



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 04:31 AM BST

PDB ID : 5W7A
Title : Rabbit acyloxyacyl hydrolase (AOAH), proteolytically processed, S262A mutant, with LPS (low quality saposin domain)
Authors : Gorelik, A.; Illes, K.; Nagar, B.
Deposited on : 2017-06-19
Resolution : 2.30 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 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 : 2.13.1
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) : 2.13.1

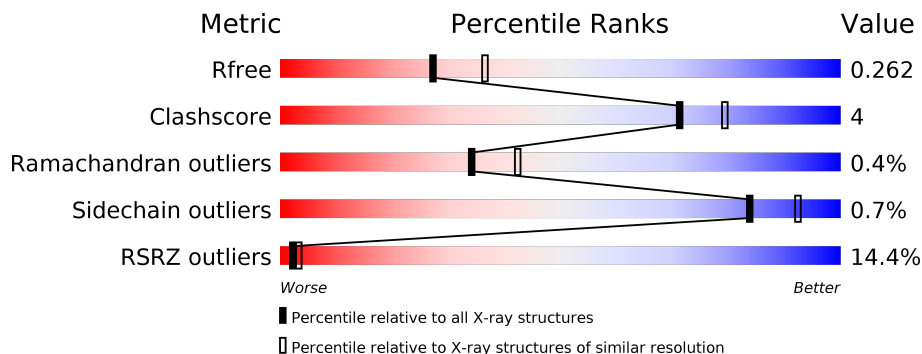
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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 $\leq 5\%$. 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	141	
2	B	422	
3	C	2	

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 9 unique types of molecules in this entry. The entry contains 7800 atoms, of which 3783 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 Acyloxyacyl hydrolase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	78	1104	366	533	96	101	8	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	ASP	-	expression tag	UNP O18823
A	14	ARG	-	expression tag	UNP O18823
A	15	HIS	-	expression tag	UNP O18823
A	16	HIS	-	expression tag	UNP O18823
A	17	HIS	-	expression tag	UNP O18823
A	18	HIS	-	expression tag	UNP O18823
A	19	HIS	-	expression tag	UNP O18823
A	20	HIS	-	expression tag	UNP O18823
A	21	LYS	-	expression tag	UNP O18823
A	22	LEU	-	expression tag	UNP O18823

- Molecule 2 is a protein called Acyloxyacyl hydrolase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	B	407	6406	2061	3156	573	603	13	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	262	ALA	SER	engineered mutation	UNP O18823

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

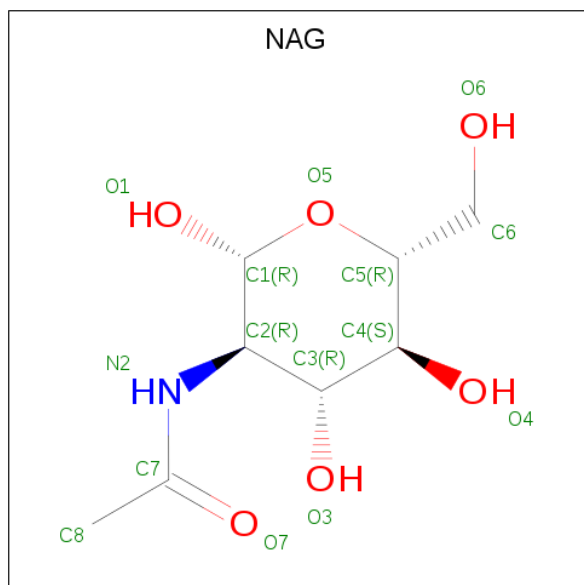


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
3	C	2	55	16	27	2	10	0	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	B	3	3	3	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



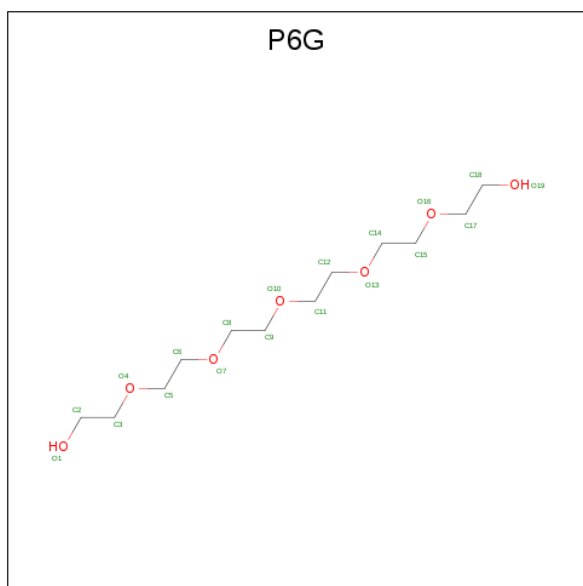
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
5	B	1	28	8	14	1	5	0	0

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P) (labeled as "Ligand of Interest" by author).



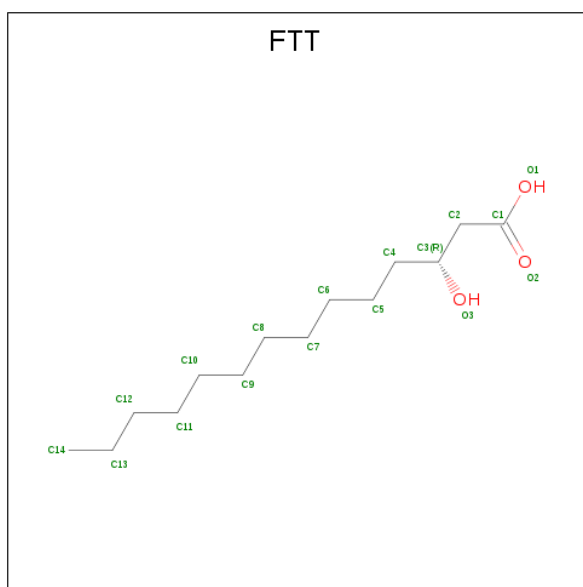
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: C₁₂H₂₆O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	H	O	0	0
			45	12	26	7		

- Molecule 8 is 3-HYDROXY-TETRADECANOIC ACID (three-letter code: FTT) (formula: C₁₄H₂₈O₃) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	H	O	0	0
			43	14	27	2		

