



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 6, 2017 – 07:34 AM EDT

PDB ID : 5N6L  
Title : Structure of the membrane integral lipoprotein N-acyltransferase Lnt C387A mutant from *E. coli*  
Authors : Huang, C.-Y.; Boland, C.; Howe, N.; Wiktor, M.; Volgeley, L.; Weichert, D.; Bailey, J.; Olieric, V.; Wang, M.; Caffrey, M.  
Deposited on : unknown  
Resolution : 2.90 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20029824

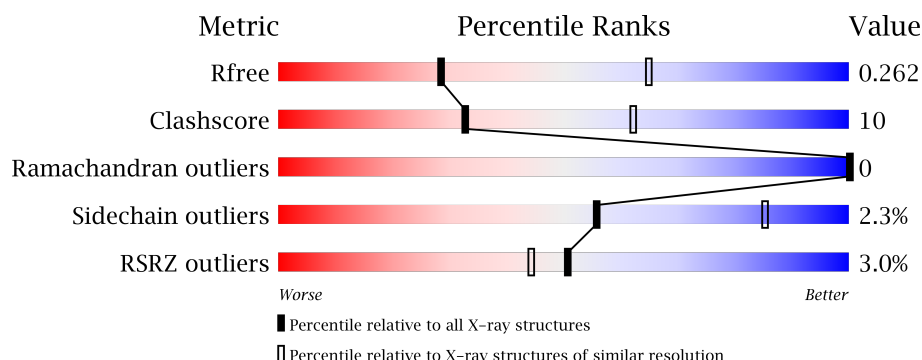
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	100719	1586 (2.90-2.90)
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	532	<div> <div>2%</div> <div>74%</div> <div>20%</div> <div>• 5%</div> </div>
1	B	532	<div> <div>4%</div> <div>66%</div> <div>25%</div> <div>• 8%</div> </div>

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
2	OLC	A	601	-	-	-	X
2	OLC	A	602	-	-	-	X
2	OLC	A	603	-	-	-	X
2	OLC	A	604	-	-	-	X
2	OLC	A	605	-	-	-	X
2	OLC	A	606	-	-	-	X
2	OLC	A	607	-	-	-	X
2	OLC	A	609	-	-	-	X
2	OLC	A	611	-	-	-	X
2	OLC	A	612	-	-	-	X
2	OLC	A	615	-	-	-	X
2	OLC	A	616	-	-	-	X
2	OLC	A	618	-	-	-	X
2	OLC	B	601	-	-	-	X
2	OLC	B	602	-	-	-	X
2	OLC	B	603	-	-	-	X
2	OLC	B	604	-	-	-	X
2	OLC	B	605	-	-	-	X
2	OLC	B	607	-	-	-	X
2	OLC	B	608	-	-	-	X
3	GOL	A	620	-	-	-	X
3	GOL	A	622	-	-	-	X
3	GOL	A	625	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8371 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 Apolipoprotein N-acyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	506	Total	C	N	O	S	0	0	0
			3982	2621	659	688	14			
1	B	491	Total	C	N	O	S	0	0	0
			3863	2540	641	669	13			

There are 42 discrepancies between the modelled and reference sequences:

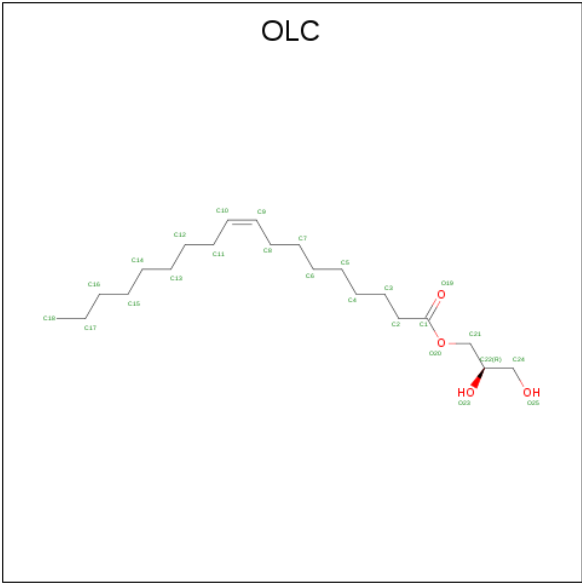
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P23930
A	-18	GLY	-	expression tag	UNP P23930
A	-17	SER	-	expression tag	UNP P23930
A	-16	SER	-	expression tag	UNP P23930
A	-15	HIS	-	expression tag	UNP P23930
A	-14	HIS	-	expression tag	UNP P23930
A	-13	HIS	-	expression tag	UNP P23930
A	-12	HIS	-	expression tag	UNP P23930
A	-11	HIS	-	expression tag	UNP P23930
A	-10	HIS	-	expression tag	UNP P23930
A	-9	SER	-	expression tag	UNP P23930
A	-8	SER	-	expression tag	UNP P23930
A	-7	GLY	-	expression tag	UNP P23930
A	-6	LEU	-	expression tag	UNP P23930
A	-5	VAL	-	expression tag	UNP P23930
A	-4	PRO	-	expression tag	UNP P23930
A	-3	ARG	-	expression tag	UNP P23930
A	-2	GLY	-	expression tag	UNP P23930
A	-1	SER	-	expression tag	UNP P23930
A	0	HIS	-	expression tag	UNP P23930
A	387	ALA	CYS	engineered mutation	UNP P23930
B	-19	MET	-	initiating methionine	UNP P23930
B	-18	GLY	-	expression tag	UNP P23930
B	-17	SER	-	expression tag	UNP P23930
B	-16	SER	-	expression tag	UNP P23930

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	HIS	-	expression tag	UNP P23930
B	-14	HIS	-	expression tag	UNP P23930
B	-13	HIS	-	expression tag	UNP P23930
B	-12	HIS	-	expression tag	UNP P23930
B	-11	HIS	-	expression tag	UNP P23930
B	-10	HIS	-	expression tag	UNP P23930
B	-9	SER	-	expression tag	UNP P23930
B	-8	SER	-	expression tag	UNP P23930
B	-7	GLY	-	expression tag	UNP P23930
B	-6	LEU	-	expression tag	UNP P23930
B	-5	VAL	-	expression tag	UNP P23930
B	-4	PRO	-	expression tag	UNP P23930
B	-3	ARG	-	expression tag	UNP P23930
B	-2	GLY	-	expression tag	UNP P23930
B	-1	SER	-	expression tag	UNP P23930
B	0	HIS	-	expression tag	UNP P23930
B	387	ALA	CYS	engineered mutation	UNP P23930

- Molecule 2 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: C<sub>21</sub>H<sub>40</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			15	11	4		
2	A	1	Total	C	O	0	0
			12	8	4		

