



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2023 – 11:03 AM EDT

PDB ID : 2I1X
Title : Bacteriorhodopsin/lipid complex, D96A mutant
Authors : Lanyi, J.K.; Schobert, B.
Deposited on : 2006-08-15
Resolution : 2.00 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

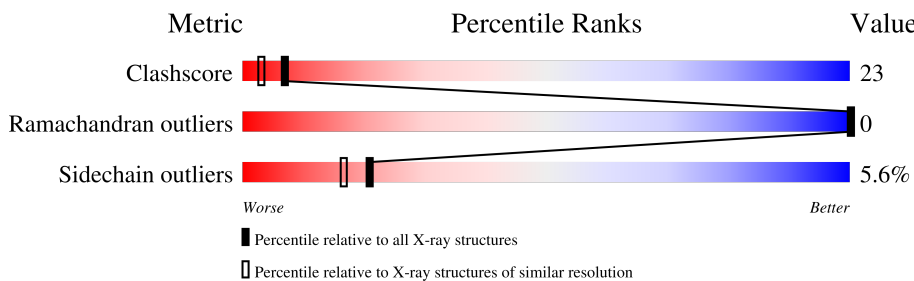
1 Overall quality at a glance

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	249	

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	LI1	A	601	X	-	-	-
3	LI1	A	602	X	-	X	-
3	LI1	A	611	X	-	-	-
3	LI1	A	613	X	-	-	-
4	SQU	A	701	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2070 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.

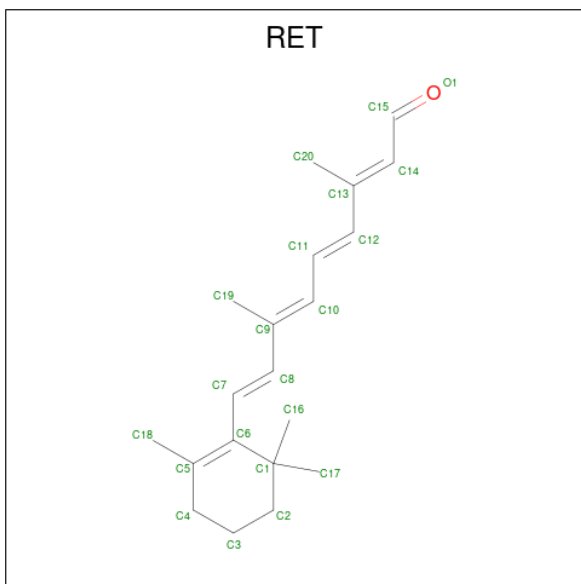
- Molecule 1 is a protein called Bacteriorhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	222	1717	1158	262	288	9	0	0	0

There is a discrepancy between the modelled and reference sequences:

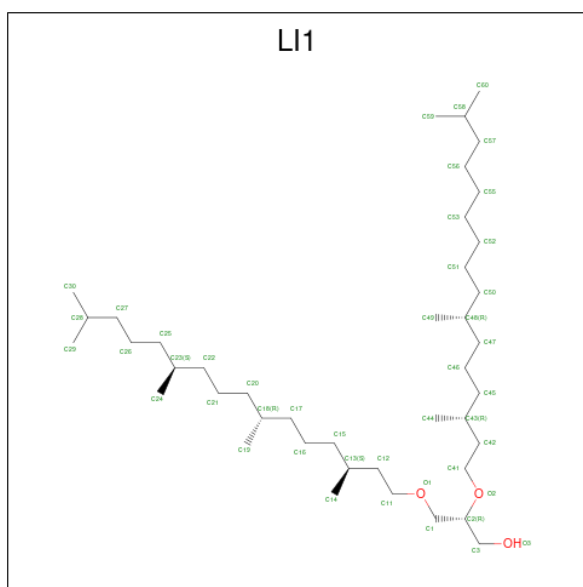
Chain	Residue	Modelled	Actual	Comment	Reference
A	96	ALA	ASP	engineered mutation	UNP P02945

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



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

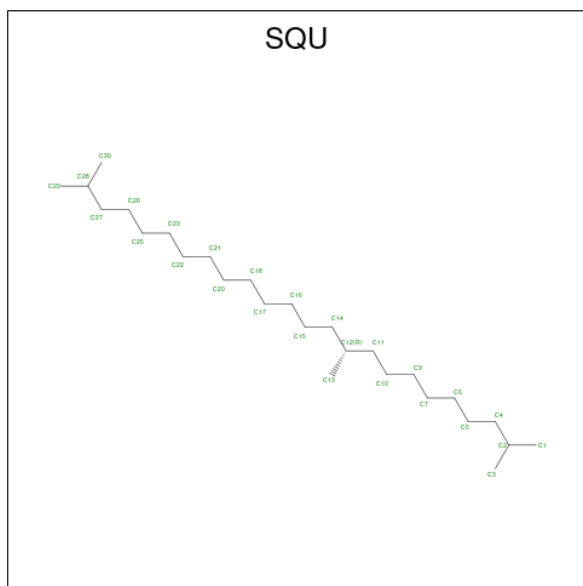
- Molecule 3 is 1-[2,6,10,14-TETRAMETHYL-HEXADECAN-16-YL]-2-[2,10,14-TRIMETHYLHEXADECAN-16-YL]GLYCEROL (three-letter code: LI1) (formula: $C_{42}H_{86}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 32 29 3	0	0
3	A	1	Total C O 41 38 3	0	0
3	A	1	Total C 18 18	0	0
3	A	1	Total C 16 16	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C O 38 35 3	0	0
3	A	1	Total C 18 18	0	0
3	A	1	Total C 16 16	0	0
3	A	1	Total C O 40 37 3	0	0
3	A	1	Total C 17 17	0	0
3	A	1	Total C 18 18	0	0
3	A	1	Total C 13 13	0	0

- Molecule 4 is 2,10,23-TRIMETHYL-TETRACOSANE (three-letter code: SQU) (formula:

C₂₇H₅₆).



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

- Molecule 5 is water.

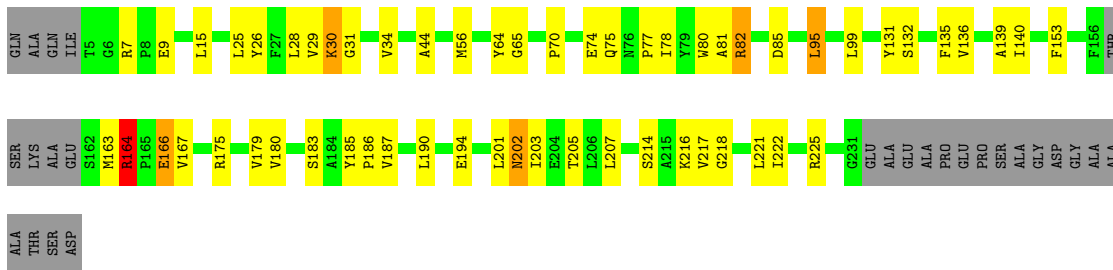
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	23	Total O 23 23	0	0

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.

- Molecule 1: Bacteriorhodopsin

Chain A:  66% 20% 11%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	60.95Å 60.95Å 109.33Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.00 23.77 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.00-2.00) 87.9 (23.77-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 1.99Å)	Xtrriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.238 , 0.299 0.186 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtrriage
Anisotropy	0.764	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 137.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.066 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2070	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.71% 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: 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	0.32	0/1764	0.93	6/2409 (0.2%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	A	164	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	A	82	ARG	NE-CZ-NH1	-6.03	117.29	120.30
1	A	216	LYS	CB-CG-CD	5.38	125.59	111.60
1	A	164	ARG	CD-NE-CZ	5.14	130.80	123.60
1	A	216	LYS	CD-CE-NZ	5.02	123.24	111.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1717	0	1777	54	0
2	A	20	0	27	2	0
3	A	283	0	447	66	0
4	A	27	0	53	7	0
5	A	23	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2070	0	2304	100	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 23.

