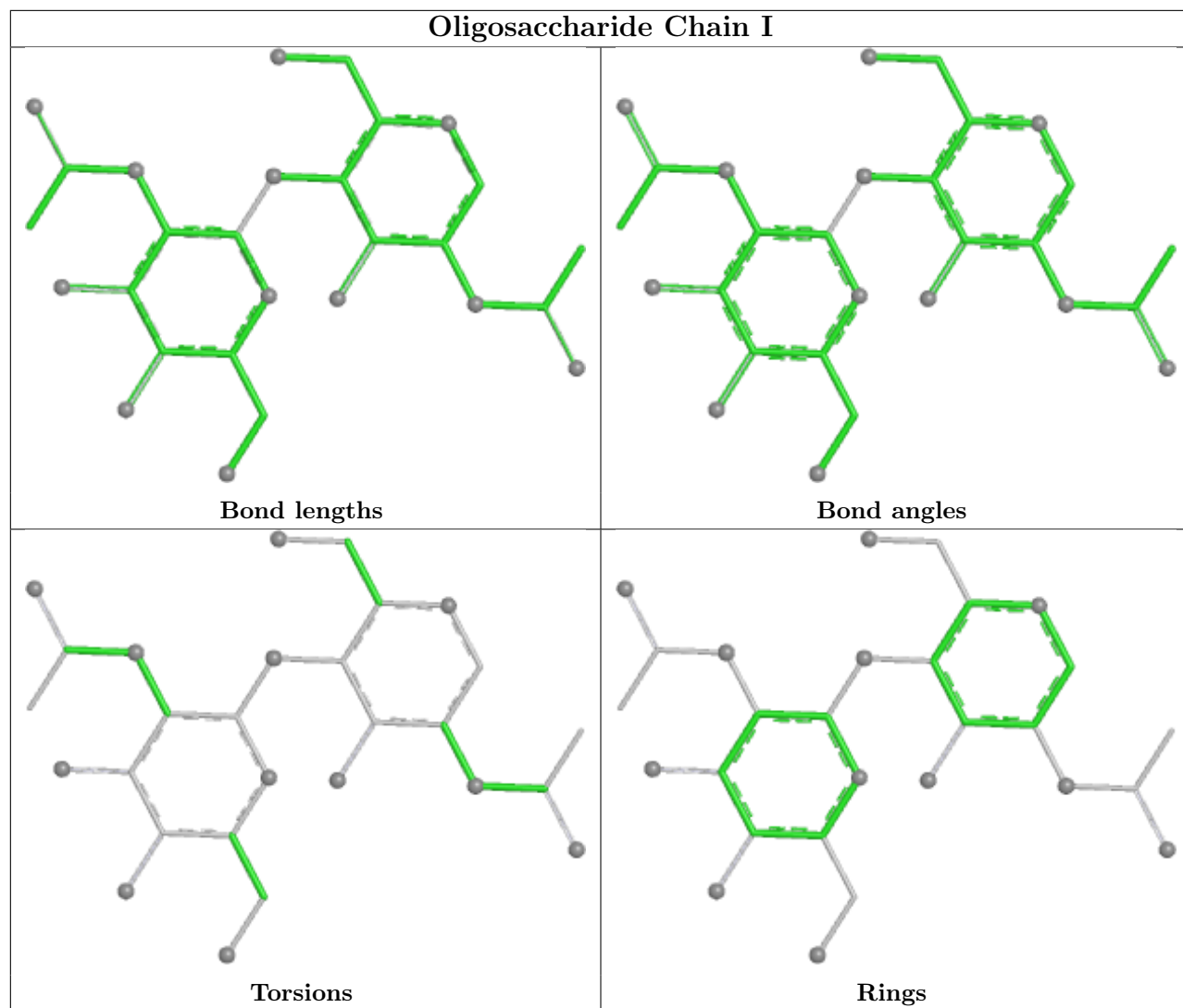
3 monomers are involved in 4 short contacts:

