



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 11:25 pm GMT

PDB ID : 8RBM
EMDB ID : EMD-19032
Title : Cryo-EM structure of the NADH:ferredoxin oxidoreductase RNF from *Azotobacter vinelandii*, ferricyanide oxidized
Authors : Zhang, L.; Einsle, O.
Deposited on : 2023-12-04
Resolution : 3.24 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.dev113
Mogul : 1.8.4, CSD as541be (2020)
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

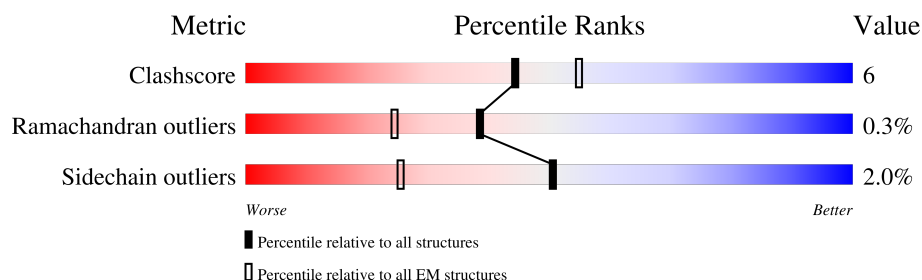
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.24 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	190	 86% 13% ..
2	C	496	 76% 14% 10%
3	D	366	 84% 10% 5%
4	E	238	 68% 18% 11%
5	G	229	 72% 12% 15%
6	B	174	 10% 11% .. 86%
6	b	174	 6% 94%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	FMN	D	411	X	-	-	-
9	FMN	G	301	X	-	-	-

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 11259 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 Ion-translocating oxidoreductase complex subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	189	Total	C	N	O	S	0	0
			1394	933	220	232	9		

- Molecule 2 is a protein called Ion-translocating oxidoreductase complex subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	446	Total	C	N	O	S	0	0
			3289	2076	581	610	22		

- Molecule 3 is a protein called Ion-translocating oxidoreductase complex subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	349	Total	C	N	O	S	0	0
			2629	1733	438	445	13		

- Molecule 4 is a protein called Ion-translocating oxidoreductase complex subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	211	Total	C	N	O	S	0	0
			1585	1032	267	273	13		

- Molecule 5 is a protein called Ion-translocating oxidoreductase complex subunit G.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	194	Total	C	N	O	S	0	0
			1482	939	259	278	6		

- Molecule 6 is a protein called Ion-translocating oxidoreductase complex subunit B.

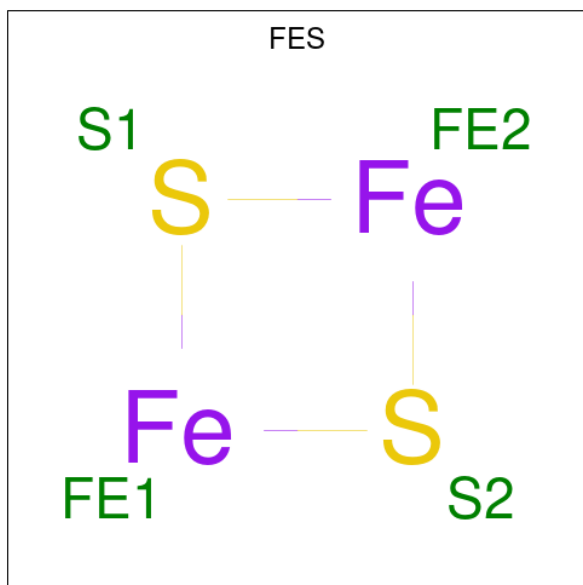
Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	25	Total	C	N	O	S	0	0
			174	114	29	29	2		

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	b	11	Total	C	N	O	0	0
			98	64	17	17		

- Molecule 7 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).

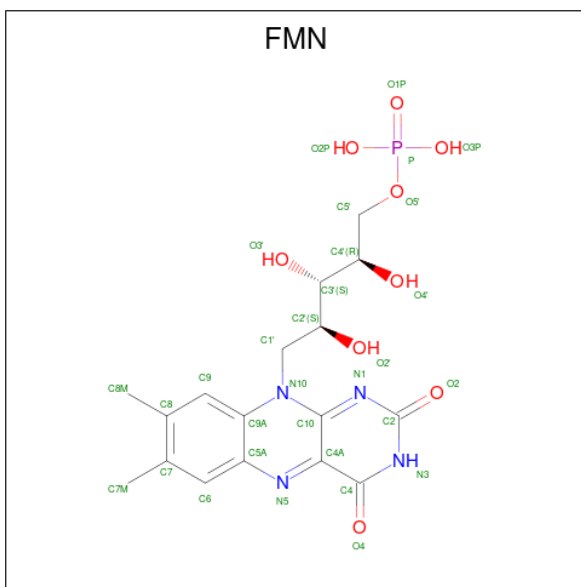


Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	Fe	S	0
			4	2	2	

- Molecule 8 is DODECYL-BETA-D-MALTOSIDE (three-letter code: LMT) (formula: $\text{C}_{24}\text{H}_{46}\text{O}_{11}$) (labeled as "Ligand of Interest" by depositor).

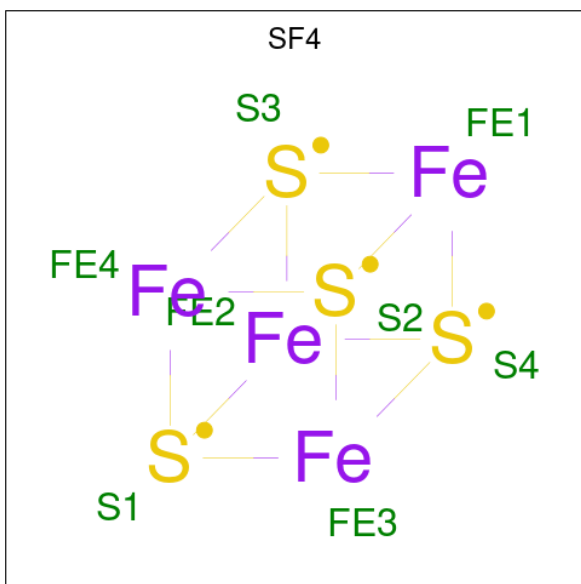


- Molecule 9 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $\text{C}_{17}\text{H}_{21}\text{N}_4\text{O}_9\text{P}$) (labeled as "Ligand of Interest" by depositor).



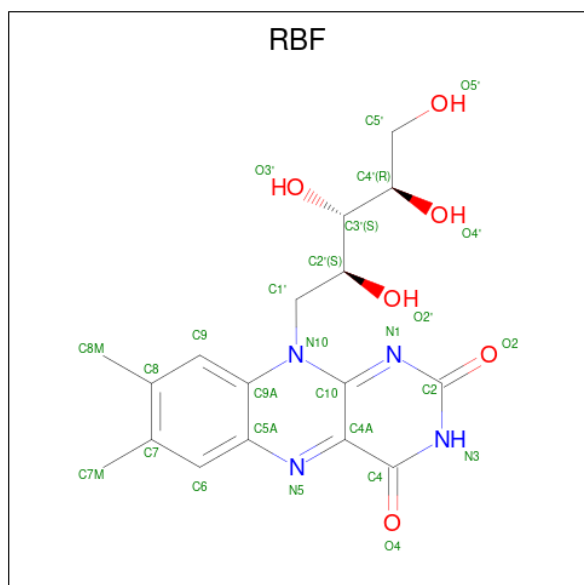
Mol	Chain	Residues	Atoms					AltConf
9	C	1	Total	C	N	O	P	0
			31	17	4	9	1	
9	D	1	Total	C	N	O	P	0
			30	17	4	8	1	
9	G	1	Total	C	N	O	P	0
			30	17	4	8	1	

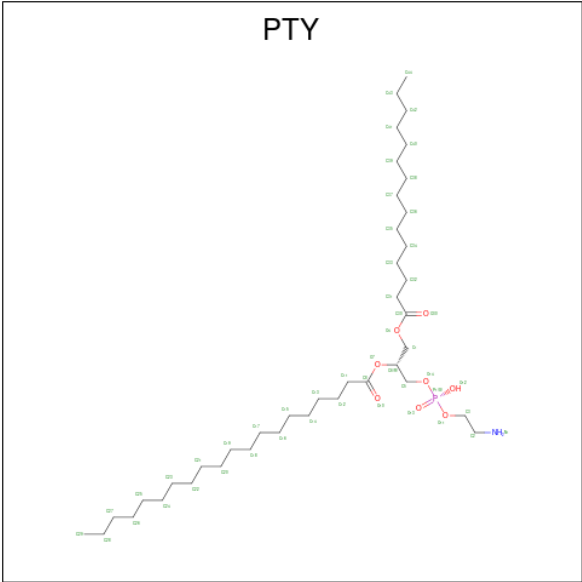
- Molecule 10 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
10	C	1	Total	Fe	S	0
			8	4	4	
10	C	1	Total	Fe	S	0
			8	4	4	

- Molecule 11 is RIBOFLAVIN (three-letter code: RBF) (formula: $C_{17}H_{20}N_4O_6$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
12	D	1	50	40	1	8	1	0

A123	V124	S130	R134	I138	L142	L155	T161	T169	L178	F182	T188	V189	I190	Q194	L197	L201	F211	L212	A215	K216	D220	R227	G1N	G1N	T1R	H1R	G1Y	G1Y	LEU	VAL	VAL	LEU	GLN													
ME1	SER	HIS	CYS	GLY	ALA	PRO	SER	VAL	PRO	GLU	PRO	GLU	LYS	LVS	VAL	P17	H18	Q19	Y20	F21	R29	L32	L36	T41	L42	A43	V44	T45	T58	V61	L62	T75	S76	T77	P78	E79	V80	R81	N82	P83	V84	V93	T96	M100	Y108	I118

- Chain G:  72% 12% 15%

Residue	Position	Sequence	Position	Sequence
E101	101	GLU	356	M35
L102	102	ASP	357	V36
G103	103	THR	358	A37
E104	104	THR	359	T38
V105	105	MET	360	Q39
L112	112	THR	361	G40
R124	124	PRO	362	L41
M136	136	GLU	363	S42
D139	139	ASN	364	L43
K143	143	ALA	365	V46
T155	155	ALA	366	C47
P156	156	ALA	367	L53
T202	202	GLY	368	R73
I203	203	LYS	369	Q83
T204	204	THR	370	Y86
P205	205	LEU	371	D87
V212	212	LEU	372	L91
F218	218	ARG	373	D99
A223	223	LEU	374	
E224	224	GLU	375	
Q225	225	LYS	376	
A228	228	TRP	377	
GLU	229	ARG	378	
		PRO	379	

- Chain B:  10% 11% .. 86%

THR	ASP	ILE	VAL	GLY	ASN	SER	GLN	VAL	THR	CYS	HIS	VAL	VAL	VAL	LEU	GLY	ASP	ALA	CYS	THR	GLY	CYS	GLY	LYS	CYS	ASP	GLU	GLY	CYS	ASP	VAL	LEU	ILE	PRO	GLN	GLY	THR	ALA	ALA	ALA	ALA
ASP	ILE	VAL	GLY	ASN	SER	GLN	VAL	THR	CYS	CYS	PRO	PRO	PRO	GLY	GLY	VAL	ASP	ALA	CYS	THR	GLY	CYS	GLY	LYS	CYS	ASP	GLU	GLY	CYS	ASP	VAL	LEU	ILE	PRO	GLN	GLY	THR	ALA	ALA	ALA	ALA

- Chain b:  6% 94%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	166974	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 ($e^-/\text{\AA}^2$)	37	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.762	Depositor
Minimum map value	-0.178	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.065	Depositor
Map size (Å)	229.59999, 229.59999, 229.59999	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PTY, LMT, FES, FMN, SF4, RBF

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	0.26	0/1423	0.47	0/1936
2	C	0.25	0/3358	0.49	0/4580
3	D	0.26	0/2702	0.47	0/3697
4	E	0.25	0/1616	0.48	0/2200
5	G	0.26	0/1503	0.47	0/2032
6	B	0.24	0/174	0.56	0/233
6	b	0.19	0/102	0.47	0/140
All	All	0.25	0/10878	0.48	0/14818

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	G	1	0

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	G	202	THR	CB

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	1394	0	1496	18	0
2	C	3289	0	3334	41	0
3	D	2629	0	2707	25	0
4	E	1585	0	1664	28	0
5	G	1482	0	1520	19	0
6	B	174	0	195	4	0
6	b	98	0	90	0	0
7	A	4	0	0	0	0
8	A	70	0	90	0	0
8	D	315	0	406	10	0
8	E	35	0	45	0	0
9	C	31	0	19	2	0
9	D	30	0	19	0	0
9	G	30	0	19	2	0
10	C	16	0	0	0	0
11	D	27	0	20	5	0
12	D	50	0	77	2	0
All	All	11259	0	11701	138	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 138 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)
4:E:197:LEU:HD11	5:G:156:PRO:HB2	1.68	0.74
3:D:88:SER:O	3:D:128:ARG:NH1	2.24	0.70
5:G:37:ALA:O	5:G:41:LEU:HB2	1.93	0.69
2:C:140:LEU:HD21	2:C:286:LEU:HD21	1.74	0.67
3:D:201:SER:HG	3:D:204:SER:HG	1.43	0.67

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	187/190 (98%)	181 (97%)	6 (3%)	0	100	100
2	C	444/496 (90%)	425 (96%)	18 (4%)	1 (0%)	44	73
3	D	347/366 (95%)	339 (98%)	8 (2%)	0	100	100
4	E	209/238 (88%)	199 (95%)	8 (4%)	2 (1%)	13	44
5	G	192/229 (84%)	186 (97%)	5 (3%)	1 (0%)	25	58
6	B	23/174 (13%)	23 (100%)	0	0	100	100
6	b	9/174 (5%)	9 (100%)	0	0	100	100
All	All	1411/1867 (76%)	1362 (96%)	45 (3%)	4 (0%)	38	67

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	75	THR
5	G	224	GLU
2	C	8	ILE
4	E	76	ILE

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	148/149 (99%)	145 (98%)	3 (2%)	50	73
2	C	348/380 (92%)	344 (99%)	4 (1%)	70	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	270/286 (94%)	267 (99%)	3 (1%)	70	84
4	E	169/194 (87%)	160 (95%)	9 (5%)	19	49
5	G	157/183 (86%)	155 (99%)	2 (1%)	65	81
6	B	17/129 (13%)	16 (94%)	1 (6%)	16	45
6	b	10/129 (8%)	10 (100%)	0	100	100
All	All	1119/1450 (77%)	1097 (98%)	22 (2%)	50	73

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	E	75	THR
4	E	212	LEU
4	E	194	GLN
4	E	220	ASP
2	C	440	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
5	G	125	ASN
5	G	225	GLN
3	D	189	ASN
4	E	19	GLN
4	E	50	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

