



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:59 AM UTC

PDB ID : 5W7A / pdb_00005w7a
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 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

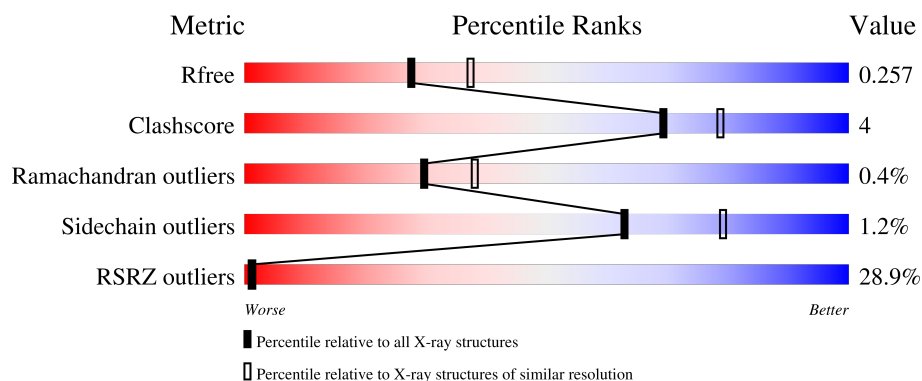
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	141	
2	B	422	
3	C	2	

2 Entry composition

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
1	A	78	Total	C	H	N	O	S	0	0	0
			1104	366	533	96	101	8			

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
2	B	407	Total	C	H	N	O	S	0	0	0
			6406	2061	3156	573	603	13			

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.

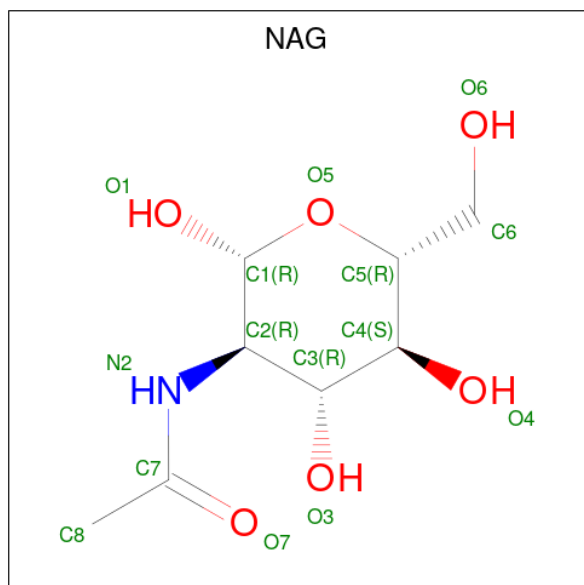


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



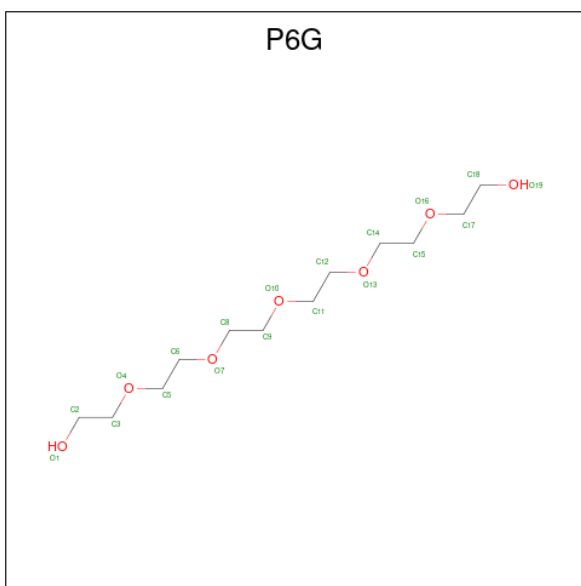
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P) (labeled as "Ligand of Interest" by depositor).



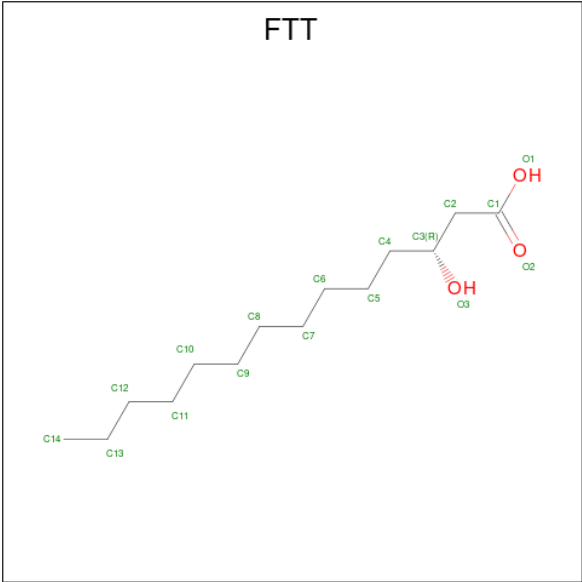
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is HEXAETHYLENE GLYCOL (CCD ID: 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 (CCD ID: FTT) (formula: C₁₄H₂₈O₃) (labeled as "Ligand of Interest" by depositor).

