



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 27, 2022 – 07:27 PM EDT

PDB ID : 6WGT  
Title : Crystal structure of HTR2A with hallucinogenic agonist  
Authors : Kim, K.L.; Che, T.; Krumm, B.E.; Roth, B.L.  
Deposited on : 2020-04-06  
Resolution : 3.40 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.31.2  
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) : 2.31.2

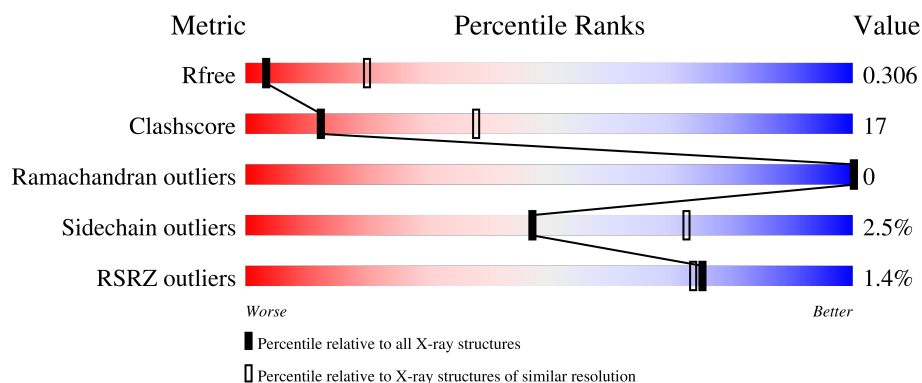
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	448	<div> <div>%</div> <div> <div></div> <div>57%</div> <div>25%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	448	<div> <div>2%</div> <div> <div></div> <div>59%</div> <div>20%</div> <div>•</div> <div>20%</div> </div> </div>
1	C	448	<div> <div>%</div> <div> <div></div> <div>58%</div> <div>25%</div> <div>•</div> <div>16%</div> </div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8100 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 5-hydroxytryptamine receptor 2A,Soluble cytochrome b562 fusion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			2692	1762	429	480	21			
1	B	358	Total	C	N	O	S	0	0	0
			2495	1623	403	448	21			
1	C	376	Total	C	N	O	S	0	0	0
			2693	1754	431	488	20			

There are 156 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	MET	-	initiating methionine	UNP P28223
A	41	LYS	-	expression tag	UNP P28223
A	42	THR	-	expression tag	UNP P28223
A	43	ILE	-	expression tag	UNP P28223
A	44	ILE	-	expression tag	UNP P28223
A	45	ALA	-	expression tag	UNP P28223
A	46	LEU	-	expression tag	UNP P28223
A	47	SER	-	expression tag	UNP P28223
A	48	TYR	-	expression tag	UNP P28223
A	49	ILE	-	expression tag	UNP P28223
A	50	PHE	-	expression tag	UNP P28223
A	51	CYS	-	expression tag	UNP P28223
A	52	LEU	-	expression tag	UNP P28223
A	53	VAL	-	expression tag	UNP P28223
A	54	PHE	-	expression tag	UNP P28223
A	55	ALA	-	expression tag	UNP P28223
A	56	ASP	-	expression tag	UNP P28223
A	57	TYR	-	expression tag	UNP P28223
A	58	LYS	-	expression tag	UNP P28223
A	59	ASP	-	expression tag	UNP P28223
A	60	ASP	-	expression tag	UNP P28223
A	61	ASP	-	expression tag	UNP P28223

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Chain	Residue	Modelled	Actual	Comment	Reference
A	62	ASP	-	expression tag	UNP P28223
A	63	GLY	-	expression tag	UNP P28223
A	64	ALA	-	expression tag	UNP P28223
A	65	PRO	-	expression tag	UNP P28223
A	247	ALA	LEU	conflict	UNP P28223
A	1007	TRP	MET	conflict	UNP P0ABE7
A	1102	ILE	HIS	conflict	UNP P0ABE7
A	1106	LEU	ARG	conflict	UNP P0ABE7
A	371	ALA	LEU	conflict	UNP P28223
A	406	GLY	-	expression tag	UNP P28223
A	407	ARG	-	expression tag	UNP P28223
A	408	PRO	-	expression tag	UNP P28223
A	409	LEU	-	expression tag	UNP P28223
A	410	GLU	-	expression tag	UNP P28223
A	411	VAL	-	expression tag	UNP P28223
A	412	LEU	-	expression tag	UNP P28223
A	413	PHE	-	expression tag	UNP P28223
A	414	GLN	-	expression tag	UNP P28223
A	415	GLY	-	expression tag	UNP P28223
A	416	PRO	-	expression tag	UNP P28223
A	417	HIS	-	expression tag	UNP P28223
A	418	HIS	-	expression tag	UNP P28223
A	419	HIS	-	expression tag	UNP P28223
A	420	HIS	-	expression tag	UNP P28223
A	421	HIS	-	expression tag	UNP P28223
A	422	HIS	-	expression tag	UNP P28223
A	423	HIS	-	expression tag	UNP P28223
A	424	HIS	-	expression tag	UNP P28223
A	425	HIS	-	expression tag	UNP P28223
A	426	HIS	-	expression tag	UNP P28223
B	40	MET	-	initiating methionine	UNP P28223
B	41	LYS	-	expression tag	UNP P28223
B	42	THR	-	expression tag	UNP P28223
B	43	ILE	-	expression tag	UNP P28223
B	44	ILE	-	expression tag	UNP P28223
B	45	ALA	-	expression tag	UNP P28223
B	46	LEU	-	expression tag	UNP P28223
B	47	SER	-	expression tag	UNP P28223
B	48	TYR	-	expression tag	UNP P28223
B	49	ILE	-	expression tag	UNP P28223
B	50	PHE	-	expression tag	UNP P28223
B	51	CYS	-	expression tag	UNP P28223

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Chain	Residue	Modelled	Actual	Comment	Reference
B	52	LEU	-	expression tag	UNP P28223
B	53	VAL	-	expression tag	UNP P28223
B	54	PHE	-	expression tag	UNP P28223
B	55	ALA	-	expression tag	UNP P28223
B	56	ASP	-	expression tag	UNP P28223
B	57	TYR	-	expression tag	UNP P28223
B	58	LYS	-	expression tag	UNP P28223
B	59	ASP	-	expression tag	UNP P28223
B	60	ASP	-	expression tag	UNP P28223
B	61	ASP	-	expression tag	UNP P28223
B	62	ASP	-	expression tag	UNP P28223
B	63	GLY	-	expression tag	UNP P28223
B	64	ALA	-	expression tag	UNP P28223
B	65	PRO	-	expression tag	UNP P28223
B	247	ALA	LEU	conflict	UNP P28223
B	1007	TRP	MET	conflict	UNP P0ABE7
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B	407	ARG	-	expression tag	UNP P28223
B	408	PRO	-	expression tag	UNP P28223
B	409	LEU	-	expression tag	UNP P28223
B	410	GLU	-	expression tag	UNP P28223
B	411	VAL	-	expression tag	UNP P28223
B	412	LEU	-	expression tag	UNP P28223
B	413	PHE	-	expression tag	UNP P28223
B	414	GLN	-	expression tag	UNP P28223
B	415	GLY	-	expression tag	UNP P28223
B	416	PRO	-	expression tag	UNP P28223
B	417	HIS	-	expression tag	UNP P28223
B	418	HIS	-	expression tag	UNP P28223
B	419	HIS	-	expression tag	UNP P28223
B	420	HIS	-	expression tag	UNP P28223
B	421	HIS	-	expression tag	UNP P28223
B	422	HIS	-	expression tag	UNP P28223
B	423	HIS	-	expression tag	UNP P28223
B	424	HIS	-	expression tag	UNP P28223
B	425	HIS	-	expression tag	UNP P28223
B	426	HIS	-	expression tag	UNP P28223
C	40	MET	-	initiating methionine	UNP P28223
C	41	LYS	-	expression tag	UNP P28223