All (100) 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)
3:A:609:LI1:C26	3:A:609:LI1:C25	1.75	1.63
3:A:611:LI1:C26	3:A:611:LI1:C25	1.74	1.62
1:A:187:VAL:HG21	3:A:610:LI1:H293	1.39	1.04
3:A:610:LI1:H122	3:A:610:LI1:H412	1.40	1.04
1:A:217:VAL:HG11	4:A:701:SQU:H201	1.52	0.92
3:A:609:LI1:C25	3:A:609:LI1:C27	2.53	0.86
3:A:611:LI1:C25	3:A:611:LI1:C27	2.52	0.86
3:A:602:LI1:H252	3:A:602:LI1:H591	1.60	0.82
3:A:609:LI1:C26	3:A:609:LI1:C23	2.58	0.81
3:A:611:LI1:C26	3:A:611:LI1:C23	2.58	0.81
4:A:701:SQU:H112	4:A:701:SQU:H171	1.63	0.80
3:A:602:LI1:H601	3:A:602:LI1:C27	2.15	0.76
3:A:610:LI1:H593	3:A:610:LI1:H502	1.69	0.75
1:A:179:VAL:HG12	3:A:610:LI1:H202	1.69	0.75
3:A:610:LI1:H122	3:A:610:LI1:C41	2.17	0.72
1:A:131:TYR:OH	3:A:602:LI1:H162	1.88	0.72
3:A:602:LI1:H592	3:A:602:LI1:H522	1.73	0.71
3:A:610:LI1:H412	3:A:610:LI1:C12	2.20	0.71
1:A:44:ALA:HA	3:A:612:LI1:H13	1.73	0.70
3:A:602:LI1:H172	3:A:602:LI1:H443	1.74	0.69
1:A:78:ILE:HD12	1:A:194:GLU:HG3	1.74	0.67
3:A:602:LI1:H592	3:A:602:LI1:H501	1.78	0.65
1:A:95:LEU:HD22	1:A:99:LEU:HG	1.79	0.64
4:A:701:SQU:H13	4:A:701:SQU:H211	1.80	0.63
3:A:602:LI1:H152	3:A:603:LI1:H141	1.79	0.62
1:A:82:ARG:HH22	1:A:205:THR:HG23	1.64	0.62
1:A:218:GLY:O	1:A:222:ILE:HD12	1.99	0.62
1:A:140:ILE:HG13	3:A:601:LI1:H272	1.82	0.61
1:A:190:LEU:HD21	3:A:603:LI1:H222	1.82	0.60
1:A:131:TYR:CE2	3:A:602:LI1:H112	2.37	0.59
1:A:26:TYR:CZ	1:A:30:LYS:HD2	2.37	0.59
1:A:64:TYR:OH	3:A:607:LI1:H32	2.02	0.59
3:A:601:LI1:O1	3:A:601:LI1:H152	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:610:LI1:H502	3:A:610:LI1:C59	2.34	0.57
1:A:135:PHE:HB3	3:A:602:LI1:H502	1.87	0.57
1:A:190:LEU:CD2	3:A:603:LI1:H222	2.35	0.56
1:A:221:LEU:O	1:A:225:ARG:HG2	2.05	0.56
1:A:153:PHE:CE2	1:A:179:VAL:HG21	2.41	0.56
1:A:26:TYR:OH	1:A:30:LYS:HD2	2.06	0.56
3:A:602:LI1:H172	3:A:602:LI1:C44	2.35	0.55
1:A:164:ARG:HG3	1:A:167:VAL:CG2	2.38	0.54
3:A:610:LI1:H593	3:A:610:LI1:C50	2.38	0.54
3:A:602:LI1:H501	3:A:602:LI1:C59	2.39	0.54
3:A:602:LI1:H592	3:A:602:LI1:C52	2.37	0.53
1:A:25:LEU:O	1:A:29:VAL:HG23	2.09	0.53
1:A:131:TYR:OH	3:A:602:LI1:H13	2.09	0.53
1:A:203:ILE:O	1:A:207:LEU:HG	2.08	0.53
1:A:183:SER:HB2	3:A:610:LI1:C23	2.40	0.51
1:A:180:VAL:HA	3:A:610:LI1:C23	2.40	0.51
1:A:31:GLY:O	1:A:34:VAL:HG23	2.10	0.51
1:A:221:LEU:HD13	4:A:701:SQU:H292	1.94	0.49
2:A:300:RET:H181	2:A:300:RET:H7	1.66	0.48
1:A:180:VAL:HA	3:A:610:LI1:H222	1.94	0.48
3:A:602:LI1:H152	3:A:603:LI1:C14	2.42	0.48
1:A:217:VAL:CG1	4:A:701:SQU:H201	2.33	0.48
1:A:65:GLY:HA3	1:A:81:ALA:HB2	1.95	0.48
1:A:135:PHE:CE1	3:A:602:LI1:H201	2.48	0.48
1:A:80:TRP:HH2	3:A:607:LI1:H451	1.78	0.47
1:A:164:ARG:HG3	1:A:167:VAL:HG23	1.95	0.47
3:A:602:LI1:H443	3:A:602:LI1:H151	1.97	0.47
1:A:56:MET:HG3	1:A:85:ASP:HB2	1.97	0.46
3:A:601:LI1:H303	3:A:608:LI1:H272	1.96	0.46
3:A:607:LI1:H511	3:A:607:LI1:H552	1.68	0.46
1:A:180:VAL:HA	3:A:610:LI1:C22	2.45	0.46
3:A:602:LI1:H241	3:A:602:LI1:H261	1.67	0.46
3:A:610:LI1:H121	3:A:610:LI1:H12	1.68	0.46
3:A:602:LI1:H241	3:A:603:LI1:H211	1.97	0.46
2:A:300:RET:H11	2:A:300:RET:H191	1.66	0.45
1:A:180:VAL:HG21	3:A:610:LI1:C48	2.47	0.45
1:A:9:GLU:HB3	1:A:202:ASN:HA	1.99	0.45
1:A:135:PHE:CD1	3:A:602:LI1:H201	2.52	0.45
3:A:613:LI1:H201	3:A:613:LI1:H162	1.45	0.45
3:A:602:LI1:H202	3:A:602:LI1:H451	1.99	0.45
1:A:175:ARG:HH21	3:A:610:LI1:C1	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:701:SQU:C1	4:A:701:SQU:H181	2.47	0.44
1:A:70:PRO:HA	1:A:74:GLU:O	2.17	0.44
1:A:77:PRO:HG2	1:A:201:LEU:HD22	1.99	0.44
4:A:701:SQU:H181	4:A:701:SQU:H11	2.00	0.44
1:A:139:ALA:CB	3:A:602:LI1:H551	2.48	0.44
3:A:602:LI1:H522	3:A:602:LI1:H562	1.33	0.44
3:A:602:LI1:H243	3:A:602:LI1:H212	1.64	0.43
3:A:610:LI1:H593	3:A:610:LI1:C51	2.48	0.43
3:A:601:LI1:H412	3:A:601:LI1:H11	1.40	0.43
3:A:601:LI1:H303	3:A:608:LI1:C27	2.48	0.43
1:A:28:LEU:HD23	1:A:28:LEU:HA	1.89	0.42
3:A:612:LI1:H221	3:A:612:LI1:H261	1.74	0.42
1:A:29:VAL:HG21	3:A:611:LI1:H161	2.01	0.42
1:A:185:TYR:N	1:A:186:PRO:HD2	2.34	0.42
1:A:164:ARG:HE	1:A:166:GLU:CD	2.22	0.42
3:A:610:LI1:H511	3:A:610:LI1:H551	1.48	0.42
1:A:135:PHE:CB	3:A:602:LI1:H502	2.48	0.42
3:A:601:LI1:H252	3:A:601:LI1:H28	1.86	0.41
1:A:136:VAL:HA	3:A:602:LI1:H532	2.02	0.41
3:A:601:LI1:H193	3:A:601:LI1:H162	1.63	0.41
1:A:56:MET:HE3	3:A:607:LI1:H521	2.02	0.41
1:A:164:ARG:HG3	1:A:167:VAL:HG21	2.01	0.41
1:A:166:GLU:H	1:A:166:GLU:HG3	1.29	0.41
1:A:202:ASN:HD22	1:A:202:ASN:H	1.68	0.41
1:A:179:VAL:CG1	3:A:610:LI1:H202	2.45	0.41
1:A:78:ILE:CD1	1:A:194:GLU:HG3	2.45	0.40

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	218/249 (88%)	217 (100%)	1 (0%)	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	177/194 (91%)	167 (94%)	10 (6%)	21 17

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	30	LYS
1	A	75	GLN
1	A	95	LEU
1	A	132	SER
1	A	163	MET
1	A	164	ARG
1	A	166	GLU
1	A	202	ASN
1	A	214	SER

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	202	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

15 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	LI1	A	610	-	39,39,44	1.07	2 (5%)	41,41,51	1.15	2 (4%)
3	LI1	A	602	-	40,40,44	1.03	2 (5%)	43,45,51	3.58	10 (23%)
3	LI1	A	613	-	12,12,44	0.46	0	12,12,51	1.09	1 (8%)
3	LI1	A	604	-	15,15,44	1.14	1 (6%)	14,14,51	1.19	2 (14%)
3	LI1	A	607	-	37,37,44	1.03	2 (5%)	37,38,51	1.08	3 (8%)
3	LI1	A	606	-	7,7,44	0.47	0	6,6,51	0.62	0
3	LI1	A	609	-	15,15,44	1.18	1 (6%)	14,14,51	1.15	2 (14%)
4	SQU	A	701	-	26,26,26	1.40	6 (23%)	28,28,28	1.81	10 (35%)
3	LI1	A	612	-	17,17,44	1.08	1 (5%)	18,18,51	1.20	1 (5%)
3	LI1	A	608	-	17,17,44	1.07	1 (5%)	18,18,51	1.29	3 (16%)
3	LI1	A	605	-	7,7,44	0.49	0	6,6,51	0.65	0
3	LI1	A	601	-	31,31,44	1.12	2 (6%)	33,33,51	1.24	4 (12%)
3	LI1	A	603	-	17,17,44	1.07	1 (5%)	18,18,51	1.16	1 (5%)
3	LI1	A	611	-	16,16,44	1.13	1 (6%)	18,18,51	4.20	5 (27%)
2	RET	A	300	1	20,20,21	0.90	1 (5%)	27,27,28	3.17	11 (40%)

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	LI1	A	610	-	-	24/39/39/49	-
3	LI1	A	602	-	1/1/6/8	24/44/44/49	-
3	LI1	A	613	-	1/1/1/8	5/11/11/49	-
3	LI1	A	604	-	-	7/13/13/49	-
3	LI1	A	607	-	-	21/38/38/49	-
3	LI1	A	606	-	-	2/5/5/49	-
3	LI1	A	609	-	-	3/13/13/49	-
4	SQU	A	701	-	-	16/25/25/25	-
3	LI1	A	612	-	-	7/16/16/49	-
3	LI1	A	608	-	-	5/16/16/49	-
3	LI1	A	605	-	-	4/5/5/49	-
3	LI1	A	601	-	2/2/3/8	18/32/32/49	-
3	LI1	A	603	-	-	10/16/16/49	-
3	LI1	A	611	-	2/2/3/8	7/17/17/49	-
2	RET	A	300	1	-	3/13/30/31	0/1/1/1

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	611	LI1	C26-C25	4.18	1.74	1.51
3	A	609	LI1	C26-C25	4.16	1.75	1.51
3	A	612	LI1	C26-C25	4.04	1.74	1.51
3	A	604	LI1	C26-C25	4.01	1.74	1.51
3	A	608	LI1	C26-C25	4.01	1.74	1.51
3	A	610	LI1	C26-C25	4.00	1.74	1.51
3	A	603	LI1	C26-C25	4.00	1.74	1.51
3	A	602	LI1	C26-C25	3.97	1.73	1.51
3	A	601	LI1	C26-C25	3.96	1.73	1.51
3	A	607	LI1	C26-C25	3.90	1.73	1.51
4	A	701	SQU	C14-C12	-3.31	1.35	1.52
3	A	610	LI1	O3-C3	3.22	1.56	1.42
3	A	602	LI1	O3-C3	3.11	1.55	1.42
4	A	701	SQU	C23-C22	-3.10	1.34	1.51
3	A	601	LI1	O3-C3	2.99	1.55	1.42
3	A	607	LI1	O3-C3	2.96	1.54	1.42
4	A	701	SQU	C18-C17	-2.91	1.35	1.51
4	A	701	SQU	C9-C7	-2.89	1.35	1.51
4	A	701	SQU	C4-C2	-2.35	1.35	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	701	SQU	C27-C28	-2.24	1.36	1.51
2	A	300	RET	C2-C3	-2.04	1.47	1.52