20 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	SF4	C	501	2	0,12,12	-	-	-		
9	FMN	D	411	3	29,32,33	0.16	0	40,47,50	0.18	0
8	LMT	E	301	-	36,36,36	1.15	5 (13%)	47,47,47	0.96	1 (2%)
8	LMT	A	203	-	36,36,36	1.15	4 (11%)	47,47,47	1.01	1 (2%)
8	LMT	D	404	-	36,36,36	1.17	4 (11%)	47,47,47	0.99	2 (4%)
9	FMN	G	301	5	29,32,33	0.15	0	40,47,50	0.18	0
10	SF4	C	502	2	0,12,12	-	-	-		
12	PTY	D	412	-	49,49,49	0.46	0	52,54,54	0.39	0
8	LMT	D	401	-	36,36,36	1.17	6 (16%)	47,47,47	1.16	2 (4%)
11	RBF	D	403	-	29,29,29	1.07	1 (3%)	41,43,43	1.20	3 (7%)
8	LMT	D	406	-	36,36,36	1.17	5 (13%)	47,47,47	0.96	2 (4%)
8	LMT	D	410	-	36,36,36	1.16	5 (13%)	47,47,47	0.96	1 (2%)
8	LMT	A	202	-	36,36,36	1.14	5 (13%)	47,47,47	1.02	2 (4%)
8	LMT	D	407	-	36,36,36	1.15	5 (13%)	47,47,47	0.97	2 (4%)
8	LMT	D	409	-	36,36,36	1.16	5 (13%)	47,47,47	1.20	4 (8%)
8	LMT	D	408	-	36,36,36	1.19	6 (16%)	47,47,47	1.04	2 (4%)
8	LMT	D	402	-	36,36,36	1.17	5 (13%)	47,47,47	0.99	2 (4%)
8	LMT	D	405	-	36,36,36	1.15	5 (13%)	47,47,47	1.20	4 (8%)
7	FES	A	201	4,1	0,4,4	-	-	-		
9	FMN	C	500	-	33,33,33	1.88	7 (21%)	48,50,50	1.24	5 (10%)

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
10	SF4	C	501	2	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	FMN	D	411	3	1/1/4/4	5/15/17/18	0/3/3/3
8	LMT	E	301	-	-	7/21/61/61	0/2/2/2
8	LMT	A	203	-	-	5/21/61/61	0/2/2/2
8	LMT	D	404	-	-	5/21/61/61	0/2/2/2
9	FMN	G	301	5	2/2/4/4	7/15/17/18	0/3/3/3
10	SF4	C	502	2	-	-	0/6/5/5
12	PTY	D	412	-	-	17/53/53/53	-
8	LMT	D	401	-	-	9/21/61/61	0/2/2/2
11	RBF	D	403	-	-	10/14/14/14	0/3/3/3
8	LMT	D	406	-	-	7/21/61/61	0/2/2/2
8	LMT	D	410	-	-	8/21/61/61	0/2/2/2
8	LMT	A	202	-	-	6/21/61/61	0/2/2/2
8	LMT	D	407	-	-	5/21/61/61	0/2/2/2
8	LMT	D	409	-	-	8/21/61/61	0/2/2/2
8	LMT	D	408	-	-	8/21/61/61	0/2/2/2
8	LMT	D	402	-	-	2/21/61/61	0/2/2/2
8	LMT	D	405	-	-	10/21/61/61	0/2/2/2
7	FES	A	201	4,1	-	-	0/1/1/1
9	FMN	C	500	-	-	10/18/18/18	0/3/3/3

The worst 5 of 68 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	500	FMN	P-O5'	6.88	1.82	1.60
9	C	500	FMN	C5'-C4'	3.57	1.56	1.51
8	D	406	LMT	O3'-C3'	-2.77	1.36	1.43
8	D	405	LMT	O3'-C3'	-2.70	1.36	1.43
8	D	404	LMT	O3'-C3'	-2.66	1.36	1.43

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	403	RBF	C5'-C4'-C3'	-4.83	101.95	112.41
11	D	403	RBF	O5'-C5'-C4'	-3.83	102.72	111.07
8	D	409	LMT	C3'-C4'-C5'	-3.69	102.47	110.93
9	C	500	FMN	C5'-C4'-C3'	-3.21	106.00	112.20
8	A	203	LMT	C3'-C4'-C5'	-3.06	103.91	110.93

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	D	411	FMN	C4'
9	G	301	FMN	C4'
9	G	301	FMN	C2'

5 of 129 torsion outliers are listed below:

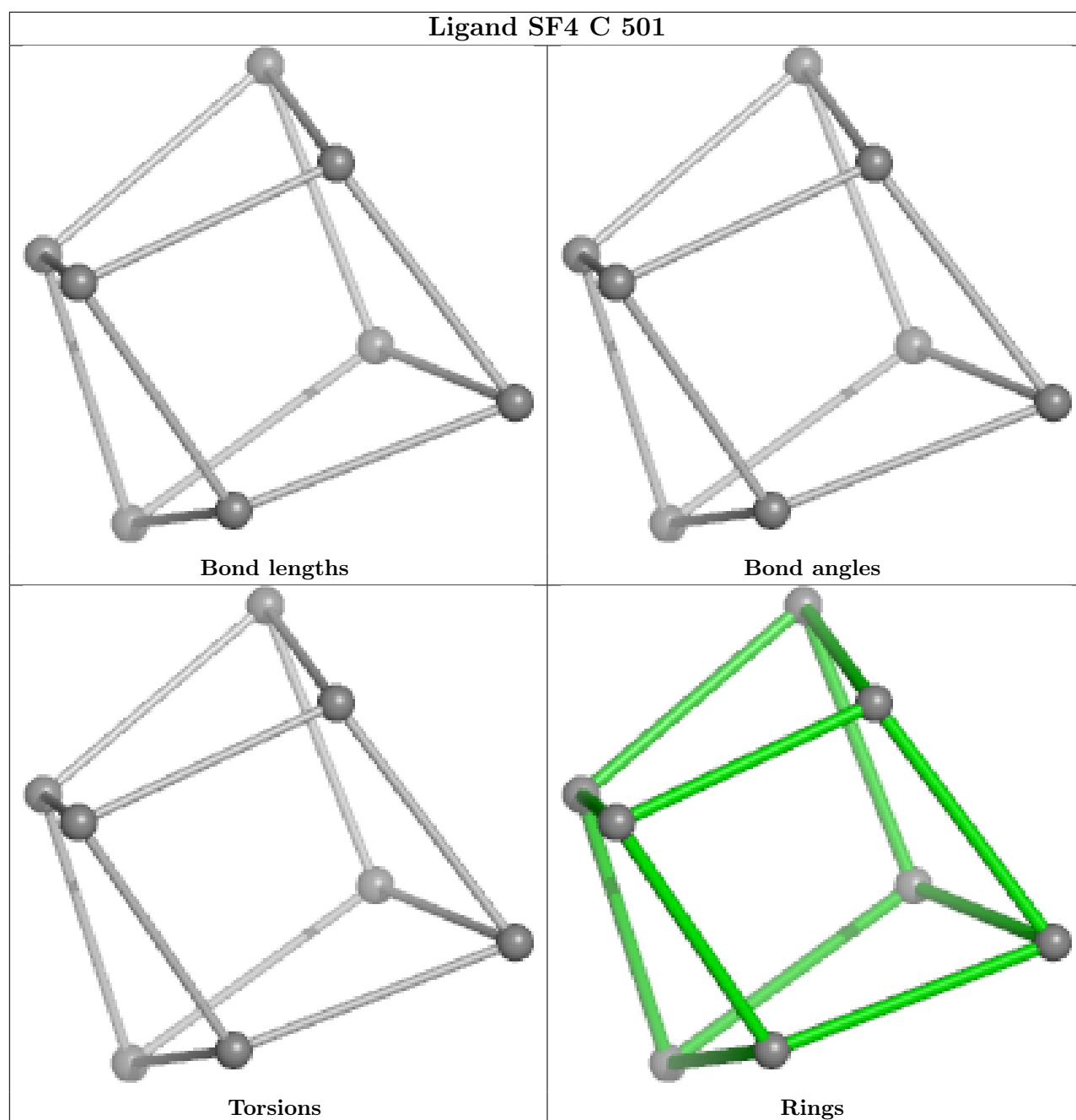
Mol	Chain	Res	Type	Atoms
8	D	401	LMT	C2'-C1'-O1'-C1
8	D	401	LMT	O5'-C1'-O1'-C1
8	D	405	LMT	C2-C1-O1'-C1'
8	D	406	LMT	C2-C1-O1'-C1'
8	D	407	LMT	O5'-C1'-O1'-C1

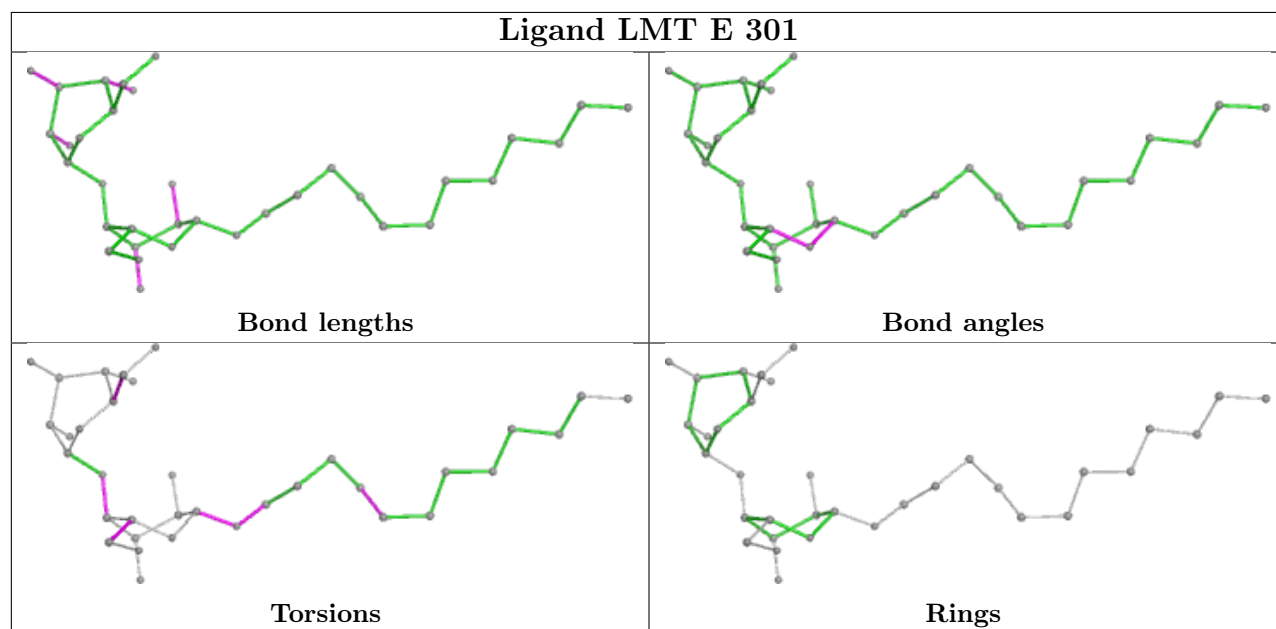
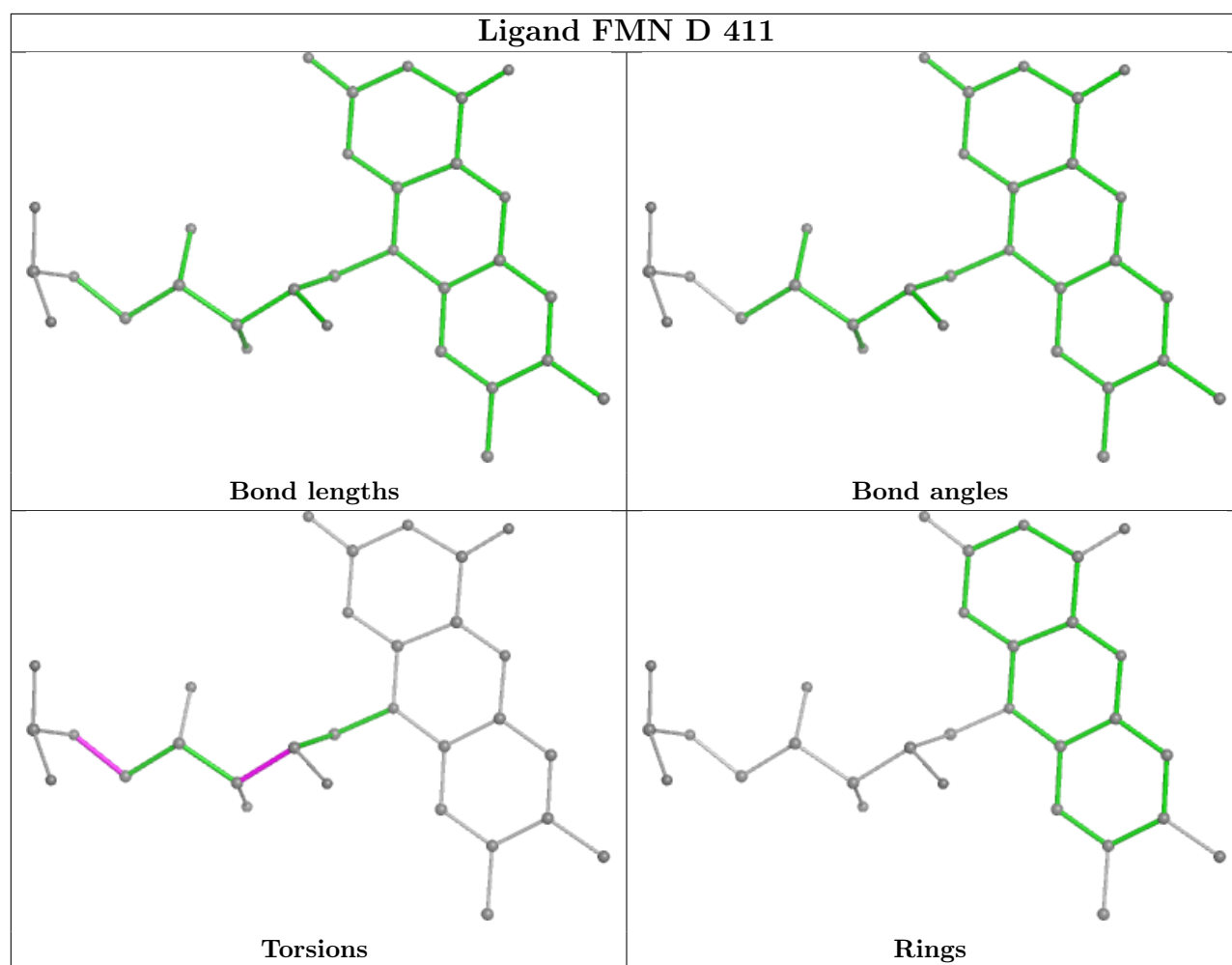
There are no ring outliers.

