



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:40 PM UTC

PDB ID : 5VCJ / pdb_00005vcj
Title : Structure of alpha-galactosylphytosphingosine bound by CD1d and in complex with the Va14Vb8.2 TCR
Authors : Wang, J.; Zajonc, D.M.
Deposited on : 2017-03-31
Resolution : 3.16 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

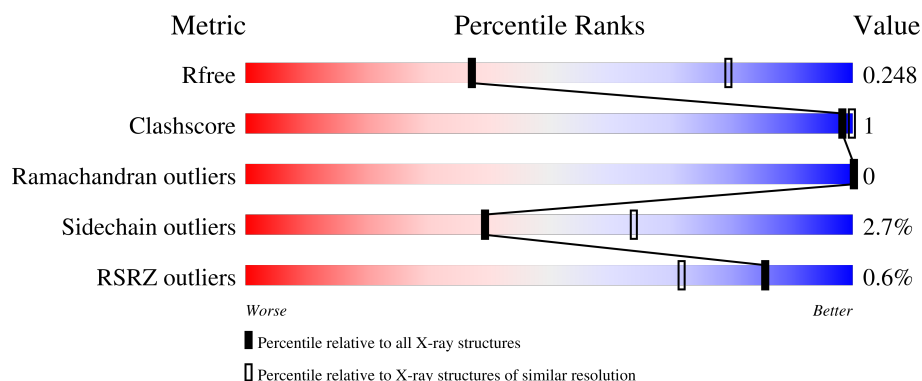
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

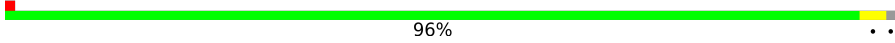
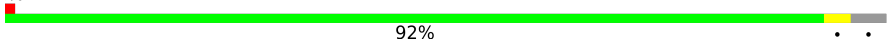
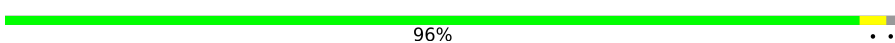
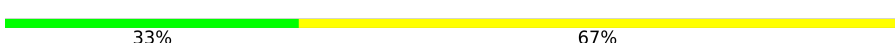
The reported resolution of this entry is 3.16 Å.

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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	285	
2	B	99	
3	C	209	
4	D	241	
5	E	6	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6511 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 Antigen-presenting glycoprotein CD1d1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2154	1374	370	397	13			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	HIS	ASP	engineered mutation	UNP P11609
A	280	HIS	-	expression tag	UNP P11609
A	281	HIS	-	expression tag	UNP P11609
A	282	HIS	-	expression tag	UNP P11609
A	283	HIS	-	expression tag	UNP P11609
A	284	HIS	-	expression tag	UNP P11609
A	285	HIS	-	expression tag	UNP P11609

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	98	Total	C	N	O	S	0	0	0
			806	514	136	149	7			

- Molecule 3 is a protein called Chimeric TCR Valpha14/Jalpha18 chain (mouse variable domain, human constant domain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	201	Total	C	N	O	S	0	0	0
			1532	949	262	313	8			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	MET	-	initiating methionine	UNP A0A0B4J1J9
C	94	ASP	-	linker	UNP A0A0B4J1J9

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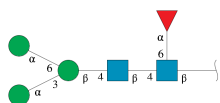
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Chain	Residue	Modelled	Actual	Comment	Reference
C	95	ARG	-	linker	UNP A0A0B4J1J9
C	96	GLY	-	linker	UNP A0A0B4J1J9
C	97	SER	-	linker	UNP A0A0B4J1J9
C	98	ALA	-	linker	UNP A0A0B4J1J9
C	99	LEU	-	linker	UNP A0A0B4J1J9
C	100	GLY	-	linker	UNP A0A0B4J1J9
C	101	ARG	-	linker	UNP A0A0B4J1J9
C	102	LEU	-	linker	UNP A0A0B4J1J9
C	103	HIS	-	linker	UNP A0A0B4J1J9
C	104	PHE	-	linker	UNP A0A0B4J1J9
C	105	GLY	-	linker	UNP A0A0B4J1J9
C	106	ALA	-	linker	UNP A0A0B4J1J9
C	107	GLY	-	linker	UNP A0A0B4J1J9
C	108	THR	-	linker	UNP A0A0B4J1J9
C	109	GLN	-	linker	UNP A0A0B4J1J9
C	110	LEU	-	linker	UNP A0A0B4J1J9
C	111	ILE	-	linker	UNP A0A0B4J1J9
C	112	VAL	-	linker	UNP A0A0B4J1J9
C	113	ILE	-	linker	UNP A0A0B4J1J9

- Molecule 4 is a protein called Chimeric TCR Vbeta8.2 chain (mouse variable domain, human constant domain).

