



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:02 AM UTC

PDB ID : 5OC9 / pdb_00005oc9
Title : Crystal Structure of human TMEM16K / Anoctamin 10
Authors : Bushell, S.R.; Pike, A.C.W.; Chu, A.; Tessitore, A.; Rotty, B.; Mukhopadhyay, S.; Kupinska, K.; Shrestha, L.; Borkowska, O.; Chalk, R.; Burgess-Brown, N.A.; Love, J.; Edwards, A.M.; Arrowsmith, C.H.; Bountra, C.; Carpenter, E.P.; Structural Genomics Consortium (SGC)
Deposited on : 2017-06-29
Resolution : 3.20 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](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

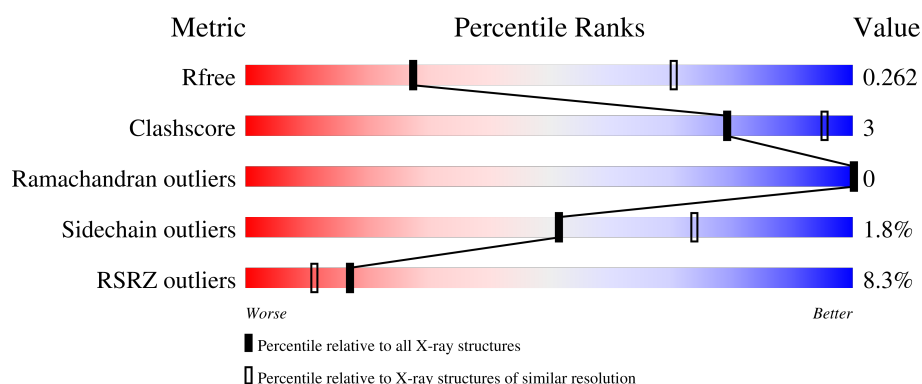
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	667	8% 83% 8% 9%
1	B	667	7% 84% 8% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10138 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 Anoctamin-10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	607	Total	C	N	O	S	0	0	0
			4860	3209	781	843	27			
1	B	616	Total	C	N	O	S	0	0	0
			4946	3268	791	860	27			

There are 14 discrepancies between the modelled and reference sequences:

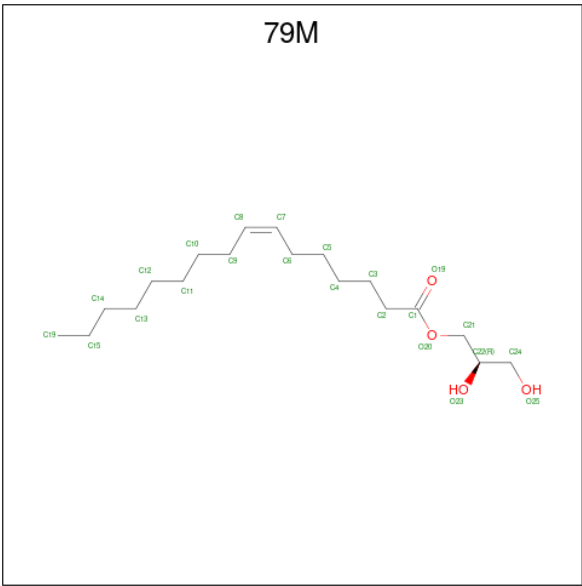
Chain	Residue	Modelled	Actual	Comment	Reference
A	661	ALA	-	expression tag	UNP Q9NW15
A	662	GLU	-	expression tag	UNP Q9NW15
A	663	ASN	-	expression tag	UNP Q9NW15
A	664	LEU	-	expression tag	UNP Q9NW15
A	665	TYR	-	expression tag	UNP Q9NW15
A	666	PHE	-	expression tag	UNP Q9NW15
A	667	GLN	-	expression tag	UNP Q9NW15
B	661	ALA	-	expression tag	UNP Q9NW15
B	662	GLU	-	expression tag	UNP Q9NW15
B	663	ASN	-	expression tag	UNP Q9NW15
B	664	LEU	-	expression tag	UNP Q9NW15
B	665	TYR	-	expression tag	UNP Q9NW15
B	666	PHE	-	expression tag	UNP Q9NW15
B	667	GLN	-	expression tag	UNP Q9NW15

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Ca	0	0
			3	3		
2	B	4	Total	Ca	0	0
			4	4		

- Molecule 3 is (2R)-2,3-dihydroxypropyl (7Z)-hexadec-7-enoate (CCD ID: 79M) (formula:

C₁₉H₃₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			23	19	4		
3	A	1	Total	C	O	0	0
			13	11	2		
3	A	1	Total	C	O	0	0
			14	10	4		
3	A	1	Total	C		0	0
			6	6			
3	A	1	Total	C	O	0	0
			20	16	4		
3	A	1	Total	C	O	0	0
			13	9	4		
3	A	1	Total	C	O	0	0
			23	19	4		
3	A	1	Total	C		0	0
			12	12			
3	A	1	Total	C		0	0
			10	10			
3	B	1	Total	C	O	0	0
			23	19	4		
3	B	1	Total	C	O	0	0
			12	10	2		
3	B	1	Total	C	O	0	0
			17	13	4		
3	B	1	Total	C	O	0	0
			19	17	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 23 19 4	0	0
3	B	1	Total C O 9 5 4	0	0
3	B	1	Total C O 14 10 4	0	0
3	B	1	Total C 8 8	0	0
3	B	1	Total C 10 10	0	0

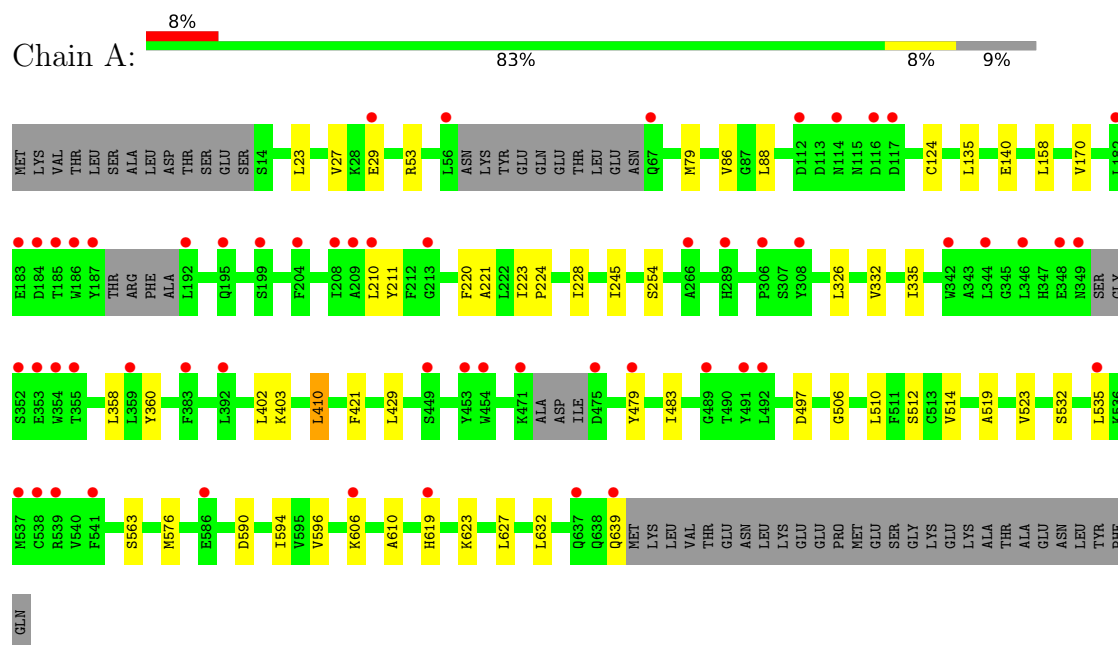
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	22	Total O 22 22	0	0
4	B	34	Total O 34 34	0	0

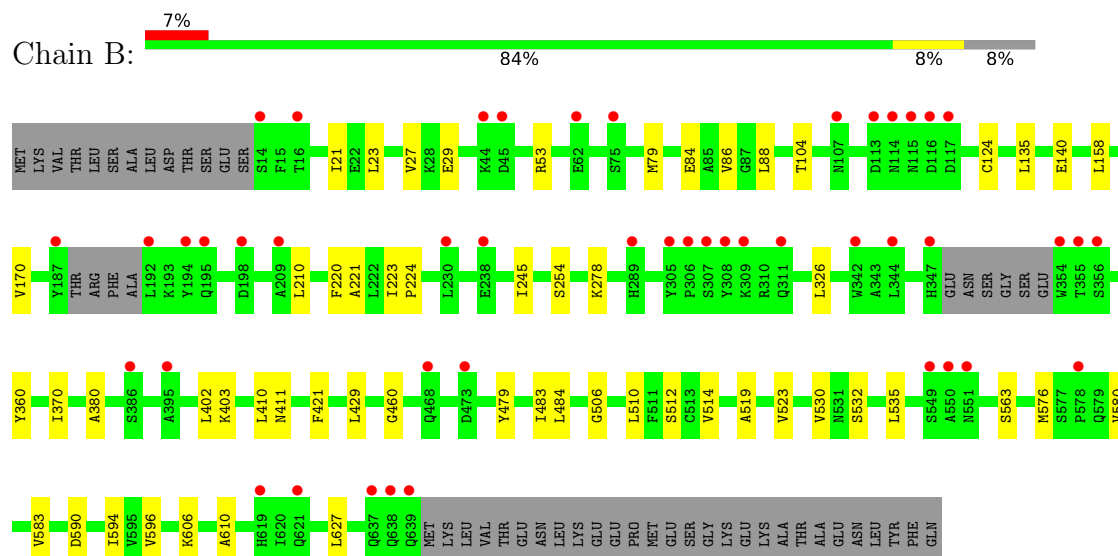
3 Residue-property plots [i](#)

