



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 04:57 am BST

PDB ID : 6TPN  
Title : Crystal structure of the Orexin-2 receptor in complex with HTL6641 at 2.61 Å resolution  
Authors : Rappas, M.; Ali, A.; Bennett, K.A.; Brown, J.D.; Bucknell, S.J.; Congreve, M.; Cooke, R.M.; Cseke, G.; de Graaf, C.; Dore, A.S.; Errey, J.C.; Jazayeri, A.; Marshall, F.H.; Mason, J.S.; Mould, R.; Patel, J.C.; Tehan, B.G.; Weir, M.; Christopher, J.A.  
Deposited on : 2019-12-13  
Resolution : 2.61 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

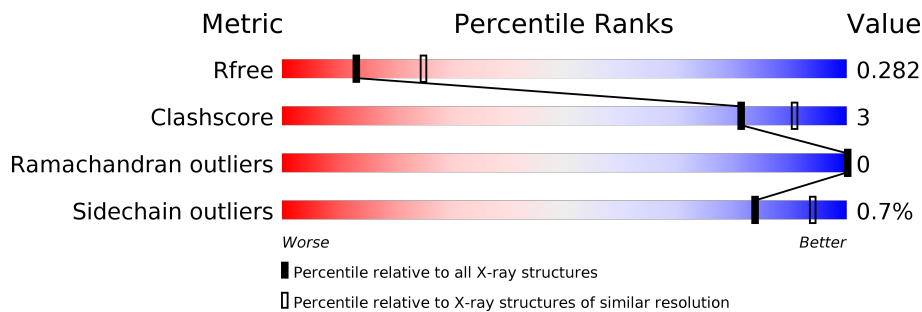
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.61 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	564	 84% 7% 10%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4269 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 Orexin receptor type 2, GlgA glycogen synthase, Orexin receptor type 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	510	4100	2691	677	702	30	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

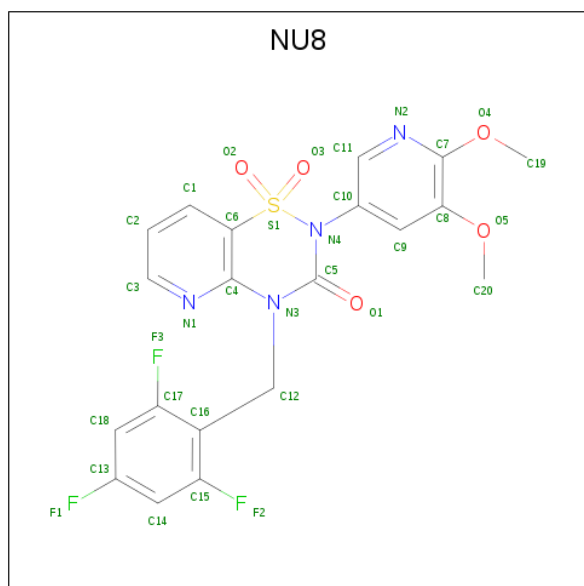
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLN	-	expression tag	UNP O43614
A	-9	ASP	-	expression tag	UNP O43614
A	-8	LEU	-	expression tag	UNP O43614
A	-7	ASP	-	expression tag	UNP O43614
A	-6	TYR	-	expression tag	UNP O43614
A	-5	LYS	-	expression tag	UNP O43614
A	-4	ASP	-	expression tag	UNP O43614
A	-3	ASP	-	expression tag	UNP O43614
A	-2	ASP	-	expression tag	UNP O43614
A	-1	ASP	-	expression tag	UNP O43614
A	0	LYS	-	expression tag	UNP O43614
A	14	ASP	ASN	engineered mutation	UNP O43614
A	22	ASP	ASN	engineered mutation	UNP O43614
A	28	LEU	PHE	engineered mutation	UNP O43614
A	30	ASP	ASN	engineered mutation	UNP O43614
A	54	ALA	GLU	engineered mutation	UNP O43614
A	91	LEU	TYR	engineered mutation	UNP O43614
A	100	ALA	ASP	engineered mutation	UNP O43614
A	142	ALA	VAL	engineered mutation	UNP O43614
A	170	LEU	ARG	engineered mutation	UNP O43614
A	202	ASP	ASN	engineered mutation	UNP O43614
A	206	ALA	LEU	engineered mutation	UNP O43614
A	219	ALA	TYR	engineered mutation	UNP O43614
A	233	ALA	MET	engineered mutation	UNP O43614
A	242	LEU	ALA	engineered mutation	UNP O43614
A	308	VAL	ILE	engineered mutation	UNP O43614