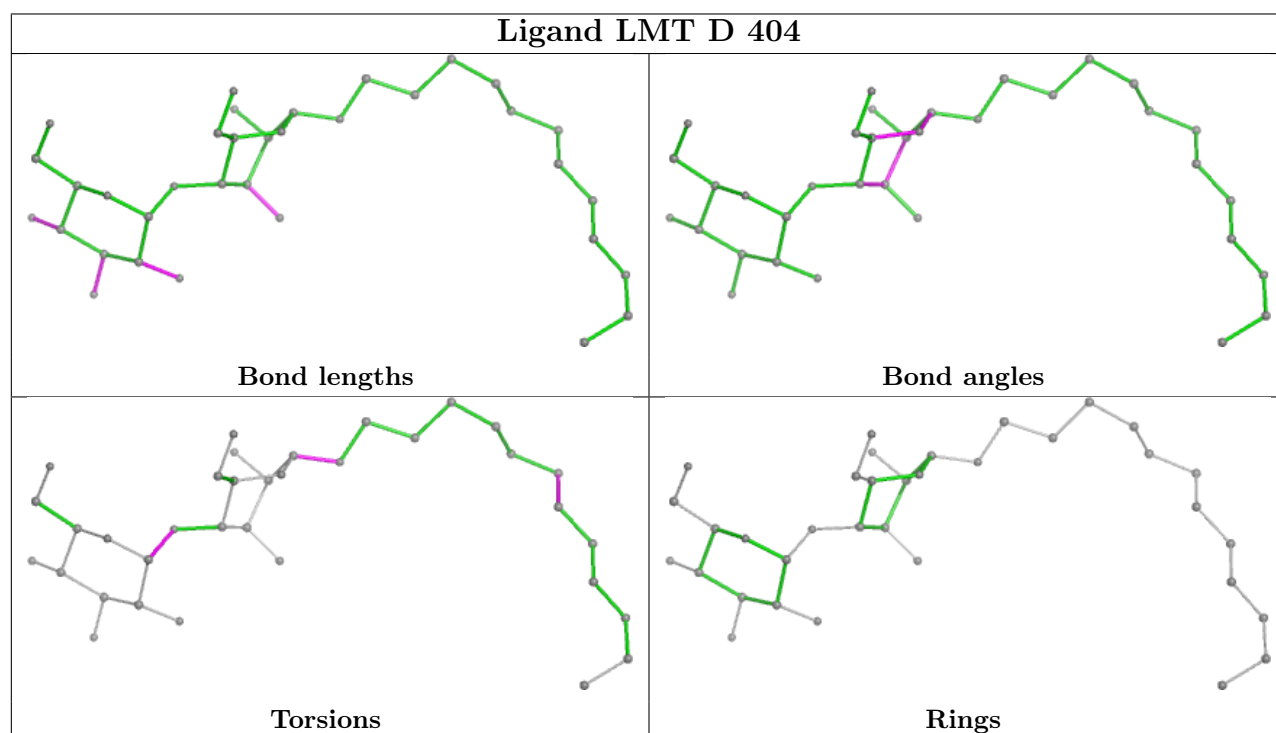
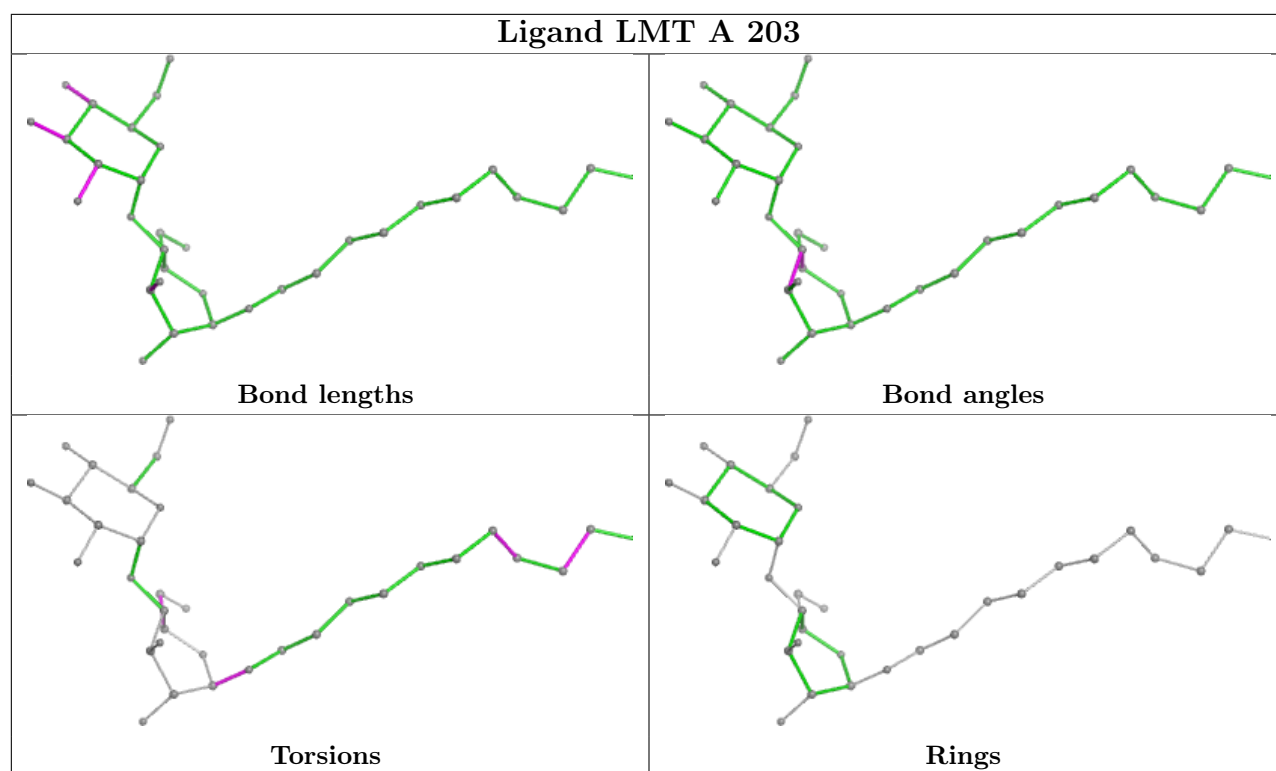
9 monomers are involved in 21 short contacts:

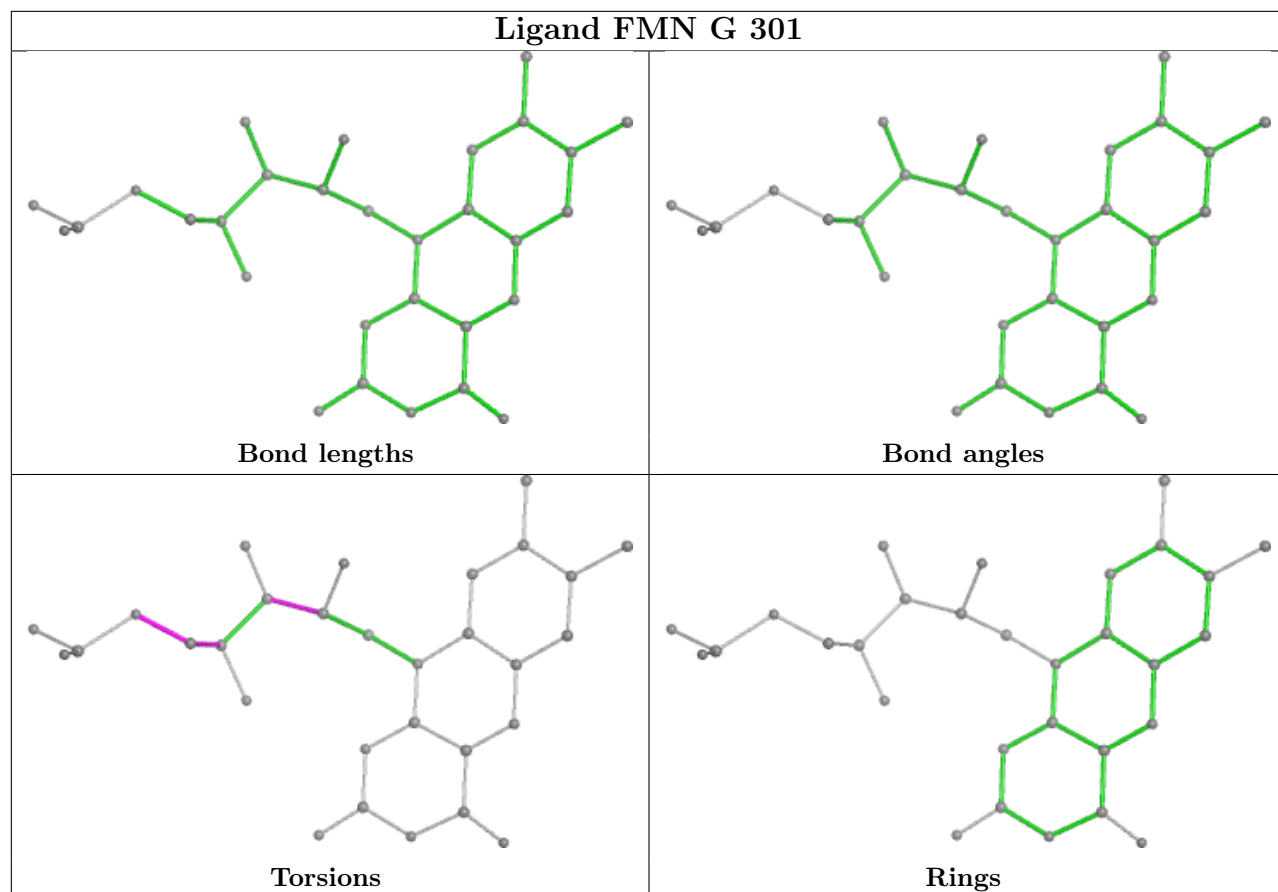
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	G	301	FMN	2	0
12	D	412	PTY	2	0
8	D	401	LMT	3	0
11	D	403	RBF	5	0
8	D	406	LMT	2	0
8	D	410	LMT	3	0
8	D	407	LMT	2	0
8	D	405	LMT	1	0
9	C	500	FMN	2	0

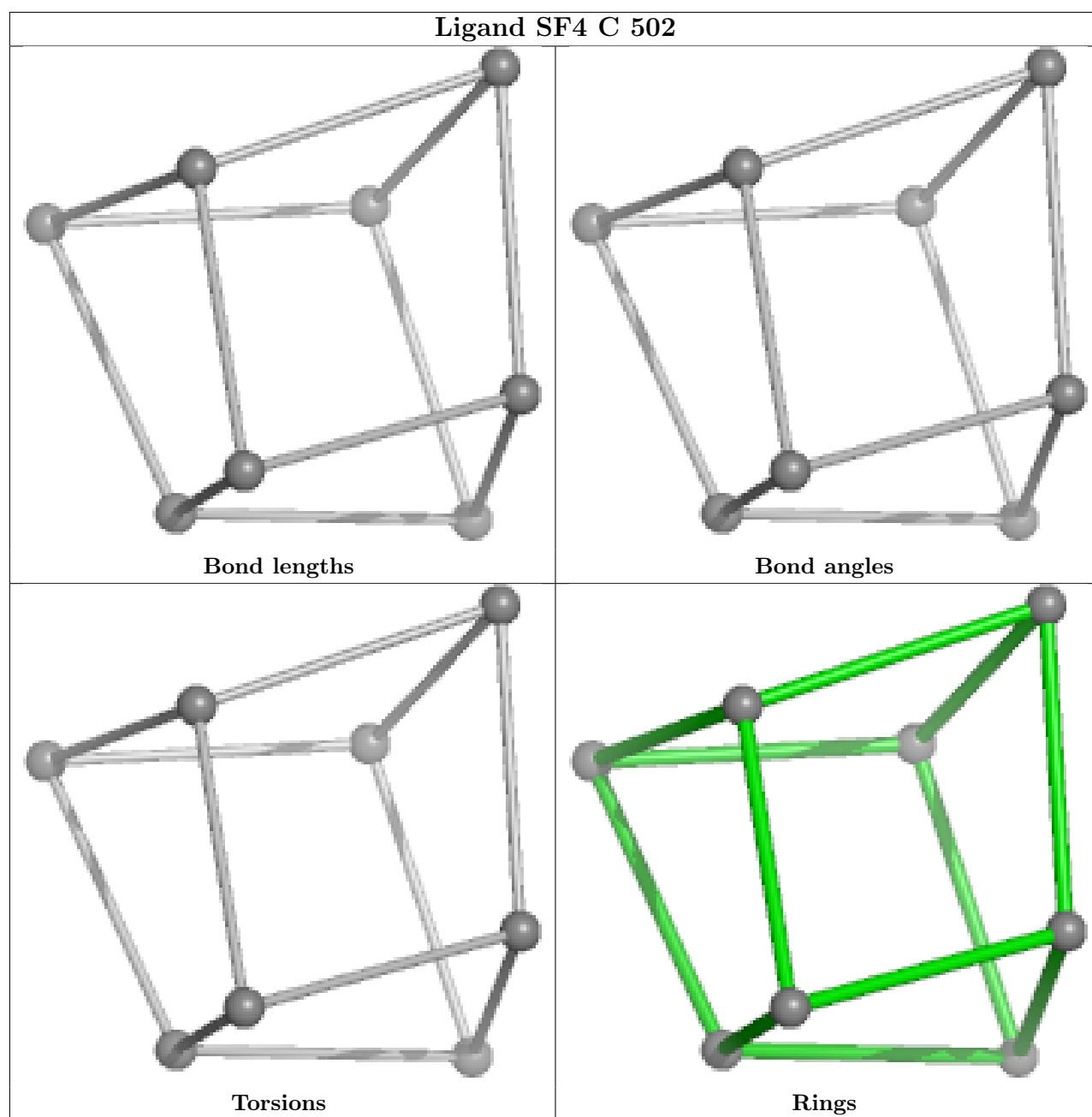
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

