Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:55 PM UTC

PDB ID	:	9H1W / pdb_00009h1w
Title	:	Grouped 150-240 ms dark structure of sensory rhodopsin-II solved by serial millisecond crystallography
Authors	:	Ortolani, G.; Bosman, R.; Branden, G.; Neutze, R.
Deposited on	:	2024-10-10
Resolution	:	2.20 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:

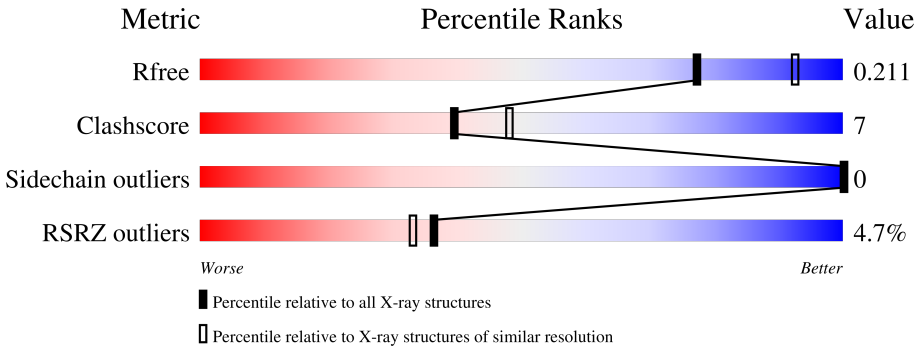
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 <=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	249	4% 76% 9% 15%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BOG	A	303	X	-	-	-
4	BOG	A	304	X	-	-	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 1951 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.

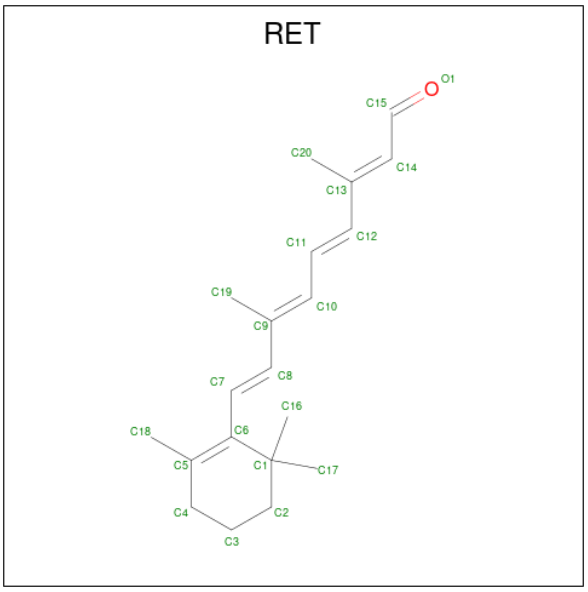
- Molecule 1 is a protein called Sensory rhodopsin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	0	0
			1603	1082	250	264	7			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	240	GLU	-	expression tag	UNP P42196
A	241	ASN	-	expression tag	UNP P42196
A	242	SER	-	expression tag	UNP P42196
A	243	HIS	-	expression tag	UNP P42196
A	244	HIS	-	expression tag	UNP P42196
A	245	HIS	-	expression tag	UNP P42196
A	246	HIS	-	expression tag	UNP P42196
A	247	HIS	-	expression tag	UNP P42196
A	248	HIS	-	expression tag	UNP P42196
A	249	HIS	-	expression tag	UNP P42196

- Molecule 2 is RETINAL (CCD ID: RET) (formula: $C_{20}H_{28}O$) (labeled as "Ligand of Interest" by depositor).

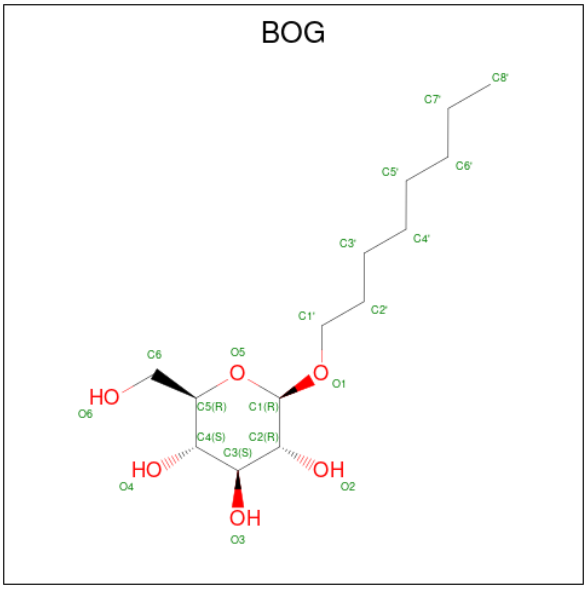


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C 20 20	0	0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

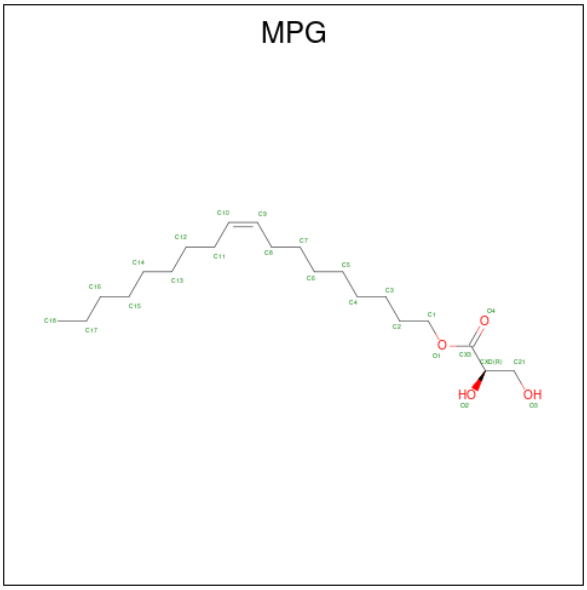
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

- Molecule 4 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: $C_{14}H_{28}O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 20 14 6	0	0
4	A	1	Total C O 20 14 6	0	0
4	A	1	Total C O 20 14 6	0	0
4	A	1	Total C O 20 14 6	0	0
4	A	1	Total C O 20 14 6	0	0
4	A	1	Total C O 20 14 6	0	0
4	A	1	Total C O 16 10 6	0	0
4	A	1	Total C O 20 14 6	0	0

- Molecule 5 is [(Z)-octadec-9-enyl] (2R)-2,3-bis(oxidanyl)propanoate (CCD ID: MPG) (formula: $C_{21}H_{40}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 25 21 4	0	0
5	A	1	Total C O 25 21 4	0	0
5	A	1	Total C O 25 21 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 18 14 4	0	0
5	A	1	Total C O 25 21 4	0	0
5	A	1	Total C O 20 16 4	0	0

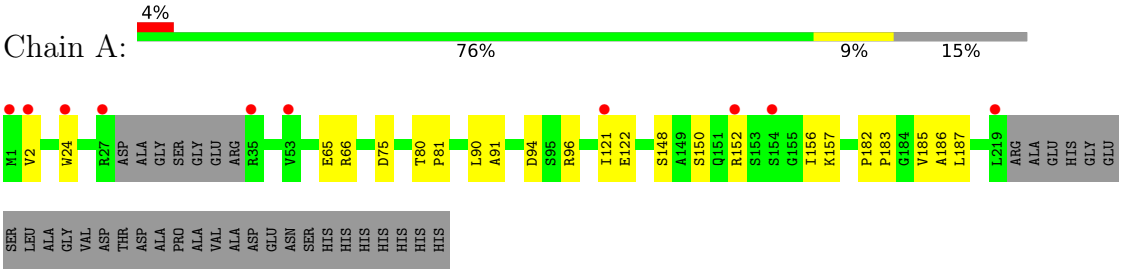
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	33	Total O 33 33	0	3

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: Sensory rhodopsin-2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	89.75Å 131.75Å 51.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.88 – 2.20 44.88 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.88-2.20) 99.7 (44.88-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.29 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.216 , 0.218 (Not available) , 0.211	Depositor DCC
R_{free} test set	1702 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å^2)	46.5	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 84.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1951	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.26% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: RET, MPG, BOG, CL

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	0.14	0/1644	0.33	0/2252

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

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	1603	0	1683	22	0
2	A	20	0	27	4	0
3	A	1	0	0	0	0
4	A	156	0	213	1	0
5	A	138	0	210	1	0
6	A	33	0	0	0	0
All	All	1951	0	2133	27	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (27) 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:94:ASP:OD1	1:A:94:ASP:C	2.28	0.76
1:A:152:ARG:HD3	1:A:156:ILE:HG21	1.71	0.72
1:A:150:SER:HA	1:A:157:LYS:NZ	2.05	0.72
2:A:301:RET:H8	2:A:301:RET:H171	1.72	0.71
1:A:150:SER:HA	1:A:157:LYS:HZ3	1.60	0.66
1:A:91:ALA:O	1:A:148:SER:OG	2.18	0.62
1:A:150:SER:O	1:A:157:LYS:NZ	2.36	0.57
1:A:121:ILE:HD12	1:A:122:GLU:N	2.20	0.56
1:A:94:ASP:OD1	1:A:94:ASP:O	2.24	0.55
1:A:2:VAL:HG13	1:A:2:VAL:O	2.05	0.55
2:A:301:RET:H171	2:A:301:RET:C8	2.38	0.54
1:A:94:ASP:OD1	1:A:96:ARG:N	2.40	0.54
1:A:185:VAL:O	1:A:185:VAL:HG23	2.10	0.51
1:A:185:VAL:O	1:A:187:LEU:N	2.46	0.49
1:A:90:LEU:O	1:A:152:ARG:HD2	2.13	0.48
1:A:66:ARG:HH11	1:A:66:ARG:HG3	1.79	0.47
1:A:150:SER:HA	1:A:157:LYS:HZ2	1.79	0.47
2:A:301:RET:H8	2:A:301:RET:H161	1.95	0.47
1:A:65:GLU:HA	1:A:65:GLU:OE1	2.15	0.46
1:A:80:THR:N	1:A:81:PRO:HD2	2.31	0.45
1:A:75:ASP:OD1	1:A:75:ASP:C	2.60	0.44
1:A:182:PRO:N	1:A:183:PRO:CD	2.82	0.43
4:A:305:BOG:H1	4:A:305:BOG:H3'2	2.01	0.43
1:A:185:VAL:O	1:A:186:ALA:C	2.62	0.42
2:A:301:RET:C8	2:A:301:RET:H161	2.48	0.42
1:A:24:TRP:CD2	5:A:312:MPG:H10	2.56	0.41
1:A:150:SER:CA	1:A:157:LYS:NZ	2.81	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

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	142/190 (75%)	142 (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 (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 for Mogul analysis.

