



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 20, 2026 – 10:31 am BST

PDB ID : 9TDL / pdb_00009tdl
Title : Complex between complement C5 and cobra venom factor, re-refined
Authors : Andersen, G.R.
Deposited on : 2025-11-24
Resolution : 4.30 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 : 1.8.4, CSD as541be (2020)
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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

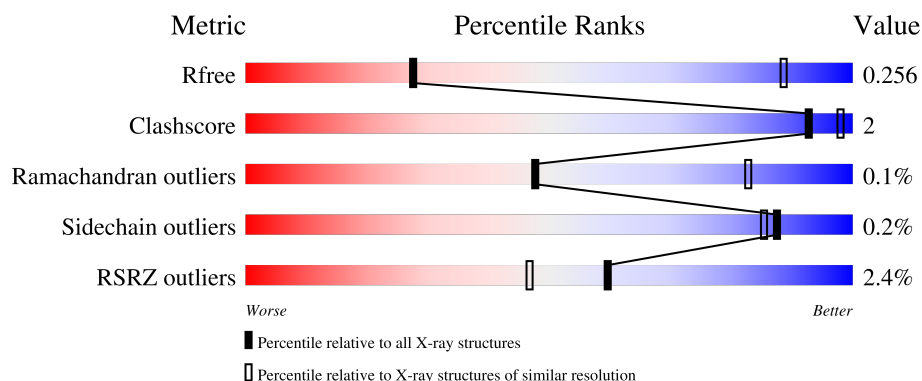
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.30 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.



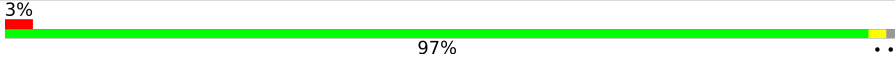
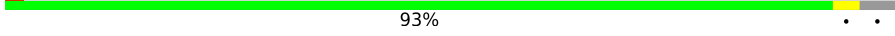
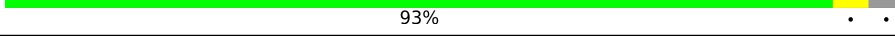
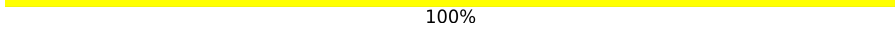
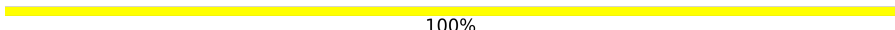
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1052 (4.70-3.90)
Clashscore	190562	1097 (4.70-3.90)
Ramachandran outliers	187476	1001 (4.70-3.90)
Sidechain outliers	187428	1007 (4.72-3.88)
RSRZ outliers	180081	1049 (4.70-3.90)

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	655	
1	B	655	
2	C	999	
2	D	999	
3	J	627	

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Mol	Chain	Length	Quality of chain
3	M	627	
4	K	252	
4	N	252	
5	L	379	
5	O	379	
6	G	2	
6	H	2	
6	I	2	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 90594 atoms, of which 45225 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 Complement C5 beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	640	Total	C	H	N	O	S	0	0	0
			10030	3245	4979	811	983	12			
1	B	640	Total	C	H	N	O	S	0	0	0
			10030	3245	4979	811	983	12			

- Molecule 2 is a protein called Complement C5 alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	996	Total	C	H	N	O	S	0	0	0
			15802	5043	7910	1318	1490	41			
2	D	995	Total	C	H	N	O	S	0	0	0
			15782	5037	7898	1317	1489	41			

- Molecule 3 is a protein called Cobra venom factor alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	J	621	Total	C	H	N	O	S	0	0	0
			9716	3104	4857	818	921	16			
3	M	622	Total	C	H	N	O	S	0	0	0
			9731	3108	4869	817	921	16			

- Molecule 4 is a protein called Cobra venom factor gamma chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	K	234	Total	C	H	N	O	S	0	0	0
			3771	1199	1906	312	349	5			
4	N	234	Total	C	H	N	O	S	0	0	0
			3771	1199	1906	312	349	5			

- Molecule 5 is a protein called Cobra venom factor beta chain.

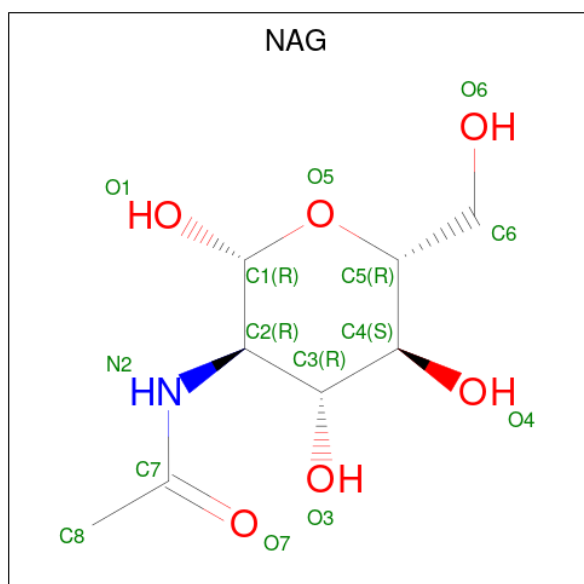
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
5	L	365	Total	C	H	N	O	S	0	0	0
			5847	1860	2897	495	576	19			
5	O	365	Total	C	H	N	O	S	0	0	0
			5847	1860	2897	495	576	19			

- Molecule 6 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
6	G	2	Total	C	H	N	O		0	0	0
			53	16	25	2	10				
6	H	2	Total	C	H	N	O		0	0	0
			53	16	25	2	10				
6	I	2	Total	C	H	N	O		0	0	0
			53	16	25	2	10				

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
7	J	1	Total	C	H	N	O		0	0
			27	8	13	1	5			

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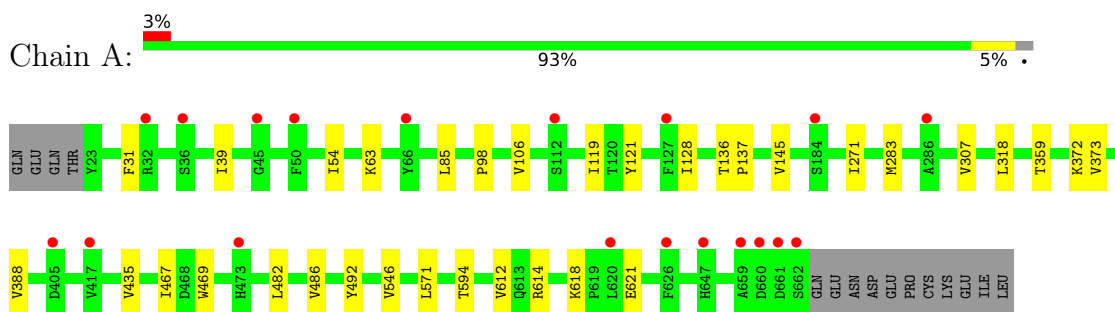
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	D	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
7	M	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
7	O	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

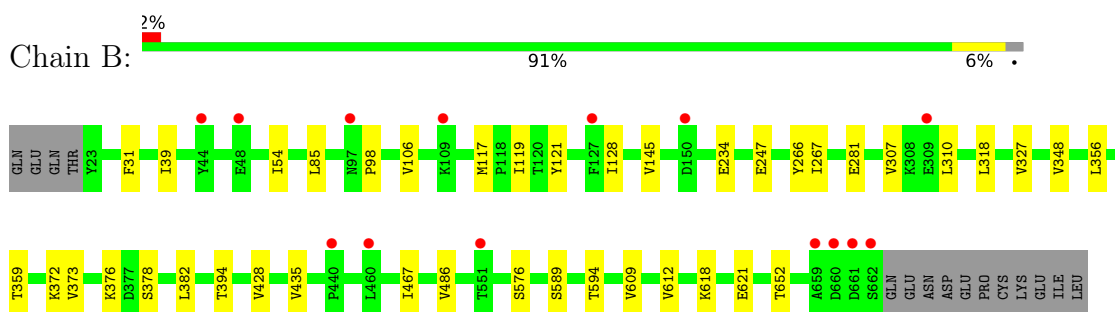
3 Residue-property plots [i](#)

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.

