W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Aug 2, 2023 – 06:51 AM EDT

PDB ID	:	1C8S
Title	:	BACTERIORHODOPSIN D96N LATE M STATE INTERMEDIATE
Authors	:	Luecke, H.
Deposited on	:	1999-07-29
Resolution	:	2.00 Å(reported)

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)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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)	:	2.34

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 2.00 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.
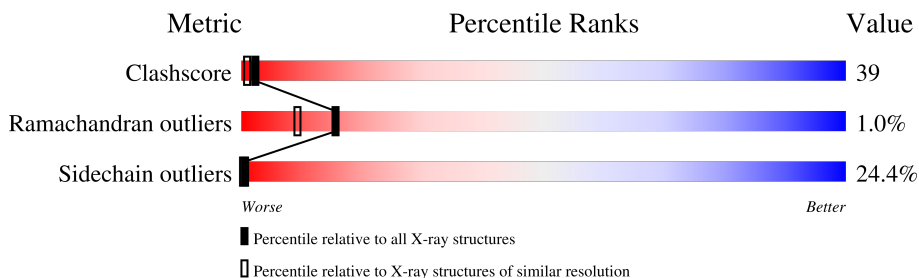
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	196	40% 45% 14% •

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
2	LI1	A	601	X	-	-	-
2	LI1	A	602	-	-	X	-
2	LI1	A	613	X	-	-	-
3	SQU	A	701	X	-	-	-

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 1821 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.
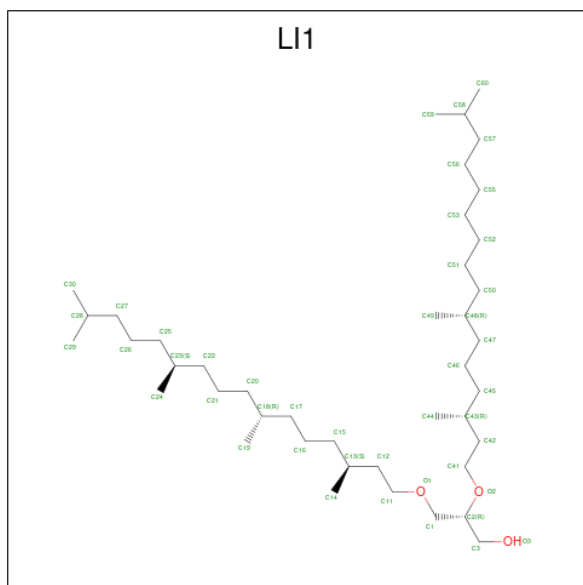
- Molecule 1 is a protein called BACTERIORHODOPSIN ("M" STATE INTERMEDIATE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total 1510	C 1021	N 224	O 257	S 8	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	ASN	ASP	engineered mutation	UNP P02945

- Molecule 2 is 1-[2,6,10.14-TETRAMETHYL-HEXADECAN-16-YL]-2-[2,10,14-TRIMETHYLHEXADECAN-16-YL]GLYCEROL (three-letter code: LI1) (formula: $C_{42}H_{86}O_3$).


LI1

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 32	C 29	O 3	0	0
2	A	1	Total 41	C 38	O 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 18	C 18		0	0
2	A	1	Total 8	C 8		0	0
2	A	1	Total 8	C 8		0	0
2	A	1	Total 38	C 35	O 3	0	0
2	A	1	Total 18	C 18		0	0
2	A	1	Total 16	C 16		0	0
2	A	1	Total 40	C 37	O 3	0	0
2	A	1	Total 18	C 18		0	0
2	A	1	Total 13	C 13		0	0