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	$\#\|Z\| > 2$
5	MPG	A	306	-	24,24,24	0.99	1 (4%)	24,25,25	1.09	2 (8%)
5	MPG	A	312	-	24,24,24	0.97	1 (4%)	24,25,25	1.13	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	MPG	A	314	-	19,19,24	1.17	1 (5%)	19,20,25	1.15	1 (5%)
4	BOG	A	316	-	20,20,20	1.33	2 (10%)	25,25,25	0.85	0
4	BOG	A	305	-	20,20,20	1.40	2 (10%)	25,25,25	1.04	2 (8%)
4	BOG	A	313	-	20,20,20	1.31	2 (10%)	25,25,25	0.73	0
4	BOG	A	304	-	20,20,20	1.08	1 (5%)	25,25,25	1.55	5 (20%)
5	MPG	A	310	-	24,24,24	1.00	1 (4%)	24,25,25	1.07	2 (8%)
4	BOG	A	308	-	20,20,20	1.32	2 (10%)	25,25,25	0.78	0
4	BOG	A	307	-	20,20,20	1.29	2 (10%)	25,25,25	0.82	1 (4%)
5	MPG	A	309	-	24,24,24	1.08	1 (4%)	24,25,25	1.12	2 (8%)
5	MPG	A	311	-	17,17,24	1.23	1 (5%)	17,18,25	1.19	2 (11%)
2	RET	A	301	1	20,20,21	0.83	1 (5%)	27,27,28	0.37	0
4	BOG	A	315	-	16,16,20	1.38	2 (12%)	21,21,25	0.99	1 (4%)
4	BOG	A	303	-	20,20,20	1.11	1 (5%)	25,25,25	0.65	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
5	MPG	A	306	-	-	11/25/25/25	-
5	MPG	A	312	-	-	12/25/25/25	-
5	MPG	A	314	-	-	5/20/20/25	-
4	BOG	A	316	-	-	10/11/31/31	0/1/1/1
4	BOG	A	305	-	-	6/11/31/31	0/1/1/1
4	BOG	A	313	-	-	4/11/31/31	0/1/1/1
4	BOG	A	304	-	2/2/5/5	7/11/31/31	0/1/1/1
5	MPG	A	310	-	-	9/25/25/25	-
4	BOG	A	308	-	-	4/11/31/31	0/1/1/1
4	BOG	A	307	-	-	4/11/31/31	0/1/1/1
5	MPG	A	309	-	-	9/25/25/25	-
5	MPG	A	311	-	-	5/18/18/25	-
2	RET	A	301	1	-	0/13/30/31	0/1/1/1
4	BOG	A	315	-	-	4/7/27/31	0/1/1/1
4	BOG	A	303	-	2/2/5/5	5/11/31/31	0/1/1/1

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	305	BOG	O5-C1	4.50	1.53	1.41
4	A	308	BOG	O5-C1	4.43	1.53	1.41
4	A	316	BOG	O5-C1	4.42	1.53	1.41
4	A	313	BOG	O5-C1	4.36	1.53	1.41
4	A	315	BOG	O5-C1	4.35	1.53	1.41
4	A	307	BOG	O5-C1	4.21	1.52	1.41
5	A	314	MPG	O1-CX3	3.97	1.41	1.33
5	A	309	MPG	O1-CX3	3.89	1.41	1.33
5	A	311	MPG	O1-CX3	3.84	1.41	1.33
4	A	303	BOG	O5-C1	3.78	1.51	1.41
4	A	304	BOG	O5-C1	3.77	1.51	1.41
5	A	306	MPG	O1-CX3	3.54	1.40	1.33
5	A	310	MPG	O1-CX3	3.53	1.40	1.33
5	A	312	MPG	O1-CX3	3.45	1.40	1.33
2	A	301	RET	C14-C13	3.22	1.36	1.33
4	A	305	BOG	O1-C1	-2.80	1.35	1.40
4	A	307	BOG	O1-C1	-2.35	1.36	1.40
4	A	316	BOG	O1-C1	-2.21	1.36	1.40
4	A	315	BOG	O1-C1	-2.14	1.36	1.40
4	A	308	BOG	O1-C1	-2.09	1.36	1.40
4	A	313	BOG	O1-C1	-2.02	1.36	1.40

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	304	BOG	C4-C3-C2	4.14	118.09	110.83
5	A	309	MPG	O1-CX3-CXD	3.67	120.26	111.78
5	A	310	MPG	O1-CX3-CXD	3.54	119.97	111.78
5	A	312	MPG	O1-CX3-CXD	3.50	119.89	111.78
5	A	306	MPG	O1-CX3-CXD	3.48	119.83	111.78
5	A	314	MPG	O1-CX3-CXD	3.47	119.81	111.78
4	A	304	BOG	O1-C1-C2	3.39	113.43	108.27
5	A	311	MPG	O1-CX3-CXD	3.28	119.37	111.78
4	A	305	BOG	O5-C5-C4	2.97	115.05	109.70
5	A	312	MPG	O1-CX3-O4	-2.54	119.50	124.14
4	A	304	BOG	O5-C1-O1	-2.41	104.34	110.04
5	A	310	MPG	O1-CX3-O4	-2.40	119.74	124.14
4	A	304	BOG	C1'-O1-C1	2.35	117.69	113.68
4	A	315	BOG	C3-C4-C5	2.19	114.20	110.23
5	A	309	MPG	O1-CX3-O4	-2.10	120.30	124.14
4	A	305	BOG	C6-C5-C4	-2.08	107.92	113.02
5	A	306	MPG	O1-CX3-O4	-2.05	120.40	124.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	307	BOG	O5-C5-C4	2.05	113.39	109.70
4	A	304	BOG	O3-C3-C4	-2.01	105.63	110.38
5	A	311	MPG	O1-CX3-O4	-2.01	120.47	124.14

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	303	BOG	C4
4	A	303	BOG	C3
4	A	304	BOG	C4
4	A	304	BOG	C3

All (95) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	304	BOG	O5-C1-O1-C1'
5	A	306	MPG	O3-C21-CXD-O2
5	A	306	MPG	O1-CX3-CXD-O2
5	A	309	MPG	O3-C21-CXD-O2
5	A	310	MPG	CXD-CX3-O1-C1
5	A	310	MPG	O4-CX3-O1-C1
5	A	310	MPG	O3-C21-CXD-O2
5	A	314	MPG	O3-C21-CXD-O2
5	A	306	MPG	O4-CX3-O1-C1
5	A	312	MPG	O4-CX3-O1-C1
4	A	315	BOG	O5-C5-C6-O6
5	A	306	MPG	CXD-CX3-O1-C1
5	A	312	MPG	CXD-CX3-O1-C1
4	A	315	BOG	C4-C5-C6-O6
4	A	305	BOG	O5-C1-O1-C1'
4	A	316	BOG	O5-C1-O1-C1'
4	A	316	BOG	O5-C5-C6-O6
4	A	303	BOG	C4-C5-C6-O6
4	A	304	BOG	C2-C1-O1-C1'
4	A	305	BOG	C2-C1-O1-C1'
4	A	316	BOG	C2-C1-O1-C1'
5	A	306	MPG	C11-C12-C13-C14
4	A	307	BOG	O5-C1-O1-C1'
4	A	303	BOG	O5-C5-C6-O6
4	A	307	BOG	C2-C1-O1-C1'
4	A	305	BOG	O5-C5-C6-O6
5	A	312	MPG	C5-C6-C7-C8

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Mol	Chain	Res	Type	Atoms
5	A	310	MPG	C1-C2-C3-C4
5	A	309	MPG	C3-C4-C5-C6
5	A	314	MPG	C1-C2-C3-C4
4	A	316	BOG	C1'-C2'-C3'-C4'
5	A	310	MPG	C14-C15-C16-C17
5	A	312	MPG	C4-C5-C6-C7
4	A	308	BOG	C4'-C5'-C6'-C7'
4	A	316	BOG	C3'-C4'-C5'-C6'
4	A	316	BOG	C4-C5-C6-O6
5	A	311	MPG	C5-C6-C7-C8
4	A	316	BOG	O1-C1'-C2'-C3'
4	A	315	BOG	C1'-C2'-C3'-C4'
5	A	306	MPG	C3-C4-C5-C6
4	A	304	BOG	C1'-C2'-C3'-C4'
4	A	308	BOG	C2'-C3'-C4'-C5'
5	A	312	MPG	O4-CX3-CXD-O2
5	A	310	MPG	C2-C3-C4-C5
4	A	308	BOG	O5-C5-C6-O6
5	A	311	MPG	O1-C1-C2-C3
5	A	309	MPG	C10-C11-C12-C13
4	A	313	BOG	C1'-C2'-C3'-C4'
4	A	307	BOG	O1-C1'-C2'-C3'
5	A	312	MPG	C2-C3-C4-C5
4	A	305	BOG	O1-C1'-C2'-C3'
5	A	309	MPG	O3-C21-CXD-CX3
4	A	307	BOG	O5-C5-C6-O6
5	A	306	MPG	C4-C5-C6-C7
5	A	310	MPG	C6-C7-C8-C9
5	A	312	MPG	C10-C11-C12-C13
4	A	304	BOG	C2'-C3'-C4'-C5'
4	A	305	BOG	C2'-C1'-O1-C1
4	A	308	BOG	C2'-C1'-O1-C1
4	A	315	BOG	O5-C1-O1-C1'
5	A	311	MPG	O4-CX3-CXD-O2
5	A	314	MPG	O4-CX3-CXD-O2
5	A	306	MPG	C1-C2-C3-C4
4	A	304	BOG	O1-C1'-C2'-C3'
4	A	304	BOG	O5-C5-C6-O6
5	A	309	MPG	C4-C5-C6-C7
5	A	309	MPG	C2-C3-C4-C5
5	A	309	MPG	C11-C12-C13-C14
5	A	309	MPG	C1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
4	A	316	BOG	C4'-C5'-C6'-C7'
5	A	306	MPG	C6-C7-C8-C9
4	A	313	BOG	C3'-C4'-C5'-C6'
4	A	316	BOG	C5'-C6'-C7'-C8'
4	A	313	BOG	C4'-C5'-C6'-C7'
4	A	303	BOG	C4'-C5'-C6'-C7'
5	A	312	MPG	O3-C21-CXD-O2
4	A	303	BOG	C2'-C3'-C4'-C5'
5	A	306	MPG	C13-C14-C15-C16
4	A	303	BOG	C3'-C4'-C5'-C6'
4	A	316	BOG	C2'-C1'-O1-C1
4	A	304	BOG	C4'-C5'-C6'-C7'
5	A	306	MPG	O4-CX3-CXD-O2
5	A	309	MPG	C7-C8-C9-C10
5	A	314	MPG	C10-C11-C12-C13
5	A	310	MPG	C9-C10-C11-C12
4	A	305	BOG	C3'-C4'-C5'-C6'
5	A	311	MPG	C6-C7-C8-C9
5	A	312	MPG	C7-C8-C9-C10
4	A	313	BOG	C4-C5-C6-O6
5	A	310	MPG	C4-C5-C6-C7
5	A	311	MPG	O4-CX3-O1-C1
5	A	312	MPG	C13-C14-C15-C16
5	A	312	MPG	C9-C10-C11-C12
5	A	312	MPG	O1-CX3-CXD-O2
5	A	314	MPG	O3-C21-CXD-CX3

There are no ring outliers.

