wwPDB X-ray Structure Validation Summary Report (i)

Oct 8, 2020 – 03:08 PM BST

PDB ID	:	6YRB
Title	:	Crystal structure of the tetramerization domain of the glycoprotein Gn (Andes virus) at pH 7.5
Authors	:	Serris, A.; Rey, F.A.; Guardado-Calvo, P.
Deposited on	:	2020-04-20
Resolution	:	2.35 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

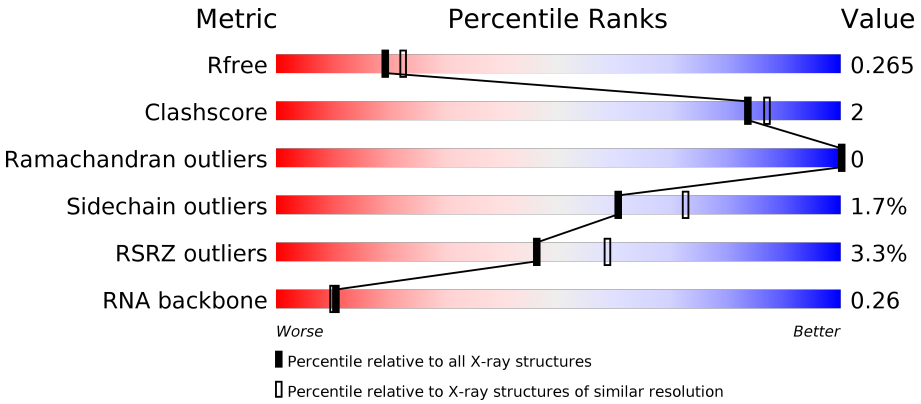
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)
RNA backbone	3102	1006 (2.74-1.98)

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 on 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 <=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	149	3%, 62%, 5%, 33%
1	B	149	%, 64%, 34%
2	C	5	80%, 20%
2	D	5	20%, 60%, 40%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	E	4	100%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 1738 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 Envelope polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	100	Total	C	N	O	S	0	0	0
			754	481	122	142	9			
1	B	99	Total	C	N	O	S	0	0	0
			744	475	119	141	9			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	485	GLY	-	expression tag	UNP Q9E006
A	486	PRO	-	expression tag	UNP Q9E006
A	487	PHE	-	expression tag	UNP Q9E006
A	488	GLU	-	expression tag	UNP Q9E006
A	489	ASP	-	expression tag	UNP Q9E006
A	490	ASP	-	expression tag	UNP Q9E006
A	491	ASP	-	expression tag	UNP Q9E006
A	492	ASP	-	expression tag	UNP Q9E006
A	493	LYS	-	expression tag	UNP Q9E006
A	494	ALA	-	expression tag	UNP Q9E006
A	495	GLY	-	expression tag	UNP Q9E006
A	496	TRP	-	expression tag	UNP Q9E006
A	497	SER	-	expression tag	UNP Q9E006
A	498	HIS	-	expression tag	UNP Q9E006
A	499	PRO	-	expression tag	UNP Q9E006
A	500	GLN	-	expression tag	UNP Q9E006
A	501	PHE	-	expression tag	UNP Q9E006
A	502	GLU	-	expression tag	UNP Q9E006
A	503	LYS	-	expression tag	UNP Q9E006
A	504	GLY	-	expression tag	UNP Q9E006
A	505	GLY	-	expression tag	UNP Q9E006
A	506	GLY	-	expression tag	UNP Q9E006
A	507	SER	-	expression tag	UNP Q9E006
A	508	GLY	-	expression tag	UNP Q9E006
A	509	GLY	-	expression tag	UNP Q9E006

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	510	GLY	-	expression tag	UNP Q9E006
A	511	SER	-	expression tag	UNP Q9E006
A	512	GLY	-	expression tag	UNP Q9E006
A	513	GLY	-	expression tag	UNP Q9E006
A	514	GLY	-	expression tag	UNP Q9E006
A	515	SER	-	expression tag	UNP Q9E006
A	516	TRP	-	expression tag	UNP Q9E006
A	517	SER	-	expression tag	UNP Q9E006
A	518	HIS	-	expression tag	UNP Q9E006
A	519	PRO	-	expression tag	UNP Q9E006
A	520	GLN	-	expression tag	UNP Q9E006
A	521	PHE	-	expression tag	UNP Q9E006
A	522	GLU	-	expression tag	UNP Q9E006
A	523	LYS	-	expression tag	UNP Q9E006
B	485	GLY	-	expression tag	UNP Q9E006
B	486	PRO	-	expression tag	UNP Q9E006
B	487	PHE	-	expression tag	UNP Q9E006
B	488	GLU	-	expression tag	UNP Q9E006
B	489	ASP	-	expression tag	UNP Q9E006
B	490	ASP	-	expression tag	UNP Q9E006
B	491	ASP	-	expression tag	UNP Q9E006
B	492	ASP	-	expression tag	UNP Q9E006
B	493	LYS	-	expression tag	UNP Q9E006
B	494	ALA	-	expression tag	UNP Q9E006
B	495	GLY	-	expression tag	UNP Q9E006
B	496	TRP	-	expression tag	UNP Q9E006
B	497	SER	-	expression tag	UNP Q9E006
B	498	HIS	-	expression tag	UNP Q9E006
B	499	PRO	-	expression tag	UNP Q9E006
B	500	GLN	-	expression tag	UNP Q9E006
B	501	PHE	-	expression tag	UNP Q9E006
B	502	GLU	-	expression tag	UNP Q9E006
B	503	LYS	-	expression tag	UNP Q9E006
B	504	GLY	-	expression tag	UNP Q9E006
B	505	GLY	-	expression tag	UNP Q9E006
B	506	GLY	-	expression tag	UNP Q9E006
B	507	SER	-	expression tag	UNP Q9E006
B	508	GLY	-	expression tag	UNP Q9E006
B	509	GLY	-	expression tag	UNP Q9E006
B	510	GLY	-	expression tag	UNP Q9E006
B	511	SER	-	expression tag	UNP Q9E006
B	512	GLY	-	expression tag	UNP Q9E006

Continued on next page...