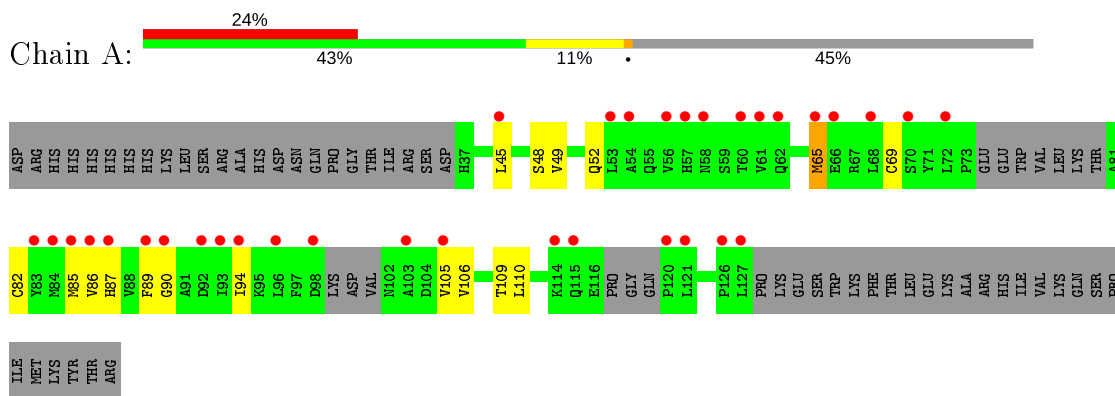
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	O	0	0
			1	1		
9	B	110	Total	O	0	0
			110	110		

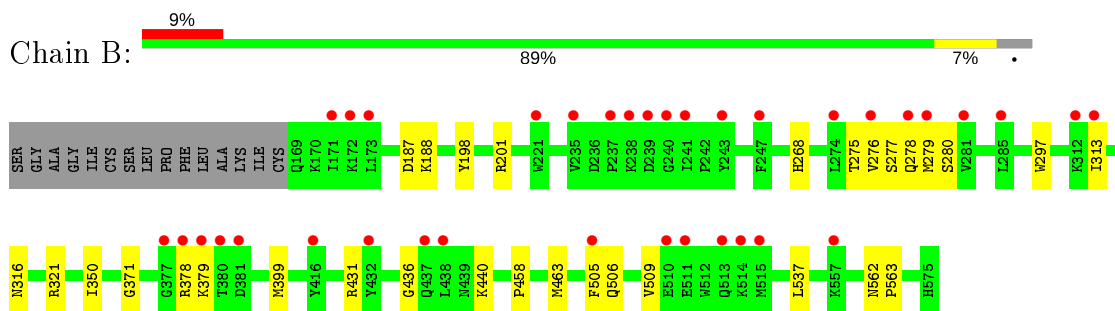
3 Residue-property plots [i](#)

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.

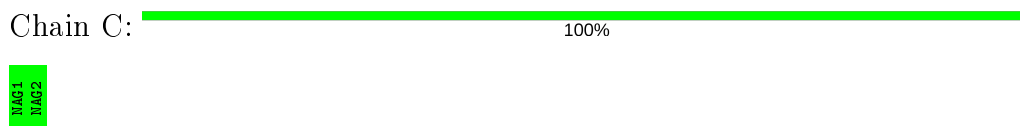
- Molecule 1: Acyloxyacyl hydrolase small subunit



- Molecule 2: Acyloxyacyl hydrolase large subunit



- Molecule 3: 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	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	89.58Å 123.20Å 125.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.69 – 2.30 34.69 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.8 (34.69-2.30) 93.5 (34.69-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.29Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.240 , 0.262 0.241 , 0.262	Depositor DCC
R_{free} test set	1530 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtrriage
Anisotropy	0.072	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 60.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7800	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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: PO4, CA, NAG, P6G, FTT

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	0.27	0/580	0.43	0/790
2	B	0.29	0/3336	0.49	0/4531
All	All	0.28	0/3916	0.48	0/5321

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	571	533	533	12	0
2	B	3250	3156	3156	16	0
3	C	28	27	25	0	0
4	B	3	0	0	0	0
5	B	14	14	13	0	0
6	B	5	0	0	1	0
7	B	19	26	26	0	0
8	B	16	27	27	0	0
9	A	1	0	0	0	0
9	B	110	0	0	0	0
All	All	4017	3783	3780	27	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (27) 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)
2:B:278:GLN:O	2:B:280:SER:N	2.03	0.90
1:A:85:MET:O	1:A:89:PHE:N	2.10	0.85
2:B:316:ASN:O	2:B:321:ARG:NH1	2.31	0.63
2:B:378:ARG:NH2	6:B:607:PO4:O1	2.33	0.61
1:A:106:VAL:O	1:A:110:LEU:N	2.36	0.52
2:B:379:LYS:O	2:B:379:LYS:HG2	2.09	0.51
1:A:69:CYS:SG	1:A:86:VAL:HG21	2.50	0.51
2:B:275:THR:CG2	2:B:277:SER:HB3	2.42	0.49
1:A:105:VAL:O	1:A:109:THR:N	2.42	0.47
2:B:350:ILE:CD1	2:B:399:MET:HG2	2.45	0.46
1:A:45:LEU:O	1:A:49:VAL:HG23	2.15	0.46
1:A:90:GLY:O	1:A:94:ILE:N	2.50	0.43
1:A:86:VAL:CG2	1:A:87:HIS:N	2.81	0.43
1:A:65:MET:HG3	1:A:86:VAL:HB	2.00	0.43
2:B:268:HIS:HB3	2:B:297:TRP:CD1	2.54	0.42
2:B:313:ILE:CD1	2:B:537:LEU:HD12	2.50	0.42
2:B:198:TYR:HA	2:B:201:ARG:O	2.20	0.42
2:B:187:ASP:O	2:B:188:LYS:HB2	2.20	0.42
2:B:458:PRO:HD2	2:B:463:MET:HE1	2.02	0.42
2:B:505:PHE:CG	2:B:506:GLN:N	2.88	0.42
1:A:52:GLN:HG2	2:B:276:VAL:HG21	2.02	0.41
1:A:90:GLY:O	1:A:94:ILE:CB	2.68	0.41
2:B:436:GLY:O	2:B:440:LYS:HA	2.21	0.41
2:B:505:PHE:O	2:B:509:VAL:HG23	2.21	0.41
2:B:562:ASN:HB2	2:B:563:PRO:HD3	2.03	0.41
1:A:48:SER:O	1:A:52:GLN:HB2	2.21	0.40
1:A:85:MET:O	1:A:89:PHE:CA	2.68	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	70/141 (50%)	67 (96%)	3 (4%)	0	100	100
2	B	405/422 (96%)	382 (94%)	21 (5%)	2 (0%)	29	35
All	All	475/563 (84%)	449 (94%)	24 (5%)	2 (0%)	34	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	279	MET
2	B	371	GLY

