



wwPDB EM Validation Summary Report ⓘ

Sep 22, 2026 – 08:49 PM EDT

PDB ID : 9ZO8 / pdb_00009zo8
EMDB ID : EMD-74471
Title : Structure of RyR1 in presence of rosuvastatin (including auxiliary transmembrane helices TMx1 and TMx2; Ca²⁺/CFF/ATP dataset; closed pore)
Authors : Weninger, G.; Marks, A.R.
Deposited on : 2025-12-15
Resolution : 2.70 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

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:

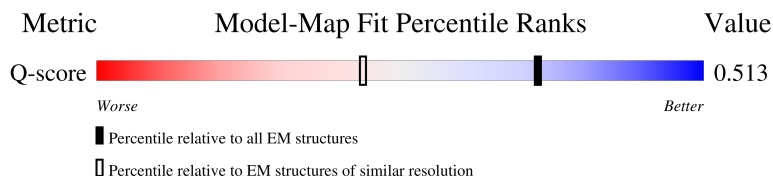
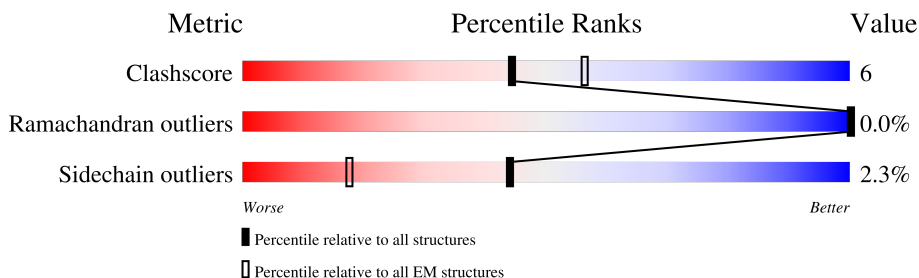
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

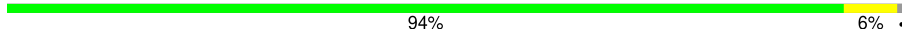
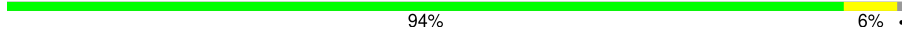
The reported resolution of this entry is 2.70 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	E	108	 93% 6% •
1	F	108	 94% 6% •
1	G	108	 94% 6% •
1	H	108	 94% 6% •

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Mol	Chain	Length	Quality of chain
2	A	5037	9% 74% 13% 12%
2	B	5037	9% 75% 13% 12%
2	C	5037	9% 74% 13% 12%
2	D	5037	9% 74% 13% 12%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 144732 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 Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	107	Total	C	N	O	S	0	0
			831	527	146	154	4		
1	F	107	Total	C	N	O	S	0	0
			831	527	146	154	4		
1	G	107	Total	C	N	O	S	0	0
			831	527	146	154	4		
1	H	107	Total	C	N	O	S	0	0
			831	527	146	154	4		

- Molecule 2 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	4433	Total	C	N	O	S	6	0
			35197	22383	6068	6509	237		
2	B	4433	Total	C	N	O	S	6	0
			35197	22383	6068	6509	237		
2	D	4433	Total	C	N	O	S	6	0
			35197	22383	6068	6509	237		
2	C	4433	Total	C	N	O	S	6	0
			35197	22383	6068	6509	237		

There are 200 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4279	UNK	ALA	conflict	UNP P11716
A	4280	UNK	GLY	conflict	UNP P11716
A	4281	UNK	ALA	conflict	UNP P11716
A	4282	UNK	GLU	conflict	UNP P11716
A	4283	UNK	GLY	conflict	UNP P11716
A	4284	UNK	ALA	conflict	UNP P11716
A	4285	UNK	ALA	conflict	UNP P11716
A	4286	UNK	GLY	conflict	UNP P11716
A	4287	UNK	THR	conflict	UNP P11716

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Chain	Residue	Modelled	Actual	Comment	Reference
A	4288	UNK	VAL	conflict	UNP P11716
A	4289	UNK	ALA	conflict	UNP P11716
A	4290	UNK	ALA	conflict	UNP P11716
A	4291	UNK	GLY	conflict	UNP P11716
A	4292	UNK	ALA	conflict	UNP P11716
A	4293	UNK	THR	conflict	UNP P11716
A	4294	UNK	ALA	conflict	UNP P11716
A	4295	UNK	ARG	conflict	UNP P11716
A	4296	UNK	LEU	conflict	UNP P11716
A	4297	UNK	ALA	conflict	UNP P11716
A	4298	UNK	ALA	conflict	UNP P11716
A	4299	UNK	ALA	conflict	UNP P11716
A	4300	UNK	ALA	conflict	UNP P11716
A	4301	UNK	ALA	conflict	UNP P11716
A	4302	UNK	ARG	conflict	UNP P11716
A	4318	UNK	ARG	conflict	UNP P11716
A	4319	UNK	LEU	conflict	UNP P11716
A	4320	UNK	ARG	conflict	UNP P11716
A	4321	UNK	ARG	conflict	UNP P11716
A	4322	UNK	LEU	conflict	UNP P11716
A	4323	UNK	THR	conflict	UNP P11716
A	4324	UNK	ALA	conflict	UNP P11716
A	4325	UNK	ARG	conflict	UNP P11716
A	4326	UNK	GLU	conflict	UNP P11716
A	4327	UNK	ALA	conflict	UNP P11716
A	4328	UNK	ALA	conflict	UNP P11716
A	4329	UNK	THR	conflict	UNP P11716
A	4330	UNK	ALA	conflict	UNP P11716
A	4331	UNK	LEU	conflict	UNP P11716
A	4332	UNK	ALA	conflict	UNP P11716
A	4333	UNK	ALA	conflict	UNP P11716
A	4334	UNK	LEU	conflict	UNP P11716
A	4335	UNK	LEU	conflict	UNP P11716
A	4336	UNK	TRP	conflict	UNP P11716
A	4337	UNK	ALA	conflict	UNP P11716
A	4338	UNK	VAL	conflict	UNP P11716
A	4339	UNK	VAL	conflict	UNP P11716
A	4340	UNK	ALA	conflict	UNP P11716
A	4341	UNK	ARG	conflict	UNP P11716
A	4342	UNK	ALA	conflict	UNP P11716
A	4343	UNK	GLY	conflict	UNP P11716
B	4279	UNK	ALA	conflict	UNP P11716

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Chain	Residue	Modelled	Actual	Comment	Reference
B	4280	UNK	GLY	conflict	UNP P11716
B	4281	UNK	ALA	conflict	UNP P11716
B	4282	UNK	GLU	conflict	UNP P11716
B	4283	UNK	GLY	conflict	UNP P11716
B	4284	UNK	ALA	conflict	UNP P11716
B	4285	UNK	ALA	conflict	UNP P11716
B	4286	UNK	GLY	conflict	UNP P11716
B	4287	UNK	THR	conflict	UNP P11716
B	4288	UNK	VAL	conflict	UNP P11716
B	4289	UNK	ALA	conflict	UNP P11716
B	4290	UNK	ALA	conflict	UNP P11716
B	4291	UNK	GLY	conflict	UNP P11716
B	4292	UNK	ALA	conflict	UNP P11716
B	4293	UNK	THR	conflict	UNP P11716
B	4294	UNK	ALA	conflict	UNP P11716
B	4295	UNK	ARG	conflict	UNP P11716
B	4296	UNK	LEU	conflict	UNP P11716
B	4297	UNK	ALA	conflict	UNP P11716
B	4298	UNK	ALA	conflict	UNP P11716
B	4299	UNK	ALA	conflict	UNP P11716
B	4300	UNK	ALA	conflict	UNP P11716
B	4301	UNK	ALA	conflict	UNP P11716
B	4302	UNK	ARG	conflict	UNP P11716
B	4318	UNK	ARG	conflict	UNP P11716
B	4319	UNK	LEU	conflict	UNP P11716
B	4320	UNK	ARG	conflict	UNP P11716
B	4321	UNK	ARG	conflict	UNP P11716
B	4322	UNK	LEU	conflict	UNP P11716
B	4323	UNK	THR	conflict	UNP P11716
B	4324	UNK	ALA	conflict	UNP P11716
B	4325	UNK	ARG	conflict	UNP P11716
B	4326	UNK	GLU	conflict	UNP P11716
B	4327	UNK	ALA	conflict	UNP P11716
B	4328	UNK	ALA	conflict	UNP P11716
B	4329	UNK	THR	conflict	UNP P11716
B	4330	UNK	ALA	conflict	UNP P11716
B	4331	UNK	LEU	conflict	UNP P11716
B	4332	UNK	ALA	conflict	UNP P11716
B	4333	UNK	ALA	conflict	UNP P11716
B	4334	UNK	LEU	conflict	UNP P11716
B	4335	UNK	LEU	conflict	UNP P11716
B	4336	UNK	TRP	conflict	UNP P11716

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Chain	Residue	Modelled	Actual	Comment	Reference
B	4337	UNK	ALA	conflict	UNP P11716
B	4338	UNK	VAL	conflict	UNP P11716
B	4339	UNK	VAL	conflict	UNP P11716
B	4340	UNK	ALA	conflict	UNP P11716
B	4341	UNK	ARG	conflict	UNP P11716
B	4342	UNK	ALA	conflict	UNP P11716
B	4343	UNK	GLY	conflict	UNP P11716
D	4279	UNK	ALA	conflict	UNP P11716
D	4280	UNK	GLY	conflict	UNP P11716
D	4281	UNK	ALA	conflict	UNP P11716
D	4282	UNK	GLU	conflict	UNP P11716
D	4283	UNK	GLY	conflict	UNP P11716
D	4284	UNK	ALA	conflict	UNP P11716
D	4285	UNK	ALA	conflict	UNP P11716
D	4286	UNK	GLY	conflict	UNP P11716
D	4287	UNK	THR	conflict	UNP P11716
D	4288	UNK	VAL	conflict	UNP P11716
D	4289	UNK	ALA	conflict	UNP P11716
D	4290	UNK	ALA	conflict	UNP P11716
D	4291	UNK	GLY	conflict	UNP P11716
D	4292	UNK	ALA	conflict	UNP P11716
D	4293	UNK	THR	conflict	UNP P11716
D	4294	UNK	ALA	conflict	UNP P11716
D	4295	UNK	ARG	conflict	UNP P11716
D	4296	UNK	LEU	conflict	UNP P11716
D	4297	UNK	ALA	conflict	UNP P11716
D	4298	UNK	ALA	conflict	UNP P11716
D	4299	UNK	ALA	conflict	UNP P11716
D	4300	UNK	ALA	conflict	UNP P11716
D	4301	UNK	ALA	conflict	UNP P11716
D	4302	UNK	ARG	conflict	UNP P11716
D	4318	UNK	ARG	conflict	UNP P11716
D	4319	UNK	LEU	conflict	UNP P11716
D	4320	UNK	ARG	conflict	UNP P11716
D	4321	UNK	ARG	conflict	UNP P11716
D	4322	UNK	LEU	conflict	UNP P11716
D	4323	UNK	THR	conflict	UNP P11716
D	4324	UNK	ALA	conflict	UNP P11716
D	4325	UNK	ARG	conflict	UNP P11716
D	4326	UNK	GLU	conflict	UNP P11716
D	4327	UNK	ALA	conflict	UNP P11716
D	4328	UNK	ALA	conflict	UNP P11716

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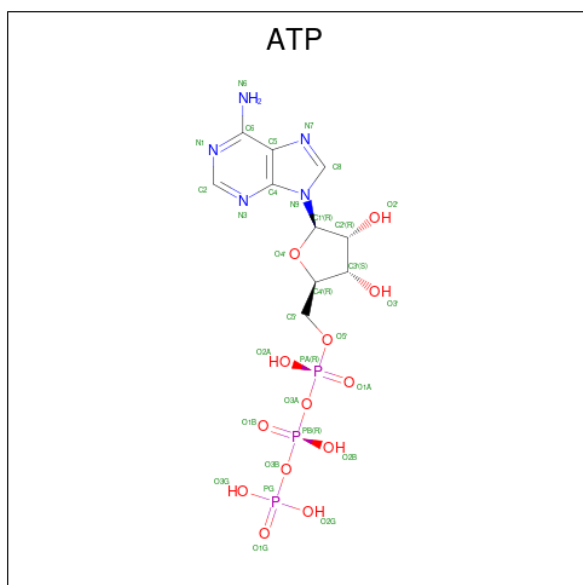
Chain	Residue	Modelled	Actual	Comment	Reference
D	4329	UNK	THR	conflict	UNP P11716
D	4330	UNK	ALA	conflict	UNP P11716
D	4331	UNK	LEU	conflict	UNP P11716
D	4332	UNK	ALA	conflict	UNP P11716
D	4333	UNK	ALA	conflict	UNP P11716
D	4334	UNK	LEU	conflict	UNP P11716
D	4335	UNK	LEU	conflict	UNP P11716
D	4336	UNK	TRP	conflict	UNP P11716
D	4337	UNK	ALA	conflict	UNP P11716
D	4338	UNK	VAL	conflict	UNP P11716
D	4339	UNK	VAL	conflict	UNP P11716
D	4340	UNK	ALA	conflict	UNP P11716
D	4341	UNK	ARG	conflict	UNP P11716
D	4342	UNK	ALA	conflict	UNP P11716
D	4343	UNK	GLY	conflict	UNP P11716
C	4279	UNK	ALA	conflict	UNP P11716
C	4280	UNK	GLY	conflict	UNP P11716
C	4281	UNK	ALA	conflict	UNP P11716
C	4282	UNK	GLU	conflict	UNP P11716
C	4283	UNK	GLY	conflict	UNP P11716
C	4284	UNK	ALA	conflict	UNP P11716
C	4285	UNK	ALA	conflict	UNP P11716
C	4286	UNK	GLY	conflict	UNP P11716
C	4287	UNK	THR	conflict	UNP P11716
C	4288	UNK	VAL	conflict	UNP P11716
C	4289	UNK	ALA	conflict	UNP P11716
C	4290	UNK	ALA	conflict	UNP P11716
C	4291	UNK	GLY	conflict	UNP P11716
C	4292	UNK	ALA	conflict	UNP P11716
C	4293	UNK	THR	conflict	UNP P11716
C	4294	UNK	ALA	conflict	UNP P11716
C	4295	UNK	ARG	conflict	UNP P11716
C	4296	UNK	LEU	conflict	UNP P11716
C	4297	UNK	ALA	conflict	UNP P11716
C	4298	UNK	ALA	conflict	UNP P11716
C	4299	UNK	ALA	conflict	UNP P11716
C	4300	UNK	ALA	conflict	UNP P11716
C	4301	UNK	ALA	conflict	UNP P11716
C	4302	UNK	ARG	conflict	UNP P11716
C	4318	UNK	ARG	conflict	UNP P11716
C	4319	UNK	LEU	conflict	UNP P11716
C	4320	UNK	ARG	conflict	UNP P11716

