



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:25 AM UTC

PDB ID : 9NRB / pdb_00009nrb
Title : Crystal structure of H5 hemagglutinin Q226L mutant from the influenza virus
A/duck/France/1611008h/16 with LSTc
Authors : Lin, T.H.; Zhu, Y.; Wilson, I.A.
Deposited on : 2025-03-14
Resolution : 2.65 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

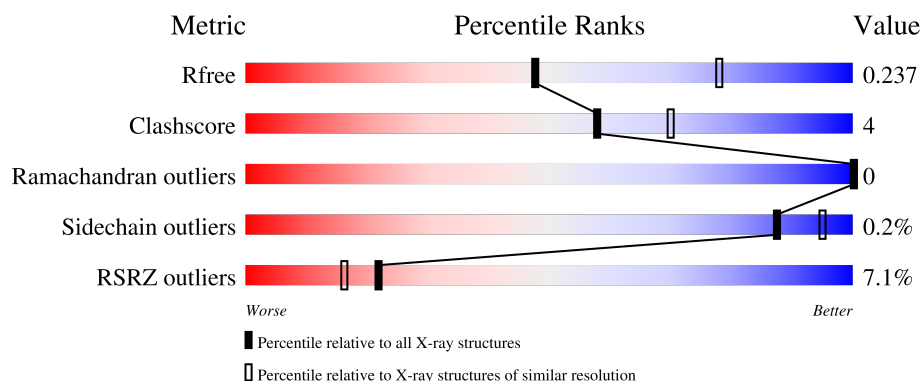
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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.



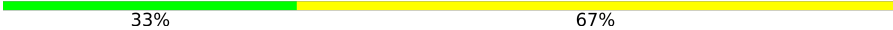
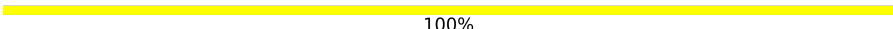
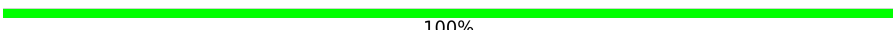
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	328	 6% 89% 9% 5%
1	C	328	 7% 80% 19% 5%
1	E	328	 4% 88% 10% 5%
2	B	177	 7% 80% 15% 5%
2	D	177	 16% 87% 8% 5%

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Mol	Chain	Length	Quality of chain
2	F	177	 5% 88% 9%
3	G	3	 33% 67%
3	H	3	 33% 67%
3	J	3	 100%
4	I	2	 100%
5	K	4	 50% 50%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12173 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 HA1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	0	0
			2547	1615	442	476	14			
1	C	324	Total	C	N	O	S	0	0	0
			2562	1624	444	480	14			
1	E	323	Total	C	N	O	S	0	0	0
			2555	1619	443	479	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	ASP	-	expression tag	UNP A0A6M2RJB8
A	9	PRO	-	expression tag	UNP A0A6M2RJB8
A	10	GLY	-	expression tag	UNP A0A6M2RJB8
A	226	LEU	GLN	engineered mutation	UNP A0A6M2RJB8
C	8	ASP	-	expression tag	UNP A0A6M2RJB8
C	9	PRO	-	expression tag	UNP A0A6M2RJB8
C	10	GLY	-	expression tag	UNP A0A6M2RJB8
C	226	LEU	GLN	engineered mutation	UNP A0A6M2RJB8
E	8	ASP	-	expression tag	UNP A0A6M2RJB8
E	9	PRO	-	expression tag	UNP A0A6M2RJB8
E	10	GLY	-	expression tag	UNP A0A6M2RJB8
E	226	LEU	GLN	engineered mutation	UNP A0A6M2RJB8

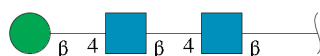
- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	169	Total	C	N	O	S	0	0	0
			1380	856	240	276	8			
2	D	169	Total	C	N	O	S	0	0	0
			1380	856	240	276	8			
2	F	172	Total	C	N	O	S	0	0	0
			1401	867	246	280	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	174	SER	-	expression tag	UNP A0A6M2RJB8
B	175	SER	-	expression tag	UNP A0A6M2RJB8
B	176	GLY	-	expression tag	UNP A0A6M2RJB8
B	177	ARG	-	expression tag	UNP A0A6M2RJB8
D	174	SER	-	expression tag	UNP A0A6M2RJB8
D	175	SER	-	expression tag	UNP A0A6M2RJB8
D	176	GLY	-	expression tag	UNP A0A6M2RJB8
D	177	ARG	-	expression tag	UNP A0A6M2RJB8
F	174	SER	-	expression tag	UNP A0A6M2RJB8
F	175	SER	-	expression tag	UNP A0A6M2RJB8
F	176	GLY	-	expression tag	UNP A0A6M2RJB8
F	177	ARG	-	expression tag	UNP A0A6M2RJB8

- Molecule 3 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
3	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



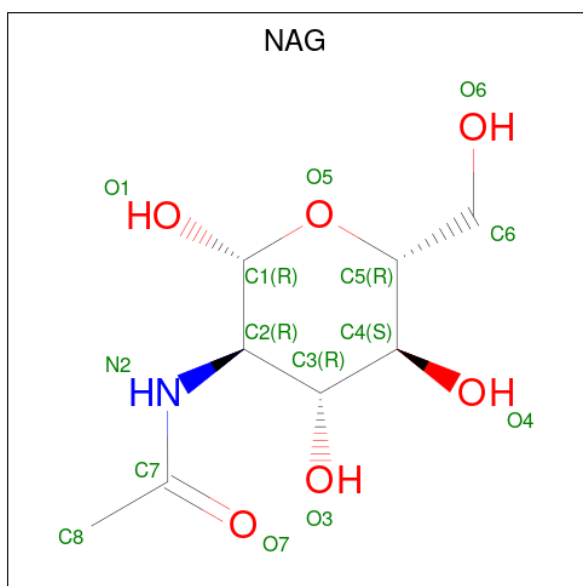
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	K	4	Total	C	N	O	0	0	0
			57	31	2	24			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



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

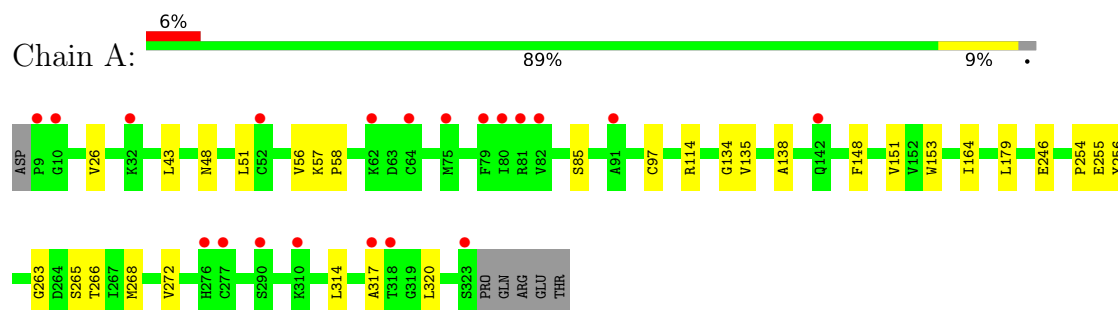
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	13	Total 13	O 13	0	0
7	B	3	Total 3	O 3	0	0
7	C	14	Total 14	O 14	0	0
7	D	3	Total 3	O 3	0	0
7	E	25	Total 25	O 25	0	0
7	F	4	Total 4	O 4	0	0

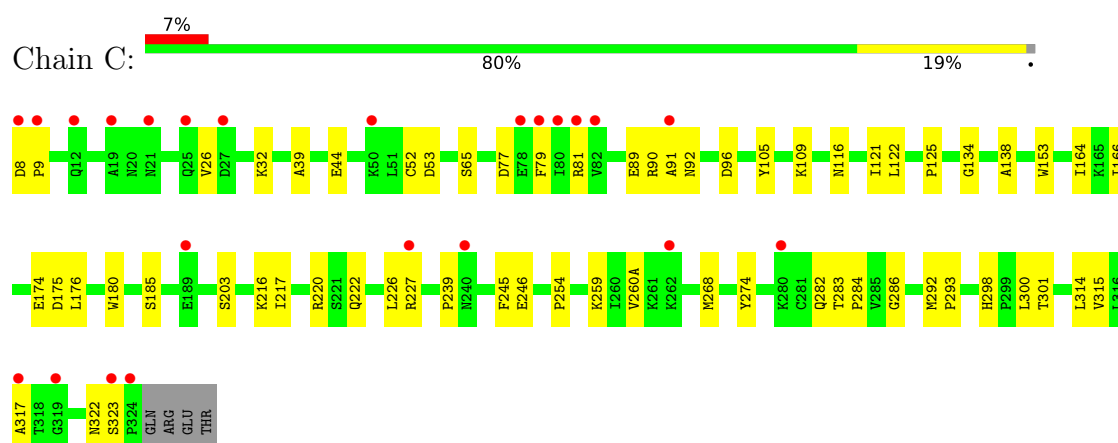
3 Residue-property plots

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.

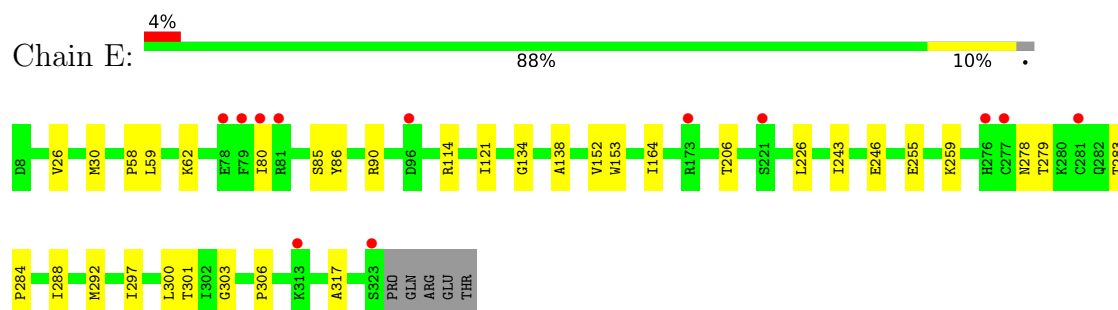
- Molecule 1: Hemagglutinin HA1 chain



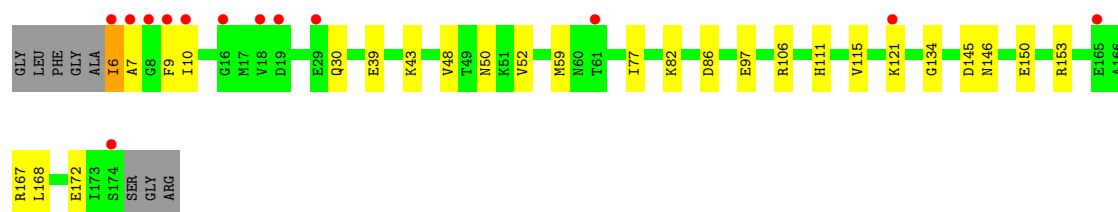
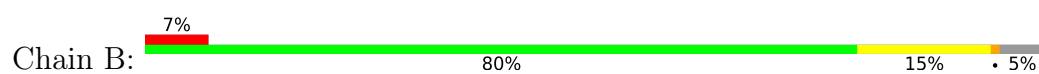
- Molecule 1: Hemagglutinin HA1 chain



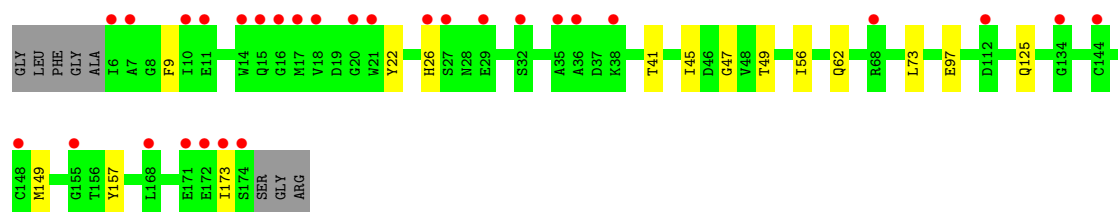
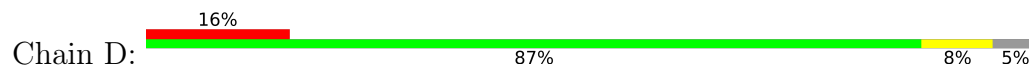
- Molecule 1: Hemagglutinin HA1 chain



