



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:06 PM UTC

PDB ID : 6N5E / pdb_00006n5e
Title : Broadly protective antibodies directed to a subdominant influenza hemagglutinin epitope
Authors : Bajic, G.; Schmidt, A.G.
Deposited on : 2018-11-21
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

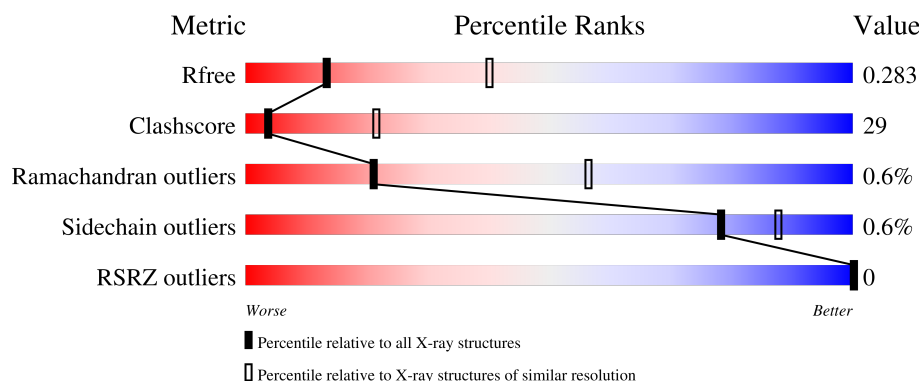
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



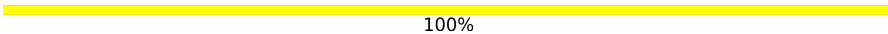
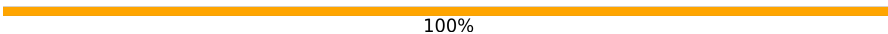
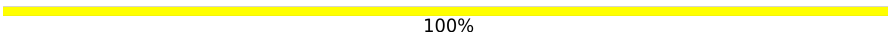
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	282	56% 43% .
1	B	282	55% 45%
1	C	282	59% 38% ..
2	E	238	51% 41% .. 5%
2	G	238	43% 46% . 7%

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Mol	Chain	Length	Quality of chain
2	H	238	 46%48%5%
3	D	217	 52%44%••
3	F	217	 47%41%•9%
3	I	217	 54%42%••
4	J	2	 50%50%
4	K	2	 100%
4	L	2	 100%
4	M	2	 100%
4	N	2	 50%50%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16381 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	A	282	Total	C	N	O	S	0	0	0
			2188	1374	382	421	11			
1	B	282	Total	C	N	O	S	0	0	0
			2188	1374	382	421	11			
1	C	277	Total	C	N	O	S	0	0	0
			2153	1353	376	413	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	188	ASP	ASN	conflict	UNP P03437
B	188	ASP	ASN	conflict	UNP P03437
C	188	ASP	ASN	conflict	UNP P03437

- Molecule 2 is a protein called FL-1066 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	225	Total	C	N	O	S	0	0	0
			1707	1080	282	337	8			
2	E	226	Total	C	N	O	S	0	0	0
			1715	1084	283	340	8			
2	G	222	Total	C	N	O	S	0	0	0
			1687	1067	279	333	8			

- Molecule 3 is a protein called FL-1066 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	211	Total	C	N	O	S	0	0	0
			1573	990	264	315	4			
3	F	197	Total	C	N	O	S	0	0	0
			1457	915	245	293	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	0	0
			1573	990	264	315	4			

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

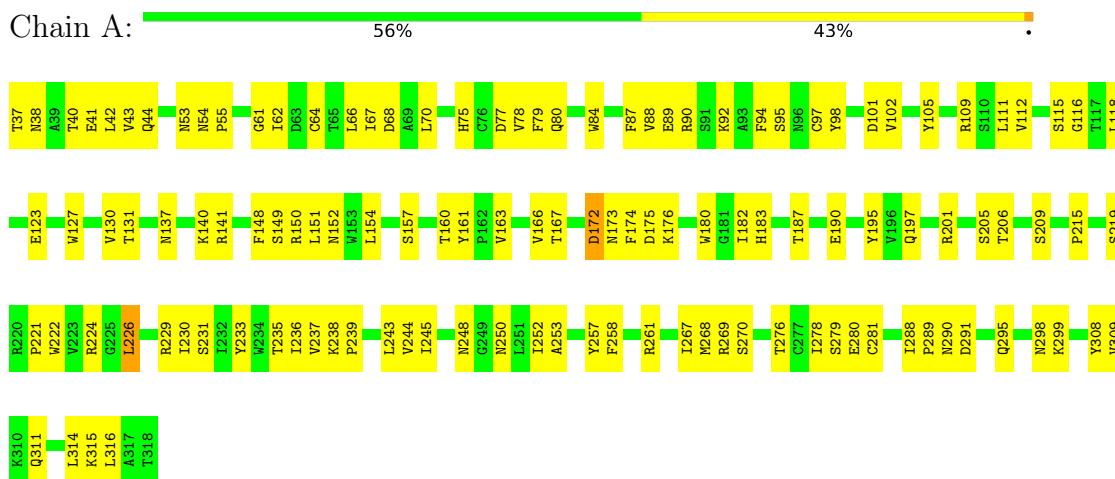


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	N	2	Total	C	N	O	0	0	0
			28	16	2	10			

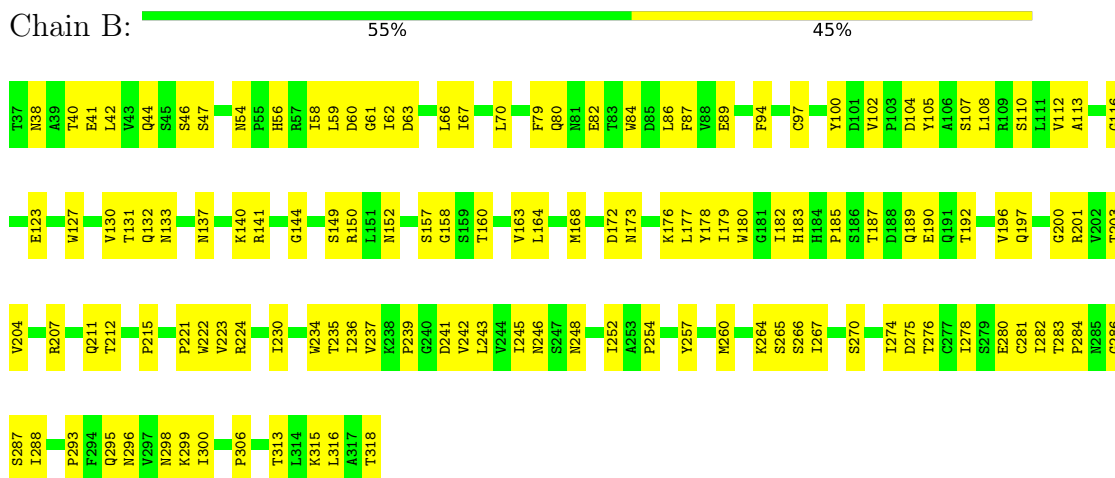
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Hemagglutinin