- Molecule 3 is 2,10,23-TRIMETHYL-TETRACOSANE (three-letter code: SQU) (formula: $C_{27}H_{56}$).
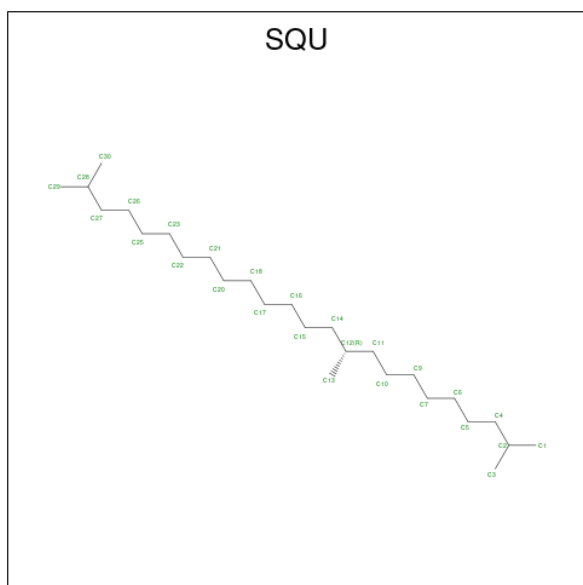
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 27	C 27	0	0

- Molecule 4 is RETINAL (three-letter code: RET) (formula: $C_{20}H_{28}O$).

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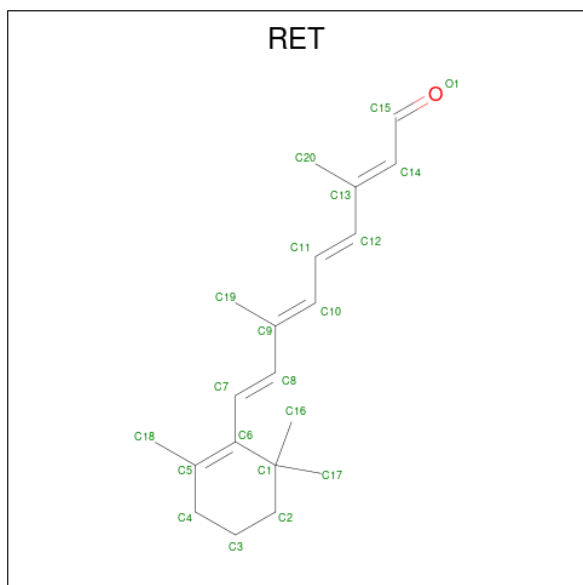
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 20	C 20	0	0

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total 14	O 14	0	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.

Note EDS was not executed.

• Molecule 1: BACTERIORHODOPSIN ("M" STATE INTERMEDIATE)
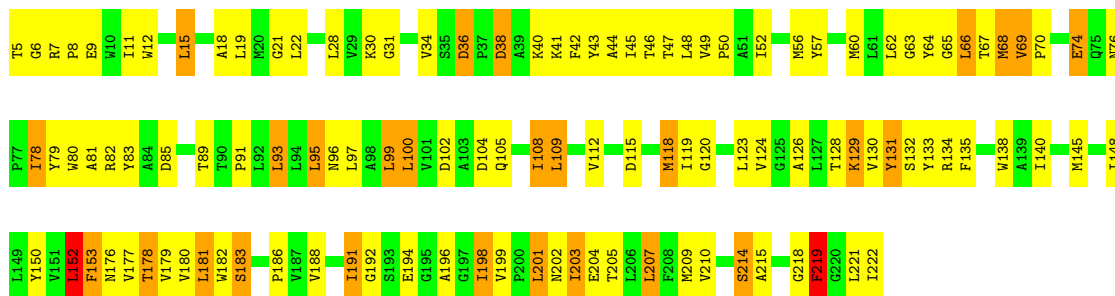
4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α, β, γ	60.63Å 60.63Å 108.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	12.00 – 2.00	Depositor
% Data completeness (in resolution range)	95.0 (12.00-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.173 , 0.219	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1821	wwPDB-VP
Average B, all atoms (Å^2)	35.0	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, LI1, SQU

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	0.38	0/1552	1.07	3/2126 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	219	PHE	CB-CG-CD1	6.05	125.03	120.80
1	A	150	TYR	CB-CG-CD1	5.52	124.31	121.00
1	A	219	PHE	CA-CB-CG	5.30	126.62	113.90

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	1510	0	1555	117	0
2	A	250	0	404	60	0
3	A	27	0	53	3	0
4	A	20	0	27	1	0
5	A	14	0	0	5	0
All	All	1821	0	2039	149	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 39.