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Chain	Residue	Modelled	Actual	Comment	Reference
C	4321	UNK	ARG	conflict	UNP P11716
C	4322	UNK	LEU	conflict	UNP P11716
C	4323	UNK	THR	conflict	UNP P11716
C	4324	UNK	ALA	conflict	UNP P11716
C	4325	UNK	ARG	conflict	UNP P11716
C	4326	UNK	GLU	conflict	UNP P11716
C	4327	UNK	ALA	conflict	UNP P11716
C	4328	UNK	ALA	conflict	UNP P11716
C	4329	UNK	THR	conflict	UNP P11716
C	4330	UNK	ALA	conflict	UNP P11716
C	4331	UNK	LEU	conflict	UNP P11716
C	4332	UNK	ALA	conflict	UNP P11716
C	4333	UNK	ALA	conflict	UNP P11716
C	4334	UNK	LEU	conflict	UNP P11716
C	4335	UNK	LEU	conflict	UNP P11716
C	4336	UNK	TRP	conflict	UNP P11716
C	4337	UNK	ALA	conflict	UNP P11716
C	4338	UNK	VAL	conflict	UNP P11716
C	4339	UNK	VAL	conflict	UNP P11716
C	4340	UNK	ALA	conflict	UNP P11716
C	4341	UNK	ARG	conflict	UNP P11716
C	4342	UNK	ALA	conflict	UNP P11716
C	4343	UNK	GLY	conflict	UNP P11716

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	C	1	Total	C	N	O	P	0
			31	10	5	13	3	

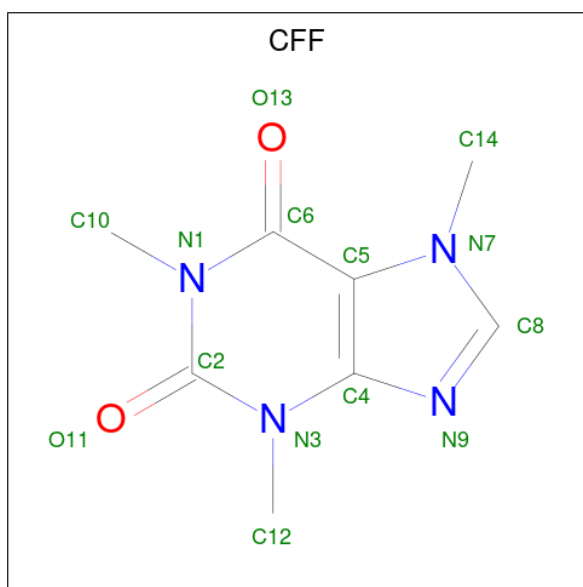
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Ca	0
			1	1	
4	B	1	Total	Ca	0
			1	1	
4	D	1	Total	Ca	0
			1	1	
4	C	1	Total	Ca	0
			1	1	

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

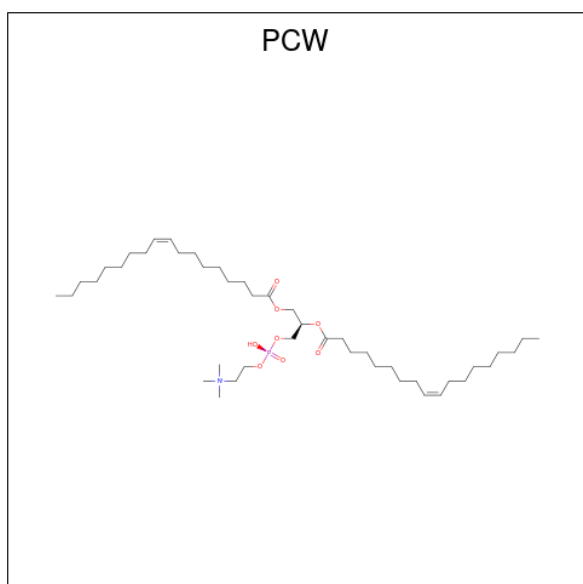
Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Zn	0
			1	1	
5	B	1	Total	Zn	0
			1	1	
5	D	1	Total	Zn	0
			1	1	
5	C	1	Total	Zn	0
			1	1	

- Molecule 6 is CAFFEINE (CCD ID: CFF) (formula: C₈H₁₀N₄O₂).



Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	4	2	
6	B	1	Total	C	N	O	0
			14	8	4	2	
6	D	1	Total	C	N	O	0
			14	8	4	2	
6	C	1	Total	C	N	O	0
			14	8	4	2	

- Molecule 7 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: $C_{44}H_{85}NO_8P$).



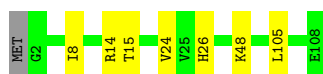
Mol	Chain	Residues	Atoms					AltConf
7	A	1	Total	C	N	O	P	0
			54	44	1	8	1	
7	A	1	Total	C	N	O	P	0
			54	44	1	8	1	
7	A	1	Total	C	N	O	P	0
			54	44	1	8	1	
7	B	1	Total	C	N	O	P	0
			54	44	1	8	1	
7	B	1	Total	C	N	O	P	0
			54	44	1	8	1	
7	D	1	Total	C	N	O	P	0
			54	44	1	8	1	
7	C	1	Total	C	N	O	P	0
			54	44	1	8	1	
7	C	1	Total	C	N	O	P	0
			54	44	1	8	1	

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 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: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain E: 

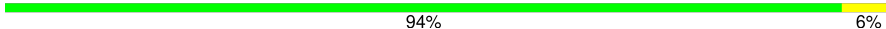


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain F: 

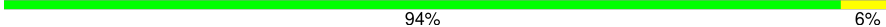


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain G: 



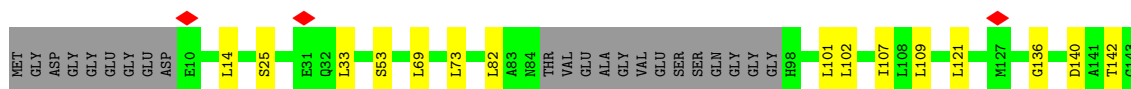
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain H: 



- Molecule 2: Ryanodine receptor 1

Chain A: 









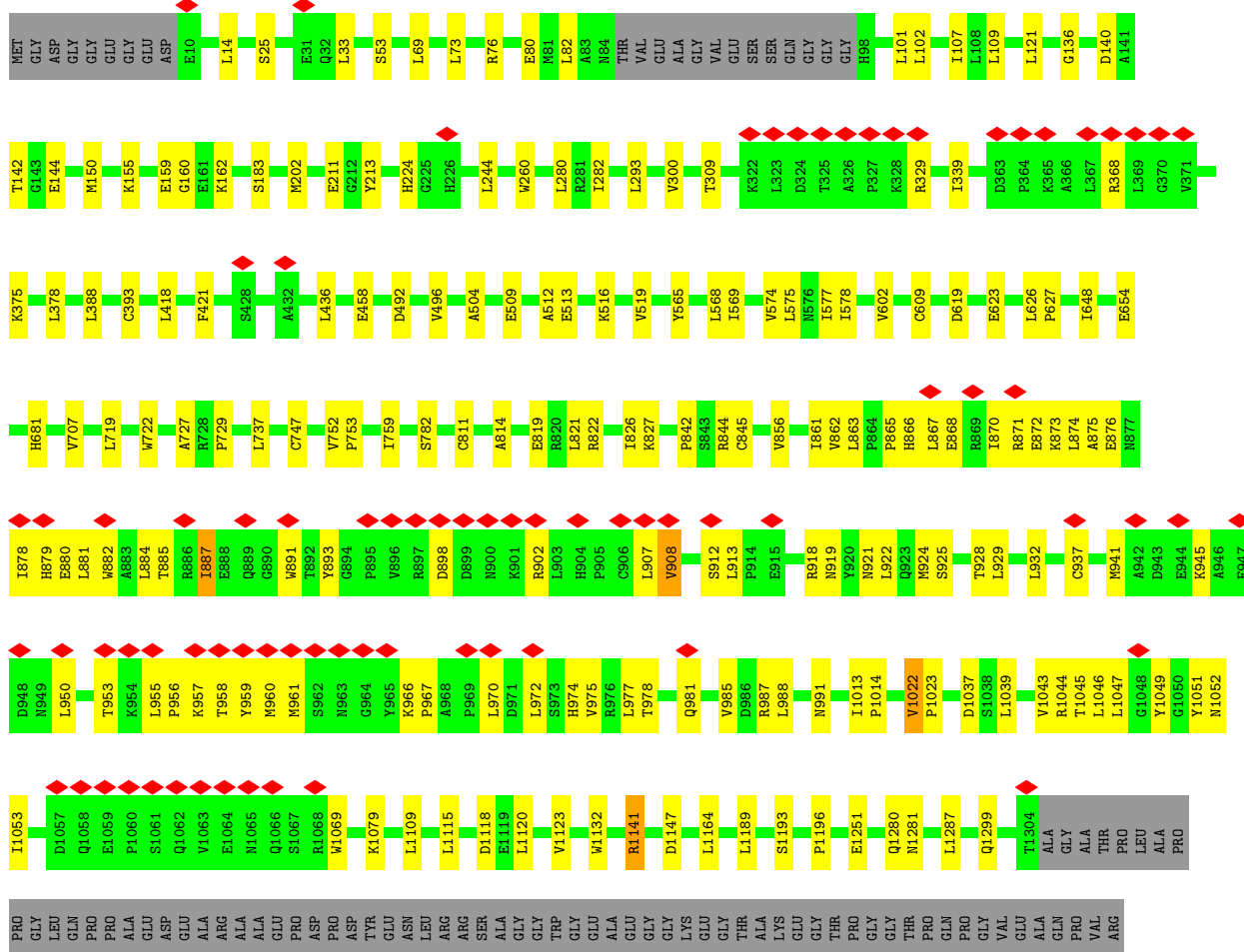
Frequency	Percentage
Very often	9%
Often	75%
Sometimes	13%
Never	12%







- Molecule 2: Ryanodine receptor 1







Chain C:







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	142752	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52.95	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.613	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	422.4, 422.4, 422.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CFF, CA, ZN, PCW, ATP

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	E	0.13	0/850	0.34	0/1146
1	F	0.13	0/850	0.34	0/1146
1	G	0.13	0/850	0.34	0/1146
1	H	0.13	0/850	0.34	0/1146
2	A	0.15	0/35759	0.38	1/48435 (0.0%)
2	B	0.16	0/35759	0.38	1/48435 (0.0%)
2	C	0.16	0/35759	0.38	1/48435 (0.0%)
2	D	0.16	0/35759	0.38	1/48435 (0.0%)
All	All	0.15	0/146436	0.38	4/198324 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3240	CYS	CA-CB-SG	5.48	127.00	114.40
2	A	3240	CYS	CA-CB-SG	5.47	126.99	114.40
2	B	3240	CYS	CA-CB-SG	5.46	126.95	114.40
2	D	3240	CYS	CA-CB-SG	5.46	126.95	114.40

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	E	831	0	828	5	0
1	F	831	0	828	4	0
1	G	831	0	828	3	0
1	H	831	0	828	3	0
2	A	35197	0	34615	455	0
2	B	35197	0	34615	447	0
2	C	35197	0	34615	457	0
2	D	35197	0	34615	453	0
3	A	31	0	12	0	0
3	B	31	0	12	0	0
3	C	31	0	12	0	0
3	D	31	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	14	0	10	0	0
6	B	14	0	10	0	0
6	C	14	0	10	0	0
6	D	14	0	10	0	0
7	A	162	0	252	6	0
7	B	108	0	168	4	0
7	C	108	0	168	5	0
7	D	54	0	84	1	0
All	All	144732	0	142532	1827	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 6.

The worst 5 of 1827 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)
2:C:2178:MET:HE3	2:C:2210:VAL:HG11	1.56	0.87
2:B:2178:MET:HE3	2:B:2210:VAL:HG11	1.56	0.86
2:A:2178:MET:HE3	2:A:2210:VAL:HG11	1.56	0.85
2:D:2178:MET:HE3	2:D:2210:VAL:HG11	1.56	0.85
2:A:955:LEU:HD22	2:A:956:PRO:HD2	1.60	0.83

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	E	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
1	F	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
1	G	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
1	H	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	A	4359/5037 (86%)	4263 (98%)	95 (2%)	1 (0%)	100	100
2	B	4359/5037 (86%)	4262 (98%)	96 (2%)	1 (0%)	100	100
2	C	4359/5037 (86%)	4263 (98%)	95 (2%)	1 (0%)	100	100
2	D	4359/5037 (86%)	4262 (98%)	96 (2%)	1 (0%)	100	100
All	All	17856/20580 (87%)	17458 (98%)	394 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	3300	ALA
2	B	3300	ALA
2	D	3300	ALA
2	C	3300	ALA

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	E	89/90 (99%)	89 (100%)	0	100	100
1	F	89/90 (99%)	89 (100%)	0	100	100
1	G	89/90 (99%)	89 (100%)	0	100	100
1	H	89/90 (99%)	89 (100%)	0	100	100
2	A	3814/4253 (90%)	3725 (98%)	89 (2%)	44	73
2	B	3814/4253 (90%)	3725 (98%)	89 (2%)	44	73
2	C	3814/4253 (90%)	3725 (98%)	89 (2%)	44	73
2	D	3814/4253 (90%)	3723 (98%)	91 (2%)	43	72
All	All	15612/17372 (90%)	15254 (98%)	358 (2%)	44	73

5 of 358 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	2897	LYS
2	C	1022	VAL
2	D	3020	THR
2	D	4082	THR
2	C	2369[A]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	3605	HIS
2	C	2881	ASN
2	D	1545	ASN
2	C	2858	GLN
2	C	3766	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 8 are monoatomic - leaving 16 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	ATP	D	5301	-	32,33,33	0.31	0	48,52,52	0.70	0
3	ATP	C	5301	-	32,33,33	0.31	0	48,52,52	0.70	0
6	CFF	B	5304	-	15,15,15	0.51	0	23,23,23	0.55	0
7	PCW	D	5305	-	53,53,53	0.50	0	59,61,61	0.48	1 (1%)
7	PCW	A	5306	-	53,53,53	0.50	0	59,61,61	0.48	1 (1%)
3	ATP	A	5301	-	32,33,33	0.31	0	48,52,52	0.70	0
6	CFF	C	5304	-	15,15,15	0.52	0	23,23,23	0.53	0
7	PCW	A	5307	-	53,53,53	0.50	0	59,61,61	0.48	0
7	PCW	C	5305	-	53,53,53	0.50	0	59,61,61	0.49	0
3	ATP	B	5301	-	32,33,33	0.31	0	48,52,52	0.70	0
7	PCW	A	5305	-	53,53,53	0.50	0	59,61,61	0.48	0
7	PCW	C	5306	-	53,53,53	0.50	0	59,61,61	0.48	1 (1%)
7	PCW	B	5306	-	53,53,53	0.50	0	59,61,61	0.49	1 (1%)
6	CFF	D	5304	-	15,15,15	0.51	0	23,23,23	0.54	0
6	CFF	A	5304	-	15,15,15	0.51	0	23,23,23	0.54	0
7	PCW	B	5305	-	53,53,53	0.50	0	59,61,61	0.48	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	ATP	D	5301	-	-	5/22/38/38	0/3/3/3
3	ATP	C	5301	-	-	5/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CFF	B	5304	-	-	-	0/2/2/2
7	PCW	D	5305	-	-	32/57/57/57	-
7	PCW	A	5306	-	-	32/57/57/57	-
3	ATP	A	5301	-	-	5/22/38/38	0/3/3/3
7	PCW	A	5307	-	-	32/57/57/57	-
7	PCW	C	5305	-	-	32/57/57/57	-
6	CFF	C	5304	-	-	-	0/2/2/2
3	ATP	B	5301	-	-	5/22/38/38	0/3/3/3
7	PCW	A	5305	-	-	32/57/57/57	-
7	PCW	C	5306	-	-	32/57/57/57	-
7	PCW	B	5306	-	-	32/57/57/57	-
6	CFF	D	5304	-	-	-	0/2/2/2
6	CFF	A	5304	-	-	-	0/2/2/2
7	PCW	B	5305	-	-	32/57/57/57	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	5306	PCW	C3-C2-C1	2.03	116.53	111.78
7	C	5306	PCW	C3-C2-C1	2.03	116.51	111.78
7	A	5306	PCW	C3-C2-C1	2.02	116.49	111.78
7	D	5305	PCW	C3-C2-C1	2.01	116.48	111.78

There are no chirality outliers.

