



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:21 AM UTC

PDB ID : 6WH4 / pdb_00006wh4
Title : Crystal structure of HTR2A with inverse agonist
Authors : Kim, K.L.; Che, T.; Krumm, B.E.; Roth, B.L.
Deposited on : 2020-04-07
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

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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

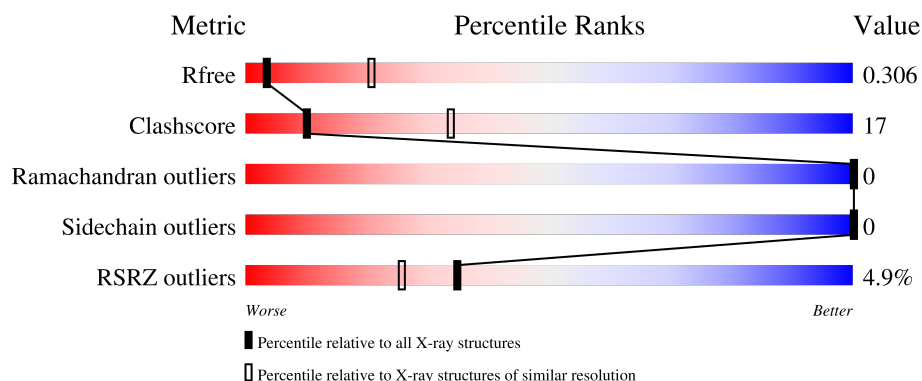
1 Overall quality at a glance

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}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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 $\leq 5\%$. 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	3% 58% 26% 16%
1	B	448	5% 57% 23% 20%
1	C	448	4% 61% 22% 16%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8108 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	378	Total	C	N	O	S	0	0	0
			2687	1752	429	486	20			
1	B	358	Total	C	N	O	S	0	0	0
			2480	1613	402	446	19			
1	C	375	Total	C	N	O	S	0	0	0
			2696	1755	432	489	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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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
B	1102	ILE	HIS	conflict	UNP P0ABE7
B	1106	LEU	ARG	conflict	UNP P0ABE7
B	371	ALA	LEU	conflict	UNP P28223
B	406	GLY	-	expression tag	UNP P28223
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

Continued on next page...

Continued from previous page...

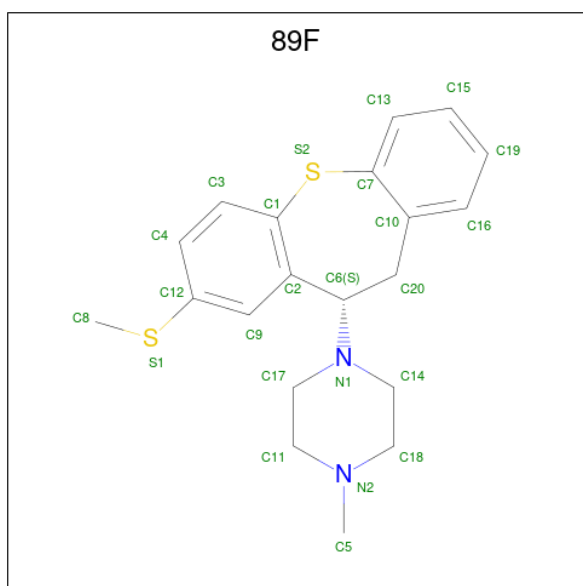
Chain	Residue	Modelled	Actual	Comment	Reference
C	42	THR	-	expression tag	UNP P28223
C	43	ILE	-	expression tag	UNP P28223
C	44	ILE	-	expression tag	UNP P28223
C	45	ALA	-	expression tag	UNP P28223
C	46	LEU	-	expression tag	UNP P28223
C	47	SER	-	expression tag	UNP P28223
C	48	TYR	-	expression tag	UNP P28223
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

Continued on next page...

Continued from previous page...

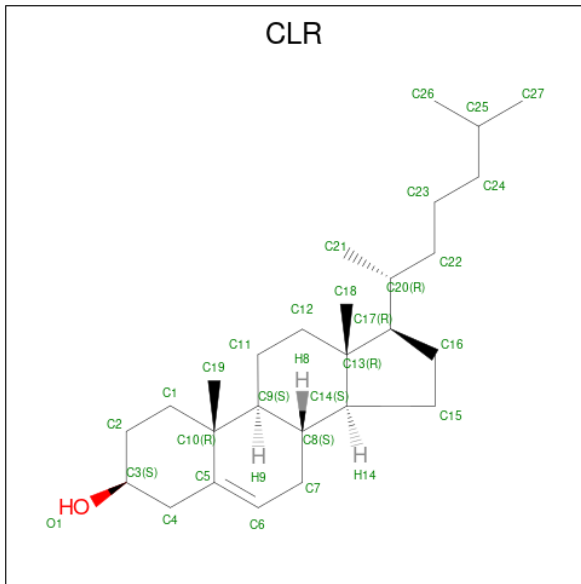
Chain	Residue	Modelled	Actual	Comment	Reference
C	419	HIS	-	expression tag	UNP P28223
C	420	HIS	-	expression tag	UNP P28223
C	421	HIS	-	expression tag	UNP P28223
C	422	HIS	-	expression tag	UNP P28223
C	423	HIS	-	expression tag	UNP P28223
C	424	HIS	-	expression tag	UNP P28223
C	425	HIS	-	expression tag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

- Molecule 2 is 1-methyl-4-[(5 {S})-3-methylsulfanyl-5,6-dihydrobenzo[b][1]benzothiepin-5-yl]piperazine (CCD ID: 89F) (formula: C₂₀H₂₄N₂S₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is OLEIC ACID (CCD ID: OLA) (formula: C₁₈H₃₄O₂).

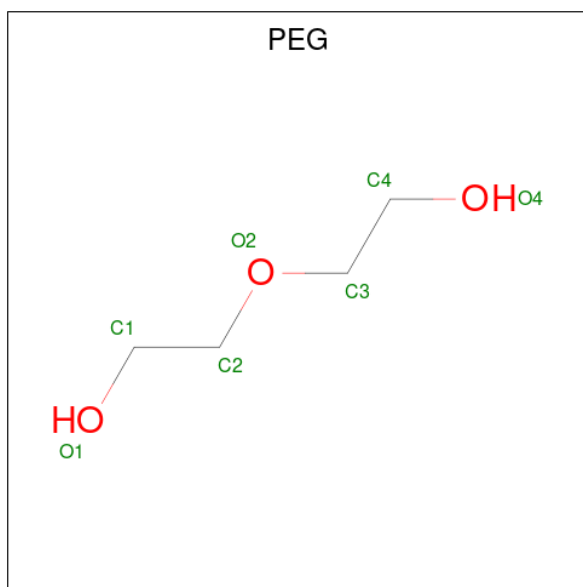


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 20	C 18	O 2	0	0
3	A	1	Total 9	C 7	O 2	0	0
3	B	1	Total 12	C 10	O 2	0	0
3	C	1	Total 20	C 18	O 2	0	0

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).