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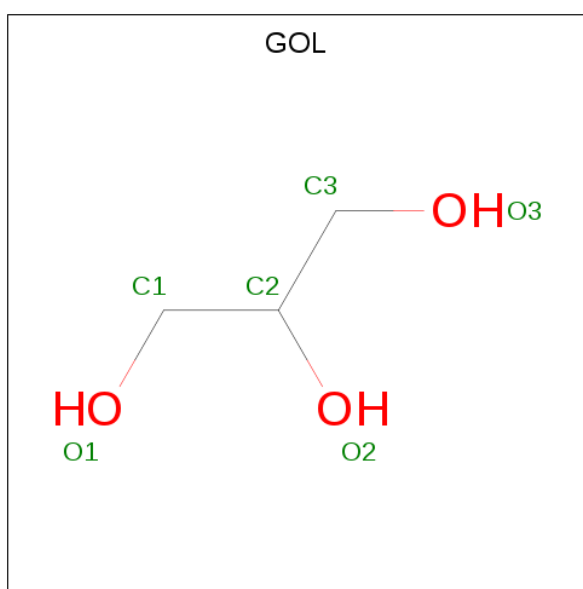
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			22	18	4		
2	A	1	Total	C	O	0	0
			14	10	4		
2	A	1	Total	C	O	0	0
			12	8	4		
2	A	1	Total	C	O	0	0
			25	21	4		
2	A	1	Total	C	O	0	0
			15	11	4		
2	A	1	Total	C	O	0	0
			14	10	4		
2	A	1	Total	C	O	0	0
			22	18	4		
2	A	1	Total	C	O	0	0
			12	8	4		
2	A	1	Total	C	O	0	0
			16	12	4		
2	A	1	Total	C	O	0	0
			22	18	4		
2	A	1	Total	C	O	0	0
			14	10	4		
2	A	1	Total	C	O	0	0
			14	10	4		
2	A	1	Total	C	O	0	0
			20	16	4		
2	A	1	Total	C	O	0	0
			13	9	4		
2	A	1	Total	C	O	0	0
			14	10	4		
2	A	1	Total	C	O	0	0
			14	10	4		
2	A	1	Total	C	O	0	0
			22	18	4		
2	B	1	Total	C	O	0	0
			14	10	4		
2	B	1	Total	C	O	0	0
			25	21	4		
2	B	1	Total	C	O	0	0
			11	7	4		
2	B	1	Total	C	O	0	0
			21	17	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			18	14	4		
2	B	1	Total	C	O	0	0
			13	9	4		
2	B	1	Total	C	O	0	0
			11	7	4		
2	B	1	Total	C	O	0	0
			16	12	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

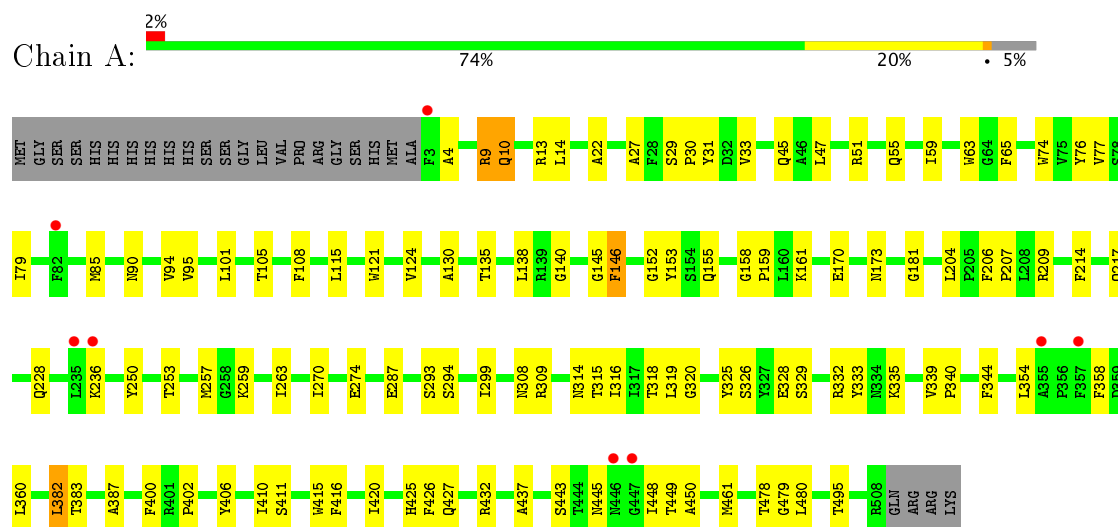
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	5	Total	O	0	0
			5	5		



