



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 07:32 AM EDT

PDB ID : 7RFC / pdb_00007rfc
Title : Crystal structure of broadly neutralizing antibody mAb1382 in complex with Hepatitis C virus envelope glycoprotein E2 ectodomain
Authors : Flyak, A.I.; Bjorkman, P.J.
Deposited on : 2021-07-14
Resolution : 3.24 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

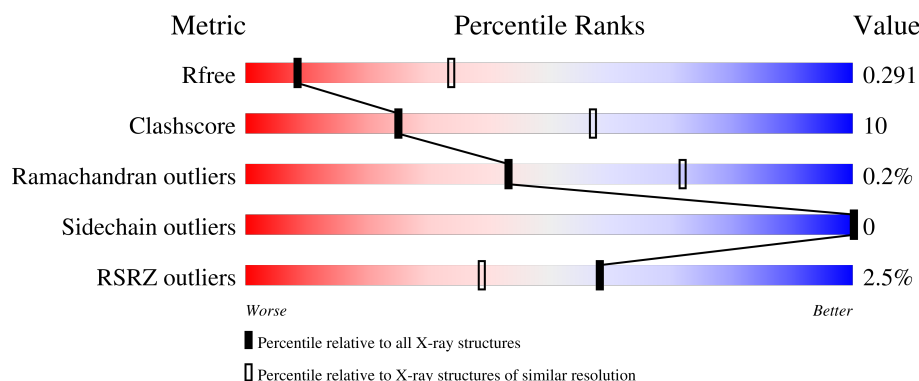
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.24 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.



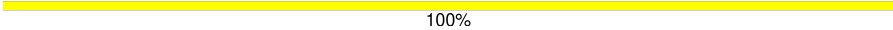
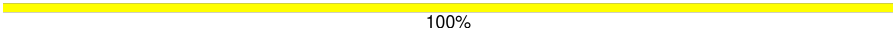
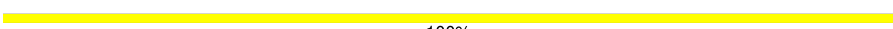
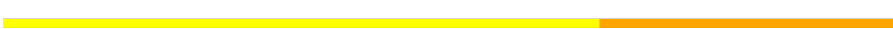
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2153 (3.28-3.20)
Clashscore	190562	2275 (3.28-3.20)
Ramachandran outliers	187476	2233 (3.28-3.20)
Sidechain outliers	187428	2232 (3.28-3.20)
RSRZ outliers	180081	2153 (3.28-3.20)

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	236	3% 72% 22% 6%
1	H	236	71% 22% 7%
2	B	216	81% 19%
2	L	216	% 81% 18% .
3	C	262	4% 62% 18% 19%

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Mol	Chain	Length	Quality of chain
3	D	262	
4	E	2	
4	F	2	
4	I	2	
4	J	2	
4	K	2	
4	M	2	
4	O	2	
5	G	3	
6	N	5	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 10362 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 mAb1382 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1634	1035	269	324	6			
1	H	220	Total	C	N	O	S	0	0	0
			1623	1029	267	321	6			

- Molecule 2 is a protein called mAb1382 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	0	0
			1673	1051	287	331	4			
2	L	214	Total	C	N	O	S	0	0	0
			1664	1046	286	328	4			

- Molecule 3 is a protein called envelope glycoprotein E2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	211	Total	C	N	O	S	0	0	0
			1673	1066	294	294	19			
3	D	223	Total	C	N	O	S	0	0	0
			1743	1108	306	310	19			

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



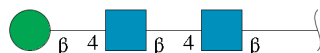
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

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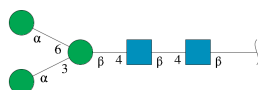
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



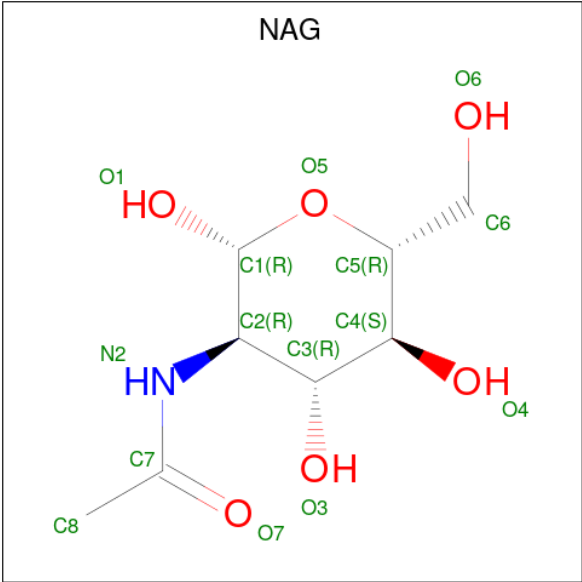
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	N	5	Total	C	N	O	0	0	0
			61	34	2	25			

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

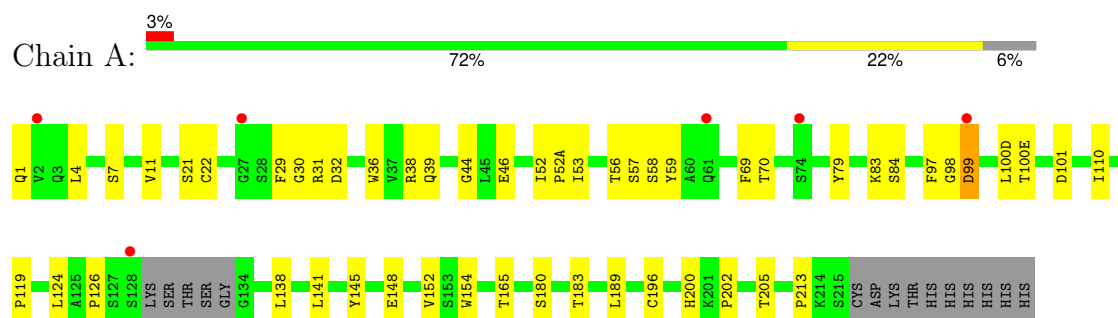


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		

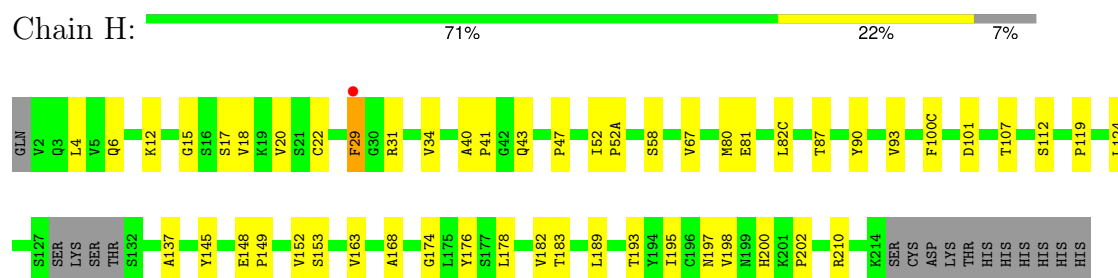
3 Residue-property plots [i](#)

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.

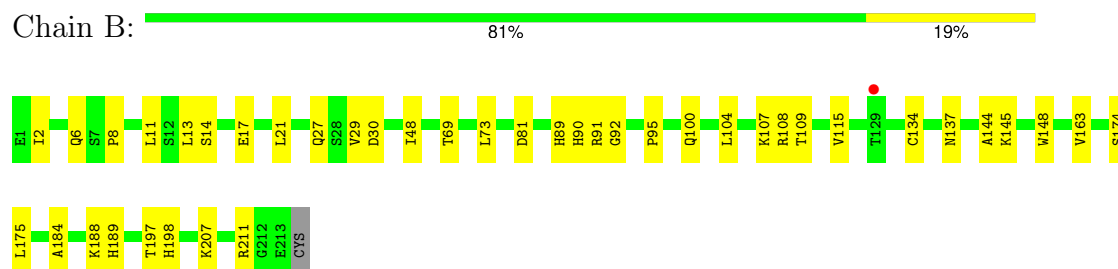
• Molecule 1: mAb1382 Heavy Chain



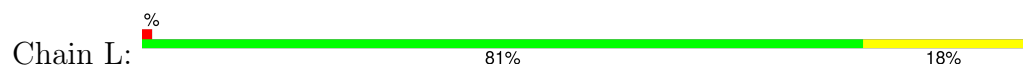
• Molecule 1: mAb1382 Heavy Chain

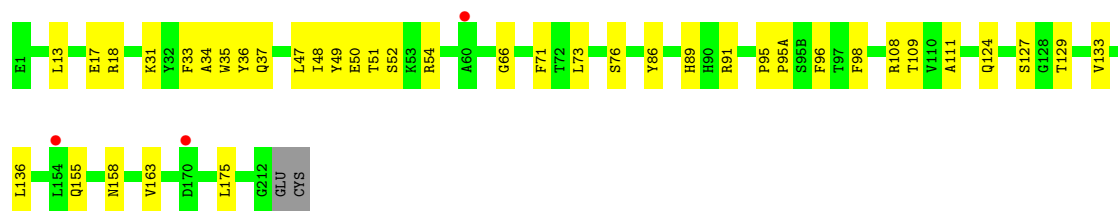


• Molecule 2: mAb1382 Light Chain

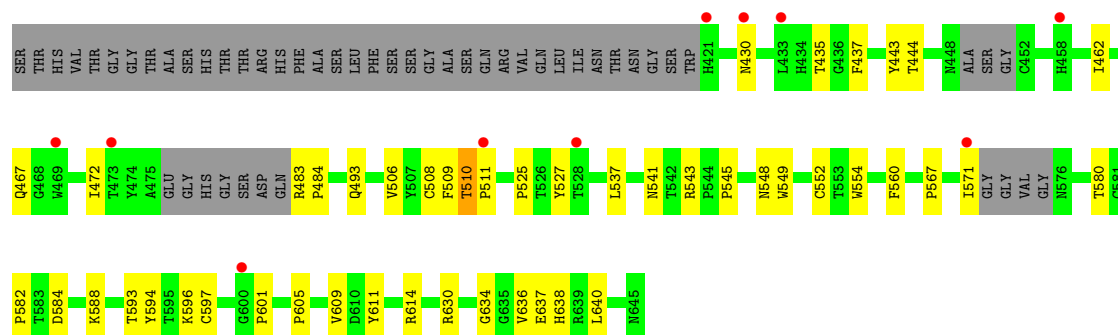


• Molecule 2: mAb1382 Light Chain

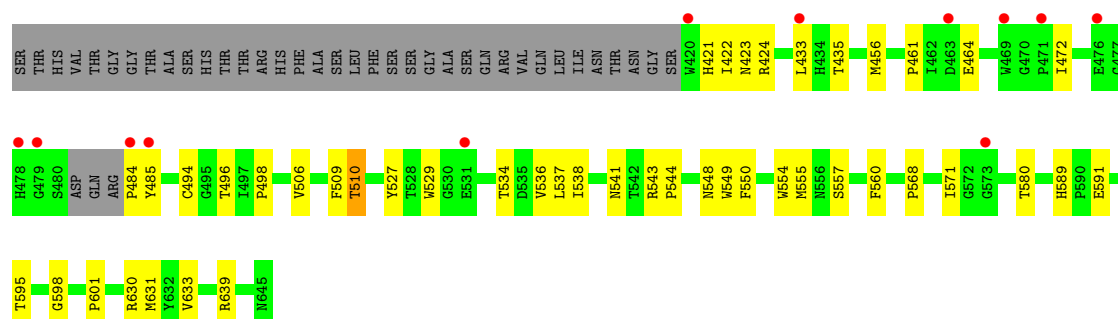




• Molecule 3: envelope glycoprotein E2



• Molecule 3: envelope glycoprotein E2



• 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



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

Chain I:  50% 50%



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

Chain J:  50% 50%

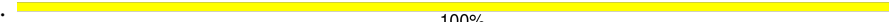


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  50% 50%



- 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 O:  50% 50%

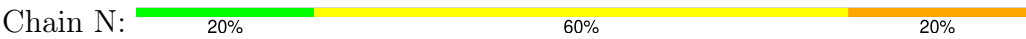


- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  67% 33%



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



MAN1
MAN2
MAN3
MAN4
MAN5

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.29Å 140.18Å 142.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.15 – 3.24 52.15 – 3.24	Depositor EDS
% Data completeness (in resolution range)	98.2 (52.15-3.24) 98.1 (52.15-3.24)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 3.26Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.233 , 0.284 0.240 , 0.291	Depositor DCC
R_{free} test set	1831 reflections (5.39%)	wwPDB-VP
Wilson B-factor (Å ²)	69.1	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 63.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	10362	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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: BMA, NAG, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.33	0/1673	0.63	0/2278
1	H	0.41	0/1662	0.72	1/2263 (0.0%)
2	B	0.38	0/1714	0.68	0/2328
2	L	0.34	0/1705	0.63	0/2316
3	C	0.35	0/1733	0.66	0/2372
3	D	0.37	0/1808	0.70	3/2476 (0.1%)
All	All	0.36	0/10295	0.67	4/14033 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	510	THR	CA-C-N	6.59	142.82	127.00
3	D	510	THR	C-N-CA	6.59	142.82	127.00
1	H	29	PHE	CB-CA-C	5.94	122.24	110.42
3	D	510	THR	C-N-CD	-5.81	107.81	120.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	99	ASP	Peptide
2	B	81	ASP	Peptide

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	1634	0	1603	39	0
1	H	1623	0	1590	39	0
2	B	1673	0	1620	32	0
2	L	1664	0	1614	33	0
3	C	1673	0	1549	35	0
3	D	1743	0	1603	32	0
4	E	28	0	25	0	0
4	F	28	0	25	0	0
4	I	28	0	25	0	0
4	J	28	0	25	1	0
4	K	28	0	25	0	0
4	M	28	0	25	0	0
4	O	28	0	25	0	0
5	G	39	0	34	1	0
6	N	61	0	52	3	0
7	C	28	0	26	0	0
7	D	28	0	26	1	0
All	All	10362	0	9892	197	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 10.

