



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 29, 2024 – 03:10 PM EST

PDB ID : 8SNP
Title : Crystal structure of mouse Netrin-1 in complex with samarium ions
Authors : Heide, F.; Legare, S.; Stetefeld, J.
Deposited on : 2023-04-27
Resolution : 3.40 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

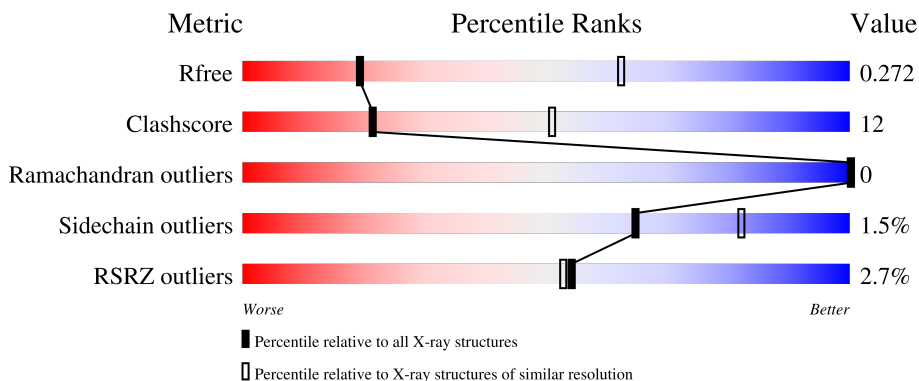
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

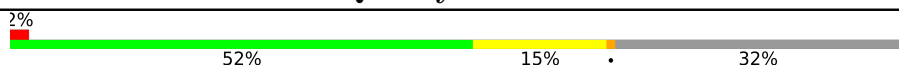


The reported resolution of this entry is 3.40 Å.

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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	604	 2% 52% 15% 32%
2	D	3	 100%
3	C	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	C	2	-	-	-	X

2 Entry composition [i](#)

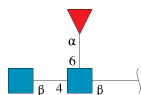
There are 5 unique types of molecules in this entry. The entry contains 6188 atoms, of which 2950 are hydrogens and 0 are deuteriums.

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 Netrin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	409	6005	1918	2865	591	592	39	0	0	0

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	D	3	72	22	34	2	14	0	0	0

- Molecule 3 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
			Total	C	H	N	O			
3	C	2	53	16	25	2	10	0	0	0

- Molecule 4 is SAMARIUM (III) ION (three-letter code: SM) (formula: Sm) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Sm	0	0
			4	4		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

MAG1
MAG2

4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	69.50Å 69.50Å 333.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	56.62 – 3.40 56.62 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (56.62-3.40) 99.4 (56.62-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 3.40Å)	Xtrriage
Refinement program	PHENIX 1.20.1-4487_4487	Depositor
R, R_{free}	0.250 , 0.268 0.252 , 0.272	Depositor DCC
R_{free} test set	614 reflections (4.50%)	wwPDB-VP
Wilson B-factor (Å ²)	90.5	Xtrriage
Anisotropy	0.785	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.068 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6188	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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, FUC, SM

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.33	0/3218	0.62	0/4369

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	ARG	Sidechain
1	A	269	ARG	Sidechain
1	A	298	ARG	Sidechain
1	A	333	ARG	Sidechain
1	A	349	ARG	Sidechain
1	A	351	ARG	Sidechain
1	A	398	ARG	Sidechain
1	A	445	ARG	Sidechain
1	A	49	ARG	Sidechain
1	A	65	ARG	Sidechain

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	3140	2865	2862	65	3
2	D	38	34	34	5	0
3	C	28	25	25	4	0
4	A	4	0	0	0	0
5	A	28	26	26	3	0
All	All	3238	2950	2947	74	3

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 12.

