

## Full wwPDB X-ray Structure Validation Report (i)

#### Feb 3, 2022 – 12:21 pm GMT

PDB ID : 708J

Title : NmHR light state structure at 20 us after photoexcitation determined by serial

femtosecond crystallography (with extrapolated, dark and light dataset)

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Deposited on : 2021-04-15

Resolution : 1.80 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 (i) symbol.

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

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as 541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.26

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0267

CCP4 : 7.1.010 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

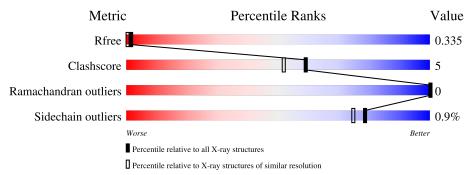
Validation Pipeline (wwPDB-VP) : 2.26

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.80 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 <=5%

Mol	Chain	Length	Quality of chain		
1	A	296	80%	9%	11%



## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2328 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 Chloride pumping rhodopsin.

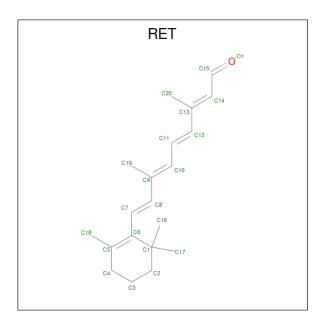
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	264	Total	С	N	О	S	0	4	0
1	A	204	2092	1394	319	363	16	0	4	

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP W8VZW3
A	-14	ALA	-	expression tag	UNP W8VZW3
A	-13	SER	-	expression tag	UNP W8VZW3
A	-12	MET	-	expression tag	UNP W8VZW3
A	-11	THR	-	expression tag	UNP W8VZW3
A	-10	GLY	-	expression tag	UNP W8VZW3
A	-9	GLY	-	expression tag	UNP W8VZW3
A	-8	GLN	-	expression tag	UNP W8VZW3
A	-7	GLN	-	expression tag	UNP W8VZW3
A	-6	MET	-	expression tag	UNP W8VZW3
A	-5	GLY	-	expression tag	UNP W8VZW3
A	-4	ARG	-	expression tag	UNP W8VZW3
A	-3	ASP	-	expression tag	UNP W8VZW3
A	-2	PRO	-	expression tag	UNP W8VZW3
A	-1	ASN	-	expression tag	UNP W8VZW3
A	0	SER	-	expression tag	UNP W8VZW3
A	273	LEU	-	expression tag	UNP W8VZW3
A	274	GLU	-	expression tag	UNP W8VZW3
A	275	HIS	-	expression tag	UNP W8VZW3
A	276	HIS	-	expression tag	UNP W8VZW3
A	277	HIS	-	expression tag	UNP W8VZW3
A	278	HIS	-	expression tag	UNP W8VZW3
A	279	HIS	-	expression tag	UNP W8VZW3
A	280	HIS	_	expression tag	UNP W8VZW3

• Molecule 2 is RETINAL (three-letter code: RET) (formula:  $C_{20}H_{28}O$ ).



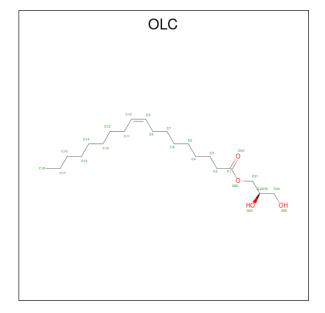


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C 20 20	0	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Cl 2 2	0	2

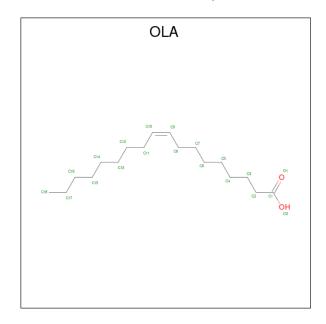
• Molecule 4 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula:  $C_{21}H_{40}O_4$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 25 21 4	0	0
4	A	1	Total C O 18 14 4	0	0
4	A	1	Total C O 12 8 4	0	0

 $\bullet$  Molecule 5 is OLEIC ACID (three-letter code: OLA) (formula:  $\mathrm{C_{18}H_{34}O_{2}}).$ 



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 20 18 2	0	0
5	A	1	Total C O 20 18 2	0	0
5	A	1	Total C O 18 16 2	0	0
5	A	1	Total C O 17 15 2	0	0
5	A	1	Total C O 20 18 2	0	0

• Molecule 6 is water.