All (197) 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:C:543:ARG:NH2	3:C:567:PRO:O	1.99	0.95
1:A:101:ASP:OD1	2:B:91:ARG:NH2	2.00	0.94
1:A:97:PHE:HA	1:A:100(E):THR:HG22	1.55	0.87
1:H:148:GLU:HG2	1:H:149:PRO:HA	1.58	0.84
3:C:525:PRO:HB2	3:C:527:TYR:HE1	1.42	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:498:PRO:HA	3:D:536:VAL:HG12	1.64	0.80
2:B:89:HIS:HE1	2:B:91:ARG:HE	1.28	0.80
3:C:543:ARG:NH1	3:C:596:LYS:O	2.15	0.79
3:C:609:VAL:HG13	3:C:640:LEU:HD12	1.70	0.71
3:D:421:HIS:CD2	4:J:1:NAG:H5	2.28	0.69
1:H:93:VAL:HG11	2:L:96:PHE:CE2	2.27	0.68
1:A:126:PRO:HG3	1:A:138:LEU:HB3	1.75	0.68
2:L:108:ARG:NH1	2:L:109:THR:O	2.28	0.67
1:A:126:PRO:HD2	1:A:213:PRO:HA	1.75	0.67
2:B:89:HIS:CE1	2:B:91:ARG:HE	2.11	0.66
1:H:4:LEU:HD23	1:H:22:CYS:SG	2.36	0.66
1:A:101:ASP:CG	2:B:91:ARG:HH22	2.02	0.66
1:A:53:ILE:HD12	1:A:53:ILE:H	1.61	0.66
1:A:38:ARG:NH2	1:A:46:GLU:OE1	2.28	0.65
1:A:124:LEU:HD21	1:A:141:LEU:HB2	1.79	0.65
1:A:52:ILE:HD11	1:A:97:PHE:CZ	2.31	0.64
2:L:33:PHE:HB3	2:L:51:THR:HG22	1.79	0.64
3:C:462:ILE:HD12	3:C:605:PRO:HG2	1.81	0.63
2:B:89:HIS:HE1	2:B:91:ARG:NE	1.95	0.63
3:D:506:VAL:HG21	3:D:537:LEU:HD22	1.79	0.63
2:L:155:GLN:HB3	2:L:158:ASN:HD21	1.64	0.63
3:C:525:PRO:HB2	3:C:527:TYR:CE1	2.30	0.63
2:B:21:LEU:HD13	2:B:73:LEU:HD23	1.81	0.61
3:D:543:ARG:NH1	3:D:598:GLY:O	2.29	0.61
1:A:58:SER:OG	2:B:95:PRO:HB2	2.00	0.61
1:H:93:VAL:HG11	2:L:96:PHE:HE2	1.66	0.60
2:B:14:SER:O	2:B:17:GLU:HG3	2.02	0.59
2:L:136:LEU:HD22	2:L:175:LEU:HD22	1.83	0.59
3:C:543:ARG:HH12	3:C:597:CYS:HA	1.67	0.59
1:H:58:SER:HB3	2:L:95:PRO:HB2	1.84	0.59
3:D:568:PRO:HB2	3:D:580:THR:HG22	1.83	0.58
1:H:29:PHE:CE2	1:H:34:VAL:HG21	2.39	0.58
2:B:29:VAL:HG13	2:B:90:HIS:CE1	2.38	0.58
1:A:52:ILE:HD11	1:A:97:PHE:CE1	2.40	0.57
3:C:509:PHE:CZ	3:C:601:PRO:HB3	2.40	0.57
1:H:148:GLU:CG	1:H:149:PRO:HA	2.32	0.57
3:C:548:ASN:HB2	3:C:549:TRP:CE3	2.39	0.57
3:C:584:ASP:HB2	3:C:594:TYR:HB2	1.87	0.56
2:L:124:GLN:HG2	2:L:129:THR:O	2.05	0.56
1:A:83:LYS:HG3	1:A:84:SER:H	1.71	0.56
1:A:31:ARG:NH1	1:A:100(D):LEU:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:584:ASP:OD1	3:C:593:THR:HA	2.05	0.56
3:D:461:PRO:HG2	3:D:464:GLU:HG2	1.88	0.56
2:B:11:LEU:HB3	2:B:104:LEU:HD23	1.86	0.55
2:L:35:TRP:CE2	2:L:73:LEU:HB2	2.41	0.55
1:H:193:THR:HG22	1:H:210:ARG:HH21	1.72	0.55
2:B:92:GLY:HA2	3:C:443:TYR:OH	2.07	0.54
1:A:7:SER:HB2	1:A:21:SER:H	1.71	0.54
2:B:163:VAL:HG22	2:B:175:LEU:HD12	1.88	0.54
2:B:184:ALA:O	2:B:188:LYS:HG3	2.07	0.54
2:B:144:ALA:HB2	2:B:198:HIS:HD2	1.73	0.53
3:D:506:VAL:HG22	3:D:554:TRP:HB3	1.90	0.53
1:H:29:PHE:CE2	1:H:52(A):PRO:HG3	2.43	0.53
2:L:49:TYR:HD1	2:L:50:GLU:HG3	1.73	0.53
2:B:137:ASN:O	2:B:174:SER:OG	2.20	0.53
1:H:41:PRO:HD3	1:H:87:THR:O	2.10	0.52
3:D:557:SER:HB2	6:N:1:NAG:H82	1.92	0.52
1:H:15:GLY:N	1:H:82(C):LEU:O	2.31	0.52
1:A:52(A):PRO:HG2	1:A:53:ILE:HD12	1.93	0.51
1:A:11:VAL:HG22	1:A:110:ILE:HB	1.92	0.51
1:A:200:HIS:CD2	1:A:202:PRO:HD2	2.45	0.51
3:D:494:CYS:HB2	3:D:541:ASN:OD1	2.10	0.51
1:A:30:GLY:C	1:A:32:ASP:H	2.18	0.51
3:D:424:ARG:HG3	3:D:527:TYR:CD2	2.45	0.51
3:D:544:PRO:HG2	3:D:550:PHE:CE1	2.45	0.51
3:C:511:PRO:HB2	3:C:638:HIS:CG	2.46	0.51
2:B:30:ASP:OD1	2:B:90:HIS:HE1	1.94	0.51
3:C:435:THR:HB	3:C:437:PHE:HD1	1.76	0.51
1:H:6:GLN:HG2	1:H:107:THR:OG1	2.11	0.51
1:H:137:ALA:HB2	1:H:183:THR:HG22	1.93	0.51
2:L:108:ARG:HH12	2:L:111:ALA:HB2	1.77	0.50
1:A:154:TRP:CZ3	1:A:196:CYS:HB3	2.47	0.50
2:L:31:LYS:O	2:L:51:THR:HG23	2.12	0.50
1:A:145:TYR:OH	1:A:148:GLU:OE2	2.21	0.49
1:A:183:THR:HG21	2:B:137:ASN:ND2	2.26	0.49
1:A:52:ILE:HG22	1:A:56:THR:HB	1.93	0.49
2:B:29:VAL:HG13	2:B:90:HIS:ND1	2.27	0.49
3:C:506:VAL:HG22	3:C:554:TRP:HB3	1.94	0.49
3:C:560:PHE:CD2	5:G:1:NAG:H5	2.48	0.49
3:D:456:MET:CE	3:D:485:TYR:HD2	2.24	0.49
3:D:589:HIS:HE1	3:D:591:GLU:HB2	1.78	0.49
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:422:ILE:H	3:D:422:ILE:HD12	1.77	0.49
1:A:57:SER:HB3	1:A:59:TYR:CZ	2.48	0.48
3:C:580:THR:O	3:C:582:PRO:HD3	2.13	0.48
2:L:18:ARG:HG3	2:L:76:SER:HA	1.95	0.48
2:B:89:HIS:CE1	2:B:91:ARG:HG3	2.49	0.48
1:A:31:ARG:O	1:A:31:ARG:HG2	2.14	0.48
1:A:189:LEU:HB3	1:A:213:PRO:HG2	1.96	0.48
2:B:108:ARG:HG2	2:B:109:THR:N	2.28	0.48
2:B:6:GLN:O	2:B:100:GLN:NE2	2.41	0.48
2:B:115:VAL:HG12	2:B:207:LYS:HG3	1.96	0.48
1:H:47:PRO:HG3	2:L:98:PHE:HD2	1.79	0.48
1:A:99:ASP:HB3	3:C:444:THR:H	1.79	0.47
2:B:8:PRO:HG3	2:B:11:LEU:HD13	1.95	0.47
3:D:433:LEU:HB2	3:D:435:THR:HG23	1.97	0.47
3:D:472:ILE:CD1	3:D:571:ILE:HG22	2.44	0.47
3:D:509:PHE:CZ	3:D:601:PRO:HB3	2.49	0.47
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.95	0.47
3:D:484:PRO:HD2	3:D:485:TYR:HD1	1.79	0.47
3:D:595:THR:HG22	3:D:633:VAL:HG22	1.96	0.47
1:A:126:PRO:HG2	1:A:213:PRO:HG3	1.96	0.47
3:D:484:PRO:HD2	3:D:485:TYR:CD1	2.50	0.47
1:A:70:THR:OG1	1:A:79:TYR:HB2	2.15	0.46
3:D:423:ASN:HA	3:D:529:TRP:CE2	2.50	0.46
2:L:48:ILE:HD13	2:L:54:ARG:HA	1.97	0.46
3:C:509:PHE:CE2	3:C:601:PRO:HB3	2.50	0.46
1:H:12:LYS:HG3	1:H:18:VAL:HB	1.97	0.46
1:A:39:GLN:HG3	1:A:44:GLY:O	2.15	0.46
3:D:534:THR:HG21	7:D:701:NAG:O6	2.16	0.46
1:H:52:ILE:HD11	2:L:95(A):PRO:HD2	1.98	0.46
3:C:510:THR:HG22	3:C:548:ASN:O	2.15	0.46
1:H:31:ARG:HE	1:H:100(C):PHE:HB3	1.81	0.46
1:A:4:LEU:HD23	1:A:22:CYS:SG	2.56	0.46
3:C:472:ILE:HG12	3:C:571:ILE:HG22	1.97	0.46
3:D:422:ILE:HG23	1:H:100(C):PHE:HE1	1.81	0.45
3:D:631:MET:HE2	3:D:631:MET:HB3	1.61	0.45
1:A:98:GLY:O	1:A:100(E):THR:HG23	2.16	0.45
3:D:496:THR:HG23	3:D:538:ILE:HA	1.99	0.45
2:L:163:VAL:HG22	2:L:175:LEU:HD12	1.98	0.45
2:B:108:ARG:NH2	2:B:109:THR:O	2.45	0.45
3:C:467:GLN:HG3	3:C:588:LYS:O	2.16	0.45
3:C:508:CYS:HA	3:C:552:CYS:HA	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:124:LEU:HD21	2:L:133:VAL:HG21	1.99	0.45
3:D:506:VAL:HG22	3:D:554:TRP:CB	2.46	0.45
3:C:506:VAL:HG22	3:C:554:TRP:CB	2.47	0.45
1:H:168:ALA:HB2	1:H:178:LEU:HD12	1.98	0.45
1:H:153:SER:OG	1:H:197:ASN:HB2	2.17	0.45
2:L:13:LEU:HA	2:L:13:LEU:HD23	1.74	0.45
1:A:119:PRO:HD2	1:A:205:THR:HG21	1.98	0.45
3:C:506:VAL:HG21	3:C:537:LEU:HD22	1.97	0.45
3:D:589:HIS:CE1	3:D:591:GLU:HB2	2.52	0.45
1:H:101:ASP:OD2	2:L:36:TYR:OH	2.33	0.45
1:A:29:PHE:HB2	1:A:52(A):PRO:HG3	1.99	0.45
2:L:136:LEU:HB2	2:L:175:LEU:HB3	1.98	0.44
1:H:145:TYR:O	1:H:176:TYR:HB2	2.18	0.44
3:C:509:PHE:C	3:C:510:THR:O	2.58	0.44
2:L:66:GLY:HA3	2:L:71:PHE:HA	1.99	0.44
6:N:3:BMA:H62	6:N:5:MAN:H2	1.79	0.44
2:B:189:HIS:O	2:B:211:ARG:NE	2.49	0.44
1:H:195:ILE:HG12	1:H:210:ARG:HA	1.98	0.44
3:C:588:LYS:HA	3:C:588:LYS:HD3	1.76	0.44
1:H:20:VAL:HG22	1:H:80:MET:HE2	1.99	0.44
1:H:200:HIS:CD2	1:H:202:PRO:HD2	2.53	0.44
6:N:1:NAG:H62	6:N:2:NAG:C7	2.47	0.44
1:H:163:VAL:HG22	1:H:182:VAL:HB	1.99	0.44
2:L:34:ALA:HB3	2:L:89:HIS:HD2	1.83	0.43
2:B:2:ILE:HD12	2:B:2:ILE:H	1.84	0.43
3:D:548:ASN:OD1	3:D:549:TRP:N	2.46	0.43
2:B:13:LEU:O	2:B:107:LYS:N	2.51	0.43
3:C:636:VAL:HG13	3:C:638:HIS:CD2	2.54	0.43
1:H:93:VAL:O	1:H:93:VAL:HG13	2.18	0.43
2:L:124:GLN:O	2:L:127:SER:OG	2.35	0.43
1:A:165:THR:HA	1:A:180:SER:HA	2.01	0.43
1:H:6:GLN:NE2	1:H:90:TYR:O	2.52	0.42
1:H:67:VAL:HA	1:H:81:GLU:O	2.18	0.42
2:L:17:GLU:HG3	2:L:18:ARG:N	2.34	0.42
1:A:30:GLY:C	1:A:32:ASP:N	2.77	0.42
1:A:152:VAL:HG11	1:A:180:SER:OG	2.19	0.42
1:H:12:LYS:HE2	1:H:17:SER:O	2.18	0.42
2:L:50:GLU:O	2:L:52:SER:N	2.47	0.42
3:C:483:ARG:HA	3:C:484:PRO:HD3	1.91	0.42
1:A:126:PRO:HD2	1:A:213:PRO:CA	2.47	0.42
2:L:108:ARG:HG2	2:L:109:THR:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:29:PHE:HE2	1:H:34:VAL:HG21	1.84	0.42
1:H:112:SER:HB2	1:H:174:GLY:HA2	2.02	0.42
1:A:36:TRP:CD1	1:A:69:PHE:CE1	3.08	0.41
2:B:134:CYS:HB2	2:B:148:TRP:CZ2	2.55	0.41
3:C:543:ARG:NH1	3:C:597:CYS:HA	2.34	0.41
3:D:555:MET:HG3	3:D:560:PHE:C	2.46	0.41
3:D:630:ARG:HB2	3:D:639:ARG:NH1	2.35	0.41
1:H:40:ALA:HB3	1:H:43:GLN:OE1	2.21	0.41
2:B:27:GLN:O	2:B:69:THR:HG22	2.21	0.41
3:C:611:TYR:CZ	3:C:614:ARG:HA	2.56	0.41
2:L:155:GLN:HB3	2:L:158:ASN:ND2	2.32	0.41
1:A:1:GLN:O	1:A:1:GLN:HG3	2.21	0.41
3:C:545:PRO:HB3	3:C:634:GLY:HA3	2.01	0.41
2:L:108:ARG:HG2	2:L:108:ARG:HH11	1.85	0.41
2:L:108:ARG:NH1	2:L:111:ALA:HB2	2.36	0.40
3:C:493:GLN:HG2	3:C:541:ASN:OD1	2.21	0.40
3:D:548:ASN:HB2	3:D:549:TRP:CE3	2.56	0.40
2:B:48:ILE:HD13	2:B:73:LEU:HD13	2.03	0.40
2:B:145:LYS:HB3	2:B:197:THR:HB	2.02	0.40
3:D:509:PHE:CE2	3:D:601:PRO:HB3	2.56	0.40
1:H:112:SER:HB2	1:H:174:GLY:CA	2.51	0.40
1:H:152:VAL:HG22	1:H:198:VAL:HG22	2.02	0.40
2:B:11:LEU:HD12	2:B:11:LEU:HA	1.76	0.40
1:H:101:ASP:HB3	2:L:91:ARG:NH1	2.36	0.40
1:H:189:LEU:HD23	1:H:189:LEU:HA	1.80	0.40
3:C:430:ASN:OD1	3:C:430:ASN:N	2.54	0.40
3:C:630:ARG:HD2	3:C:637:GLU:OE2	2.21	0.40
2:L:47:LEU:HD11	2:L:86:TYR:HE1	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	217/236 (92%)	203 (94%)	14 (6%)	0	100	100
1	H	216/236 (92%)	203 (94%)	13 (6%)	0	100	100
2	B	213/216 (99%)	203 (95%)	10 (5%)	0	100	100
2	L	212/216 (98%)	201 (95%)	11 (5%)	0	100	100
3	C	203/262 (78%)	195 (96%)	7 (3%)	1 (0%)	24	56
3	D	219/262 (84%)	206 (94%)	12 (6%)	1 (0%)	24	56
All	All	1280/1428 (90%)	1211 (95%)	67 (5%)	2 (0%)	43	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	510	THR
3	D	510	THR