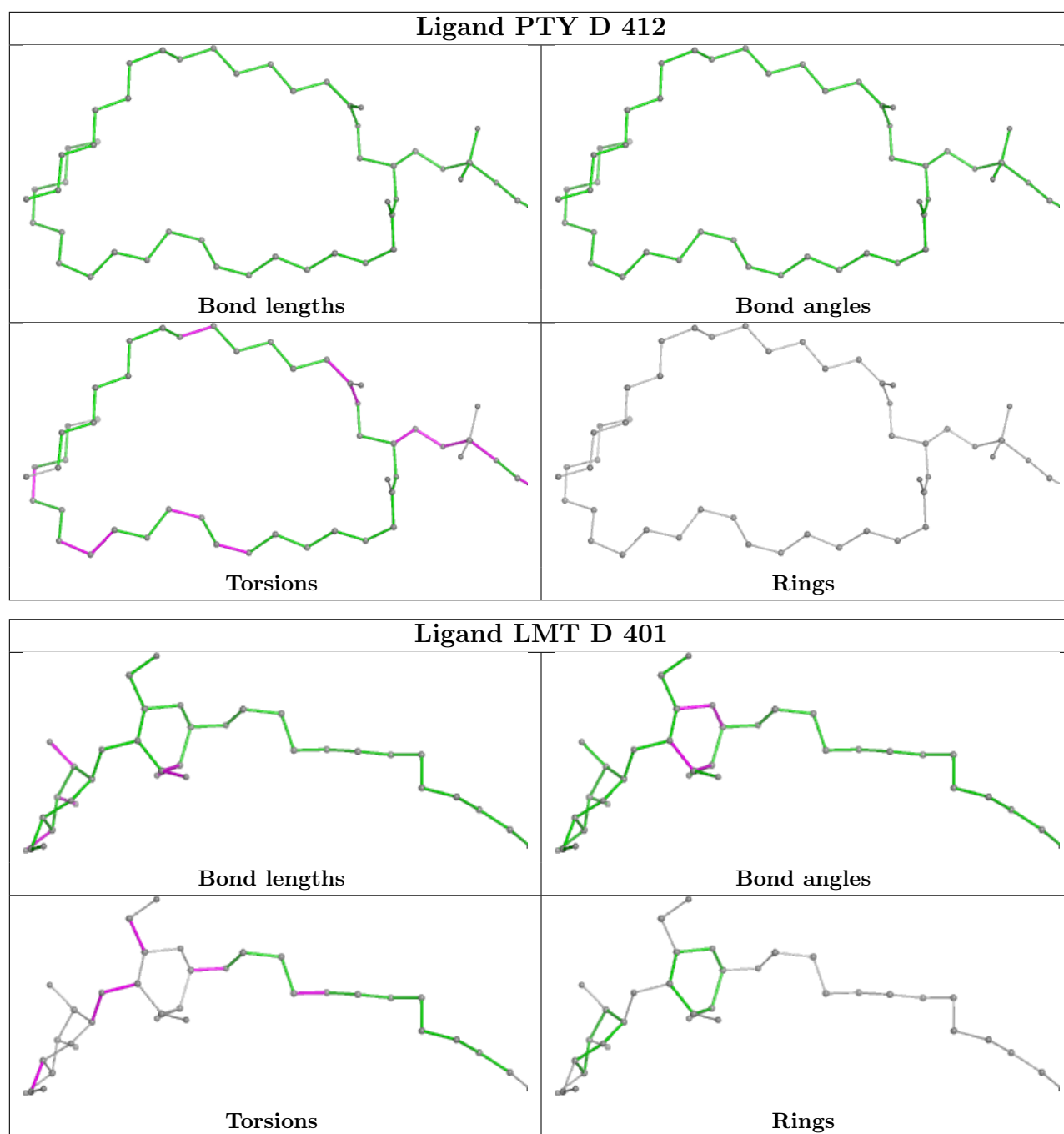


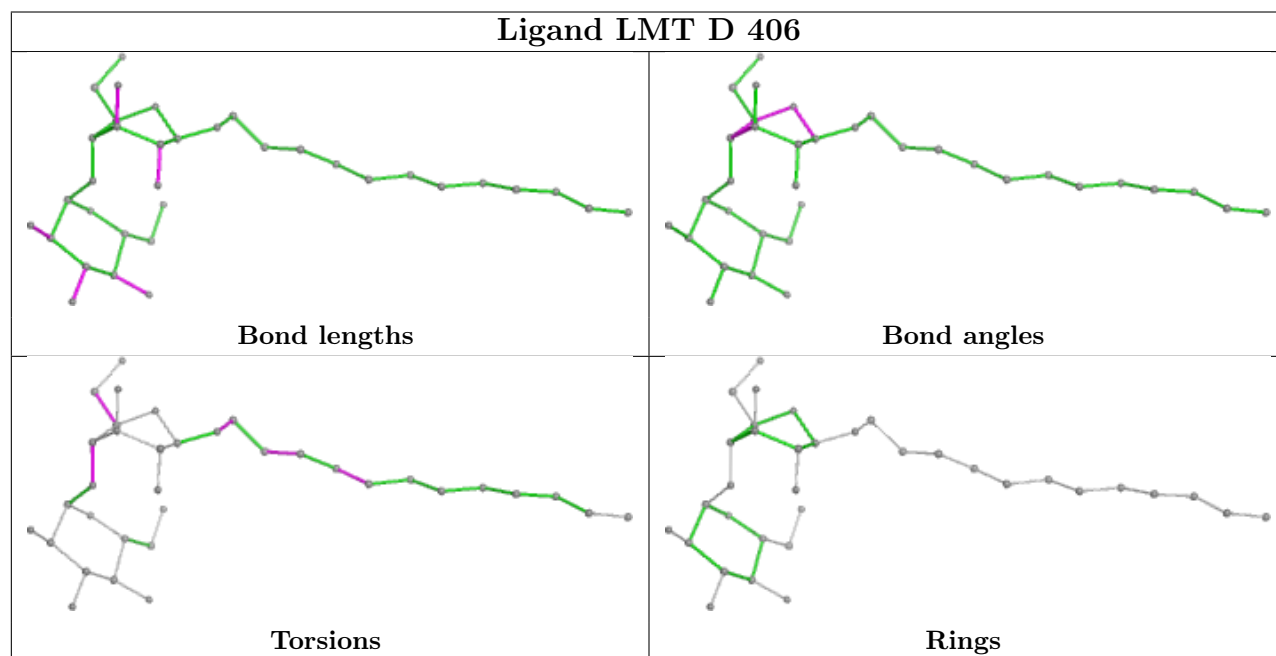
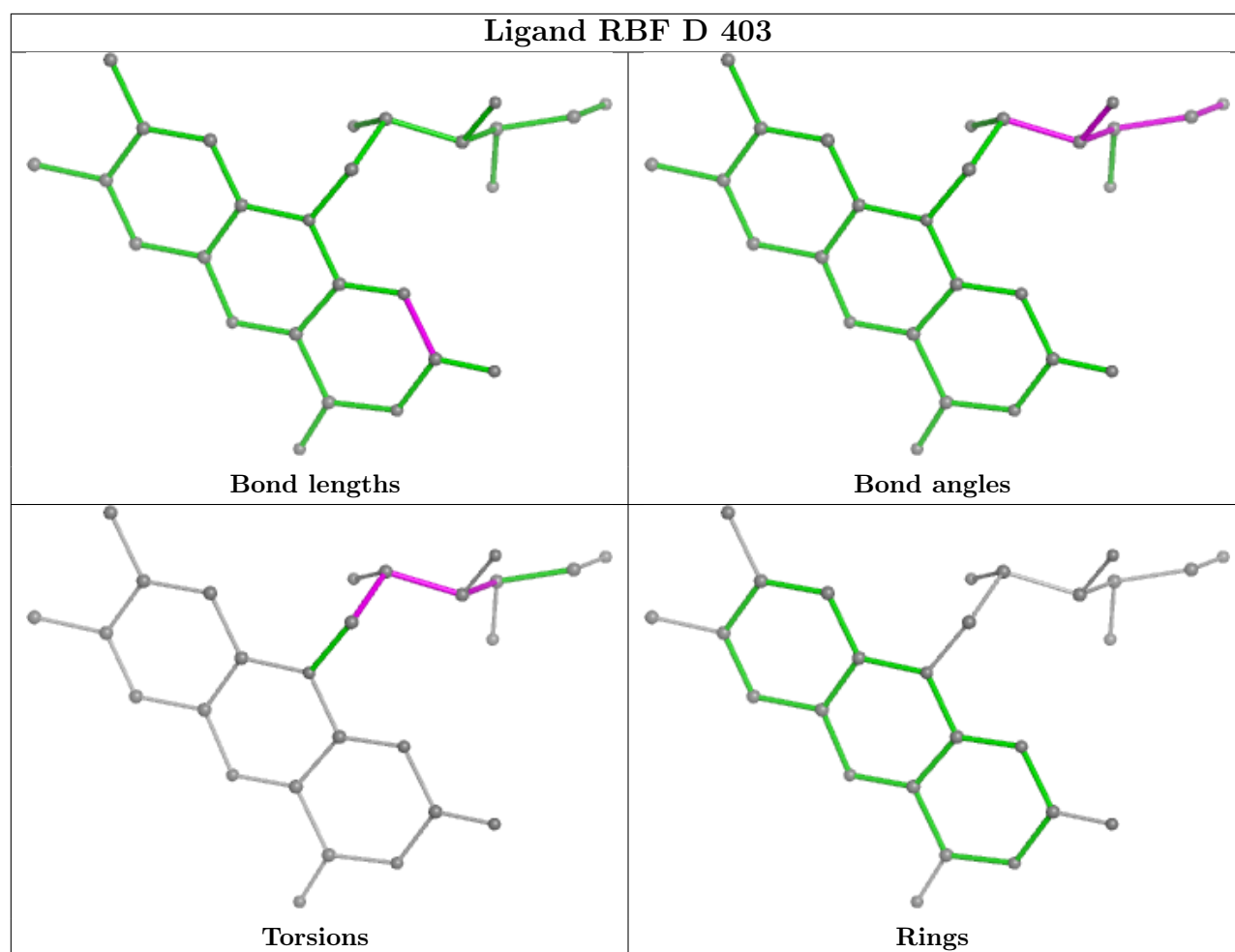


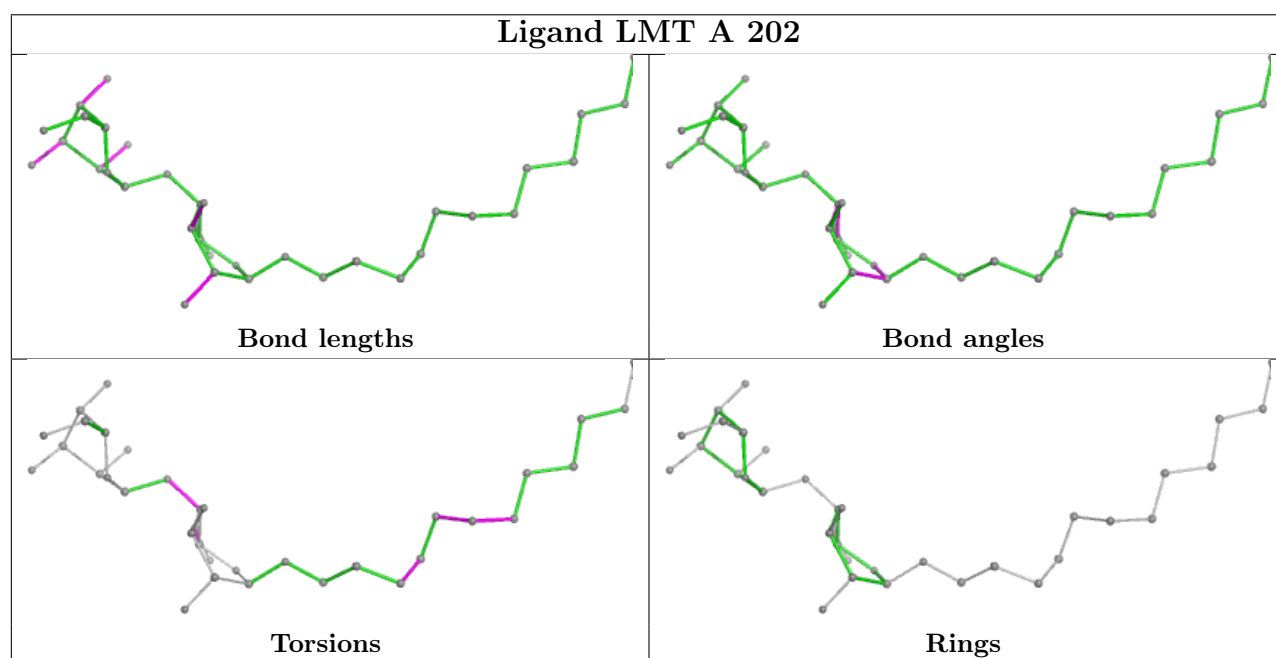
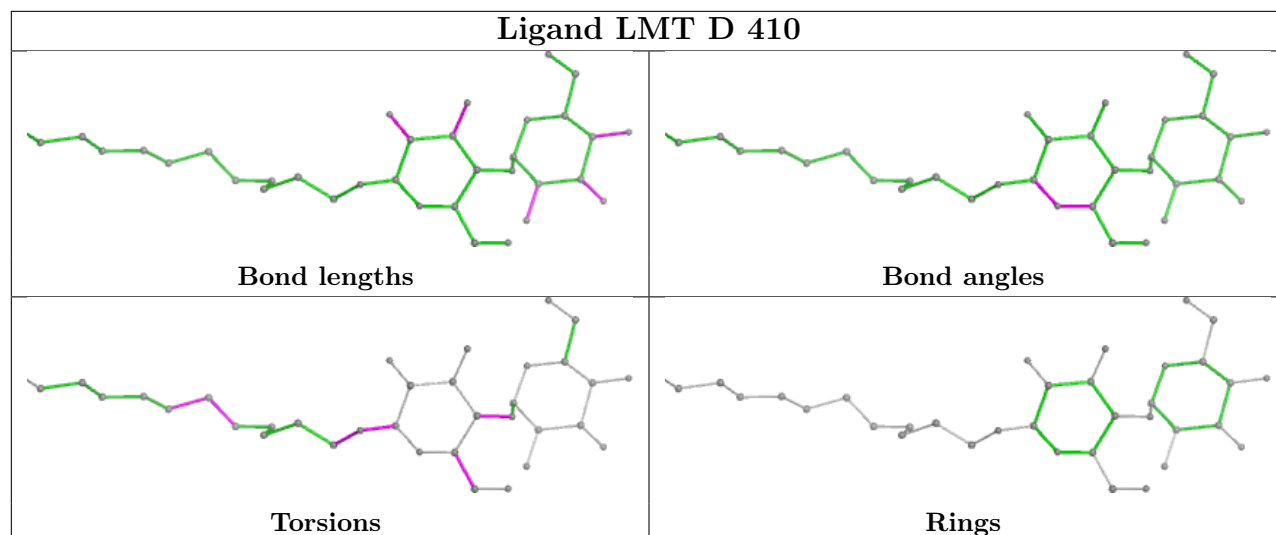


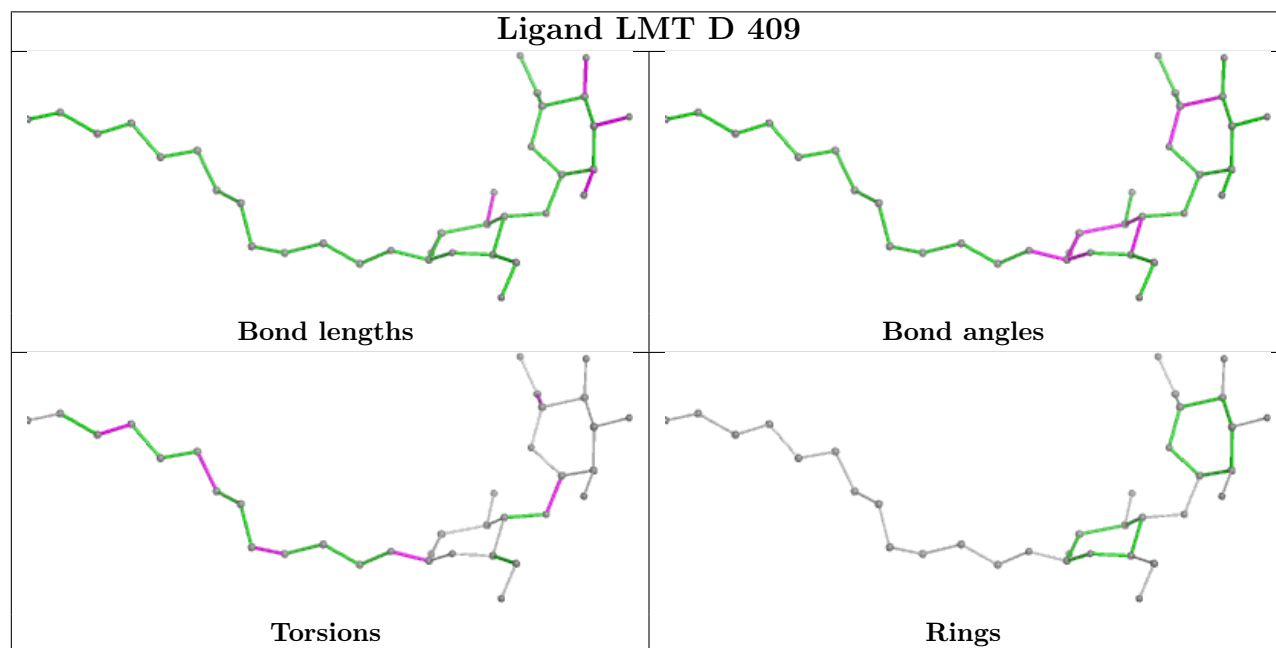
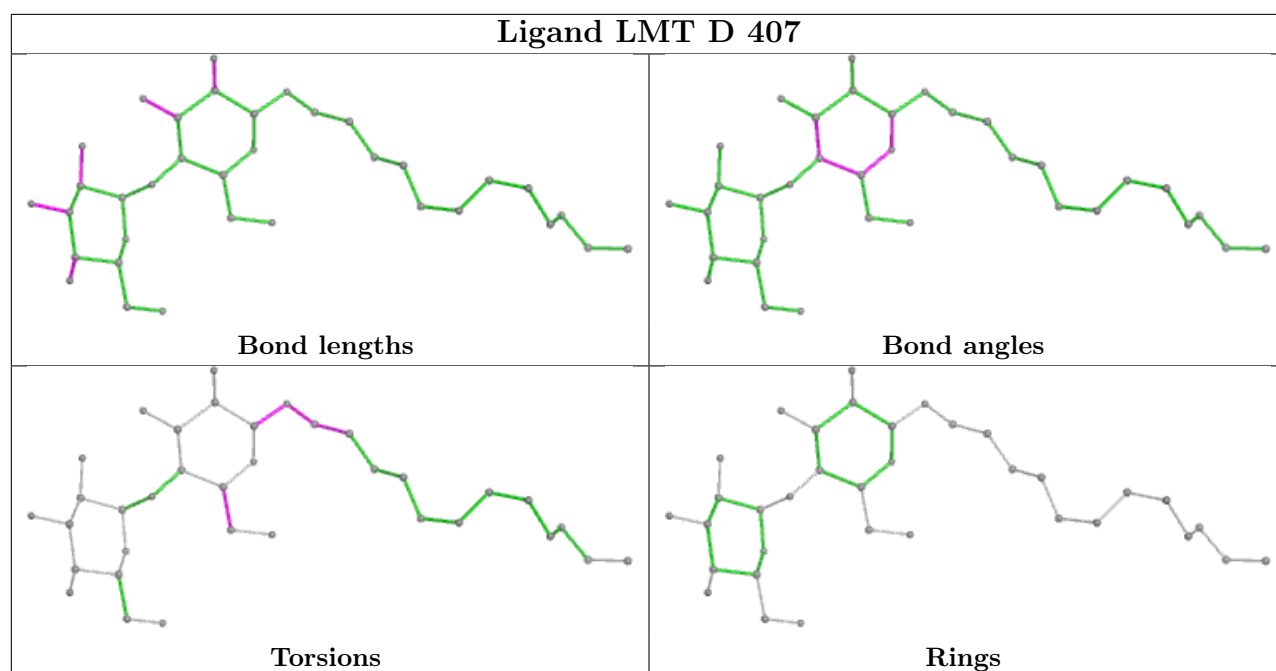