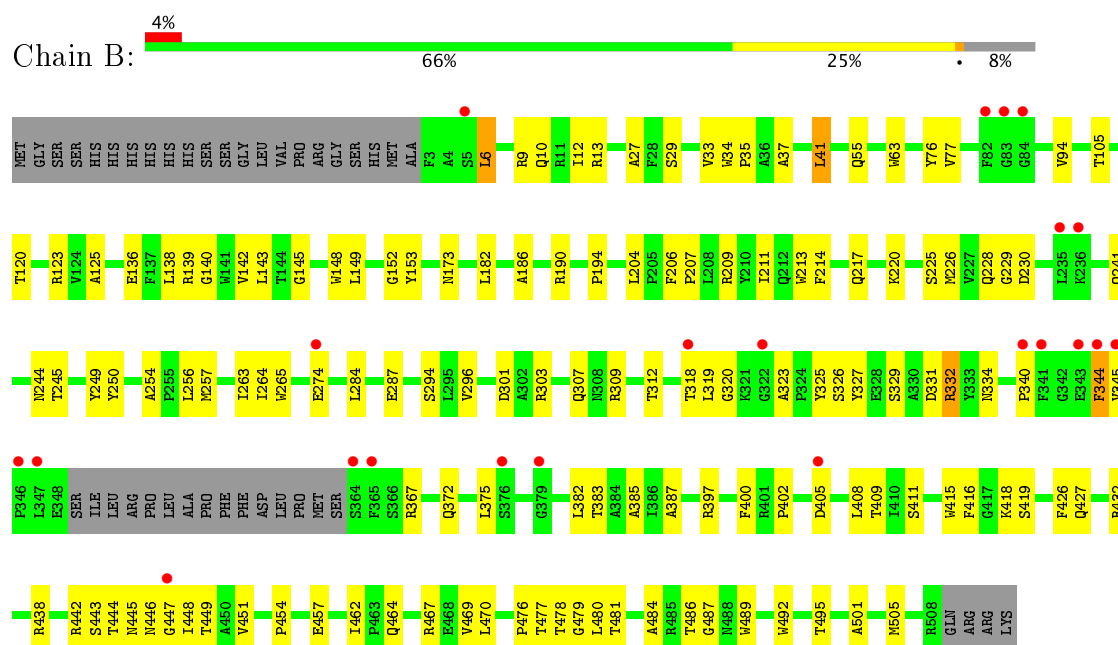
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Apolipoprotein N-acyltransferase



#### • Molecule 1: Apolipoprotein N-acyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.22Å 142.95Å 197.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.79 – 2.90 49.85 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (49.79-2.90) 97.7 (49.85-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 2.91Å)	Xtriage
Refinement program	BUSTER, PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.227 , 0.263 0.238 , 0.262	Depositor DCC
$R_{free}$ test set	1699 reflections (5.13%)	DCC
Wilson B-factor (Å <sup>2</sup> )	86.6	Xtriage
Anisotropy	0.341	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 51.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8371	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, OLC

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	0.31	1/4097 (0.0%)	0.51	0/5598
1	B	0.27	0/3972	0.51	0/5425
All	All	0.29	1/8069 (0.0%)	0.51	0/11023

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	146	PHE	C-N	8.32	1.50	1.34

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	3982	0	4051	74	0
1	B	3863	0	3926	92	0
2	A	312	0	406	12	0
2	B	129	0	167	2	0
3	A	48	0	64	2	0
3	B	24	0	32	0	0
4	A	8	0	0	0	0
4	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8371	0	8646	169	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 10.

The worst 5 of 169 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:A:612:OLC:H2	2:A:613:OLC:H21A	1.66	0.76
1:B:214:PHE:HA	1:B:479:GLY:HA3	1.66	0.75
1:A:85:MET:HB2	1:A:90:ASN:HD21	1.51	0.75
1:A:214:PHE:HA	1:A:479:GLY:HA3	1.71	0.71
1:A:153:TYR:OH	1:A:432:ARG:NH2	2.25	0.69

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	504/532 (95%)	488 (97%)	16 (3%)	0	100	100
1	B	487/532 (92%)	479 (98%)	8 (2%)	0	100	100
All	All	991/1064 (93%)	967 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	421/443 (95%)	410 (97%)	11 (3%)	51	83
1	B	407/443 (92%)	399 (98%)	8 (2%)	60	87
All	All	828/886 (94%)	809 (98%)	19 (2%)	56	85

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	382	LEU
1	A	425	HIS
1	B	332	ARG
1	A	358	PHE
1	B	344	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	90	ASN
1	A	223	GLN
1	B	228	GLN