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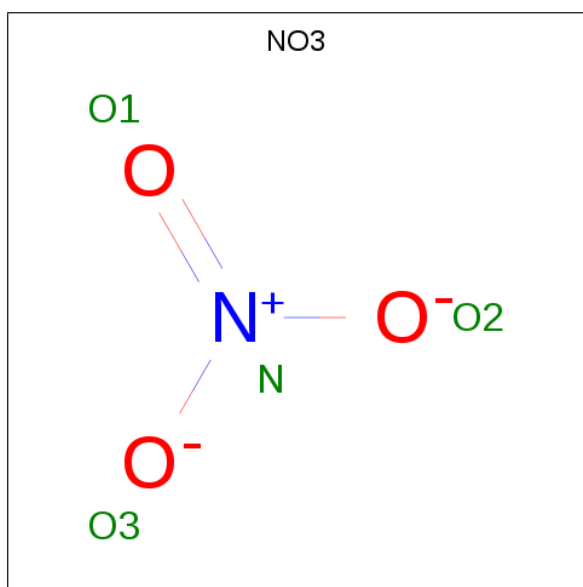
Chain	Residue	Modelled	Actual	Comment	Reference
A	310	VAL	LEU	engineered mutation	UNP O43614
A	318	ALA	LEU	engineered mutation	UNP O43614
A	347	ALA	THR	engineered mutation	UNP O43614
A	381	TRP	CYS	engineered mutation	UNP O43614
A	382	TRP	CYS	engineered mutation	UNP O43614
A	383	TRP	CYS	engineered mutation	UNP O43614
A	389	HIS	-	expression tag	UNP O43614
A	390	HIS	-	expression tag	UNP O43614
A	391	HIS	-	expression tag	UNP O43614
A	392	HIS	-	expression tag	UNP O43614
A	393	HIS	-	expression tag	UNP O43614
A	394	HIS	-	expression tag	UNP O43614
A	395	HIS	-	expression tag	UNP O43614
A	396	HIS	-	expression tag	UNP O43614

- Molecule 2 is 2-(5,6-dimethoxypyridin-3-yl)-1,1-bis(oxidanylidene)-4-[[2,4,6-tris(fluoro)phenyl)methyl]pyrido[2,3-e][1,2,4]thiadiazin-3-one (three-letter code: NU8) (formula: C<sub>20</sub>H<sub>15</sub>F<sub>3</sub>N<sub>4</sub>O<sub>5</sub>S) (labeled as "Ligand of Interest" by author).



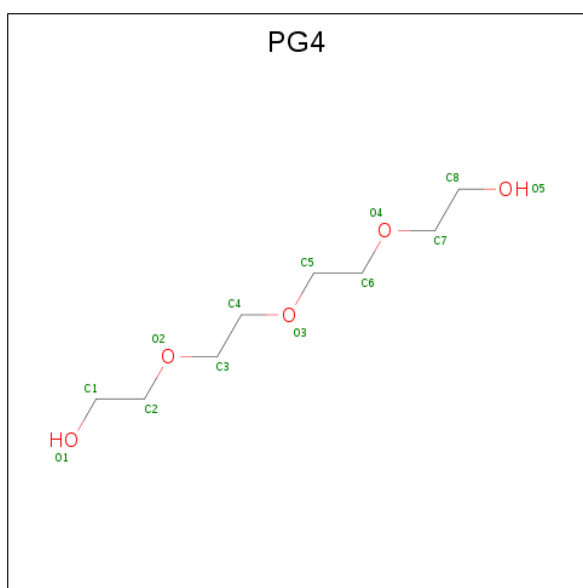
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
2	A	1	33	20	3	4	5	1	0	0

- Molecule 3 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>).