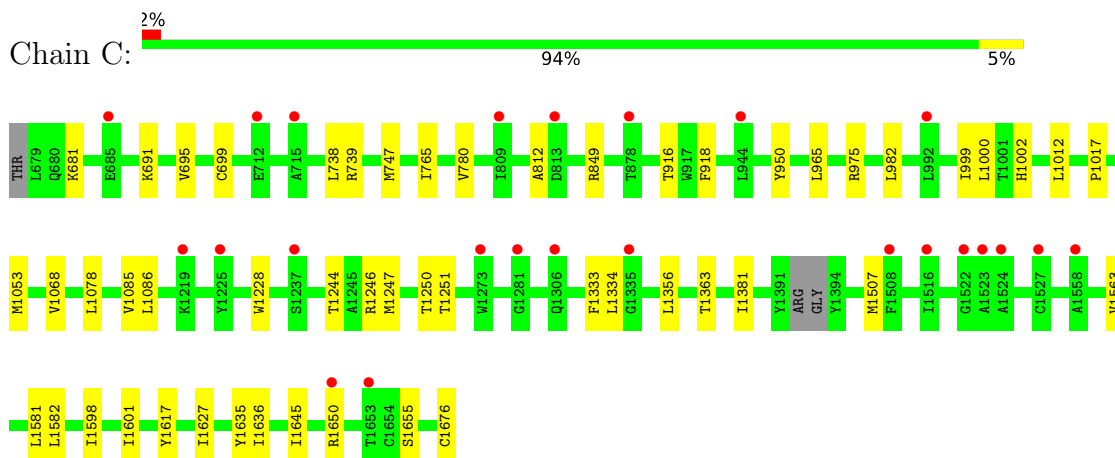
- Molecule 1: Complement C5 beta chain



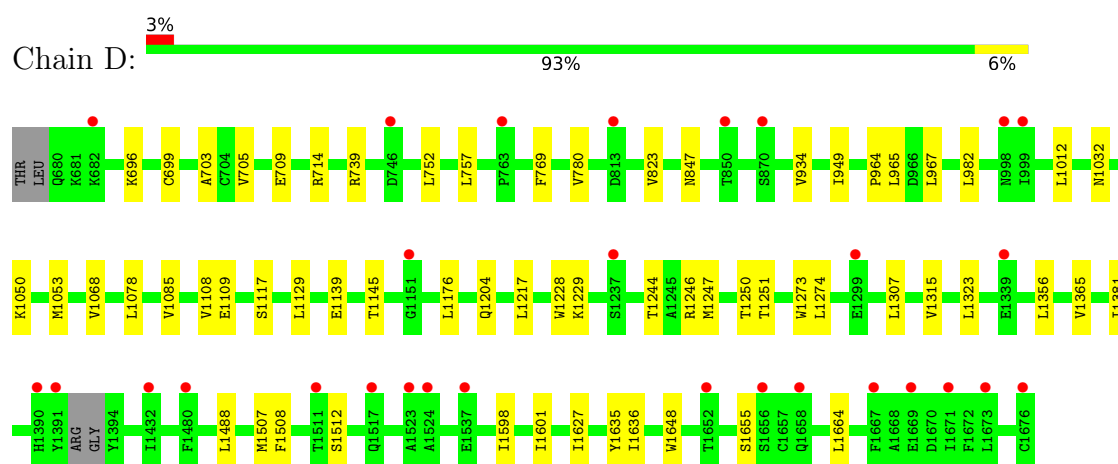
- Molecule 1: Complement C5 beta chain



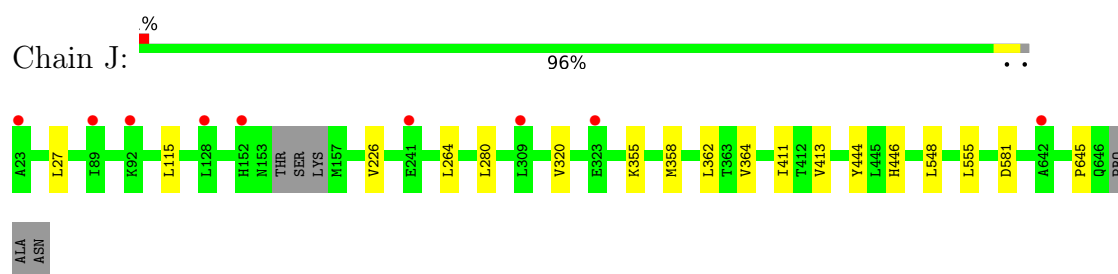
- Molecule 2: Complement C5 alpha chain



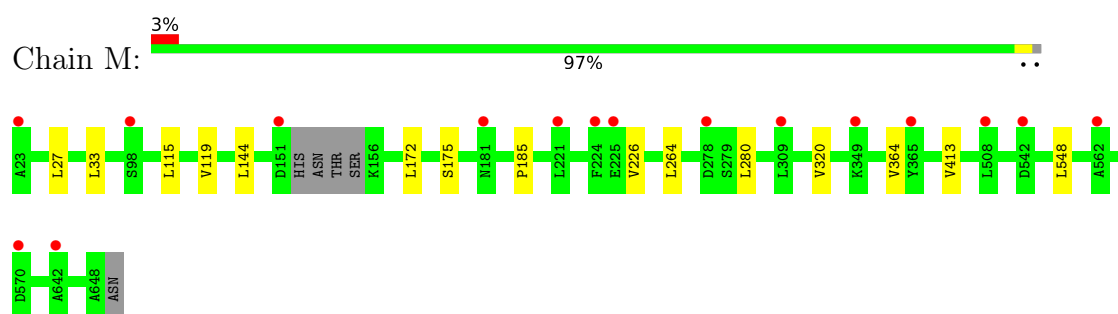
- Molecule 2: Complement C5 alpha chain



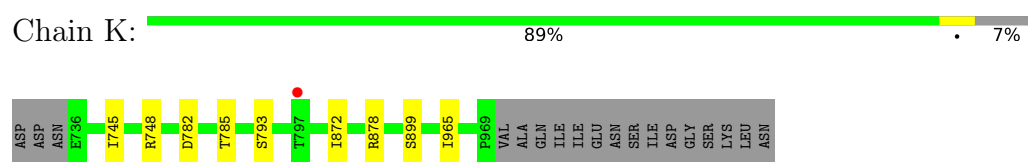
• Molecule 3: Cobra venom factor alpha chain



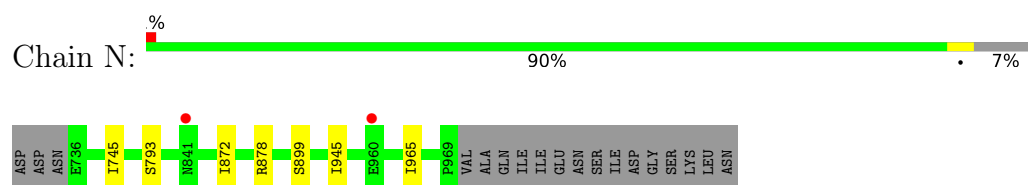
• Molecule 3: Cobra venom factor alpha chain