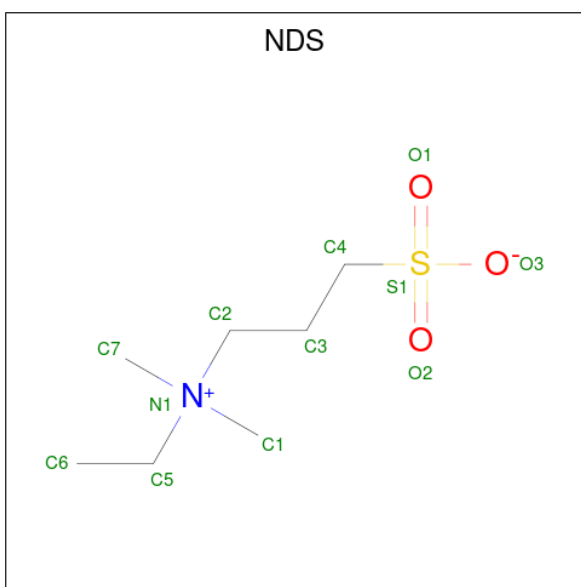
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			28	27	1		
4	C	1	Total	C	O	0	0
			28	27	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



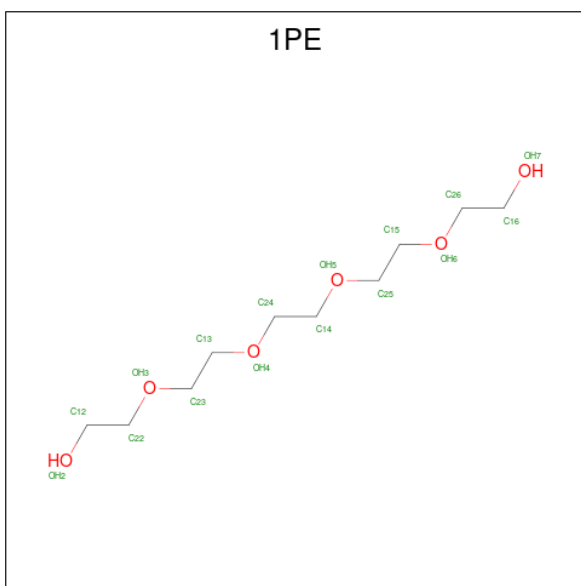
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is ETHYL DIMETHYL AMMONIO PROPANE SULFONATE (CCD ID: NDS) (formula: $C_7H_{17}NO_3S$).

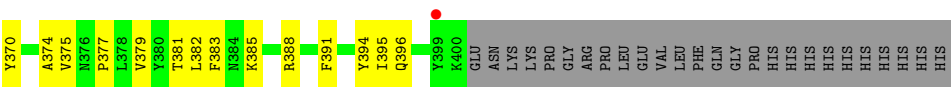


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	S	0	0
			12	7	1	3	1		

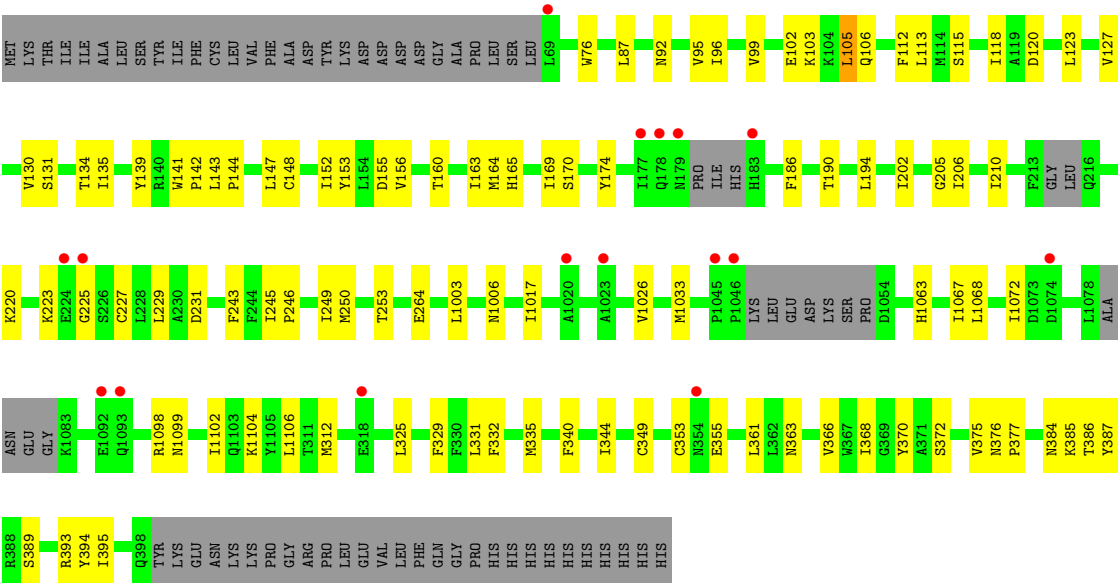
- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



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



● 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, α , β , γ	82.38Å 177.31Å 280.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.50 – 3.40 33.50 – 3.40	Depositor EDS
% Data completeness (in resolution range)	90.8 (33.50-3.40) 90.8 (33.50-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.258 , 0.304 0.260 , 0.306	Depositor DCC
R_{free} test set	1448 reflections (3.15%)	wwPDB-VP
Wilson B-factor (Å ²)	69.4	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 69.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	8108	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, NDS, 89F, OLA, CLR

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	0.55	0/2740	0.85	1/3760 (0.0%)
1	B	0.51	0/2526	0.80	0/3467
1	C	0.55	0/2748	0.86	4/3758 (0.1%)
All	All	0.54	0/8014	0.84	5/10985 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	CYS	CA-CB-SG	-8.47	94.92	114.40
1	C	227	CYS	CA-CB-SG	-7.55	97.03	114.40
1	C	148	CYS	CA-CB-SG	-6.93	98.47	114.40
1	C	113	LEU	CB-CG-CD2	-6.74	90.47	110.70
1	C	105	LEU	CB-CG-CD2	-5.57	93.99	110.70

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	2687	0	2479	92	1
1	B	2480	0	2223	89	0
1	C	2696	0	2495	88	1

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	24	0	0	1	0
2	B	24	0	0	0	0
2	C	24	0	0	0	0
3	A	29	0	43	7	0
3	B	12	0	15	1	0
3	C	20	0	33	4	0
4	A	28	0	46	3	0
4	C	28	0	46	2	0
5	A	7	0	10	0	0
5	B	7	0	10	0	0
5	C	14	0	20	0	0
6	C	12	0	17	1	0
7	C	16	0	22	3	0
All	All	8108	0	7459	270	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 270 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:1065:PHE:CE1	1:A:1094:LEU:HD13	1.93	1.04
1:A:1068:LEU:HD12	1:A:1094:LEU:HD23	1.47	0.95
1:A:1068:LEU:HD12	1:A:1094:LEU:CD2	2.00	0.91
1:C:1068:LEU:H	1:C:1068:LEU:HD12	1.39	0.87
1:B:92:ASN:HB3	1:B:117:ALA:HB1	1.59	0.83

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:A:351:GLU:O	1:C:225:GLY:N[7_555]	2.19	0.01

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	370/448 (83%)	359 (97%)	11 (3%)	0	100	100
1	B	346/448 (77%)	334 (96%)	12 (4%)	0	100	100
1	C	365/448 (82%)	351 (96%)	14 (4%)	0	100	100
All	All	1081/1344 (80%)	1044 (97%)	37 (3%)	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	248/390 (64%)	248 (100%)	0	100	100
1	B	216/390 (55%)	216 (100%)	0	100	100
1	C	251/390 (64%)	251 (100%)	0	100	100
All	All	715/1170 (61%)	715 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	1041	GLN
1	B	1013	ASN
1	C	1103	GLN
1	C	363	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