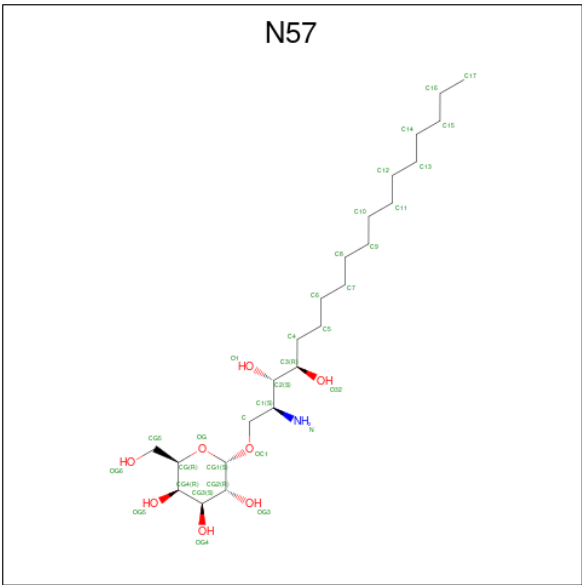
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	239	Total	C	N	O	S	0	0	0
			1869	1174	333	356	6			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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.



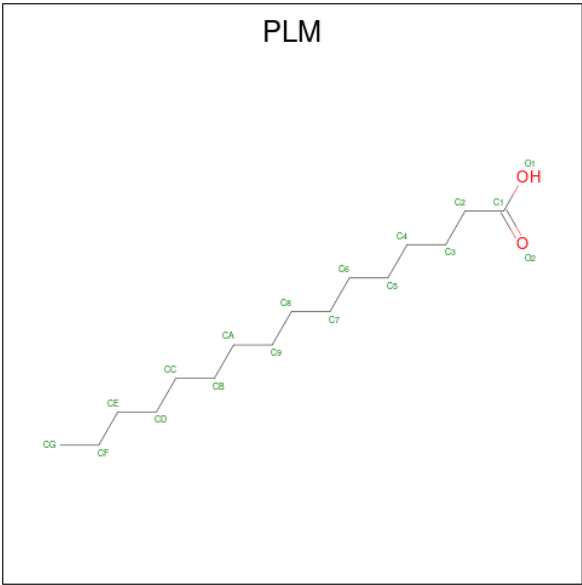
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	6	Total	C	N	O	0	0	0
			71	40	2	29			

- Molecule 6 is (2S,3S,4R)-2-amino-3,4-dihydroxyoctadecyl alpha-D-galactopyranoside (CCD ID: N57) (formula: C₂₄H₄₉NO₈).



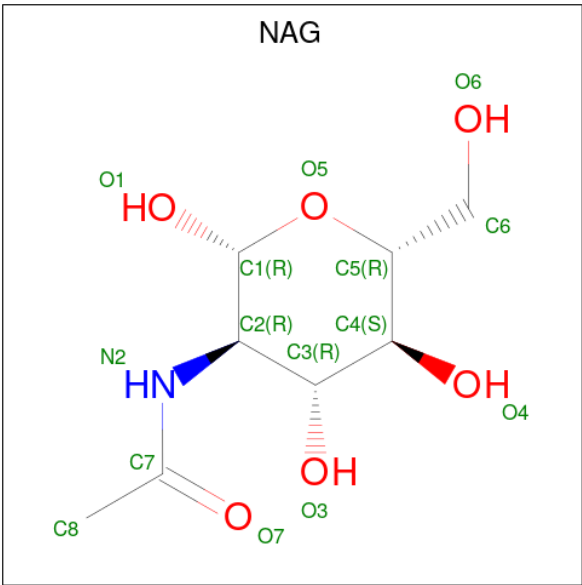
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			33	24	1	8		

- Molecule 7 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			18	16	2		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

3 Residue-property plots [i](#)

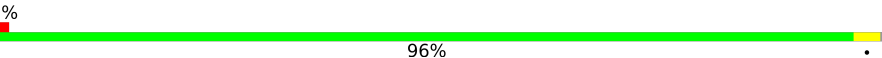
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

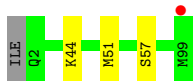
- Molecule 1: Antigen-presenting glycoprotein CD1d1

Chain A: 