All (74) 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:319:LYS:HG3	1:A:320:PRO:HD2	1.62	0.82
1:A:303:VAL:HG23	1:A:313:PRO:HA	1.70	0.73
1:A:322:HIS:HA	1:A:340:ALA:HA	1.71	0.72
1:A:297:ASP:OD1	1:A:298:ARG:N	2.30	0.64
1:A:319:LYS:CG	1:A:320:PRO:HD2	2.27	0.64
1:A:260:GLU:HA	1:A:264:ASP:N	2.13	0.62
1:A:66:VAL:HG12	1:A:134:LEU:HD22	1.82	0.60
1:A:113:ASN:ND2	1:A:115:HIS:O	2.35	0.59
1:A:142:PHE:O	1:A:243:THR:HA	2.03	0.58
1:A:221:SER:HB2	1:A:224:ASP:HB2	1.84	0.58
1:A:319:LYS:HG3	1:A:320:PRO:CD	2.31	0.58
1:A:193:ILE:CD1	1:A:193:ILE:O	2.51	0.58
1:A:193:ILE:O	1:A:193:ILE:HD12	2.04	0.58
1:A:53:PRO:O	1:A:284:ARG:NH1	2.37	0.58
3:C:1:NAG:H61	3:C:2:NAG:C1	2.35	0.56
1:A:260:GLU:OE2	1:A:265:SER:OG	2.20	0.55
5:A:705:NAG:O4	5:A:706:NAG:C1	2.55	0.55
2:D:1:NAG:C6	2:D:2:NAG:C1	2.86	0.53
1:A:242:VAL:O	1:A:242:VAL:HG23	2.09	0.53
1:A:353:ASN:ND2	1:A:356:LEU:HD23	2.24	0.52
1:A:325:ARG:HG3	1:A:326:PRO:HD2	1.90	0.52
1:A:39:ASP:HB3	1:A:42:SER:HB2	1.90	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:TYR:O	1:A:352:PHE:HD2	1.94	0.51
1:A:425:CYS:HB3	1:A:429:VAL:HG13	1.91	0.51
1:A:260:GLU:HA	1:A:264:ASP:CA	2.41	0.51
1:A:417:ASN:ND2	3:C:1:NAG:O7	2.45	0.50
1:A:163:LYS:HB3	1:A:174:PHE:CD2	2.47	0.50
1:A:144:VAL:HG23	1:A:222:THR:HG21	1.95	0.49
1:A:47:HIS:HB3	1:A:48:PRO:HD2	1.94	0.49
3:C:1:NAG:C6	3:C:2:NAG:C1	2.91	0.49
1:A:221:SER:CB	1:A:224:ASP:HB2	2.43	0.49
1:A:238:LEU:O	1:A:242:VAL:HG22	2.13	0.48
1:A:43:ASP:HB2	1:A:49:ARG:HB2	1.94	0.48
1:A:410:GLY:HA3	1:A:434:CYS:O	2.13	0.47
1:A:303:VAL:CG2	1:A:313:PRO:HA	2.42	0.47
2:D:2:NAG:HN2	2:D:2:NAG:H5	1.79	0.47
1:A:163:LYS:HD3	1:A:174:PHE:CE2	2.50	0.46
1:A:231:ASP:HB2	1:A:234:ASN:OD1	2.14	0.46
1:A:324:ASP:HB3	1:A:339:VAL:HG23	1.98	0.46
1:A:131:ASN:OD1	1:A:131:ASN:O	2.32	0.46
1:A:107:PHE:CD2	1:A:118:THR:HG23	2.51	0.46
1:A:163:LYS:NZ	1:A:241:TRP:O	2.47	0.46
1:A:297:ASP:HB2	1:A:303:VAL:CG1	2.45	0.45
1:A:97:SER:HB2	5:A:705:NAG:H5	1.98	0.45
1:A:287:CYS:SG	1:A:291:ALA:HB3	2.56	0.45
1:A:153:SER:HB2	1:A:154:PRO:HD2	1.98	0.45
1:A:239:GLN:O	1:A:243:THR:CG2	2.64	0.45
1:A:298:ARG:O	1:A:299:ASP:CG	2.56	0.44
1:A:430:THR:HG22	1:A:431:GLY:N	2.33	0.44
1:A:313:PRO:HG2	1:A:314:GLU:OE1	2.17	0.44
1:A:163:LYS:HB3	1:A:174:PHE:HD2	1.83	0.44
1:A:307:ARG:HB3	1:A:307:ARG:NH1	2.32	0.44
1:A:184:MET:CG	1:A:253:ARG:HH21	2.31	0.44
1:A:346:HIS:CD2	1:A:375:THR:HG21	2.53	0.44
5:A:705:NAG:C4	5:A:706:NAG:C1	2.96	0.44
1:A:430:THR:CG2	1:A:431:GLY:N	2.82	0.43
1:A:406:CYS:HA	1:A:433:THR:HG23	2.00	0.43
1:A:174:PHE:CD1	1:A:220:PHE:CE2	3.07	0.42
1:A:182:ARG:HH11	1:A:182:ARG:HG2	1.85	0.42
2:D:2:NAG:H5	2:D:2:NAG:N2	2.35	0.42
2:D:1:NAG:H62	2:D:2:NAG:C1	2.49	0.42
1:A:174:PHE:CD1	1:A:220:PHE:HE2	2.38	0.42
1:A:260:GLU:HG2	1:A:265:SER:OG	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:PHE:CG	1:A:118:THR:CG2	3.03	0.41
1:A:124:ASN:ND2	1:A:270:ASP:O	2.51	0.41
1:A:145:THR:N	1:A:282:GLY:O	2.51	0.41
1:A:133:THR:HG21	2:D:3:FUC:C6	2.50	0.41
1:A:350:CYS:SG	1:A:351:ARG:N	2.93	0.41
3:C:1:NAG:O4	3:C:2:NAG:H83	2.20	0.41
1:A:141:LYS:HD2	1:A:314:GLU:OE2	2.21	0.41
1:A:321:PHE:CD2	1:A:321:PHE:O	2.74	0.41
1:A:325:ARG:CG	1:A:326:PRO:HD2	2.50	0.41
1:A:95:ASN:HB3	1:A:98:ASP:HB3	2.03	0.40
1:A:281:VAL:O	1:A:281:VAL:HG23	2.21	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:GLU:OE2	1:A:221:SER:OG[4_645]	1.91	0.29
1:A:264:ASP:OD2	1:A:435:ASN:ND2[2_544]	1.95	0.25
1:A:264:ASP:OD2	1:A:435:ASN:HD22[2_544]	1.44	0.16

