



## wwPDB EM Validation Summary Report ⓘ

May 25, 2024 – 09:29 PM EDT

PDB ID : 7RXG  
EMDB ID : EMD-24730  
Title : afTMEM16 in C18 lipid nanodiscs with MSP1E3 scaffold protein in the presence of Ca<sup>2+</sup>, full dimer  
Authors : Falzone, M.E.; Accardi, A.  
Deposited on : 2021-08-23  
Resolution : 2.28 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ 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.dev92  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

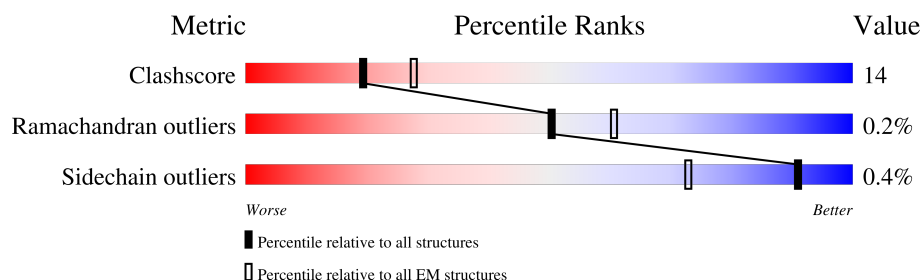
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.28 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	735	<div> <div>7%</div> <div>64%</div> <div>24%</div> <div>12%</div> </div>
1	B	735	<div> <div>7%</div> <div>65%</div> <div>24%</div> <div>12%</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 11380 atoms, of which 96 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.

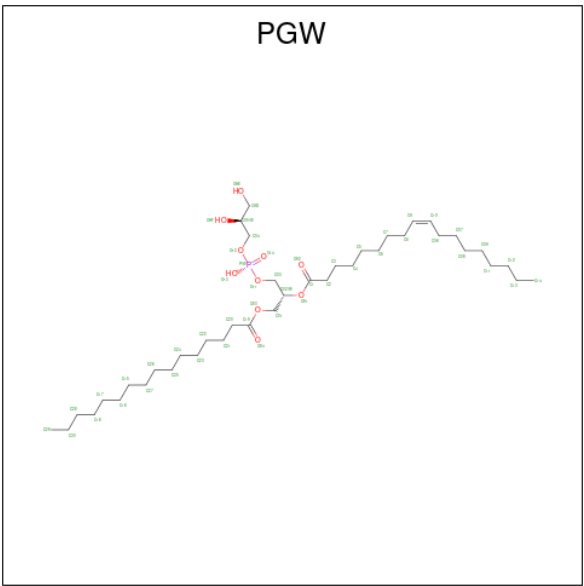
- Molecule 1 is a protein called afTMEM16 lipid scramblase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	650	Total	C	N	O	S	0	0
			5258	3429	883	927	19		
1	A	650	Total	C	N	O	S	0	0
			5258	3429	883	927	19		

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
2	B	2	Total	Ca	0
			2	2	
2	A	2	Total	Ca	0
			2	2	

- Molecule 3 is (1R)-2-{[(S)-{[(2S)-2,3-dihydroxypropyl]oxy}(hydroxy)phosphoryl]oxy}-1-[(hexadecanoyloxy)methyl]ethyl (9Z)-octadec-9-enoate (three-letter code: PGW) (formula: C<sub>40</sub>H<sub>77</sub>O<sub>10</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	B	1	Total	C	O	P	0
			45	34	10	1	
3	B	1	Total	C	O	P	0
			25	16	8	1	
3	B	1	Total	C	O		0
			38	33	5		
3	B	1	Total	C	O	P	0
			31	22	8	1	
3	B	1	Total	C	O	P	0
			25	15	9	1	
3	B	1	Total	C	O	P	0
			32	23	8	1	
3	B	1	Total	C	O	P	0
			27	18	8	1	
3	B	1	Total	C	O	P	0
			28	19	8	1	
3	B	1	Total	C	O	P	0
			29	20	8	1	
3	B	1	Total	C	O	P	0
			44	33	10	1	
3	A	1	Total	C	O	P	0
			34	25	8	1	
3	A	1	Total	C	O	P	0
			44	33	10	1	
3	A	1	Total	C	O	P	0
			45	34	10	1	
3	A	1	Total	C	O	P	0
			25	16	8	1	
3	A	1	Total	C	O	P	0
			34	25	8	1	
3	A	1	Total	C	O		0
			38	33	5		
3	A	1	Total	C	O	P	0
			31	22	8	1	
3	A	1	Total	C	O	P	0
			25	15	9	1	
3	A	1	Total	C	O	P	0
			32	23	8	1	
3	A	1	Total	C	O	P	0
			27	18	8	1	
3	A	1	Total	C	O	P	0
			28	19	8	1	
3	A	1	Total	C	O	P	0
			29	20	8	1	

- Molecule 4 is water.

Mol	Chain	Residues	Atoms			AltConf
4	B	24	Total 72	H 48	O 24	0
4	A	24	Total 72	H 48	O 24	0



GLN GLN	SER	ASP	ASP	ASP	ALA	ASP	GLU	VAL	LYS	GLY	VAL	SER	SER	SER	ILE	PRO	PRO	SER	GLU	GLU	ILE	THR	ARG	GLU	GLY	SER	LEU	GLU	GLN	GLY	THR	ASP	ALA	ALA	ARG	ASP	TRP	SER	SER	LYS	GLN	GLY	THR	ASP	P701	R708	E714	E717	V718	G719	L720	I723	T724	LYS	ALA	LYS	GLY	ASP	GLU	THR	LYS	LYS
	N539	N540	N541	L544	E554	R562	I566	N569	L570	T583	V588	Y589	M590	N593	G594	H595	E596	G597	P598	N599	T603	T604	I605	R606	C607	W608	A609	L610	L611	L612	T613	E618	H619	L620	R625	R641	R642	I645	E646	R647	R653	S660	ALA	GLU																		
	V117	F118	K119	G123	D137	D144	T147	Q150	C151	M152	R153	E154	W155	L161	Y180	L184	Q185	F188	R189	F190	P194	F197	S207	F208	S209	I210	I211	Y212	T213	V214	W219	I224	W227	K228	E231	R237	T240	V243	R250																							
	F253	K254	K257	E258	I259	R260	D261	E262	S263	T264	G265	E266	V267	R268	A273	R276	M277	V284	P285	A291	L294	F302	A303	I304	E305	I306	E310	N313	G314	P315	L316	K317	G318	Y319	L320	V321	F322	I323	P324	V328	I332	T341	K345	L346	N347	N351																
	Y352	E353	L362	V368	V369	N370	F371	I372	Y375	V386	P387	F388	A389	I392	V393	P394	H400	L401	T402	V403	R404	P405	F406	V407	S408	K409	E410	H411	A412	I413	K414	A415	R416	T417	E418	F419	S420	I421	D424	R425	K428	Q438	L444	V448	P449	F450	V451	K452	Q453													
	R454	V455	F456	R457	E458	Y459	K460	E461	Y462	T463	LYS	LYS	GLN	HIS	ALA	LYS	ALA	GLU	PRO	GLY	ASN	GLY	ALA	GLY	GLY	GLU	LYS	THR	VAL	D487	E488	L494	T495	R496	V497	R498	W499	E500	A501	D505	D511	L512	R513	C516	I517	Q518	F519	G520	S526	F536												

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	994187	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	42.8227	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.139	Depositor
Minimum map value	-0.072	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0169	Depositor
Map size (Å)	271.3728, 271.3728, 271.3728	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7067, 0.7067, 0.7067	Depositor



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, PGW

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	0.31	0/5398	0.43	0/7340
1	B	0.32	0/5398	0.43	0/7340
All	All	0.31	0/10796	0.43	0/14680

There are no bond length outliers.

There are no bond angle outliers.

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	5258	0	5207	165	0
1	B	5258	0	5207	157	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	392	0	462	39	0
3	B	324	0	380	27	0
4	A	24	48	0	4	0
4	B	24	48	0	3	0
All	All	11284	96	11256	316	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 14.

The worst 5 of 316 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:33:ILE:CD1	1:A:723:ILE:HD12	1.71	1.20
1:B:33:ILE:HD13	1:A:723:ILE:HD12	1.12	1.05
1:B:33:ILE:HD13	1:A:723:ILE:CD1	1.85	1.05
1:A:719:GLY:O	1:A:723:ILE:HG13	1.67	0.94
1:B:604:THR:HG22	3:B:803:PGW:HAD	1.56	0.87

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	644/735 (88%)	627 (97%)	16 (2%)	1 (0%)	47	57
1	B	644/735 (88%)	627 (97%)	16 (2%)	1 (0%)	47	57
All	All	1288/1470 (88%)	1254 (97%)	32 (2%)	2 (0%)	50	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	420	SER
1	A	420	SER

### 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 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	560/646 (87%)	558 (100%)	2 (0%)	91	95
1	B	560/646 (87%)	558 (100%)	2 (0%)	91	95
All	All	1120/1292 (87%)	1116 (100%)	4 (0%)	91	95

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	417	THR
1	B	505	ASP
1	A	417	THR
1	A	505	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	370	ASN
1	A	453	GLN
1	A	593	ASN
1	A	438	GLN
1	B	593	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](#)

Of 26 ligands modelled in this entry, 4 are monoatomic - leaving 22 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	PGW	B	812	-	43,43,50	1.01	4 (9%)	46,49,56	1.09	2 (4%)
3	PGW	B	805	-	37,37,50	0.98	3 (8%)	39,39,56	1.19	2 (5%)
3	PGW	A	1111	-	31,31,50	1.16	4 (12%)	35,36,56	1.20	2 (5%)
3	PGW	B	807	-	24,24,50	1.06	1 (4%)	26,29,56	1.03	1 (3%)
3	PGW	A	1102	-	43,43,50	1.00	4 (9%)	46,49,56	1.09	2 (4%)
3	PGW	A	1101	-	33,33,50	1.14	4 (12%)	37,38,56	1.18	2 (5%)
3	PGW	A	1107	-	33,33,50	1.14	4 (12%)	37,38,56	1.18	2 (5%)
3	PGW	B	811	-	28,28,50	1.25	5 (17%)	32,33,56	1.23	2 (6%)
3	PGW	A	1113	-	27,27,50	1.24	5 (18%)	31,32,56	1.23	2 (6%)
3	PGW	A	1108	-	37,37,50	0.98	3 (8%)	39,39,56	1.20	2 (5%)
3	PGW	A	1114	-	28,28,50	1.25	5 (17%)	32,33,56	1.23	2 (6%)
3	PGW	B	803	-	44,44,50	0.98	3 (6%)	46,50,56	1.12	2 (4%)
3	PGW	B	808	-	31,31,50	1.16	4 (12%)	35,36,56	1.20	2 (5%)
3	PGW	A	1109	-	30,30,50	1.22	4 (13%)	34,35,56	1.20	2 (5%)
3	PGW	A	1106	-	24,24,50	1.32	4 (16%)	28,29,56	1.31	3 (10%)
3	PGW	A	1105	-	44,44,50	0.98	3 (6%)	46,50,56	1.12	2 (4%)
3	PGW	A	1110	-	24,24,50	1.06	1 (4%)	26,29,56	1.03	1 (3%)
3	PGW	B	810	-	27,27,50	1.24	5 (18%)	31,32,56	1.23	2 (6%)
3	PGW	A	1112	-	26,26,50	1.29	4 (15%)	30,31,56	1.28	2 (6%)
3	PGW	B	806	-	30,30,50	1.22	4 (13%)	34,35,56	1.20	2 (5%)
3	PGW	B	804	-	24,24,50	1.31	4 (16%)	28,29,56	1.30	3 (10%)
3	PGW	B	809	-	26,26,50	1.29	4 (15%)	30,31,56	1.28	2 (6%)

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	PGW	B	812	-	-	23/48/48/55	-
3	PGW	B	805	-	-	14/39/39/55	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PGW	A	1111	-	-	17/33/33/55	-
3	PGW	B	807	-	-	12/28/28/55	-
3	PGW	A	1102	-	-	23/48/48/55	-
3	PGW	A	1101	-	-	16/35/35/55	-
3	PGW	A	1107	-	-	16/35/35/55	-
3	PGW	B	811	-	-	18/30/30/55	-
3	PGW	A	1113	-	-	17/29/29/55	-
3	PGW	A	1108	-	-	14/39/39/55	-
3	PGW	A	1114	-	-	18/30/30/55	-
3	PGW	B	803	-	-	23/49/49/55	-
3	PGW	B	808	-	-	17/33/33/55	-
3	PGW	A	1109	-	-	10/32/32/55	-
3	PGW	A	1106	-	-	11/26/26/55	-
3	PGW	A	1105	-	-	23/49/49/55	-
3	PGW	A	1110	-	-	12/28/28/55	-
3	PGW	B	810	-	-	17/29/29/55	-
3	PGW	A	1112	-	-	16/28/28/55	-
3	PGW	B	806	-	-	10/32/32/55	-
3	PGW	B	804	-	-	11/26/26/55	-
3	PGW	B	809	-	-	16/28/28/55	-

The worst 5 of 82 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	809	PGW	O01-C1	3.09	1.43	1.34
3	A	1112	PGW	O01-C1	3.09	1.43	1.34
3	A	1109	PGW	O01-C1	2.97	1.42	1.34
3	B	806	PGW	O01-C1	2.95	1.42	1.34
3	A	1111	PGW	O01-C1	2.95	1.42	1.34

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	809	PGW	O01-C1-C2	4.18	120.51	111.50
3	A	1112	PGW	O01-C1-C2	4.18	120.50	111.50
3	A	1106	PGW	O01-C1-C2	4.16	120.46	111.50
3	B	804	PGW	O01-C1-C2	4.14	120.43	111.50
3	A	1108	PGW	O01-C1-C2	4.13	120.40	111.50

There are no chirality outliers.

