wwPDB EM Validation Summary Report

May 29, 2024 – 10:30 AM EDT

PDB ID	:	2AT9
Title	:	STRUCTURE OF BACTERIORHODOPSIN AT 3.0 ANGSTROM BY ELECTRON CRYSTALLOGRAPHY
Authors	:	Mitsuoka, K.; Hirai, T.; Murata, K.; Miyazawa, A.; Kidera, A.; Kimura, Y.; Fujiyoshi, Y.
Deposited on	:	1998-12-17
Resolution	:	3.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

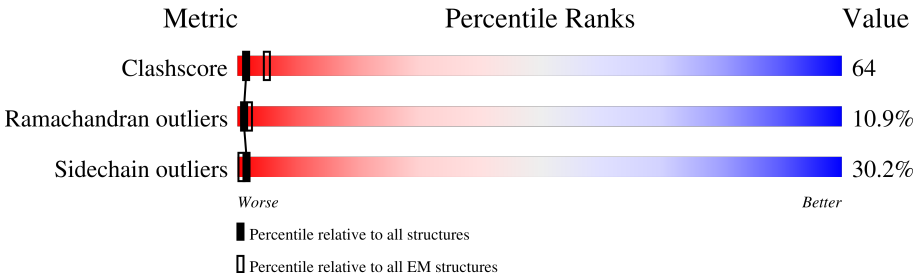
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON CRYSTALLOGRAPHY

The reported resolution of this entry is 3.00 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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%

Mol	Chain	Length	Quality of chain
1	A	248	16% 50% 23% • 10%

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
3	2DP	A	261	X	-	-	-
3	2DP	A	262	X	-	-	-
3	2DP	A	263	X	-	-	-
3	2DP	A	264	X	-	-	-
3	2DP	A	265	X	-	-	-
3	2DP	A	267	X	-	-	-
3	2DP	A	268	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	2DP	A	269	X	-	-	-

2 Entry composition (i)

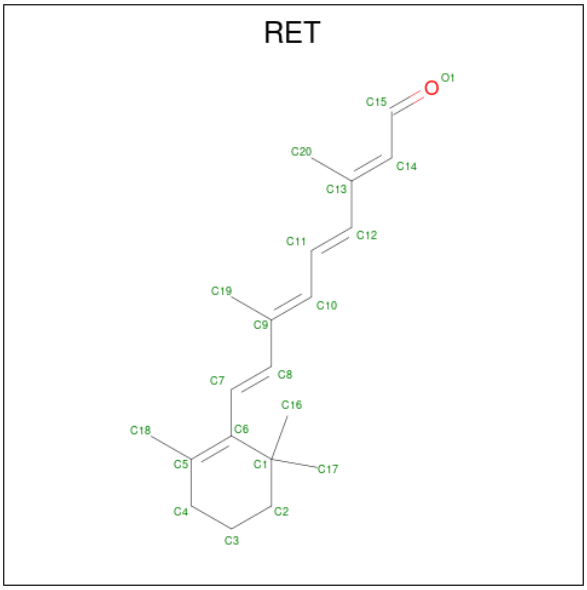
There are 4 unique types of molecules in this entry. The entry contains 2223 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 BACTERIORHODOPSIN.

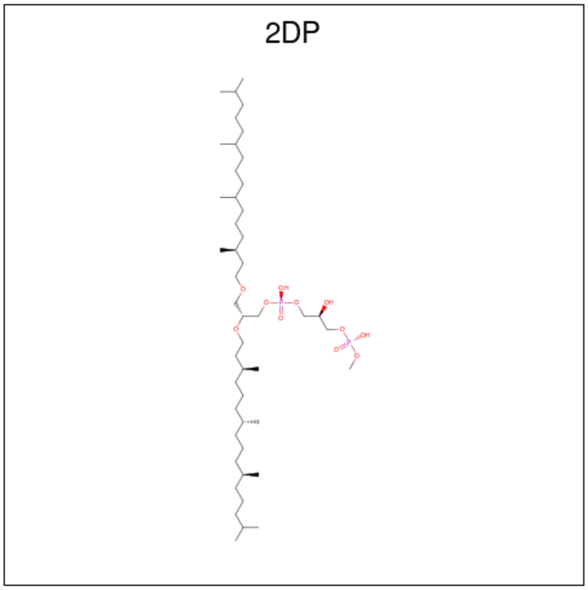
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	222	1721	1156	263	293	9	0	0

- Molecule 2 is RETINAL (three-letter code: RET) (formula: $C_{20}H_{28}O$).