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	LI1	C49-C48-C47	-19.39	41.08	111.29
3	A	611	LI1	C24-C23-C25	-16.90	50.10	111.29
2	A	300	RET	C11-C10-C9	-11.20	111.32	127.31
3	A	602	LI1	C49-C48-C50	-9.59	76.56	111.29
2	A	300	RET	C7-C8-C9	5.27	134.20	126.23
2	A	300	RET	C20-C13-C12	5.03	126.01	118.08
2	A	300	RET	C10-C11-C12	-4.98	107.68	123.22
4	A	701	SQU	C15-C14-C12	4.63	130.89	115.92
3	A	608	LI1	C25-C26-C27	-3.62	100.82	113.62
3	A	612	LI1	C25-C26-C27	-3.61	100.84	113.62
3	A	610	LI1	C25-C26-C27	-3.59	100.93	113.62
3	A	603	LI1	C25-C26-C27	-3.57	101.01	113.62
3	A	602	LI1	C24-C23-C25	3.49	123.92	111.29
3	A	602	LI1	O3-C3-C2	-3.46	102.60	111.78
3	A	601	LI1	C25-C26-C27	-3.46	101.40	113.62
2	A	300	RET	C20-C13-C14	-3.40	113.66	123.71
2	A	300	RET	C7-C6-C5	-3.20	113.71	121.46
2	A	300	RET	C8-C9-C10	-3.17	114.08	118.94
3	A	601	LI1	O3-C3-C2	-3.05	103.70	111.78
2	A	300	RET	C1-C6-C7	2.97	124.17	115.78
3	A	610	LI1	O3-C3-C2	-2.96	103.92	111.78
4	A	701	SQU	C10-C9-C7	2.90	129.17	114.42
4	A	701	SQU	C23-C22-C21	2.80	128.65	114.42
4	A	701	SQU	C25-C23-C22	2.77	128.50	114.42
3	A	609	LI1	C27-C26-C25	-2.73	100.55	114.42
3	A	607	LI1	O3-C3-C2	-2.73	104.55	111.78
4	A	701	SQU	C5-C4-C2	2.73	128.82	115.98
3	A	602	LI1	C26-C25-C23	-2.69	102.99	115.86
3	A	601	LI1	C21-C20-C18	-2.68	107.27	115.92
3	A	604	LI1	C27-C26-C25	-2.65	100.99	114.42
3	A	611	LI1	C27-C26-C25	-2.64	100.53	113.29
3	A	611	LI1	C26-C25-C23	-2.57	103.55	115.86
3	A	602	LI1	C27-C26-C25	-2.56	100.92	113.29
3	A	613	LI1	C21-C20-C18	-2.45	108.00	115.92
3	A	602	LI1	C46-C45-C43	-2.40	108.16	115.92
2	A	300	RET	C18-C5-C4	-2.40	109.01	113.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	701	SQU	C20-C18-C17	2.37	126.46	114.42
4	A	701	SQU	C18-C17-C16	2.37	126.46	114.42
3	A	602	LI1	C51-C50-C48	-2.36	108.29	115.92
3	A	602	LI1	C46-C47-C48	-2.34	108.37	115.92
3	A	611	LI1	C21-C22-C23	-2.32	108.43	115.92
3	A	608	LI1	C21-C20-C18	-2.31	108.45	115.92
3	A	611	LI1	C21-C20-C18	-2.29	108.52	115.92
3	A	602	LI1	C21-C22-C23	-2.23	108.72	115.92
4	A	701	SQU	C9-C7-C6	2.21	125.66	114.42
3	A	607	LI1	C46-C45-C43	-2.21	108.78	115.92
4	A	701	SQU	C14-C12-C11	2.20	123.69	112.13
3	A	609	LI1	C26-C25-C23	-2.18	103.33	114.42
3	A	604	LI1	C26-C25-C23	-2.05	104.02	114.42
4	A	701	SQU	C26-C27-C28	2.04	125.57	115.98
2	A	300	RET	C3-C4-C5	-2.03	110.45	114.08
3	A	607	LI1	C26-C25-C23	-2.03	104.14	114.42
3	A	608	LI1	C26-C25-C23	-2.02	104.18	114.42
3	A	601	LI1	C26-C25-C23	-2.01	104.23	114.42
2	A	300	RET	C2-C1-C6	2.00	113.56	110.48

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	601	LI1	C18
3	A	601	LI1	C2
3	A	602	LI1	C48
3	A	611	LI1	C13
3	A	611	LI1	C23
3	A	613	LI1	C18

All (156) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	RET	C20-C13-C14-C15
3	A	601	LI1	C1-C2-O2-C41
3	A	602	LI1	C1-C2-C3-O3
3	A	602	LI1	O2-C2-C3-O3
3	A	602	LI1	C11-C12-C13-C14
3	A	607	LI1	C44-C43-C45-C46
3	A	611	LI1	C16-C17-C18-C19
3	A	610	LI1	C55-C56-C57-C58
3	A	610	LI1	C12-C11-O1-C1

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Mol	Chain	Res	Type	Atoms
4	A	701	SQU	C5-C6-C7-C9
3	A	604	LI1	C20-C21-C22-C23
3	A	602	LI1	C52-C53-C55-C56
3	A	602	LI1	C49-C48-C50-C51
3	A	602	LI1	C21-C22-C23-C24
3	A	612	LI1	C14-C13-C15-C16
3	A	610	LI1	O2-C41-C42-C43
3	A	601	LI1	C18-C20-C21-C22
3	A	613	LI1	C15-C16-C17-C18
3	A	601	LI1	C15-C16-C17-C18
3	A	602	LI1	C55-C56-C57-C58
3	A	602	LI1	C45-C46-C47-C48
3	A	610	LI1	C25-C26-C27-C28
4	A	701	SQU	C2-C4-C5-C6
3	A	602	LI1	C23-C25-C26-C27
4	A	701	SQU	C12-C14-C15-C16
3	A	603	LI1	C18-C20-C21-C22
3	A	612	LI1	C23-C25-C26-C27
3	A	610	LI1	C52-C53-C55-C56
3	A	608	LI1	C26-C27-C28-C30
3	A	609	LI1	C20-C21-C22-C23
3	A	601	LI1	C16-C17-C18-C19
3	A	602	LI1	C53-C55-C56-C57
3	A	604	LI1	C25-C26-C27-C28
3	A	605	LI1	C17-C18-C20-C21
4	A	701	SQU	C23-C25-C26-C27
3	A	602	LI1	C42-C41-O2-C2
3	A	607	LI1	C42-C41-O2-C2
3	A	605	LI1	C15-C16-C17-C18
3	A	607	LI1	C45-C46-C47-C48
3	A	607	LI1	C53-C55-C56-C57
4	A	701	SQU	C26-C27-C28-C29
3	A	601	LI1	C45-C46-C47-C48
3	A	610	LI1	C53-C55-C56-C57
3	A	604	LI1	C22-C23-C25-C26
3	A	601	LI1	C21-C22-C23-C25
3	A	610	LI1	C17-C18-C20-C21
3	A	612	LI1	C22-C23-C25-C26
4	A	701	SQU	C11-C10-C9-C7
3	A	601	LI1	C20-C21-C22-C23
3	A	608	LI1	C20-C21-C22-C23
3	A	602	LI1	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
3	A	610	LI1	C16-C17-C18-C20
3	A	610	LI1	C22-C23-C25-C26
3	A	607	LI1	O2-C41-C42-C43
3	A	612	LI1	C25-C26-C27-C28
3	A	611	LI1	C13-C15-C16-C17
4	A	701	SQU	C16-C17-C18-C20
3	A	610	LI1	C56-C57-C58-C60
3	A	608	LI1	C22-C23-C25-C26
3	A	603	LI1	C21-C22-C23-C25
3	A	607	LI1	C12-C11-O1-C1
3	A	601	LI1	C13-C15-C16-C17
3	A	607	LI1	O1-C11-C12-C13
3	A	607	LI1	C23-C25-C26-C27
3	A	608	LI1	C12-C13-C15-C16
3	A	610	LI1	C56-C57-C58-C59
3	A	601	LI1	C22-C23-C25-C26
3	A	607	LI1	C47-C48-C50-C51
4	A	701	SQU	C3-C2-C4-C5
3	A	610	LI1	C47-C48-C50-C51
4	A	701	SQU	C21-C22-C23-C25
3	A	601	LI1	C26-C27-C28-C30
3	A	602	LI1	O1-C1-C2-C3
3	A	603	LI1	C22-C23-C25-C26
3	A	605	LI1	C18-C20-C21-C22
3	A	613	LI1	C21-C22-C23-C24
3	A	607	LI1	C12-C13-C15-C16
3	A	604	LI1	C16-C17-C18-C20
3	A	603	LI1	C16-C17-C18-C20
3	A	610	LI1	C51-C52-C53-C55
3	A	601	LI1	O1-C1-C2-O2
3	A	602	LI1	C42-C43-C45-C46
3	A	611	LI1	C21-C22-C23-C25
3	A	611	LI1	C22-C23-C25-C26
3	A	612	LI1	C12-C13-C15-C16
3	A	613	LI1	C16-C17-C18-C20
3	A	602	LI1	C44-C43-C45-C46
3	A	602	LI1	C46-C47-C48-C49
3	A	602	LI1	C24-C23-C25-C26
4	A	701	SQU	C6-C7-C9-C10
2	A	300	RET	C12-C13-C14-C15
3	A	613	LI1	C11-C12-C13-C15
3	A	607	LI1	C55-C56-C57-C58

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Mol	Chain	Res	Type	Atoms
3	A	609	LI1	C22-C23-C25-C26
4	A	701	SQU	C22-C23-C25-C26
3	A	601	LI1	C26-C27-C28-C29
3	A	602	LI1	C11-C12-C13-C15
4	A	701	SQU	C26-C27-C28-C30
3	A	610	LI1	O1-C1-C2-C3
3	A	602	LI1	O1-C1-C2-O2
4	A	701	SQU	C25-C26-C27-C28
3	A	610	LI1	C23-C25-C26-C27
3	A	601	LI1	O2-C41-C42-C43
3	A	606	LI1	C15-C16-C17-C18
3	A	606	LI1	C13-C15-C16-C17
3	A	608	LI1	C26-C27-C28-C29
3	A	610	LI1	C21-C22-C23-C25
3	A	607	LI1	C42-C43-C45-C46
3	A	611	LI1	C16-C17-C18-C20
4	A	701	SQU	C10-C11-C12-C14
3	A	601	LI1	O1-C1-C2-C3
3	A	607	LI1	C2-C1-O1-C11
3	A	607	LI1	C46-C47-C48-C50
3	A	610	LI1	O1-C1-C2-O2
3	A	610	LI1	C15-C16-C17-C18
3	A	603	LI1	C25-C26-C27-C28
3	A	612	LI1	C16-C17-C18-C20
3	A	603	LI1	C12-C13-C15-C16
3	A	602	LI1	O1-C11-C12-C13
3	A	603	LI1	C14-C13-C15-C16
3	A	607	LI1	C22-C23-C25-C26
3	A	610	LI1	C48-C50-C51-C52
3	A	601	LI1	C12-C11-O1-C1
3	A	602	LI1	C16-C17-C18-C20
3	A	609	LI1	C11-C12-C13-C15
3	A	603	LI1	C26-C27-C28-C30
3	A	612	LI1	C15-C16-C17-C18
3	A	607	LI1	C18-C20-C21-C22
4	A	701	SQU	C13-C12-C14-C15
3	A	607	LI1	C15-C16-C17-C18
3	A	602	LI1	C17-C18-C20-C21
3	A	607	LI1	C52-C53-C55-C56
2	A	300	RET	C7-C8-C9-C19
3	A	605	LI1	C13-C15-C16-C17
3	A	607	LI1	C48-C50-C51-C52