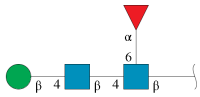
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	513	GLY	-	expression tag	UNP Q9E006
B	514	GLY	-	expression tag	UNP Q9E006
B	515	SER	-	expression tag	UNP Q9E006
B	516	TRP	-	expression tag	UNP Q9E006
B	517	SER	-	expression tag	UNP Q9E006
B	518	HIS	-	expression tag	UNP Q9E006
B	519	PRO	-	expression tag	UNP Q9E006
B	520	GLN	-	expression tag	UNP Q9E006
B	521	PHE	-	expression tag	UNP Q9E006
B	522	GLU	-	expression tag	UNP Q9E006
B	523	LYS	-	expression tag	UNP Q9E006

- Molecule 2 is a RNA chain called RNA (5'-D(*())-R(P*UP*UP*UP*())-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	P	0	0	1
			65	27	6	28	4			
2	D	5	Total	C	N	O	P	0	0	1
			65	27	6	28	4			

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-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
3	E	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 4 is IODIDE ION (three-letter code: IOD) (formula: I) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total	I	0	0
			3	3		
4	A	3	Total	I	0	0
			3	3		

- Molecule 5 is water.

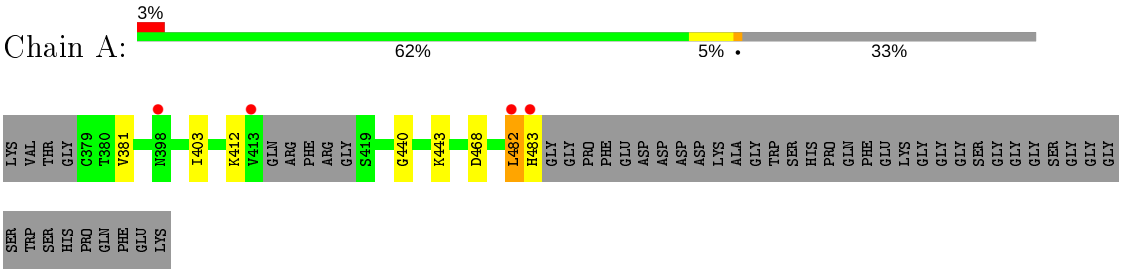
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	31	Total O 31 31	0	0
5	B	21	Total O 21 21	0	0
5	C	1	Total O 1 1	0	0
5	D	2	Total O 2 2	0	0

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.

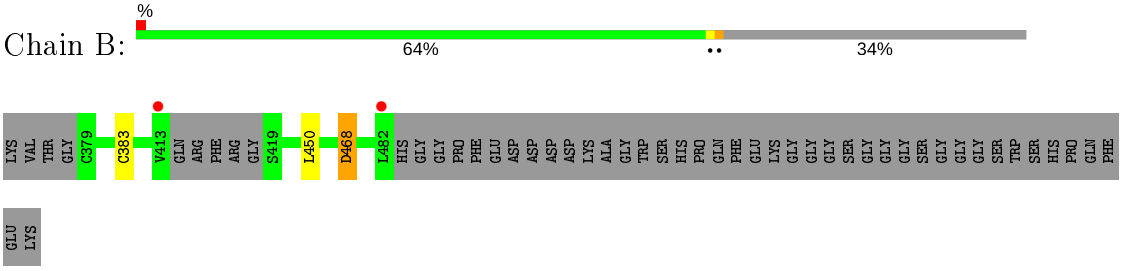
• Molecule 1: Envelope polyprotein

Chain A:



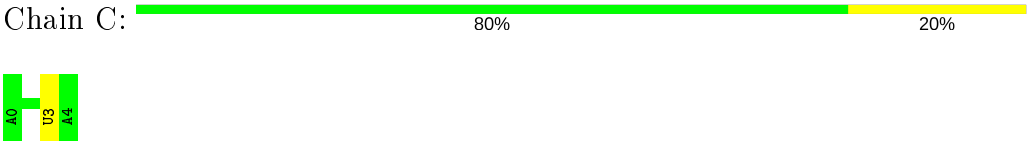
• Molecule 1: Envelope polyprotein

Chain B:



• Molecule 2: RNA (5'-D(*())-R(P*UP*UP*UP*())-3')

Chain C:

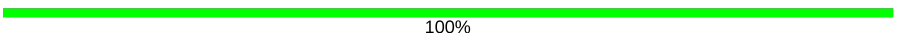


• Molecule 2: RNA (5'-D(*())-R(P*UP*UP*UP*())-3')

Chain D:

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

Chain E:




NAG1
NAG2
BMA3
FUC4

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α, β, γ	67.85Å 67.85Å 121.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.70 – 2.35 37.70 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.6 (37.70-2.35) 99.6 (37.70-2.35)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.07 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.14rc3	Depositor
R, R_{free}	0.226 , 0.266 0.226 , 0.265	Depositor DCC
R_{free} test set	570 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	43.1	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 27.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.259 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1738	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.10% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: FUC, IOD, BMA, 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	0.25	0/766	0.44	0/1040
1	B	0.24	0/755	0.42	0/1025
2	C	0.27	0/70	1.30	1/108 (0.9%)
2	D	0.27	0/70	1.33	2/108 (1.9%)
All	All	0.25	0/1661	0.58	3/2281 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	3	U	C2-N1-C1'	6.08	124.99	117.70
2	C	3	U	C2-N1-C1'	5.95	124.84	117.70
2	D	3	U	N1-C2-O2	5.26	126.48	122.80

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	754	0	752	6	0
1	B	744	0	746	2	0
2	C	65	0	30	0	0
2	D	65	0	30	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	49	0	43	0	0
4	A	3	0	0	2	0
4	B	3	0	0	1	0
5	A	31	0	0	0	0
5	B	21	0	0	0	0
5	C	1	0	0	0	0
5	D	2	0	0	0	0
All	All	1738	0	1601	8	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 8 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:468:ASP:HB2	4:A:606:IOD:I	2.70	0.62
1:B:468:ASP:HB2	4:B:601:IOD:I	2.73	0.58
1:A:381:VAL:HG23	1:A:443:LYS:HD3	1.89	0.54
1:A:440:GLY:HA2	4:A:605:IOD:I	2.79	0.52
1:A:443:LYS:NZ	2:D:4:A:OP1	2.41	0.51

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	96/149 (64%)	93 (97%)	3 (3%)	0	100	100
1	B	95/149 (64%)	93 (98%)	2 (2%)	0	100	100
All	All	191/298 (64%)	186 (97%)	5 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	89/123 (72%)	87 (98%)	2 (2%)	52 63
1	B	88/123 (72%)	87 (99%)	1 (1%)	73 84
All	All	177/246 (72%)	174 (98%)	3 (2%)	60 72

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

Mol	Chain	Res	Type
1	A	482	LEU
1	A	483	HIS
1	B	468	ASP

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

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	2/5 (40%)	0	0
2	D	3/5 (60%)	0	0
All	All	5/10 (50%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

4 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	E	1	1,3	14,14,15	0.23	0	17,19,21	0.44	0
3	NAG	E	2	3	14,14,15	0.21	0	17,19,21	0.41	0
3	BMA	E	3	3	11,11,12	0.57	0	15,15,17	0.72	0
3	FUC	E	4	3	10,10,11	0.72	0	14,14,16	0.77	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	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	1/2/19/22	0/1/1/1
3	FUC	E	4	3	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

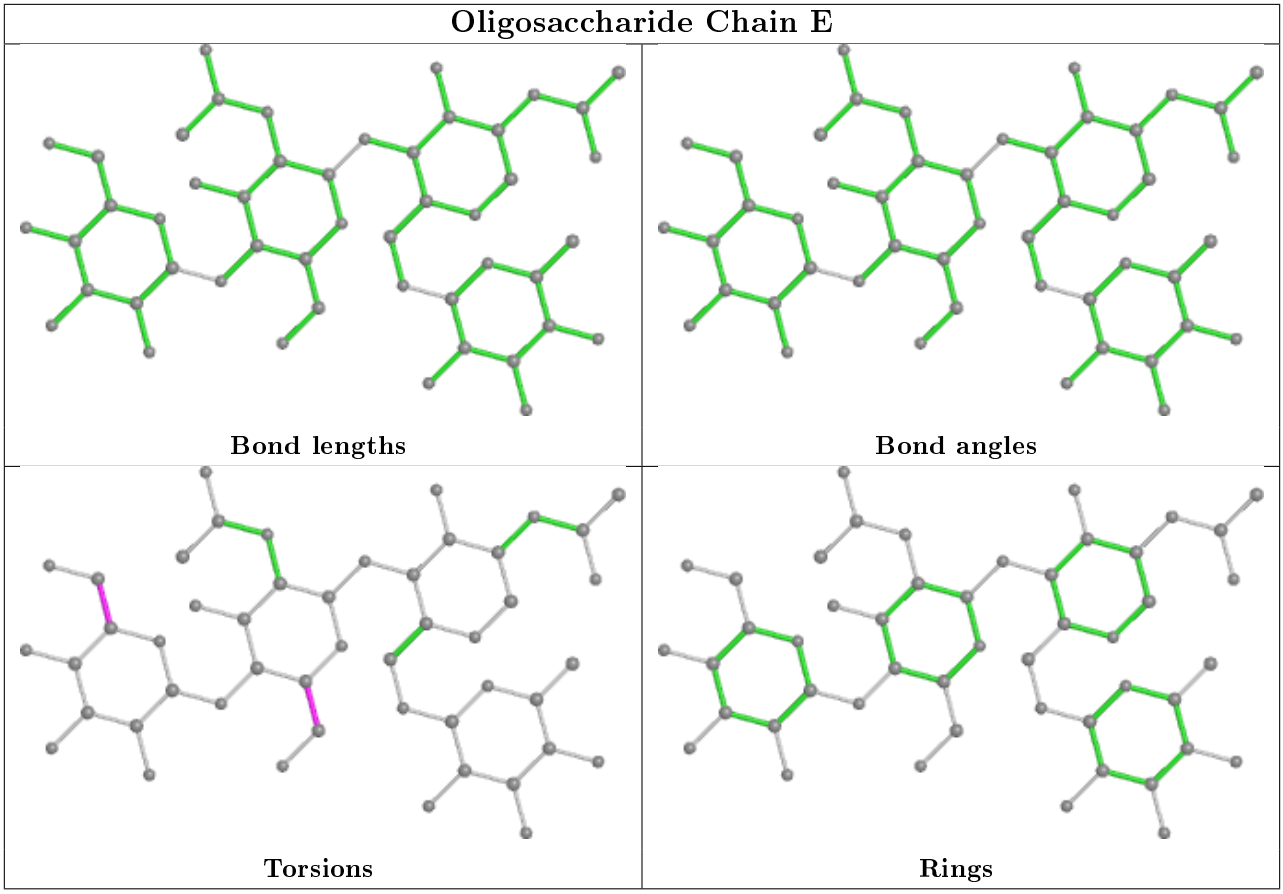
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
3	E	3	BMA	O5-C5-C6-O6