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	61/130 (47%)	59 (97%)	2 (3%)	38	53
2	B	354/366 (97%)	353 (100%)	1 (0%)	92	97
All	All	415/496 (84%)	412 (99%)	3 (1%)	84	92

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

Mol	Chain	Res	Type
1	A	65	MET
1	A	82	CYS
2	B	431	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	169	GLN
2	B	406	HIS

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](#)

2 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	3,2	14,14,15	0.29	0	17,19,21	0.74	0
3	NAG	C	2	3	14,14,15	0.35	0	17,19,21	0.53	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	C	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

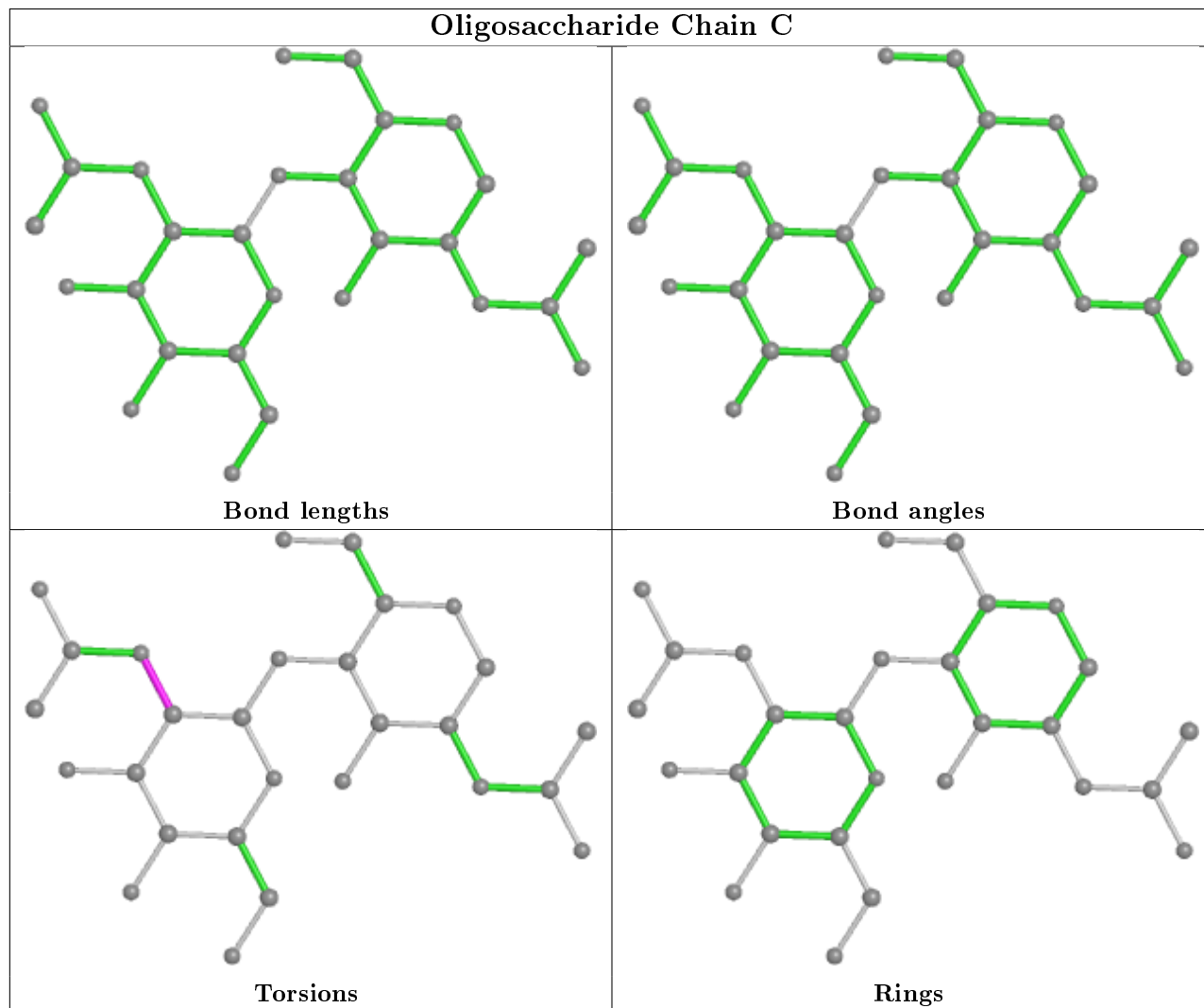
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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
8	FTT	B	609	-	15,15,16	0.61	0	15,15,17	0.88	0
6	PO4	B	607	-	4,4,4	0.91	0	6,6,6	0.41	0
7	P6G	B	608	-	18,18,18	0.53	0	17,17,17	0.38	0
5	NAG	B	606	2	14,14,15	0.62	0	17,19,21	0.76	1 (5%)

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
8	FTT	B	609	-	-	4/14/14/15	-
7	P6G	B	608	-	-	7/16/16/16	-
5	NAG	B	606	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	606	NAG	C1-O5-C5	2.78	115.95	112.19

There are no chirality outliers.