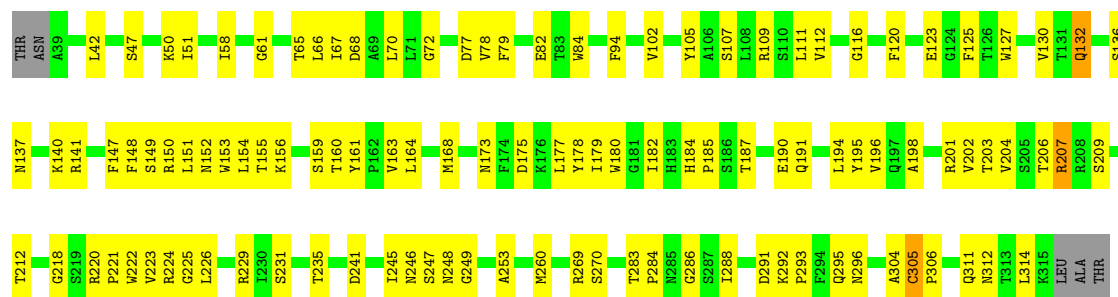


• Molecule 1: Hemagglutinin



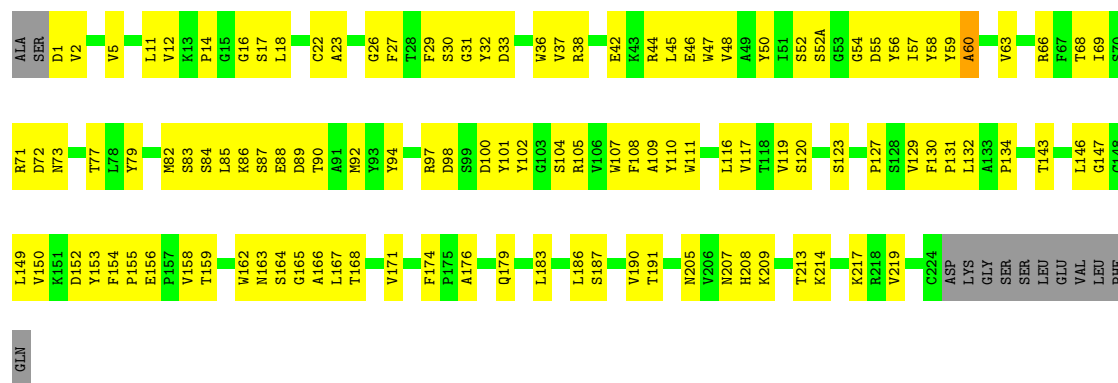
• Molecule 1: Hemagglutinin





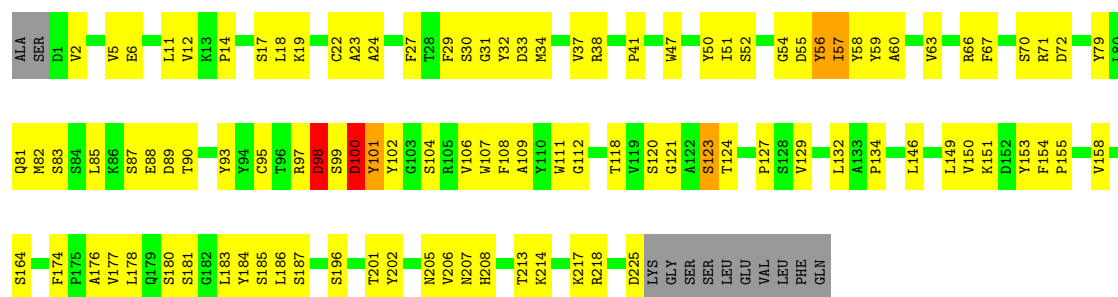
• Molecule 2: FL-1066 heavy chain

Chain H: 46% 48% 5%



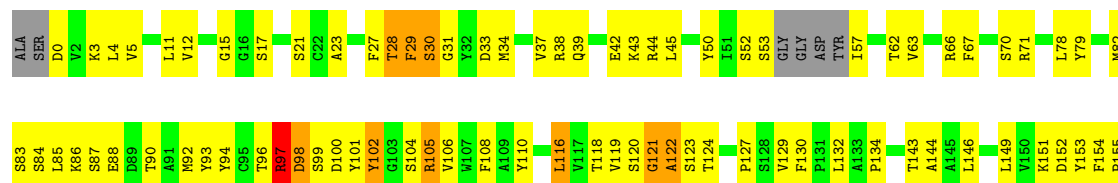
• Molecule 2: FL-1066 heavy chain

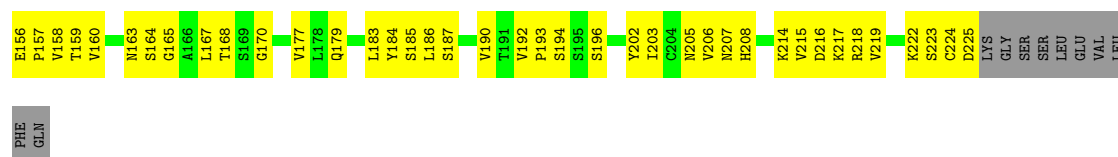
Chain E: 51% 41% 5%



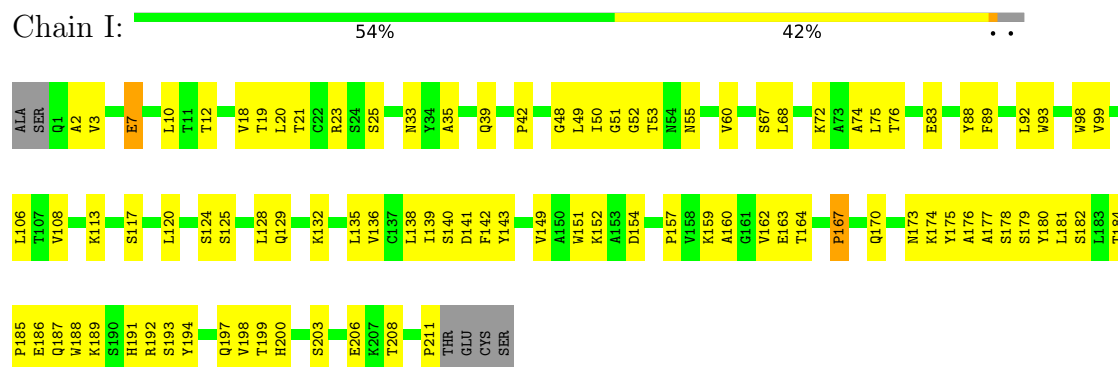
• Molecule 2: FL-1066 heavy chain

Chain G: 43% 46% 7%

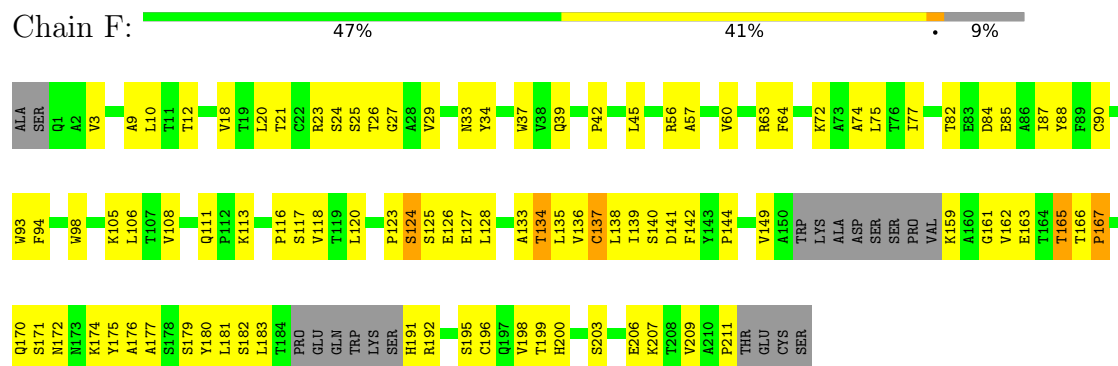




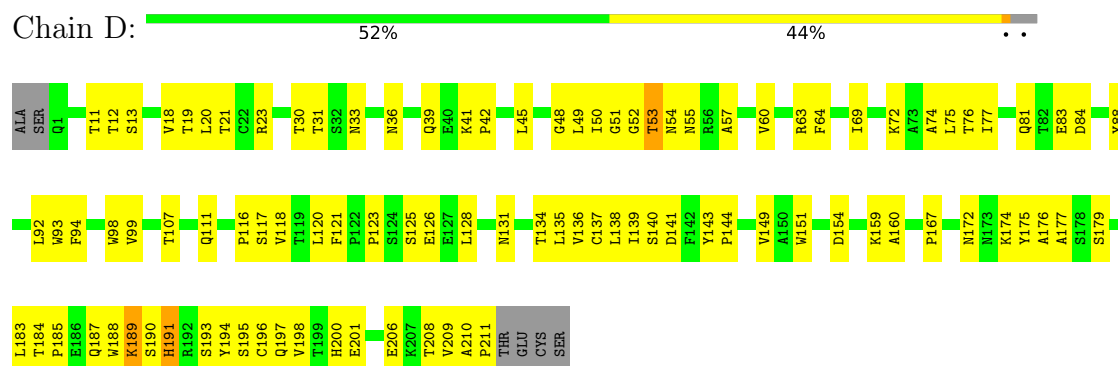
• Molecule 3: FL-1066 light chain



• Molecule 3: FL-1066 light chain



• Molecule 3: FL-1066 light chain



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





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

Chain K:  100%



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

Chain L:  100%



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

Chain M:  100%



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

Chain N:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	153.56Å 153.56Å 91.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.33 – 3.00 44.33 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.33-3.00) 99.8 (44.33-3.00)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.249 , 0.287 0.246 , 0.283	Depositor DCC
R_{free} test set	2303 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	60.7	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 28.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.088 for -h,-k,l 0.094 for h,-h-k,-l 0.398 for -k,-h,-l	Xtriage
Reported twinning fraction	0.490 for -k,-h,-l	Depositor
Outliers	0 of 48395 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16381	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.29	0/2240	0.67	5/3051 (0.2%)
1	B	0.32	0/2240	0.66	2/3051 (0.1%)
1	C	0.32	0/2205	0.66	3/3002 (0.1%)
2	E	0.42	0/1758	0.85	3/2391 (0.1%)
2	G	0.48	0/1728	0.96	11/2349 (0.5%)
2	H	0.34	0/1750	0.70	0/2380
3	D	0.39	0/1612	0.86	3/2206 (0.1%)
3	F	0.45	0/1488	0.94	6/2032 (0.3%)
3	I	0.30	0/1612	0.71	1/2206 (0.0%)
All	All	0.37	0/16633	0.78	34/22668 (0.1%)

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	30	SER	N-CA-C	-8.86	101.70	111.36
2	E	98	ASP	CB-CA-C	7.47	123.29	109.54
3	F	165	THR	CA-C-N	6.97	130.01	120.67
