



wwPDB EM Validation Summary Report ⓘ

Nov 10, 2024 – 09:35 AM EST

PDB ID : 6WEJ
EMDB ID : EMD-21649
Title : Structure of cGMP-unbound WT TAX-4 reconstituted in lipid nanodiscs
Authors : Zheng, X.; Fu, Z.; Su, D.; Zhang, Y.; Li, M.; Pan, Y.; Li, H.; Li, S.; Grassucci, R.A.; Ren, Z.; Hu, Z.; Li, X.; Zhou, M.; Li, G.; Frank, J.; Yang, J.
Deposited on : 2020-04-02
Resolution : 2.60 Å(reported)
Based on initial model : 5H3O

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

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

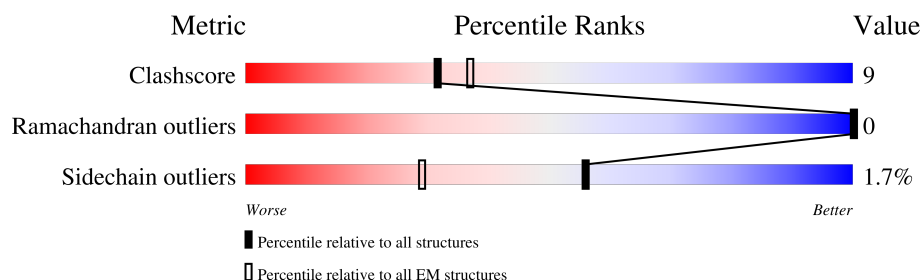
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	733	
1	B	733	
1	C	733	
1	D	733	

2 Entry composition [i](#)

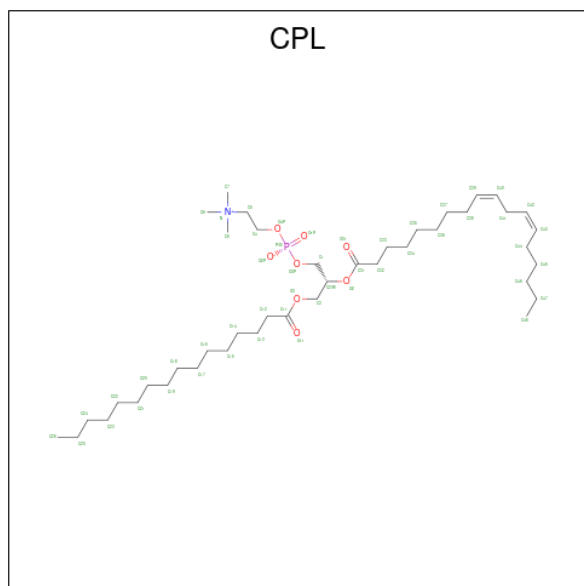
There are 4 unique types of molecules in this entry. The entry contains 17665 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cyclic nucleotide-gated cation channel.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	513	Total	C	N	O	S	0	0
			4241	2757	715	745	24		
1	B	513	Total	C	N	O	S	0	0
			4241	2757	715	745	24		
1	C	513	Total	C	N	O	S	0	0
			4241	2757	715	745	24		
1	D	513	Total	C	N	O	S	0	0
			4241	2757	715	745	24		

- Molecule 2 is 1-PALMITOYL-2-LINOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: CPL) (formula: C₄₂H₈₀NO₈P).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			47	37	1	8	1	
2	A	1	Total	C	O	P		0
			38	29	8	1		

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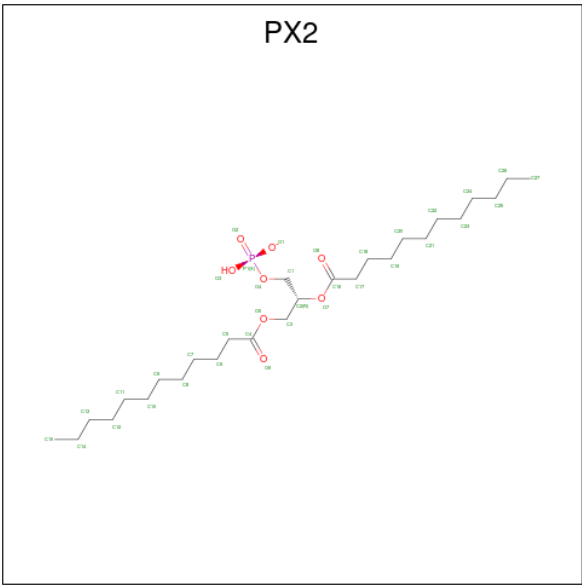
Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total C 9 9	0
2	A	1	Total C 9 9	0
2	A	1	Total C 12 12	0
2	A	1	Total C 12 12	0
2	B	1	Total C N O P 47 37 1 8 1	0
2	B	1	Total C O P 38 29 8 1	0
2	B	1	Total C 9 9	0
2	B	1	Total C 9 9	0
2	B	1	Total C 12 12	0
2	B	1	Total C 12 12	0
2	C	1	Total C N O P 47 37 1 8 1	0
2	C	1	Total C O P 38 29 8 1	0
2	C	1	Total C 9 9	0
2	C	1	Total C 9 9	0
2	C	1	Total C 12 12	0
2	C	1	Total C 12 12	0
2	D	1	Total C N O P 47 37 1 8 1	0
2	D	1	Total C O P 38 29 8 1	0
2	D	1	Total C 9 9	0
2	D	1	Total C 9 9	0
2	D	1	Total C 12 12	0

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Mol	Chain	Residues	Atoms		AltConf
2	D	1	Total	C	0
			12	12	

- Molecule 3 is 1,2-DILAUROYL-SN-GLYCERO-3-PHOSPHATE (three-letter code: PX2) (formula: C₂₇H₅₂O₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			23	14	8	1	
3	A	1	Total	C	O	P	0
			25	16	8	1	
3	B	1	Total	C	O	P	0
			23	14	8	1	
3	B	1	Total	C	O	P	0
			25	16	8	1	
3	C	1	Total	C	O	P	0
			23	14	8	1	
3	C	1	Total	C	O	P	0
			25	16	8	1	
3	D	1	Total	C	O	P	0
			23	14	8	1	
3	D	1	Total	C	O	P	0
			25	16	8	1	

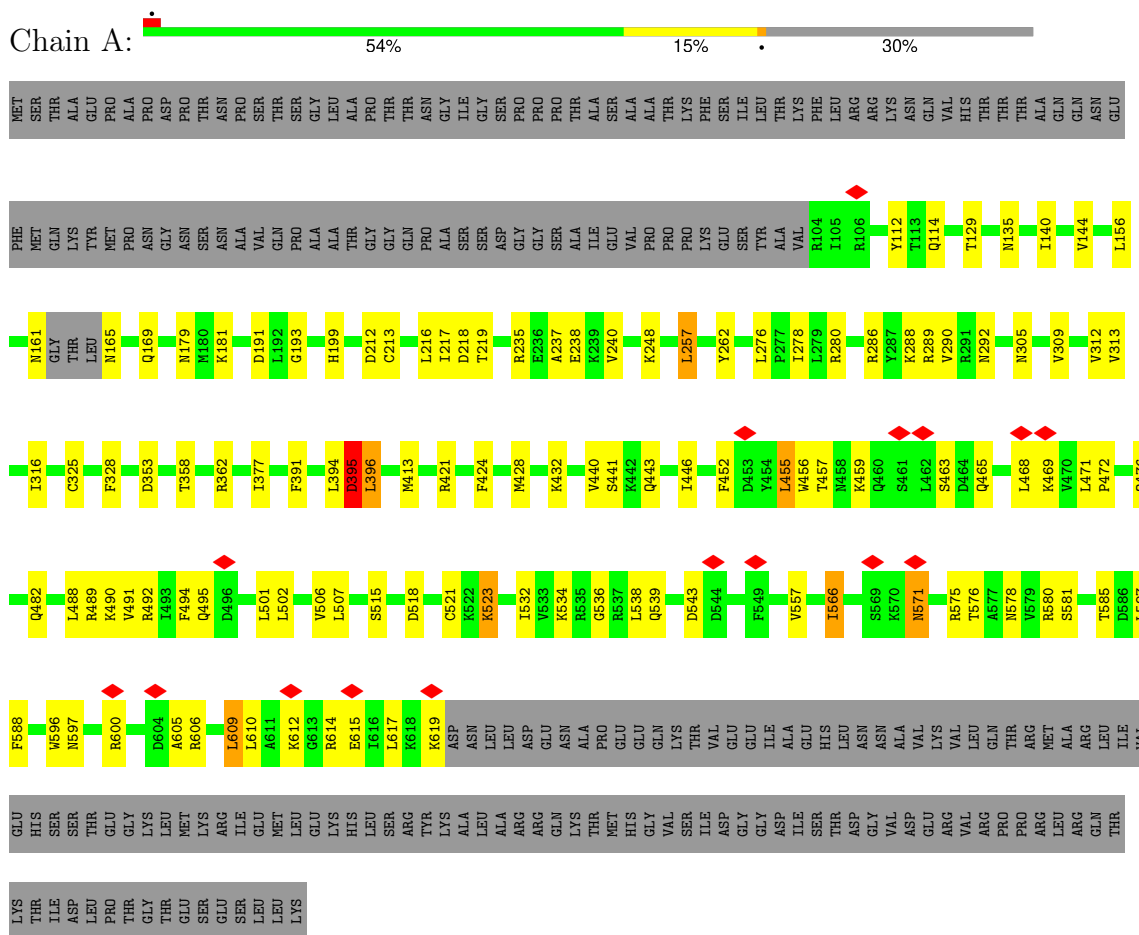
- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Na 1	0

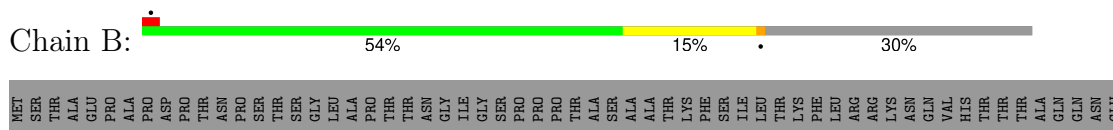
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: Cyclic nucleotide-gated cation channel



• Molecule 1: Cyclic nucleotide-gated cation channel



ARG
LEU
ARG
GLN
ALA
THR
LYS
THR
THR
ILE
ASP
LEU
PRO
THR
GLY
THR
GLU
SER
SER
LEU
LEU
LYS

● Molecule 1: Cyclic nucleotide-gated cation channel



MET
SER
THR
GLN
ALA
GLU
MET
PRO
ALA
PRO
ASP
THR
PRO
ASN
THR
GLY
THR
GLU
SER
SER
GLU
SER
LEU
LEU
LYS

PHE
MET
GLN
LYS
TYR
GLY
MET
PRO
ASN
GLY
ASN
SER
SER
ASN
ALA
VAL
GLN
PRO
SER
ALA
THR
GLY
GLN
THR
PRO
ASN
ALA
SER
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ASP
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ALA
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R104
R105
R106

L156
L161
GLY
THR
LEU
N165
Q169
N179
D191
L192
G193
Y197
M198
H199
D212
C213
L216
L217
D218
T219
R235
E236
A237
E238
K239
V240
L257
Y262
L276
P277
L278
L279
R280
R286
R289
V290
K291
K292
N305
V309
V312
V313

I316
C325
F328
D353
T358
R362
I377
F391
L394
D395
L396
M413
F424
M428
K432
Q433
V440
Q443
T446
W451
F452
L455
W456
T457
S461
L462
S463
D464
Q465
L468
K469
W470
L471
Q476
Q482
L488
R489
K490

V491
R492
T493
Q495
D496
L501
L502
V506
L507
S515
D518
C521
K522
K523
G524
D525
I532
V533
K534
R535
G536
R537
L538
Q539
D543
D544
F549
V557
T566
A567
G568
S569
K570
N571
R575
T576
A577
N578
T579
R580
S581
T585
D586
L587
F588
W596

N597
R600
A605
R606
L609
L610
A611
G612
G613
R614
E615
T616
L617
K618
K619
ASP
ASN
LEU
LEU
LEU
ASP
GLU
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LEU
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	163525	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	66.03	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	6.851	Depositor
Minimum map value	-4.665	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.139	Depositor
Recommended contour level	0.574	Depositor
Map size (\AA)	316.72, 316.72, 316.72	wwPDB
Map dimensions	296, 296, 296	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PX2, NA, CPL

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	0.64	9/4343 (0.2%)	0.59	8/5889 (0.1%)
1	B	0.64	9/4343 (0.2%)	0.59	8/5889 (0.1%)
1	C	0.64	9/4343 (0.2%)	0.59	8/5889 (0.1%)
1	D	0.64	9/4343 (0.2%)	0.59	8/5889 (0.1%)
All	All	0.64	36/17372 (0.2%)	0.59	32/23556 (0.1%)

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	395	ASP	CB-CG	-10.77	1.29	1.51
1	D	395	ASP	CB-CG	-10.77	1.29	1.51
1	A	395	ASP	CB-CG	-10.76	1.29	1.51
1	B	395	ASP	CB-CG	-10.75	1.29	1.51
1	A	394	LEU	C-O	-10.06	1.04	1.23

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	292	ASN	CB-CA-C	-8.39	93.62	110.40
1	A	292	ASN	CB-CA-C	-8.38	93.65	110.40
1	C	292	ASN	CB-CA-C	-8.37	93.67	110.40
1	D	292	ASN	CB-CA-C	-8.37	93.67	110.40
1	A	395	ASP	CB-CG-OD1	7.81	125.33	118.30

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	4241	0	4283	74	0
1	B	4241	0	4283	74	0
1	C	4241	0	4283	73	0
1	D	4241	0	4283	72	0
2	A	127	0	186	6	0
2	B	127	0	186	6	0
2	C	127	0	186	7	0
2	D	127	0	186	6	0
3	A	48	0	43	1	0
3	B	48	0	43	1	0
3	C	48	0	43	2	0
3	D	48	0	43	2	0
4	A	1	0	0	0	0
All	All	17665	0	18048	304	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 9.