• Molecule 4: Cobra venom factor gamma chain



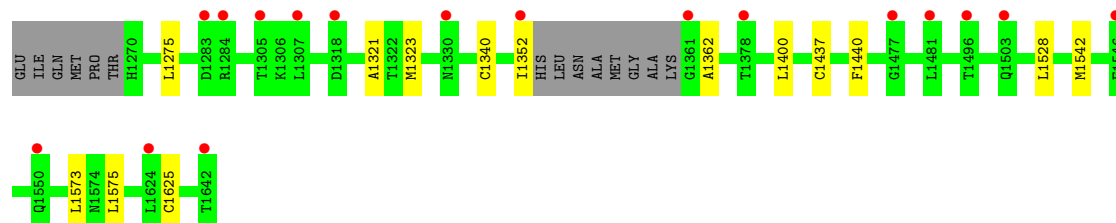
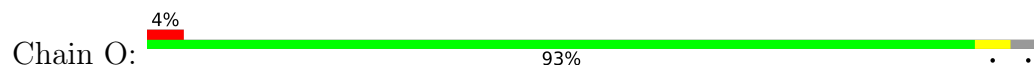
• Molecule 4: Cobra venom factor gamma chain



• Molecule 5: Cobra venom factor beta chain



- Molecule 5: Cobra venom factor beta chain



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	176.52Å 179.20Å 389.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.47 – 4.30 49.47 – 4.30	Depositor EDS
% Data completeness (in resolution range)	94.2 (49.47-4.30) 94.2 (49.47-4.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 4.29Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.202 , 0.257 0.201 , 0.256	Depositor DCC
R_{free} test set	1734 reflections (2.05%)	wwPDB-VP
Wilson B-factor (Å ²)	135.2	Xtriage
Anisotropy	0.503	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 190.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.026 for k,h,-l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	90594	wwPDB-VP
Average B, all atoms (Å ²)	213.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.26	0/5170	0.51	0/7033
1	B	0.27	0/5170	0.53	0/7033
2	C	0.28	0/8055	0.53	0/10908
2	D	0.27	0/8047	0.54	0/10897
3	J	0.26	0/4968	0.51	0/6758
3	M	0.26	0/4971	0.50	0/6762
4	K	0.26	0/1903	0.48	0/2582
4	N	0.27	0/1903	0.49	0/2582
5	L	0.27	0/3002	0.55	0/4060
5	O	0.29	0/3002	0.56	0/4060
All	All	0.27	0/46191	0.53	0/62675

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
2	C	0	1
2	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	1655	SER	Peptide

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Mol	Chain	Res	Type	Group
2	D	1655	SER	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5051	4979	4979	19	0
1	B	5051	4979	4979	25	0
2	C	7892	7910	7910	28	0
2	D	7884	7898	7898	35	0
3	J	4859	4857	4857	12	0
3	M	4862	4869	4869	8	0
4	K	1865	1906	1906	7	0
4	N	1865	1906	1906	5	0
5	L	2950	2897	2897	7	0
5	O	2950	2897	2897	8	0
6	G	28	25	25	0	0
6	H	28	25	25	1	0
6	I	28	25	25	0	0
7	D	14	13	13	0	0
7	J	14	13	13	0	0
7	M	14	13	13	0	0
7	O	14	13	13	0	0
All	All	45369	45225	45225	139	0

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

The worst 5 of 139 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:B:594:THR:HG21	2:D:780:VAL:HG21	1.66	0.77
3:J:358:MET:HE1	3:J:444:TYR:HB3	1.76	0.67
1:A:594:THR:HG21	2:C:780:VAL:HG21	1.78	0.64
1:A:373:VAL:HG11	1:A:435:VAL:HG11	1.82	0.62
2:D:1247:MET:HA	2:D:1250:THR:HG22	1.81	0.62

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	638/655 (97%)	608 (95%)	29 (4%)	1 (0%)	43	77
1	B	638/655 (97%)	609 (96%)	29 (4%)	0	100	100
2	C	992/999 (99%)	942 (95%)	49 (5%)	1 (0%)	48	83
2	D	991/999 (99%)	941 (95%)	49 (5%)	1 (0%)	48	83
3	J	617/627 (98%)	595 (96%)	21 (3%)	1 (0%)	43	77
3	M	618/627 (99%)	598 (97%)	20 (3%)	0	100	100
4	K	232/252 (92%)	223 (96%)	9 (4%)	0	100	100
4	N	232/252 (92%)	222 (96%)	10 (4%)	0	100	100
5	L	361/379 (95%)	347 (96%)	14 (4%)	0	100	100
5	O	361/379 (95%)	348 (96%)	13 (4%)	0	100	100
All	All	5680/5824 (98%)	5433 (96%)	243 (4%)	4 (0%)	48	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	982	LEU
3	J	645	PRO
1	A	614	ARG
2	D	982	LEU

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	565/580 (97%)	565 (100%)	0	100	100
1	B	565/580 (97%)	565 (100%)	0	100	100
2	C	884/886 (100%)	882 (100%)	2 (0%)	87	85
2	D	883/886 (100%)	882 (100%)	1 (0%)	88	88
3	J	543/548 (99%)	543 (100%)	0	100	100
3	M	543/548 (99%)	543 (100%)	0	100	100
4	K	211/227 (93%)	211 (100%)	0	100	100
4	N	211/227 (93%)	211 (100%)	0	100	100
5	L	334/345 (97%)	331 (99%)	3 (1%)	70	76
5	O	334/345 (97%)	331 (99%)	3 (1%)	70	76
All	All	5073/5172 (98%)	5064 (100%)	9 (0%)	87	85

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	O	1437	CYS
5	O	1625	CYS
5	L	1437	CYS
5	L	1625	CYS
2	D	699	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
3	M	385	HIS
3	M	507	ASN
5	O	1622	GLN
3	J	407	GLN
3	J	385	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

6 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
6	NAG	G	1	2,6	14,14,15	0.82	0	17,19,21	1.36	2 (11%)
6	NAG	G	2	6	14,14,15	1.38	3 (21%)	17,19,21	1.19	1 (5%)
6	NAG	H	1	5,6	14,14,15	0.97	0	17,19,21	1.59	4 (23%)
6	NAG	H	2	6	14,14,15	0.77	0	17,19,21	0.81	0
6	NAG	I	1	2,6	14,14,15	0.79	0	17,19,21	1.09	1 (5%)
6	NAG	I	2	6	14,14,15	0.87	0	17,19,21	1.20	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	G	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	G	2	6	-	0/6/23/26	0/1/1/1
6	NAG	H	1	5,6	-	0/6/23/26	0/1/1/1
6	NAG	H	2	6	-	0/6/23/26	0/1/1/1
6	NAG	I	1	2,6	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	G	2	NAG	O5-C1	-3.79	1.37	1.43
6	G	2	NAG	C1-C2	-2.23	1.49	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	G	2	NAG	C2-N2	-2.04	1.42	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	1	NAG	C4-C3-C2	-3.71	105.58	111.02
6	H	1	NAG	O4-C4-C3	-2.97	103.48	110.35
6	I	2	NAG	O5-C1-C2	-2.78	106.89	111.29
6	G	1	NAG	C1-O5-C5	2.67	115.81	112.19
6	H	1	NAG	C6-C5-C4	2.34	118.47	113.00

There are no chirality outliers.

