



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 22, 2024 – 09:46 pm GMT

PDB ID : 8C9W  
Title : Crystal structure of the adenosine A2A receptor (construct A2A-PSB2-bRIL) complexed with Etrumadenant at the orthosteric pocket  
Authors : Strater, N.; Claff, T.; Schlegel, J.G.; Voss, J.H.; Vaassen, V.; Muller, C.E.  
Deposited on : 2023-01-23  
Resolution : 2.11 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
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)	:	2.36

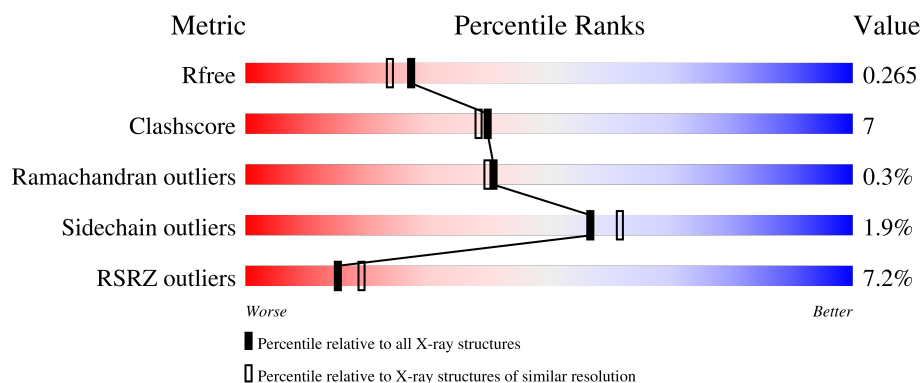
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.11 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	431	<div> <div>6%</div> <div> <div></div> <div>78%</div> <div>11%</div> <div>10%</div> </div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6633 atoms, of which 3259 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 Adenosine receptor A2a,Soluble cytochrome b562.

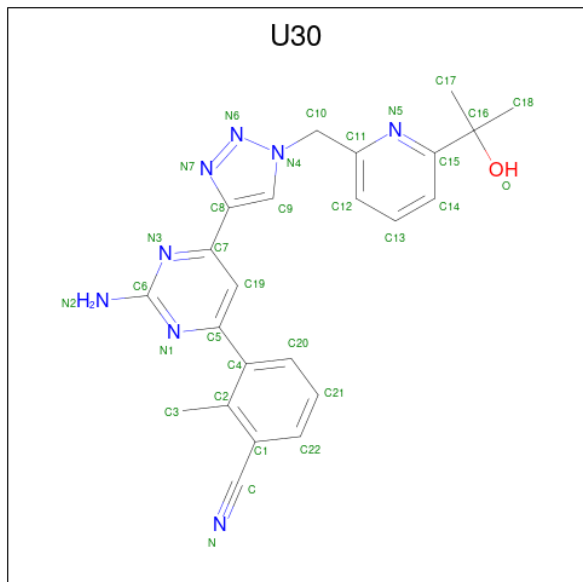
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	387	Total	C	H	N	O	S	0	14	0
			6157	2001	3099	516	519	22			

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP P29274
A	-7	TYR	-	expression tag	UNP P29274
A	-6	LYS	-	expression tag	UNP P29274
A	-5	ASP	-	expression tag	UNP P29274
A	-4	ASP	-	expression tag	UNP P29274
A	-3	ASP	-	expression tag	UNP P29274
A	-2	ASP	-	expression tag	UNP P29274
A	-1	GLY	-	expression tag	UNP P29274
A	0	ALA	-	expression tag	UNP P29274
A	1	PRO	-	expression tag	UNP P29274
A	91	LYS	SER	conflict	UNP P29274
A	154	ALA	ASN	conflict	UNP P29274
A	1007	TRP	MET	conflict	UNP P0ABE7
A	1102	ILE	HIS	conflict	UNP P0ABE7
A	1106	LEU	ARG	conflict	UNP P0ABE7
A	317	HIS	-	expression tag	UNP P29274
A	318	HIS	-	expression tag	UNP P29274
A	319	HIS	-	expression tag	UNP P29274
A	320	HIS	-	expression tag	UNP P29274
A	321	HIS	-	expression tag	UNP P29274
A	322	HIS	-	expression tag	UNP P29274
A	323	HIS	-	expression tag	UNP P29274
A	324	HIS	-	expression tag	UNP P29274
A	325	HIS	-	expression tag	UNP P29274
A	326	HIS	-	expression tag	UNP P29274

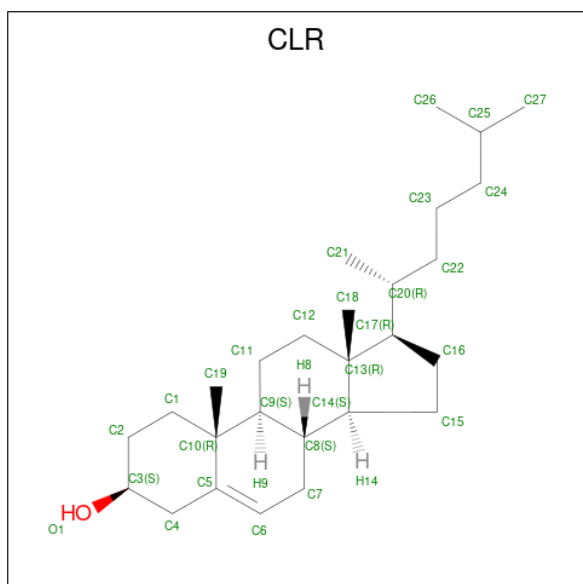
- Molecule 2 is 3-[2-azanyl-6-[1-[[6-(2-oxidanylpropan-2-yl)pyridin-2-yl]methyl]-1,2,3-tri

azol-4-yl]pyrimidin-4-yl]-2-methyl-benzenecarbonitrile (three-letter code: U30) (formula:  $C_{23}H_{22}N_8O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			54	23	22	8	1		

- Molecule 3 is CHOLESTEROL (three-letter code: CLR) (formula:  $C_{27}H_{46}O$ ).