5 of 276 torsion outliers are listed below:

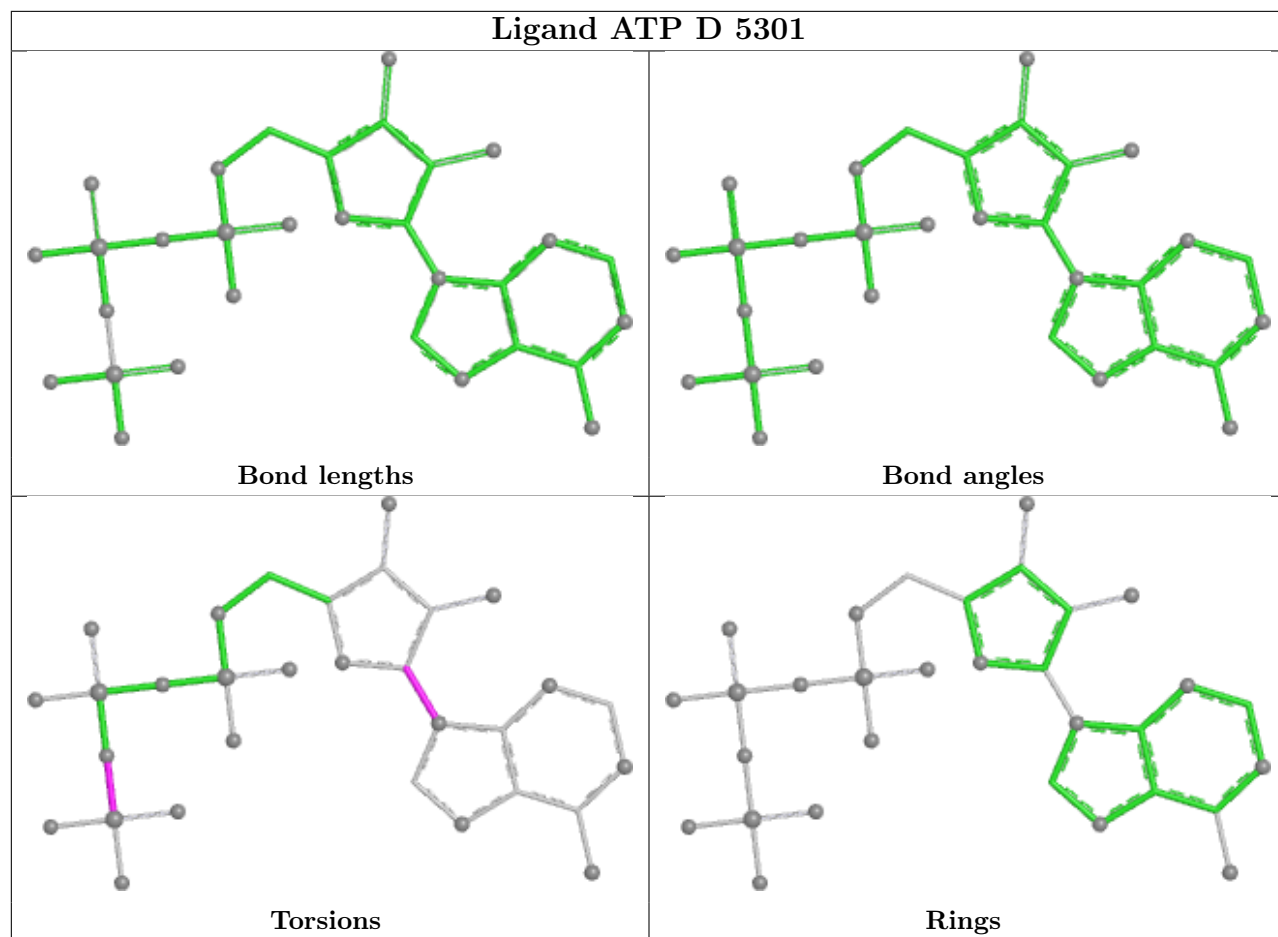
Mol	Chain	Res	Type	Atoms
7	A	5305	PCW	O4P-C4-C5-N
7	A	5305	PCW	C1-O3P-P-O2P
7	A	5305	PCW	C4-O4P-P-O2P
7	A	5305	PCW	C4-O4P-P-O3P
7	A	5306	PCW	C32-C31-O2-C2

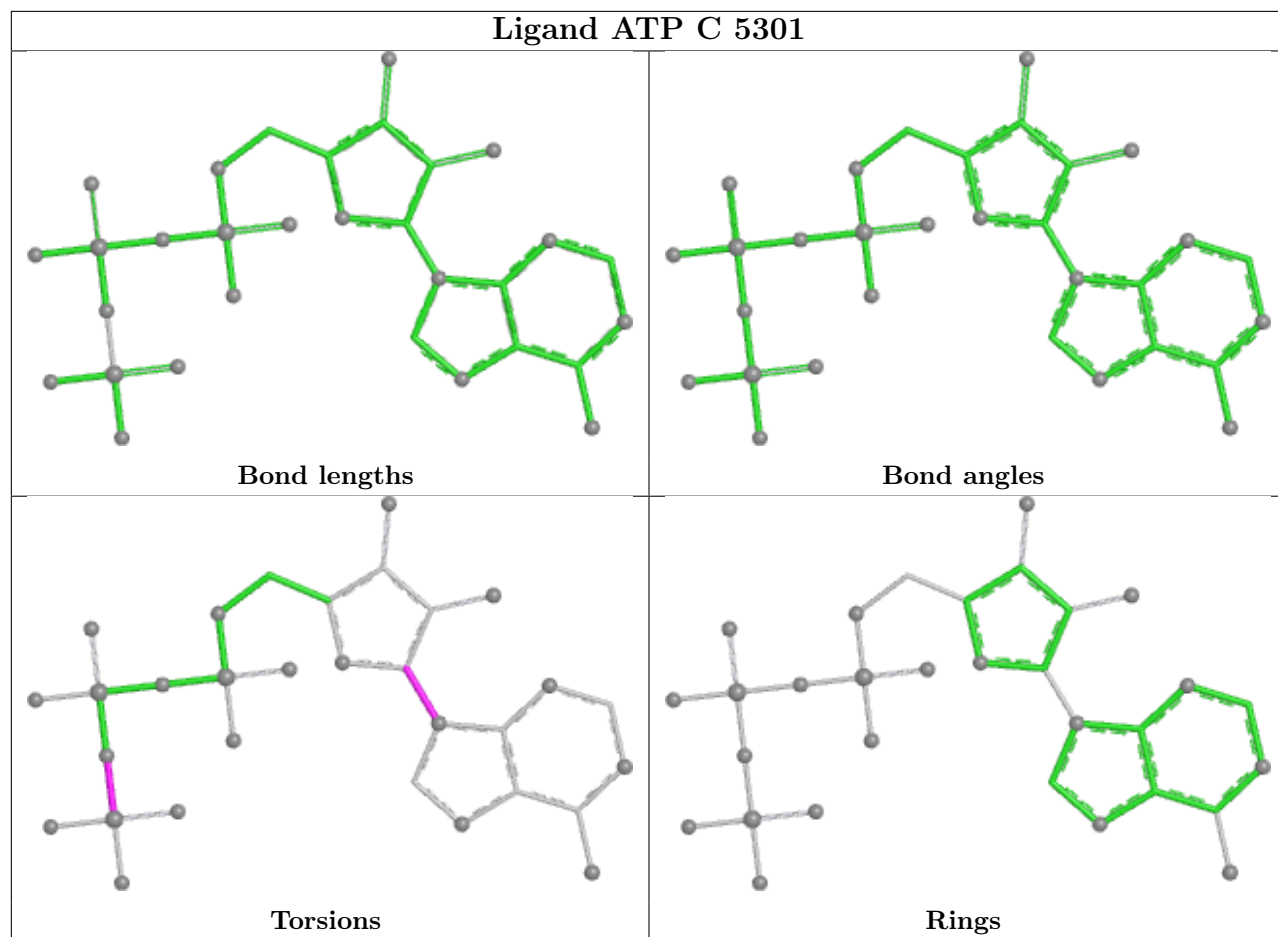
There are no ring outliers.

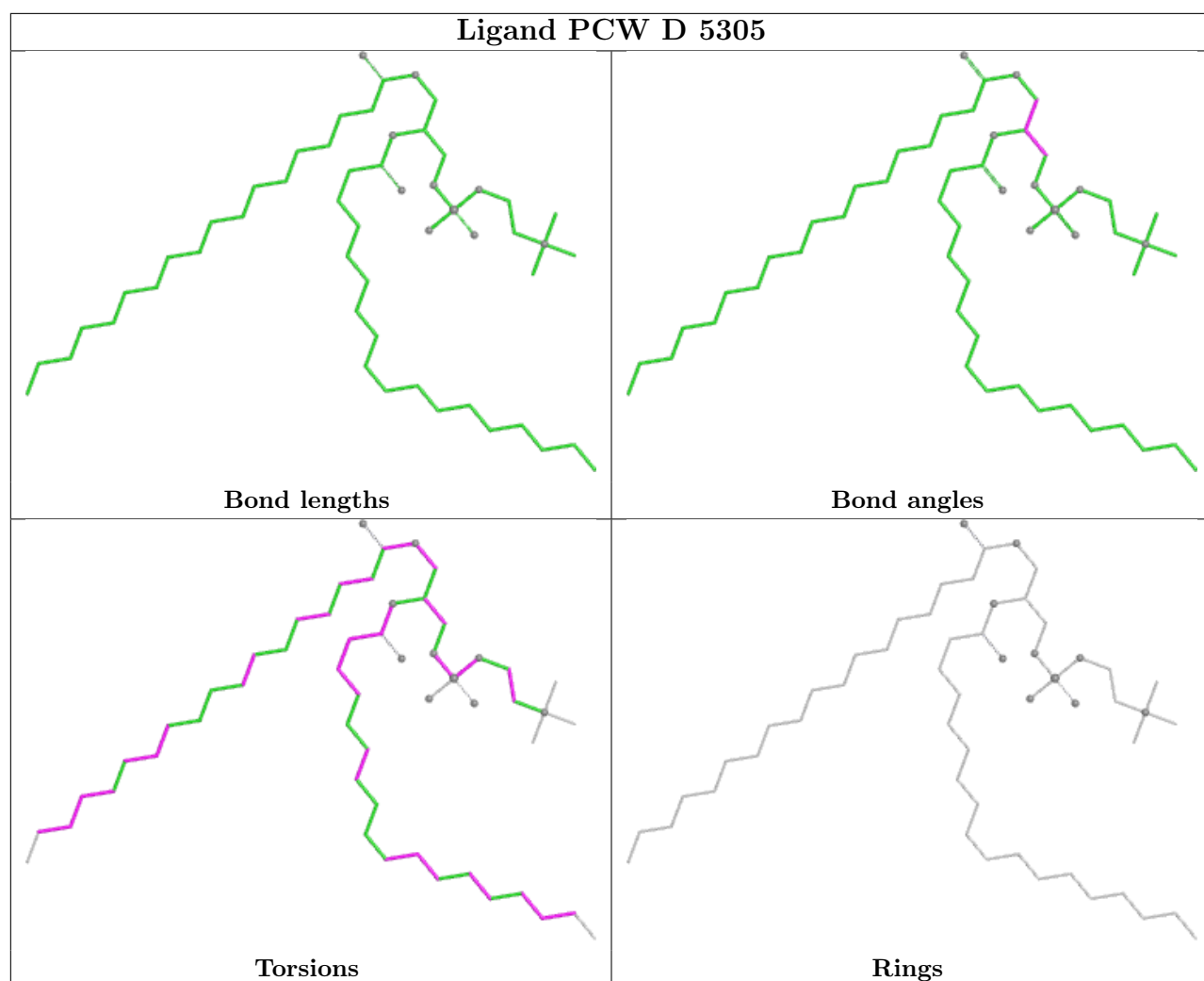
8 monomers are involved in 13 short contacts:

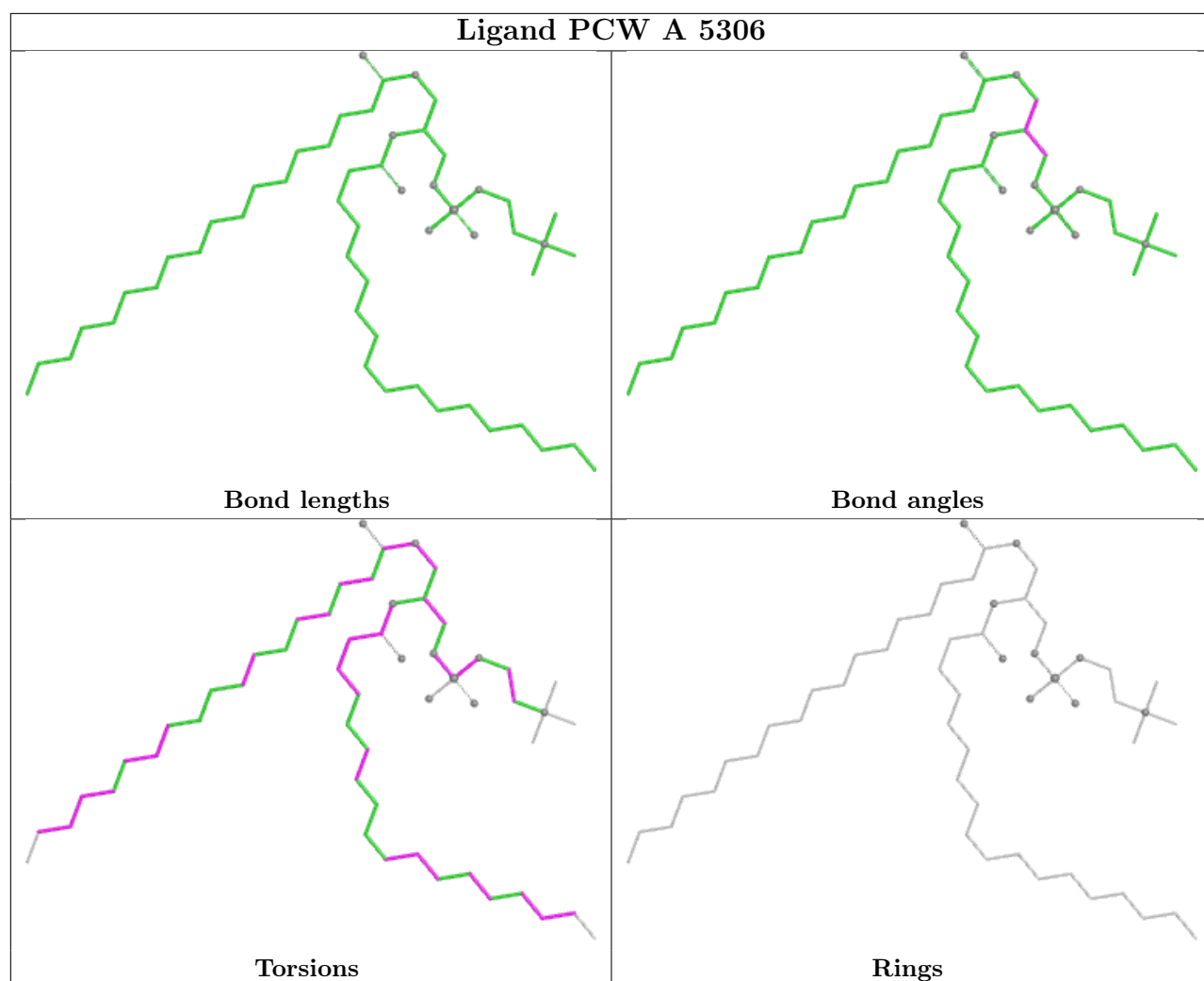
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	5305	PCW	1	0
7	A	5306	PCW	1	0
7	A	5307	PCW	3	0
7	C	5305	PCW	4	0
7	A	5305	PCW	3	0
7	C	5306	PCW	1	0
7	B	5306	PCW	1	0
7	B	5305	PCW	3	0

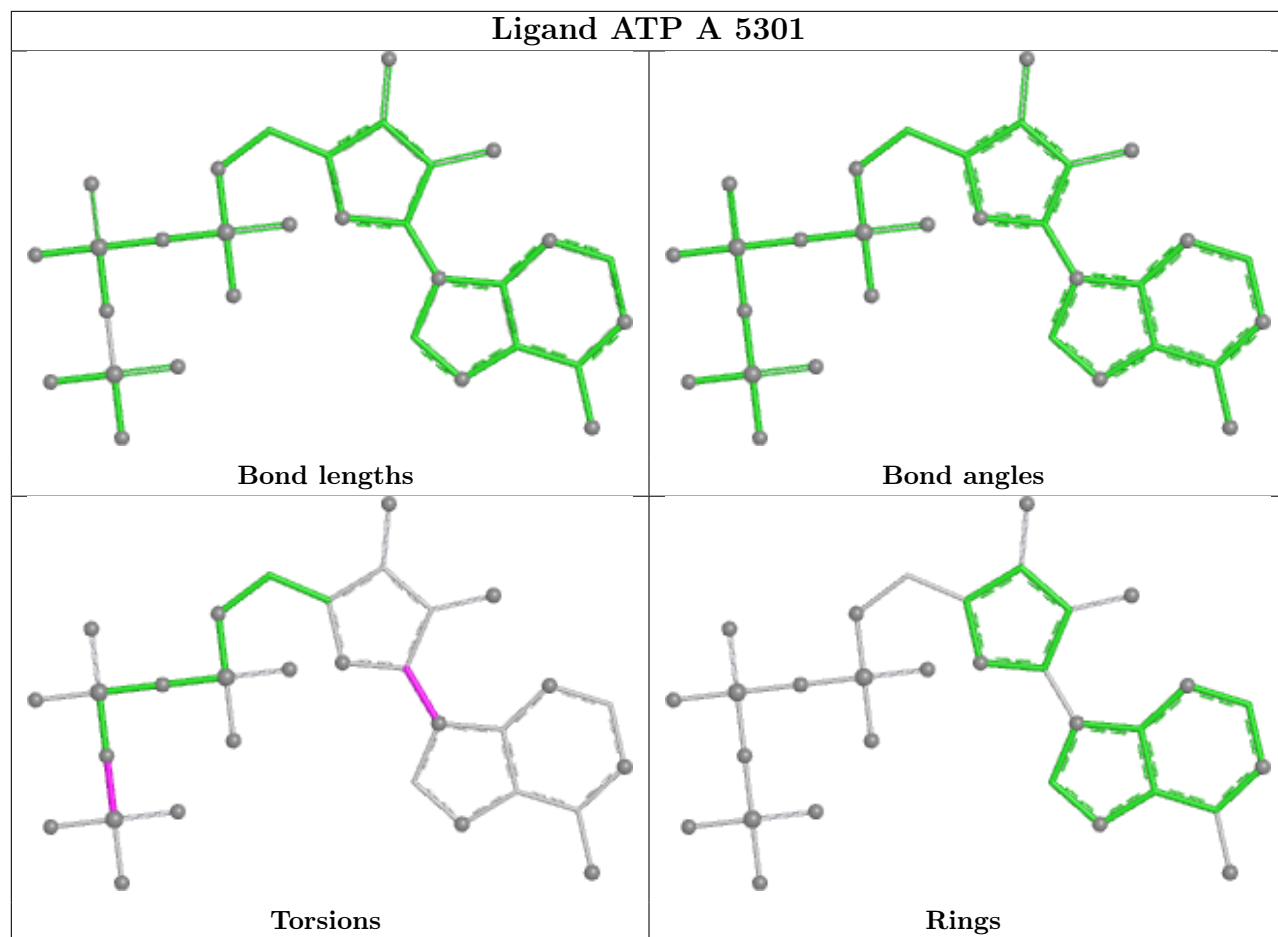
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