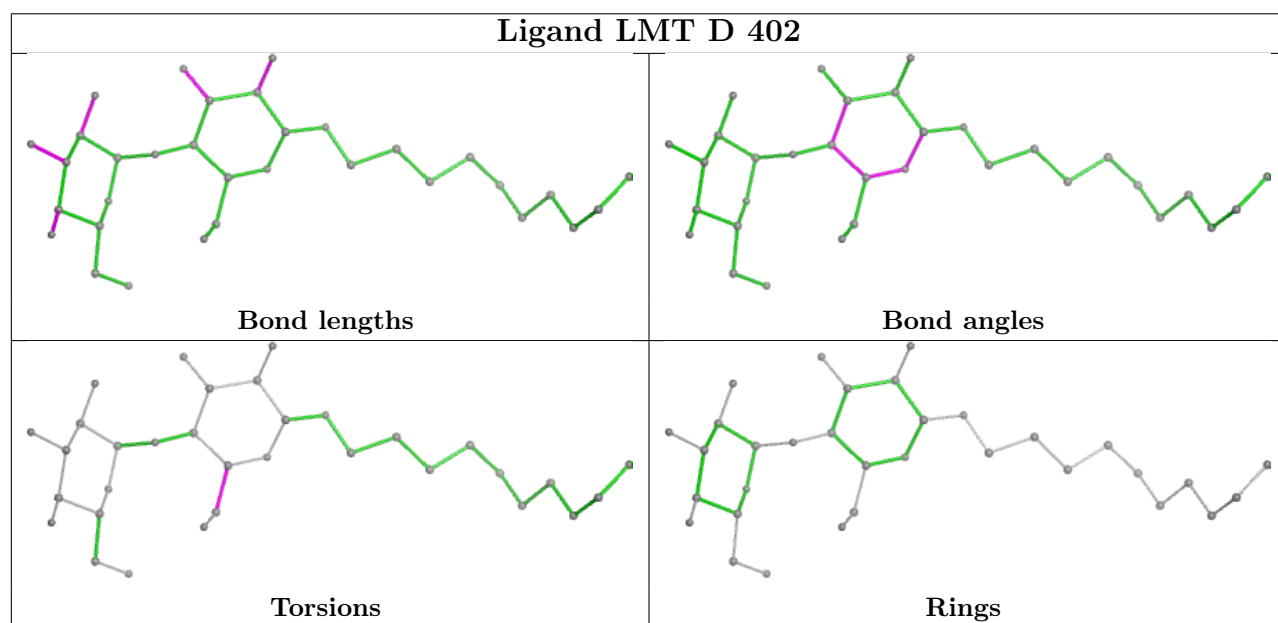
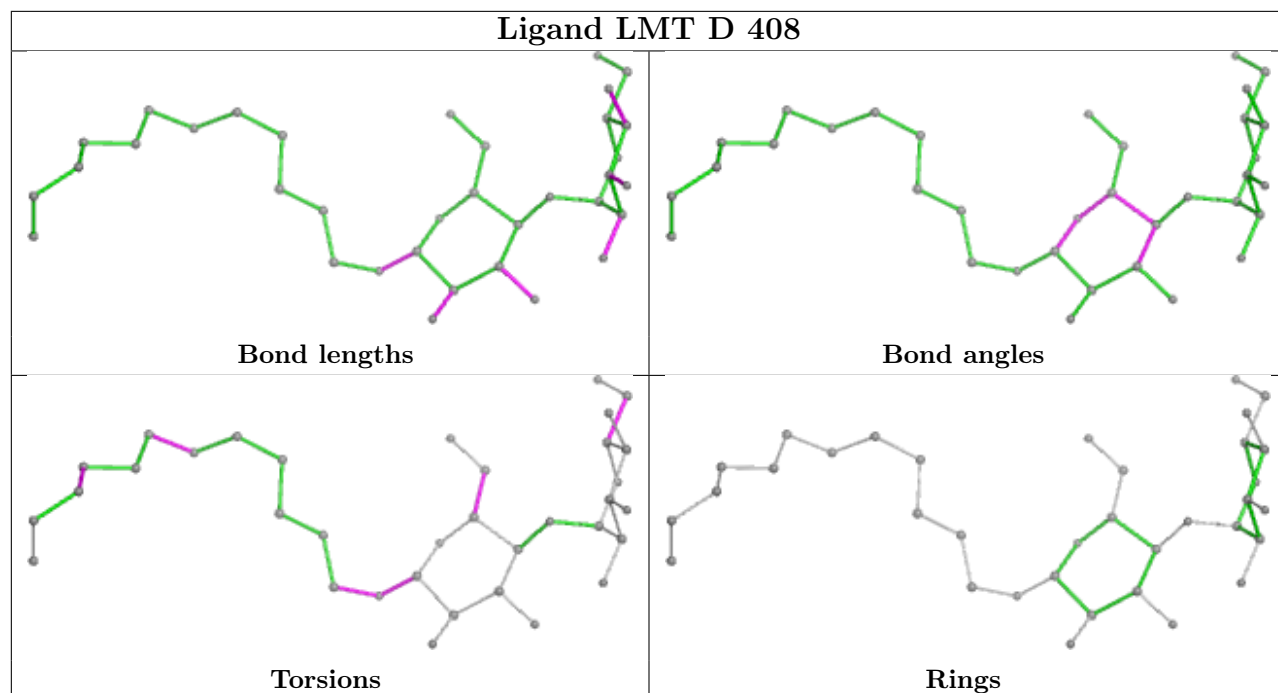


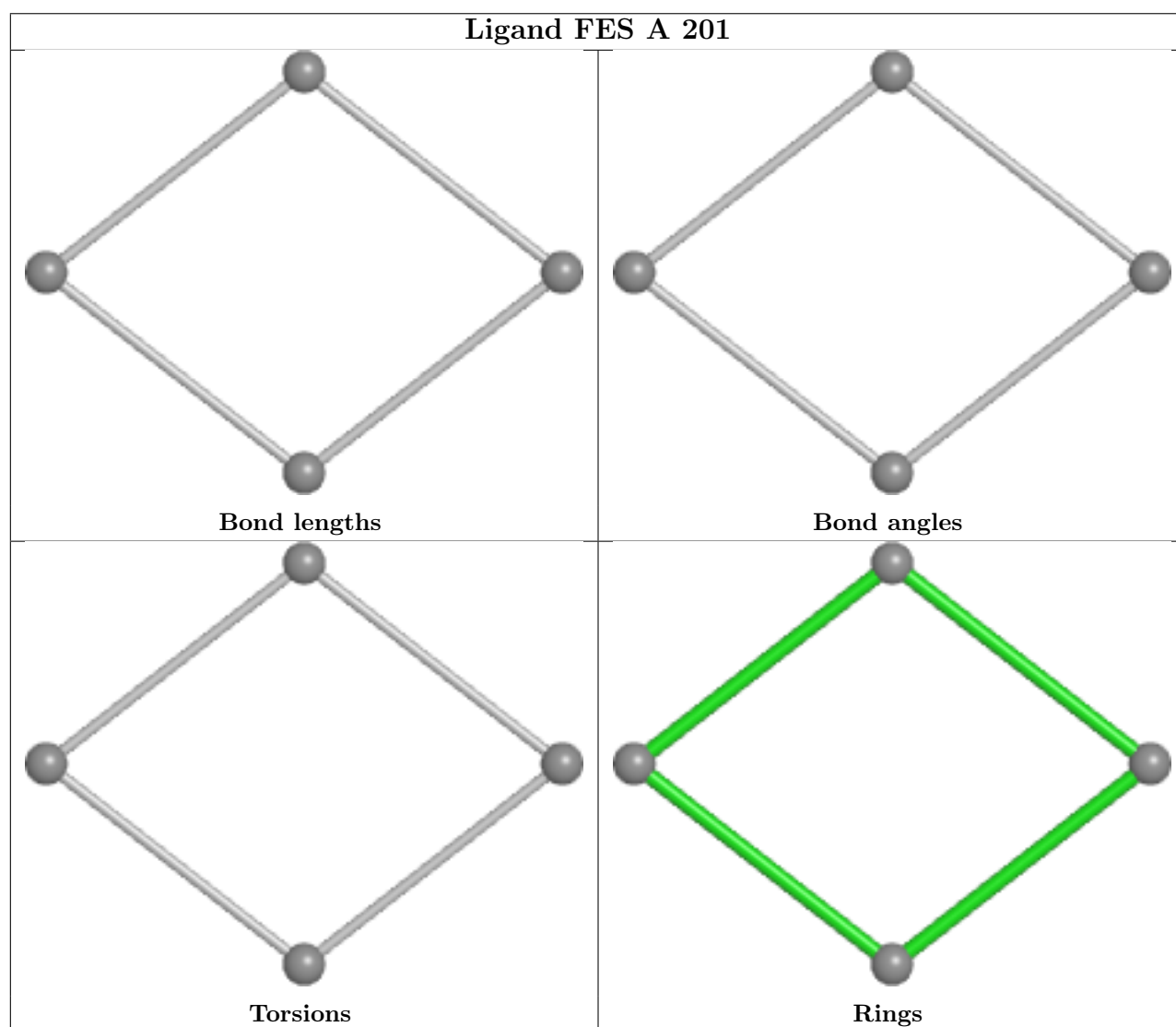
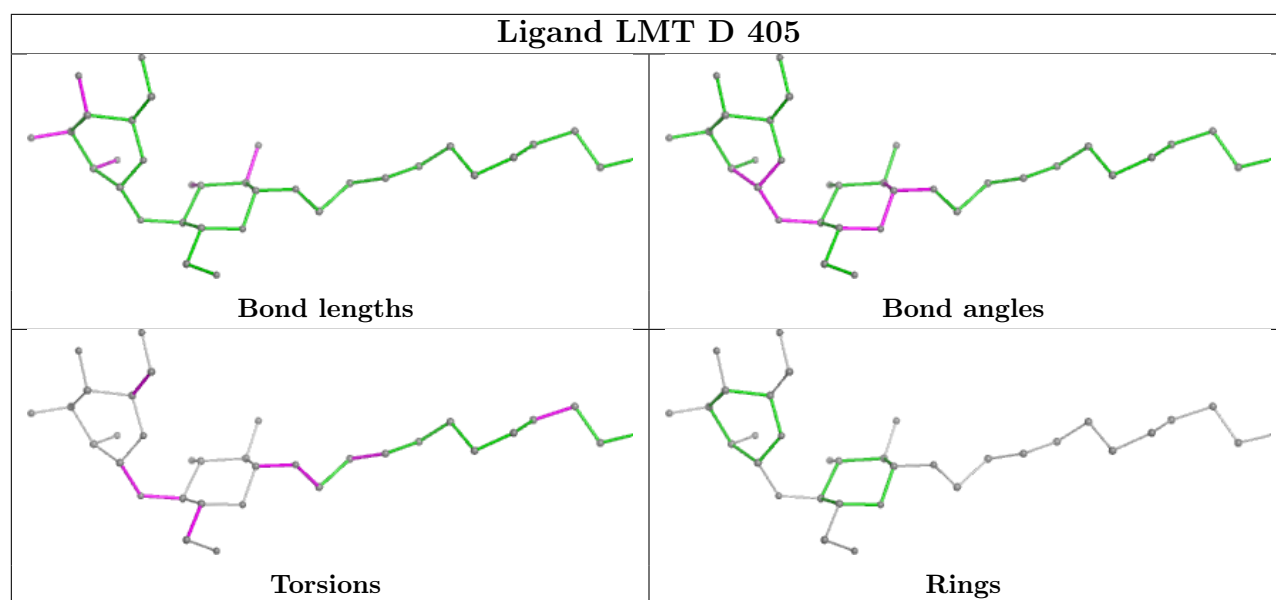