15 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	$\# Z > 2$
4	CLR	A	1204	-	31,31,31	0.64	0	48,48,48	1.66	11 (22%)
2	89F	B	1201	-	26,27,27	0.43	0	32,38,38	1.04	3 (9%)
3	OLA	B	1203	-	11,11,19	1.12	1 (9%)	11,11,19	0.87	0
2	89F	C	1201	-	26,27,27	0.31	0	32,38,38	0.84	0
3	OLA	A	1203	-	8,8,19	0.70	0	8,8,19	1.48	1 (12%)
5	PEG	A	1205	-	6,6,6	0.30	0	5,5,5	0.21	0
6	NDS	C	1205	-	11,11,11	0.41	0	15,16,16	0.69	1 (6%)
7	1PE	C	1207	-	15,15,15	0.55	0	14,14,14	0.50	0
3	OLA	C	1206	-	19,19,19	0.88	1 (5%)	19,19,19	0.80	1 (5%)
3	OLA	A	1202	-	19,19,19	0.82	1 (5%)	19,19,19	1.00	0
4	CLR	C	1202	-	31,31,31	0.66	0	48,48,48	1.53	10 (20%)
5	PEG	C	1204	-	6,6,6	0.13	0	5,5,5	0.13	0
5	PEG	C	1203	-	6,6,6	0.14	0	5,5,5	0.13	0
2	89F	A	1201	-	26,27,27	0.34	0	32,38,38	0.85	0
5	PEG	B	1202	-	6,6,6	0.13	0	5,5,5	0.15	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	CLR	A	1204	-	-	7/10/68/68	0/4/4/4
2	89F	B	1201	-	-	5/6/28/28	0/3/4/4
3	OLA	B	1203	-	-	4/9/9/17	-
2	89F	C	1201	-	-	0/6/28/28	0/3/4/4
3	OLA	A	1203	-	-	5/6/6/17	-
5	PEG	A	1205	-	-	2/4/4/4	-
6	NDS	C	1205	-	-	0/11/11/11	-
7	1PE	C	1207	-	-	6/13/13/13	-
3	OLA	C	1206	-	-	9/17/17/17	-
3	OLA	A	1202	-	-	7/17/17/17	-
4	CLR	C	1202	-	-	2/10/68/68	0/4/4/4
5	PEG	C	1204	-	-	1/4/4/4	-
5	PEG	C	1203	-	-	2/4/4/4	-
2	89F	A	1201	-	-	2/6/28/28	0/3/4/4
5	PEG	B	1202	-	-	1/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1203	OLA	C10-C9	2.86	1.47	1.29
3	C	1206	OLA	C10-C9	2.82	1.47	1.31
3	A	1202	OLA	C10-C9	2.76	1.47	1.31

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1204	CLR	C17-C13-C14	3.90	104.57	100.10
4	C	1202	CLR	C13-C14-C8	-3.63	109.26	114.41
4	C	1202	CLR	C17-C13-C14	3.63	104.26	100.10
4	A	1204	CLR	C13-C14-C8	-3.46	109.50	114.41
4	A	1204	CLR	C8-C7-C6	-3.34	108.13	112.76

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1201	89F	C2-C6-N1-C17
2	B	1201	89F	C20-C6-N1-C14
2	B	1201	89F	C20-C6-N1-C17
7	C	1207	1PE	C24-C14-OH5-C25

Continued on next page...

Continued from previous page...

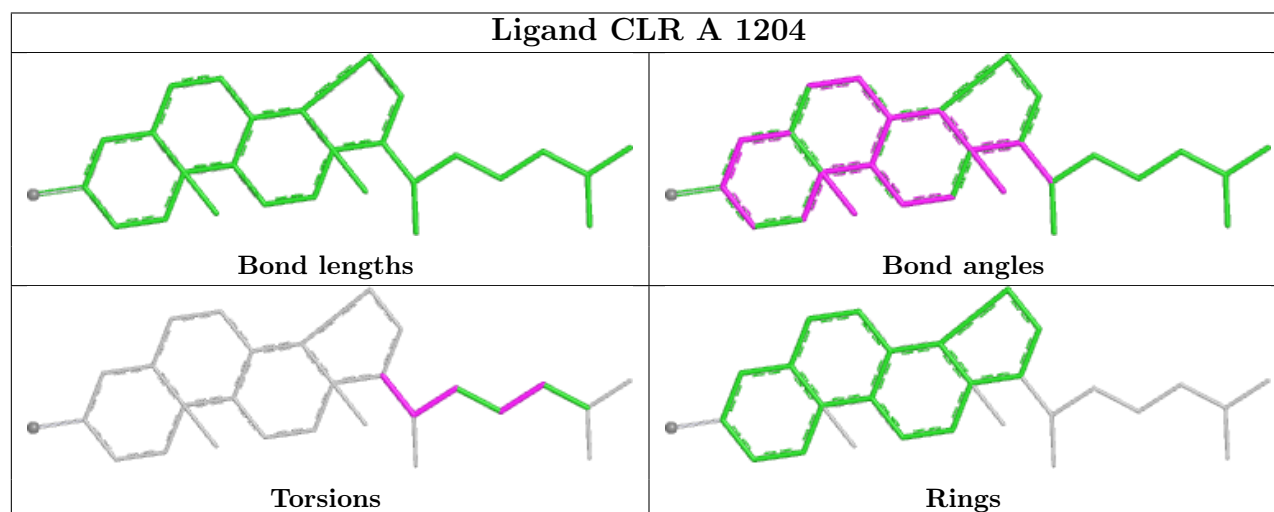
Mol	Chain	Res	Type	Atoms
4	A	1204	CLR	C17-C20-C22-C23

There are no ring outliers.

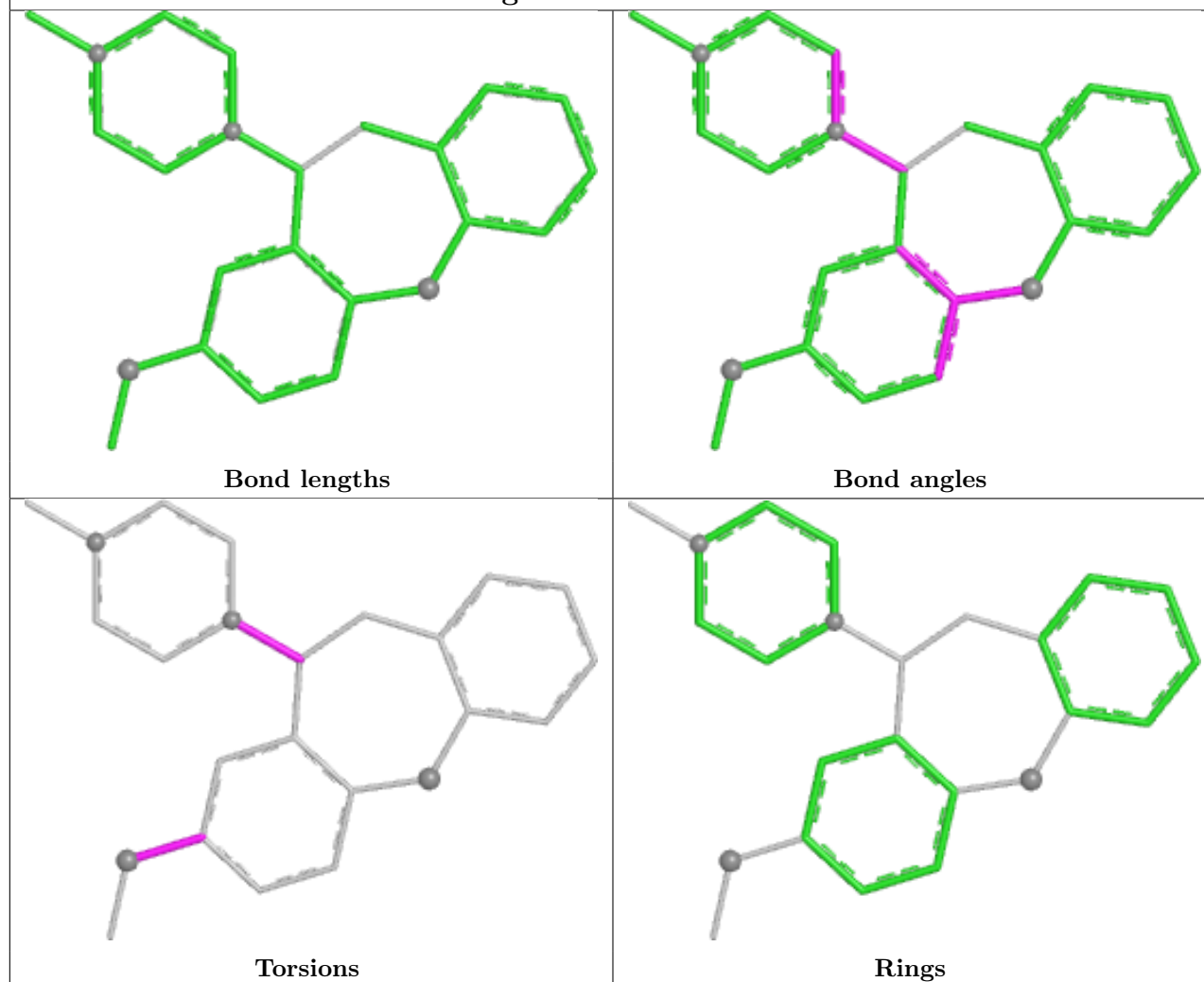
9 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1204	CLR	3	0
3	B	1203	OLA	1	0
3	A	1203	OLA	2	0
6	C	1205	NDS	1	0
7	C	1207	1PE	3	0
3	C	1206	OLA	4	0
3	A	1202	OLA	5	0
4	C	1202	CLR	2	0
2	A	1201	89F	1	0