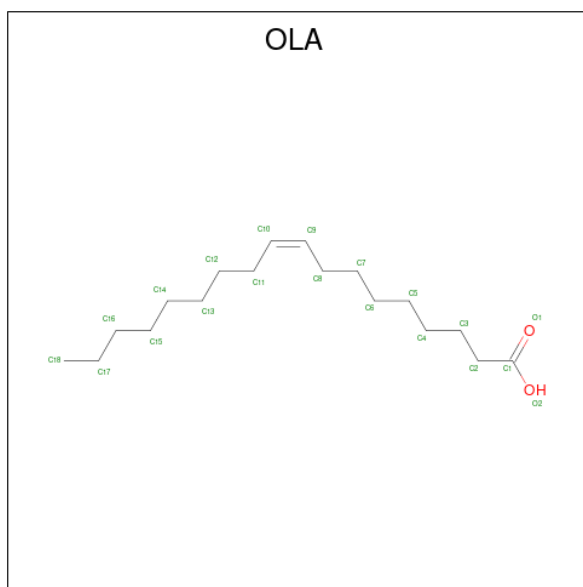
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			74	27	46	1		

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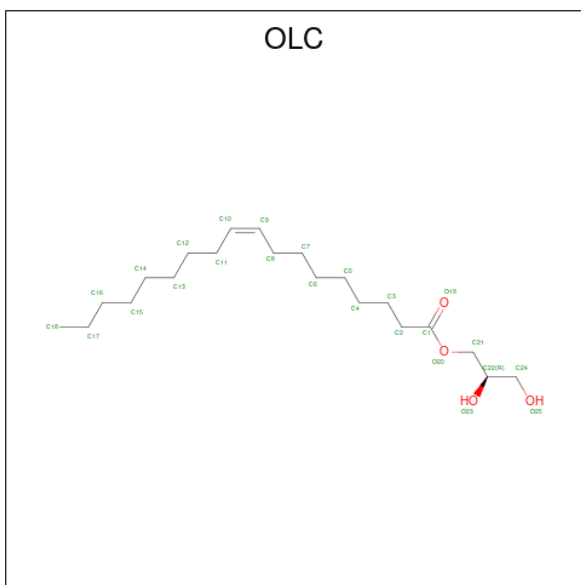
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			74	27	46	1		
3	A	1	Total	C	H	O	0	0
			74	27	46	1		

- Molecule 4 is OLEIC ACID (three-letter code: OLA) (formula:  $C_{18}H_{34}O_2$ ).



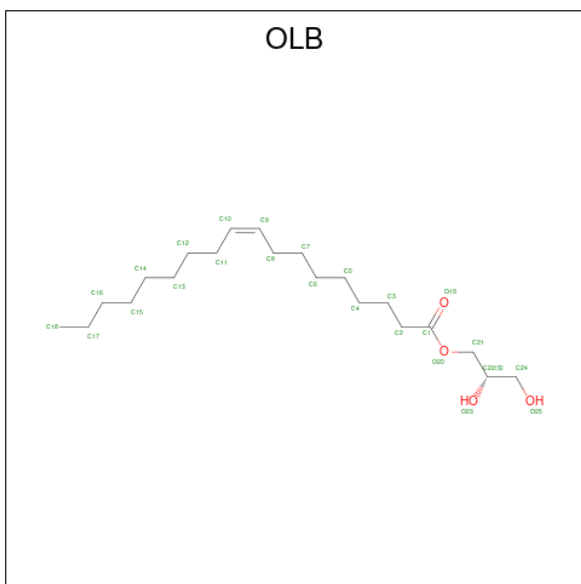
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			15	13	2		
4	A	1	Total	C	O	0	0
			17	15	2		
4	A	1	Total	C	O	0	0
			9	7	2		
4	A	1	Total	C	O	0	0
			20	18	2		
4	A	1	Total	C	O	0	0
			19	17	2		

- Molecule 5 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula:  $C_{21}H_{40}O_4$ ).



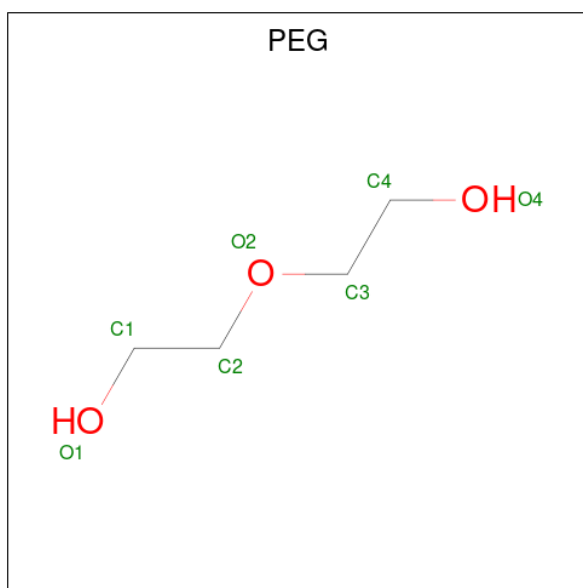
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			22	18	4		
5	A	1	Total	C	O	0	0
			16	12	4		

- Molecule 6 is (2S)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLB) (formula: C<sub>21</sub>H<sub>40</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			18	14	4		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			7	4	3		


- Molecule 8 is water.

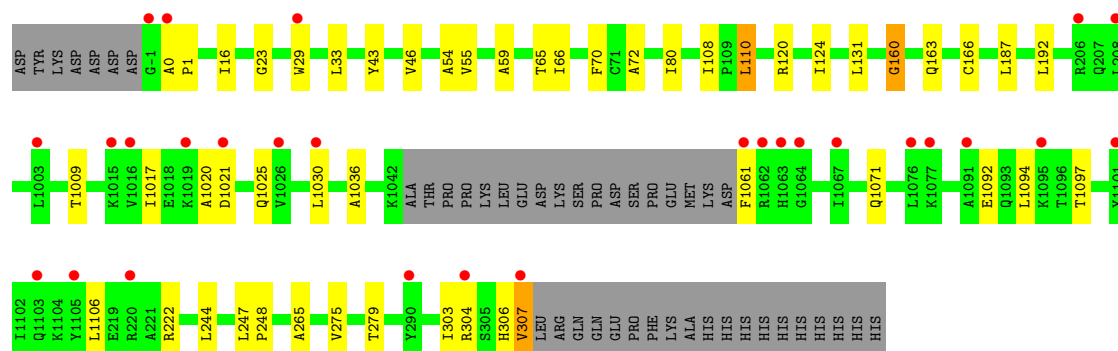
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	57	Total	O	0	0
			57	57		

### 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: Adenosine receptor A2a,Soluble cytochrome b562

Chain A: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.16Å 178.23Å 139.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.24 – 2.11 38.24 – 2.11	Depositor EDS
% Data completeness (in resolution range)	74.8 (38.24-2.11) 74.8 (38.24-2.11)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.31 (at 2.12Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, $R_{free}$	0.197 , 0.267 0.198 , 0.265	Depositor DCC
$R_{free}$ test set	994 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.1	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 65.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6633	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.49% 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: U30, PEG, OLB, CLR, OLC, OLA

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	0.61	0/3191	0.73	0/4341

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	3058	3099	3096	42	0
2	A	32	22	0	1	0
3	A	84	138	138	7	0
4	A	80	0	115	5	0
5	A	38	0	52	5	0
6	A	18	0	23	2	0
7	A	7	0	10	1	0
8	A	57	0	0	1	0
All	All	3374	3259	3434	50	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 7.