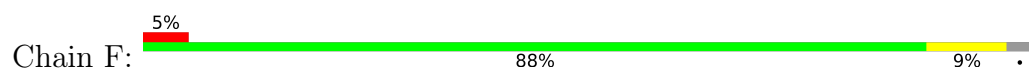
- Molecule 2: Hemagglutinin HA2 chain



- Molecule 2: Hemagglutinin HA2 chain



- Molecule 2: Hemagglutinin HA2 chain



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



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



- Molecule 3: beta-D-mannopyranose-(1-4)-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:  100%

 MAG1
MAG2

- Molecule 5: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose

Chain K:  50% 50%

 GAL1
MAG2
GAL3
SIA4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.92Å 176.40Å 226.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.81 – 2.65 26.81 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.2 (26.81-2.65) 99.0 (26.81-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.65Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.209 , 0.238 0.208 , 0.237	Depositor DCC
R_{free} test set	5546 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12173	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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, SIA, BMA, GAL

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	0.11	0/2611	0.30	0/3551
1	C	0.11	0/2627	0.29	0/3575
1	E	0.11	0/2619	0.29	0/3563
2	B	0.09	0/1406	0.23	0/1890
2	D	0.10	0/1406	0.24	0/1890
2	F	0.09	0/1427	0.24	0/1917
All	All	0.11	0/12096	0.28	0/16386

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 [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	2547	0	2504	16	0
1	C	2562	0	2514	40	0
1	E	2555	0	2508	18	0
2	B	1380	0	1285	20	0
2	D	1380	0	1284	13	0
2	F	1401	0	1305	12	0
3	G	39	0	34	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	39	0	34	0	0
3	J	39	0	34	0	0
4	I	28	0	25	0	0
5	K	57	0	49	0	0
6	A	28	0	26	1	0
6	C	28	0	26	0	0
6	D	14	0	13	0	0
6	E	14	0	13	0	0
7	A	13	0	0	0	0
7	B	3	0	0	0	0
7	C	14	0	0	0	0
7	D	3	0	0	0	0
7	E	25	0	0	0	0
7	F	4	0	0	0	0
All	All	12173	0	11654	106	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 4.

All (106) 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:52:CYS:H	1:C:282:GLN:HE22	1.35	0.71
1:A:26:VAL:HG21	1:A:317:ALA:HB2	1.74	0.70
2:B:77:ILE:HD11	2:F:77:ILE:HD13	1.75	0.68
1:E:26:VAL:HG21	1:E:317:ALA:HB2	1.75	0.66
1:C:90:ARG:HD2	1:C:91:ALA:H	1.61	0.65
2:B:167:ARG:NH1	2:D:173:ILE:O	2.31	0.63
1:C:283:THR:HG22	1:C:301:THR:HG22	1.80	0.63
1:C:203:SER:HB2	1:C:246:GLU:HB3	1.80	0.62
1:C:216:LYS:O	1:C:220:ARG:NH2	2.32	0.62
1:C:44:GLU:HG2	1:C:292:MET:HB2	1.81	0.62
1:C:26:VAL:HG21	1:C:317:ALA:HB2	1.81	0.61
2:B:134:GLY:HA2	2:F:124:LEU:HD13	1.82	0.61
1:C:52:CYS:H	1:C:282:GLN:NE2	1.99	0.60
1:C:222:GLN:HG3	1:C:227:ARG:HG2	1.83	0.60
1:E:138:ALA:HB2	1:E:226:LEU:HD23	1.85	0.59
1:C:77:ASP:OD2	1:C:77:ASP:N	2.35	0.59
1:C:79:PHE:HD1	1:C:81:ARG:HB2	1.68	0.58
1:E:62:LYS:O	1:E:90:ARG:HD3	2.03	0.57
1:E:283:THR:HG22	1:E:301:THR:HG22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:85:SER:HA	1:E:114:ARG:HD3	1.88	0.56
1:C:322:ASN:HD22	1:C:323:SER:H	1.54	0.55
2:B:82:LYS:NZ	2:B:86:ASP:OD2	2.40	0.54
2:B:145:ASP:OD2	2:B:145:ASP:N	2.36	0.54
1:A:51:LEU:HD22	1:A:272:VAL:HG12	1.89	0.53
2:B:9:PHE:CZ	2:F:124:LEU:HD11	2.42	0.53
1:A:114:ARG:NH1	1:A:263:GLY:HA3	2.24	0.53
2:B:150:GLU:OE1	2:B:153:ARG:NH1	2.42	0.53
1:E:59:LEU:HD11	1:E:80:ILE:HD11	1.89	0.53
1:E:121:ILE:HG21	1:E:259:LYS:HD3	1.90	0.53
1:C:138:ALA:HB2	1:C:226:LEU:HD23	1.91	0.52
1:C:122:LEU:HD21	1:C:125:PRO:HB3	1.92	0.52
2:F:23:GLY:HA3	2:F:36:ALA:HA	1.92	0.52
2:D:22:TYR:H	2:D:41:THR:HG22	1.75	0.51
2:D:45:ILE:O	2:D:49:THR:OG1	2.22	0.51
1:C:116:ASN:HB3	1:C:260(A):VAL:HG12	1.92	0.50
2:B:48:VAL:O	2:B:52:VAL:HG23	2.12	0.50
1:A:134:GLY:HA3	1:A:153:TRP:HB3	1.94	0.49
1:C:65:SER:OG	1:C:96:ASP:OD1	2.25	0.49
2:B:6:ILE:HG13	2:B:7:ALA:H	1.78	0.49
1:C:174:GLU:OE1	1:C:259:LYS:HE3	2.12	0.49
2:D:26:HIS:HB2	2:D:149:MET:HE3	1.95	0.49
1:C:105:TYR:CZ	1:C:109:LYS:HD2	2.47	0.49
2:F:165:GLU:OE2	2:F:169:LYS:NZ	2.46	0.49
2:B:6:ILE:HD13	2:B:115:VAL:HB	1.95	0.48
1:C:134:GLY:HA3	1:C:153:TRP:HB3	1.95	0.48
2:F:167:ARG:O	2:F:171:GLU:HG3	2.13	0.48
1:E:152:VAL:HG23	1:E:255:GLU:HB2	1.96	0.48
1:A:255:GLU:HG2	1:A:256:TYR:CD2	2.49	0.47
1:C:53:ASP:OD1	1:C:274:TYR:OH	2.30	0.47
1:E:58:PRO:HB3	1:E:86:TYR:CE1	2.50	0.47
1:A:148:PHE:HB2	1:A:151:VAL:HG12	1.97	0.47
1:E:134:GLY:HA3	1:E:153:TRP:HB3	1.97	0.47
2:B:50:ASN:ND2	1:C:32:LYS:HG3	2.30	0.47
2:D:62:GLN:NE2	2:F:90:ASP:OD2	2.46	0.47
1:E:206:THR:HG22	1:E:243:ILE:HA	1.97	0.47
2:B:9:PHE:HB3	2:B:10:ILE:HD12	1.97	0.47
2:B:30:GLN:HE22	2:B:146:ASN:H	1.64	0.46
1:A:268:MET:HE3	1:A:268:MET:HB2	1.87	0.46
1:E:164:ILE:O	1:E:246:GLU:HA	2.15	0.46
1:A:97:CYS:HB2	1:A:138:ALA:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:ILE:HG22	1:C:245:PHE:HB2	1.98	0.45
1:C:293:PRO:HD3	2:D:56:ILE:HG12	1.99	0.45
2:D:22:TYR:H	2:D:41:THR:CG2	2.29	0.45
1:C:284:PRO:HD3	1:C:300:LEU:O	2.16	0.45
1:A:48:ASN:HB3	6:A:402:NAG:H81	1.99	0.45
1:C:268:MET:HE3	1:C:268:MET:HB2	1.79	0.44
1:C:314:LEU:HD21	2:D:97:GLU:HG2	1.99	0.44
2:B:39:GLU:O	2:B:43:LYS:HG3	2.16	0.44
1:A:265:SER:OG	1:A:266:THR:N	2.50	0.44
1:C:79:PHE:CD1	1:C:81:ARG:HB2	2.52	0.44
2:D:9:PHE:C	2:D:9:PHE:CD2	2.95	0.44
1:C:164:ILE:O	1:C:246:GLU:HA	2.17	0.44
1:C:298:HIS:HE1	1:C:300:LEU:HD12	1.84	0.43
1:C:90:ARG:HD2	1:C:91:ALA:N	2.32	0.43
1:C:90:ARG:NH2	1:C:92:ASN:HB2	2.34	0.43
1:A:320:LEU:HD22	2:B:111:HIS:CG	2.53	0.43
1:E:278:ASN:OD1	1:E:279:THR:N	2.52	0.43
1:A:56:VAL:HB	1:A:85:SER:HB3	1.99	0.43
2:B:59:MET:HE3	2:B:59:MET:HA	2.00	0.43
2:B:168:LEU:O	2:B:172:GLU:HG3	2.18	0.43
1:E:288:ILE:HG21	1:E:297:ILE:HD13	2.00	0.43
1:C:185:SER:HB2	1:C:217:ILE:HG12	2.01	0.43
1:A:43:LEU:HB2	1:A:314:LEU:HB2	2.01	0.42
1:C:175:ASP:OD1	1:C:239:PRO:HD3	2.20	0.42
1:C:39:ALA:HB1	1:C:315:VAL:HG12	2.02	0.42
1:C:180:TRP:HB3	1:C:254:PRO:HG3	2.01	0.42
1:C:121:ILE:HG21	1:C:259:LYS:HD3	2.00	0.42
2:B:121:LYS:HD3	2:B:121:LYS:HA	1.67	0.42
2:D:125:GLN:NE2	2:D:157:TYR:H	2.17	0.42
2:F:29:GLU:OE2	2:F:143:LYS:HE2	2.20	0.42
2:B:97:GLU:HB3	2:F:58:LYS:HD2	2.01	0.42
1:E:284:PRO:HD3	1:E:300:LEU:O	2.19	0.42
1:A:57:LYS:HG2	1:A:58:PRO:HD2	2.01	0.41
1:E:303:GLY:HA2	2:F:63:PHE:CD2	2.55	0.41
1:A:164:ILE:O	1:A:246:GLU:HA	2.20	0.41
1:C:176:LEU:HD12	1:C:176:LEU:HA	1.91	0.41
1:E:292:MET:O	1:E:306:PRO:HB3	2.20	0.41
2:B:106:ARG:HG3	2:F:106:ARG:HH21	1.86	0.41
1:C:322:ASN:HD22	1:C:323:SER:N	2.17	0.41
2:F:7:ALA:HB1	2:F:11:GLU:HG3	2.01	0.41
1:A:179:LEU:O	1:A:254:PRO:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:47:GLY:C	1:E:30:MET:HG2	2.46	0.41
2:D:125:GLN:HE22	2:D:157:TYR:H	1.67	0.41
1:C:8:ASP:N	1:C:9:PRO:HD2	2.36	0.40
2:D:73:LEU:HD23	2:D:73:LEU:HA	1.91	0.40
1:C:283:THR:OG1	1:C:286:GLY:O	2.25	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	320/328 (98%)	308 (96%)	12 (4%)	0	100	100
1	C	322/328 (98%)	312 (97%)	10 (3%)	0	100	100
1	E	321/328 (98%)	310 (97%)	11 (3%)	0	100	100
2	B	167/177 (94%)	166 (99%)	1 (1%)	0	100	100
2	D	167/177 (94%)	166 (99%)	1 (1%)	0	100	100
2	F	170/177 (96%)	169 (99%)	1 (1%)	0	100	100
All	All	1467/1515 (97%)	1431 (98%)	36 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	287/293 (98%)	286 (100%)	1 (0%)	86	94
1	C	289/293 (99%)	288 (100%)	1 (0%)	86	94
1	E	288/293 (98%)	288 (100%)	0	100	100
2	B	147/151 (97%)	146 (99%)	1 (1%)	76	86
2	D	147/151 (97%)	147 (100%)	0	100	100
2	F	149/151 (99%)	149 (100%)	0	100	100
All	All	1307/1332 (98%)	1304 (100%)	3 (0%)	87	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	135	VAL
2	B	6	ILE
1	C	89	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	55	ASN
1	A	92	ASN
1	A	103	ASN
1	A	117	HIS
1	A	158	ASN
1	A	172	ASN
1	A	210	ASN
1	A	322	ASN
2	B	30	GLN
2	B	42	GLN
2	B	50	ASN
2	B	95	ASN
2	B	117	ASN
1	C	12	GLN
1	C	116	ASN
1	C	172	ASN
1	C	244	HIS
1	C	276	HIS
1	C	282	GLN
1	C	322	ASN
2	D	30	GLN

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Mol	Chain	Res	Type
2	D	125	GLN
1	E	40	GLN
1	E	55	ASN
1	E	150	ASN
1	E	244	HIS
2	F	42	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 ⓘ