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Mol	Chain	Res	Type	Atoms
4	A	701	SQU	C20-C21-C22-C23
3	A	603	LI1	C11-C12-C13-C14
3	A	604	LI1	C23-C25-C26-C27
3	A	610	LI1	C2-C1-O1-C11
3	A	610	LI1	C41-C42-C43-C45
3	A	613	LI1	C13-C15-C16-C17
3	A	604	LI1	C21-C22-C23-C25
3	A	610	LI1	C12-C13-C15-C16
3	A	603	LI1	C11-C12-C13-C15
3	A	602	LI1	C12-C11-O1-C1
3	A	610	LI1	C50-C51-C52-C53
3	A	601	LI1	C46-C47-C48-C50
3	A	602	LI1	C20-C21-C22-C23
3	A	601	LI1	C12-C13-C15-C16
3	A	611	LI1	C17-C18-C20-C21
3	A	610	LI1	C45-C46-C47-C48
3	A	607	LI1	C21-C22-C23-C25
3	A	607	LI1	C56-C57-C58-C60
3	A	604	LI1	C11-C12-C13-C15
3	A	611	LI1	C19-C18-C20-C21
3	A	601	LI1	C42-C43-C45-C46

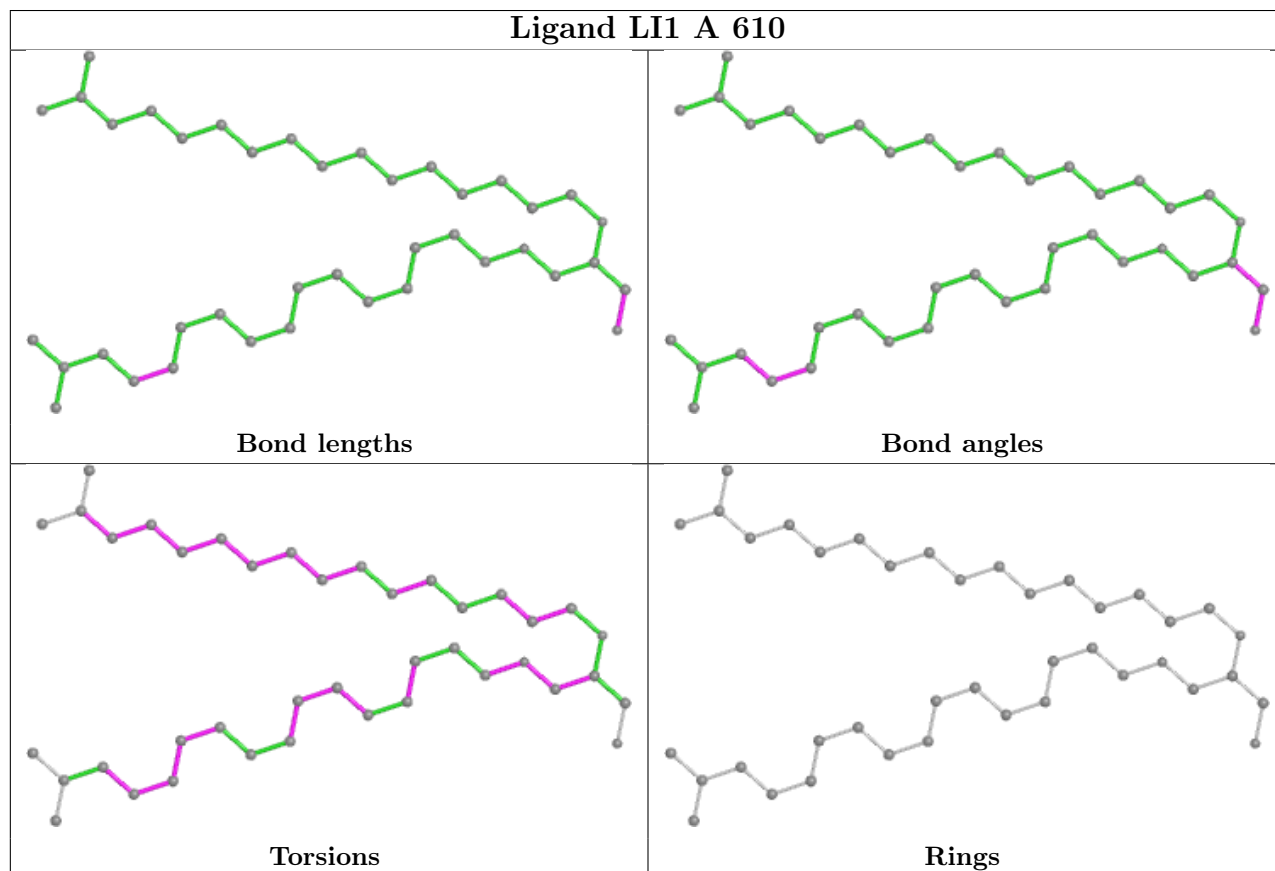
There are no ring outliers.

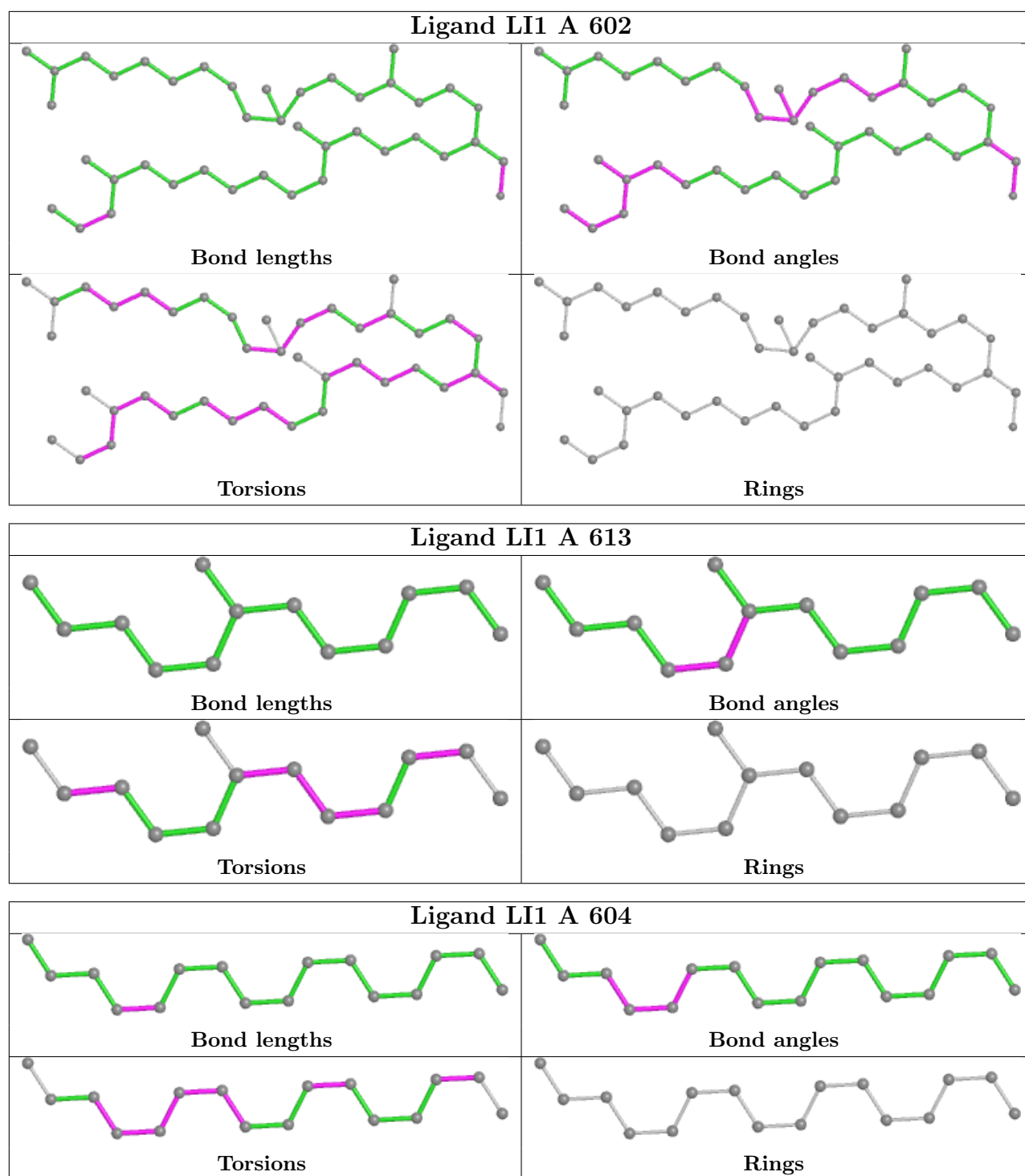
12 monomers are involved in 75 short contacts:

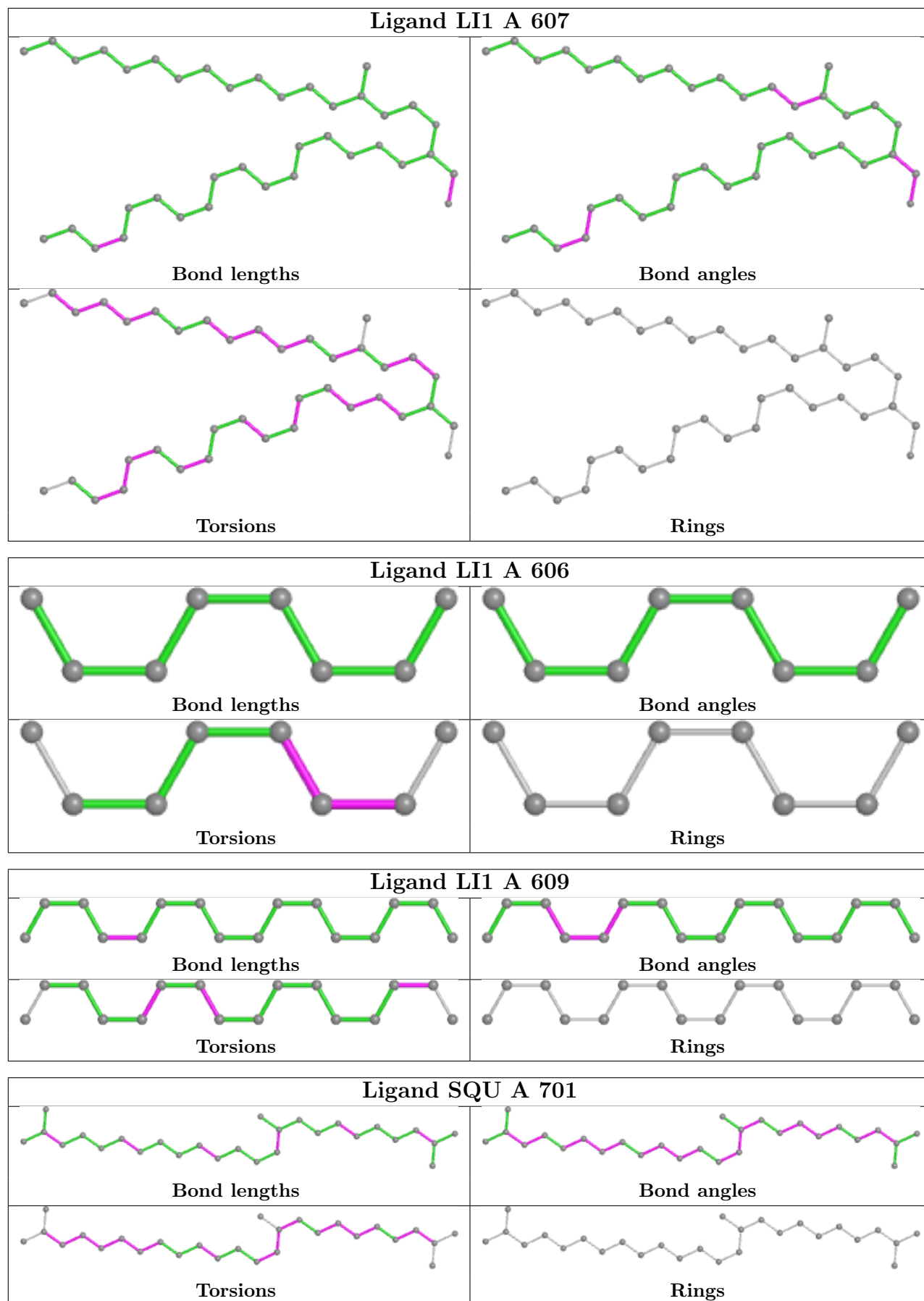
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	610	LI1	18	0
3	A	602	LI1	25	0
3	A	613	LI1	1	0
3	A	607	LI1	4	0
3	A	609	LI1	3	0
4	A	701	SQU	7	0
3	A	612	LI1	2	0
3	A	608	LI1	2	0
3	A	601	LI1	7	0
3	A	603	LI1	5	0
3	A	611	LI1	4	0
2	A	300	RET	2	0