The worst 5 of 304 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:B:571:ASN:O	1:B:571:ASN:ND2	2.10	0.85
1:C:571:ASN:ND2	1:C:571:ASN:O	2.10	0.85
1:A:571:ASN:O	1:A:571:ASN:ND2	2.10	0.84
1:D:571:ASN:O	1:D:571:ASN:ND2	2.10	0.84
1:A:305:ASN:HB3	1:A:413:MET:HG3	1.61	0.81

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 PDB entries followed by that with respect to all EM

entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	509/733 (69%)	487 (96%)	22 (4%)	0	100	100
1	B	509/733 (69%)	487 (96%)	22 (4%)	0	100	100
1	C	509/733 (69%)	487 (96%)	22 (4%)	0	100	100
1	D	509/733 (69%)	487 (96%)	22 (4%)	0	100	100
All	All	2036/2932 (69%)	1948 (96%)	88 (4%)	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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	465/651 (71%)	457 (98%)	8 (2%)	56	78
1	B	465/651 (71%)	457 (98%)	8 (2%)	56	78
1	C	465/651 (71%)	457 (98%)	8 (2%)	56	78
1	D	465/651 (71%)	457 (98%)	8 (2%)	56	78
All	All	1860/2604 (71%)	1828 (98%)	32 (2%)	56	78

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	457	THR
1	D	523	LYS
1	B	457	THR
1	B	455	LEU
1	D	576	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	425	GLN
1	D	179	ASN
1	C	482	GLN
1	C	578	ASN
1	D	386	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 1 is monoatomic - leaving 32 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
2	CPL	B	804	-	8,8,51	0.28	0	7,7,59	0.79	0
3	PX2	A	803	-	22,22,35	1.60	6 (27%)	25,27,40	2.66	8 (32%)
2	CPL	C	805	-	8,8,51	0.17	0	7,7,59	0.47	0
2	CPL	A	801	-	46,46,51	1.39	7 (15%)	52,54,59	2.29	14 (26%)
2	CPL	C	804	-	8,8,51	0.28	0	7,7,59	0.78	0
2	CPL	A	804	-	8,8,51	0.28	0	7,7,59	0.79	0
2	CPL	B	801	-	46,46,51	1.39	7 (15%)	52,54,59	2.29	14 (26%)
2	CPL	C	806	-	11,11,51	0.69	0	10,10,59	0.64	0
3	PX2	B	803	-	22,22,35	1.59	6 (27%)	25,27,40	2.66	8 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CPL	B	806	-	11,11,51	0.68	0	10,10,59	0.64	0
2	CPL	C	807	-	11,11,51	0.18	0	10,10,59	0.76	0
3	PX2	C	803	-	22,22,35	1.60	6 (27%)	25,27,40	2.65	8 (32%)
2	CPL	A	806	-	11,11,51	0.69	0	10,10,59	0.64	0
2	CPL	B	802	-	37,37,51	1.66	4 (10%)	40,42,59	2.15	12 (30%)
2	CPL	D	807	-	11,11,51	0.18	0	10,10,59	0.76	0
2	CPL	B	807	-	11,11,51	0.18	0	10,10,59	0.76	0
2	CPL	A	805	-	8,8,51	0.18	0	7,7,59	0.46	0
2	CPL	D	804	-	8,8,51	0.28	0	7,7,59	0.79	0
2	CPL	A	802	-	37,37,51	1.66	4 (10%)	40,42,59	2.15	12 (30%)
2	CPL	A	807	-	11,11,51	0.18	0	10,10,59	0.76	0
2	CPL	D	802	-	37,37,51	1.66	4 (10%)	40,42,59	2.15	12 (30%)
2	CPL	C	802	-	37,37,51	1.66	4 (10%)	40,42,59	2.15	12 (30%)
2	CPL	D	801	-	46,46,51	1.40	7 (15%)	52,54,59	2.29	14 (26%)
3	PX2	D	803	-	22,22,35	1.59	6 (27%)	25,27,40	2.65	8 (32%)
2	CPL	D	806	-	11,11,51	0.68	0	10,10,59	0.64	0
2	CPL	C	801	-	46,46,51	1.40	7 (15%)	52,54,59	2.29	13 (25%)
2	CPL	D	805	-	8,8,51	0.18	0	7,7,59	0.47	0
3	PX2	B	808	-	24,24,35	1.18	4 (16%)	27,29,40	1.28	2 (7%)
2	CPL	B	805	-	8,8,51	0.18	0	7,7,59	0.46	0
3	PX2	A	808	-	24,24,35	1.18	4 (16%)	27,29,40	1.29	2 (7%)
3	PX2	C	808	-	24,24,35	1.18	4 (16%)	27,29,40	1.29	2 (7%)
3	PX2	D	808	-	24,24,35	1.19	4 (16%)	27,29,40	1.29	2 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CPL	B	804	-	-	3/6/6/55	-
3	PX2	A	803	-	-	8/24/24/37	-
2	CPL	C	805	-	-	4/6/6/55	-
2	CPL	A	801	-	-	31/50/50/55	-
2	CPL	C	804	-	-	3/6/6/55	-
2	CPL	A	804	-	-	3/6/6/55	-
2	CPL	B	801	-	-	31/50/50/55	-
2	CPL	C	806	-	-	4/9/9/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PX2	B	803	-	-	8/24/24/37	-
2	CPL	B	806	-	-	4/9/9/55	-
2	CPL	C	807	-	-	5/9/9/55	-
3	PX2	C	803	-	-	8/24/24/37	-
2	CPL	A	806	-	-	4/9/9/55	-
2	CPL	B	802	-	-	19/41/41/55	-
2	CPL	D	807	-	-	5/9/9/55	-
2	CPL	B	807	-	-	5/9/9/55	-
2	CPL	A	805	-	-	4/6/6/55	-
2	CPL	D	804	-	-	3/6/6/55	-
2	CPL	A	802	-	-	19/41/41/55	-
2	CPL	A	807	-	-	5/9/9/55	-
2	CPL	D	802	-	-	19/41/41/55	-
2	CPL	C	802	-	-	19/41/41/55	-
2	CPL	D	801	-	-	31/50/50/55	-
3	PX2	D	803	-	-	8/24/24/37	-
2	CPL	D	806	-	-	4/9/9/55	-
2	CPL	C	801	-	-	31/50/50/55	-
2	CPL	D	805	-	-	4/6/6/55	-
3	PX2	B	808	-	-	16/26/26/37	-
2	CPL	B	805	-	-	4/6/6/55	-
3	PX2	A	808	-	-	16/26/26/37	-
3	PX2	C	808	-	-	16/26/26/37	-
3	PX2	D	808	-	-	16/26/26/37	-

The worst 5 of 84 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	802	CPL	O2-C31	6.95	1.53	1.34
2	C	802	CPL	O2-C31	6.93	1.53	1.34
2	D	802	CPL	O2-C31	6.93	1.53	1.34
2	A	802	CPL	O2-C31	6.93	1.53	1.34
2	C	801	CPL	O2-C31	4.65	1.47	1.34

The worst 5 of 143 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	801	CPL	O2-C31-C32	7.92	128.62	111.48
2	B	801	CPL	O2-C31-C32	7.91	128.60	111.48
2	A	801	CPL	O2-C31-C32	7.91	128.60	111.48
2	D	801	CPL	O2-C31-C32	7.91	128.60	111.48
2	B	801	CPL	O3-C11-C12	6.72	132.34	111.83

There are no chirality outliers.

5 of 360 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	CPL	C5-C4-O4P-P
2	A	801	CPL	O31-C31-O2-C2
2	A	801	CPL	C39-C40-C41-C42
2	A	801	CPL	C1-O3P-P-O1P
2	A	801	CPL	C1-O3P-P-O2P

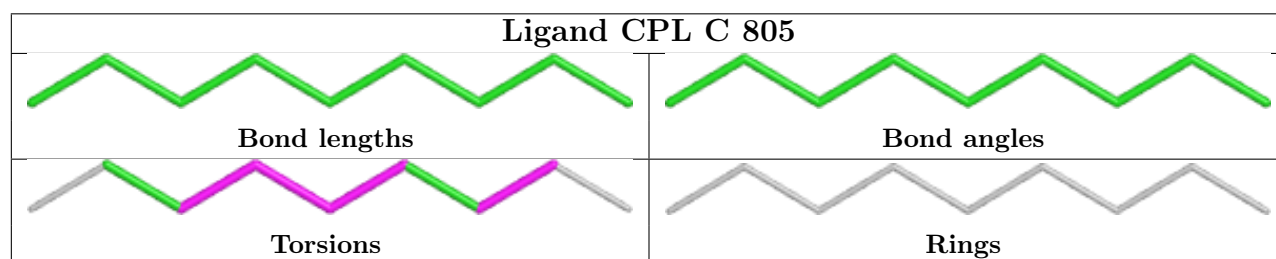
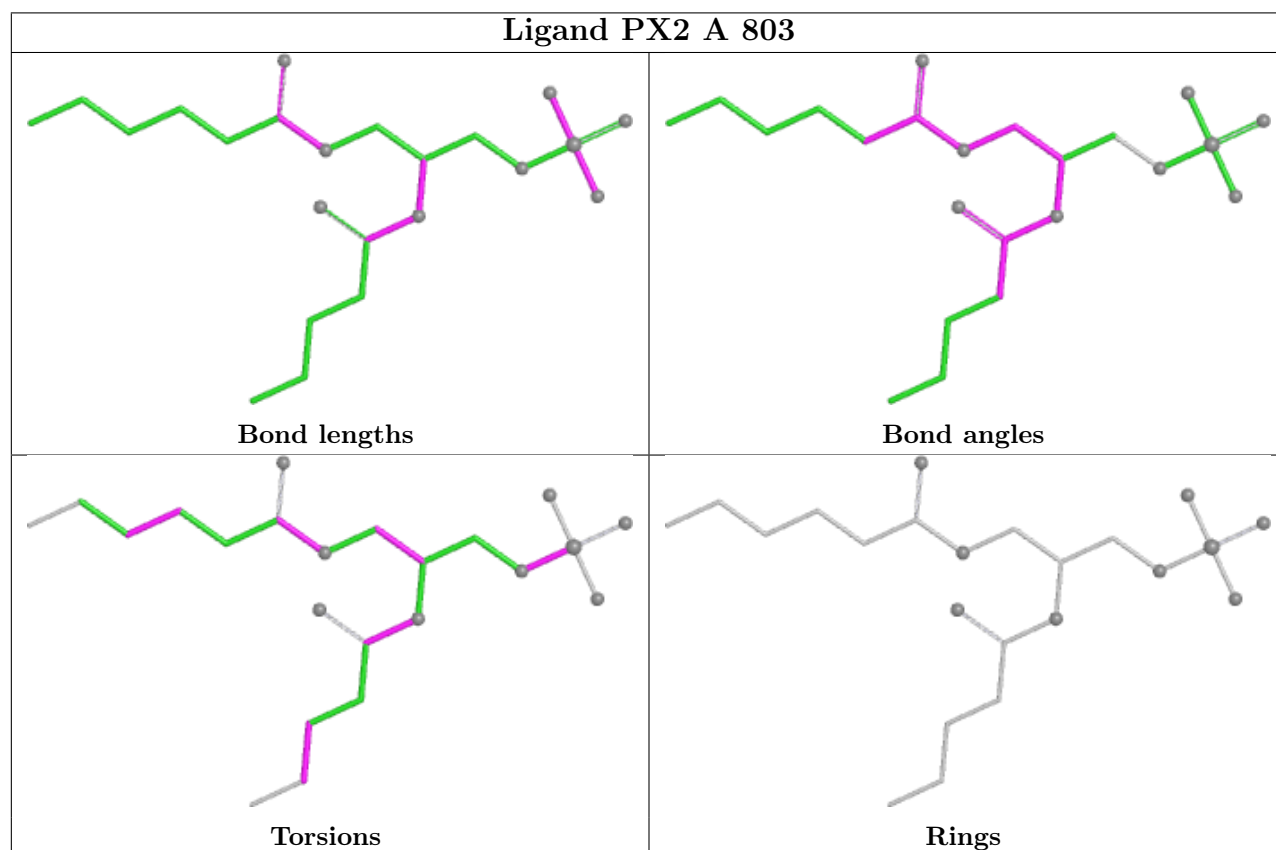
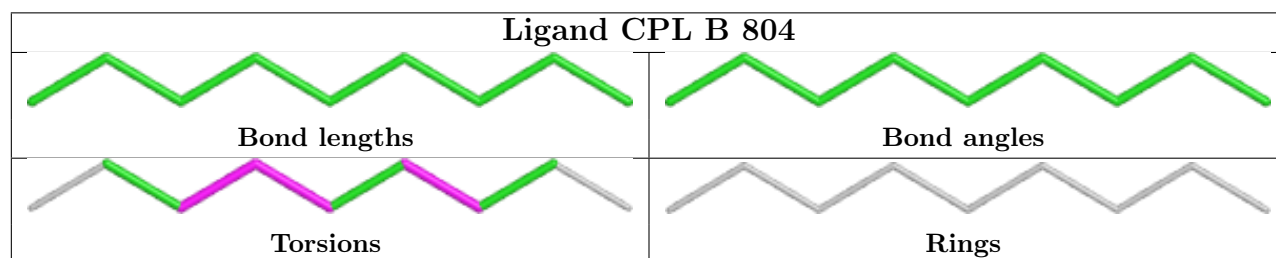
There are no ring outliers.

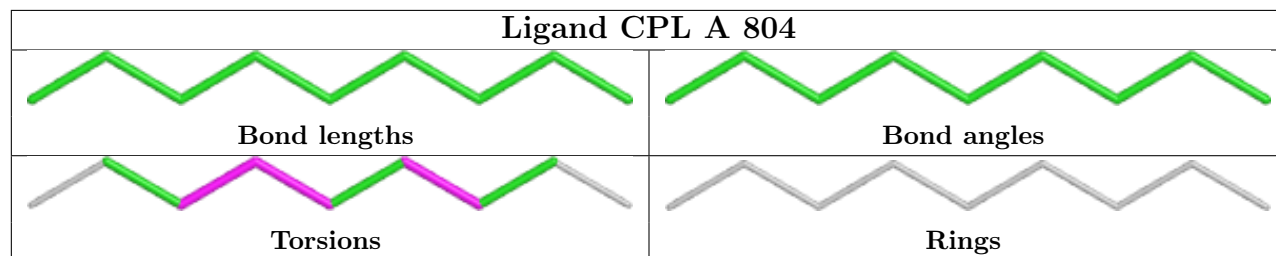
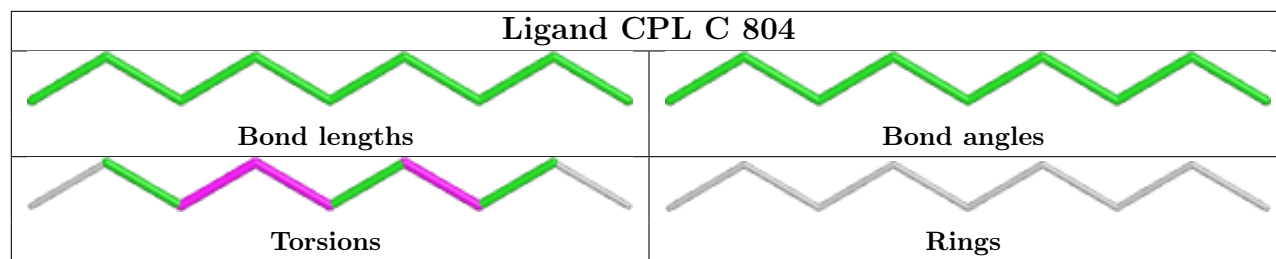
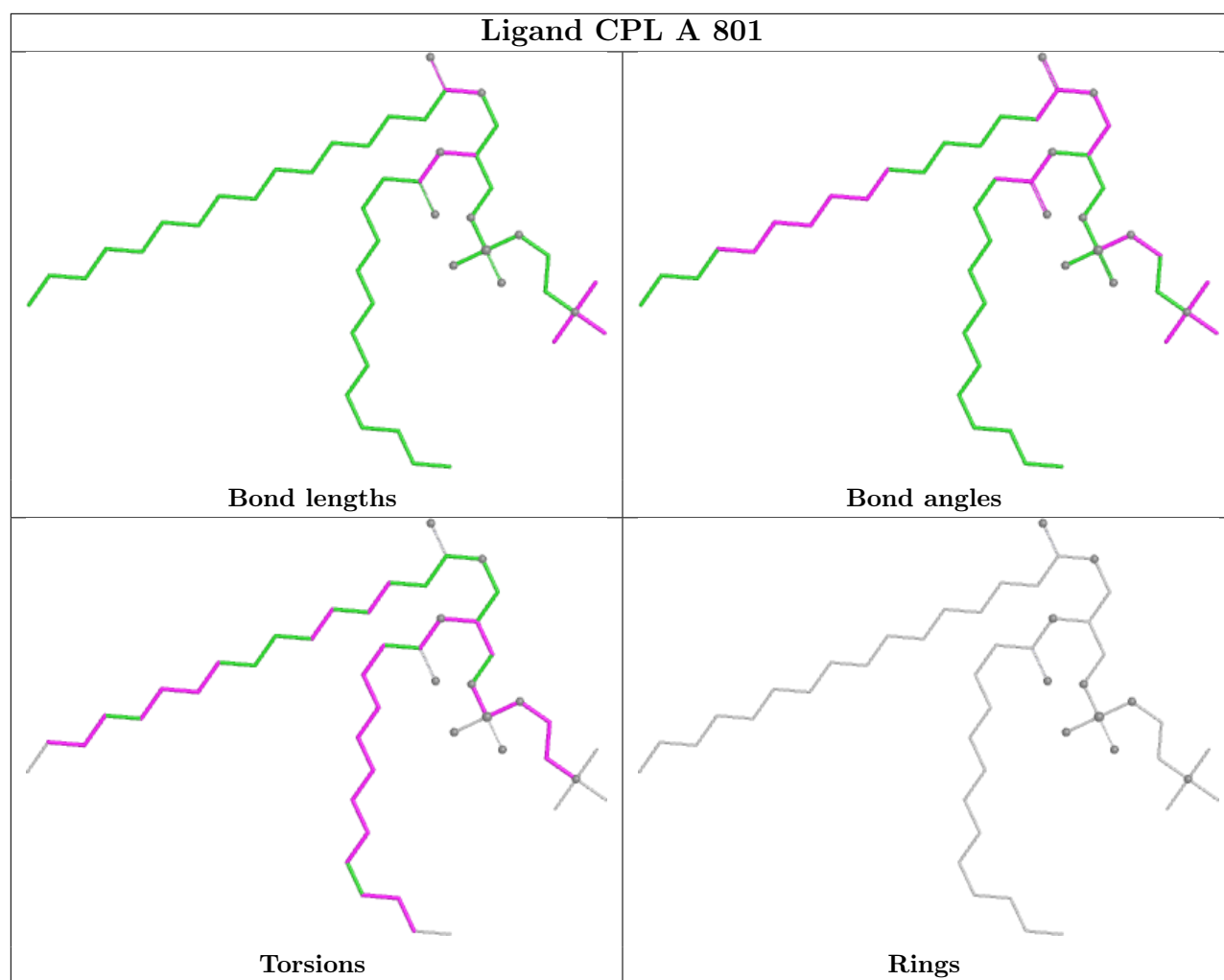
12 monomers are involved in 31 short contacts:

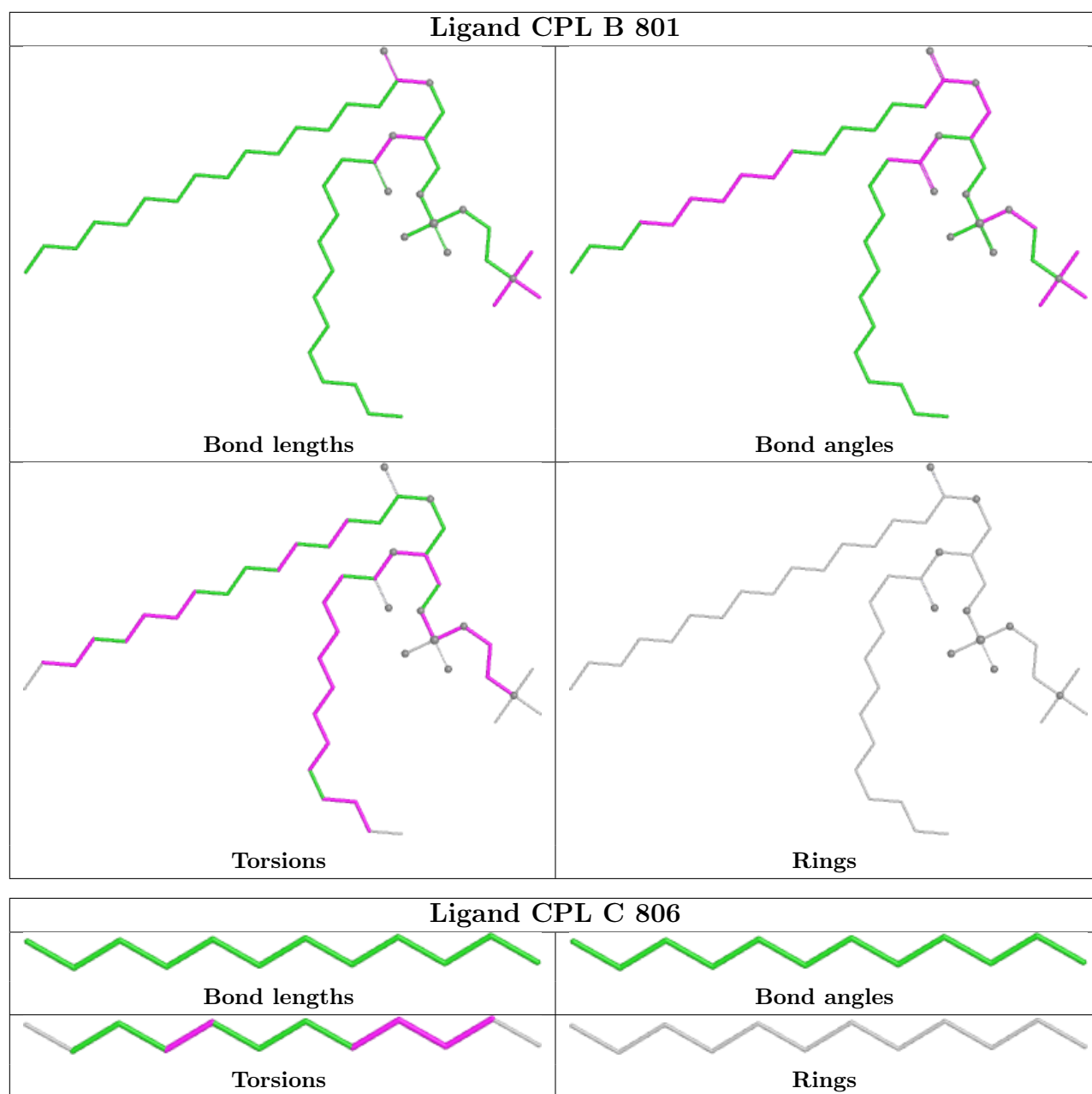
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	803	PX2	1	0
2	A	801	CPL	5	0
2	B	801	CPL	5	0
2	C	806	CPL	1	0
3	B	803	PX2	1	0
2	B	806	CPL	1	0
3	C	803	PX2	2	0
2	A	806	CPL	1	0
2	D	801	CPL	5	0
3	D	803	PX2	2	0
2	D	806	CPL	1	0
2	C	801	CPL	6	0

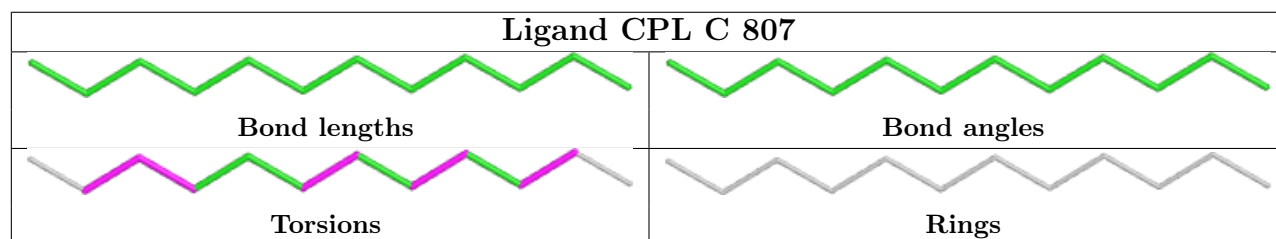
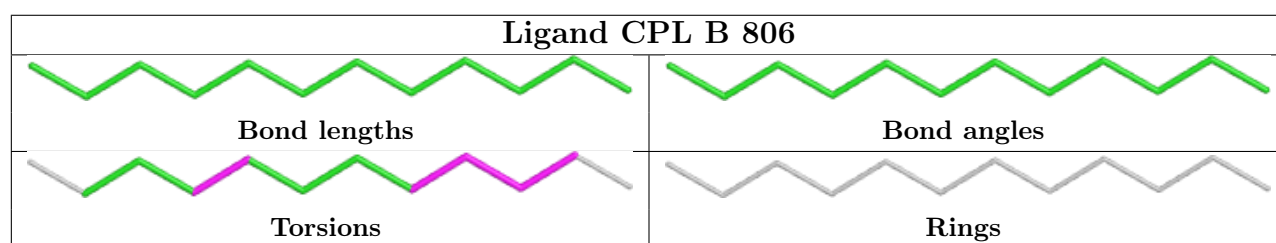
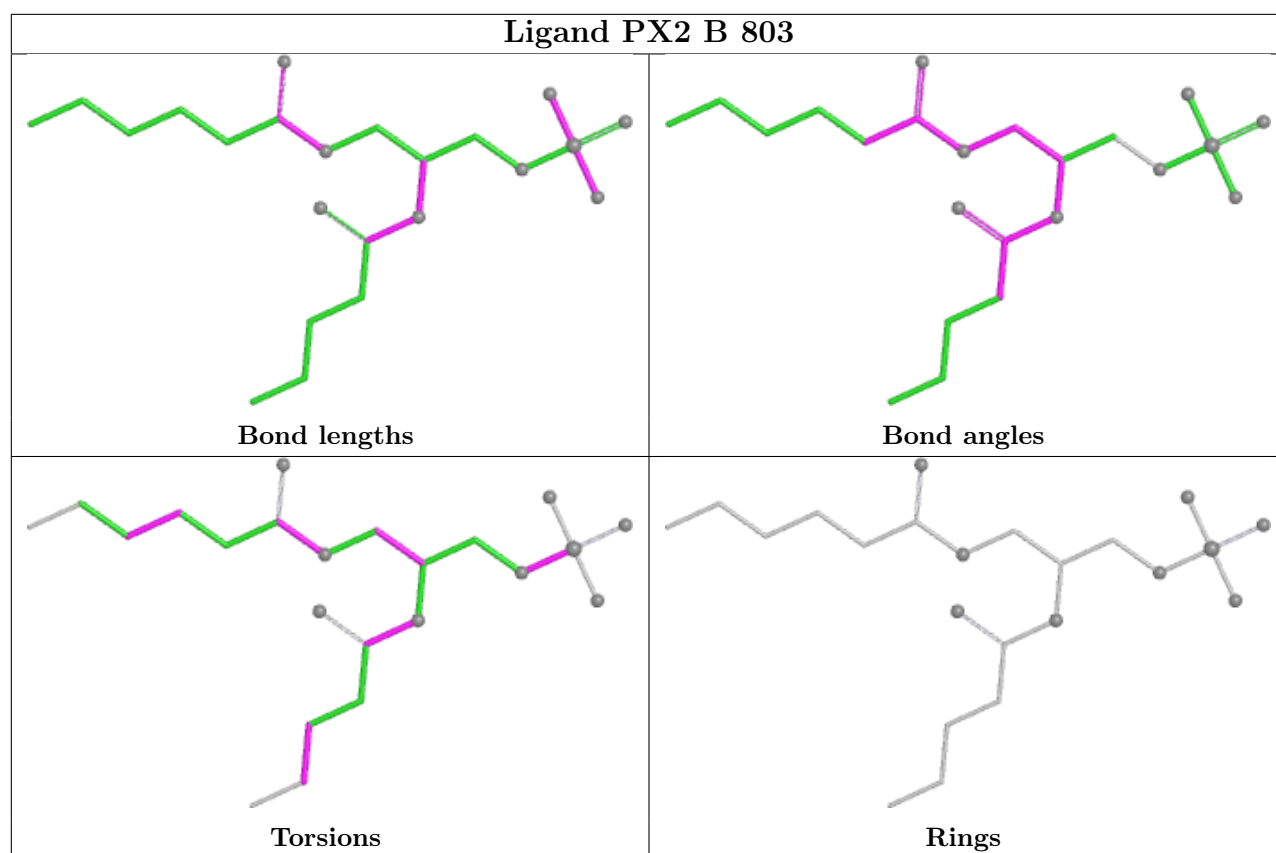
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

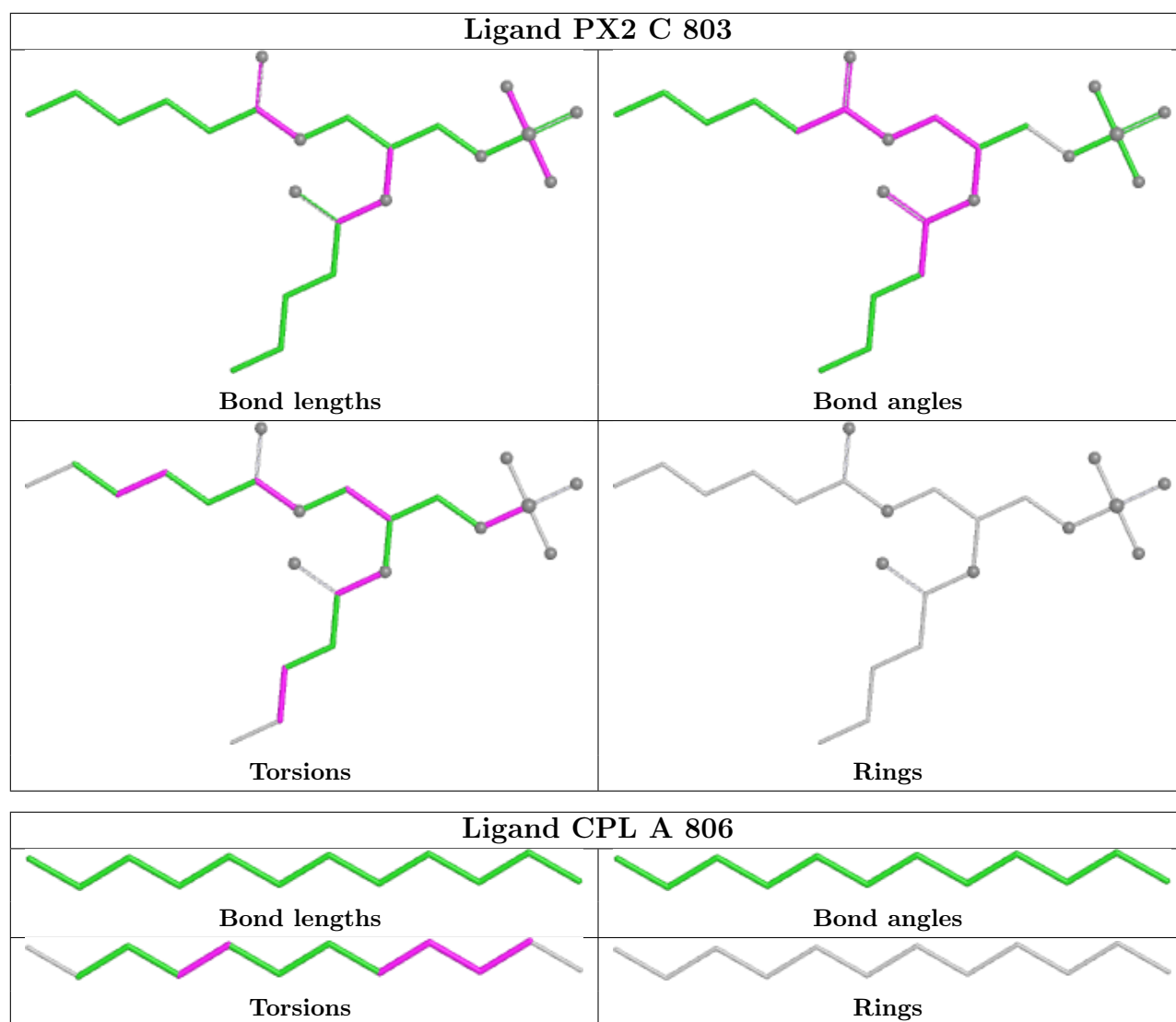
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