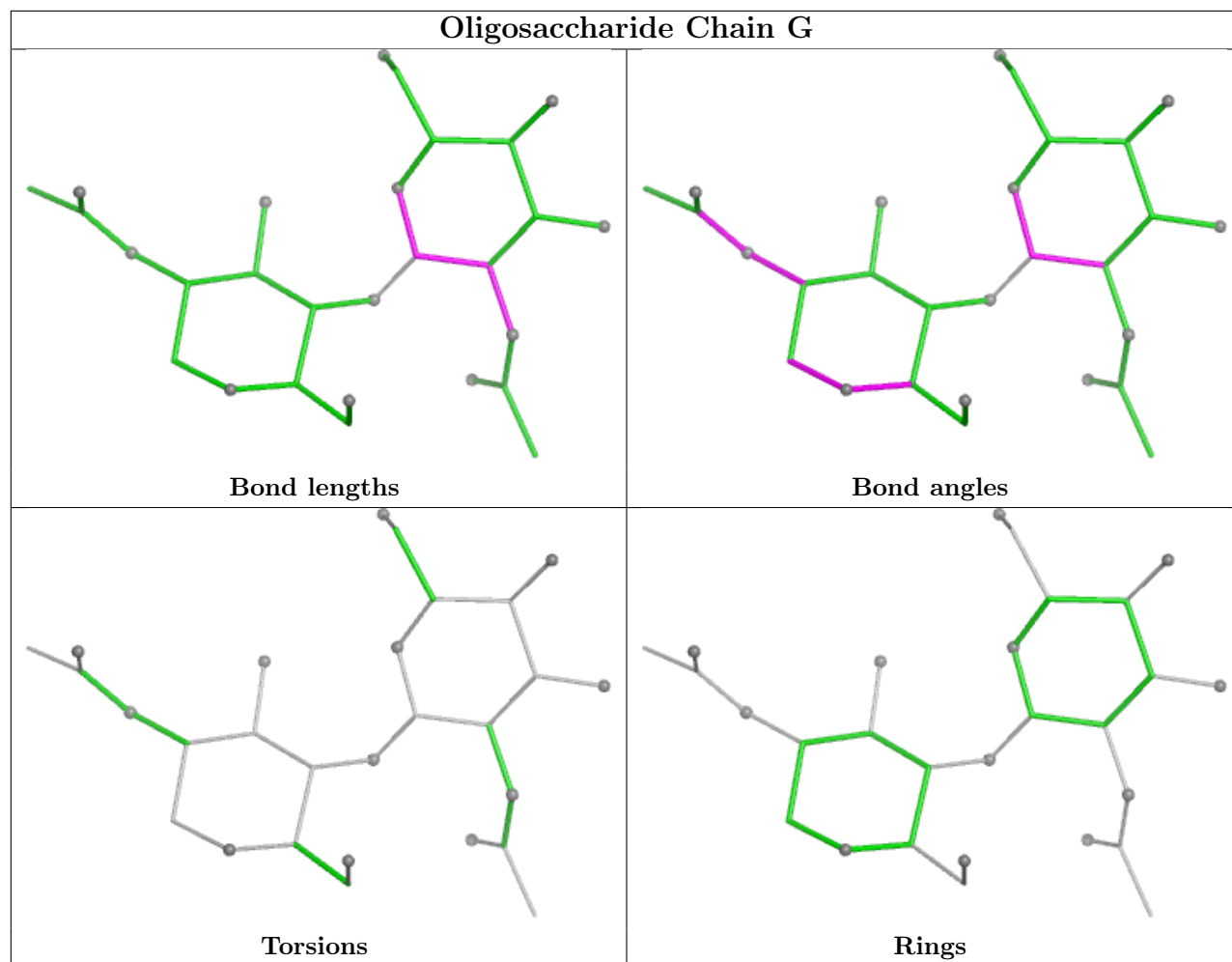
There are no torsion outliers.

There are no ring outliers.

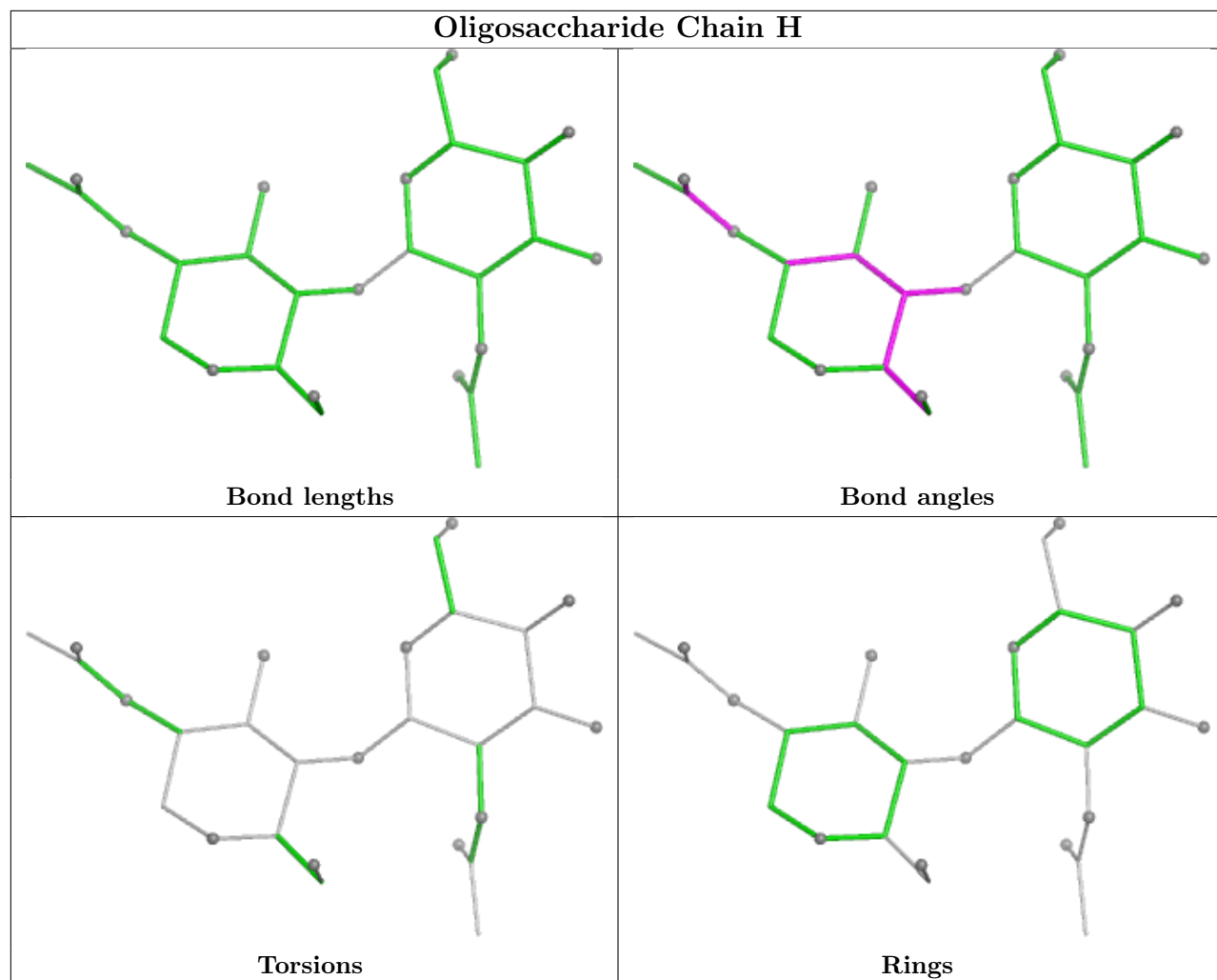
1 monomer is involved in 1 short contact:

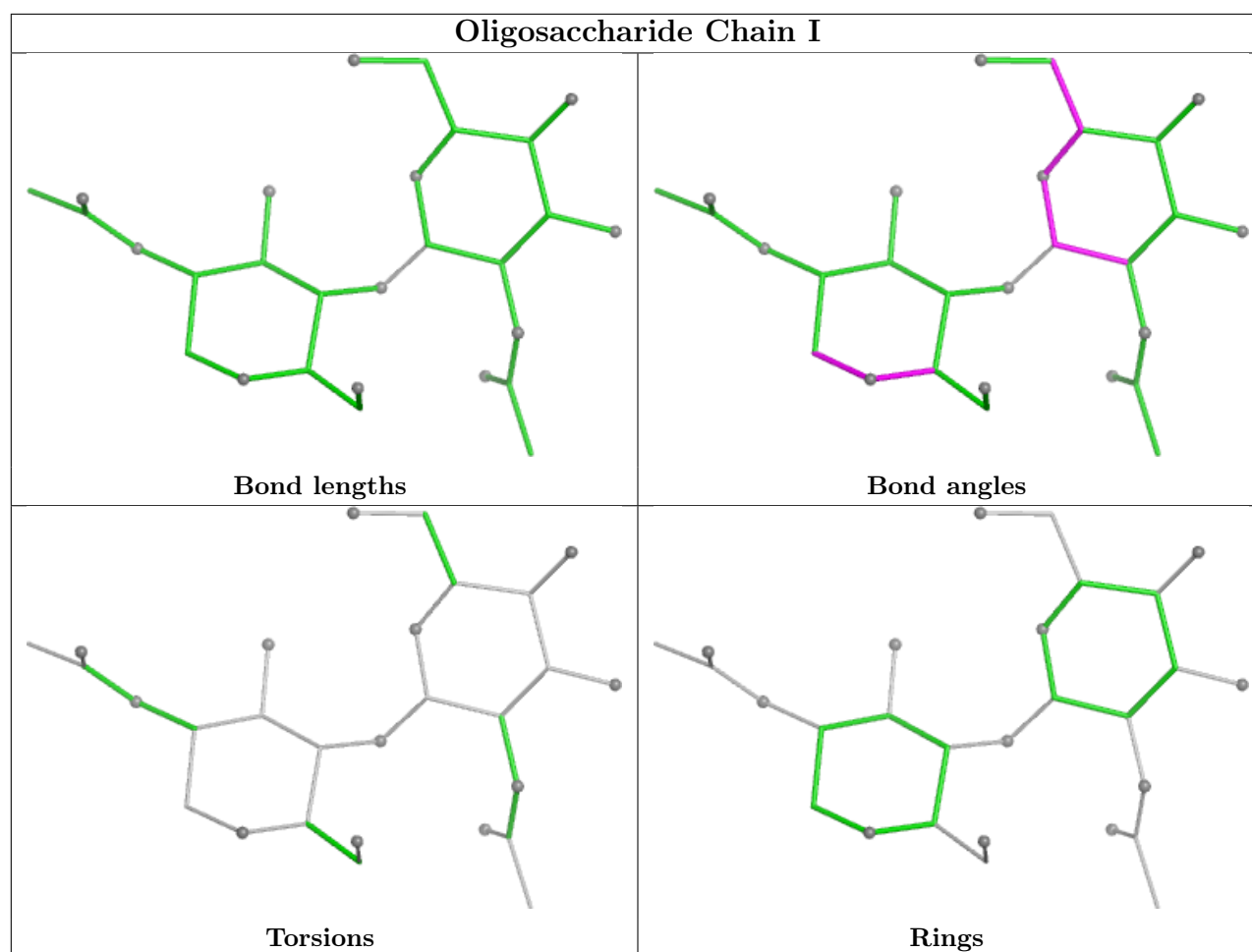
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	1	NAG	1	0

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



Oligosaccharide Chain H





5.6 Ligand geometry [i](#)

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	O	1701	5	14,14,15	0.71	0	17,19,21	1.73	4 (23%)
7	NAG	D	1701	2	14,14,15	0.99	1 (7%)	17,19,21	3.11	5 (29%)
7	NAG	M	1701	3	14,14,15	0.67	0	17,19,21	1.08	1 (5%)
7	NAG	J	1701	3	14,14,15	0.81	0	17,19,21	1.29	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
7	NAG	O	1701	5	-	3/6/23/26	0/1/1/1
7	NAG	D	1701	2	-	1/6/23/26	0/1/1/1
7	NAG	M	1701	3	-	0/6/23/26	0/1/1/1
7	NAG	J	1701	3	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	1701	NAG	O5-C1	-2.67	1.39	1.43

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	1701	NAG	C1-O5-C5	-10.56	97.89	112.19
7	O	1701	NAG	C2-N2-C7	4.42	129.20	122.90
7	J	1701	NAG	C2-N2-C7	3.98	128.56	122.90
7	D	1701	NAG	C6-C5-C4	3.65	121.54	113.00
7	D	1701	NAG	O4-C4-C3	-3.27	102.79	110.35

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

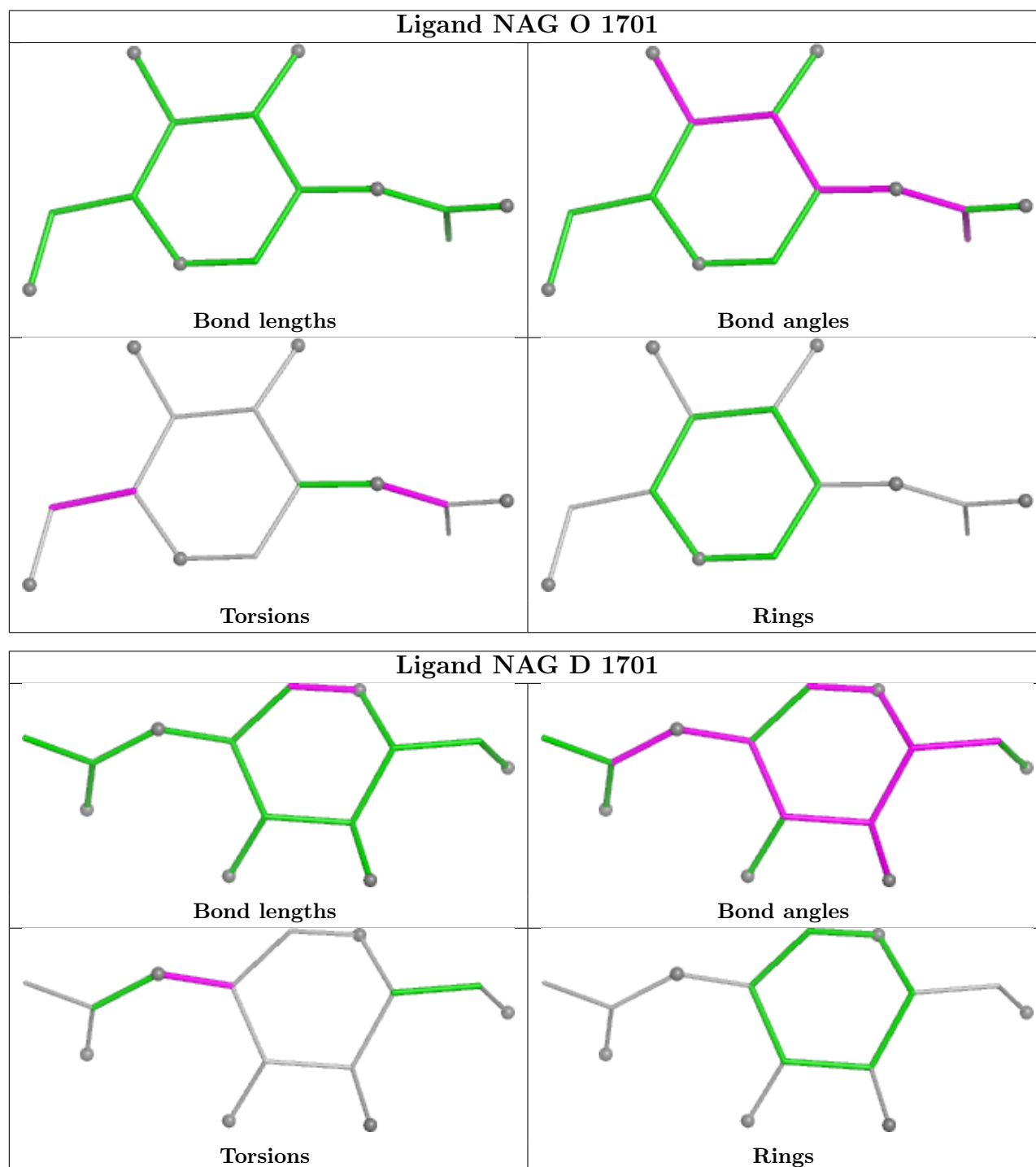
Mol	Chain	Res	Type	Atoms
7	D	1701	NAG	C1-C2-N2-C7
7	J	1701	NAG	C8-C7-N2-C2
7	J	1701	NAG	O7-C7-N2-C2
7	O	1701	NAG	C8-C7-N2-C2
7	O	1701	NAG	O7-C7-N2-C2