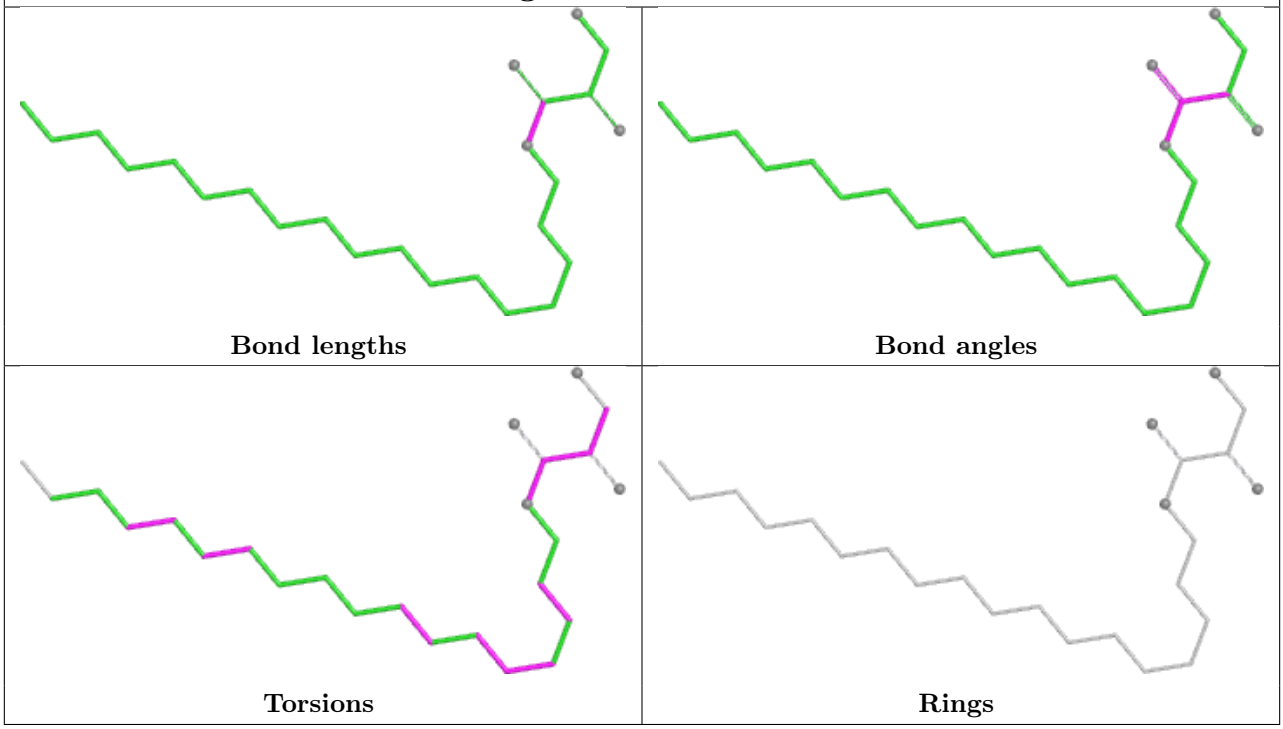
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	312	MPG	1	0
4	A	305	BOG	1	0
2	A	301	RET	4	0

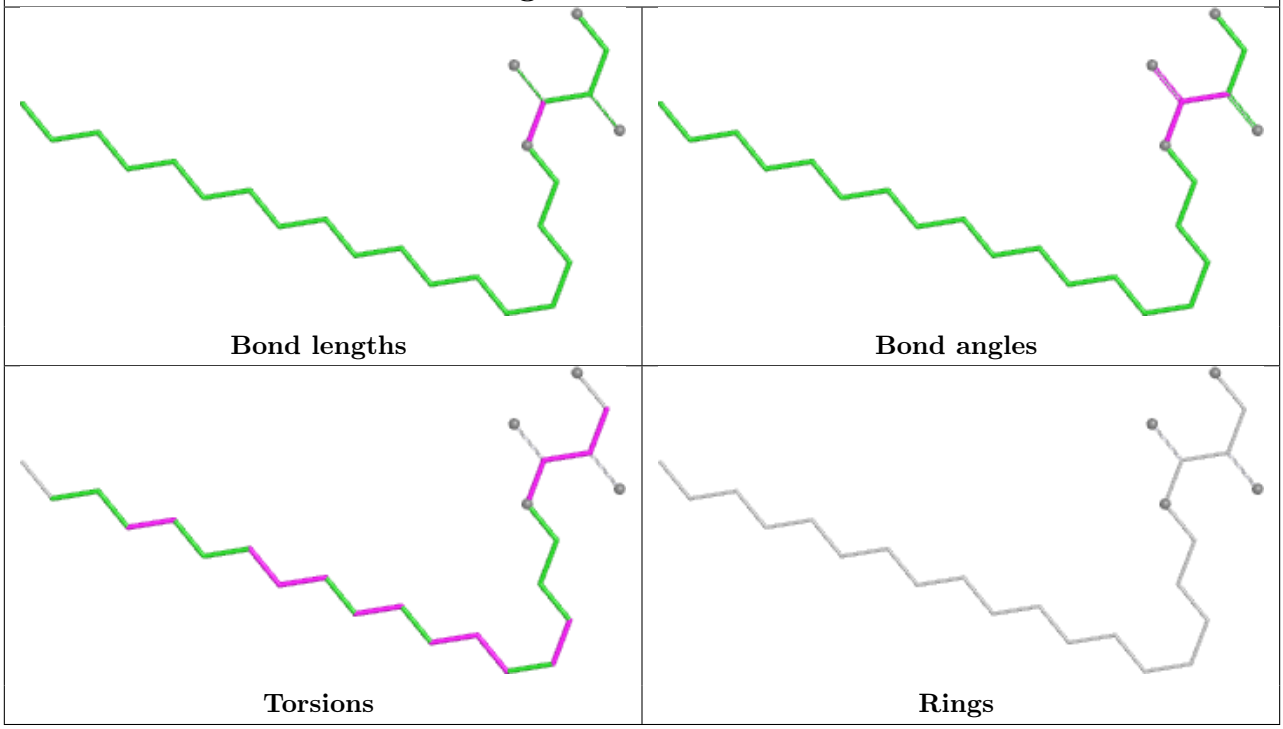
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

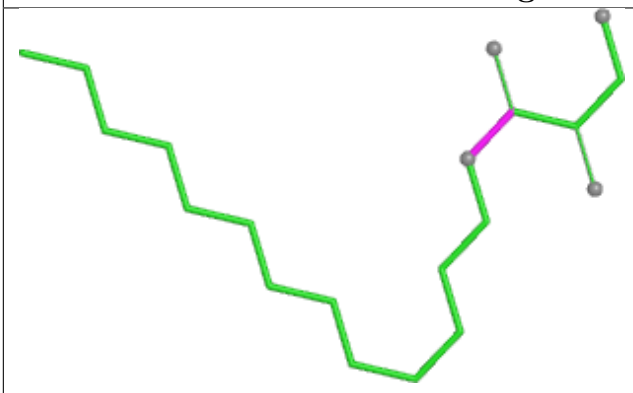
Ligand MPG A 306



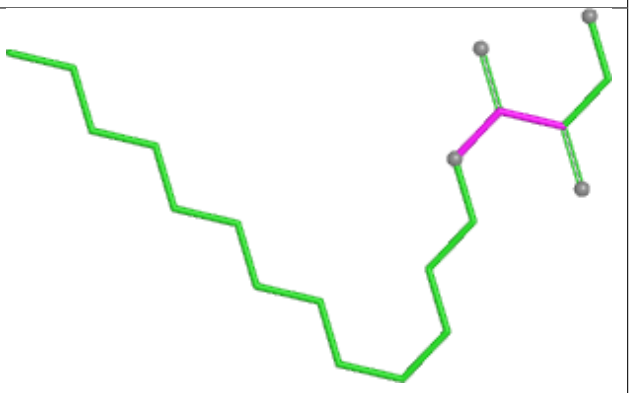
Ligand MPG A 312



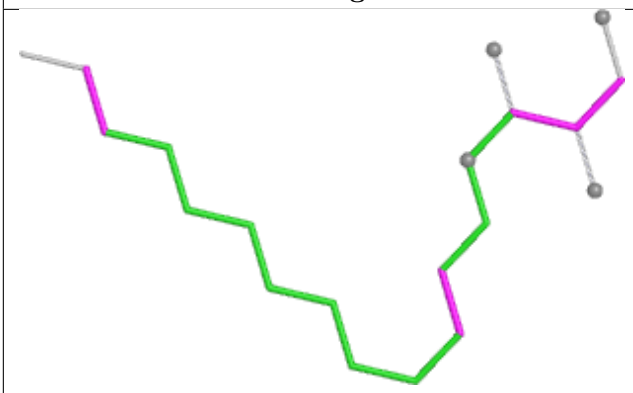
Ligand MPG A 314



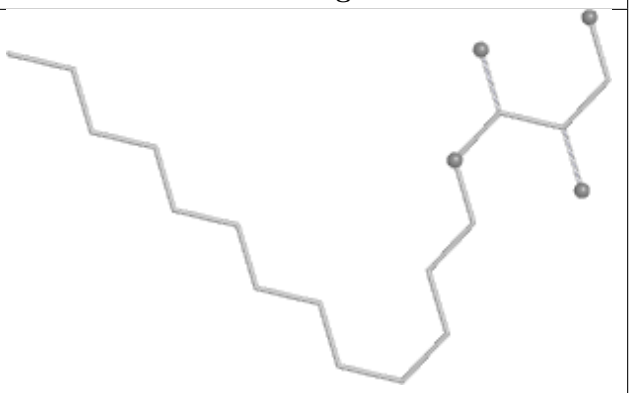
Bond lengths



Bond angles

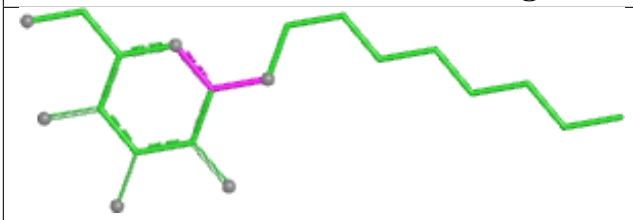


Torsions

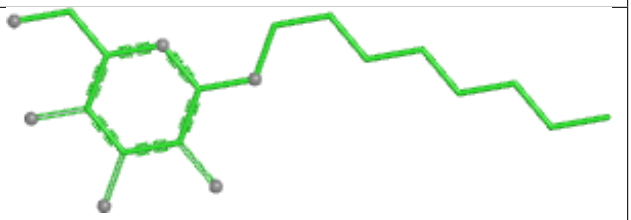


Rings

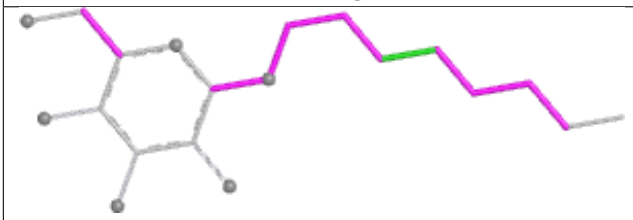
Ligand BOG A 316



Bond lengths



Bond angles



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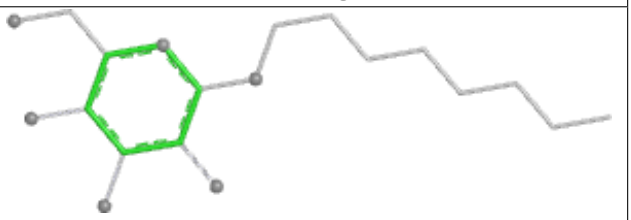