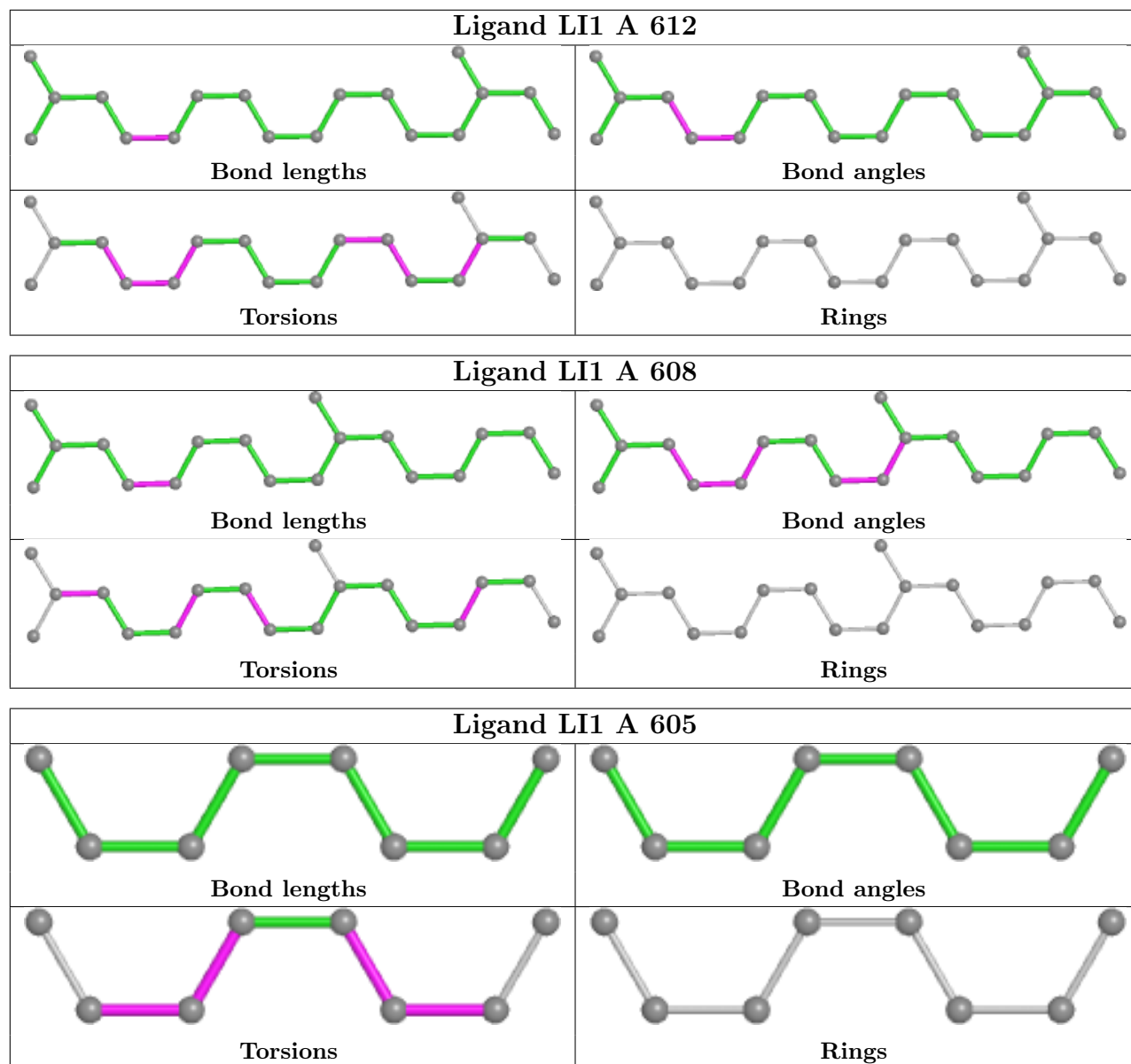
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

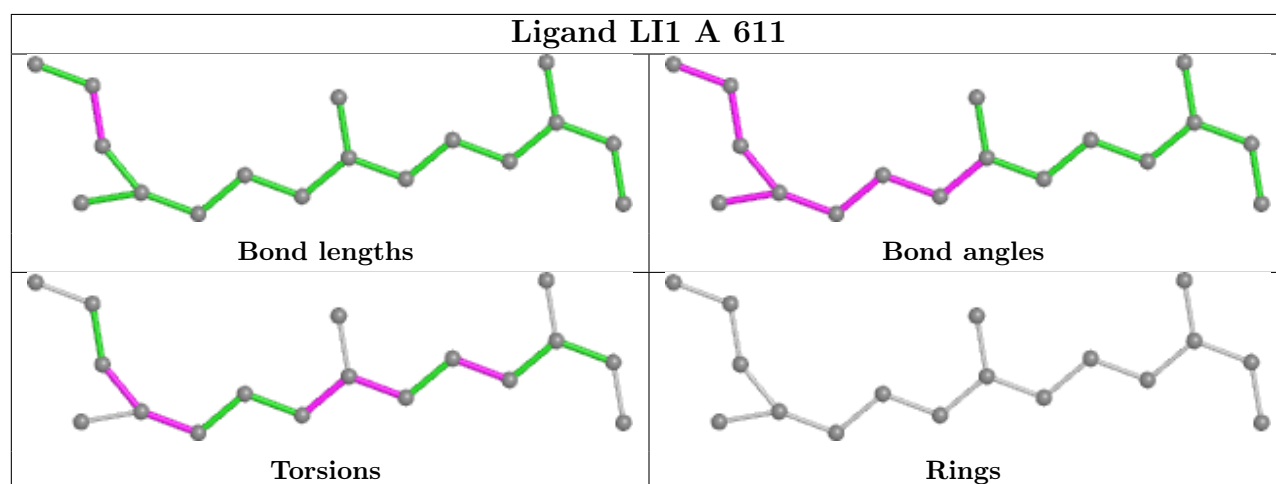
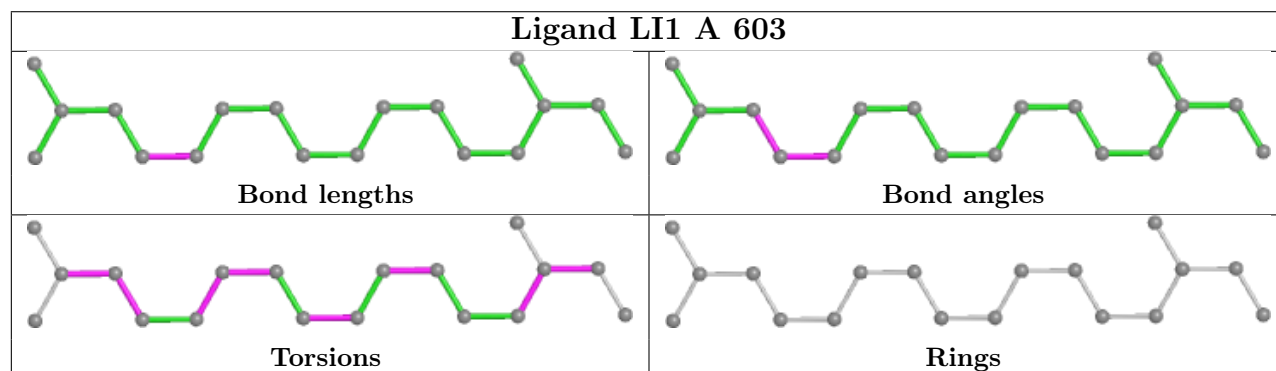
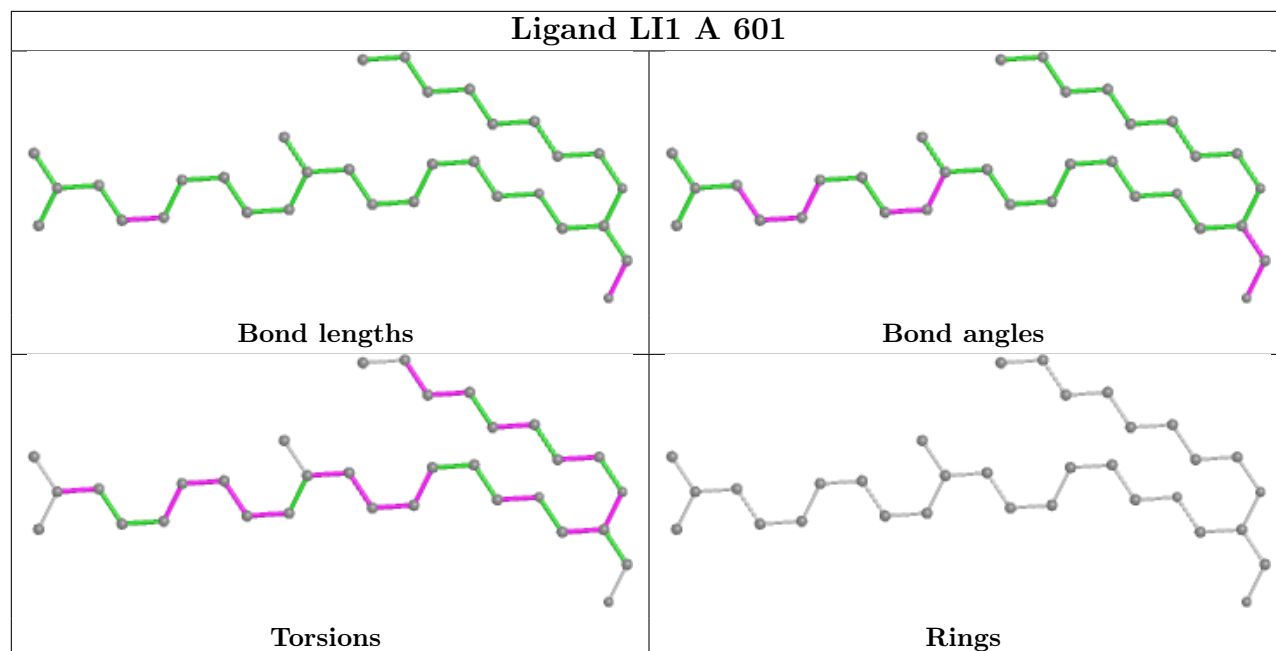
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.