All (13) torsion outliers are listed below:

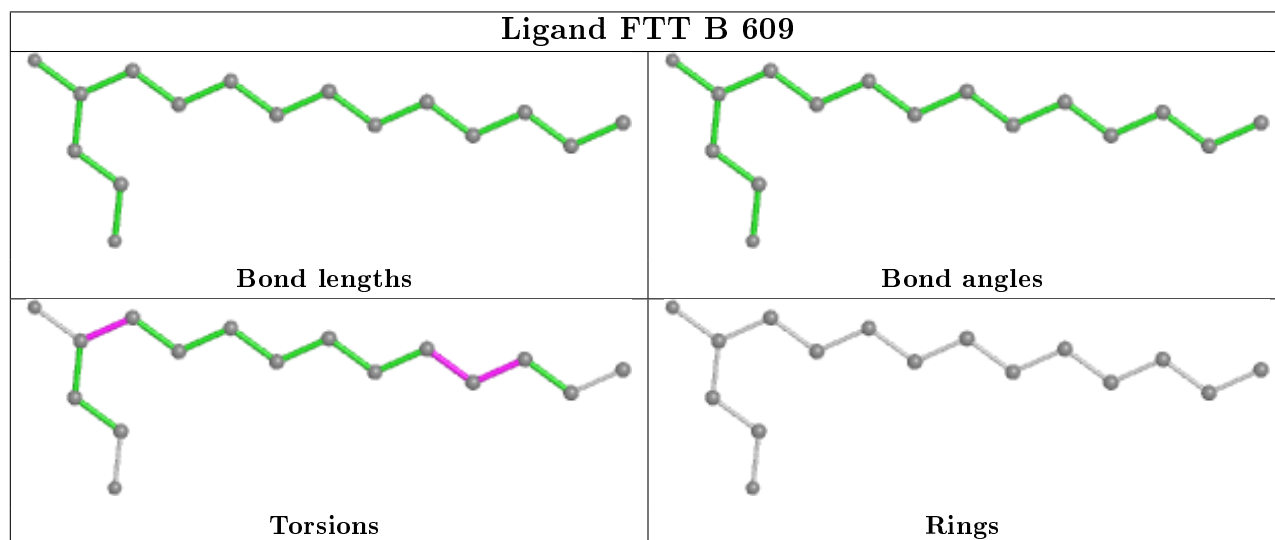
Mol	Chain	Res	Type	Atoms
8	B	609	FTT	C2-C3-C4-C5
5	B	606	NAG	C4-C5-C6-O6
5	B	606	NAG	O5-C5-C6-O6
8	B	609	FTT	C9-C10-C11-C12
8	B	609	FTT	O3-C3-C4-C5
8	B	609	FTT	C10-C11-C12-C13
7	B	608	P6G	C6-C5-O4-C3
7	B	608	P6G	O4-C5-C6-O7
7	B	608	P6G	O16-C17-C18-O19
7	B	608	P6G	O1-C2-C3-O4
7	B	608	P6G	C9-C8-O7-C6
7	B	608	P6G	C2-C3-O4-C5
7	B	608	P6G	O10-C11-C12-O13

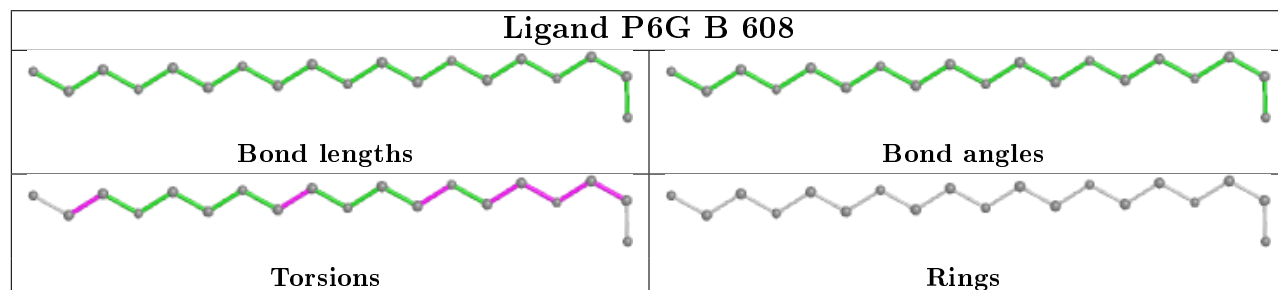
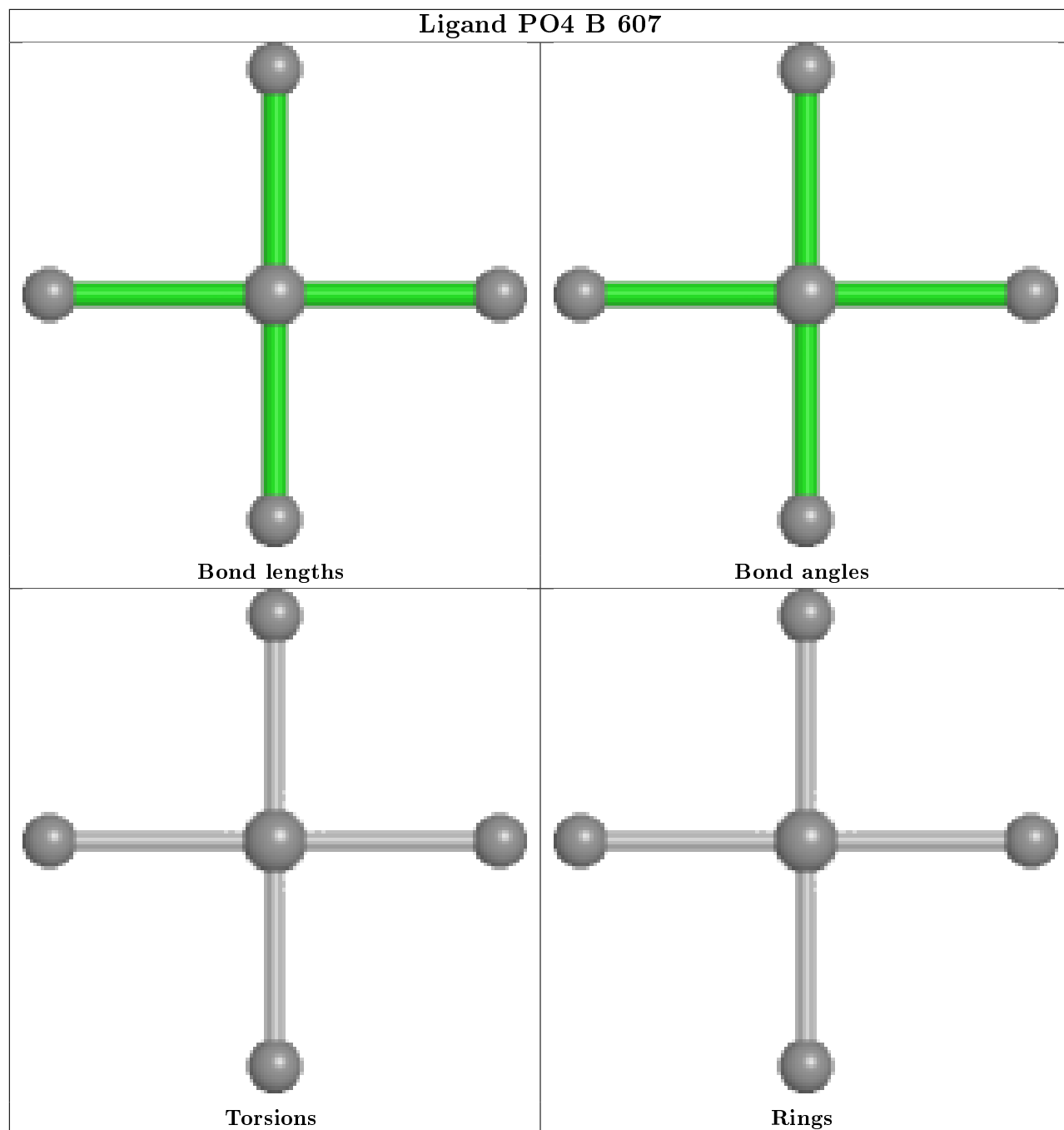
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	607	PO4	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