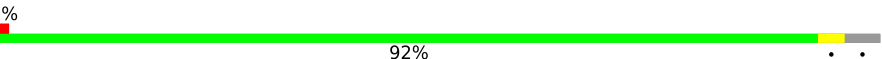


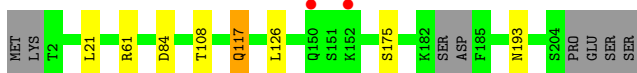
- Molecule 2: Beta-2-microglobulin

Chain B: 

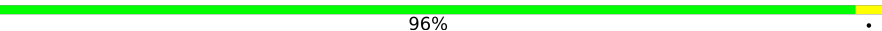


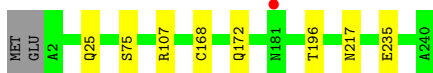
- Molecule 3: Chimeric TCR Valpha14/Jalpha18 chain (mouse variable domain, human constant domain)

Chain C: 

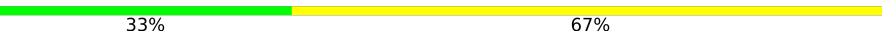


- Molecule 4: Chimeric TCR Vbeta8.2 chain (mouse variable domain, human constant domain)

Chain D: 



- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamid o-2-deoxy-beta-D-glucopyranose

Chain E: 

MAG1
MAG2
BMA3
MAN4
MAN5
FUC6

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	79.26Å 191.61Å 151.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.81 – 3.16 95.81 – 3.16	Depositor EDS
% Data completeness (in resolution range)	97.8 (95.81-3.16) 97.9 (95.81-3.16)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.189 , 0.248 0.193 , 0.248	Depositor DCC
R_{free} test set	959 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	52.2	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 19.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6511	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 3.81% 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: PLM, N57, BMA, NAG, MAN, FUC

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	0.53	0/2216	0.74	0/3011
2	B	0.53	0/832	0.70	0/1129
3	C	0.56	0/1559	0.73	0/2121
4	D	0.53	0/1920	0.71	0/2618
All	All	0.54	0/6527	0.72	0/8879

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	2154	0	2063	5	0
2	B	806	0	772	0	0
3	C	1532	0	1447	3	0
4	D	1869	0	1772	0	0
5	E	71	0	61	0	0
6	A	33	0	0	0	0
7	A	18	0	31	0	0
8	A	28	0	26	0	0
All	All	6511	0	6172	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 1.

All (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:88:MET:HE1	1:A:145:LEU:HD23	1.69	0.74
1:A:87:MET:HE1	1:A:149:VAL:HG21	1.87	0.56
3:C:21:LEU:HG	3:C:108:THR:HG21	1.98	0.45
1:A:221:MET:HE2	1:A:228:GLU:HB3	1.99	0.45
3:C:117:GLN:HE21	3:C:117:GLN:HA	1.82	0.44
1:A:107:TYR:HB2	1:A:111:ALA:HB3	2.01	0.43
3:C:61:ARG:NH2	3:C:84:ASP:OD2	2.53	0.41
1:A:124:TYR:CZ	1:A:136:VAL:HG11	2.56	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	263/285 (92%)	253 (96%)	10 (4%)	0	100	100
2	B	96/99 (97%)	93 (97%)	3 (3%)	0	100	100
3	C	197/209 (94%)	189 (96%)	8 (4%)	0	100	100
4	D	237/241 (98%)	230 (97%)	7 (3%)	0	100	100
All	All	793/834 (95%)	765 (96%)	28 (4%)	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	234/249 (94%)	230 (98%)	4 (2%)	53	70
2	B	91/93 (98%)	88 (97%)	3 (3%)	33	60
3	C	174/188 (93%)	170 (98%)	4 (2%)	44	66
4	D	201/208 (97%)	193 (96%)	8 (4%)	28	56
All	All	700/738 (95%)	681 (97%)	19 (3%)	39	64

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	SER
1	A	134	GLN
1	A	182	ASP
1	A	252	ASP
2	B	44	LYS
2	B	51	MET
2	B	57	SER
3	C	117	GLN
3	C	126	LEU
3	C	175	SER
3	C	193	ASN
4	D	25	GLN
4	D	75	SER
4	D	107	ARG
4	D	168	CYS
4	D	172	GLN
4	D	196	THR
4	D	217	ASN
4	D	235	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	14	GLN
1	A	117	HIS
1	A	229	GLN

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Mol	Chain	Res	Type
1	A	248	GLN
2	B	13	HIS
3	C	38	GLN
3	C	117	GLN
3	C	193	ASN
4	D	24	ASN
4	D	37	GLN
4	D	134	HIS
4	D	208	GLN