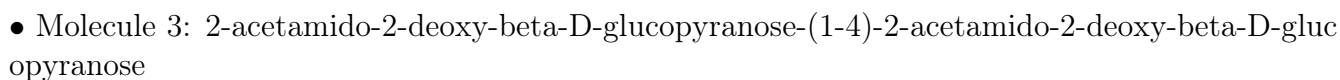
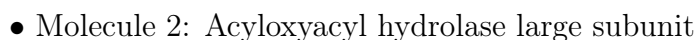


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	H	O	0	0
			43	14	27	2		

- 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		

- Molecule 1: Acyloxyacyl hydrolase small subunit



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)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.240 , 0.262 (Not available) , 0.257	Depositor DCC
R_{free} test set	1530 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 57.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
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

Xtriage'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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, P6G, PO4, CA, 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	0.15	0/580	0.34	0/790
2	B	0.19	0/3336	0.40	0/4531
All	All	0.19	0/3916	0.39	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

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:HG2	2:B:379:LYS:O	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: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
2:B:429:HIS:O	2:B:445:THR:OG1	2.30	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

5.3.1 Protein backbone

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%)	24	31
All	All	475/563 (84%)	449 (94%)	24 (5%)	2 (0%)	30	38

All (2) Ramachandran outliers are listed below:

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

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	61/130 (47%)	59 (97%)	2 (3%)	33	50
2	B	354/366 (97%)	351 (99%)	3 (1%)	73	86
All	All	415/496 (84%)	410 (99%)	5 (1%)	63	79

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

Mol	Chain	Res	Type
1	A	82	CYS
1	A	86	VAL
2	B	431	ARG
2	B	507	GLU
2	B	549	ARG

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	55	GLN

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Mol	Chain	Res	Type
1	A	115	GLN
2	B	169	GLN
2	B	361	HIS
2	B	406	HIS
2	B	439	ASN
2	B	575	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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	0.37	0	17,19,21	0.54	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.

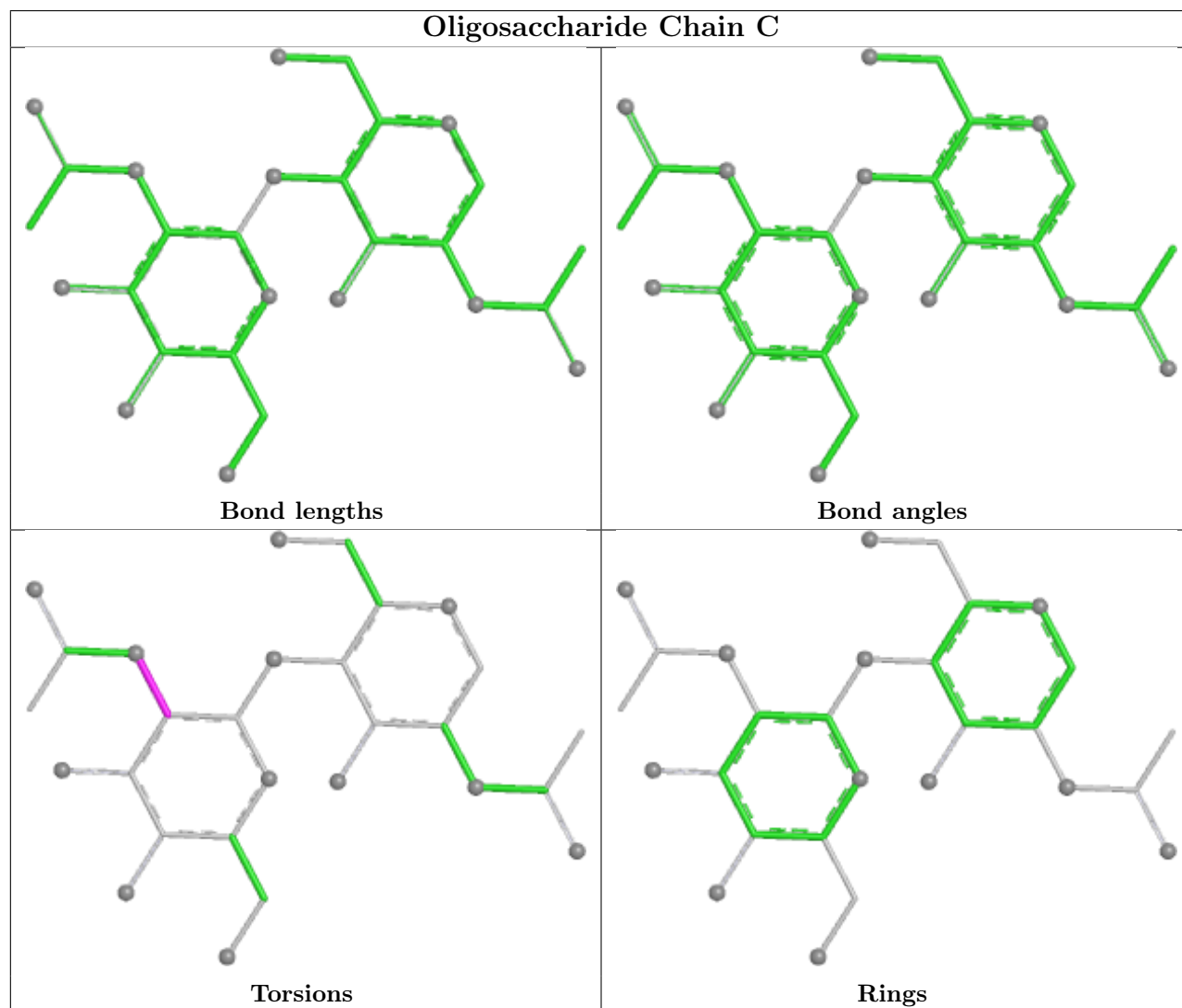
All (1) torsion outliers are listed below:

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

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	-	14,15,16	0.61	0	15,15,17	0.88	0
7	P6G	B	608	-	18,18,18	0.54	0	17,17,17	0.38	0
5	NAG	B	606	2	14,14,15	0.62	0	17,19,21	0.78	1 (5%)
6	PO4	B	607	-	4,4,4	0.96	0	6,6,6	0.44	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
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	2.81	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	O3-C3-C4-C5