The worst 5 of 149 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:180:VAL:HG22	2:A:610:LI1:H211	1.49	0.92
1:A:181:LEU:HD21	1:A:215:ALA:HB2	1.61	0.83
1:A:21:GLY:HA2	2:A:612:LI1:H291	1.59	0.82
2:A:602:LI1:H171	2:A:602:LI1:H451	1.60	0.82
1:A:78:ILE:HD13	1:A:194:GLU:HG2	1.63	0.80

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	192/196 (98%)	179 (93%)	11 (6%)	2 (1%)	15	9

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	ASP
1	A	152	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	156/156 (100%)	118 (76%)	38 (24%)	0	0

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	178	THR
1	A	207	LEU
1	A	181	LEU
1	A	198	ILE
1	A	219	PHE

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 ⓘ

13 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	$\#|Z| > 2$
2	LI1	A	609	-	15,15,44	0.50	0	14,14,51	0.94	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
4	RET	A	301	1	20,20,21	0.74	0	27,27,28	1.36	3 (11%)
2	LI1	A	605	-	7,7,44	0.50	0	6,6,51	0.82	0
3	SQU	A	701	-	26,26,26	1.40	6 (23%)	28,28,28	1.78	10 (35%)
2	LI1	A	601	-	31,31,44	0.82	1 (3%)	33,33,51	1.13	3 (9%)
2	LI1	A	603	-	17,17,44	0.51	0	18,18,51	1.16	1 (5%)
2	LI1	A	613	-	12,12,44	0.51	0	12,12,51	1.39	2 (16%)
2	LI1	A	607	-	37,37,44	0.80	1 (2%)	37,38,51	1.05	1 (2%)
2	LI1	A	610	-	39,39,44	0.79	1 (2%)	41,41,51	1.02	1 (2%)
2	LI1	A	606	-	7,7,44	0.49	0	6,6,51	0.87	0
2	LI1	A	602	-	40,40,44	0.75	1 (2%)	43,45,51	1.14	3 (6%)
2	LI1	A	612	-	17,17,44	0.47	0	18,18,51	1.02	1 (5%)
2	LI1	A	608	-	17,17,44	0.50	0	18,18,51	1.21	2 (11%)

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
2	LI1	A	609	-	-	11/13/13/49	-
4	RET	A	301	1	-	0/13/30/31	0/1/1/1
3	SQU	A	701	-	1/1/3/3	14/25/25/25	-
2	LI1	A	605	-	-	4/5/5/49	-
2	LI1	A	601	-	2/2/3/8	17/32/32/49	-
2	LI1	A	613	-	1/1/1/8	5/11/11/49	-
2	LI1	A	603	-	-	10/16/16/49	-
2	LI1	A	607	-	-	18/38/38/49	-
2	LI1	A	610	-	-	30/39/39/49	-
2	LI1	A	606	-	-	4/5/5/49	-
2	LI1	A	602	-	-	21/44/44/49	-
2	LI1	A	612	-	-	8/16/16/49	-
2	LI1	A	608	-	-	7/16/16/49	-

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	SQU	C14-C12	-3.33	1.35	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	SQU	C9-C7	-2.94	1.35	1.51
3	A	701	SQU	C23-C22	-2.92	1.35	1.51
2	A	607	LI1	O3-C3	2.91	1.54	1.42
3	A	701	SQU	C18-C17	-2.88	1.35	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	701	SQU	C15-C14-C12	4.41	130.16	115.92
4	A	301	RET	C11-C12-C13	-3.66	116.12	126.42
2	A	613	LI1	C16-C17-C18	-2.96	106.36	115.92
2	A	602	LI1	O3-C3-C2	-2.85	104.22	111.78
2	A	607	LI1	O3-C3-C2	-2.83	104.29	111.78

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	601	LI1	C18
2	A	601	LI1	C2
2	A	613	LI1	C18
3	A	701	SQU	C12

5 of 149 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	602	LI1	O2-C2-C3-O3
2	A	602	LI1	C1-C2-O2-C41
2	A	602	LI1	C41-C42-C43-C44
2	A	607	LI1	O2-C2-C3-O3
2	A	607	LI1	C42-C41-O2-C2

There are no ring outliers.