5 of 354 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	803	PGW	C04-C05-CAD-OAE
3	B	803	PGW	O03-C01-C02-O01
3	B	804	PGW	C03-O11-P-O12
3	B	804	PGW	C03-O11-P-O14
3	B	805	PGW	C01-C02-C03-O11

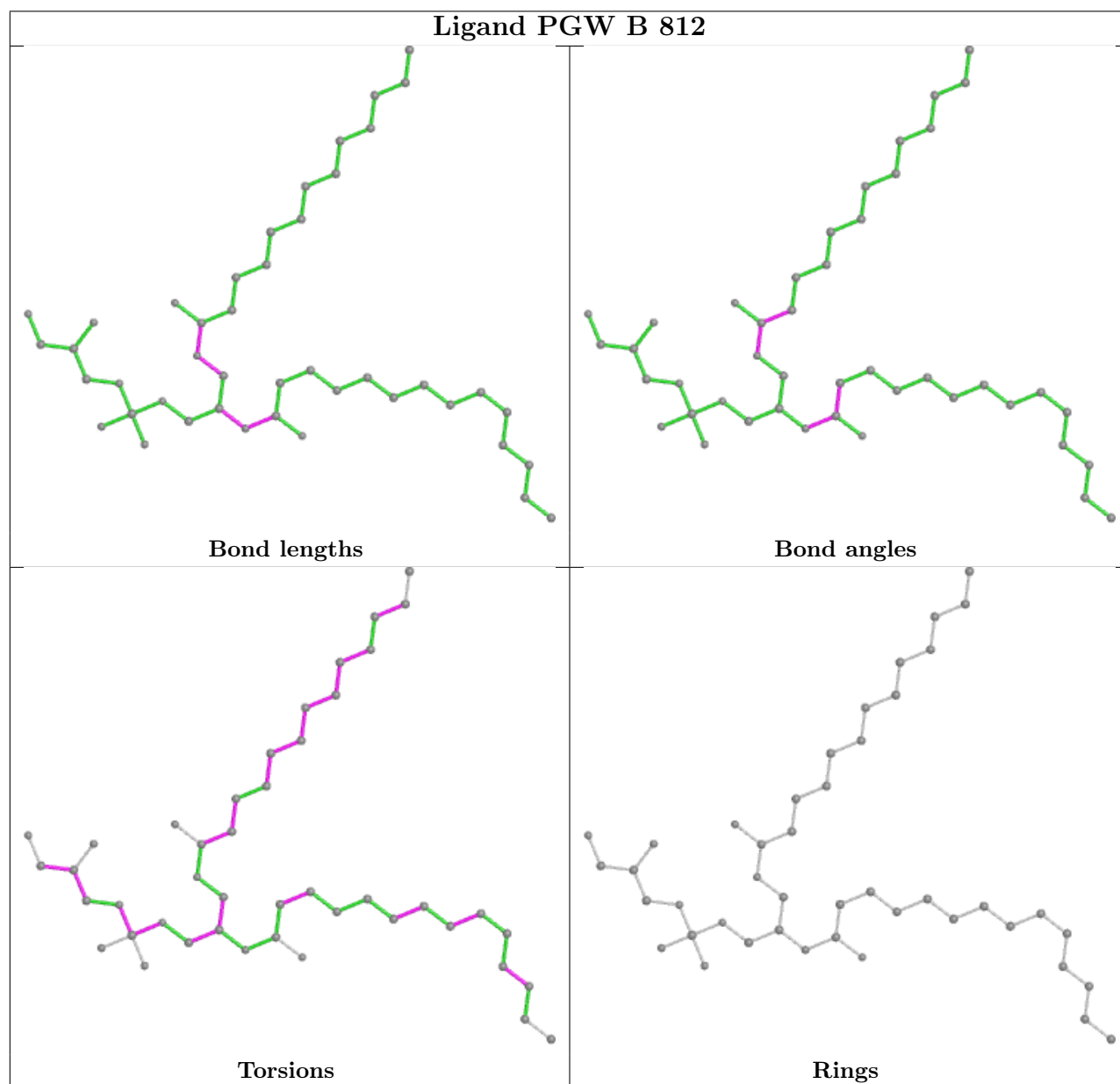
There are no ring outliers.

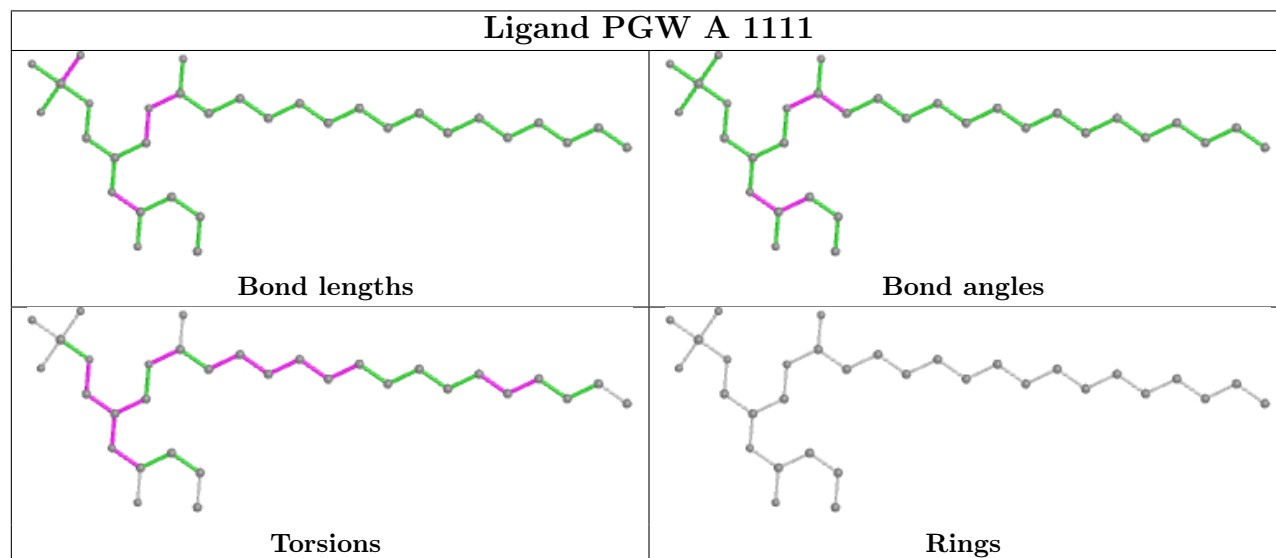
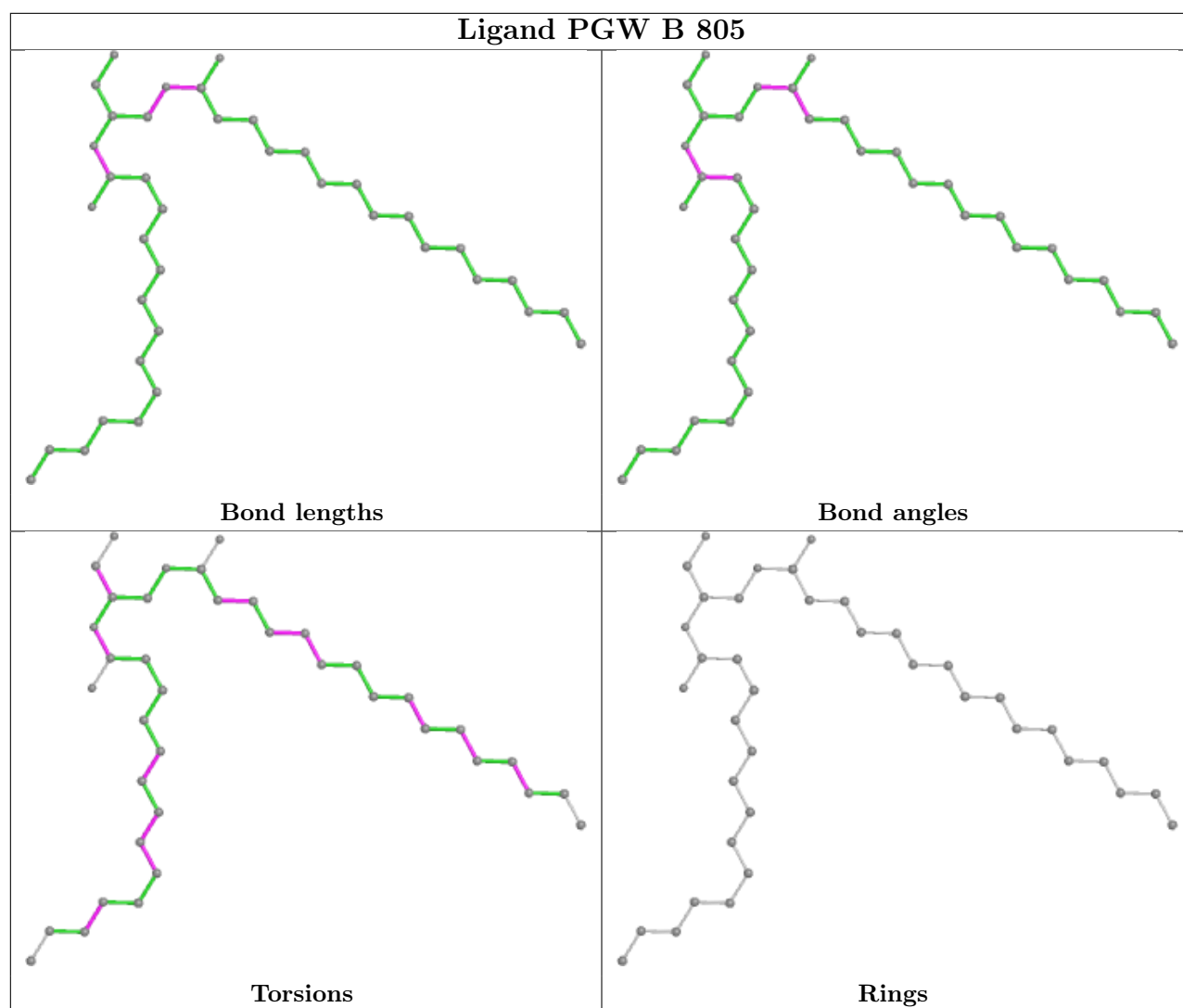
19 monomers are involved in 63 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	812	PGW	5	0
3	B	805	PGW	5	0
3	A	1111	PGW	3	0
3	B	807	PGW	4	0
3	A	1102	PGW	5	0
3	A	1101	PGW	7	0
3	A	1107	PGW	7	0
3	B	811	PGW	1	0
3	A	1113	PGW	1	0
3	A	1108	PGW	6	0
3	A	1114	PGW	1	0
3	B	803	PGW	7	0
3	B	808	PGW	3	0
3	A	1109	PGW	1	0
3	A	1105	PGW	6	0
3	A	1110	PGW	4	0
3	A	1112	PGW	2	0
3	B	806	PGW	1	0
3	B	809	PGW	2	0

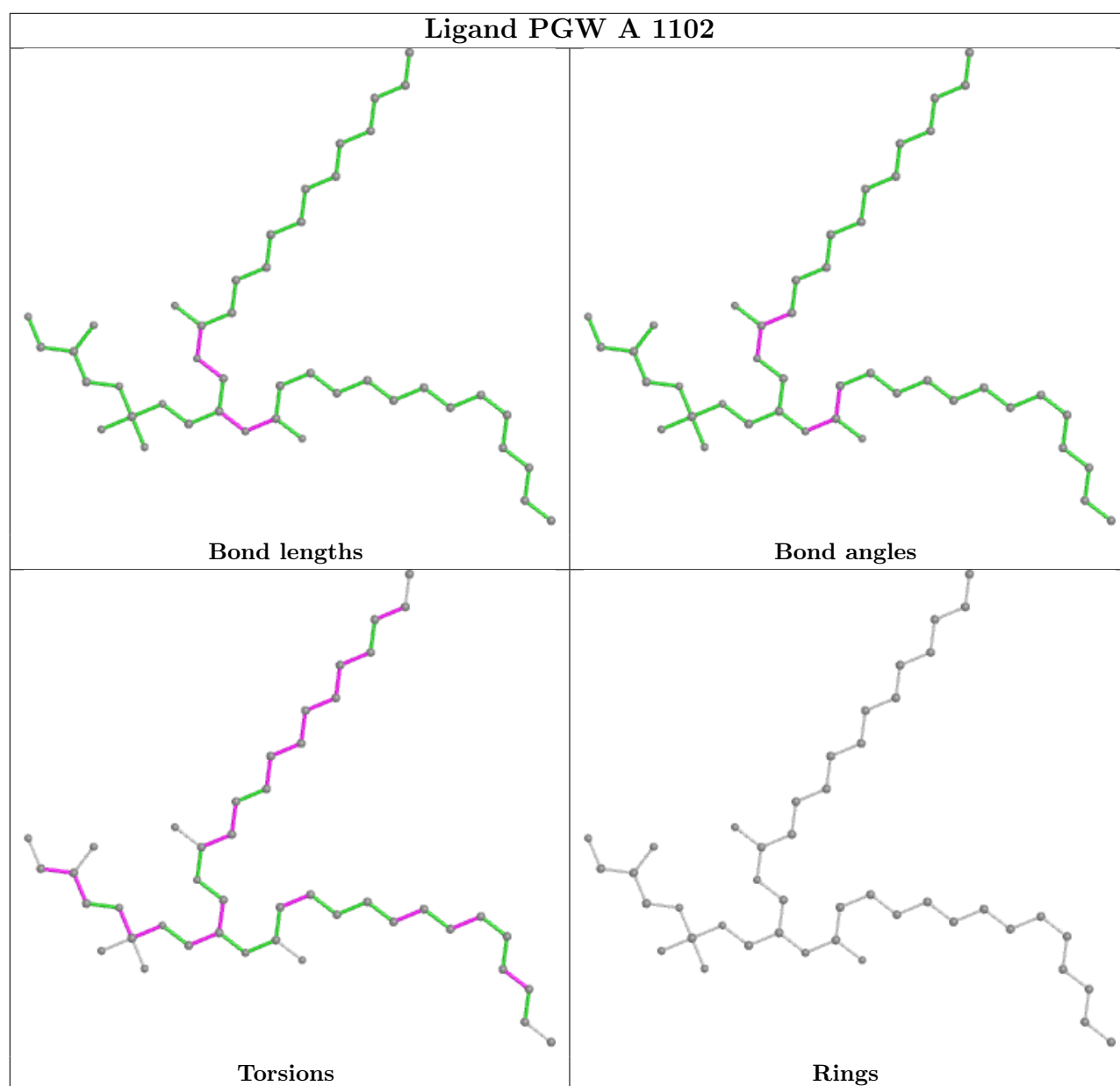
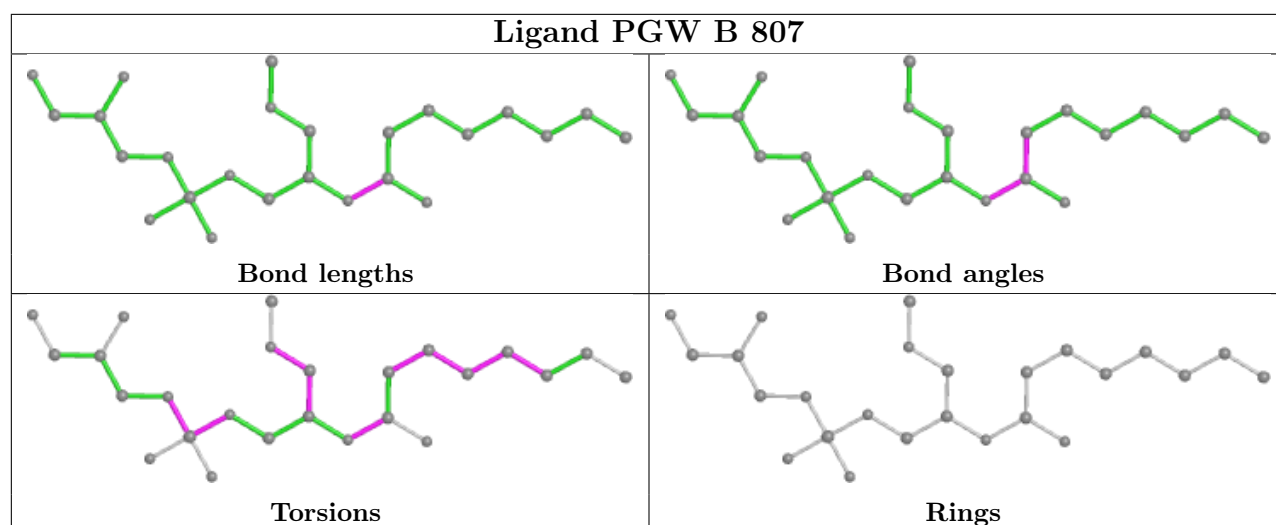
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