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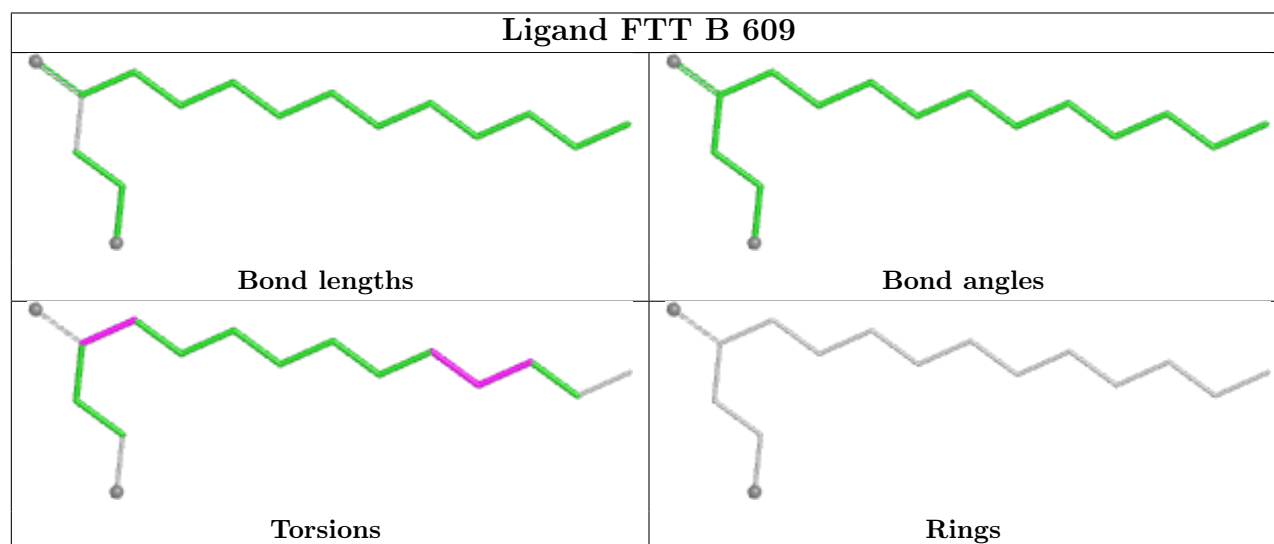
Mol	Chain	Res	Type	Atoms
8	B	609	FTT	C9-C10-C11-C12
8	B	609	FTT	C10-C11-C12-C13
7	B	608	P6G	C6-C5-O4-C3
7	B	608	P6G	O16-C17-C18-O19
7	B	608	P6G	O4-C5-C6-O7
7	B	608	P6G	O1-C2-C3-O4
7	B	608	P6G	C9-C8-O7-C6
7	B	608	P6G	C2-C3-O4-C5
7	B	608	P6G	O10-C11-C12-O13

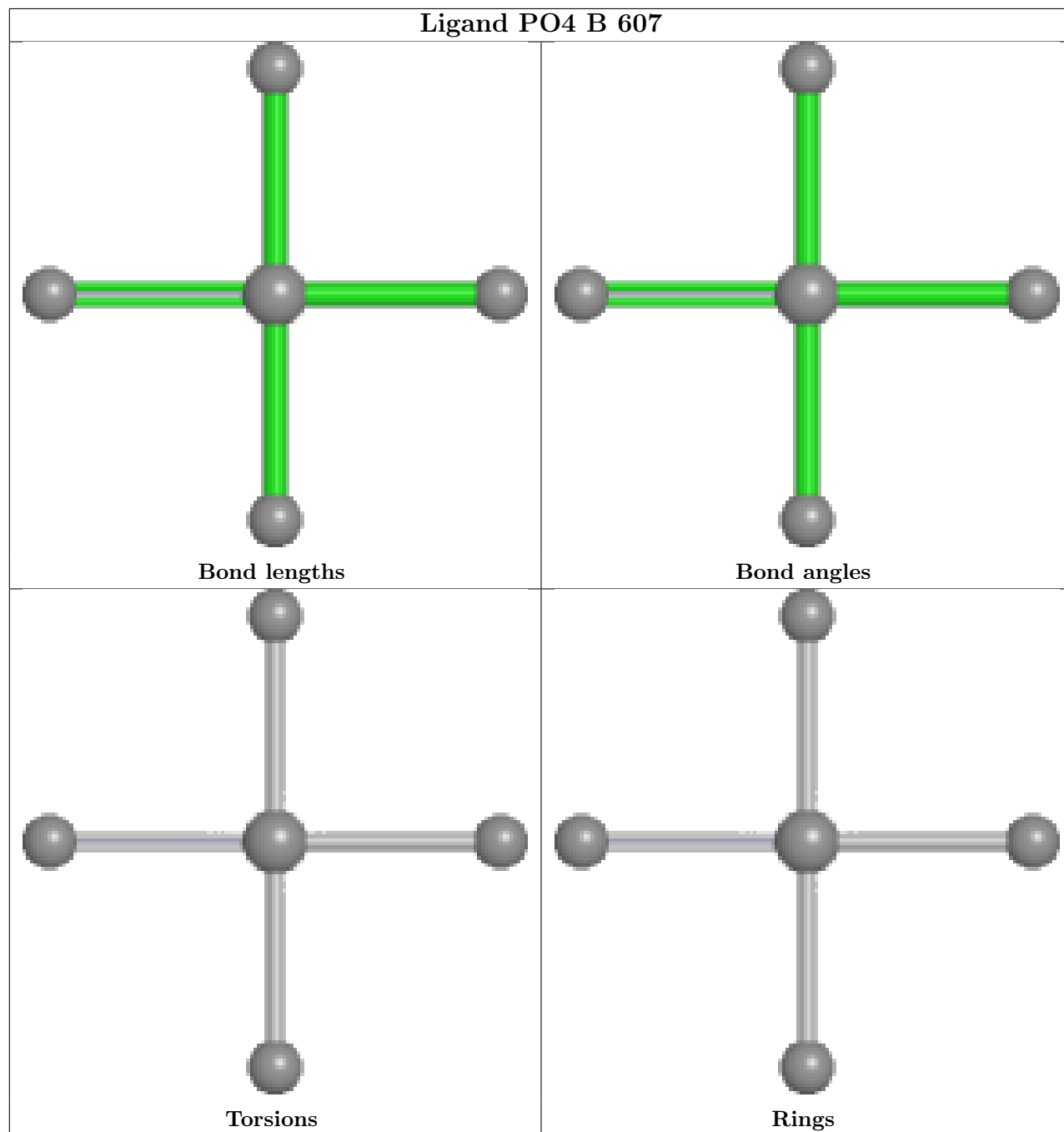
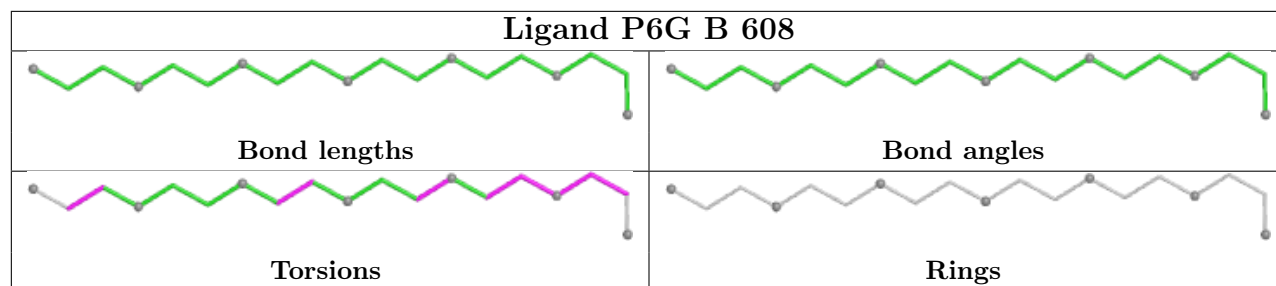
There are no ring outliers.