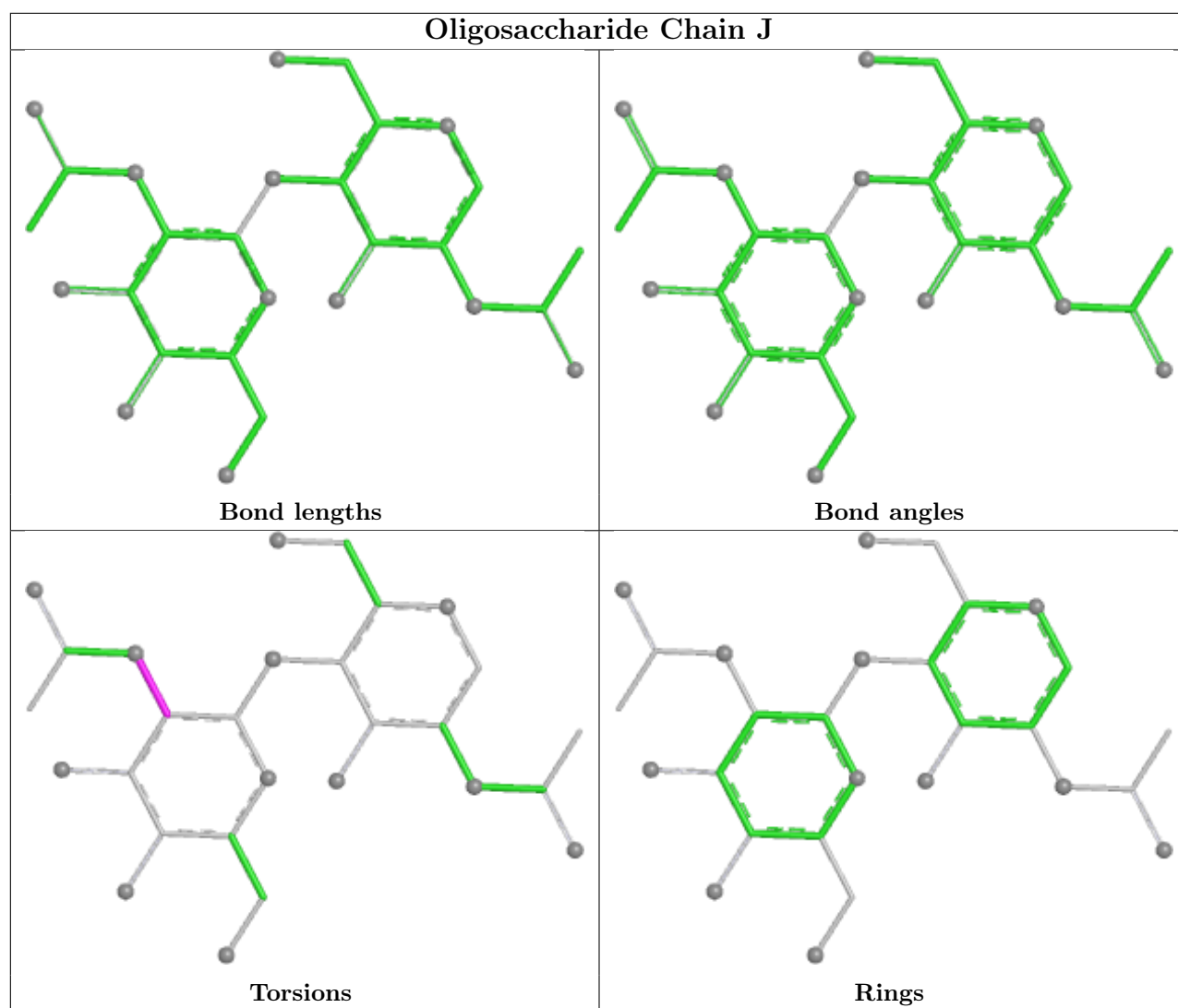
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	2	NAG	2	0
2	L	1	NAG	1	0
2	H	1	NAG	1	0

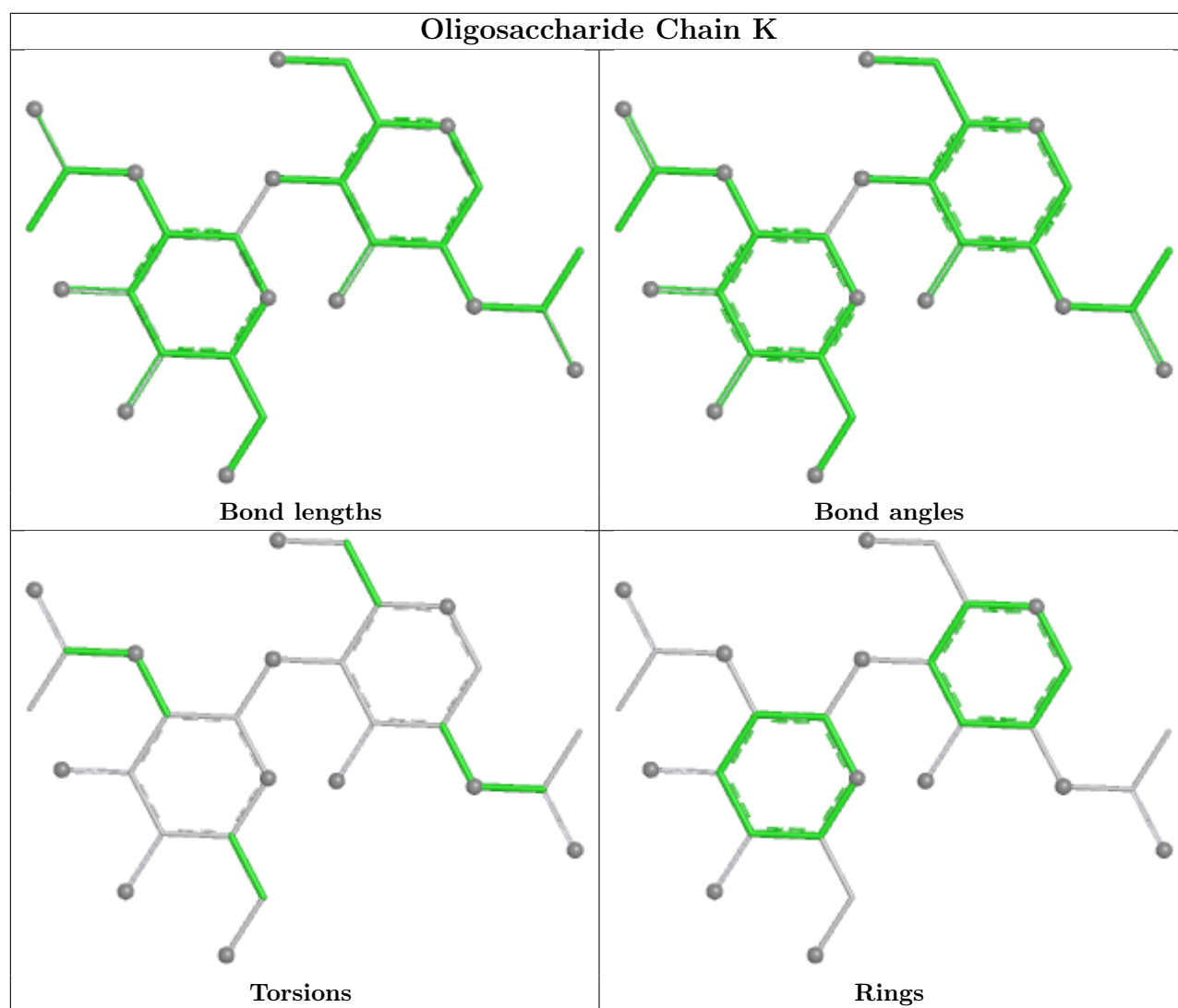
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