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

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers

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

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, 95^{th} 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	100/149 (67%)	-0.25	4 (4%) 38 51	29, 40, 74, 107	0
1	B	99/149 (66%)	-0.15	2 (2%) 65 75	31, 43, 84, 99	0
2	C	5/5 (100%)	-0.13	0 100 100	40, 45, 64, 109	0
2	D	5/5 (100%)	1.10	1 (20%) 1 2	38, 50, 88, 109	0
All	All	209/308 (67%)	-0.17	7 (3%) 46 59	29, 42, 83, 109	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	413	VAL	7.0
1	A	482	LEU	5.6
2	D	0	A	4.9
1	B	482	LEU	4.1
1	A	413	VAL	3.9

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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, 95^{th} 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.

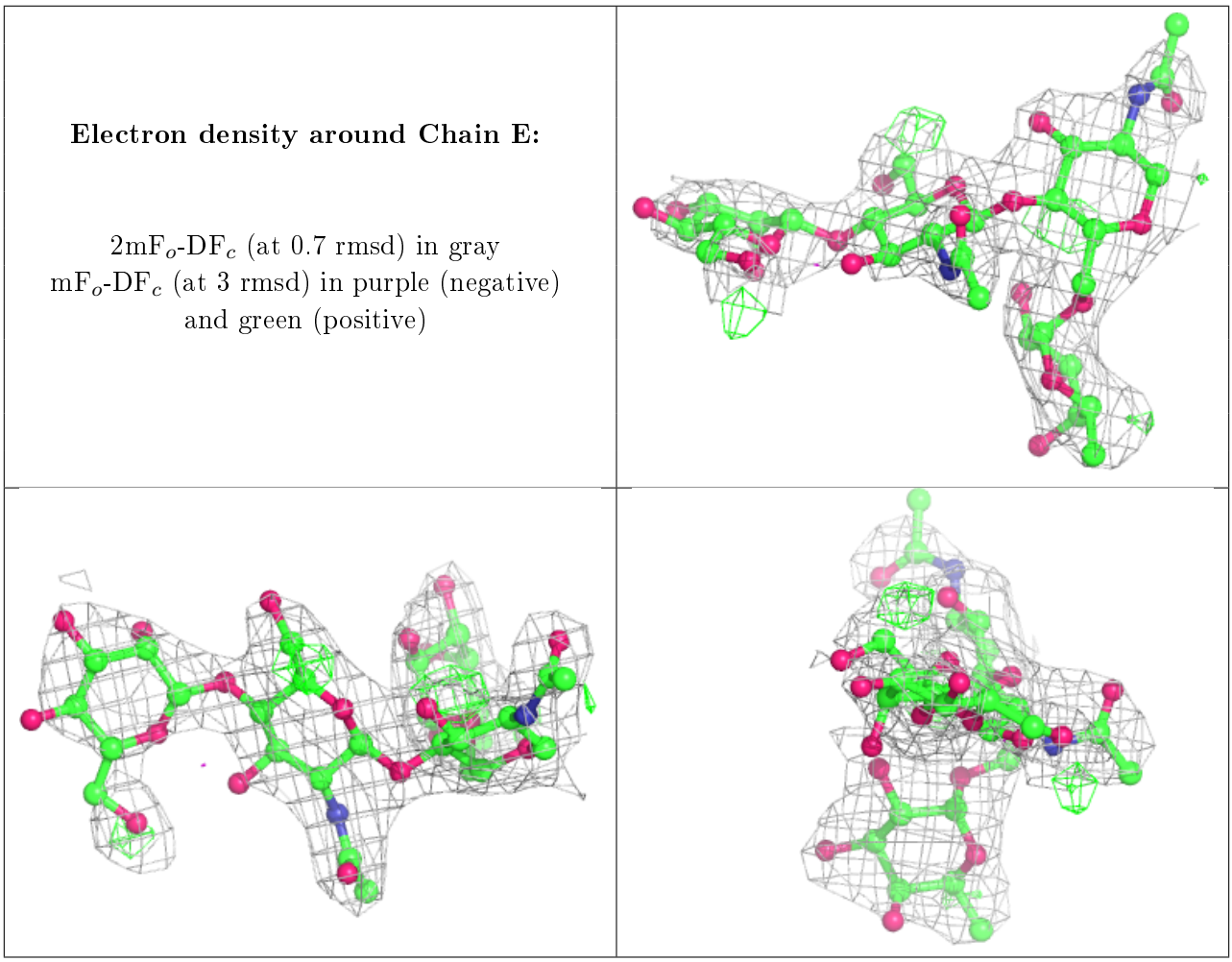
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	BMA	E	3	11/12	0.83	0.32	67,85,89,90	0
3	NAG	E	1	14/15	0.86	0.17	46,65,69,71	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FUC	E	4	10/11	0.86	0.23	56,66,72,77	0
3	NAG	E	2	14/15	0.88	0.23	60,72,76,77	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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	IOD	A	607	1/1	0.91	0.09	118,118,118,118	0
4	IOD	B	601	1/1	0.96	0.07	116,116,116,116	0

Continued on next page...