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	184/198 (93%)	184 (100%)	0	100	100
1	H	182/198 (92%)	182 (100%)	0	100	100
2	B	187/188 (100%)	187 (100%)	0	100	100
2	L	186/188 (99%)	186 (100%)	0	100	100
3	C	182/219 (83%)	182 (100%)	0	100	100
3	D	187/219 (85%)	187 (100%)	0	100	100
All	All	1108/1210 (92%)	1108 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	GLN

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Mol	Chain	Res	Type
1	A	171	GLN
1	A	192	GLN
2	B	89	HIS
2	B	90	HIS
2	B	158	ASN
2	B	160	GLN
3	D	421	HIS
3	D	434	HIS
1	H	192	GLN

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 ⓘ

22 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	E	1	4,3	14,14,15	0.67	0	17,19,21	1.69	4 (23%)
4	NAG	E	2	4	14,14,15	0.49	0	17,19,21	1.38	5 (29%)
4	NAG	F	1	4,3	14,14,15	0.43	0	17,19,21	1.04	1 (5%)
4	NAG	F	2	4	14,14,15	0.47	0	17,19,21	1.08	2 (11%)
5	NAG	G	1	3,5	14,14,15	0.48	0	17,19,21	1.08	1 (5%)
5	NAG	G	2	5	14,14,15	0.57	0	17,19,21	1.02	1 (5%)
5	BMA	G	3	5	11,11,12	0.56	0	15,15,17	0.83	1 (6%)
4	NAG	I	1	4,3	14,14,15	0.49	0	17,19,21	1.12	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	I	2	4	14,14,15	0.47	0	17,19,21	0.78	0
4	NAG	J	1	4,3	14,14,15	0.57	0	17,19,21	1.16	3 (17%)
4	NAG	J	2	4	14,14,15	0.35	0	17,19,21	0.86	0
4	NAG	K	1	4,3	14,14,15	0.48	0	17,19,21	0.75	0
4	NAG	K	2	4	14,14,15	0.73	1 (7%)	17,19,21	0.81	0
4	NAG	M	1	4,3	14,14,15	0.39	0	17,19,21	1.00	2 (11%)
4	NAG	M	2	4	14,14,15	0.79	1 (7%)	17,19,21	1.00	1 (5%)
6	NAG	N	1	6,3	14,14,15	0.55	0	17,19,21	0.94	0
6	NAG	N	2	6	14,14,15	0.59	0	17,19,21	0.86	0
6	BMA	N	3	6	11,11,12	0.27	0	15,15,17	0.91	1 (6%)
6	MAN	N	4	6	11,11,12	0.66	0	15,15,17	0.75	0
6	MAN	N	5	6	11,11,12	0.66	0	15,15,17	0.76	0
4	NAG	O	1	4,3	14,14,15	0.51	0	17,19,21	0.98	1 (5%)
4	NAG	O	2	4	14,14,15	0.60	0	17,19,21	0.67	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	1	4,3	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	5/6/23/26	0/1/1/1
4	NAG	F	1	4,3	-	4/6/23/26	0/1/1/1
4	NAG	F	2	4	-	4/6/23/26	0/1/1/1
5	NAG	G	1	3,5	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	4/6/23/26	0/1/1/1
5	BMA	G	3	5	-	2/2/19/22	0/1/1/1
4	NAG	I	1	4,3	-	3/6/23/26	0/1/1/1
4	NAG	I	2	4	-	5/6/23/26	0/1/1/1
4	NAG	J	1	4,3	-	2/6/23/26	0/1/1/1
4	NAG	J	2	4	-	1/6/23/26	0/1/1/1
4	NAG	K	1	4,3	-	0/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	M	1	4,3	-	4/6/23/26	0/1/1/1
4	NAG	M	2	4	-	1/6/23/26	0/1/1/1
6	NAG	N	1	6,3	-	2/6/23/26	0/1/1/1
6	NAG	N	2	6	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BMA	N	3	6	-	1/2/19/22	0/1/1/1
6	MAN	N	4	6	-	1/2/19/22	0/1/1/1
6	MAN	N	5	6	-	0/2/19/22	0/1/1/1
4	NAG	O	1	4,3	-	3/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	2	NAG	C1-C2	2.59	1.55	1.52
4	K	2	NAG	C1-C2	2.11	1.55	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1	NAG	C1-O5-C5	3.49	116.86	112.19
4	E	1	NAG	O4-C4-C3	3.38	118.35	110.38
4	E	1	NAG	O5-C5-C6	-3.29	101.27	107.66
4	I	1	NAG	C2-N2-C7	3.07	127.01	122.90
5	G	1	NAG	O5-C1-C2	-3.03	106.60	111.29
4	O	1	NAG	C1-O5-C5	2.97	116.17	112.19
4	J	1	NAG	O5-C5-C6	2.82	113.15	107.66
4	E	2	NAG	C1-O5-C5	2.70	115.81	112.19
4	E	2	NAG	C2-N2-C7	2.70	126.52	122.90
4	F	2	NAG	C2-N2-C7	2.70	126.52	122.90
4	M	1	NAG	C2-N2-C7	-2.39	119.70	122.90
4	F	1	NAG	O5-C1-C2	-2.34	107.67	111.29
5	G	2	NAG	O5-C5-C6	2.30	112.14	107.66
4	E	2	NAG	C4-C3-C2	-2.28	107.67	111.02
4	M	1	NAG	O3-C3-C2	-2.14	104.95	109.40
4	M	2	NAG	O5-C1-C2	-2.14	107.99	111.29
4	E	2	NAG	O5-C1-C2	-2.10	108.04	111.29
4	F	2	NAG	C1-O5-C5	2.10	115.00	112.19
4	E	1	NAG	O4-C4-C5	-2.07	104.24	109.32
4	J	1	NAG	C1-O5-C5	2.04	114.92	112.19
4	J	1	NAG	C1-C2-N2	-2.04	107.22	110.43
5	G	3	BMA	O2-C2-C1	2.02	113.84	109.22
4	E	2	NAG	C6-C5-C4	-2.01	108.08	113.02
6	N	3	BMA	O3-C3-C2	-2.01	105.94	110.05