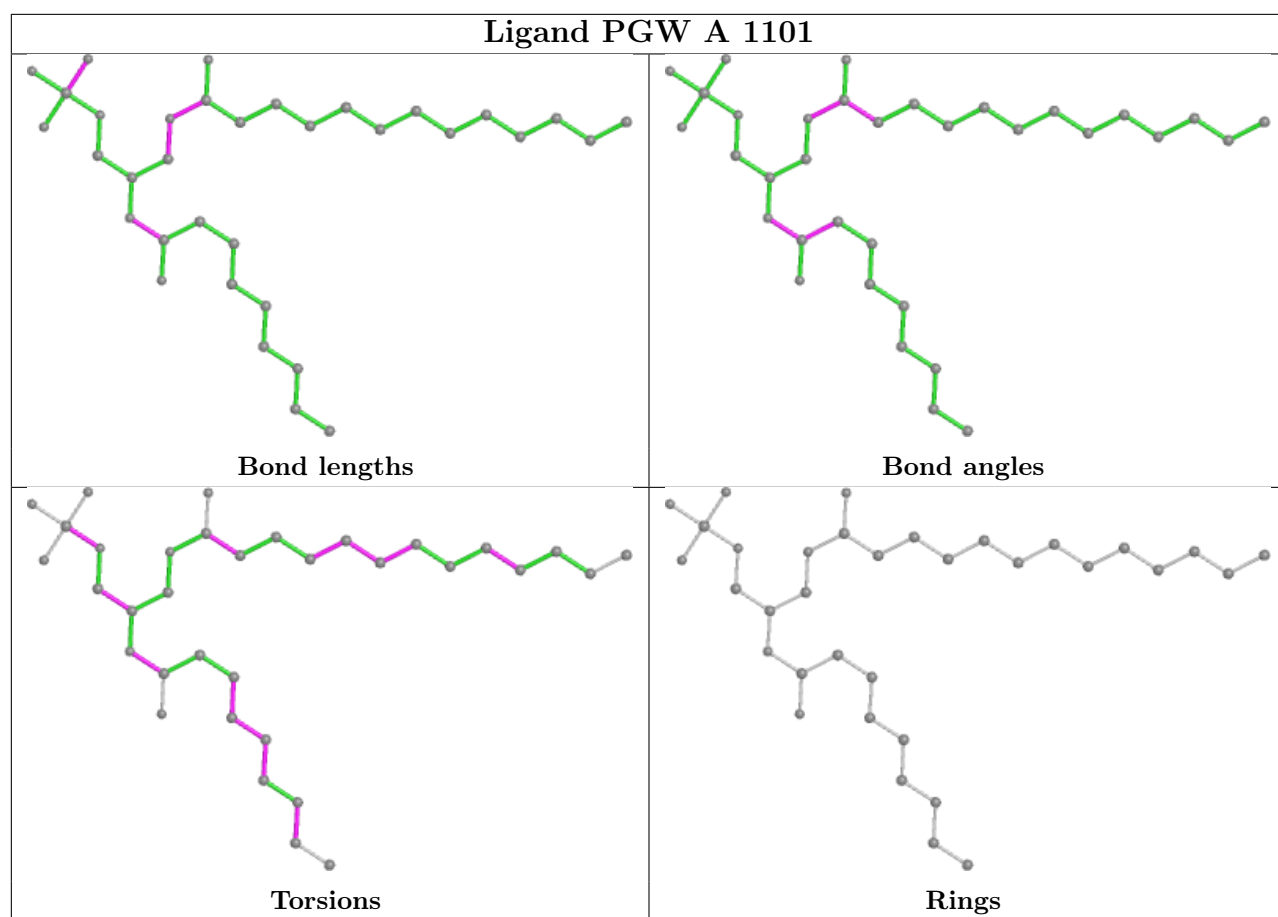
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

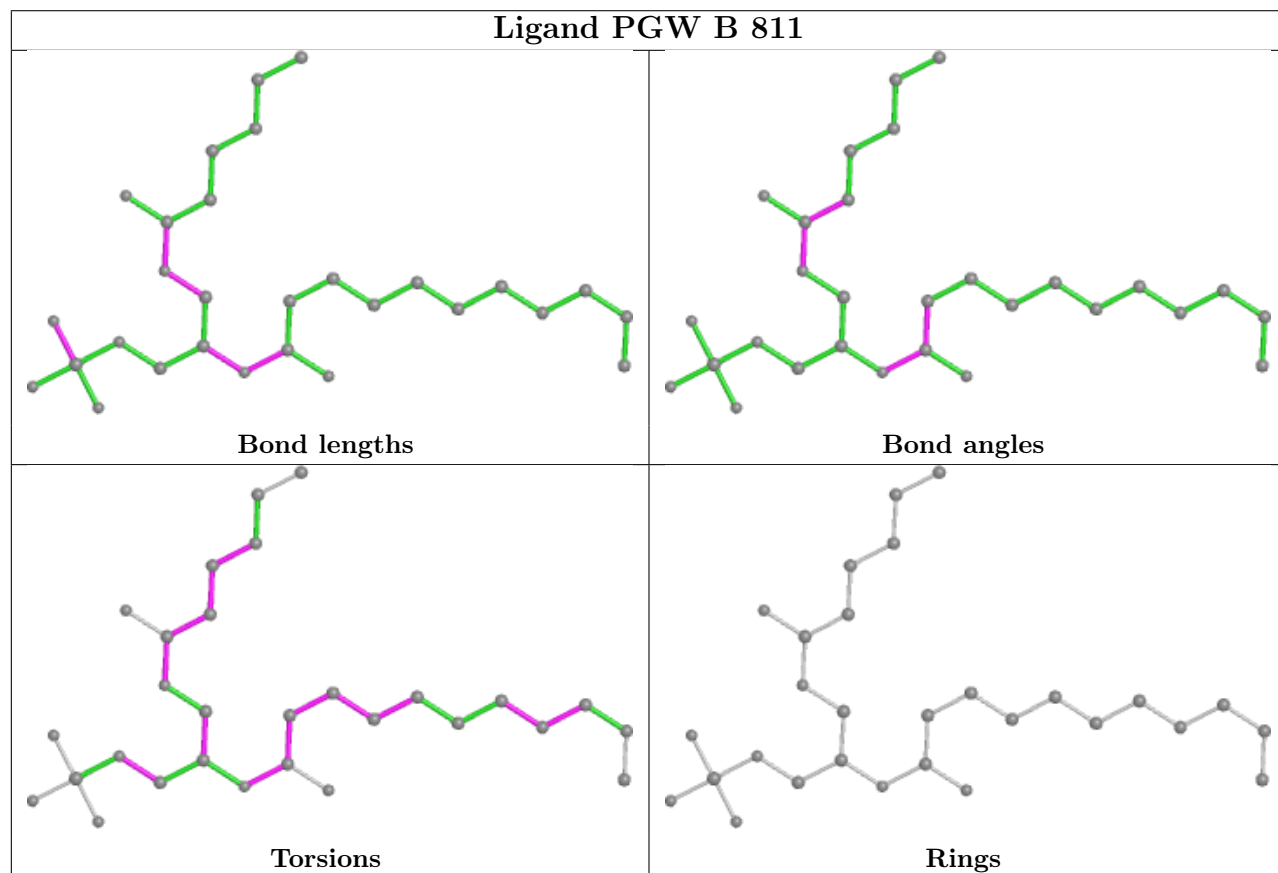
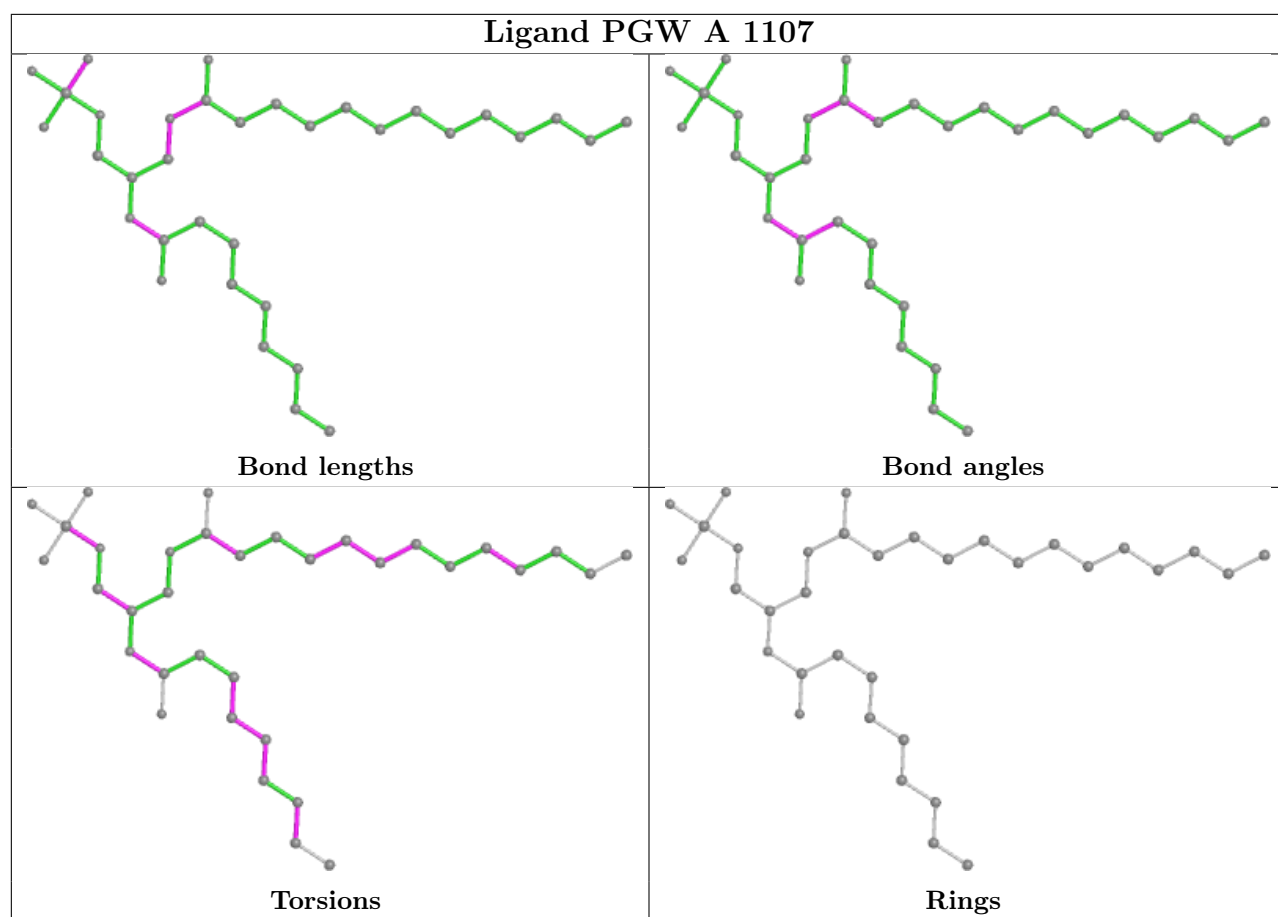