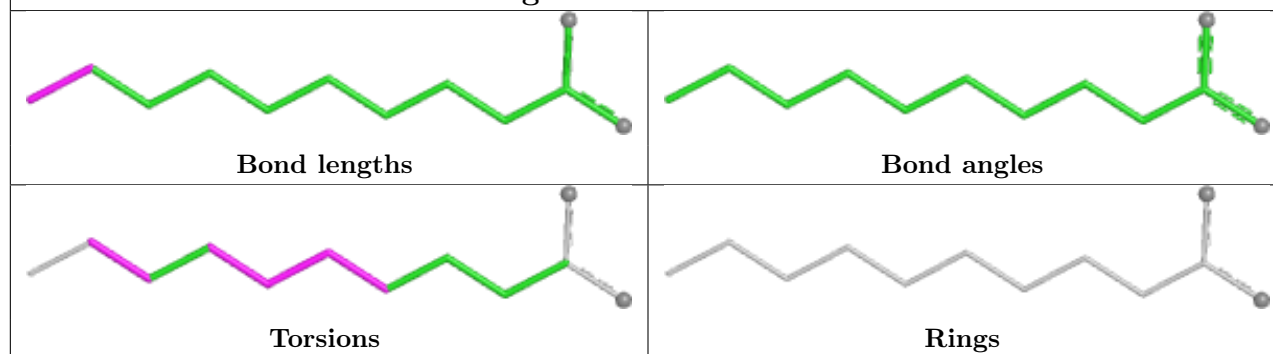
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