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 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: Anoctamin-10



• Molecule 1: Anoctamin-10



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.15Å 153.59Å 218.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.79 – 3.20 76.79 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (76.79-3.20) 99.9 (76.79-3.20)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 3.19Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.228 , 0.245 0.242 , 0.262	Depositor DCC
R_{free} test set	1699 reflections (4.49%)	wwPDB-VP
Wilson B-factor (Å ²)	58.2	Xtriage
Anisotropy	0.583	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 51.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	10138	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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: 79M, CA

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	0.76	0/4977	1.34	4/6751 (0.1%)
1	B	0.77	0/5067	1.33	8/6874 (0.1%)
All	All	0.76	0/10044	1.33	12/13625 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	360	TYR	CA-C-N	7.77	127.89	120.43
1	A	360	TYR	C-N-CA	7.77	127.89	120.43
1	B	360	TYR	CA-C-N	7.73	127.85	120.43
1	B	360	TYR	C-N-CA	7.73	127.85	120.43
1	B	535	LEU	CA-C-N	6.22	128.52	120.44
1	B	535	LEU	C-N-CA	6.22	128.52	120.44
1	A	29	GLU	CA-C-N	5.29	127.38	120.28
1	A	29	GLU	C-N-CA	5.29	127.38	120.28
1	B	29	GLU	CA-C-N	5.26	127.33	120.28
1	B	29	GLU	C-N-CA	5.26	127.33	120.28
1	B	84	GLU	CA-C-N	5.08	127.04	120.44
1	B	84	GLU	C-N-CA	5.08	127.04	120.44

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	4860	0	4862	27	0
1	B	4946	0	4947	29	0
2	A	3	0	0	0	0
2	B	4	0	0	0	0
3	A	134	0	195	8	0
3	B	135	0	192	10	0
4	A	22	0	0	0	0
4	B	34	0	0	0	0
All	All	10138	0	10196	54	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 3.

All (54) 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:245:ILE:HD11	3:A:705:79M:H22C	1.78	0.65
1:B:245:ILE:HD11	3:B:706:79M:H22C	1.77	0.64
1:A:429:LEU:HD23	1:A:514:VAL:HG11	1.84	0.60
1:B:429:LEU:HD23	1:B:514:VAL:HG11	1.84	0.59
1:A:326:LEU:HG	1:A:410:LEU:HD13	1.85	0.58
1:B:606:LYS:HG2	3:B:709:79M:H241	1.86	0.58
1:A:606:LYS:HG2	3:A:708:79M:H241	1.88	0.55
1:A:506:GLY:O	1:A:510:LEU:HB2	2.08	0.54
1:A:228:ILE:HD13	3:A:704:79M:H101	1.90	0.52
1:A:211:TYR:CZ	1:A:497:ASP:HB3	2.46	0.50
1:B:402:LEU:HD23	3:B:711:79M:H211	1.93	0.50
1:A:402:LEU:HD23	3:A:710:79M:H211	1.92	0.50
1:A:79:MET:HE2	1:A:124:CYS:HA	1.94	0.50
1:B:583:VAL:HG21	3:B:708:79M:H32C	1.92	0.49
1:B:79:MET:HE2	1:B:124:CYS:HA	1.95	0.49
1:A:220:PHE:HA	1:A:223:ILE:HD12	1.95	0.48
1:A:519:ALA:O	1:A:523:VAL:HG23	2.12	0.48
1:B:220:PHE:HA	1:B:223:ILE:HD12	1.95	0.48
1:B:519:ALA:O	1:B:523:VAL:HG23	2.12	0.48
1:B:326:LEU:HG	1:B:410:LEU:HD13	1.96	0.48
1:A:619:HIS:HB2	1:A:623:LYS:NZ	2.29	0.48
1:B:254:SER:HB3	1:B:563:SER:HB2	1.95	0.48
1:B:506:GLY:O	1:B:510:LEU:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:ALA:O	1:B:224:PRO:HD2	2.14	0.48
1:B:610:ALA:HB2	3:B:709:79M:H242	1.96	0.47
1:A:254:SER:HB3	1:A:563:SER:HB2	1.95	0.47
1:A:221:ALA:O	1:A:224:PRO:HD2	2.14	0.47
1:A:596:VAL:HG21	1:B:596:VAL:HG21	1.97	0.47
1:A:590:ASP:O	1:A:594:ILE:HG12	2.15	0.47
1:B:590:ASP:O	1:B:594:ILE:HG12	2.15	0.46
1:A:23:LEU:HD23	1:A:27:VAL:HG11	1.97	0.46
1:B:21:ILE:HG12	1:B:170:VAL:HG22	1.98	0.46
1:B:370:ILE:HD12	1:B:411:ASN:HB3	1.98	0.45
1:A:639:GLN:HG3	1:B:104:THR:HG21	1.99	0.45
1:B:380:ALA:HB2	3:B:713:79M:H102	1.99	0.45
1:A:403:LYS:HD2	3:A:710:79M:H241	1.99	0.45
1:A:421:PHE:HA	1:A:576:MET:HE1	1.99	0.44
1:B:403:LYS:HD2	3:B:711:79M:H241	1.99	0.44
3:A:708:79M:H51C	3:B:709:79M:H52C	1.99	0.43
1:B:86:VAL:HG23	1:B:88:LEU:HG	1.99	0.43
1:B:421:PHE:HA	1:B:576:MET:HE1	1.99	0.43
1:A:86:VAL:HG23	1:A:88:LEU:HG	2.00	0.43
1:A:332:VAL:HA	1:A:335:ILE:HD12	2.00	0.43
1:B:460:GLY:HA2	1:B:484:LEU:HD11	2.01	0.43
1:A:610:ALA:HB2	3:A:708:79M:H242	2.01	0.42
1:B:479:TYR:O	1:B:483:ILE:HG12	2.20	0.42
1:A:479:TYR:O	1:A:483:ILE:HG12	2.20	0.42
1:A:632:LEU:HD21	1:B:278:LYS:HE2	2.01	0.42
1:B:580:VAL:HG13	3:B:708:79M:H31C	2.01	0.41
1:A:158:LEU:HD11	1:A:170:VAL:HG21	2.02	0.41
1:A:245:ILE:HG13	3:A:706:79M:H31C	2.02	0.41
1:B:23:LEU:HD23	1:B:27:VAL:HG11	2.03	0.41
1:B:245:ILE:HG13	3:B:707:79M:H31C	2.02	0.40
1:B:158:LEU:HD11	1:B:170:VAL:HG21	2.02	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	597/667 (90%)	578 (97%)	19 (3%)	0	100	100
1	B	610/667 (92%)	590 (97%)	20 (3%)	0	100	100
All	All	1207/1334 (90%)	1168 (97%)	39 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	509/591 (86%)	499 (98%)	10 (2%)	48	72
1	B	516/591 (87%)	508 (98%)	8 (2%)	55	75
All	All	1025/1182 (87%)	1007 (98%)	18 (2%)	51	74

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ARG
1	A	135	LEU
1	A	140	GLU
1	A	210	LEU
1	A	358	LEU
1	A	410	LEU
1	A	512	SER
1	A	532	SER
1	A	535	LEU
1	A	627	LEU
1	B	53	ARG
1	B	135	LEU
1	B	140	GLU
1	B	210	LEU
1	B	512	SER

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Mol	Chain	Res	Type
1	B	530	VAL
1	B	532	SER
1	B	627	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
1	A	411	ASN
1	A	456	GLN
1	B	49	GLN
1	B	66	ASN
1	B	67	GLN
1	B	95	ASN
1	B	148	GLN

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 25 ligands modelled in this entry, 7 are monoatomic - leaving 18 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
3	79M	B	707	-	16,16,22	0.27	0	17,17,23	0.28	0
3	79M	B	713	-	9,9,22	0.25	0	8,8,23	0.10	0
3	79M	A	707	-	5,5,22	0.18	0	4,4,23	0.11	0
3	79M	A	708	-	19,19,22	0.26	0	20,20,23	0.32	0
3	79M	B	706	-	11,11,22	0.36	0	11,11,23	0.40	0
3	79M	A	705	-	12,12,22	0.35	0	12,12,23	0.42	0
3	79M	A	712	-	9,9,22	0.27	0	8,8,23	0.12	0
3	79M	A	710	-	22,22,22	0.19	0	23,23,23	0.17	0
3	79M	A	704	-	22,22,22	0.23	0	23,23,23	0.20	0
3	79M	A	706	-	13,13,22	0.25	0	14,14,23	0.30	0
3	79M	B	712	-	7,7,22	0.25	0	6,6,23	0.15	0
3	79M	A	709	-	12,12,22	0.28	0	13,13,23	0.23	0
3	79M	A	711	-	11,11,22	0.28	0	10,10,23	0.13	0
3	79M	B	708	-	18,18,22	0.23	0	18,18,23	0.33	0
3	79M	B	709	-	22,22,22	0.21	0	23,23,23	0.23	0
3	79M	B	710	-	8,8,22	0.10	0	9,9,23	0.31	0
3	79M	B	705	-	22,22,22	0.25	0	23,23,23	0.24	0
3	79M	B	711	-	13,13,22	0.18	0	14,14,23	0.23	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
3	79M	B	707	-	-	3/16/16/22	-
3	79M	B	713	-	-	2/7/7/22	-
3	79M	A	707	-	-	0/3/3/22	-
3	79M	A	708	-	-	2/19/19/22	-
3	79M	B	706	-	-	3/10/10/22	-
3	79M	A	705	-	-	3/11/11/22	-
3	79M	A	712	-	-	3/7/7/22	-
3	79M	A	710	-	-	2/22/22/22	-
3	79M	A	704	-	-	6/22/22/22	-
3	79M	A	706	-	-	1/13/13/22	-
3	79M	B	712	-	-	2/5/5/22	-
3	79M	A	709	-	-	2/12/12/22	-
3	79M	A	711	-	-	4/9/9/22	-
3	79M	B	708	-	-	2/17/17/22	-
3	79M	B	709	-	-	2/22/22/22	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	79M	B	710	-	-	0/7/7/22	-
3	79M	B	705	-	-	5/22/22/22	-
3	79M	B	711	-	-	1/13/13/22	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	709	79M	O20-C21-C22-C24
3	A	709	79M	O20-C21-C22-O23
3	B	705	79M	C1-C2-C3-C4
3	B	705	79M	O20-C21-C22-O23
3	B	709	79M	C11-C12-C13-C14
3	A	710	79M	C2-C3-C4-C5
3	A	708	79M	C2-C3-C4-C5
3	B	711	79M	C2-C3-C4-C5
3	A	711	79M	C5-C6-C7-C8
3	B	707	79M	C7-C8-C9-C10
3	A	712	79M	C10-C11-C12-C13
3	A	712	79M	C11-C12-C13-C14
3	A	711	79M	C11-C10-C9-C8
3	B	705	79M	C7-C8-C9-C10
3	B	705	79M	C12-C13-C14-C15
3	A	708	79M	C1-C2-C3-C4
3	A	704	79M	C11-C10-C9-C8
3	B	706	79M	C5-C6-C7-C8
3	B	705	79M	O20-C21-C22-C24
3	A	710	79M	C7-C8-C9-C10
3	B	708	79M	C3-C4-C5-C6
3	B	709	79M	C10-C11-C12-C13
3	A	705	79M	C5-C6-C7-C8
3	A	704	79M	C2-C3-C4-C5
3	B	712	79M	C11-C12-C13-C14
3	B	706	79M	C2-C3-C4-C5
3	A	712	79M	C7-C8-C9-C10
3	A	711	79M	C11-C12-C13-C14
3	B	708	79M	C7-C8-C9-C10
3	A	705	79M	C22-C21-O20-C1
3	A	711	79M	C10-C11-C12-C13