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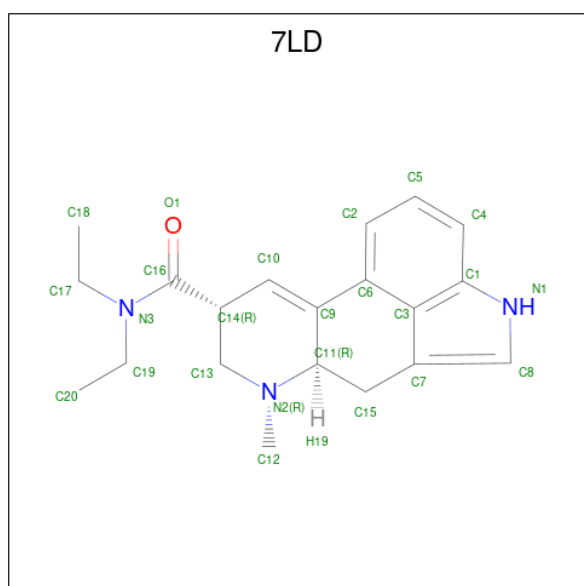
Chain	Residue	Modelled	Actual	Comment	Reference
C	42	THR	-	expression tag	UNP P28223
C	43	ILE	-	expression tag	UNP P28223
C	44	ILE	-	expression tag	UNP P28223
C	45	ALA	-	expression tag	UNP P28223
C	46	LEU	-	expression tag	UNP P28223
C	47	SER	-	expression tag	UNP P28223
C	48	TYR	-	expression tag	UNP P28223
C	49	ILE	-	expression tag	UNP P28223
C	50	PHE	-	expression tag	UNP P28223
C	51	CYS	-	expression tag	UNP P28223
C	52	LEU	-	expression tag	UNP P28223
C	53	VAL	-	expression tag	UNP P28223
C	54	PHE	-	expression tag	UNP P28223
C	55	ALA	-	expression tag	UNP P28223
C	56	ASP	-	expression tag	UNP P28223
C	57	TYR	-	expression tag	UNP P28223
C	58	LYS	-	expression tag	UNP P28223
C	59	ASP	-	expression tag	UNP P28223
C	60	ASP	-	expression tag	UNP P28223
C	61	ASP	-	expression tag	UNP P28223
C	62	ASP	-	expression tag	UNP P28223
C	63	GLY	-	expression tag	UNP P28223
C	64	ALA	-	expression tag	UNP P28223
C	65	PRO	-	expression tag	UNP P28223
C	247	ALA	LEU	conflict	UNP P28223
C	1007	TRP	MET	conflict	UNP P0ABE7
C	1102	ILE	HIS	conflict	UNP P0ABE7
C	1106	LEU	ARG	conflict	UNP P0ABE7
C	371	ALA	LEU	conflict	UNP P28223
C	406	GLY	-	expression tag	UNP P28223
C	407	ARG	-	expression tag	UNP P28223
C	408	PRO	-	expression tag	UNP P28223
C	409	LEU	-	expression tag	UNP P28223
C	410	GLU	-	expression tag	UNP P28223
C	411	VAL	-	expression tag	UNP P28223
C	412	LEU	-	expression tag	UNP P28223
C	413	PHE	-	expression tag	UNP P28223
C	414	GLN	-	expression tag	UNP P28223
C	415	GLY	-	expression tag	UNP P28223
C	416	PRO	-	expression tag	UNP P28223
C	417	HIS	-	expression tag	UNP P28223
C	418	HIS	-	expression tag	UNP P28223

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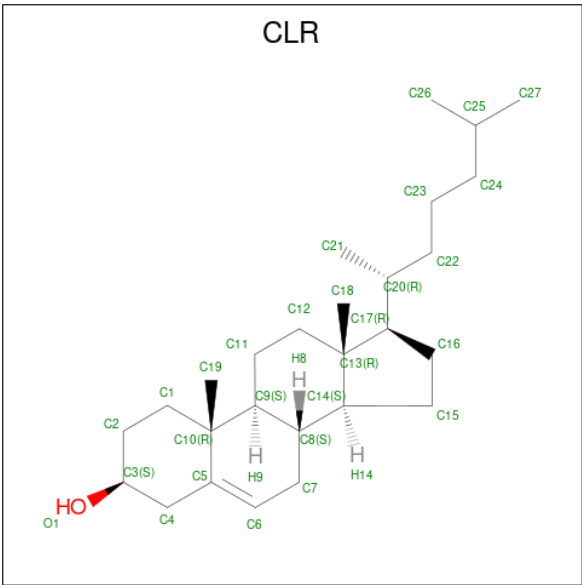
Chain	Residue	Modelled	Actual	Comment	Reference
C	419	HIS	-	expression tag	UNP P28223
C	420	HIS	-	expression tag	UNP P28223
C	421	HIS	-	expression tag	UNP P28223
C	422	HIS	-	expression tag	UNP P28223
C	423	HIS	-	expression tag	UNP P28223
C	424	HIS	-	expression tag	UNP P28223
C	425	HIS	-	expression tag	UNP P28223
C	426	HIS	-	expression tag	UNP P28223

- Molecule 2 is (8alpha)-N,N-diethyl-6-methyl-9,10-didehydroergoline-8-carboxamide (three-letter code: 7LD) (formula: C<sub>20</sub>H<sub>25</sub>N<sub>3</sub>O) (labeled as "Ligand of Interest" by depositor).



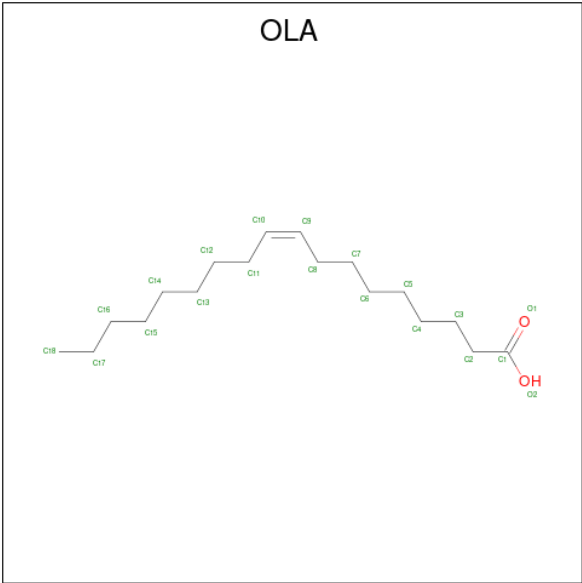
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			24	20	3	1		
2	B	1	Total	C	N	O	0	0
			24	20	3	1		
2	C	1	Total	C	N	O	0	0
			24	20	3	1		

- Molecule 3 is CHOLESTEROL (three-letter code: CLR) (formula: C<sub>27</sub>H<sub>46</sub>O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			28	27	1		
3	A	1	Total	C	O	0	0
			28	27	1		

- Molecule 4 is OLEIC ACID (three-letter code: OLA) (formula: C<sub>18</sub>H<sub>34</sub>O<sub>2</sub>).



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

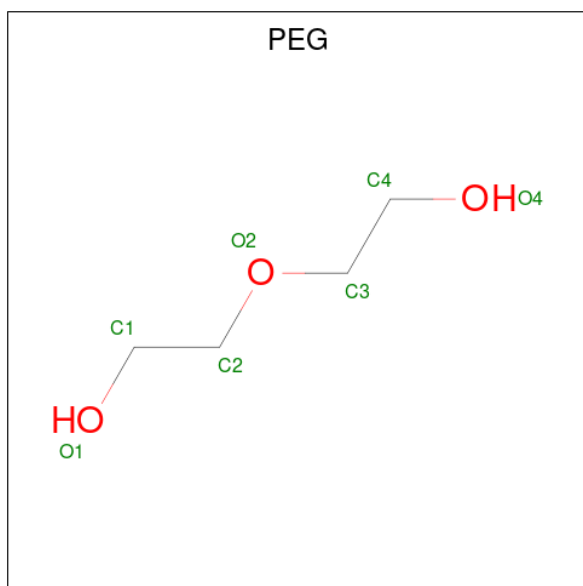
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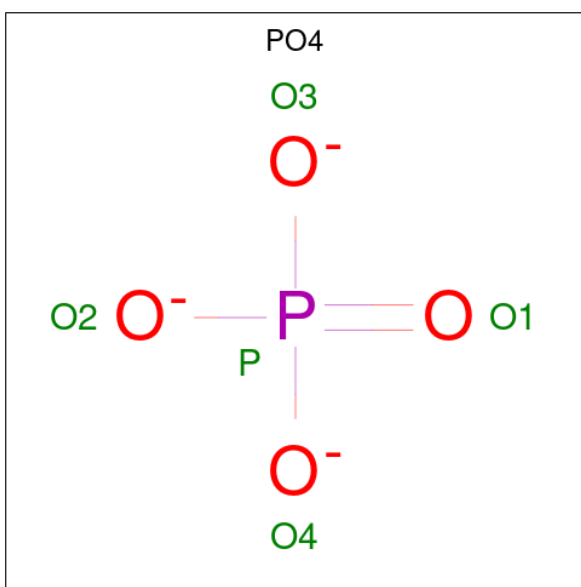
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	C	0	0
			10	10		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



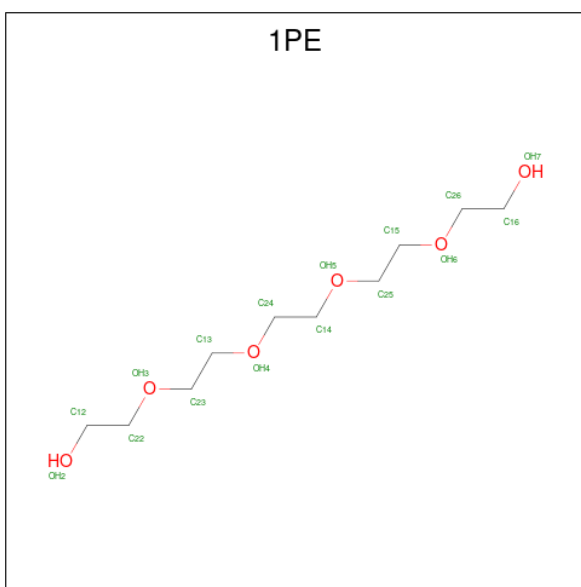
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	P	0	0
			5	4	1		
6	B	1	Total	O	P	0	0
			5	4	1		
6	C	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula:  $C_{10}H_{22}O_6$ ).