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

- Molecule 3 is 3-[[3-METHYLPHOSPHONO-GLYCEROLYL]PHOSPHONYL]-[1,2-DI[2,6,10,14-TETRAMETHYL-HEXADECAN-16-YL]GLYCEROL (three-letter code: 2DP) (formula: $C_{47}H_{98}O_{11}P_2$).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total 60	C 47	O 11	P 2	0
3	A	1	Total 60	C 47	O 11	P 2	0
3	A	1	Total 60	C 47	O 11	P 2	0
3	A	1	Total 60	C 47	O 11	P 2	0
3	A	1	Total 60	C 47	O 11	P 2	0
3	A	1	Total 60	C 47	O 11	P 2	0
3	A	1	Total 60	C 47	O 11	P 2	0
3	A	1	Total 60	C 47	O 11	P 2	0

- Molecule 4 is water.

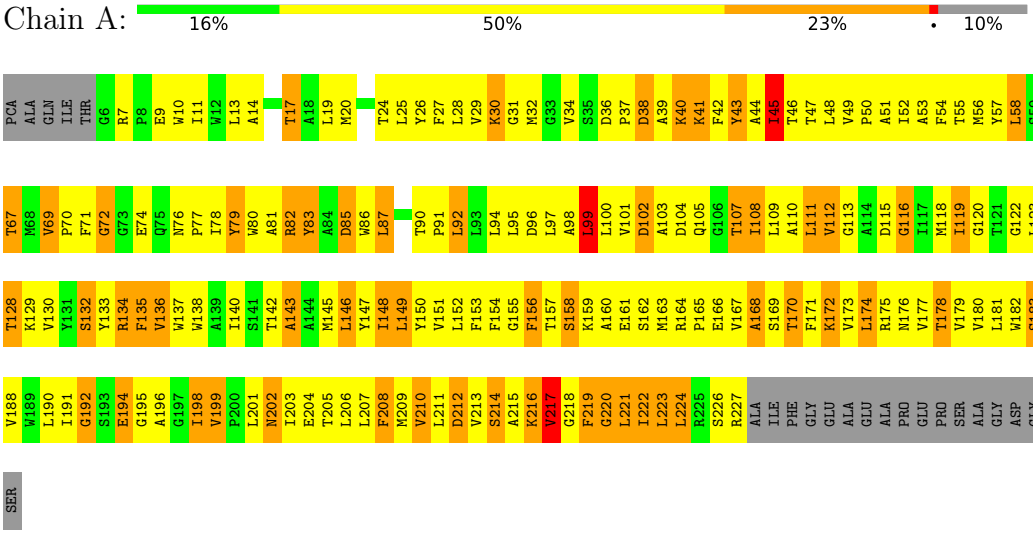
Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total 2	O 2	0

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. 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. 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: BACTERIORHODOPSIN

Chain A:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α, β, γ	62.45Å 62.45Å 100.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 3.00	Depositor
% Data completeness (in resolution range)	73.7 (8.00-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.237 , 0.330	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2223	wwPDB-VP
Average B, all atoms (Å^2)	15.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: RET, 2DP

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	0.56	0/1768	0.81	0/2415

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	147	TYR	Sidechain

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	1721	0	1777	280	0
2	A	20	0	27	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	480	0	752	40	0
4	A	2	0	0	0	0
All	All	2223	0	2556	308	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 64.

The worst 5 of 308 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:56:MET:HG3	1:A:85:ASP:HB2	1.44	0.99
1:A:168:ALA:O	1:A:172:LYS:HD2	1.64	0.97
1:A:67:THR:HG22	1:A:80:TRP:HD1	1.34	0.92
1:A:168:ALA:C	1:A:172:LYS:HD2	1.91	0.90
1:A:169:SER:O	1:A:173:VAL:HG22	1.73	0.89

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 PDB entries followed by that with respect to all EM entries.

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	220/248 (89%)	150 (68%)	46 (21%)	24 (11%)	0 2

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	ARG
1	A	135	PHE
1	A	158	SER
1	A	160	ALA
1	A	168	ALA

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 PDB entries followed by that with respect to all EM entries.

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	179/193 (93%)	125 (70%)	54 (30%)	0 1

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	132	SER
1	A	163	MET
1	A	221	LEU
1	A	136	VAL
1	A	148	ILE

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

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

9 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	$\#\|Z\| > 2$
3	2DP	A	264	-	59,59,59	1.18	3 (5%)	67,74,74	1.15	8 (11%)
3	2DP	A	268	-	59,59,59	1.32	6 (10%)	67,74,74	1.12	7 (10%)
3	2DP	A	269	-	59,59,59	1.37	9 (15%)	67,74,74	1.08	6 (8%)
3	2DP	A	267	-	59,59,59	1.44	6 (10%)	67,74,74	1.10	7 (10%)
3	2DP	A	262	-	59,59,59	1.17	2 (3%)	67,74,74	1.04	4 (5%)
2	RET	A	249(A)	1	20,20,21	0.89	1 (5%)	27,27,28	1.03	2 (7%)
3	2DP	A	261	-	59,59,59	1.30	7 (11%)	67,74,74	1.11	5 (7%)
3	2DP	A	265	-	59,59,59	1.35	8 (13%)	67,74,74	1.09	5 (7%)
3	2DP	A	263	-	59,59,59	1.21	6 (10%)	67,74,74	1.01	5 (7%)