The worst 5 of 50 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:1106:LEU:HD11	1:A:222:ARG:HH21	1.40	0.85
4:A:1206:OLA:H142	5:A:1209:OLC:H13A	1.62	0.82
1:A:160:GLY:N	1:A:163:GLN:OE1	2.20	0.74
1:A:124:ILE:HD13	4:A:1207:OLA:H31	1.73	0.70
1:A:275[A]:VAL:HG12	4:A:1213:OLA:H162	1.76	0.68

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	397/431 (92%)	388 (98%)	8 (2%)	1 (0%)	41 40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	160	GLY

### 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	329/359 (92%)	323 (98%)	6 (2%)	59 63

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1092	GLU
1	A	306	HIS
1	A	307	VAL
1	A	1021	ASP
1	A	110	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

13 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	$\# Z  > 2$
6	OLB	A	1210	-	17,17,24	0.35	0	18,18,25	0.56	0
4	OLA	A	1207	-	8,8,19	0.64	0	8,8,19	1.63	3 (37%)
4	OLA	A	1208	-	19,19,19	0.86	1 (5%)	19,19,19	0.95	2 (10%)
4	OLA	A	1205	-	14,14,19	1.02	1 (7%)	14,14,19	0.96	2 (14%)
4	OLA	A	1206	-	16,16,19	0.87	1 (6%)	16,16,19	0.90	1 (6%)
3	CLR	A	1204	-	31,31,31	0.28	0	48,48,48	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	U30	A	1201	-	33,35,35	0.52	0	40,51,51	0.55	0
4	OLA	A	1213	-	18,18,19	0.80	1 (5%)	18,18,19	0.97	1 (5%)
5	OLC	A	1209	-	21,21,24	0.51	0	22,22,25	0.47	0
5	OLC	A	1211	-	15,15,24	0.33	0	16,16,25	0.57	0
3	CLR	A	1203	-	31,31,31	0.23	0	48,48,48	0.46	0
3	CLR	A	1202	-	31,31,31	0.23	0	48,48,48	0.58	0
7	PEG	A	1212	-	6,6,6	0.23	0	5,5,5	0.34	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
6	OLB	A	1210	-	-	6/17/17/24	-
4	OLA	A	1207	-	-	3/6/6/17	-
4	OLA	A	1208	-	-	7/17/17/17	-
4	OLA	A	1205	-	-	8/12/12/17	-
4	OLA	A	1206	-	-	8/14/14/17	-
3	CLR	A	1204	-	-	0/10/68/68	0/4/4/4
2	U30	A	1201	-	-	4/18/20/20	0/4/4/4
4	OLA	A	1213	-	-	8/16/16/17	-
5	OLC	A	1209	-	-	8/21/21/24	-
5	OLC	A	1211	-	-	4/15/15/24	-
3	CLR	A	1203	-	-	0/10/68/68	0/4/4/4
3	CLR	A	1202	-	-	0/10/68/68	0/4/4/4
7	PEG	A	1212	-	-	3/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1205	OLA	C10-C9	2.96	1.48	1.31
4	A	1208	OLA	C10-C9	2.78	1.47	1.31
4	A	1206	OLA	C10-C9	2.74	1.47	1.31
4	A	1213	OLA	C10-C9	2.62	1.47	1.31

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1207	OLA	O2-C1-C2	2.87	123.24	114.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1208	OLA	O2-C1-O1	-2.63	116.74	123.30
4	A	1207	OLA	O2-C1-O1	-2.62	116.76	123.30
4	A	1205	OLA	O2-C1-O1	-2.28	117.61	123.30
4	A	1208	OLA	O2-C1-C2	2.24	121.22	114.03

There are no chirality outliers.

5 of 59 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1201	U30	N3-C7-C8-C9
2	A	1201	U30	C19-C7-C8-C9
2	A	1201	U30	N5-C15-C16-C17
2	A	1201	U30	N5-C15-C16-O
5	A	1211	OLC	C21-C22-C24-O25

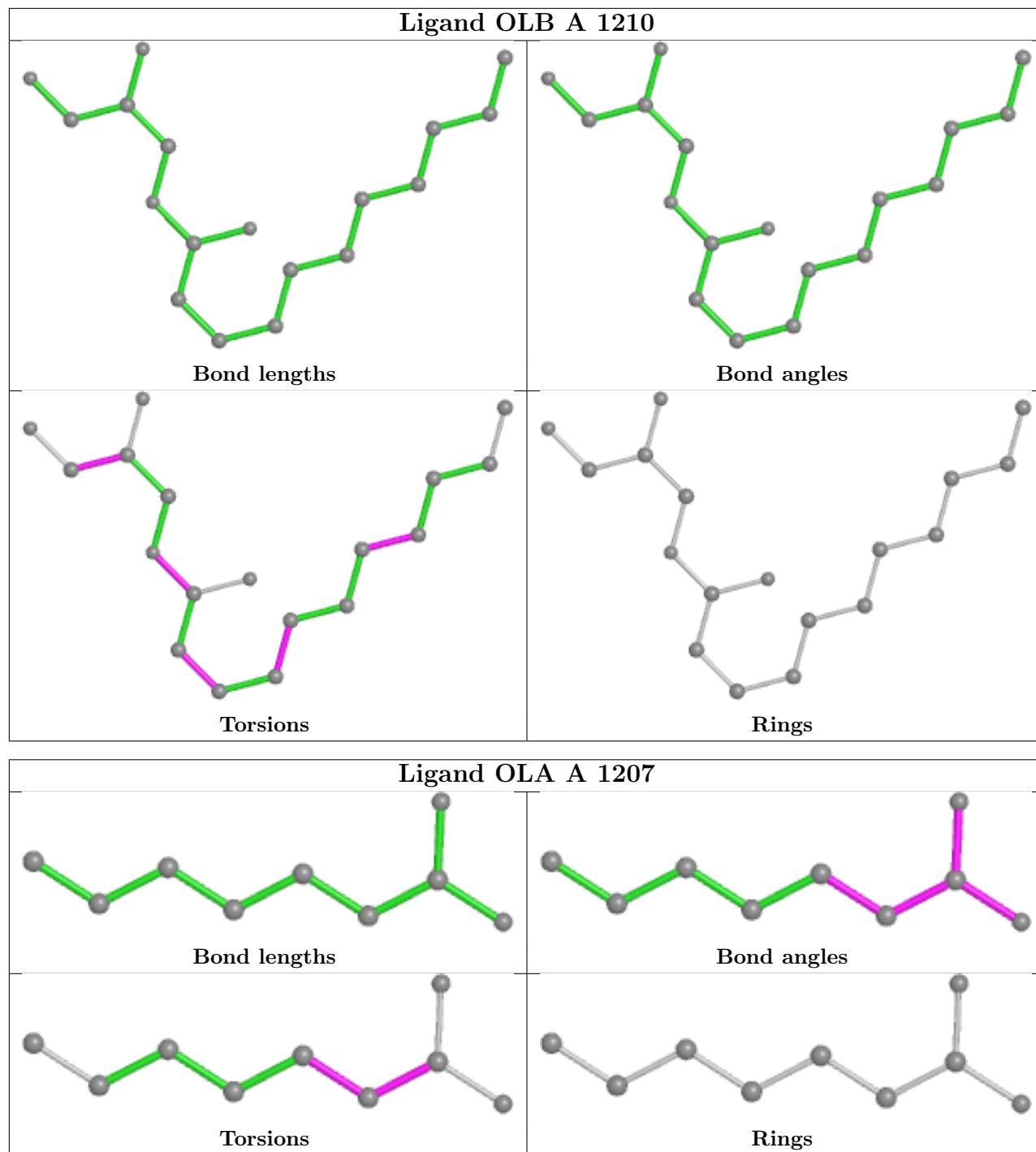
There are no ring outliers.

