



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:14 PM UTC

PDB ID : 5WQC / pdb_00005wqc
Title : Crystal structure of human orexin 2 receptor bound to the selective antagonist EMPA determined by the synchrotron light source at SPring-8.
Authors : Suno, R.; Hirata, K.; Yamashita, K.; Tsujimoto, H.; Sasanuma, M.; Horita, S.; Yamamoto, M.; Rosenbaum, D.M.; Iwata, S.; Shimamura, T.; Kobayashi, T.
Deposited on : 2016-11-25
Resolution : 1.96 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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

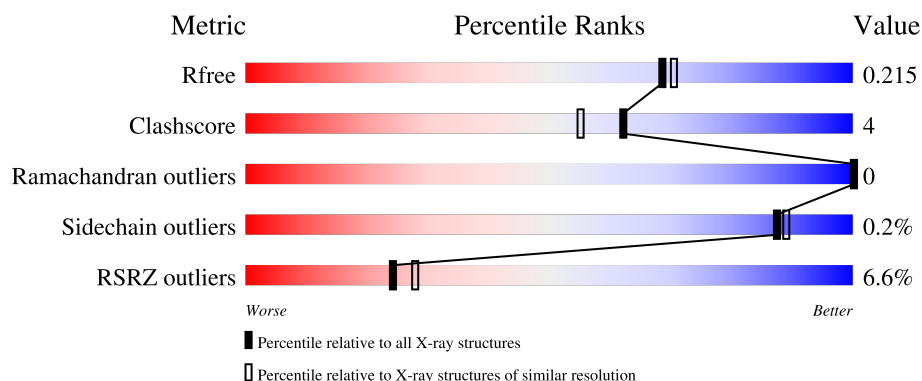
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	560	6% 81% 8% 11%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4302 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

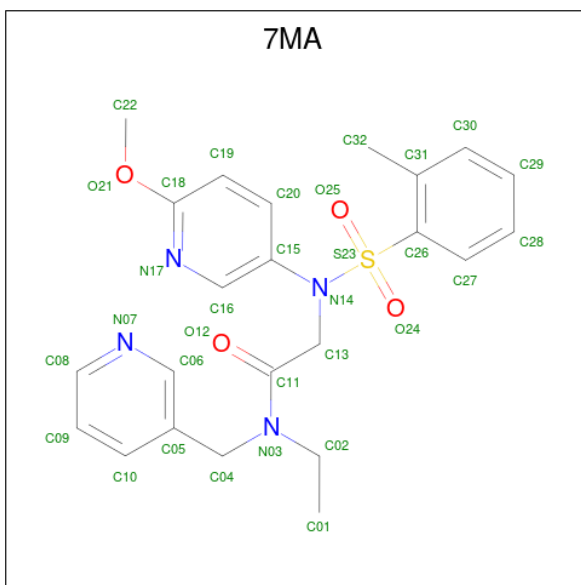
- Molecule 1 is a protein called Orexin receptor type 2, GlgA glycogen synthase, Orexin receptor type 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	6	0
			4043	2652	666	690	35			

There are 20 discrepancies between the modelled and reference sequences:

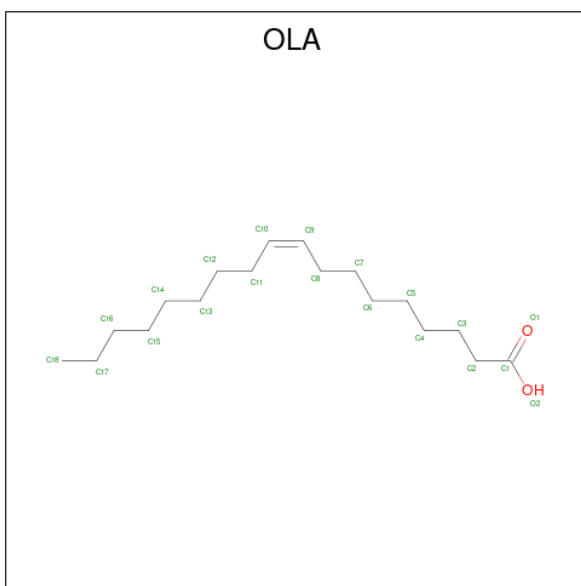
Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	ASP	-	expression tag	UNP O43614
A	-5	TYR	-	expression tag	UNP O43614
A	-4	LYS	-	expression tag	UNP O43614
A	-3	ASP	-	expression tag	UNP O43614
A	-2	ASP	-	expression tag	UNP O43614
A	-1	ASP	-	expression tag	UNP O43614
A	0	ASP	-	expression tag	UNP O43614
A	1	ALA	-	expression tag	UNP O43614
A	2	MET	-	expression tag	UNP O43614
A	308	VAL	ILE	variant	UNP O43614
A	387	HIS	-	expression tag	UNP O43614
A	388	HIS	-	expression tag	UNP O43614
A	389	HIS	-	expression tag	UNP O43614
A	390	HIS	-	expression tag	UNP O43614
A	391	HIS	-	expression tag	UNP O43614
A	392	HIS	-	expression tag	UNP O43614
A	393	HIS	-	expression tag	UNP O43614
A	394	HIS	-	expression tag	UNP O43614
A	395	HIS	-	expression tag	UNP O43614
A	396	HIS	-	expression tag	UNP O43614

- Molecule 2 is N-ethyl-2-[(6-methoxypyridin-3-yl)-(2-methylphenyl)sulfonyl-amino]-N-(pyridin-3-ylmethyl)ethanamide (CCD ID: 7MA) (formula: C₂₃H₂₆N₄O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			32	23	4	4	1		

- Molecule 3 is OLEIC ACID (CCD ID: OLA) (formula: $C_{18}H_{34}O_2$).