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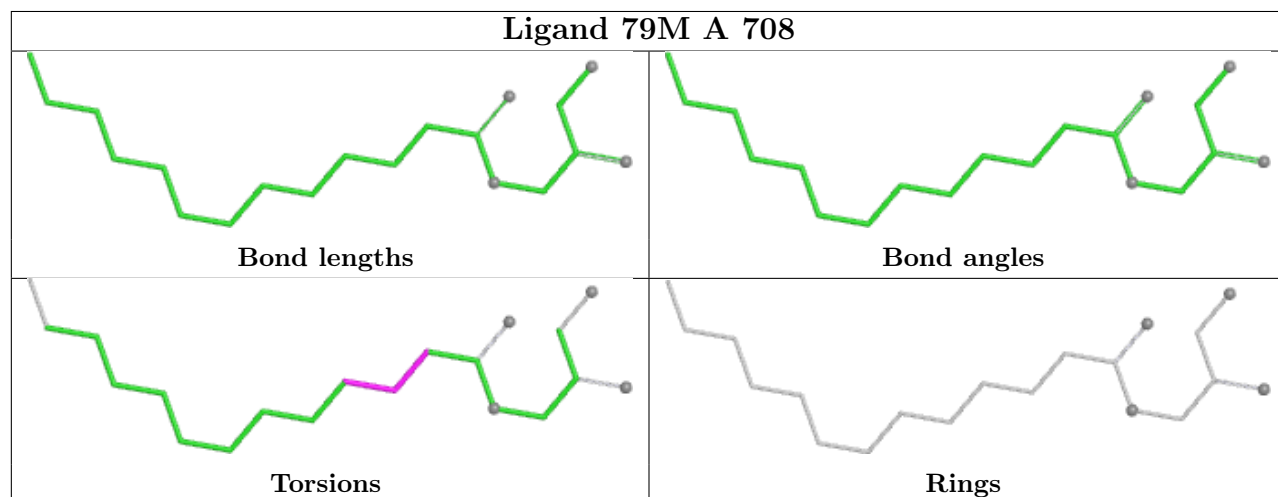
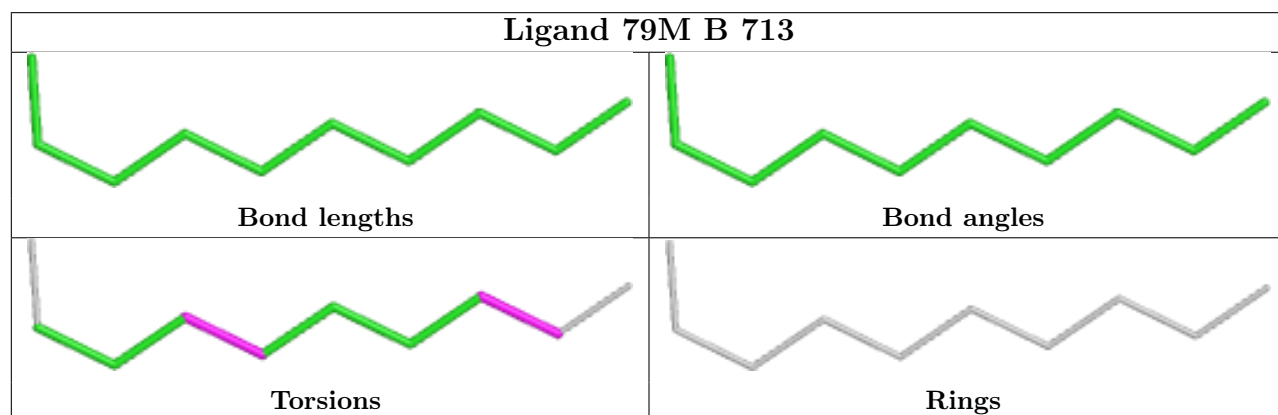
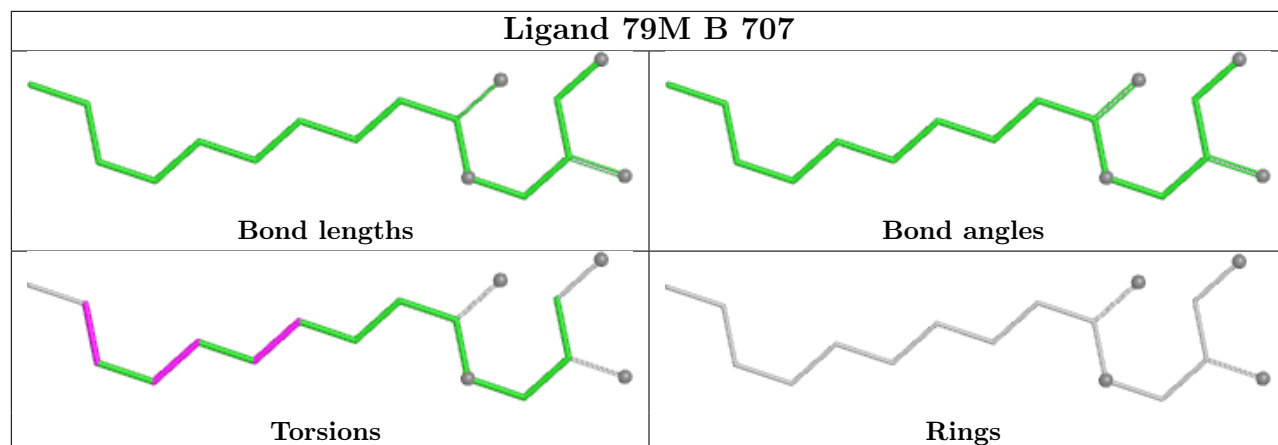
Mol	Chain	Res	Type	Atoms
3	B	706	79M	C22-C21-O20-C1
3	A	705	79M	C2-C3-C4-C5
3	B	712	79M	C10-C11-C12-C13
3	A	704	79M	C10-C11-C12-C13
3	A	704	79M	C5-C6-C7-C8
3	B	707	79M	C5-C6-C7-C8
3	B	707	79M	C3-C4-C5-C6
3	A	704	79M	C9-C10-C11-C12
3	A	706	79M	C3-C4-C5-C6
3	B	713	79M	C7-C8-C9-C10
3	A	704	79M	C3-C4-C5-C6
3	B	713	79M	C11-C12-C13-C14