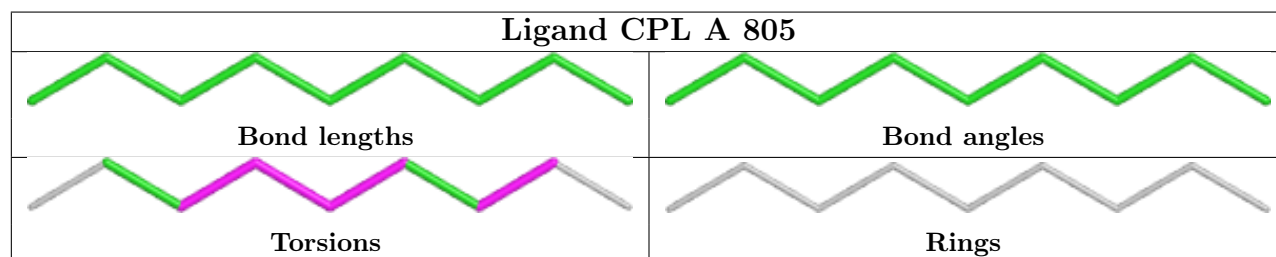
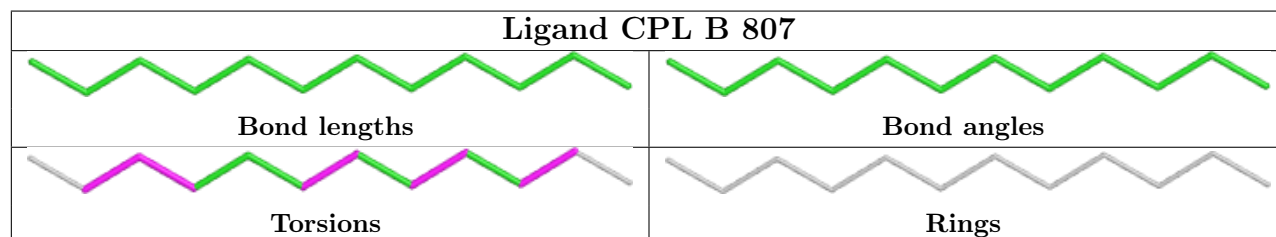
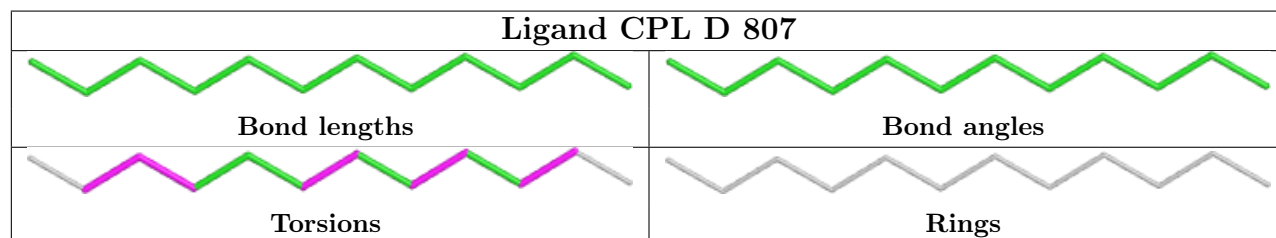
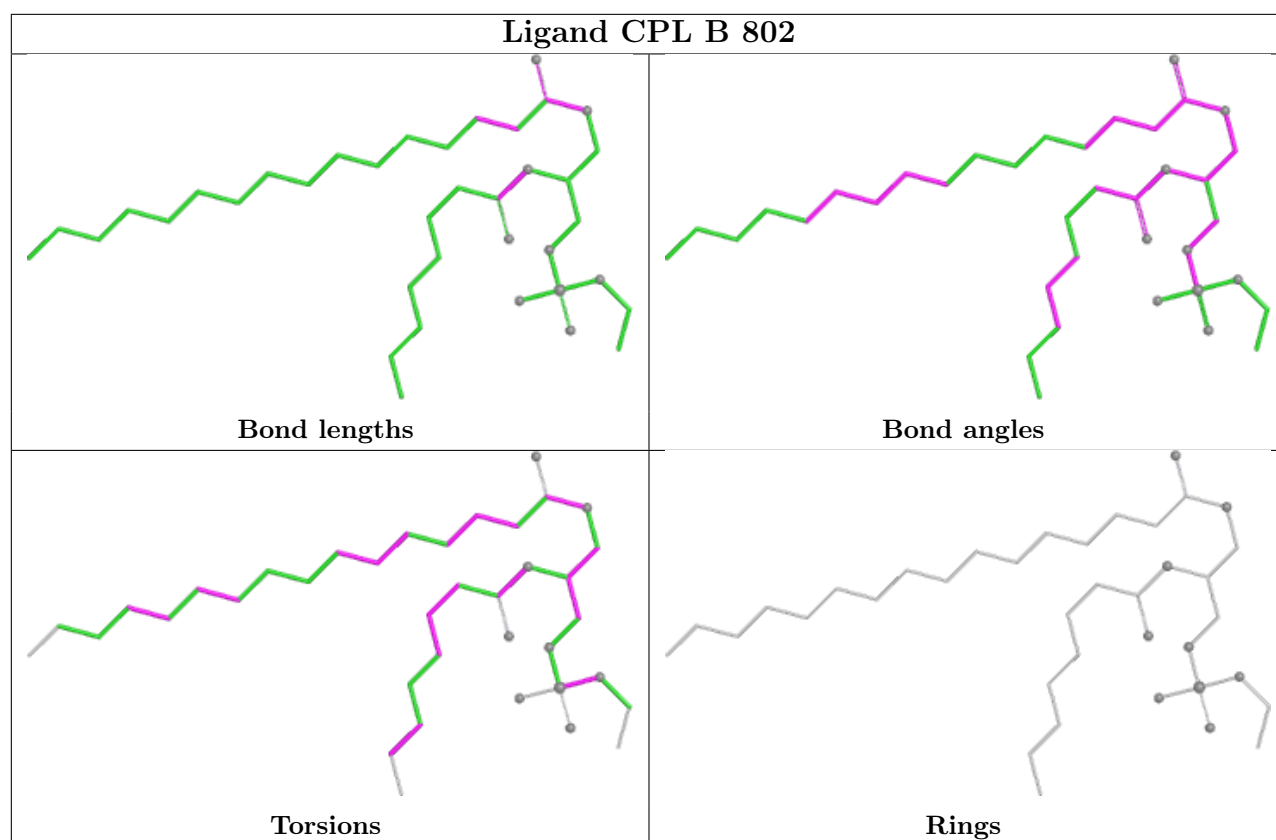


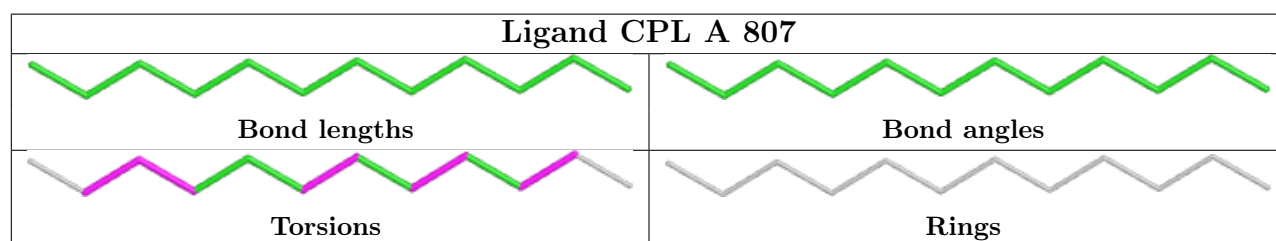
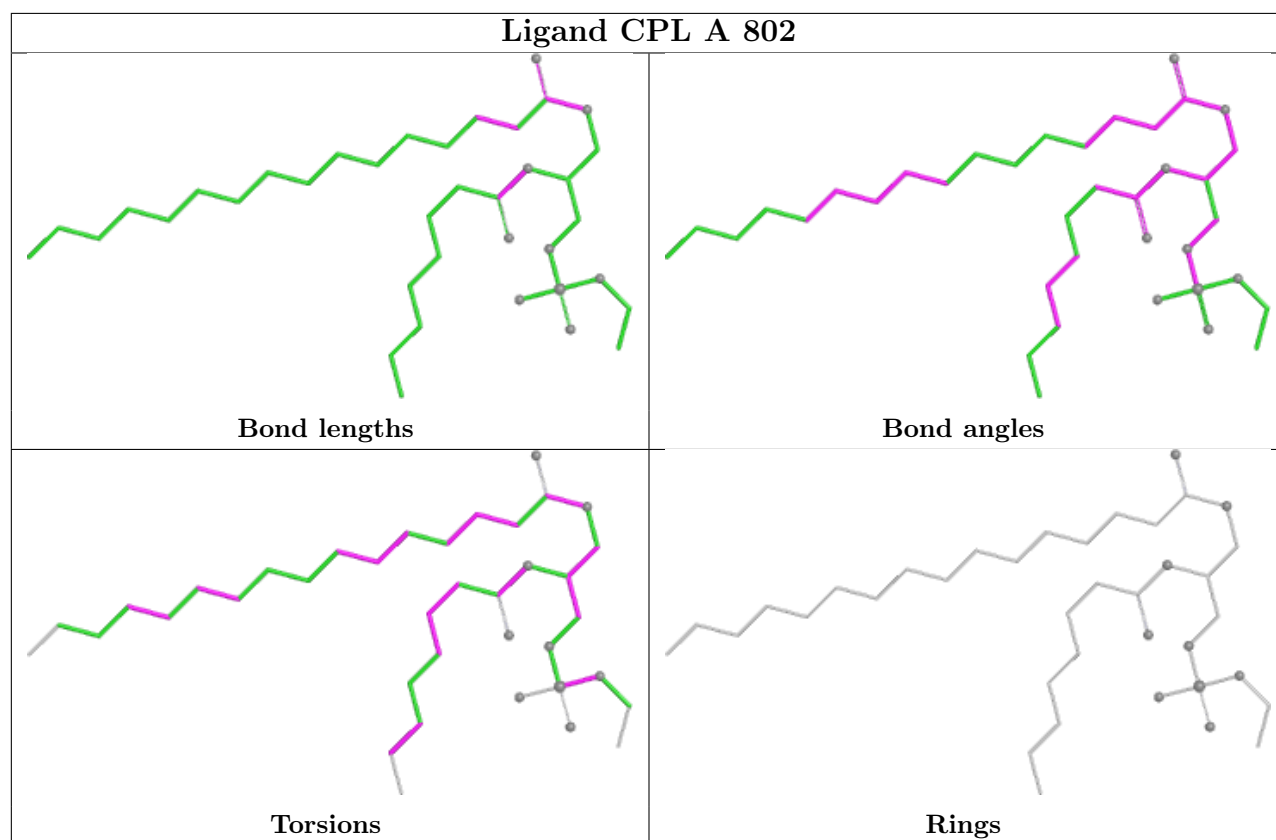
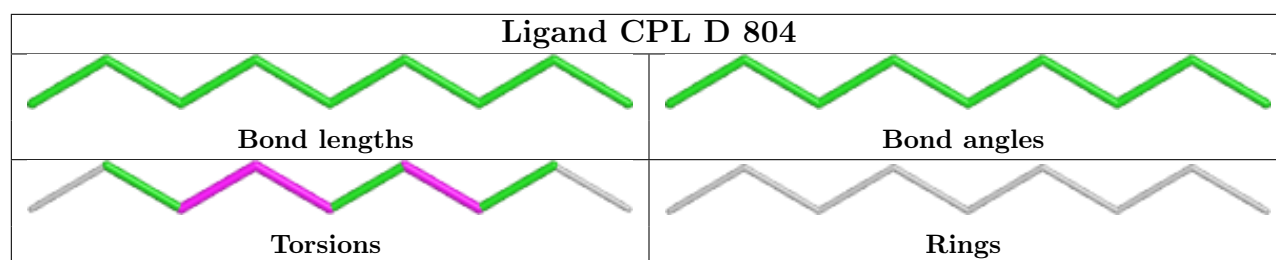