3	F	165	THR	C-N-CA	6.97	130.01	120.67
3	I	7	GLU	CA-CB-CG	6.88	127.86	114.10

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	2188	0	2140	108	1
1	B	2188	0	2137	112	0
1	C	2153	0	2100	95	1
2	E	1715	0	1662	112	0
2	G	1687	0	1642	110	1
2	H	1707	0	1658	115	0
3	D	1573	0	1531	86	0
3	F	1457	0	1424	134	0
3	I	1573	0	1531	98	1
4	J	28	0	25	1	0
4	K	28	0	25	1	0
4	L	28	0	25	3	0
4	M	28	0	25	2	0
4	N	28	0	25	0	0
All	All	16381	0	15950	932	2

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 29.

The worst 5 of 932 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)
3:F:118:VAL:CB	3:F:139:ILE:HD13	1.37	1.50
3:F:118:VAL:HB	3:F:139:ILE:CD1	1.48	1.44
2:E:99:SER:HB2	2:E:106:VAL:O	1.04	1.18
2:E:178:LEU:HD23	2:E:184:TYR:CE1	1.79	1.17
3:F:117:SER:O	3:F:140:SER:OG	1.60	1.17

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:THR:OG1	2:G:194:SER:OG[2_655]	2.06	0.14
1:C:50:LYS:NZ	3:I:83:GLU:OE2[3_654]	2.13	0.07

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	280/282 (99%)	261 (93%)	18 (6%)	1 (0%)	30	65
1	B	280/282 (99%)	262 (94%)	18 (6%)	0	100	100
1	C	275/282 (98%)	261 (95%)	13 (5%)	1 (0%)	30	65
2	E	224/238 (94%)	203 (91%)	16 (7%)	5 (2%)	5	26
2	G	218/238 (92%)	200 (92%)	17 (8%)	1 (0%)	24	60
2	H	223/238 (94%)	200 (90%)	21 (9%)	2 (1%)	14	48
3	D	209/217 (96%)	189 (90%)	20 (10%)	0	100	100
3	F	191/217 (88%)	175 (92%)	15 (8%)	1 (0%)	24	60
3	I	209/217 (96%)	199 (95%)	9 (4%)	1 (0%)	24	60
All	All	2109/2211 (95%)	1950 (92%)	147 (7%)	12 (1%)	21	56

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	57	ILE
2	E	181	SER
2	G	105	ARG
1	A	226	LEU
1	C	132	GLN

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	249/249 (100%)	248 (100%)	1 (0%)	84	90
1	B	249/249 (100%)	249 (100%)	0	100	100
1	C	245/249 (98%)	244 (100%)	1 (0%)	84	90
2	E	192/202 (95%)	188 (98%)	4 (2%)	47	75
2	G	190/202 (94%)	186 (98%)	4 (2%)	47	75
2	H	191/202 (95%)	191 (100%)	0	100	100
3	D	173/178 (97%)	172 (99%)	1 (1%)	78	88
3	F	160/178 (90%)	160 (100%)	0	100	100
3	I	173/178 (97%)	173 (100%)	0	100	100
All	All	1822/1887 (97%)	1811 (99%)	11 (1%)	78	88

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	30	SER
2	G	97	ARG
3	D	189	LYS
2	G	100	ASP
2	E	101	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	54	ASN
3	F	172	ASN
1	C	298	ASN
3	I	197	GLN
1	C	152	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 ⓘ