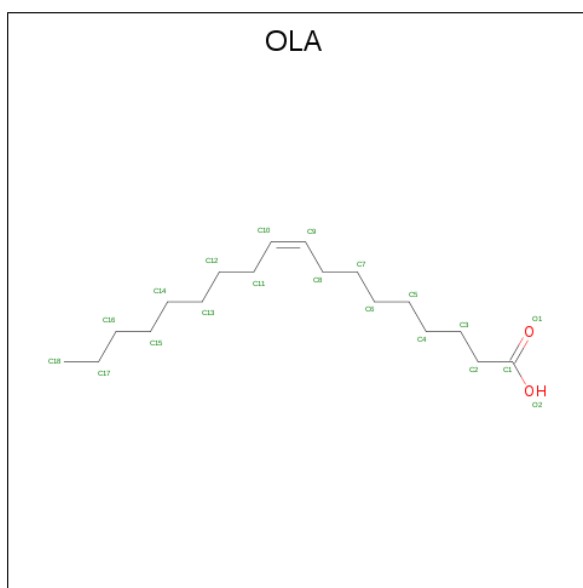
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	N	O	0	0
			4	1	3		
3	A	1	Total	N	O	0	0
			4	1	3		

- Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is OLEIC ACID (three-letter code: OLA) (formula:  $C_{18}H_{34}O_2$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	C O	0	0
			13	11 2		
5	A	1	Total	C O	0	0
			10	8 2		
5	A	1	Total	C O	0	0
			20	18 2		
5	A	1	Total	C O	0	0
			13	11 2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	46	Total	O	0	0
			46	46		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.94Å 173.95Å 78.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.48 – 2.61 48.89 – 1.99	Depositor EDS
% Data completeness (in resolution range)	60.5 (41.48-2.61) 52.0 (48.89-1.99)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	-0.04 (at 1.98Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, $R_{free}$	0.214 , 0.251 0.252 , 0.282	Depositor DCC
$R_{free}$ test set	2145 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	8.6	Xtrriage
Anisotropy	0.488	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.24 , -34.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.75	EDS
Total number of atoms	4269	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.42% 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: OLA, PG4, YCM, NU8, NO3

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	0.30	0/4192	0.44	1/5681 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1074	LYS	CB-CA-C	5.50	121.41	110.40

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	4100	0	4176	22	0
2	A	33	0	0	1	0
3	A	8	0	0	0	0
4	A	26	0	36	0	0
5	A	56	0	77	0	0
6	A	46	0	0	2	0
All	All	4269	0	4289	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 3.

The worst 5 of 22 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:1078:GLU:HG3	6:A:1320:HOH:O	1.85	0.76
1:A:380:SER:CB	1:A:387:HIS:ND1	2.70	0.55
1:A:380:SER:HB2	1:A:387:HIS:ND1	2.22	0.55
1:A:134:GLN:O	1:A:134:GLN:HG2	2.07	0.53
1:A:346:PHE:O	1:A:350:HIS:HD2	1.91	0.52

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	505/564 (90%)	491 (97%)	14 (3%)	0	<a href="#">100</a> <a href="#">100</a>

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	441/491 (90%)	438 (99%)	3 (1%)	<a href="#">84</a> <a href="#">94</a>

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

Mol	Chain	Res	Type
1	A	36	ASP
1	A	56	VAL
1	A	254	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1008	ASN
1	A	324	ASN
1	A	350	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
1	YCM	A	1004	1	7,9,10	1.10	0	4,10,12	0.45	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
1	YCM	A	1004	1	-	0/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