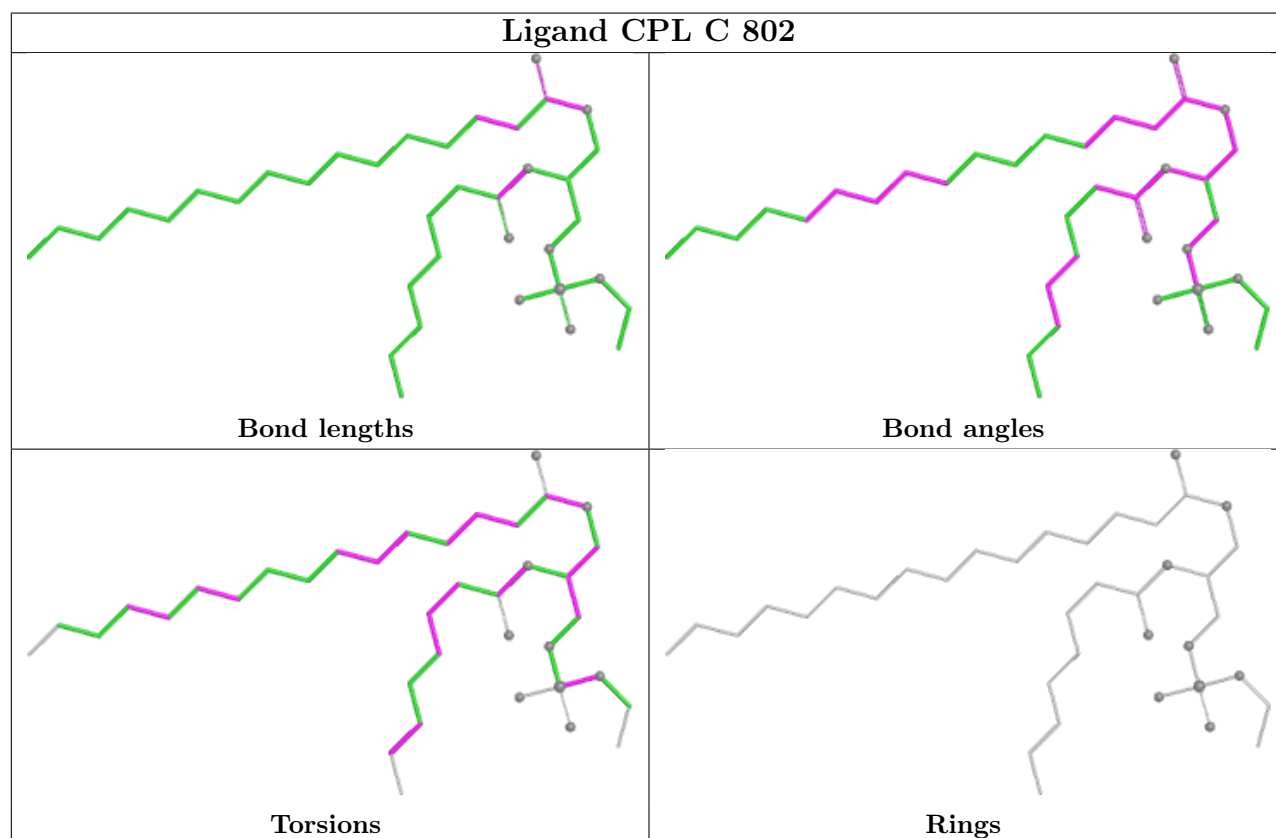
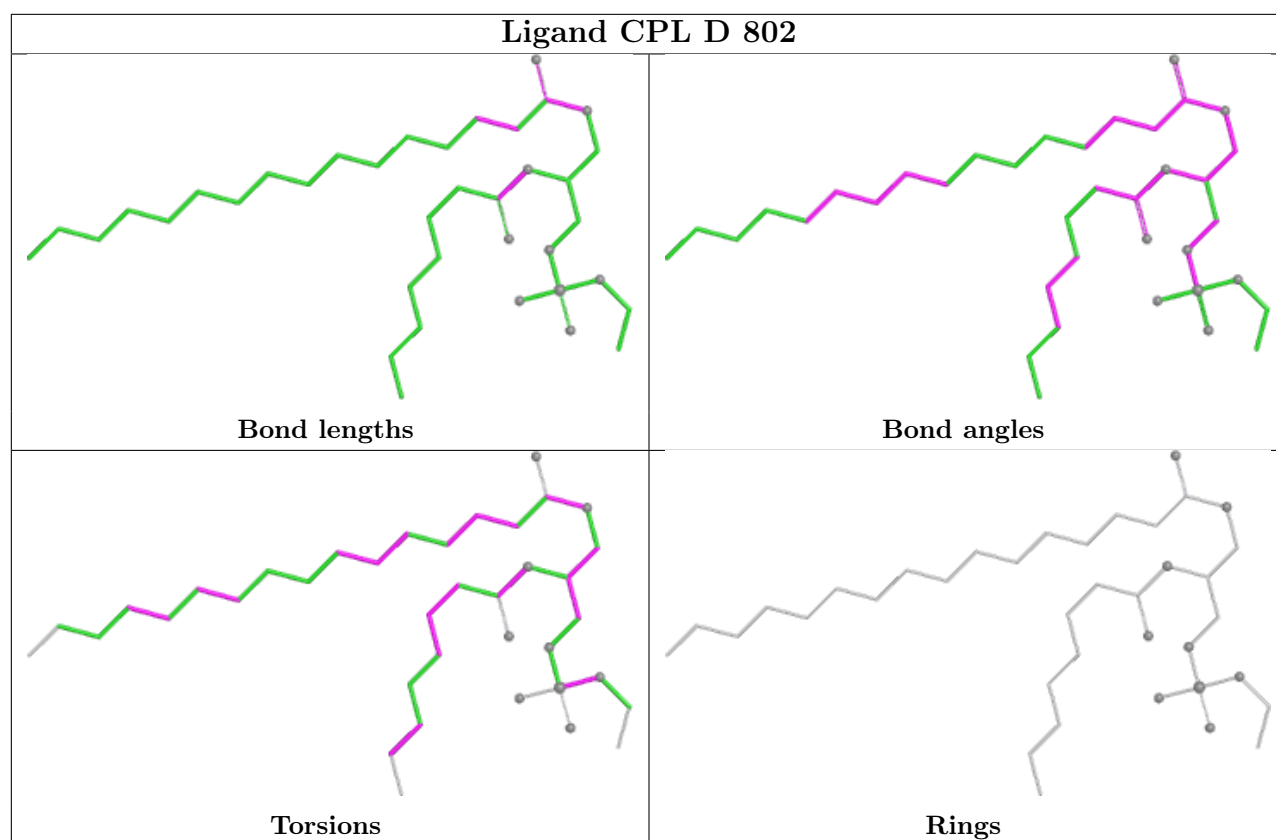