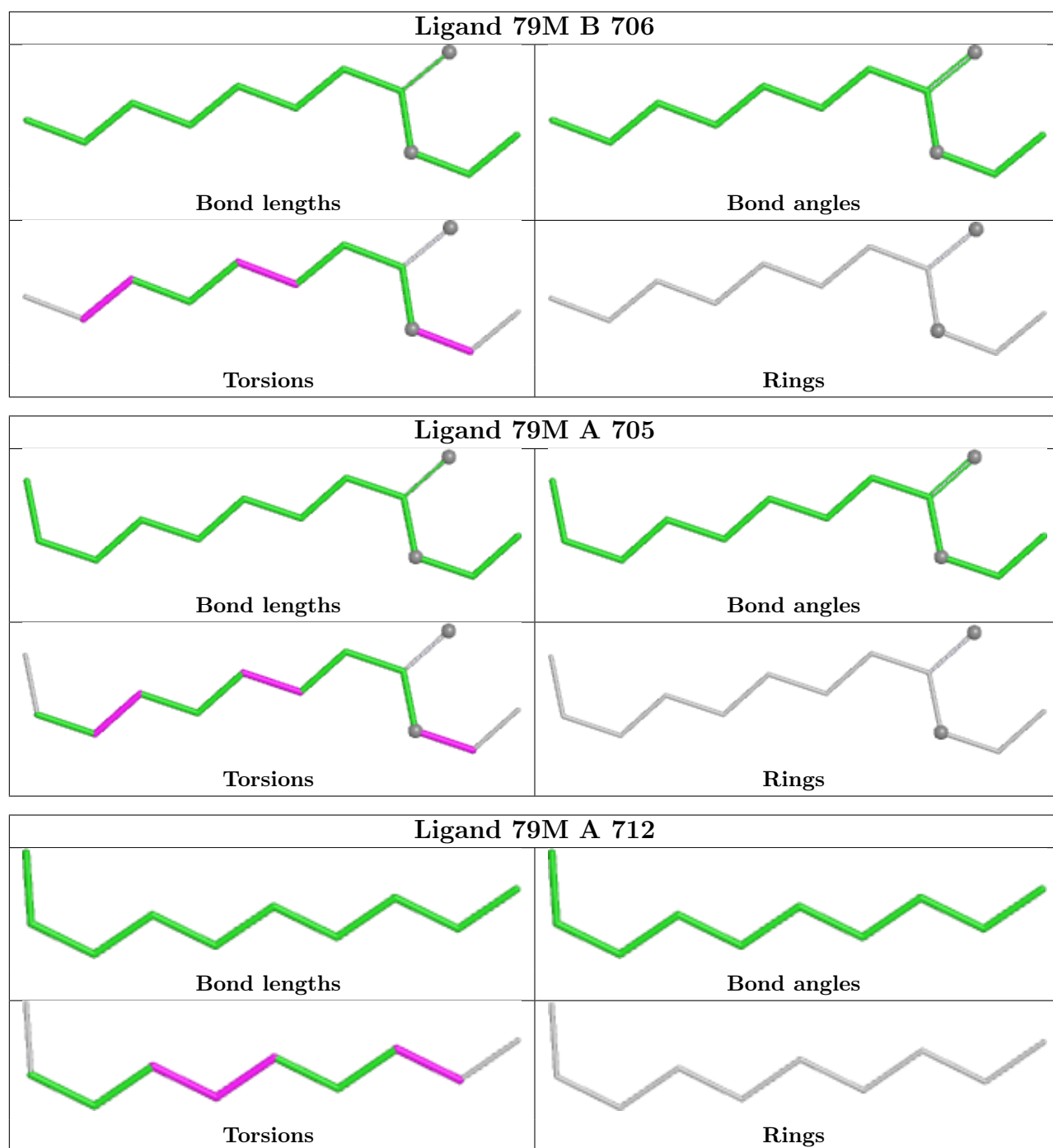
There are no ring outliers.

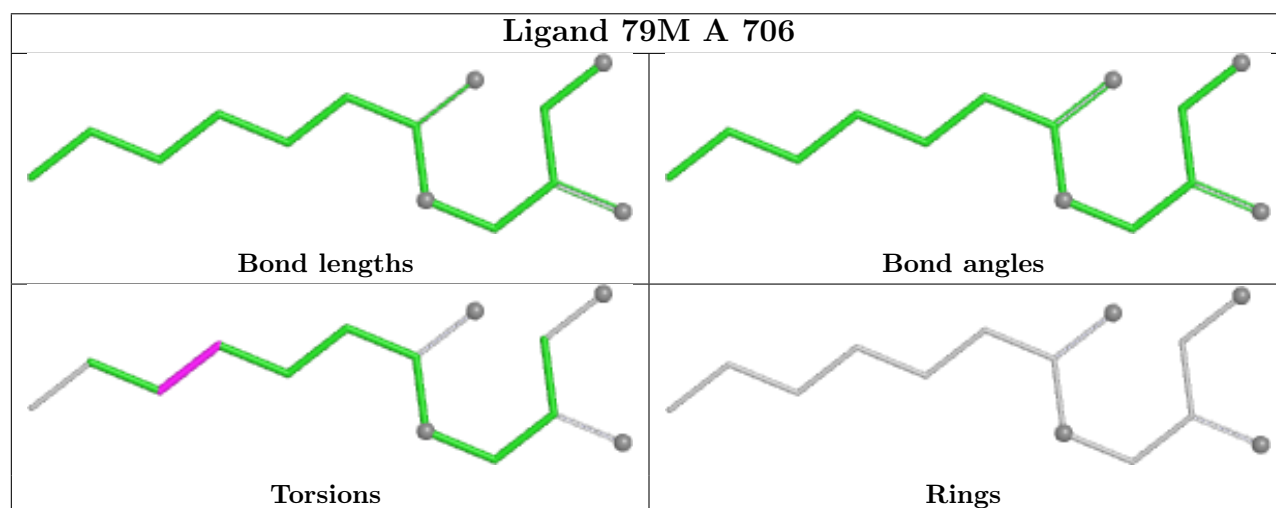
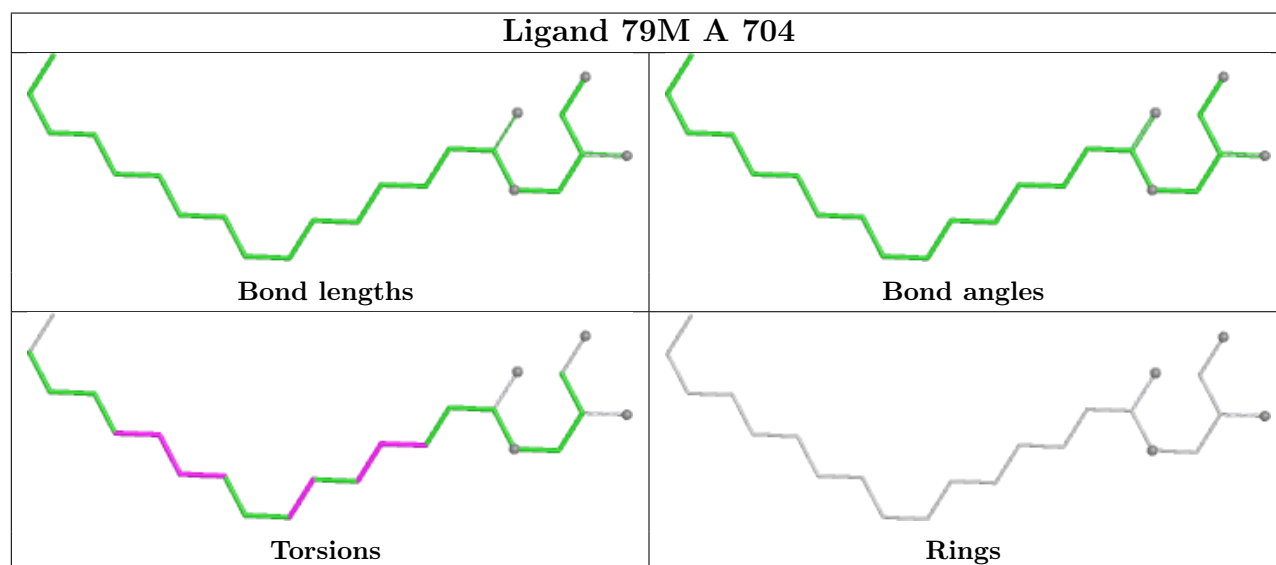
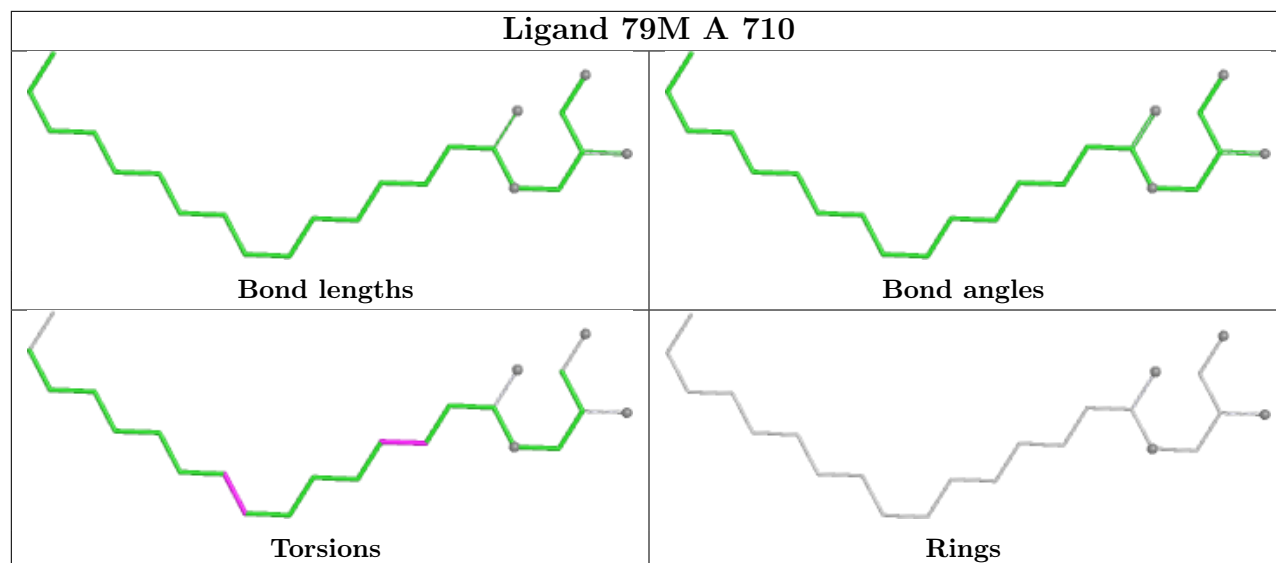
11 monomers are involved in 17 short contacts:

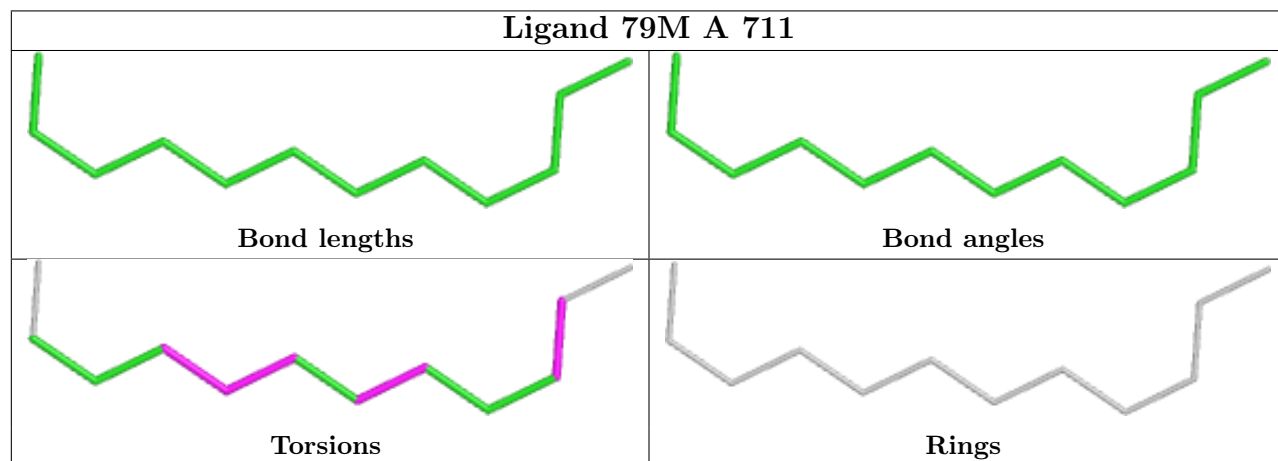
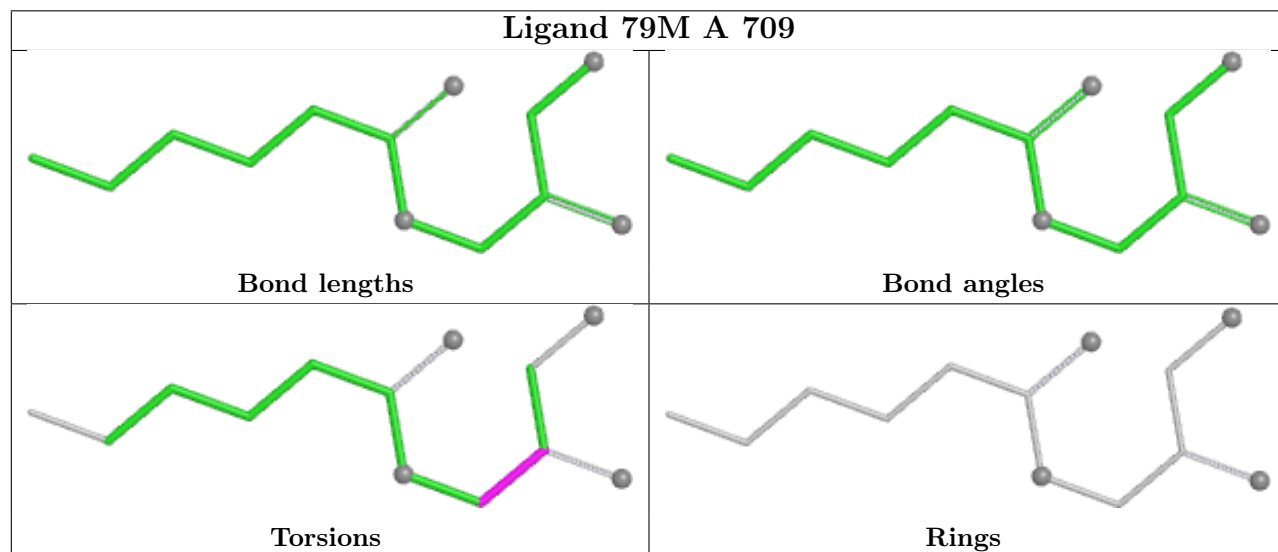
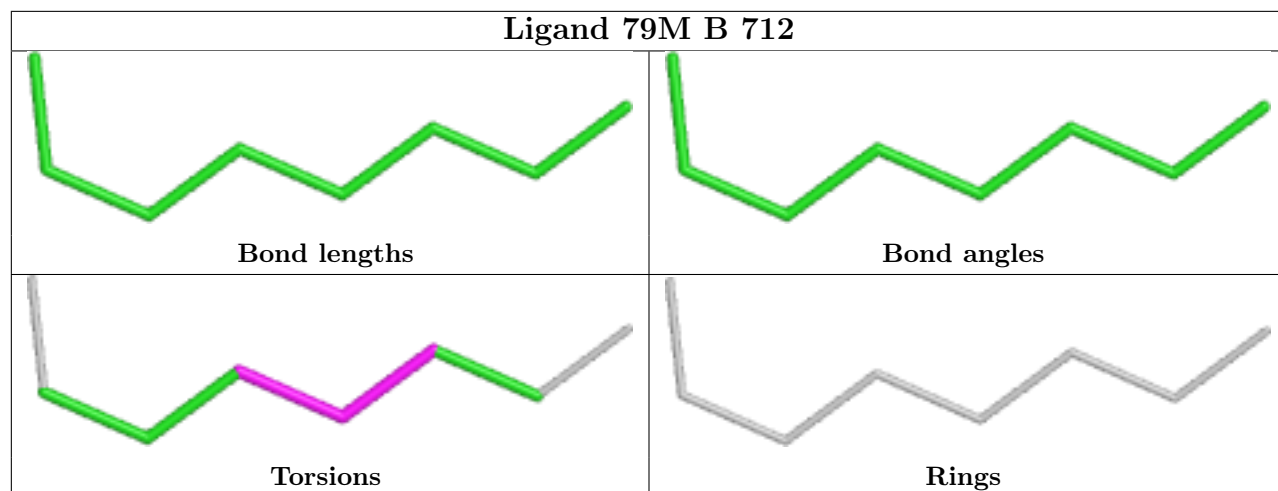
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	707	79M	1	0
3	B	713	79M	1	0
3	A	708	79M	3	0
3	B	706	79M	1	0
3	A	705	79M	1	0
3	A	710	79M	2	0
3	A	704	79M	1	0
3	A	706	79M	1	0
3	B	708	79M	2	0
3	B	709	79M	3	0
3	B	711	79M	2	0

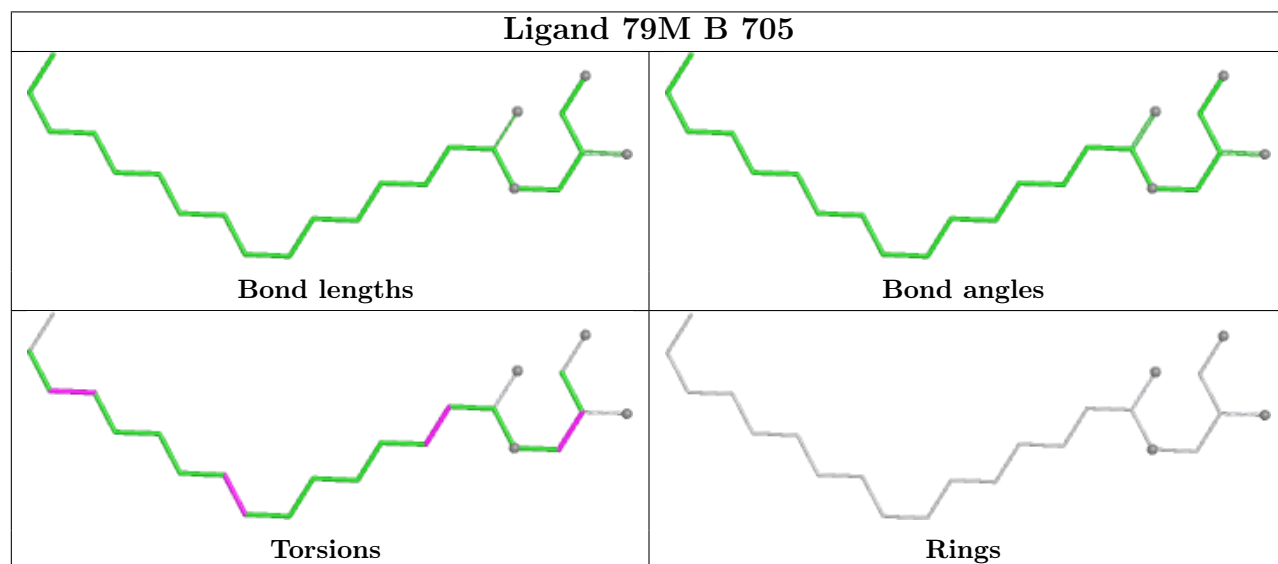
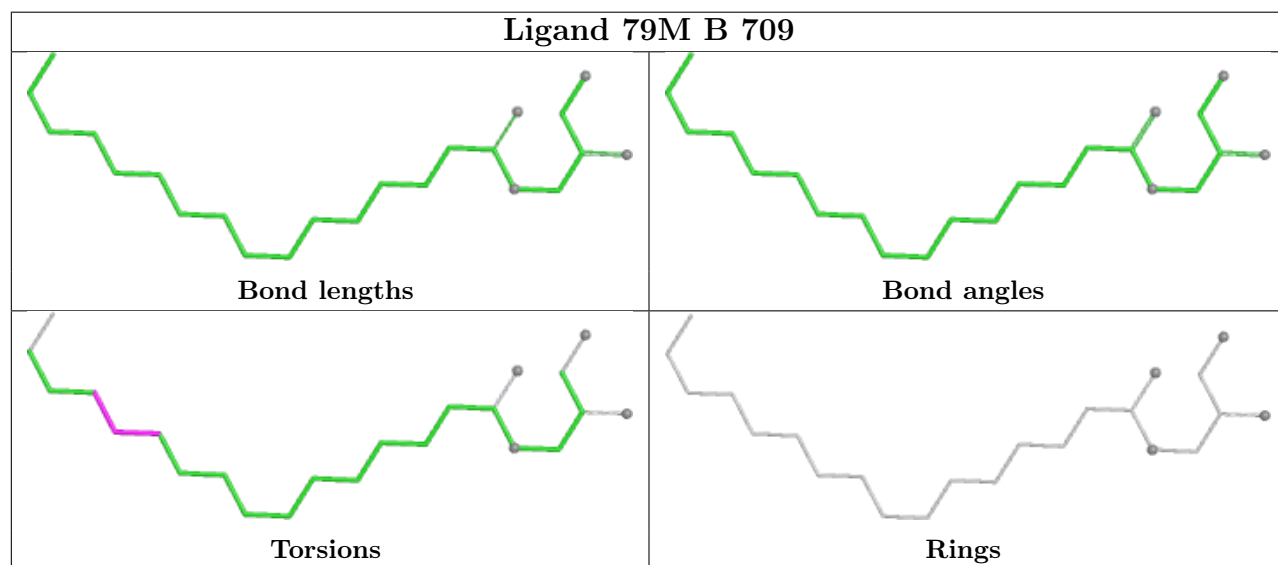
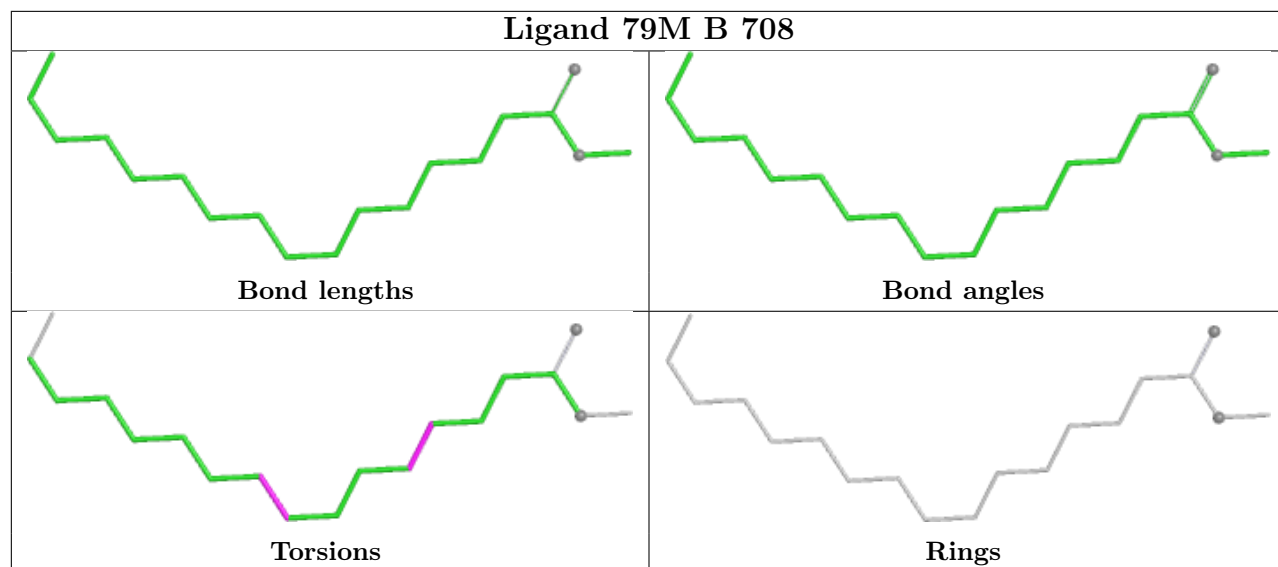
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