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	401/604 (66%)	380 (95%)	21 (5%)	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	338/514 (66%)	333 (98%)	5 (2%)	65 82

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	ASP
1	A	127	GLN
1	A	174	PHE
1	A	333	ARG
1	A	423	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

5 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	C	1	3,1	14,14,15	1.06	2 (14%)	17,19,21	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	C	2	3	14,14,15	0.83	1 (7%)	17,19,21	0.58	0
2	NAG	D	1	1,2	14,14,15	0.31	0	17,19,21	1.68	2 (11%)
2	NAG	D	2	2	14,14,15	1.09	2 (14%)	17,19,21	0.82	1 (5%)
2	FUC	D	3	2	10,10,11	1.12	1 (10%)	14,14,16	0.91	1 (7%)

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	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	3/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	FUC	D	3	2	-	-	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NAG	C1-C2	3.18	1.57	1.52
3	C	1	NAG	O5-C1	-3.09	1.38	1.43
2	D	3	FUC	C1-C2	2.62	1.58	1.52
2	D	2	NAG	O5-C1	2.42	1.47	1.43
3	C	2	NAG	O5-C1	2.34	1.47	1.43
3	C	1	NAG	C1-C2	2.22	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	C1-O5-C5	5.64	119.83	112.19
2	D	2	NAG	C1-O5-C5	2.83	116.03	112.19
2	D	3	FUC	O2-C2-C1	2.26	113.78	109.15
2	D	1	NAG	O4-C4-C3	-2.23	105.20	110.35

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	O5-C5-C6-O6

Continued on next page...

Continued from previous page...

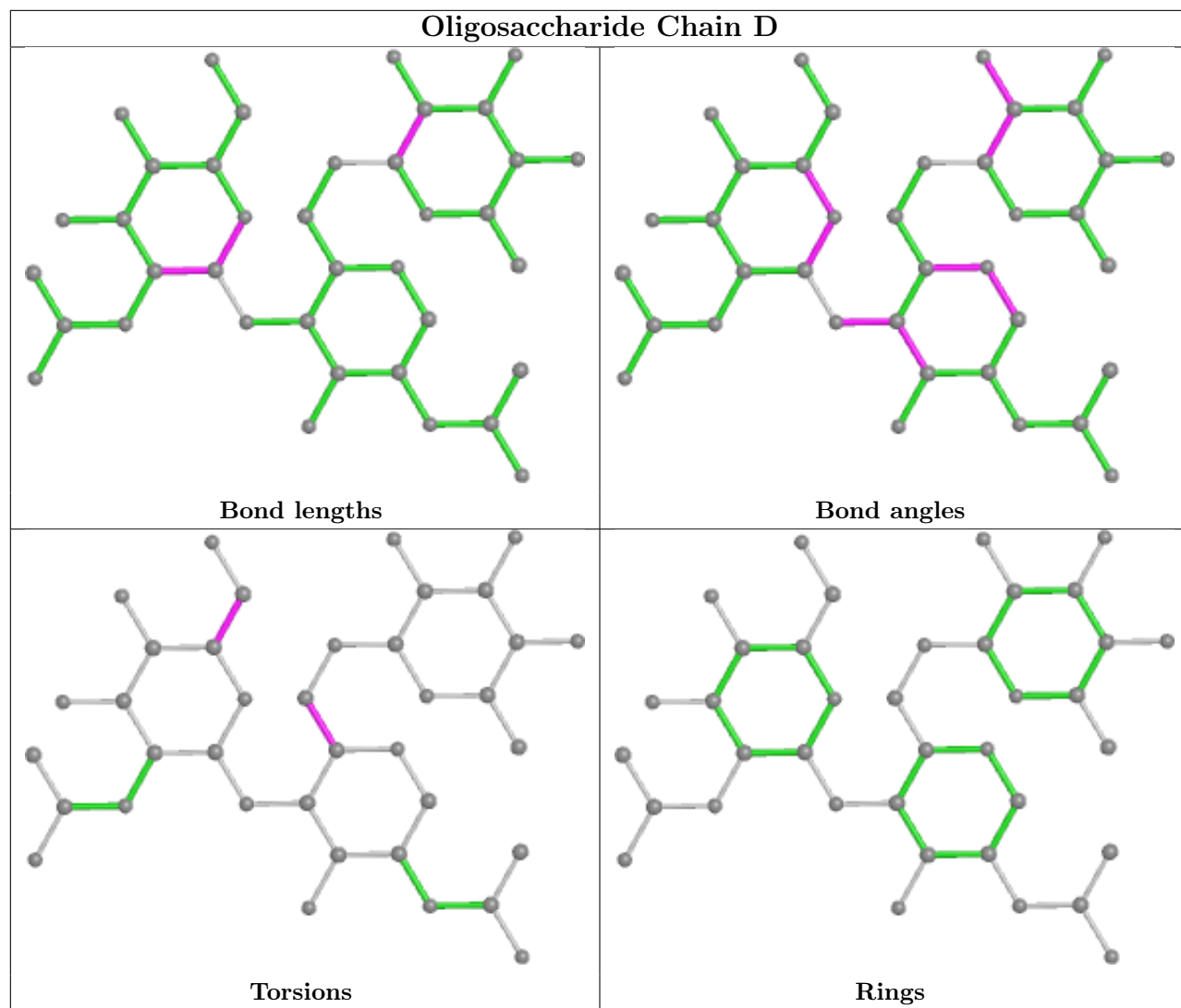
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
2	D	1	NAG	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6