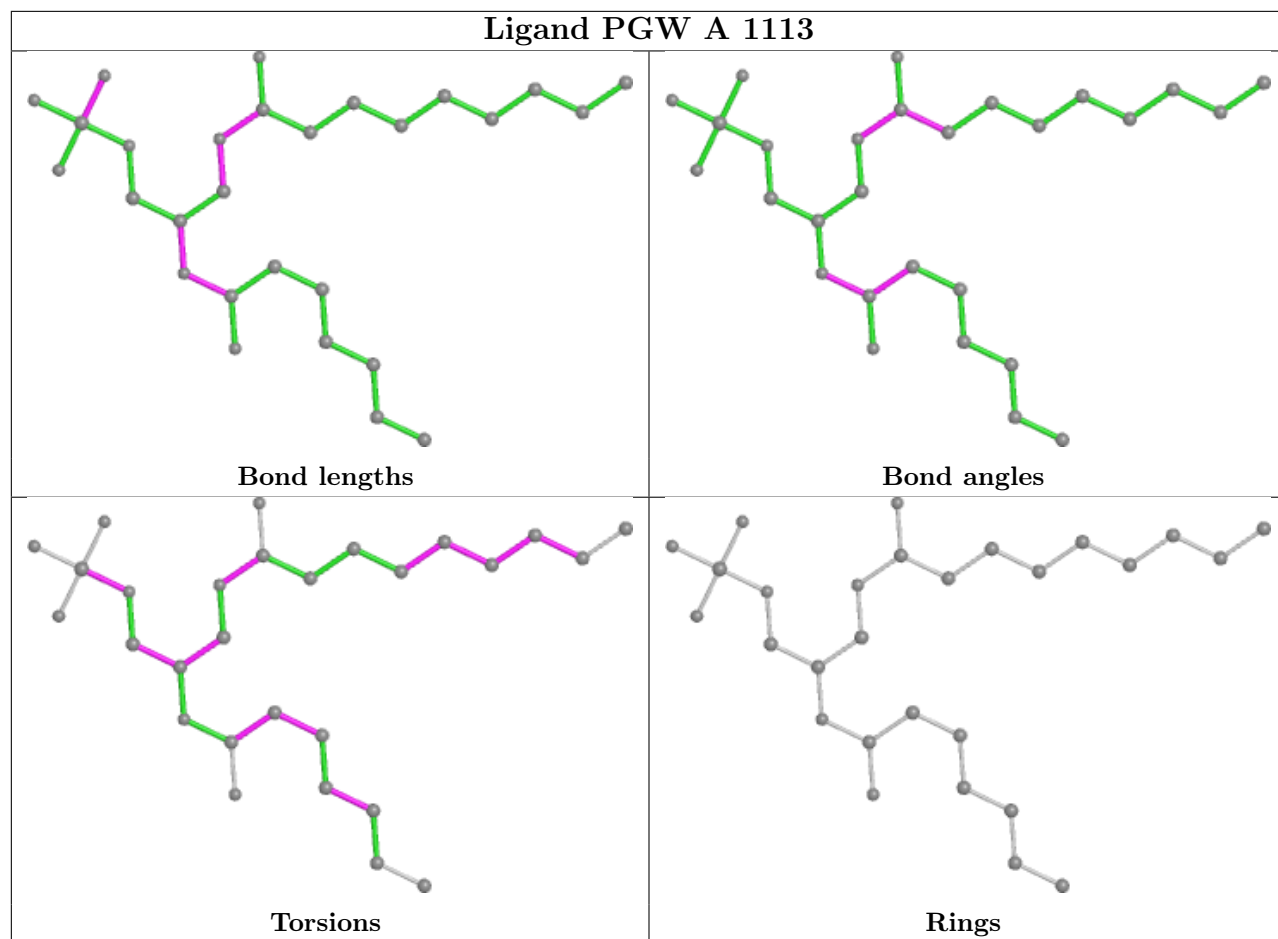


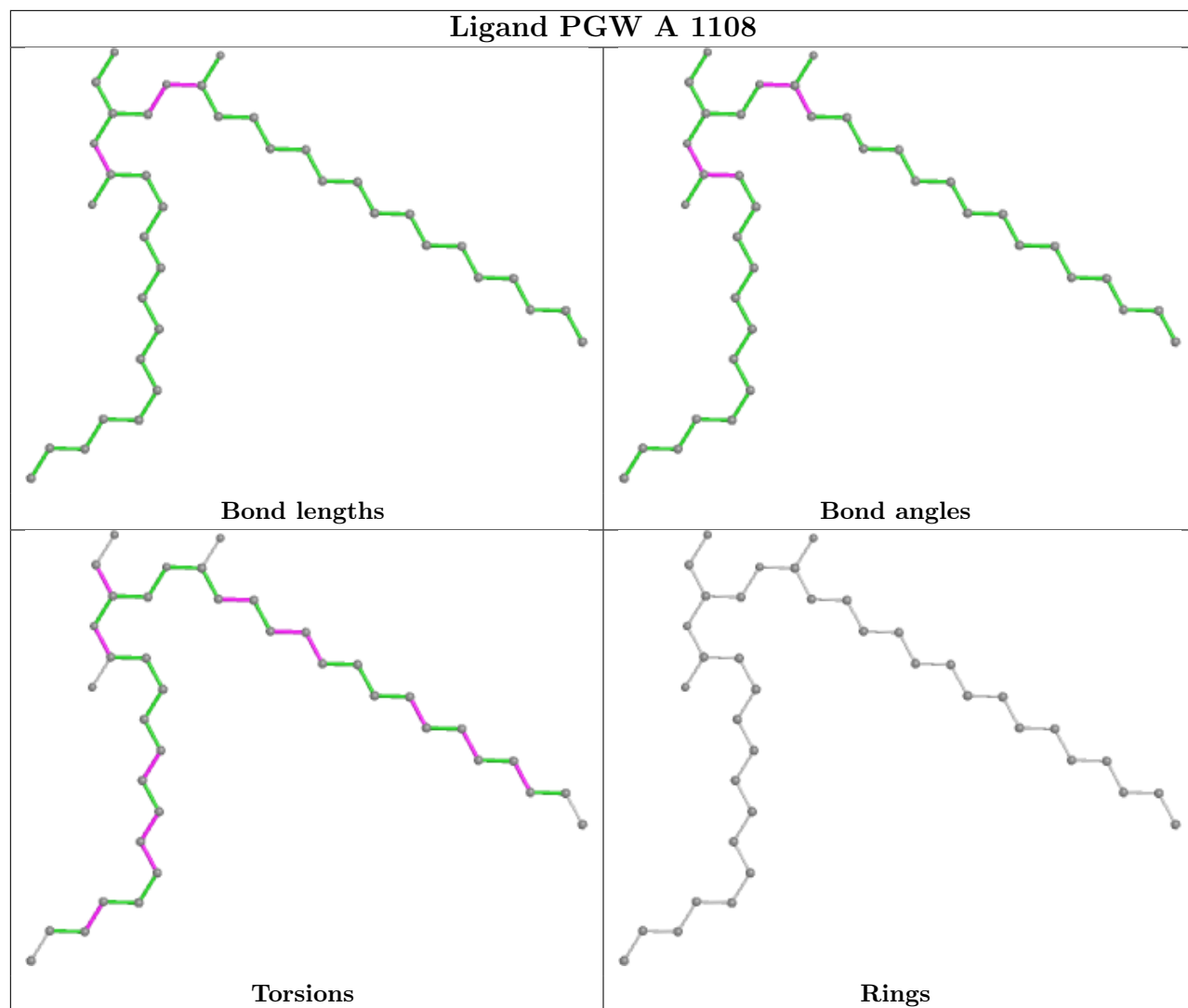


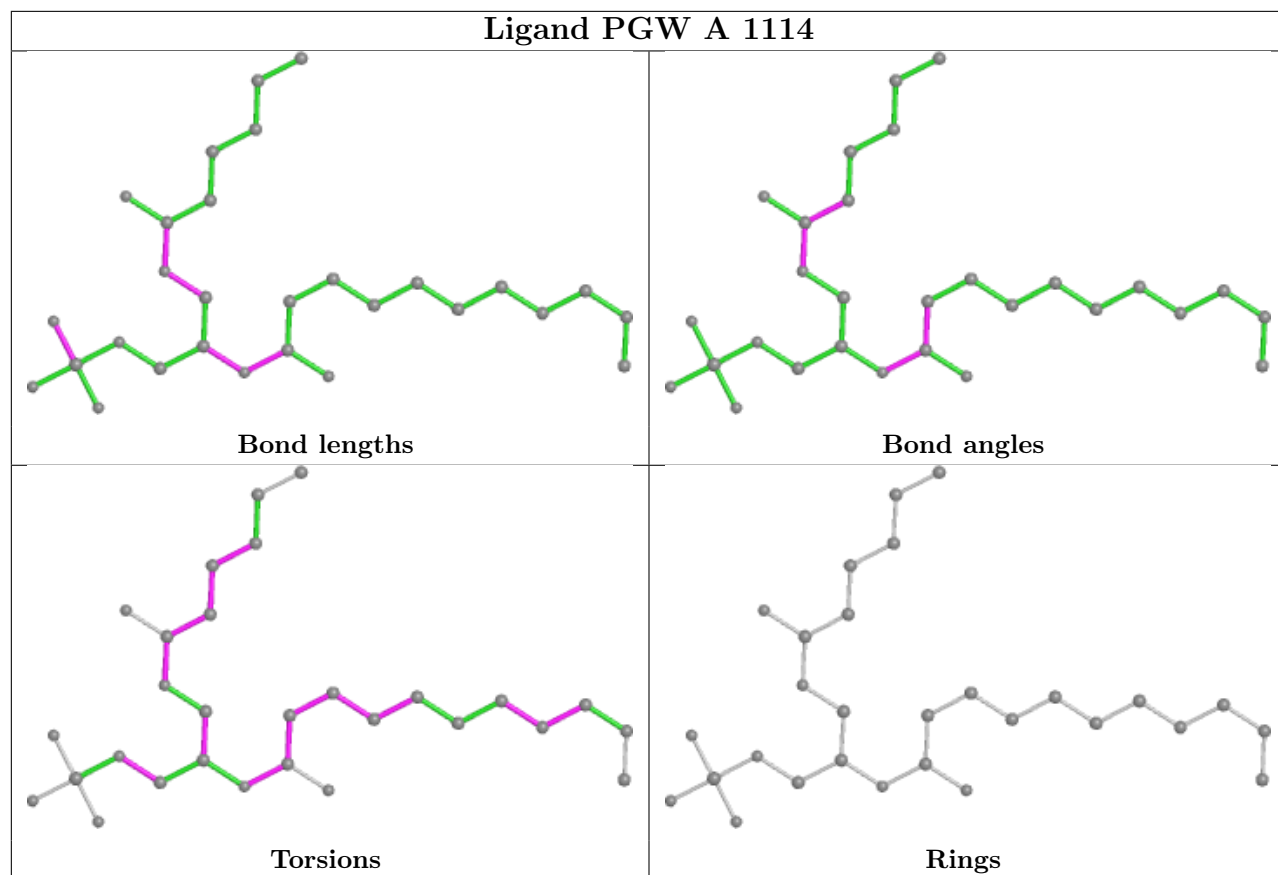