Rings

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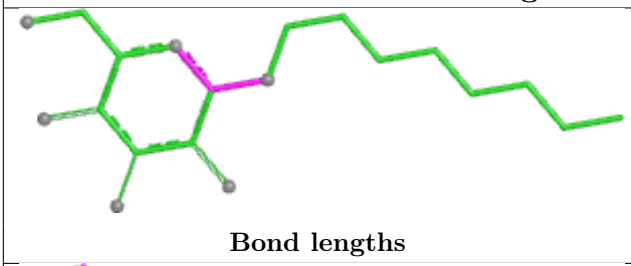
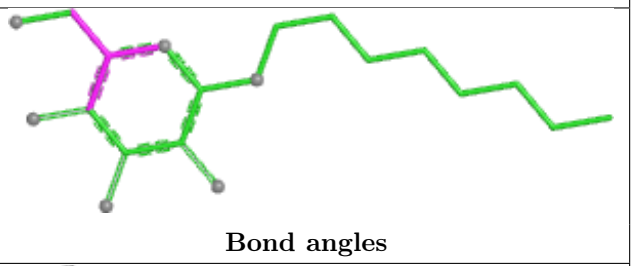
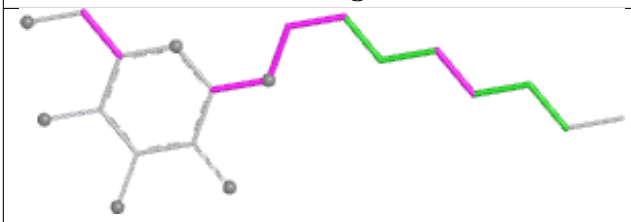


Bond lengths



Bond angles



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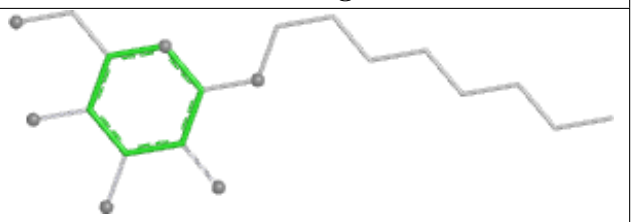
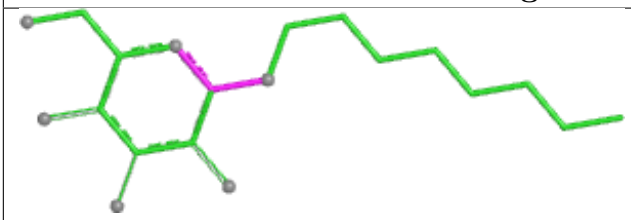


Rings

Ligand BOG A 313



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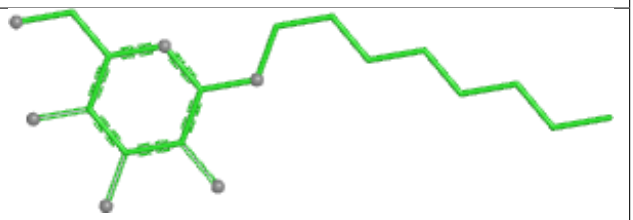
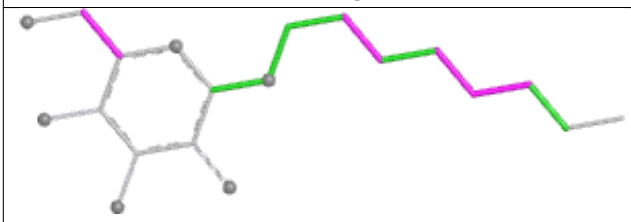


Bond angles



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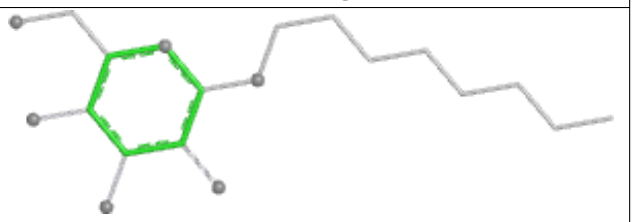

Rings

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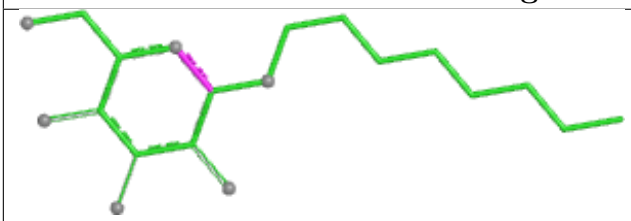

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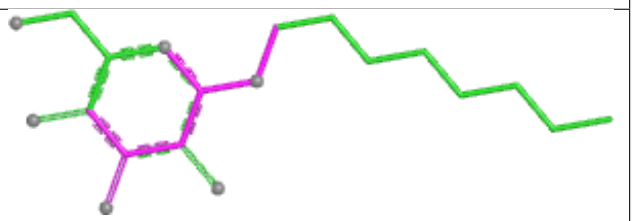
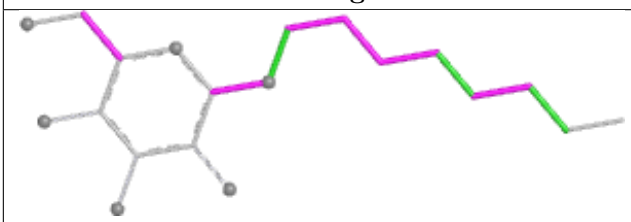


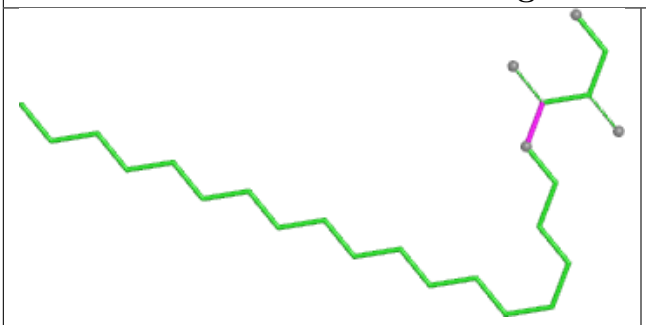
Bond angles



Torsions

Rings

Ligand MPG A 310



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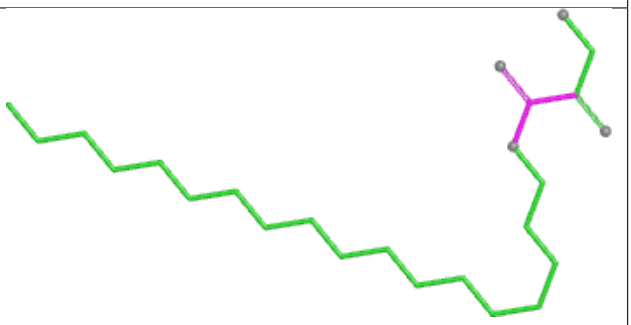
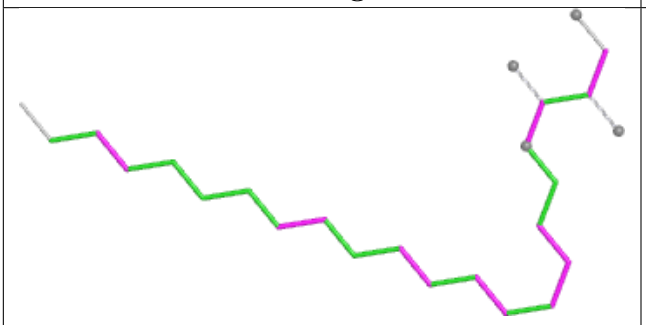


Bond angles



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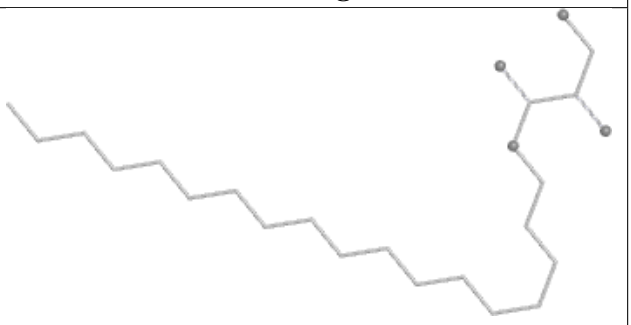
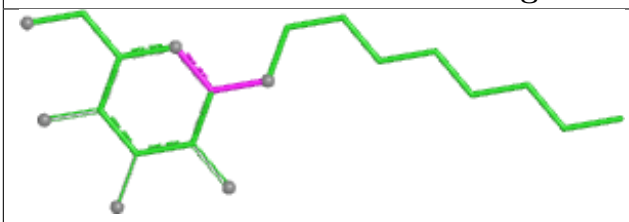


Rings

Ligand BOG A 308



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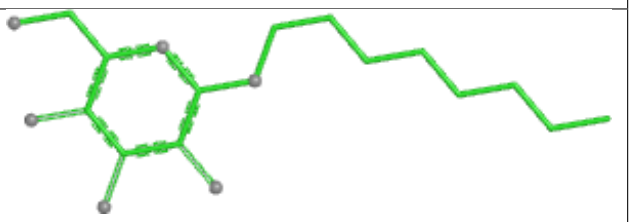
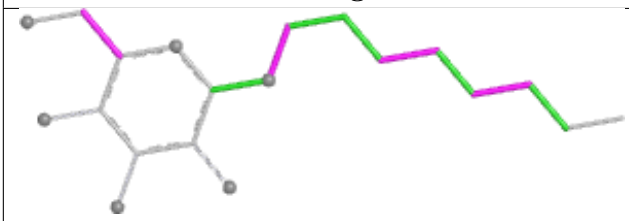