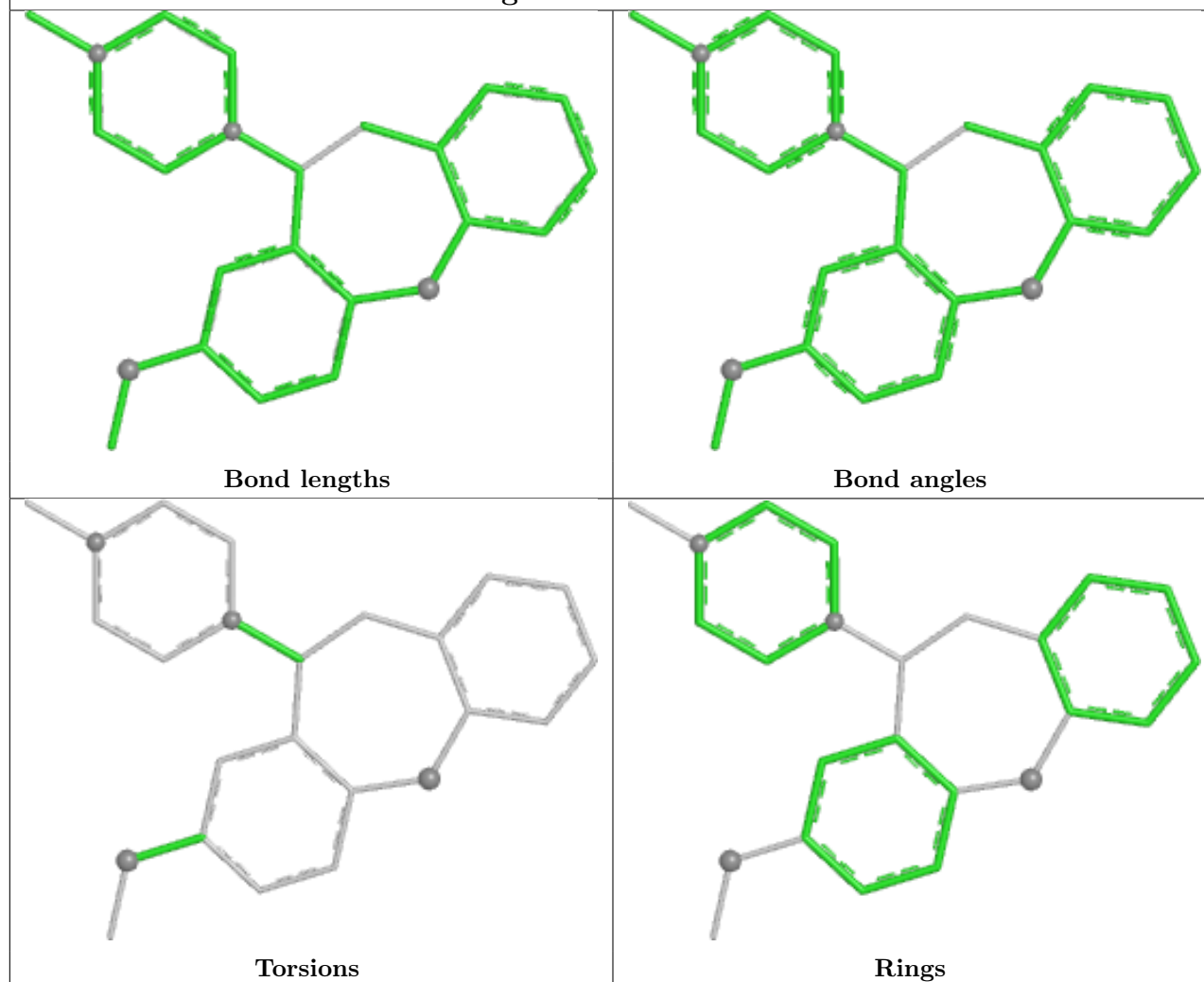
Ligand 89F B 1201



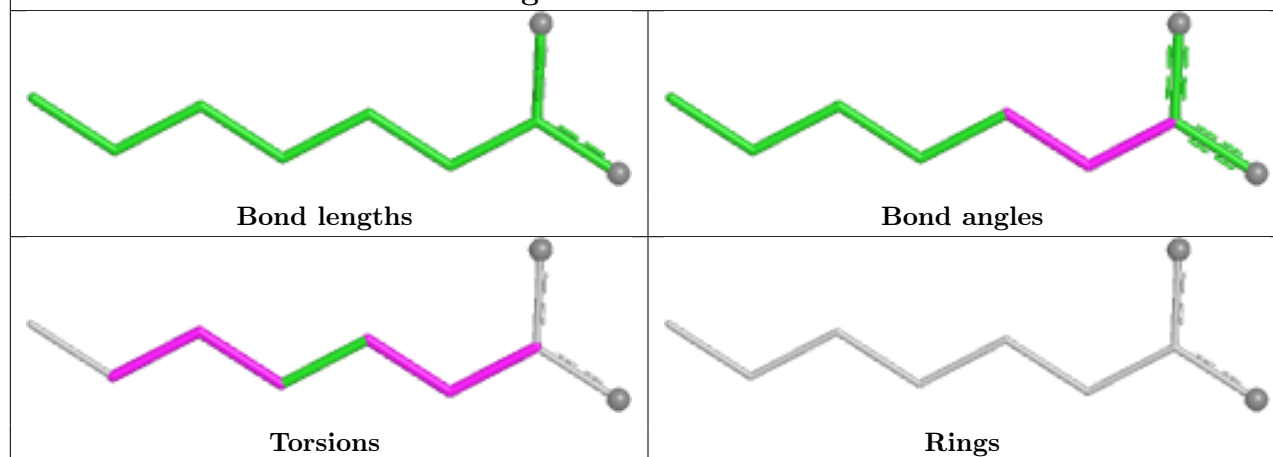
Ligand OLA B 1203

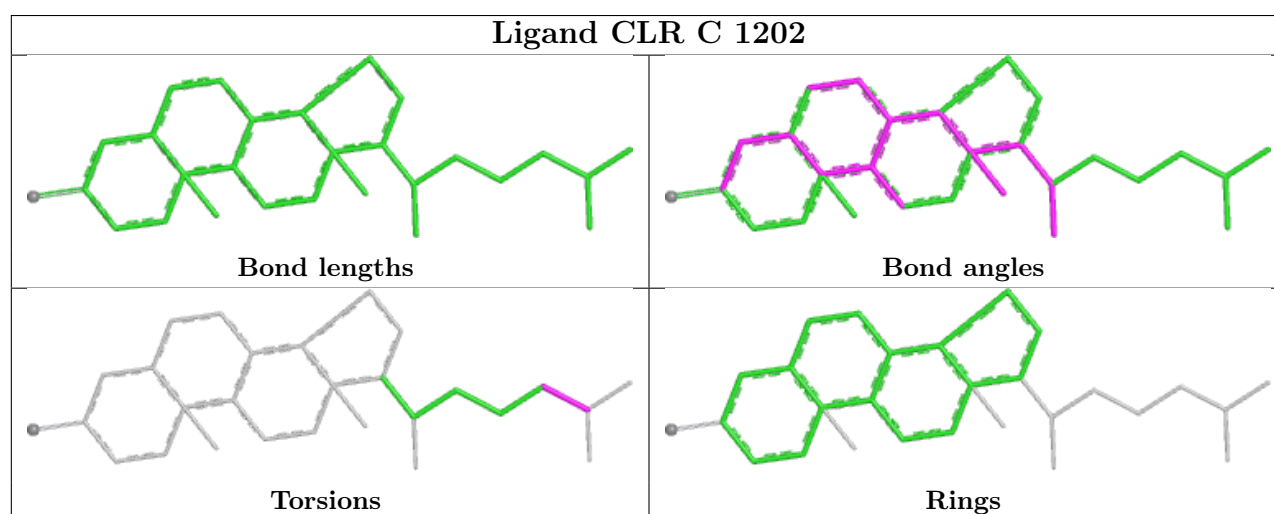
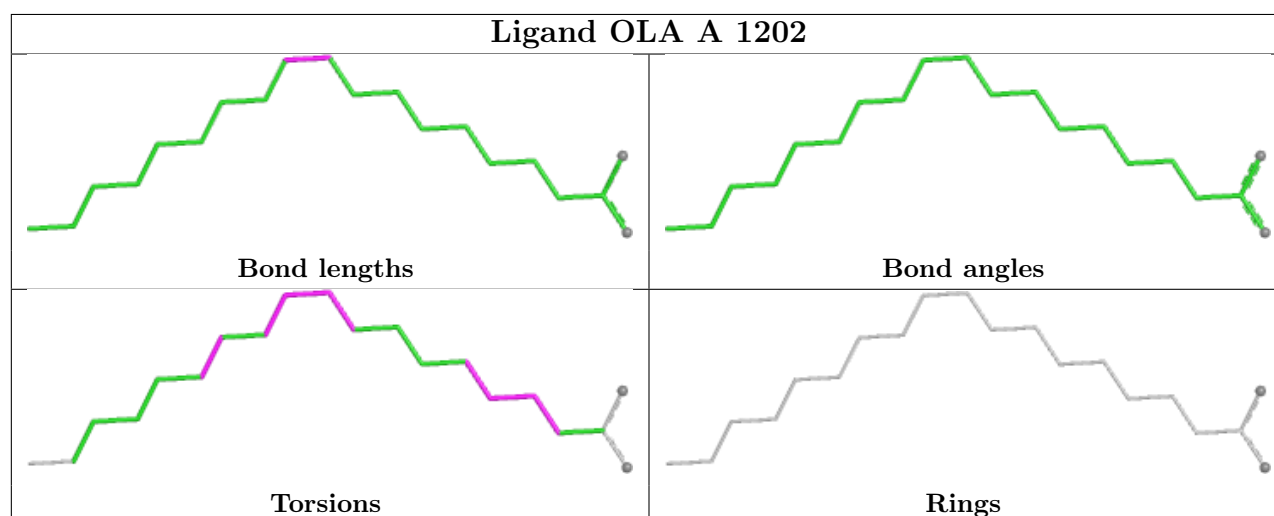
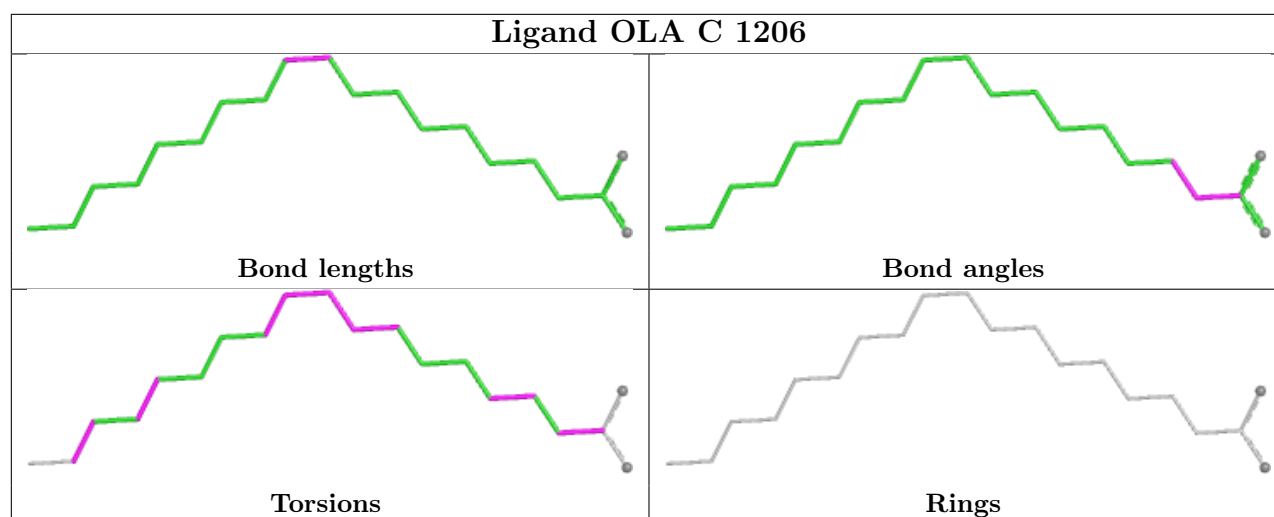