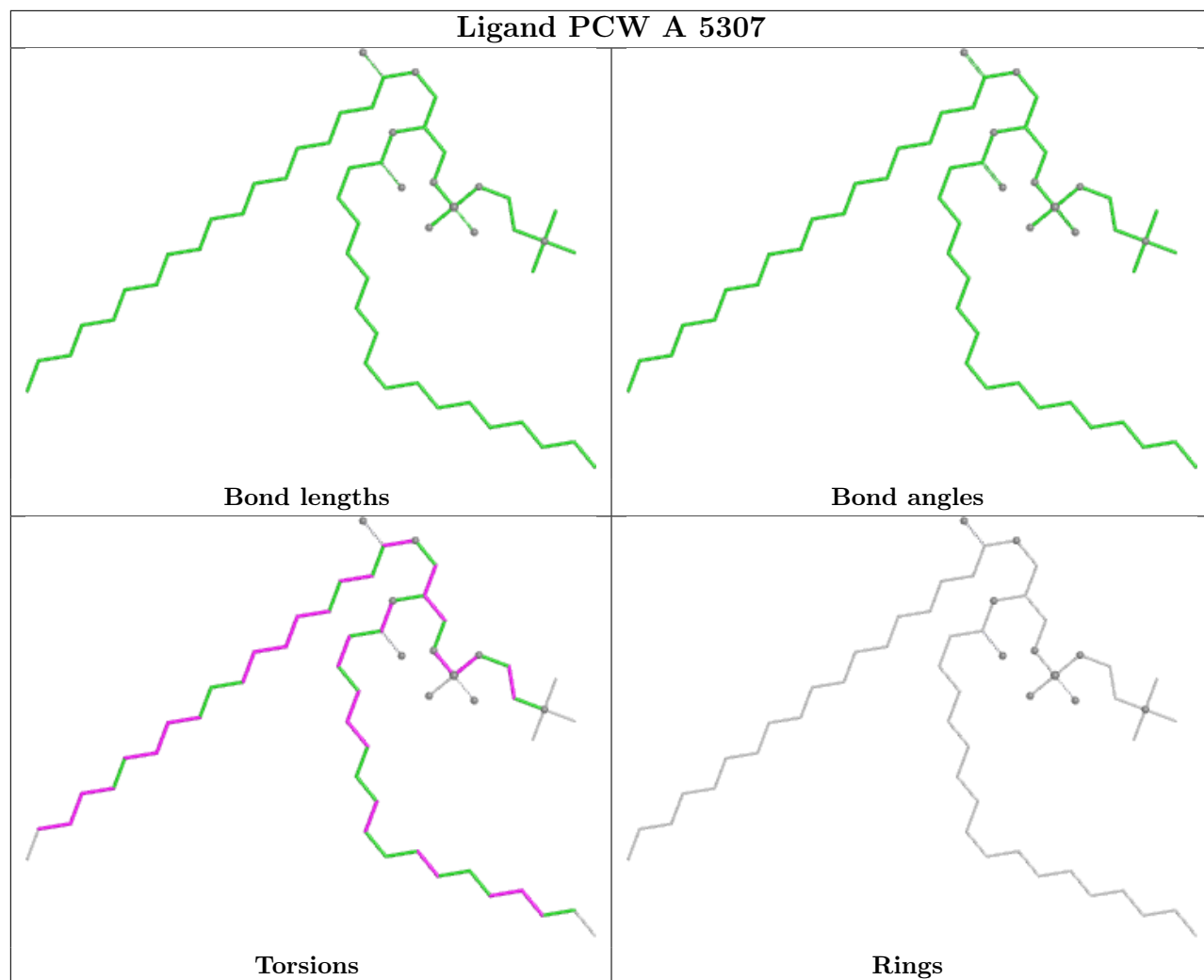


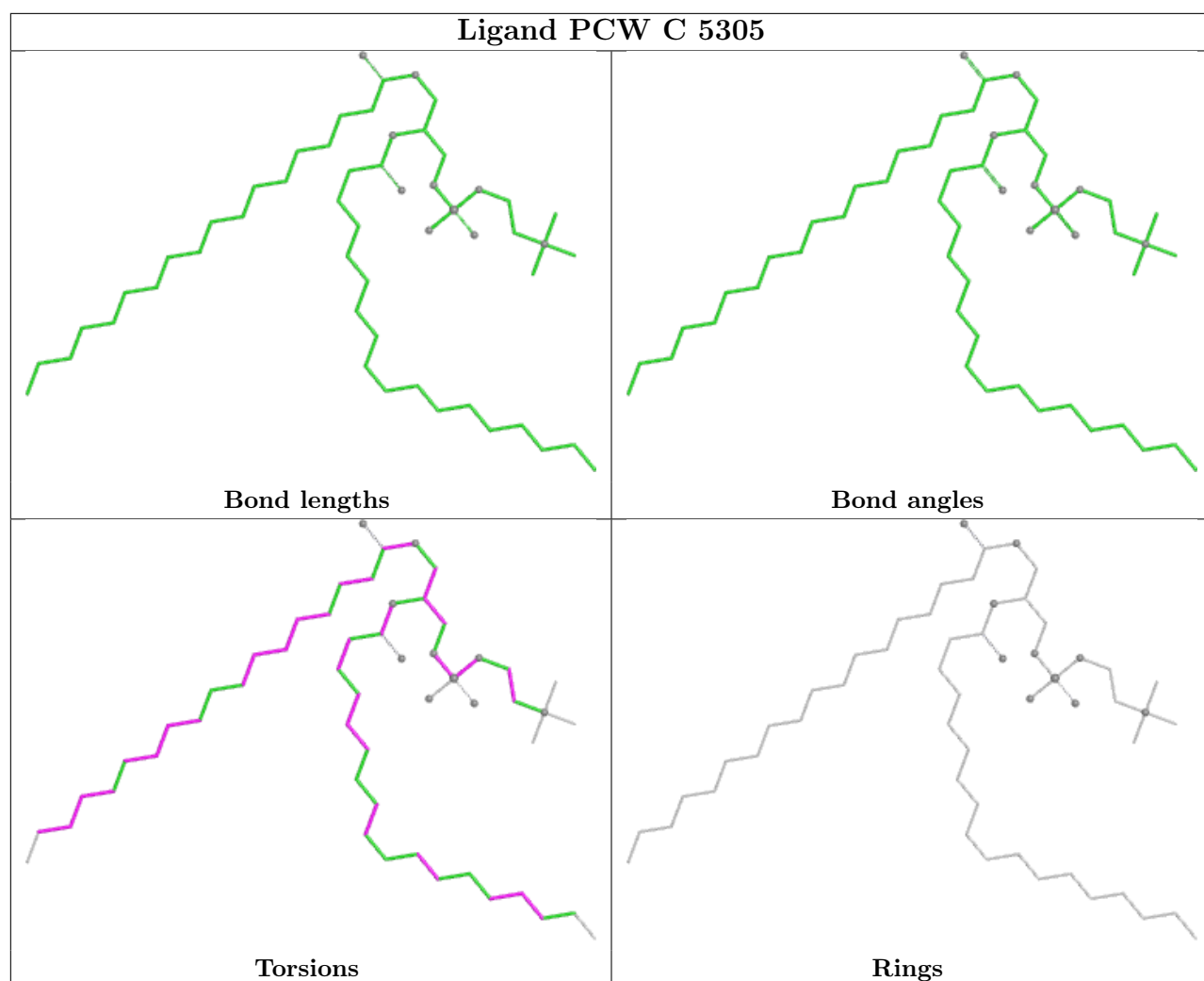


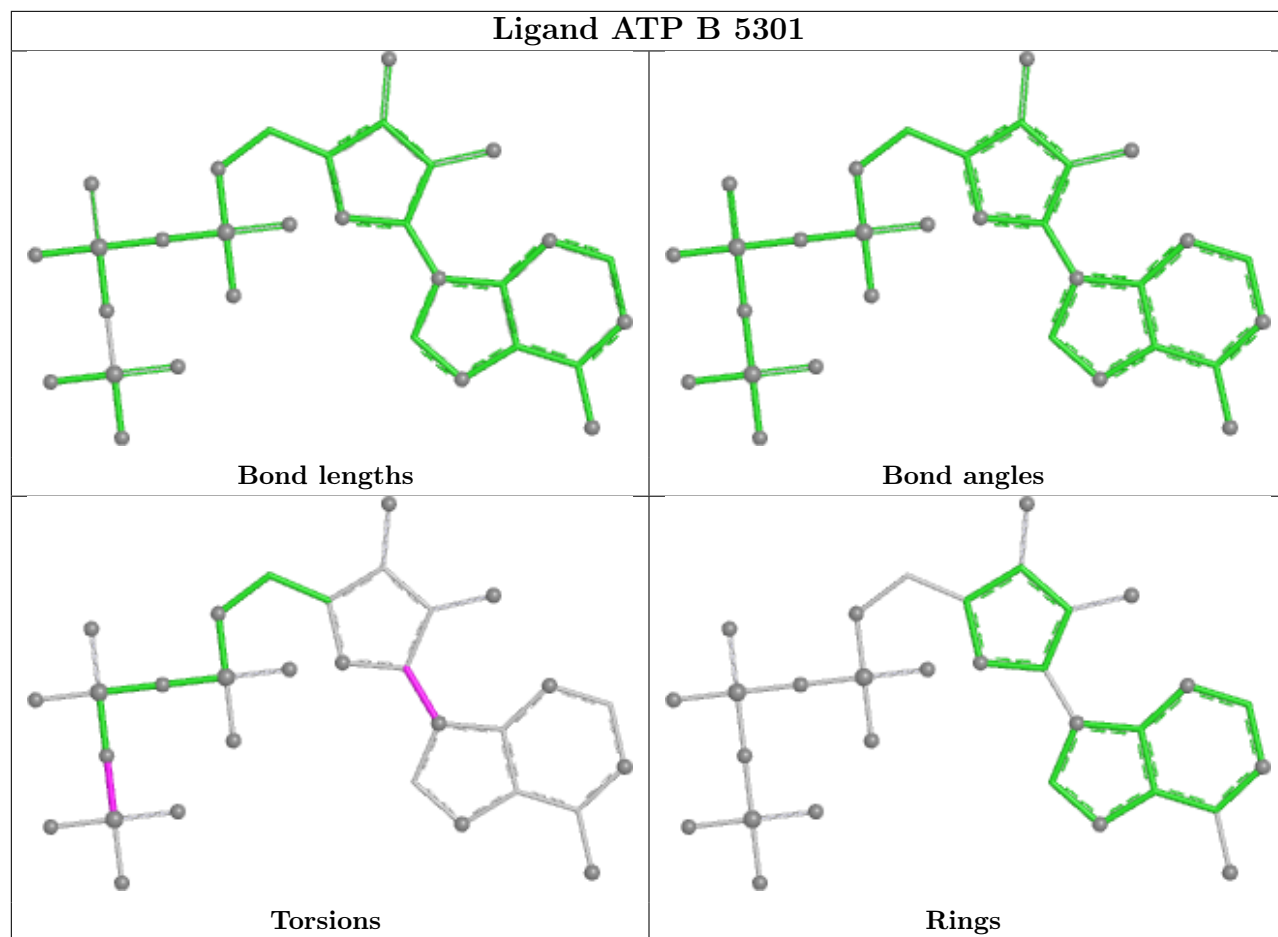


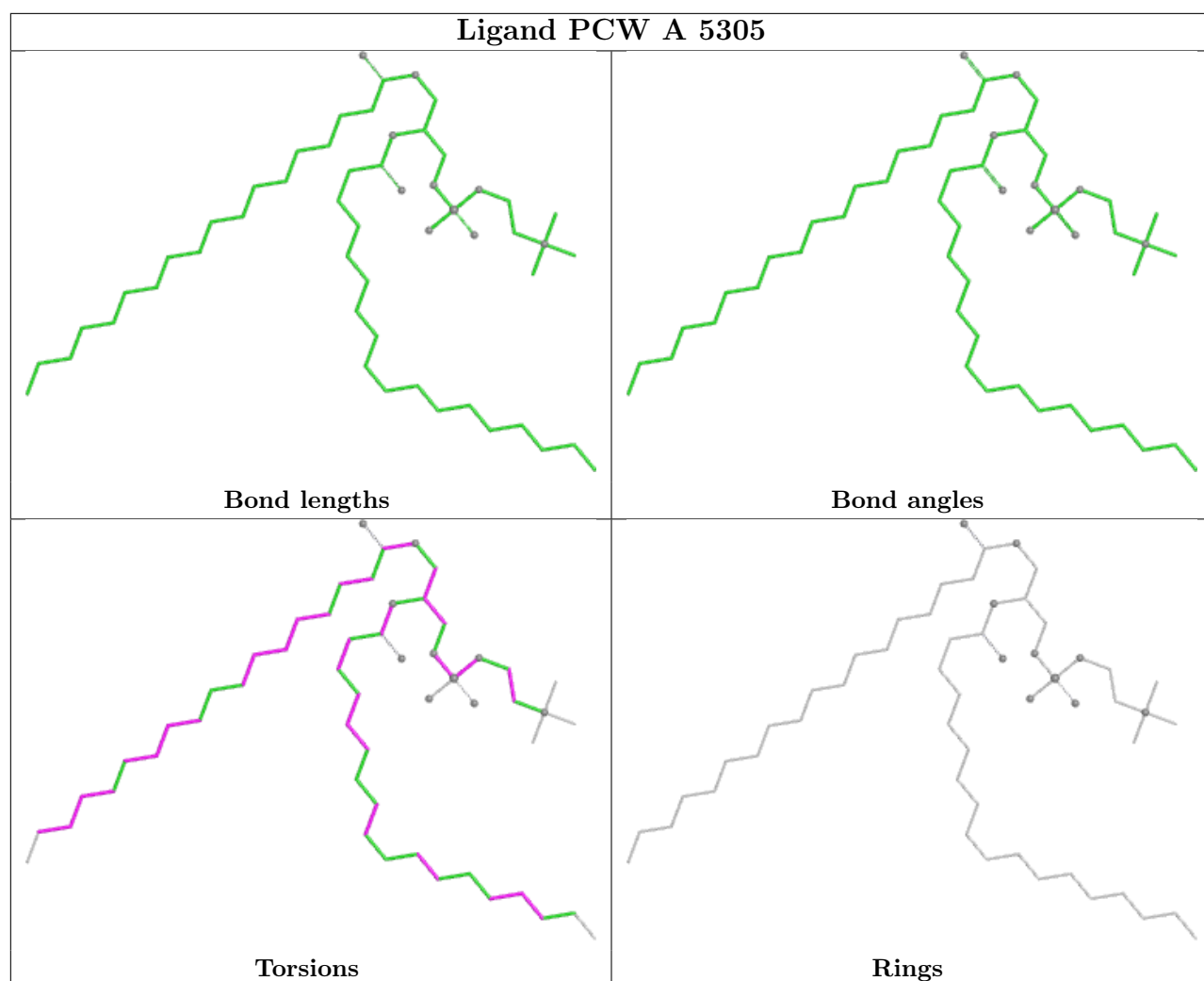


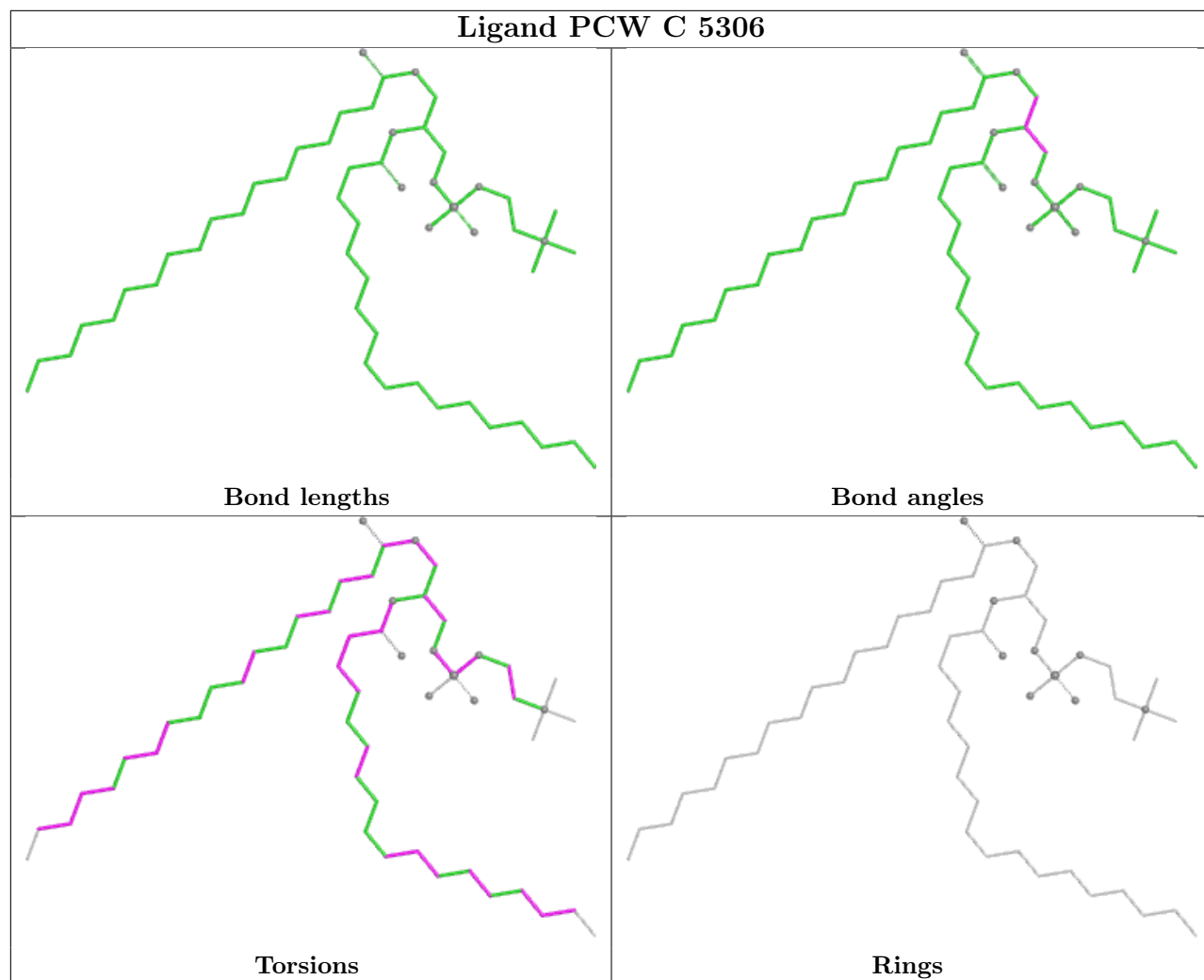


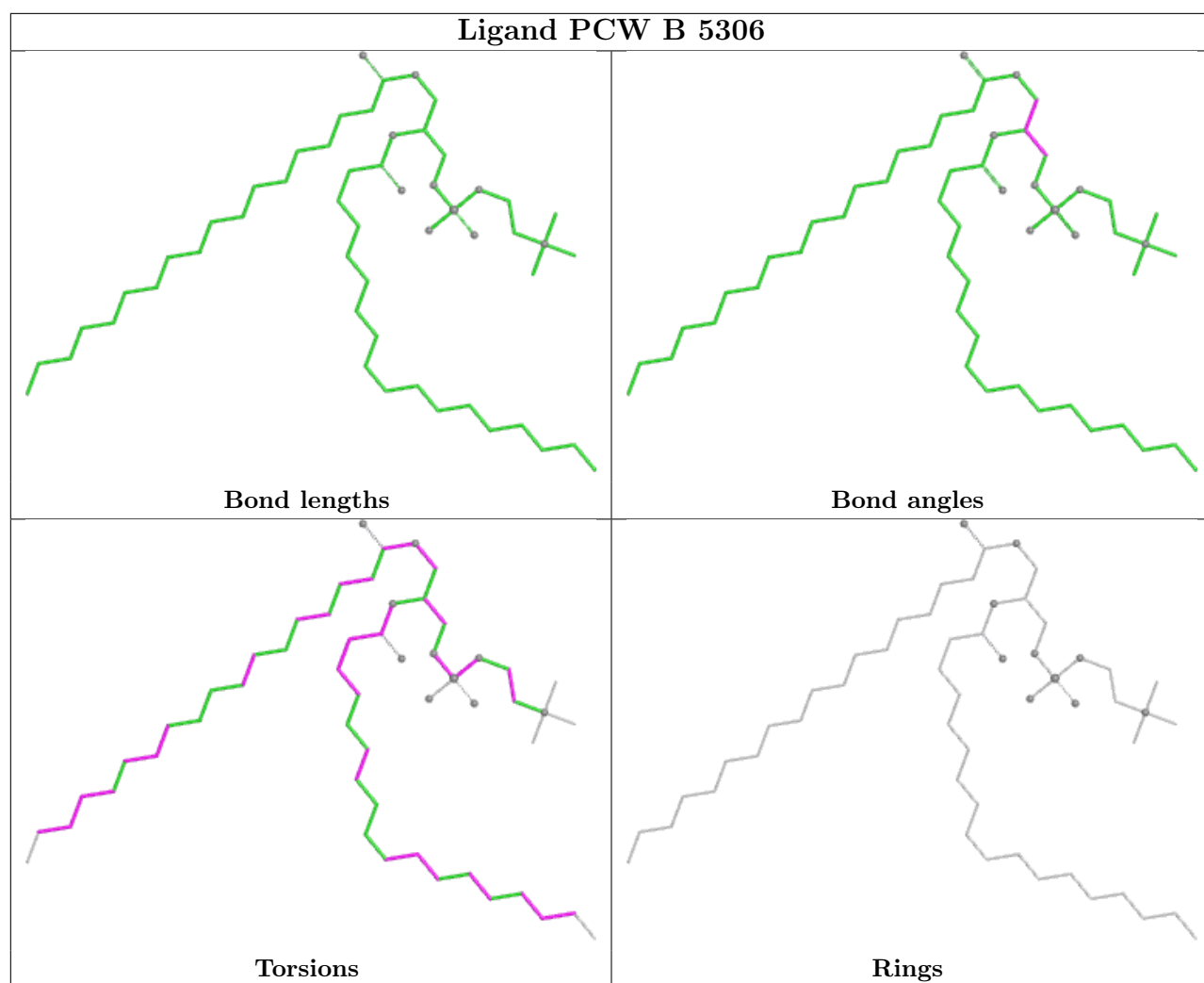


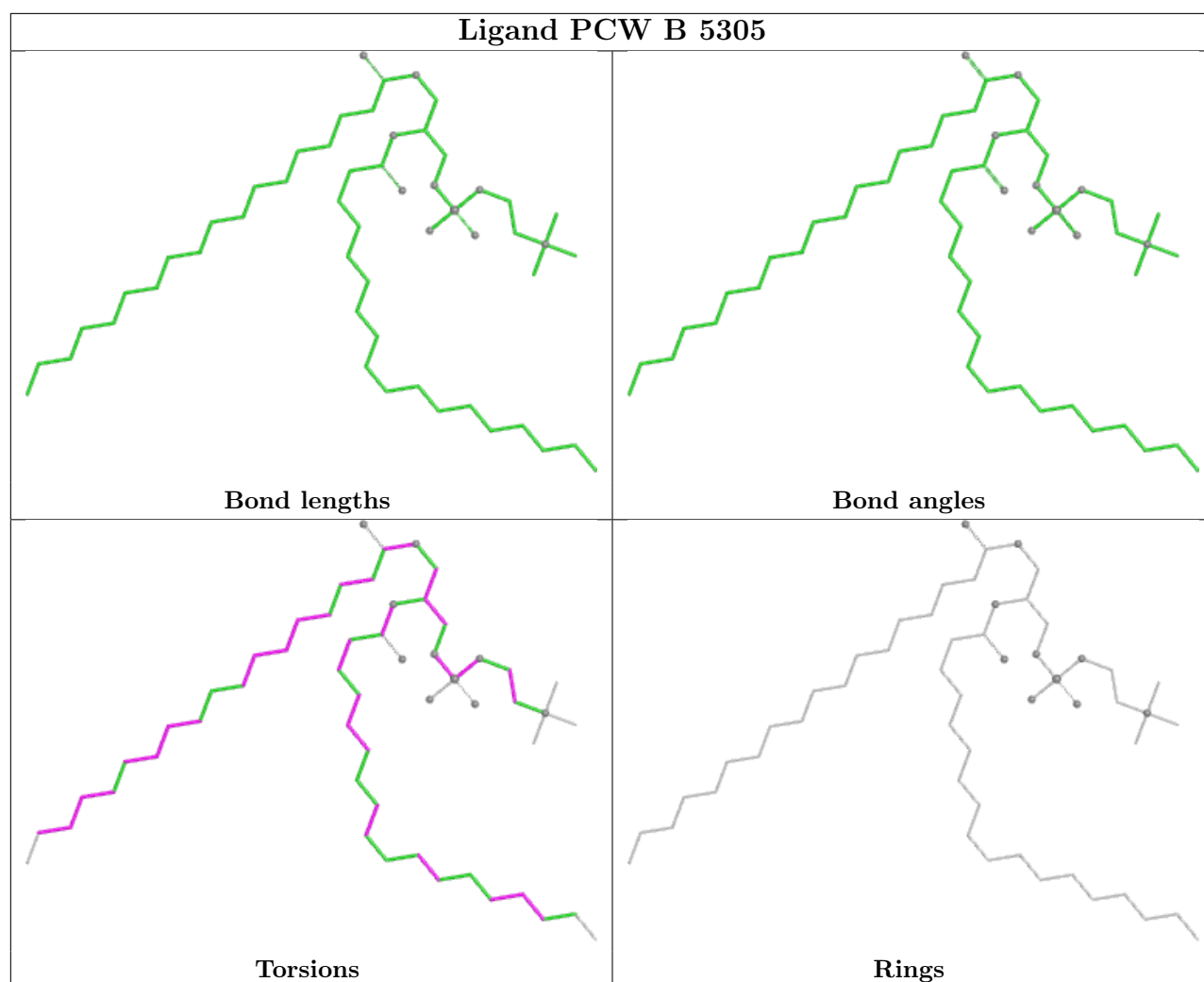












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

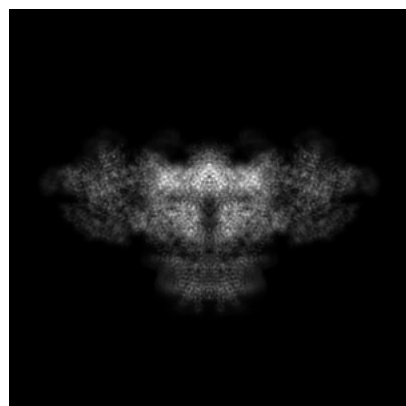
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74471. These allow visual inspection of the internal detail of the map and identification of artifacts.

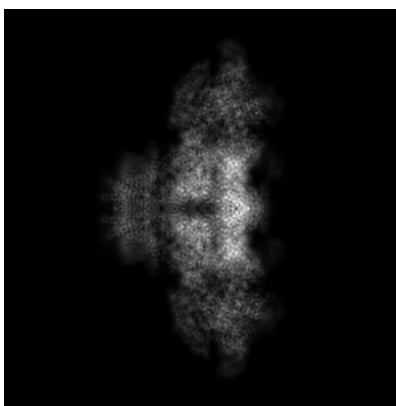
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

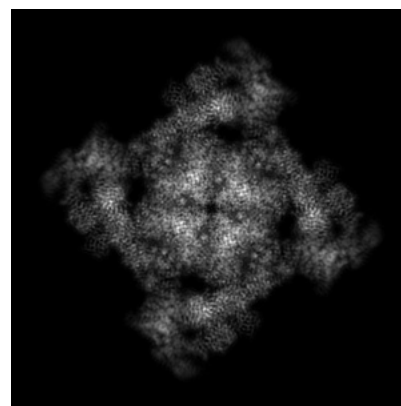
6.1.1 Primary map



X

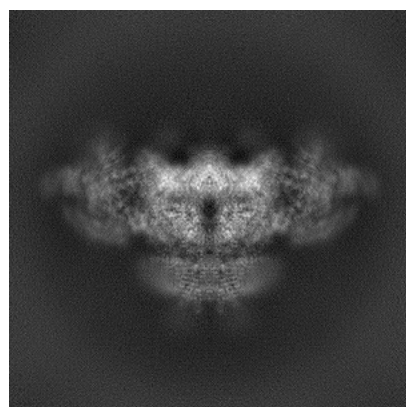


Y

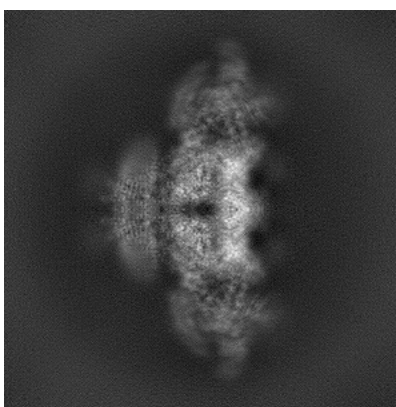


Z

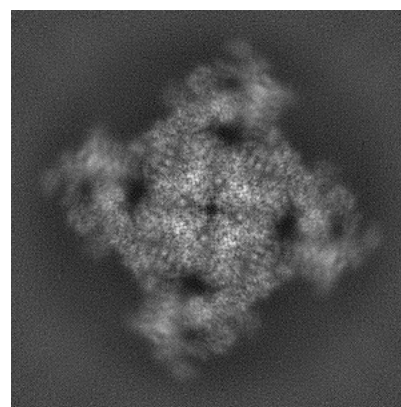
6.1.2 Raw map



X



Y



Z

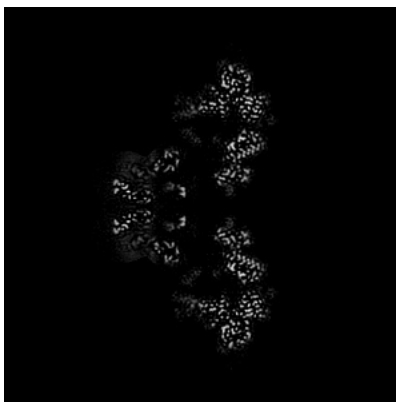