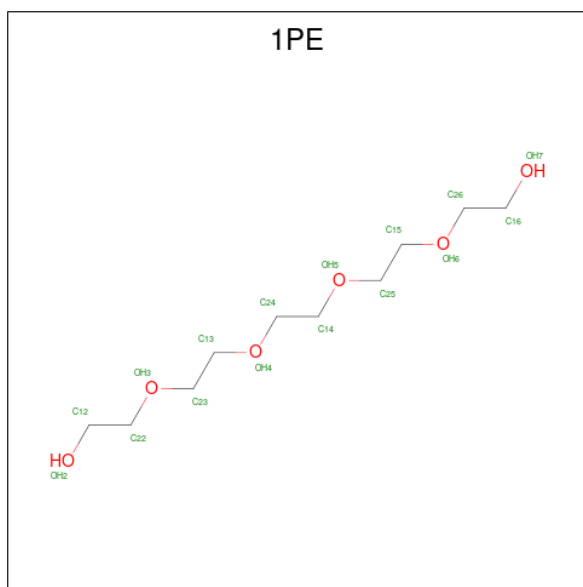
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	12	2		
3	A	1	Total	C	O	0	0
			20	18	2		
3	A	1	Total	C	O	0	0
			14	12	2		

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

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



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

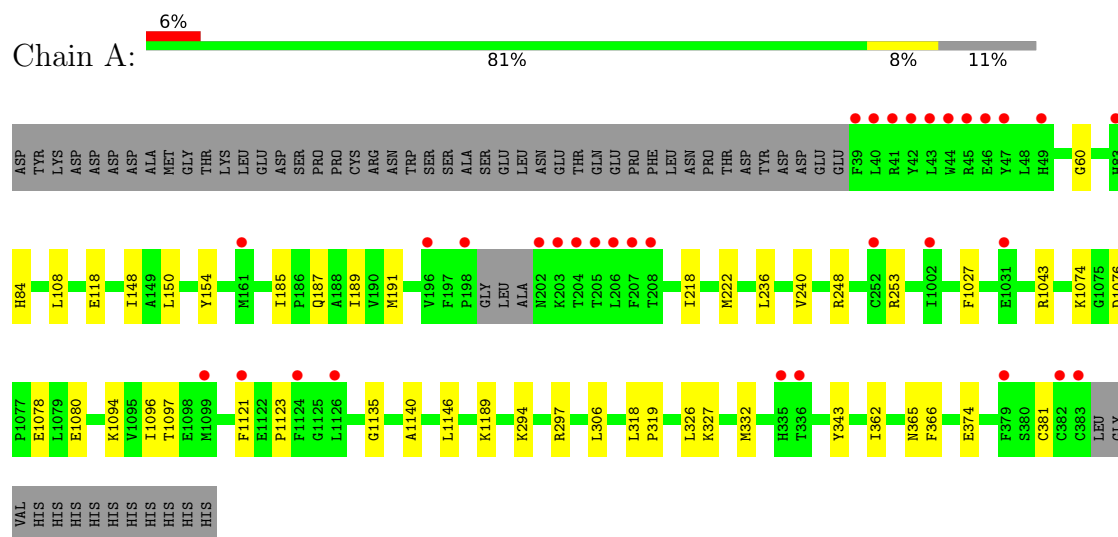
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	126	Total	O	0	0
			126	126		

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: Orexin receptor type 2,GlgA glycogen synthase,Orexin receptor type 2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	94.13Å 75.52Å 95.93Å 90.00° 111.39° 90.00°	Depositor
Resolution (Å)	46.64 – 1.96 46.64 – 1.96	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.64-1.96) 99.9 (46.64-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 1.97Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.181 , 0.215 0.182 , 0.215	Depositor DCC
R_{free} test set	2273 reflections (4.60%)	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.674	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4302	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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: OLA, 7MA, 1PE

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	0.63	0/4154	0.69	0/5622

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	4043	0	4158	35	0
2	A	32	0	0	0	0
3	A	88	0	135	6	0
4	A	13	0	17	1	0
5	A	126	0	0	3	0
All	All	4302	0	4310	35	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 4.