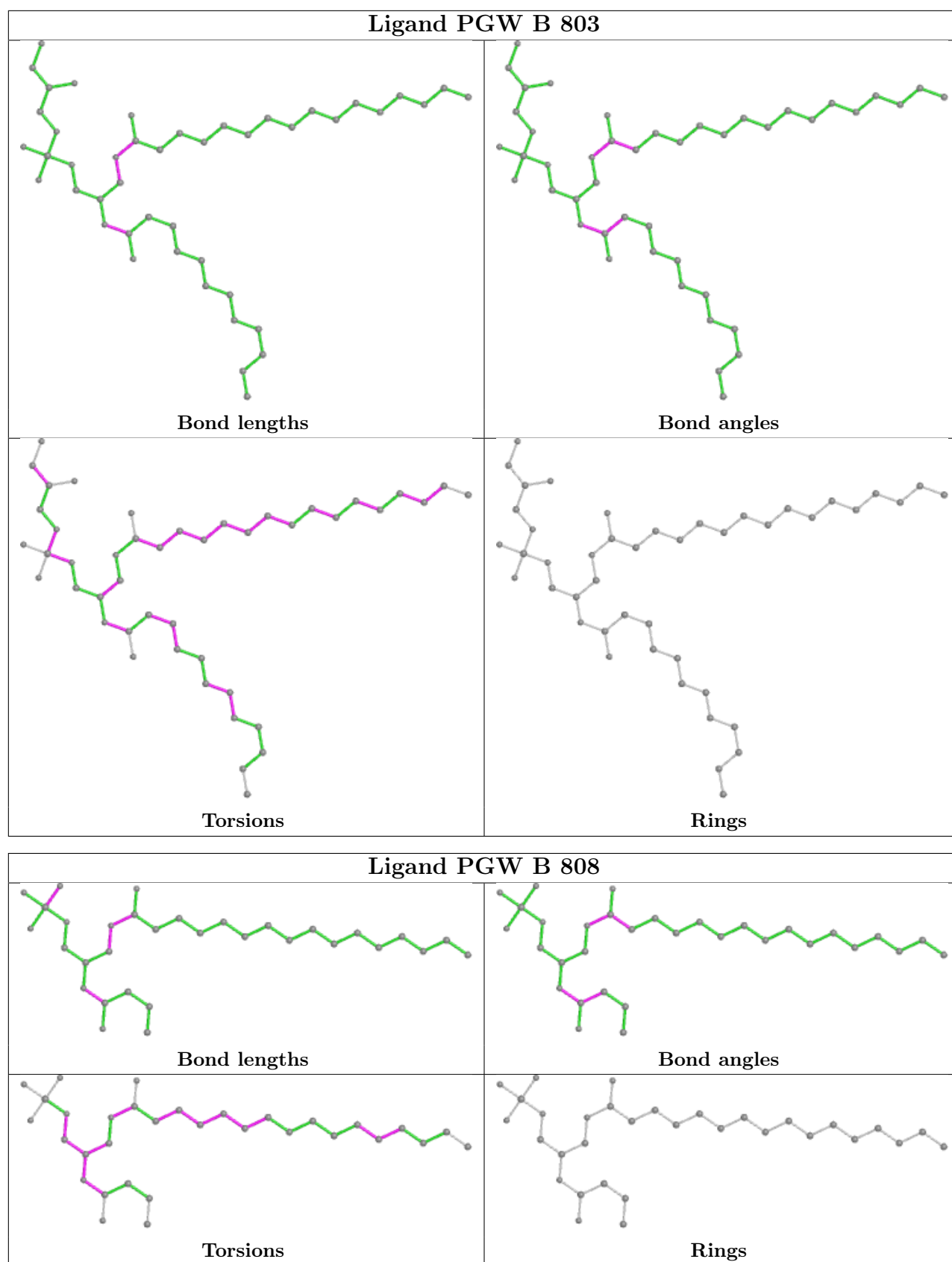


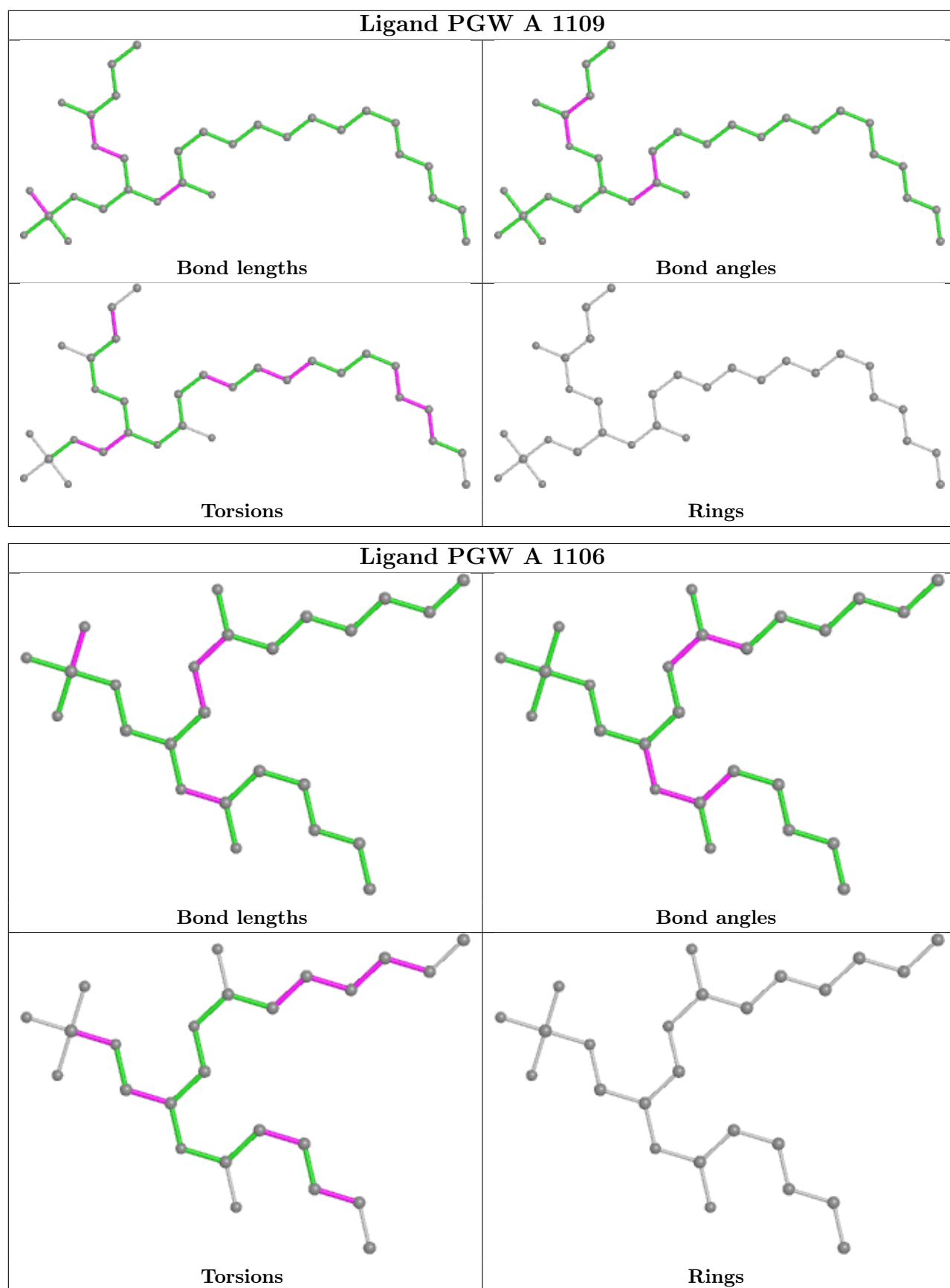




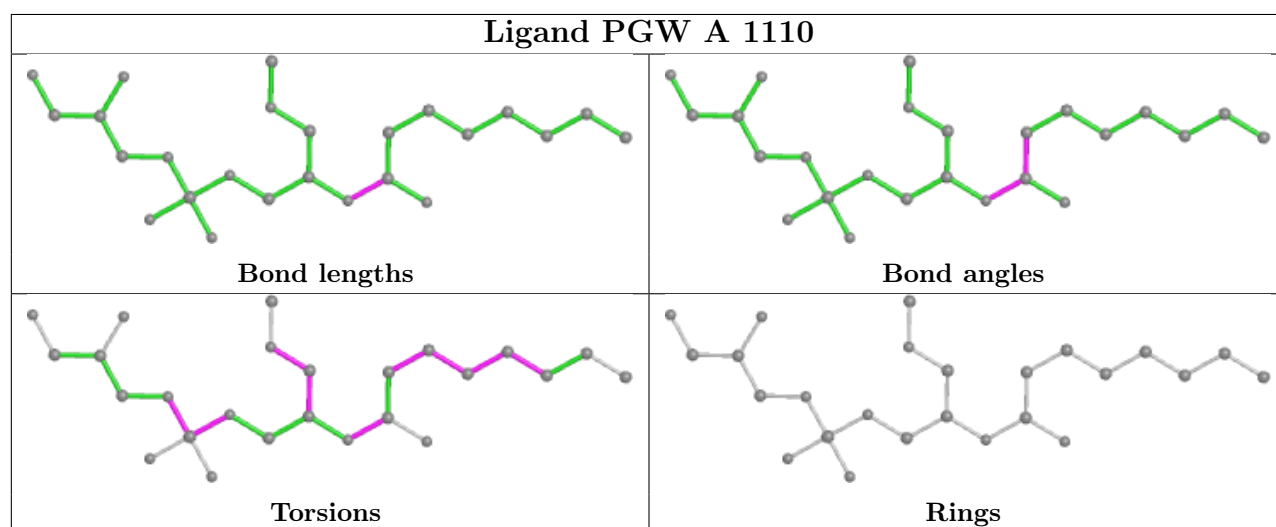
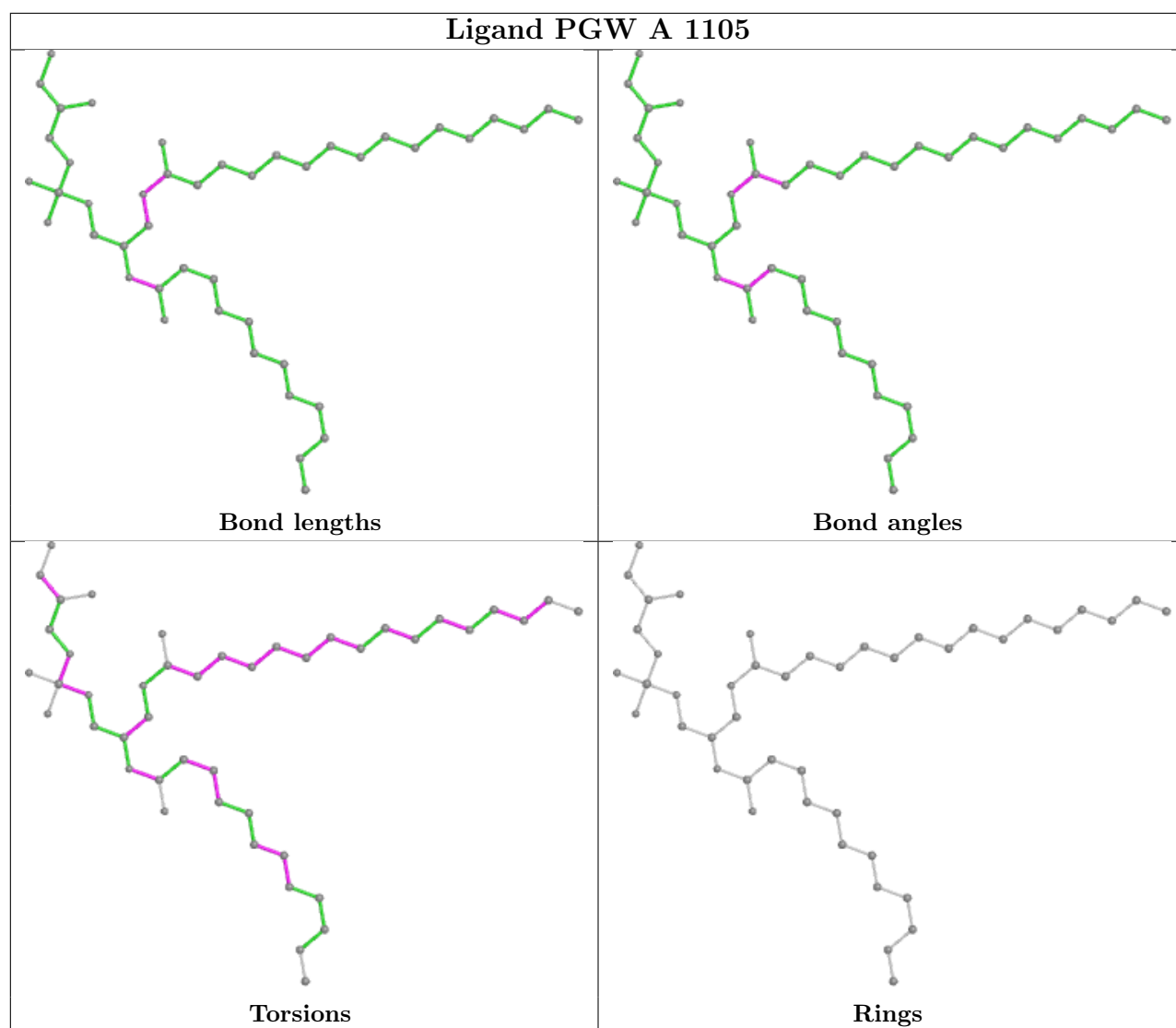