### 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](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

39 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$
2	OLC	A	601	-	14,14,24	0.87	1 (7%)	15,15,25	1.06	1 (6%)
2	OLC	A	602	-	11,11,24	0.98	1 (9%)	12,12,25	1.09	1 (8%)
2	OLC	A	603	-	21,21,24	0.75	1 (4%)	22,22,25	1.11	2 (9%)
2	OLC	A	604	-	13,13,24	0.93	1 (7%)	14,14,25	1.15	1 (7%)
2	OLC	A	605	-	11,11,24	0.98	1 (9%)	12,12,25	1.21	1 (8%)
2	OLC	A	606	-	24,24,24	0.70	1 (4%)	25,25,25	1.20	1 (4%)
2	OLC	A	607	-	14,14,24	0.87	1 (7%)	15,15,25	1.06	1 (6%)
2	OLC	A	608	-	13,13,24	0.93	1 (7%)	14,14,25	1.09	1 (7%)
2	OLC	A	609	-	21,21,24	0.76	1 (4%)	22,22,25	0.96	1 (4%)
2	OLC	A	610	-	11,11,24	1.00	1 (9%)	12,12,25	1.15	1 (8%)
2	OLC	A	611	-	15,15,24	0.87	1 (6%)	16,16,25	0.97	1 (6%)
2	OLC	A	612	-	21,21,24	0.74	1 (4%)	22,22,25	1.03	1 (4%)
2	OLC	A	613	-	13,13,24	0.91	1 (7%)	14,14,25	1.12	1 (7%)
2	OLC	A	614	-	13,13,24	0.91	1 (7%)	14,14,25	1.17	1 (7%)
2	OLC	A	615	-	19,19,24	0.80	1 (5%)	20,20,25	1.54	3 (15%)
2	OLC	A	616	-	12,12,24	0.89	1 (8%)	13,13,25	1.30	1 (7%)
2	OLC	A	617	-	13,13,24	0.88	1 (7%)	14,14,25	1.15	1 (7%)
2	OLC	A	618	-	13,13,24	0.85	1 (7%)	14,14,25	1.26	1 (7%)
2	OLC	A	619	-	21,21,24	0.73	1 (4%)	22,22,25	0.98	1 (4%)
3	GOL	A	620	-	5,5,5	0.38	0	5,5,5	0.25	0
3	GOL	A	621	-	5,5,5	0.37	0	5,5,5	0.24	0
3	GOL	A	622	-	5,5,5	0.38	0	5,5,5	0.31	0
3	GOL	A	623	-	5,5,5	0.39	0	5,5,5	0.32	0
3	GOL	A	624	-	5,5,5	0.35	0	5,5,5	0.19	0
3	GOL	A	625	-	5,5,5	0.25	0	5,5,5	0.28	0
3	GOL	A	626	-	5,5,5	0.29	0	5,5,5	0.23	0
3	GOL	A	627	-	5,5,5	0.29	0	5,5,5	0.18	0
2	OLC	B	601	-	13,13,24	0.90	1 (7%)	14,14,25	0.98	1 (7%)
2	OLC	B	602	-	24,24,24	0.69	1 (4%)	25,25,25	1.00	1 (4%)
2	OLC	B	603	-	10,10,24	1.05	1 (10%)	11,11,25	1.19	1 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	OLC	B	604	-	20,20,24	0.77	1 (5%)	21,21,25	1.08	1 (4%)
2	OLC	B	605	-	17,17,24	0.83	1 (5%)	18,18,25	1.13	1 (5%)
2	OLC	B	606	-	12,12,24	0.93	1 (8%)	13,13,25	1.37	2 (15%)
2	OLC	B	607	-	10,10,24	0.96	1 (10%)	11,11,25	1.13	1 (9%)
2	OLC	B	608	-	15,15,24	0.81	1 (6%)	16,16,25	0.94	1 (6%)
3	GOL	B	609	-	5,5,5	0.37	0	5,5,5	0.27	0
3	GOL	B	610	-	5,5,5	0.37	0	5,5,5	0.22	0
3	GOL	B	611	-	5,5,5	0.42	0	5,5,5	0.11	0
3	GOL	B	612	-	5,5,5	0.28	0	5,5,5	0.61	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
2	OLC	A	601	-	-	0/14/14/24	0/0/0/0
2	OLC	A	602	-	-	0/11/11/24	0/0/0/0
2	OLC	A	603	-	-	0/21/21/24	0/0/0/0
2	OLC	A	604	-	-	0/13/13/24	0/0/0/0
2	OLC	A	605	-	-	0/11/11/24	0/0/0/0
2	OLC	A	606	-	-	0/24/24/24	0/0/0/0
2	OLC	A	607	-	-	0/14/14/24	0/0/0/0
2	OLC	A	608	-	-	0/13/13/24	0/0/0/0
2	OLC	A	609	-	-	0/21/21/24	0/0/0/0
2	OLC	A	610	-	-	0/11/11/24	0/0/0/0
2	OLC	A	611	-	-	0/15/15/24	0/0/0/0
2	OLC	A	612	-	-	0/21/21/24	0/0/0/0
2	OLC	A	613	-	-	0/13/13/24	0/0/0/0
2	OLC	A	614	-	-	0/13/13/24	0/0/0/0
2	OLC	A	615	-	-	0/19/19/24	0/0/0/0
2	OLC	A	616	-	-	0/12/12/24	0/0/0/0
2	OLC	A	617	-	-	0/13/13/24	0/0/0/0
2	OLC	A	618	-	-	0/13/13/24	0/0/0/0
2	OLC	A	619	-	-	0/21/21/24	0/0/0/0
3	GOL	A	620	-	-	0/4/4/4	0/0/0/0
3	GOL	A	621	-	-	0/4/4/4	0/0/0/0
3	GOL	A	622	-	-	0/4/4/4	0/0/0/0
3	GOL	A	623	-	-	0/4/4/4	0/0/0/0
3	GOL	A	624	-	-	0/4/4/4	0/0/0/0
3	GOL	A	625	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	626	-	-	0/4/4/4	0/0/0/0
3	GOL	A	627	-	-	0/4/4/4	0/0/0/0
2	OLC	B	601	-	-	0/13/13/24	0/0/0/0
2	OLC	B	602	-	-	0/24/24/24	0/0/0/0
2	OLC	B	603	-	-	0/10/10/24	0/0/0/0
2	OLC	B	604	-	-	0/20/20/24	0/0/0/0
2	OLC	B	605	-	-	0/17/17/24	0/0/0/0
2	OLC	B	606	-	-	0/12/12/24	0/0/0/0
2	OLC	B	607	-	-	0/10/10/24	0/0/0/0
2	OLC	B	608	-	-	0/15/15/24	0/0/0/0
3	GOL	B	609	-	-	0/4/4/4	0/0/0/0
3	GOL	B	610	-	-	0/4/4/4	0/0/0/0
3	GOL	B	611	-	-	0/4/4/4	0/0/0/0
3	GOL	B	612	-	-	0/4/4/4	0/0/0/0