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, 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	78/141 (55%)	2.04	34 (43%) 0 0	59, 86, 109, 114	0
2	B	407/422 (96%)	0.61	36 (8%) 10 13	11, 38, 79, 102	0
All	All	485/563 (86%)	0.84	70 (14%) 2 3	11, 42, 96, 114	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	86	VAL	7.1
1	A	87	HIS	6.8
1	A	96	LEU	6.4
1	A	89	PHE	5.8
2	B	379	LYS	5.6
2	B	312	LYS	5.5
1	A	72	LEU	4.9
2	B	241	ILE	4.6
2	B	172	LYS	4.5
2	B	237	PRO	4.4
2	B	437	GLN	4.3
1	A	61	VAL	4.3
1	A	54	ALA	4.3
1	A	58	ASN	4.2
2	B	240	GLY	4.2
2	B	171	ILE	4.1
2	B	239	ASP	4.1
1	A	66	GLU	3.7
1	A	127	LEU	3.7
2	B	276	VAL	3.7
2	B	513	GLN	3.6
2	B	380	THR	3.6
1	A	83	TYR	3.6
1	A	62	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	56	VAL	3.5
1	A	85	MET	3.5
2	B	432	TYR	3.5
2	B	235	VAL	3.3
1	A	120	PRO	3.2
2	B	514	LYS	3.2
1	A	68	LEU	3.2
2	B	377	GLY	3.1
2	B	281	VAL	3.0
2	B	416	TYR	3.0
1	A	115	GLN	3.0
2	B	381	ASP	3.0
1	A	65	MET	2.9
2	B	313	ILE	2.9
1	A	126	PRO	2.9
2	B	438	LEU	2.8
2	B	221	TRP	2.7
2	B	510	GLU	2.7
2	B	511	GLU	2.6
1	A	70	SER	2.6
2	B	278	GLN	2.6
2	B	173	LEU	2.6
1	A	53	LEU	2.5
1	A	90	GLY	2.5
1	A	93	ILE	2.5
2	B	274	LEU	2.5
1	A	92	ASP	2.5
2	B	285	LEU	2.4
1	A	84	MET	2.4
1	A	105	VAL	2.4
1	A	98	ASP	2.3
1	A	103	ALA	2.3
2	B	238	LYS	2.3
1	A	45	LEU	2.3
1	A	60	THR	2.3
2	B	378	ARG	2.3
2	B	279	MET	2.2
2	B	247	PHE	2.2
1	A	57	HIS	2.2
2	B	557	LYS	2.2
2	B	515	MET	2.1
1	A	121	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	505	PHE	2.1
1	A	94	ILE	2.1
2	B	243	TYR	2.0
1	A	114	LYS	2.0

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

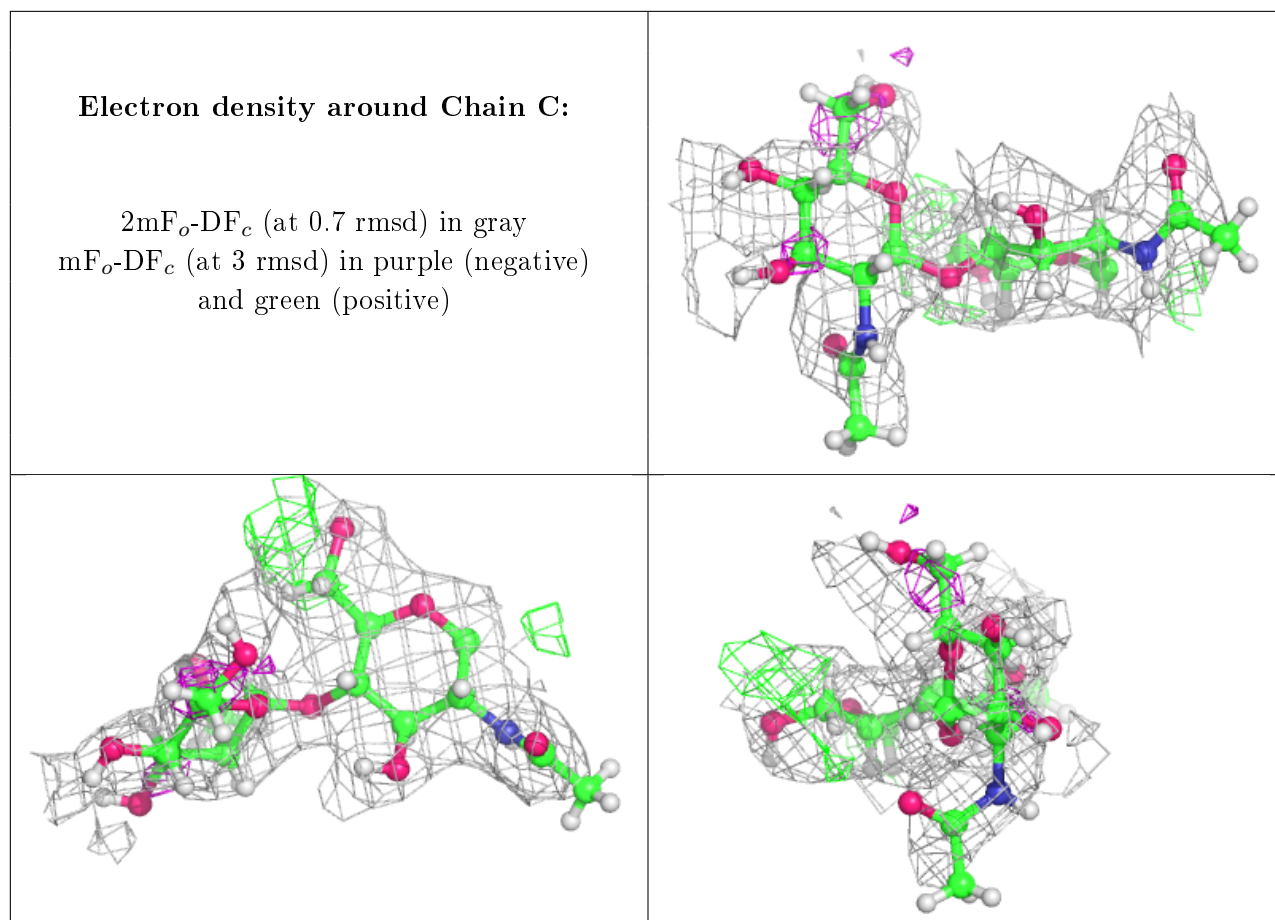
There are no non-standard protein/DNA/RNA residues in this entry.