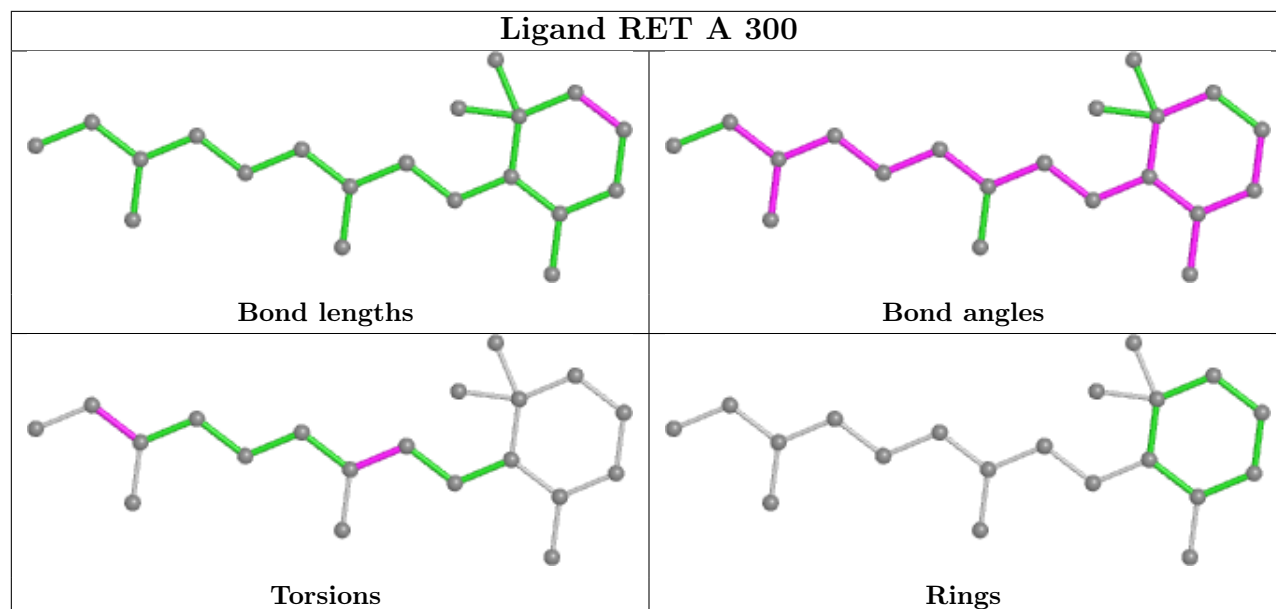












5.7 Other polymers [i](#)

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

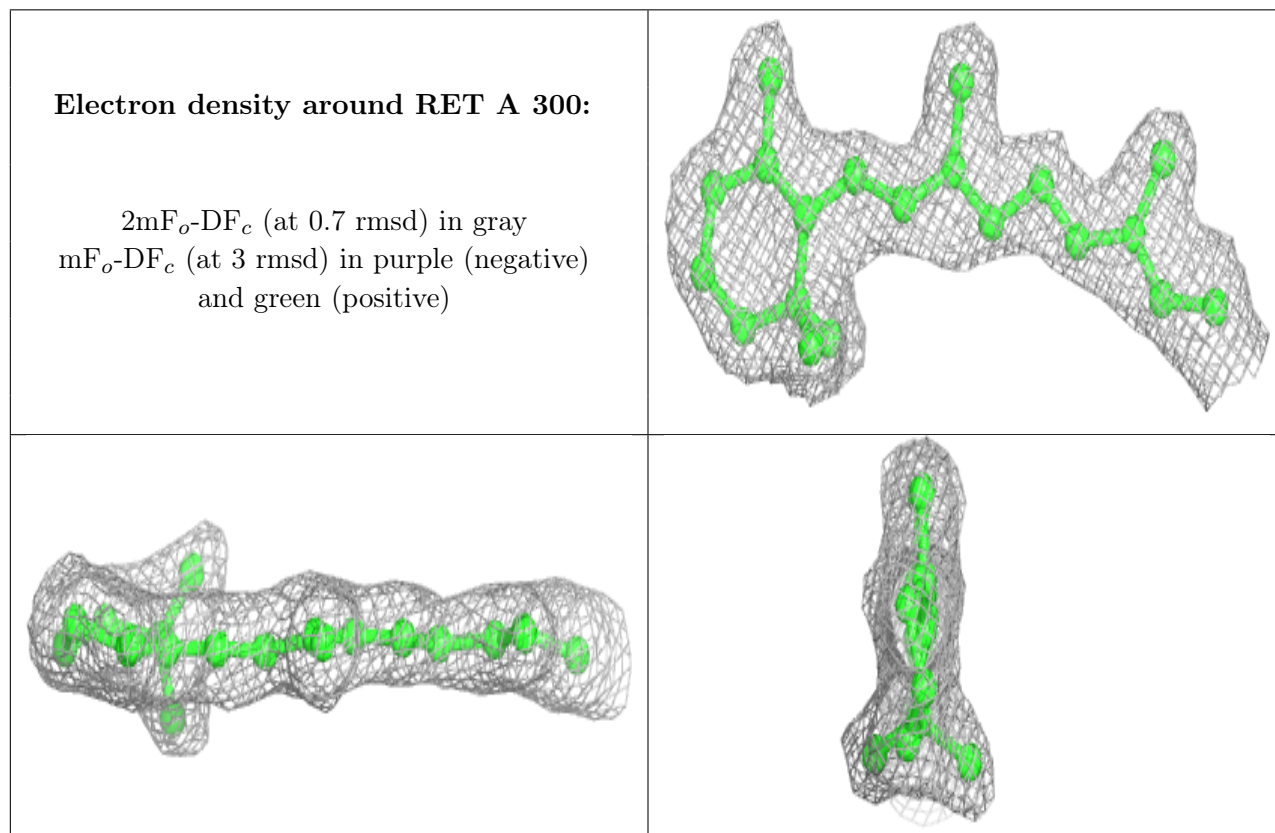
6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

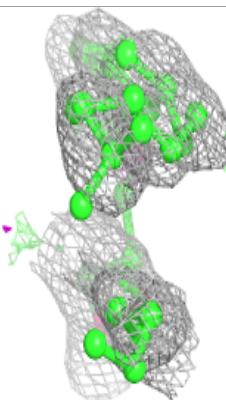
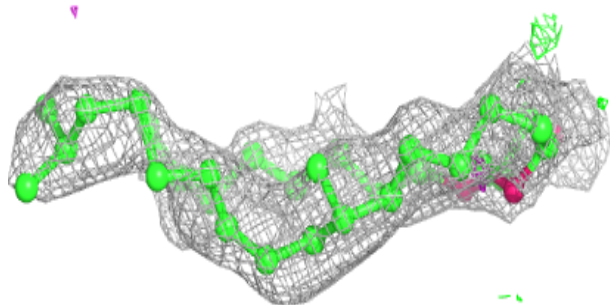
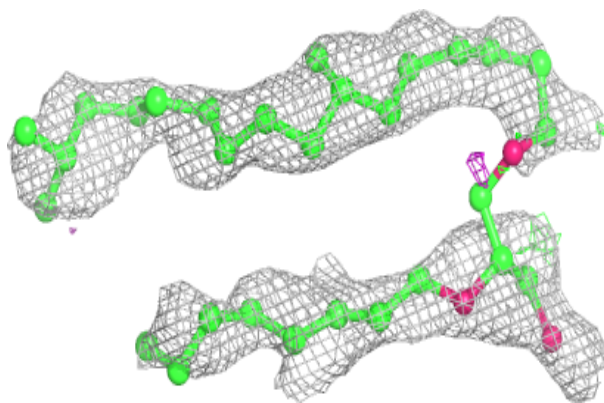
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

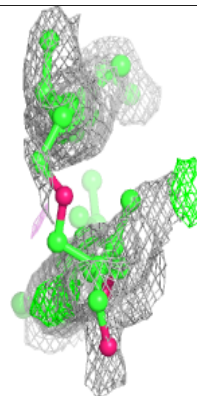
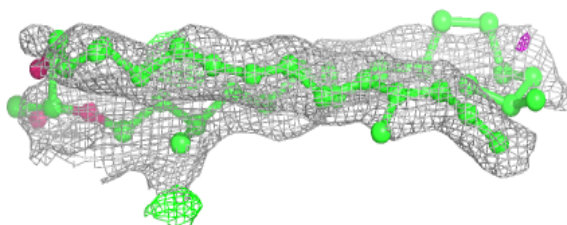
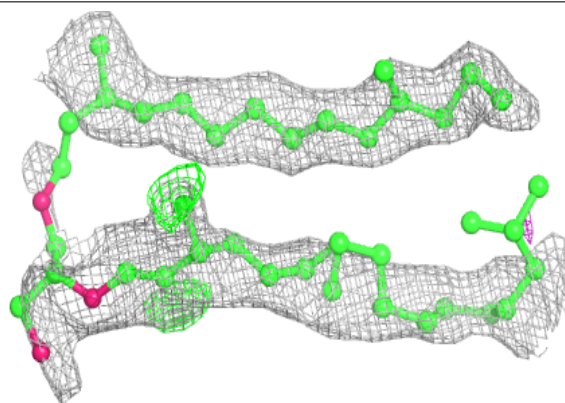


Electron density around LI1 A 601:

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

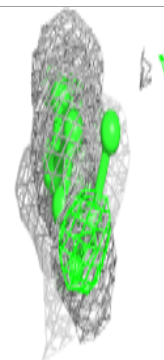
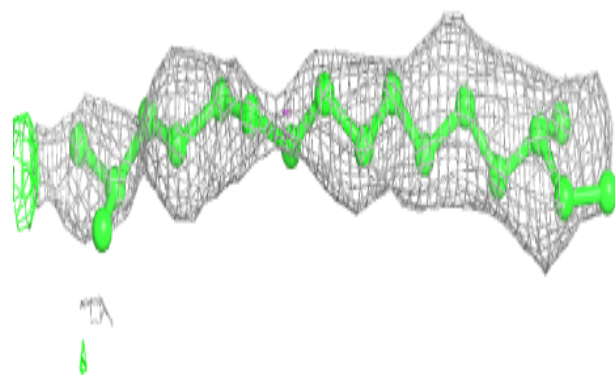
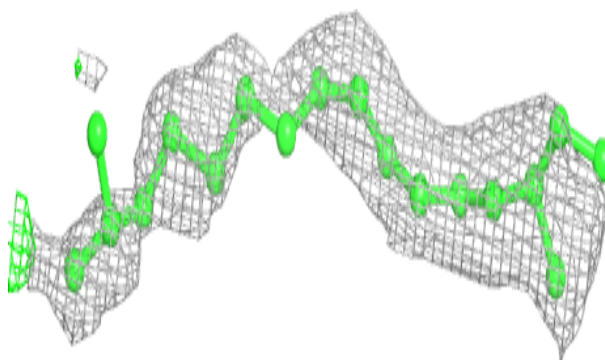
**Electron density around LI1 A 602:**

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

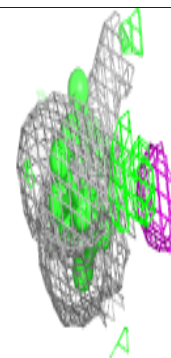
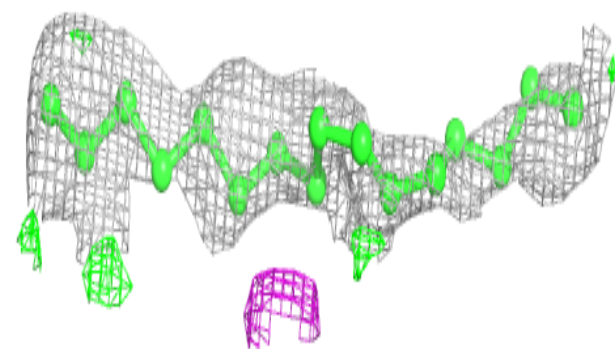
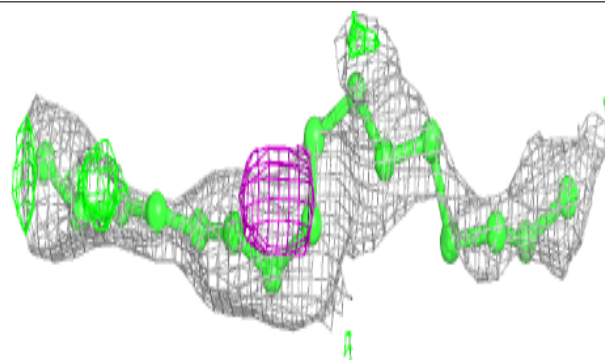


Electron density around LI1 A 603:

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

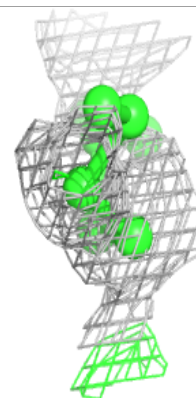
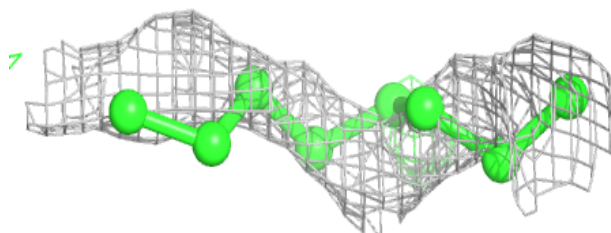
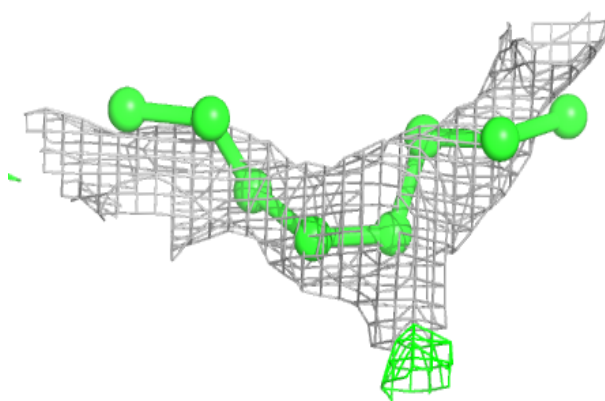
**Electron density around LI1 A 604:**

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

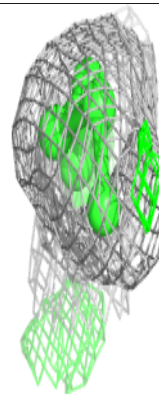
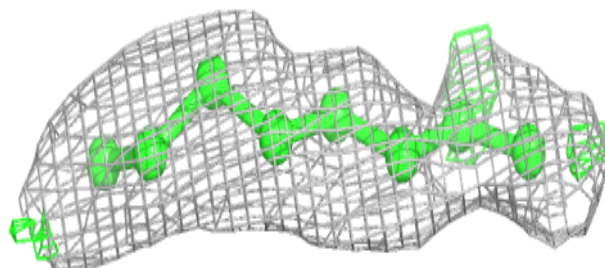
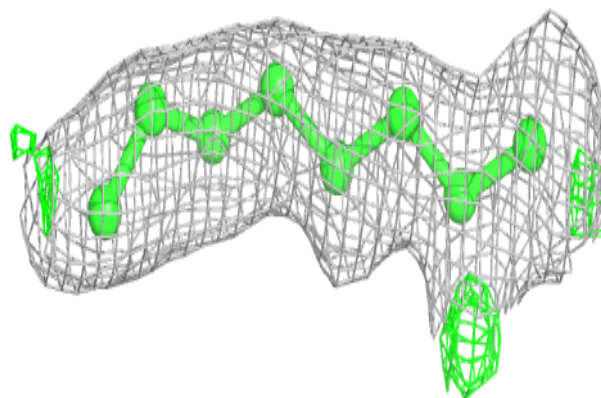


Electron density around LI1 A 605:

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

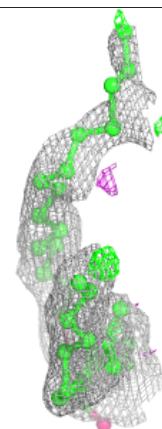
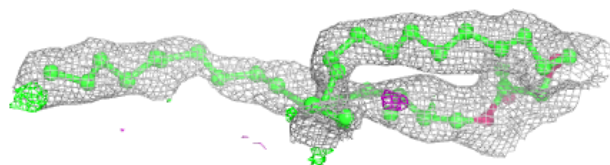
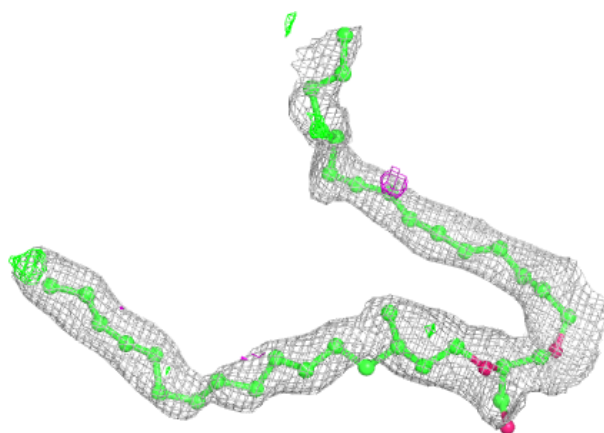
**Electron density around LI1 A 606:**

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

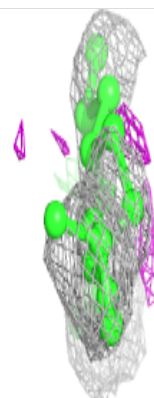
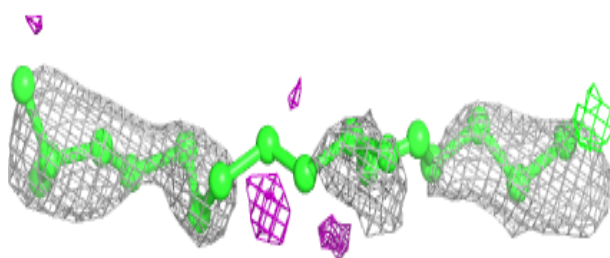
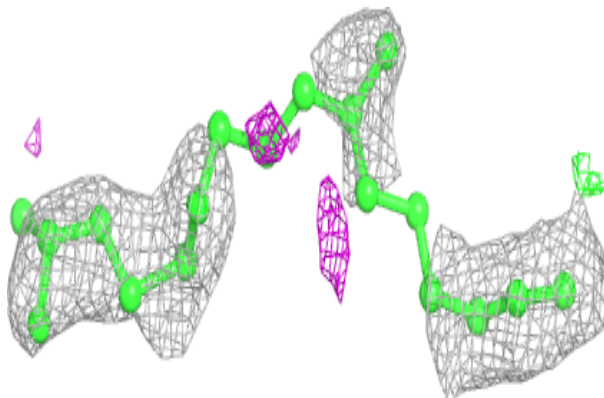


Electron density around LI1 A 607:

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

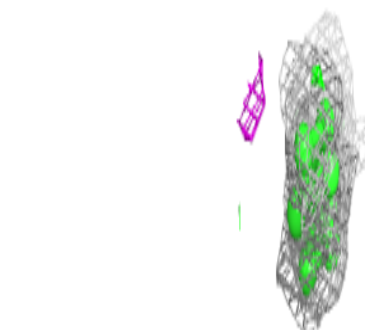
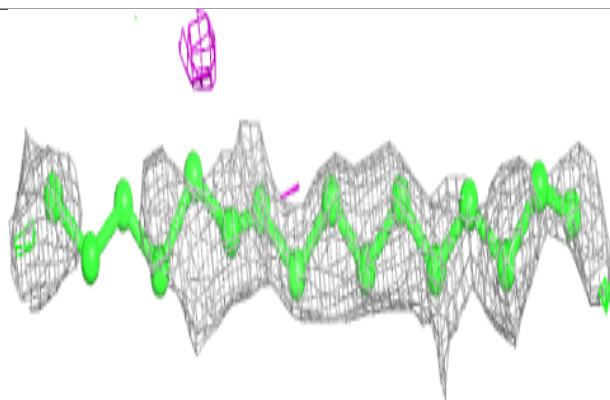
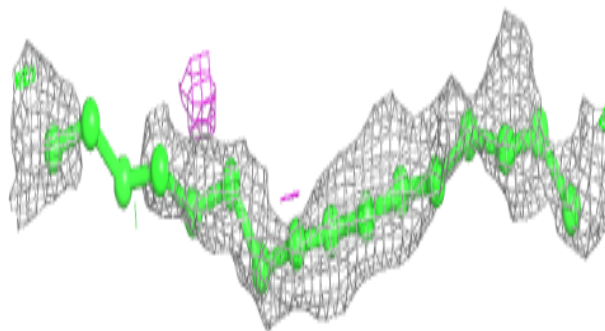
**Electron density around LI1 A 608:**