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
3	2DP	A	264	-	2/2/12/12	44/70/70/70	-
3	2DP	A	268	-	2/2/12/12	46/70/70/70	-
3	2DP	A	269	-	2/2/12/12	42/70/70/70	-
3	2DP	A	267	-	2/2/12/12	42/70/70/70	-
3	2DP	A	262	-	2/2/12/12	39/70/70/70	-
2	RET	A	249(A)	1	-	0/13/30/31	0/1/1/1
3	2DP	A	261	-	2/2/12/12	40/70/70/70	-
3	2DP	A	265	-	2/2/12/12	35/70/70/70	-
3	2DP	A	263	-	2/2/12/12	43/70/70/70	-

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	267	2DP	C6-C5	3.50	1.63	1.51
3	A	267	2DP	C4-C5	3.45	1.63	1.51
3	A	263	2DP	C4-C5	3.28	1.62	1.51
3	A	262	2DP	C4-C5	3.23	1.62	1.51
3	A	269	2DP	C4-C5	3.15	1.62	1.51

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	268	2DP	C41-O2-C2	3.54	123.54	115.40
3	A	261	2DP	C41-O2-C2	3.46	123.36	115.40
3	A	264	2DP	O2-C41-C42	-3.05	102.37	108.77
3	A	264	2DP	C41-O2-C2	3.04	122.40	115.40
3	A	267	2DP	C21-C22-C23	2.93	125.39	115.92

5 of 16 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	261	2DP	C23
3	A	261	2DP	C18
3	A	262	2DP	C23
3	A	262	2DP	C18
3	A	263	2DP	C23

5 of 331 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	261	2DP	O1-C1-C2-O2
3	A	261	2DP	C5-C4-O6-P1
3	A	261	2DP	C6-O8-P2-O9
3	A	261	2DP	C6-O8-P2-O10
3	A	261	2DP	C6-O8-P2-O11

There are no ring outliers.

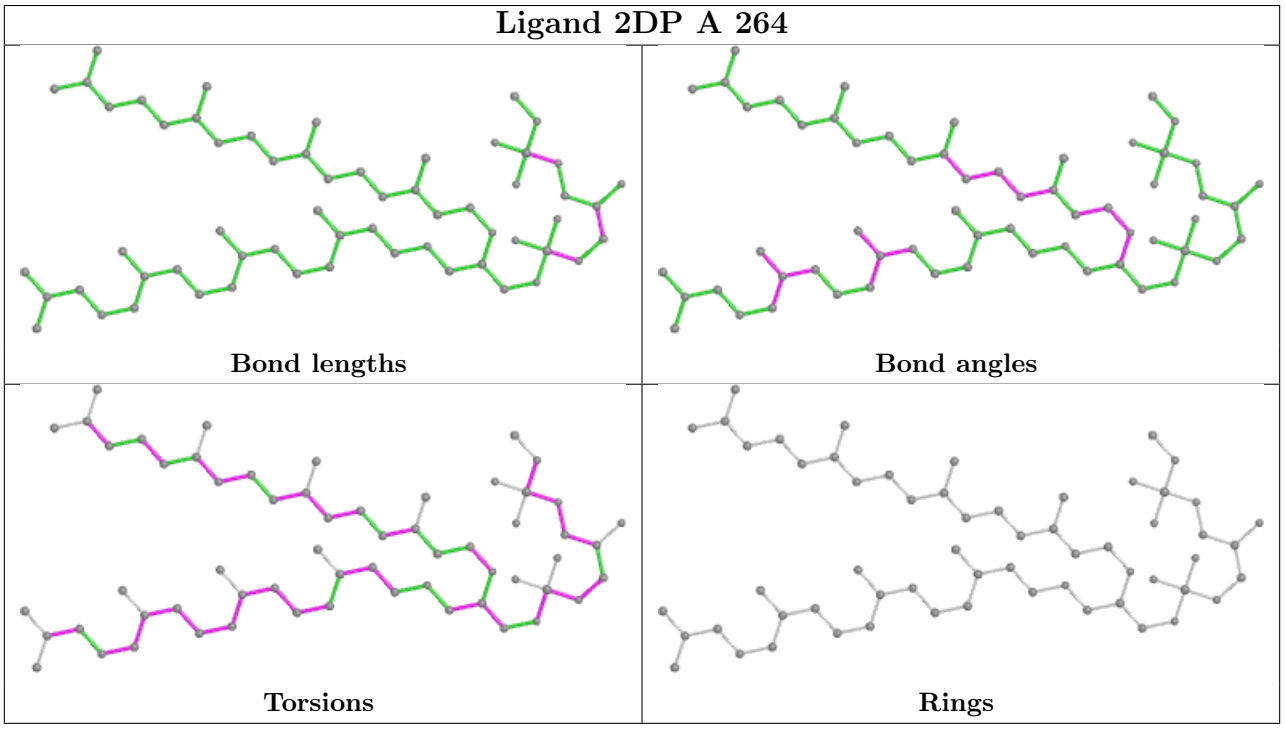
9 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	264	2DP	5	0
3	A	268	2DP	6	0
3	A	269	2DP	6	0
3	A	267	2DP	8	0
3	A	262	2DP	10	0
2	A	249(A)	RET	6	0
3	A	261	2DP	4	0
3	A	265	2DP	2	0
3	A	263	2DP	7	0