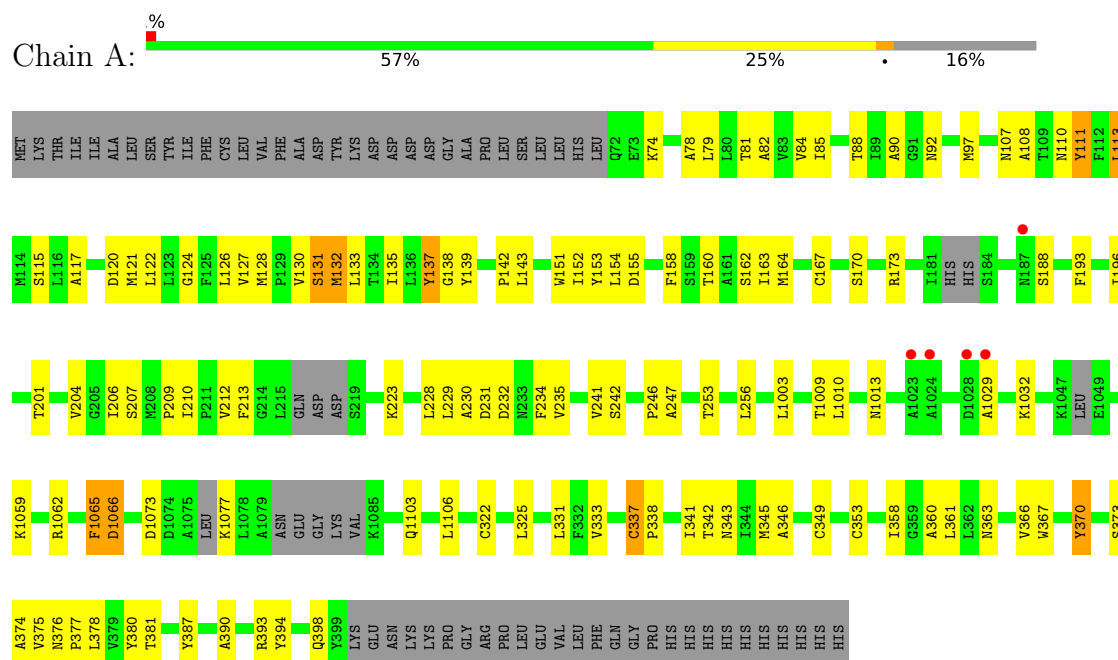


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			16	10	6		

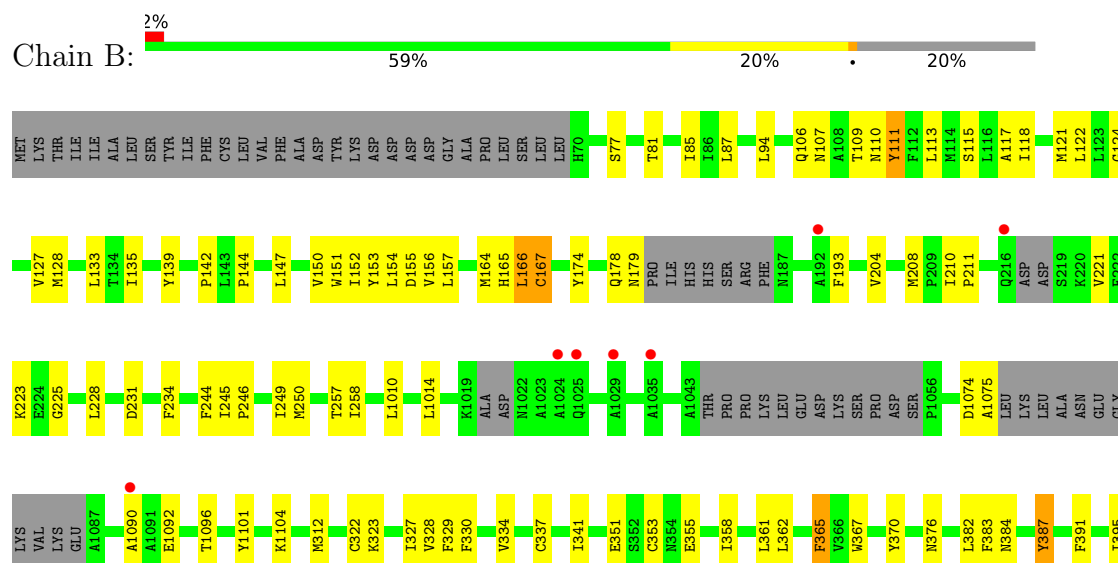
### 3 Residue-property plots

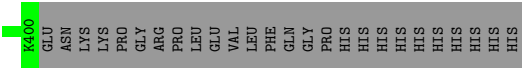
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: 5-hydroxytryptamine receptor 2A,Soluble cytochrome b562 fusion

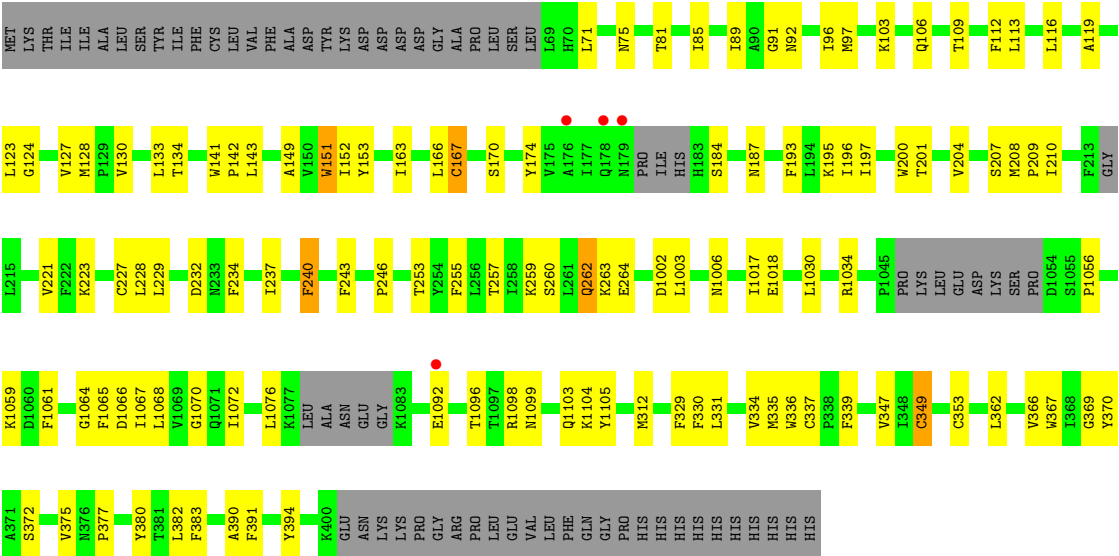


- Molecule 1: 5-hydroxytryptamine receptor 2A,Soluble cytochrome b562 fusion





● Molecule 1: 5-hydroxytryptamine receptor 2A,Soluble cytochrome b562 fusion



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.64Å 175.26Å 280.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.54 – 3.40 34.54 – 3.40	Depositor EDS
% Data completeness (in resolution range)	94.2 (34.54-3.40) 94.3 (34.54-3.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.38 (at 3.39Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.265 , 0.305 0.265 , 0.306	Depositor DCC
$R_{free}$ test set	1350 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	68.1	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 65.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	8100	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 5.37% 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: PEG, 1PE, CLR, PO4, 7LD, 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	0.64	2/2745 (0.1%)	0.82	6/3758 (0.2%)
1	B	0.58	4/2542 (0.2%)	0.71	3/3484 (0.1%)
1	C	0.61	3/2744 (0.1%)	0.75	0/3756
All	All	0.61	9/8031 (0.1%)	0.76	9/10998 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	167	CYS	CB-SG	-6.31	1.71	1.82
1	C	167	CYS	CB-SG	-5.78	1.72	1.81
1	A	337	CYS	CB-SG	-5.63	1.72	1.81
1	C	349	CYS	CB-SG	-5.58	1.72	1.81
1	B	337	CYS	CB-SG	-5.44	1.73	1.81

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	87	LEU	CB-CG-CD2	-6.43	100.06	111.00
1	A	113	LEU	CB-CG-CD2	6.43	121.93	111.00
1	A	1106	LEU	CA-CB-CG	6.09	129.31	115.30
1	B	166	LEU	CB-CG-CD2	6.00	121.21	111.00
1	B	122	LEU	CB-CG-CD1	-5.96	100.86	111.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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	2692	0	2493	102	0
1	B	2495	0	2226	64	1
1	C	2693	0	2490	90	0
2	A	24	0	0	0	0
2	B	24	0	0	1	0
2	C	24	0	0	0	0
3	A	56	0	92	17	0
4	A	37	0	61	6	0
4	B	10	0	14	0	0
5	A	7	0	10	1	0
5	C	7	0	10	0	0
6	B	10	0	0	1	0
6	C	5	0	0	0	0
7	C	16	0	22	3	0
All	All	8100	0	7418	262	1

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 17.