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 ⓘ

6 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	$\# Z > 2$
5	NAG	E	1	5,1	14,14,15	0.38	0	17,19,21	0.78	0
5	NAG	E	2	5	14,14,15	0.35	0	17,19,21	0.89	0
5	BMA	E	3	5	11,11,12	0.45	0	15,15,17	1.31	2 (13%)
5	MAN	E	4	5	11,11,12	0.33	0	15,15,17	0.99	1 (6%)
5	MAN	E	5	5	11,11,12	0.40	0	15,15,17	1.04	2 (13%)
5	FUC	E	6	5	10,10,11	0.48	0	14,14,16	0.92	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
5	NAG	E	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1
5	BMA	E	3	5	-	2/2/19/22	0/1/1/1
5	MAN	E	4	5	-	0/2/19/22	0/1/1/1
5	MAN	E	5	5	-	2/2/19/22	0/1/1/1
5	FUC	E	6	5	-	-	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	3	BMA	C1-C2-C3	3.14	114.22	109.64
5	E	5	MAN	C1-O5-C5	2.92	116.09	112.19
5	E	3	BMA	C1-O5-C5	2.74	115.86	112.19
5	E	4	MAN	C1-O5-C5	2.56	115.61	112.19
5	E	5	MAN	C1-C2-C3	2.16	112.78	109.64
5	E	6	FUC	O5-C5-C6	2.10	111.96	107.40

There are no chirality outliers.

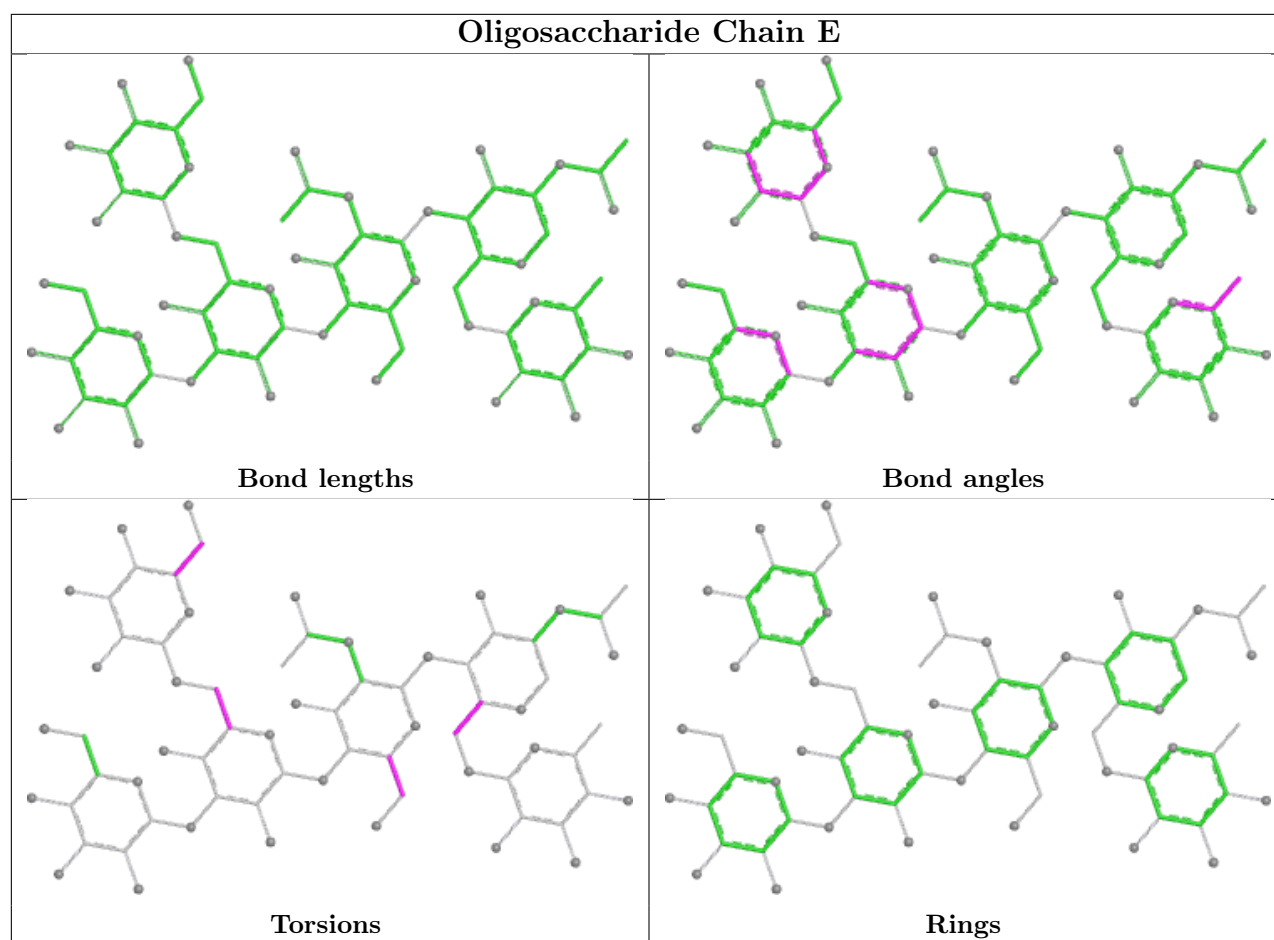
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	2	NAG	O5-C5-C6-O6
5	E	5	MAN	C4-C5-C6-O6
5	E	3	BMA	O5-C5-C6-O6
5	E	5	MAN	O5-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6
5	E	3	BMA	C4-C5-C6-O6
5	E	1	NAG	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 [i](#)