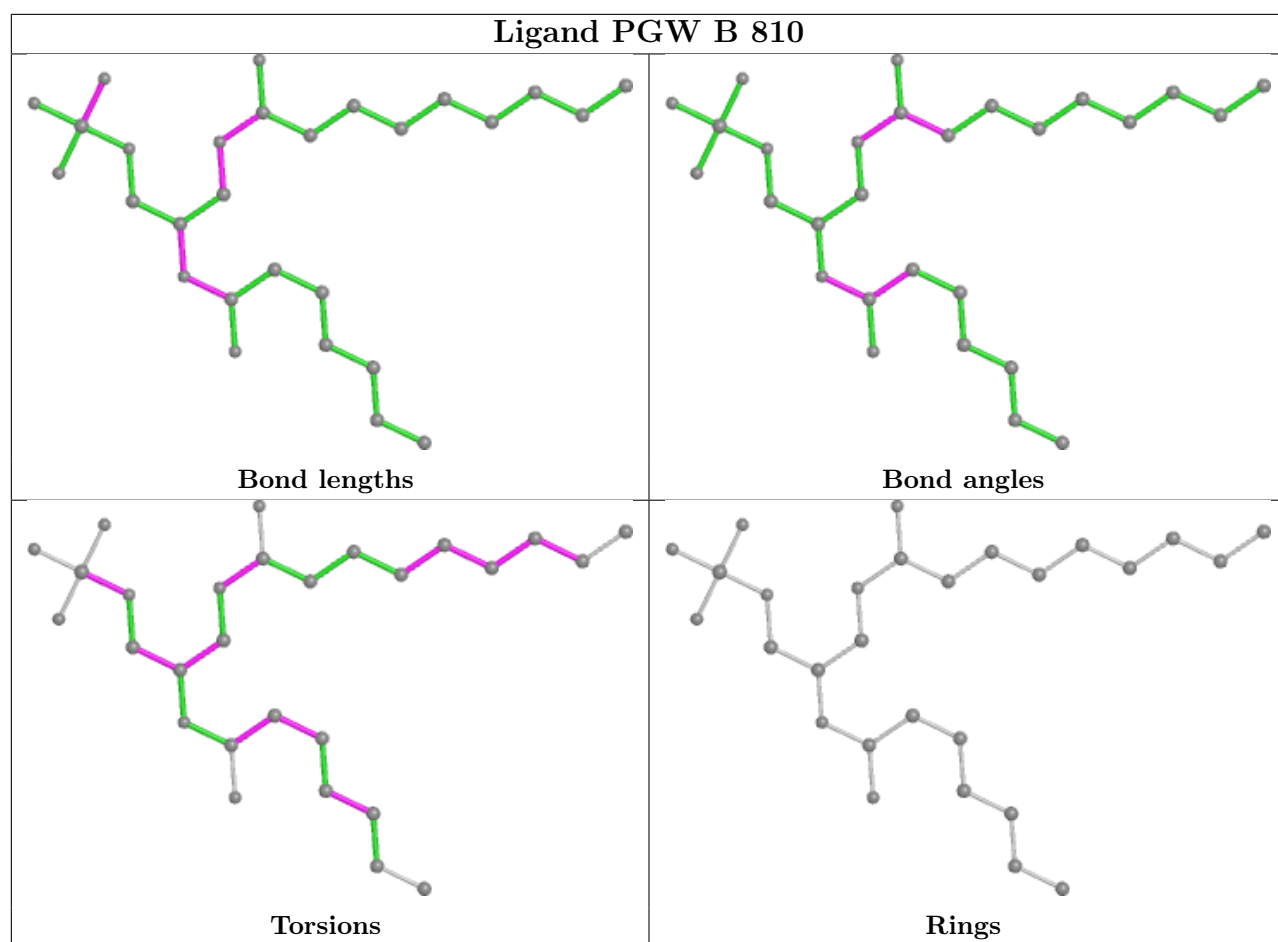




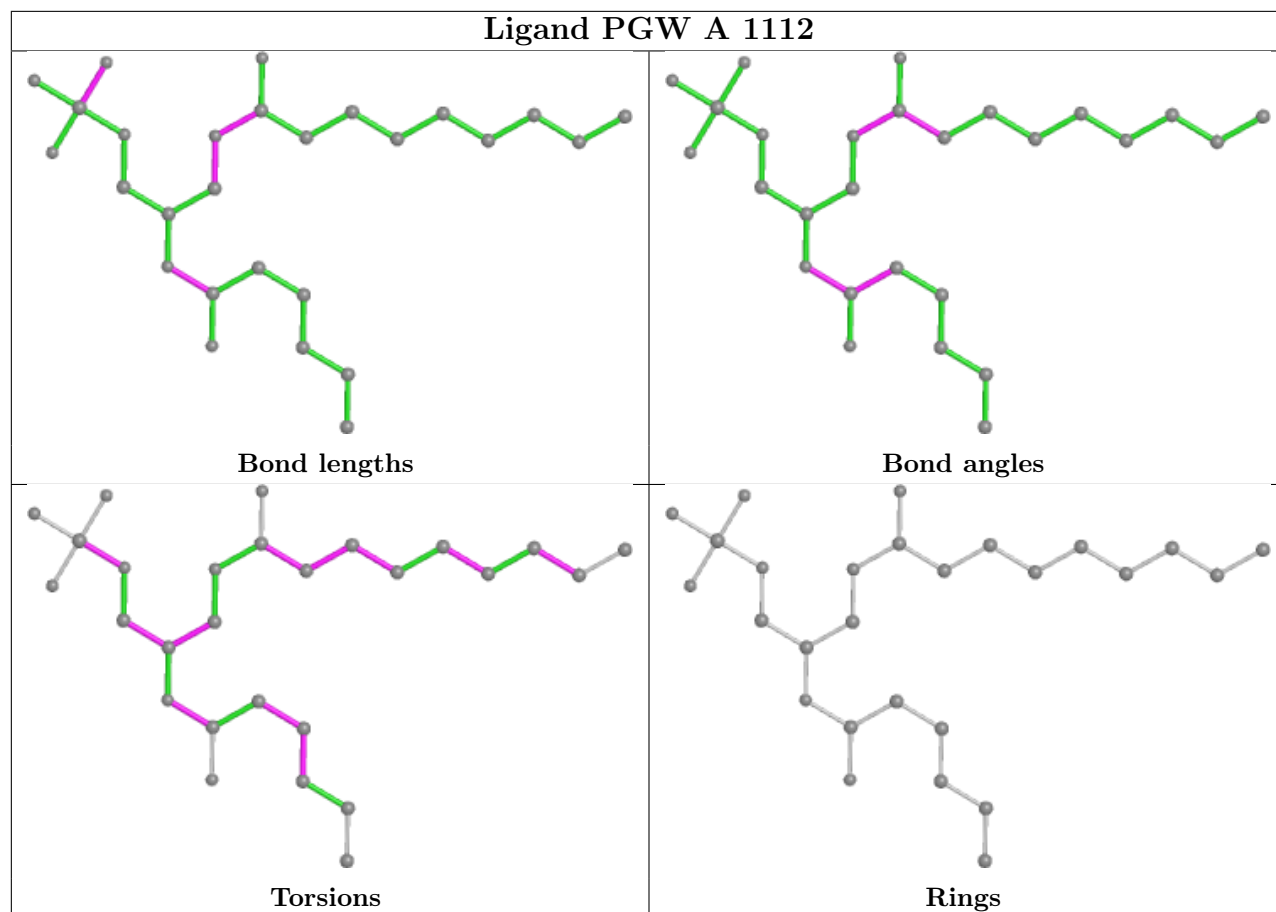




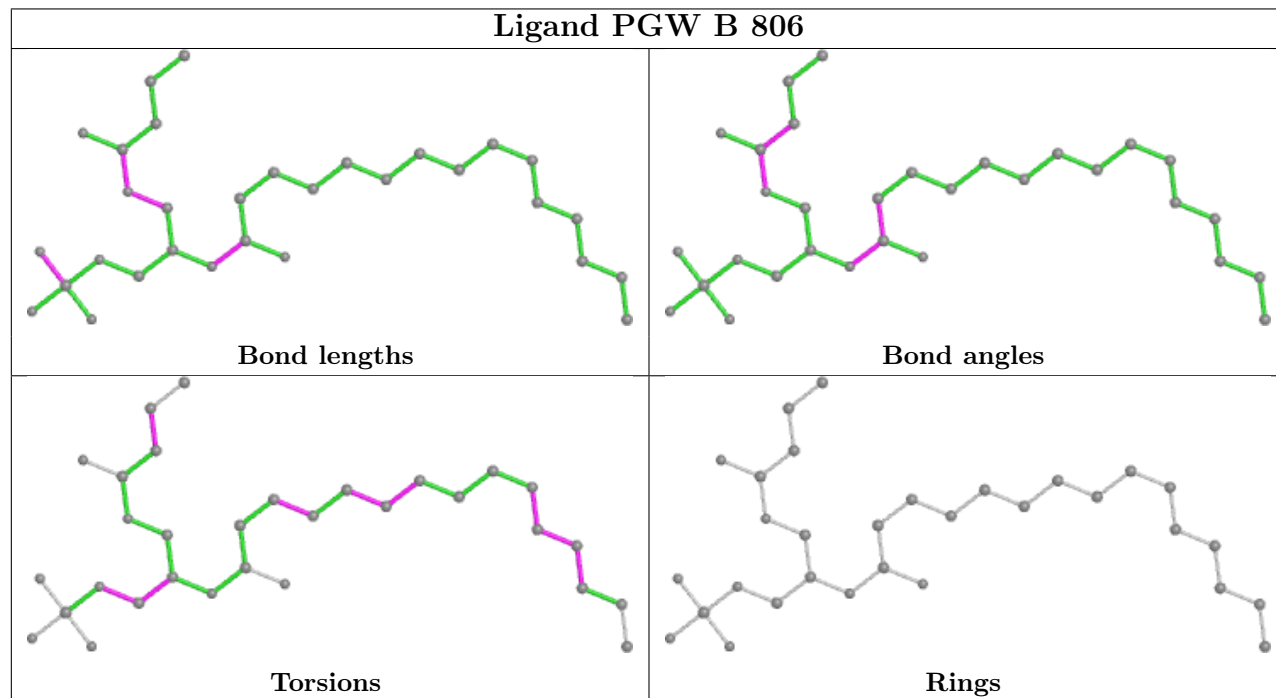


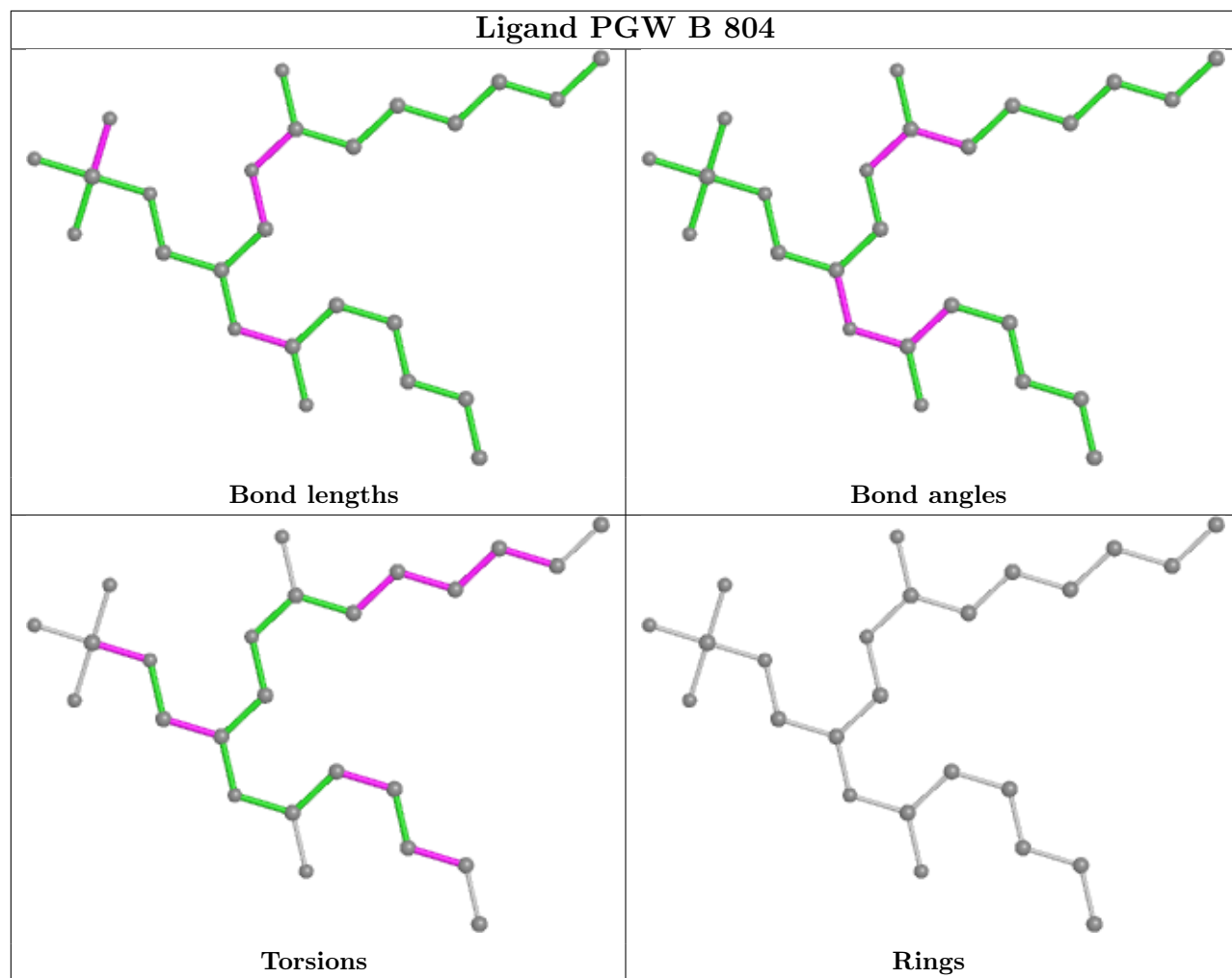


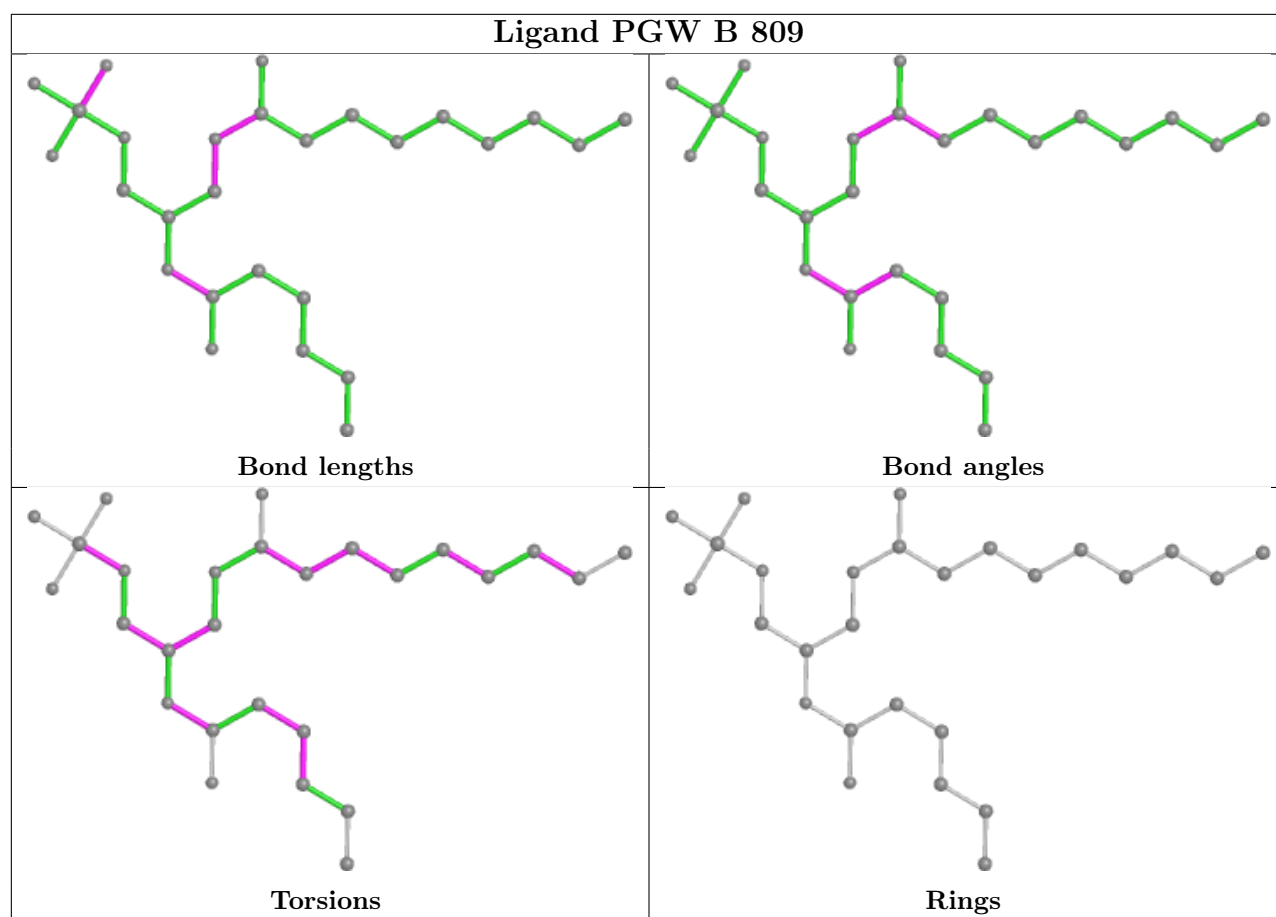
## Ligand PGW A 1112



## Ligand PGW B 806







## 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.

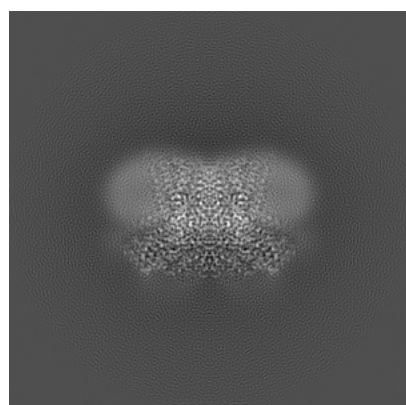
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24730. These allow visual inspection of the internal detail of the map and identification of artifacts.

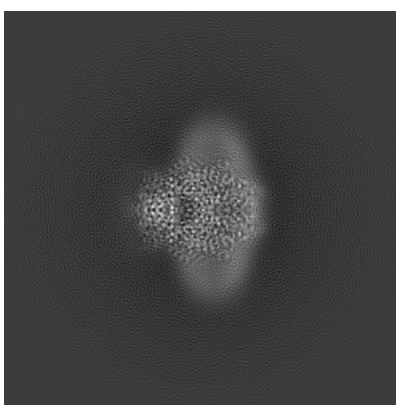
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

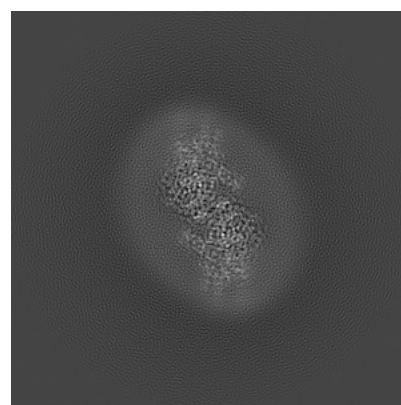
#### 6.1.1 Primary map



X



Y

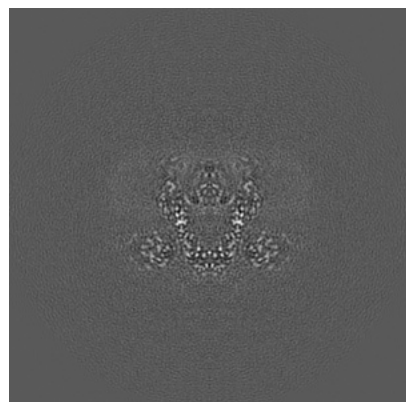


Z

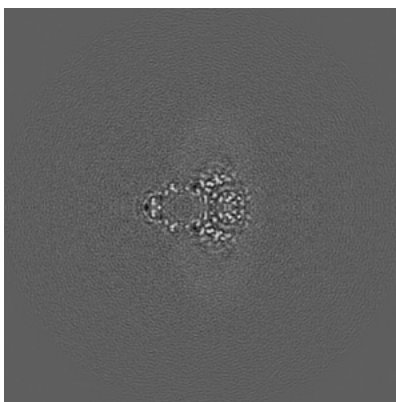
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

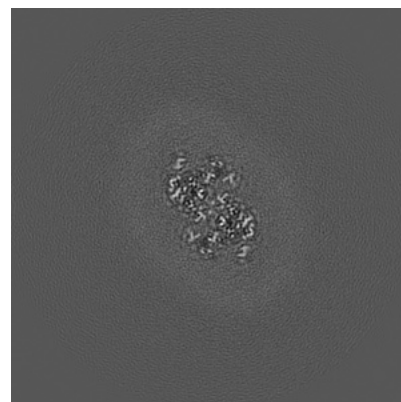
#### 6.2.1 Primary map



X Index: 192



Y Index: 192

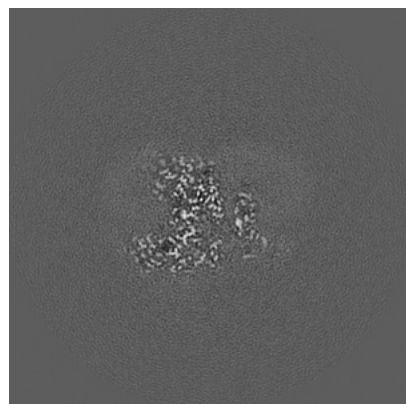


Z Index: 192

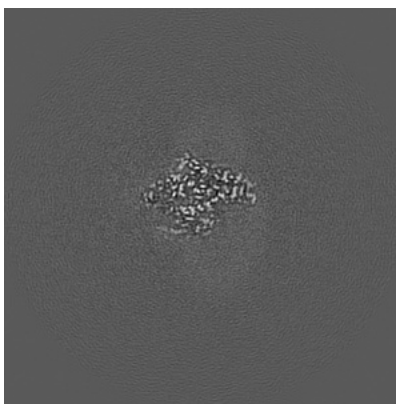
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