9 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
3	NO3	A	1202	-	1,3,3	0.70	0	0,3,3	0.00	-
4	PG4	A	1204	-	12,12,12	0.45	0	11,11,11	0.36	0
3	NO3	A	1203	-	1,3,3	0.52	0	0,3,3	0.00	-
2	NU8	A	1201	-	33,36,36	1.54	5 (15%)	42,54,54	2.74	17 (40%)
5	OLA	A	1206	-	9,12,19	0.31	0	8,12,19	0.72	0
5	OLA	A	1208	-	16,19,19	0.23	0	15,19,19	0.60	0
5	OLA	A	1207	-	6,9,19	0.24	0	5,9,19	0.59	0
5	OLA	A	1209	-	9,12,19	0.30	0	8,12,19	0.76	0
4	PG4	A	1205	-	12,12,12	0.45	0	11,11,11	0.32	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
4	PG4	A	1204	-	-	3/10/10/10	-
2	NU8	A	1201	-	-	1/12/36/36	0/3/4/4
5	OLA	A	1206	-	-	6/8/10/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	OLA	A	1208	-	-	8/15/17/17	-
5	OLA	A	1207	-	-	3/5/7/17	-
5	OLA	A	1209	-	-	4/8/10/17	-
4	PG4	A	1205	-	-	0/10/10/10	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	NU8	C10-N4	-4.86	1.39	1.45
2	A	1201	NU8	C5-N3	-3.25	1.33	1.37
2	A	1201	NU8	O4-C7	2.83	1.39	1.35
2	A	1201	NU8	C7-N2	2.56	1.37	1.32
2	A	1201	NU8	C6-S1	-2.19	1.72	1.75

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	NU8	C19-O4-C7	7.64	124.78	117.21
2	A	1201	NU8	C14-C15-C16	-7.36	119.42	124.59
2	A	1201	NU8	O3-S1-N4	-5.69	102.69	107.89
2	A	1201	NU8	O4-C7-N2	-5.05	114.47	120.35
2	A	1201	NU8	O4-C7-C8	4.19	124.21	116.93

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1209	OLA	C1-C2-C3-C4
2	A	1201	NU8	C16-C12-N3-C5
5	A	1206	OLA	C2-C3-C4-C5
5	A	1207	OLA	C4-C5-C6-C7
5	A	1208	OLA	C3-C4-C5-C6

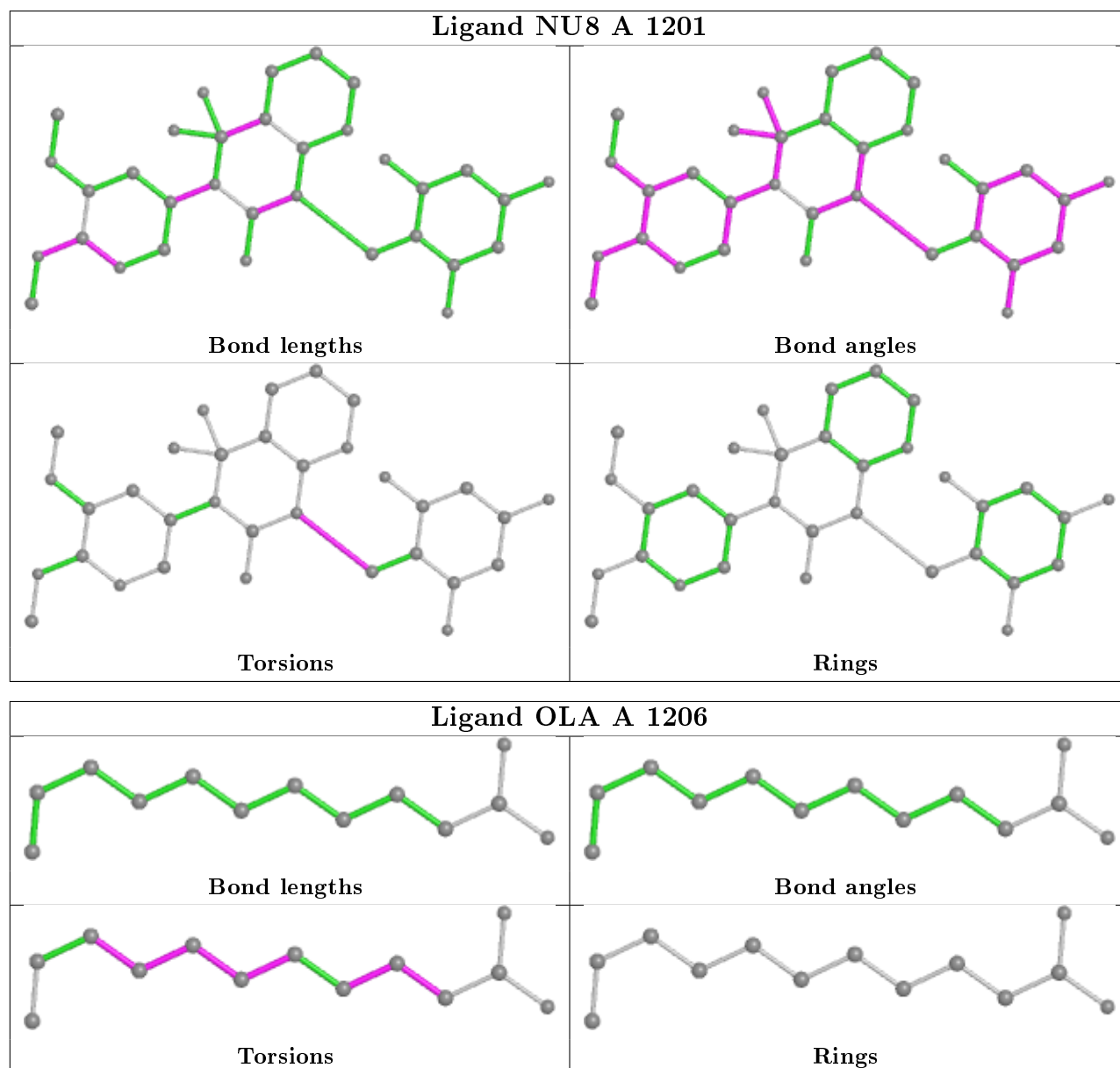
There are no ring outliers.