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	2	NAG	C8-C7-N2-C2
4	E	2	NAG	O7-C7-N2-C2
4	M	1	NAG	O7-C7-N2-C2
5	G	2	NAG	C8-C7-N2-C2
5	G	2	NAG	O7-C7-N2-C2
5	G	2	NAG	O5-C5-C6-O6
4	M	1	NAG	C8-C7-N2-C2
4	E	1	NAG	O7-C7-N2-C2
5	G	2	NAG	C4-C5-C6-O6
4	E	1	NAG	C8-C7-N2-C2
4	J	1	NAG	C8-C7-N2-C2
4	J	1	NAG	O7-C7-N2-C2
4	O	1	NAG	C8-C7-N2-C2
4	I	2	NAG	O5-C5-C6-O6
5	G	3	BMA	O5-C5-C6-O6
4	I	2	NAG	C4-C5-C6-O6
4	F	1	NAG	C8-C7-N2-C2
4	F	1	NAG	O5-C5-C6-O6
5	G	3	BMA	C4-C5-C6-O6
6	N	1	NAG	O5-C5-C6-O6
4	F	1	NAG	O7-C7-N2-C2
4	O	1	NAG	O7-C7-N2-C2
4	O	2	NAG	C8-C7-N2-C2
5	G	1	NAG	C8-C7-N2-C2
5	G	1	NAG	O7-C7-N2-C2
6	N	2	NAG	C8-C7-N2-C2
4	I	2	NAG	C8-C7-N2-C2
4	K	2	NAG	C8-C7-N2-C2
4	O	2	NAG	O7-C7-N2-C2
6	N	2	NAG	O7-C7-N2-C2
4	F	2	NAG	O5-C5-C6-O6
4	M	1	NAG	O5-C5-C6-O6
4	K	2	NAG	O7-C7-N2-C2
4	I	2	NAG	O7-C7-N2-C2
4	E	2	NAG	O5-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6
4	O	1	NAG	O5-C5-C6-O6
4	J	2	NAG	O5-C5-C6-O6
6	N	1	NAG	C4-C5-C6-O6
6	N	3	BMA	O5-C5-C6-O6
6	N	4	MAN	O5-C5-C6-O6
4	F	2	NAG	C8-C7-N2-C2

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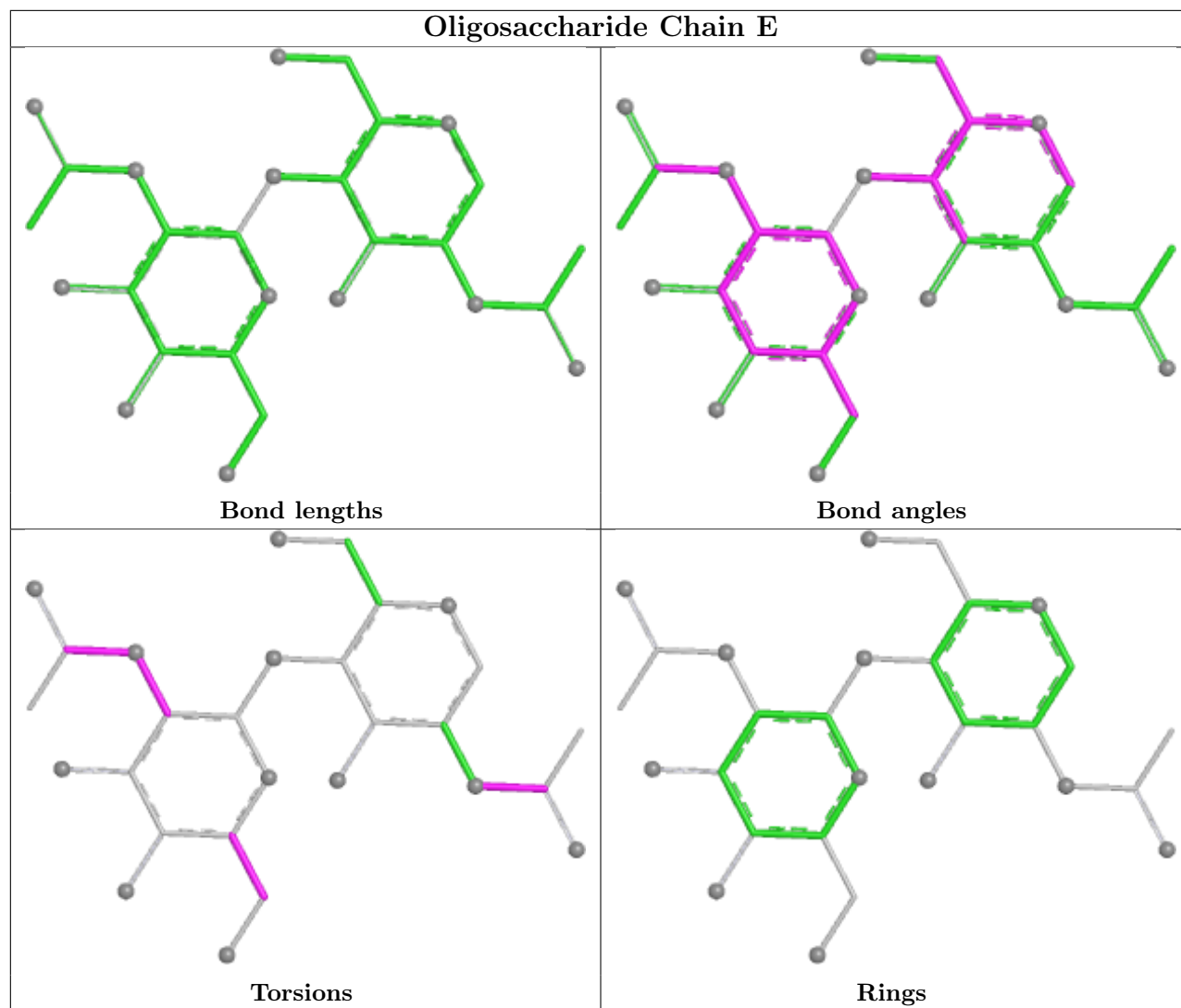
Mol	Chain	Res	Type	Atoms
4	E	2	NAG	C1-C2-N2-C7
4	I	1	NAG	C8-C7-N2-C2
4	I	1	NAG	O7-C7-N2-C2
4	F	1	NAG	C4-C5-C6-O6
4	F	2	NAG	O7-C7-N2-C2
4	I	1	NAG	C3-C2-N2-C7
4	F	2	NAG	C4-C5-C6-O6
4	I	2	NAG	C1-C2-N2-C7
4	M	1	NAG	C4-C5-C6-O6
4	E	2	NAG	C3-C2-N2-C7

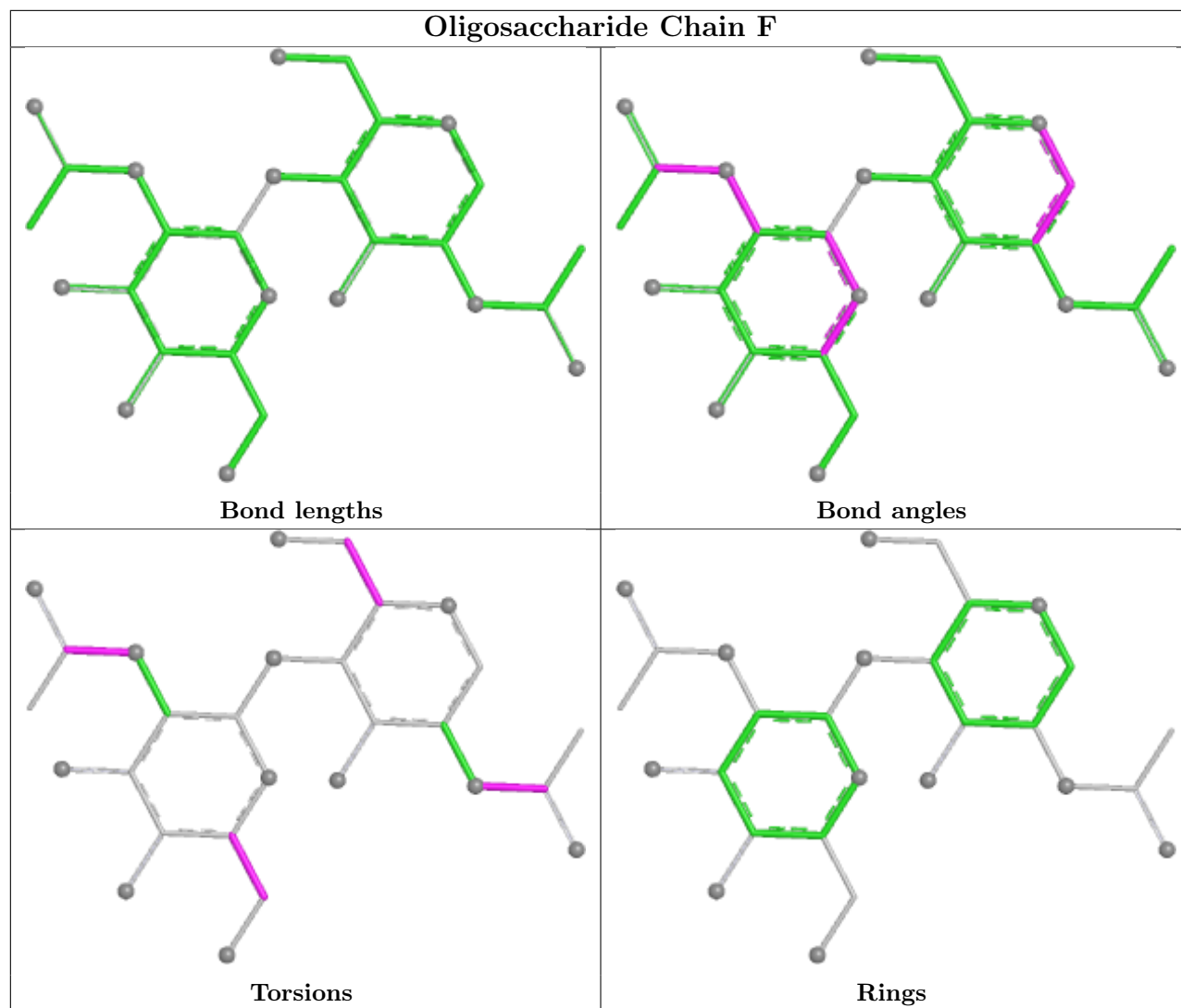
There are no ring outliers.

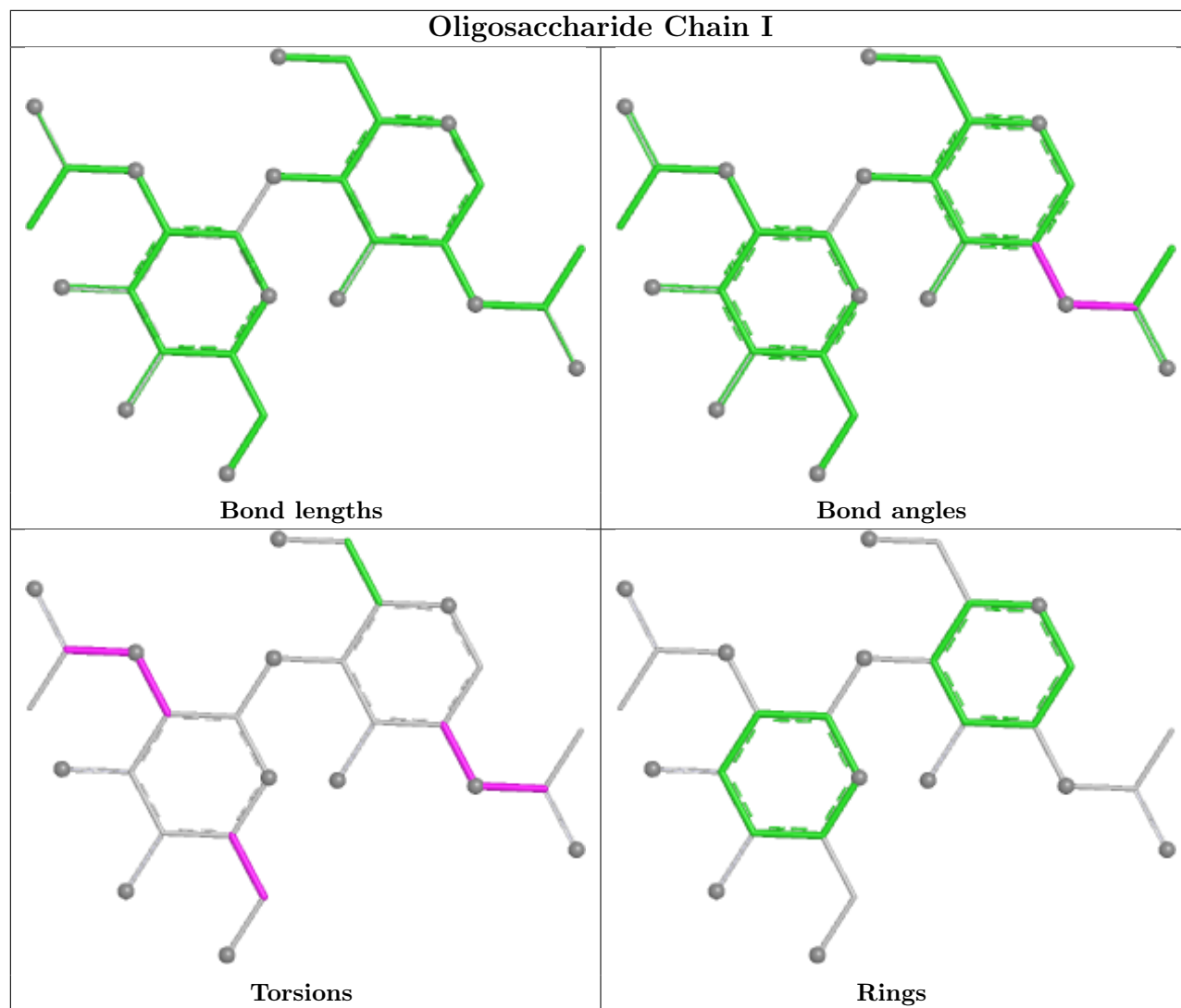
6 monomers are involved in 5 short contacts:

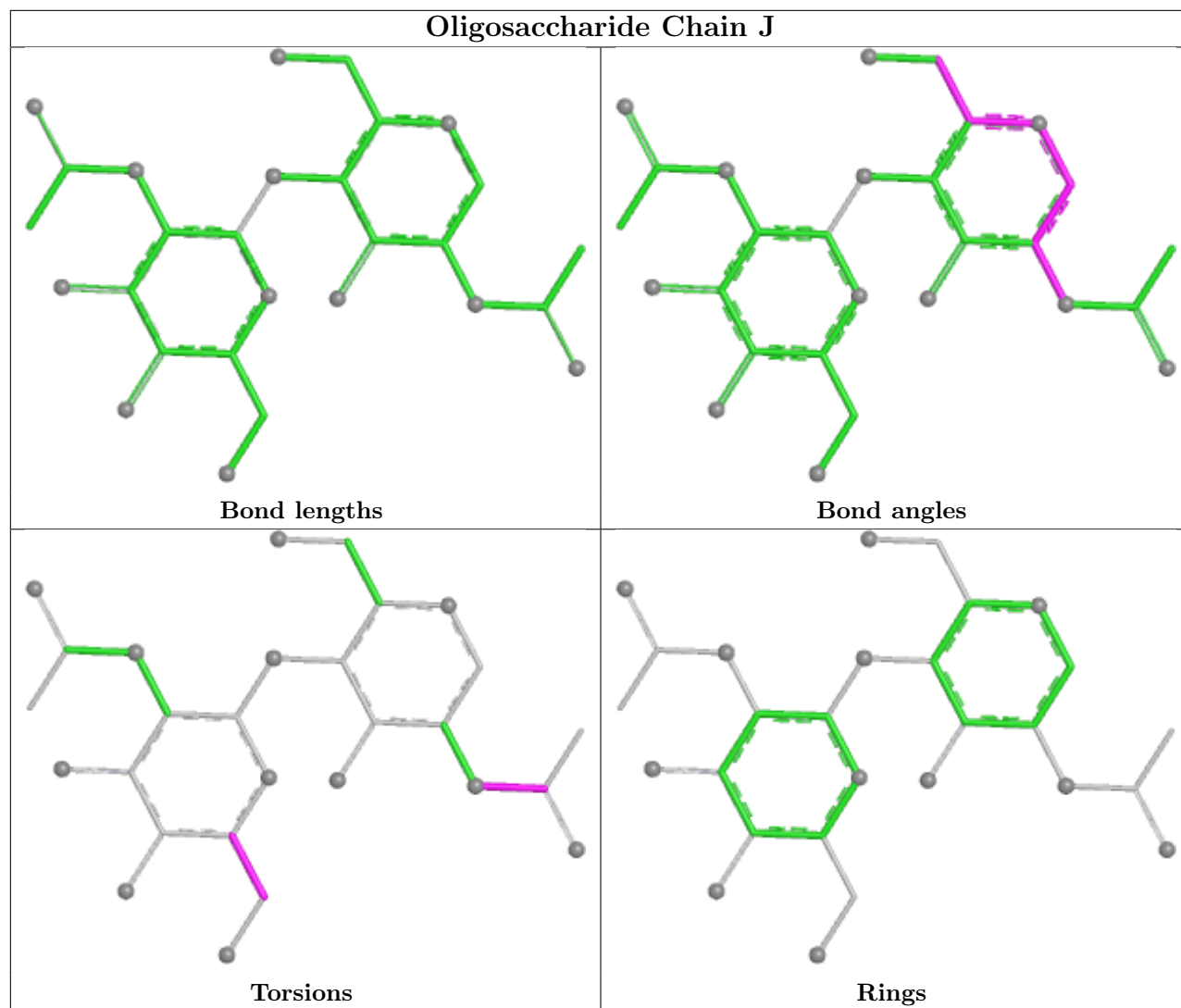
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	1	NAG	1	0
6	N	1	NAG	2	0
6	N	5	MAN	1	0
5	G	1	NAG	1	0
6	N	2	NAG	1	0
6	N	3	BMA	1	0

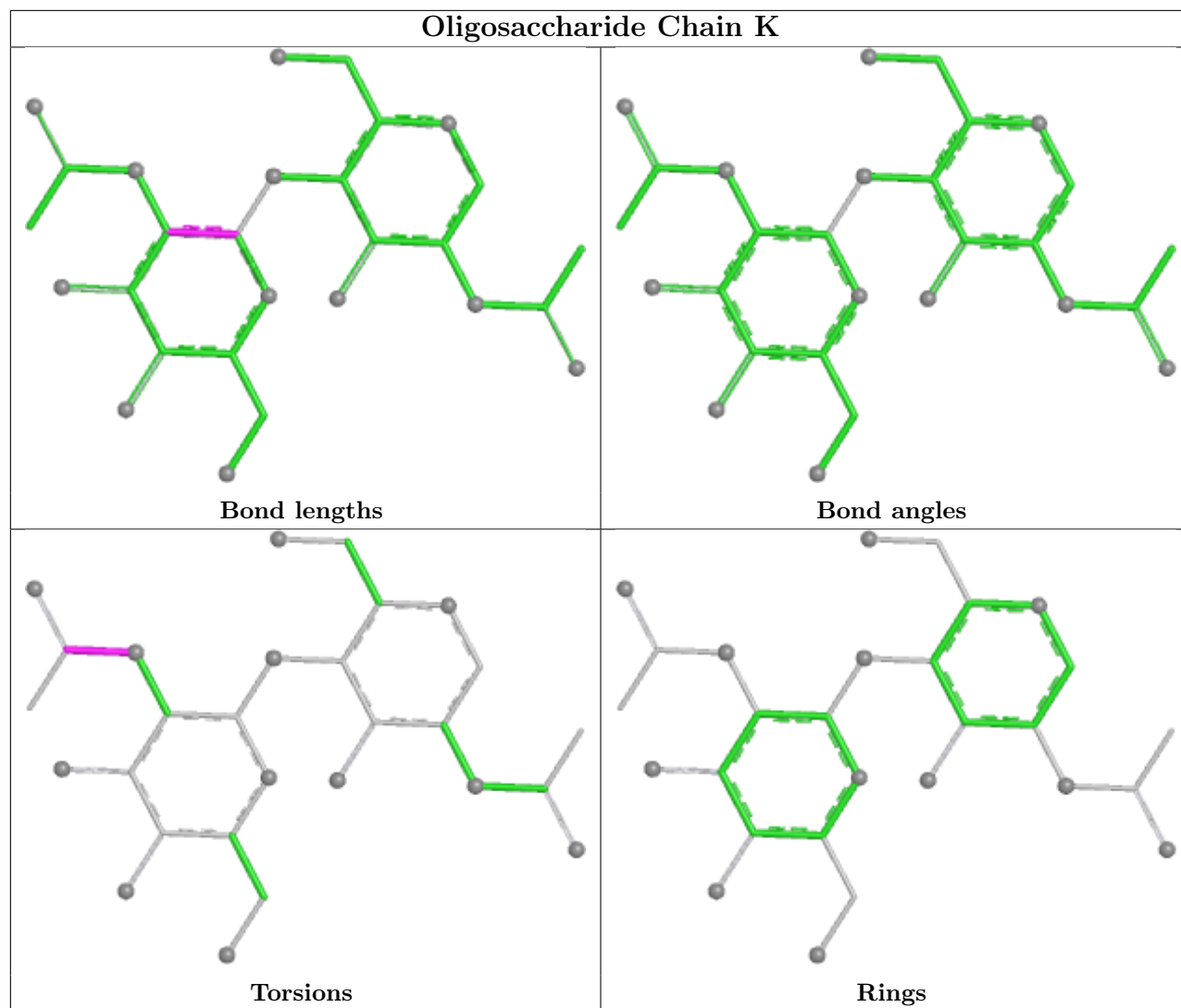
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