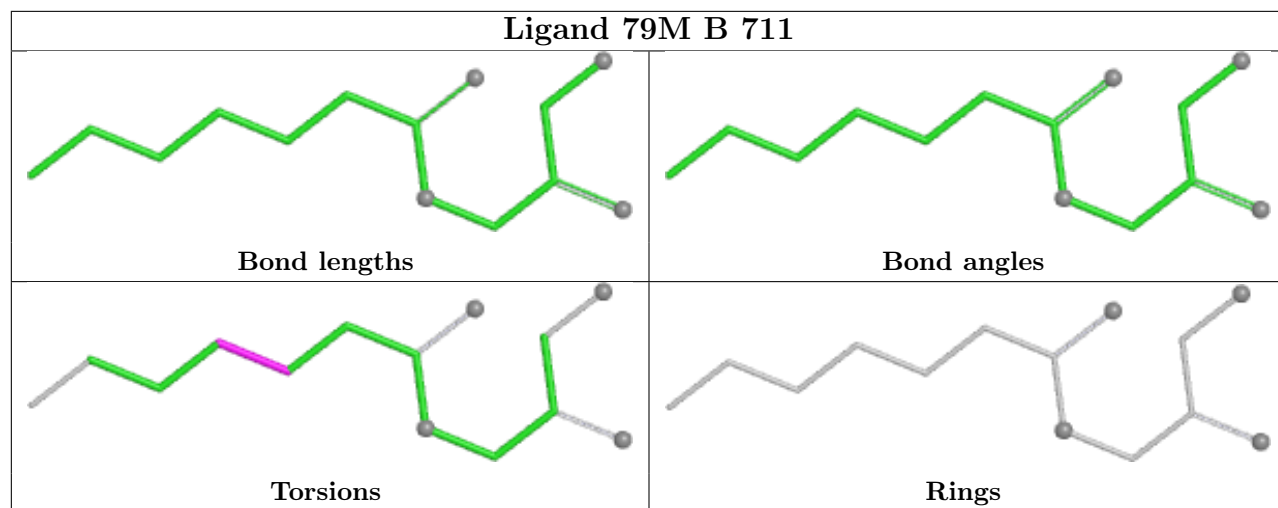












5.7 Other polymers [i](#)

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

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	607/667 (91%)	0.63	56 (9%)	14 9	37, 53, 91, 165	0
1	B	616/667 (92%)	0.57	46 (7%)	20 13	34, 55, 83, 141	0
All	All	1223/1334 (91%)	0.60	102 (8%)	17 11	34, 54, 86, 165	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	116	ASP	5.2
1	B	45	ASP	4.6
1	A	67	GLN	4.5
1	B	114	ASN	4.4
1	B	194	TYR	4.3
1	A	471	LYS	4.3
1	A	489	GLY	4.3
1	A	354	TRP	4.2
1	B	347	HIS	4.2
1	B	354	TRP	4.2
1	B	355	THR	4.1
1	A	56	LEU	4.0
1	A	353	GLU	4.0
1	A	348	GLU	3.5
1	A	208	ILE	3.5
1	A	183	GLU	3.4
1	A	586	GLU	3.4
1	A	112	ASP	3.4
1	A	114	ASN	3.3
1	A	383	PHE	3.3
1	A	637	GLN	3.3
1	B	308	TYR	3.2
1	A	306	PRO	3.2
1	A	349	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	352	SER	3.2
1	A	185	THR	3.2
1	A	187	TYR	3.1
1	B	637	GLN	3.1
1	B	14	SER	3.1
1	A	204	PHE	3.1
1	A	539	ARG	3.1
1	A	538	CYS	3.1
1	B	307	SER	3.0
1	B	473	ASP	3.0
1	A	355	THR	3.0
1	A	342	TRP	3.0
1	B	44	LYS	2.9
1	A	454	TRP	2.9
1	A	199	SER	2.9
1	A	117	ASP	2.8
1	A	541	PHE	2.8
1	A	184	ASP	2.8
1	A	210	LEU	2.8
1	B	305	TYR	2.8
1	A	195	GLN	2.8
1	B	549	SER	2.7
1	B	115	ASN	2.7
1	A	186	TRP	2.7
1	A	182	LEU	2.7
1	B	107	ASN	2.7
1	B	551	ASN	2.7
1	B	192	LEU	2.7
1	B	619	HIS	2.6
1	B	198	ASP	2.6
1	B	356	SER	2.6
1	B	117	ASP	2.5
1	B	306	PRO	2.5
1	B	113	ASP	2.5
1	A	346	LEU	2.5
1	B	550	ALA	2.4
1	A	192	LEU	2.4
1	B	344	LEU	2.4
1	A	491	TYR	2.4
1	B	395	ALA	2.4
1	B	468	GLN	2.4
1	A	535	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	453	TYR	2.3
1	B	311	GLN	2.3
1	B	75	SER	2.3
1	B	209	ALA	2.3
1	B	386	SER	2.3
1	B	187	TYR	2.3
1	A	209	ALA	2.3
1	B	342	TRP	2.3
1	A	344	LEU	2.3
1	B	195	GLN	2.3
1	B	309	LYS	2.3
1	A	266	ALA	2.2
1	A	492	LEU	2.2
1	B	116	ASP	2.2
1	A	639	GLN	2.2
1	B	62	GLU	2.2
1	A	537	MET	2.2
1	A	29	GLU	2.2
1	A	213	GLY	2.2
1	A	475	ASP	2.2
1	B	639	GLN	2.1
1	A	619	HIS	2.1
1	A	308	TYR	2.1
1	B	230	LEU	2.1
1	B	621	GLN	2.1
1	B	578	PRO	2.1
1	A	289	HIS	2.1
1	B	238	GLU	2.1
1	A	479	TYR	2.1
1	A	606	LYS	2.0
1	A	359	LEU	2.0
1	A	392	LEU	2.0
1	B	16	THR	2.0
1	A	449	SER	2.0
1	B	289	HIS	2.0
1	B	638	GLN	2.0