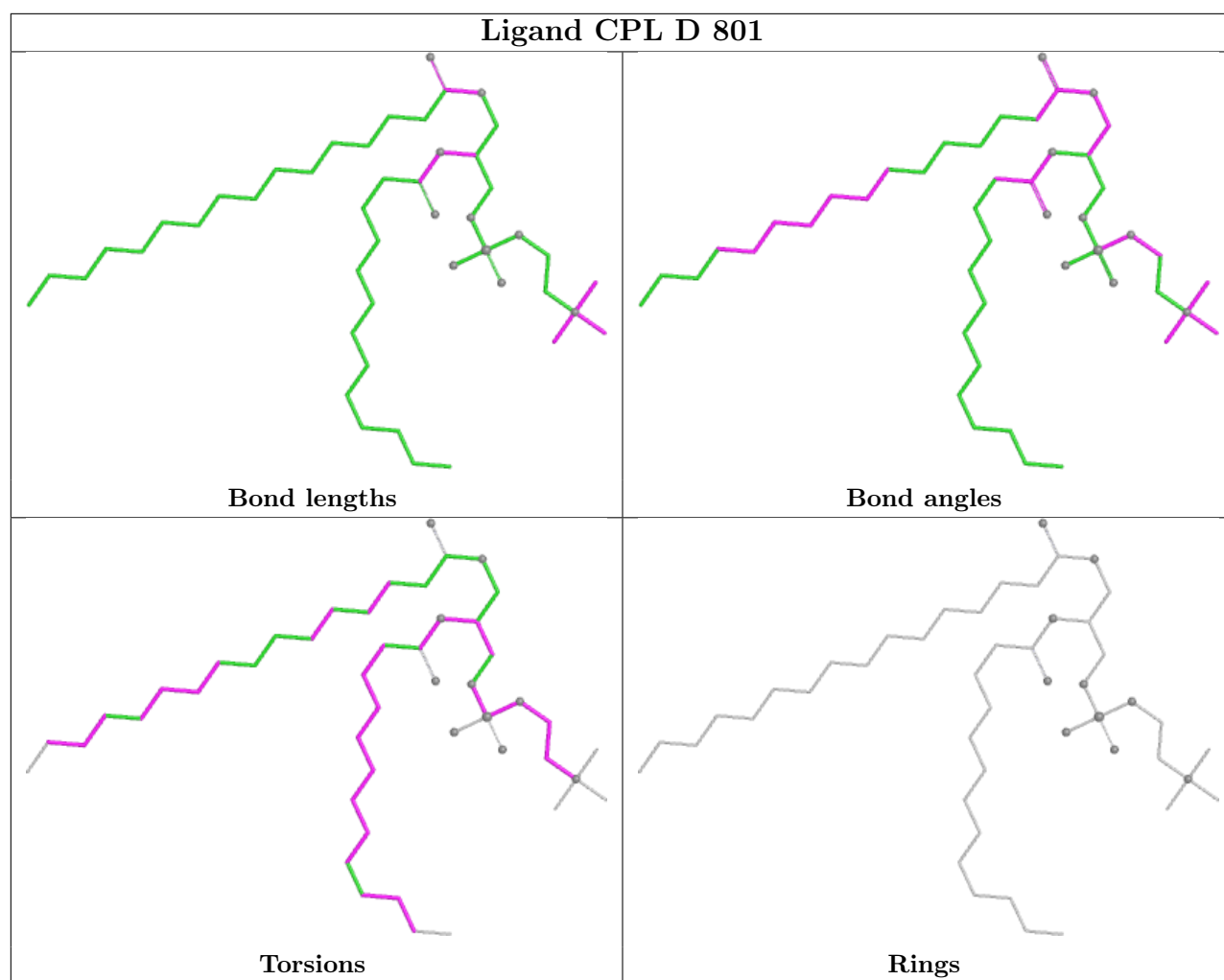


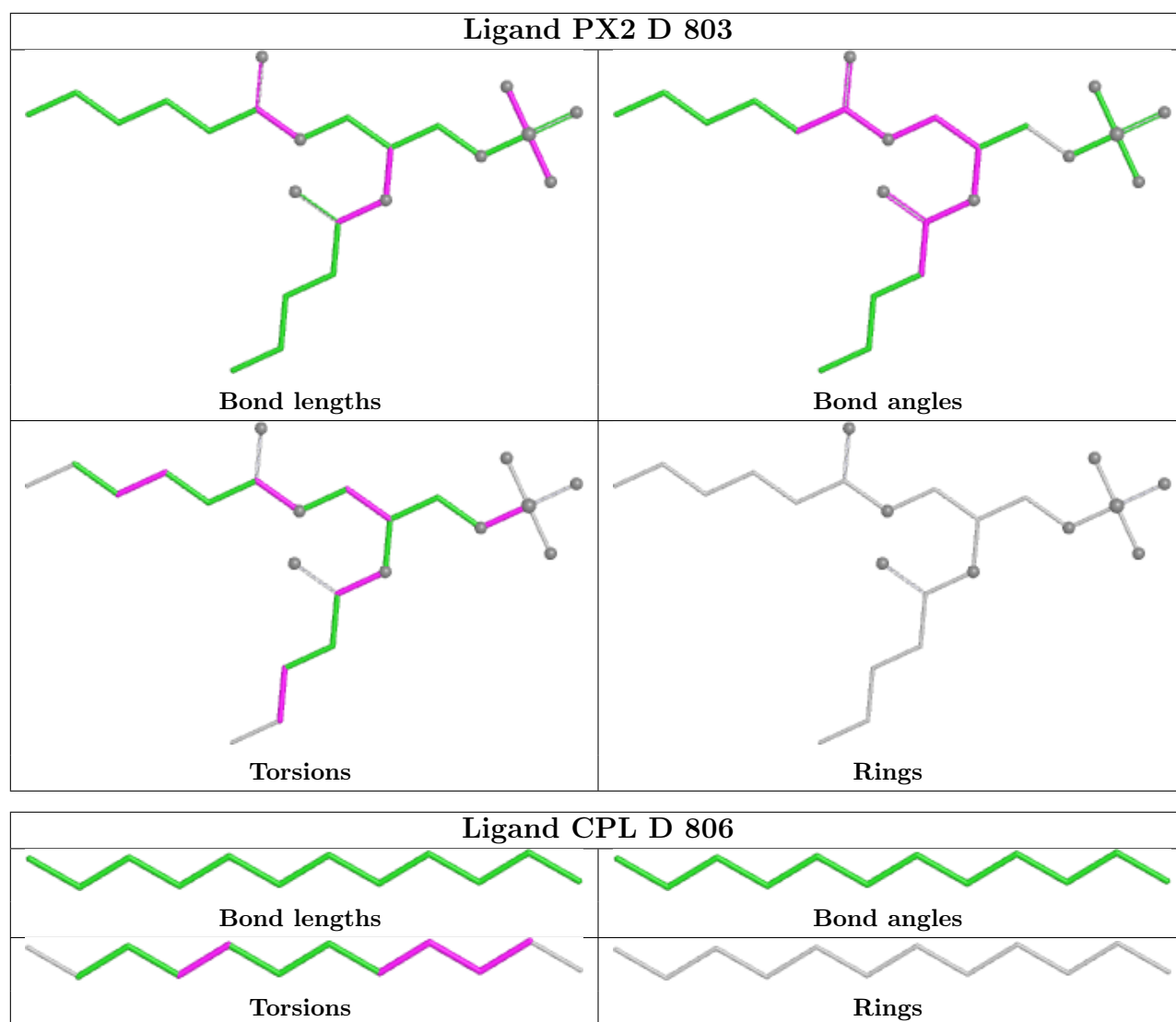


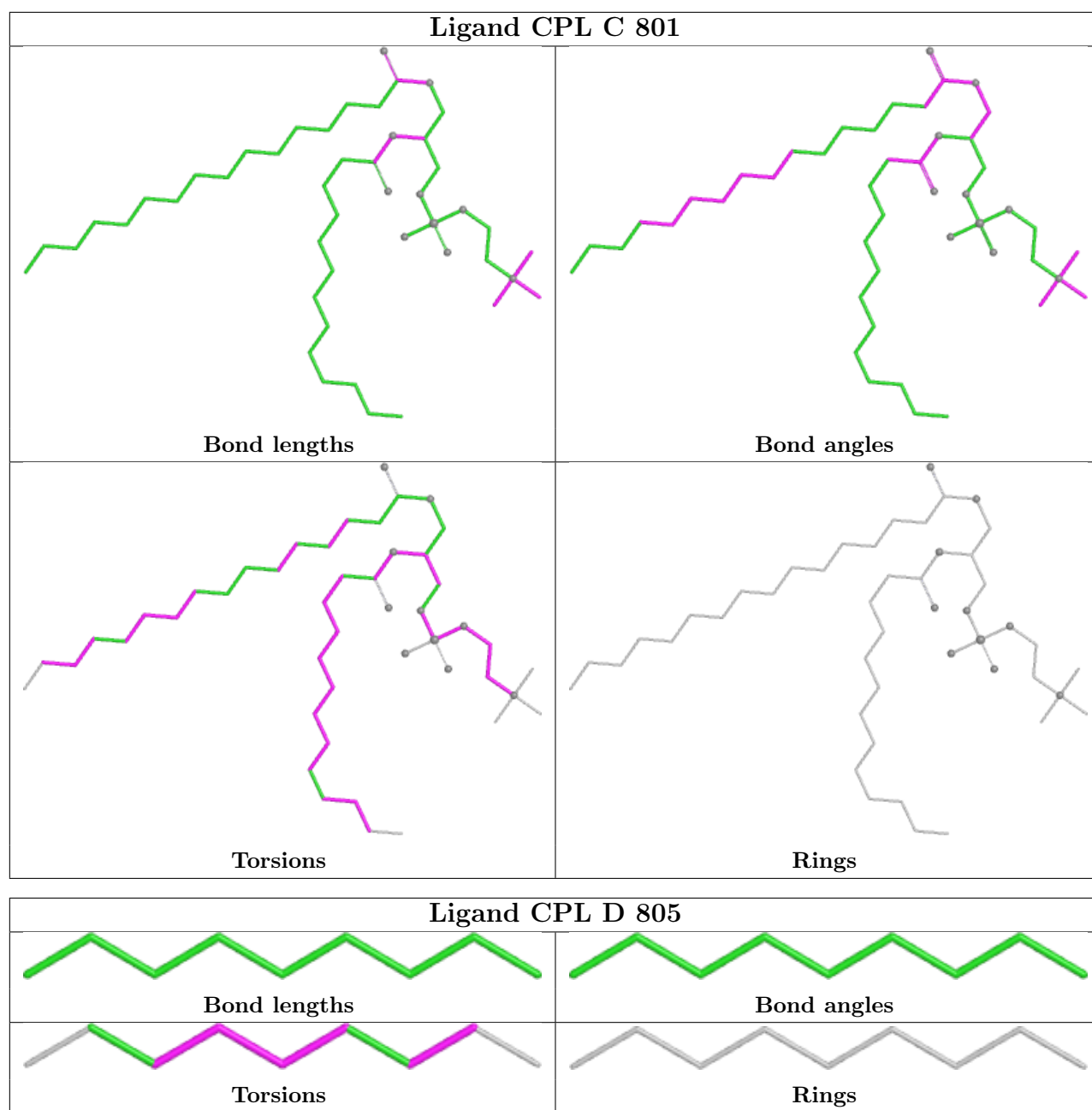


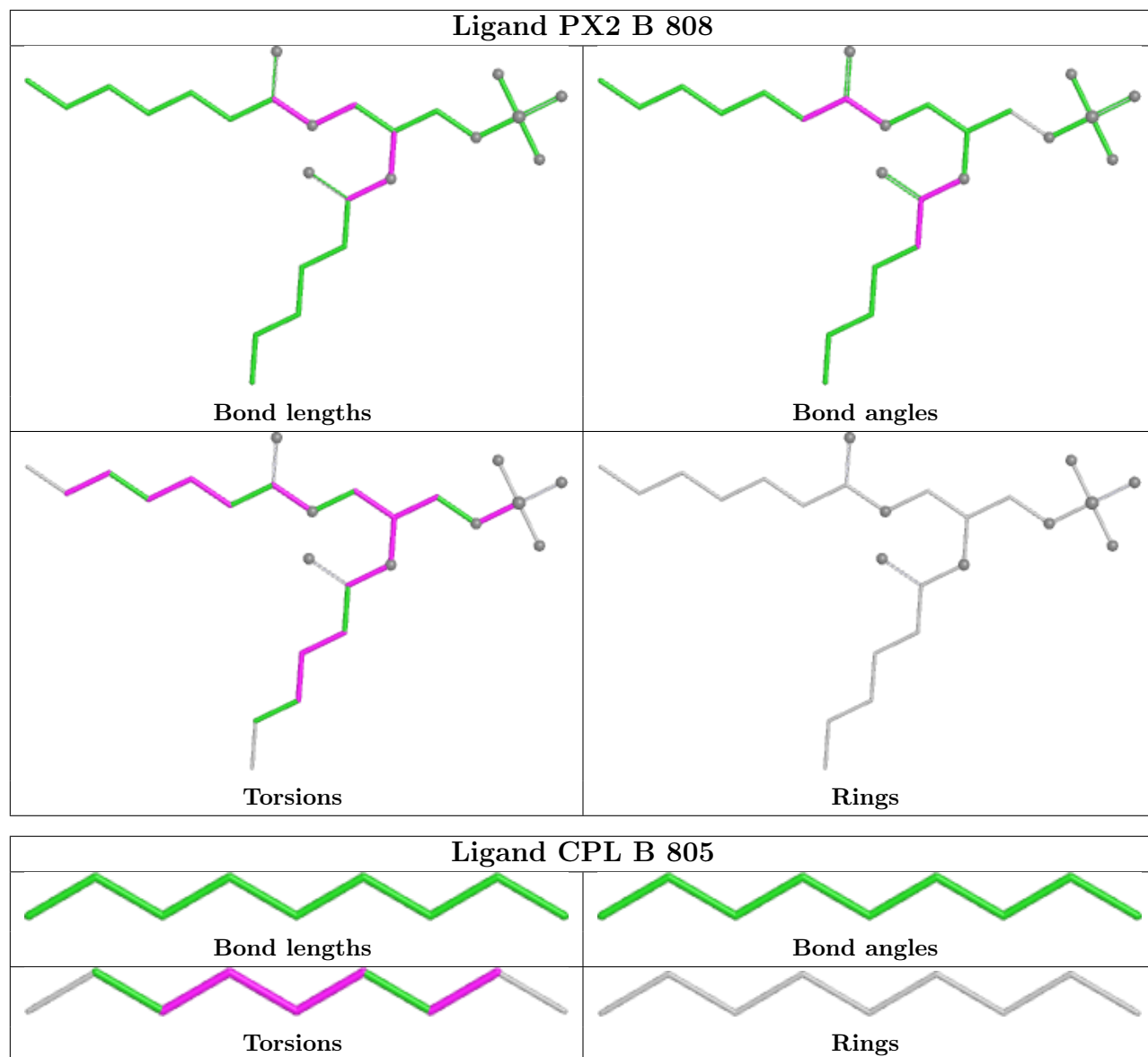


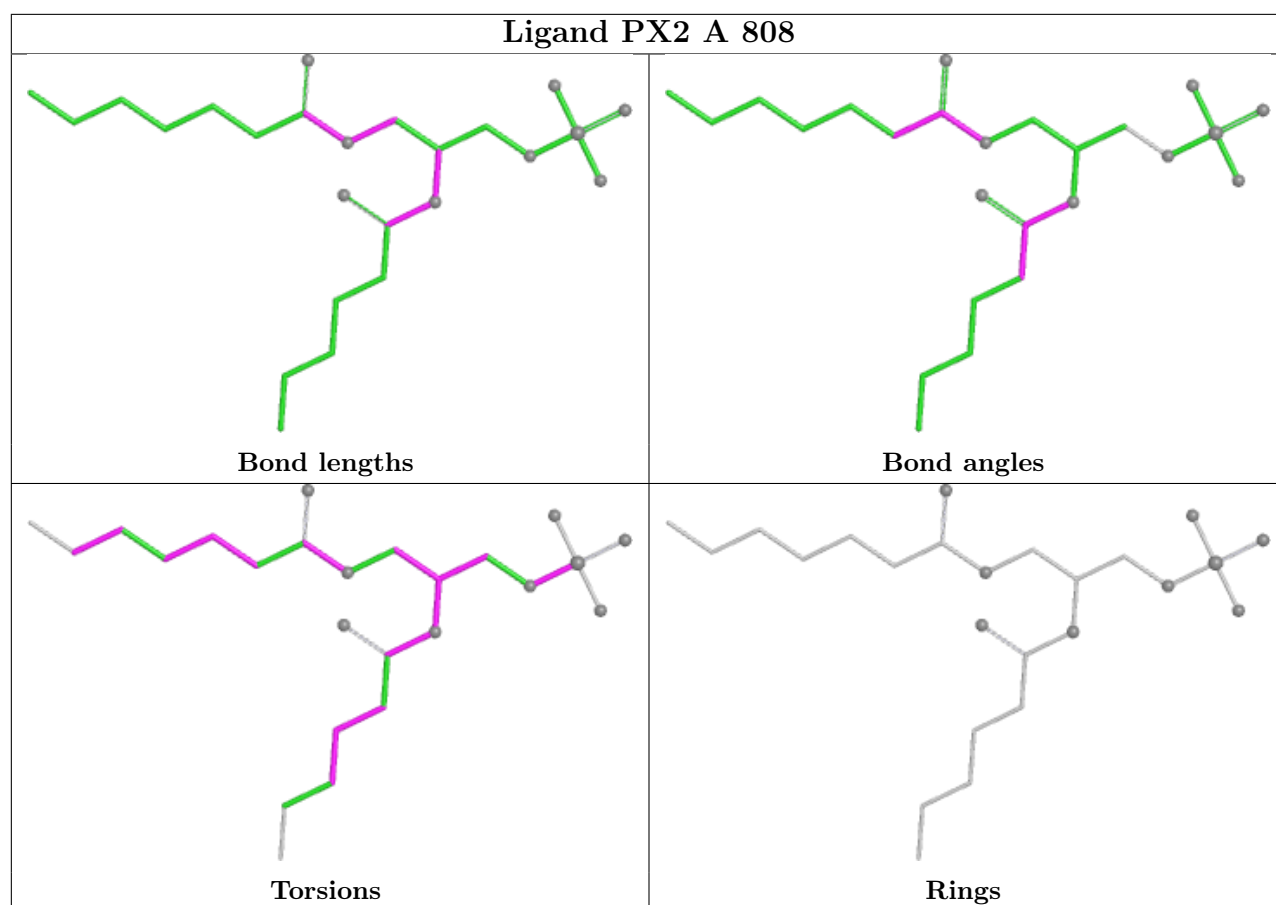


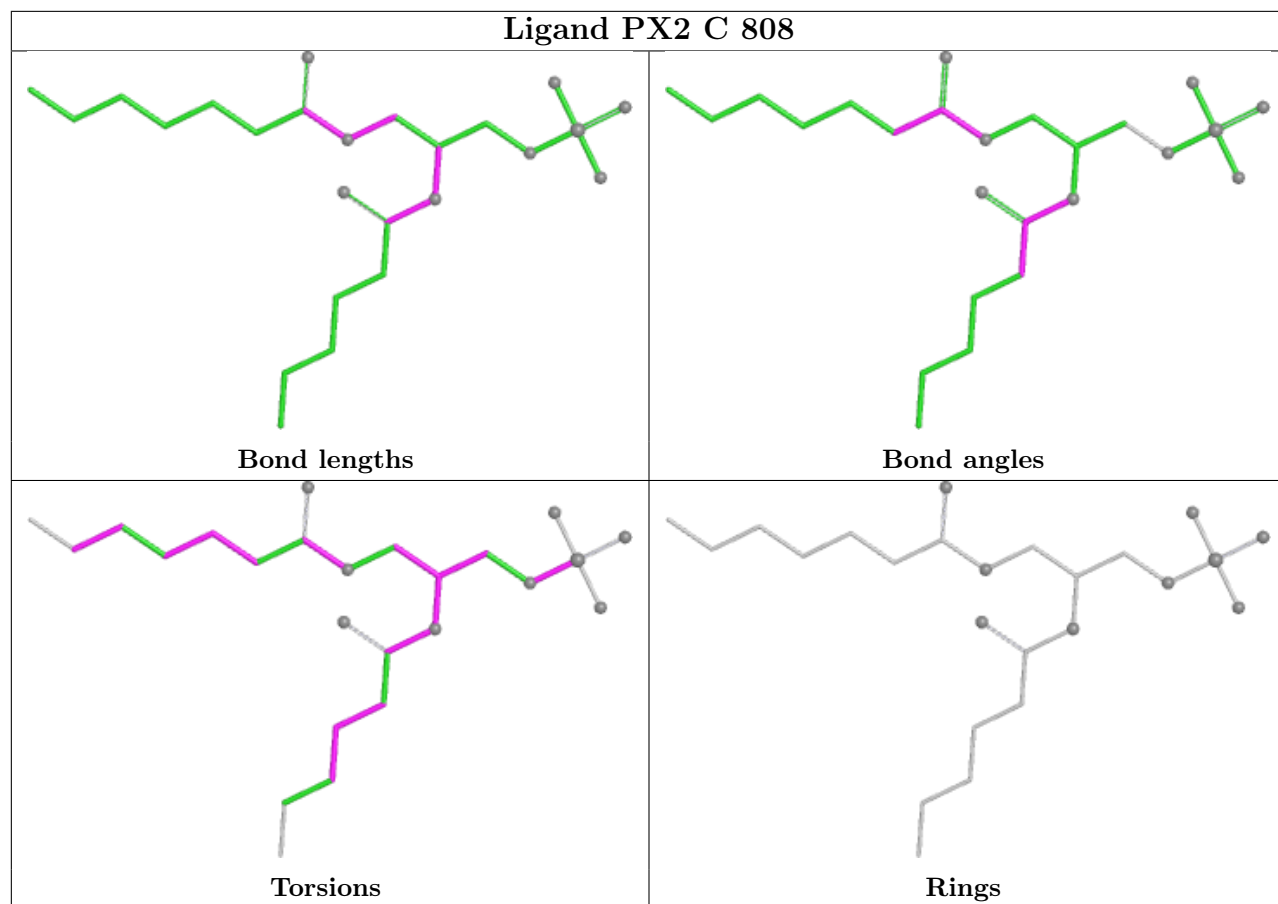


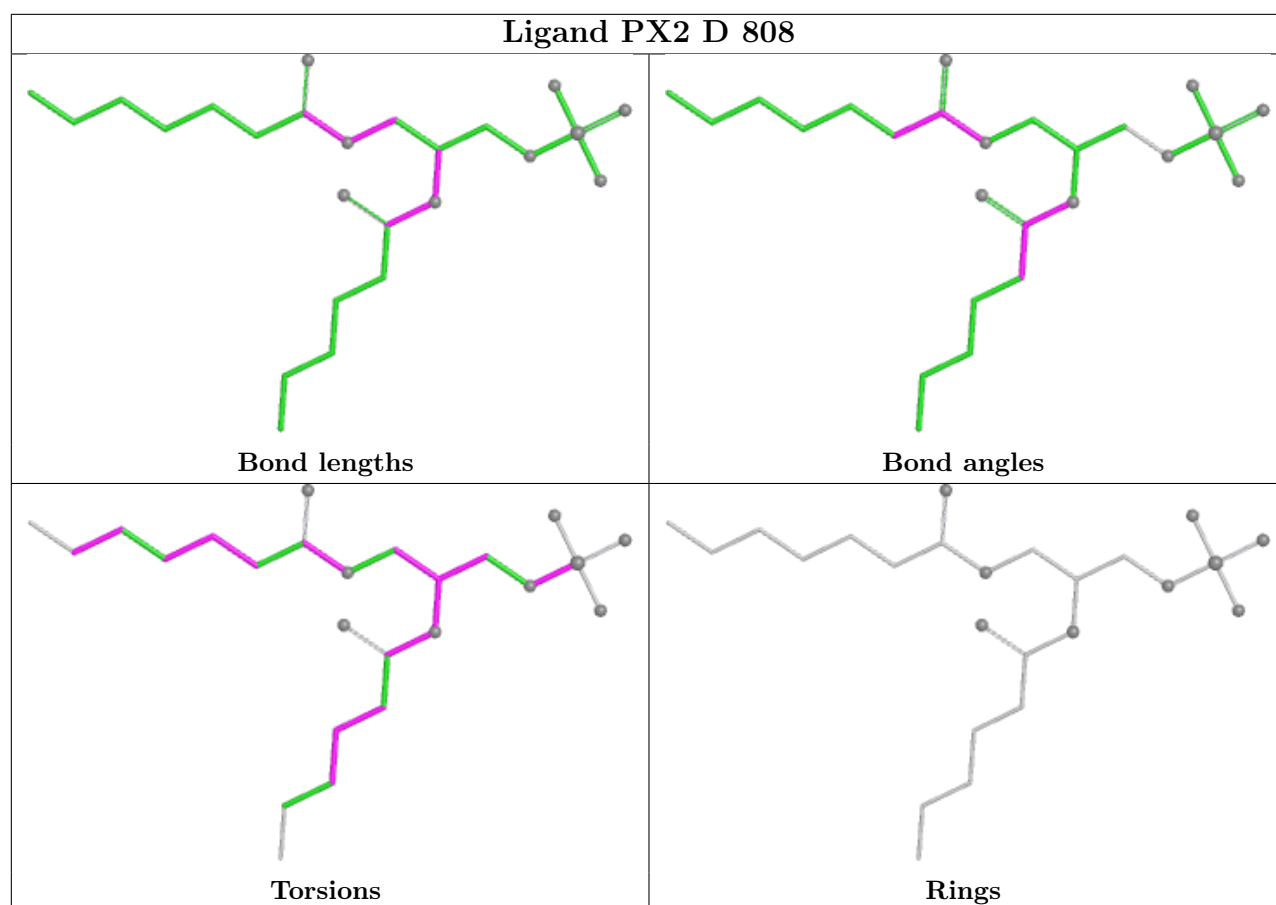












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

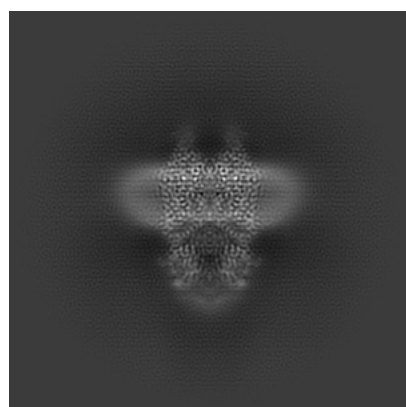
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21649. These allow visual inspection of the internal detail of the map and identification of artifacts.