4 ligands 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	$\# Z > 2$
8	NAG	A	604	1	14,14,15	0.57	0	17,19,21	1.42	2 (11%)
7	PLM	A	602	-	17,17,17	0.83	0	17,17,17	0.68	0
8	NAG	A	603	1	14,14,15	0.39	0	17,19,21	0.95	0
6	N57	A	601	-	33,33,33	0.73	1 (3%)	37,41,41	0.67	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	A	604	1	-	2/6/23/26	0/1/1/1
7	PLM	A	602	-	-	5/15/15/15	-
8	NAG	A	603	1	-	2/6/23/26	0/1/1/1
6	N57	A	601	-	-	8/29/49/49	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	601	N57	OC1-CG1	2.52	1.44	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	604	NAG	C1-O5-C5	3.54	116.93	112.19
8	A	604	NAG	O5-C1-C2	-2.54	107.36	111.29

There are no chirality outliers.

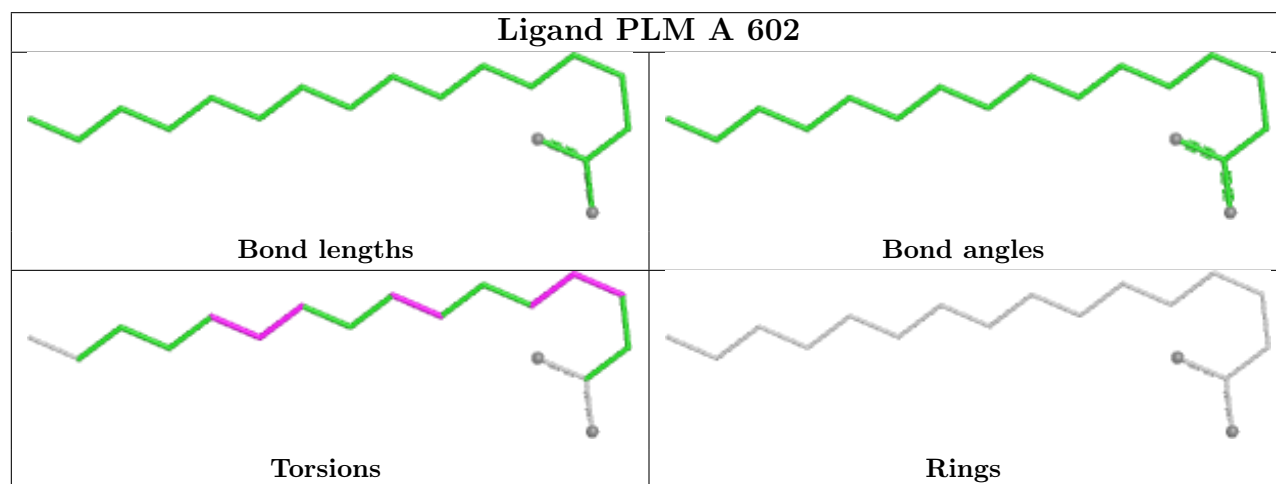
All (17) torsion outliers are listed below:

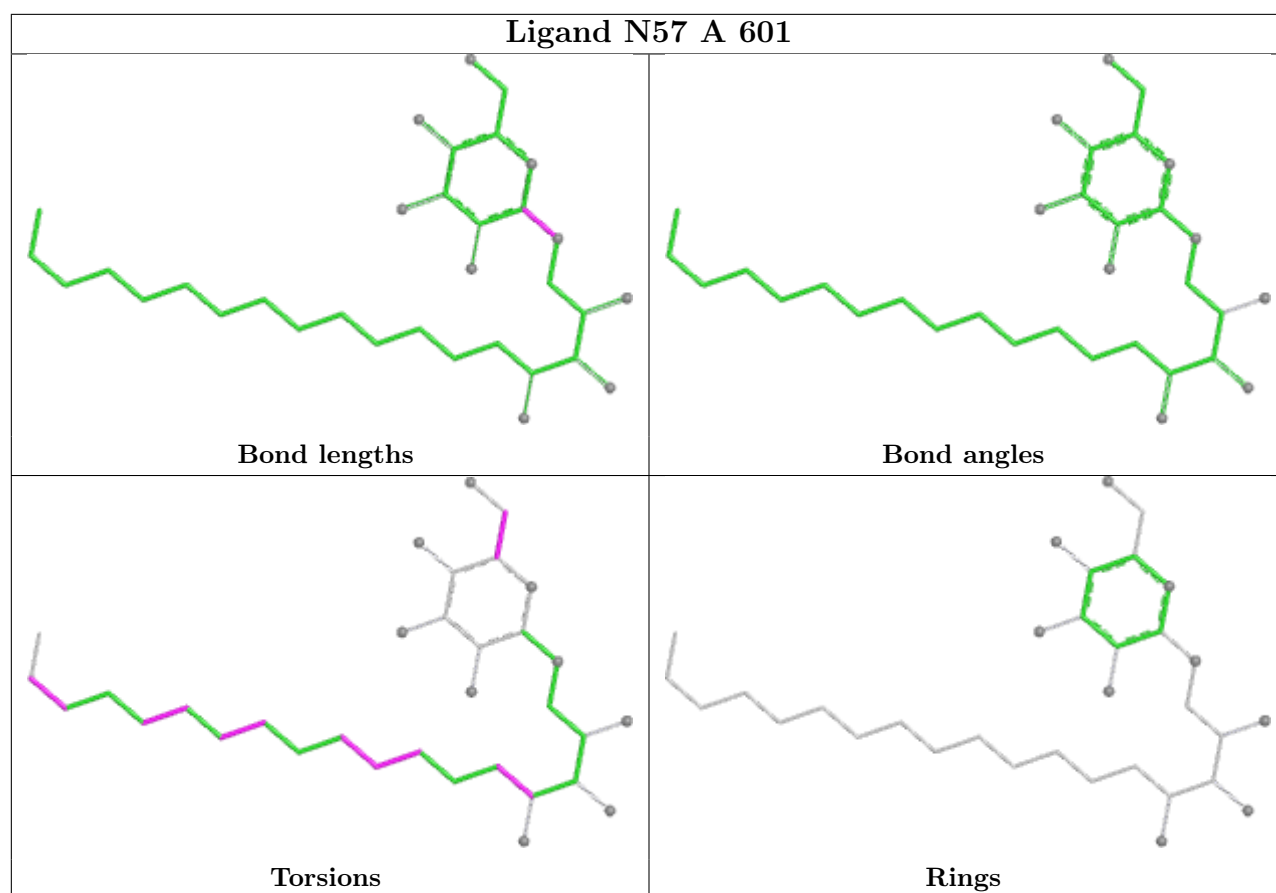
Mol	Chain	Res	Type	Atoms
6	A	601	N57	O32-C3-C4-C5
8	A	603	NAG	O5-C5-C6-O6
8	A	603	NAG	C4-C5-C6-O6
8	A	604	NAG	O5-C5-C6-O6
6	A	601	N57	CG4-CG-CG5-OG6
6	A	601	N57	C9-C10-C11-C12
7	A	602	PLM	C9-CA-CB-CC
6	A	601	N57	OG-CG-CG5-OG6
6	A	601	N57	C5-C6-C7-C8
7	A	602	PLM	C2-C3-C4-C5
8	A	604	NAG	C4-C5-C6-O6
7	A	602	PLM	C3-C4-C5-C6
6	A	601	N57	C11-C12-C13-C14
7	A	602	PLM	CA-CB-CC-CD
7	A	602	PLM	C6-C7-C8-C9
6	A	601	N57	C14-C15-C16-C17
6	A	601	N57	C6-C7-C8-C9

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 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 [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	267/285 (93%)	-0.17	1 (0%) 88 78	33, 49, 83, 109	0
2	B	98/99 (98%)	-0.01	1 (1%) 79 62	41, 59, 82, 128	0
3	C	201/209 (96%)	-0.11	2 (0%) 79 62	33, 52, 87, 111	0
4	D	239/241 (99%)	-0.28	1 (0%) 88 78	33, 46, 64, 81	0
All	All	805/834 (96%)	-0.17	5 (0%) 85 72	33, 49, 83, 128	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	99	MET	3.3
4	D	181	ASN	2.2
3	C	150	GLN	2.1
1	A	255	ALA	2.1
3	C	152	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.