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 ⓘ

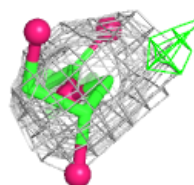
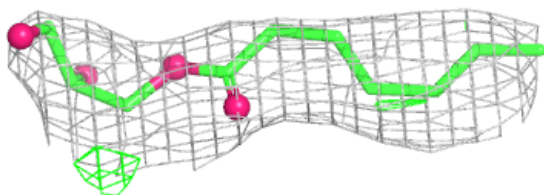
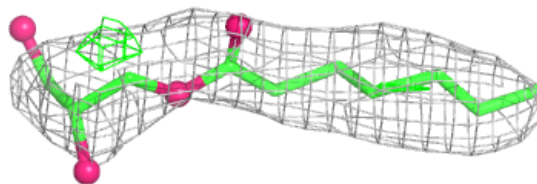
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	79M	A	706	14/23	0.65	0.33	82,89,91,91	0
3	79M	B	707	17/23	0.75	0.26	71,80,88,88	0
3	79M	B	706	12/23	0.76	0.27	68,72,77,77	0
3	79M	A	710	23/23	0.76	0.28	78,83,88,90	0
3	79M	A	705	13/23	0.78	0.30	80,81,87,87	0
3	79M	B	705	23/23	0.80	0.23	69,71,72,72	0
3	79M	A	712	10/23	0.83	0.19	46,48,49,49	0
3	79M	B	711	14/23	0.83	0.21	50,61,65,66	0
3	79M	B	712	8/23	0.83	0.21	44,48,55,56	0
3	79M	B	708	19/23	0.85	0.21	45,55,72,72	0
3	79M	A	709	13/23	0.85	0.26	89,95,96,97	0
3	79M	A	704	23/23	0.85	0.24	73,77,79,80	0
3	79M	B	710	9/23	0.87	0.23	99,100,100,100	0
3	79M	A	711	12/23	0.87	0.18	50,57,59,59	0
3	79M	A	708	20/23	0.87	0.19	53,66,74,74	0
3	79M	B	713	10/23	0.88	0.16	39,40,40,40	0
3	79M	B	709	23/23	0.90	0.18	60,63,67,68	0
3	79M	A	707	6/23	0.94	0.16	43,44,44,45	0
2	CA	B	704	1/1	0.97	0.14	43,43,43,43	0
2	CA	A	703	1/1	0.98	0.03	53,53,53,53	0
2	CA	B	702	1/1	0.98	0.09	41,41,41,41	0
2	CA	A	702	1/1	0.98	0.05	45,45,45,45	0
2	CA	A	701	1/1	0.99	0.05	36,36,36,36	0
2	CA	B	703	1/1	0.99	0.06	33,33,33,33	0
2	CA	B	701	1/1	0.99	0.08	46,46,46,46	0

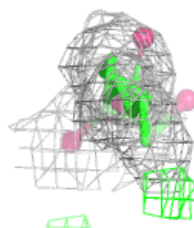
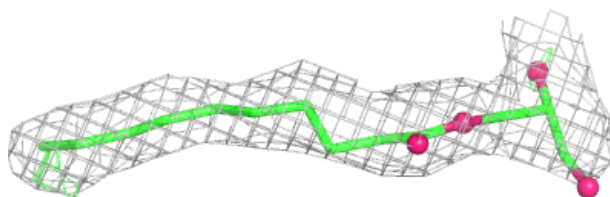
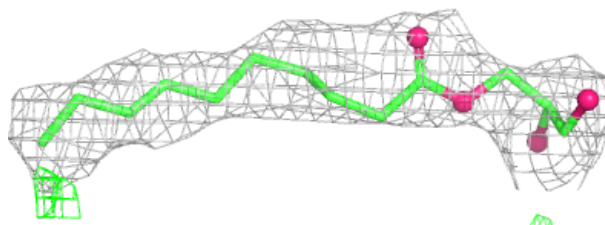
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 79M A 706:

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

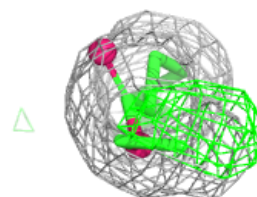
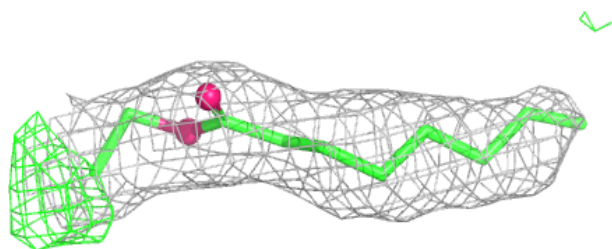
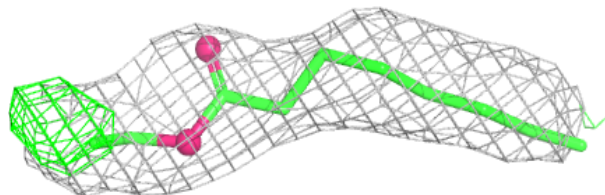
**Electron density around 79M B 707:**

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

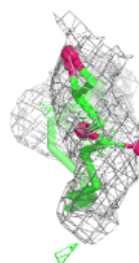
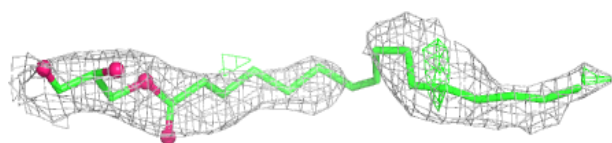
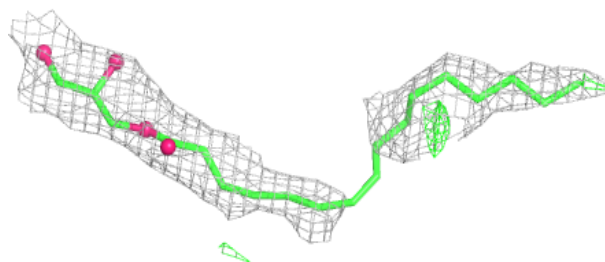


Electron density around 79M B 706:

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

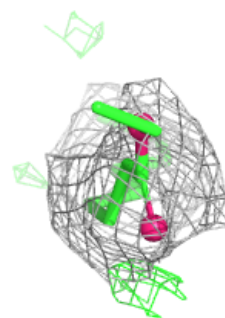
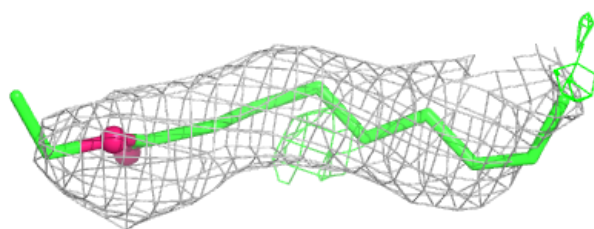
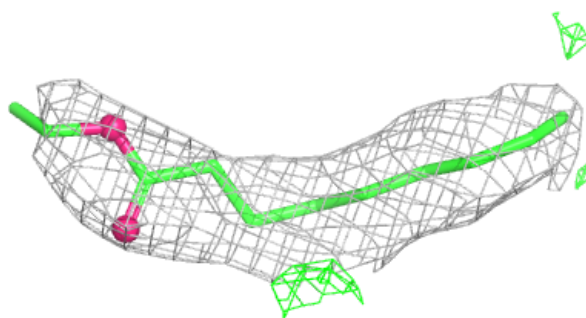
**Electron density around 79M A 710:**

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and green (positive)

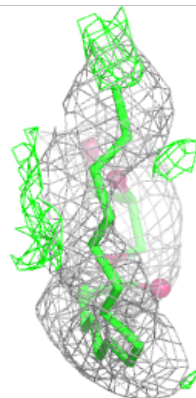
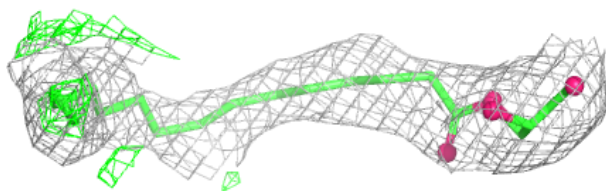
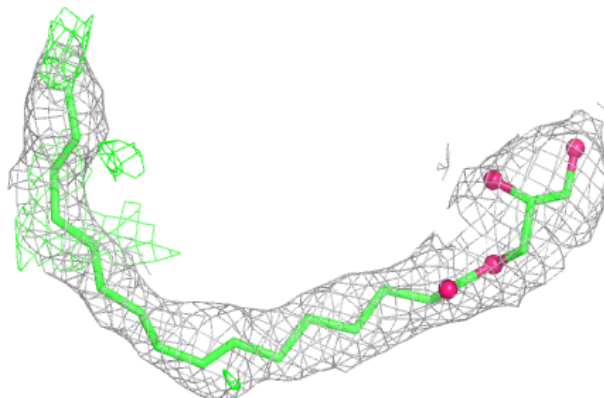


Electron density around 79M A 705:

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

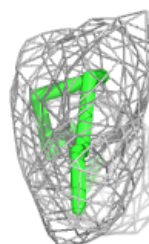
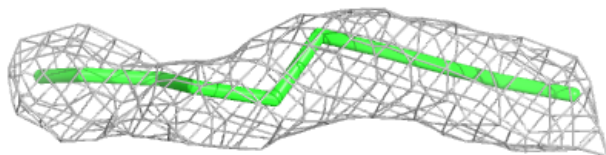
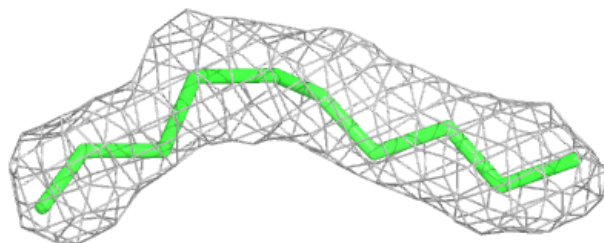
**Electron density around 79M B 705:**