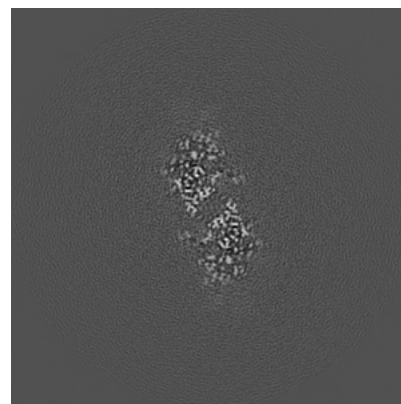
### 6.3.1 Primary map



X Index: 203



Y Index: 165

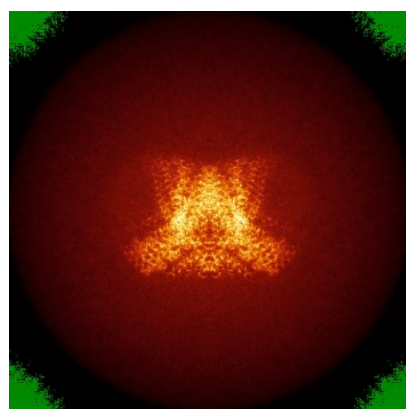


Z Index: 161

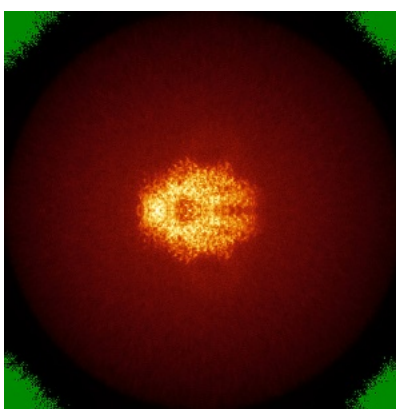
The images above show the largest variance slices of the map in three orthogonal directions.

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

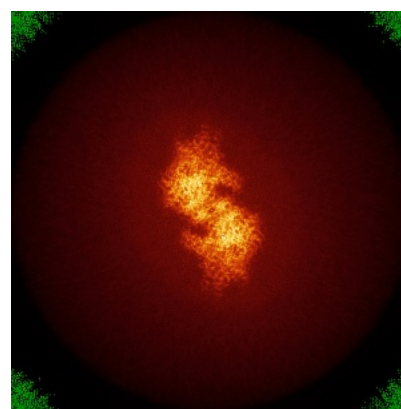
### 6.4.1 Primary map



X



Y

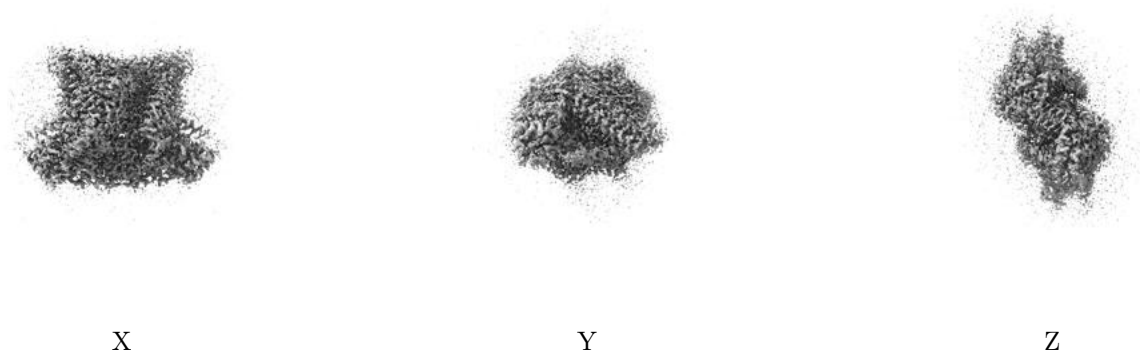


Z

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 0.0169. 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](#)

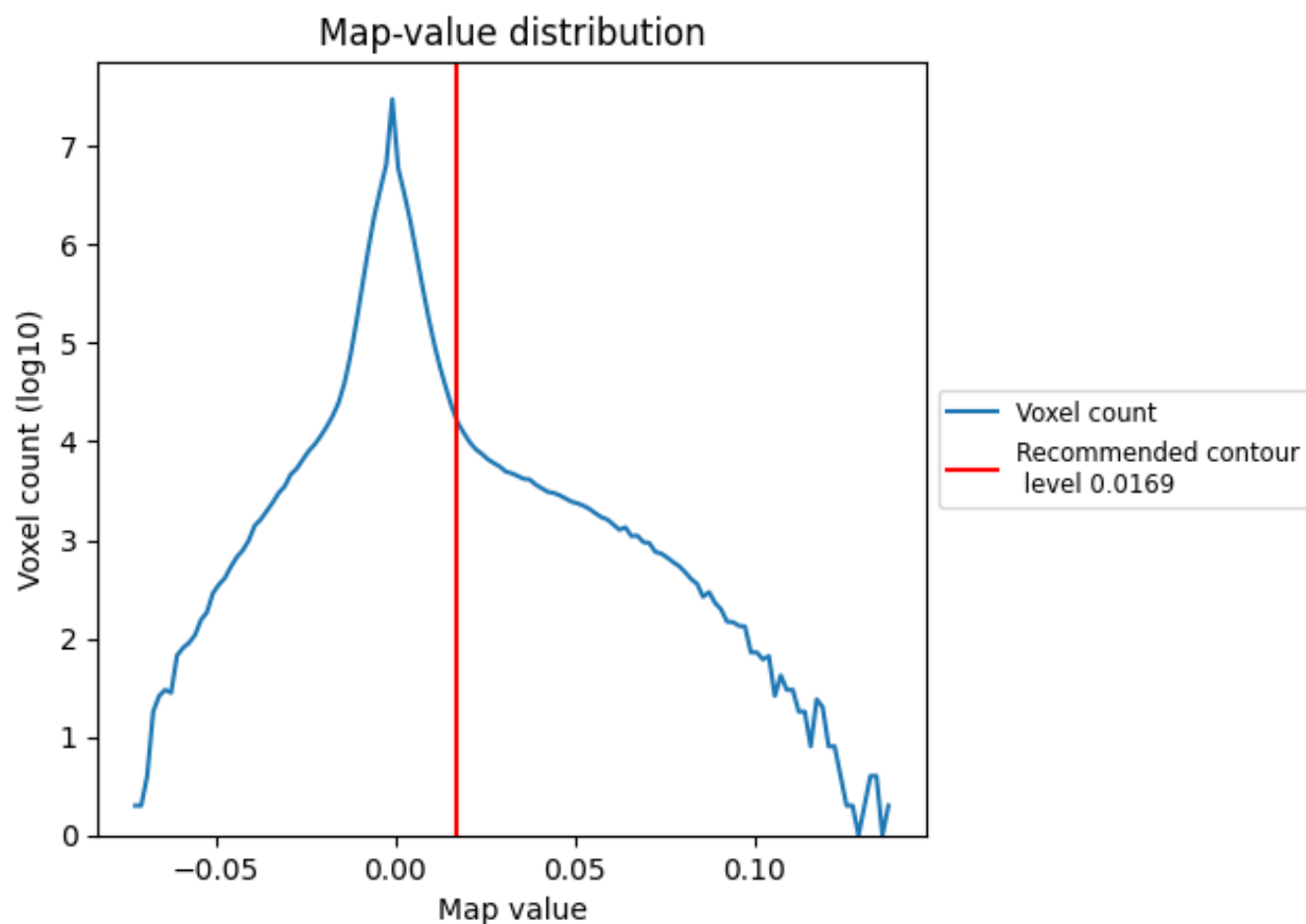
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

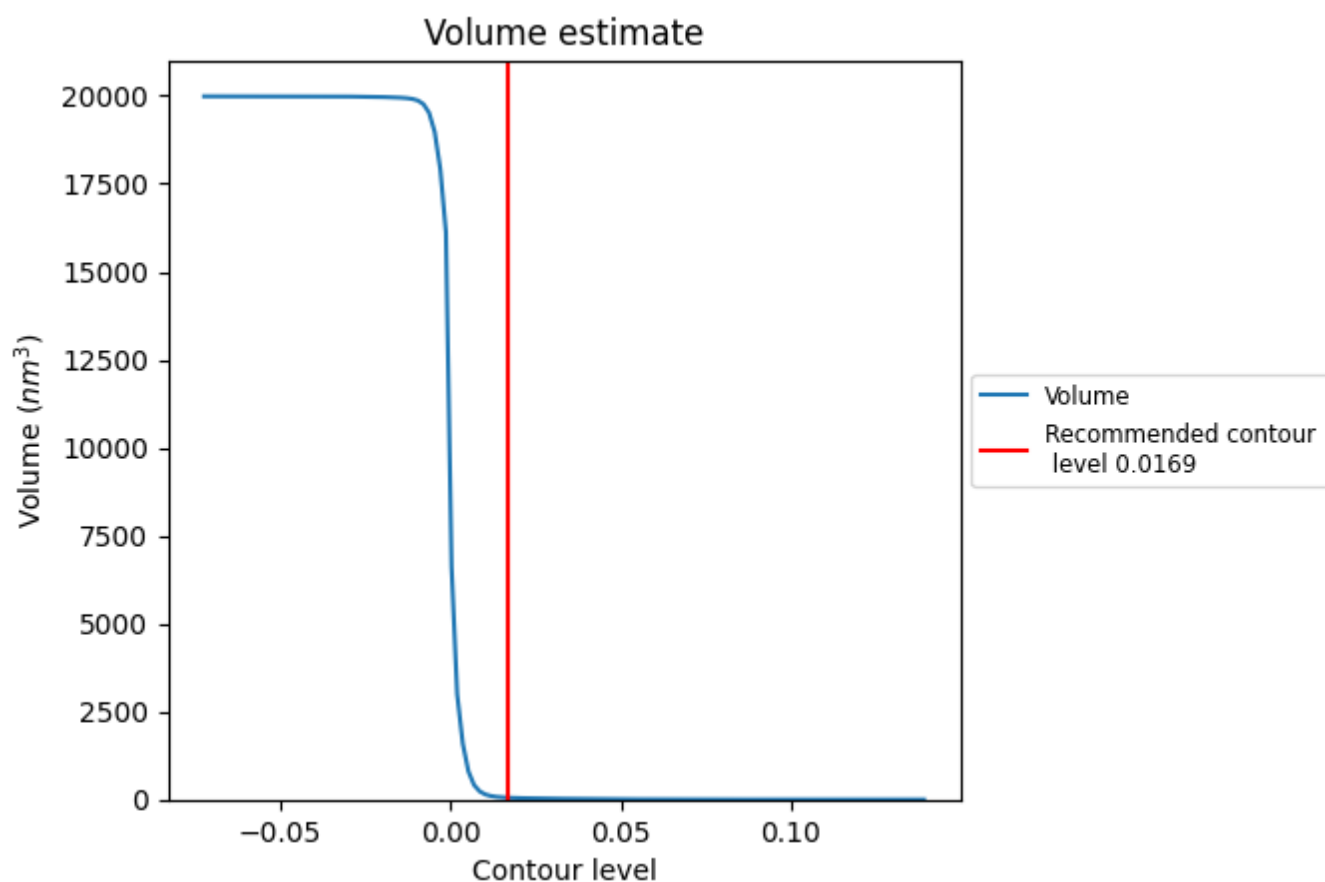
This section contains the results of statistical analysis of the map.

### 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.

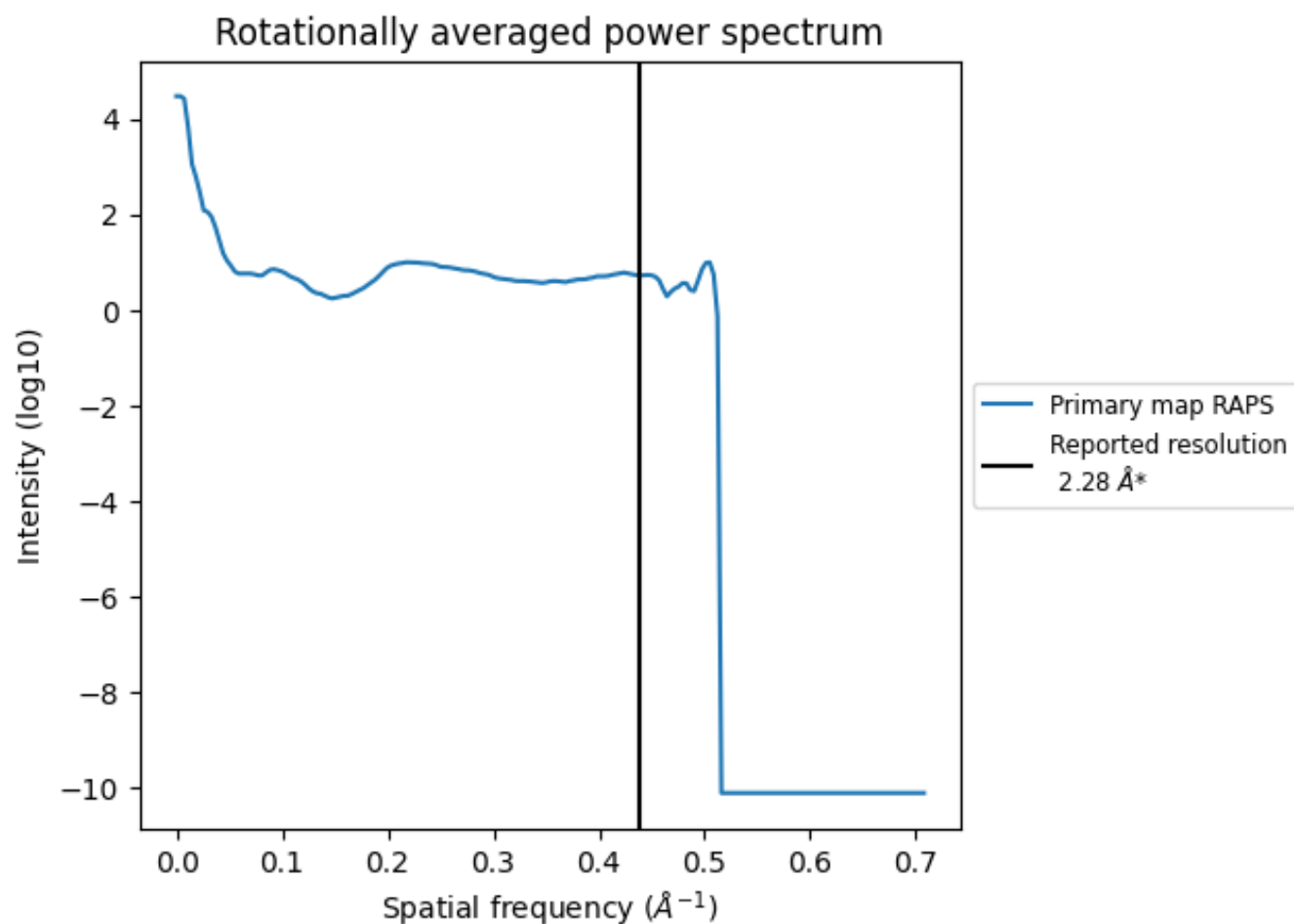
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 52  $\text{nm}^3$ ; this corresponds to an approximate mass of 47 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 ⓘ