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	618	OLC	O20-C1	2.47	1.40	1.33
2	B	607	OLC	O20-C1	2.48	1.40	1.33
2	A	617	OLC	O20-C1	2.57	1.40	1.33
2	B	608	OLC	O20-C1	2.58	1.40	1.33
2	A	619	OLC	O20-C1	2.59	1.40	1.33

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	615	OLC	C21-O20-C1	-2.98	108.16	117.13
2	B	606	OLC	C3-C2-C1	-2.10	105.90	113.58
2	A	603	OLC	O20-C1-O19	-2.03	118.52	123.55
2	B	608	OLC	O20-C1-C2	2.19	118.28	111.90
2	A	615	OLC	O20-C21-C22	2.26	116.81	105.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	OLC	1	0
2	A	602	OLC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	603	OLC	1	0
2	A	611	OLC	1	0
2	A	612	OLC	4	0
2	A	613	OLC	1	0
2	A	615	OLC	3	0
2	A	618	OLC	1	0
3	A	624	GOL	2	0
2	B	603	OLC	1	0
2	B	606	OLC	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	506/532 (95%)	-0.15	8 (1%) 72 70	52, 73, 121, 160	0
1	B	491/532 (92%)	0.20	22 (4%) 34 29	66, 87, 123, 156	0
All	All	997/1064 (93%)	0.02	30 (3%) 51 44	52, 81, 123, 160	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	345	VAL	6.0
1	B	344	PHE	4.4
1	B	82	PHE	4.2
1	B	343	GLU	4.1
1	B	347	LEU	3.8

### 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](#)

There are no carbohydrates in this entry.