All (35) 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:365:ASN:ND2	3:A:3005:OLA:H22	2.01	0.76
1:A:1074:LYS:HG3	1:A:1080:GLU:OE1	1.95	0.66
1:A:365:ASN:HD22	3:A:3005:OLA:H22	1.59	0.66
1:A:150[B]:LEU:HG	1:A:154:TYR:CE2	2.30	0.66
1:A:294:LYS:HE3	1:A:297:ARG:HH21	1.63	0.63
1:A:366:PHE:CE1	3:A:3005:OLA:H21	2.33	0.63
1:A:1043[A]:ARG:HH22	1:A:1078:GLU:HB3	1.65	0.62
1:A:218:ILE:HG22	1:A:222:MET:HE2	1.83	0.61
1:A:1094:LYS:NZ	5:A:4008:HOH:O	2.37	0.58
1:A:1140:ALA:HB1	1:A:1146:LEU:HD13	1.86	0.56
1:A:374:GLU:OE2	5:A:4001:HOH:O	2.19	0.52
1:A:60:GLY:HA3	3:A:3004:OLA:H142	1.93	0.51
1:A:1027:PHE:HE2	1:A:1096:ILE:HD11	1.76	0.51
1:A:1027:PHE:CE2	1:A:1096:ILE:HD11	2.46	0.51
1:A:1074:LYS:HD2	1:A:1097:THR:HB	1.94	0.50
1:A:1043[A]:ARG:NH2	1:A:1078:GLU:HB3	2.27	0.49
1:A:248:ARG:HE	1:A:253:ARG:NH2	2.12	0.48
1:A:366:PHE:CZ	3:A:3005:OLA:H21	2.48	0.48
1:A:1043[A]:ARG:NH1	1:A:1076:ASP:OD2	2.46	0.48
1:A:318:LEU:HB3	1:A:319:PRO:HD3	1.97	0.47
1:A:327:LYS:HE3	4:A:3501:1PE:H121	1.97	0.46
1:A:326:LEU:HD13	1:A:332:MET:HE2	1.97	0.46
1:A:84:HIS:HE1	5:A:4096:HOH:O	2.00	0.43
1:A:108:LEU:C	1:A:108:LEU:HD23	2.43	0.43
1:A:248:ARG:HE	1:A:253:ARG:HH21	1.66	0.43
1:A:187:GLN:O	1:A:191:MET:HG2	2.18	0.43
1:A:362:ILE:HG12	3:A:3005:OLA:H82	2.00	0.42
1:A:185:ILE:O	1:A:189:ILE:HG12	2.20	0.42
1:A:236:LEU:O	1:A:240:VAL:HG23	2.18	0.42
1:A:118:GLU:HG2	1:A:343:TYR:CZ	2.55	0.42
1:A:1135:GLY:CA	1:A:1189:LYS:HE3	2.50	0.41
1:A:118:GLU:HG2	1:A:343:TYR:OH	2.21	0.41
1:A:1121:PHE:CZ	1:A:1123:PRO:HG3	2.56	0.40
1:A:294:LYS:HE3	1:A:297:ARG:NH2	2.31	0.40
1:A:148:ILE:HG21	1:A:306:LEU:HD22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	501/560 (90%)	493 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	445/494 (90%)	444 (100%)	1 (0%)	87	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	381	CYS

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	134	GLN
1	A	1090	HIS
1	A	324	ASN
1	A	356	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 ⓘ

7 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	1PE	A	3501	-	12,12,15	0.47	0	11,11,14	0.71	0
3	OLA	A	3002	-	19,19,19	0.81	1 (5%)	19,19,19	0.98	0
3	OLA	A	3004	-	19,19,19	0.82	1 (5%)	19,19,19	0.96	1 (5%)
3	OLA	A	3005	-	19,19,19	0.83	1 (5%)	19,19,19	0.81	1 (5%)
2	7MA	A	2001	-	34,34,34	4.35	10 (29%)	46,47,47	2.23	18 (39%)
3	OLA	A	3003	-	13,13,19	0.96	1 (7%)	13,13,19	1.33	1 (7%)
3	OLA	A	3001	-	13,13,19	0.99	1 (7%)	13,13,19	1.34	2 (15%)

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	1PE	A	3501	-	-	2/10/10/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OLA	A	3002	-	-	11/17/17/17	-
3	OLA	A	3004	-	-	11/17/17/17	-
3	OLA	A	3005	-	-	11/17/17/17	-
2	7MA	A	2001	-	-	7/32/32/32	0/3/3/3
3	OLA	A	3003	-	-	5/11/11/17	-
3	OLA	A	3001	-	-	5/11/11/17	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	7MA	S23-N14	16.85	1.89	1.65
2	A	2001	7MA	O24-S23	12.49	1.56	1.43
2	A	2001	7MA	O25-S23	9.44	1.53	1.43
2	A	2001	7MA	C32-C31	-5.20	1.41	1.51
2	A	2001	7MA	C15-N14	-4.83	1.37	1.44
2	A	2001	7MA	C04-C05	-4.42	1.43	1.51
2	A	2001	7MA	C06-N07	3.42	1.41	1.34
3	A	3005	OLA	C10-C9	2.95	1.48	1.31
3	A	3001	OLA	C10-C9	2.91	1.48	1.31
3	A	3002	OLA	C10-C9	2.76	1.47	1.31
3	A	3004	OLA	C10-C9	2.73	1.47	1.31
3	A	3003	OLA	C10-C9	2.73	1.47	1.31
2	A	2001	7MA	C13-N14	-2.52	1.44	1.48
2	A	2001	7MA	C26-S23	2.47	1.81	1.78
2	A	2001	7MA	C19-C20	2.31	1.42	1.38