15 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	G	1	3,1	14,14,15	0.65	0	17,19,21	0.86	0
3	NAG	G	2	3	14,14,15	0.77	0	17,19,21	1.29	3 (17%)
3	BMA	G	3	3	11,11,12	0.74	0	15,15,17	2.58	6 (40%)
3	NAG	H	1	3,1	14,14,15	0.66	0	17,19,21	1.19	1 (5%)
3	NAG	H	2	3	14,14,15	0.68	0	17,19,21	0.84	0
3	BMA	H	3	3	11,11,12	0.73	0	15,15,17	2.42	4 (26%)
4	NAG	I	1	4,1	14,14,15	0.67	0	17,19,21	1.12	0
4	NAG	I	2	4	14,14,15	0.68	0	17,19,21	0.77	0
3	NAG	J	1	3,2	14,14,15	0.65	0	17,19,21	1.23	2 (11%)
3	NAG	J	2	3	14,14,15	0.68	0	17,19,21	0.99	1 (5%)
3	BMA	J	3	3	11,11,12	0.79	0	15,15,17	2.21	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GAL	K	1	5	12,12,12	0.64	0	17,17,17	0.84	0
5	NAG	K	2	5	14,14,15	0.73	0	17,19,21	0.88	0
5	GAL	K	3	5	11,11,12	0.74	0	15,15,17	1.38	2 (13%)
5	SIA	K	4	5	20,20,21	1.49	1 (5%)	21,28,31	1.61	4 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
3	NAG	H	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	3/6/23/26	0/1/1/1
3	BMA	H	3	3	-	0/2/19/22	0/1/1/1
4	NAG	I	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
3	NAG	J	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
3	BMA	J	3	3	-	1/2/19/22	0/1/1/1
5	GAL	K	1	5	-	1/2/22/22	0/1/1/1
5	NAG	K	2	5	-	2/6/23/26	0/1/1/1
5	GAL	K	3	5	-	0/2/19/22	0/1/1/1
5	SIA	K	4	5	-	0/18/34/38	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	K	4	SIA	C2-C1	5.24	1.58	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	3	BMA	C1-O5-C5	8.10	123.04	112.19
3	H	3	BMA	C1-O5-C5	7.52	122.27	112.19
3	J	3	BMA	C1-O5-C5	6.40	120.76	112.19
5	K	4	SIA	O1A-C1-C2	-3.94	114.34	122.85
5	K	3	GAL	O3-C3-C2	-3.69	102.52	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	2	NAG	O3-C3-C2	-3.57	101.98	109.40
5	K	4	SIA	O6-C2-C3	-3.37	106.03	110.56
3	J	1	NAG	O5-C1-C2	-3.22	106.30	111.29
5	K	3	GAL	O3-C3-C4	3.01	117.46	110.38
3	J	3	BMA	C2-C3-C4	2.91	115.98	110.86
3	H	3	BMA	C2-C3-C4	2.75	115.69	110.86
3	G	3	BMA	C2-C3-C4	2.65	115.52	110.86
5	K	4	SIA	O1B-C1-O1A	2.62	130.01	124.08
3	G	3	BMA	O3-C3-C2	-2.44	105.07	110.05
3	H	3	BMA	O3-C3-C2	-2.43	105.09	110.05
3	J	1	NAG	O4-C4-C3	-2.41	104.70	110.38
3	J	3	BMA	O3-C3-C2	-2.37	105.22	110.05
3	H	1	NAG	C1-O5-C5	2.34	115.33	112.19
5	K	4	SIA	C6-C5-N5	-2.30	107.24	110.91
3	J	2	NAG	O5-C1-C2	-2.26	107.80	111.29
3	G	2	NAG	O4-C4-C3	2.25	115.68	110.38
3	G	2	NAG	O5-C1-C2	-2.19	107.90	111.29
3	J	3	BMA	C3-C4-C5	2.14	114.12	110.23
3	G	3	BMA	O5-C5-C4	2.14	116.03	110.83
3	J	3	BMA	O4-C4-C3	-2.12	105.39	110.38
3	G	3	BMA	C3-C4-C5	2.08	114.01	110.23
3	H	3	BMA	O4-C4-C3	-2.08	105.47	110.38
3	G	3	BMA	O4-C4-C3	-2.07	105.48	110.38

There are no chirality outliers.

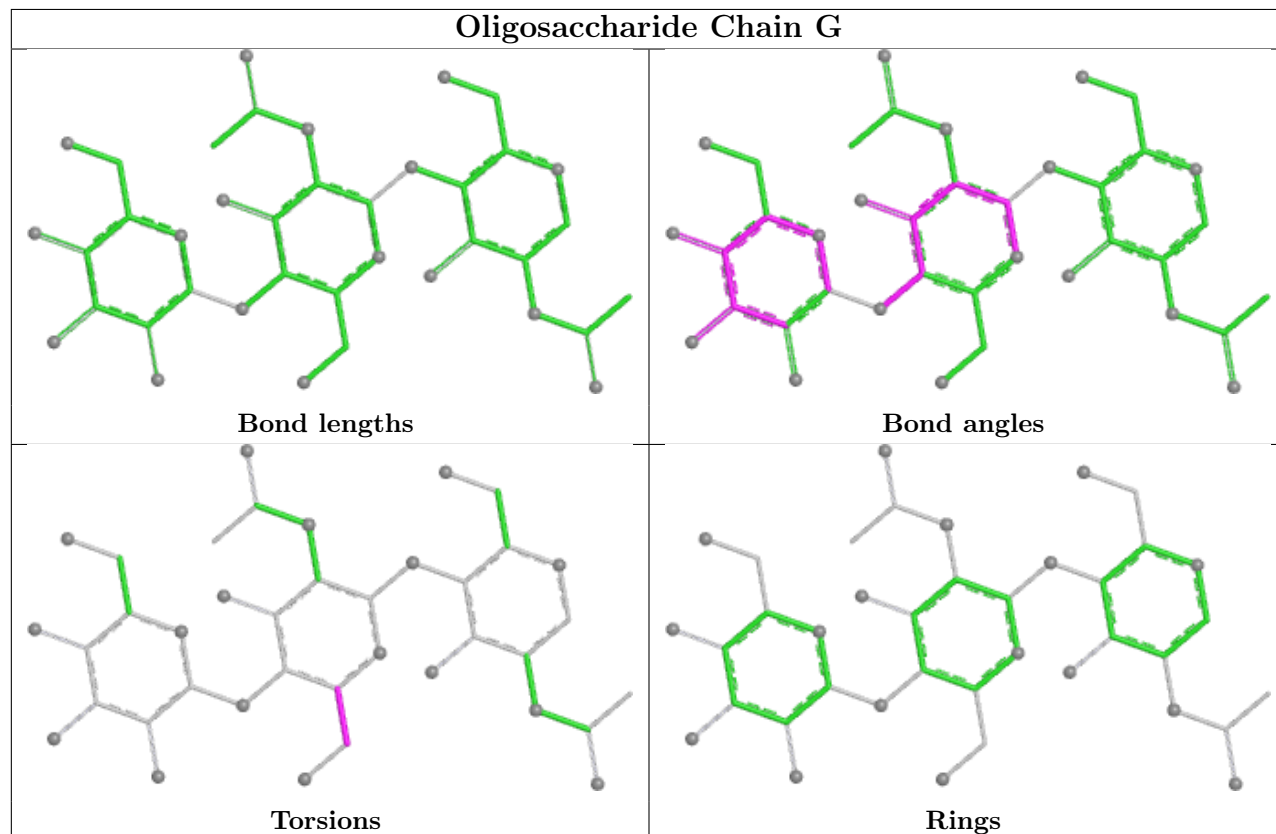
All (13) torsion outliers are listed below:

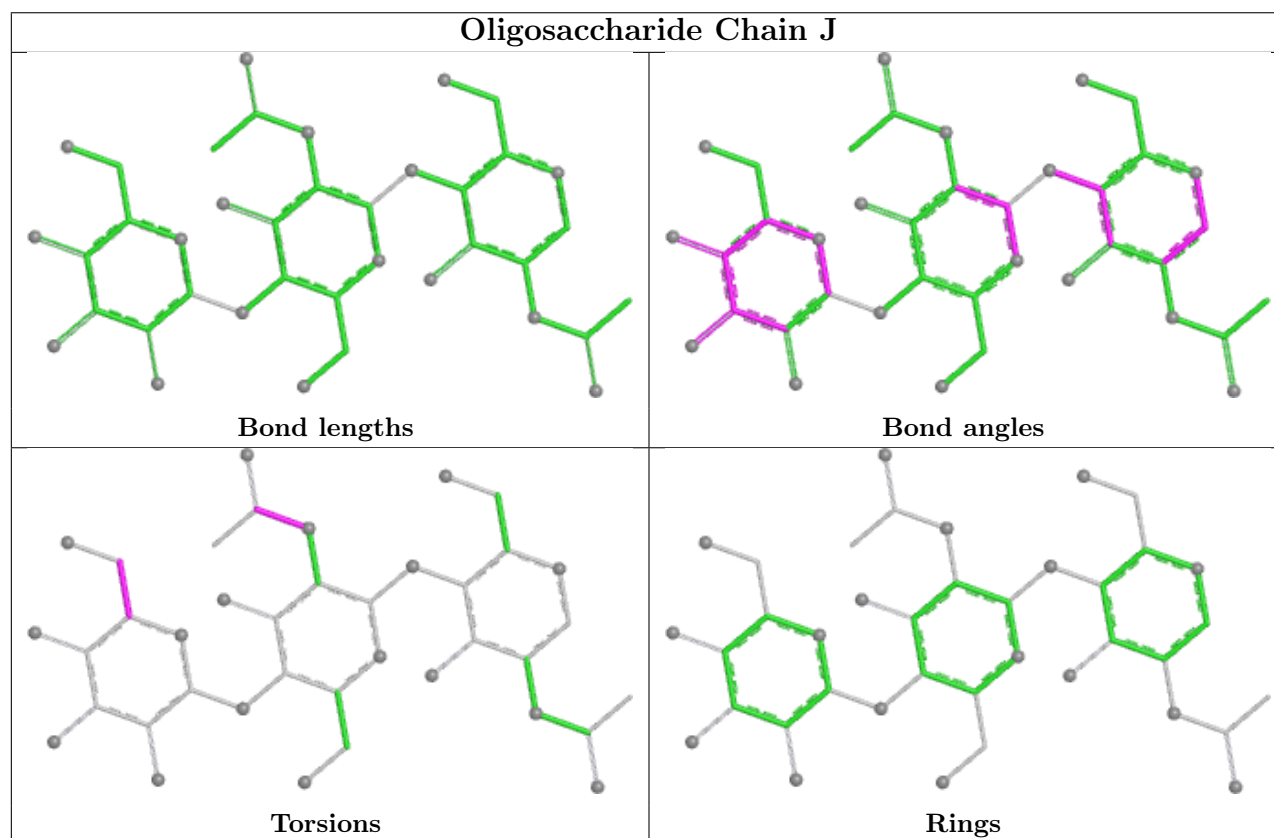
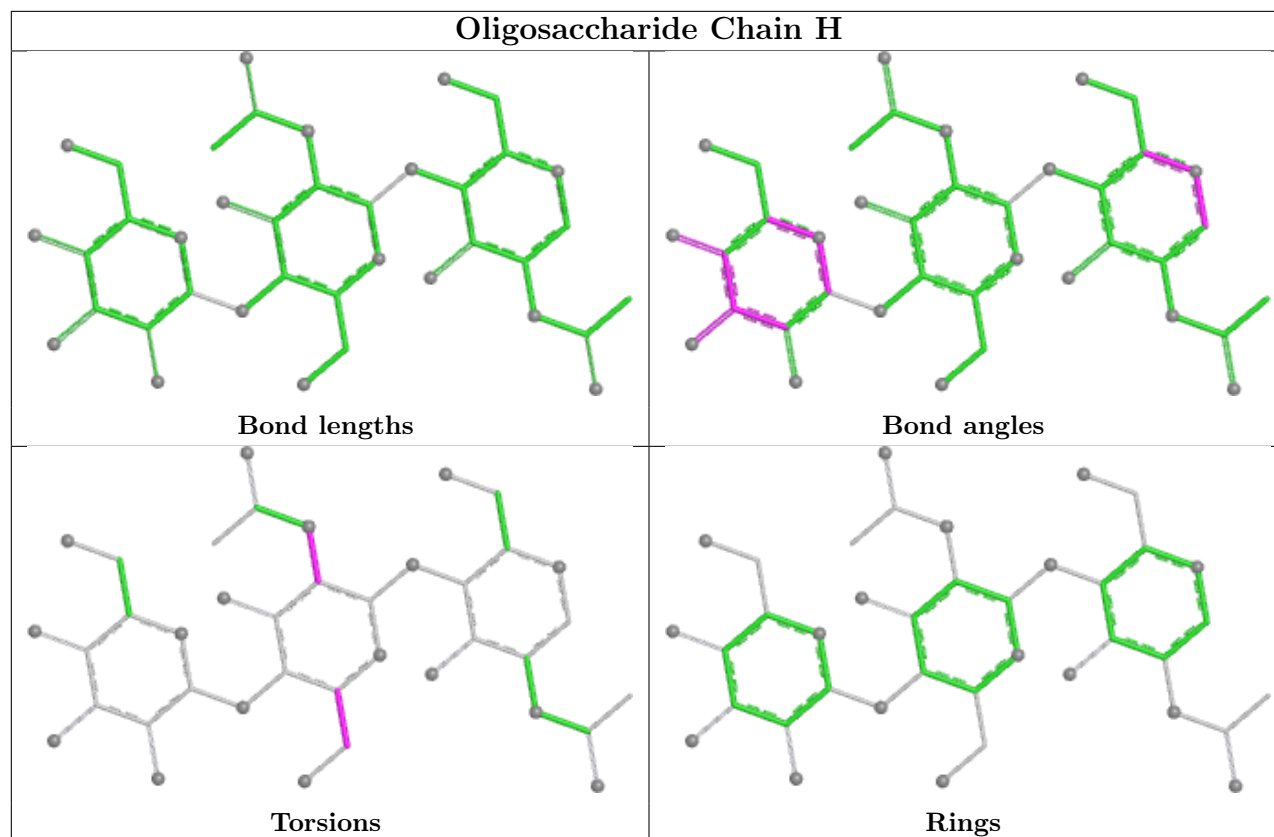
Mol	Chain	Res	Type	Atoms
5	K	2	NAG	C4-C5-C6-O6
3	J	2	NAG	C8-C7-N2-C2
3	J	2	NAG	O7-C7-N2-C2
4	I	1	NAG	C8-C7-N2-C2
4	I	1	NAG	O7-C7-N2-C2
3	G	2	NAG	O5-C5-C6-O6
5	K	2	NAG	O5-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
5	K	1	GAL	O5-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	J	3	BMA	O5-C5-C6-O6
3	H	2	NAG	C1-C2-N2-C7