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

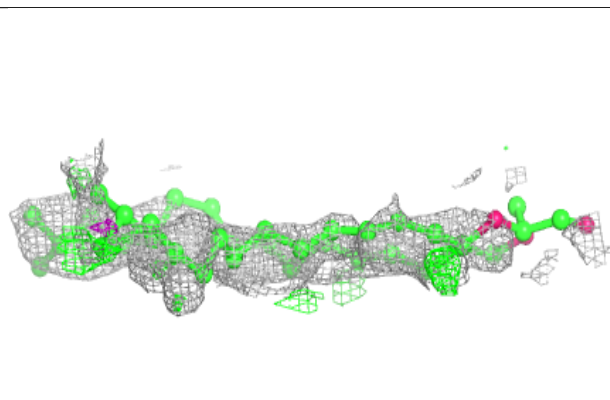
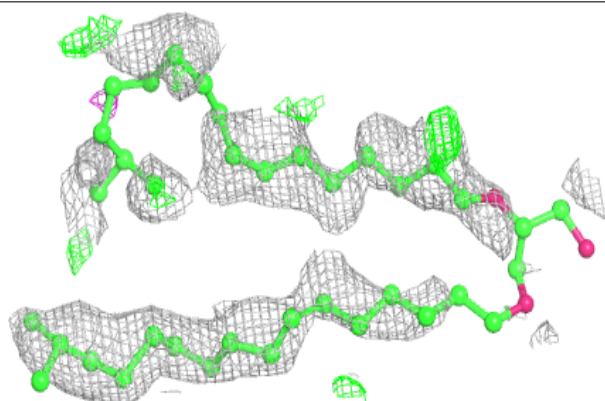


Electron density around LI1 A 609:

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

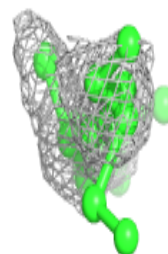
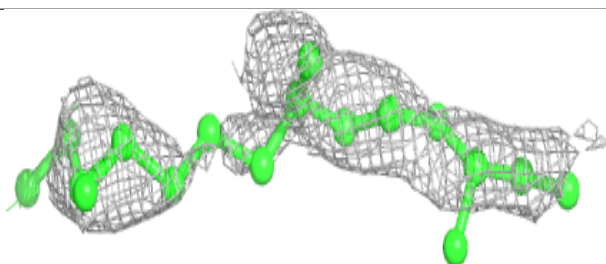
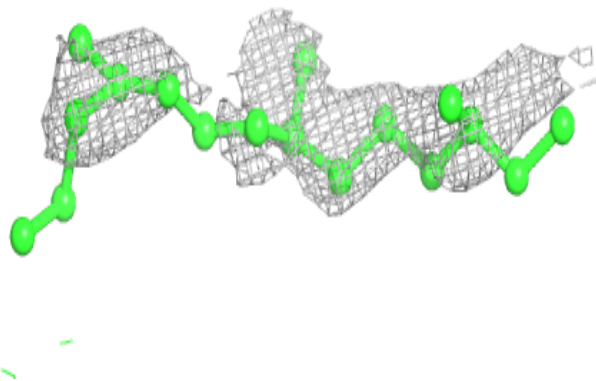
**Electron density around LI1 A 610:**

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

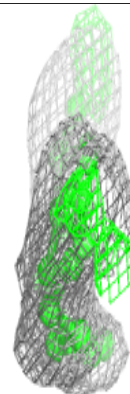
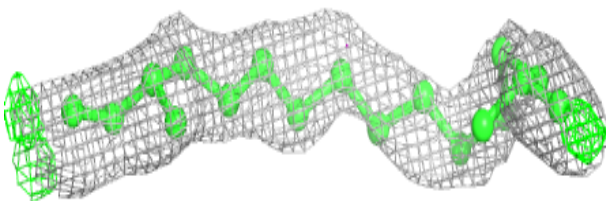
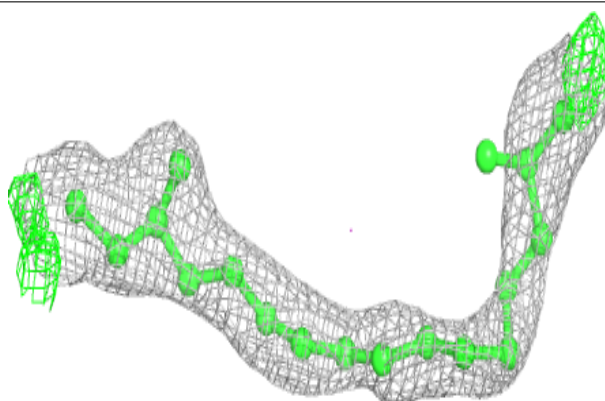


Electron density around LI1 A 611:

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

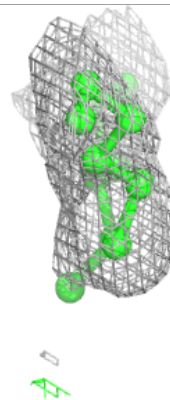
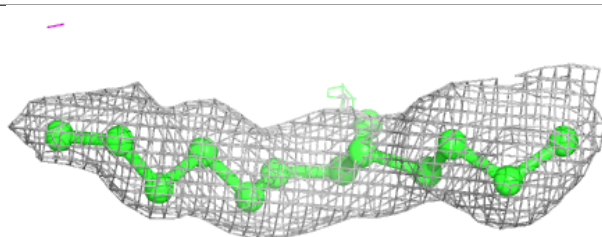
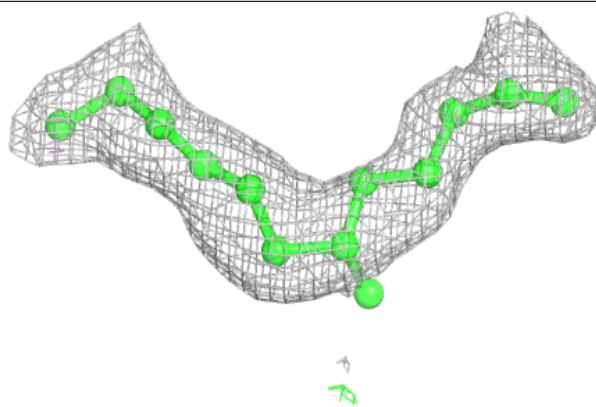
**Electron density around LI1 A 612:**

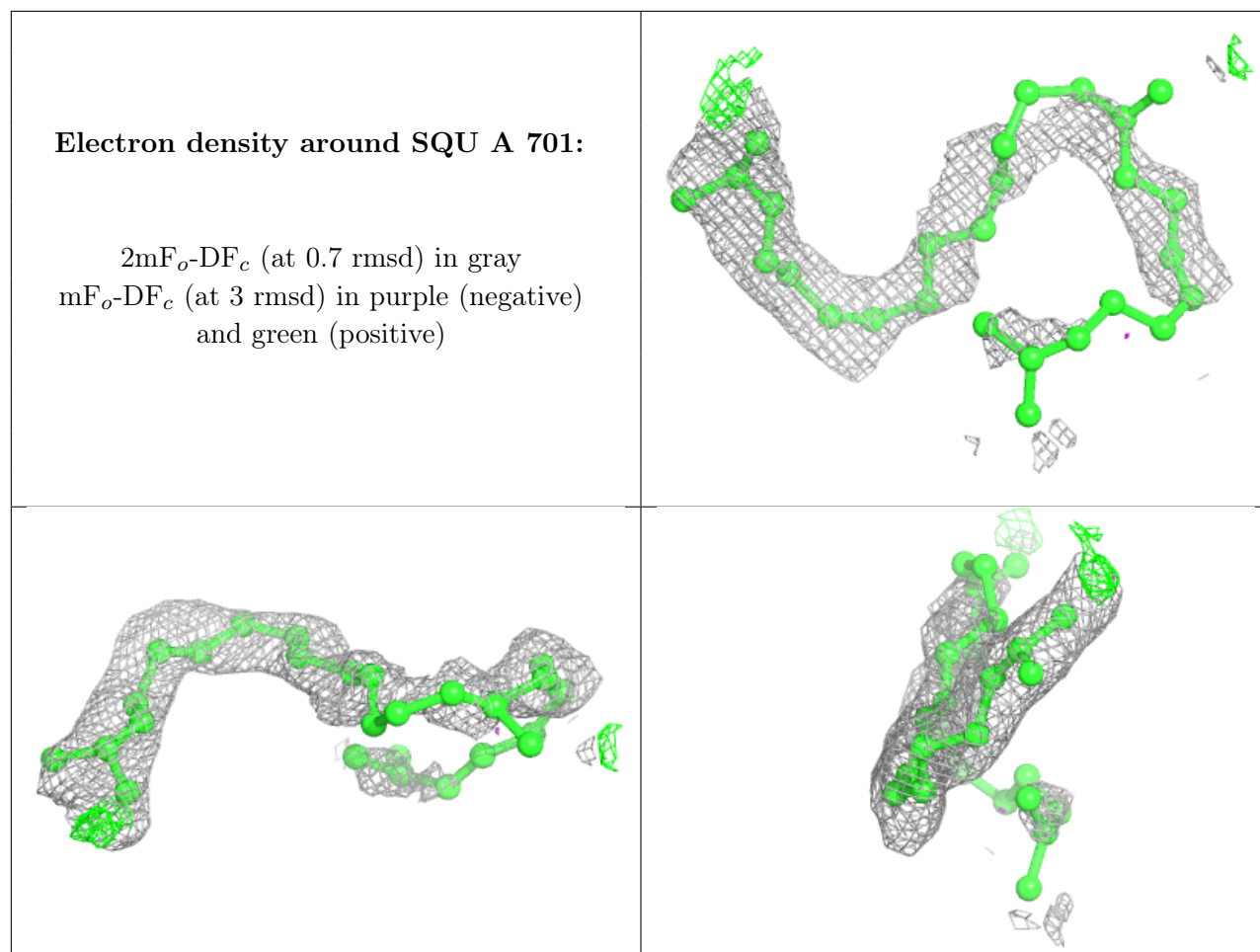
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around LI1 A 613:

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





6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.