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2001	7MA	C20-C15-N14	6.31	129.34	120.15
2	A	2001	7MA	O25-S23-O24	-5.15	111.55	119.59
2	A	2001	7MA	C13-N14-C15	4.12	122.20	116.67
2	A	2001	7MA	O21-C18-C19	3.78	123.46	116.77
2	A	2001	7MA	C13-C11-N03	3.49	121.27	117.04
2	A	2001	7MA	C26-S23-N14	3.47	112.26	106.16
2	A	2001	7MA	C05-C06-N07	-3.11	117.81	123.75
3	A	3001	OLA	O2-C1-C2	3.05	123.63	114.00
2	A	2001	7MA	C19-C18-N17	-3.03	119.92	124.65
2	A	2001	7MA	C30-C31-C26	2.92	119.35	116.27
3	A	3004	OLA	C3-C2-C1	-2.88	106.99	114.51
2	A	2001	7MA	O12-C11-C13	-2.75	116.50	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2001	7MA	C20-C19-C18	2.67	121.11	117.71
3	A	3003	OLA	C3-C2-C1	-2.64	107.63	114.51
2	A	2001	7MA	C16-N17-C18	2.56	119.05	116.72
2	A	2001	7MA	C19-C20-C15	-2.55	117.07	120.30
3	A	3001	OLA	O2-C1-O1	-2.52	116.84	123.33
2	A	2001	7MA	C13-N14-S23	-2.51	112.38	117.47
2	A	2001	7MA	C08-N07-C06	2.46	121.17	116.85
2	A	2001	7MA	C04-C05-C10	-2.26	116.59	120.75
2	A	2001	7MA	C10-C05-C06	2.15	120.26	117.10
2	A	2001	7MA	C15-N14-S23	-2.13	113.44	117.72
3	A	3005	OLA	O2-C1-C2	2.11	120.65	114.00

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2001	7MA	O12-C11-C13-N14
2	A	2001	7MA	N03-C11-C13-N14
2	A	2001	7MA	C15-N14-S23-C26
3	A	3002	OLA	C11-C10-C9-C8
3	A	3004	OLA	C11-C10-C9-C8
3	A	3005	OLA	C1-C2-C3-C4
3	A	3001	OLA	C11-C10-C9-C8
2	A	2001	7MA	C13-N14-S23-O25
3	A	3002	OLA	C12-C13-C14-C15
3	A	3005	OLA	C10-C11-C12-C13
3	A	3004	OLA	C14-C15-C16-C17
3	A	3005	OLA	C5-C6-C7-C8
3	A	3002	OLA	C1-C2-C3-C4
3	A	3002	OLA	C13-C14-C15-C16
3	A	3005	OLA	C14-C15-C16-C17
2	A	2001	7MA	C15-N14-S23-O25
3	A	3005	OLA	C11-C12-C13-C14
3	A	3001	OLA	C5-C6-C7-C8
4	A	3501	1PE	C15-C25-OH5-C14
3	A	3004	OLA	C11-C12-C13-C14
3	A	3004	OLA	C6-C7-C8-C9
3	A	3001	OLA	C4-C5-C6-C7
3	A	3004	OLA	C13-C14-C15-C16
3	A	3003	OLA	C6-C7-C8-C9
3	A	3005	OLA	C6-C7-C8-C9
3	A	3002	OLA	C4-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
3	A	3005	OLA	C15-C16-C17-C18
3	A	3004	OLA	C3-C4-C5-C6
3	A	3002	OLA	C3-C4-C5-C6
3	A	3002	OLA	C5-C6-C7-C8
3	A	3003	OLA	C9-C10-C11-C12
3	A	3005	OLA	C13-C14-C15-C16
3	A	3002	OLA	C10-C11-C12-C13
2	A	2001	7MA	C13-N14-S23-C26
3	A	3003	OLA	C5-C6-C7-C8
3	A	3005	OLA	C2-C3-C4-C5
3	A	3004	OLA	C7-C8-C9-C10
2	A	2001	7MA	C13-N14-S23-O24
3	A	3001	OLA	C9-C10-C11-C12
4	A	3501	1PE	C13-C23-OH3-C22
3	A	3003	OLA	C11-C10-C9-C8
3	A	3002	OLA	O1-C1-C2-C3
3	A	3002	OLA	O2-C1-C2-C3
3	A	3005	OLA	C4-C5-C6-C7
3	A	3004	OLA	C2-C3-C4-C5
3	A	3003	OLA	C7-C8-C9-C10
3	A	3005	OLA	C9-C10-C11-C12
3	A	3001	OLA	C7-C8-C9-C10
3	A	3002	OLA	C9-C10-C11-C12
3	A	3004	OLA	C9-C10-C11-C12
3	A	3004	OLA	O2-C1-C2-C3
3	A	3004	OLA	O1-C1-C2-C3