11 monomers are involved in 64 short contacts:

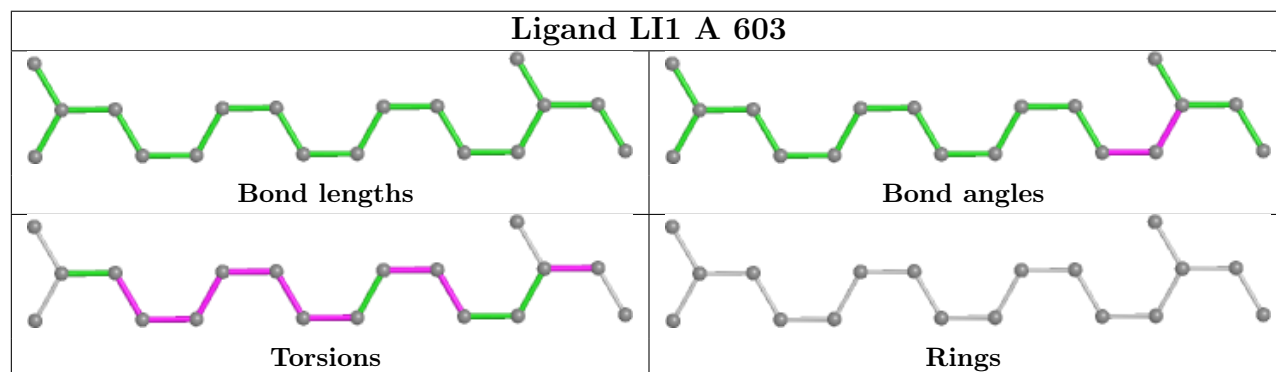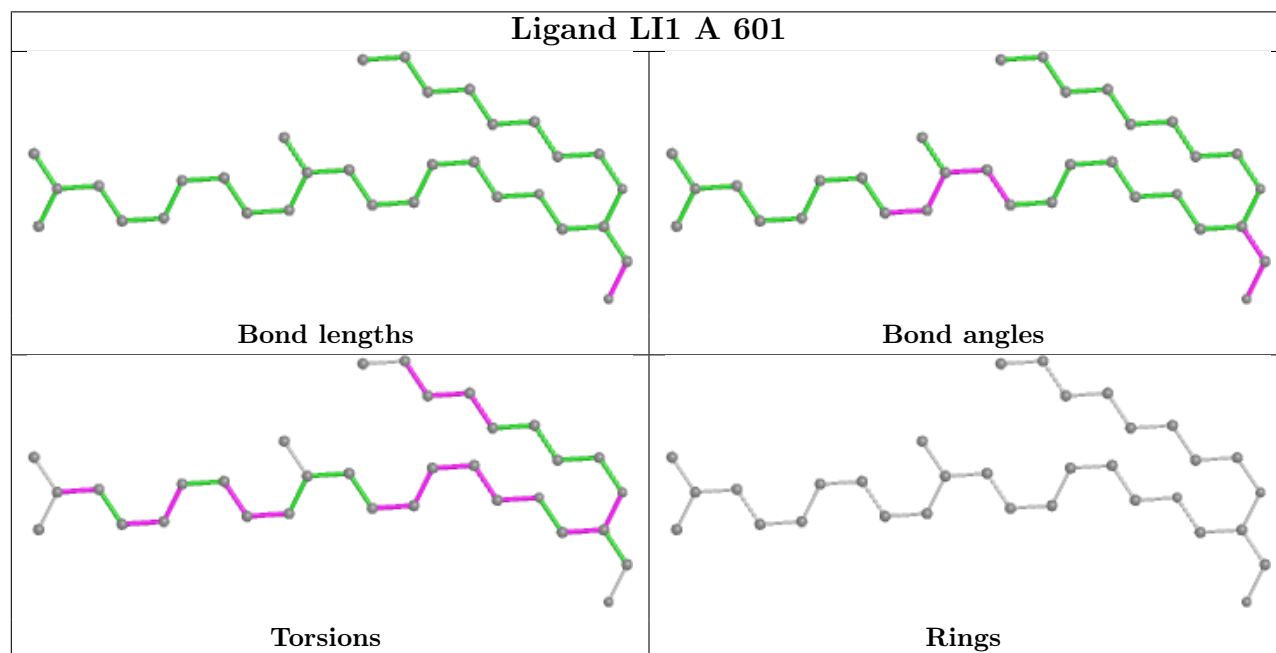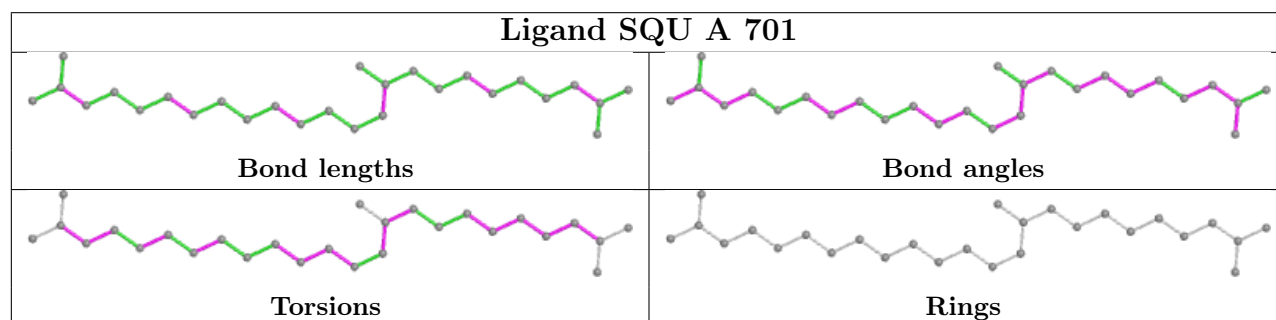