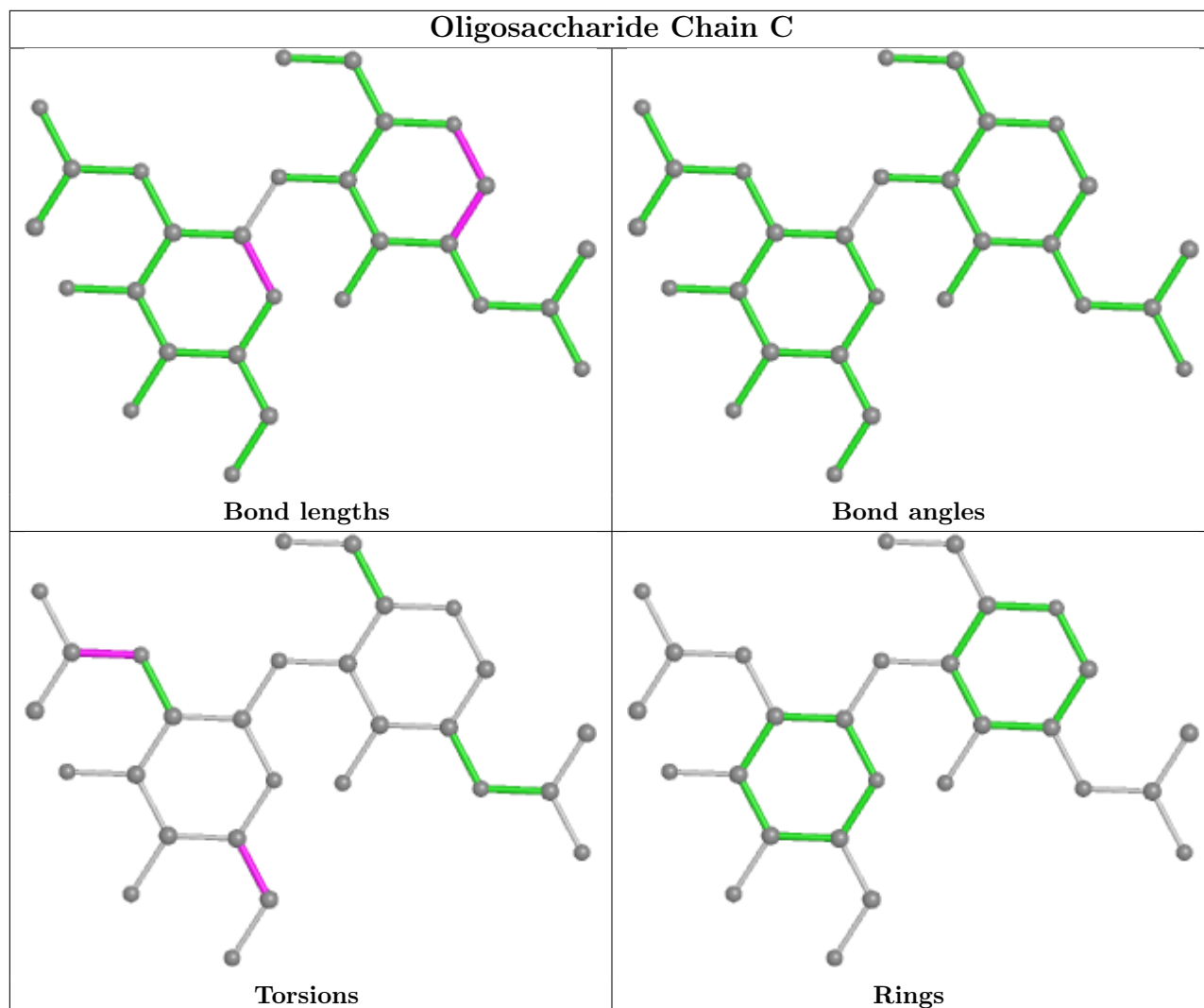
There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3	FUC	1	0
2	D	1	NAG	2	0
2	D	2	NAG	4	0
3	C	2	NAG	3	0
3	C	1	NAG	4	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 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	$\# Z > 2$
5	NAG	A	706	-	14,14,15	0.30	0	17,19,21	0.66	0
5	NAG	A	705	1	14,14,15	0.30	0	17,19,21	0.76	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
5	NAG	A	706	-	-	0/6/23/26	0/1/1/1
5	NAG	A	705	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	706	NAG	2	0
5	A	705	NAG	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	409/604 (67%)	0.32	11 (2%) 54 53	75, 108, 150, 190	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	89	ARG	2.9
1	A	213	LEU	2.8
1	A	333	ARG	2.7
1	A	80	VAL	2.5
1	A	134	LEU	2.4
1	A	214	SER	2.4
1	A	279	LEU	2.3
1	A	251	PHE	2.3
1	A	174	PHE	2.2
1	A	249	VAL	2.2
1	A	215	GLY	2.1

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.