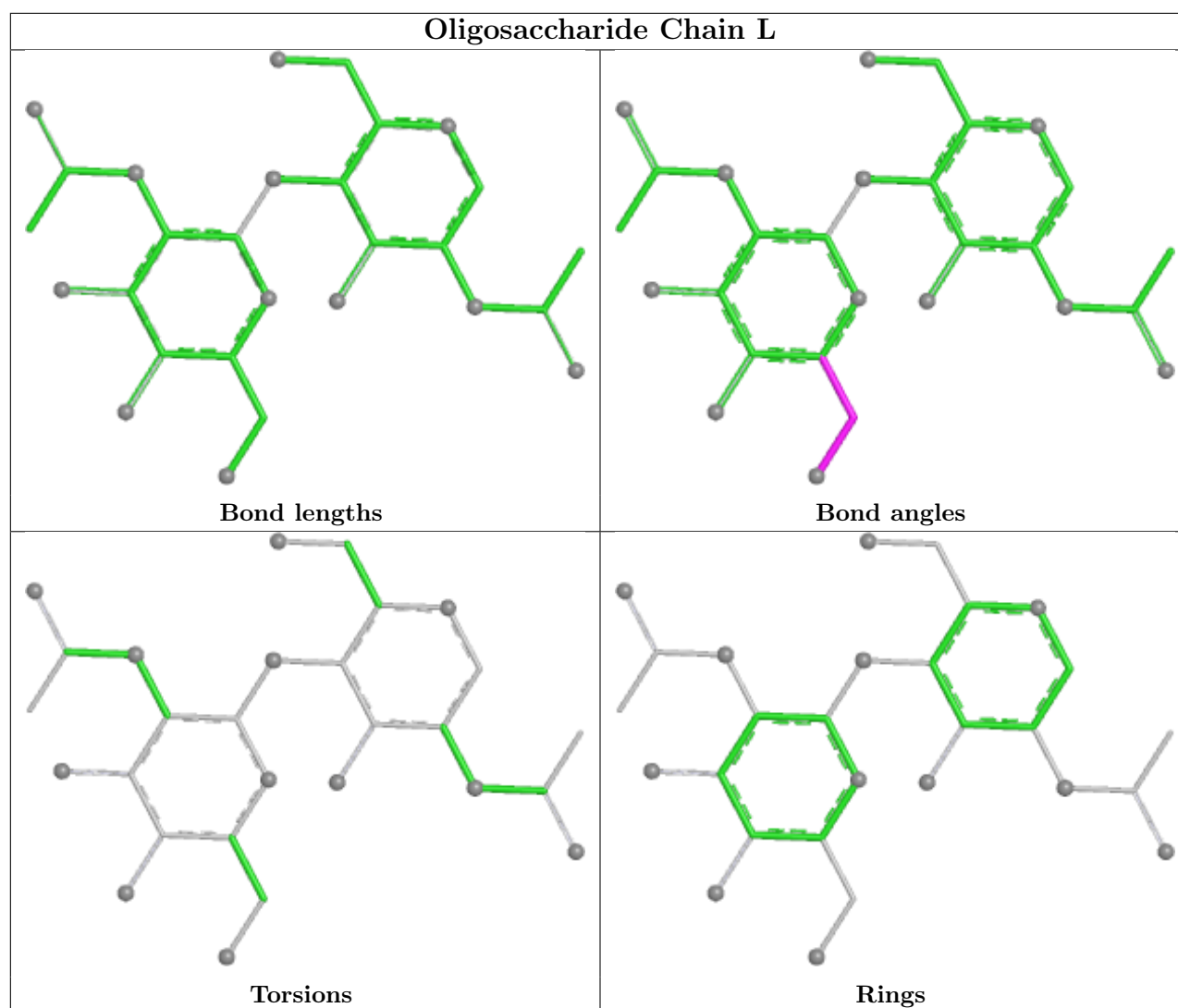












5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 10 are monoatomic - leaving 11 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	NDG	F	304	-	15,15,15	0.36	0	21,21,21	0.70	0
4	NDG	F	305	-	15,15,15	0.54	0	21,21,21	0.86	1 (4%)
5	1PE	E	305	-	15,15,15	0.44	0	14,14,14	0.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NDG	A	304	-	15,15,15	0.55	0	21,21,21	0.73	0
4	NDG	B	304	-	15,15,15	0.52	0	21,21,21	0.86	0
4	NDG	D	304	-	15,15,15	0.53	0	21,21,21	0.66	0
4	NDG	B	305	-	15,15,15	0.60	0	21,21,21	0.87	0
5	1PE	A	305	-	15,15,15	0.46	0	14,14,14	0.81	1 (7%)
7	NAG	C	304	-	15,15,15	0.42	0	21,21,21	0.80	0
7	NAG	C	305	-	15,15,15	0.40	0	21,21,21	0.79	0
7	NAG	E	304	-	15,15,15	0.42	0	21,21,21	1.25	1 (4%)

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	NDG	F	304	-	-	0/6/26/26	0/1/1/1
4	NDG	F	305	-	-	0/6/26/26	0/1/1/1
5	1PE	E	305	-	-	7/13/13/13	-
4	NDG	A	304	-	-	2/6/26/26	0/1/1/1
4	NDG	B	304	-	-	0/6/26/26	0/1/1/1
4	NDG	D	304	-	-	2/6/26/26	0/1/1/1
4	NDG	B	305	-	-	2/6/26/26	0/1/1/1
5	1PE	A	305	-	-	7/13/13/13	-
7	NAG	C	304	-	-	0/6/26/26	0/1/1/1
7	NAG	C	305	-	-	2/6/26/26	0/1/1/1
7	NAG	E	304	-	-	0/6/26/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	304	NAG	C1-C2-C3	-3.86	105.29	110.54
4	F	305	NDG	O5-C1-C2	2.62	112.15	109.52
5	A	305	1PE	C25-OH5-C14	-2.03	104.36	113.26

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	305	NAG	O5-C5-C6-O6
4	B	305	NDG	O5-C5-C6-O6
5	A	305	1PE	C14-C24-OH4-C13
7	C	305	NAG	C4-C5-C6-O6
4	B	305	NDG	C4-C5-C6-O6
4	D	304	NDG	C4-C5-C6-O6
4	D	304	NDG	O5-C5-C6-O6
5	A	305	1PE	OH7-C16-C26-OH6