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	NAG	J	1	4,1	14,14,15	0.28	0	17,19,21	1.54	3 (17%)
4	NAG	J	2	4	14,14,15	0.28	0	17,19,21	0.69	0
4	NAG	K	1	4,1	14,14,15	0.47	0	17,19,21	0.83	0
4	NAG	K	2	4	14,14,15	0.30	0	17,19,21	0.47	0
4	NAG	L	1	4,1	14,14,15	0.67	1 (7%)	17,19,21	1.09	2 (11%)
4	NAG	L	2	4	14,14,15	0.78	1 (7%)	17,19,21	0.73	1 (5%)
4	NAG	M	1	4,1	14,14,15	0.28	0	17,19,21	0.75	0
4	NAG	M	2	4	14,14,15	0.75	0	17,19,21	0.61	0
4	NAG	N	1	4,1	14,14,15	0.44	0	17,19,21	2.48	2 (11%)
4	NAG	N	2	4	14,14,15	0.26	0	17,19,21	0.39	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	J	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	J	2	4	-	4/6/23/26	0/1/1/1
4	NAG	K	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	L	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	L	2	4	-	1/6/23/26	0/1/1/1
4	NAG	M	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	M	2	4	-	2/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	4/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	2	NAG	O5-C1	-2.25	1.39	1.43
4	L	1	NAG	C1-C2	2.18	1.55	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	1	NAG	C1-O5-C5	9.52	124.94	112.19
4	J	1	NAG	C2-N2-C7	4.78	129.31	122.90
4	L	1	NAG	C1-O5-C5	2.77	115.90	112.19
4	J	1	NAG	O4-C4-C5	-2.49	103.18	109.32
4	L	1	NAG	C1-C2-N2	2.46	114.31	110.43

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

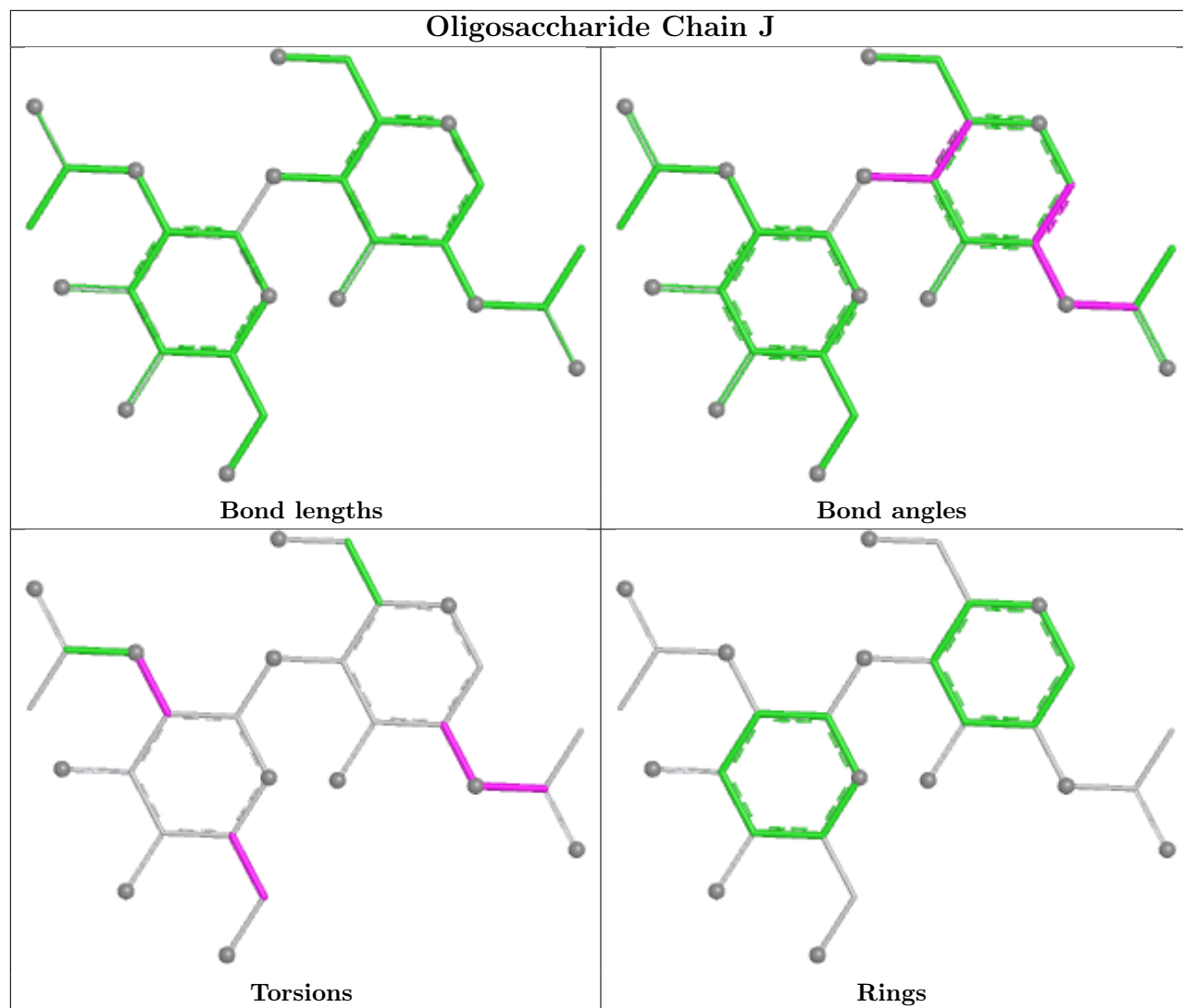
Mol	Chain	Res	Type	Atoms
4	M	2	NAG	O5-C5-C6-O6
4	K	1	NAG	C4-C5-C6-O6
4	M	2	NAG	C4-C5-C6-O6
4	J	2	NAG	O5-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6