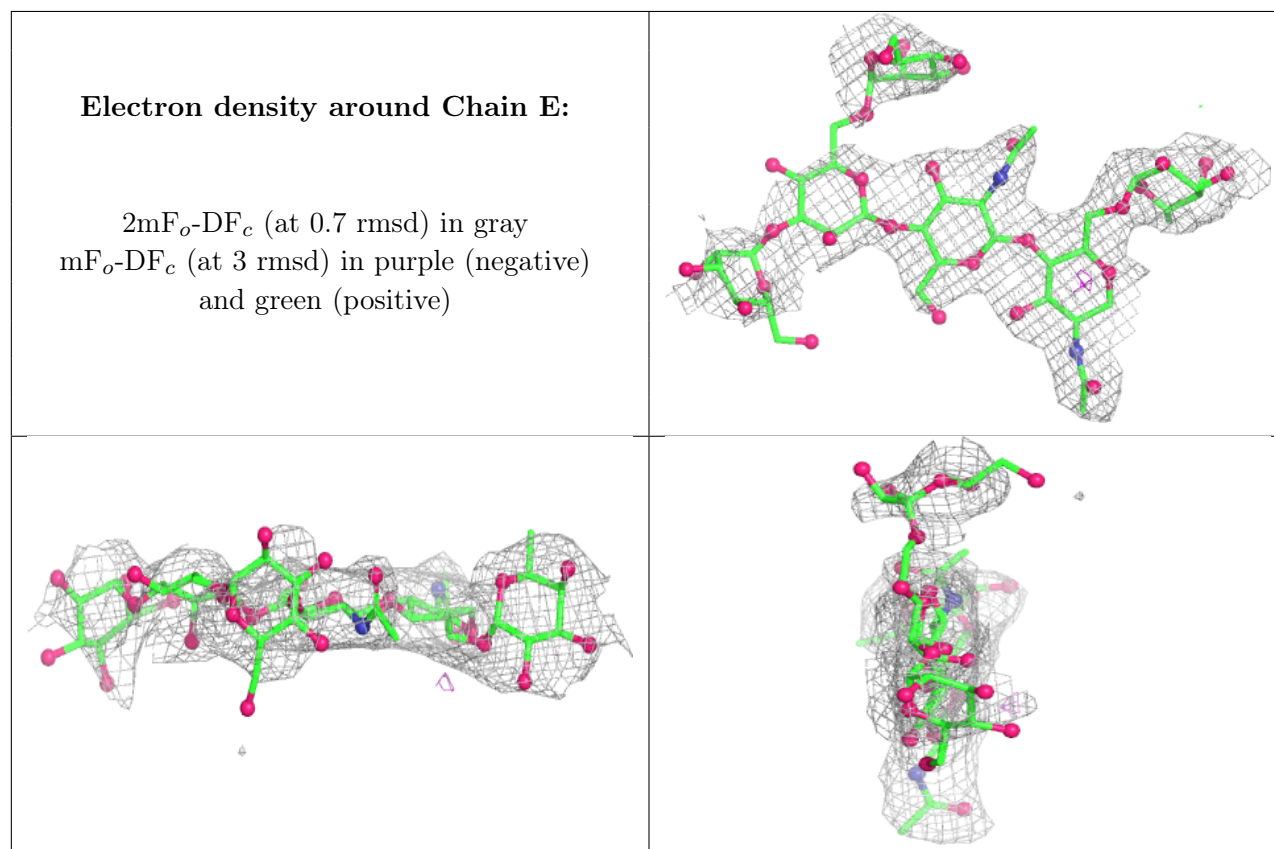
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MAN	E	4	11/12	0.29	0.14	124,127,129,129	0
5	BMA	E	3	11/12	0.64	0.12	104,116,119,124	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	MAN	E	5	11/12	0.66	0.13	110,115,119,119	0
5	NAG	E	2	14/15	0.90	0.10	66,69,77,91	0
5	FUC	E	6	10/11	0.91	0.11	59,63,65,67	0
5	NAG	E	1	14/15	0.95	0.07	50,51,60,61	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.