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 [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	78/141 (55%)	3.50	68 (87%) 0 0	64, 95, 118, 128	0
2	B	407/422 (96%)	0.82	72 (17%) 4 4	12, 42, 87, 113	0
All	All	485/563 (86%)	1.25	140 (28%) 1 1	12, 47, 104, 128	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	465	ALA	8.5
1	A	81	ALA	7.8
1	A	37	HIS	7.7
2	B	466	ASN	7.3
1	A	86	VAL	6.9
1	A	85	MET	6.1
1	A	93	ILE	6.1
1	A	116	GLU	6.0
1	A	89	PHE	5.8
1	A	98	ASP	5.8
1	A	61	VAL	5.1
1	A	113	CYS	5.0
1	A	72	LEU	5.0
1	A	73	PRO	4.9
1	A	88	VAL	4.8
1	A	83	TYR	4.8
1	A	96	LEU	4.7
1	A	94	ILE	4.5
1	A	60	THR	4.5
1	A	82	CYS	4.5
1	A	68	LEU	4.5
2	B	377	GLY	4.5
1	A	87	HIS	4.4
1	A	63	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	66	GLU	4.4
2	B	505	PHE	4.3
2	B	274	LEU	4.3
2	B	284	PHE	4.3
1	A	103	ALA	4.3
1	A	112	PHE	4.2
1	A	65	MET	4.1
2	B	313	ILE	4.1
1	A	54	ALA	4.0
1	A	90	GLY	4.0
1	A	92	ASP	3.9
1	A	48	SER	3.9
2	B	277	SER	3.8
2	B	504	ALA	3.8
2	B	241	ILE	3.8
1	A	56	VAL	3.8
1	A	127	LEU	3.8
2	B	278	GLN	3.8
2	B	279	MET	3.8
1	A	97	PHE	3.7
1	A	51	GLU	3.6
2	B	276	VAL	3.6
2	B	281	VAL	3.6
2	B	571	ASP	3.6
1	A	62	GLN	3.5
1	A	115	GLN	3.5
2	B	379	LYS	3.4
1	A	67	ARG	3.4
2	B	308	ASP	3.4
1	A	91	ALA	3.4
1	A	71	TYR	3.4
1	A	64	SER	3.3
2	B	437	GLN	3.3
2	B	239	ASP	3.2
1	A	53	LEU	3.2
1	A	109	THR	3.2
1	A	95	LYS	3.1
1	A	58	ASN	3.1
1	A	105	VAL	3.1
1	A	84	MET	3.1
2	B	376	ASN	3.1
1	A	49	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	312	LYS	3.1
2	B	206	ASN	3.1
2	B	378	ARG	3.1
2	B	247	PHE	3.0
2	B	280	SER	3.0
1	A	120	PRO	3.0
2	B	467	GLU	3.0
2	B	310	ALA	2.9
2	B	560	PRO	2.9
1	A	108	HIS	2.9
2	B	221	TRP	2.9
1	A	50	ILE	2.8
2	B	218	PRO	2.8
2	B	171	ILE	2.8
1	A	40	CYS	2.8
2	B	219	ASP	2.8
1	A	70	SER	2.8
1	A	111	GLU	2.8
1	A	110	LEU	2.8
2	B	283	SER	2.7
2	B	380	THR	2.7
2	B	285	LEU	2.7
2	B	416	TYR	2.6
2	B	430	SER	2.6
2	B	558	GLU	2.6
2	B	217	ARG	2.6
2	B	237	PRO	2.6
1	A	59	SER	2.6
2	B	251	SER	2.6
1	A	121	LEU	2.5
2	B	328	CYS	2.5
1	A	126	PRO	2.5
1	A	57	HIS	2.5
1	A	102	ASN	2.5
1	A	107	CYS	2.5
2	B	438	LEU	2.5
2	B	314	LYS	2.5
2	B	275	THR	2.4
1	A	106	VAL	2.4
2	B	503	PHE	2.4
1	A	47	VAL	2.4
2	B	220	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	69	CYS	2.4
2	B	176	LYS	2.4
2	B	243	TYR	2.4
2	B	273	TRP	2.4
2	B	382	PRO	2.3
1	A	122	CYS	2.3
2	B	464	SER	2.3
2	B	250	GLY	2.3
2	B	169	GLN	2.3
1	A	39	THR	2.3
2	B	235	VAL	2.3
1	A	38	TYR	2.2
2	B	518	GLN	2.2
2	B	175	ILE	2.2
1	A	45	LEU	2.2
2	B	565	ILE	2.2
2	B	439	ASN	2.2
2	B	172	LYS	2.2
1	A	114	LYS	2.2
2	B	233	TRP	2.1
2	B	307	LEU	2.1
2	B	561	PHE	2.1
2	B	513	GLN	2.1
2	B	510	GLU	2.1
2	B	406	HIS	2.1
2	B	205	CYS	2.1
2	B	238	LYS	2.1
1	A	125	TYR	2.1
2	B	442	VAL	2.1
2	B	381	ASP	2.0
2	B	287	LEU	2.0
2	B	557	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.