The worst 5 of 262 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:81:THR:HB	1:A:132:MET:HE2	1.36	1.03
1:A:337:CYS:O	1:A:341:ILE:HG13	1.71	0.88
1:A:345:MET:HG2	3:A:1202:CLR:H121	1.59	0.83
1:B:1075:ALA:HB3	1:B:1090:ALA:HB2	1.60	0.82
1:A:137:TYR:CD2	1:A:142:PRO:HB3	2.14	0.82

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:GLY:N	1:B:351:GLU:O[3_555]	2.18	0.02

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	365/448 (82%)	350 (96%)	15 (4%)	0	100	100
1	B	346/448 (77%)	339 (98%)	7 (2%)	0	100	100
1	C	366/448 (82%)	361 (99%)	5 (1%)	0	100	100
All	All	1077/1344 (80%)	1050 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	247/390 (63%)	238 (96%)	9 (4%)	35	63
1	B	216/390 (55%)	212 (98%)	4 (2%)	57	78
1	C	249/390 (64%)	244 (98%)	5 (2%)	55	77
All	All	712/1170 (61%)	694 (98%)	18 (2%)	47	72

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	240	PHE
1	C	391	PHE
1	C	262	GLN
1	A	370	TYR
1	C	167	CYS



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

Mol	Chain	Res	Type
1	A	92	ASN
1	A	1013	ASN
1	B	396	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

14 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	PO4	B	1203	-	4,4,4	0.86	0	6,6,6	0.62	0
4	OLA	A	1203	-	16,16,19	0.91	1 (6%)	15,15,19	0.93	1 (6%)
6	PO4	B	1204	-	4,4,4	0.77	0	6,6,6	0.53	0
5	PEG	A	1205	-	6,6,6	0.44	0	5,5,5	0.30	0
2	7LD	C	1201	-	24,27,27	6.71	10 (41%)	27,40,40	4.09	10 (37%)
2	7LD	B	1201	-	24,27,27	6.36	10 (41%)	27,40,40	2.56	6 (22%)
3	CLR	A	1206	-	31,31,31	0.67	0	48,48,48	1.78	12 (25%)
3	CLR	A	1202	-	31,31,31	0.74	1 (3%)	48,48,48	1.98	19 (39%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	1PE	C	1204	-	15,15,15	0.58	0	14,14,14	0.55	0
5	PEG	C	1202	-	6,6,6	0.16	0	5,5,5	0.24	0
2	7LD	A	1201	-	24,27,27	6.44	10 (41%)	27,40,40	2.60	7 (25%)
4	OLA	A	1204	-	19,19,19	0.82	1 (5%)	19,19,19	0.94	1 (5%)
4	OLA	B	1202	-	9,9,19	1.01	1 (11%)	8,8,19	0.37	0
6	PO4	C	1203	-	4,4,4	0.74	0	6,6,6	0.60	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	OLA	A	1203	-	-	9/14/14/17	-
5	PEG	A	1205	-	-	2/4/4/4	-
2	7LD	C	1201	-	-	5/12/36/36	0/3/4/4
2	7LD	B	1201	-	-	1/12/36/36	0/3/4/4
3	CLR	A	1206	-	-	10/10/68/68	0/4/4/4
3	CLR	A	1202	-	-	7/10/68/68	0/4/4/4
7	1PE	C	1204	-	-	7/13/13/13	-
5	PEG	C	1202	-	-	2/4/4/4	-
2	7LD	A	1201	-	-	2/12/36/36	0/3/4/4
4	OLA	A	1204	-	-	13/17/17/17	-
4	OLA	B	1202	-	-	3/7/7/17	-

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1201	7LD	C10-C9	22.17	1.57	1.33
2	A	1201	7LD	C10-C9	20.87	1.56	1.33
2	B	1201	7LD	C10-C9	19.68	1.54	1.33
2	C	1201	7LD	C13-C14	13.61	1.66	1.52
2	A	1201	7LD	C13-C14	11.86	1.64	1.52

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1201	7LD	C12-N2-C11	-14.74	95.81	111.62
2	B	1201	7LD	C14-C10-C9	-8.46	111.56	123.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	7LD	C6-C9-C10	-7.71	113.96	123.07
2	B	1201	7LD	C6-C9-C10	-7.48	114.23	123.07
2	C	1201	7LD	C6-C9-C10	-7.15	114.61	123.07

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

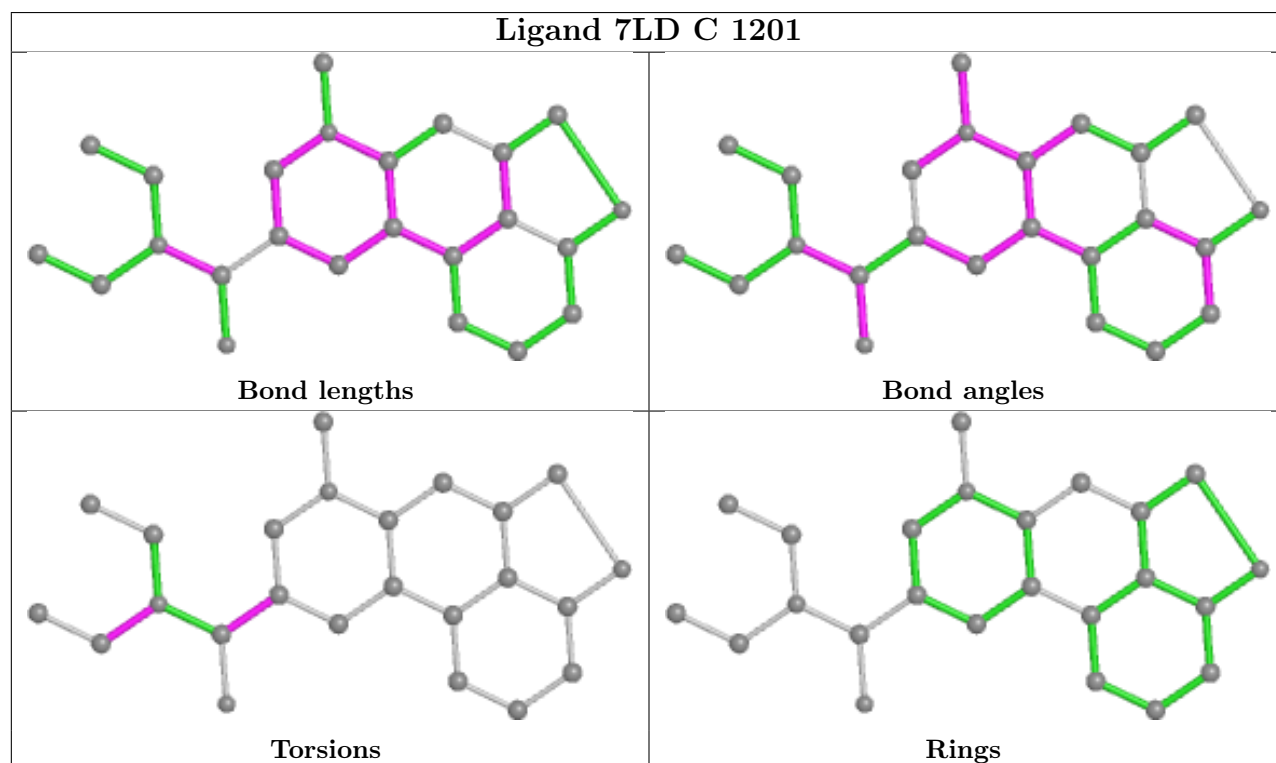
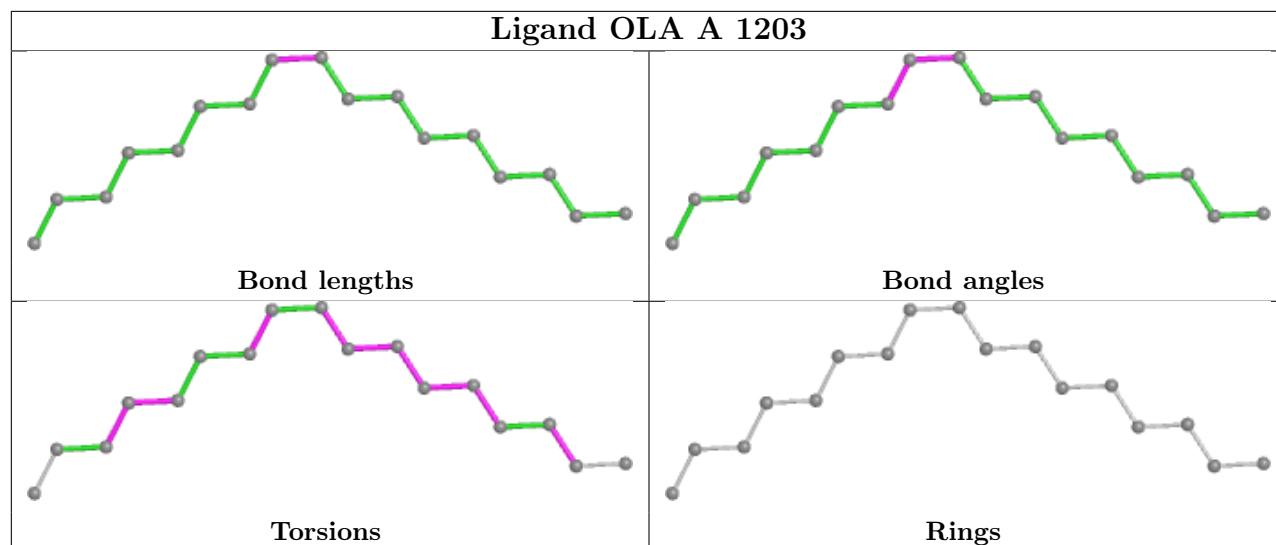
Mol	Chain	Res	Type	Atoms
2	C	1201	7LD	C13-C14-C16-N3
2	C	1201	7LD	C13-C14-C16-O1
3	A	1202	CLR	C13-C17-C20-C21
3	A	1202	CLR	C13-C17-C20-C22
3	A	1206	CLR	C16-C17-C20-C21