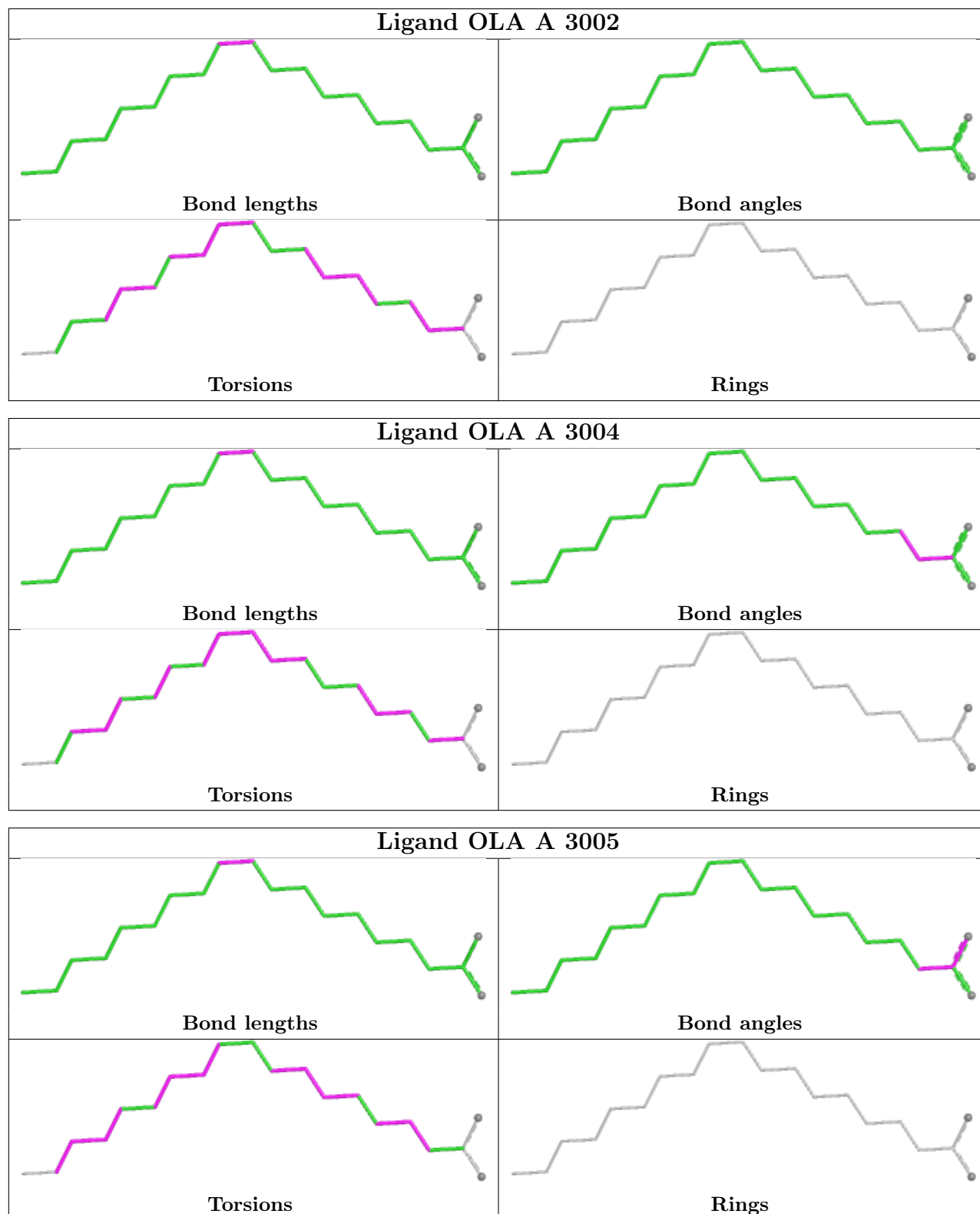
There are no ring outliers.

3 monomers are involved in 7 short contacts:

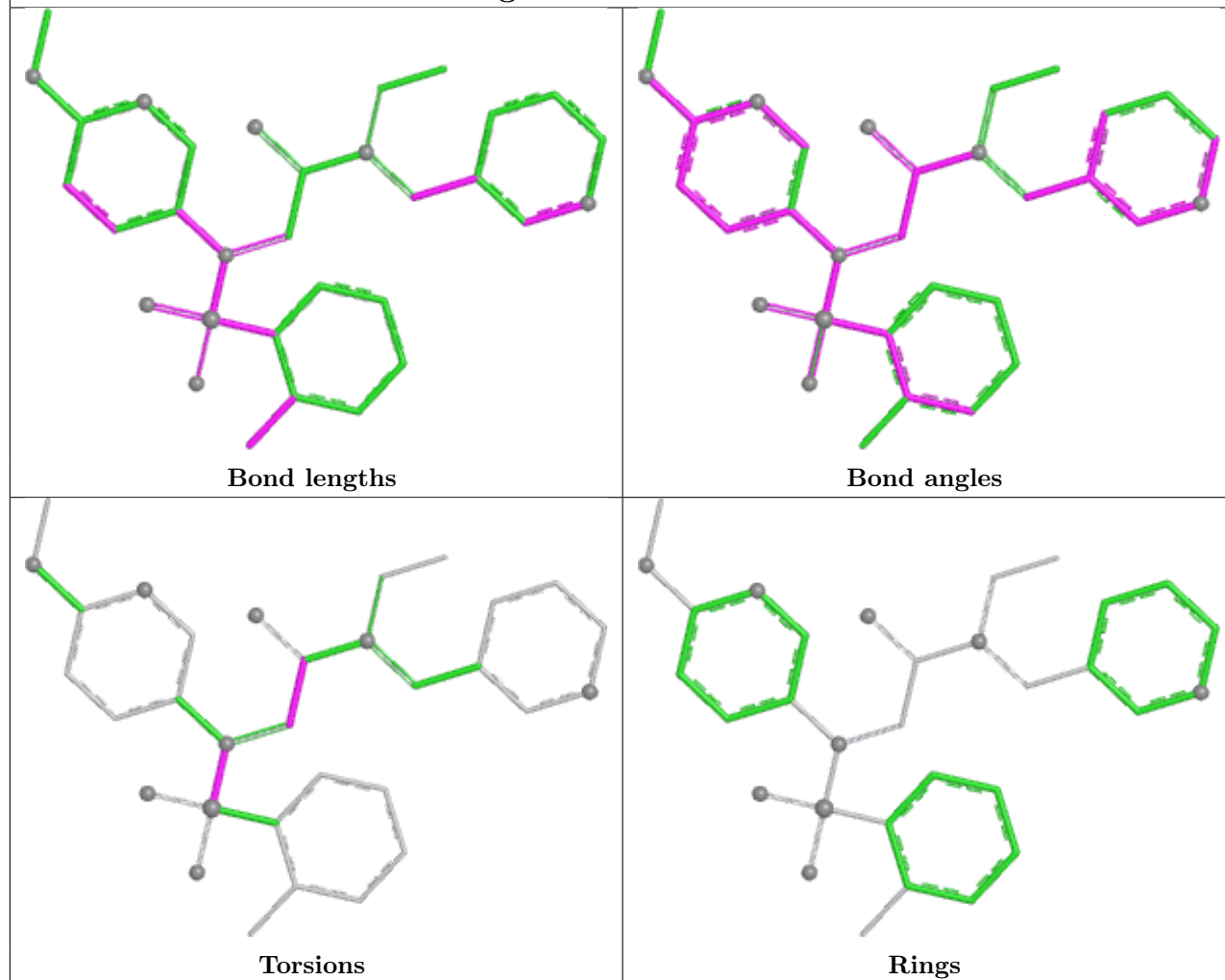
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	3501	1PE	1	0
3	A	3004	OLA	1	0
3	A	3005	OLA	5	0

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

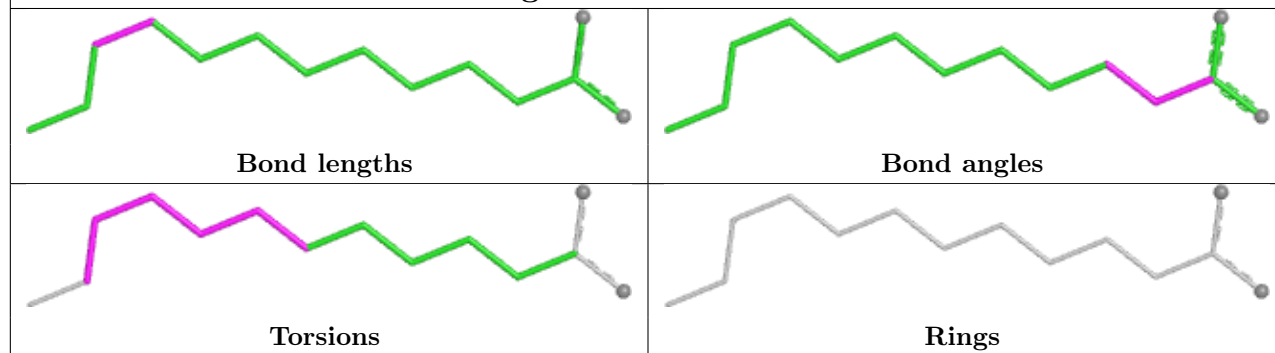
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