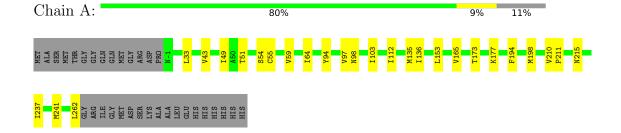
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	64	Total O 64 64	0	0



## 3 Residue-property plots (i)

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





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	104.48Å 51.18Å 78.33Å	Donogitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $131.78^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	13.45 - 1.80	Depositor
Resolution (A)	13.45 - 1.80	EDS
% Data completeness	90.5 (13.45-1.80)	Depositor
(in resolution range)	90.6 (13.45-1.80)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.26  (at  1.80Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
D.D.	0.284 , 0.327	Depositor
$R, R_{free}$	0.295 , $0.335$	DCC
$R_{free}$ test set	1328 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.9	Xtriage
Anisotropy	0.724	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	2328	wwPDB-VP
Average B, all atoms $(\mathring{A}^2)$	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.34% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: RET, OLA, CL, 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	$\mathbf{lengths}$	Bond angles		
			RMSZ	# Z  > 5	RMSZ	# Z  > 5	
	1	A	0.26	0/2157	0.43	0/2941	

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	2092	0	2133	18	0
2	A	20	0	27	5	0
3	A	2	0	0	1	0
4	A	55	0	76	1	0
5	A	95	0	149	0	0
6	A	64	0	0	2	0
All	All	2328	0	2385	22	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 5.

All (22) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\mathring{\mathbf{A}}) \end{array}$	Clash overlap (Å)
1:A:103:ILE:HD12	1:A:136:ILE:HD11	1.64	0.77
1:A:49:ILE:HG23	1:A:112:ILE:HD13	1.69	0.74
1:A:33:LEU:HD22	1:A:59:VAL:HG22	1.75	0.67
1:A:94:TYR:O	1:A:97:VAL:HG22	1.95	0.66
2:A:301:RET:H171	2:A:301:RET:H8	1.84	0.60
1:A:64:ILE:HG13	1:A:98:ASN:HB2	1.86	0.58
1:A:215:ASN:ND2	6:A:406:HOH:O	2.40	0.55
1:A:43:VAL:HG21	1:A:51[A]:THR:HG21	1.93	0.51
1:A:98:ASN:ND2	6:A:409:HOH:O	2.43	0.51
1:A:54:SER:OG	3:A:302[A]:CL:CL	2.57	0.49
1:A:135:MET:SD	2:A:301:RET:H192	2.53	0.48
1:A:194:PHE:O	1:A:198:MET:HG2	2.14	0.47
2:A:301:RET:H8	2:A:301:RET:H161	1.96	0.47
1:A:49:ILE:CG2	1:A:112:ILE:HD13	2.42	0.47
1:A:94:TYR:HA	1:A:97:VAL:HG22	1.97	0.47
2:A:301:RET:H161	2:A:301:RET:C8	2.47	0.45
2:A:301:RET:H7	2:A:301:RET:H181	1.76	0.43
1:A:165:VAL:HG13	4:A:304:OLC:H8A	2.01	0.42
1:A:173:THR:HG22	1:A:177:LYS:HD2	2.01	0.42
1:A:55:CYS:O	1:A:59:VAL:HG23	2.21	0.41
1:A:210:VAL:N	1:A:211:PRO:CD	2.84	0.40
1:A:237:ILE:O	1:A:241:MET:HG3	2.21	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	266/296 (90%)	263 (99%)	3 (1%)	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	222/242 (92%)	220 (99%)	2 (1%)	78 75