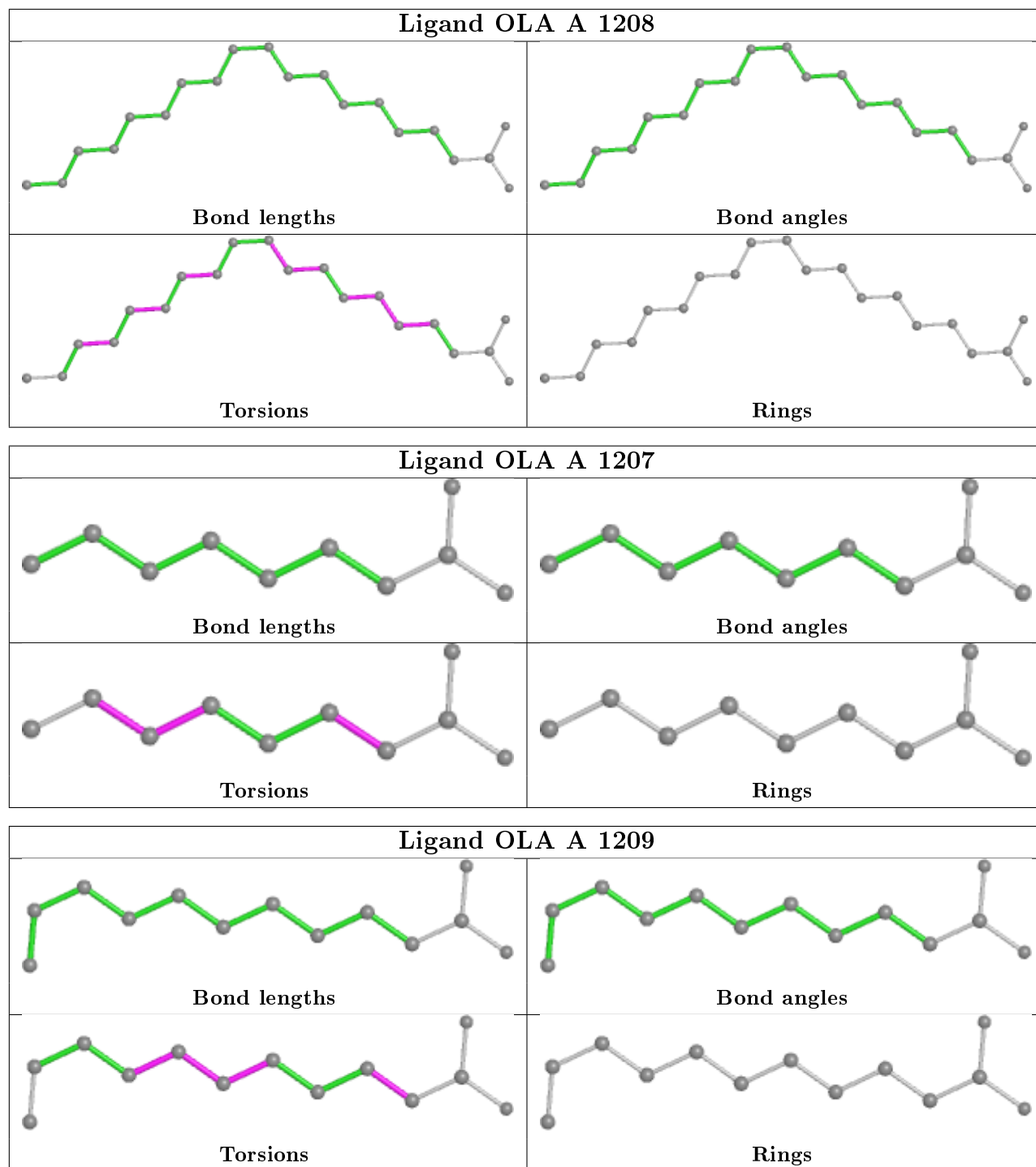
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	NU8	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 [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.