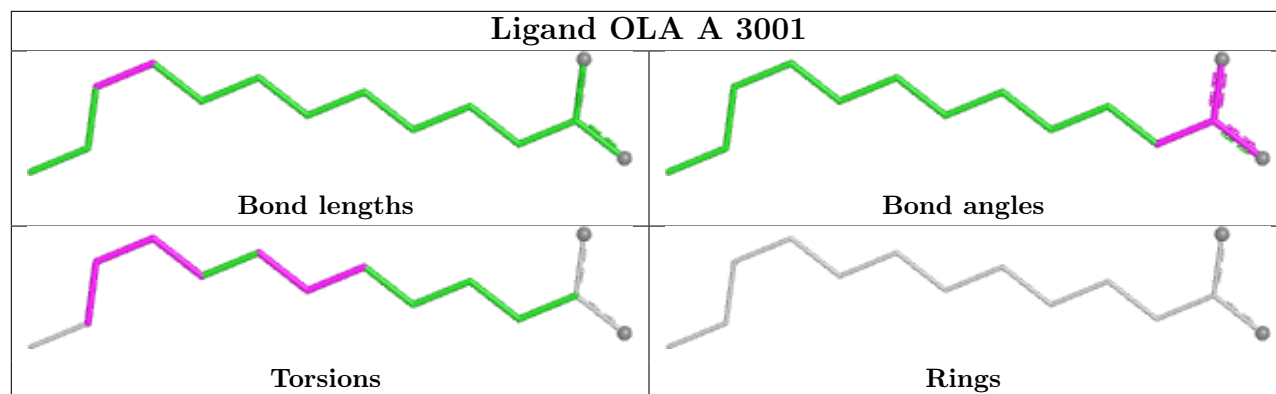


Ligand 7MA A 2001



Ligand OLA A 3003





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	499/560 (89%)	0.32	33 (6%) 24 28	15, 35, 72, 110	6 (1%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	47	TYR	6.7
1	A	40	LEU	6.0
1	A	44	TRP	5.4
1	A	39	PHE	5.4
1	A	1124	PHE	4.7
1	A	198	PRO	4.5
1	A	43	LEU	4.3
1	A	207	PHE	4.3
1	A	196	VAL	4.1
1	A	161	MET	4.1
1	A	383	CYS	3.6
1	A	206	LEU	3.5
1	A	45	ARG	3.4
1	A	204	THR	3.2
1	A	42	TYR	3.1
1	A	335	HIS	3.1
1	A	382	CYS	3.0
1	A	379	PHE	2.8
1	A	203	LYS	2.7
1	A	252	CYS	2.5
1	A	46	GLU	2.5
1	A	202	ASN	2.5
1	A	83	HIS	2.4
1	A	1126	LEU	2.4
1	A	1031	GLU	2.4
1	A	1121	PHE	2.3
1	A	1002	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	208	THR	2.2
1	A	41	ARG	2.2
1	A	205	THR	2.2
1	A	49	HIS	2.1
1	A	336	THR	2.1
1	A	1099	MET	2.0

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](#)

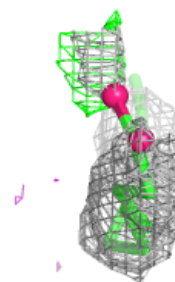
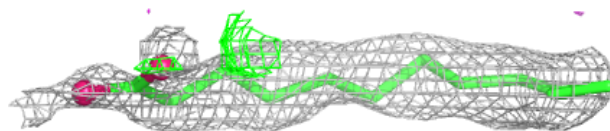
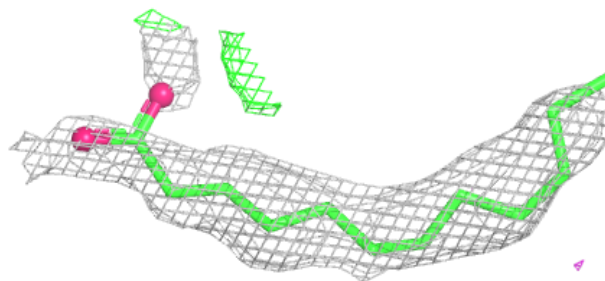
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	3003	14/20	0.79	0.22	56,62,83,84	0
3	OLA	A	3005	20/20	0.82	0.20	54,65,80,82	0
4	1PE	A	3501	13/16	0.82	0.17	47,57,69,71	0
3	OLA	A	3001	14/20	0.83	0.19	46,52,64,65	0
3	OLA	A	3004	20/20	0.86	0.18	47,59,76,77	0
3	OLA	A	3002	20/20	0.87	0.17	47,58,71,71	0
2	7MA	A	2001	32/32	0.90	0.14	24,38,69,77	0

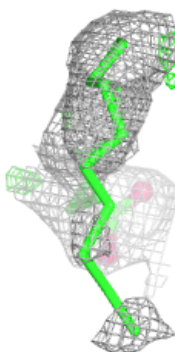
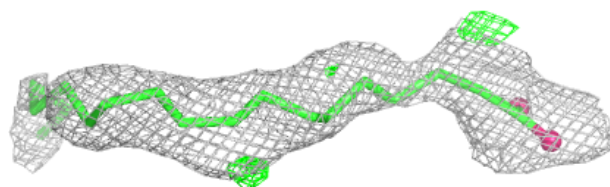
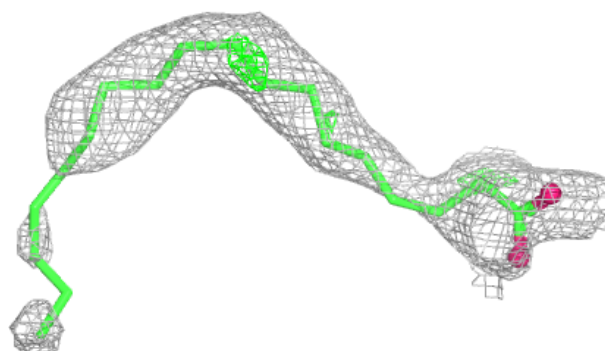
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OLA A 3003:

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

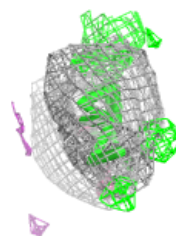
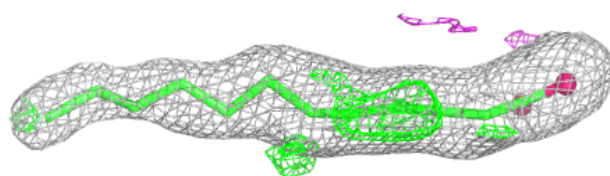
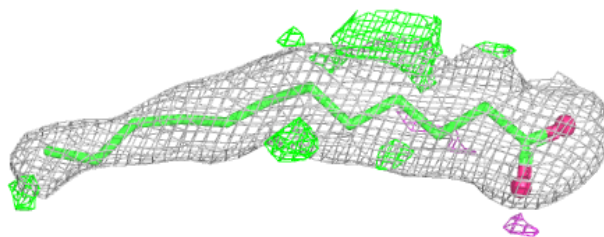
**Electron density around OLA A 3005:**

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

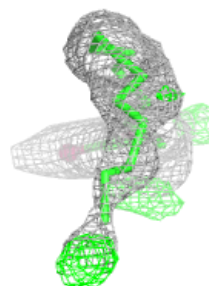
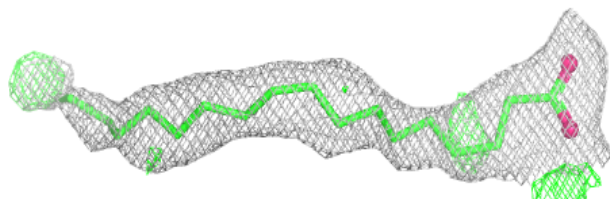
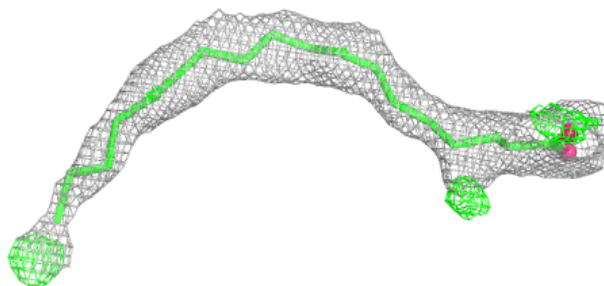


Electron density around OLA A 3001:

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

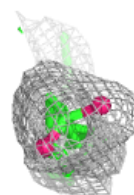
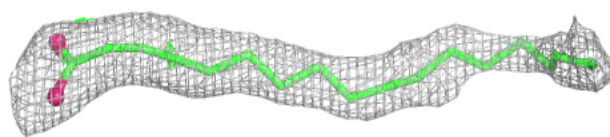
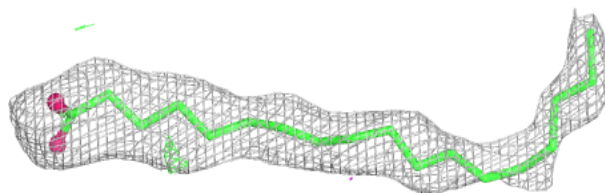
**Electron density around OLA A 3004:**

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



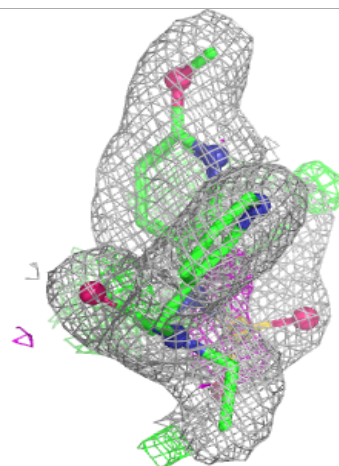
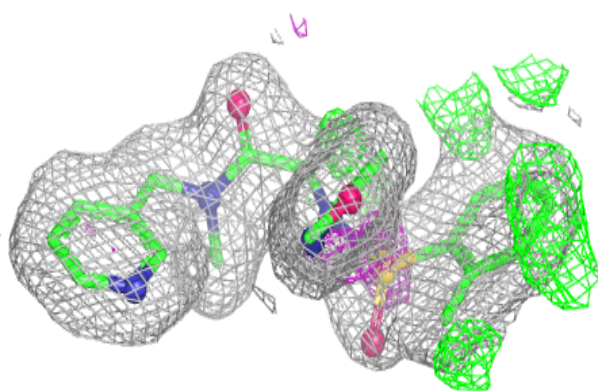
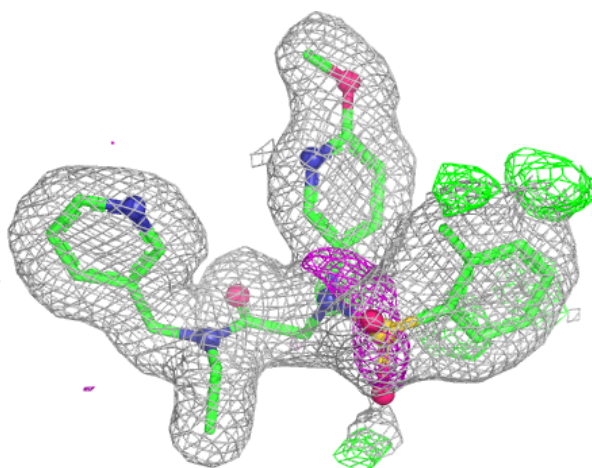
Electron density around OLA A 3002:

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



Electron density around 7MA A 2001:

$2mF_o-DF_c$ (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.