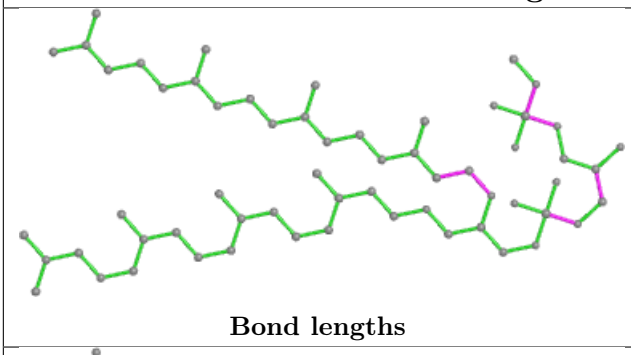
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

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.

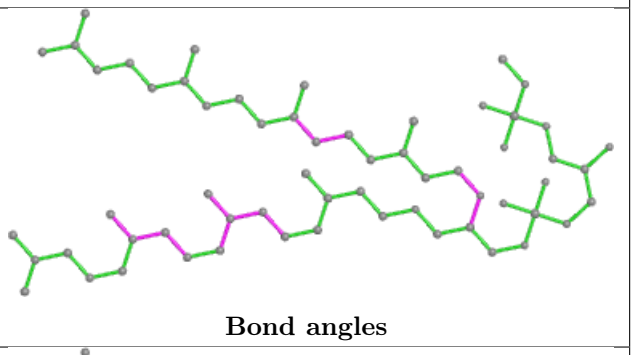
Ligand 2DP A 264



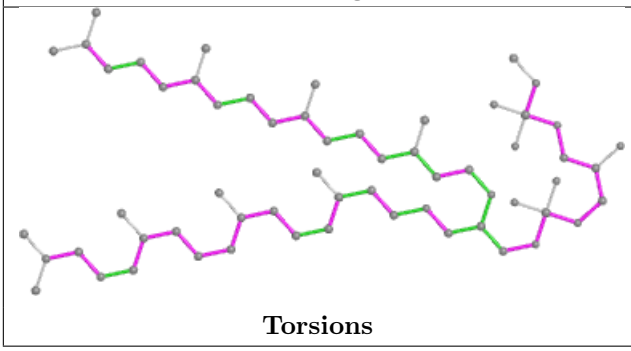
Ligand 2DP A 268



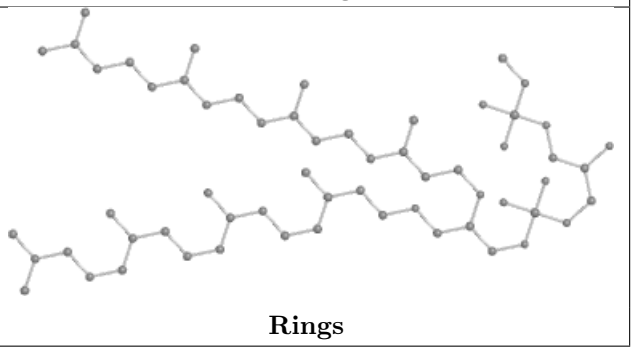
Bond lengths



Bond angles