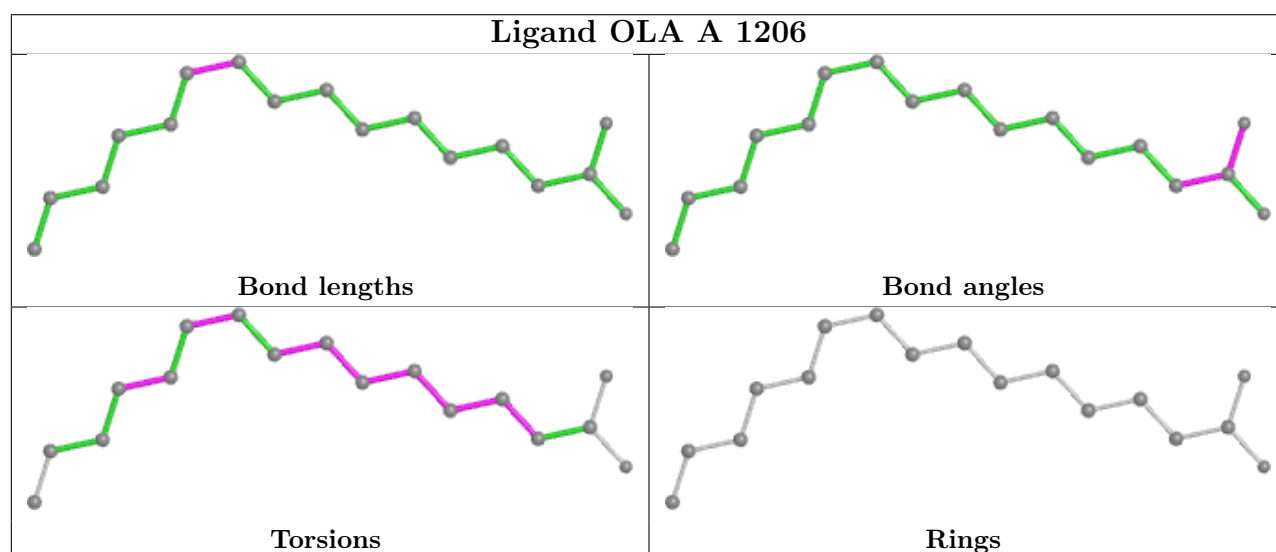
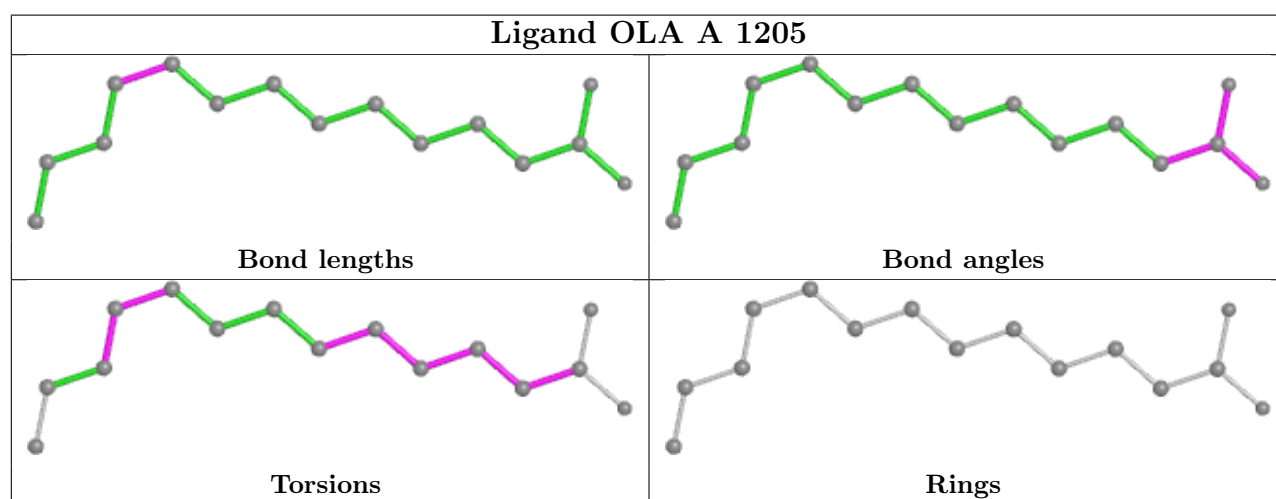
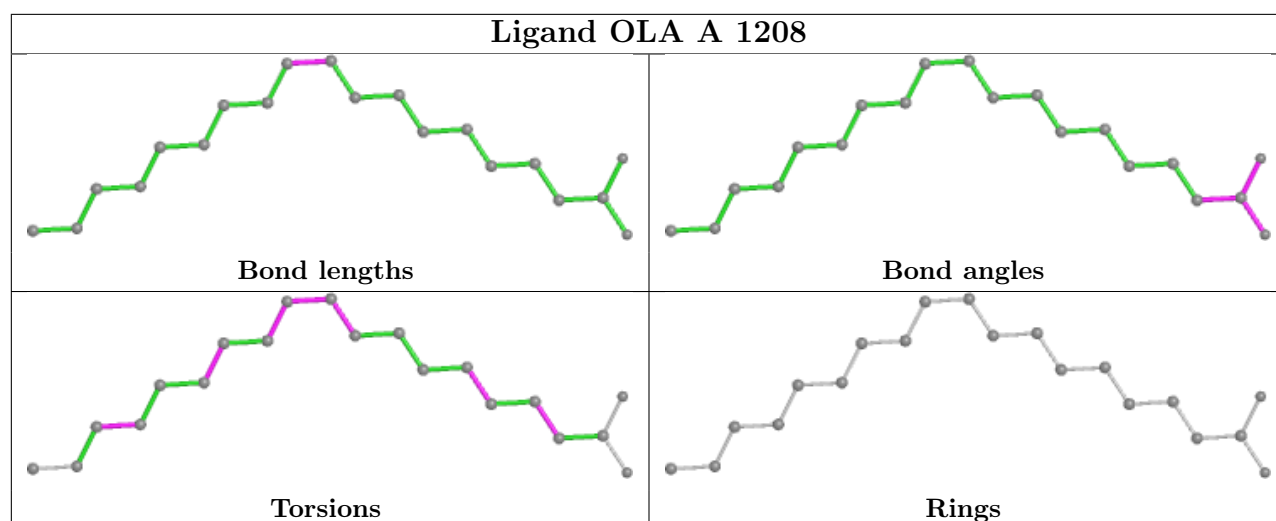
11 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1210	OLB	2	0
4	A	1207	OLA	1	0
4	A	1206	OLA	2	0
3	A	1204	CLR	4	0
2	A	1201	U30	1	0
4	A	1213	OLA	2	0
5	A	1209	OLC	2	0
5	A	1211	OLC	3	0
3	A	1203	CLR	2	0
3	A	1202	CLR	1	0
7	A	1212	PEG	1	0