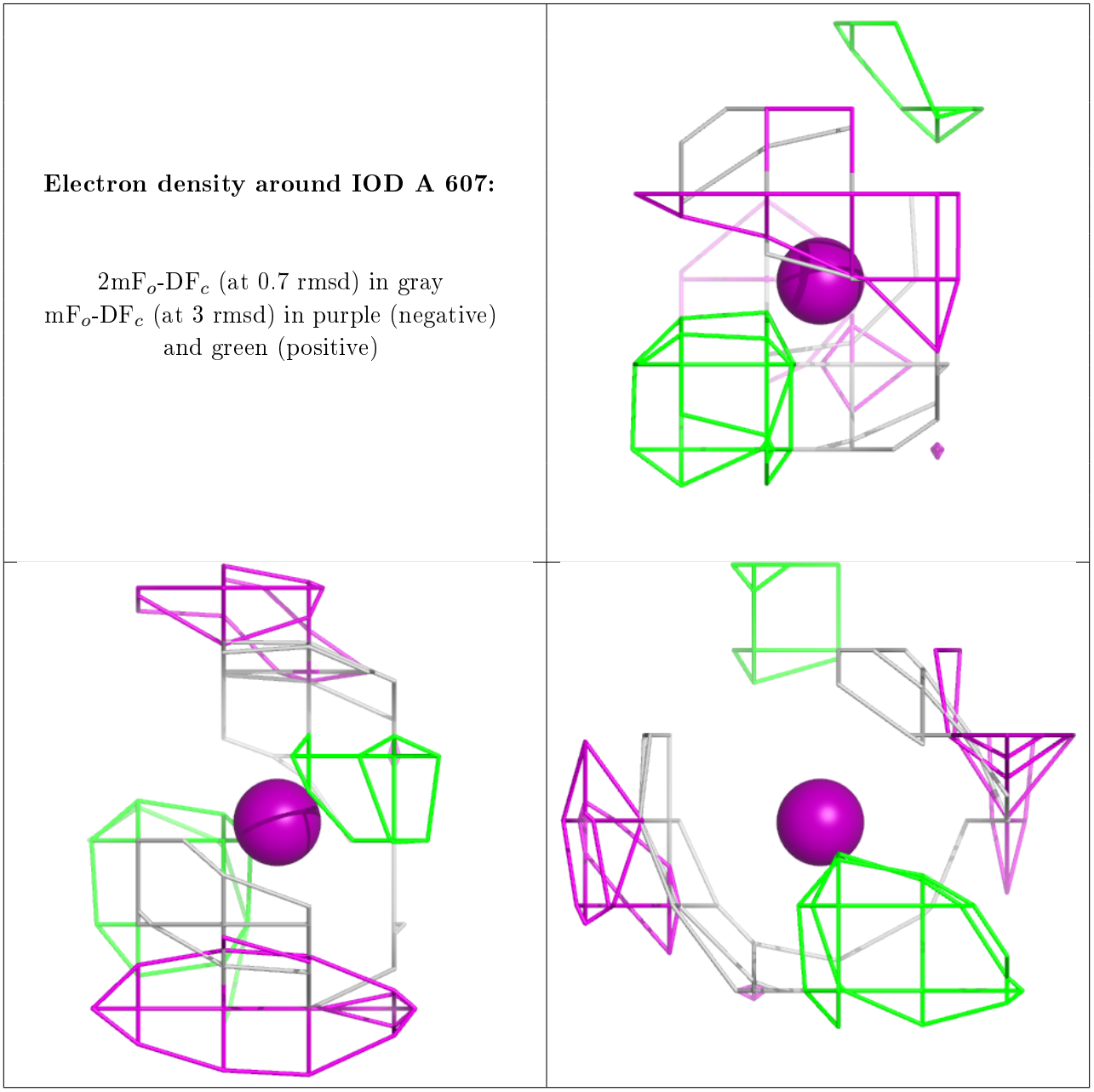
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	IOD	A	606	1/1	0.96	0.06	103,103,103,103	0
4	IOD	B	603	1/1	0.96	0.09	159,159,159,159	0
4	IOD	B	602	1/1	0.98	0.09	117,117,117,117	0
4	IOD	A	605	1/1	0.99	0.06	80,80,80,80	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.