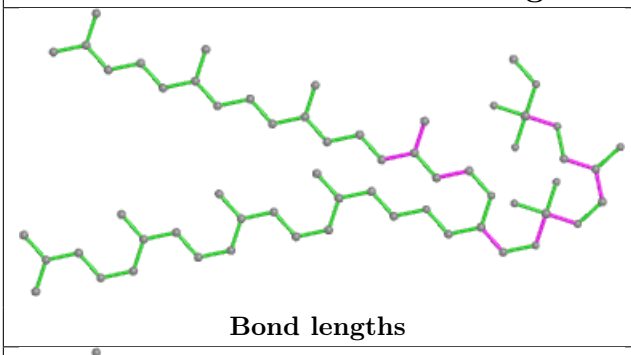


Torsions

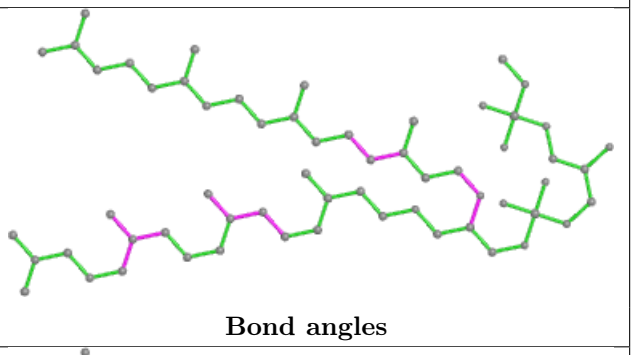


Rings

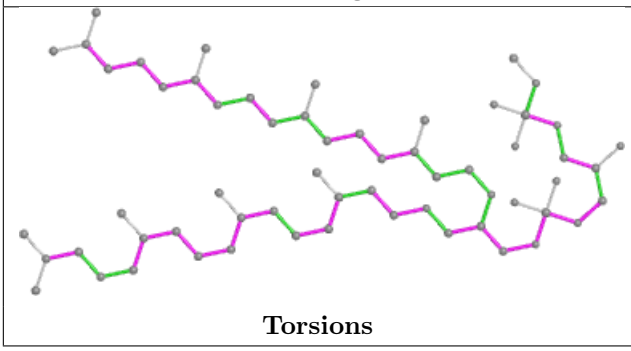
Ligand 2DP A 269



Bond lengths



Bond angles



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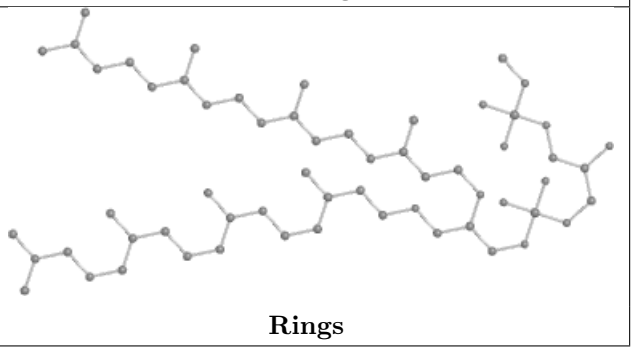
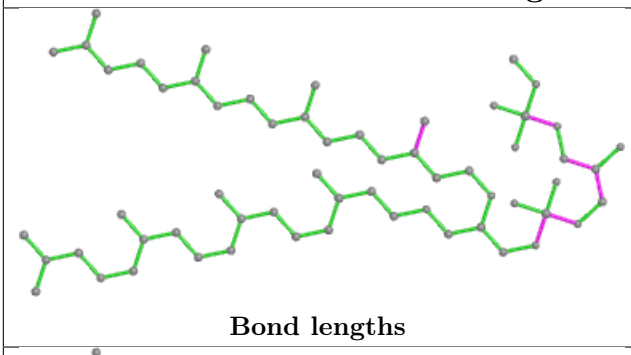
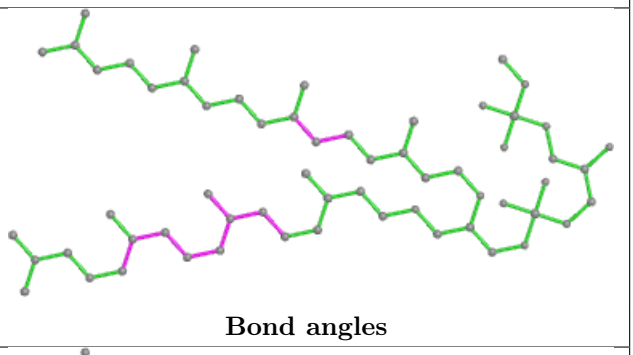