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

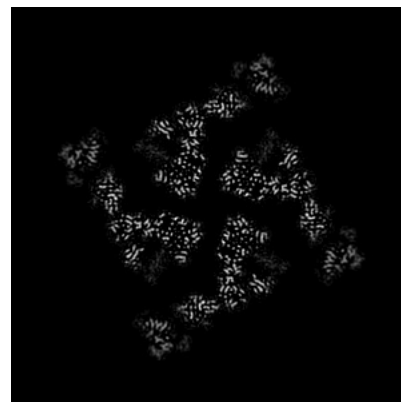
6.2.1 Primary map



X Index: 256

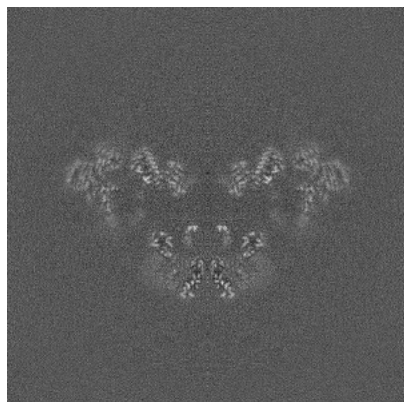


Y Index: 256

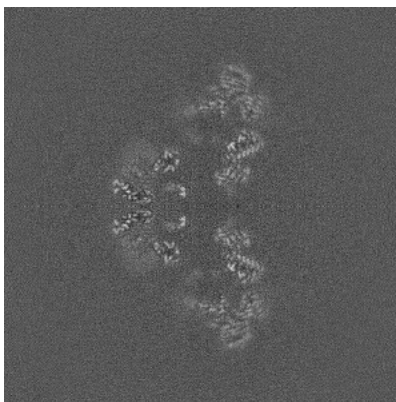


Z Index: 256

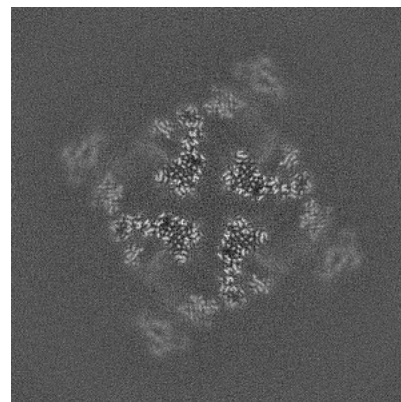
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

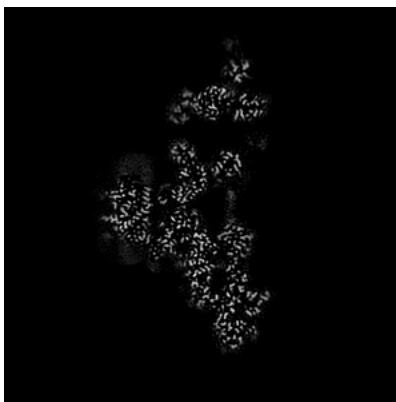
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

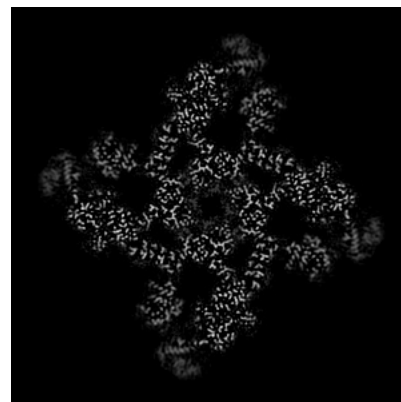
6.3.1 Primary map



X Index: 238

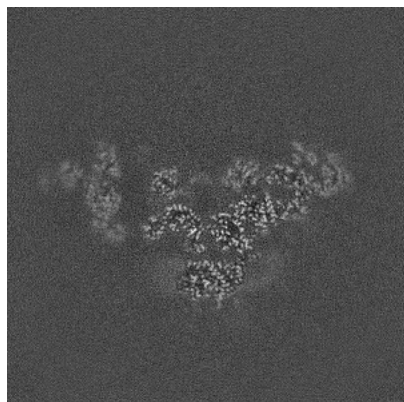


Y Index: 238

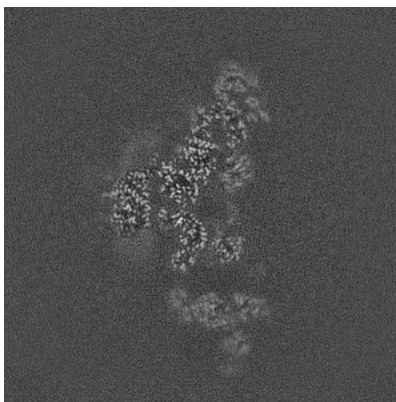


Z Index: 287

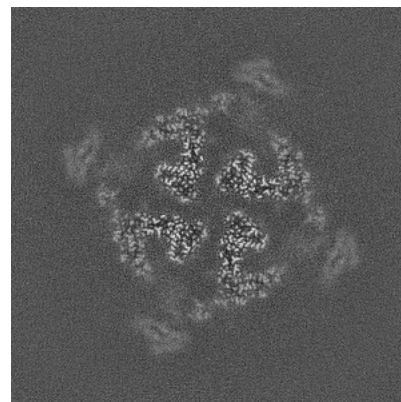
6.3.2 Raw map



X Index: 237



Y Index: 275

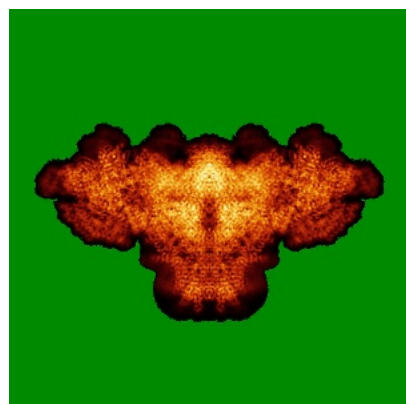


Z Index: 249

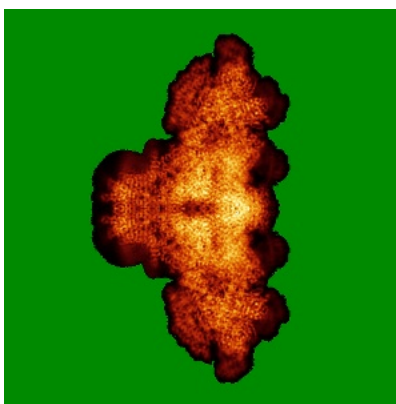
The images above show the largest variance slices of the map in three orthogonal directions.