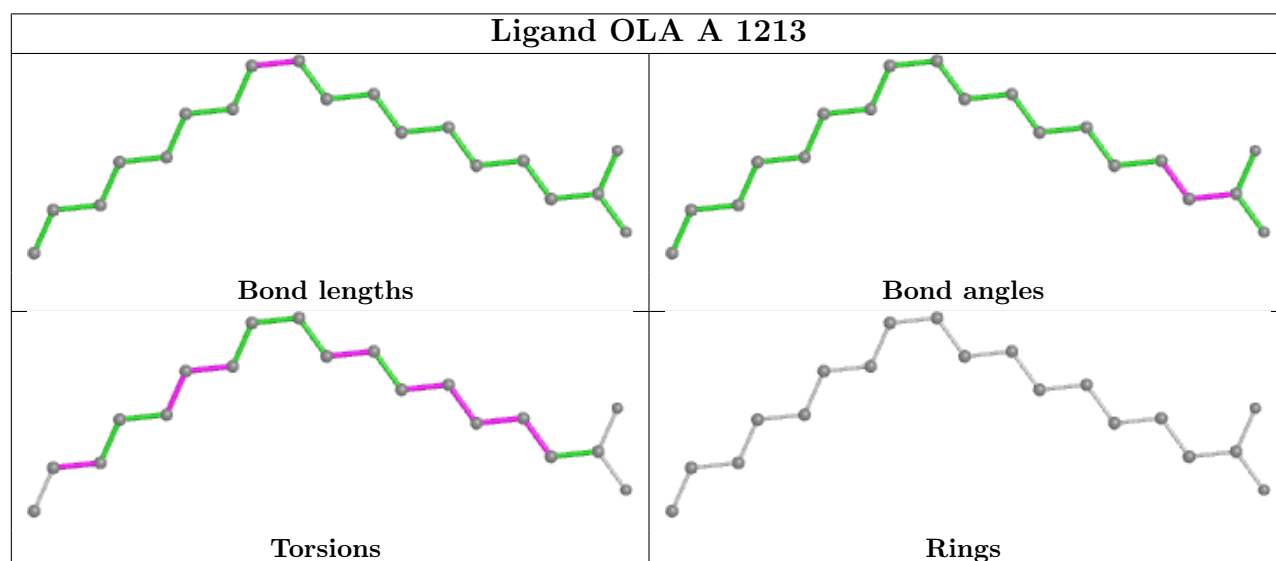
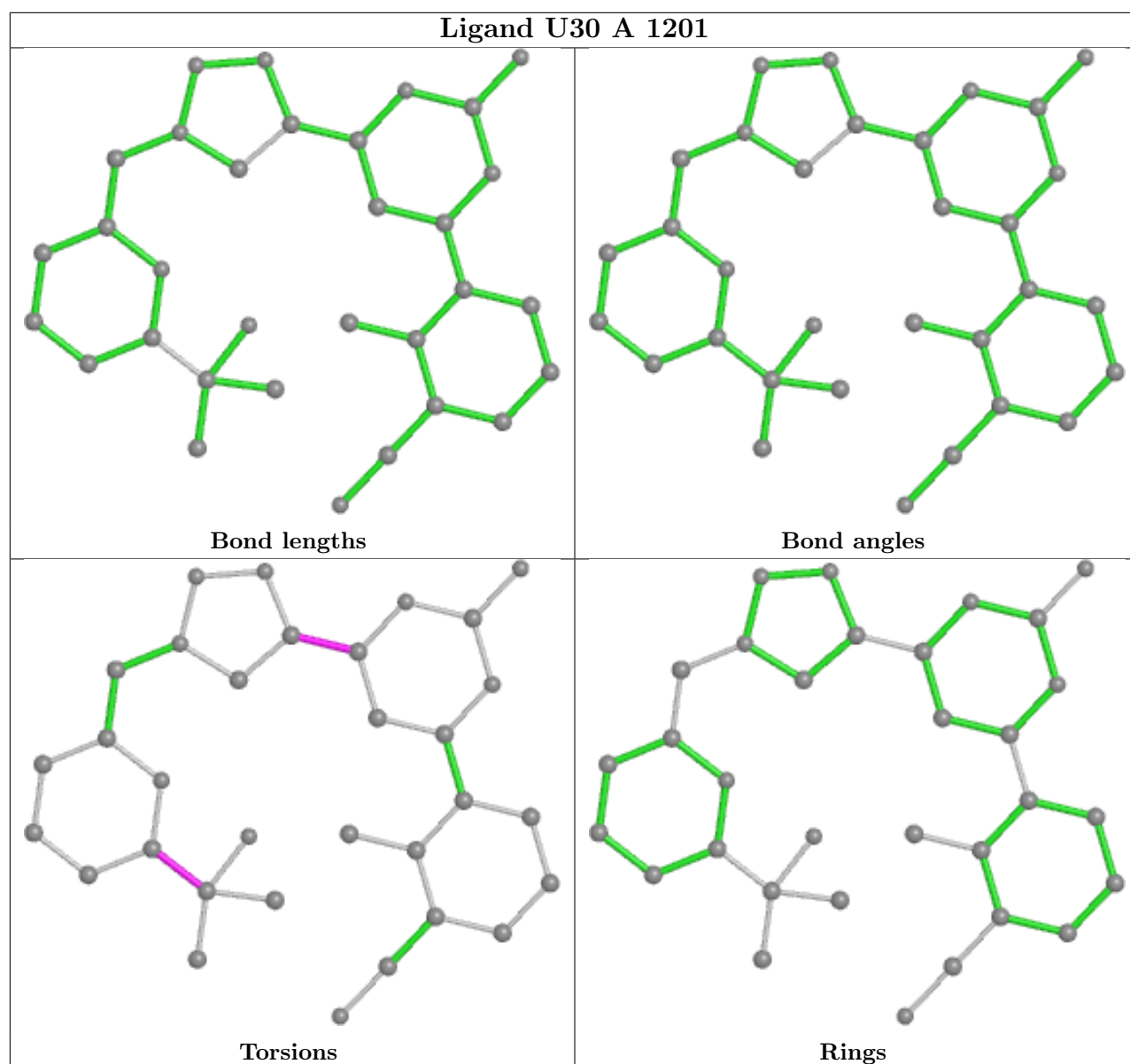
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