Rings

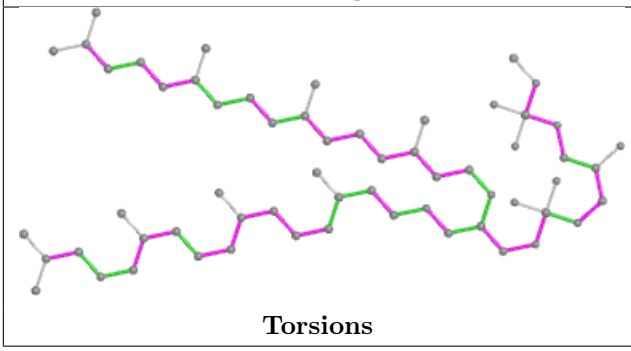
Ligand 2DP A 267



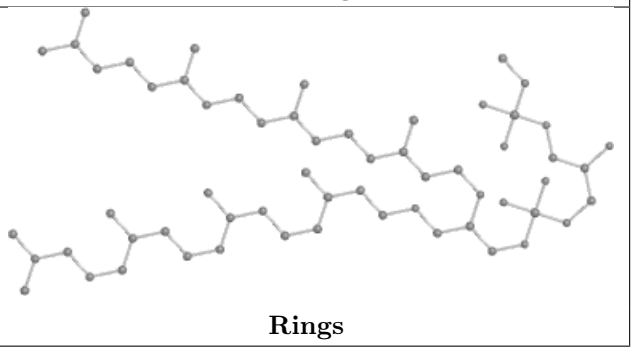
Bond lengths



Bond angles

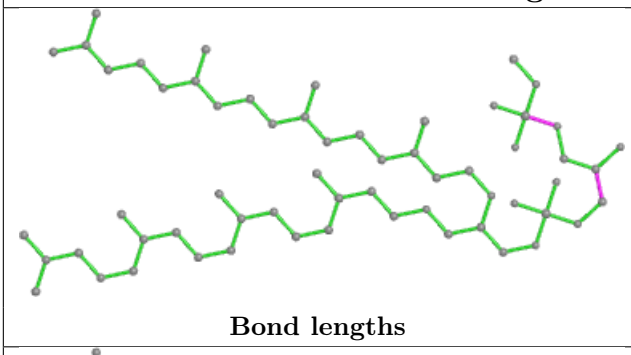


Torsions

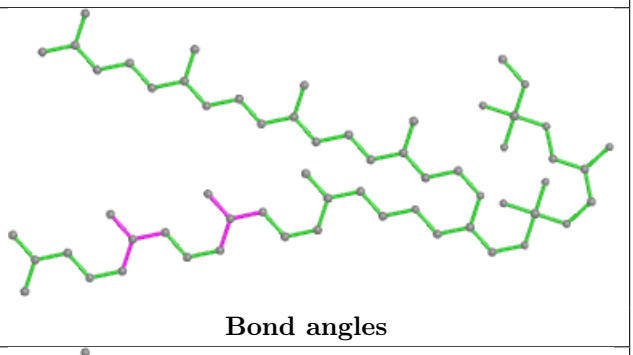


Rings

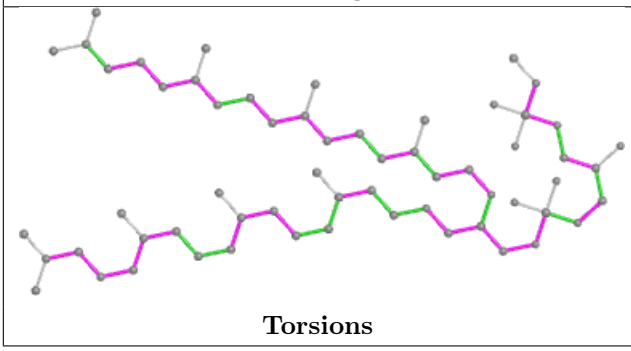
Ligand 2DP A 262



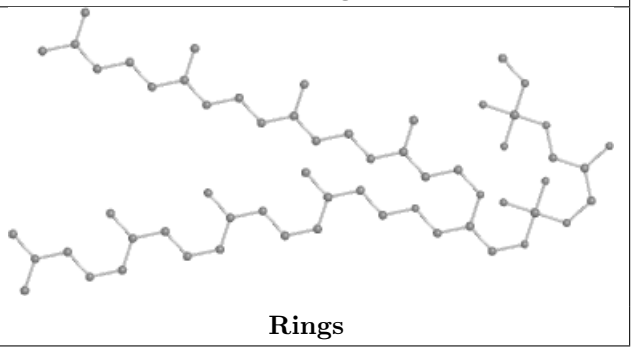