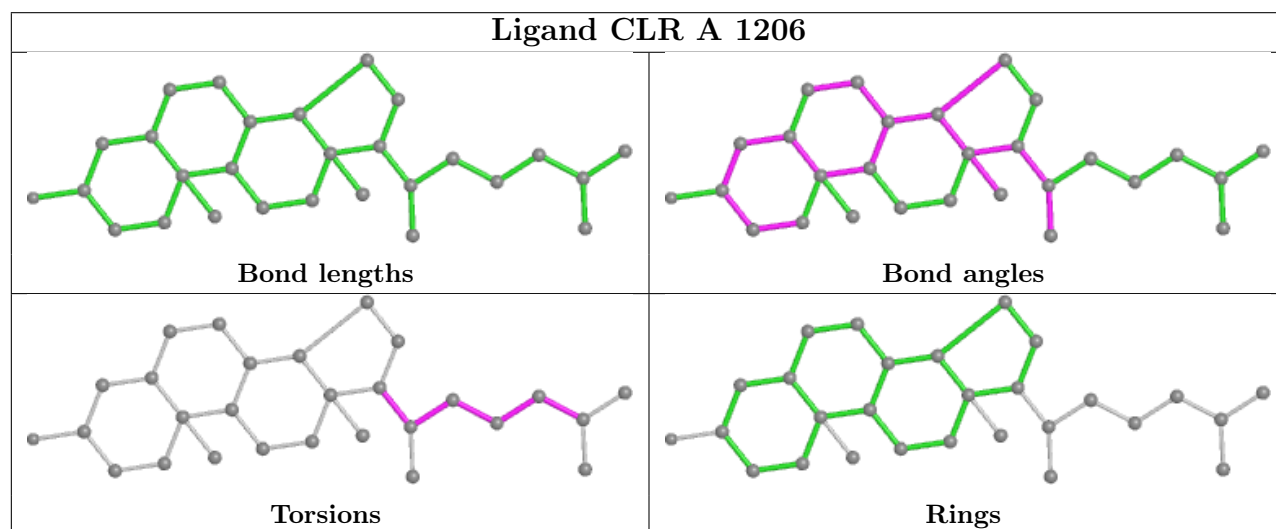
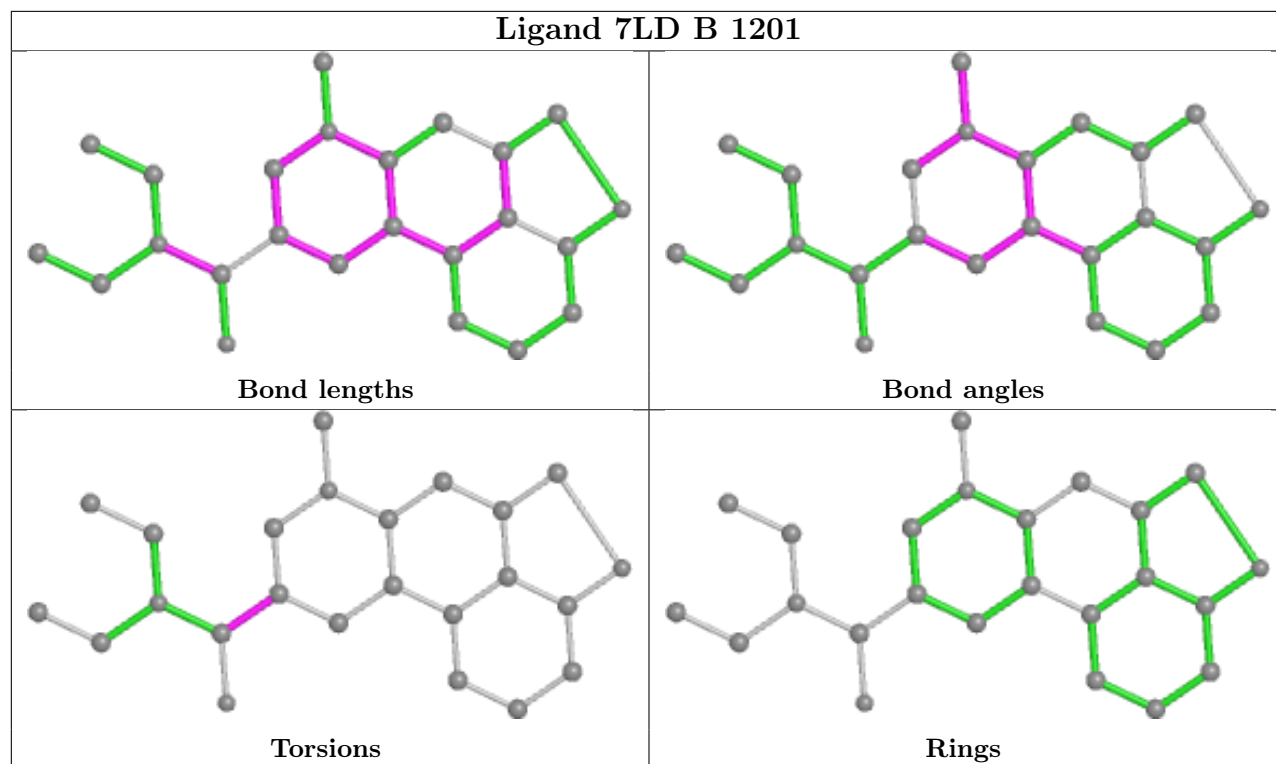
There are no ring outliers.