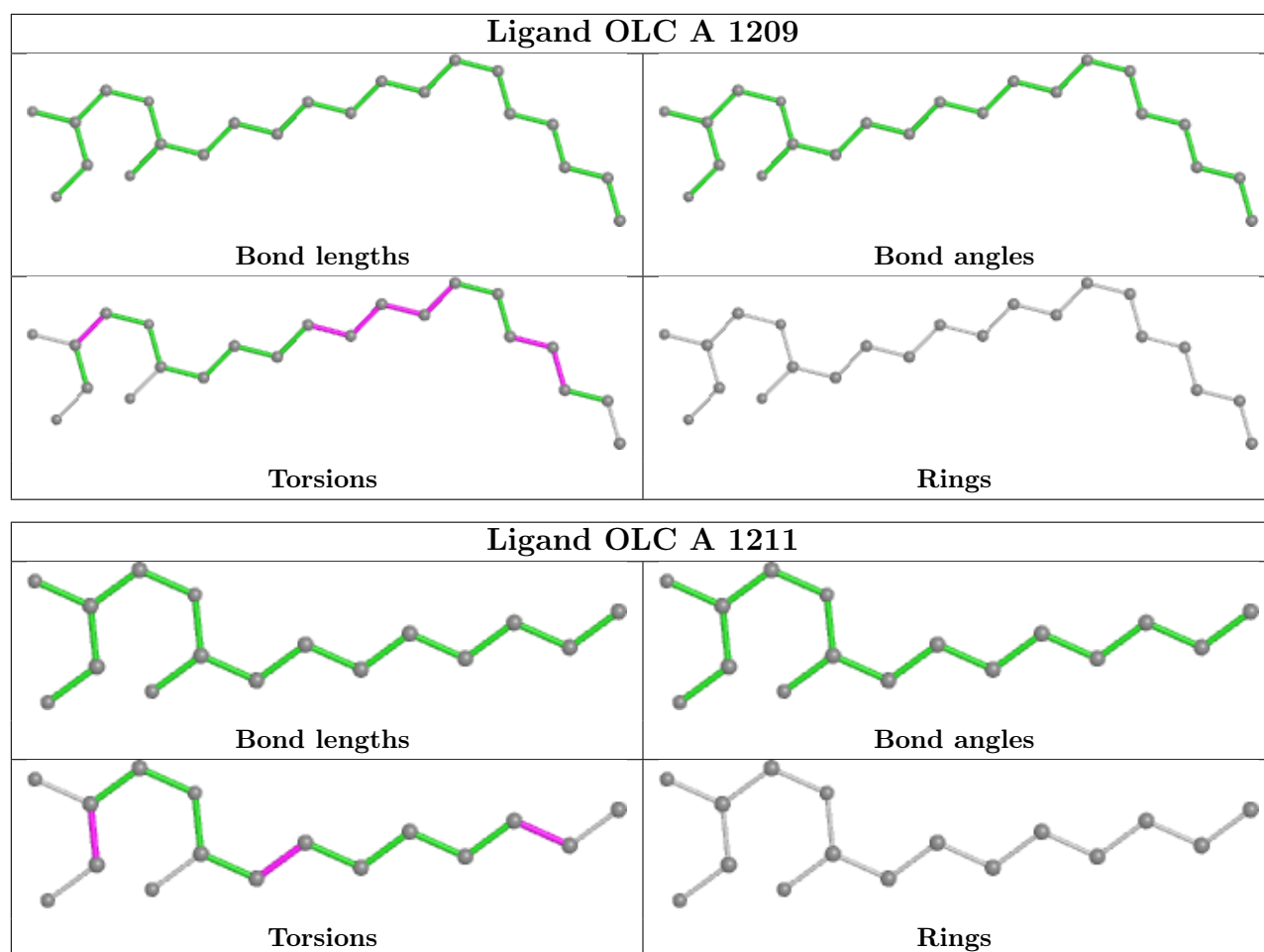
equivalents in the CSD to analyse the geometry.











## 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](#)

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	387/431 (89%)	0.39	28 (7%) 15 19	24, 40, 83, 136	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1061	PHE	7.6
1	A	1063	HIS	6.3
1	A	1062	ARG	4.6
1	A	1030	LEU	4.0
1	A	307	VAL	3.7

### 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 monosaccharides 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. 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.

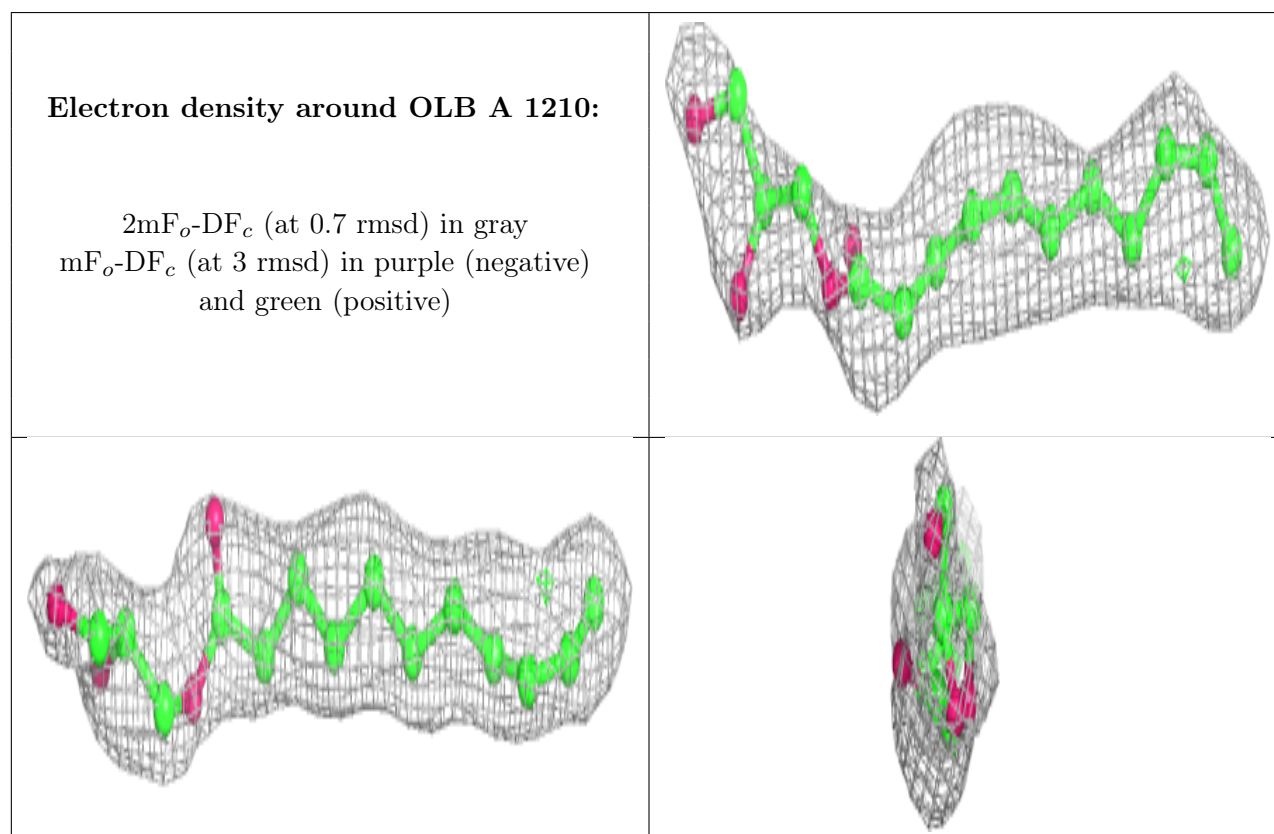
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	OLB	A	1210	18/25	0.79	0.20	37,55,76,81	0
4	OLA	A	1208	20/20	0.81	0.28	48,57,82,100	0