Bond lengths



Bond angles

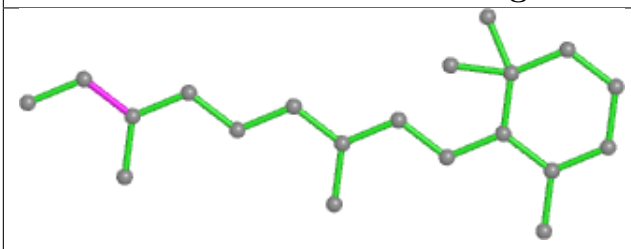


Torsions

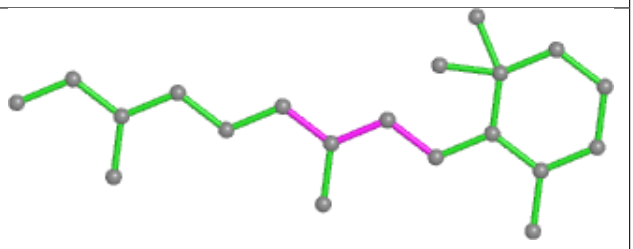


Rings

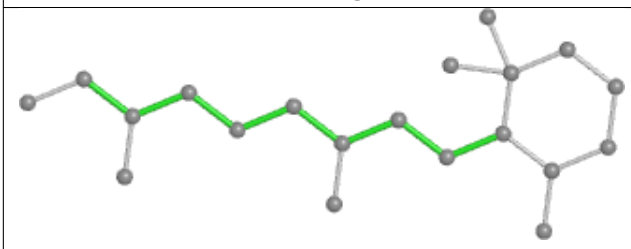
Ligand RET A 249A



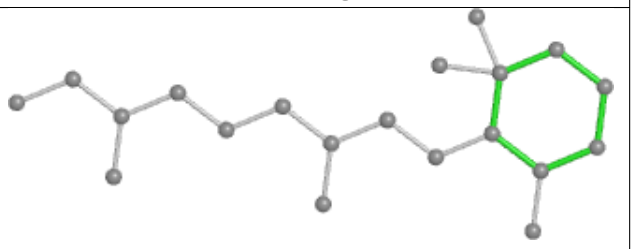
Bond lengths



Bond angles

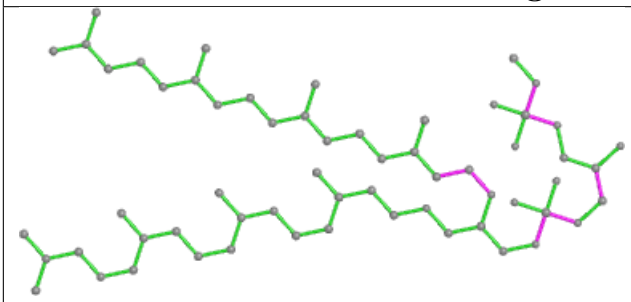


Torsions

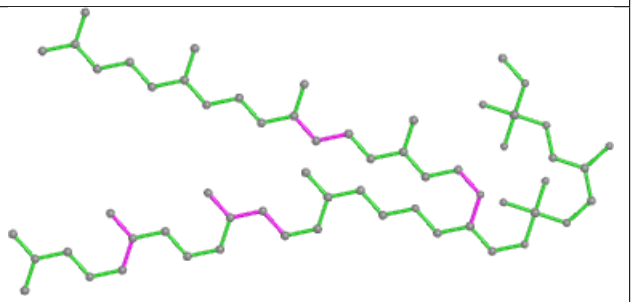