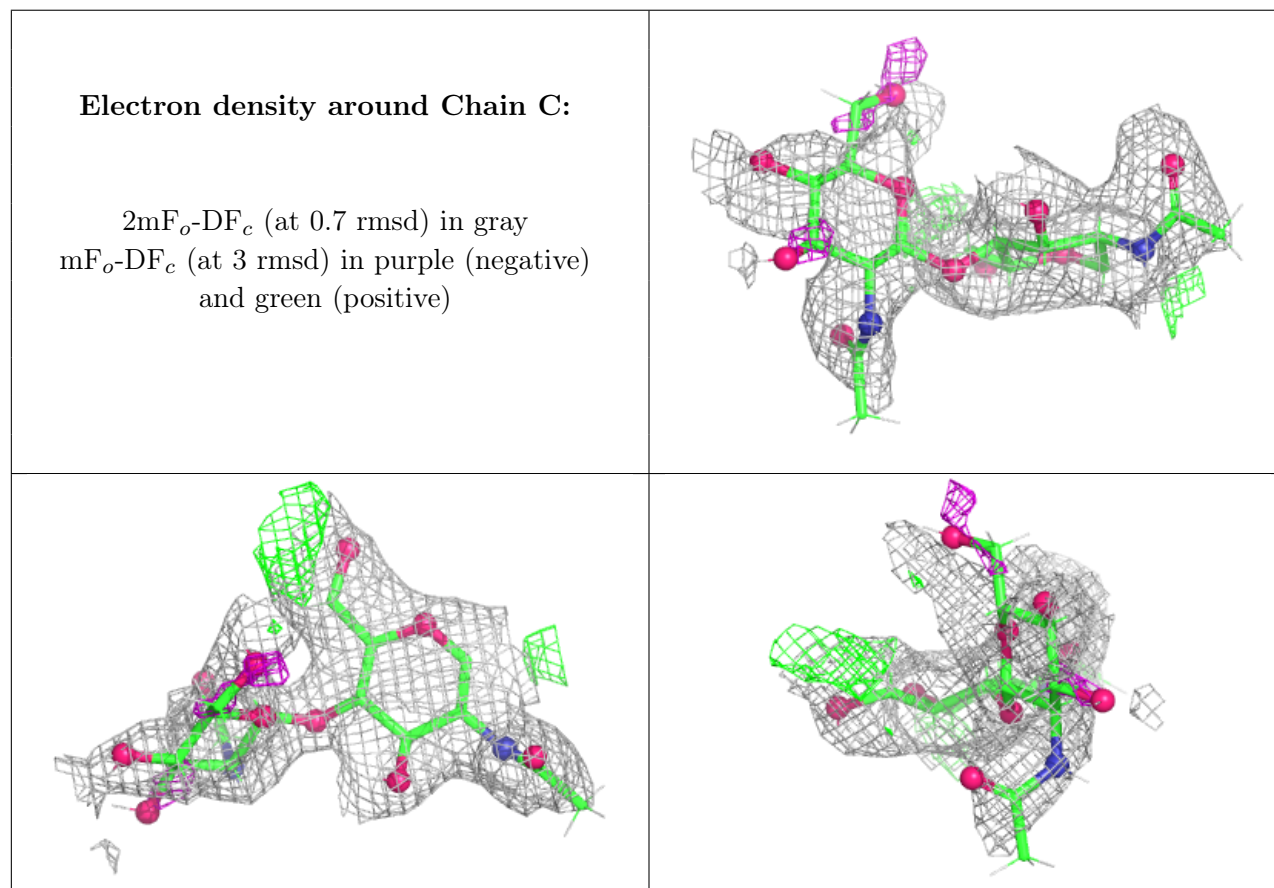
6.3 Carbohydrates [i](#)