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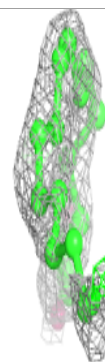
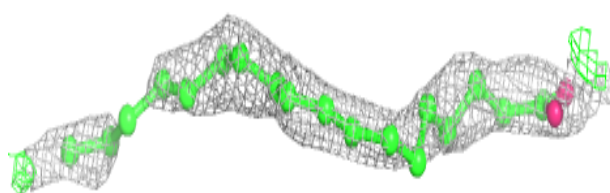
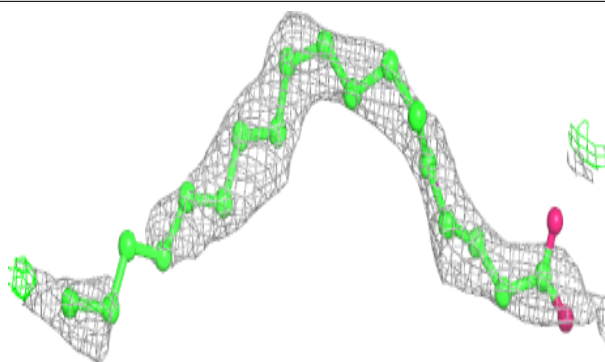
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	OLA	A	1213	19/20	0.84	0.19	33,48,69,70	0
7	PEG	A	1212	7/7	0.84	0.26	57,65,76,77	0
5	OLC	A	1209	22/25	0.86	0.20	38,54,69,77	0
4	OLA	A	1205	15/20	0.90	0.15	39,54,79,82	0
4	OLA	A	1207	9/20	0.92	0.21	43,52,58,59	0
5	OLC	A	1211	16/25	0.92	0.18	32,46,69,70	0
4	OLA	A	1206	17/20	0.93	0.16	29,46,73,75	0
3	CLR	A	1203	28/28	0.94	0.15	31,55,72,80	0
3	CLR	A	1202	28/28	0.95	0.14	24,43,67,81	0
3	CLR	A	1204	28/28	0.97	0.13	28,43,73,75	0
2	U30	A	1201	32/32	0.97	0.13	20,32,55,57	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.

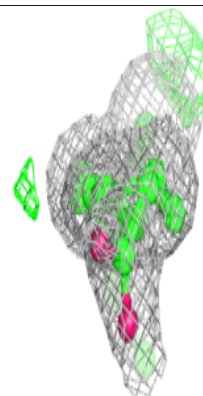
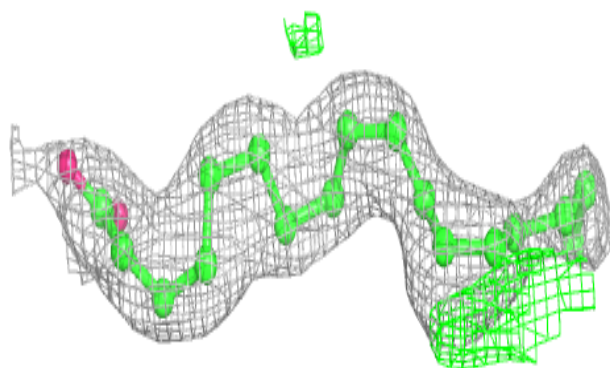
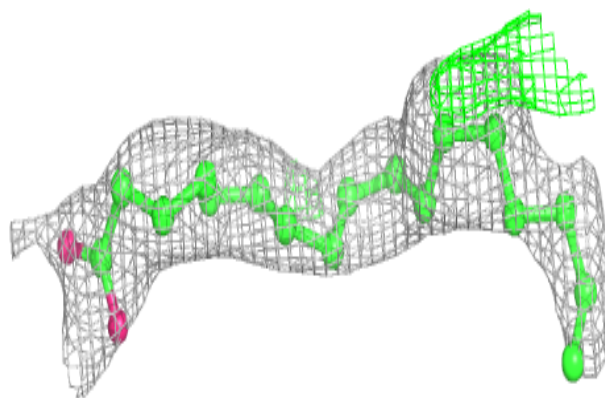


**Electron density around OLA A 1208:**

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

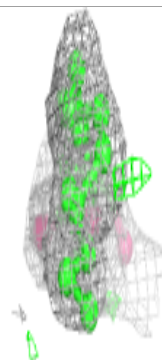
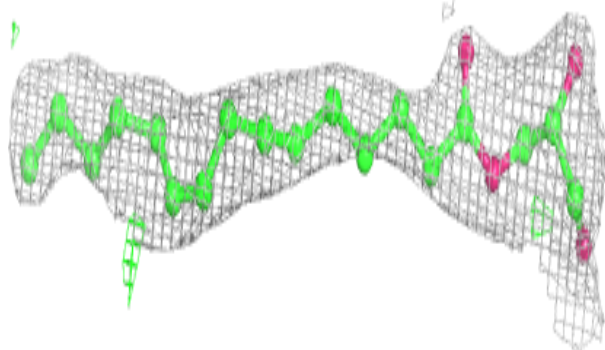
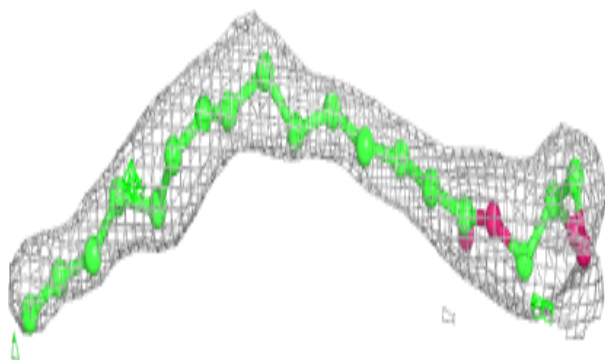
**Electron density around OLA A 1213:**

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

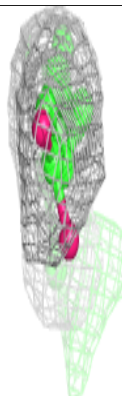
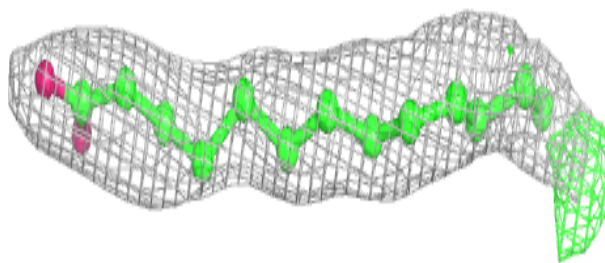
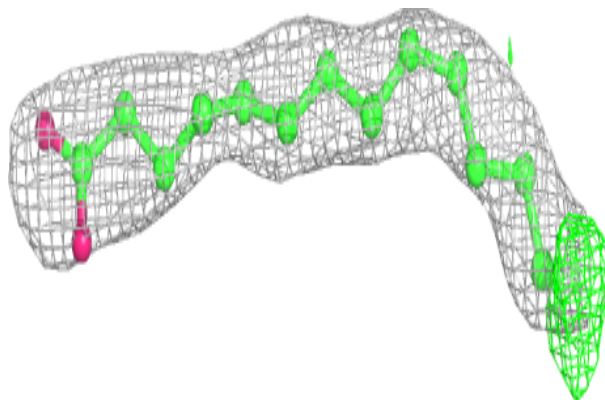