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	OLC	A	607	15/25	0.76	0.49	11.61	102,104,114,116	0
2	OLC	A	616	13/25	0.86	0.42	10.19	66,81,102,105	0
2	OLC	A	611	16/25	0.82	0.56	9.86	91,94,97,112	0
2	OLC	A	606	25/25	0.87	0.36	7.02	67,86,96,105	0
2	OLC	B	605	18/25	0.73	0.56	6.24	116,119,128,128	0
2	OLC	A	618	14/25	0.86	0.45	6.00	80,85,99,103	0
3	GOL	A	622	6/6	0.63	0.42	5.82	114,121,124,128	0
2	OLC	A	603	22/25	0.85	0.31	5.60	72,91,107,112	0
2	OLC	B	602	25/25	0.91	0.39	5.44	54,86,104,107	0
2	OLC	A	605	12/25	0.76	0.30	5.10	101,112,125,138	0
2	OLC	A	609	22/25	0.72	0.37	3.79	91,101,112,126	0
2	OLC	B	604	21/25	0.77	0.36	3.79	103,114,124,129	0
3	GOL	A	620	6/6	0.71	0.29	3.77	122,122,124,125	0
2	OLC	B	607	11/25	0.73	0.33	3.77	75,100,110,112	0
2	OLC	B	603	11/25	0.79	0.51	3.51	114,123,129,133	0
2	OLC	A	612	22/25	0.87	0.35	3.37	76,86,109,112	0
2	OLC	B	601	14/25	0.86	0.28	2.70	94,104,113,118	0
2	OLC	A	604	14/25	0.81	0.28	2.58	100,108,119,120	0
2	OLC	A	601	15/25	0.91	0.30	2.37	74,82,89,94	0
2	OLC	A	602	12/25	0.90	0.24	2.36	87,94,102,111	0
2	OLC	A	615	20/25	0.73	0.47	2.21	64,92,116,119	0
2	OLC	B	608	16/25	0.77	0.20	2.07	73,94,118,125	0
3	GOL	A	625	6/6	0.83	0.21	2.06	65,76,80,89	0
2	OLC	A	610	12/25	0.91	0.35	1.96	108,119,129,141	0
3	GOL	B	610	6/6	0.81	0.32	1.96	111,113,115,128	0
2	OLC	A	619	22/25	0.89	0.19	1.53	60,72,115,124	0
2	OLC	A	608	14/25	0.80	0.25	1.36	81,96,105,106	0
2	OLC	A	613	14/25	0.88	0.28	0.81	87,104,113,117	0
2	OLC	B	606	13/25	0.81	0.22	0.76	69,90,104,108	0
3	GOL	A	624	6/6	0.65	0.20	-0.30	99,106,110,113	0
3	GOL	B	609	6/6	0.83	0.16	-	88,98,104,110	0
3	GOL	B	612	6/6	0.84	0.28	-	94,97,102,108	0
3	GOL	A	627	6/6	0.83	0.38	-	78,84,86,98	0
3	GOL	A	623	6/6	0.77	0.53	-	85,88,93,101	0
3	GOL	B	611	6/6	0.74	0.34	-	75,89,96,96	0
3	GOL	A	621	6/6	0.87	0.27	-	79,88,97,103	0
2	OLC	A	617	14/25	0.82	0.30	-	85,93,101,114	0
2	OLC	A	614	14/25	0.75	0.31	-	100,109,114,121	0
3	GOL	A	626	6/6	0.63	0.48	-	81,83,93,102	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.