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	C	2	14/15	0.76	0.45	55,60,71,72	0
3	NAG	C	1	14/15	0.81	0.21	43,49,56,56	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](#)

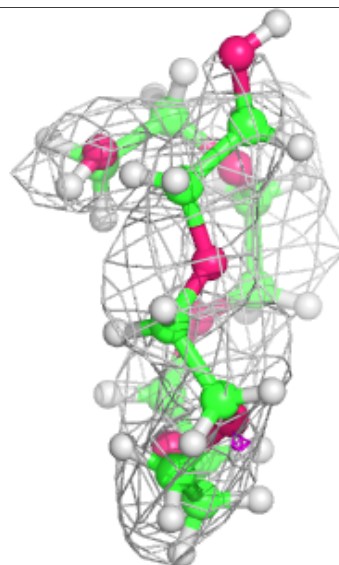
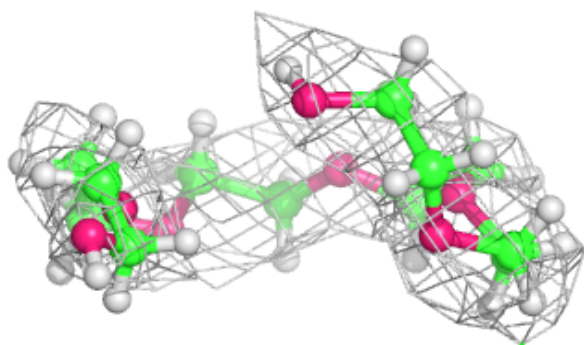
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	B	606	14/15	0.66	0.22	66,72,84,84	0
7	P6G	B	608	19/19	0.80	0.24	62,75,80,81	0
6	PO4	B	607	5/5	0.82	0.25	85,85,87,87	0
8	FTT	B	609	16/17	0.84	0.28	52,64,70,70	0
4	CA	B	603	1/1	0.98	0.12	28,28,28,28	0
4	CA	B	601	1/1	0.99	0.07	16,16,16,16	0
4	CA	B	602	1/1	0.99	0.07	17,17,17,17	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.

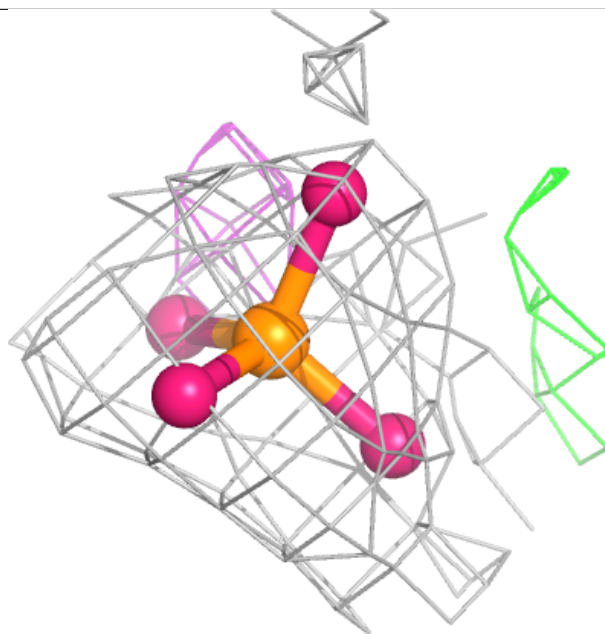
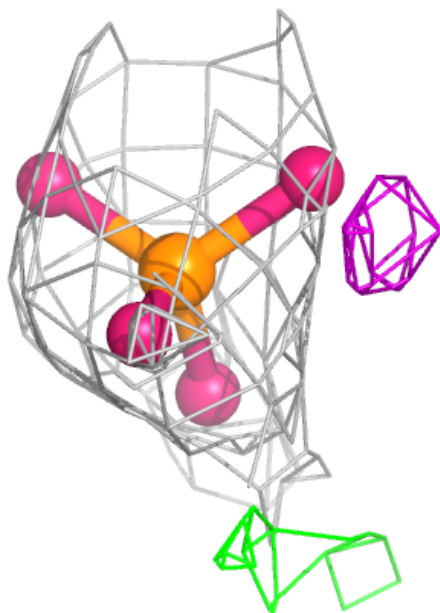
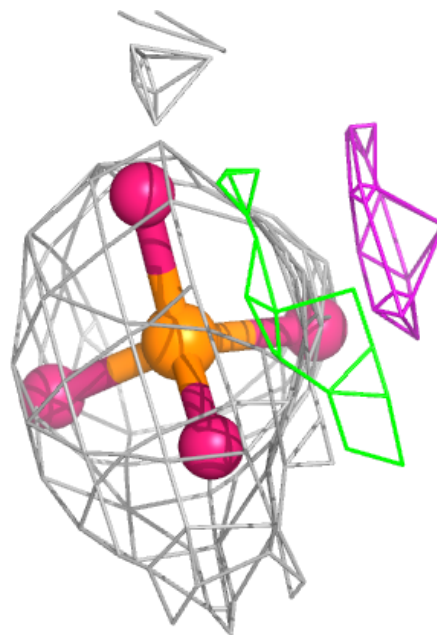
Electron density around P6G B 608:

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



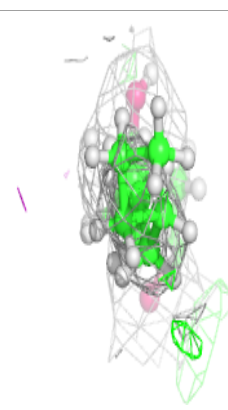
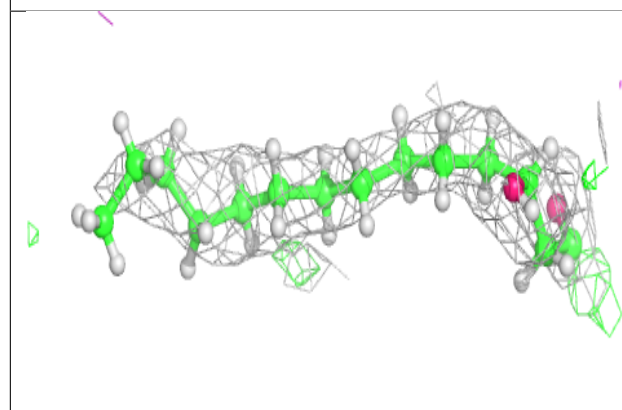
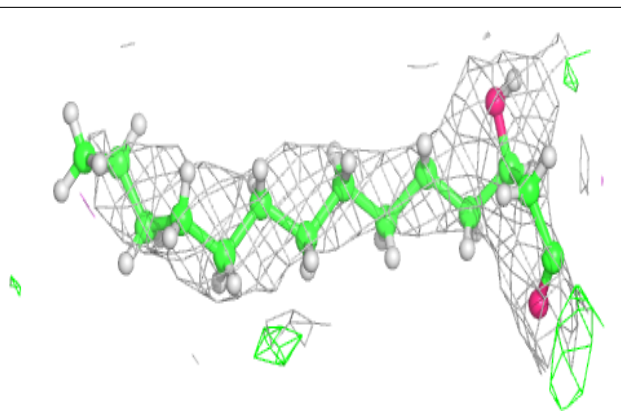
Electron density around PO4 B 607:

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



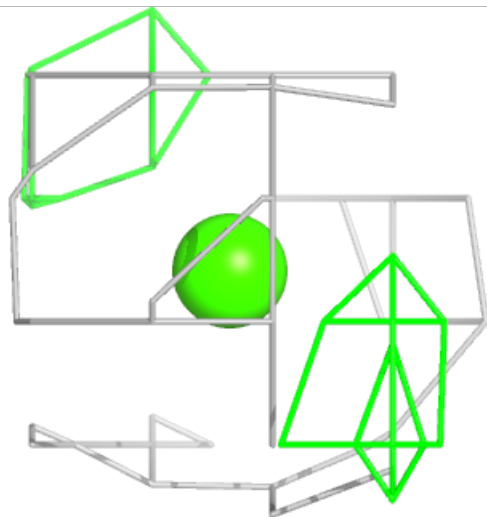
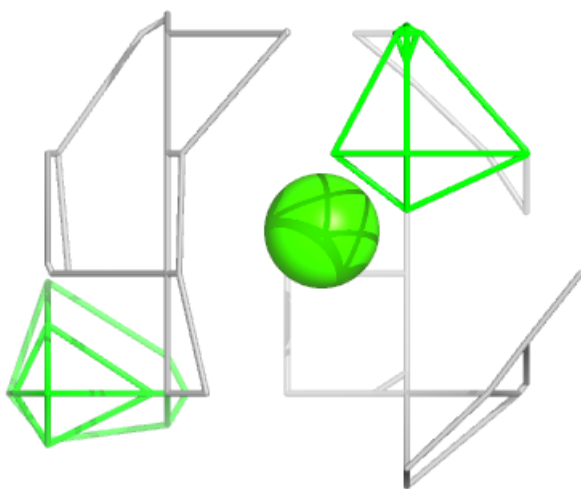
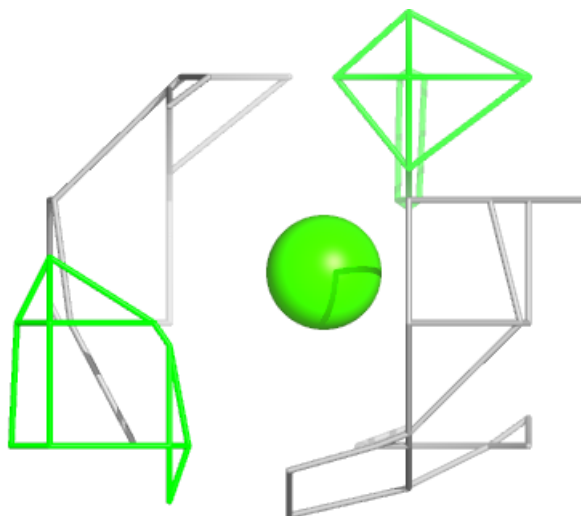
Electron density around FTT B 609:

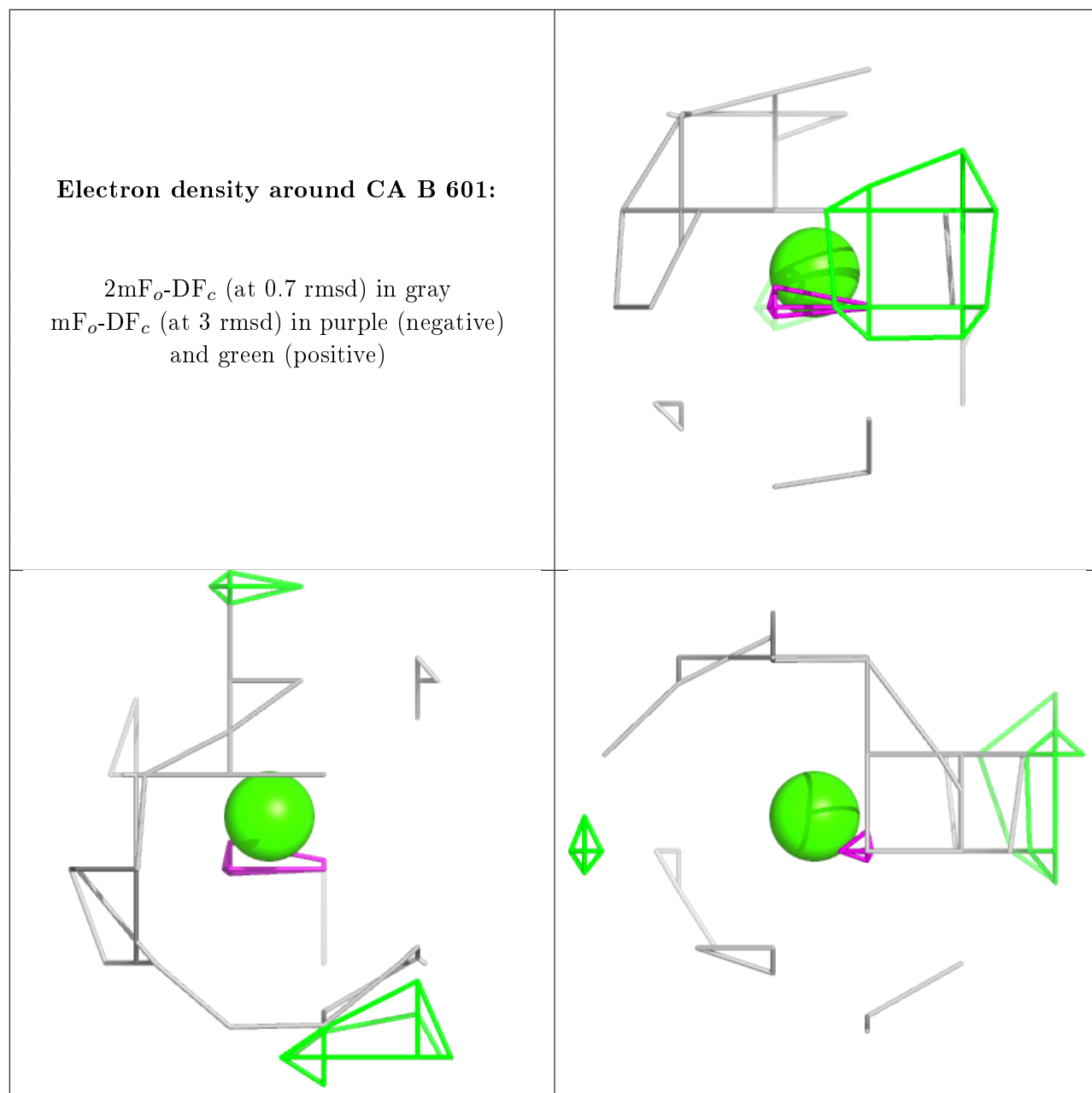
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

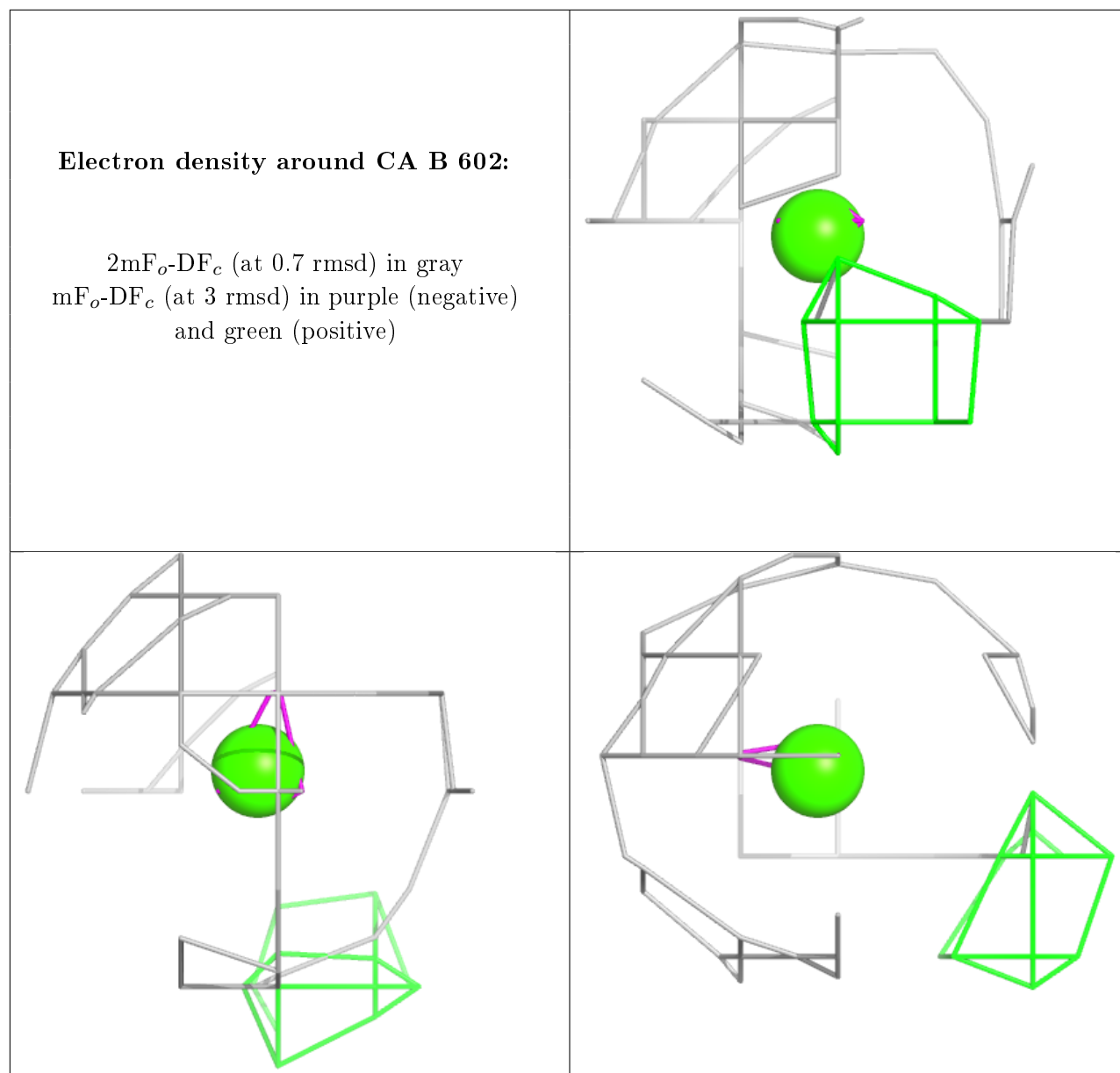


Electron density around CA B 603:

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







6.5 Other polymers [i](#)

There are no such residues in this entry.