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

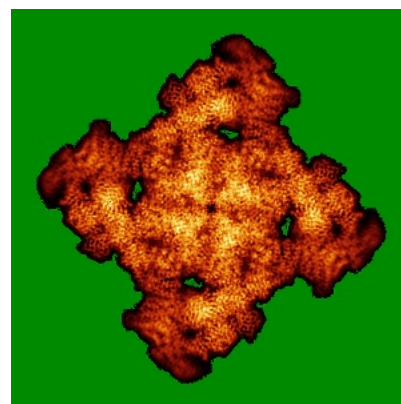
6.4.1 Primary map



X

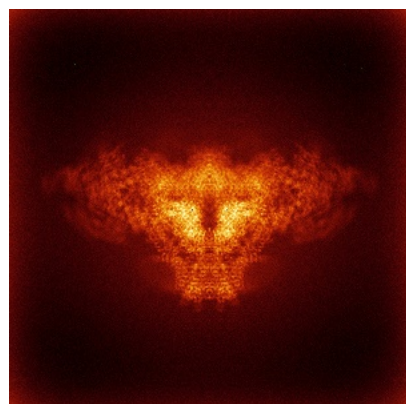


Y

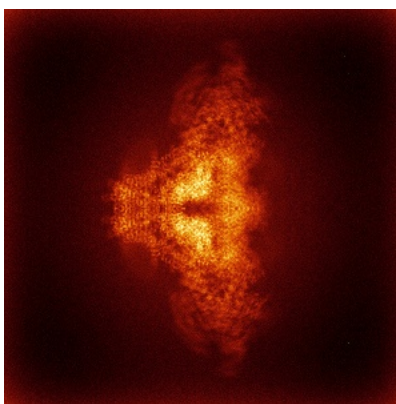


Z

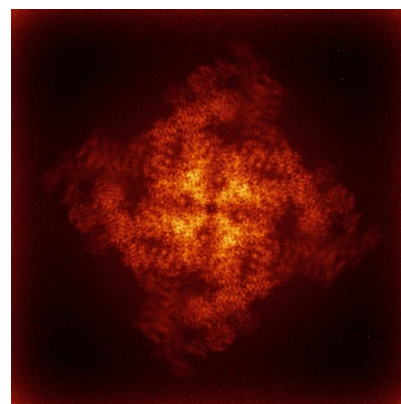
6.4.2 Raw map



X



Y

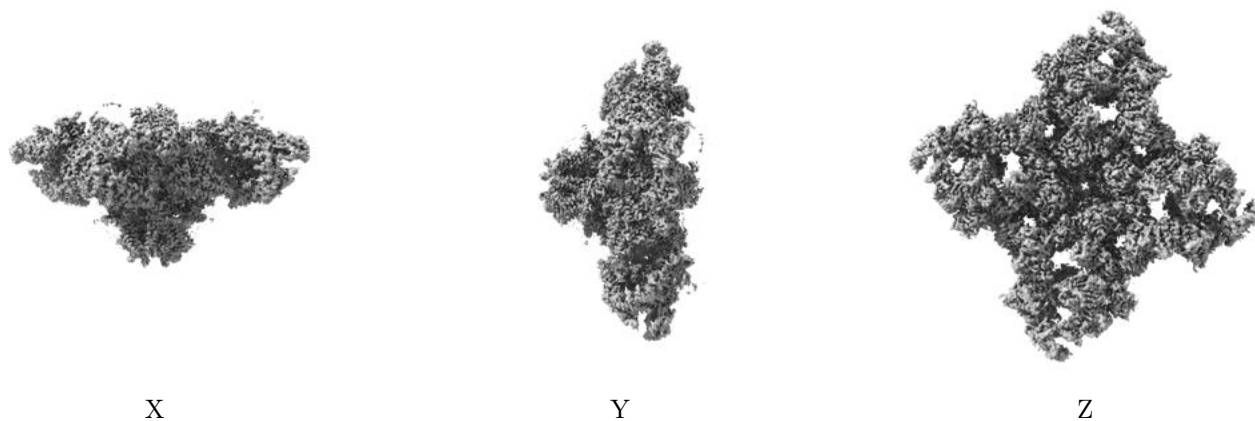


Z

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.

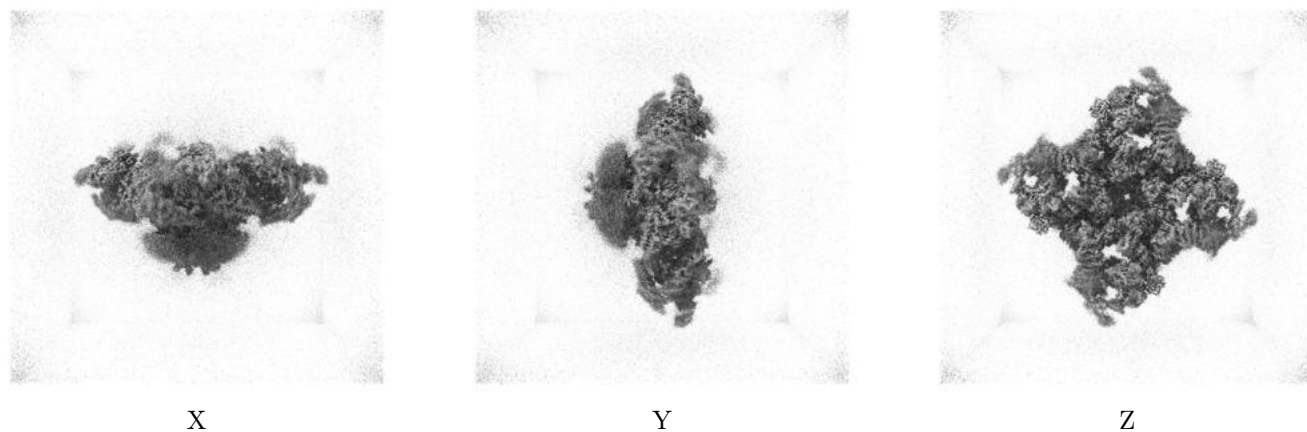
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

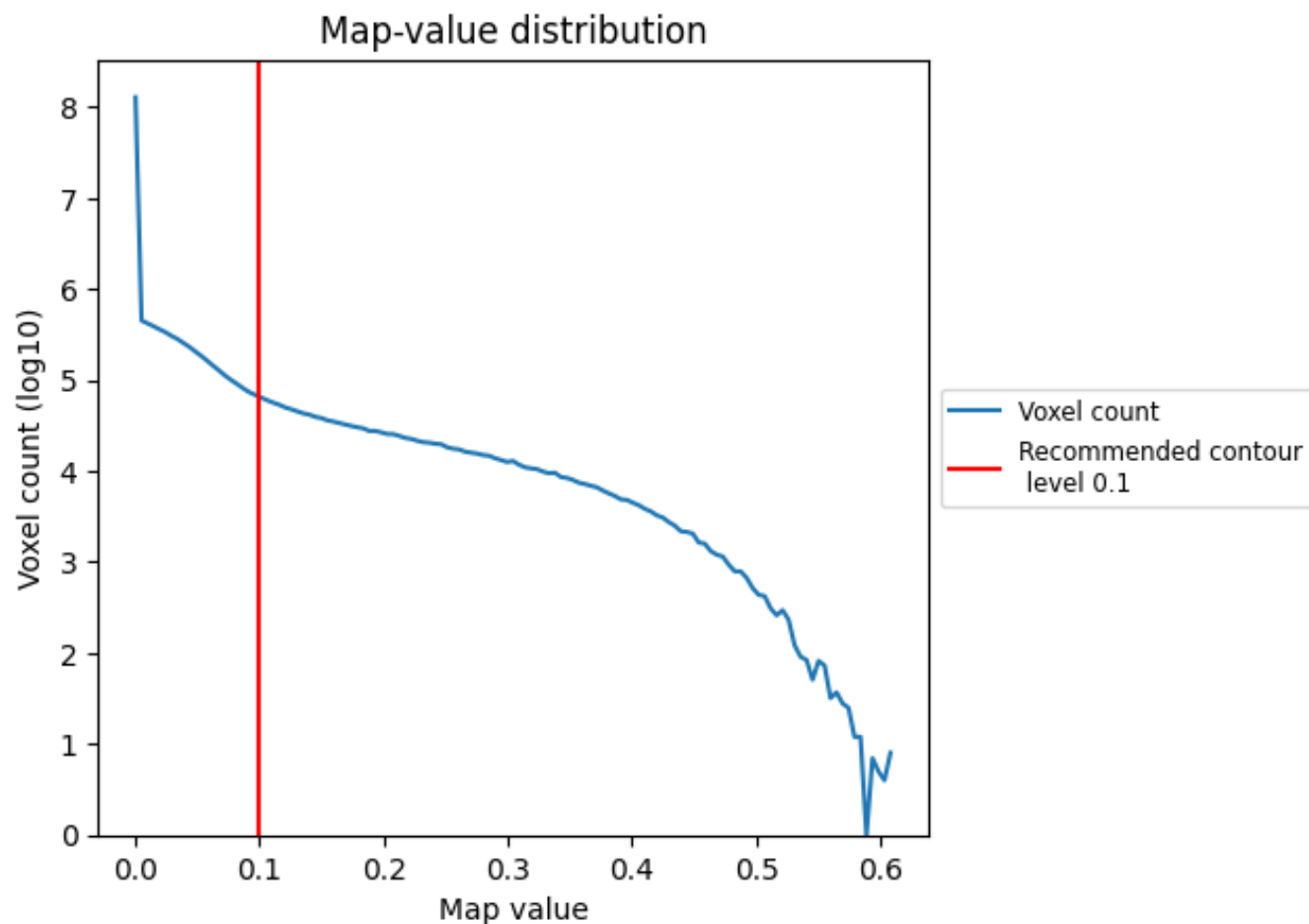
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

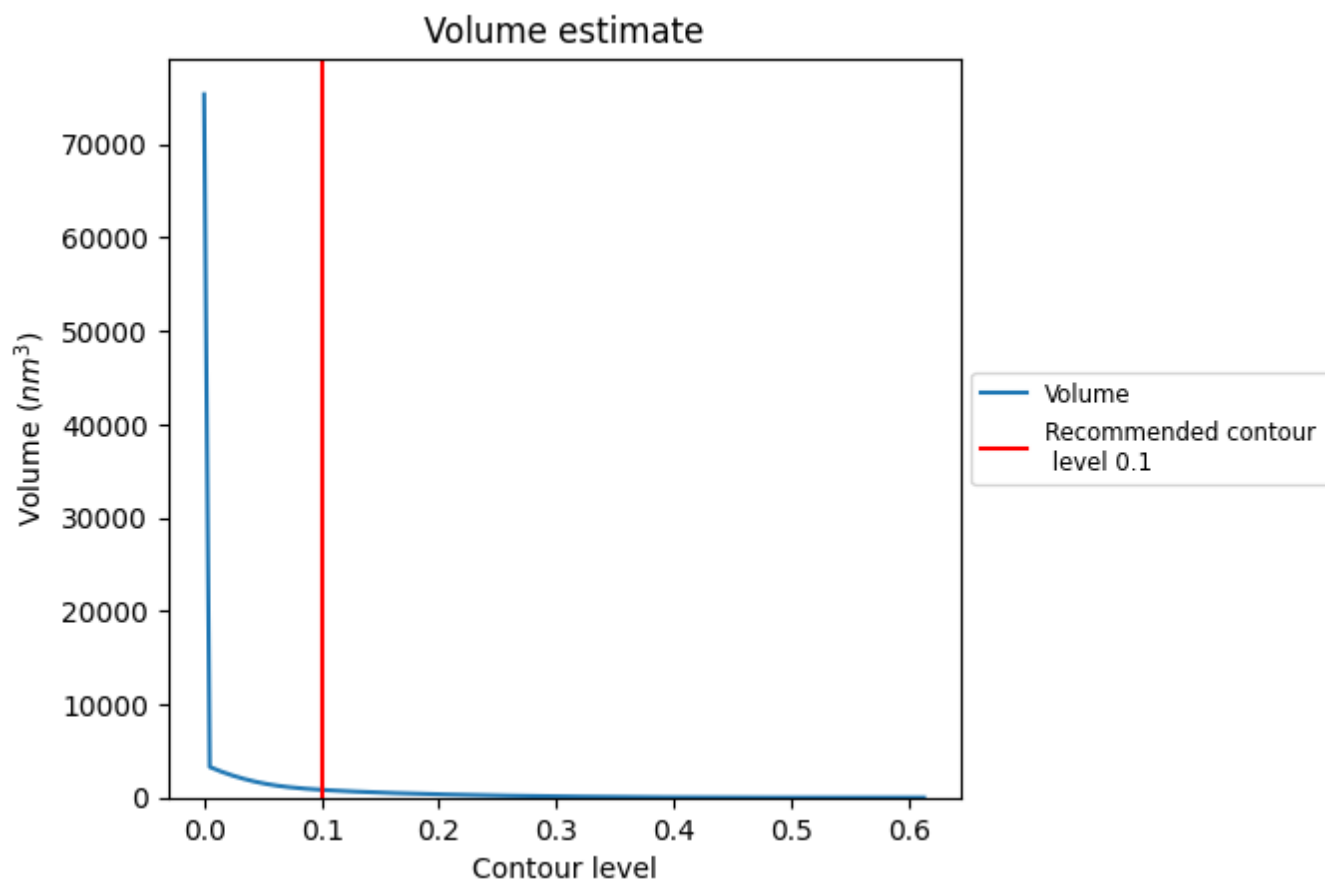
This section contains the results of statistical analysis of the map.

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.

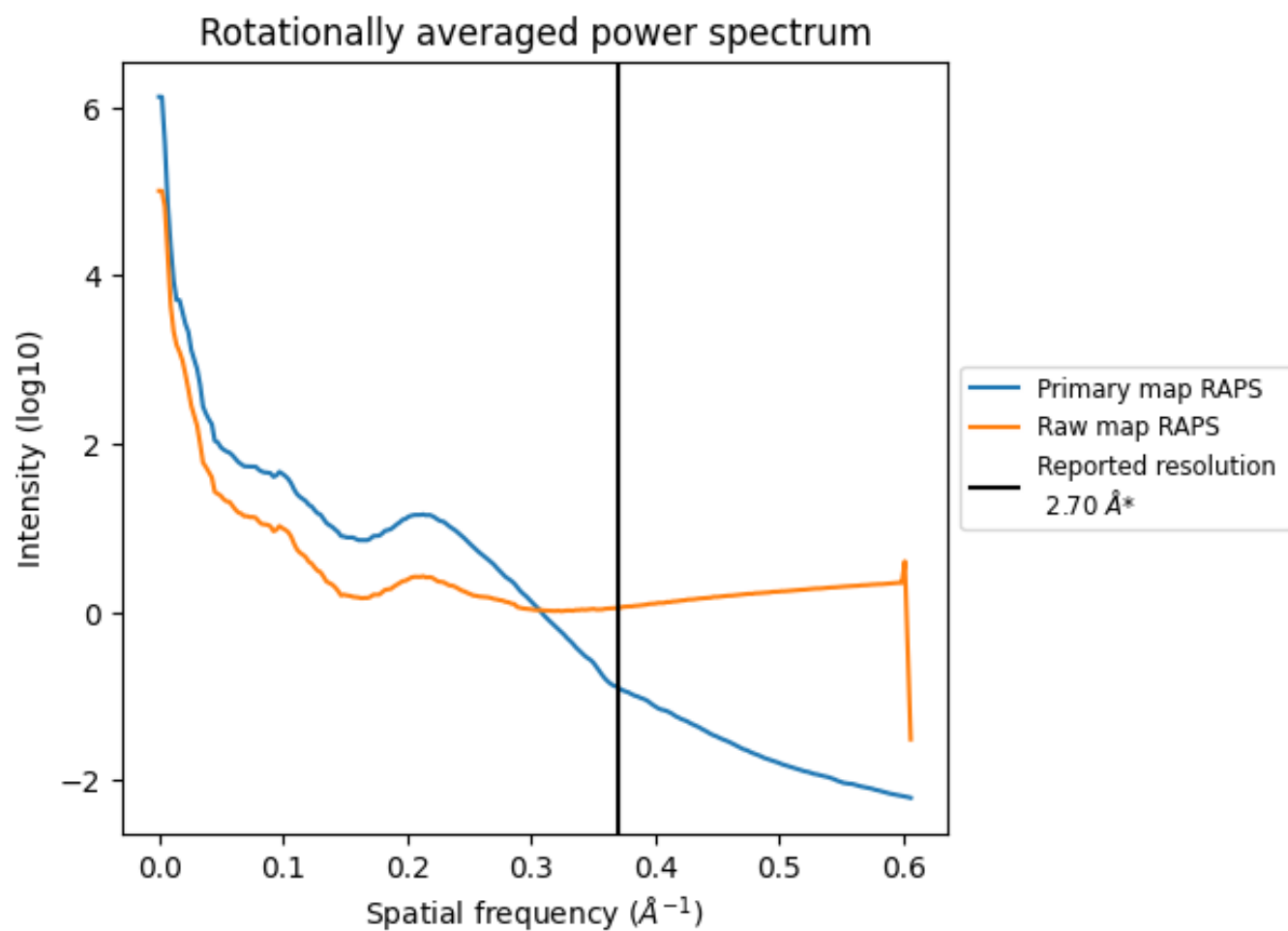
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 830 nm³; this corresponds to an approximate mass of 749 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 ⓘ