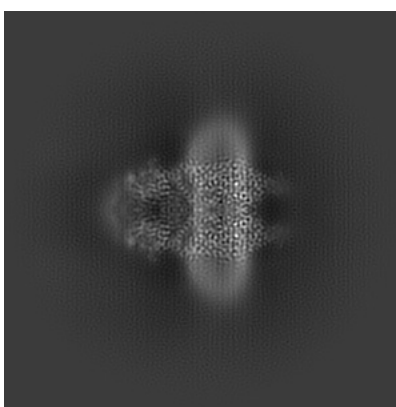
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

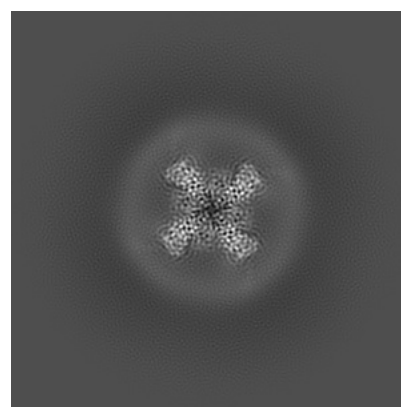
6.1.1 Primary map



X



Y

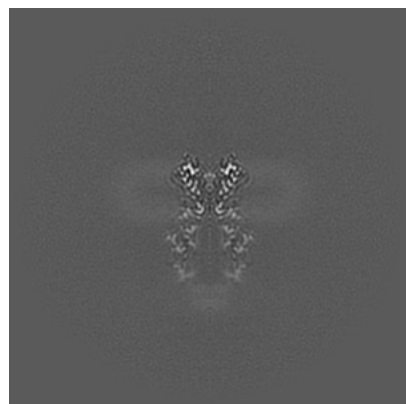


Z

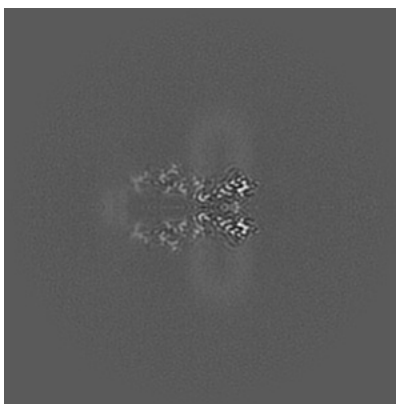
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

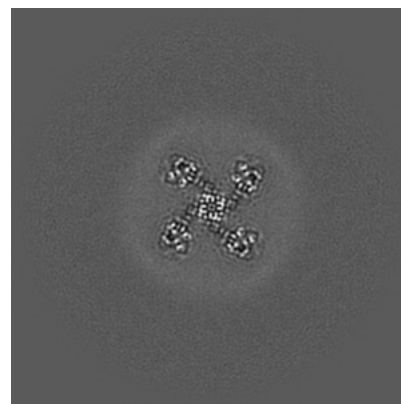
6.2.1 Primary map



X Index: 148



Y Index: 148

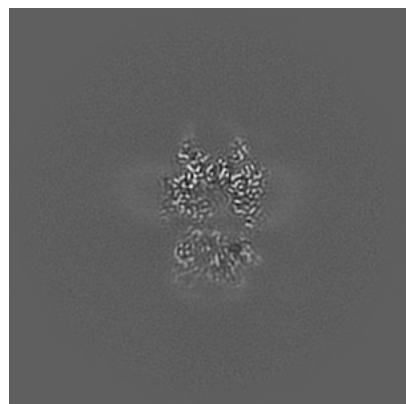


Z Index: 148

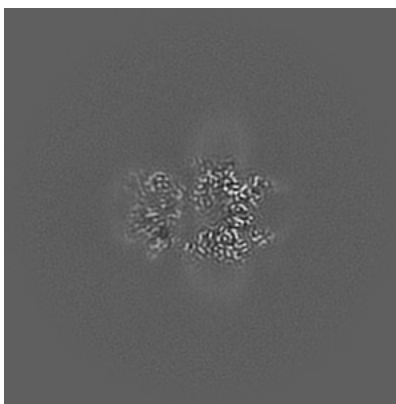
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

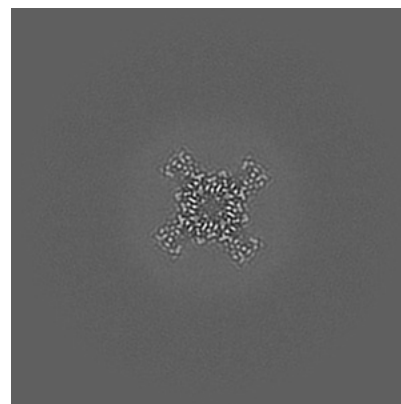
6.3.1 Primary map



X Index: 129



Y Index: 129

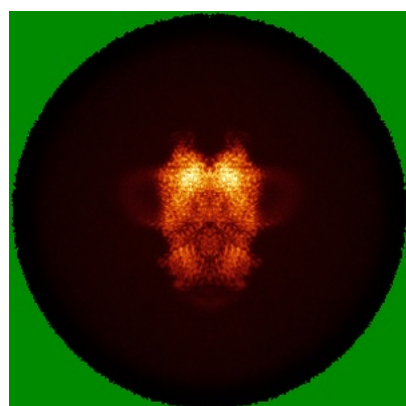


Z Index: 174

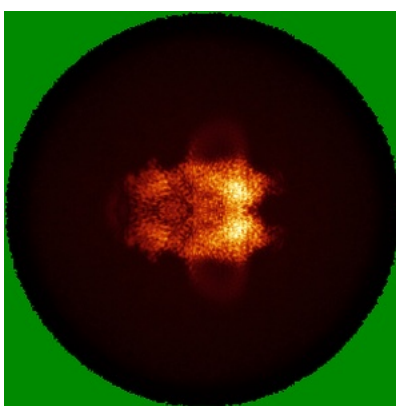
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

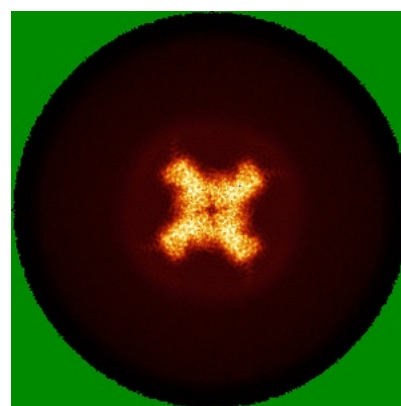
6.4.1 Primary map



X



Y

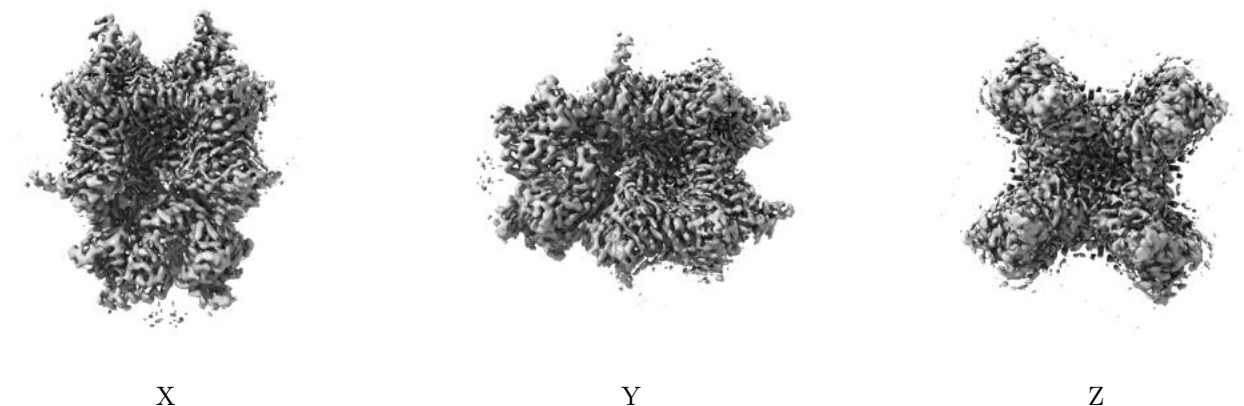


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.574. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

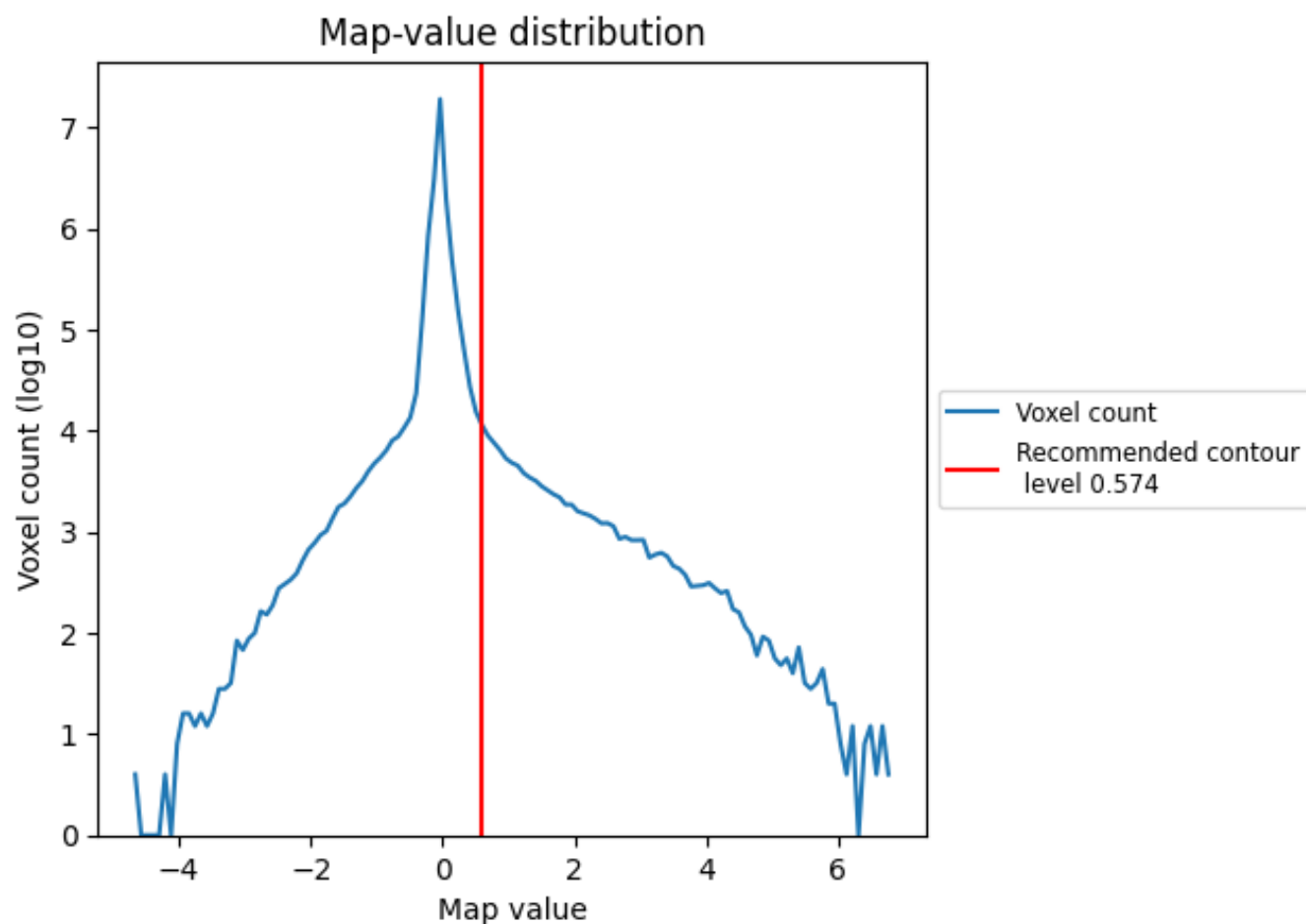
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

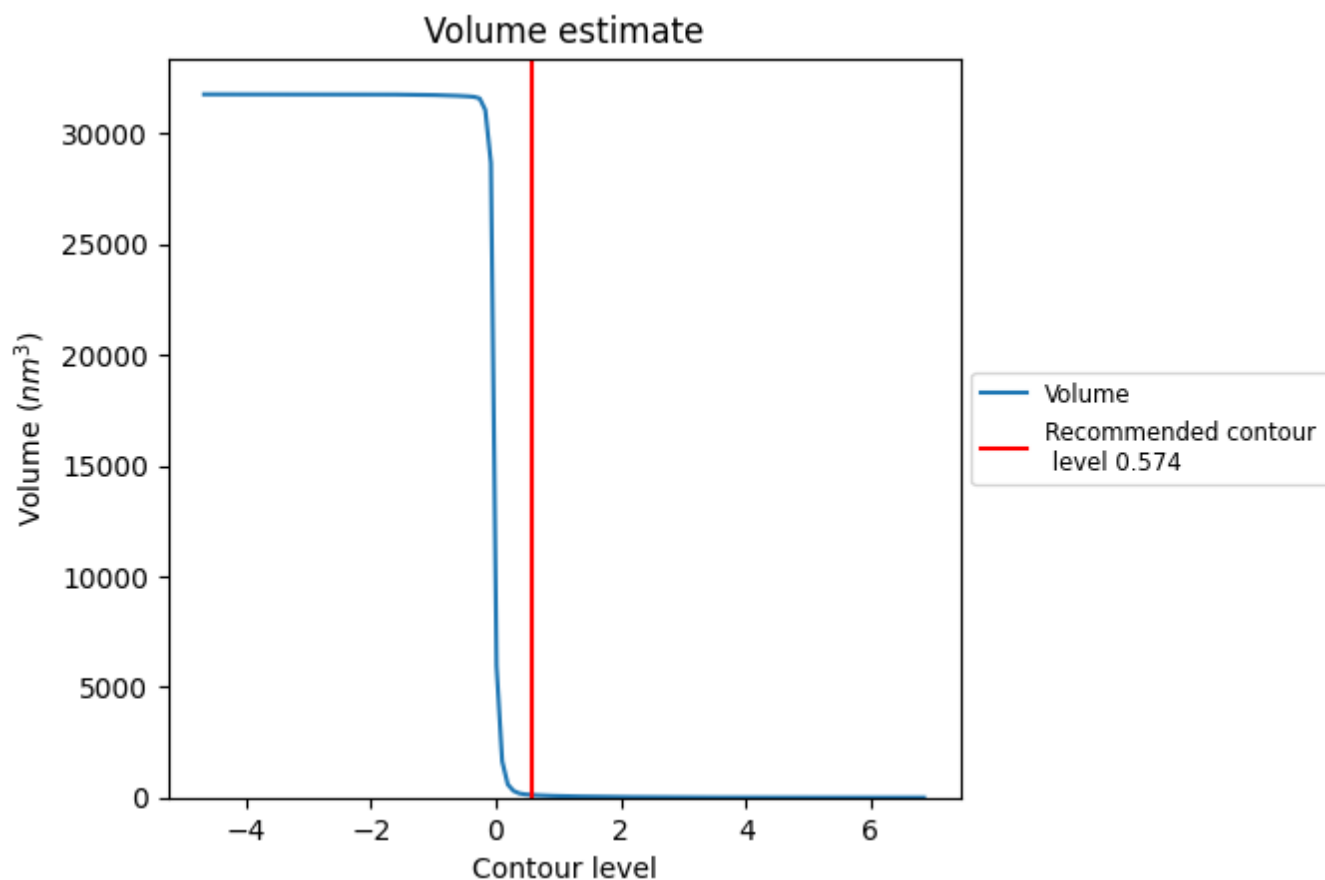
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