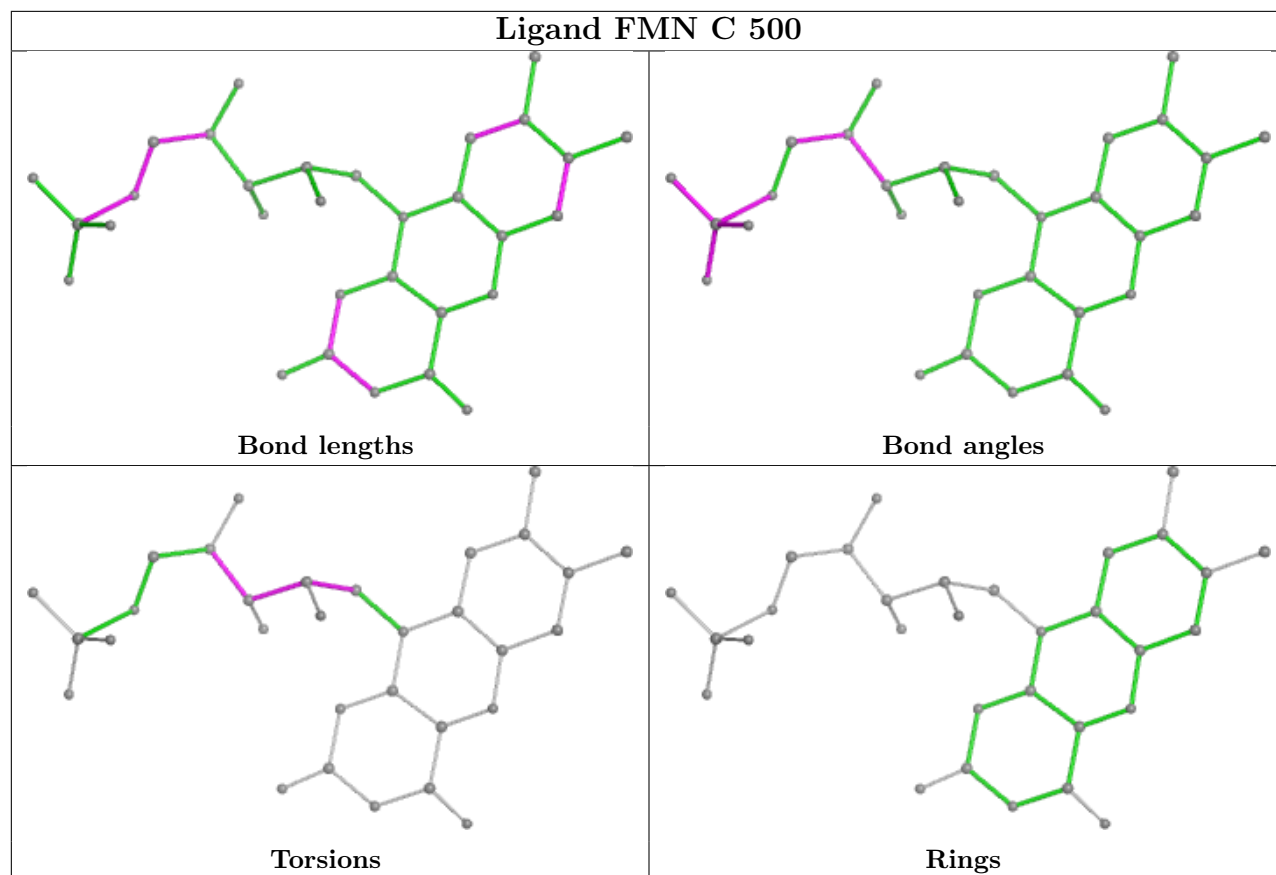












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

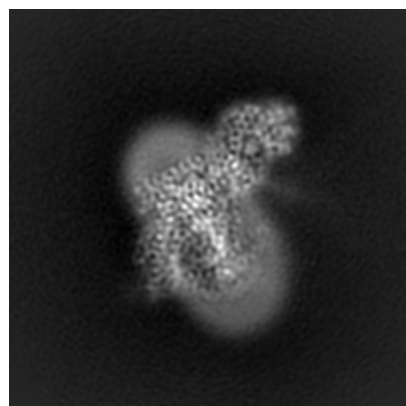
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19032. These allow visual inspection of the internal detail of the map and identification of artifacts.

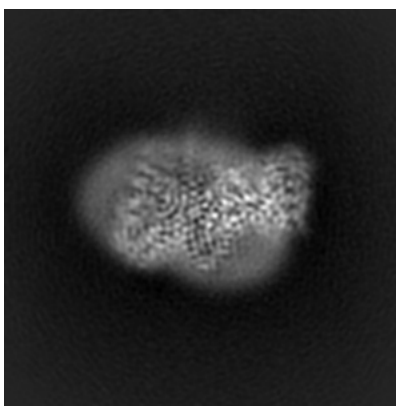
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

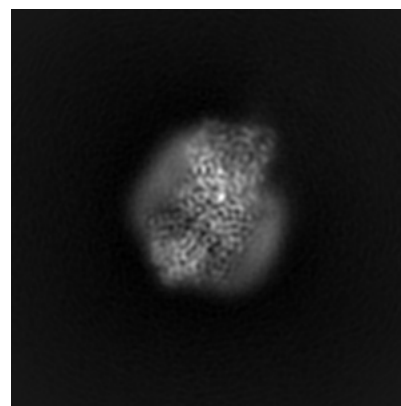
6.1.1 Primary map



X

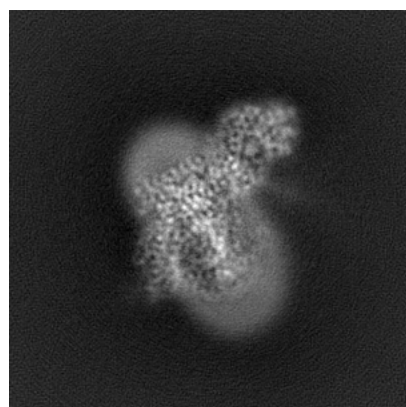


Y

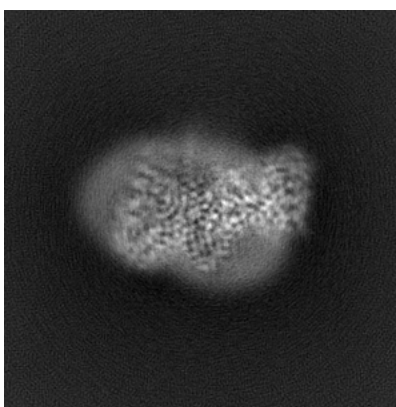


Z

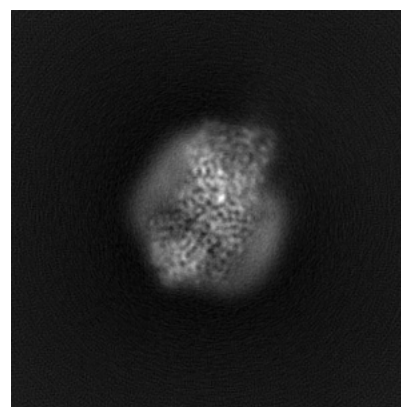
6.1.2 Raw map



X



Y

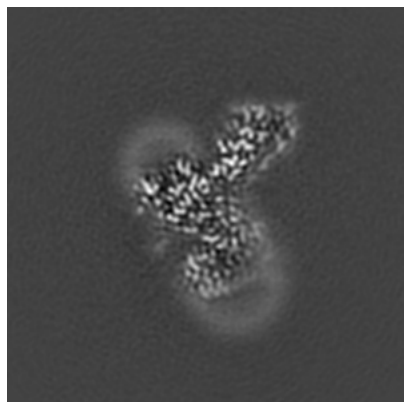


Z

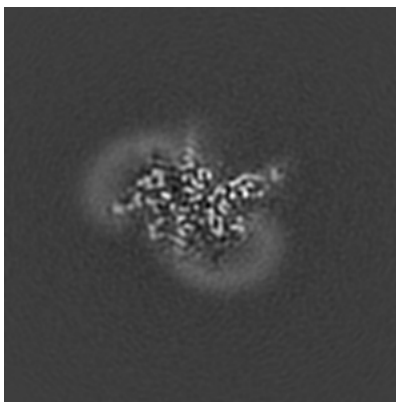
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

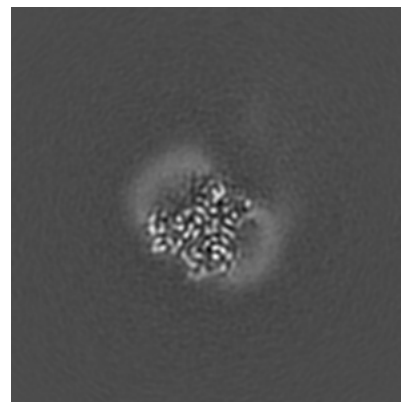
6.2.1 Primary map



X Index: 140

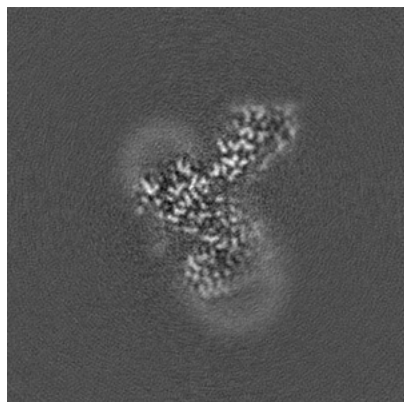


Y Index: 140

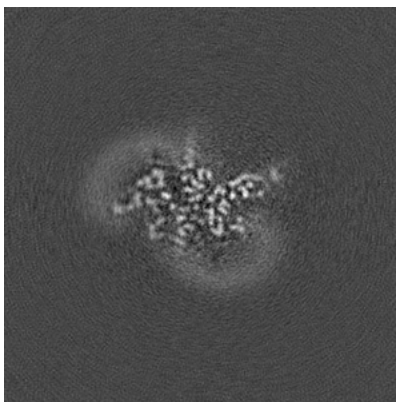


Z Index: 140

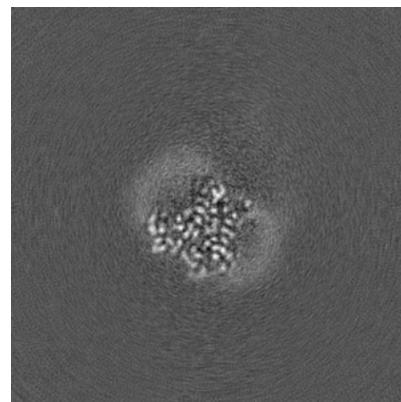
6.2.2 Raw map



X Index: 140



Y Index: 140

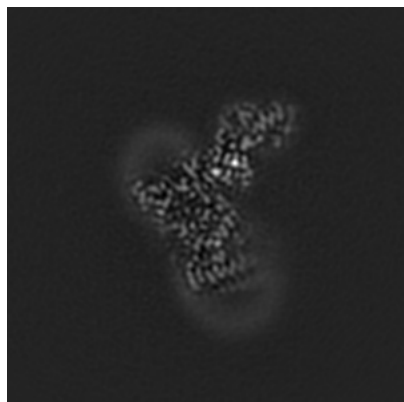


Z Index: 140

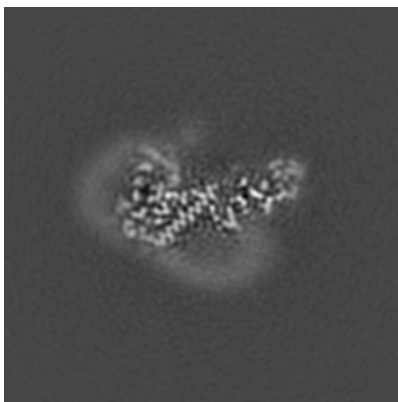
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

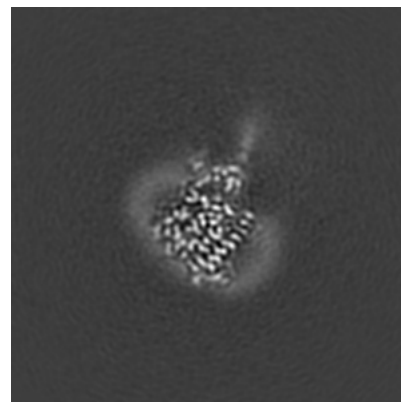
6.3.1 Primary map



X Index: 146

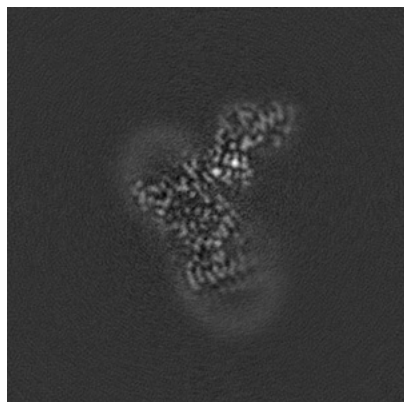


Y Index: 149

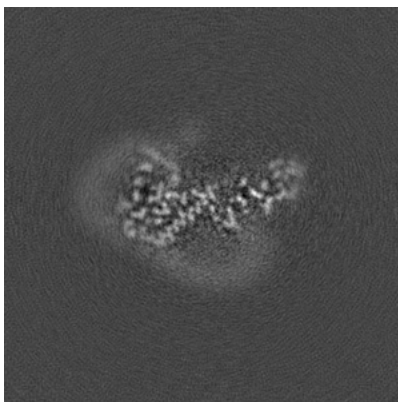


Z Index: 154

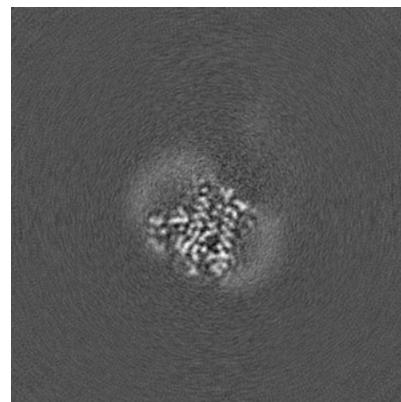
6.3.2 Raw map



X Index: 146



Y Index: 149

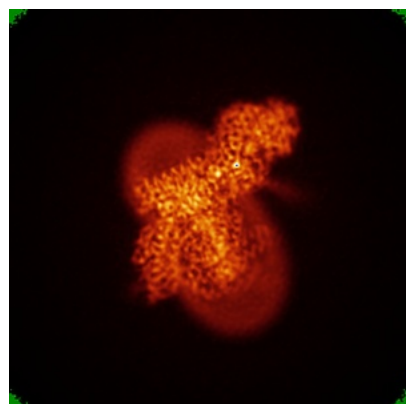


Z Index: 143

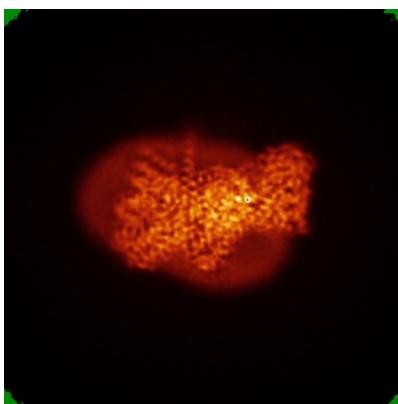
The images above show the largest variance slices of the map in three orthogonal directions.