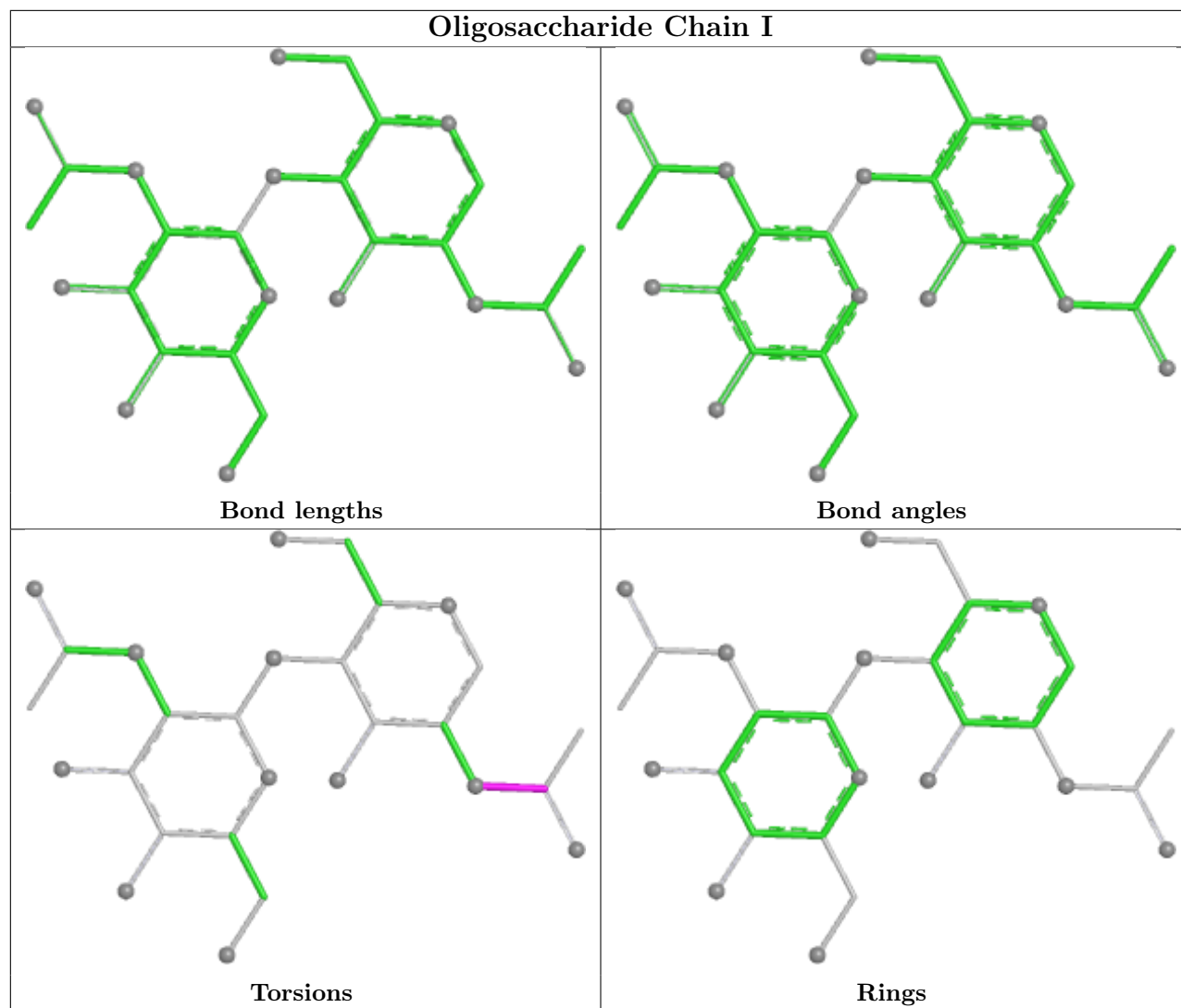
There are no ring outliers.

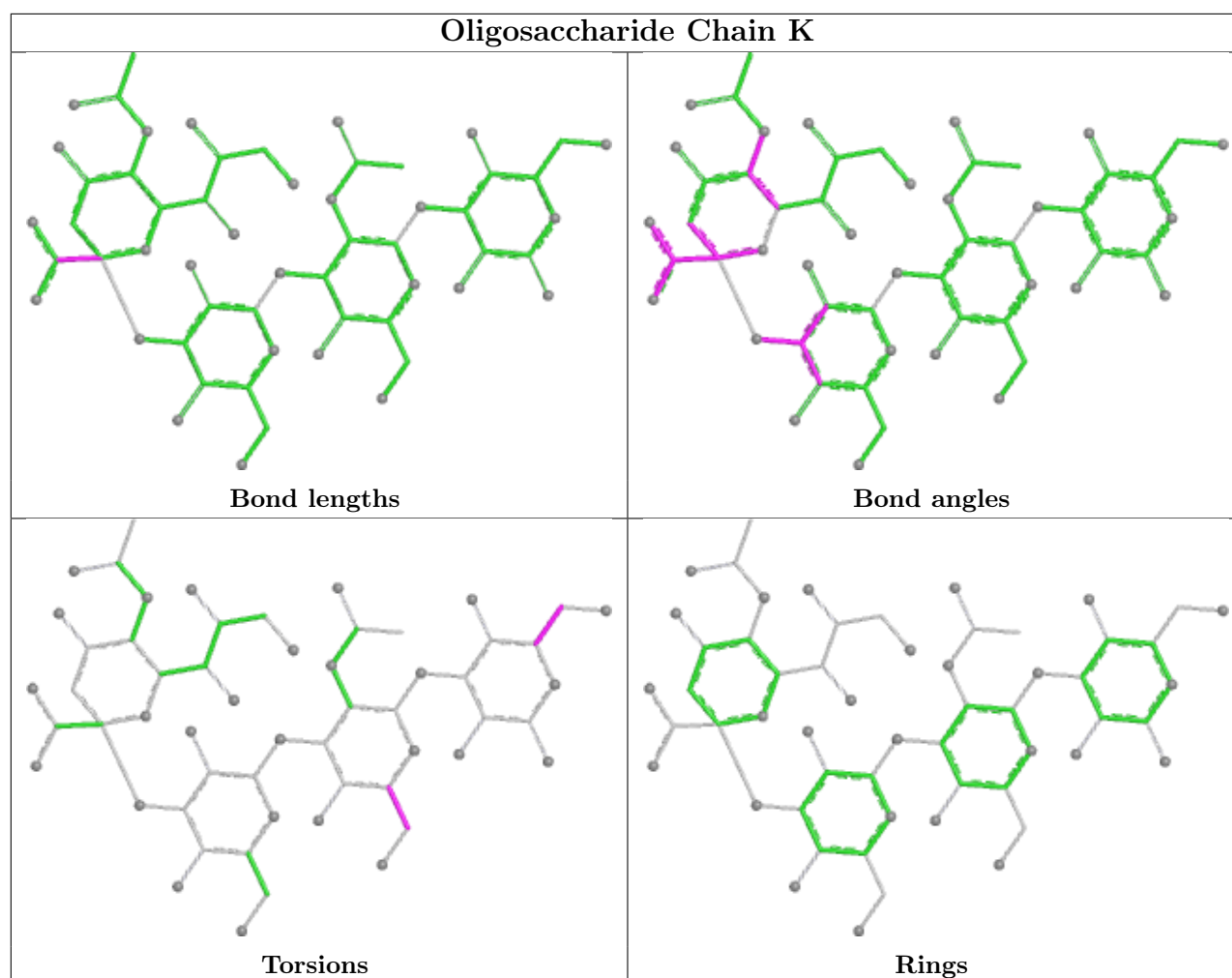
No monomer is involved in short contacts.

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](#)

6 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	$\# Z > 2$
6	NAG	A	401	1	14,14,15	0.65	0	17,19,21	0.95	0
6	NAG	A	402	1	14,14,15	0.69	0	17,19,21	2.67	2 (11%)
6	NAG	E	401	1	14,14,15	0.65	0	17,19,21	0.95	1 (5%)
6	NAG	D	201	2	14,14,15	0.61	0	17,19,21	0.91	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	C	401	1	14,14,15	0.78	0	17,19,21	1.17	2 (11%)
6	NAG	C	402	1	14,14,15	0.65	0	17,19,21	2.72	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	401	1	-	2/6/23/26	0/1/1/1
6	NAG	A	402	1	-	6/6/23/26	0/1/1/1
6	NAG	E	401	1	-	0/6/23/26	0/1/1/1
6	NAG	D	201	2	-	0/6/23/26	0/1/1/1
6	NAG	C	401	1	-	2/6/23/26	0/1/1/1
6	NAG	C	402	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	402	NAG	C2-N2-C7	9.85	136.11	122.90
6	A	402	NAG	C2-N2-C7	9.71	135.91	122.90
6	C	402	NAG	C8-C7-N2	3.54	122.00	116.12
6	A	402	NAG	C8-C7-N2	3.50	121.92	116.12
6	E	401	NAG	C1-O5-C5	2.44	115.45	112.19
6	C	401	NAG	O5-C1-C2	-2.35	107.66	111.29
6	C	401	NAG	C2-N2-C7	2.35	126.04	122.90
6	D	201	NAG	O5-C1-C2	-2.20	107.88	111.29

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	401	NAG	O5-C5-C6-O6
6	A	401	NAG	C4-C5-C6-O6
6	A	402	NAG	C8-C7-N2-C2
6	A	402	NAG	O7-C7-N2-C2
6	C	402	NAG	C8-C7-N2-C2
6	C	402	NAG	O7-C7-N2-C2
6	A	402	NAG	O5-C5-C6-O6