**Electron density around OLC A 1209:**

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

**Electron density around OLA A 1205:**

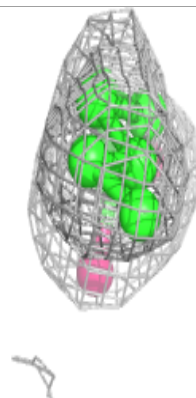
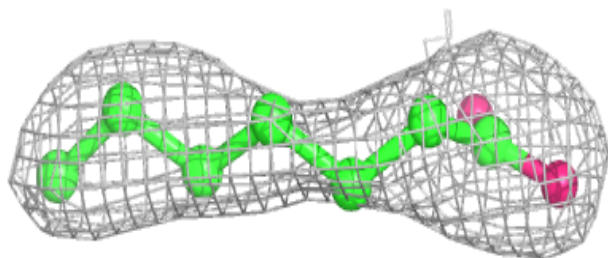
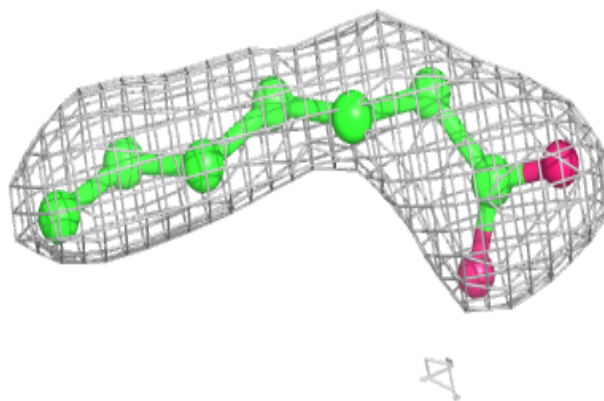
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



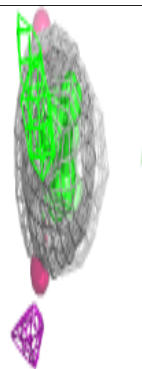
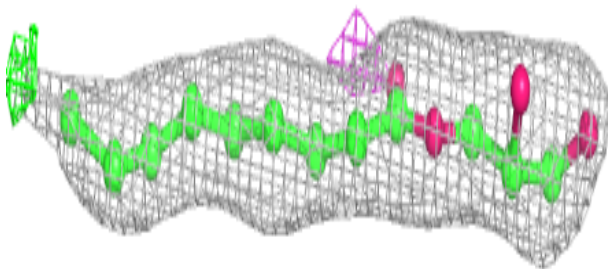
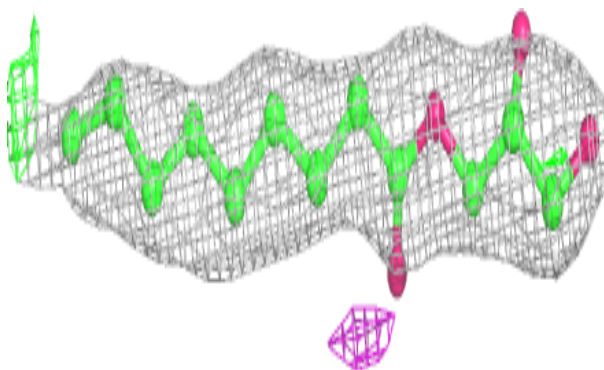


**Electron density around OLA A 1207:**

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

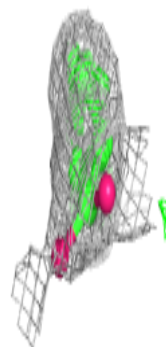
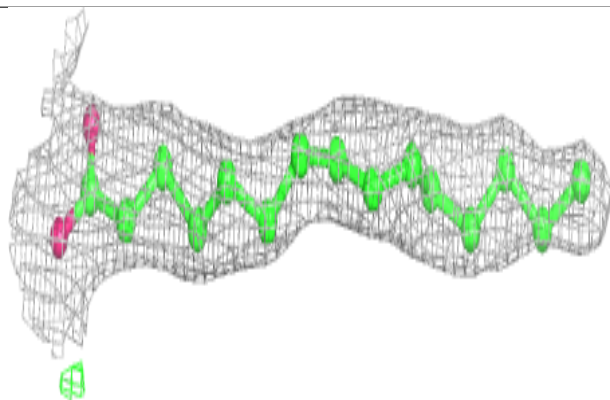
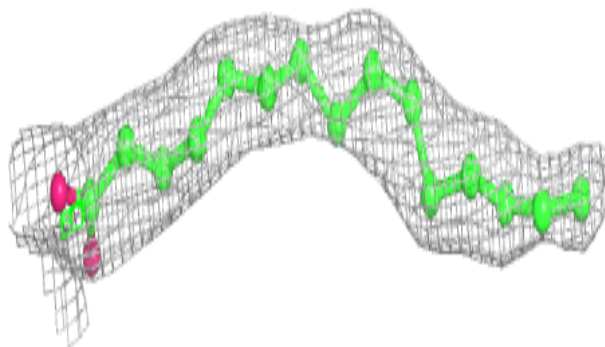
**Electron density around OLC A 1211:**

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

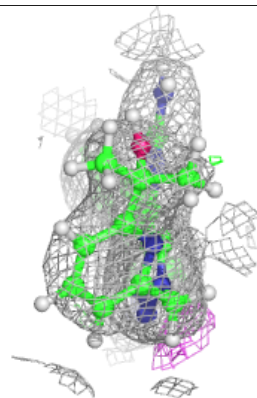
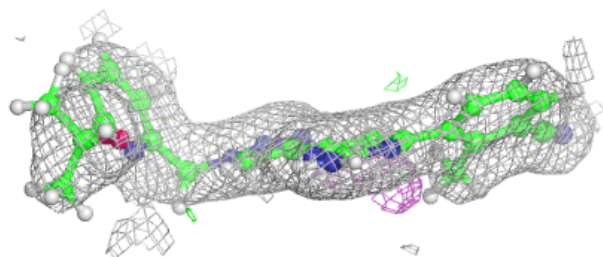
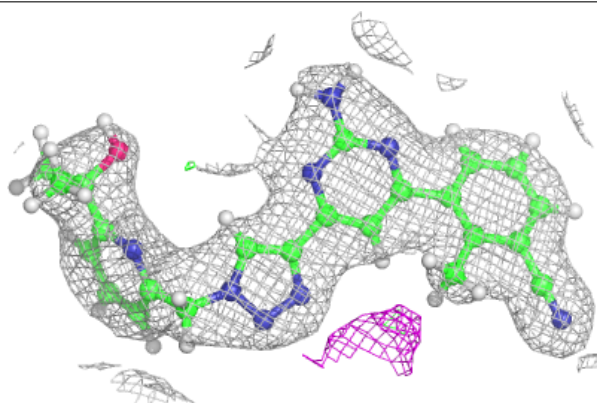


**Electron density around OLA A 1206:**

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

**Electron density around U30 A 1201:**

$2mF_o-DF_c$  (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.