Bond angles



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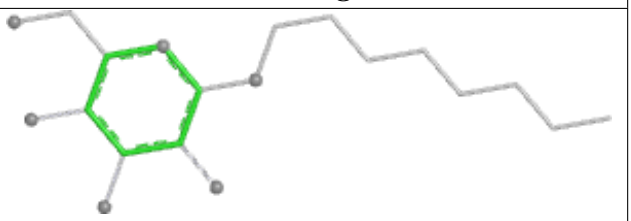

Rings

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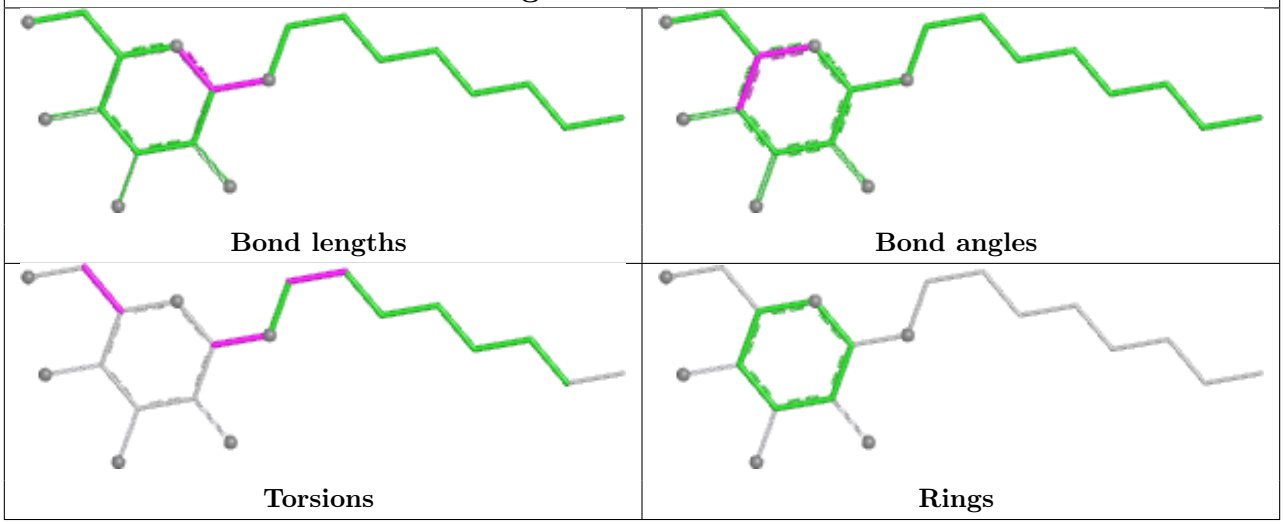

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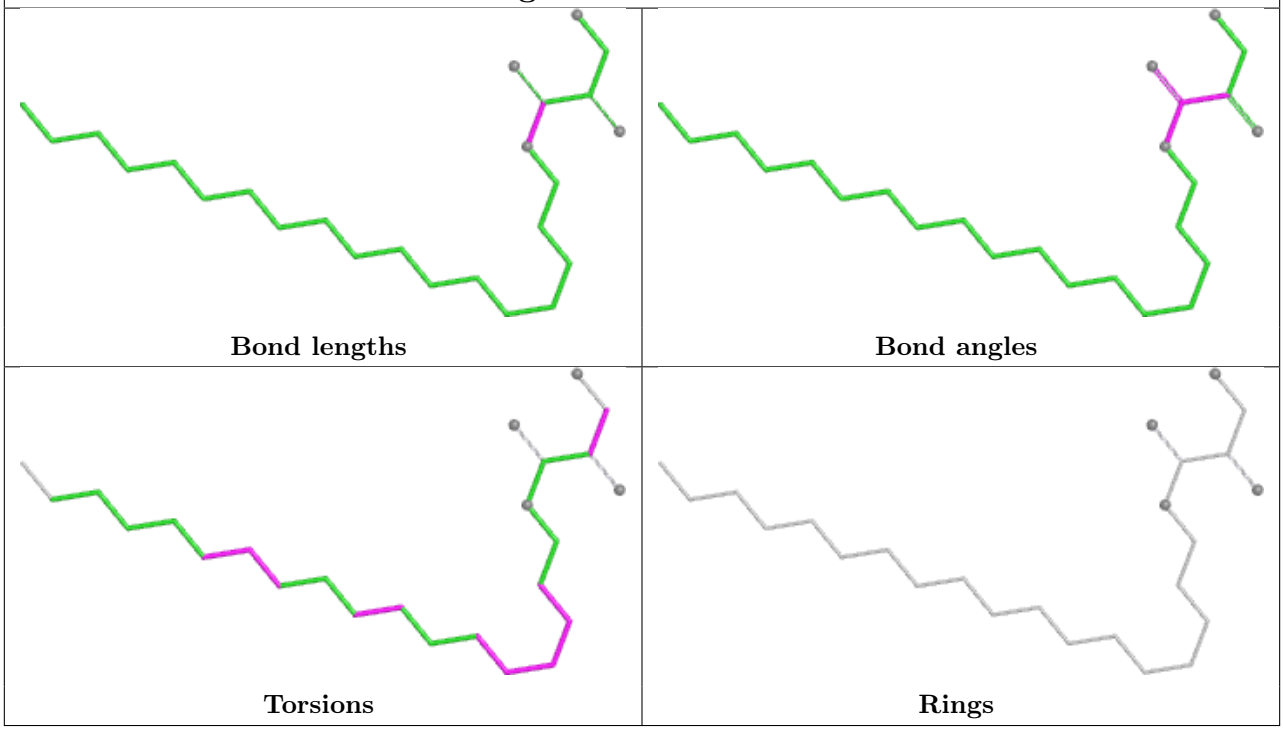

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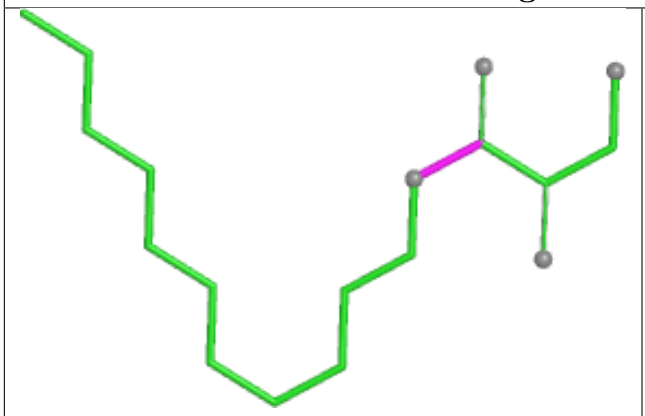
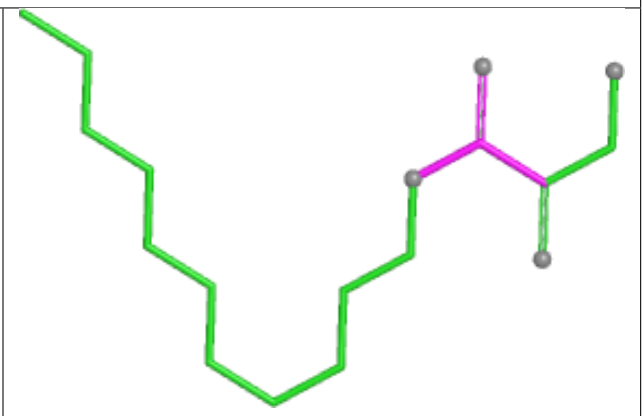
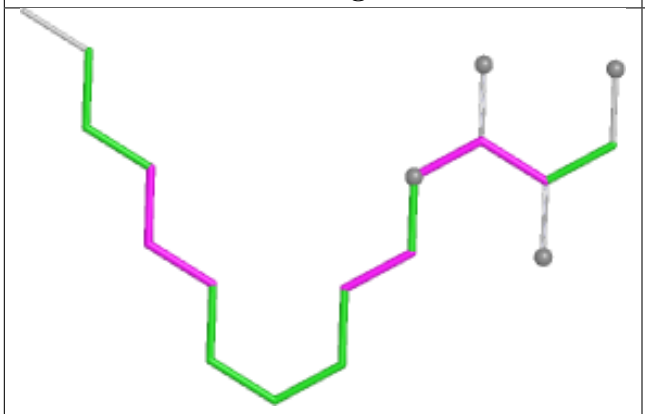


Bond lengths



Bond angles



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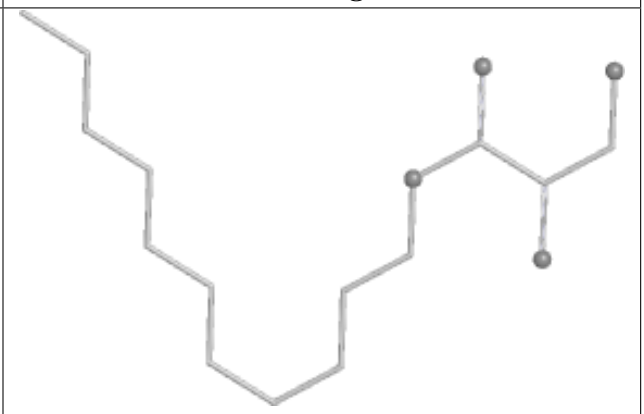
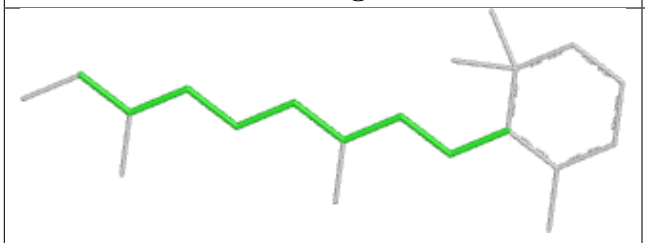