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	LEU
1	A	262	LEU

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

Mol	Chain	Res	Type
1	A	86	GLN
1	A	98	ASN

#### 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 monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	Trino	Chain	Res	Link	Во	ond leng	ths	В	ond ang	cles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	OLA	A	310	-	13,16,19	0.80	1 (7%)	12,16,19	0.51	0
5	OLA	A	307	-	16,19,19	0.72	1 (6%)	15,19,19	0.60	0
5	OLA	A	311	-	16,19,19	0.72	1 (6%)	15,19,19	0.57	0
5	OLA	A	306	-	16,19,19	0.74	1 (6%)	15,19,19	0.52	0
5	OLA	A	308	-	14,17,19	0.77	1 (7%)	13,17,19	0.52	0
4	OLC	A	304	-	24,24,24	0.84	2 (8%)	25,25,25	0.94	1 (4%)
4	OLC	A	305	-	17,17,24	0.96	2 (11%)	18,18,25	1.07	1 (5%)
4	OLC	A	309	-	11,11,24	1.16	2 (18%)	12,12,25	1.00	1 (8%)
2	RET	A	301	1	20,20,21	0.71	0	27,27,28	1.55	5 (18%)

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	OLA	A	310	-	-	5/12/14/17	-
5	OLA	A	307	-	-	7/15/17/17	-
5	OLA	A	311	-	-	8/15/17/17	-
5	OLA	A	306	-	-	9/15/17/17	-
5	OLA	A	308	-	-	9/13/15/17	-
4	OLC	A	304	-	-	7/24/24/24	-
4	OLC	A	305	-	-	7/17/17/24	-
4	OLC	A	309	-	-	3/11/11/24	-
2	RET	A	301	1	-	0/13/30/31	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
5	A	306	OLA	C10-C9	2.79	1.47	1.31
5	A	310	OLA	C10-C9	2.76	1.47	1.31
5	A	308	OLA	C10-C9	2.73	1.47	1.31
5	A	311	OLA	C10-C9	2.73	1.47	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(\text{\AA})$
5	A	307	OLA	C10-C9	2.71	1.47	1.31
4	A	309	OLC	O20-C1	2.50	1.40	1.33
4	A	304	OLC	O20-C21	-2.41	1.39	1.45
4	A	305	OLC	O20-C1	2.41	1.40	1.33
4	A	304	OLC	O20-C1	2.32	1.40	1.33
4	A	305	OLC	O20-C21	-2.13	1.40	1.45
4	A	309	OLC	O20-C21	-2.07	1.40	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
2	A	301	RET	C11-C12-C13	-4.26	114.45	126.42
4	A	305	OLC	O20-C1-C2	2.64	120.20	111.91
2	A	301	RET	C3-C4-C5	-2.63	109.38	114.08
2	A	301	RET	C7-C8-C9	-2.62	122.28	126.23
4	A	309	OLC	O20-C1-C2	2.53	119.85	111.91
4	A	304	OLC	O20-C1-C2	2.37	119.36	111.91
2	A	301	RET	C4-C5-C6	2.09	125.77	122.73
2	A	301	RET	C18-C5-C6	-2.03	122.25	124.53

There are no chirality outliers.

All (55) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	306	OLA	C1-C2-C3-C4
5	A	307	OLA	C1-C2-C3-C4
5	A	308	OLA	C1-C2-C3-C4
5	A	311	OLA	C1-C2-C3-C4
4	A	309	OLC	O19-C1-O20-C21
4	A	305	OLC	C2-C1-O20-C21
4	A	309	OLC	C2-C1-O20-C21
4	A	305	OLC	O19-C1-O20-C21
4	A	305	OLC	O20-C21-C22-O23
5	A	306	OLA	C11-C12-C13-C14
5	A	306	OLA	C12-C13-C14-C15
4	A	305	OLC	O20-C21-C22-C24
5	A	310	OLA	C5-C6-C7-C8
4	A	304	OLC	C21-C22-C24-O25
4	A	309	OLC	C1-C2-C3-C4
5	A	308	OLA	C6-C7-C8-C9
5	A	308	OLA	C11-C12-C13-C14
5	A	311	OLA	C3-C4-C5-C6