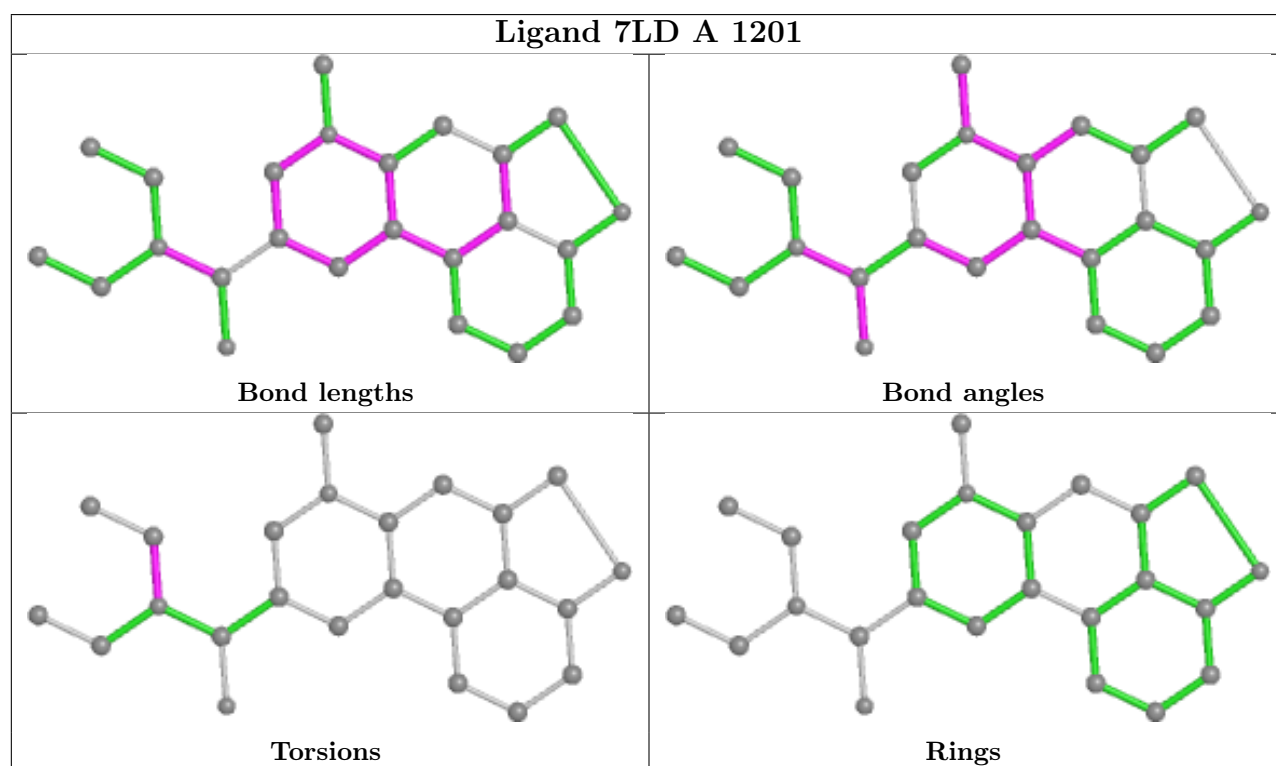
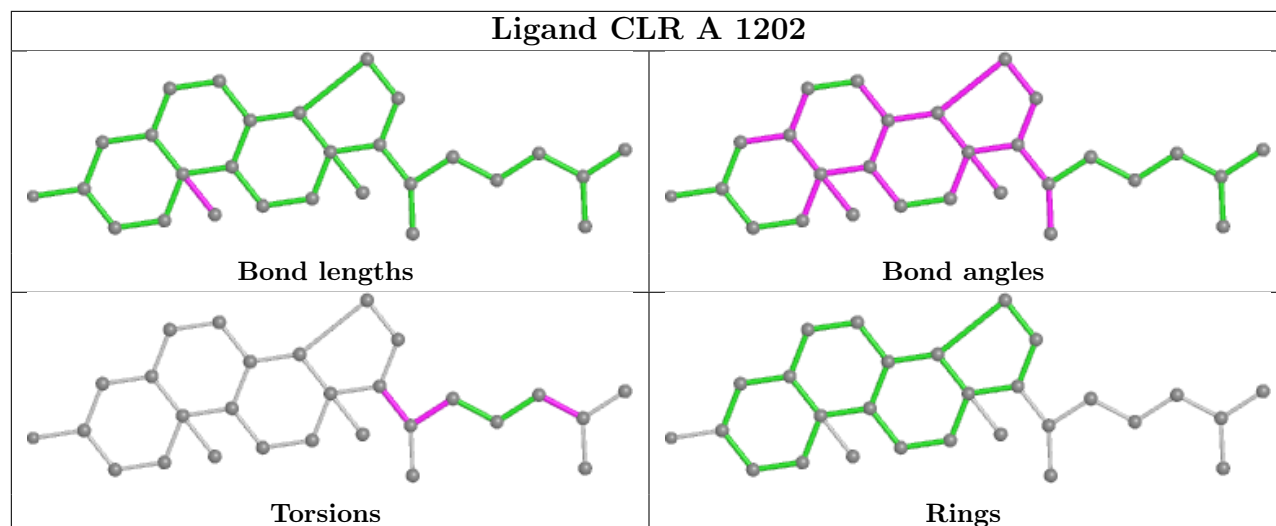
8 monomers are involved in 29 short contacts:

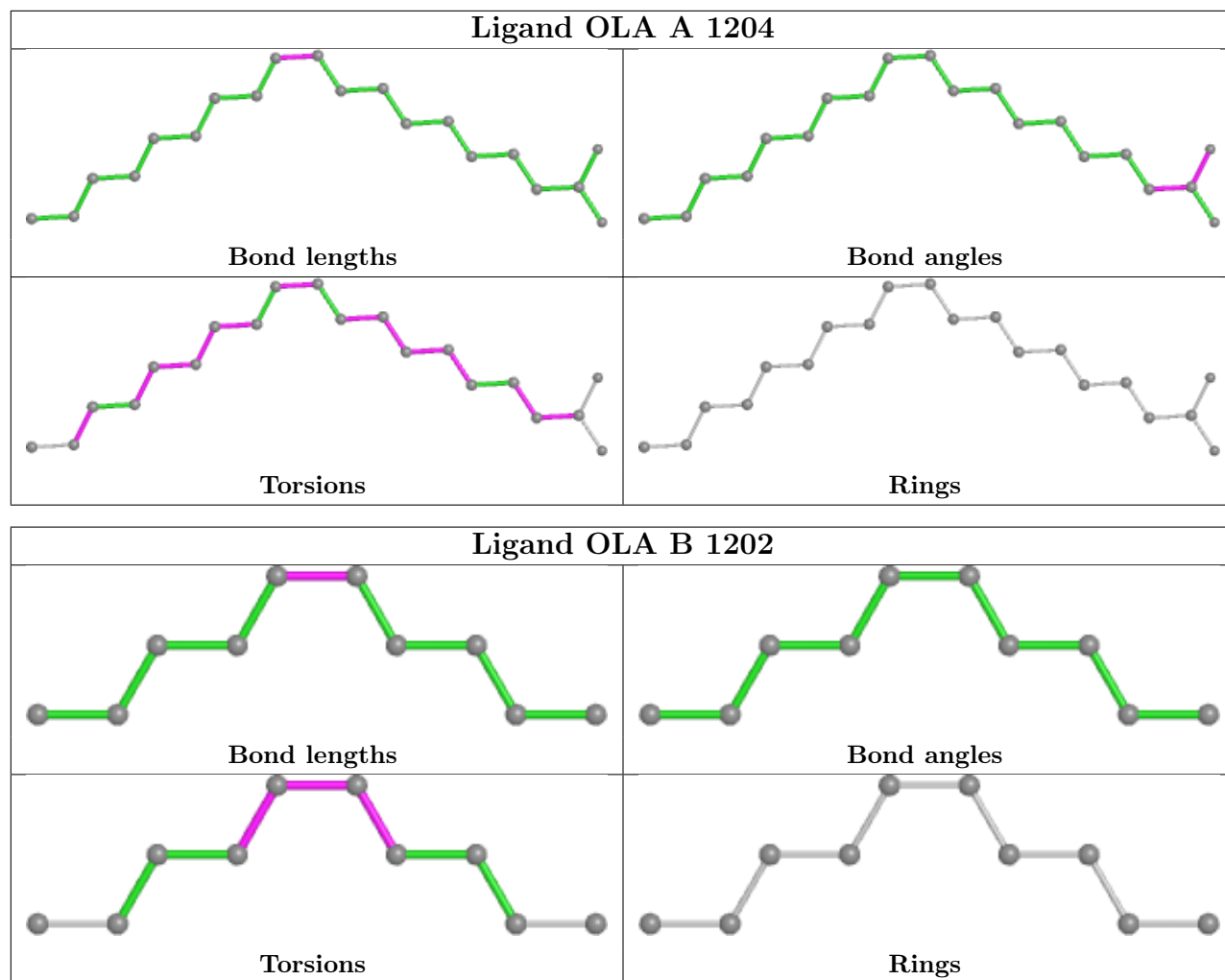
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1203	OLA	3	0
6	B	1204	PO4	1	0
5	A	1205	PEG	1	0
2	B	1201	7LD	1	0
3	A	1206	CLR	9	0
3	A	1202	CLR	8	0
7	C	1204	1PE	3	0
4	A	1204	OLA	3	0