5	A	305	1PE	OH6-C15-C25-OH5
5	E	305	1PE	OH5-C14-C24-OH4
5	E	305	1PE	C24-C14-OH5-C25
5	A	305	1PE	C24-C14-OH5-C25
5	E	305	1PE	C14-C24-OH4-C13
5	E	305	1PE	OH4-C13-C23-OH3
5	E	305	1PE	OH6-C15-C25-OH5
5	A	305	1PE	C25-C15-OH6-C26
5	E	305	1PE	C16-C26-OH6-C15
4	A	304	NDG	C4-C5-C6-O6
5	A	305	1PE	C16-C26-OH6-C15
5	A	305	1PE	C12-C22-OH3-C23
5	E	305	1PE	C25-C15-OH6-C26
4	A	304	NDG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	305	1PE	1	0
5	A	305	1PE	9	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 ⓘ

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	237/238 (99%)	-0.33	2 (0%) 82 85	8, 13, 19, 28	0
1	B	235/238 (98%)	-0.13	7 (2%) 52 56	9, 15, 26, 39	0
1	C	236/238 (99%)	0.10	6 (2%) 58 62	12, 20, 34, 45	0
1	D	237/238 (99%)	-0.04	8 (3%) 48 52	10, 17, 31, 45	0
1	E	237/238 (99%)	-0.04	4 (1%) 69 73	9, 17, 30, 39	0
1	F	237/238 (99%)	0.14	8 (3%) 48 52	13, 20, 35, 60	0
All	All	1419/1428 (99%)	-0.05	35 (2%) 58 62	8, 17, 31, 60	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	236	LEU	4.8
1	F	237	THR	4.6
1	B	235	ILE	4.4
1	C	235	ILE	4.4
1	F	112	SER	4.1
1	F	236	LEU	4.0
1	F	235	ILE	4.0
1	B	210	ASN	3.8
1	D	113	ASN	3.5
1	F	2	ASP	3.3
1	F	1	LEU	3.1
1	D	237	THR	3.1
1	C	1	LEU	3.0
1	E	113	ASN	3.0
1	C	112	SER	2.9
1	D	120	ASN	2.7
1	D	114	THR	2.7
1	E	1	LEU	2.7
1	B	113	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	157	GLY	2.7
1	B	112	SER	2.6
1	A	113	ASN	2.6
1	B	1	LEU	2.6
1	B	209	PRO	2.6
1	F	195	SER	2.5
1	C	209	PRO	2.4
1	F	111	SER	2.3
1	E	237	THR	2.3
1	A	237	THR	2.2
1	D	111	SER	2.1
1	D	201	ASP	2.1
1	D	112	SER	2.1
1	D	1	LEU	2.1
1	C	210	ASN	2.0
1	E	151	ASN	2.0