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

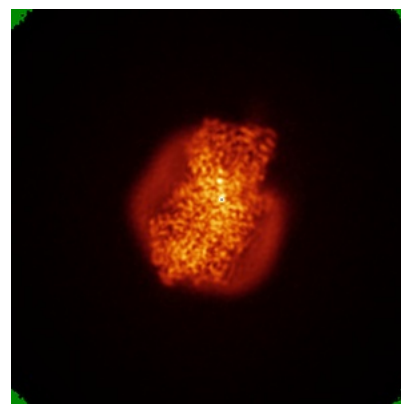
6.4.1 Primary map



X

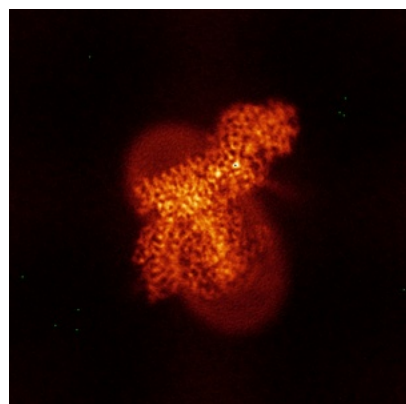


Y

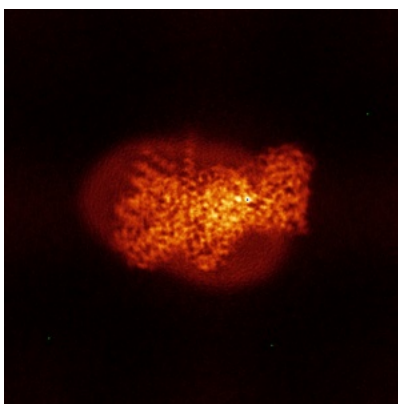


Z

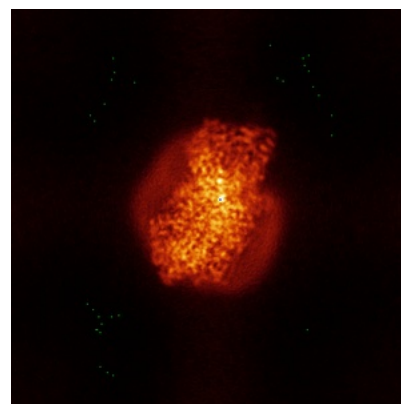
6.4.2 Raw map



X



Y

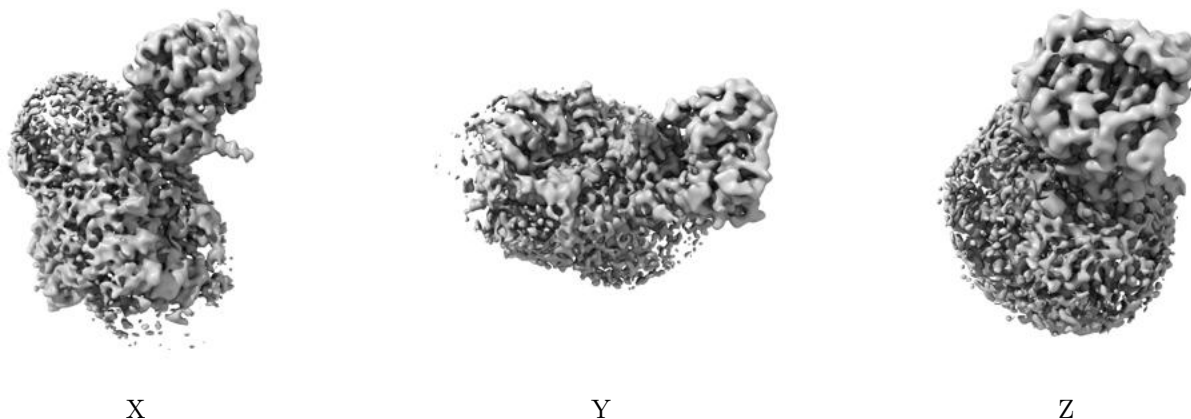


Z

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.

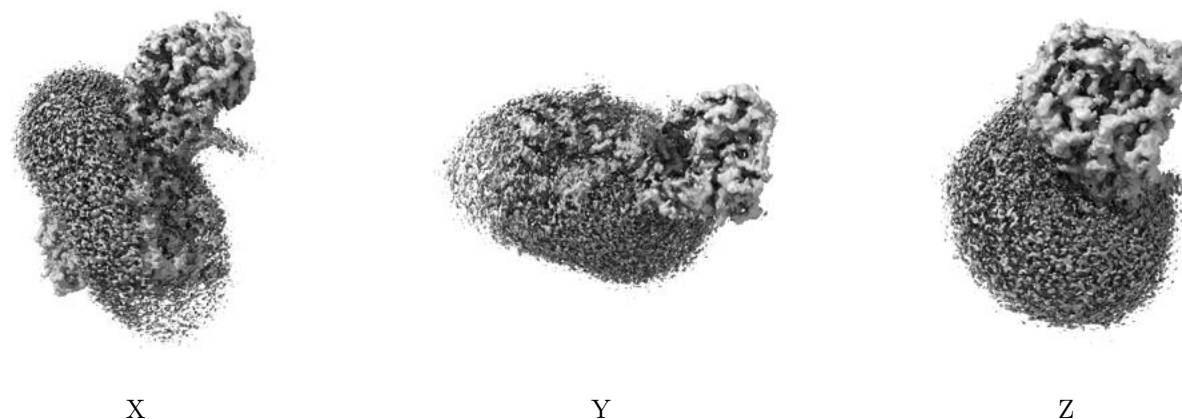
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.065. 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.

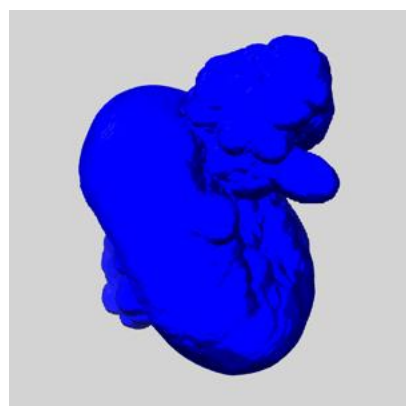
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

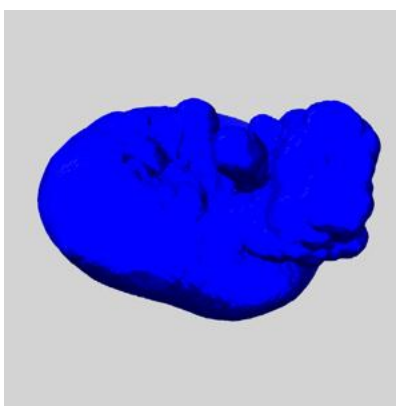
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

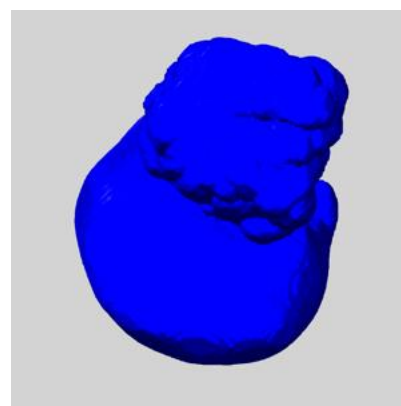
6.6.1 emd_19032_msk_1.map [i](#)



X



Y

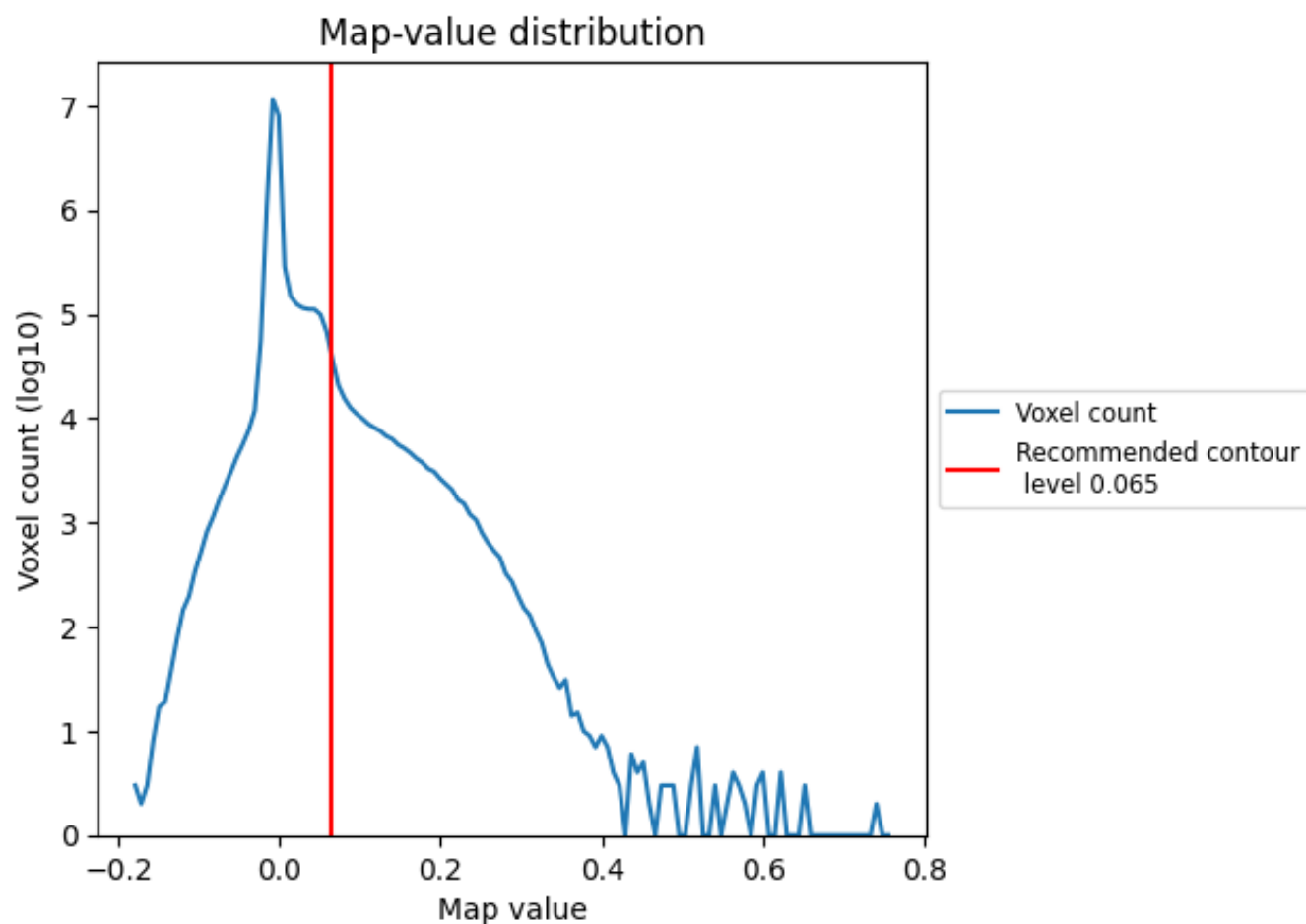


Z

7 Map analysis [i](#)

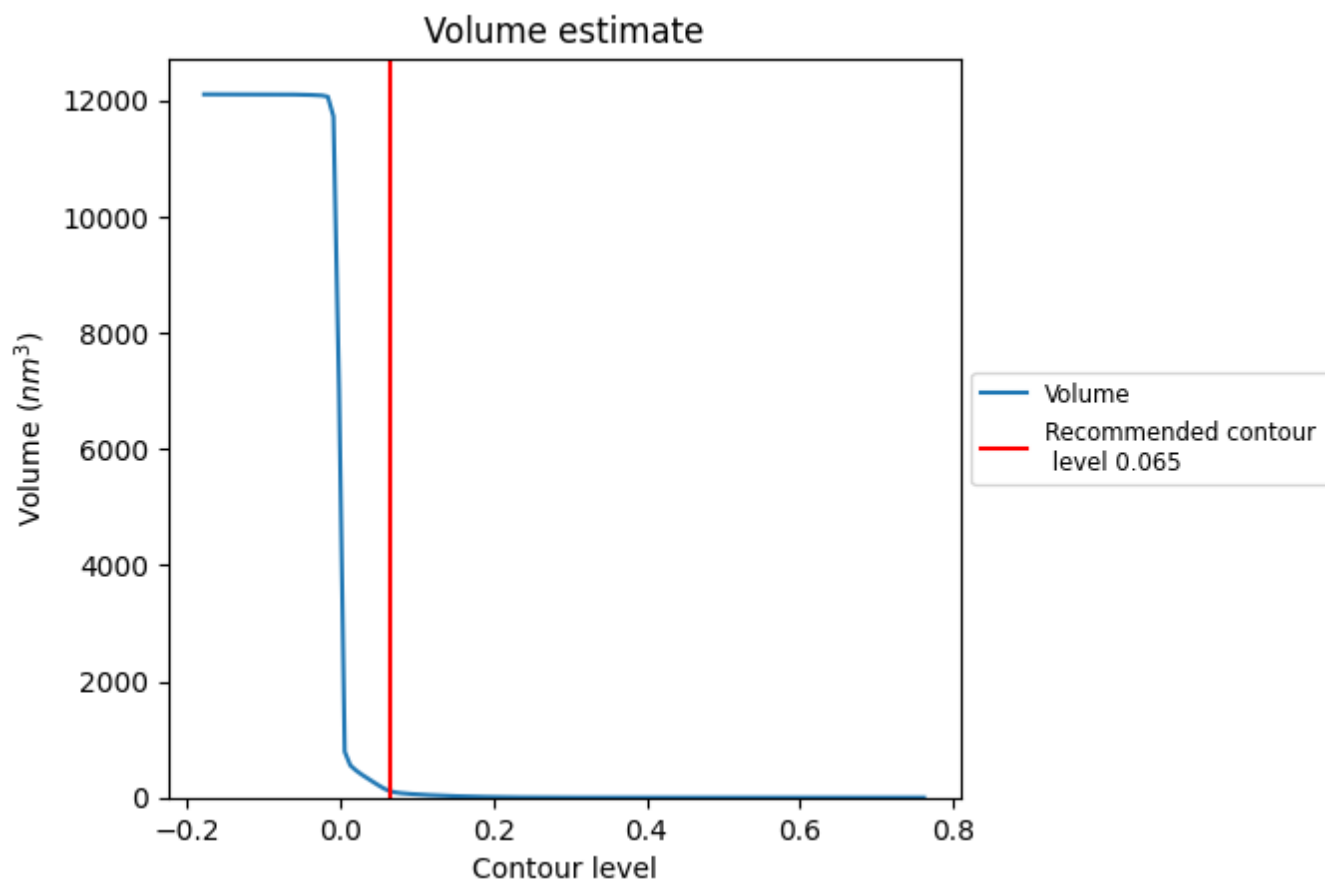
This section contains the results of statistical analysis of the map.

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.

