



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:54 PM UTC

PDB ID : 8IF2 / pdb_00008if2
Title : Crystal structure of the receptor binding domain of SARS-CoV-2 Omicron BQ.1.1 variant spike protein in complex with its receptor ACE2
Authors : Kimura, K.; Suzuki, T.; Hashiguchi, T.
Deposited on : 2023-02-17
Resolution : 2.78 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

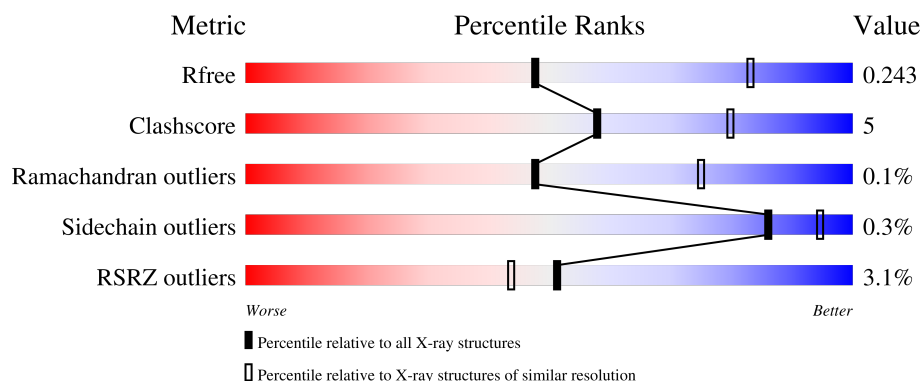
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	608	4% 84% 14% .
2	B	224	83% 5% 11%
3	J	3	100%
3	N	3	100%
3	O	3	33% 67%

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Mol	Chain	Length	Quality of chain
4	K	7	43% 43% 14%
5	L	2	50% 50%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6713 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 Processed angiotensin-converting enzyme 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	0	0
			4857	3108	804	916	29			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	618	GLY	-	expression tag	UNP Q9BYF1
A	619	THR	-	expression tag	UNP Q9BYF1
A	620	LYS	-	expression tag	UNP Q9BYF1
A	621	HIS	-	expression tag	UNP Q9BYF1
A	622	HIS	-	expression tag	UNP Q9BYF1
A	623	HIS	-	expression tag	UNP Q9BYF1
A	624	HIS	-	expression tag	UNP Q9BYF1
A	625	HIS	-	expression tag	UNP Q9BYF1
A	626	HIS	-	expression tag	UNP Q9BYF1

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	199	Total	C	N	O	S	0	0	0
			1583	1023	264	288	8			

There are 29 discrepancies between the modelled and reference sequences:

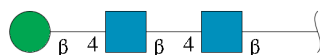
Chain	Residue	Modelled	Actual	Comment	Reference
B	339	ASP	GLY	variant	UNP P0DTC2
B	346	THR	ARG	variant	UNP P0DTC2
B	371	PHE	SER	variant	UNP P0DTC2
B	373	PRO	SER	variant	UNP P0DTC2
B	375	PHE	SER	variant	UNP P0DTC2
B	376	ALA	THR	variant	UNP P0DTC2
B	405	ASN	ASP	variant	UNP P0DTC2

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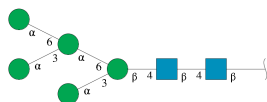
Chain	Residue	Modelled	Actual	Comment	Reference
B	408	SER	ARG	variant	UNP P0DTC2
B	417	ASN	LYS	variant	UNP P0DTC2
B	440	LYS	ASN	variant	UNP P0DTC2
B	444	THR	LYS	variant	UNP P0DTC2
B	452	ARG	LEU	variant	UNP P0DTC2
B	460	LYS	ASN	variant	UNP P0DTC2
B	477	ASN	SER	variant	UNP P0DTC2
B	478	LYS	THR	variant	UNP P0DTC2
B	484	ALA	GLU	variant	UNP P0DTC2
B	486	VAL	PHE	variant	UNP P0DTC2
B	498	ARG	GLN	variant	UNP P0DTC2
B	501	TYR	ASN	variant	UNP P0DTC2
B	505	HIS	TYR	variant	UNP P0DTC2
B	537	GLY	-	expression tag	UNP P0DTC2
B	538	THR	-	expression tag	UNP P0DTC2
B	539	LYS	-	expression tag	UNP P0DTC2
B	540	HIS	-	expression tag	UNP P0DTC2
B	541	HIS	-	expression tag	UNP P0DTC2
B	542	HIS	-	expression tag	UNP P0DTC2
B	543	HIS	-	expression tag	UNP P0DTC2
B	544	HIS	-	expression tag	UNP P0DTC2
B	545	HIS	-	expression tag	UNP P0DTC2

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

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]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
4	K	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 5 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
5	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Zn	0	0
			1	1		

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

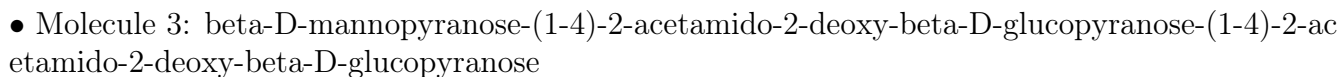
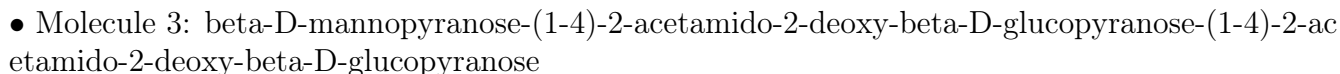


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	13	Total	O	0	0
			13	13		
8	B	17	Total	O	0	0
			17	17		

- Molecule 1: Processed angiotensin-converting enzyme 2





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



- Molecule 5: 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 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	120.05Å 120.05Å 167.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.17 – 2.78 49.17 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.17-2.78) 99.8 (49.17-2.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.200 , 0.245 0.201 , 0.243	Depositor DCC
R_{free} test set	1733 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	72.3	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6713	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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: ZN, NAG, MAN, BMA

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	0/4994	0.32	0/6785
2	B	0.10	0/1632	0.29	0/2225
All	All	0.11	0/6626	0.31	0/9010

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4857	0	4628	52	0
2	B	1583	0	1504	7	0
3	J	39	0	34	0	0
3	N	39	0	34	0	0
3	O	39	0	34	1	0
4	K	83	0	70	1	0
5	L	28	0	25	0	0
6	A	1	0	0	0	0
7	A	14	0	13	1	0
8	A	13	0	0	0	0
8	B	17	0	0	0	0
All	All	6713	0	6342	59	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 5.