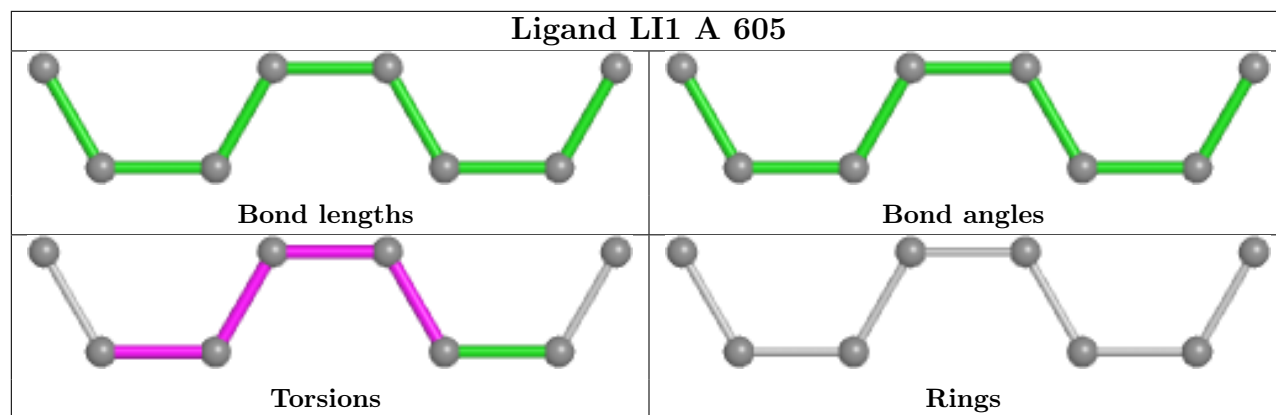| Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	301	RET	1	0
3	A	701	SQU	3	0
2	A	601	LI1	8	0
2	A	603	LI1	2	0
2	A	613	LI1	1	0
2	A	607	LI1	5	0