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	0.58	0.18	55,60,71,72	0
3	NAG	C	1	14/15	0.71	0.15	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 ⓘ

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	0.71	0.19	66,72,84,84	0
6	PO4	B	607	5/5	0.73	0.23	85,85,87,87	0
7	P6G	B	608	19/19	0.79	0.19	62,75,80,81	0

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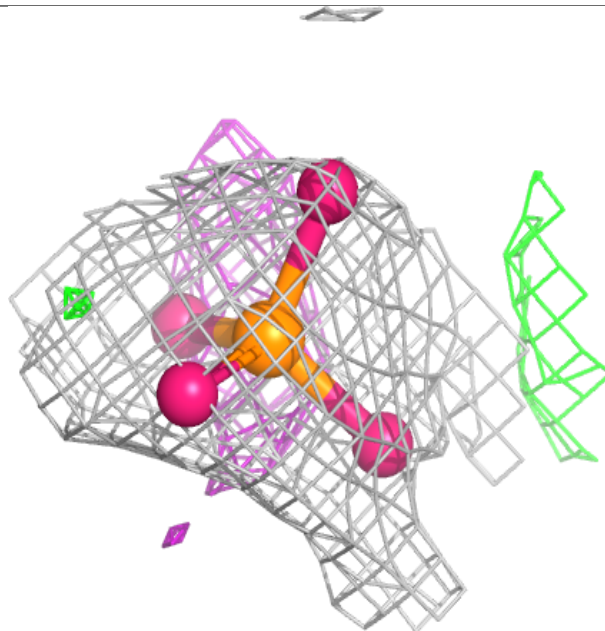
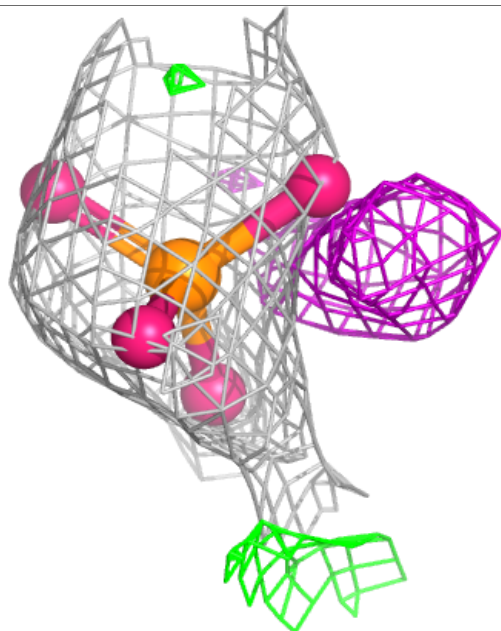
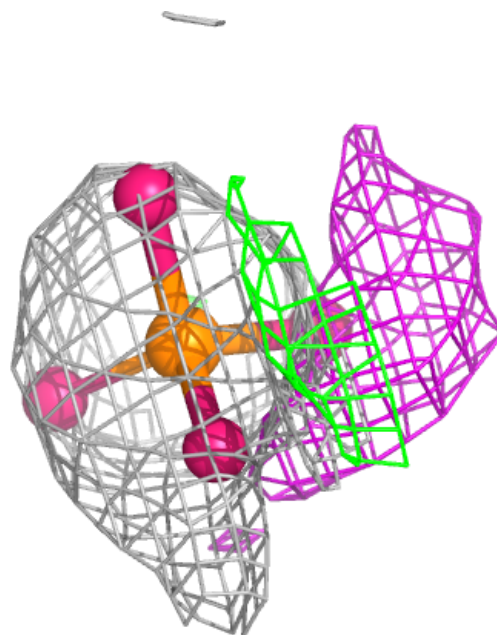
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	FTT	B	609	16/17	0.82	0.18	52,64,70,70	0
4	CA	B	603	1/1	0.97	0.04	28,28,28,28	0
4	CA	B	602	1/1	0.99	0.04	17,17,17,17	0
4	CA	B	601	1/1	0.99	0.04	16,16,16,16	0

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.

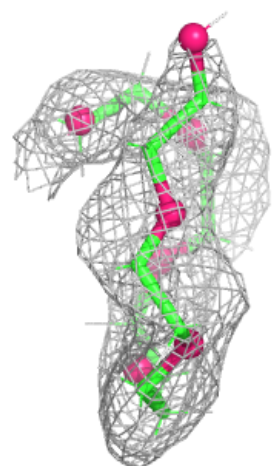
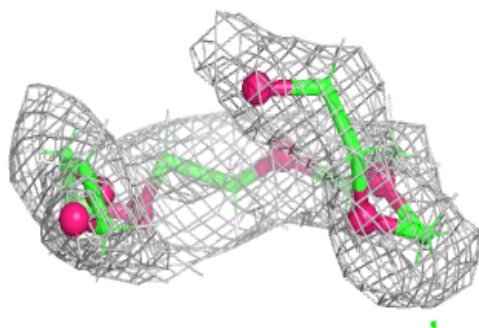
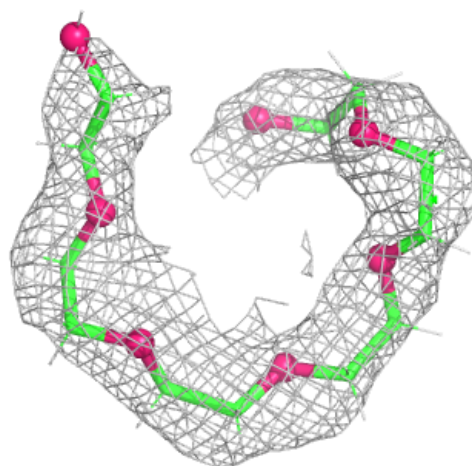
Electron density around PO4 B 607:

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



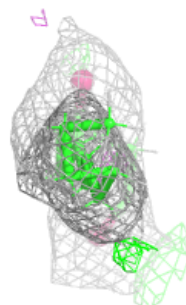
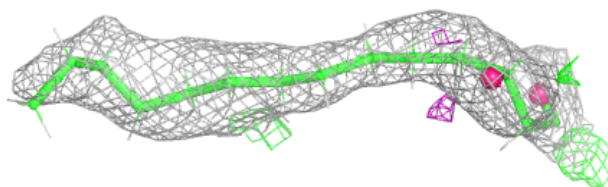
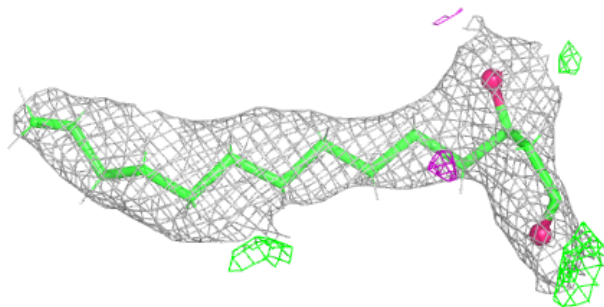
Electron density around P6G B 608:

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



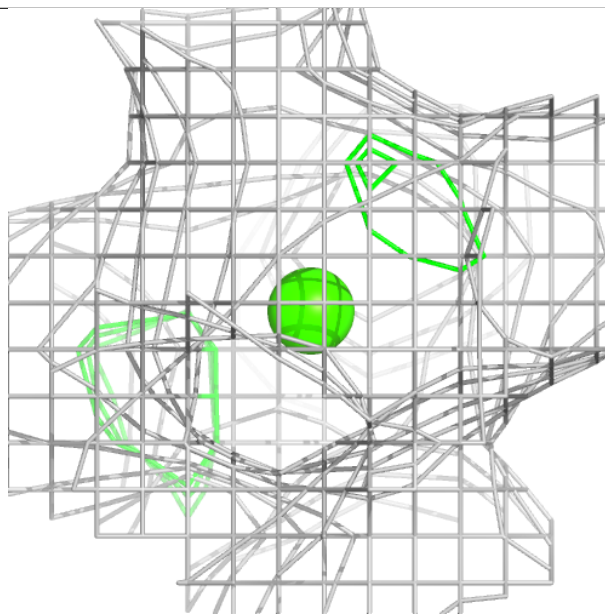
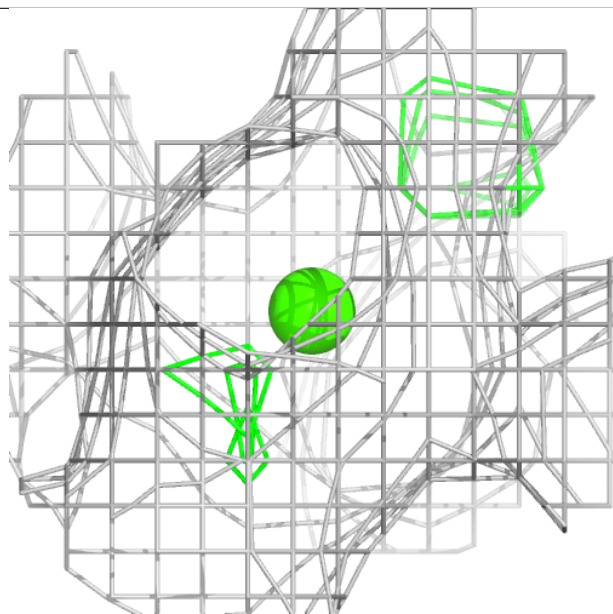
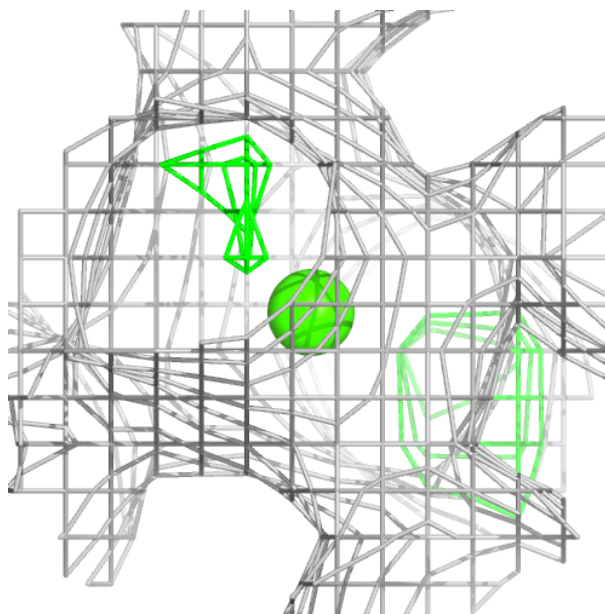
Electron density around FTT B 609:

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



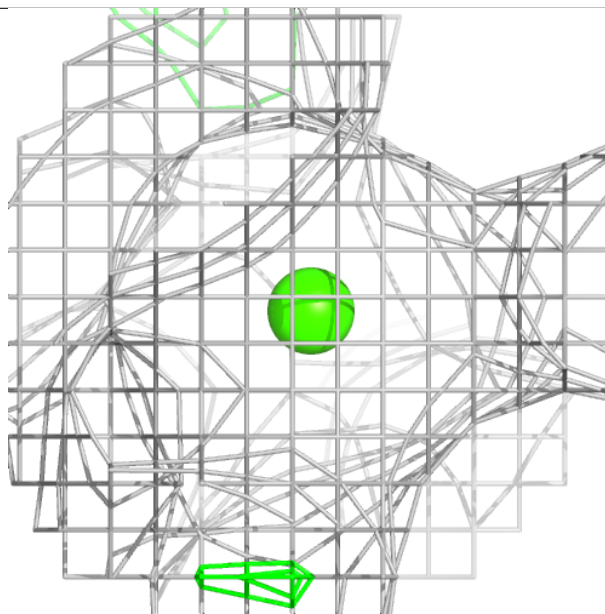
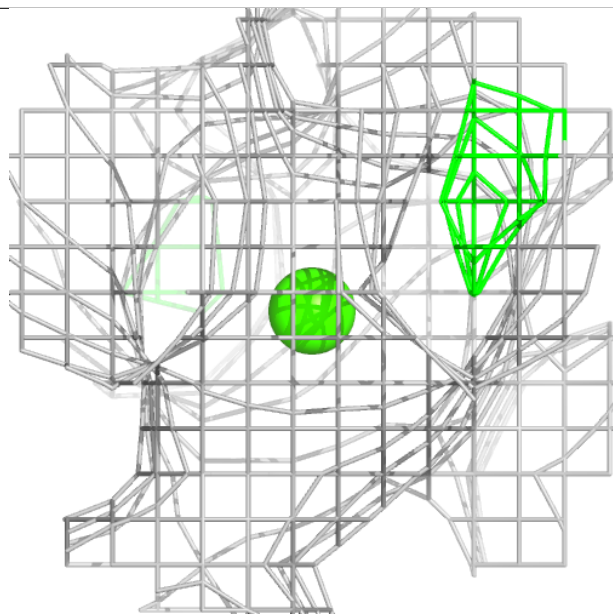
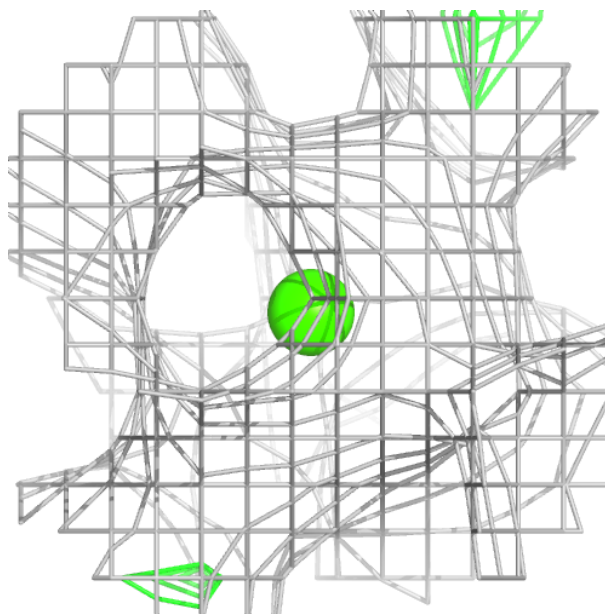
Electron density around CA B 603:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



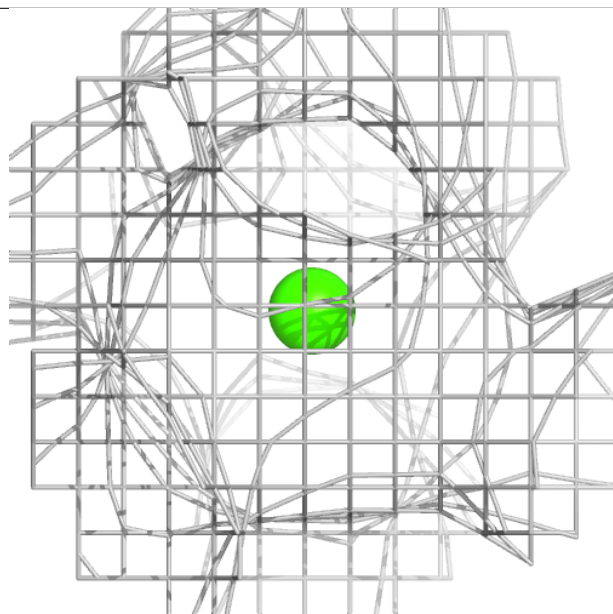
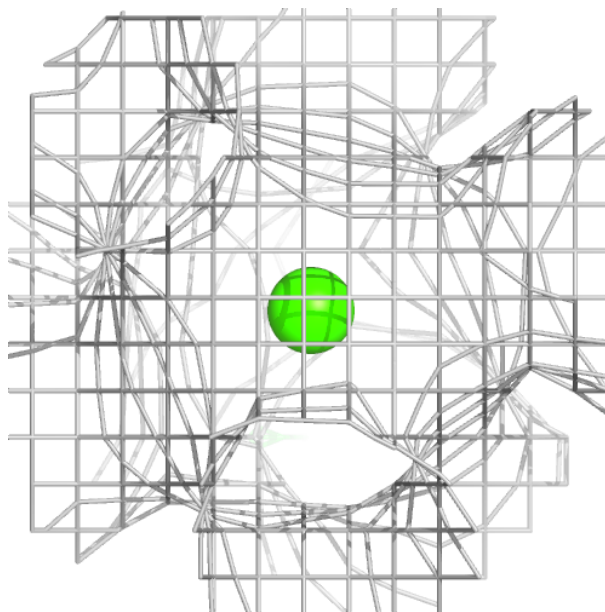
Electron density around CA B 602:

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



Electron density around CA 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)



6.5 Other polymers ⓘ

There are no such residues in this entry.