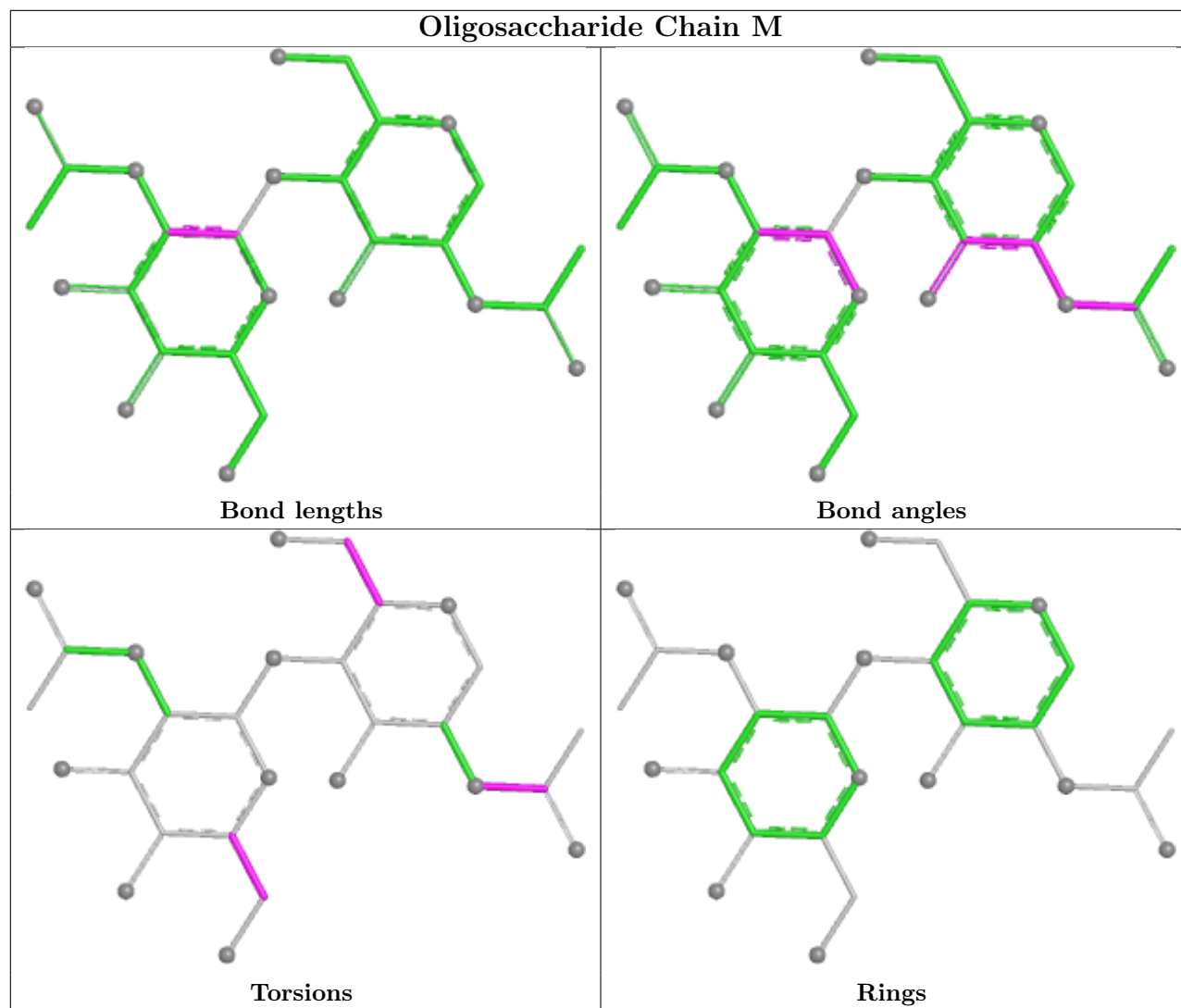


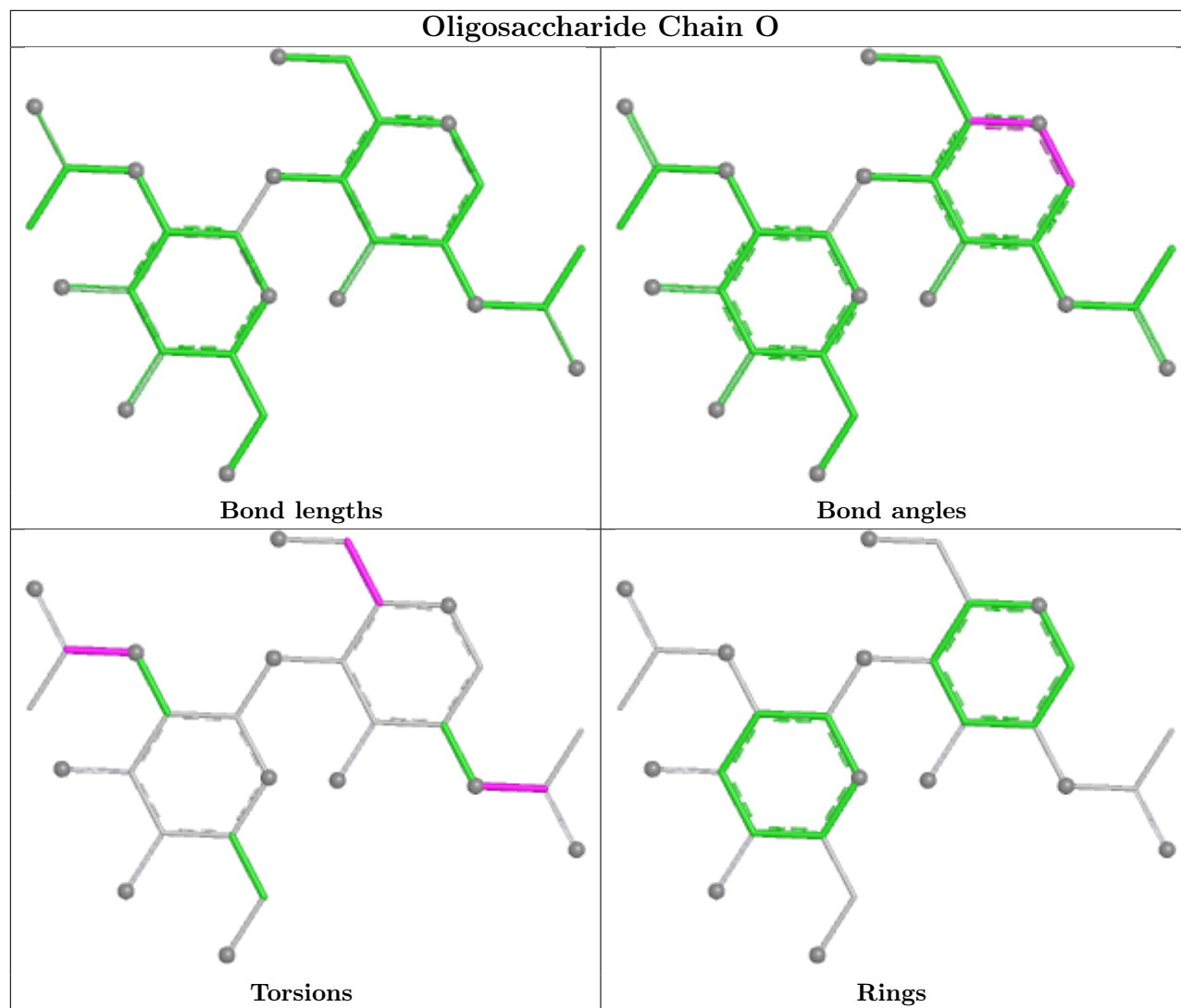


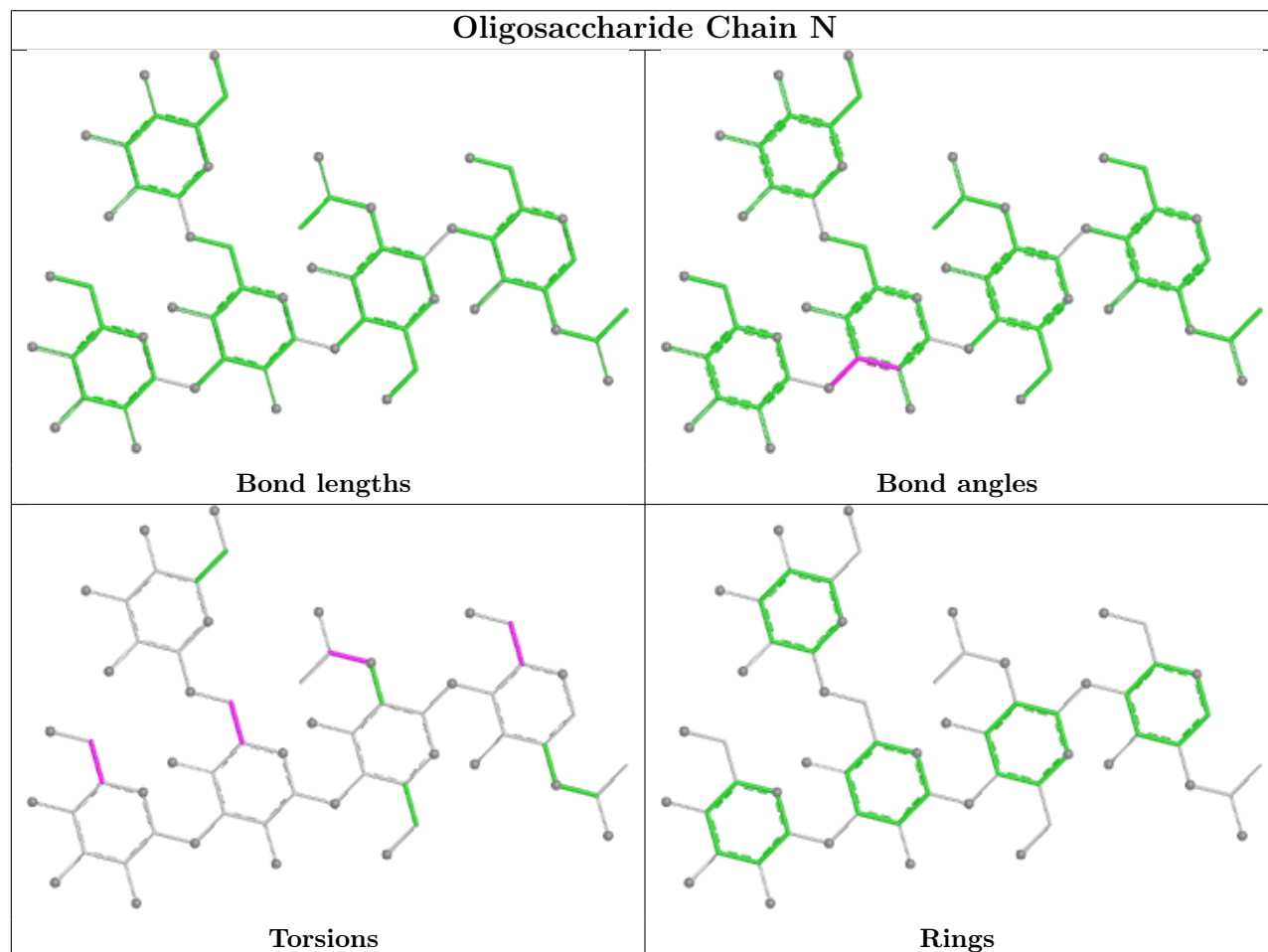
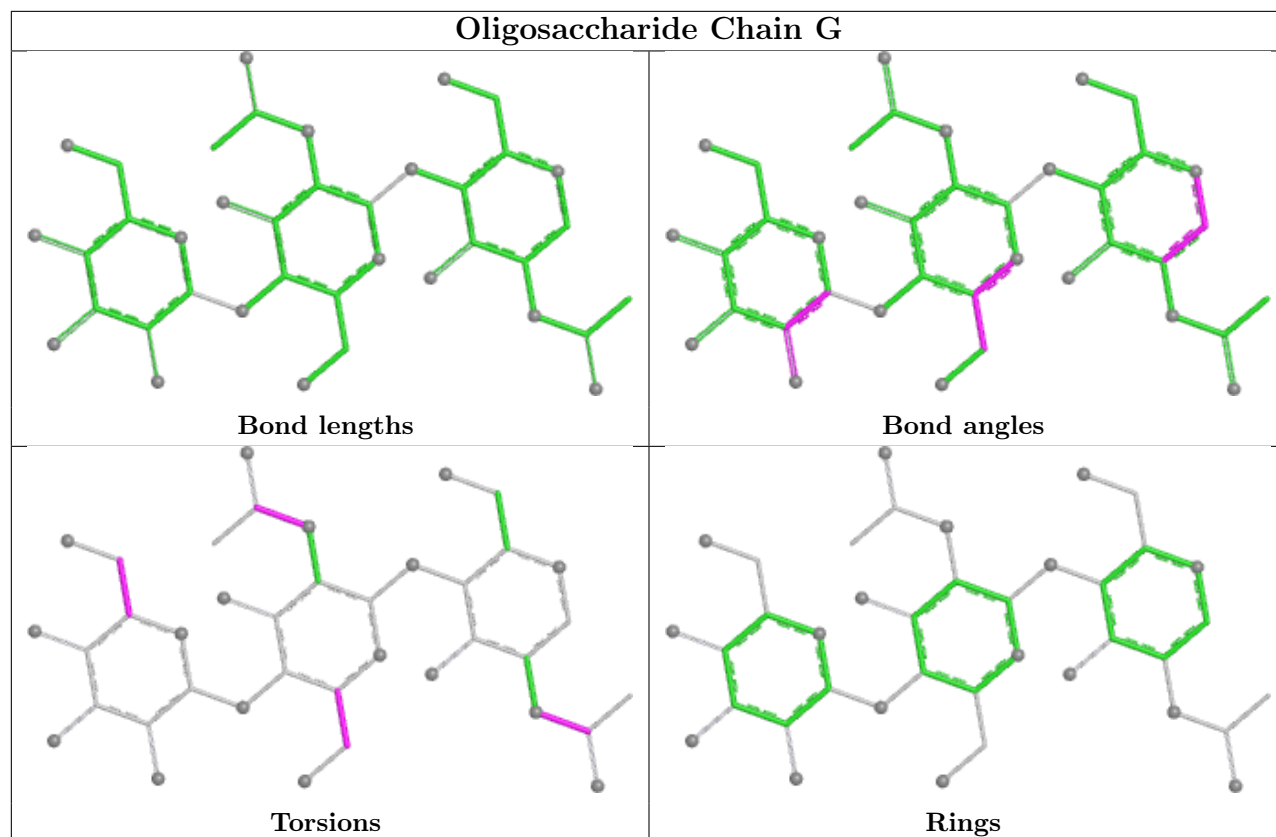












5.6 Ligand geometry

4 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	C	4302	3	14,14,15	0.36	0	17,19,21	0.90	0
7	NAG	D	702	3	14,14,15	0.61	0	17,19,21	1.44	2 (11%)
7	NAG	D	701	3	14,14,15	0.51	0	17,19,21	1.15	1 (5%)
7	NAG	C	4301	3	14,14,15	0.65	0	17,19,21	1.38	3 (17%)

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	C	4302	3	-	3/6/23/26	0/1/1/1
7	NAG	D	702	3	-	3/6/23/26	0/1/1/1
7	NAG	D	701	3	-	2/6/23/26	0/1/1/1
7	NAG	C	4301	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	4301	NAG	C1-O5-C5	3.37	116.70	112.19
7	D	702	NAG	C2-N2-C7	2.89	126.77	122.90
7	D	701	NAG	O5-C5-C6	2.76	113.03	107.66
7	C	4301	NAG	O5-C1-C2	-2.50	107.42	111.29
7	D	702	NAG	O4-C4-C5	2.48	115.44	109.32
7	C	4301	NAG	O5-C5-C6	2.22	111.99	107.66

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	4302	NAG	C1-C2-N2-C7
7	C	4302	NAG	C8-C7-N2-C2
7	C	4302	NAG	O7-C7-N2-C2
7	D	702	NAG	C1-C2-N2-C7
7	D	702	NAG	O7-C7-N2-C2
7	D	702	NAG	C8-C7-N2-C2
7	D	701	NAG	C8-C7-N2-C2
7	D	701	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	701	NAG	1	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	221/236 (93%)	0.33	6 (2%)	56 37	41, 65, 90, 120	0
1	H	220/236 (93%)	0.17	1 (0%)	87 76	40, 54, 81, 109	0
2	B	215/216 (99%)	0.30	1 (0%)	87 76	43, 65, 92, 120	0
2	L	214/216 (99%)	0.38	3 (1%)	73 54	47, 66, 97, 126	0
3	C	211/262 (80%)	0.72	10 (4%)	36 23	54, 91, 127, 182	0
3	D	223/262 (85%)	0.57	12 (5%)	31 20	43, 75, 111, 138	0
All	All	1304/1428 (91%)	0.41	33 (2%)	58 39	40, 68, 109, 182	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	433	LEU	4.6
3	D	478	HIS	3.6
3	D	469	TRP	3.0
3	C	600	GLY	3.0
3	C	469	TRP	2.9
3	D	420	TRP	2.9
1	A	27	GLY	2.9
3	C	571	ILE	2.8
2	L	170	ASP	2.8
3	D	479	GLY	2.8
3	C	430	ASN	2.7
1	A	99	ASP	2.7
3	D	463	ASP	2.7
1	H	29	PHE	2.6
3	D	573	GLY	2.5
3	C	433	LEU	2.4
3	C	528	THR	2.4
1	A	61	GLN	2.4
3	C	473	THR	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	129	THR	2.3
1	A	128	SER	2.3
2	L	154	LEU	2.2
1	A	74	SER	2.2
2	L	60	ALA	2.2
3	C	421	HIS	2.2
3	D	531	GLU	2.2
3	C	458	HIS	2.2
3	D	485	TYR	2.1
3	D	471	PRO	2.1
1	A	2	VAL	2.1
3	C	511	PRO	2.0
3	D	484	PRO	2.0
3	D	476	GLU	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.

