



wwPDB EM Validation Summary Report ⓘ

Nov 24, 2024 – 01:58 AM JST

PDB ID : 8IC5
EMDB ID : EMD-35355
Title : Respiratory complex CIII2, focus-refined of type I, PERK -/- mouse under cold temperature
Authors : Shin, Y.-C.; Liao, M.
Deposited on : 2023-02-10
Resolution : 4.10 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 : 1.8.5 (274361), 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) : 2.40

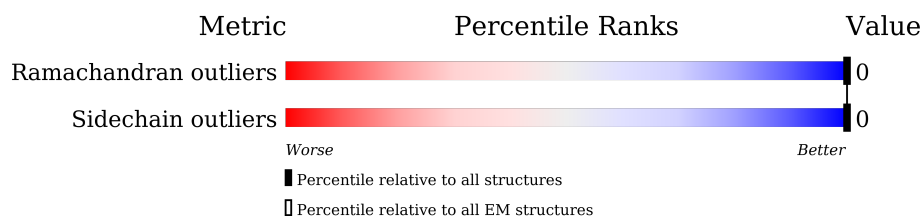
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

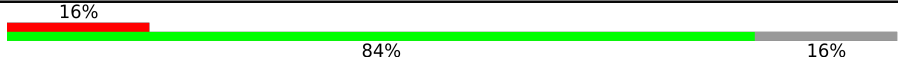

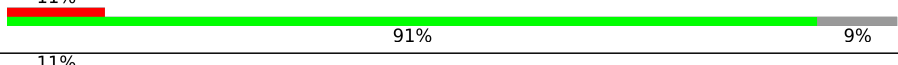
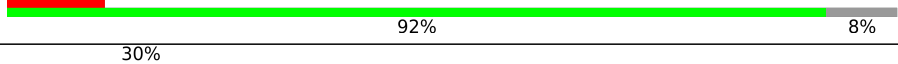
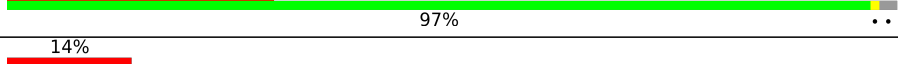
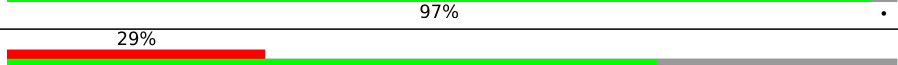
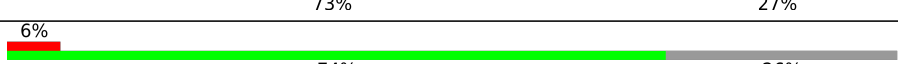


The reported resolution of this entry is 4.10 Å.

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)
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	AA	480	
1	Aa	480	
2	AB	453	
2	Ab	453	
3	AC	381	
3	Ac	381	
4	AD	325	
4	Ad	325	
5	AE	274	

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Mol	Chain	Length	Quality of chain
5	AI	274	
5	Ae	274	
6	AF	111	
6	Af	111	
7	AG	82	
7	Ag	82	
8	AH	89	
8	Ah	89	
9	AJ	64	
9	Aj	64	
10	AK	56	
10	Ak	56	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 31445 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 Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	403	Total	C	N	O	S	0	0
			3157	1971	562	608	16		
1	Aa	400	Total	C	N	O	S	0	0
			3131	1957	554	604	16		

- Molecule 2 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	413	Total	C	N	O	S	0	0
			3097	1949	542	597	9		
2	Ab	417	Total	C	N	O	S	0	0
			3128	1965	550	604	9		

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	373	Total	C	N	O	S	0	0
			2988	2018	461	489	20		
3	Ac	369	Total	C	N	O	S	0	0
			2956	1995	457	484	20		

- Molecule 4 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	238	Total	C	N	O	S	0	0
			1896	1211	326	345	14		
4	Ad	240	Total	C	N	O	S	0	0
			1912	1221	328	349	14		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	181	Total	C	N	O	S	0	0
			1397	885	243	263	6		
5	AI	48	Total	C	N	O		0	0
			328	210	61	57			
5	Ae	186	Total	C	N	O	S	0	0
			1436	907	251	271	7		

- Molecule 6 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	97	Total	C	N	O	S	0	0
			855	546	152	154	3		
6	Af	98	Total	C	N	O	S	0	0
			864	552	154	155	3		