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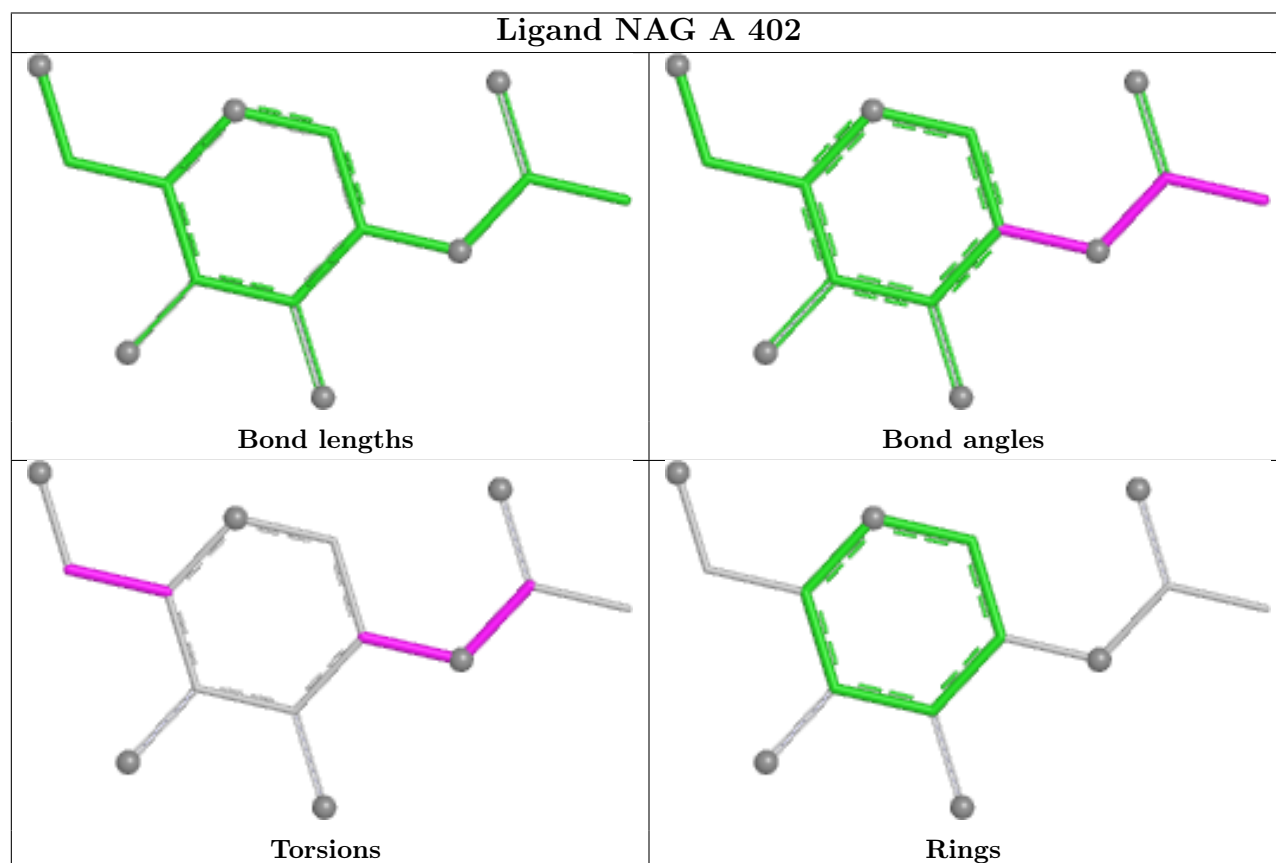
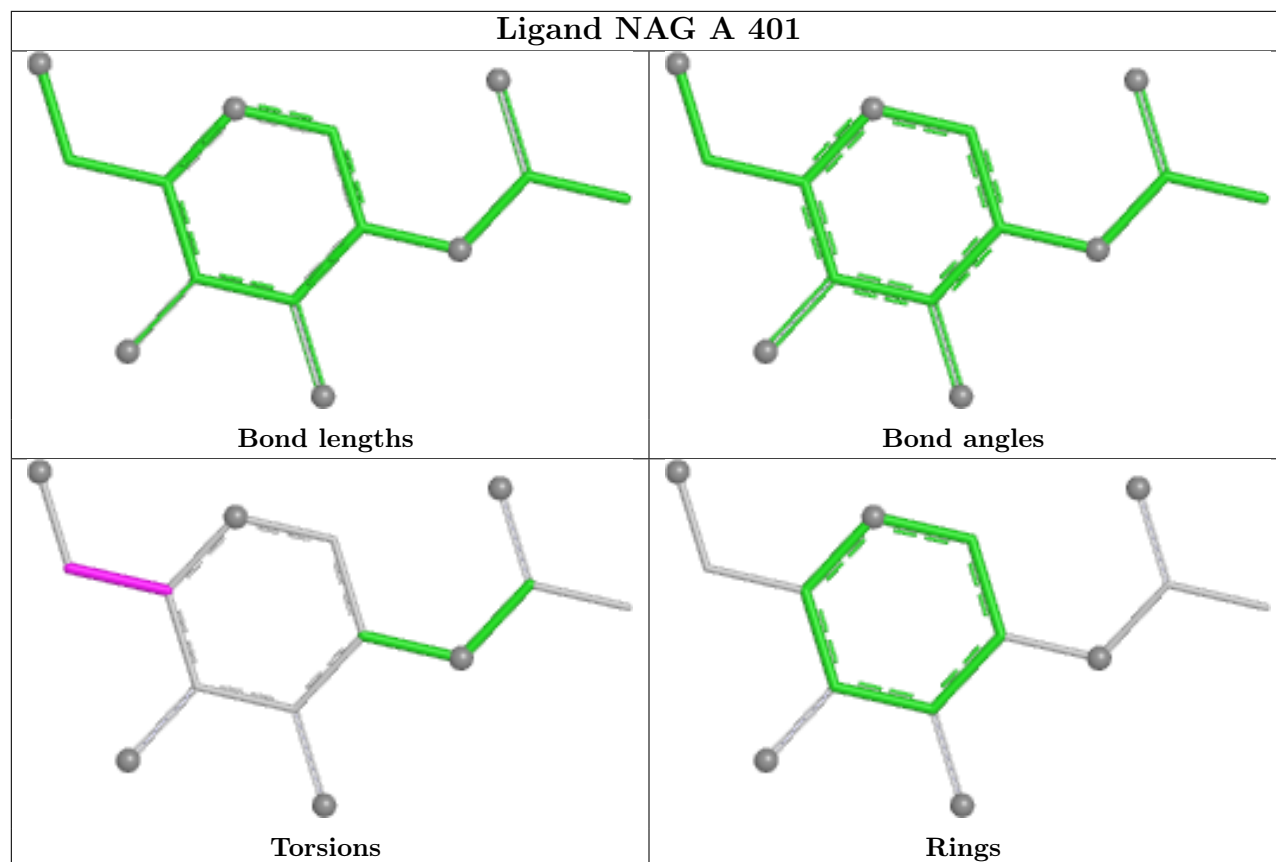
Mol	Chain	Res	Type	Atoms
6	C	401	NAG	O5-C5-C6-O6
6	A	402	NAG	C4-C5-C6-O6
6	A	402	NAG	C1-C2-N2-C7
6	C	402	NAG	C1-C2-N2-C7
6	A	402	NAG	C3-C2-N2-C7
6	C	401	NAG	C3-C2-N2-C7
6	C	402	NAG	C3-C2-N2-C7

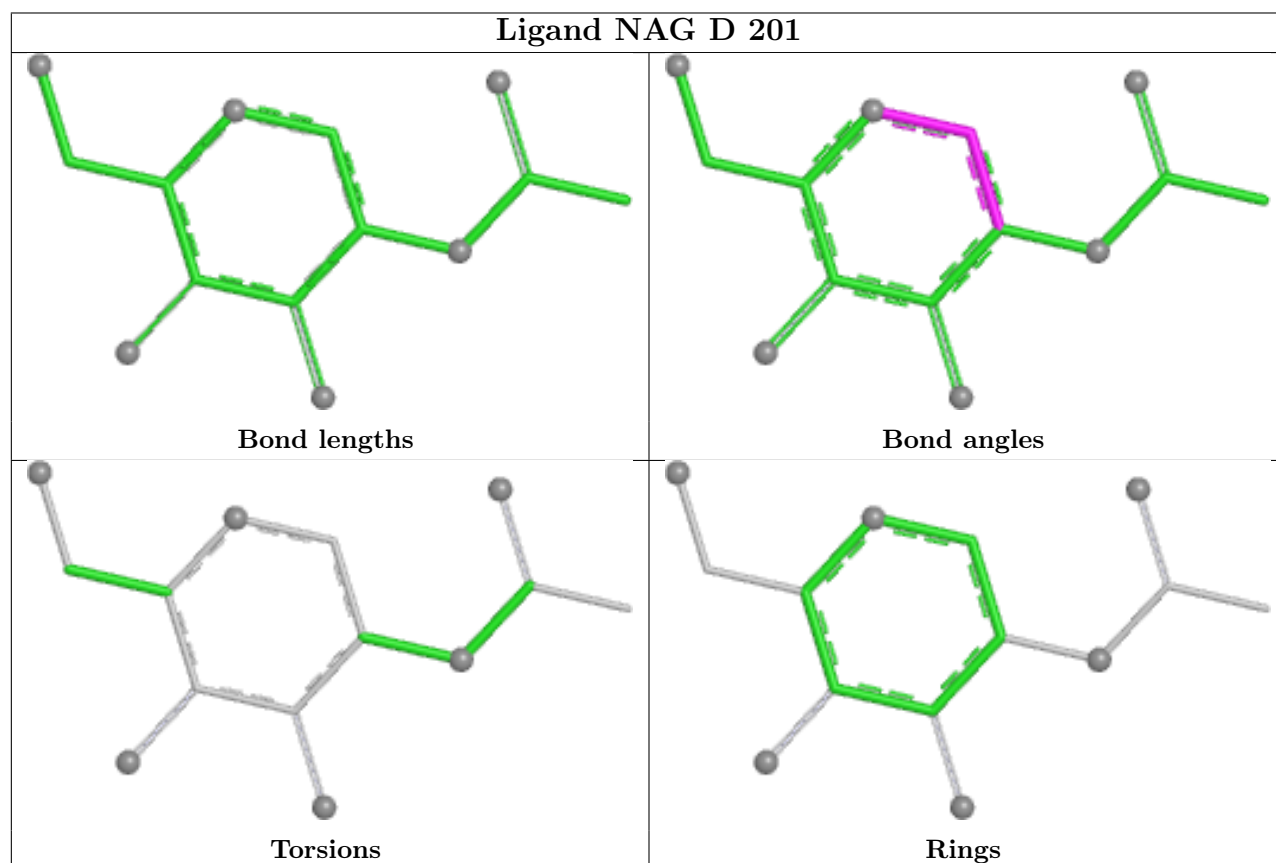
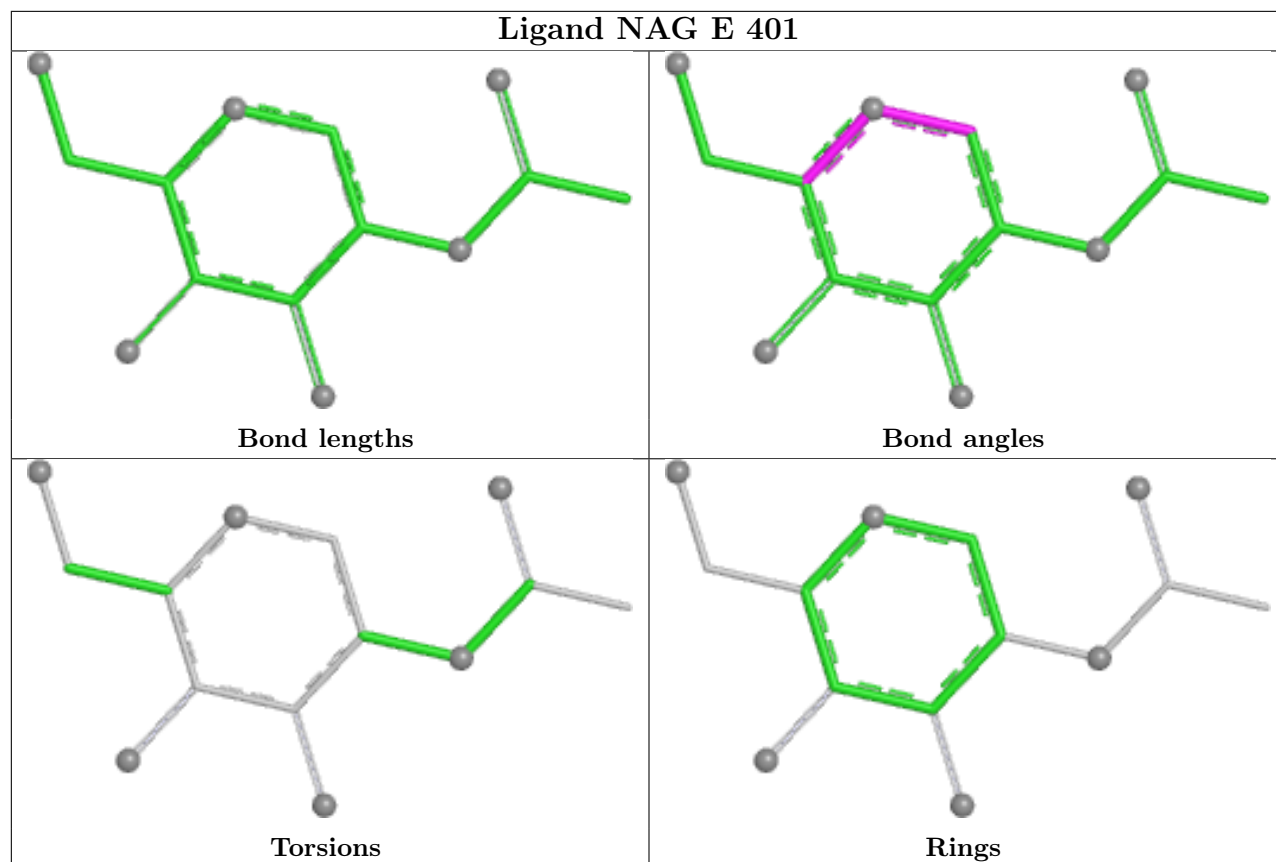
There are no ring outliers.