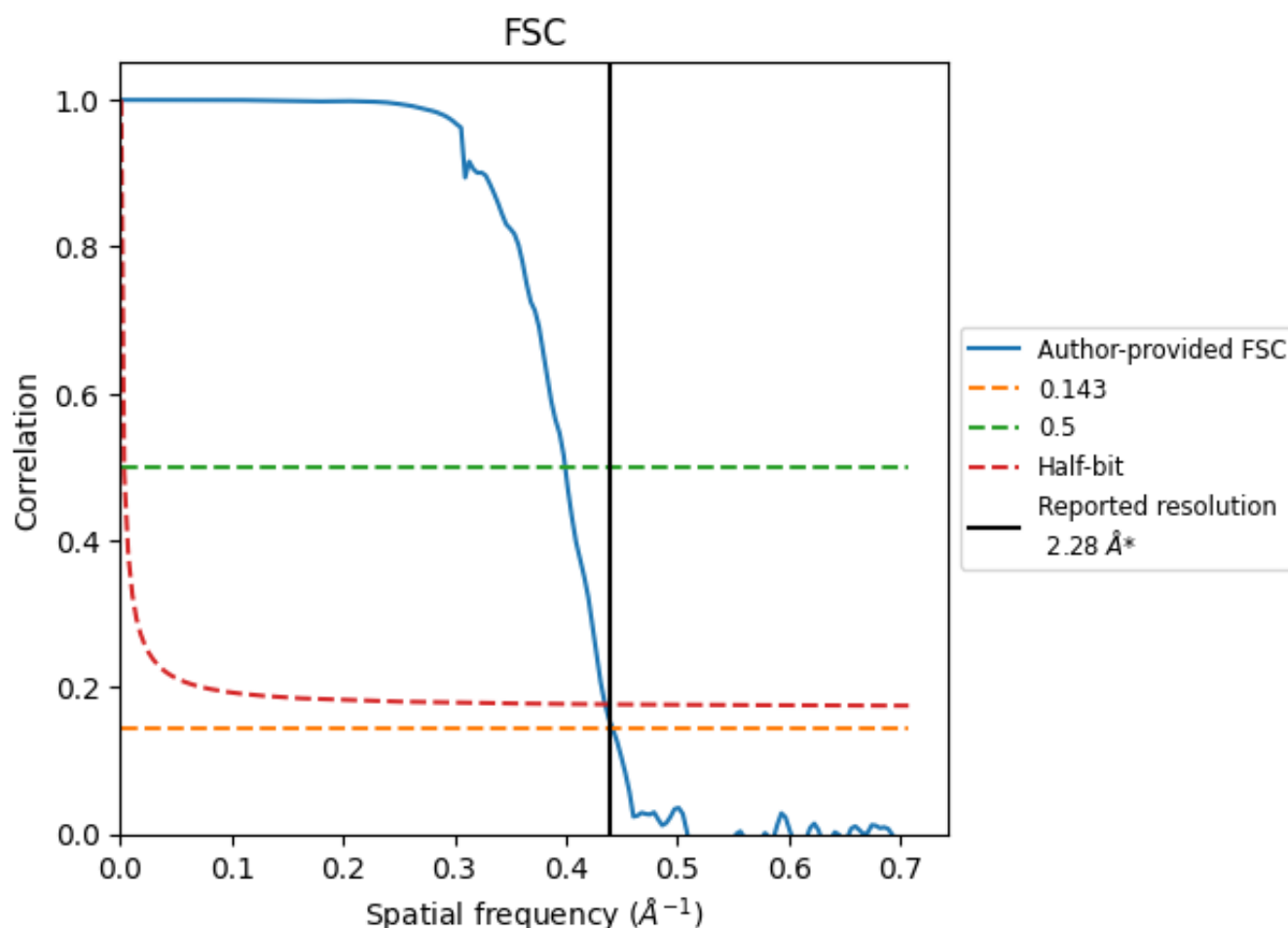


\*Reported resolution corresponds to spatial frequency of 0.439 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.439 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

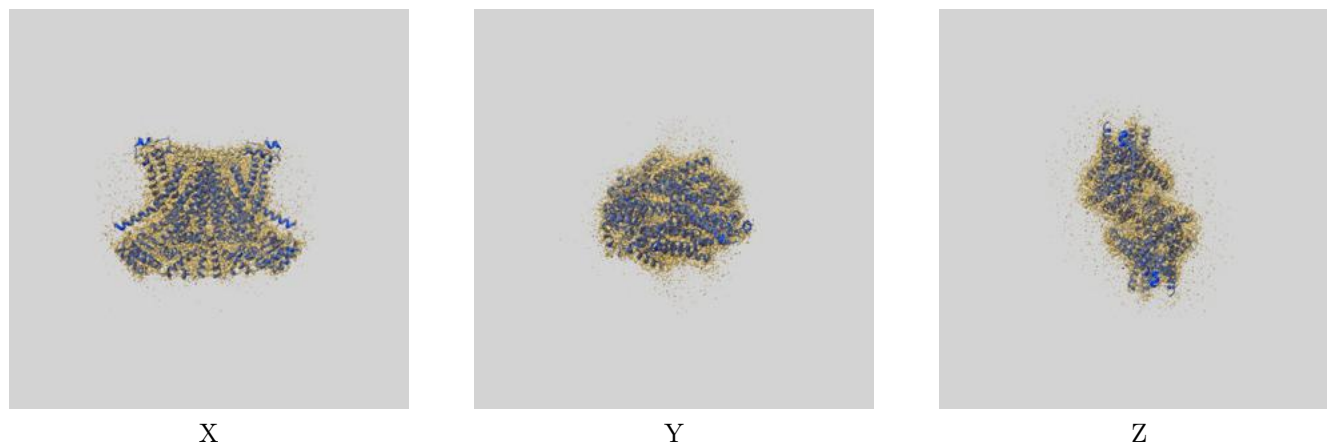
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.28	-	-
Author-provided FSC curve	2.26	2.50	2.30
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

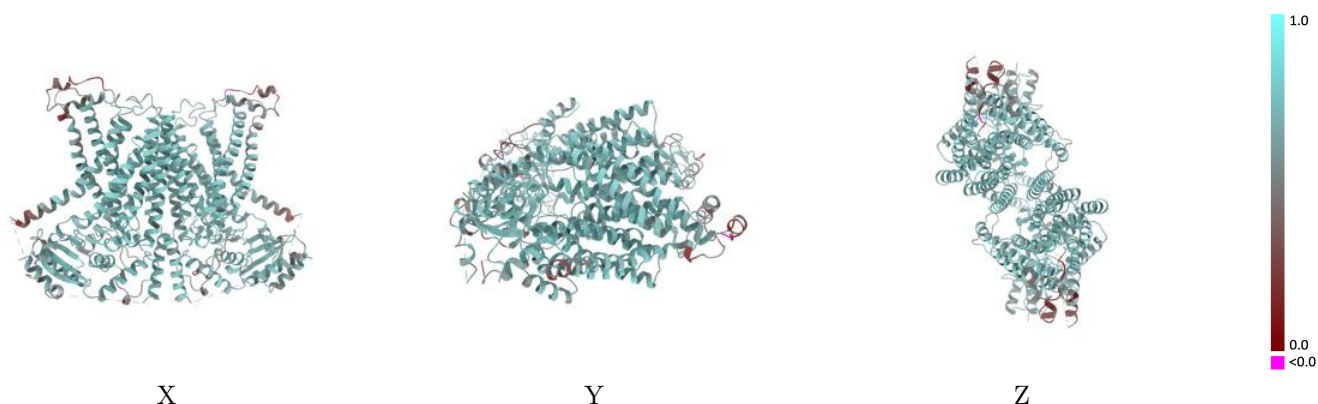
This section contains information regarding the fit between EMDB map EMD-24730 and PDB model 7RXG. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

### 9.1 Map-model overlay [i](#)



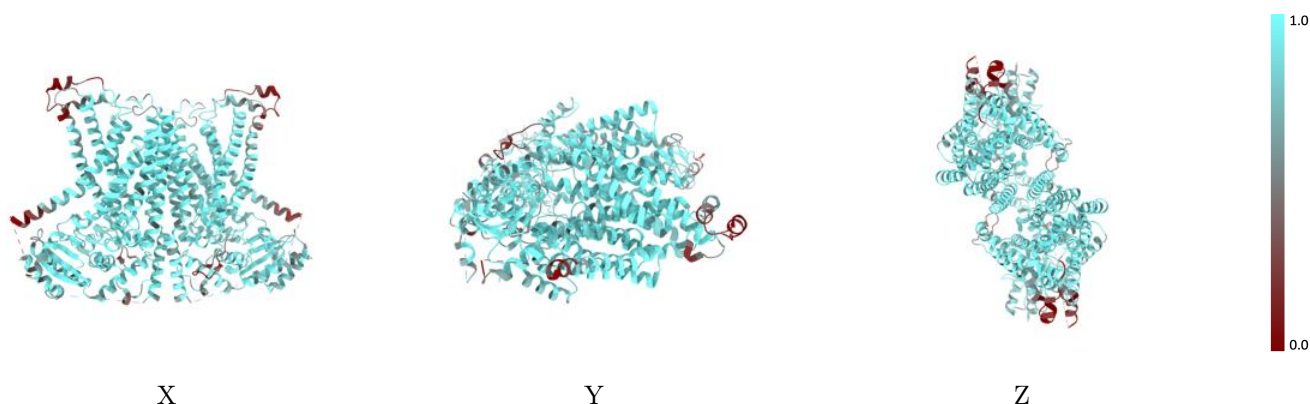
The images above show the 3D surface view of the map at the recommended contour level 0.0169 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



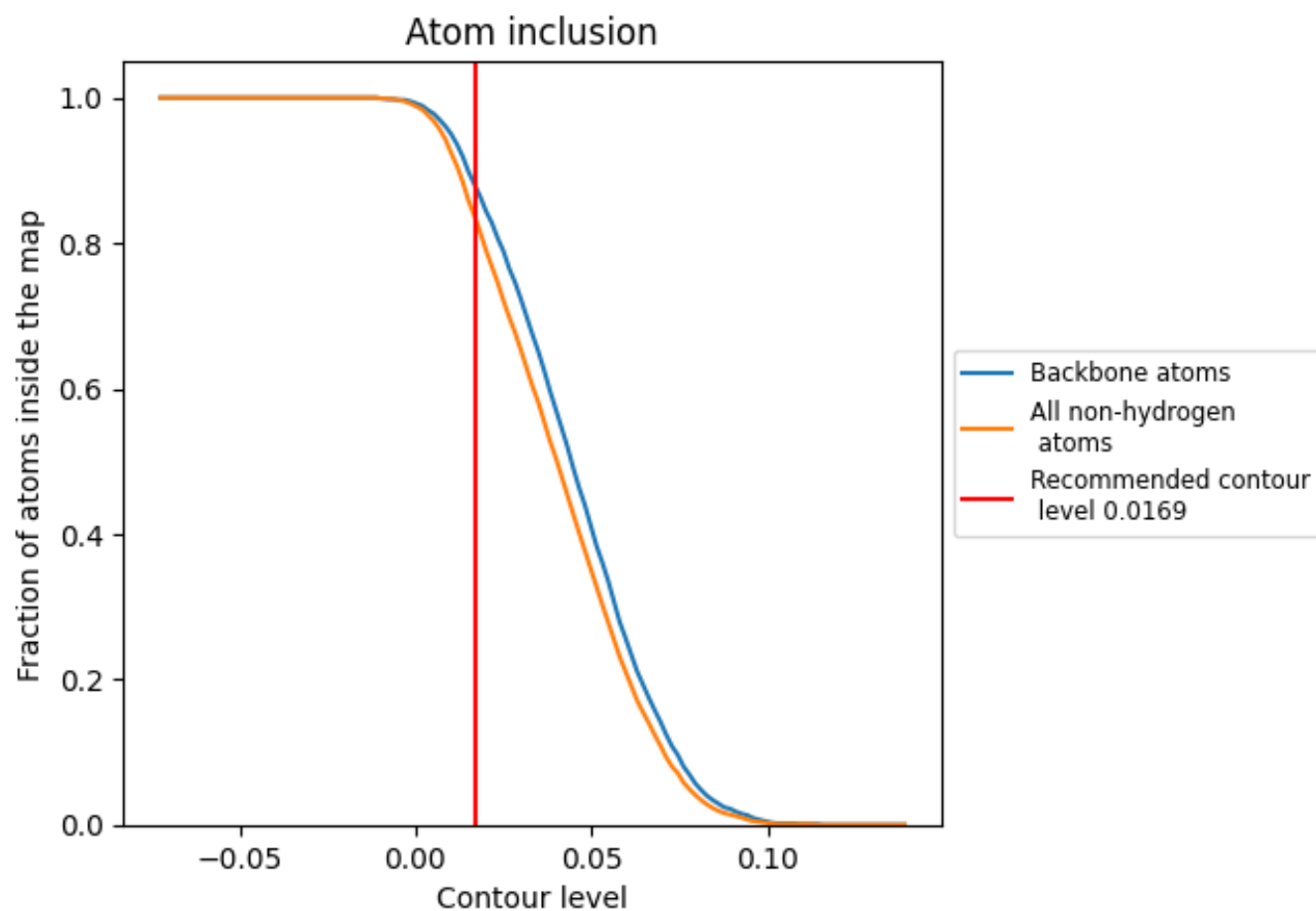
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0169).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.0169) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8360	<div></div> 0.6480
A	<div></div> 0.8360	<div></div> 0.6470
B	<div></div> 0.8410	<div></div> 0.6490