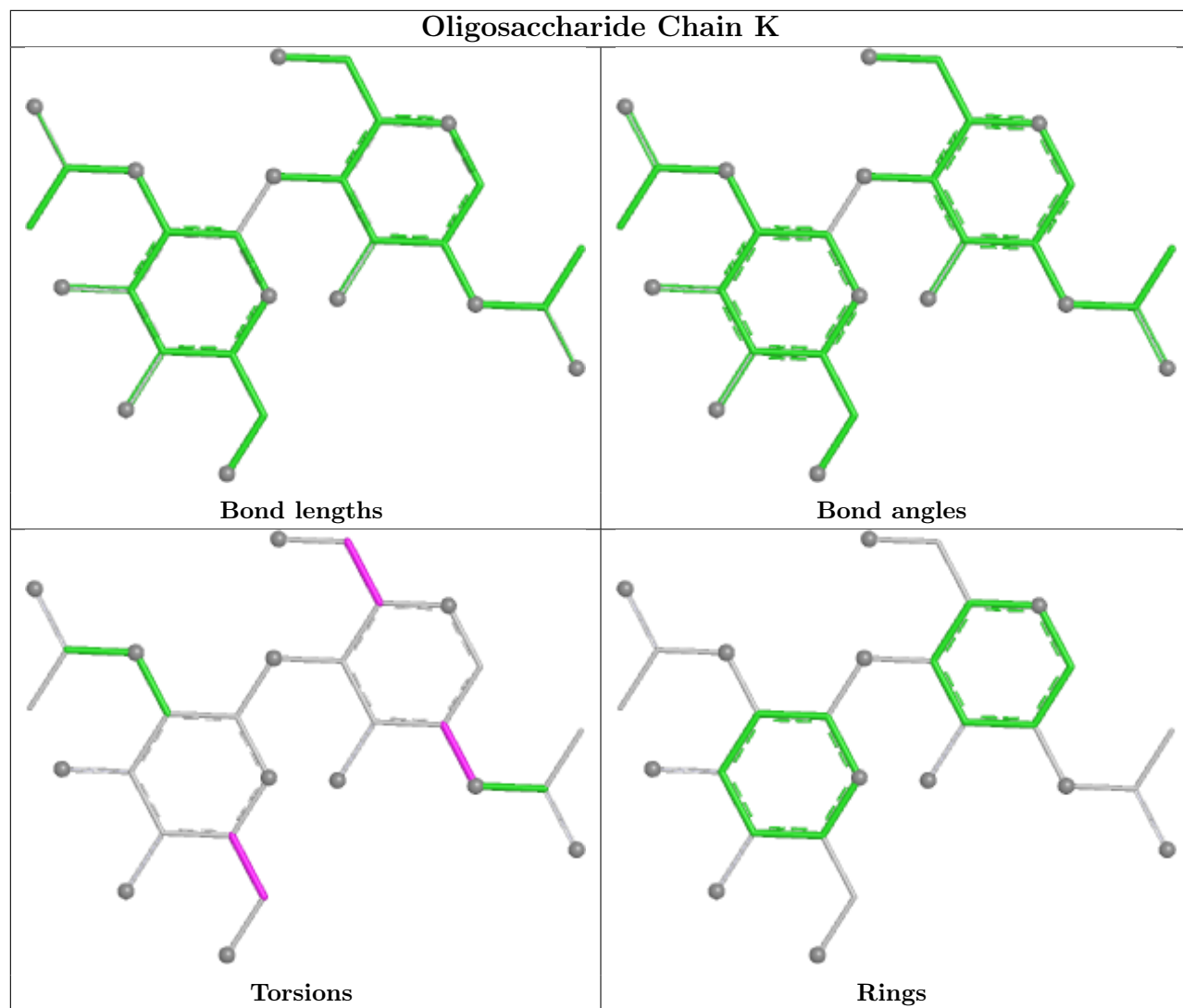
There are no ring outliers.

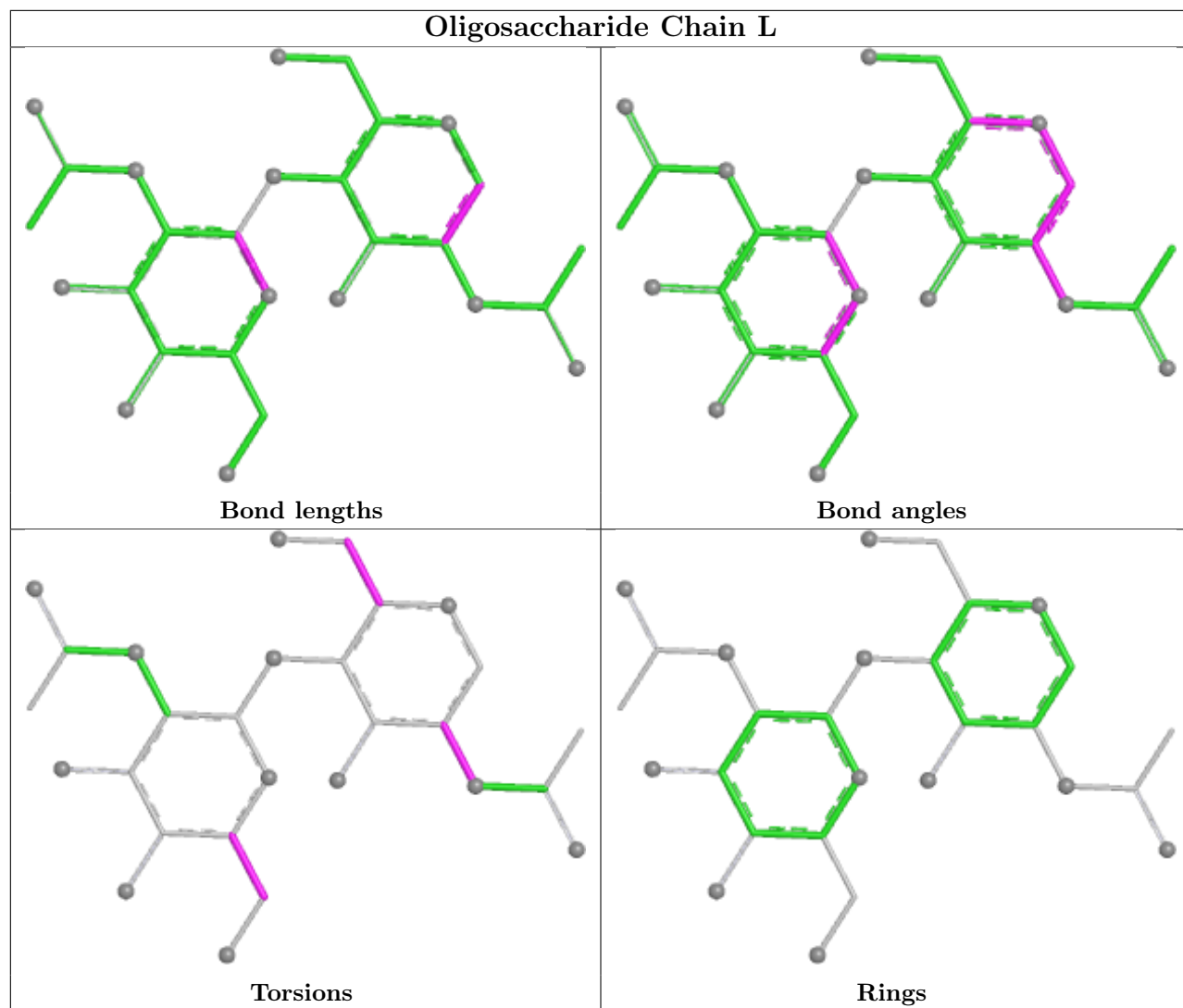
7 monomers are involved in 7 short contacts:

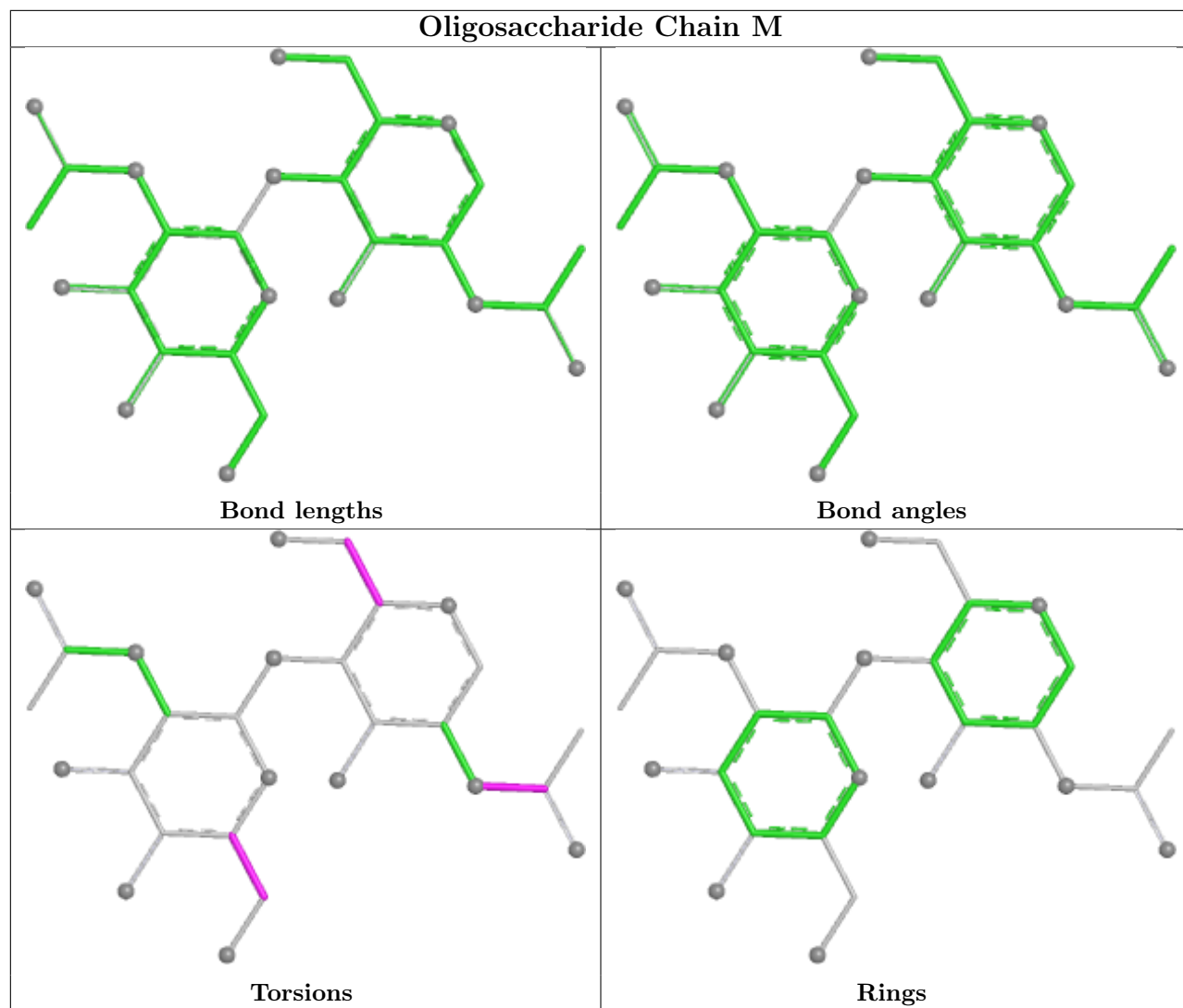
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	K	2	NAG	1	0
4	J	1	NAG	1	0
4	K	1	NAG	1	0
4	L	2	NAG	2	0
4	M	2	NAG	2	0
4	L	1	NAG	3	0
4	M	1	NAG	2	0

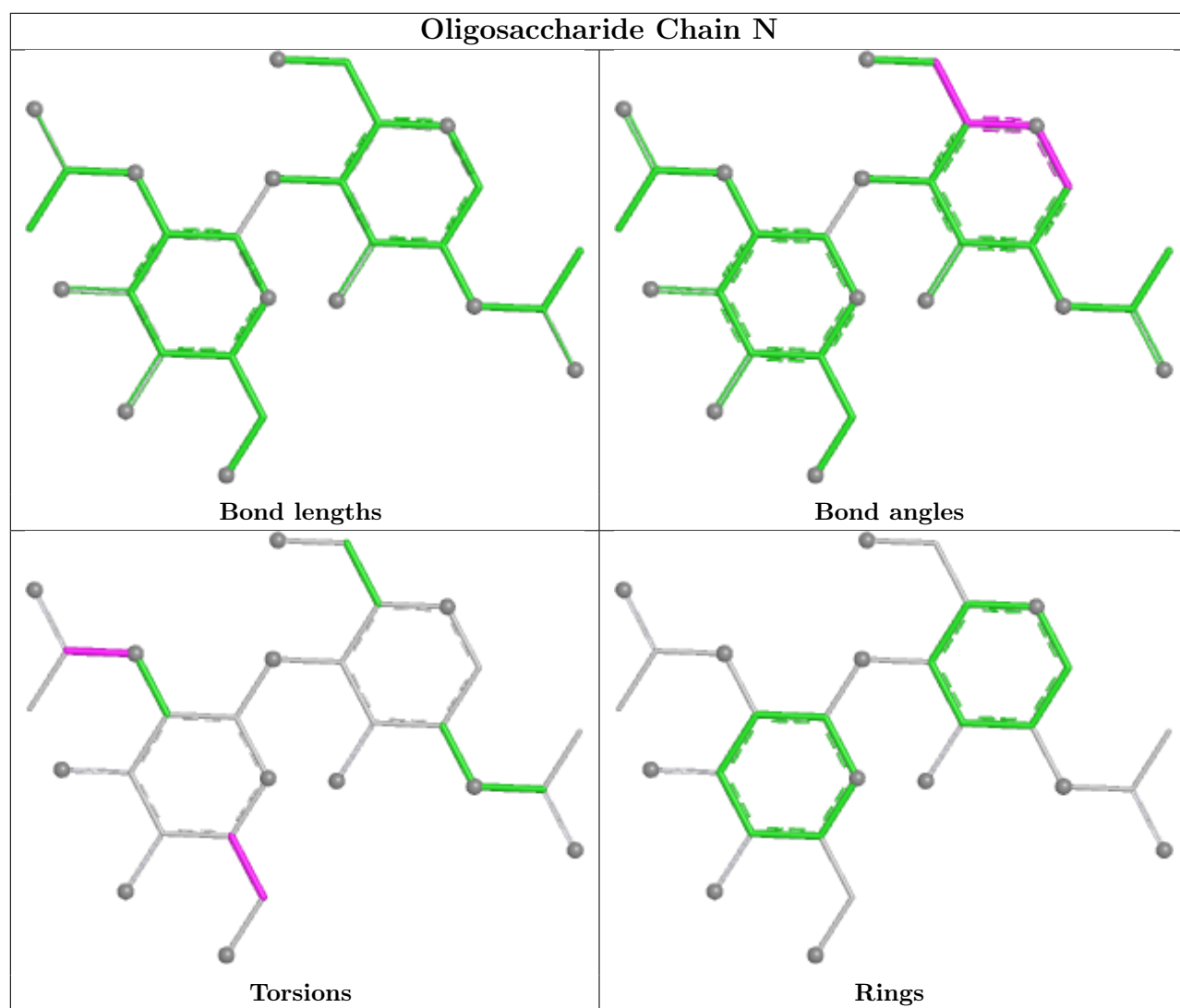
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	282/282 (100%)	-1.36	0 100 100	37, 49, 68, 87	0
1	B	282/282 (100%)	-1.37	0 100 100	32, 47, 71, 82	0
1	C	277/282 (98%)	-1.35	0 100 100	38, 49, 64, 98	0
2	E	226/238 (94%)	-1.27	0 100 100	35, 50, 70, 88	0
2	G	222/238 (93%)	-1.16	0 100 100	41, 57, 93, 114	0
2	H	225/238 (94%)	-1.31	0 100 100	35, 44, 70, 97	0
3	D	211/217 (97%)	-1.24	0 100 100	43, 59, 85, 104	0
3	F	197/217 (90%)	-1.09	0 100 100	42, 64, 118, 129	0
3	I	211/217 (97%)	-1.28	0 100 100	37, 53, 77, 101	0
All	All	2133/2211 (96%)	-1.28	0 100 100	32, 51, 89, 129	0

There are no RSRZ outliers to report.