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Mol	$\begin{array}{ c c c c }\hline Chain \end{array}$	Res	Type	Atoms
5	A	306	OLA	C6-C7-C8-C9
4	A	305	OLC	C4-C5-C6-C7
5	A	311	OLA	C11-C12-C13-C14
4	A	304	OLC	C2-C1-O20-C21
5	A	308	OLA	C4-C5-C6-C7
5	A	307	OLA	C2-C3-C4-C5
5	A	311	OLA	C11-C10-C9-C8
4	A	304	OLC	C15-C16-C17-C18
5	A	306	OLA	C3-C4-C5-C6
4	A	304	OLC	O19-C1-O20-C21
5	A	310	OLA	C11-C10-C9-C8
5	A	307	OLA	C11-C12-C13-C14
5	A	307	OLA	C11-C10-C9-C8
4	A	304	OLC	C5-C6-C7-C8
5	A	306	OLA	C4-C5-C6-C7
5	A	308	OLA	C11-C10-C9-C8
5	A	310	OLA	C4-C5-C6-C7
5	A	307	OLA	C14-C15-C16-C17
5	A	311	OLA	C15-C16-C17-C18
5	A	311	OLA	C4-C5-C6-C7
5	A	308	OLA	C5-C6-C7-C8
5	A	307	OLA	C10-C11-C12-C13
5	A	306	OLA	C13-C14-C15-C16
5	A	307	OLA	C12-C13-C14-C15
4	A	305	OLC	C7-C8-C9-C10
5	A	308	OLA	C9-C10-C11-C12
5	A	308	OLA	C3-C4-C5-C6
4	A	305	OLC	C1-C2-C3-C4
5	A	311	OLA	C9-C10-C11-C12
4	A	304	OLC	O23-C22-C24-O25
5	A	308	OLA	C2-C3-C4-C5
4	A	304	OLC	C7-C8-C9-C10
5	A	306	OLA	C7-C8-C9-C10
5	A	310	OLA	C7-C8-C9-C10
5	A	311	OLA	C12-C13-C14-C15
5	A	306	OLA	C9-C10-C11-C12
5	A	310	OLA	C11-C12-C13-C14

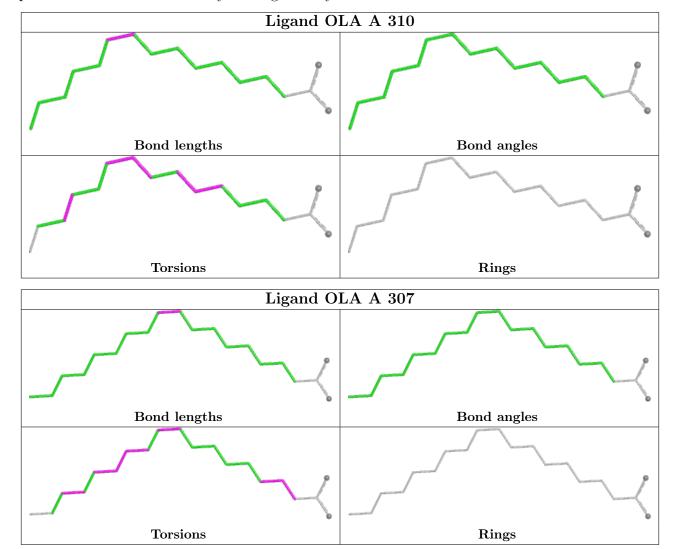
There are no ring outliers.