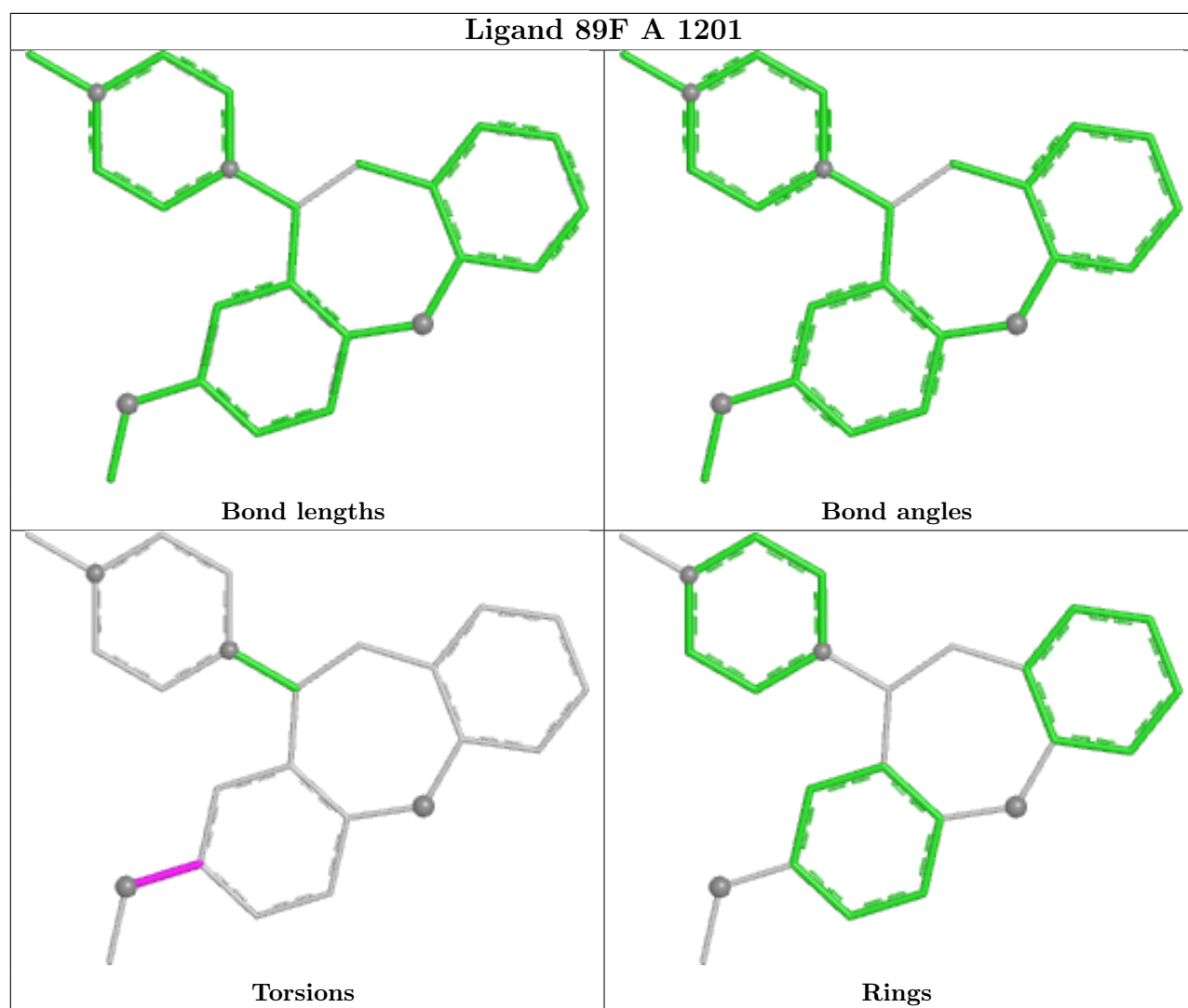
Ligand 89F C 1201



Ligand OLA A 1203







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, 95th 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 ²)	Q<0.9
1	A	378/448 (84%)	0.38	15 (3%) 42 30	16, 39, 89, 112	0
1	B	358/448 (79%)	0.68	23 (6%) 25 20	23, 56, 98, 121	0
1	C	375/448 (83%)	0.32	16 (4%) 40 29	17, 42, 76, 104	0
All	All	1111/1344 (82%)	0.46	54 (4%) 35 26	16, 46, 90, 121	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	353	CYS	4.2
1	A	1029	ALA	4.0
1	B	1025	GLN	3.9
1	C	1092	GLU	3.8
1	C	178	GLN	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](#)

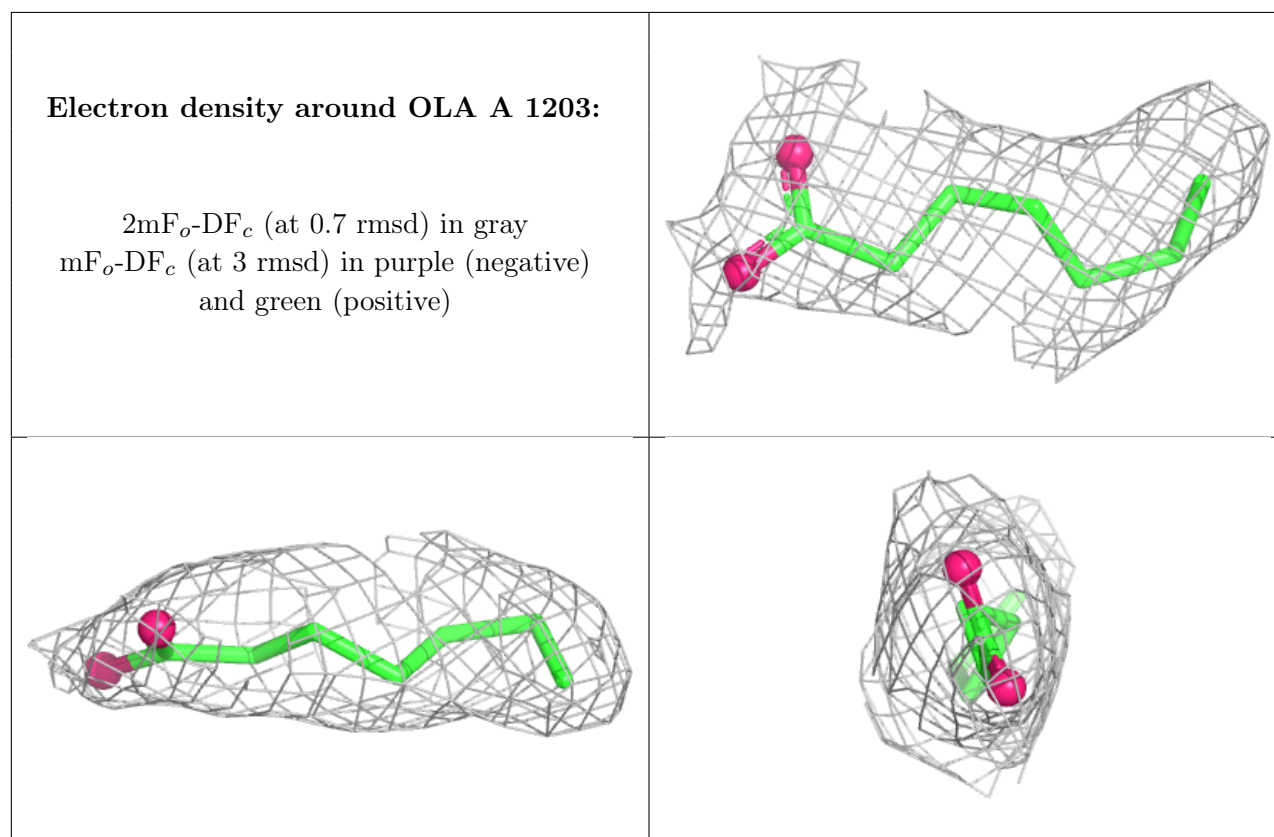
There are no oligosaccharides in this entry.