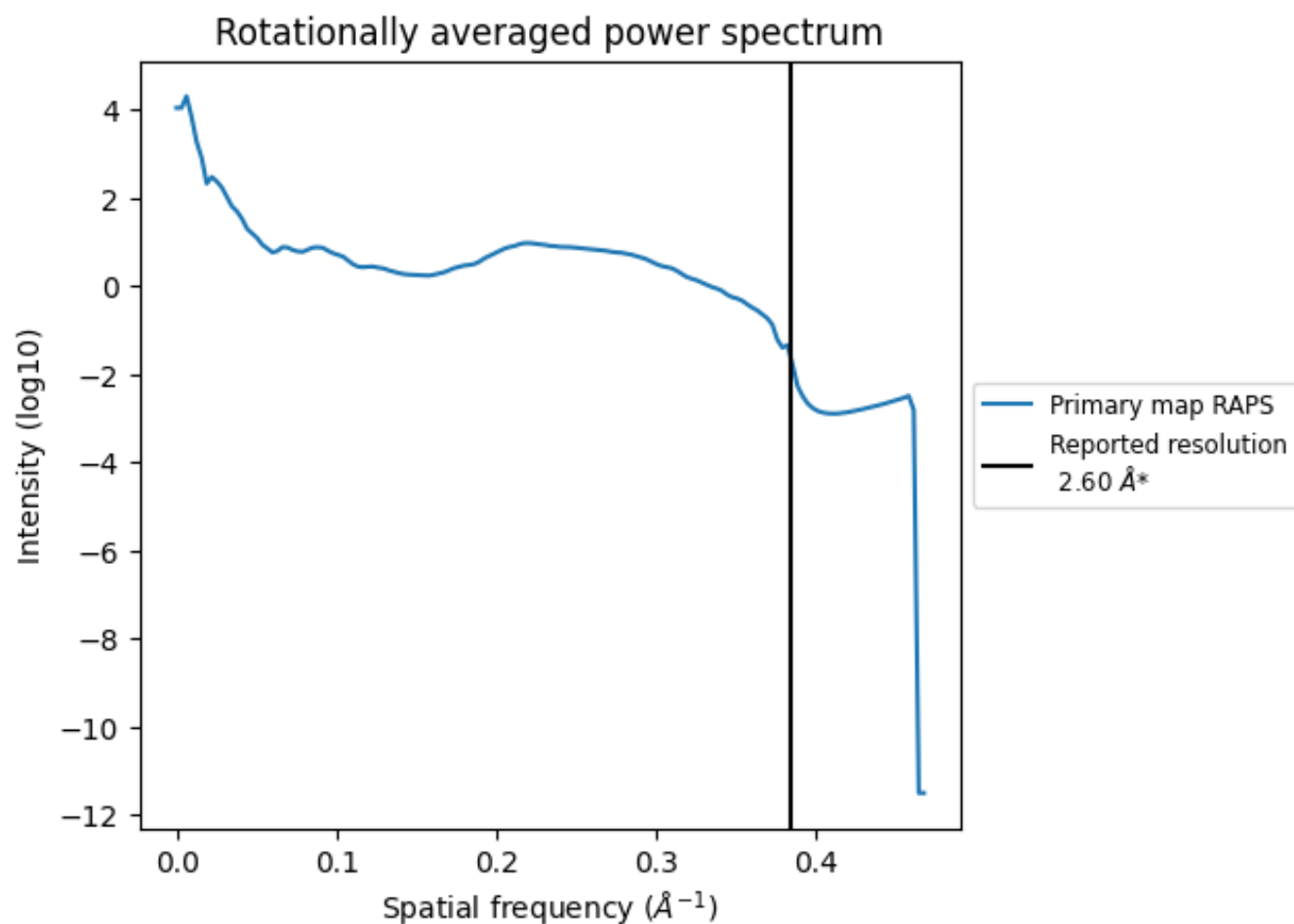
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 119 nm^3 ; this corresponds to an approximate mass of 107 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.385 \AA^{-1}

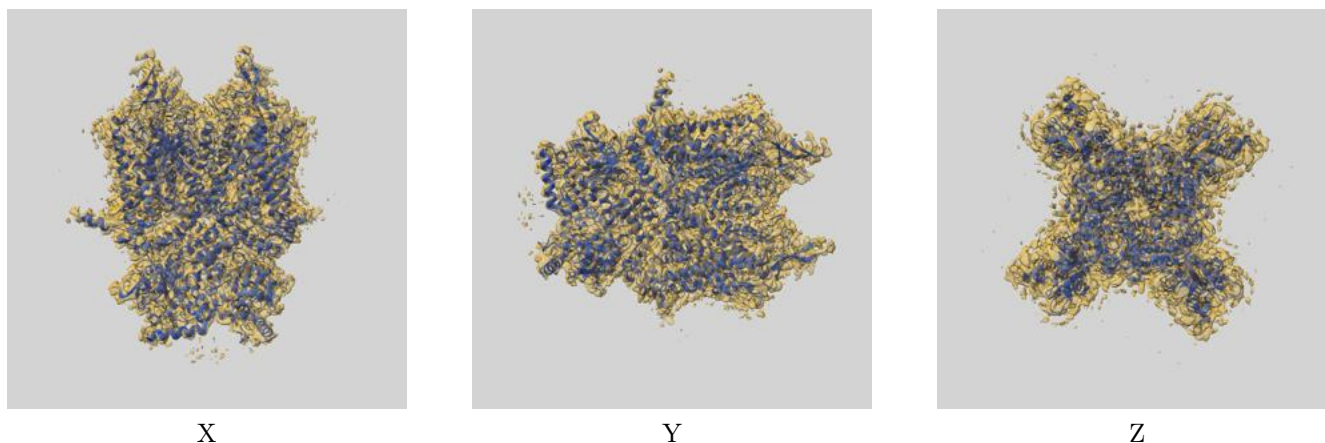
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

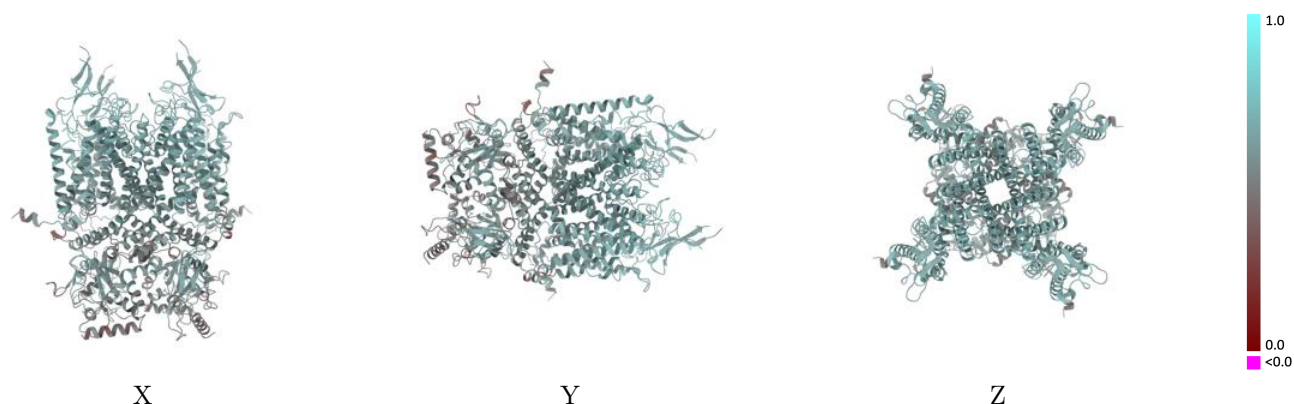
This section contains information regarding the fit between EMDB map EMD-21649 and PDB model 6WEJ. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



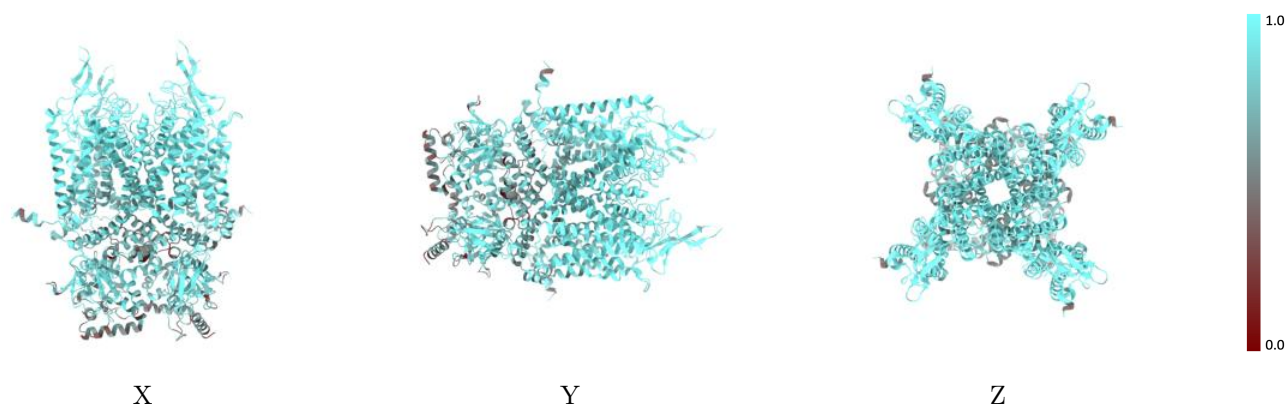
The images above show the 3D surface view of the map at the recommended contour level 0.574 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



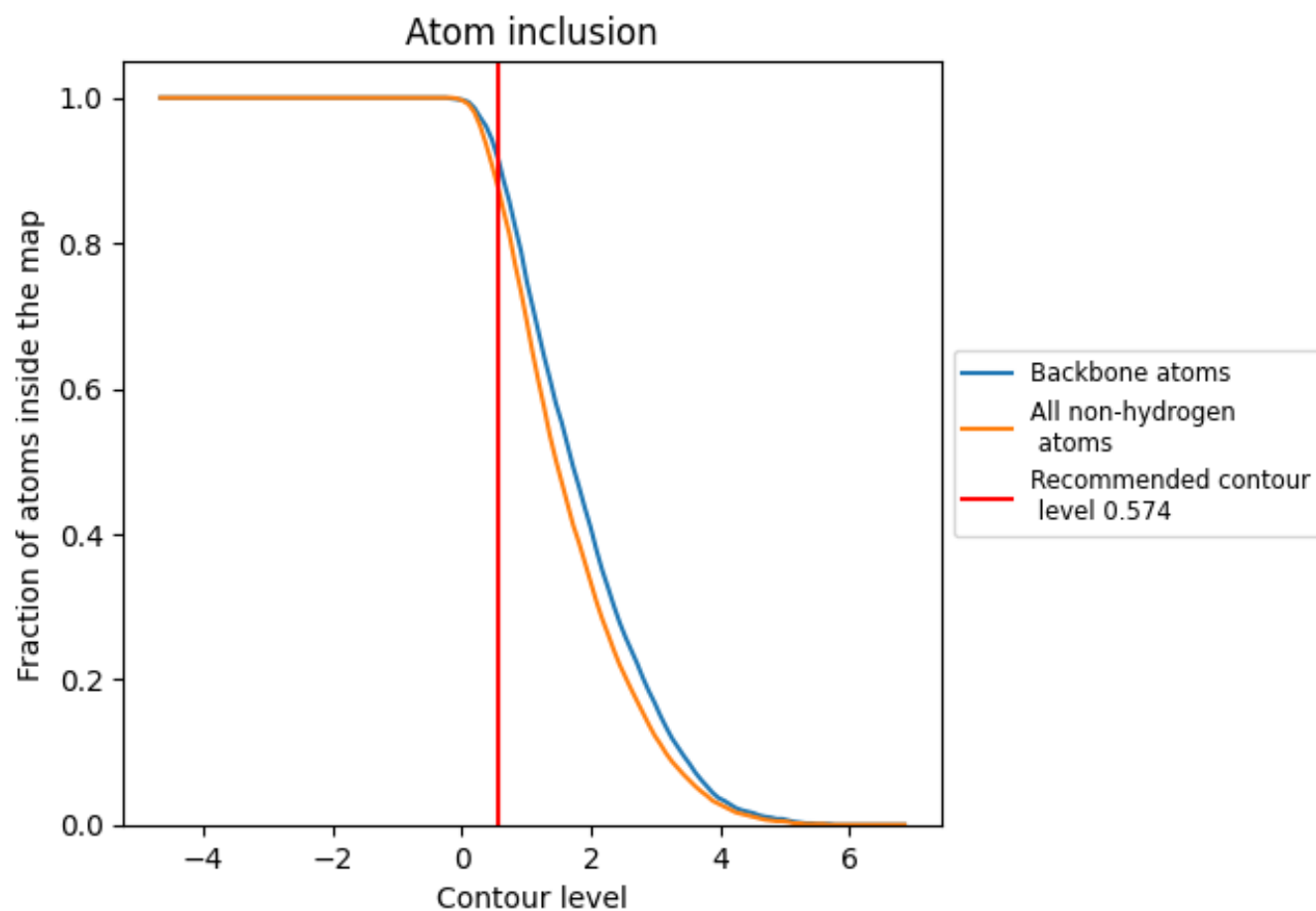
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.574).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.574) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8720	<div></div> 0.5820
A	<div></div> 0.8730	<div></div> 0.5830
B	<div></div> 0.8690	<div></div> 0.5810
C	<div></div> 0.8740	<div></div> 0.5830
D	<div></div> 0.8740	<div></div> 0.5820