2 monomers are involved in 6 short contacts:

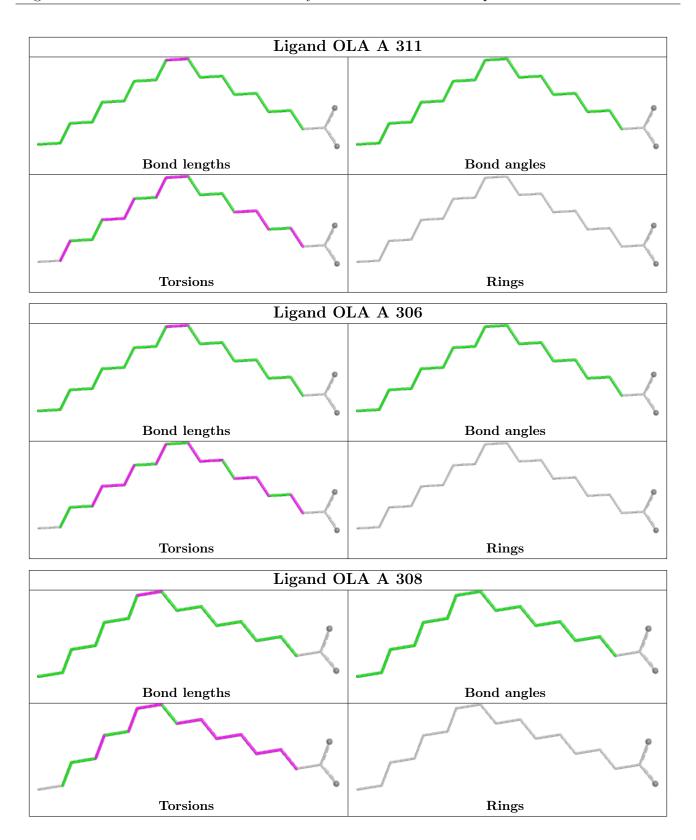


Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	304	OLC	1	0
2	A	301	RET	5	0

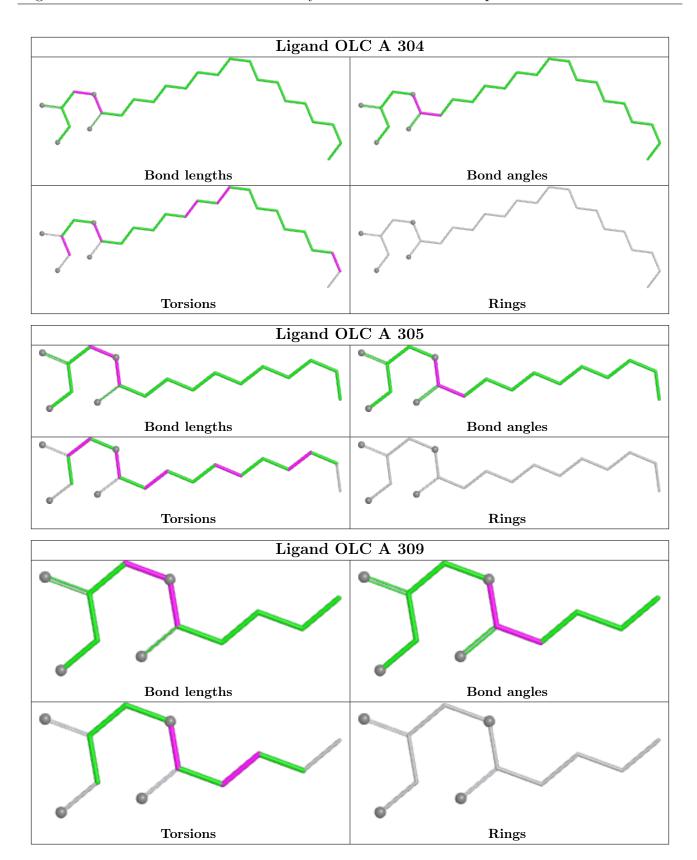
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.