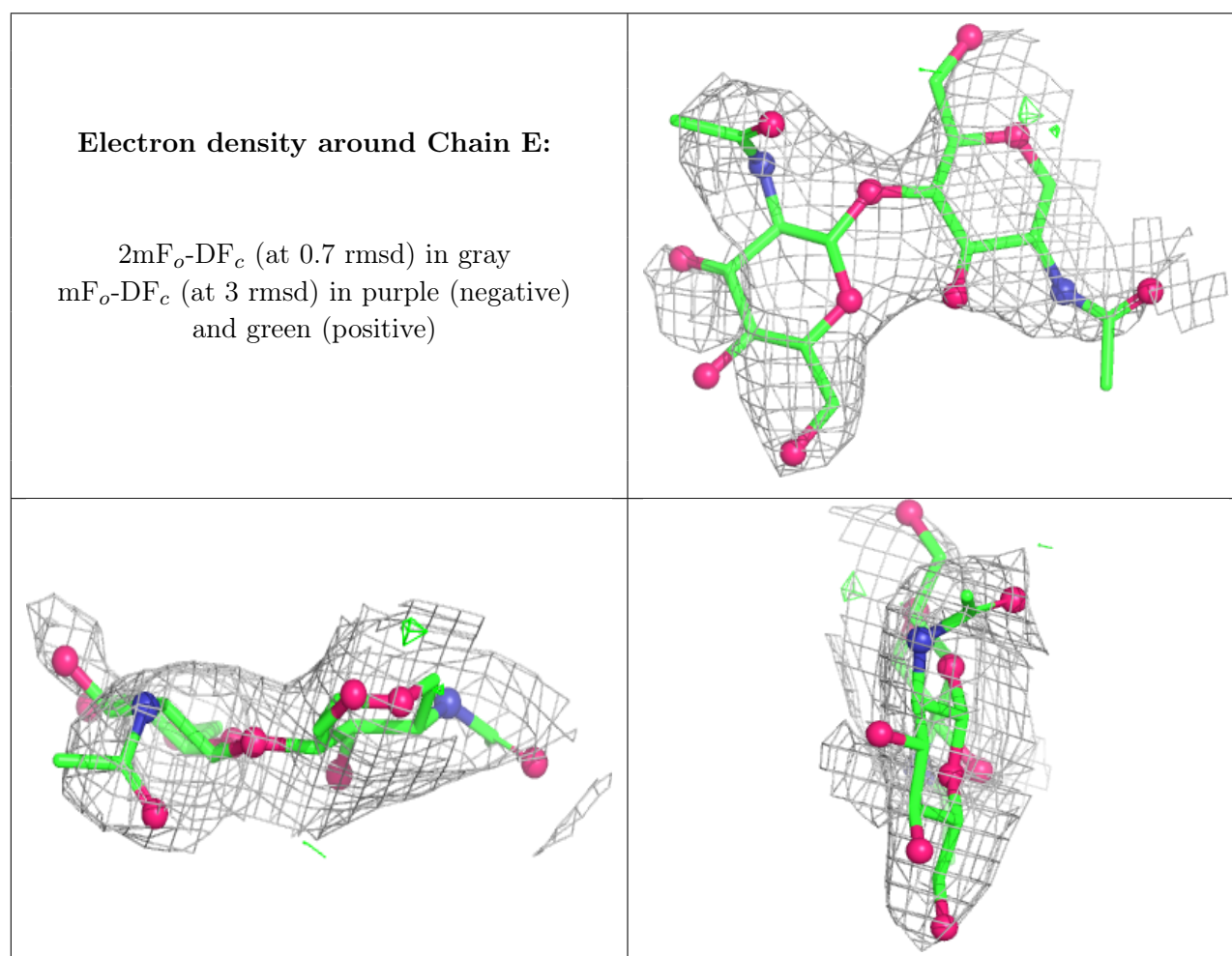
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	E	1	14/15	-	-	83,91,97,97	0
4	NAG	E	2	14/15	-	-	95,99,106,107	0
4	NAG	F	1	14/15	-	-	111,118,122,124	0
4	NAG	F	2	14/15	-	-	105,118,122,124	0
6	BMA	N	3	11/12	0.33	0.15	122,123,128,131	0
6	MAN	N	4	11/12	0.37	0.15	110,123,131,131	0
4	NAG	J	2	14/15	0.38	0.19	92,99,103,104	0
4	NAG	M	2	14/15	0.45	0.18	102,114,119,121	0
6	MAN	N	5	11/12	0.45	0.13	118,122,126,129	0
5	NAG	G	2	14/15	0.46	0.14	92,107,115,119	0
6	NAG	N	2	14/15	0.48	0.19	79,103,114,119	0
4	NAG	K	2	14/15	0.48	0.16	100,113,117,120	0
4	NAG	I	2	14/15	0.54	0.17	88,109,116,116	0
4	NAG	K	1	14/15	0.57	0.19	87,102,112,112	0

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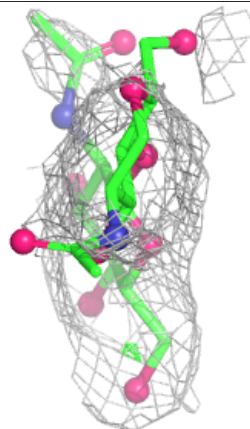
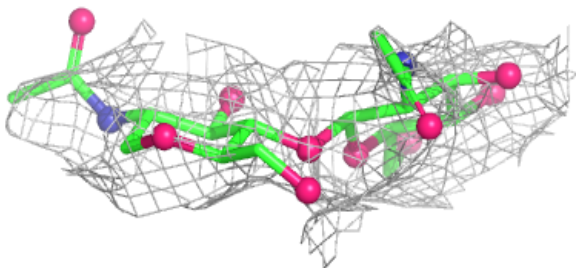
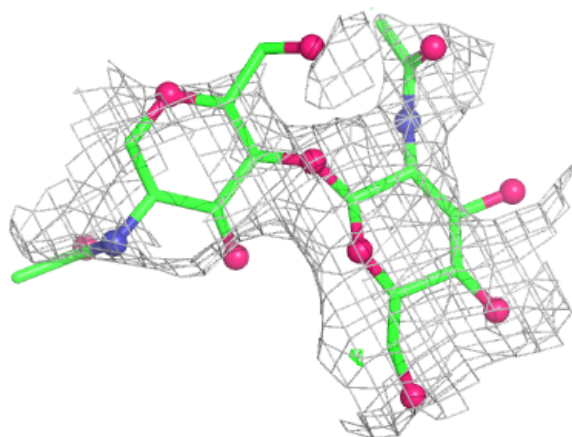
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	M	1	14/15	0.60	0.16	105,113,117,120	0
4	NAG	O	2	14/15	0.67	0.13	89,96,103,103	0
5	BMA	G	3	11/12	-	-	101,114,120,120	0
4	NAG	J	1	14/15	0.69	0.18	79,91,98,99	0
5	NAG	G	1	14/15	0.71	0.15	88,93,101,101	0
4	NAG	I	1	14/15	0.71	0.17	87,98,105,106	0
6	NAG	N	1	14/15	0.76	0.14	72,78,85,93	0
4	NAG	O	1	14/15	0.79	0.13	79,91,94,97	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.



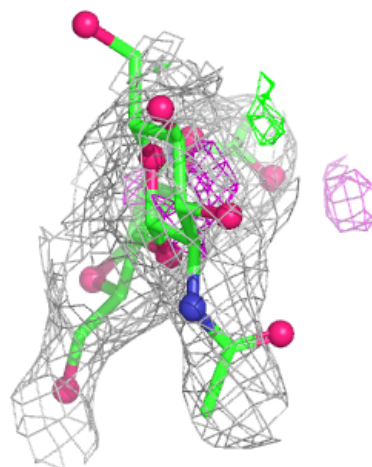
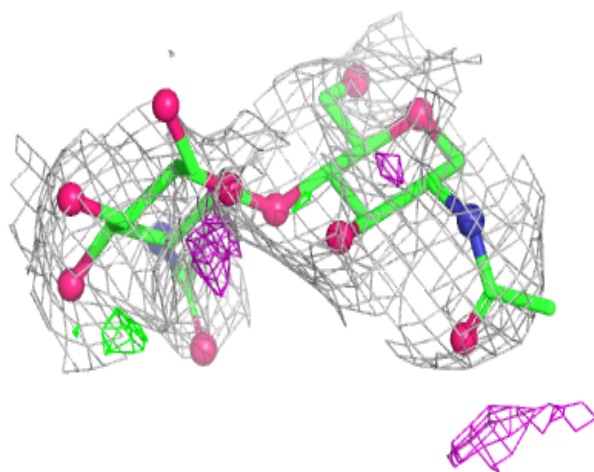
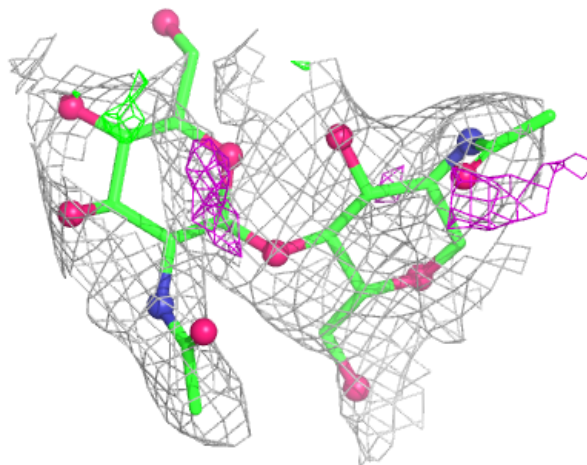
Electron density around Chain F:

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



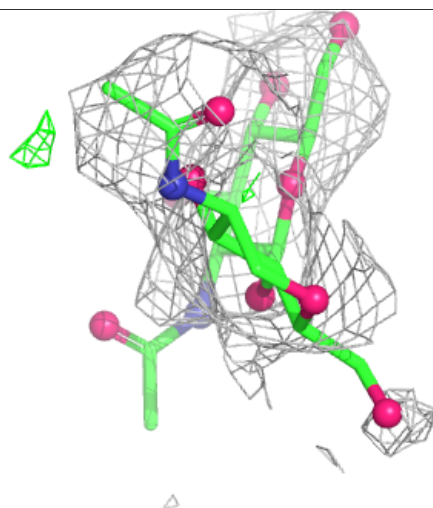
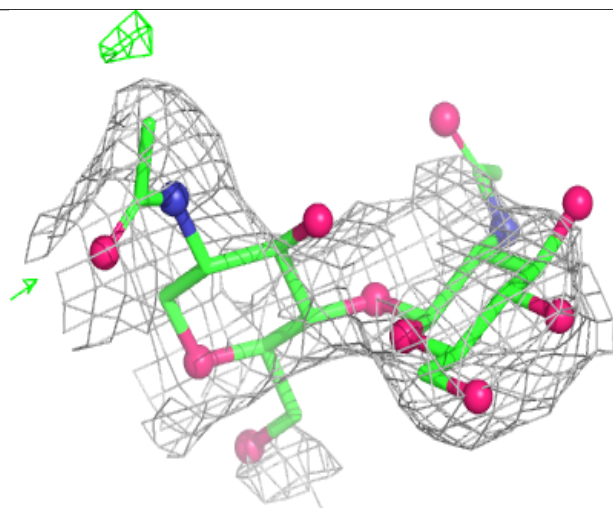
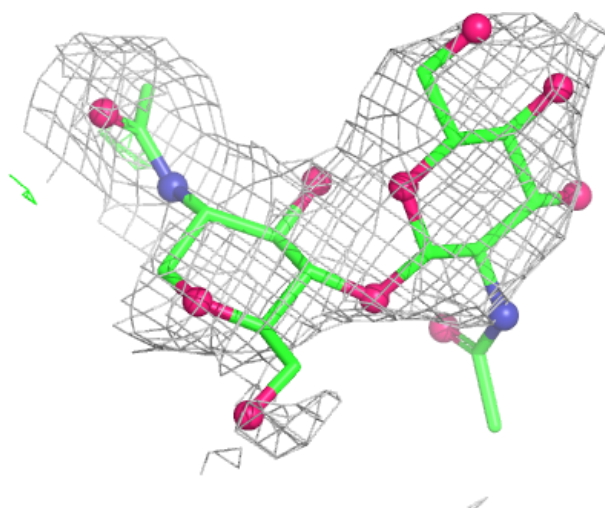
Electron density around Chain I:

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



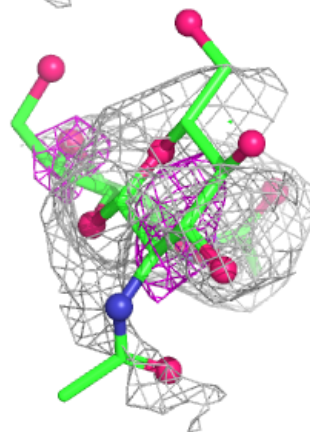
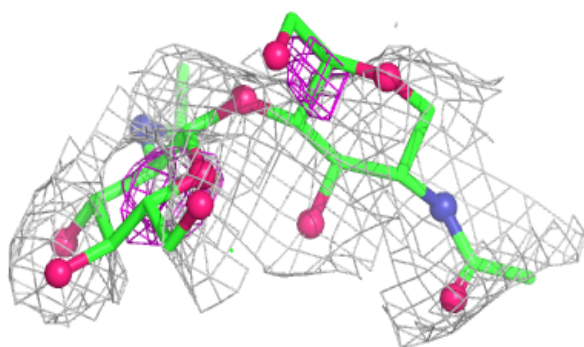
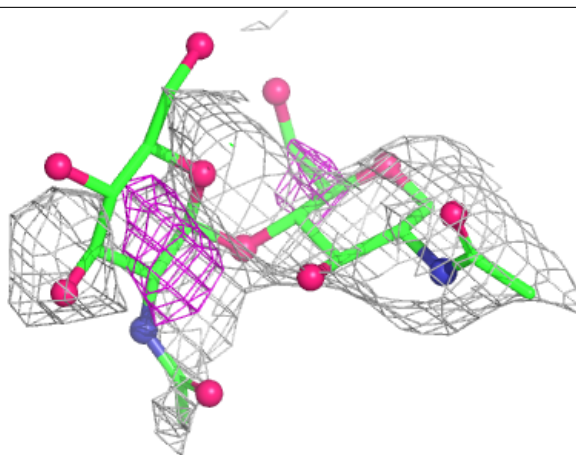
Electron density around Chain J:

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



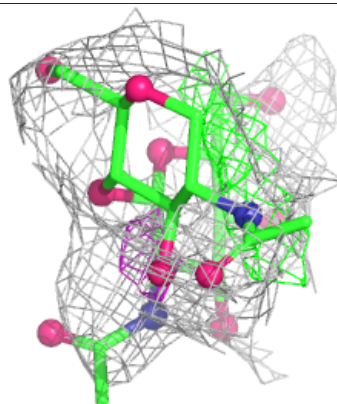
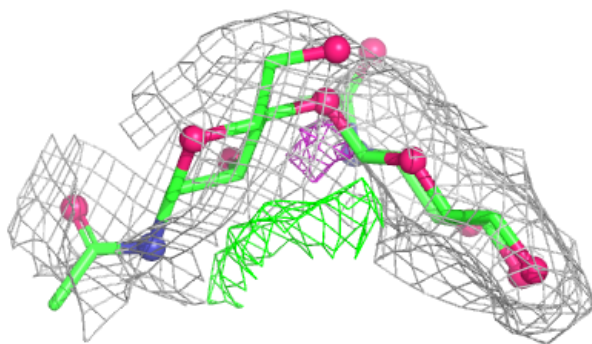
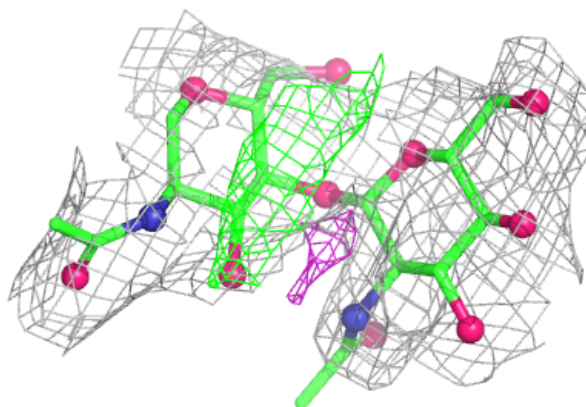
Electron density around Chain K:

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



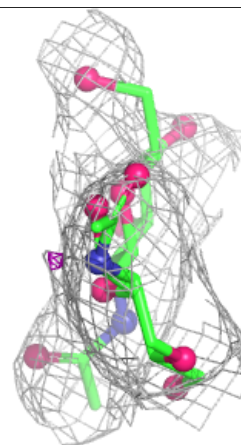
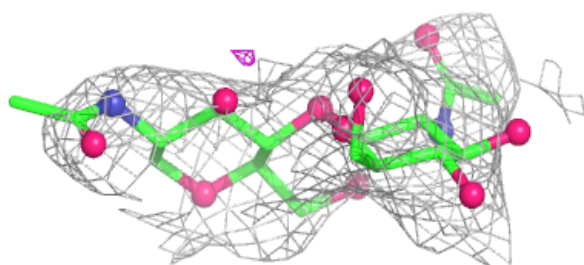
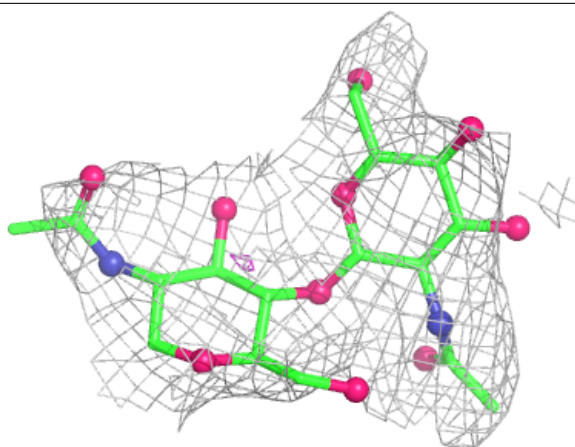
Electron density around Chain M:

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

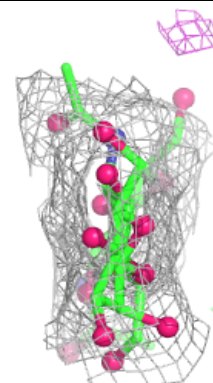
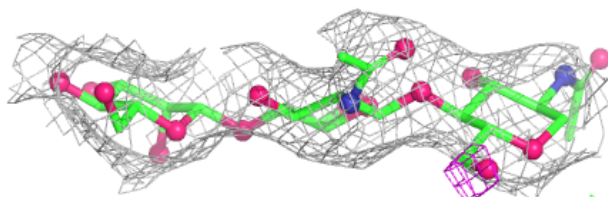
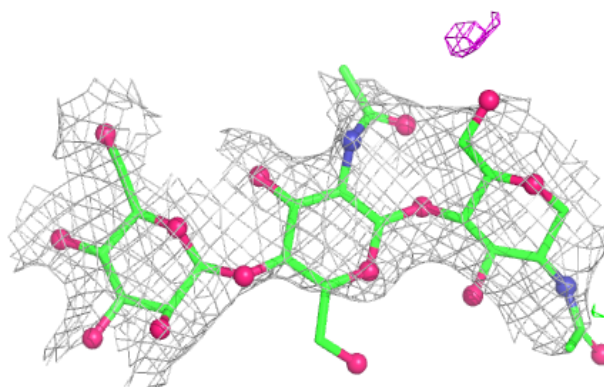


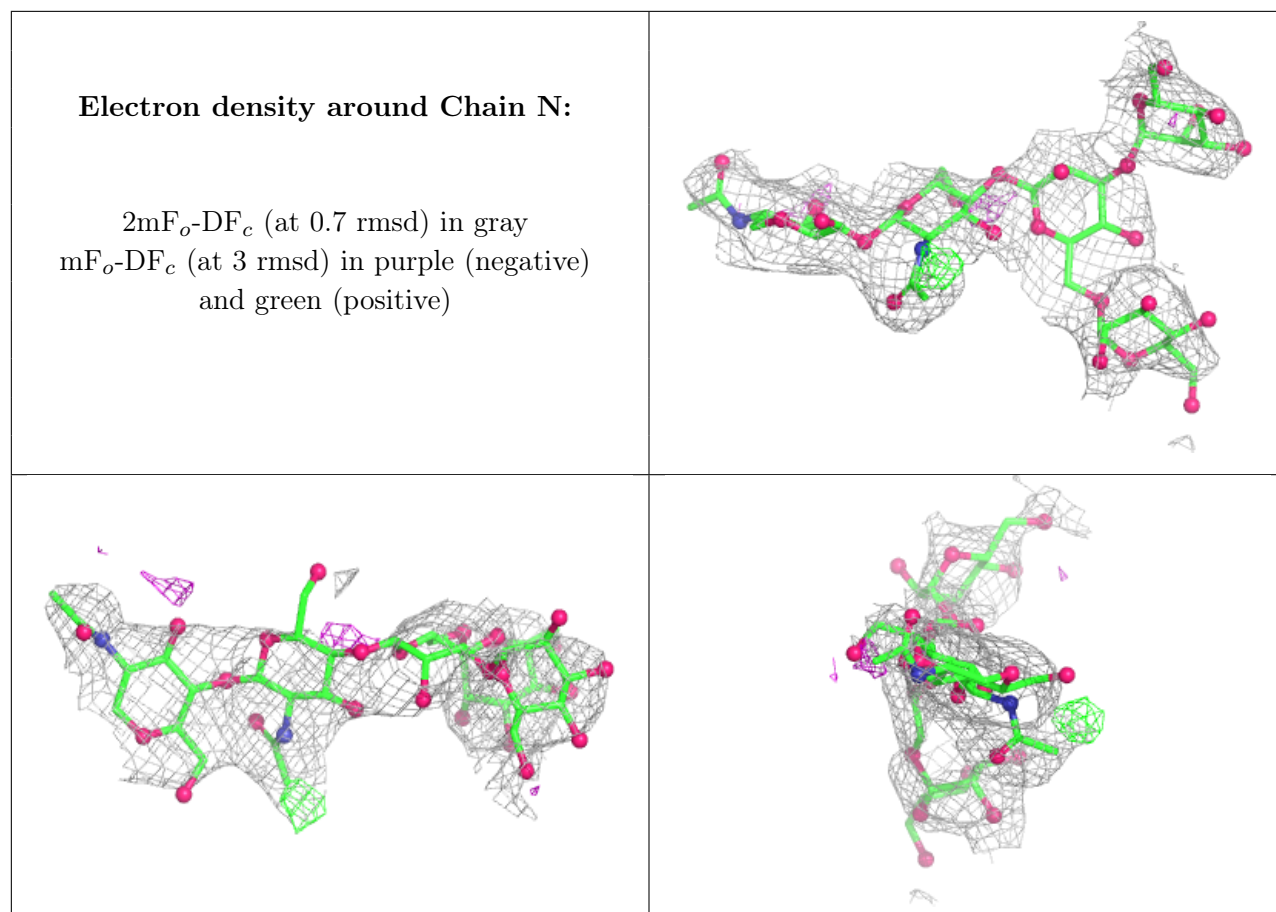
Electron density around Chain O:

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

**Electron density around Chain G:**

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	C	4301	14/15	0.51	0.18	116,126,134,135	0
7	NAG	D	701	14/15	0.59	0.16	103,107,112,113	0
7	NAG	D	702	14/15	0.70	0.14	69,76,80,80	0
7	NAG	C	4302	14/15	0.79	0.12	80,93,97,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.