Rings

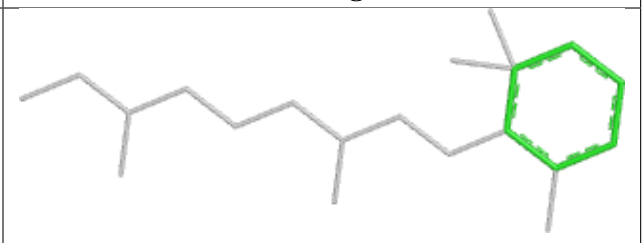
Ligand RET A 301

Bond lengths

Bond angles

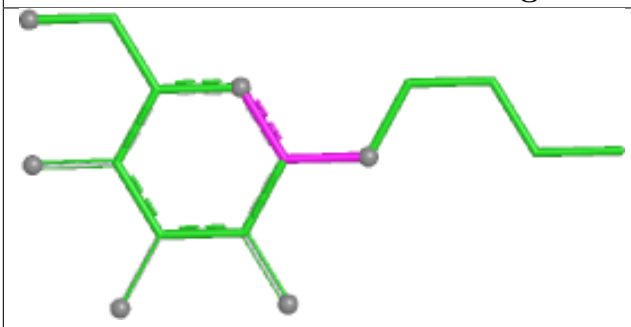


Torsions

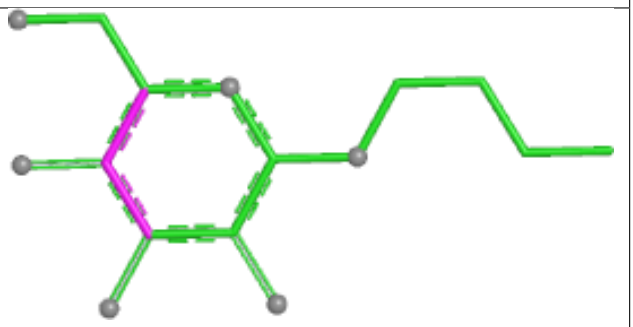


Rings

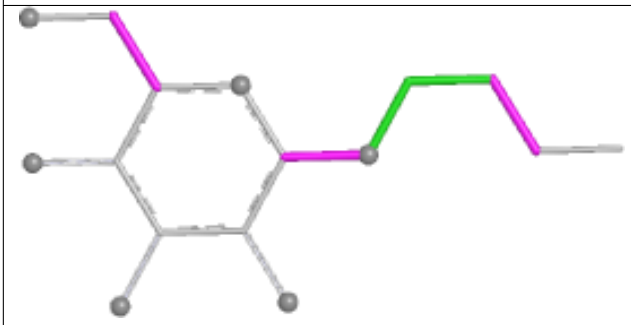
Ligand BOG A 315



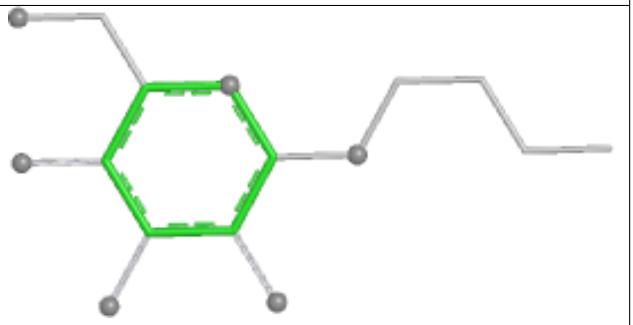
Bond lengths



Bond angles

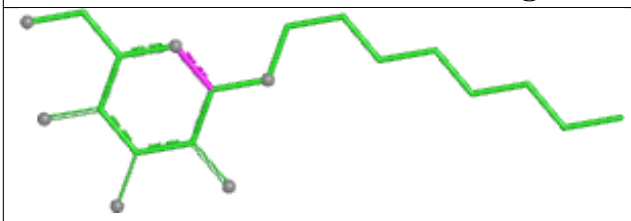


Torsions

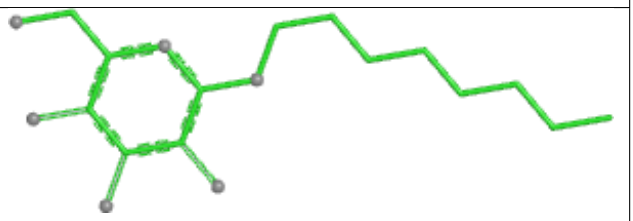


Rings

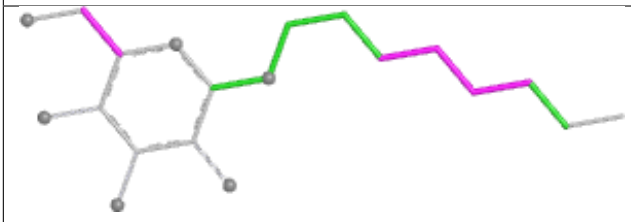
Ligand BOG A 303



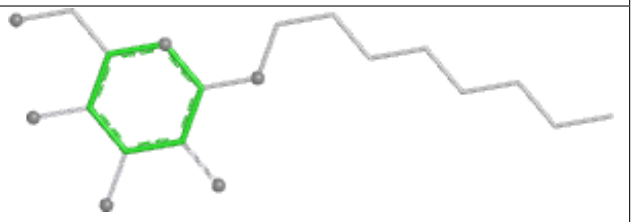
Bond lengths



Bond angles



Torsions



Rings

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

6.1 Protein, DNA and RNA chains

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^{th} 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	212/249 (85%)	0.12	10 (4%) 36 33	21, 38, 82, 156	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	154	SER	3.0
1	A	219	LEU	2.9
1	A	35	ARG	2.5
1	A	1	MET	2.5
1	A	2	VAL	2.4
1	A	53	VAL	2.4
1	A	152	ARG	2.3
1	A	24	TRP	2.3
1	A	27	ARG	2.2
1	A	121	ILE	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

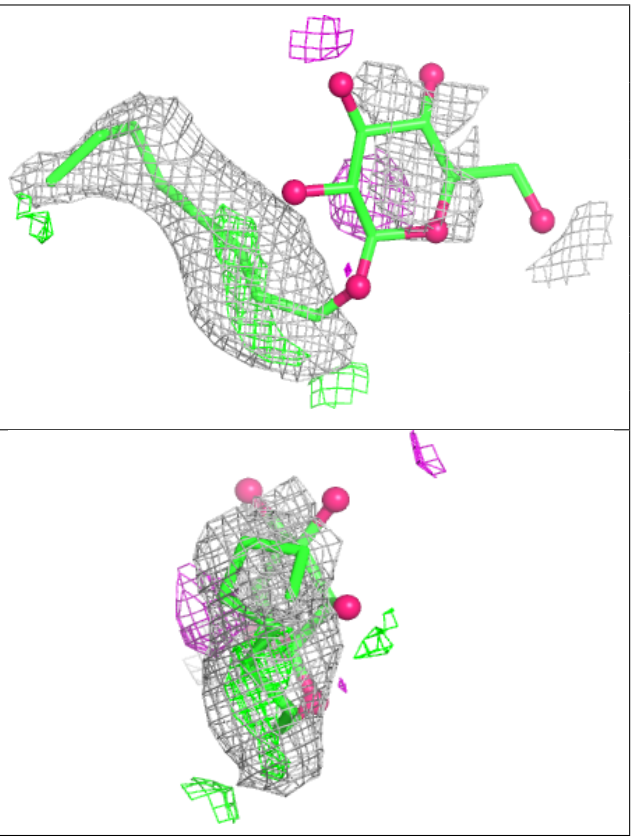
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	BOG	A	305	20/20	0.51	0.27	110,131,151,157	0
4	BOG	A	313	20/20	0.55	0.26	129,140,148,149	0
4	BOG	A	308	20/20	0.56	0.20	108,124,137,147	0
4	BOG	A	315	16/20	0.61	0.24	104,118,137,138	0
4	BOG	A	303	20/20	0.71	0.20	63,116,156,159	0
5	MPG	A	314	20/25	0.71	0.32	88,107,116,117	0
5	MPG	A	309	25/25	0.72	0.30	82,100,112,115	0
4	BOG	A	316	20/20	0.74	0.26	106,131,171,188	0
5	MPG	A	310	25/25	0.75	0.26	89,100,114,126	0
4	BOG	A	307	20/20	0.76	0.20	109,122,137,137	0
4	BOG	A	304	20/20	0.76	0.22	79,97,121,124	0
5	MPG	A	312	25/25	0.77	0.29	94,108,132,146	0
5	MPG	A	306	25/25	0.78	0.25	73,96,107,114	0
5	MPG	A	311	18/25	0.78	0.22	72,85,117,117	0
2	RET	A	301	20/21	0.94	0.06	18,21,23,25	0
3	CL	A	302	1/1	0.95	0.06	49,49,49,49	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.

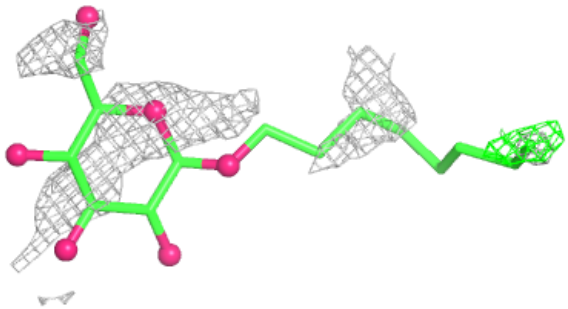
Electron density around BOG A 305:

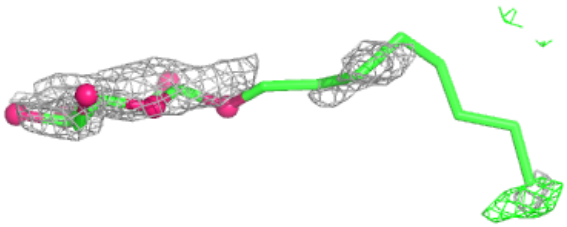
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

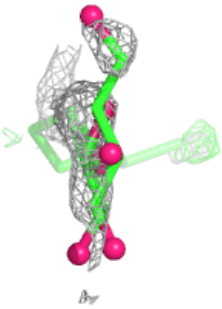


Electron density around BOG A 313:

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

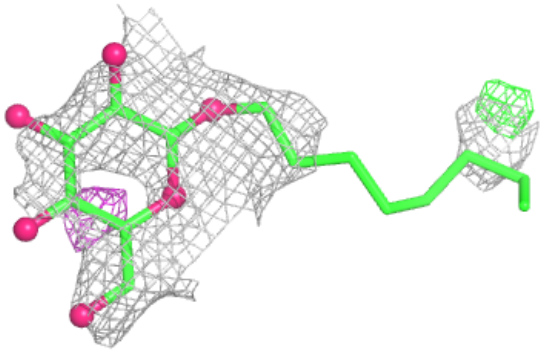


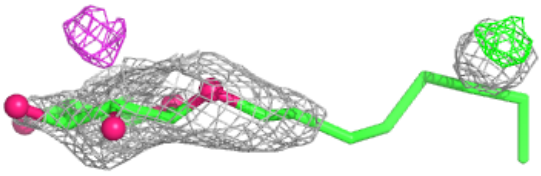


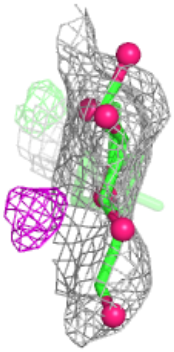


Electron density around BOG A 308:

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

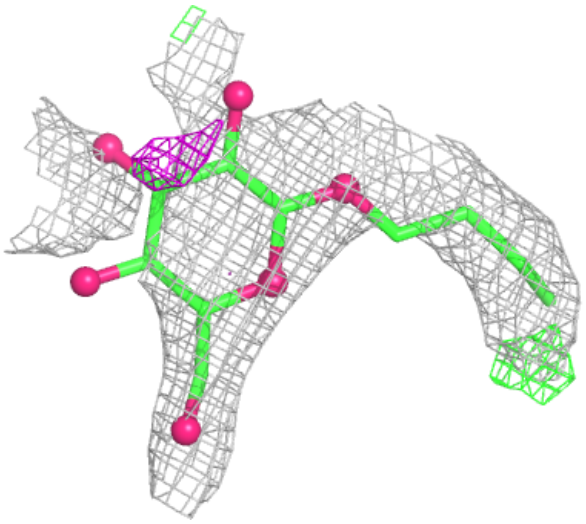


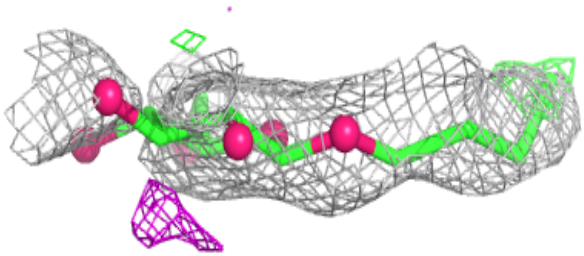


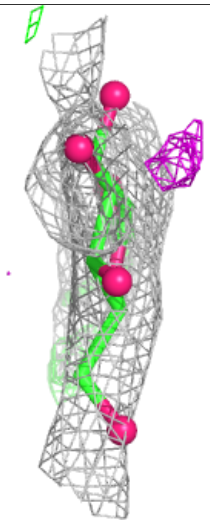


Electron density around BOG A 315:

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

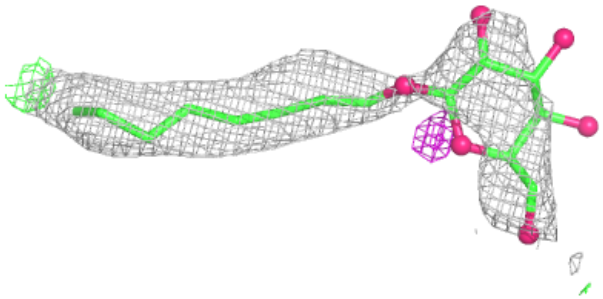


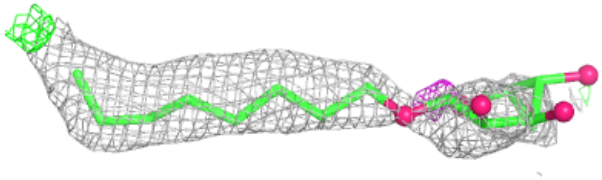


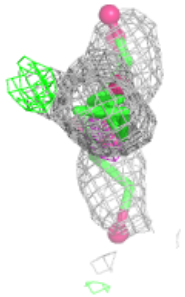


Electron density around BOG A 303:

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

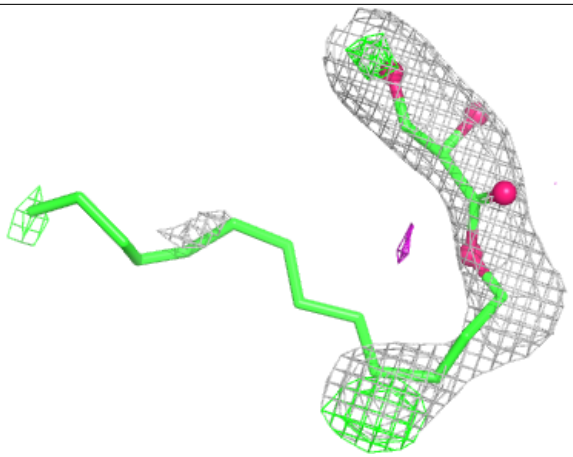


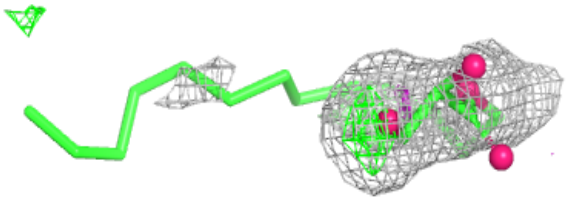


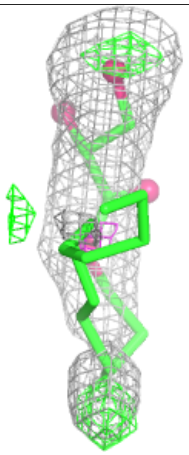


Electron density around MPG A 314:

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

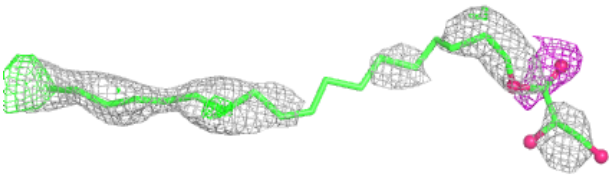


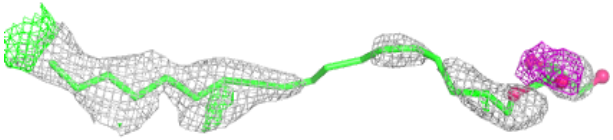


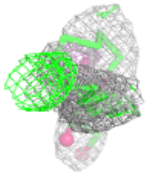


Electron density around MPG A 309:

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

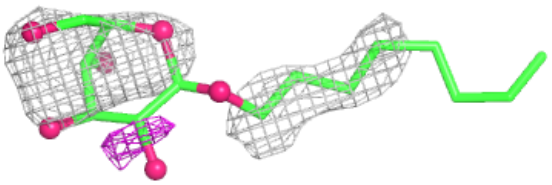


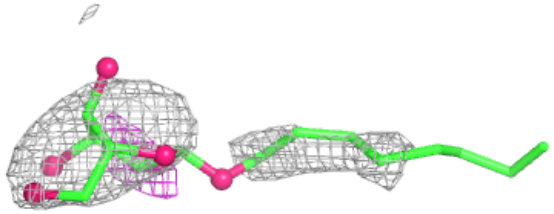


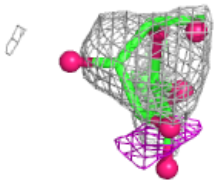


Electron density around BOG A 316:

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

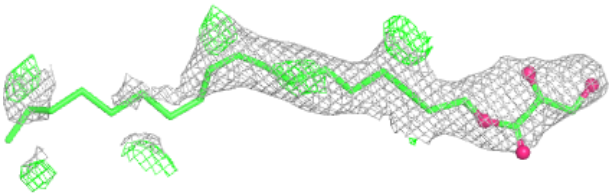


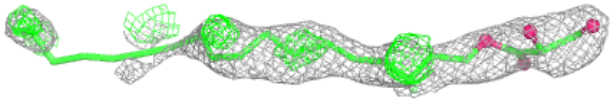


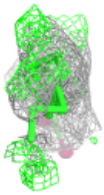


Electron density around MPG A 310:

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

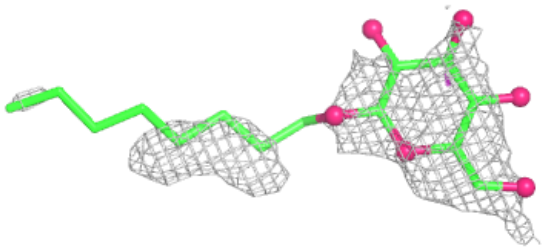


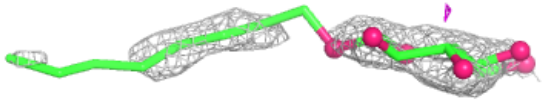


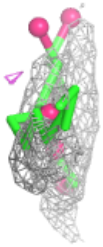


Electron density around BOG A 307:

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

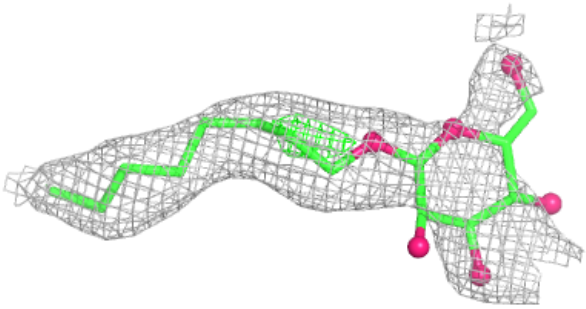


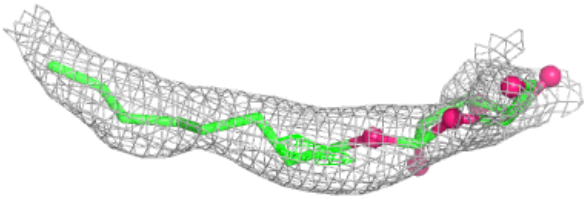


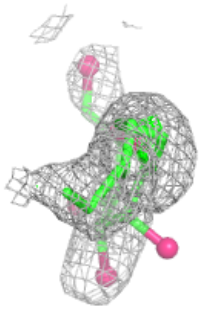


Electron density around BOG A 304:

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

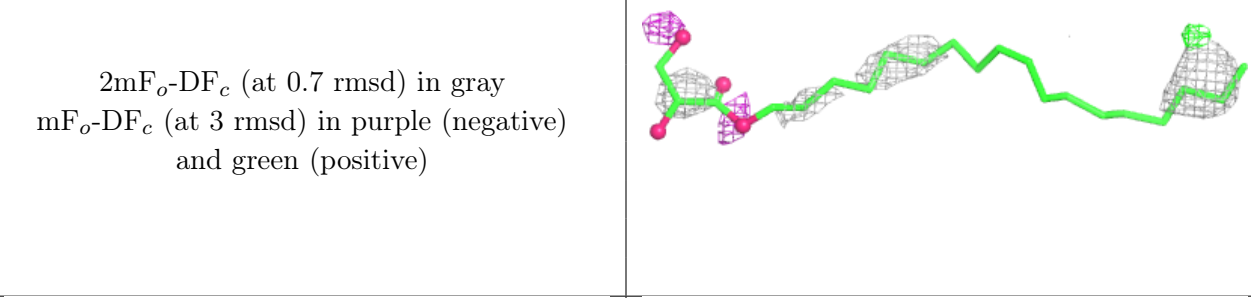


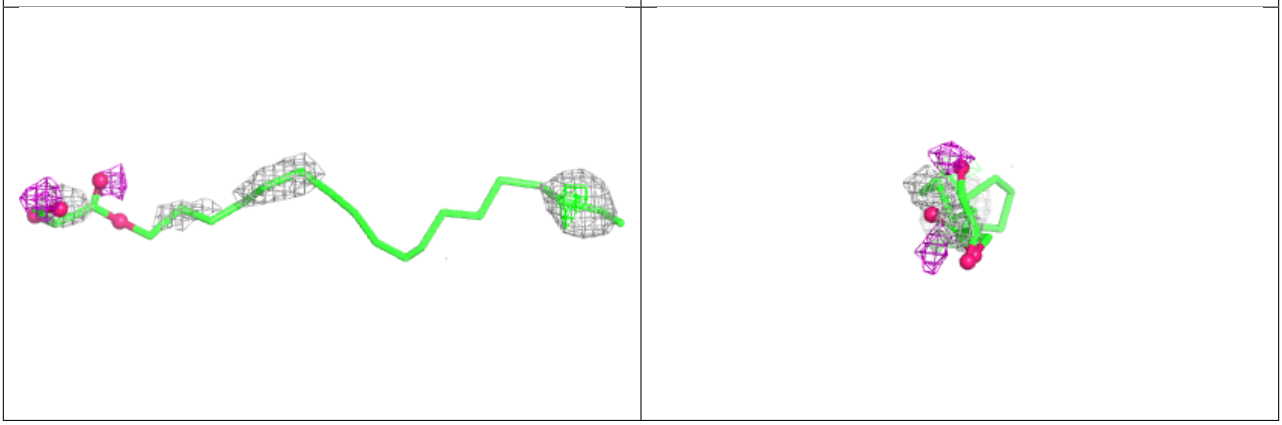




Electron density around MPG A 312:

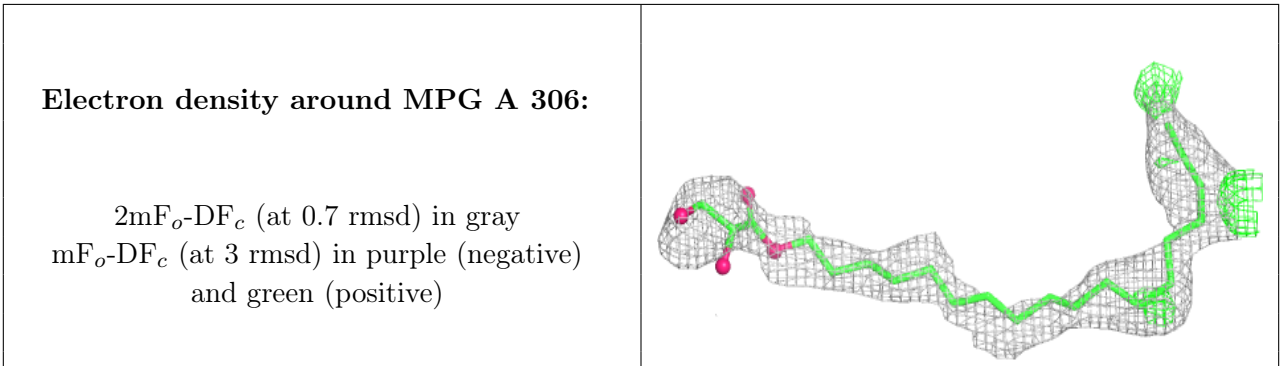
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

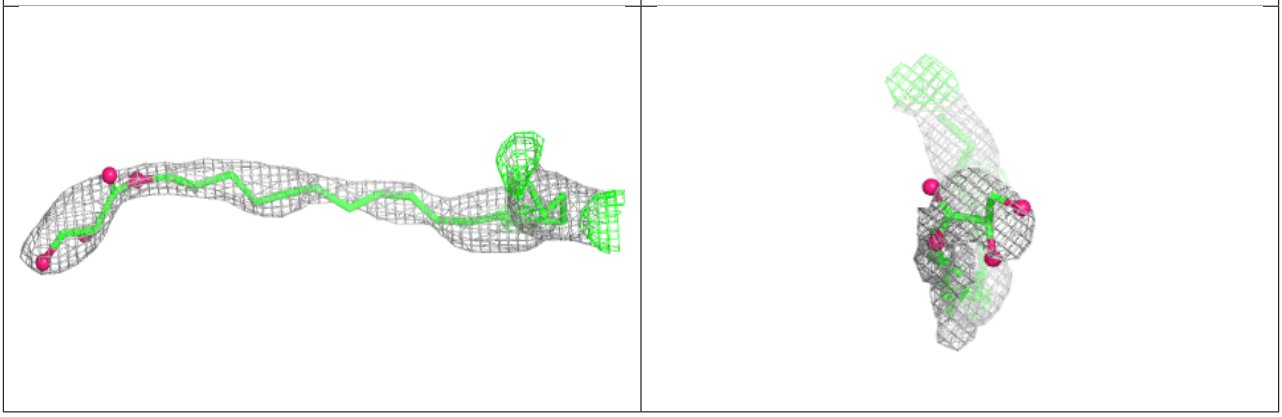




Electron density around MPG A 306:

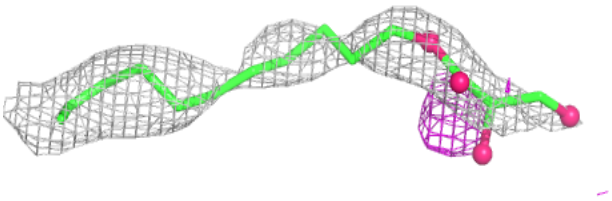
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

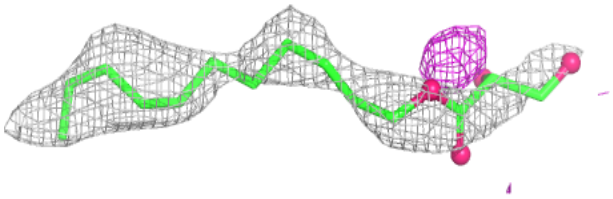


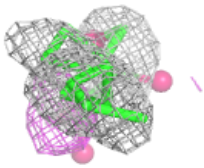


Electron density around MPG A 311:

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

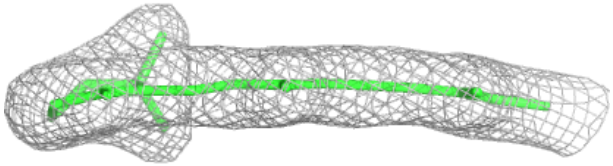


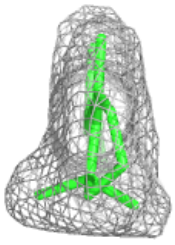




Electron density around RET A 301:

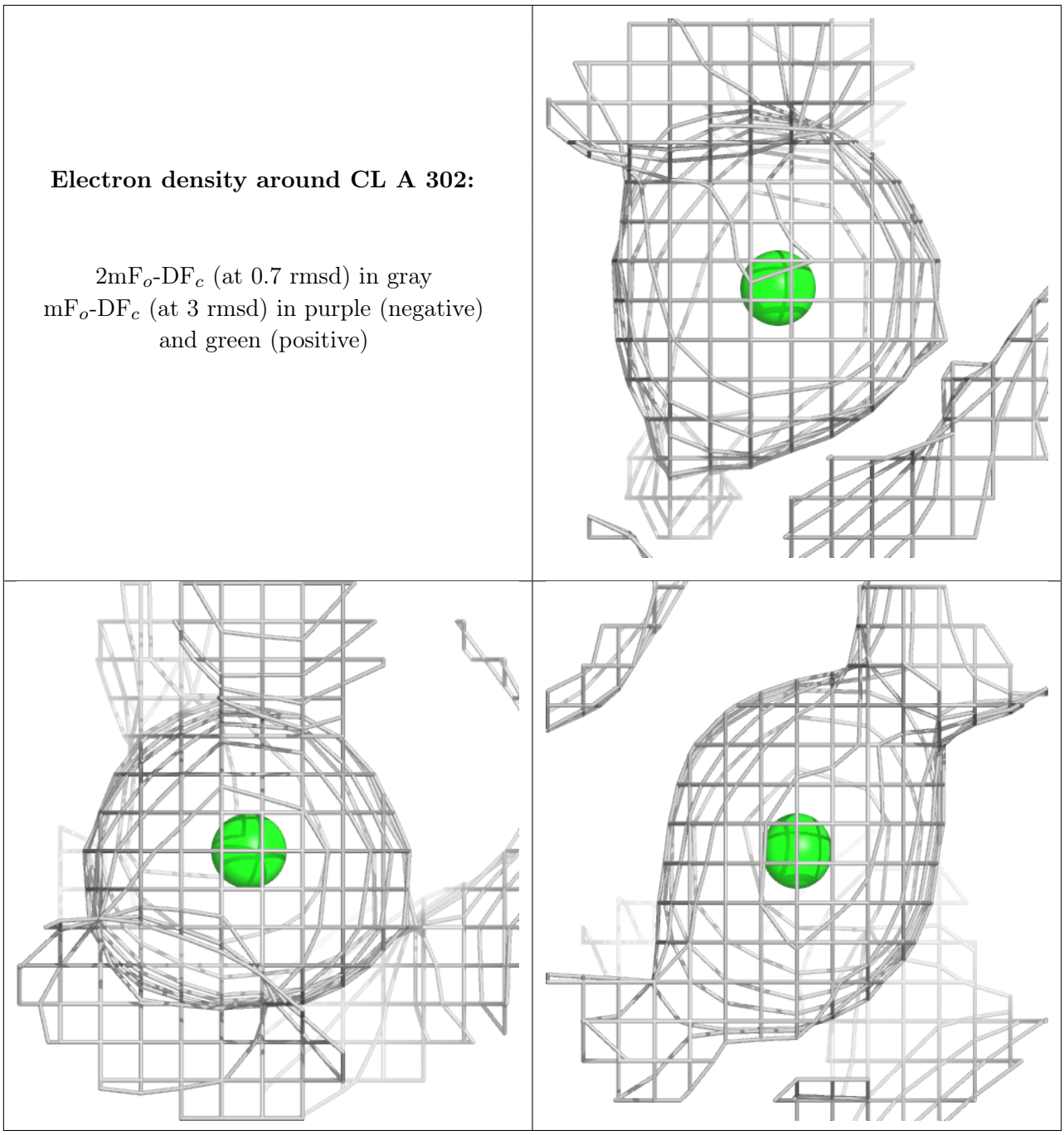
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around CL A 302:

$2mF_o$-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

There are no such residues in this entry.