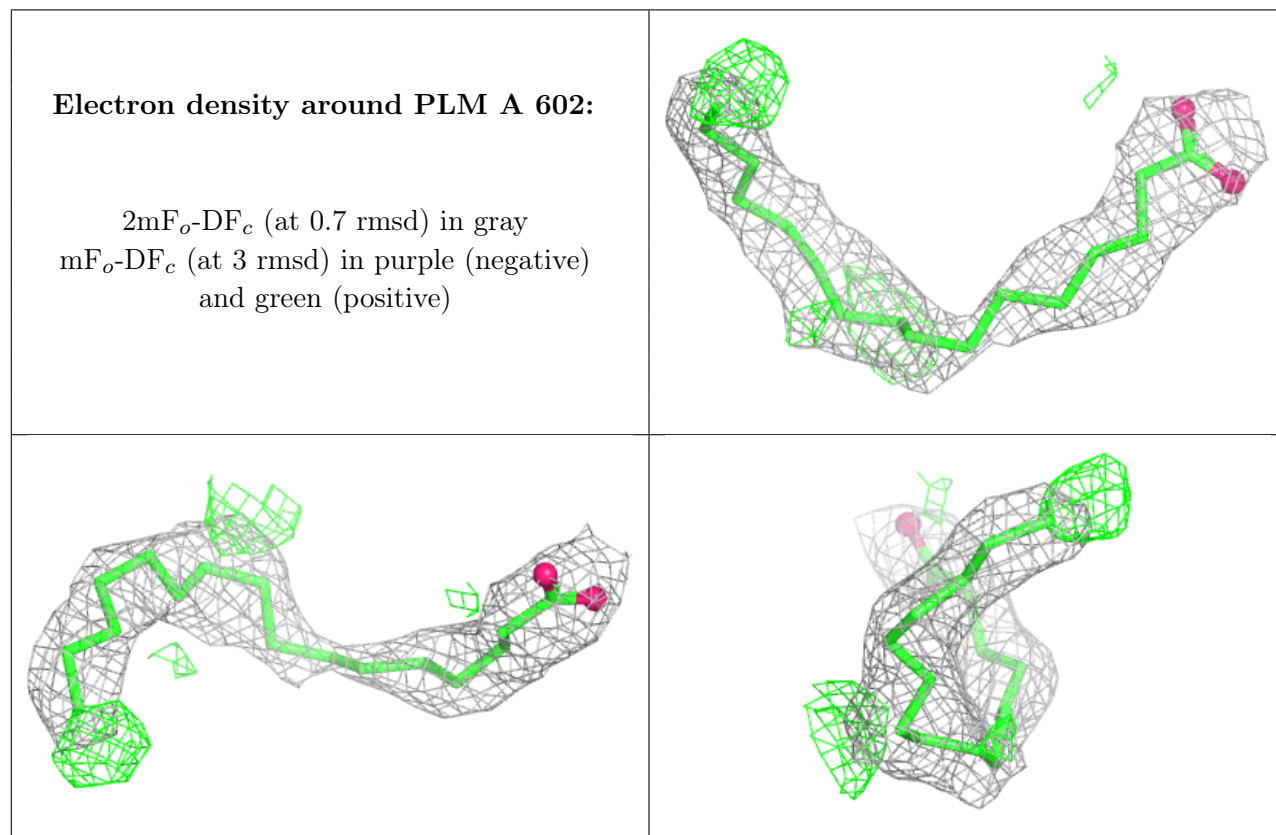


6.4 Ligands ⓘ

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.

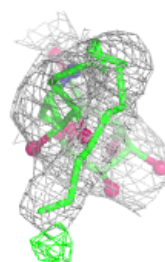
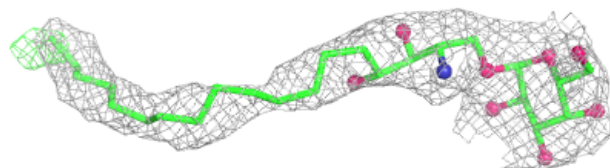
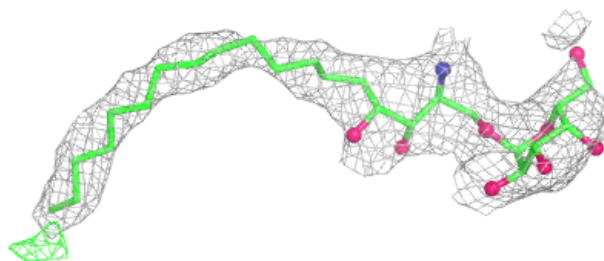
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	NAG	A	603	14/15	0.87	0.10	67,76,78,79	0
8	NAG	A	604	14/15	0.88	0.09	46,48,51,51	0
7	PLM	A	602	18/18	0.92	0.20	58,66,68,68	0
6	N57	A	601	33/33	0.94	0.13	50,53,59,59	0

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 N57 A 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 [i](#)

There are no such residues in this entry.