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	377/448 (84%)	-0.24	5 (1%) 77 76	19, 43, 97, 120	0
1	B	358/448 (79%)	-0.16	7 (1%) 65 64	22, 56, 106, 126	0
1	C	376/448 (83%)	-0.18	4 (1%) 80 79	20, 46, 85, 105	0
All	All	1111/1344 (82%)	-0.20	16 (1%) 75 74	19, 48, 100, 126	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1024	ALA	3.9
1	C	179	ASN	3.7
1	B	1035	ALA	3.6
1	B	1029	ALA	3.2
1	C	178	GLN	3.2

### 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.

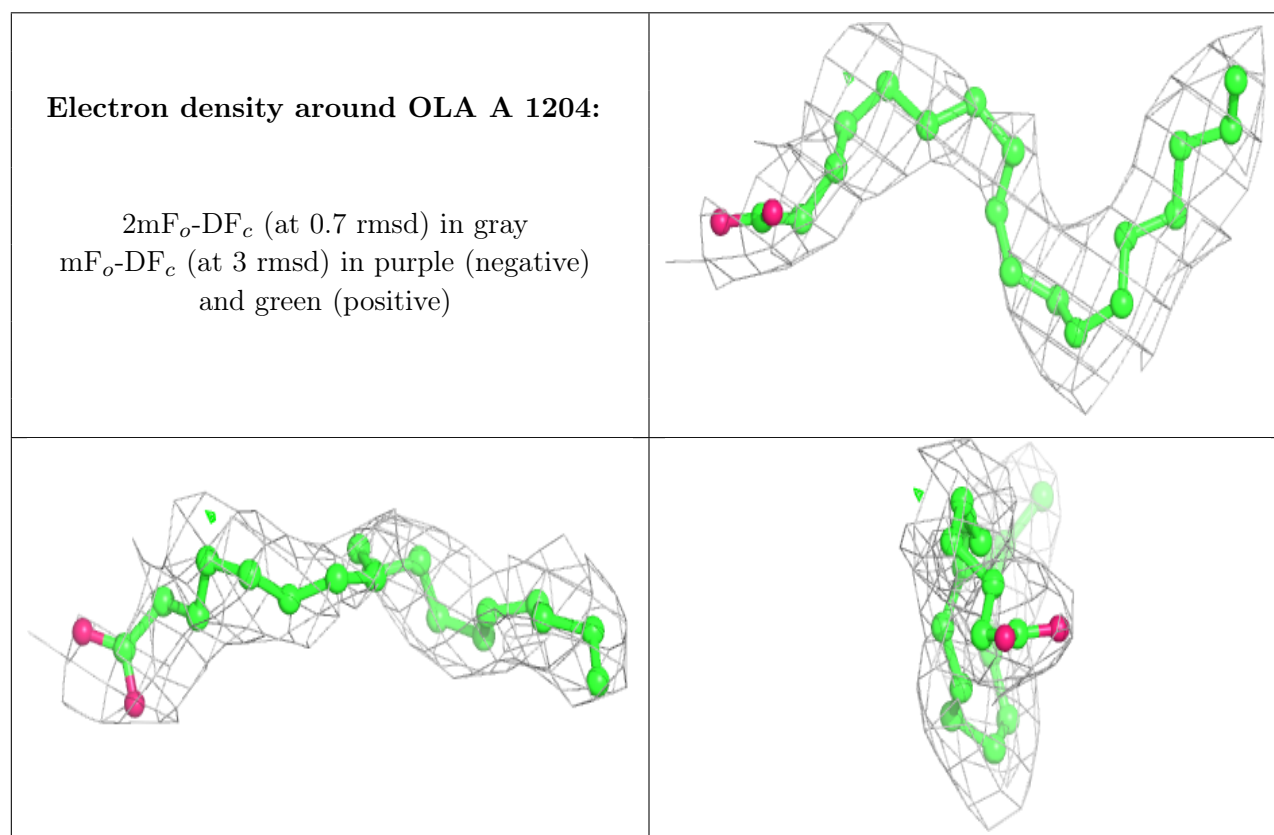
### 6.4 Ligands [i](#)

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.



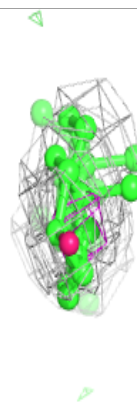
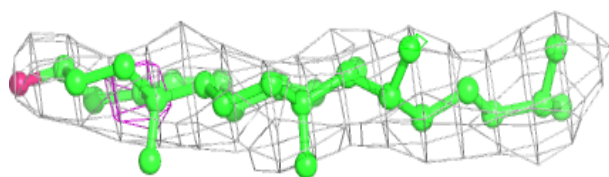
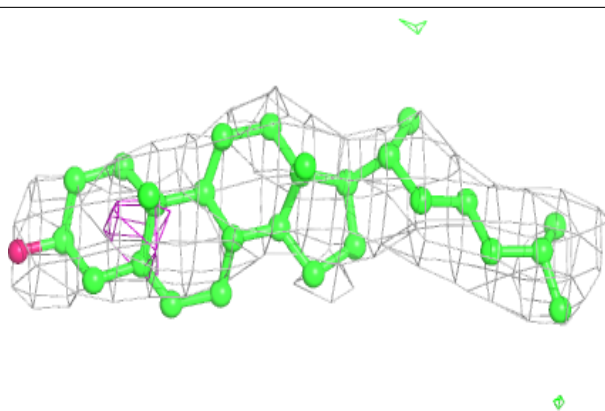
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	OLA	A	1204	20/20	0.82	0.29	23,48,74,75	0
5	PEG	C	1202	7/7	0.86	0.26	29,32,41,48	0
3	CLR	A	1202	28/28	0.87	0.32	19,53,62,64	0
4	OLA	A	1203	17/20	0.87	0.46	21,25,33,40	0
6	PO4	C	1203	5/5	0.88	0.23	78,79,93,105	0
5	PEG	A	1205	7/7	0.89	0.22	28,34,41,41	0
2	7LD	C	1201	24/24	0.89	0.28	28,36,55,62	0
2	7LD	B	1201	24/24	0.89	0.27	37,43,57,64	0
6	PO4	B	1203	5/5	0.90	0.38	59,70,86,91	0
3	CLR	A	1206	28/28	0.90	0.52	45,51,63,67	0
2	7LD	A	1201	24/24	0.92	0.21	24,31,35,40	0
7	1PE	C	1204	16/16	0.92	0.25	43,49,76,80	0
4	OLA	B	1202	10/20	0.93	0.16	23,27,35,37	0
6	PO4	B	1204	5/5	0.94	0.32	65,70,89,97	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.

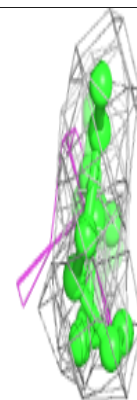
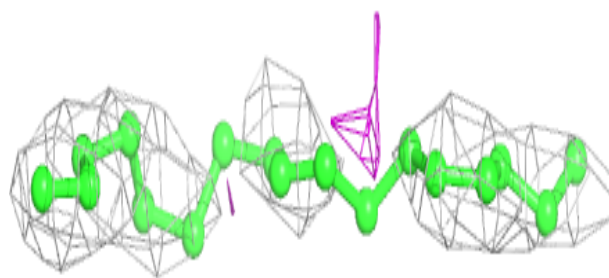
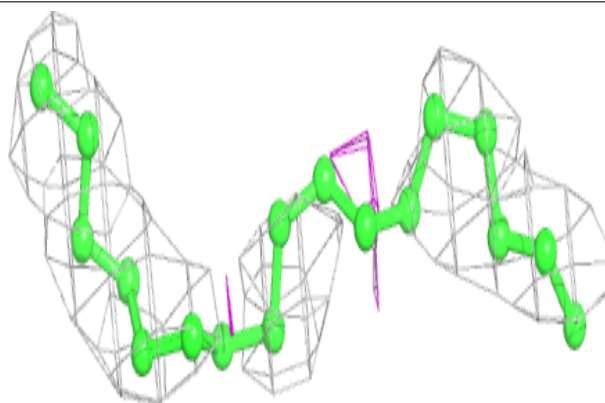