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

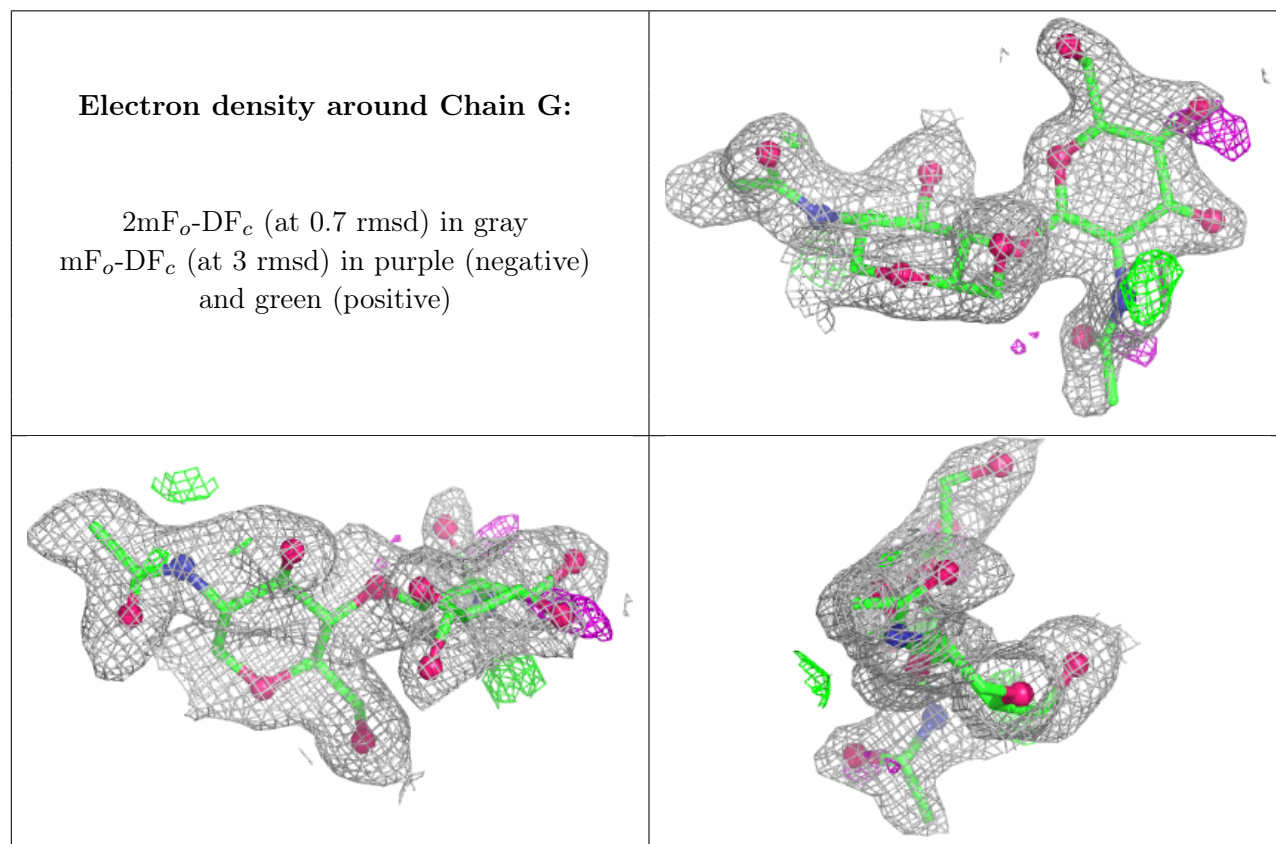
There are no non-standard protein/DNA/RNA residues in this entry.