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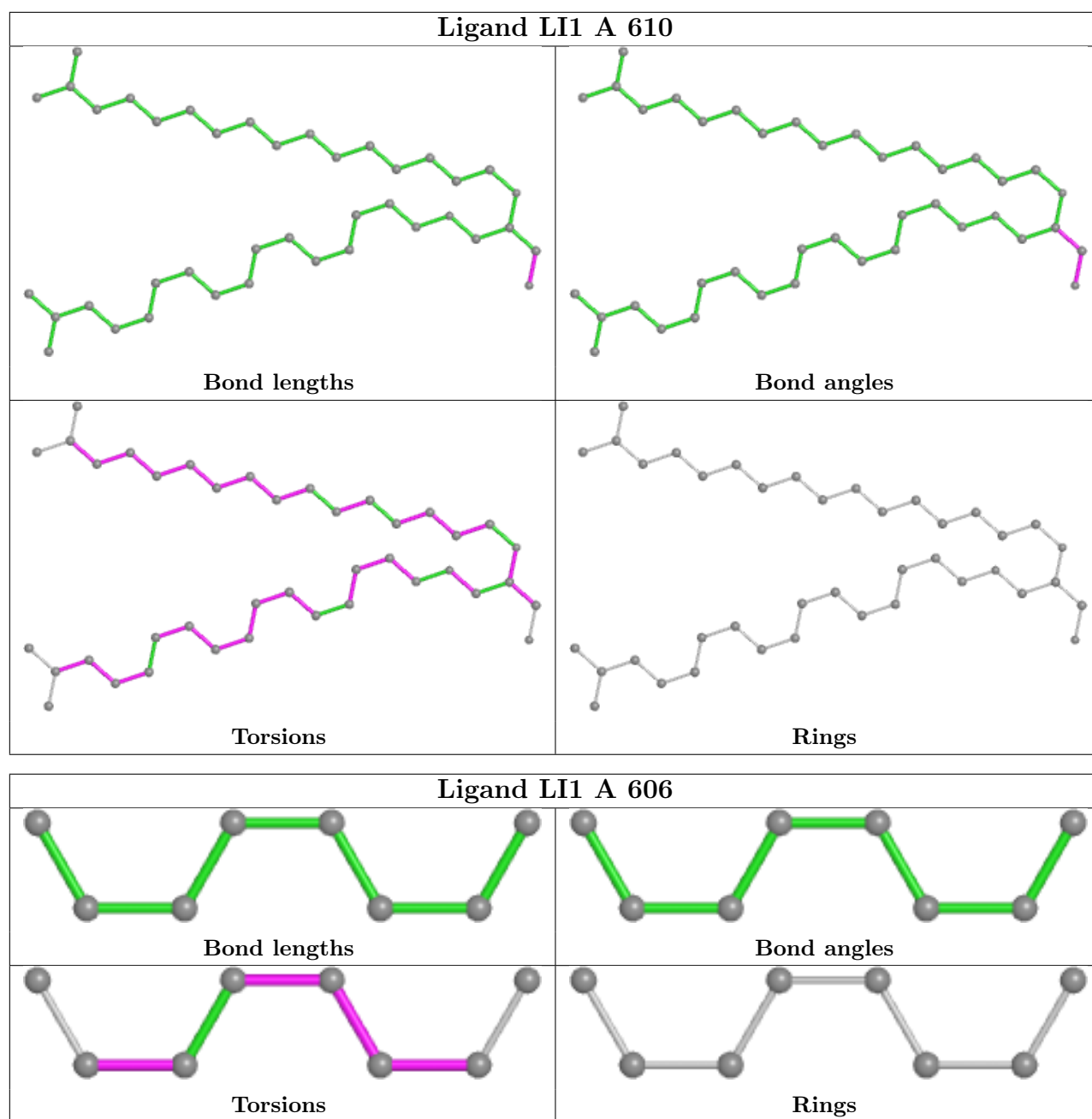| Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	610	LI1	12	0
2	A	606	LI1	2	0
2	A	602	LI1	22	0
2	A	612	LI1	7	0
2	A	608	LI1	7	0