Rings

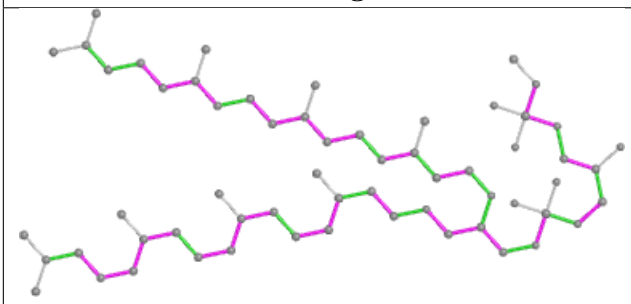
Ligand 2DP A 261



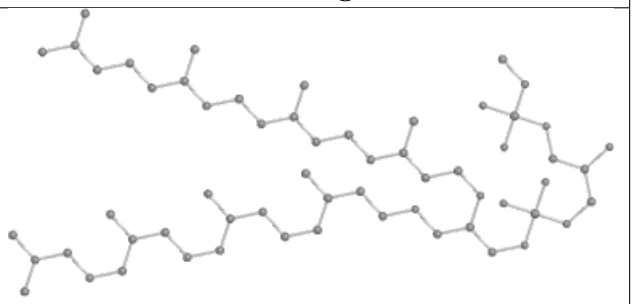
Bond lengths



Bond angles

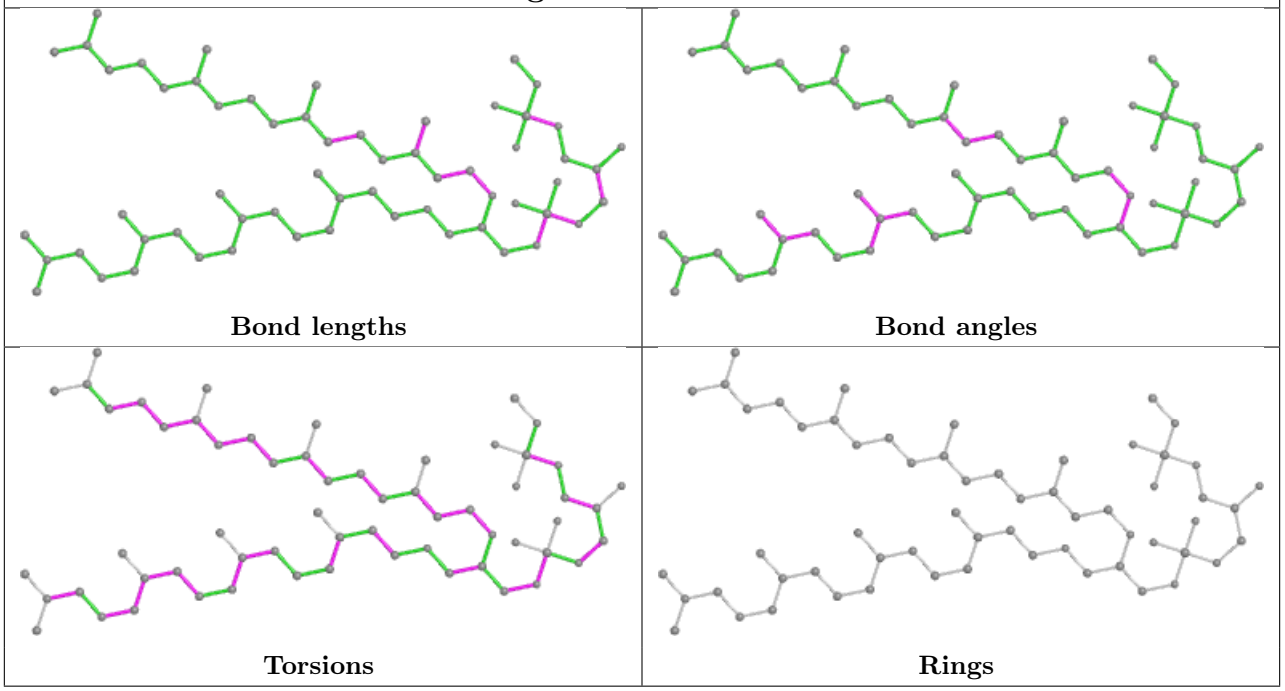


Torsions

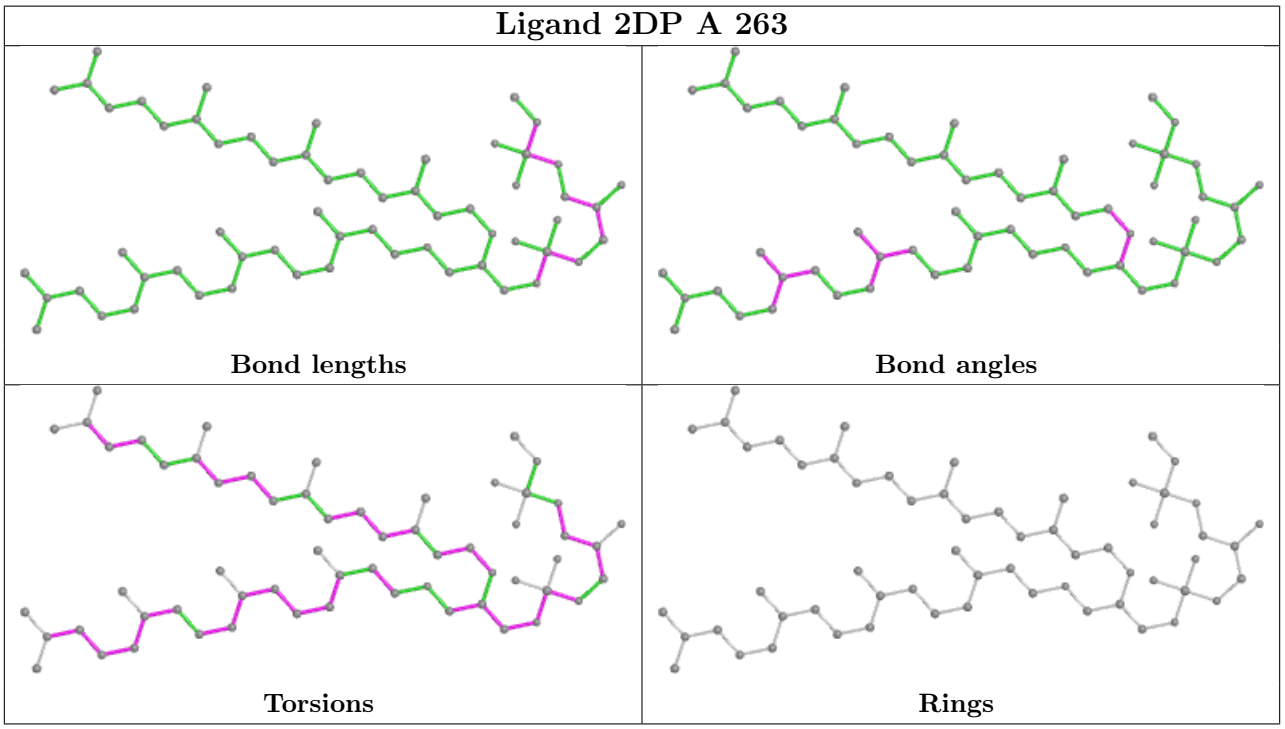


Rings

Ligand 2DP A 265



Ligand 2DP A 263



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.