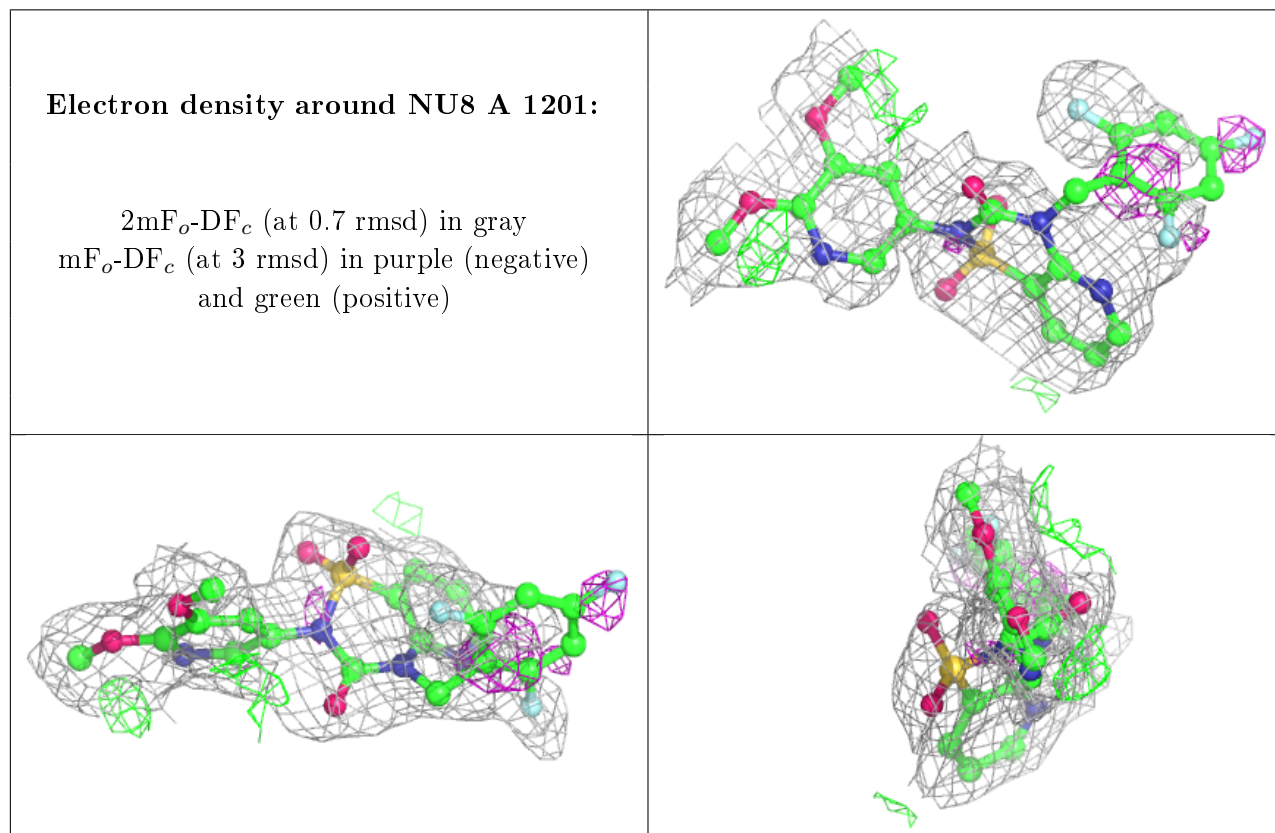
### 6.3 Carbohydrates [i](#)