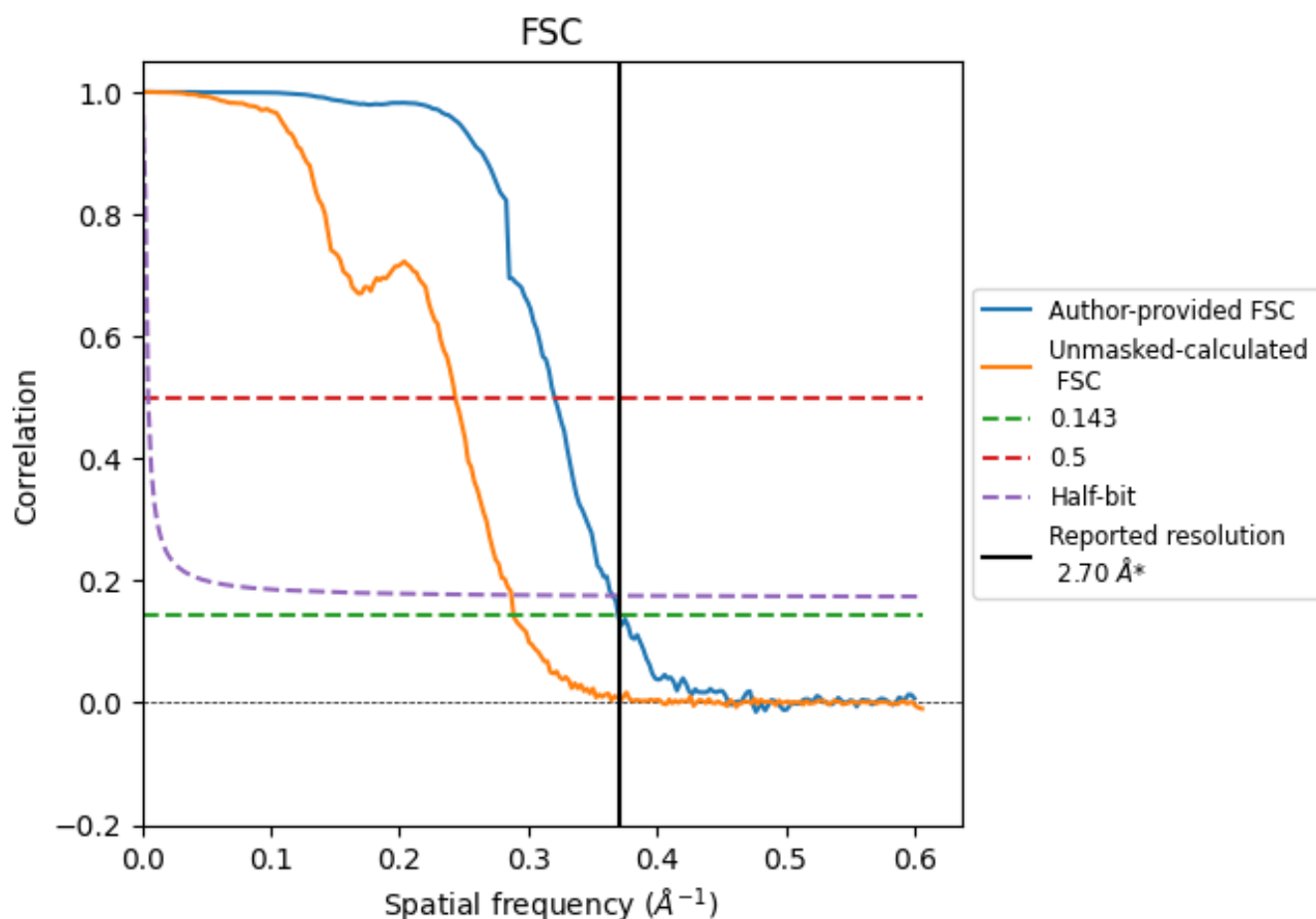


*Reported resolution corresponds to spatial frequency of $0.370 \text{ \AA}^{-1}$

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 $0.370 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

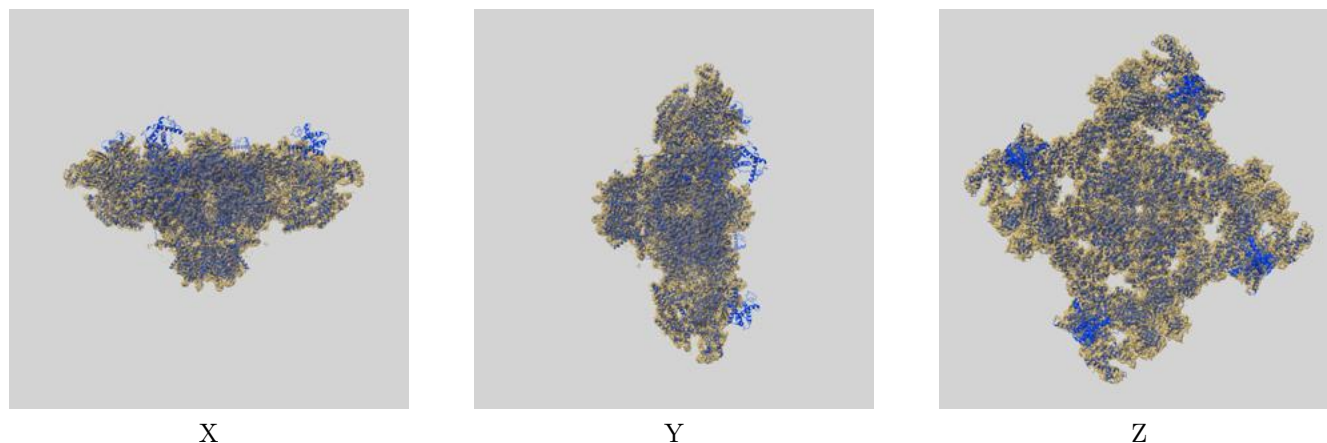
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	3.12	2.73
Unmasked-calculated*	3.46	4.11	3.49

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.46 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

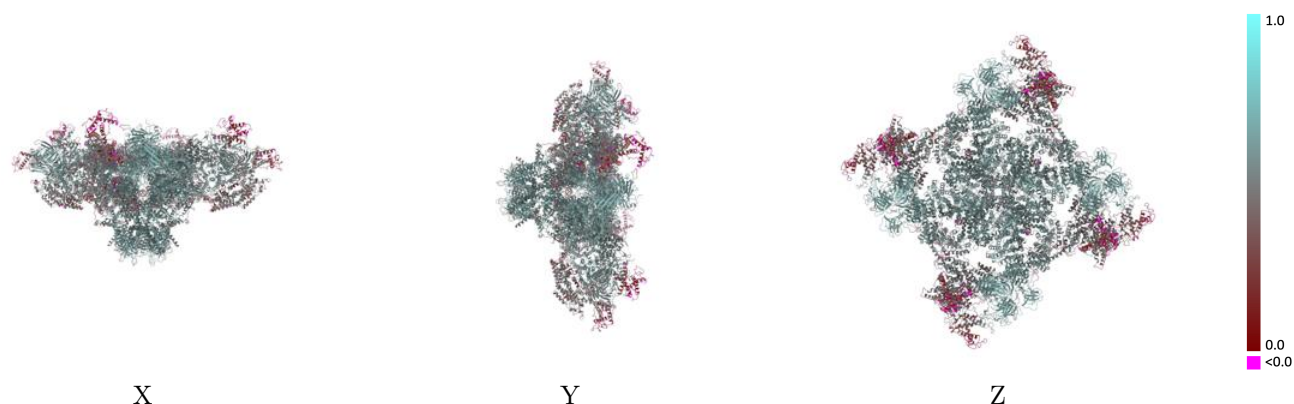
This section contains information regarding the fit between EMDB map EMD-74471 and PDB model 9ZO8. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



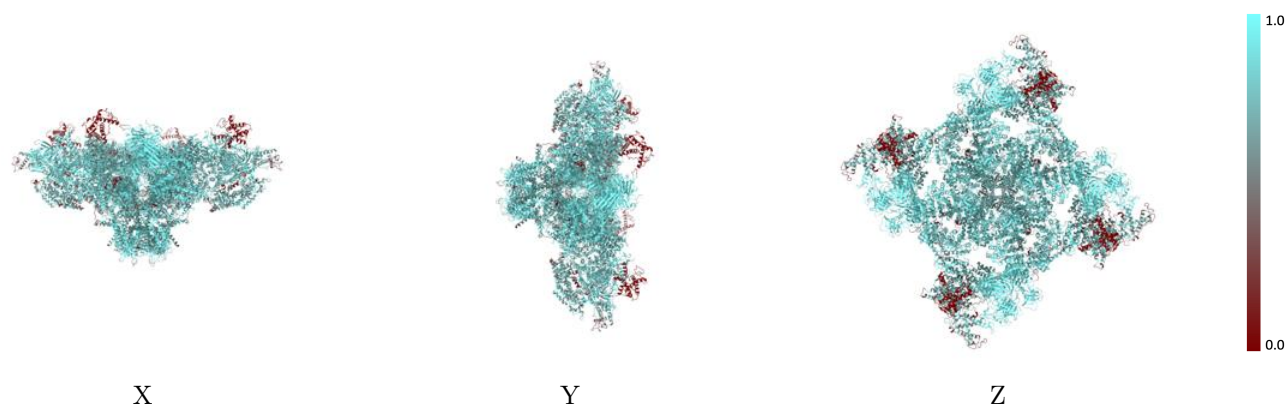
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



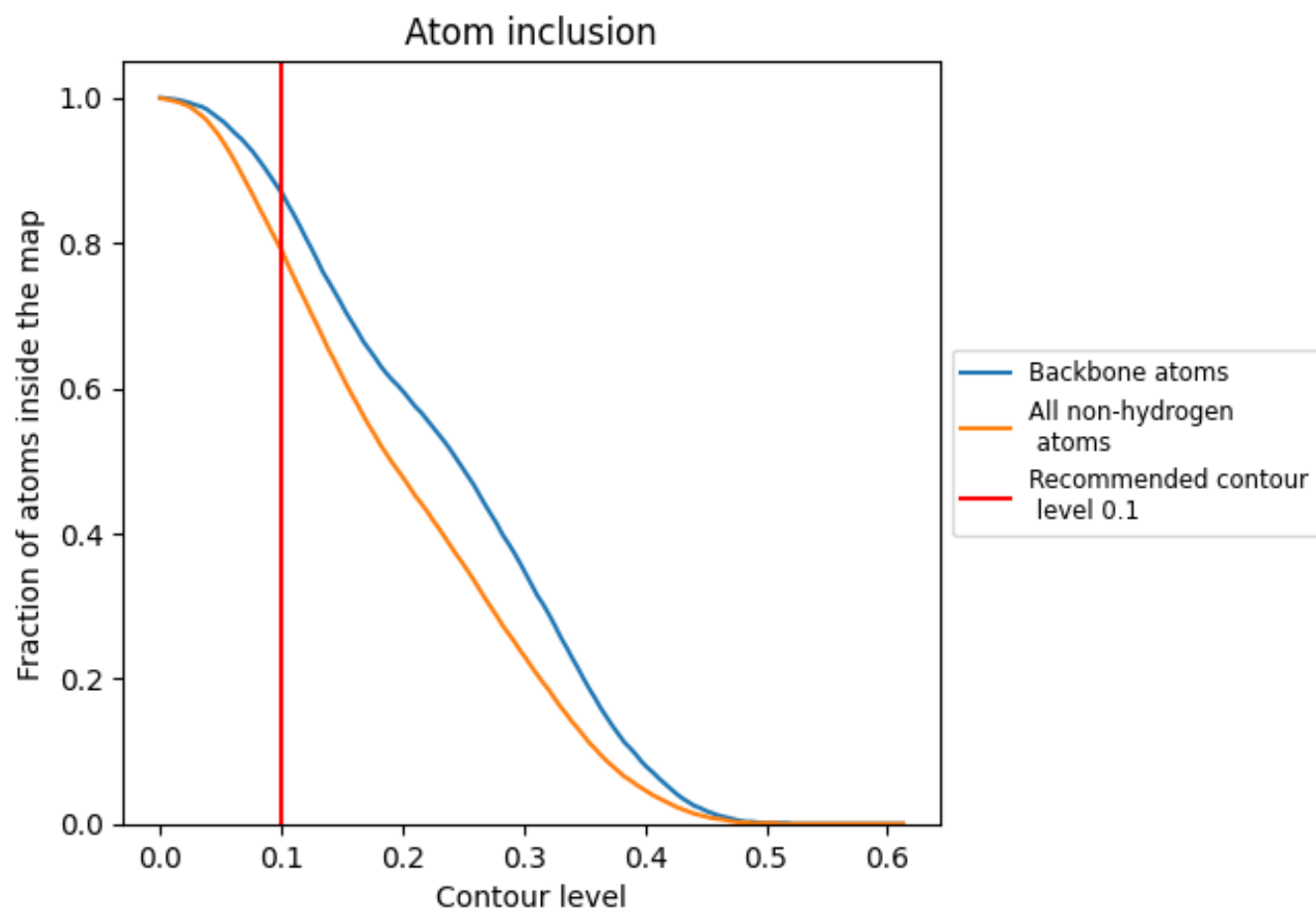
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 79% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7900	0.5130
A	0.7870	0.5120
B	0.7870	0.5110
C	0.7870	0.5110
D	0.7880	0.5120
E	0.8920	0.5970
F	0.8880	0.5970
G	0.8870	0.5960
H	0.8880	0.5970

1.0

0.0

<0.0