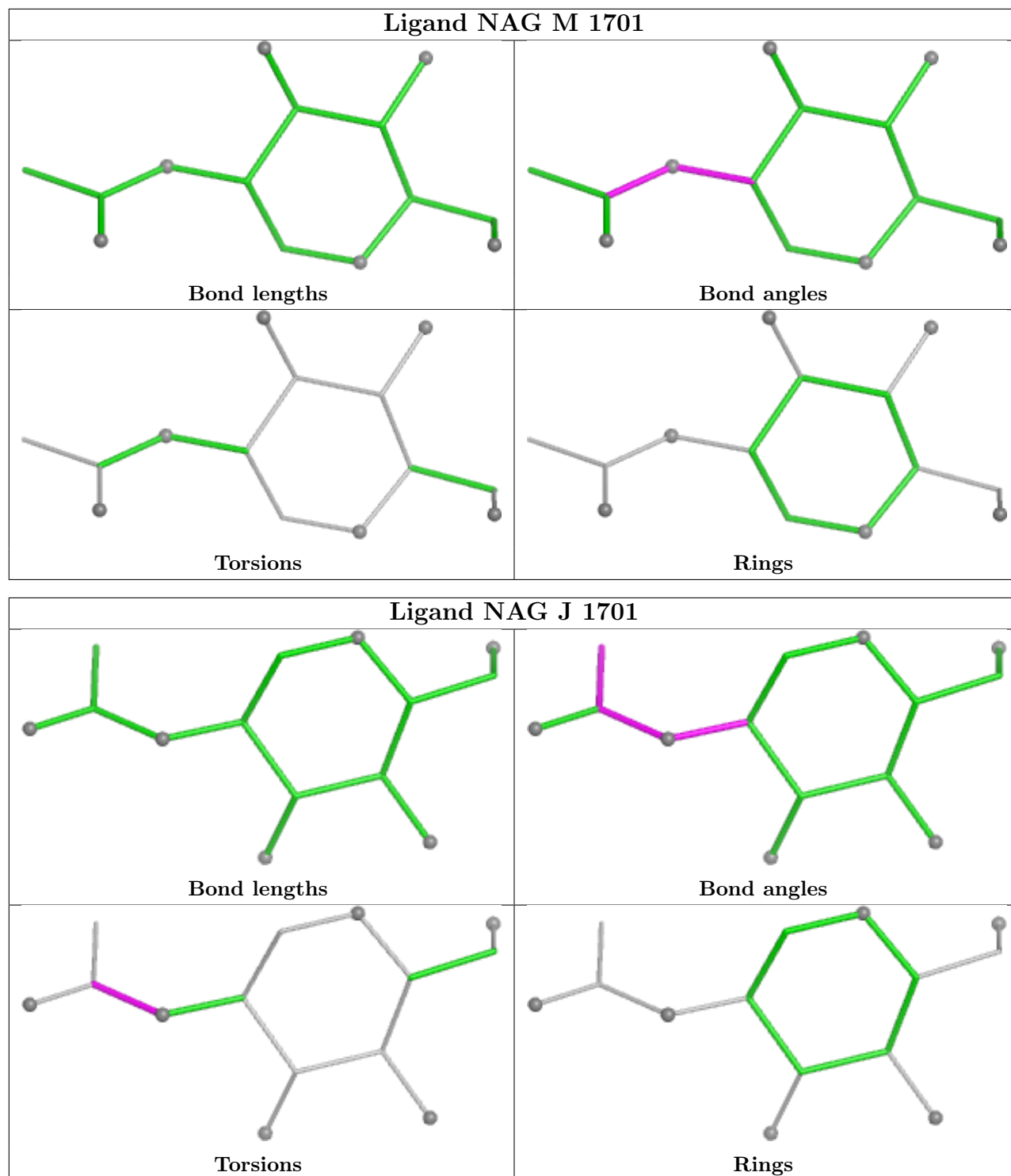
There are no ring outliers.

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 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 ⓘ

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	640/655 (97%)	0.42	19 (2%)	52	40	147, 210, 259, 290	0
1	B	640/655 (97%)	0.41	14 (2%)	62	48	149, 208, 259, 311	0
2	C	996/999 (99%)	0.51	24 (2%)	59	47	138, 211, 326, 393	0
2	D	995/999 (99%)	0.46	29 (2%)	53	41	142, 208, 317, 405	0
3	J	621/627 (99%)	0.37	9 (1%)	73	58	145, 199, 256, 296	0
3	M	622/627 (99%)	0.40	16 (2%)	57	44	152, 205, 255, 306	0
4	K	234/252 (92%)	0.28	1 (0%)	88	77	147, 191, 247, 272	0
4	N	234/252 (92%)	0.33	2 (0%)	81	66	153, 197, 246, 281	0
5	L	365/379 (96%)	0.48	7 (1%)	66	51	147, 215, 255, 291	0
5	O	365/379 (96%)	0.51	17 (4%)	36	32	165, 219, 257, 278	0
All	All	5712/5824 (98%)	0.43	138 (2%)	59	47	138, 207, 278, 405	0

The worst 5 of 138 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	662	SER	4.8
3	M	151	ASP	4.1
2	D	1523	ALA	4.0
5	L	1642	THR	3.8
3	M	349	LYS	3.5