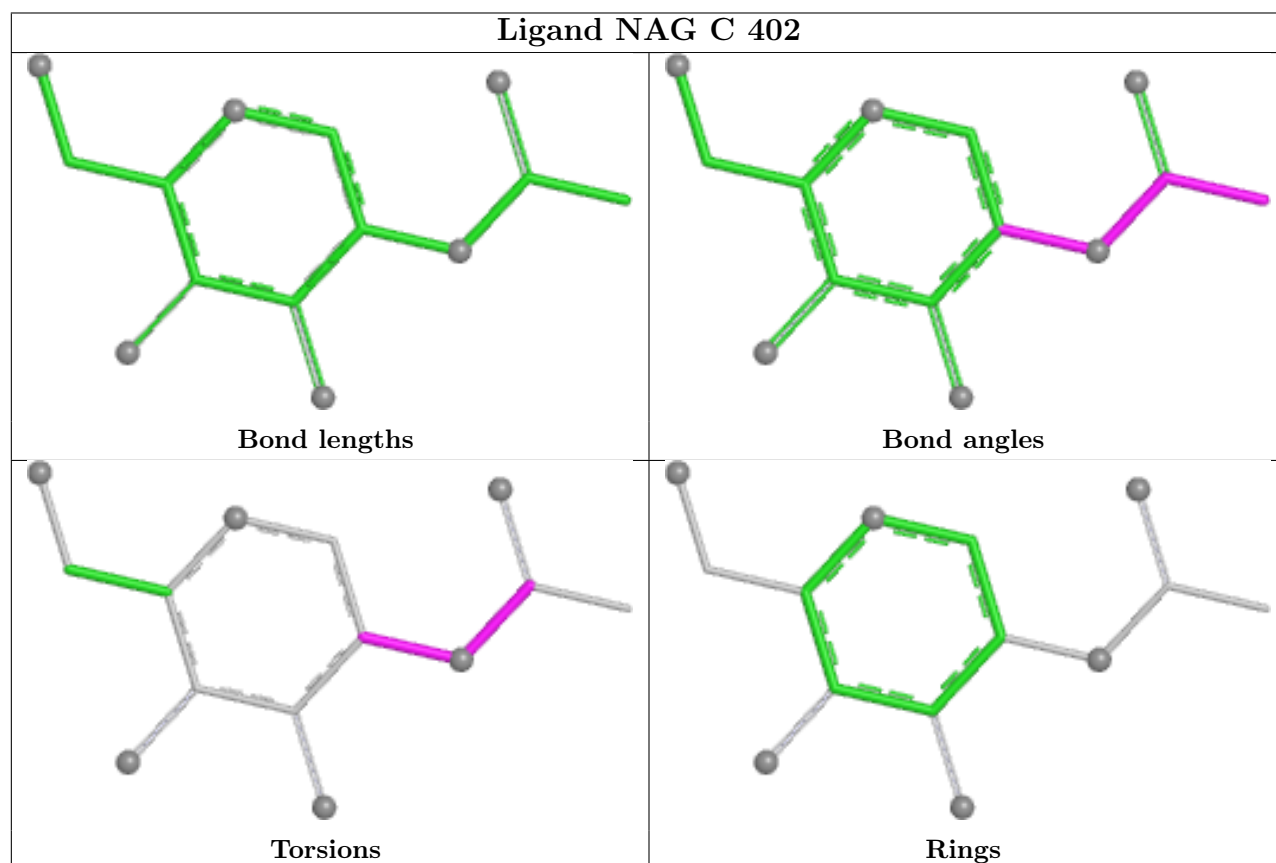
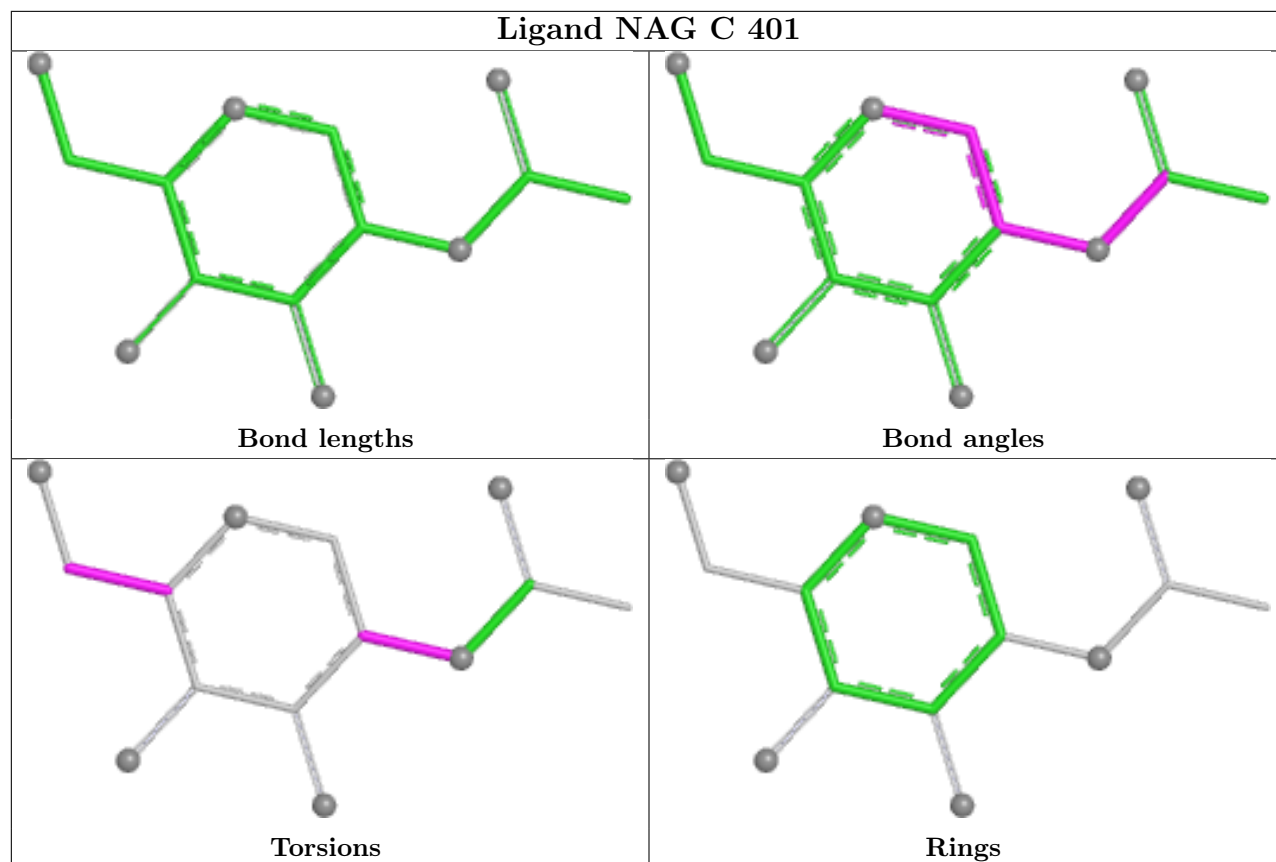
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	402	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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	322/328 (98%)	0.40	20 (6%)	26	20	45, 68, 99, 147	0
1	C	324/328 (98%)	0.43	23 (7%)	22	16	42, 67, 103, 150	0
1	E	323/328 (98%)	0.22	12 (3%)	45	37	43, 63, 93, 149	0
2	B	169/177 (95%)	0.61	13 (7%)	19	14	52, 75, 111, 137	0
2	D	169/177 (95%)	1.05	29 (17%)	4	3	51, 92, 122, 135	0
2	F	172/177 (97%)	0.48	8 (4%)	36	28	57, 73, 98, 122	0
All	All	1479/1515 (97%)	0.48	105 (7%)	22	16	42, 70, 106, 150	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	173	ILE	8.9
1	C	80	ILE	8.1
2	B	7	ALA	7.2
1	A	79	PHE	7.0
1	E	79	PHE	6.9
2	B	8	GLY	6.5
2	B	174	SER	6.5
1	C	9	PRO	5.5
2	D	6	ILE	5.5
1	A	9	PRO	5.2
2	D	10	ILE	4.9
2	D	7	ALA	4.9
1	C	324	PRO	4.7
1	C	319	GLY	4.6
1	C	8	ASP	4.2
1	C	78	GLU	4.2
1	C	79	PHE	4.2
1	A	323	SER	4.1
2	D	18	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
2	D	38	LYS	4.1
2	B	9	PHE	4.1
1	A	318	THR	4.1
2	F	10	ILE	4.0
2	F	155	GLY	3.8
1	A	91	ALA	3.8
1	E	81	ARG	3.5
1	E	323	SER	3.5
1	A	277	CYS	3.5
2	F	8	GLY	3.4
2	D	21	TRP	3.4
1	A	82	VAL	3.3
1	A	80	ILE	3.2
1	C	21	ASN	3.2
1	E	80	ILE	3.2
1	C	81	ARG	3.1
2	D	68	ARG	3.1
1	C	189	GLU	3.1
2	D	172	GLU	3.1
2	B	6	ILE	3.1
2	B	10	ILE	3.1
2	D	144	CYS	3.1
2	F	6	ILE	3.1
1	E	78	GLU	3.1
2	B	19	ASP	3.1
2	D	36	ALA	3.1
1	E	173	ARG	3.1
1	C	262	LYS	3.0
1	E	96	ASP	2.9
1	A	62	LYS	2.9
2	D	17	MET	2.8
2	B	121	LYS	2.7
1	E	221	SER	2.7
2	D	35	ALA	2.7
2	D	168	LEU	2.7
2	B	16	GLY	2.7
2	D	148	CYS	2.6
1	A	32	LYS	2.6
1	A	64	CYS	2.6
2	D	15	GLN	2.6
1	A	81	ARG	2.6
2	D	134	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	323	SER	2.5
2	D	174	SER	2.5
1	C	227	ARG	2.4
2	B	165	GLU	2.4
2	D	171	GLU	2.4
1	C	19	ALA	2.4
2	F	172	GLU	2.4
1	A	10	GLY	2.4
2	D	11	GLU	2.4
1	C	280	LYS	2.4
2	D	29	GLU	2.4
2	D	14	TRP	2.4
1	E	276	HIS	2.3
1	E	281	CYS	2.3
1	A	276	HIS	2.3
2	D	26	HIS	2.3
2	B	61	THR	2.3
1	C	12	GLN	2.3
2	D	155	GLY	2.3
1	C	82	VAL	2.3
2	F	17	MET	2.3
1	A	290	SER	2.3
1	A	317	ALA	2.2
1	E	277	CYS	2.2
1	A	75	MET	2.2
1	C	91	ALA	2.2
2	D	32	SER	2.2
1	C	50	LYS	2.1
1	A	52	CYS	2.1
2	D	16	GLY	2.1
2	D	20	GLY	2.1
2	D	27	SER	2.1
1	A	310	LYS	2.1
2	B	29	GLU	2.1
2	F	11	GLU	2.1
1	C	240	ASN	2.1
1	C	27	ASP	2.0
2	D	112	ASP	2.0
1	C	317	ALA	2.0
1	E	313	LYS	2.0
1	A	142	GLN	2.0
2	B	18	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
2	F	144	CYS	2.0
1	C	25	GLN	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](#)