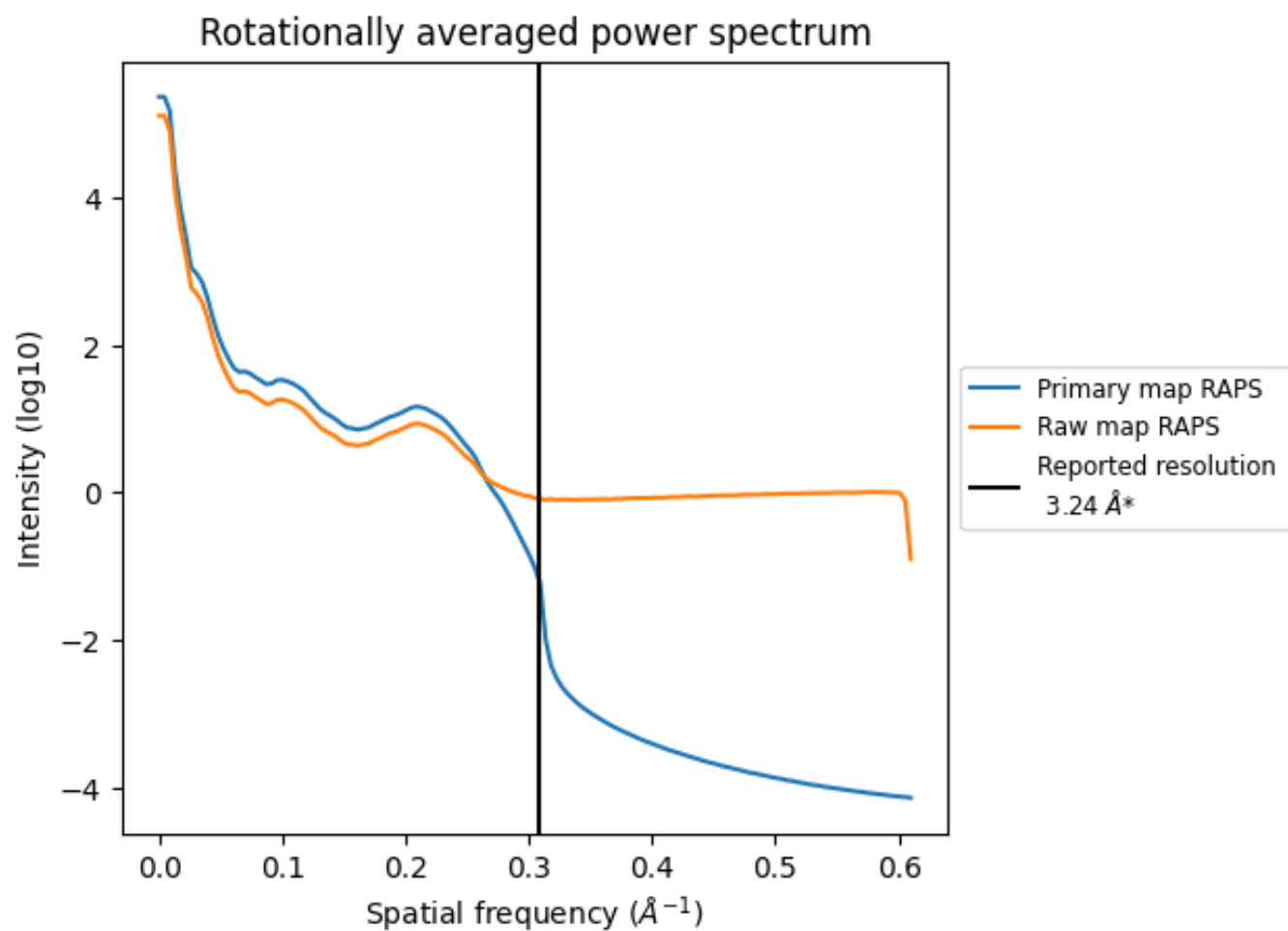
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 110 nm³; this corresponds to an approximate mass of 99 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 ⓘ

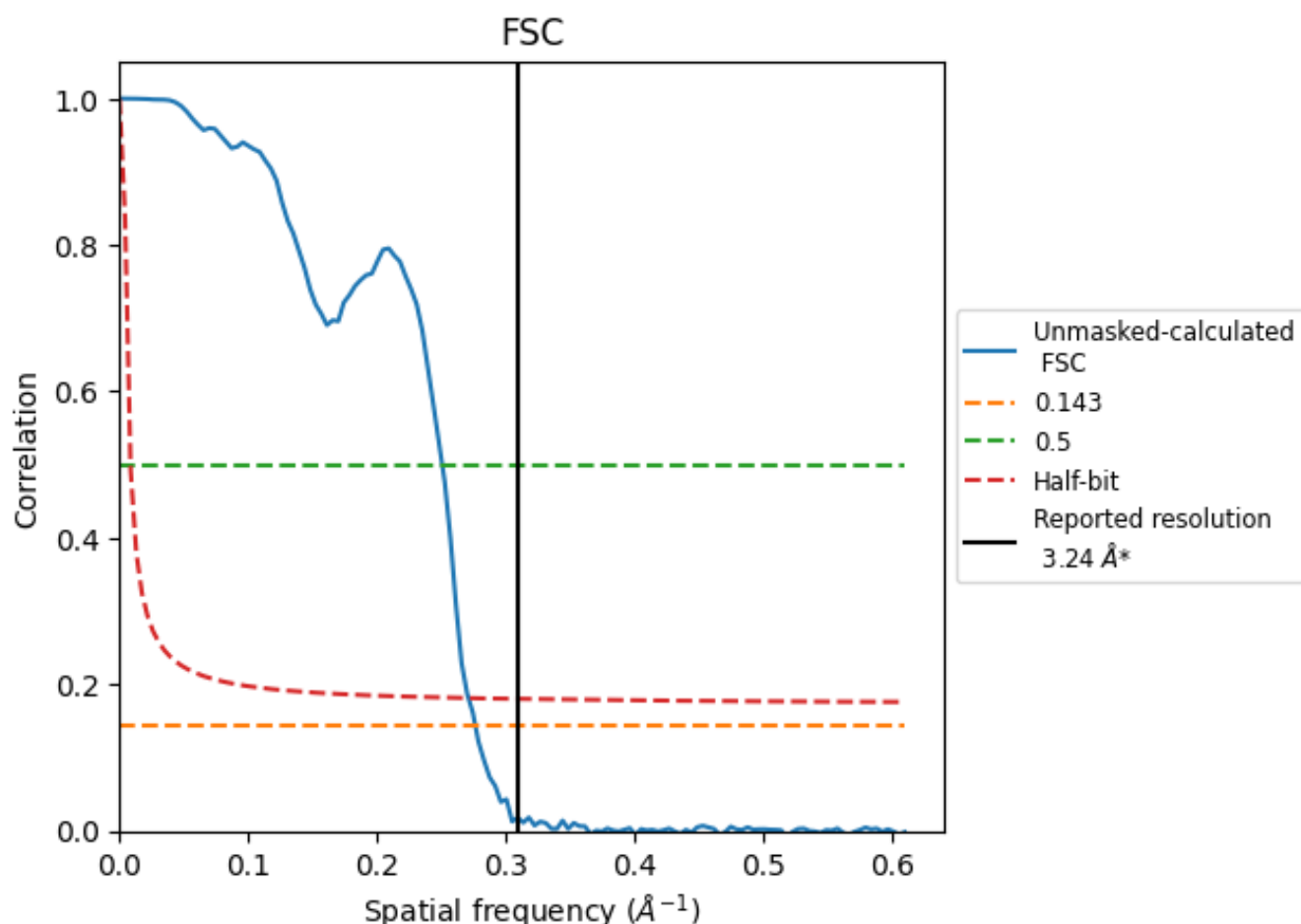


*Reported resolution corresponds to spatial frequency of 0.309 \AA^{-1}

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 0.309 \AA^{-1}

8.2 Resolution estimates [i](#)

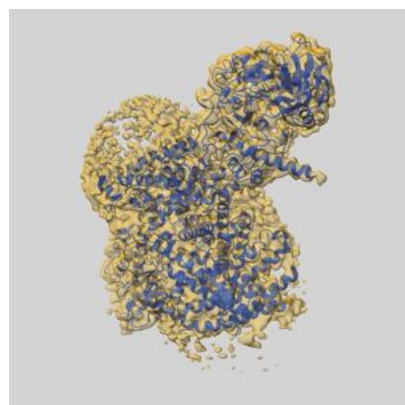
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.24	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.62	3.99	3.69

*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 3.62 differs from the reported value 3.24 by more than 10 %

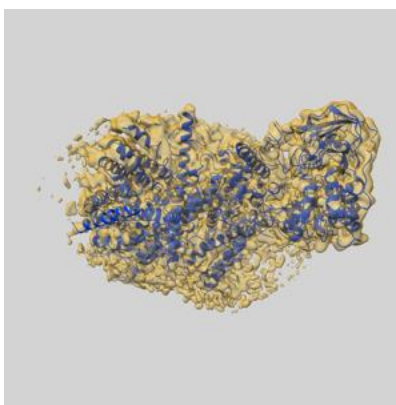
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19032 and PDB model 8RBM. Per-residue inclusion information can be found in section [3](#) on page [10](#).

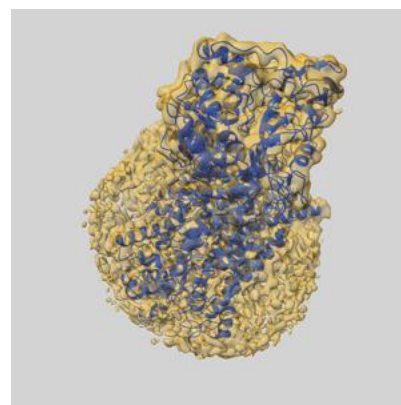
9.1 Map-model overlay [i](#)



X



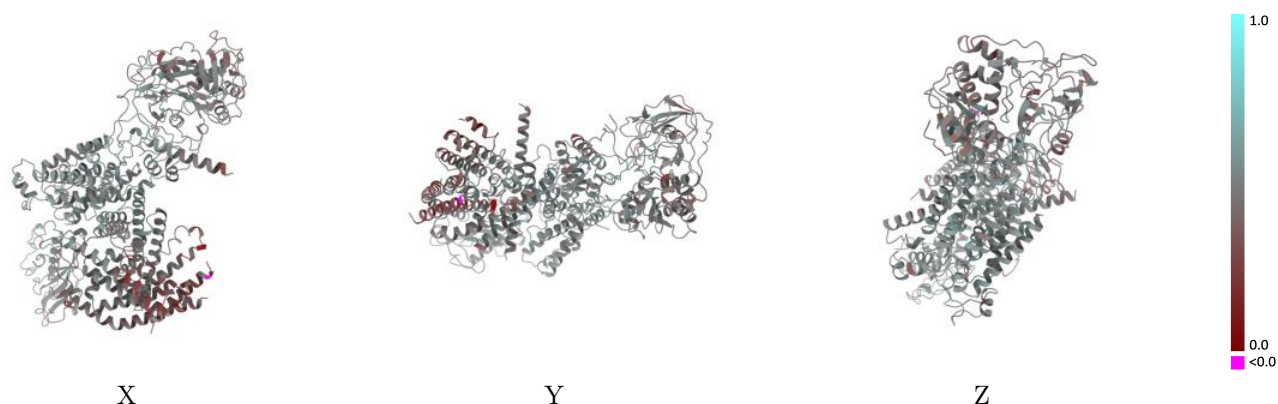
Y



Z

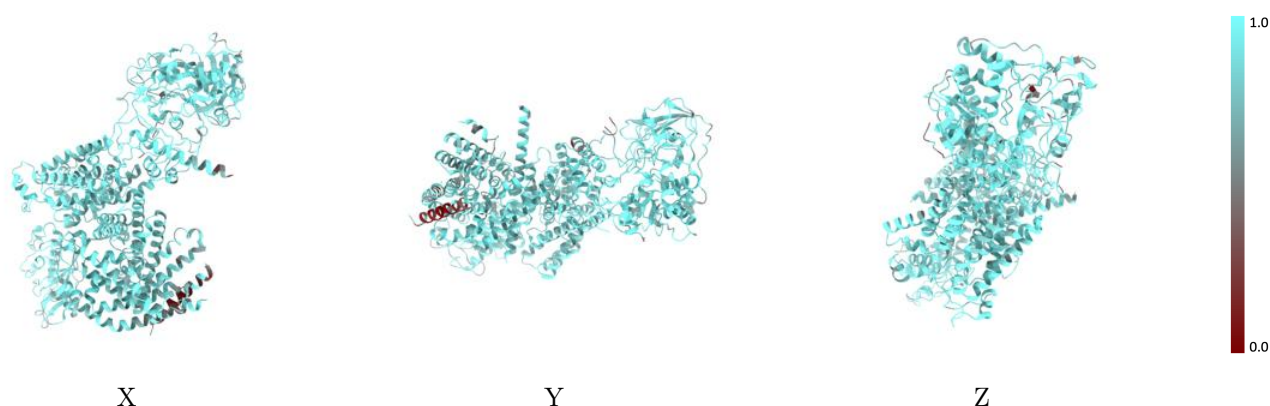
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



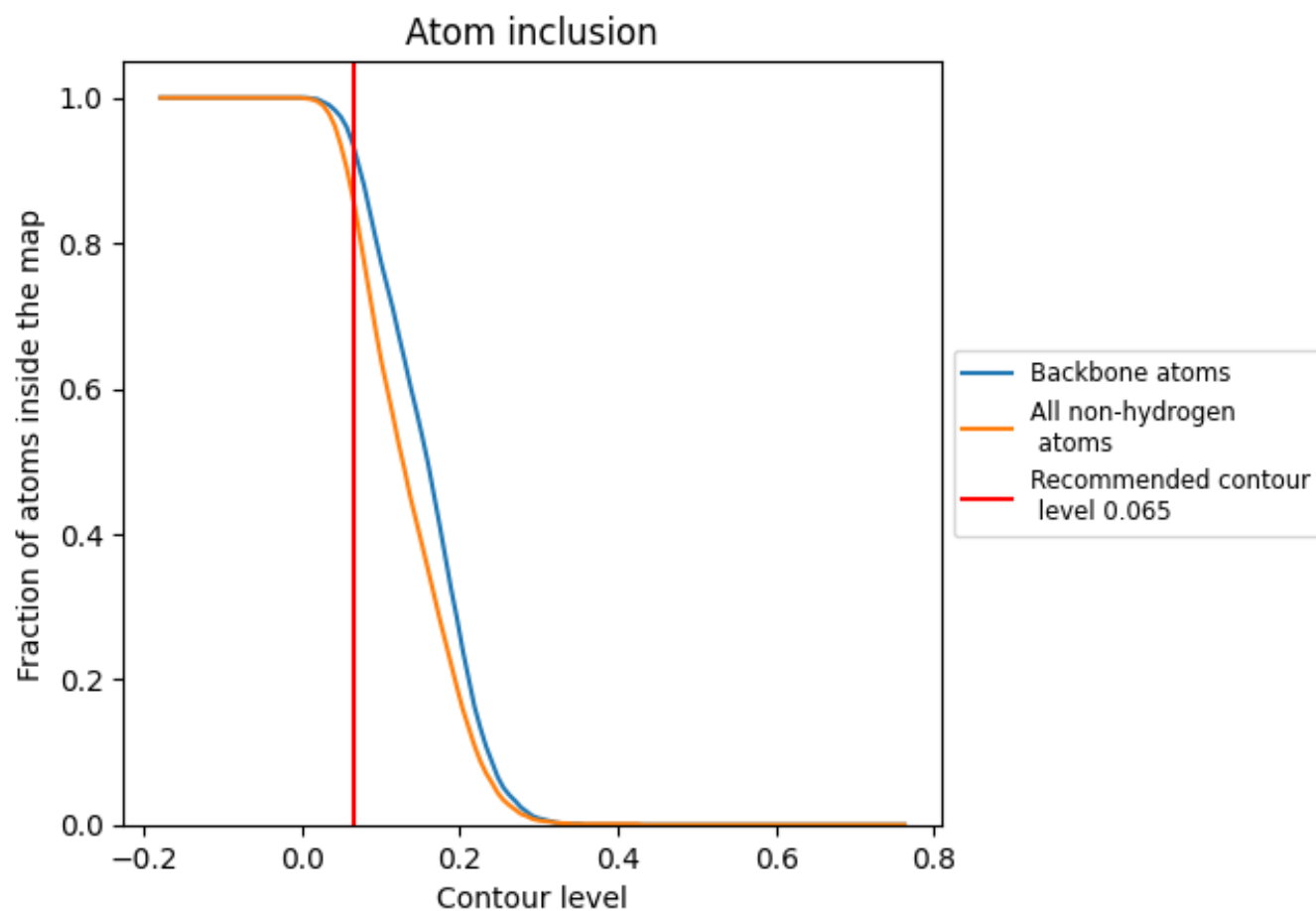
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 86% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8620</div>	<div><div></div>0.4730</div>
A	<div><div></div>0.8770</div>	<div><div></div>0.4750</div>
B	<div><div></div>0.3020</div>	<div><div></div>0.2650</div>
C	<div><div></div>0.8740</div>	<div><div></div>0.4720</div>
D	<div><div></div>0.8880</div>	<div><div></div>0.5110</div>
E	<div><div></div>0.8480</div>	<div><div></div>0.4320</div>
G	<div><div></div>0.8530</div>	<div><div></div>0.4640</div>
b	<div><div></div>0.7550</div>	<div><div></div>0.4590</div>

1.0

0.0

<0.0