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

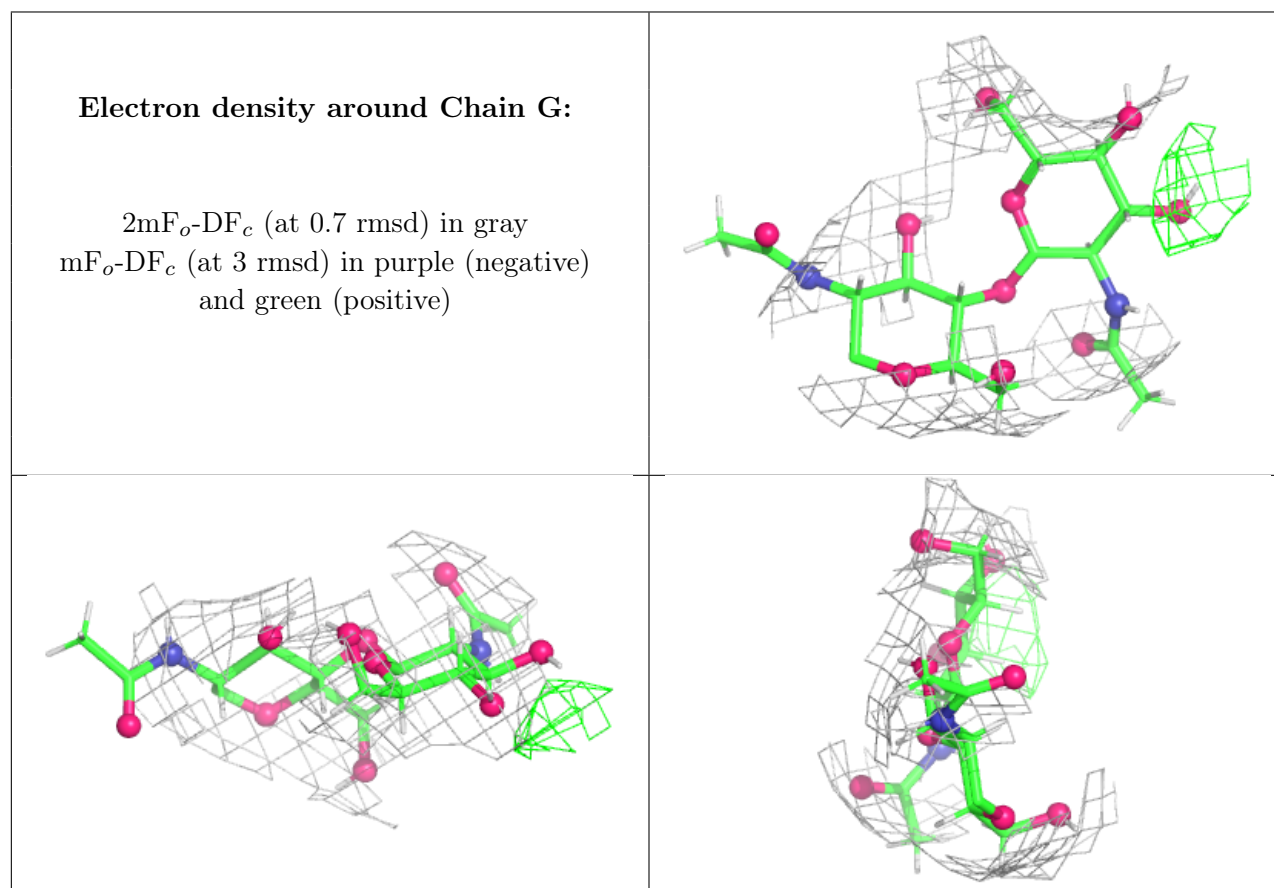
There are no non-standard protein/DNA/RNA residues in this entry.

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.

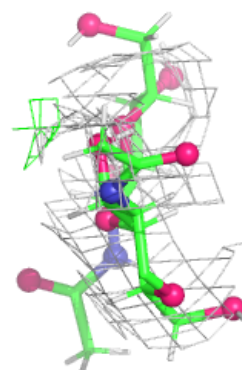
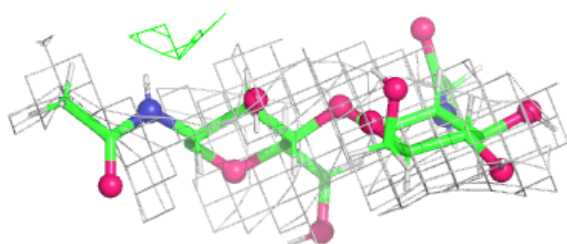
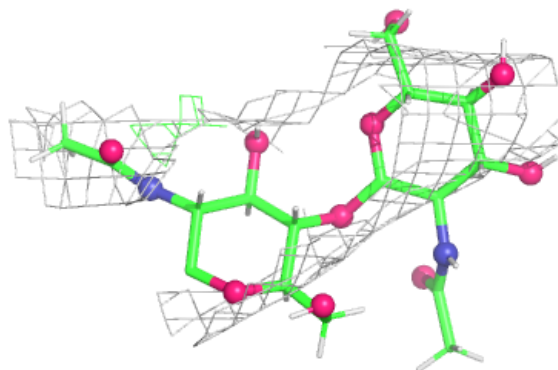
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	G	1	14/15	-	-	227,260,301,333	0
6	NAG	G	2	14/15	-	-	248,299,366,380	0
6	NAG	H	1	14/15	-	-	240,272,306,316	0
6	NAG	H	2	14/15	-	-	233,274,326,335	0
6	NAG	I	1	14/15	-	-	216,261,302,313	0
6	NAG	I	2	14/15	-	-	258,301,358,376	0

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

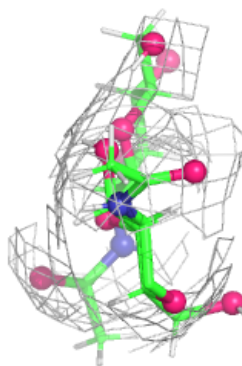
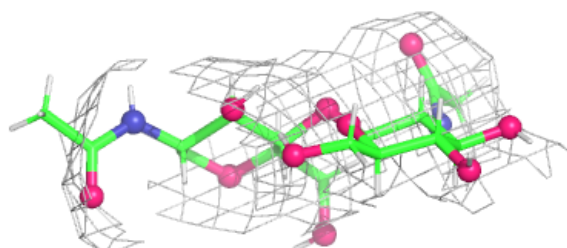
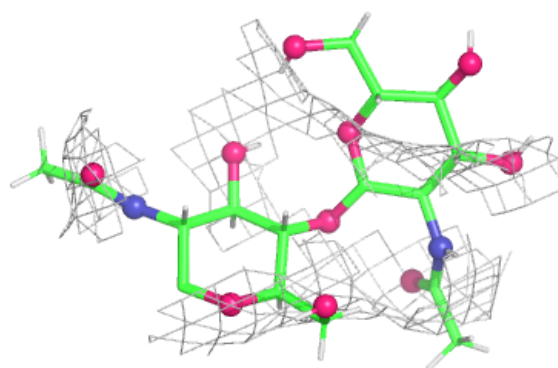


Electron density around Chain H:

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

**Electron density around Chain I:**

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

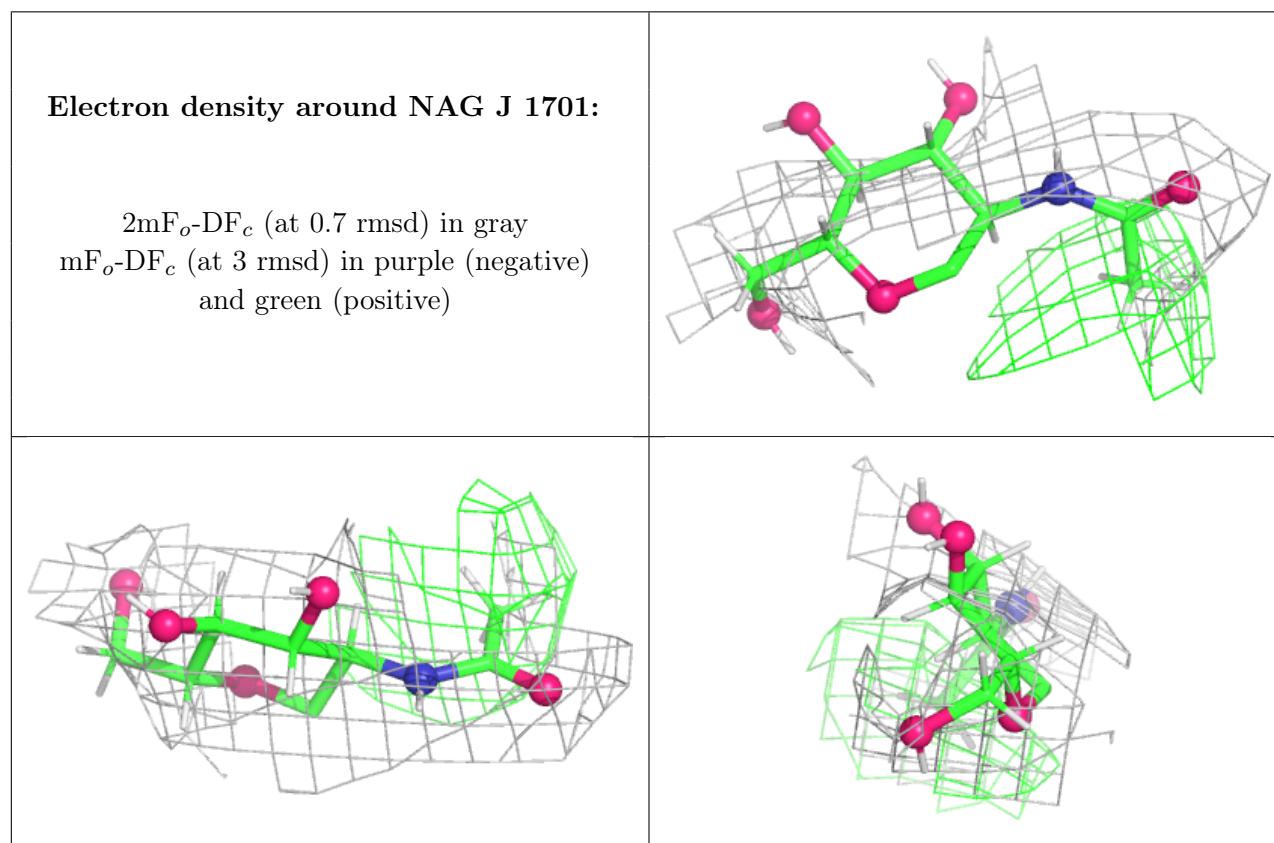


6.4 Ligands [i](#)

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

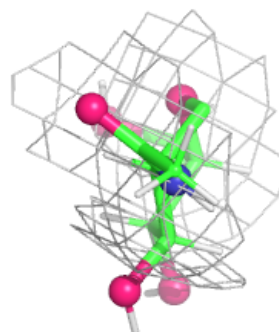
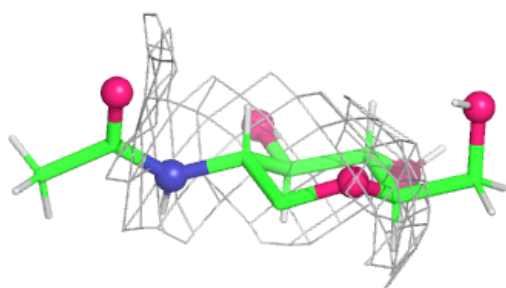
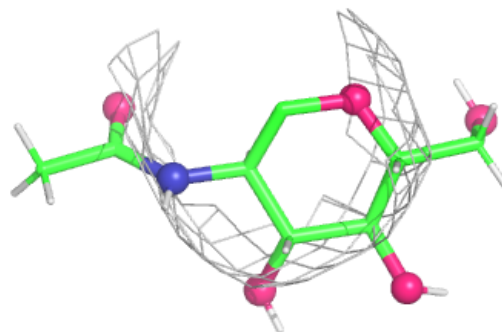
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	NAG	J	1701	14/15	0.29	0.21	297,335,393,404	0
7	NAG	M	1701	14/15	0.50	0.20	343,378,452,454	0
7	NAG	O	1701	14/15	0.57	0.18	230,277,332,353	0
7	NAG	D	1701	14/15	0.68	0.17	243,279,323,343	0

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.



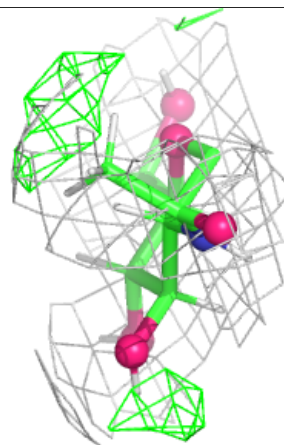
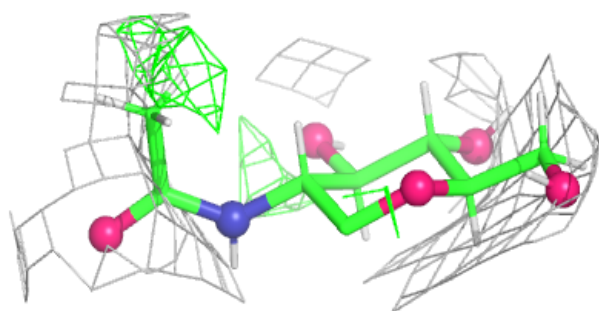
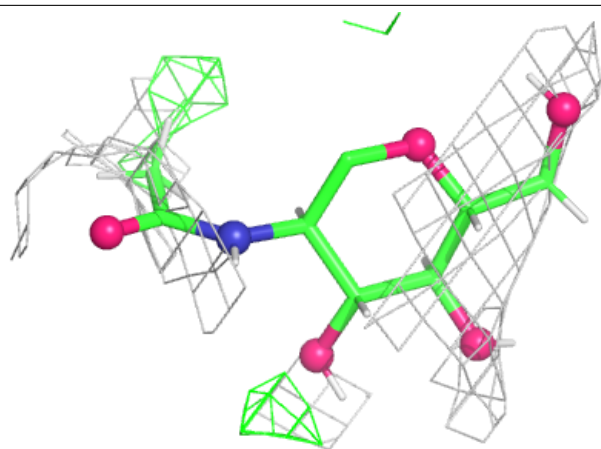
Electron density around NAG M 1701:

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



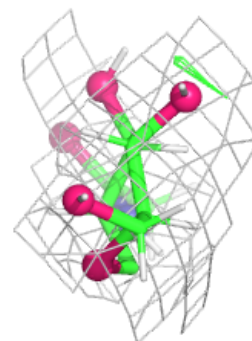
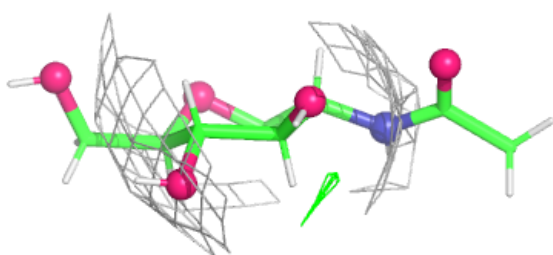
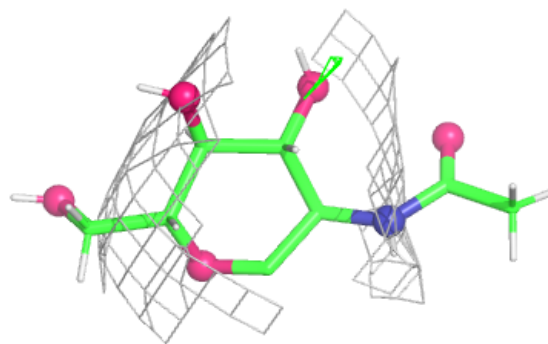
Electron density around NAG O 1701:

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



Electron density around NAG D 1701:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.