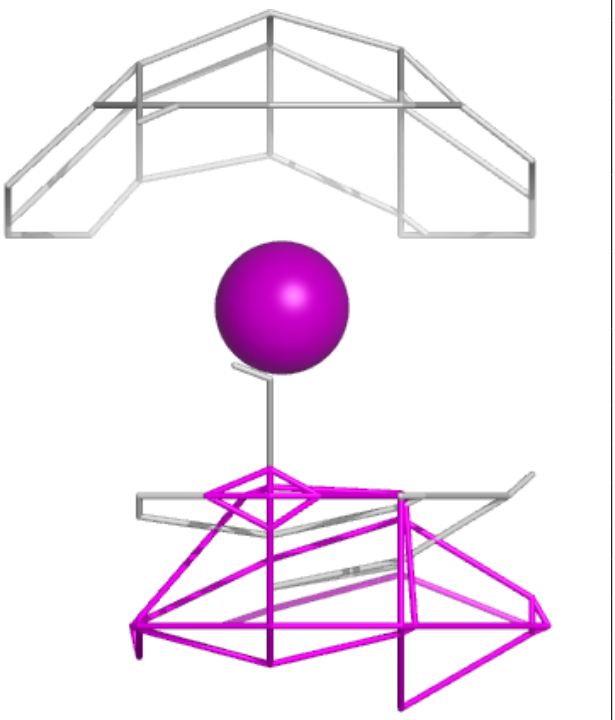
Electron density around IOD A 607:

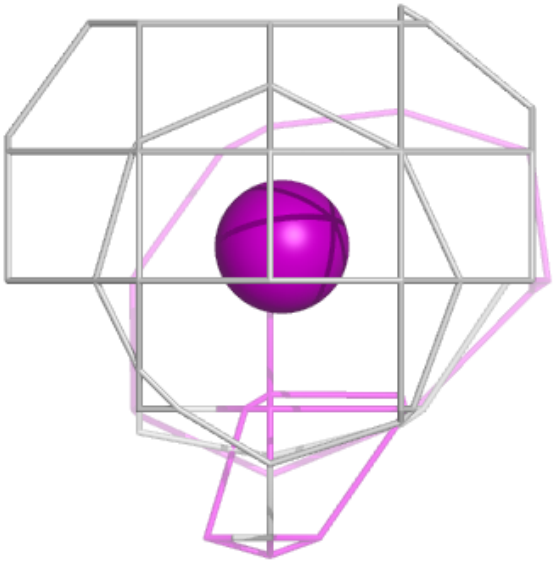
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

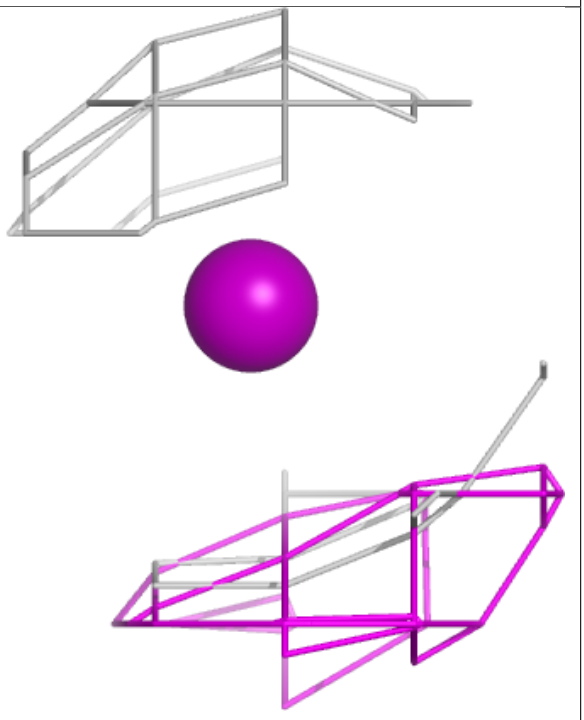


Electron density around IOD B 601:

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

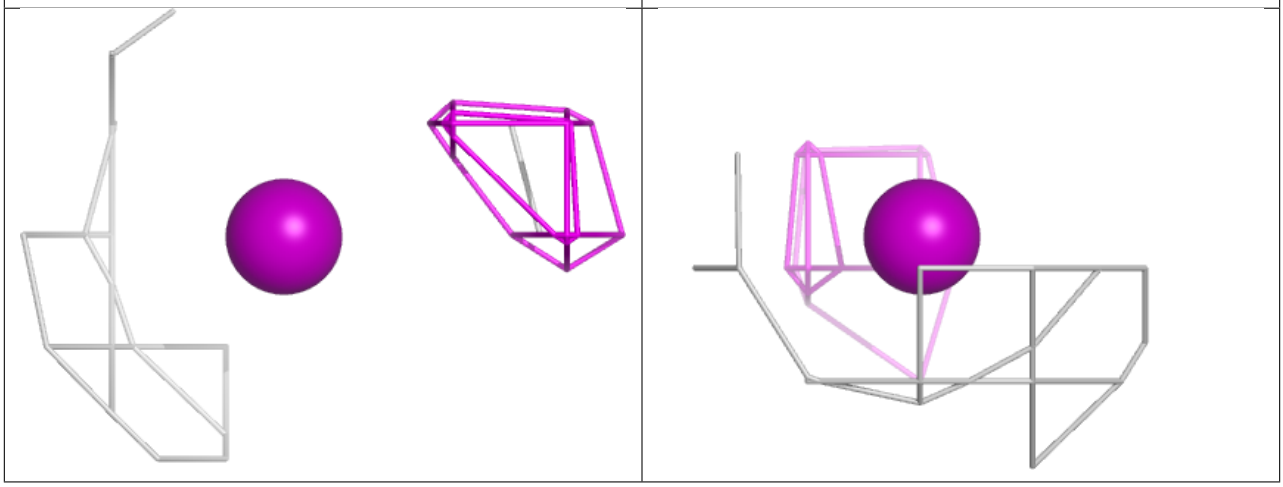






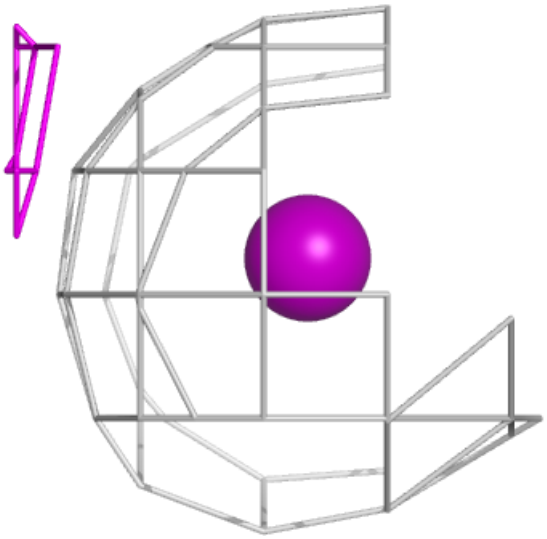
Electron density around IOD A 606:

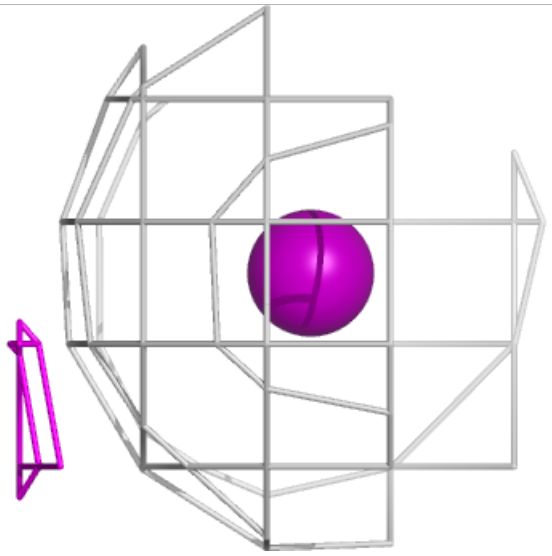
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

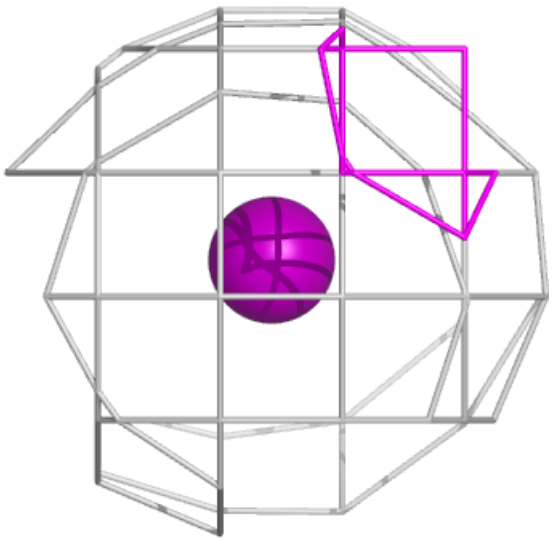


Electron density around IOD B 603:

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

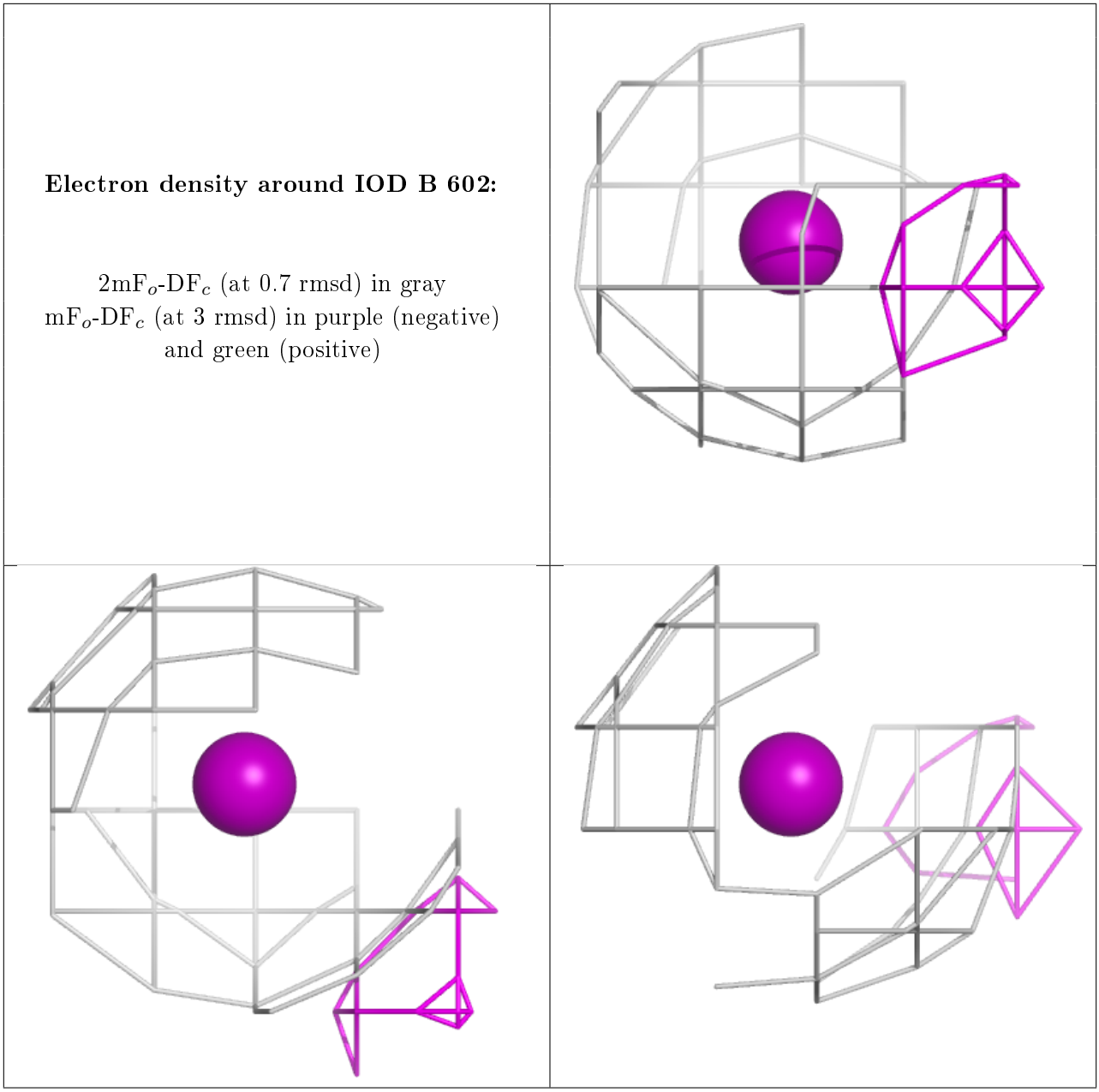






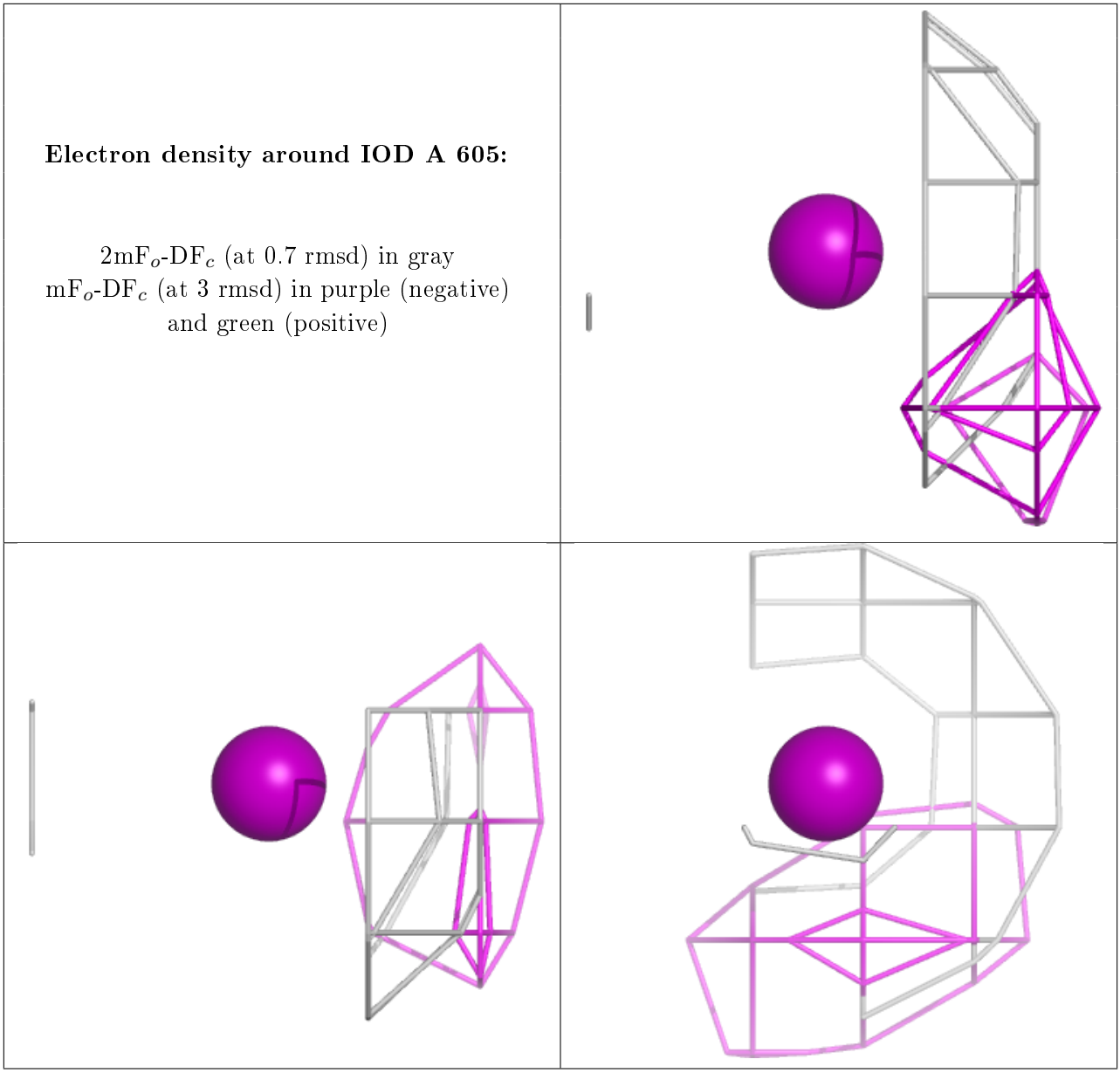
Electron density around IOD B 602:

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



Electron density around IOD A 605:

$2mF_o$-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.