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, 95th 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.

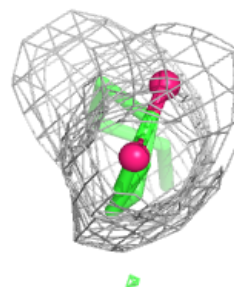
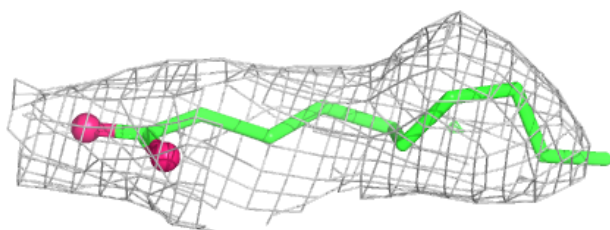
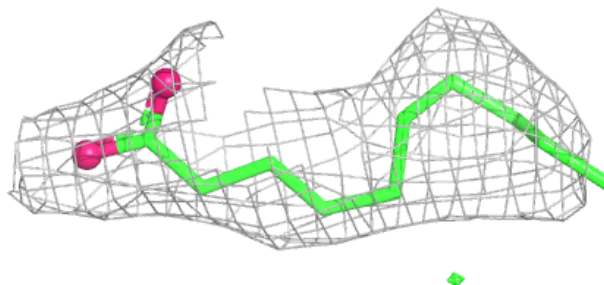
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	OLA	A	1203	9/20	0.62	0.21	41,50,69,69	0
6	NDS	C	1205	12/12	0.72	0.28	51,61,82,90	0
3	OLA	B	1203	12/20	0.74	0.20	38,47,61,61	0
5	PEG	C	1203	7/7	0.77	0.18	44,56,64,76	0
4	CLR	C	1202	28/28	0.81	0.17	66,91,105,105	0
5	PEG	C	1204	7/7	0.83	0.10	52,52,56,57	0
4	CLR	A	1204	28/28	0.86	0.17	64,74,83,84	0
3	OLA	C	1206	20/20	0.89	0.14	29,36,48,50	0
3	OLA	A	1202	20/20	0.89	0.15	25,36,59,60	0
2	89F	B	1201	24/24	0.93	0.15	34,46,52,55	0
7	1PE	C	1207	16/16	0.93	0.13	37,47,73,80	0
5	PEG	A	1205	7/7	0.95	0.11	25,30,35,36	0
2	89F	A	1201	24/24	0.96	0.10	25,28,31,36	0
5	PEG	B	1202	7/7	0.96	0.09	34,43,50,52	0
2	89F	C	1201	24/24	0.97	0.08	16,21,27,30	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.

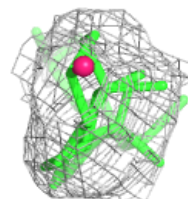
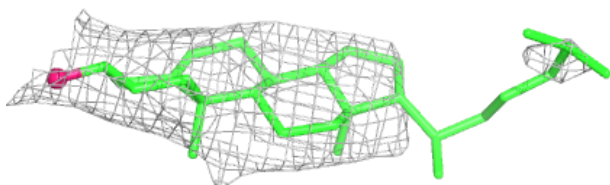
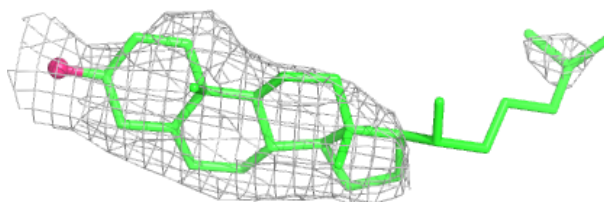


Electron density around OLA B 1203:

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

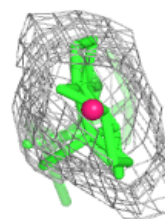
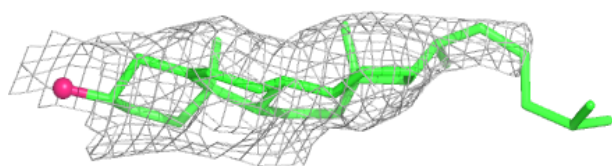
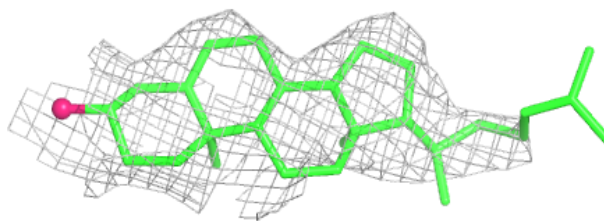
**Electron density around CLR C 1202:**

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

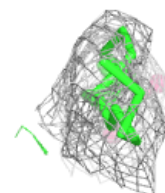
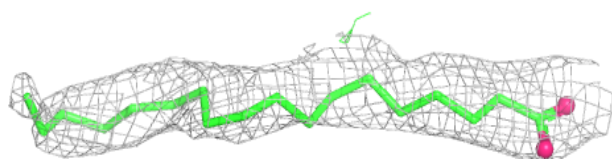


Electron density around CLR A 1204:

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

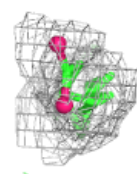
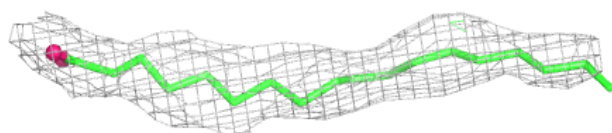
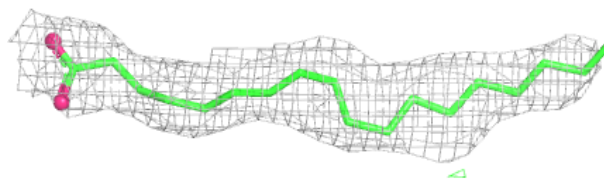
**Electron density around OLA C 1206:**