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.

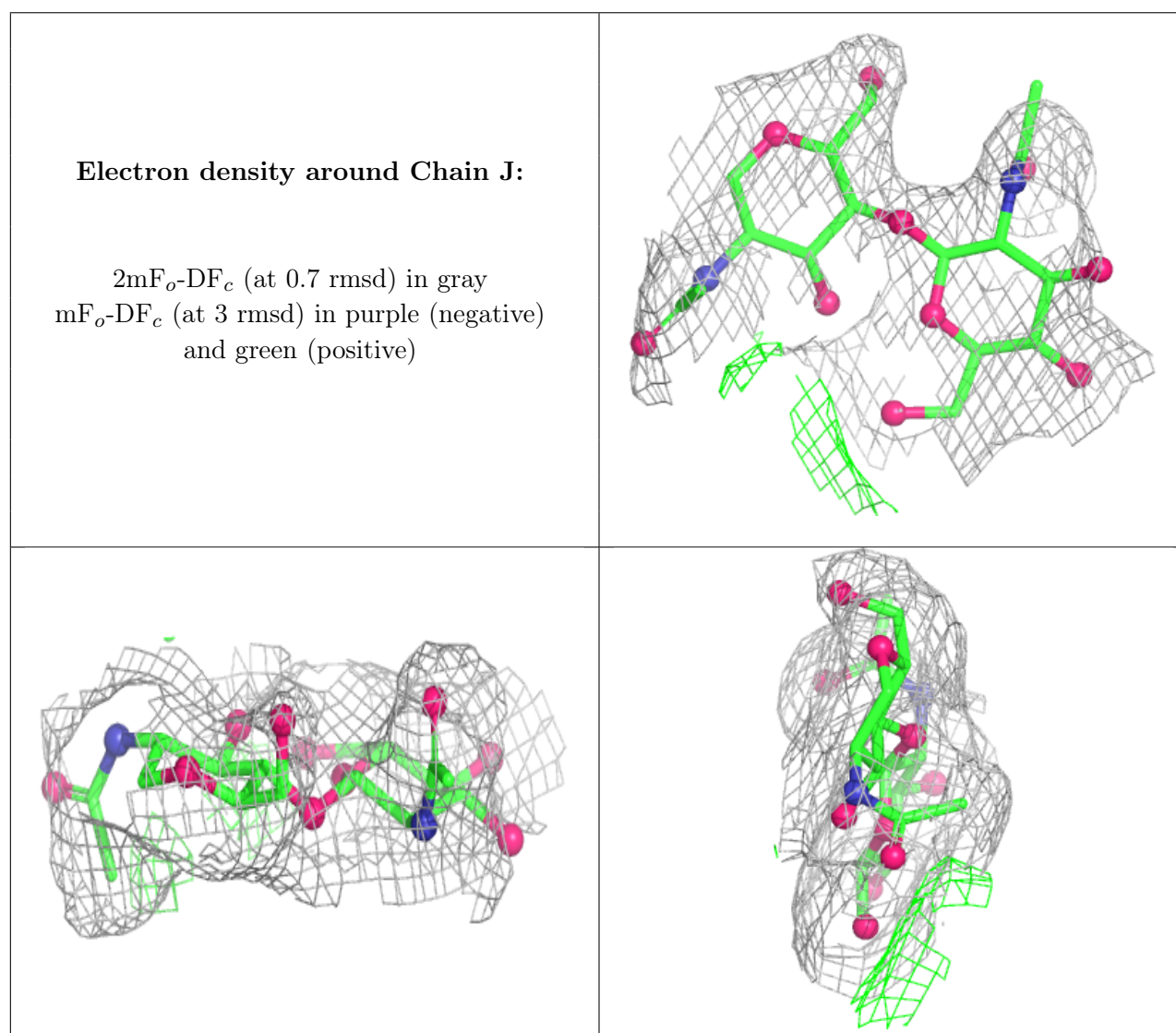
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	K	1	14/15	0.96	0.05	63,65,70,70	0
4	NAG	M	2	14/15	0.96	0.06	81,86,89,89	0

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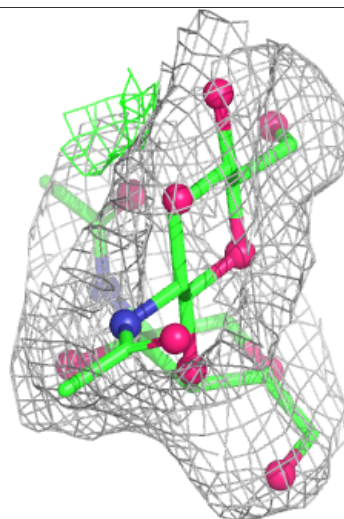
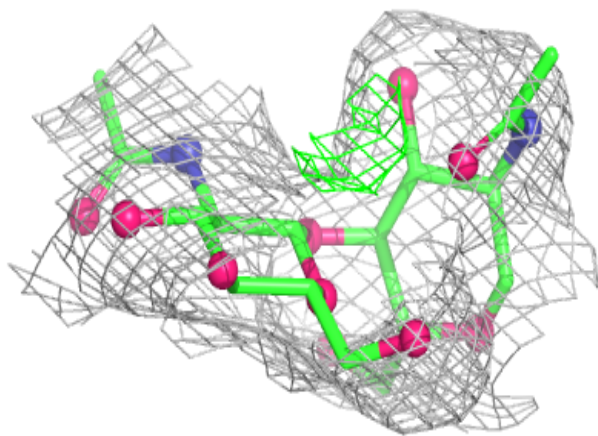
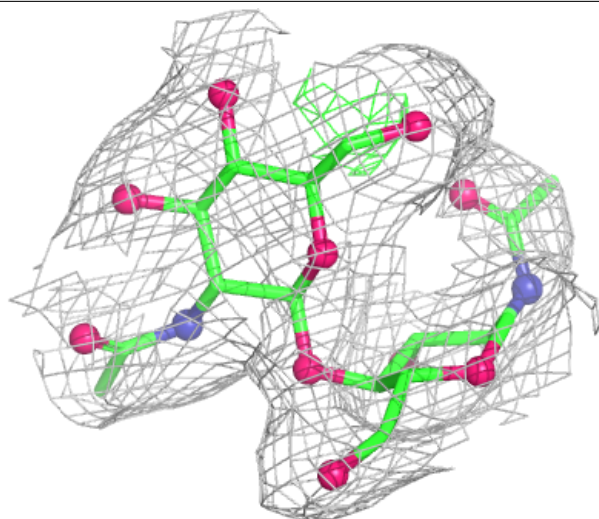
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	K	2	14/15	0.97	0.04	62,66,69,80	0
4	NAG	M	1	14/15	0.97	0.05	63,72,81,83	0
4	NAG	J	1	14/15	0.97	0.04	52,53,55,55	0
4	NAG	L	2	14/15	0.98	0.03	72,74,77,78	0
4	NAG	J	2	14/15	0.98	0.04	55,57,59,60	0
4	NAG	L	1	14/15	0.98	0.04	65,68,74,79	0
4	NAG	N	2	14/15	0.98	0.03	50,52,54,55	0
4	NAG	N	1	14/15	0.99	0.03	48,52,57,58	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.