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.

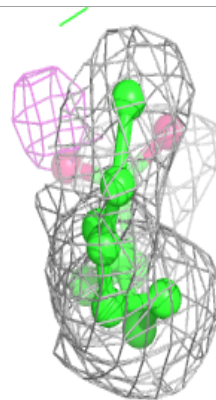
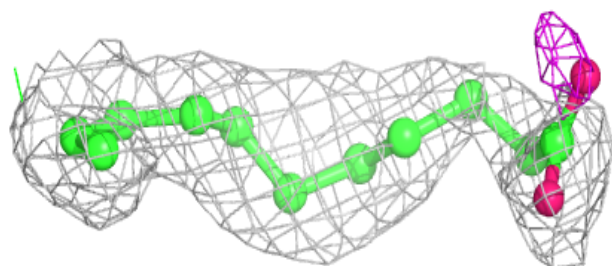
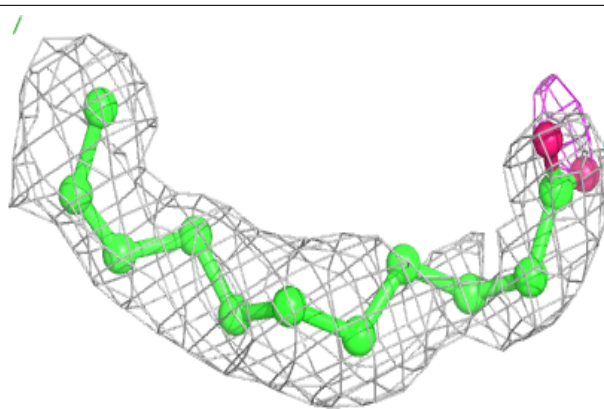
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



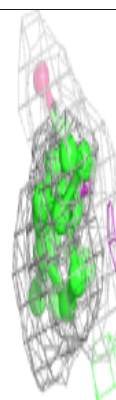
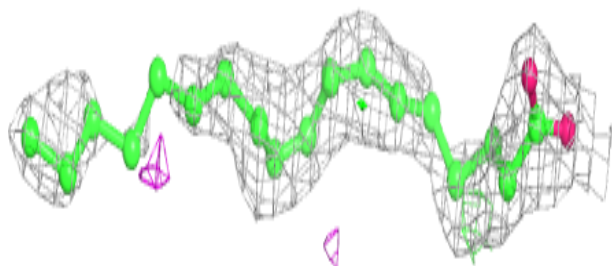
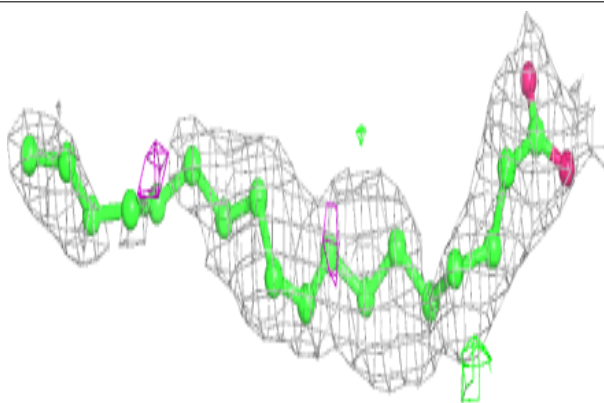