All (59) 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:A:289:PRO:HB3	1:A:434:THR:HG22	1.66	0.77
1:A:284:PRO:HD3	1:A:440:LEU:HD22	1.77	0.66
1:A:323:MET:HE1	1:A:379:ILE:HG21	1.79	0.65
2:B:409:GLN:HE22	4:K:6:MAN:H2	1.65	0.60
1:A:457:GLU:HG2	1:A:513:ILE:HB	1.81	0.60
1:A:436:ILE:HG13	7:A:702:NAG:H81	1.84	0.59
1:A:524:GLN:HB3	1:A:574:VAL:HG11	1.88	0.56
2:B:360:ASN:H	2:B:523:THR:HG23	1.72	0.54
1:A:323:MET:HE2	1:A:327:PHE:CD1	2.43	0.53
1:A:403:ALA:HB2	1:A:518:ARG:HB2	1.90	0.53
3:O:1:NAG:H61	3:O:2:NAG:H83	1.90	0.53
1:A:284:PRO:HB3	1:A:594:TRP:CH2	2.44	0.53
2:B:461:LEU:HD22	2:B:465:GLU:HB3	1.92	0.52
1:A:21:ILE:HD11	1:A:87:GLU:HB3	1.92	0.52
1:A:169:ARG:NH1	1:A:270:MET:HE3	2.25	0.51
1:A:374:HIS:HA	1:A:405:GLY:HA3	1.93	0.50
1:A:293:VAL:HG22	1:A:294:THR:H	1.77	0.50
1:A:402:GLU:HG3	1:A:514:ARG:HD3	1.94	0.50
1:A:165:TRP:HA	1:A:270:MET:HE1	1.95	0.48
1:A:288:LYS:HB3	1:A:289:PRO:HD3	1.94	0.48
1:A:268:GLY:O	1:A:277:ASN:ND2	2.36	0.48
1:A:455:MET:HE2	1:A:455:MET:HB3	1.82	0.48
1:A:188:ASN:HB3	1:A:192:ARG:NH1	2.30	0.47
1:A:37:GLU:HB3	1:A:353:LYS:HE2	1.95	0.47
1:A:161:ARG:NH1	1:A:265:HIS:O	2.43	0.47
1:A:91:LEU:O	1:A:95:LEU:HG	2.15	0.47
1:A:416:LYS:HD3	1:A:430:GLU:OE2	2.15	0.47
1:A:416:LYS:NZ	1:A:430:GLU:OE1	2.34	0.46
1:A:204:ARG:HG2	1:A:222:LEU:HD23	1.97	0.46
1:A:475:LYS:HG2	1:A:495:GLU:OE2	2.15	0.46
1:A:180:TYR:O	1:A:184:VAL:HG13	2.16	0.45
1:A:19:SER:N	2:B:477:ASN:HD21	2.15	0.45
1:A:535:HIS:CD2	1:A:542:CYS:HB2	2.51	0.45
1:A:431:ASP:OD1	1:A:434:THR:HG23	2.17	0.44
1:A:90:ASN:OD1	1:A:92:THR:HG22	2.17	0.44
1:A:169:ARG:HH12	1:A:270:MET:HE3	1.82	0.44
1:A:71:ALA:HA	1:A:74:LYS:HE2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ILE:HG22	1:A:172:VAL:HG13	2.00	0.44
1:A:523:PHE:CE2	1:A:584:LEU:HD13	2.53	0.44
2:B:517:LEU:HD12	2:B:517:LEU:HA	1.84	0.44
1:A:152:MET:O	1:A:161:ARG:NH2	2.51	0.43
1:A:381:TYR:CE1	1:A:558:LEU:HA	2.54	0.43
1:A:456:LEU:O	1:A:460:ARG:HG3	2.19	0.43
1:A:402:GLU:O	1:A:518:ARG:HD3	2.19	0.42
1:A:471:ASP:OD1	1:A:471:ASP:N	2.53	0.42
1:A:439:LEU:HD11	1:A:540:HIS:CG	2.55	0.42
2:B:502:GLY:O	2:B:506:GLN:HG3	2.19	0.42
1:A:134:ASN:HB3	1:A:137:ASN:O	2.20	0.42
1:A:593:THR:HA	1:A:596:LYS:HD2	2.01	0.42
2:B:403:ARG:HG2	2:B:505:HIS:HA	2.01	0.41
1:A:582:ARG:HB3	1:A:583:PRO:HD3	2.02	0.41
1:A:180:TYR:HA	1:A:183:TYR:HB3	2.01	0.41
1:A:594:TRP:CZ3	1:A:598:GLN:HG3	2.56	0.41
1:A:72:PHE:O	1:A:76:GLN:HG2	2.21	0.41
1:A:252:TYR:HA	1:A:253:PRO:HD3	1.91	0.41
1:A:456:LEU:HD22	1:A:512:PHE:CD2	2.56	0.41
1:A:499:ASP:N	1:A:500:PRO:HD2	2.35	0.40
1:A:398:GLU:OE1	1:A:511:SER:OG	2.33	0.40
1:A:581:VAL:HG12	1:A:585:LEU:HG	2.03	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	593/608 (98%)	572 (96%)	20 (3%)	1 (0%)	43	70
2	B	197/224 (88%)	193 (98%)	4 (2%)	0	100	100
All	All	790/832 (95%)	765 (97%)	24 (3%)	1 (0%)	48	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	PRO

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	526/537 (98%)	525 (100%)	1 (0%)	87	96
2	B	171/195 (88%)	170 (99%)	1 (1%)	78	91
All	All	697/732 (95%)	695 (100%)	2 (0%)	86	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	455	MET
2	B	387	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	175	GLN
1	A	210	ASN
1	A	290	ASN
1	A	345	HIS
1	A	552	GLN
2	B	487	ASN

5.3.3 RNA [i](#)

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 ⓘ

18 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	J	1	3,1	14,14,15	0.50	0	17,19,21	0.56	0
3	NAG	J	2	3	14,14,15	0.39	0	17,19,21	0.44	0
3	BMA	J	3	3	11,11,12	0.89	0	15,15,17	0.85	0
4	NAG	K	1	4,1	14,14,15	0.37	0	17,19,21	0.58	0
4	NAG	K	2	4	14,14,15	0.28	0	17,19,21	0.42	0
4	BMA	K	3	4	11,11,12	0.53	0	15,15,17	0.84	0
4	MAN	K	4	4	11,11,12	0.76	0	15,15,17	0.91	2 (13%)
4	MAN	K	5	4	11,11,12	0.79	1 (9%)	15,15,17	1.05	2 (13%)
4	MAN	K	6	4	11,11,12	0.74	0	15,15,17	1.29	1 (6%)
4	MAN	K	7	4	11,11,12	0.64	0	15,15,17	0.89	1 (6%)
5	NAG	L	1	5,1	14,14,15	0.38	0	17,19,21	0.69	1 (5%)
5	NAG	L	2	5	14,14,15	0.51	0	17,19,21	0.50	0
3	NAG	N	1	3,1	14,14,15	0.42	0	17,19,21	0.59	0
3	NAG	N	2	3	14,14,15	0.21	0	17,19,21	0.49	0
3	BMA	N	3	3	11,11,12	0.82	0	15,15,17	0.72	0
3	NAG	O	1	2,3	14,14,15	0.32	0	17,19,21	0.56	0
3	NAG	O	2	3	14,14,15	0.37	0	17,19,21	0.45	0
3	BMA	O	3	3	11,11,12	0.60	0	15,15,17	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
3	NAG	J	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	4/6/23/26	0/1/1/1
3	BMA	J	3	3	-	0/2/19/22	0/1/1/1
4	NAG	K	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	BMA	K	3	4	-	0/2/19/22	0/1/1/1
4	MAN	K	4	4	-	2/2/19/22	0/1/1/1
4	MAN	K	5	4	-	2/2/19/22	0/1/1/1
4	MAN	K	6	4	-	2/2/19/22	1/1/1/1
4	MAN	K	7	4	-	0/2/19/22	0/1/1/1
5	NAG	L	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	L	2	5	-	2/6/23/26	0/1/1/1
3	NAG	N	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	N	2	3	-	0/6/23/26	0/1/1/1
3	BMA	N	3	3	-	2/2/19/22	0/1/1/1
3	NAG	O	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	O	2	3	-	3/6/23/26	0/1/1/1
3	BMA	O	3	3	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	5	MAN	C1-C2	2.00	1.57	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	6	MAN	C1-O5-C5	3.76	117.23	112.19
4	K	5	MAN	C1-O5-C5	2.70	115.80	112.19
5	L	1	NAG	C1-O5-C5	2.20	115.14	112.19
4	K	4	MAN	C1-O5-C5	2.17	115.09	112.19
4	K	4	MAN	O2-C2-C3	-2.14	105.72	110.15
4	K	7	MAN	O2-C2-C3	-2.11	105.79	110.15
4	K	5	MAN	O2-C2-C3	-2.01	105.99	110.15