**Electron density around CLR A 1202:**

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

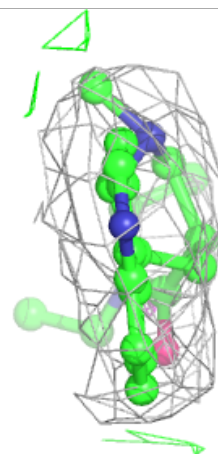
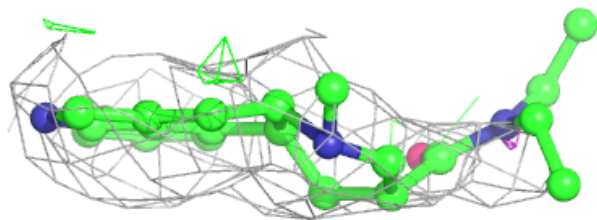
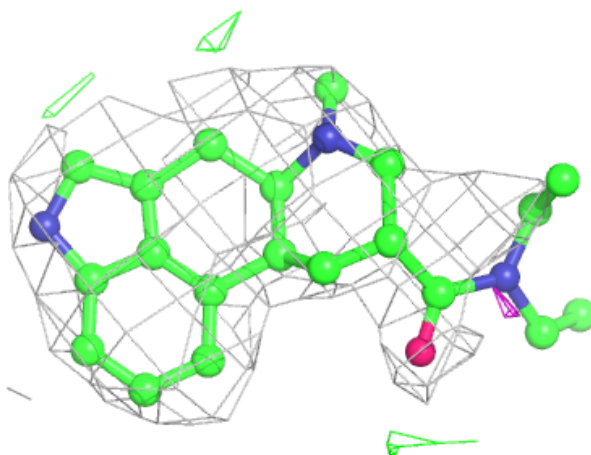
**Electron density around OLA A 1203:**

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



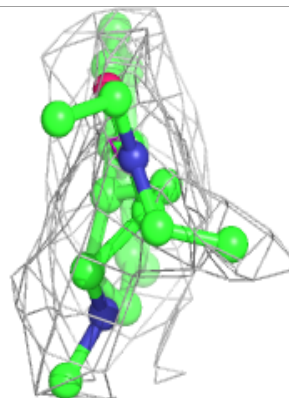
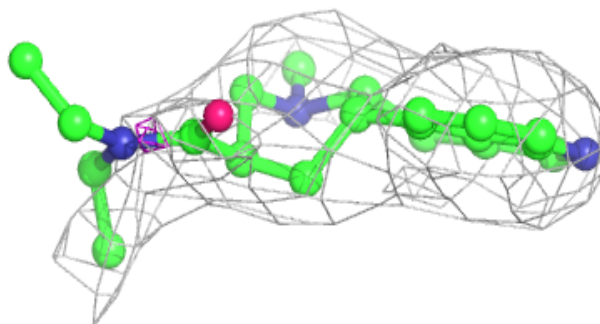
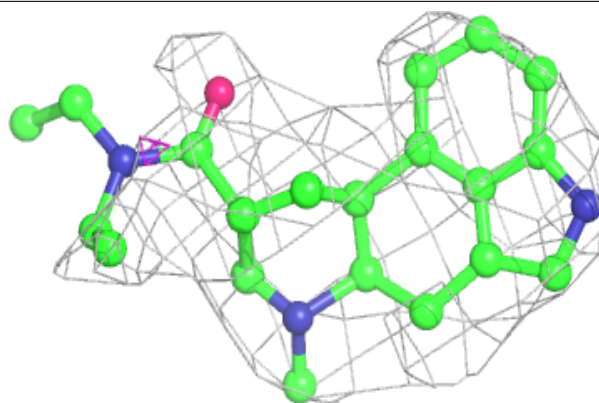
**Electron density around 7LD C 1201:**

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

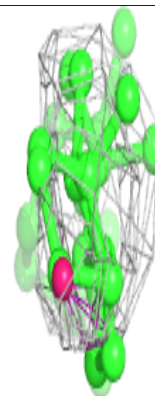
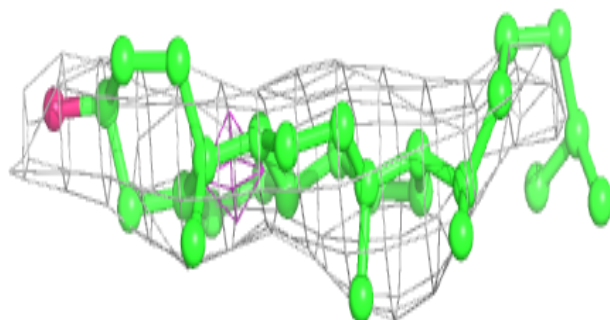
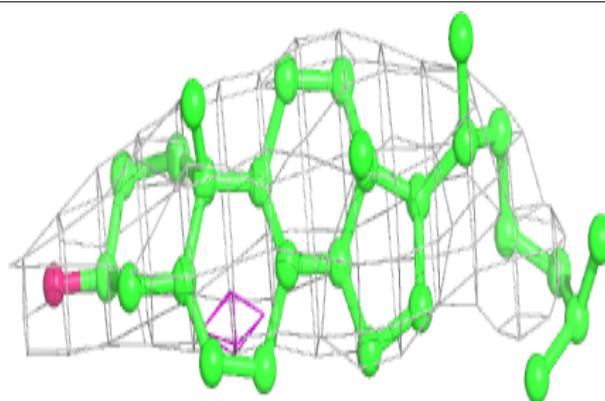


**Electron density around 7LD B 1201:**

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

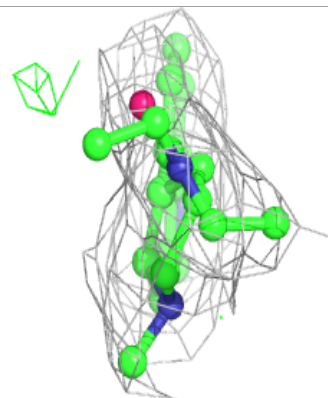
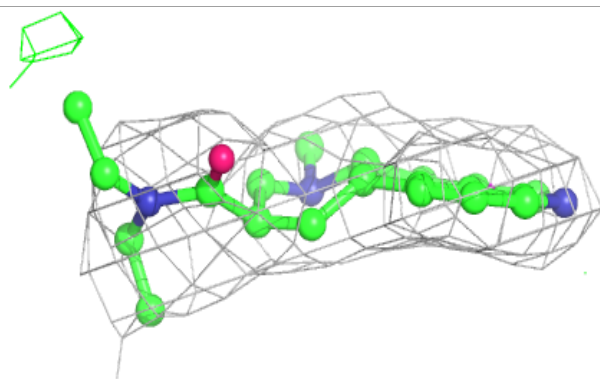
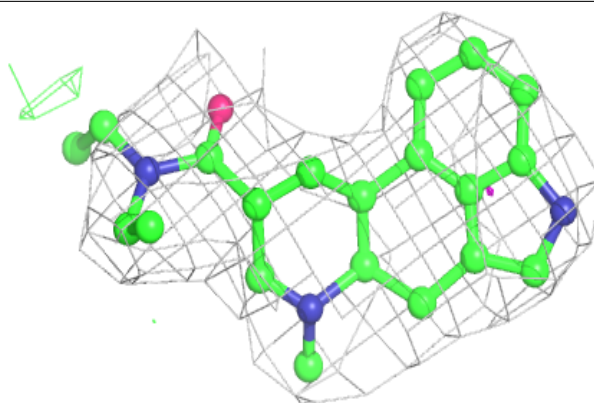
**Electron density around CLR A 1206:**

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

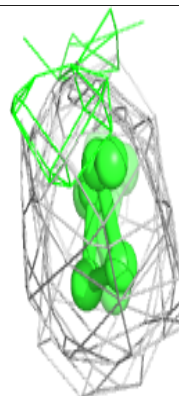
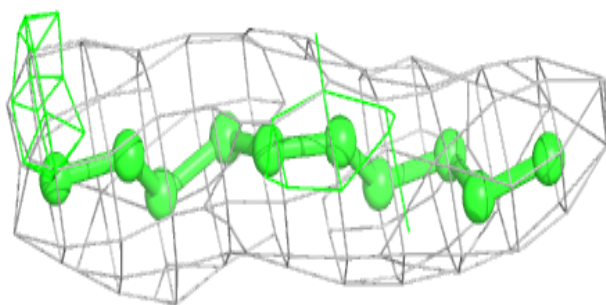
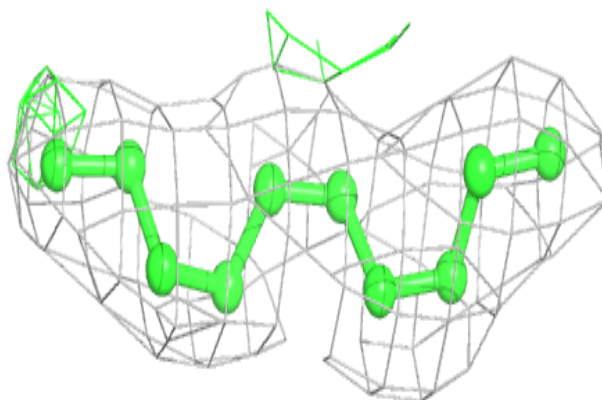


**Electron density around 7LD A 1201:**

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

**Electron density around OLA B 1202:**

$2mF_o-DF_c$  (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.