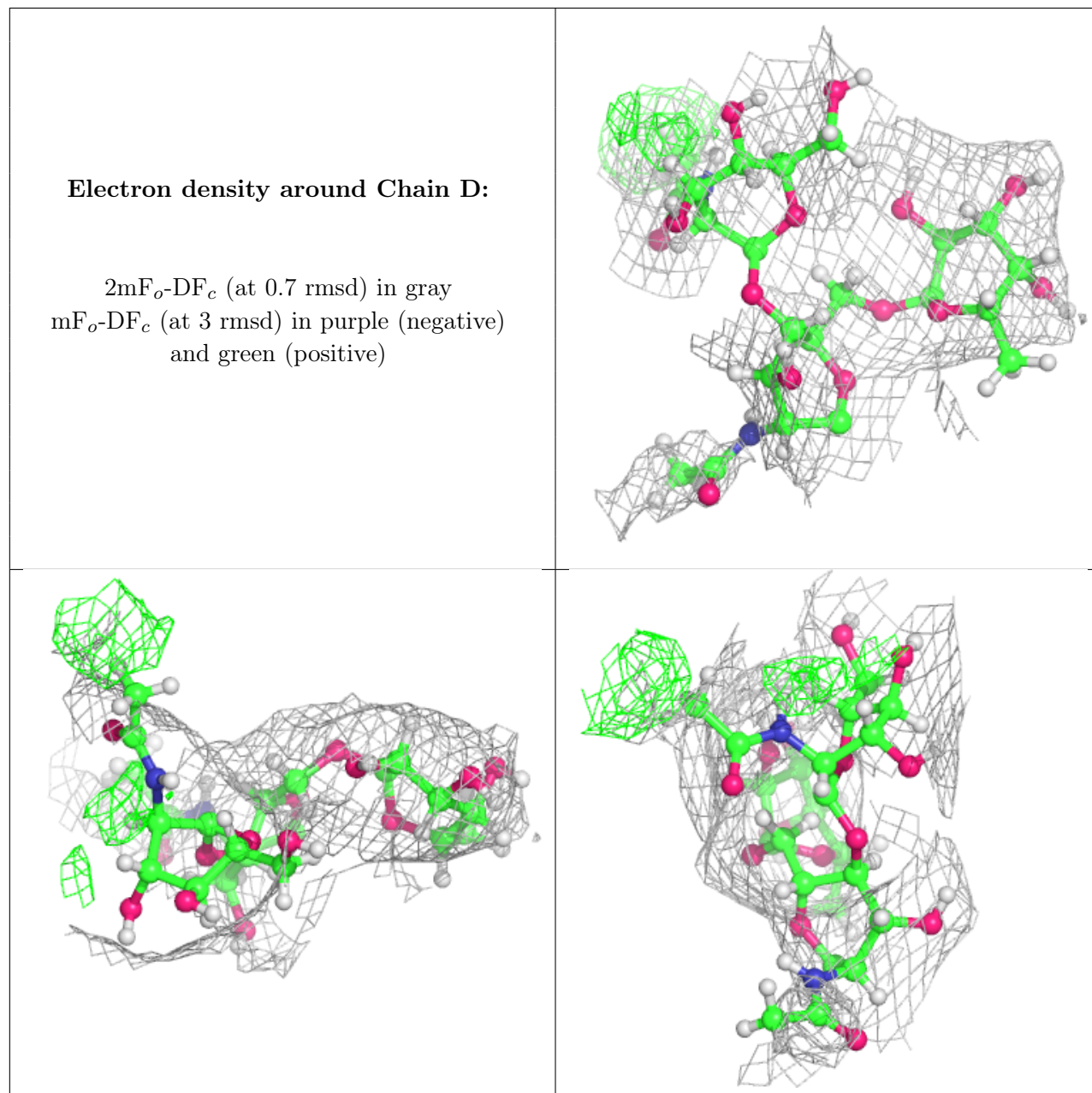
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	C	2	14/15	0.47	0.45	126,186,225,228	0