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	J	1	NAG	O5-C5-C6-O6

Continued on next page...

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

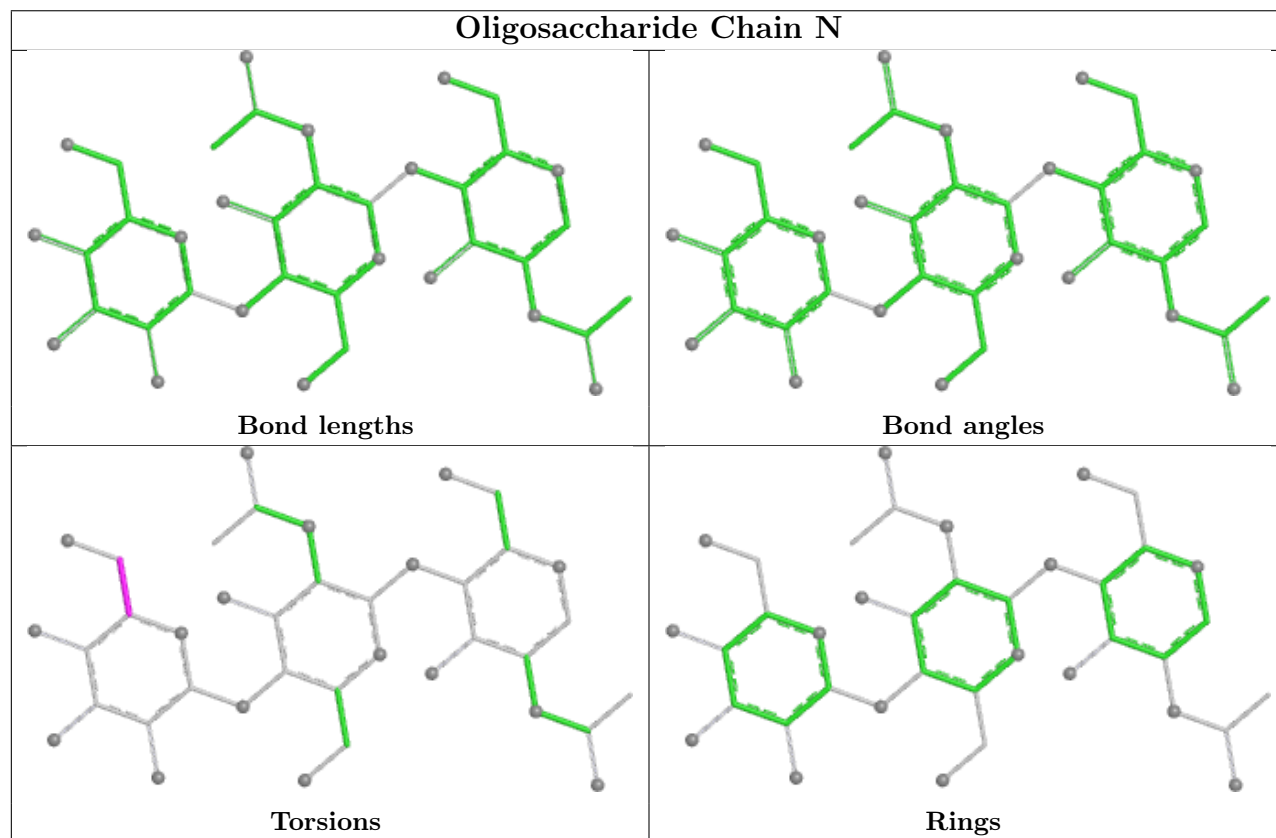
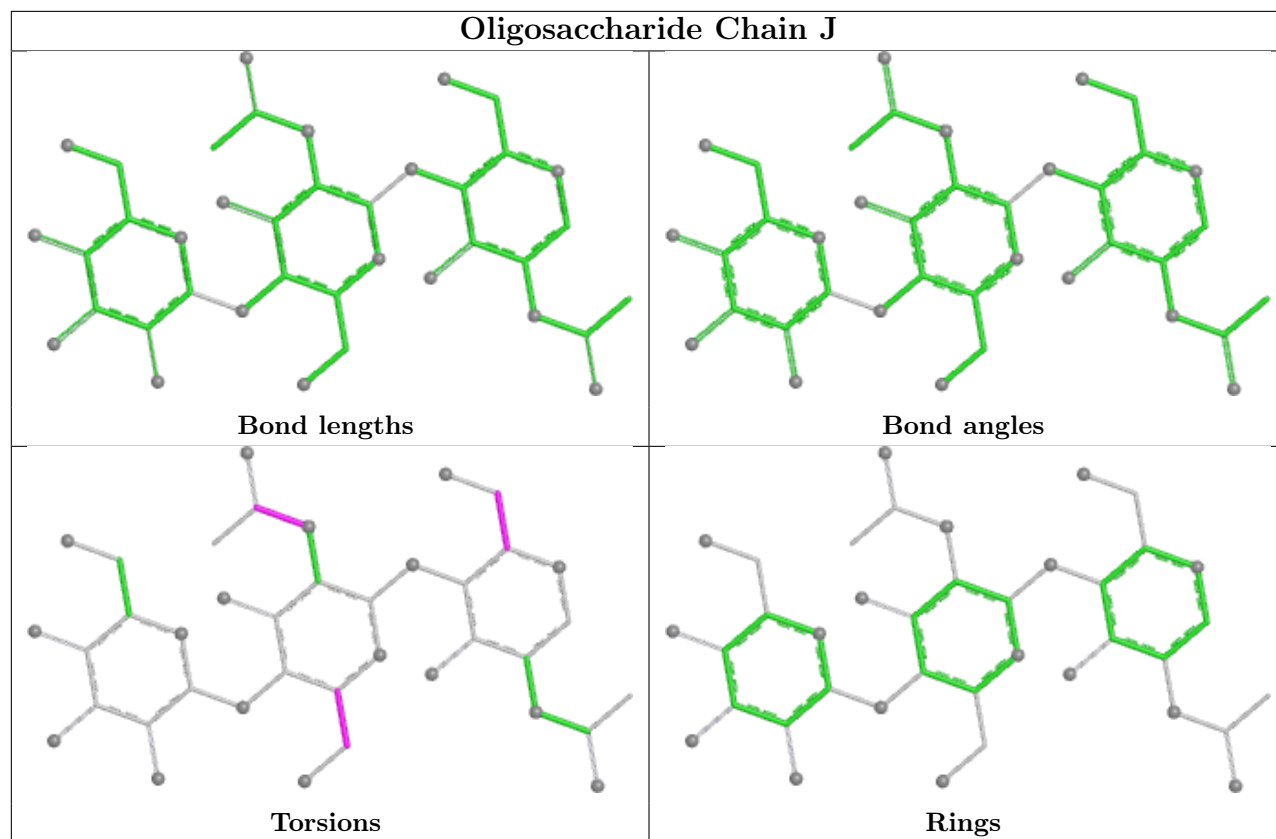
All (1) ring outliers are listed below:

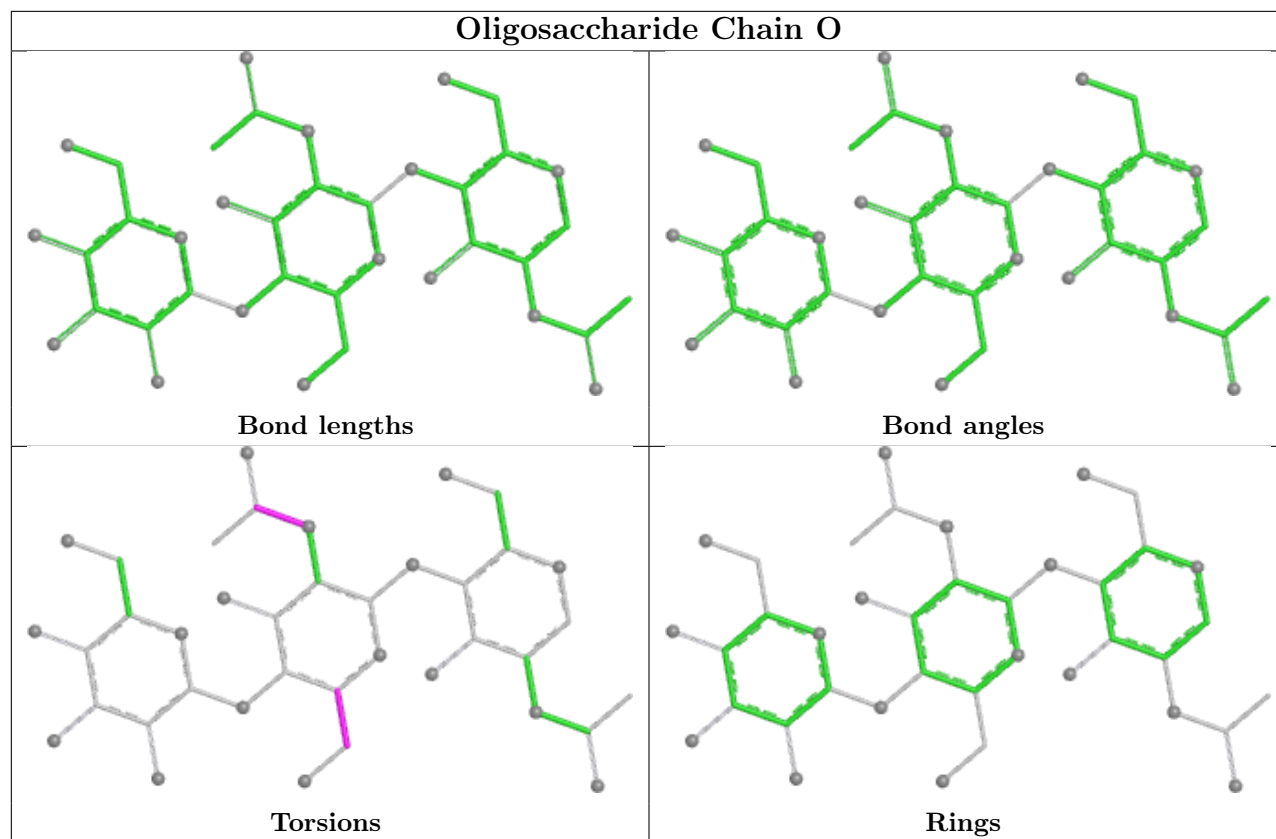
Mol	Chain	Res	Type	Atoms
4	K	6	MAN	C1-C2-C3-C4-C5-O5

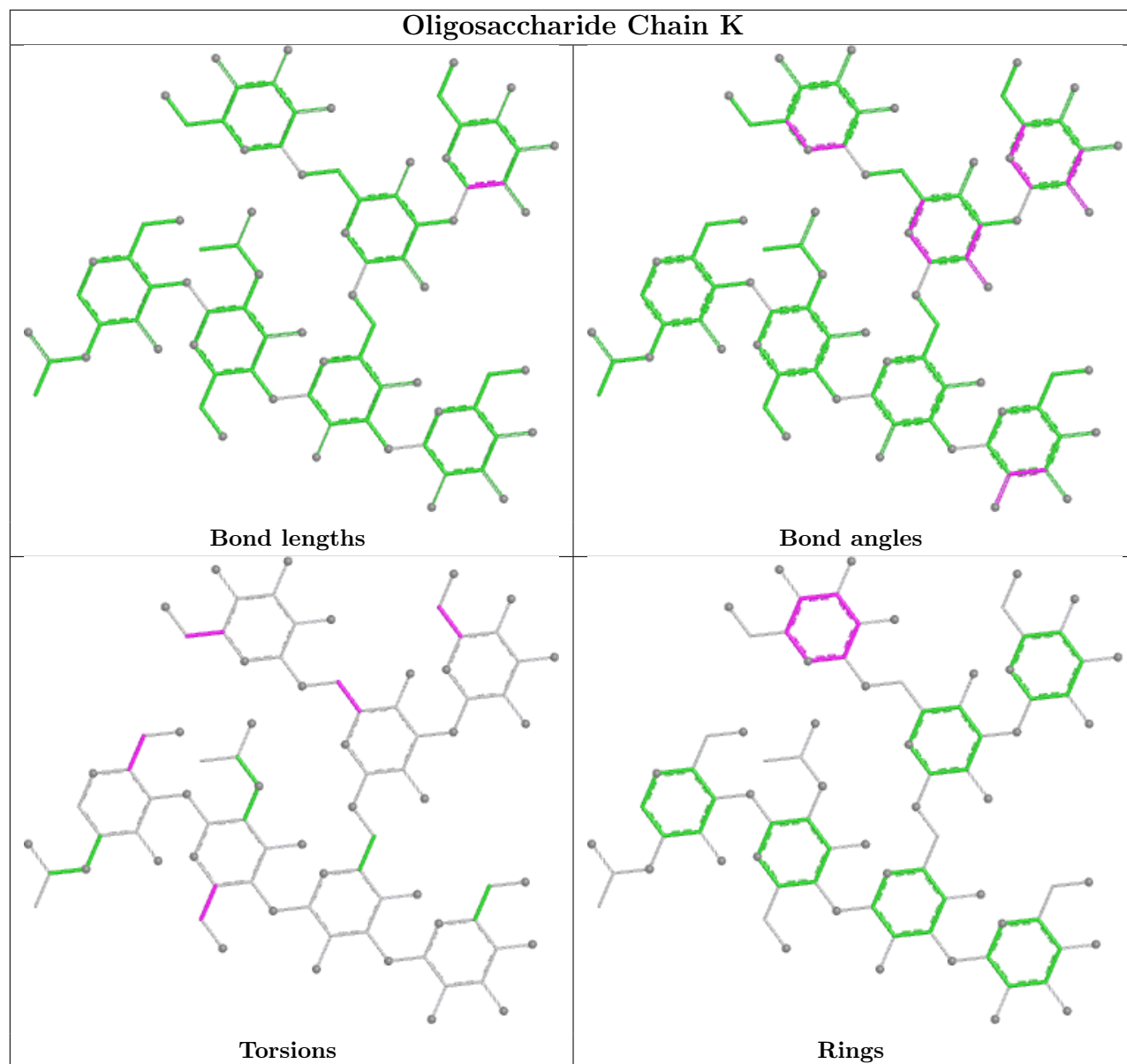
3 monomers are involved in 2 short contacts:

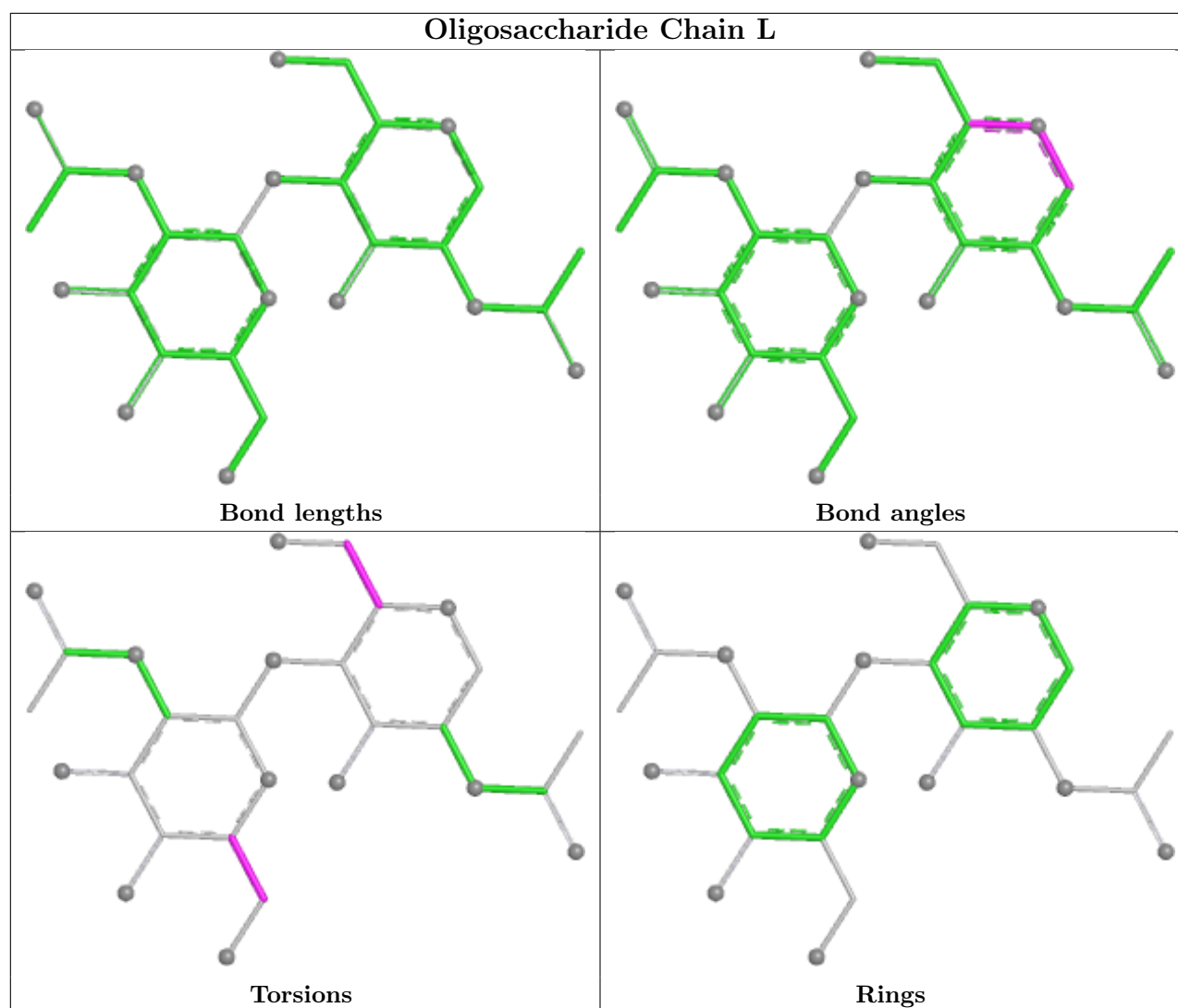
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	O	1	NAG	1	0
4	K	6	MAN	1	0
3	O	2	NAG	1	0

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









5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	NAG	A	702	1	14,14,15	0.41	0	17,19,21	0.40	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
7	NAG	A	702	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