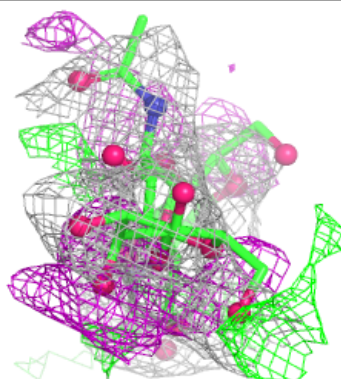
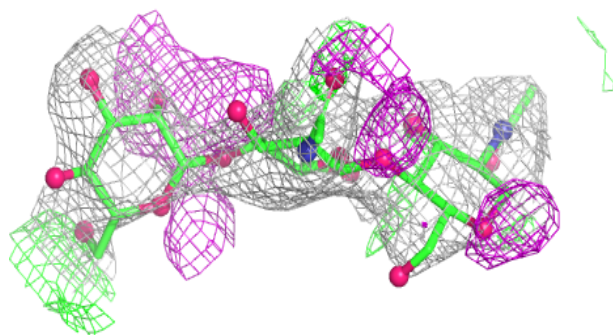
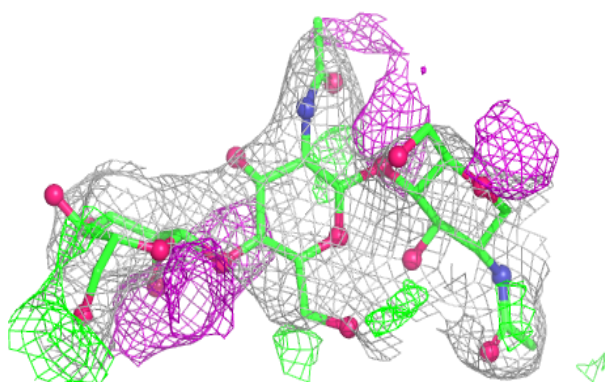
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BMA	J	3	11/12	0.53	0.14	103,129,137,138	0
4	NAG	I	2	14/15	0.56	0.20	109,130,139,144	0
3	BMA	G	3	11/12	0.58	0.32	74,125,142,148	0
5	GAL	K	1	12/12	0.59	0.13	124,161,176,179	0
3	NAG	G	2	14/15	0.69	0.24	87,113,124,129	0
3	BMA	H	3	11/12	0.71	0.19	73,102,121,125	0
3	NAG	J	1	14/15	0.77	0.16	78,99,109,110	0
5	NAG	K	2	14/15	0.79	0.14	97,121,135,135	0
3	NAG	J	2	14/15	0.81	0.17	90,105,125,129	0
3	NAG	G	1	14/15	0.83	0.20	76,91,105,118	0
3	NAG	H	2	14/15	0.87	0.15	71,86,93,93	0
3	NAG	H	1	14/15	0.87	0.15	59,82,101,111	0
4	NAG	I	1	14/15	0.90	0.12	78,92,111,128	0
5	GAL	K	3	11/12	0.90	0.11	66,80,90,97	0
5	SIA	K	4	20/21	0.94	0.12	48,67,83,85	0

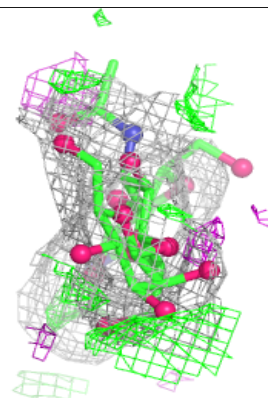
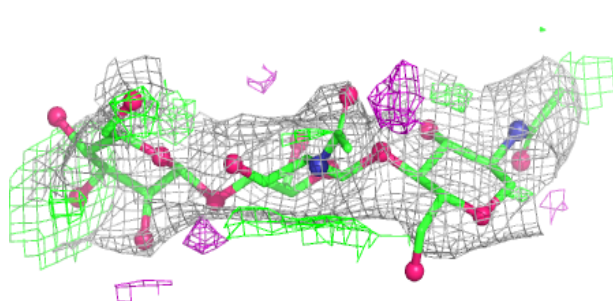
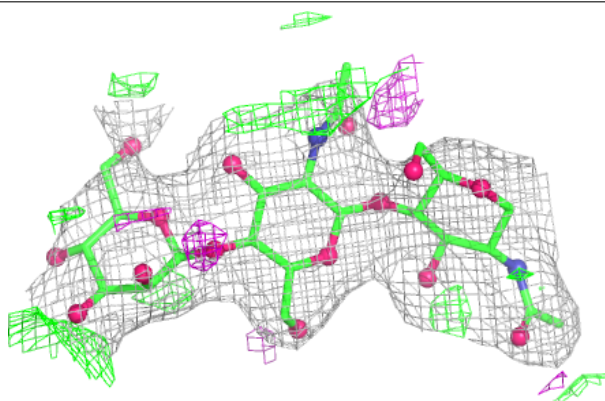
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain G:

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

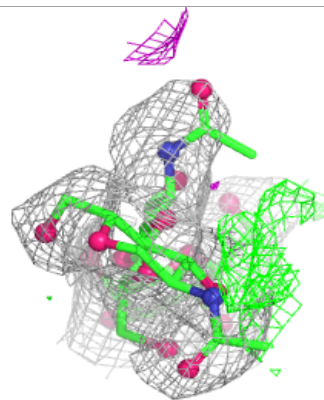
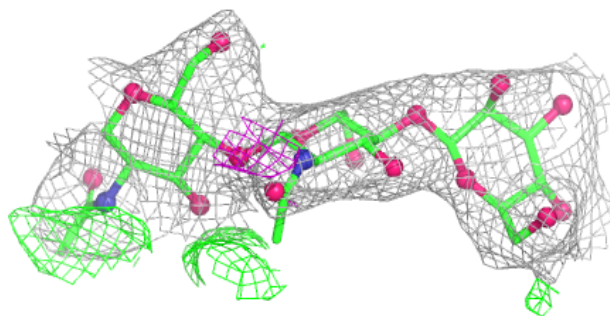
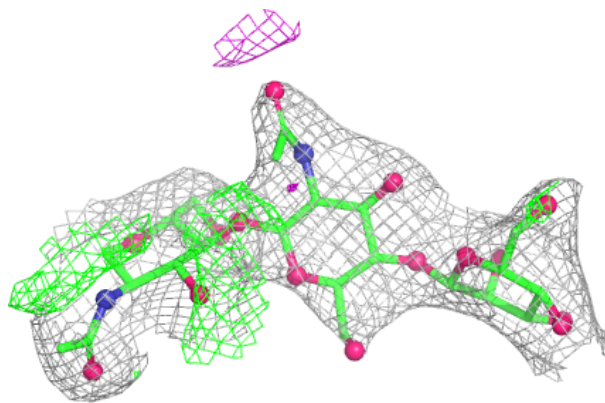
**Electron density around Chain H:**

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



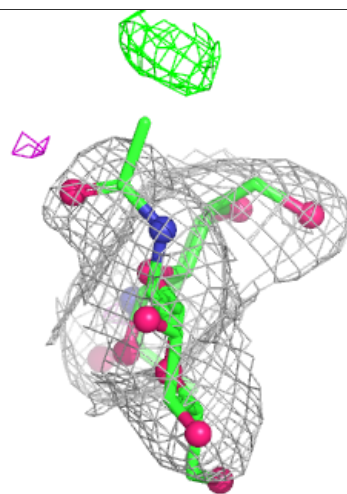
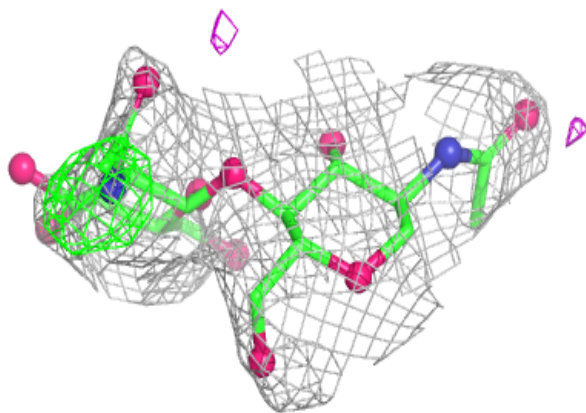
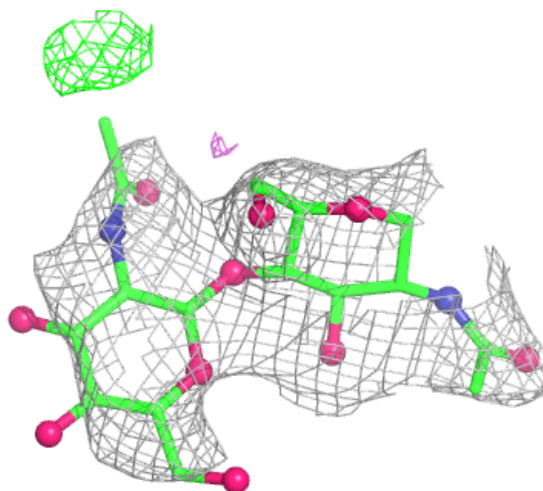
Electron density around Chain J:

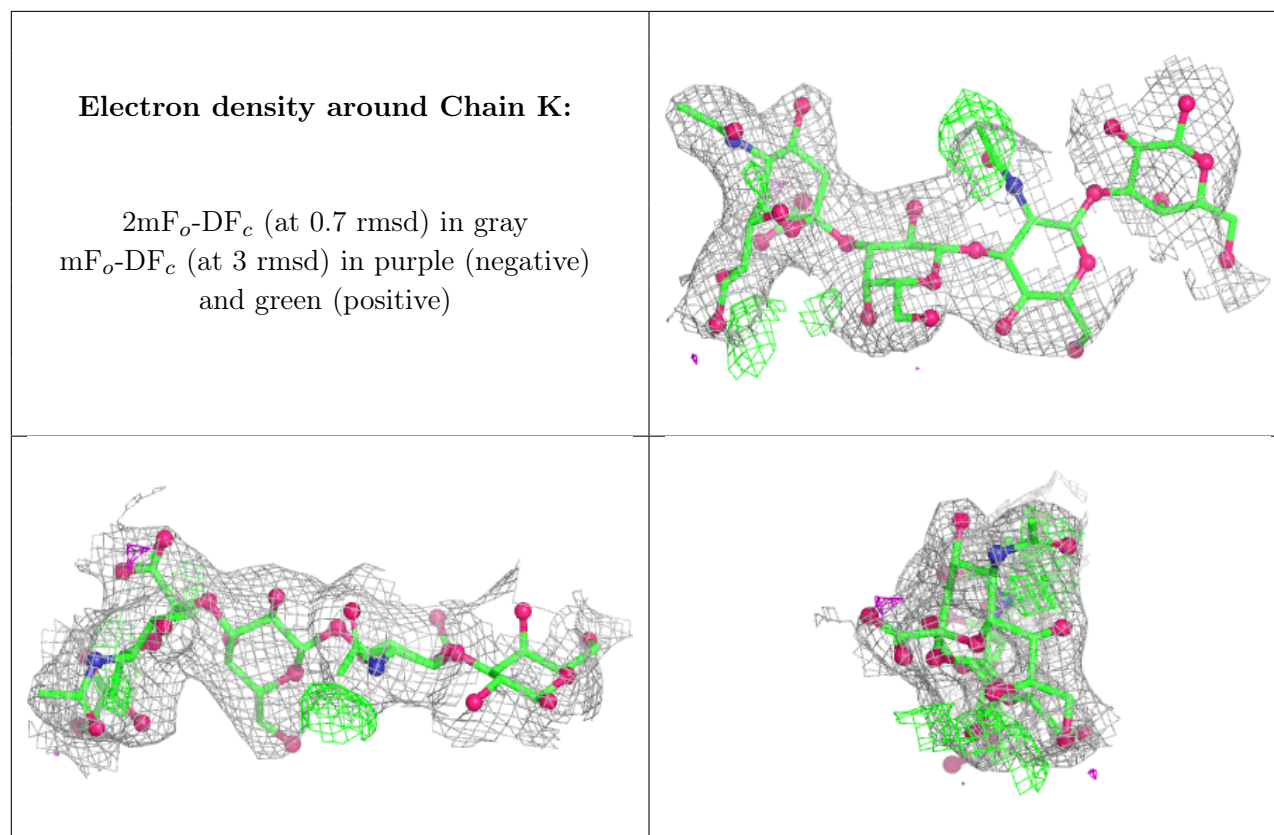
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain I:

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





6.4 Ligands [i](#)

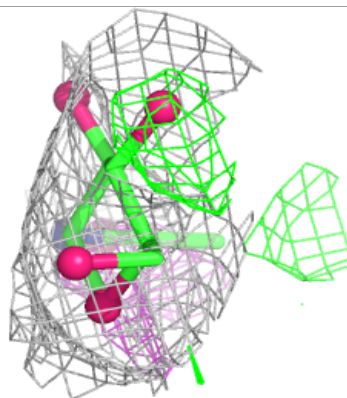
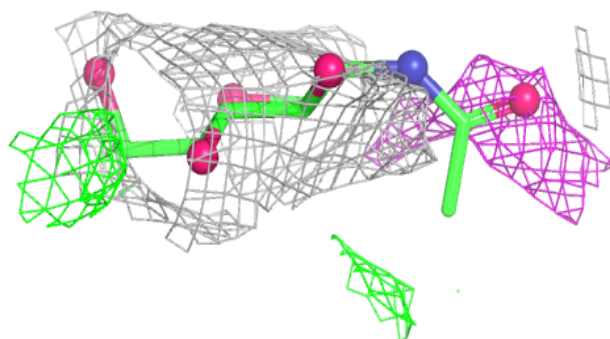
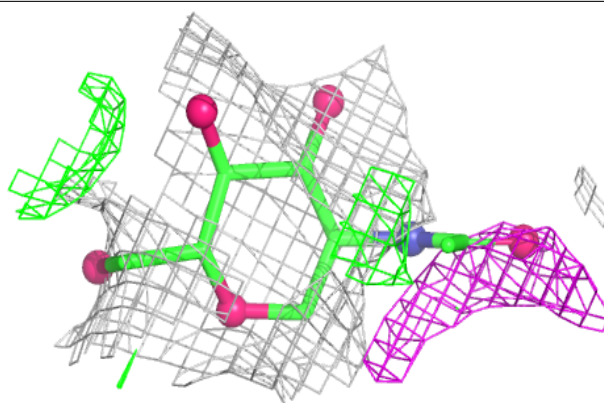
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NAG	C	402	14/15	0.58	0.22	96,135,143,145	0
6	NAG	D	201	14/15	0.63	0.18	109,126,143,149	0
6	NAG	C	401	14/15	0.65	0.17	92,118,129,133	0
6	NAG	A	402	14/15	0.67	0.26	106,116,141,148	0
6	NAG	E	401	14/15	0.71	0.18	91,119,132,133	0
6	NAG	A	401	14/15	0.78	0.16	104,118,130,131	0

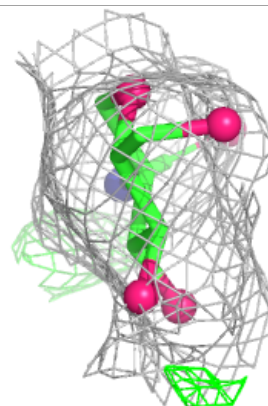
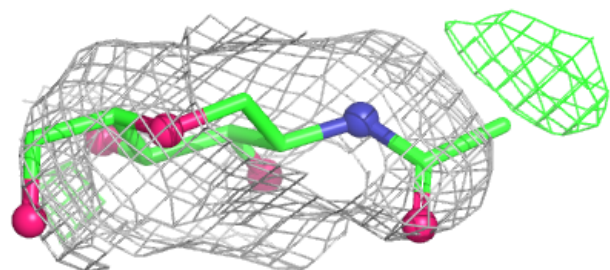
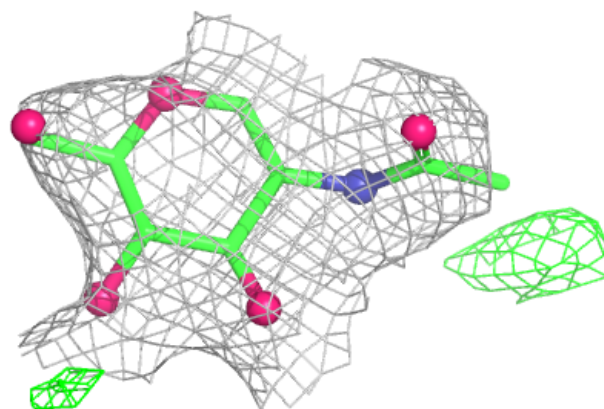
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NAG C 402:

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

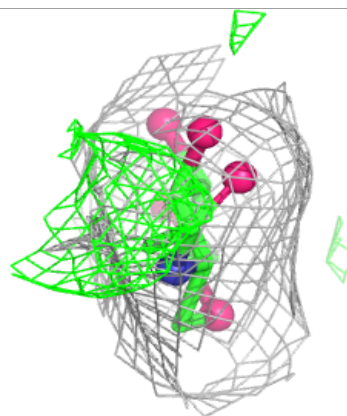
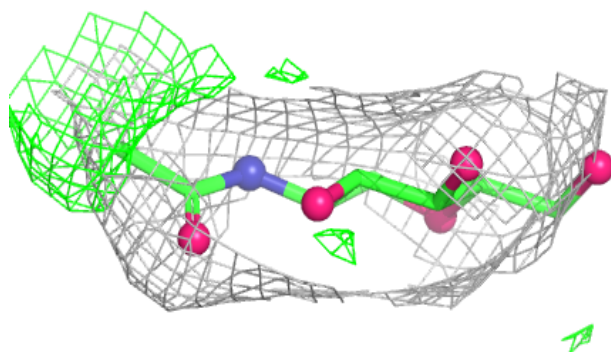
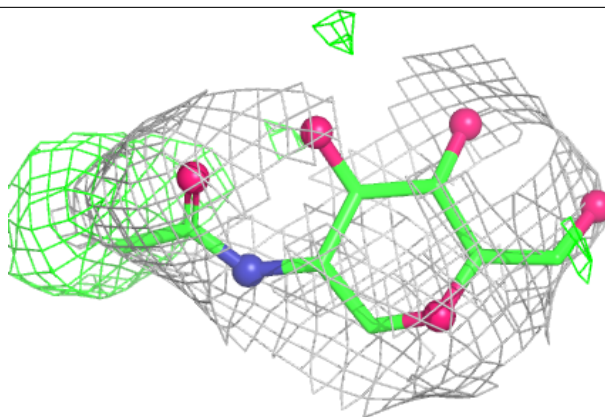
**Electron density around NAG D 201:**

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

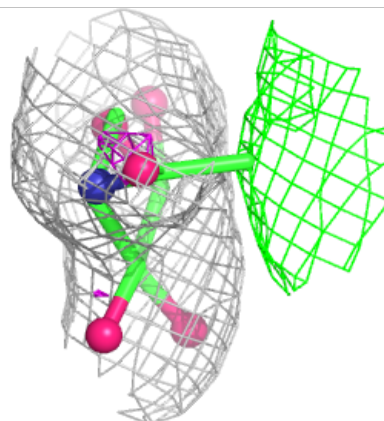
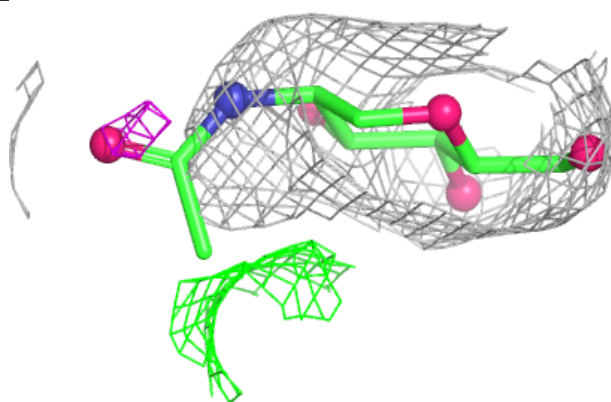
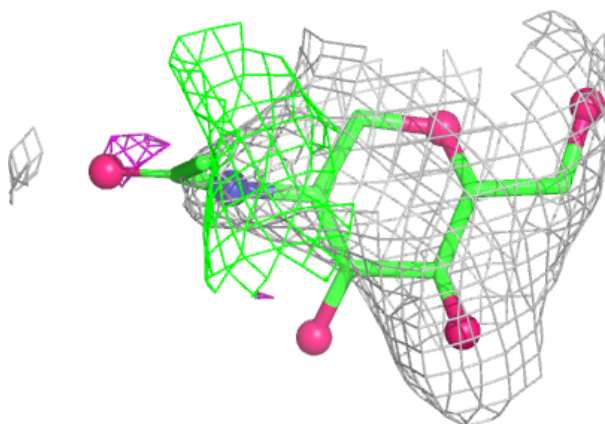


Electron density around NAG C 401:

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

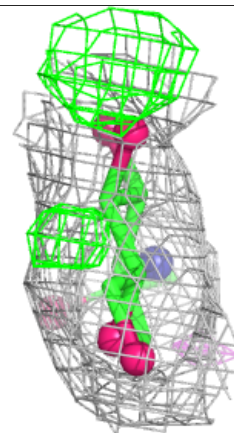
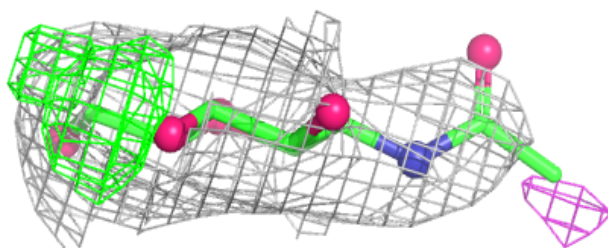
**Electron density around NAG A 402:**

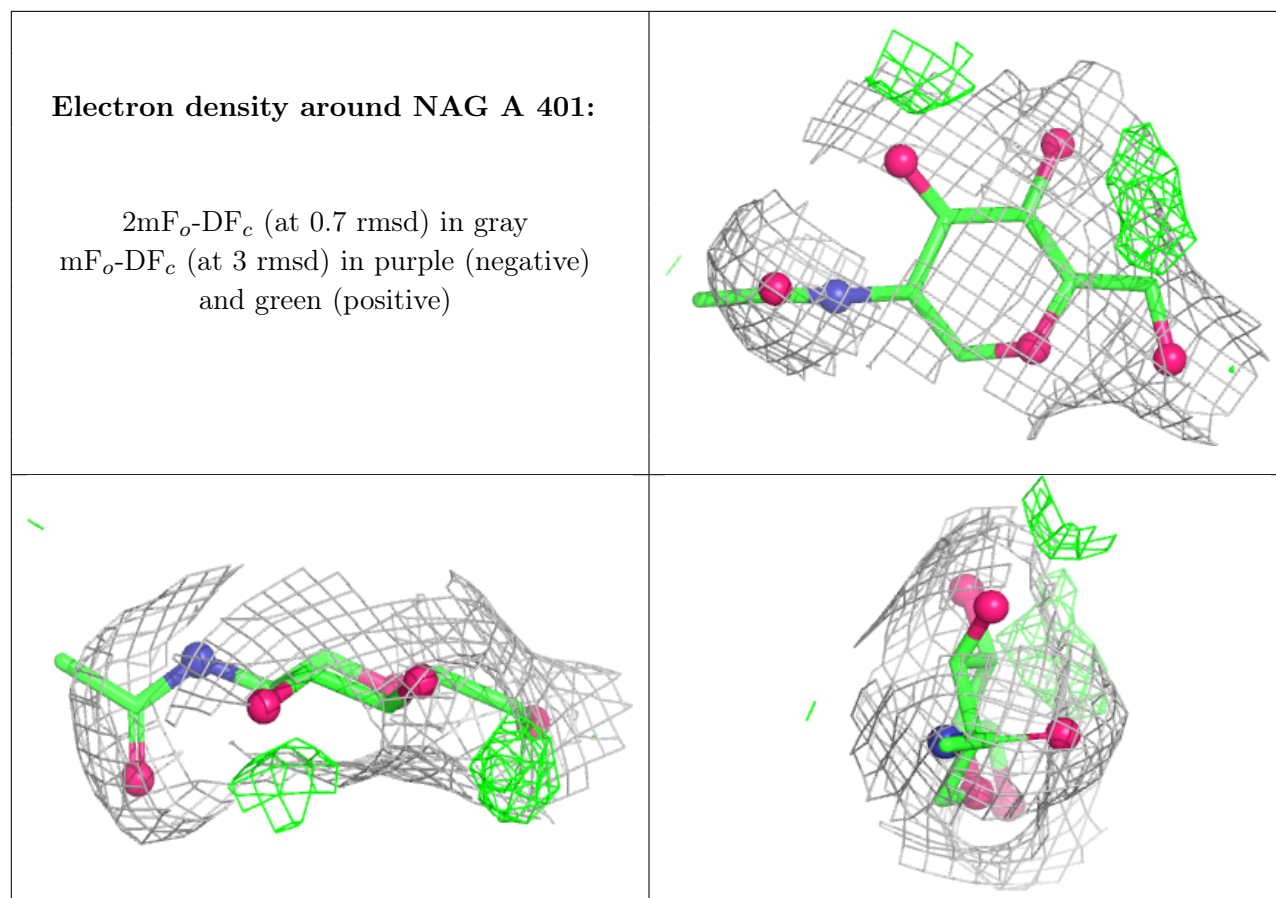
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around NAG E 401:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.