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

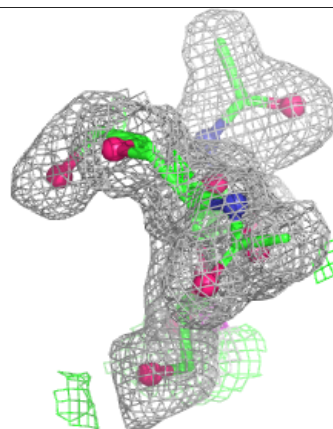
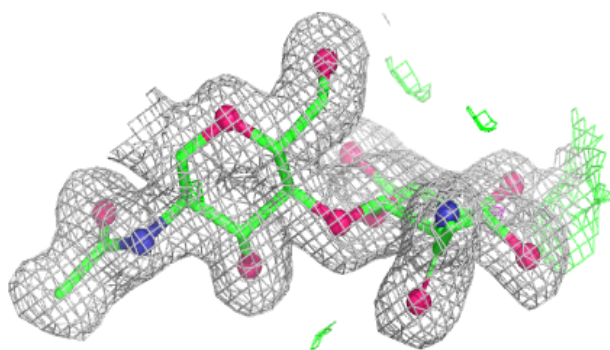
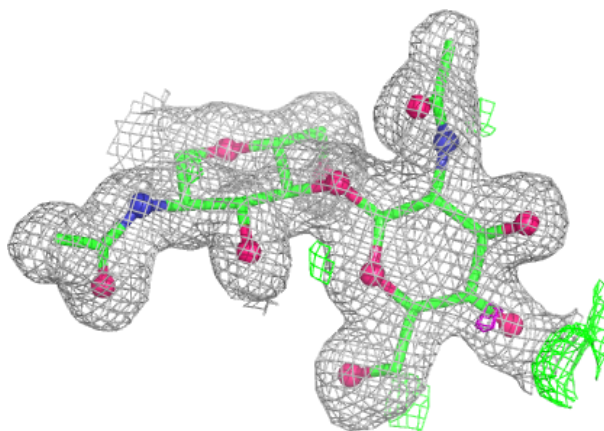
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	J	2	14/15	0.81	0.14	27,33,35,36	0
2	NAG	G	2	14/15	0.82	0.14	31,35,37,39	0
2	NAG	L	2	14/15	0.87	0.12	28,31,33,33	0
2	NAG	K	2	14/15	0.88	0.11	25,29,30,33	0
2	NAG	H	2	14/15	0.93	0.08	22,24,26,26	0
2	NAG	G	1	14/15	0.93	0.08	20,22,24,27	0
2	NAG	J	1	14/15	0.94	0.09	16,19,23,24	0
2	NAG	K	1	14/15	0.94	0.07	16,18,21,21	0
2	NAG	I	2	14/15	0.95	0.08	21,23,24,25	0
2	NAG	H	1	14/15	0.96	0.06	17,19,19,20	0
2	NAG	L	1	14/15	0.96	0.07	21,22,23,26	0
2	NAG	I	1	14/15	0.96	0.07	17,18,19,20	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.



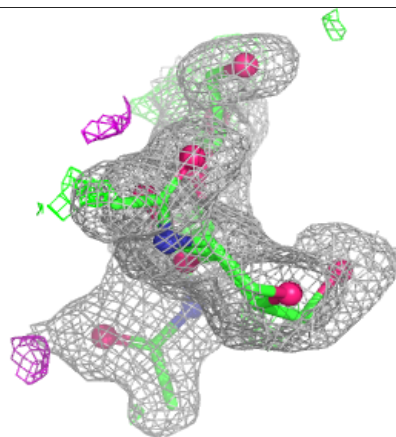
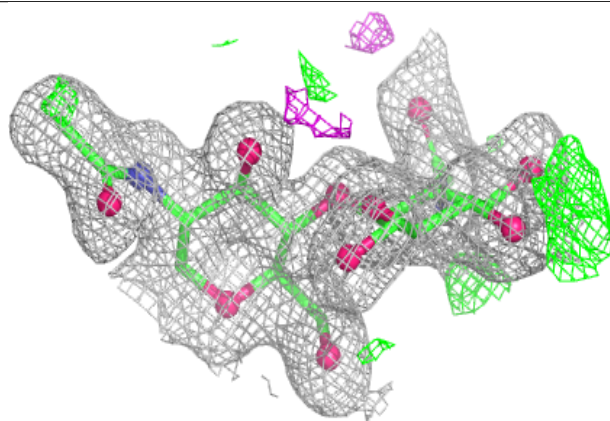
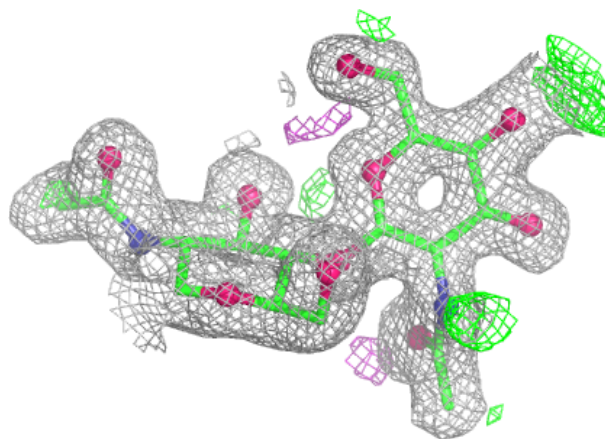
Electron density around Chain H:

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



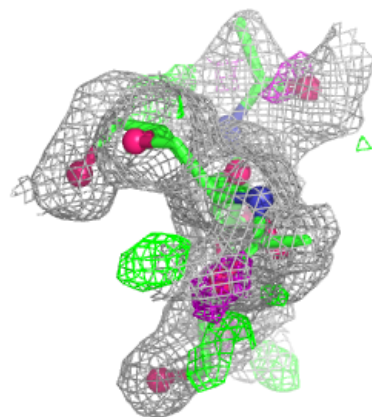
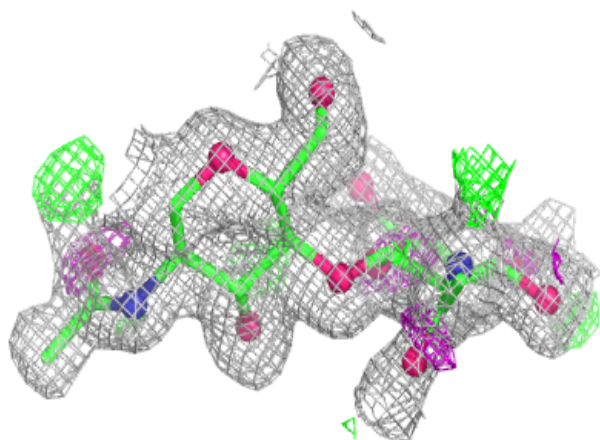
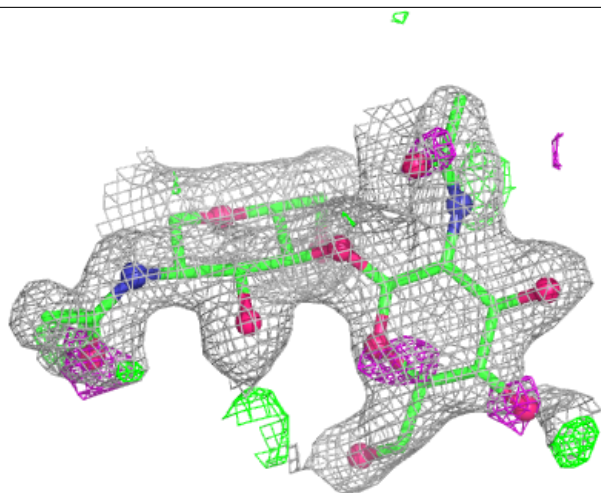
Electron density around Chain I:

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



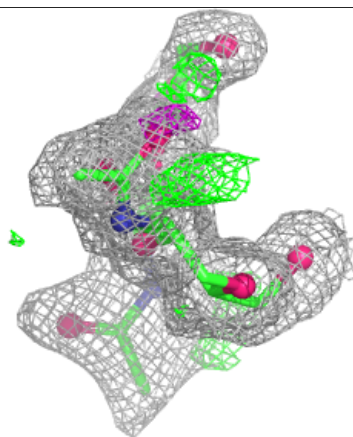
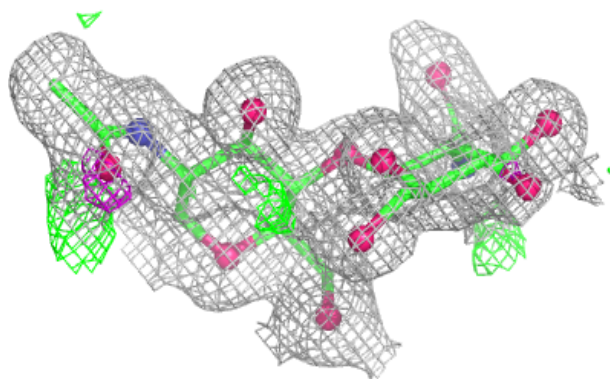
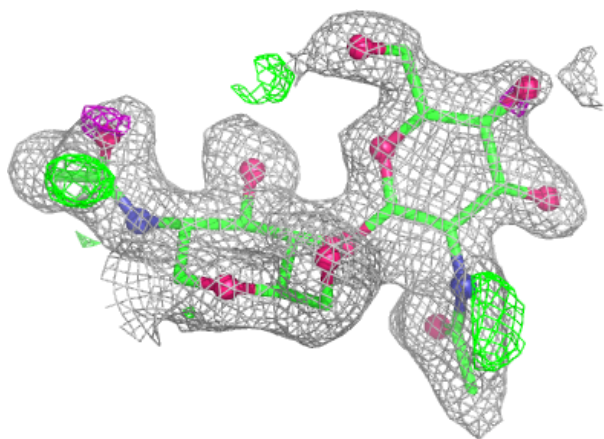
Electron density around Chain J:

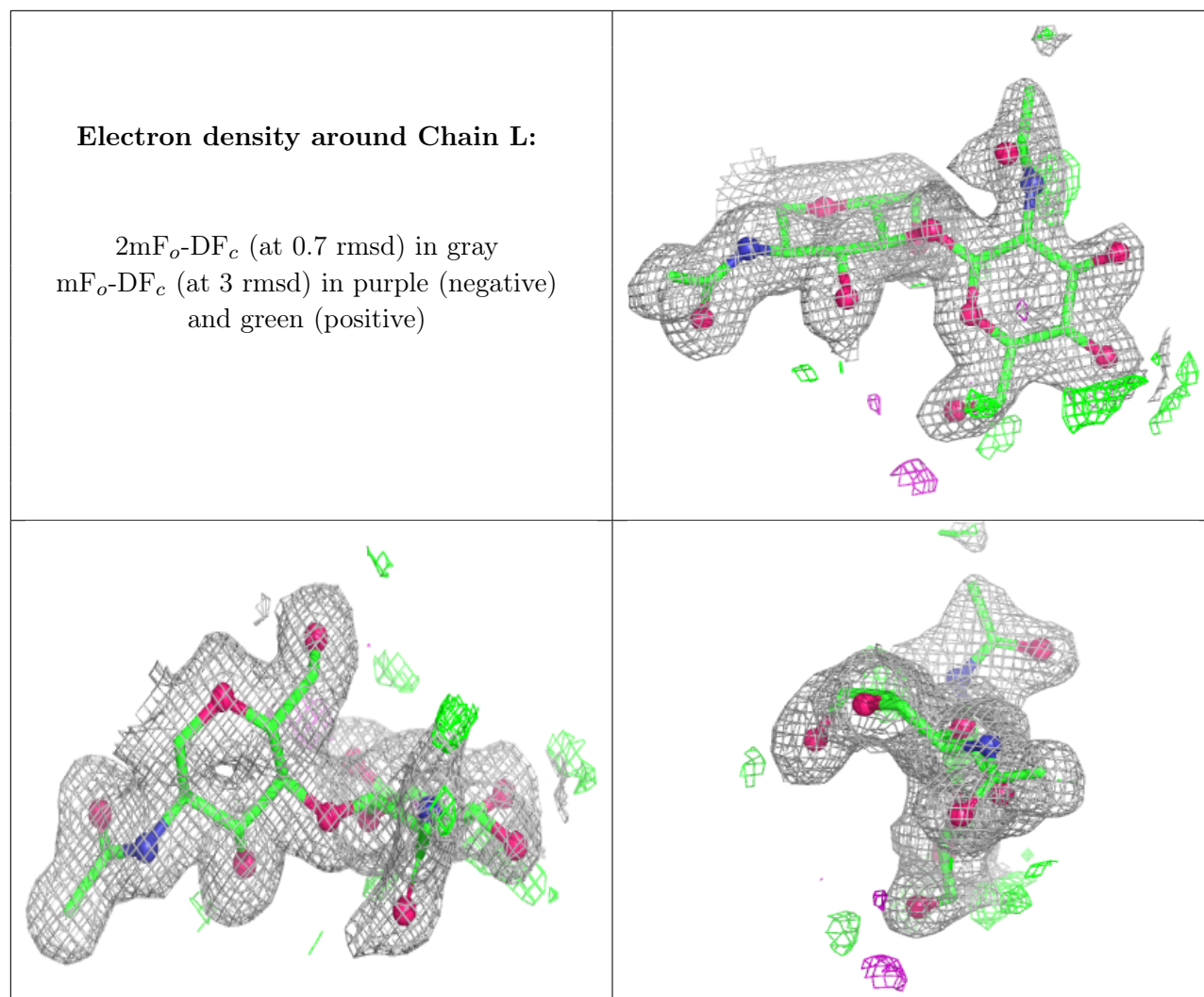
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain K:

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





6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	1PE	A	305	16/16	0.78	0.18	21,23,26,29	0
4	NDG	D	304	15/15	0.84	0.12	30,37,41,43	0
4	NDG	F	305	15/15	0.85	0.13	33,39,42,43	0
5	1PE	E	305	16/16	0.86	0.13	19,20,21,22	16
7	NAG	C	304	15/15	0.86	0.11	28,33,37,39	0
7	NAG	C	305	15/15	0.87	0.11	35,41,45,45	0
7	NAG	E	304	15/15	0.87	0.12	30,35,40,44	0
4	NDG	B	305	15/15	0.90	0.10	29,34,38,40	0
4	NDG	F	304	15/15	0.91	0.09	22,27,30,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NDG	B	304	15/15	0.92	0.09	20,26,29,30	0
4	NDG	A	304	15/15	0.93	0.09	18,24,28,31	0
6	MG	A	307	1/1	0.94	0.09	35,35,35,35	0
6	MG	E	306	1/1	0.96	0.05	16,16,16,16	0
6	MG	C	306	1/1	0.97	0.05	23,23,23,23	0
6	MG	A	306	1/1	0.99	0.06	7,7,7,7	0
3	CA	D	303	1/1	1.00	0.02	12,12,12,12	0
3	CA	E	303	1/1	1.00	0.01	13,13,13,13	0
3	CA	F	303	1/1	1.00	0.02	15,15,15,15	0
3	CA	A	303	1/1	1.00	0.02	8,8,8,8	0
3	CA	B	303	1/1	1.00	0.02	11,11,11,11	0
3	CA	C	303	1/1	1.00	0.03	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.