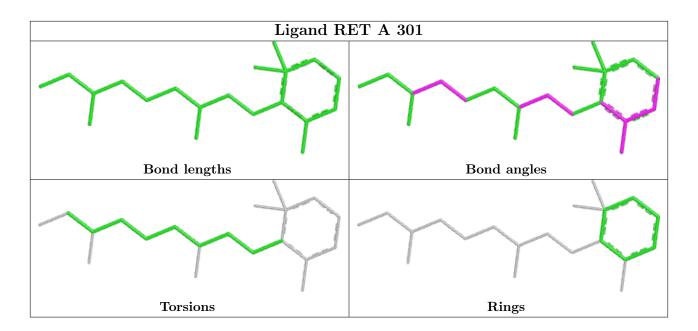












## 5.7 Other polymers (i)

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

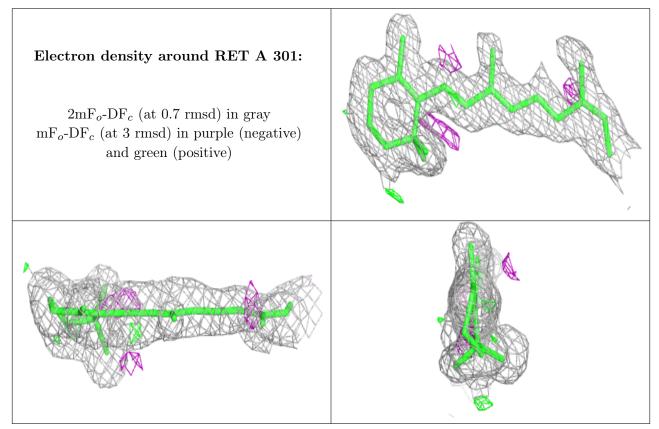
#### 6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

#### 6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

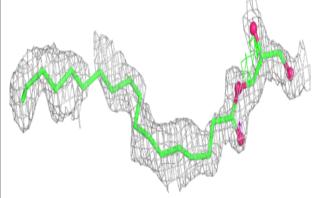
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

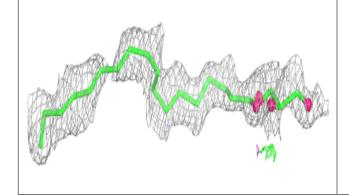


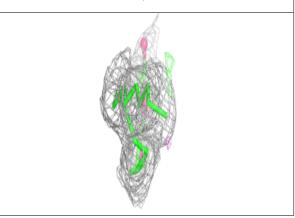


#### Electron density around OLC A 304:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 0.7 rmsd) in gray  $\mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)

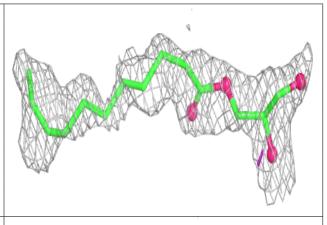


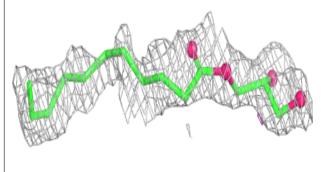


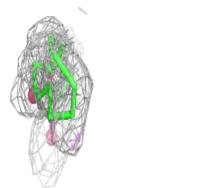


#### Electron density around OLC A 305:

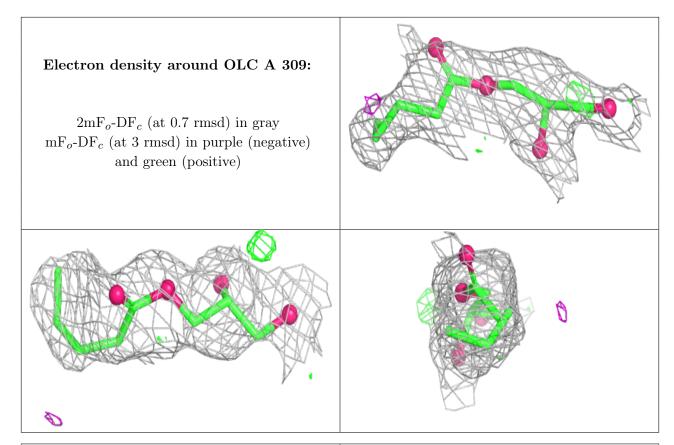
 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 0.7 rmsd) in gray  $\mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)