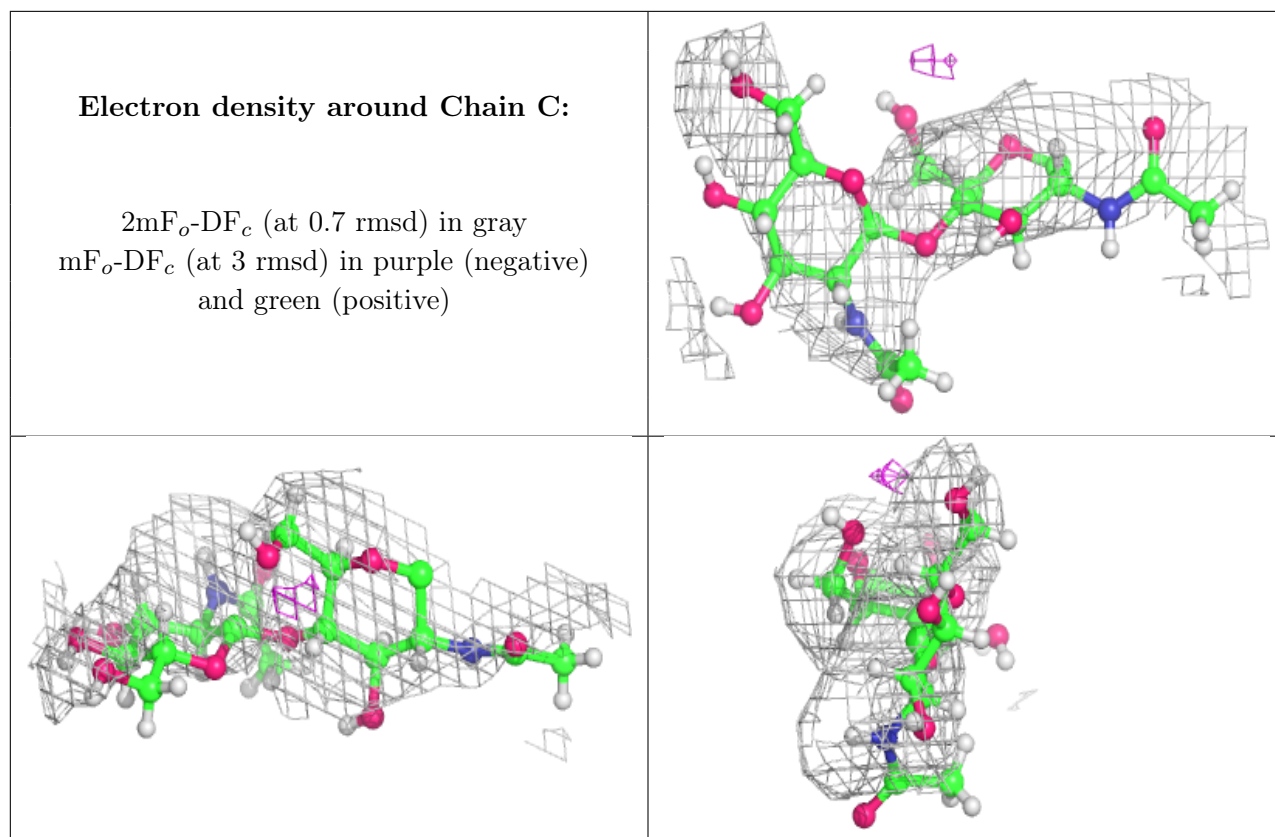
Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	C	1	14/15	0.74	0.39	131,176,213,220	0
2	NAG	D	1	14/15	0.78	0.20	125,187,229,242	0
2	NAG	D	2	14/15	0.78	0.19	145,186,224,232	0
2	FUC	D	3	10/11	0.79	0.22	140,170,191,194	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.





6.4 Ligands [i](#)

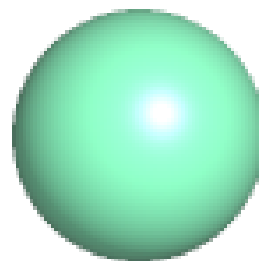
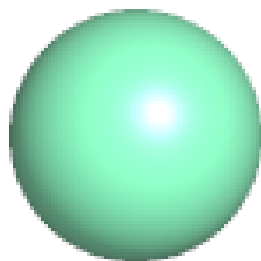
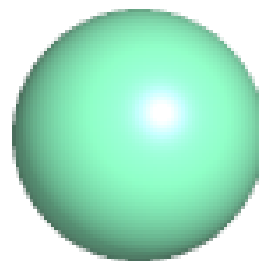
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	A	705	14/15	0.82	0.23	92,155,196,203	0
5	NAG	A	706	14/15	0.89	0.17	120,151,187,200	0
4	SM	A	703	1/1	0.90	0.29	207,207,207,207	0
4	SM	A	702	1/1	0.94	0.33	200,200,200,200	0
4	SM	A	701	1/1	0.97	0.29	171,171,171,171	0
4	SM	A	704	1/1	0.98	0.22	141,141,141,141	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.