**Electron density around OLA A 1206:**

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

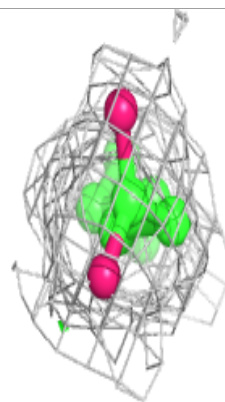
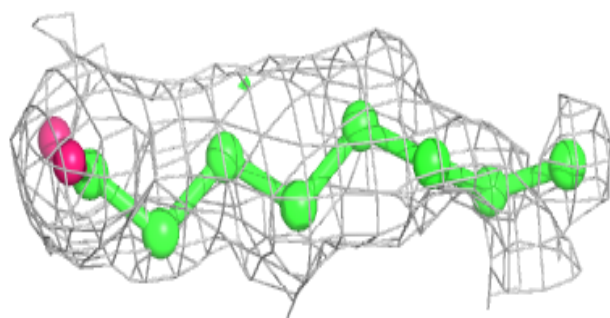
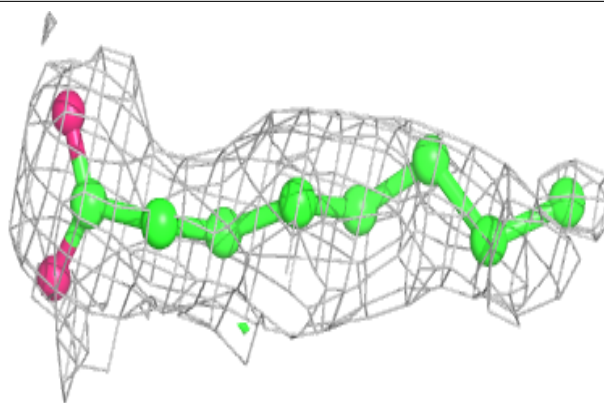
**Electron density around OLA A 1208:**

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

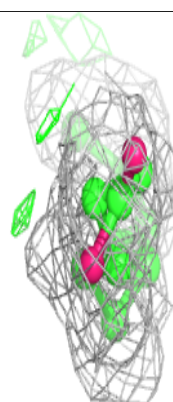
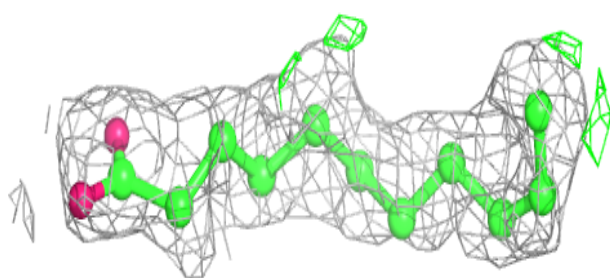
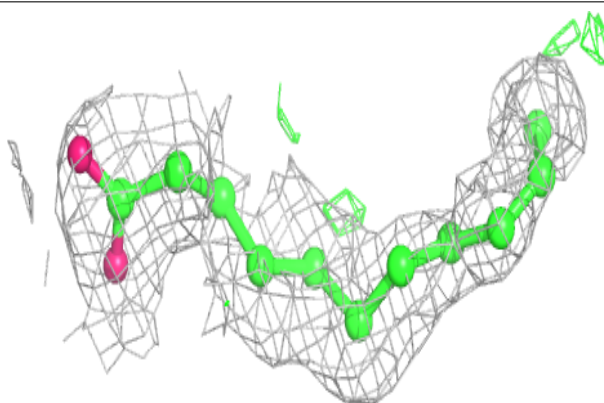


**Electron density around OLA A 1207:**

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

**Electron density around OLA A 1209:**

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



## 6.5 Other polymers

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