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 LI1 A 609

Ligand RET A 301

Ligand LI1 A 605

Bond lengths

Bond angles

Torsions

Rings

Ligand SQU A 701

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 601

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 603

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 613

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 607

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 610

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 606

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 602

Bond lengths

Bond angles

Torsions

Rings

Ligand LI1 A 612

Bond lengths

Bond angles

Torsions

Rings

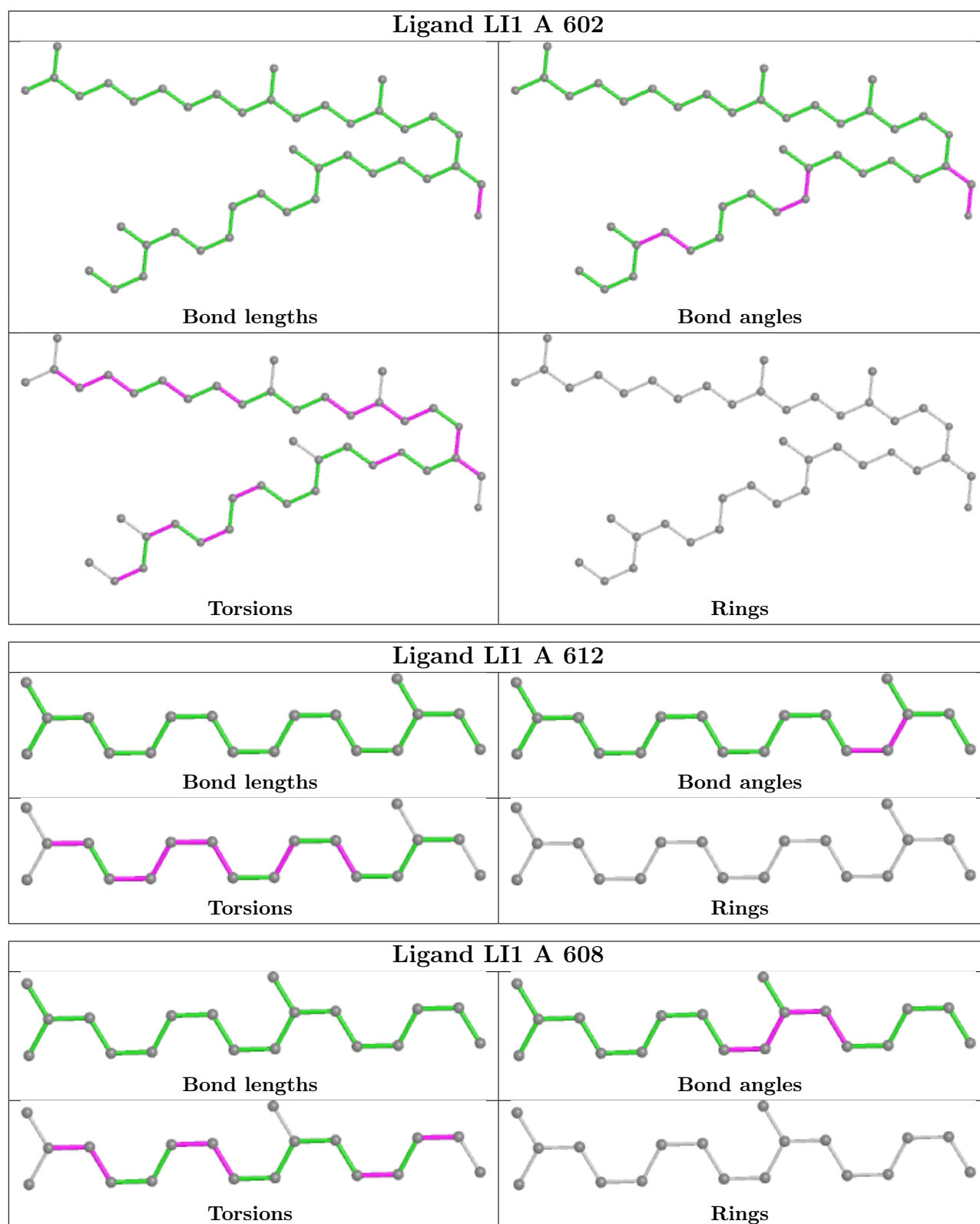## Ligand LI1 A 608

Bond lengths

Bond angles

Torsions

Rings

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	153:PHE	C	176:ASN	N	9.48

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.