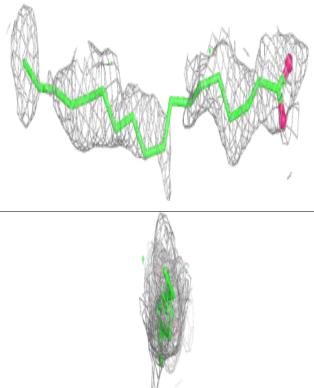


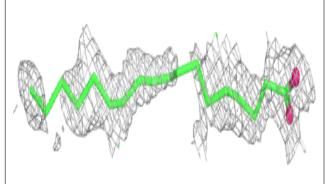




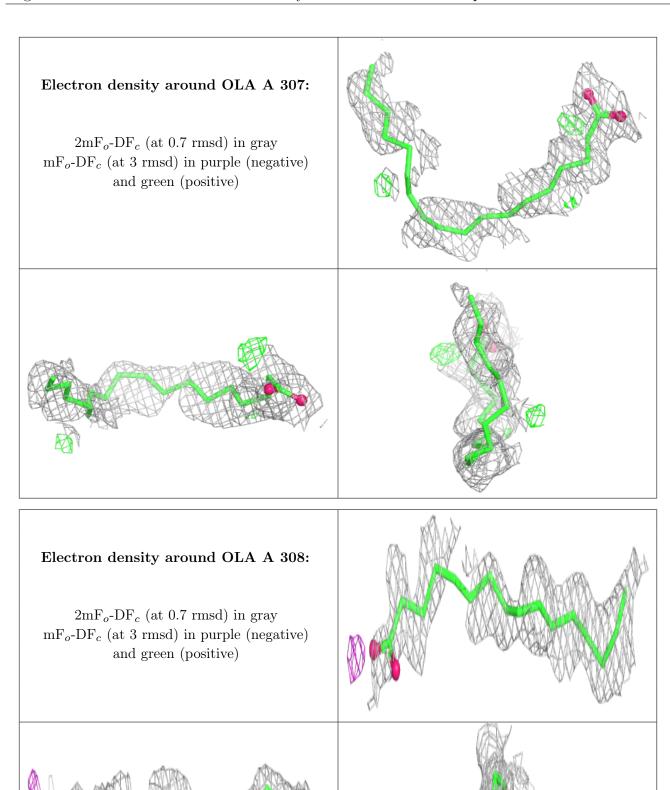
## Electron density around OLA A 306:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$  (at 0.7 rmsd) in gray  ${\rm mF}_o\text{-}{\rm DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)



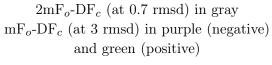


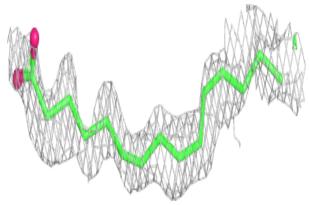


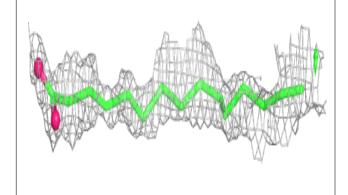


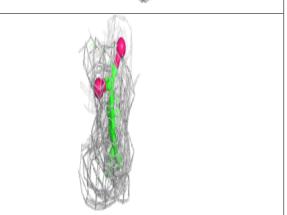


# Electron density around OLA A 310:



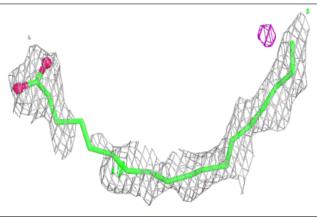


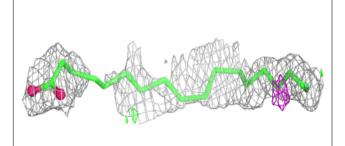


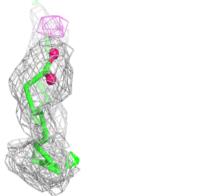


#### Electron density around OLA A 311:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 0.7 rmsd) in gray  $\mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)









## 6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