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

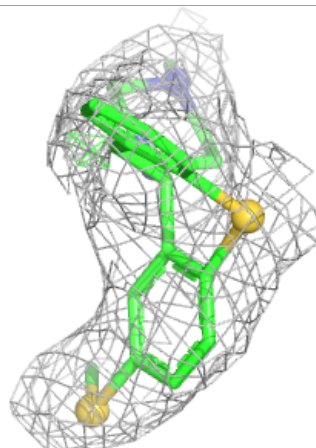
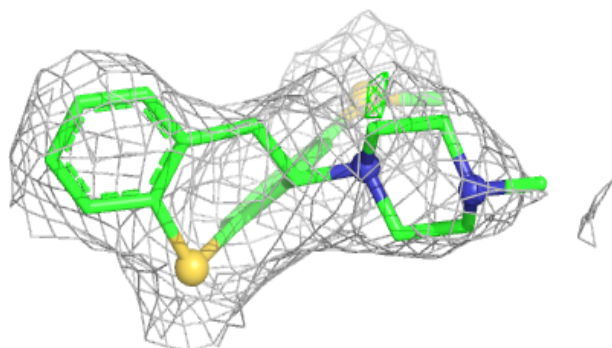
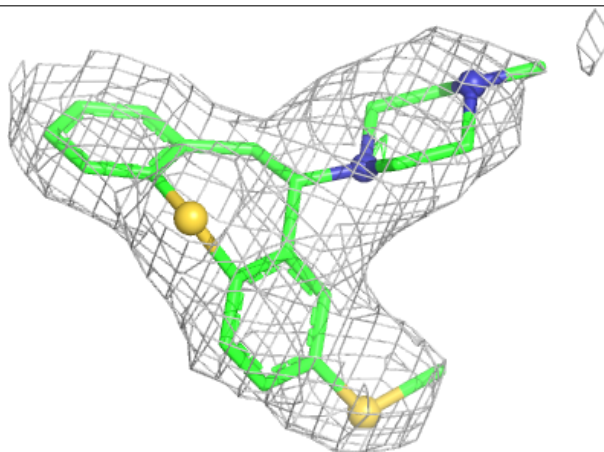


Electron density around OLA A 1202:

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

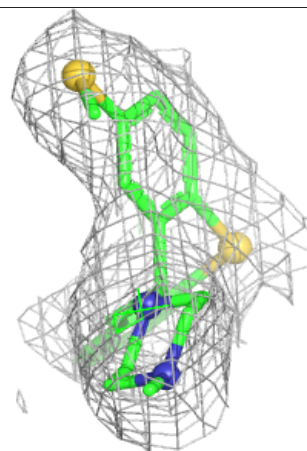
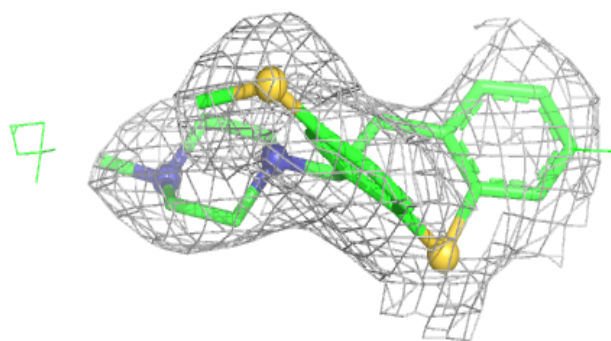
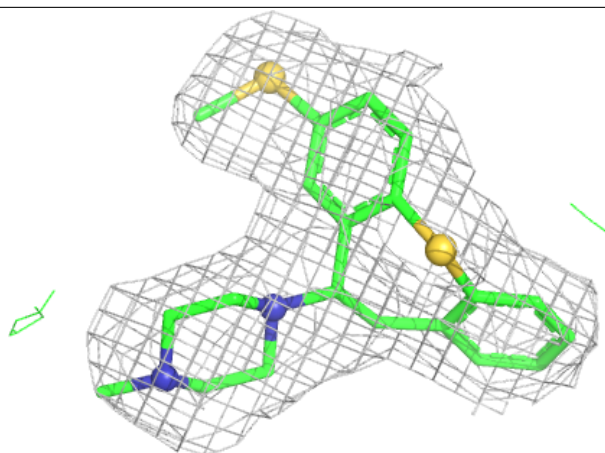
**Electron density around 89F B 1201:**

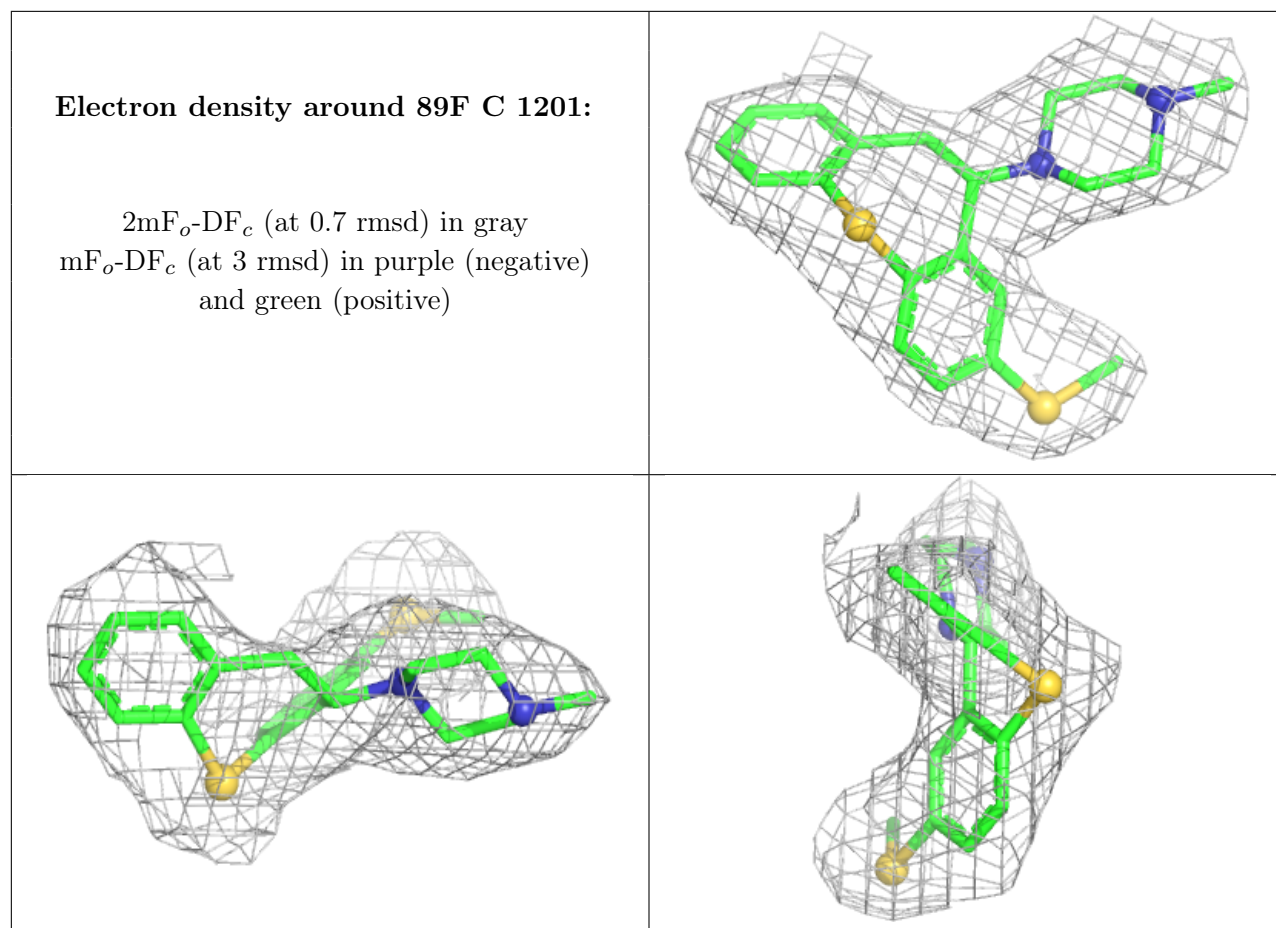
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 89F 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.