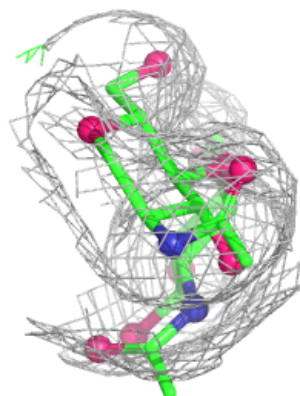
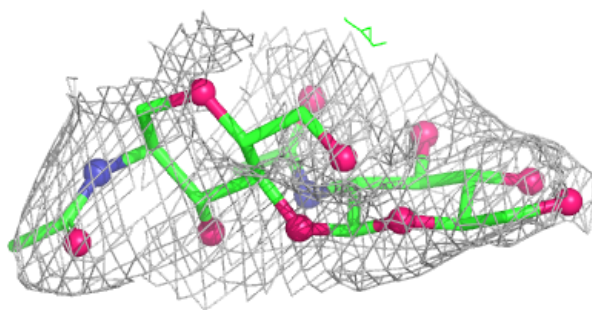
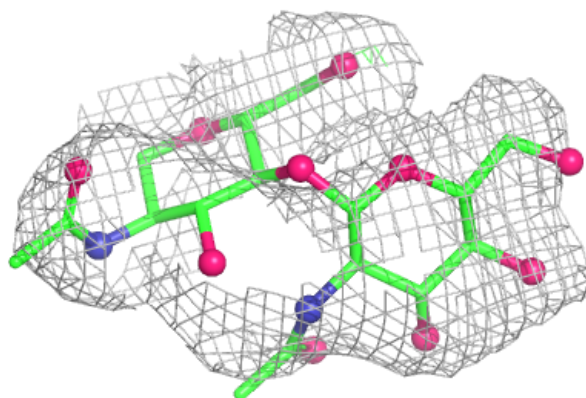
Electron density around Chain K:

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

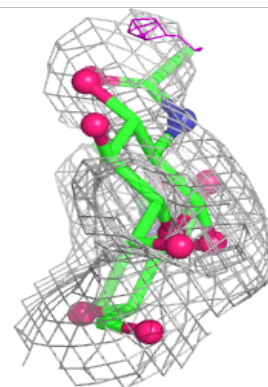
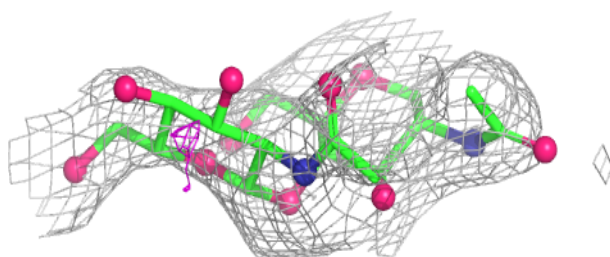
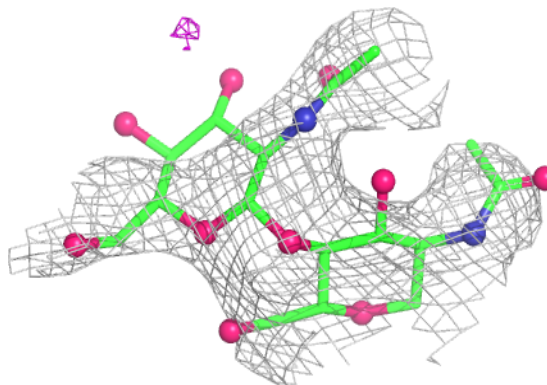


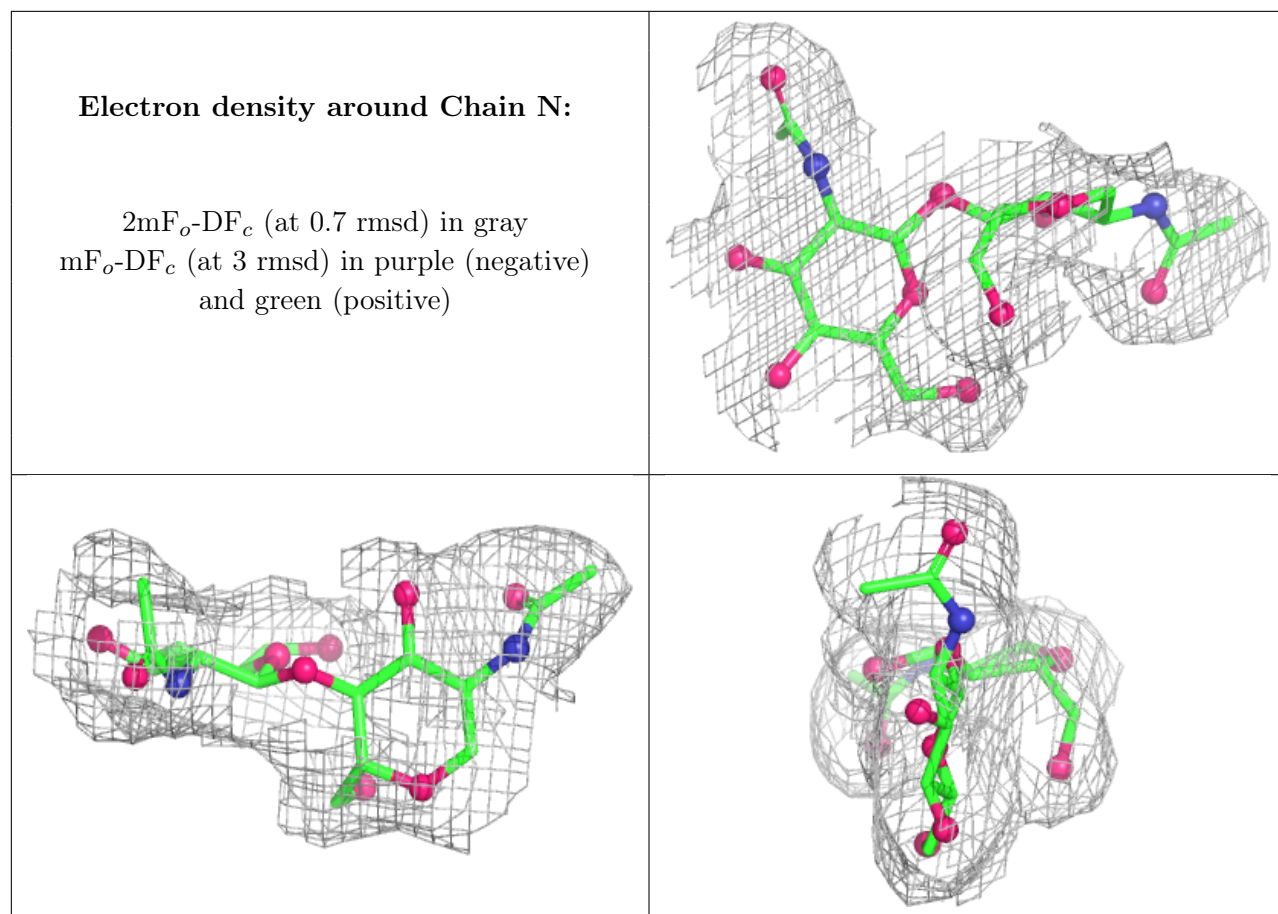
Electron density around Chain L:

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

**Electron density around Chain M:**

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.