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

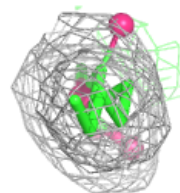
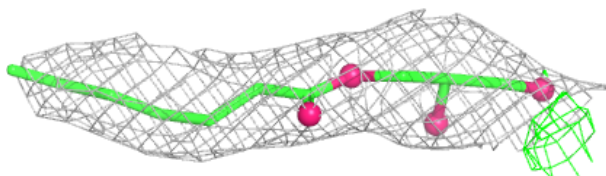
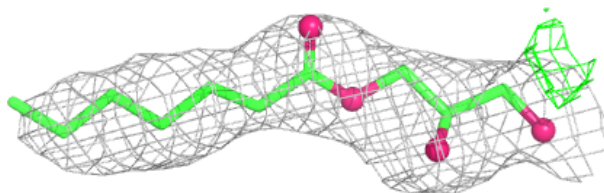


Electron density around 79M A 712:

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

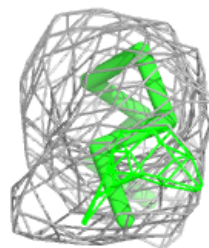
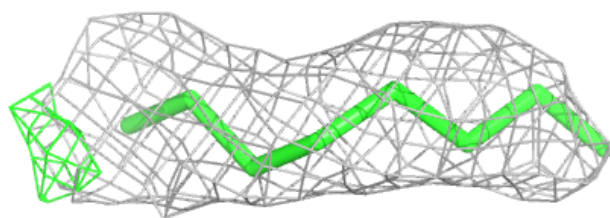
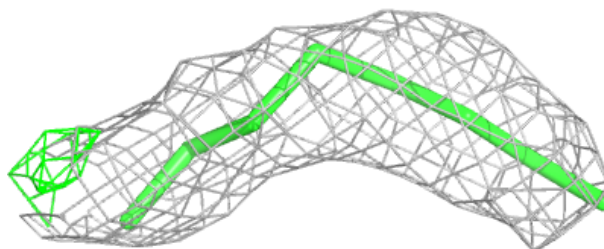
**Electron density around 79M B 711:**

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

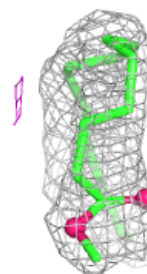
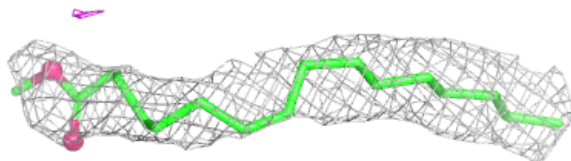
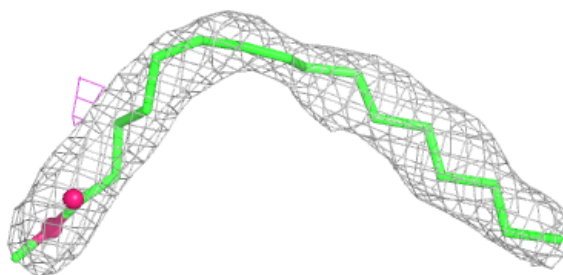


Electron density around 79M B 712:

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

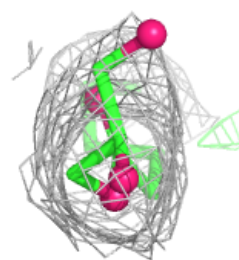
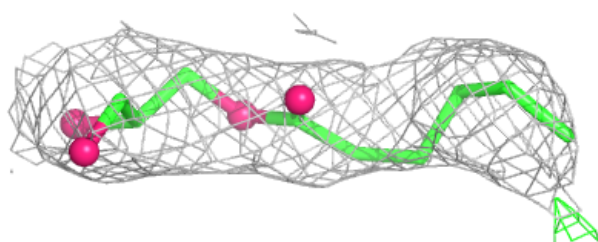
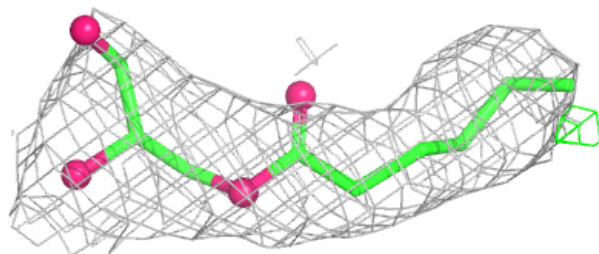
**Electron density around 79M B 708:**

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

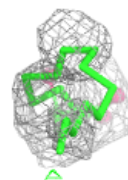
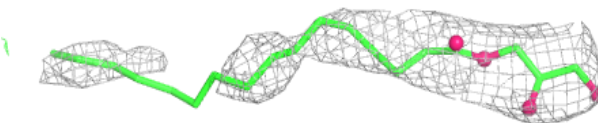
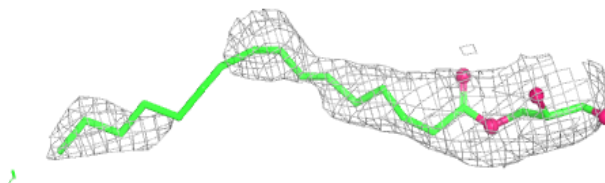


Electron density around 79M A 709:

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

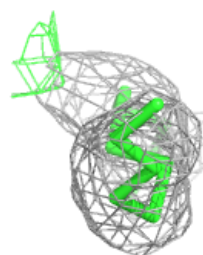
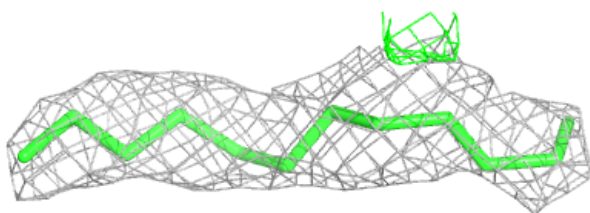
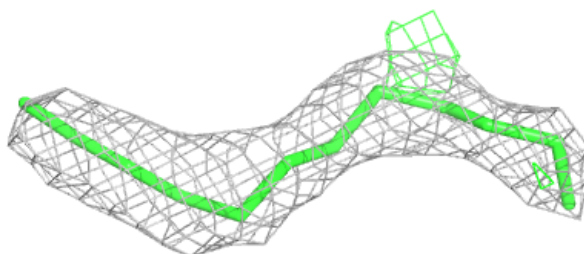
**Electron density around 79M A 704:**

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

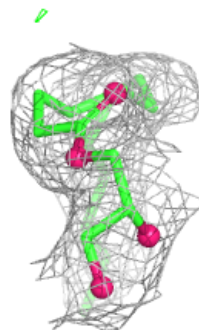
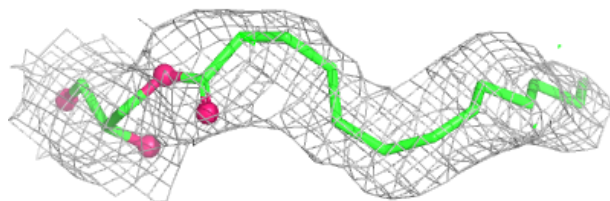
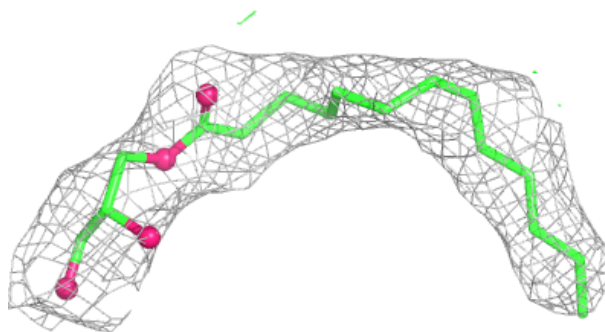


Electron density around 79M A 711:

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

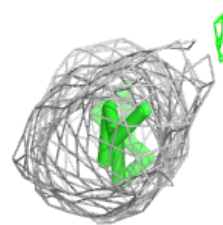
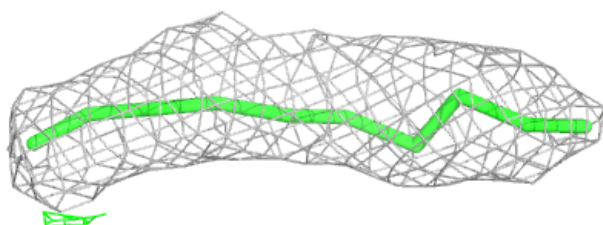
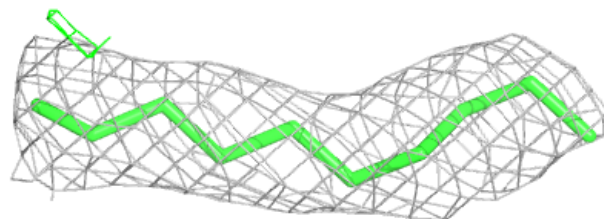
**Electron density around 79M A 708:**

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

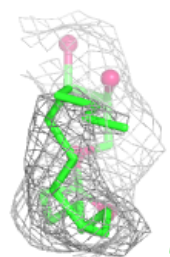
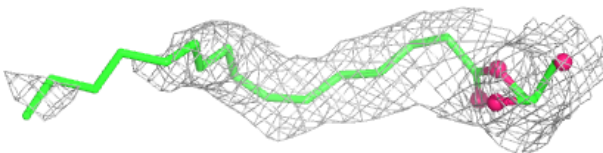
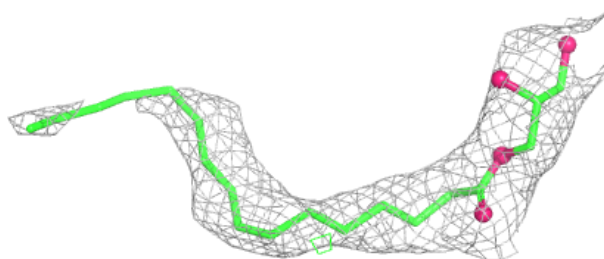


Electron density around 79M B 713:

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

**Electron density around 79M B 709:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.