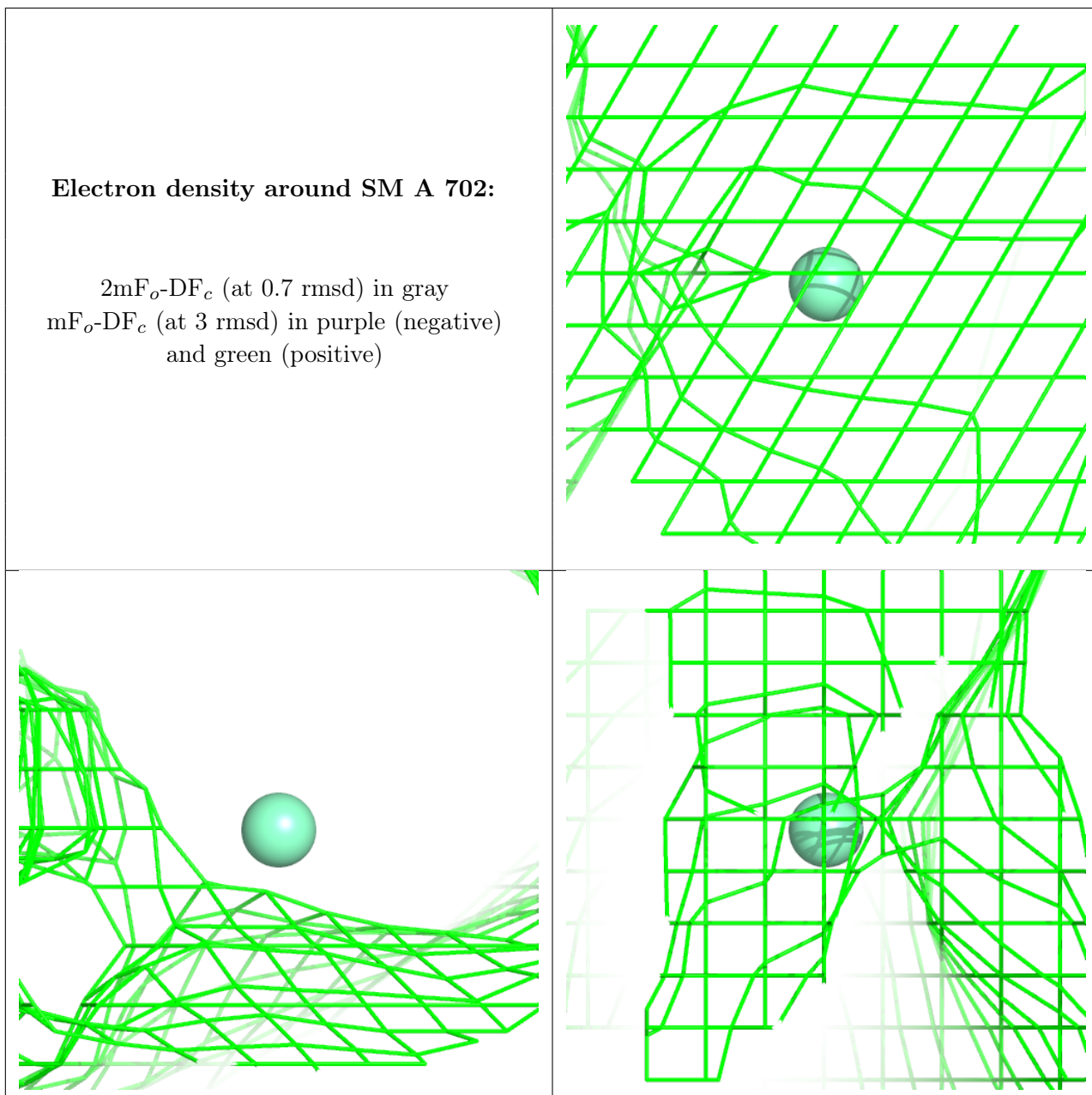
Electron density around SM A 703:

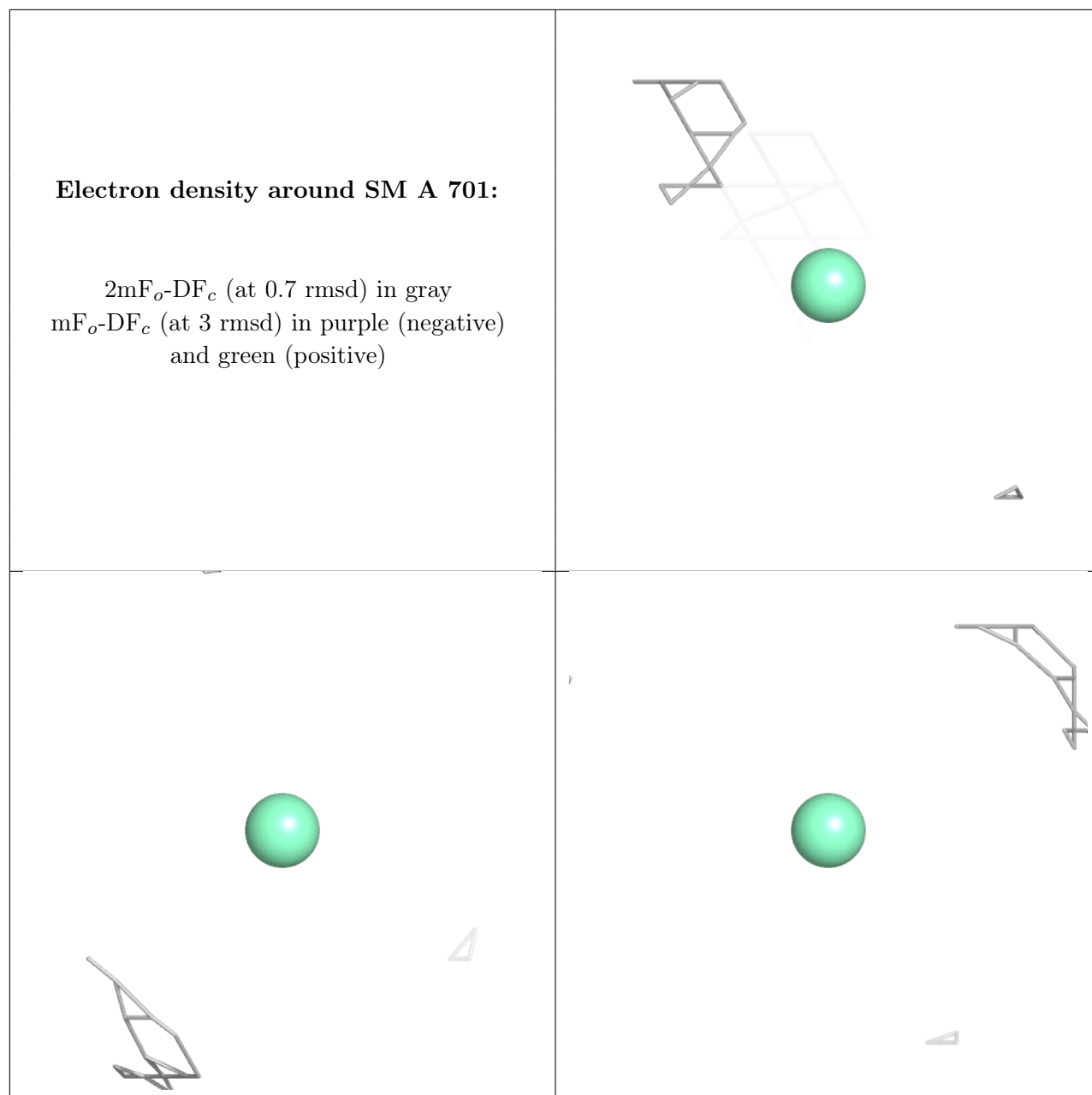
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