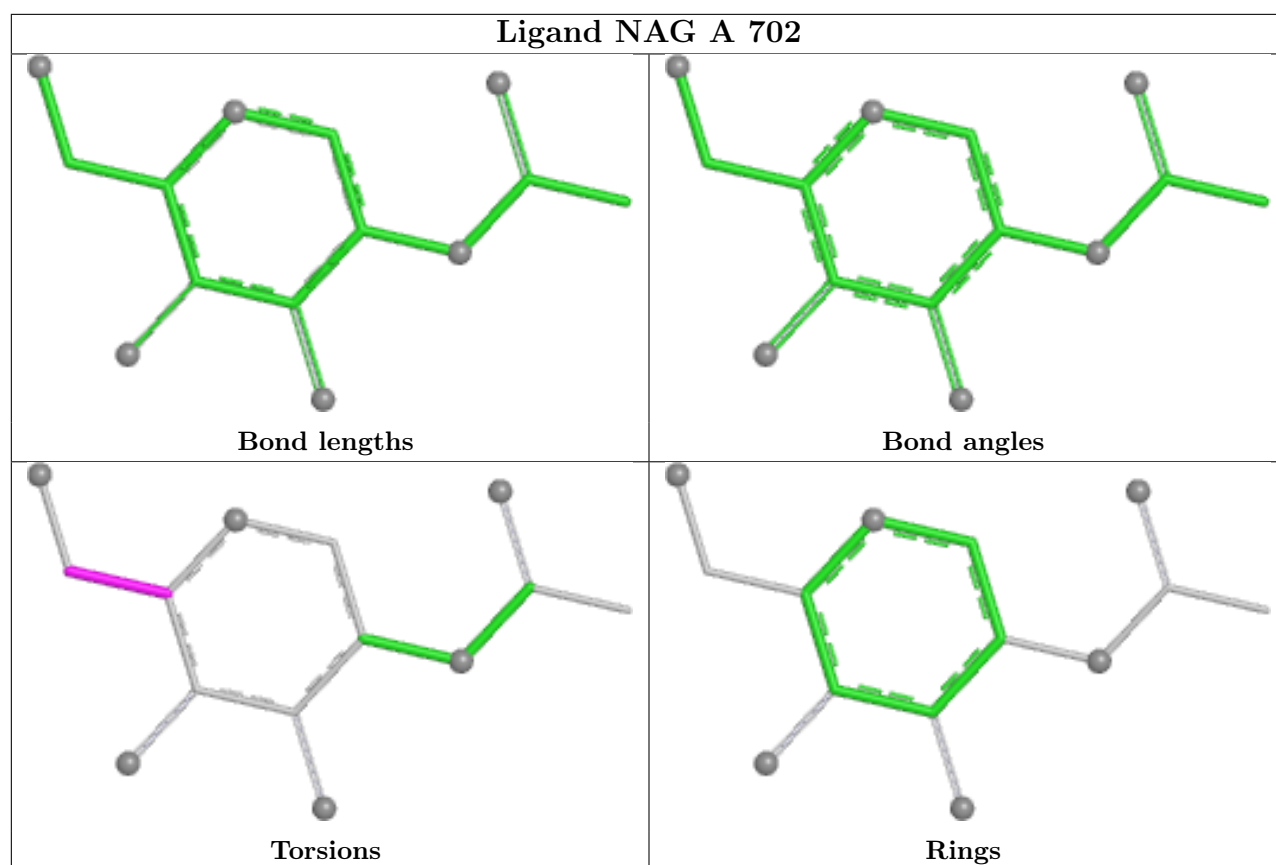
Mol	Chain	Res	Type	Atoms
7	A	702	NAG	O5-C5-C6-O6
7	A	702	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	702	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	595/608 (97%)	0.08	24 (4%) 42 36	44, 86, 130, 167	0
2	B	199/224 (88%)	-0.35	1 (0%) 87 83	40, 60, 102, 137	0
All	All	794/832 (95%)	-0.03	25 (3%) 51 44	40, 79, 128, 167	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	145	GLU	5.9
1	A	293	VAL	5.4
1	A	107	VAL	3.4
1	A	291	ILE	3.1
2	B	332	ILE	3.1
1	A	557	MET	2.9
1	A	89	GLN	2.8
1	A	104	GLY	2.6
1	A	253	PRO	2.6
1	A	102	GLN	2.6
1	A	146	PRO	2.5
1	A	292	ASP	2.4
1	A	466	GLY	2.3
1	A	21	ILE	2.3
1	A	613	TYR	2.3
1	A	288	LYS	2.3
1	A	294	THR	2.3
1	A	20	THR	2.2
1	A	612	PRO	2.2
1	A	19	SER	2.2
1	A	103	ASN	2.1
1	A	601	ASN	2.1
1	A	539	LEU	2.0
1	A	256	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	87	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](#)

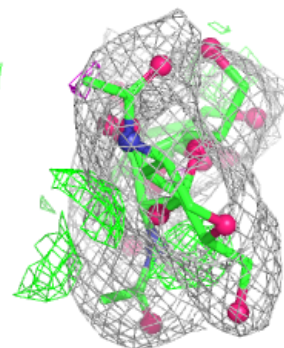
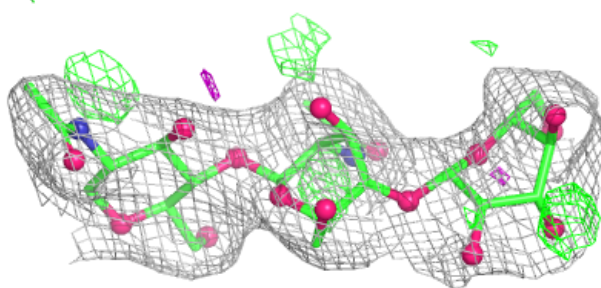
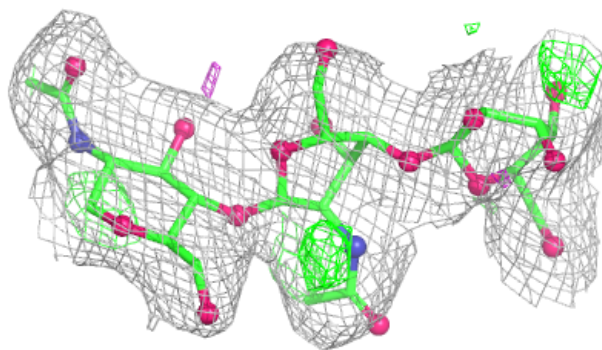
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	J	1	14/15	-	-	47,64,75,79	0
3	NAG	J	2	14/15	-	-	66,104,118,133	0
3	BMA	J	3	11/12	-	-	106,127,138,150	0
3	NAG	N	1	14/15	-	-	96,112,134,151	0
3	NAG	N	2	14/15	-	-	108,145,164,169	0
3	BMA	N	3	11/12	-	-	135,167,174,175	0
3	NAG	O	1	14/15	-	-	47,61,80,88	0
3	NAG	O	2	14/15	-	-	52,86,120,134	0
3	BMA	O	3	11/12	-	-	69,95,107,115	0
4	NAG	K	1	14/15	-	-	99,118,122,124	0
4	NAG	K	2	14/15	-	-	115,129,138,144	0
4	BMA	K	3	11/12	-	-	110,134,144,148	0
4	MAN	K	4	11/12	-	-	121,155,162,162	0
4	MAN	K	5	11/12	-	-	128,155,159,160	0
4	MAN	K	6	11/12	-	-	124,131,135,159	0
4	MAN	K	7	11/12	-	-	127,139,148,150	0
5	NAG	L	1	14/15	-	-	67,85,119,126	0
5	NAG	L	2	14/15	-	-	101,133,149,150	0

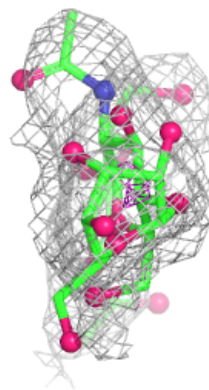
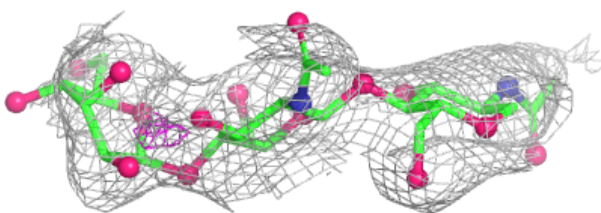
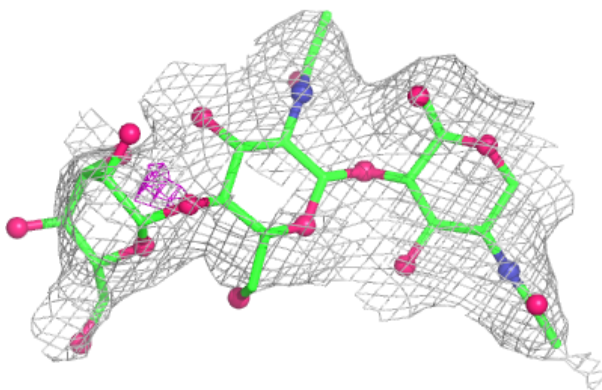
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain J:

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

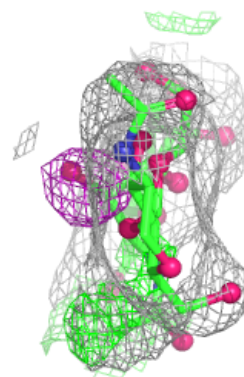
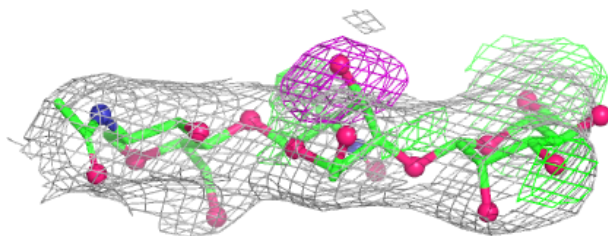
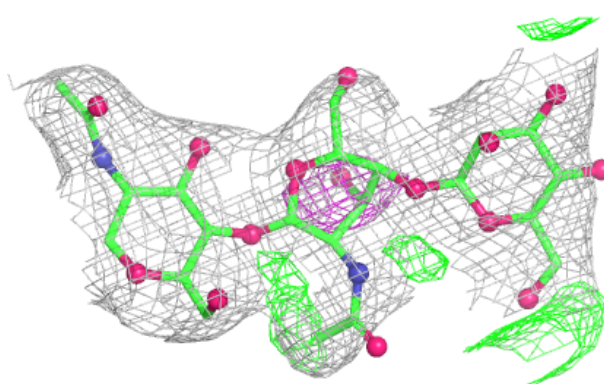
**Electron density around Chain N:**

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



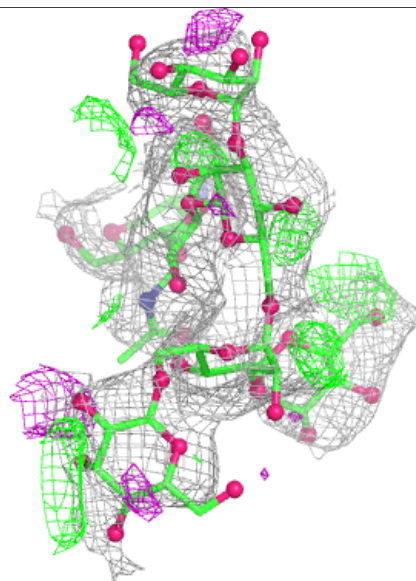
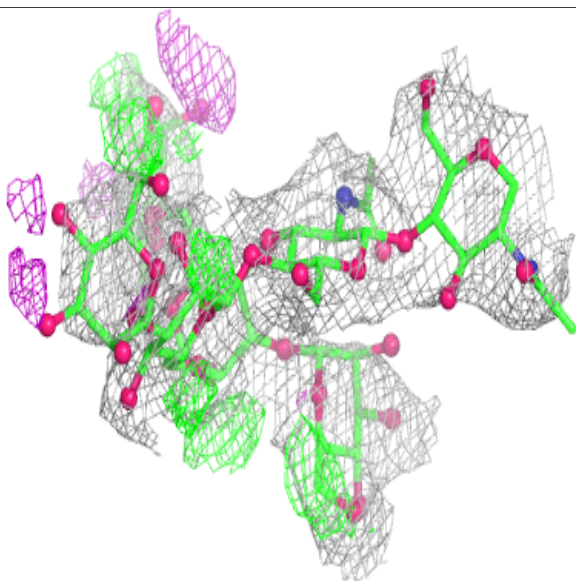
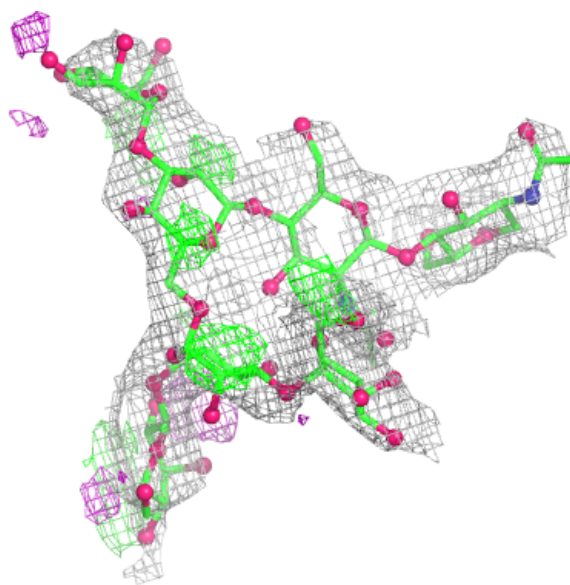
Electron density around Chain O:

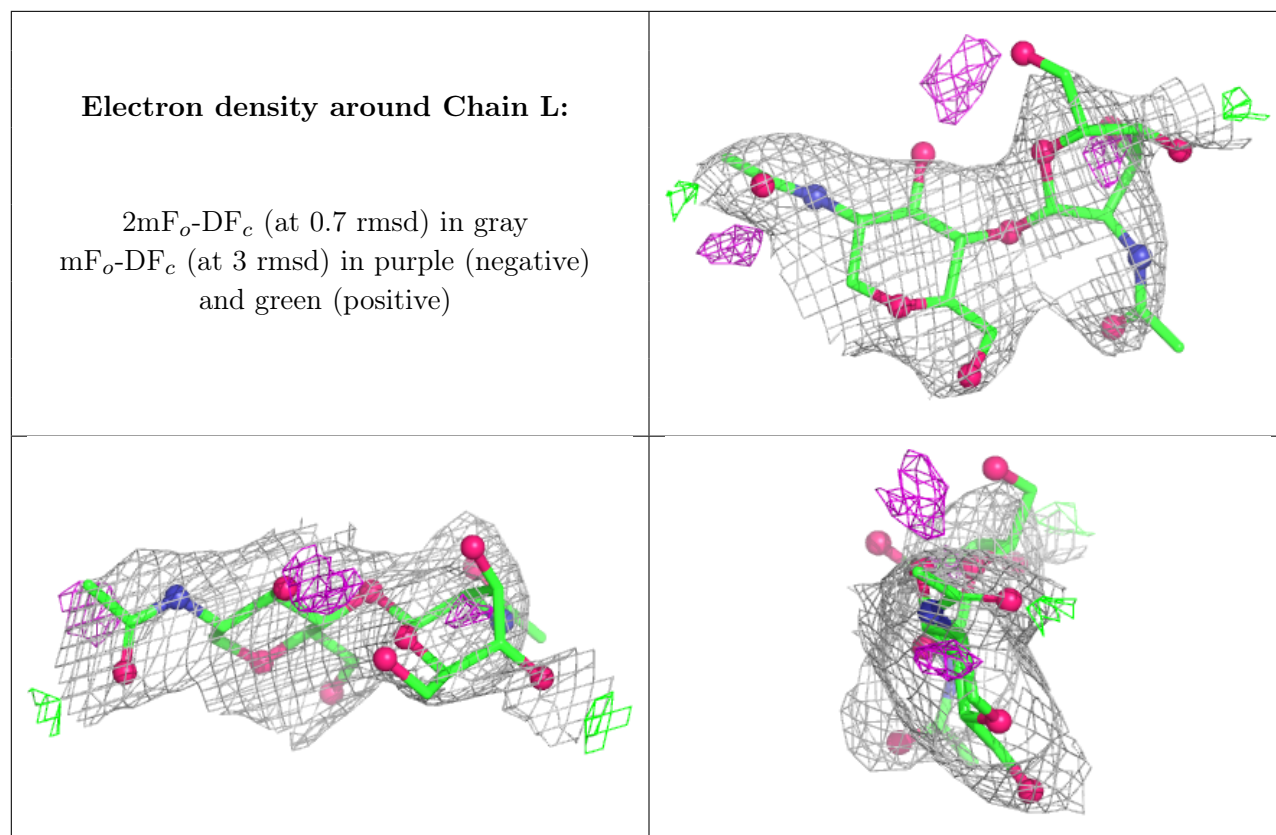
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain K:

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





6.4 Ligands [i](#)

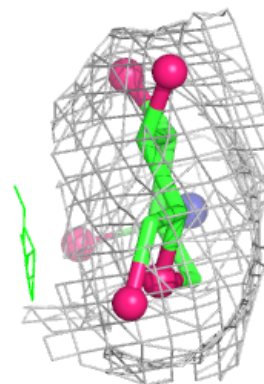
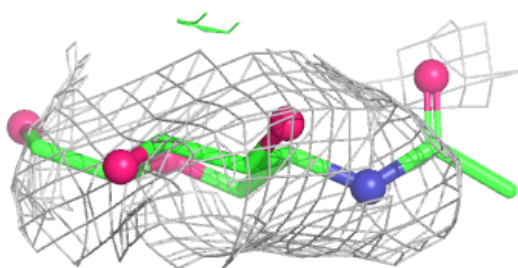
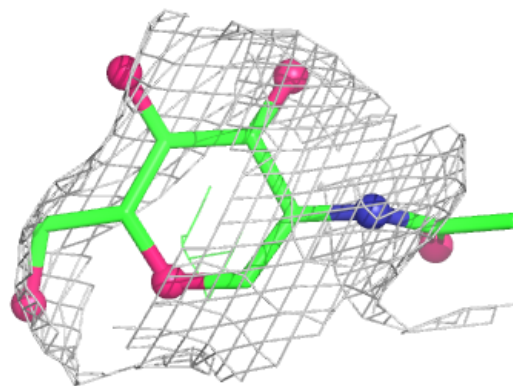
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	A	702	14/15	0.62	0.14	130,143,151,152	0
6	ZN	A	701	1/1	0.98	0.13	64,64,64,64	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.

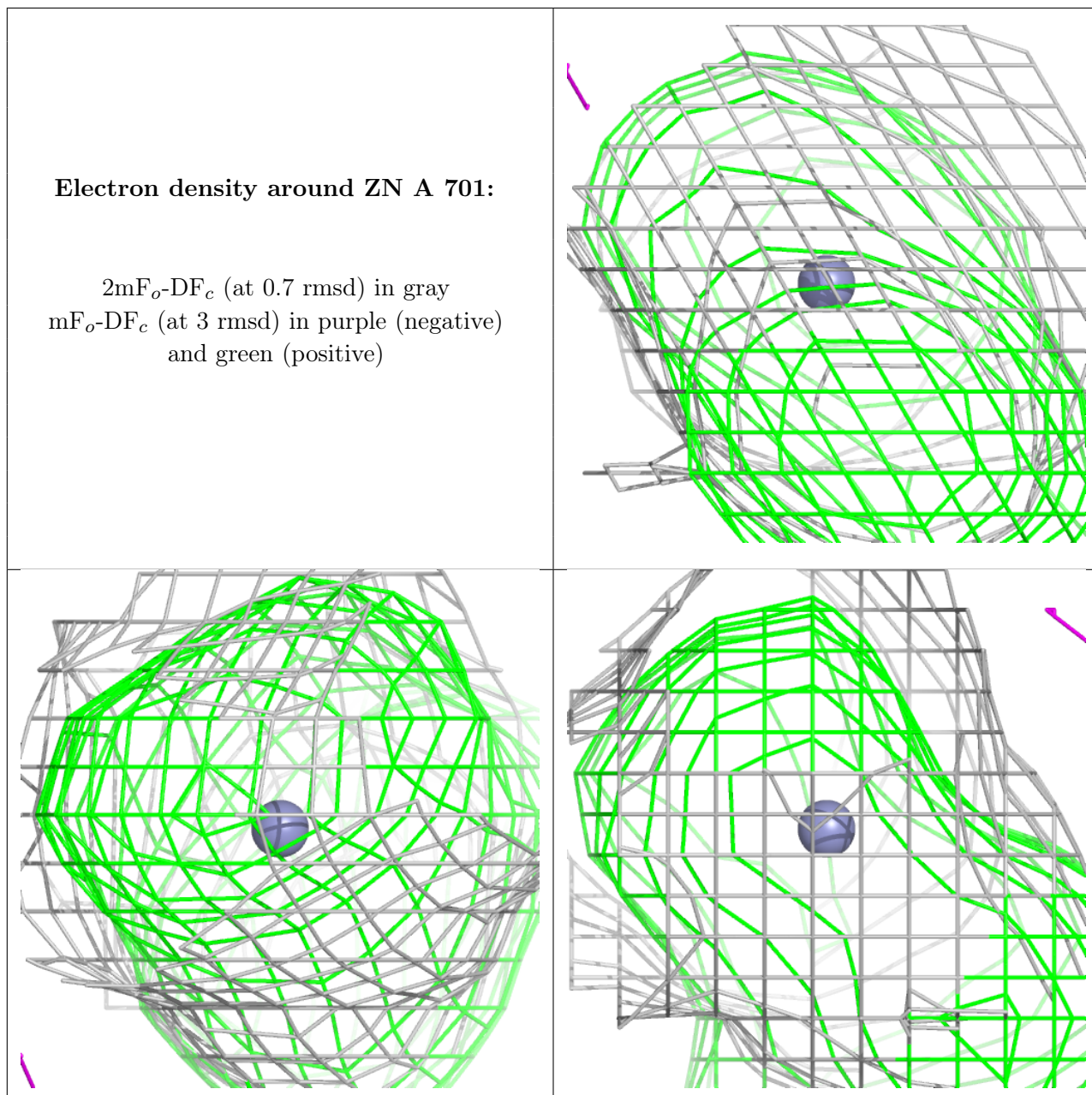
Electron density around NAG A 702:

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



Electron density around ZN A 701:

$2mF_o-DF_c$ (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.