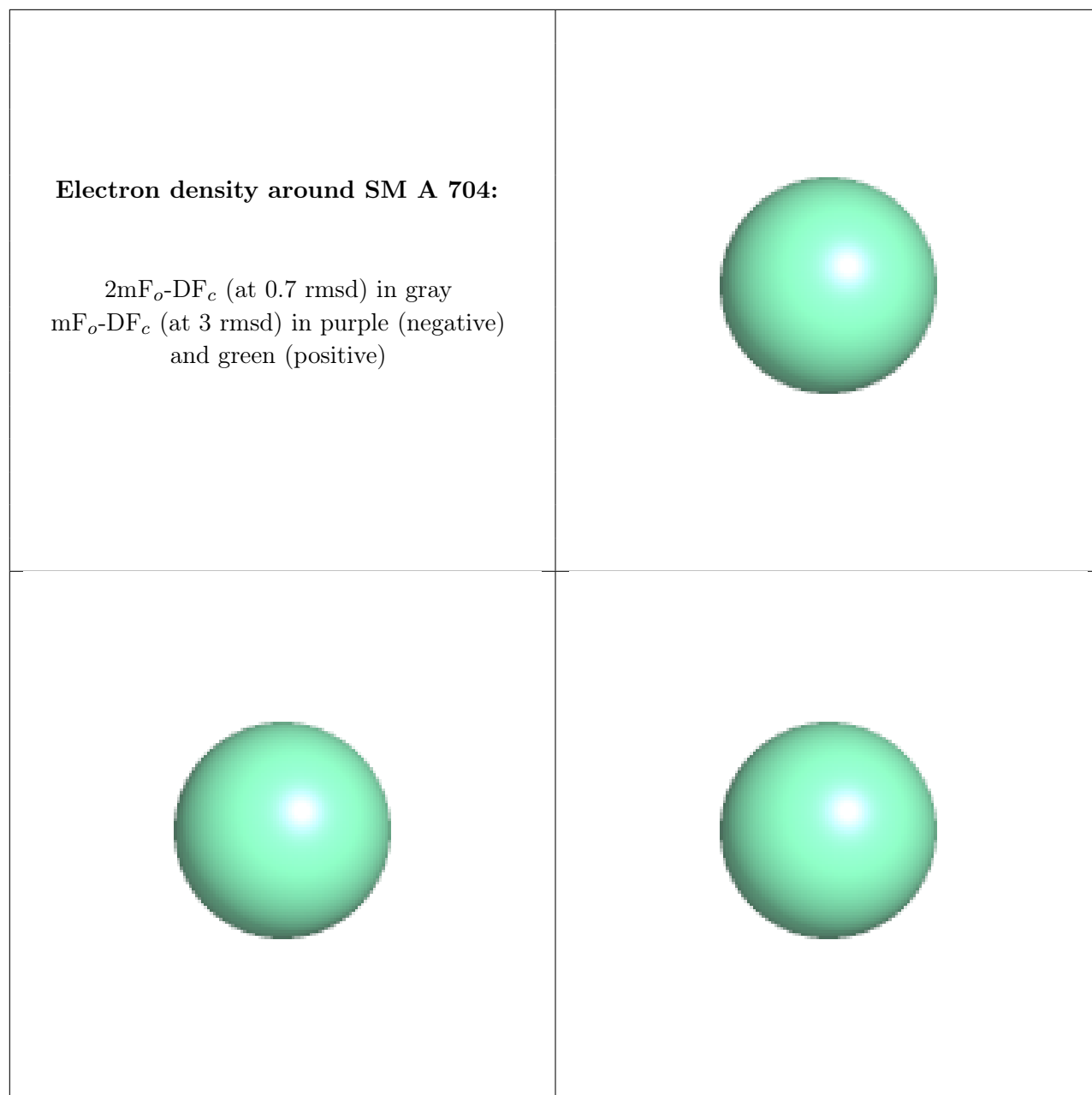


Electron density around SM A 702:

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







6.5 Other polymers [i](#)

There are no such residues in this entry.