- Molecule 7 is a protein called Cytochrome b-c1 complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	75	Total	C	N	O	S	0	0
			634	413	115	105	1		
7	Ag	76	Total	C	N	O	S	0	0
			643	418	116	108	1		

- Molecule 8 is a protein called Cytochrome b-c1 complex subunit 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	64	Total	C	N	O	S	0	0
			527	321	98	103	5		
8	Ah	64	Total	C	N	O	S	0	0
			527	321	98	103	5		

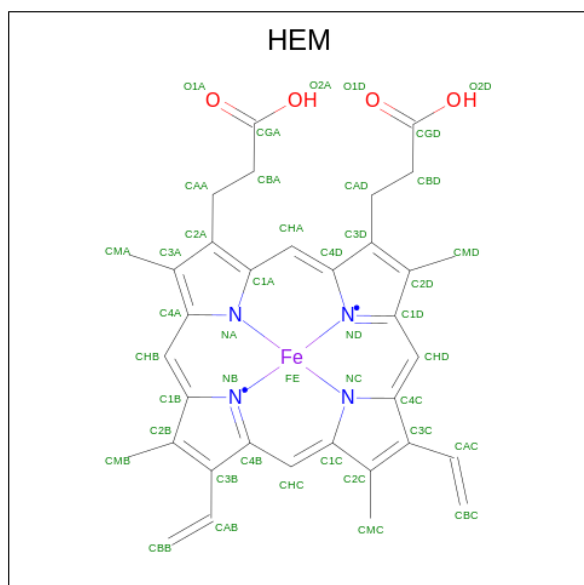
- Molecule 9 is a protein called Cytochrome b-c1 complex subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AJ	41	Total	C	N	O	0	0
			332	216	57	59		
9	Aj	41	Total	C	N	O	0	0
			332	216	57	59		

- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 10.

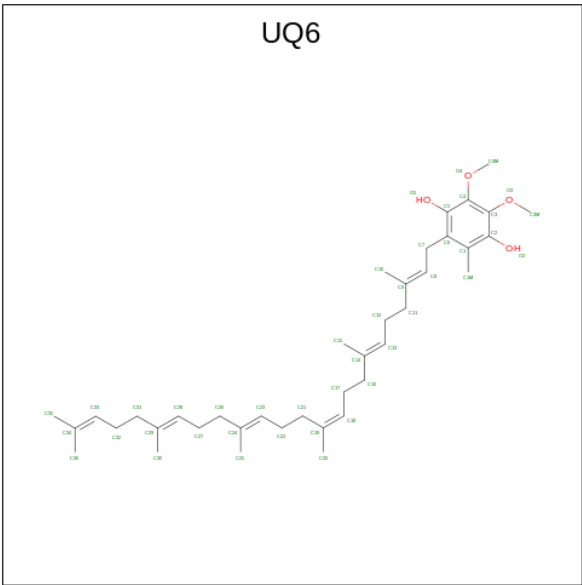
Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	43	Total	C	N	O	S	0	0
			355	235	64	55	1		
10	AK	45	Total	C	N	O	S	0	0
			365	242	64	58	1		

- Molecule 11 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



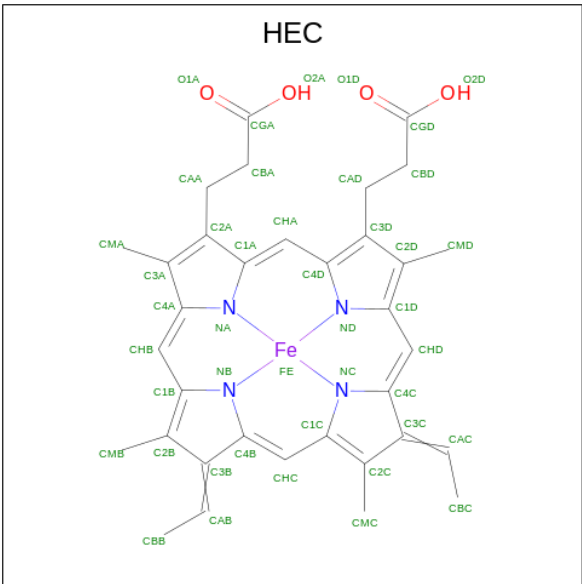
Mol	Chain	Residues	Atoms					AltConf
11	AC	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
11	AC	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
11	Ac	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
11	Ac	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 12 is 5-(3,7,11,15,19,23-HEXAMETHYL-TETRACOSA-2,6,10,14,18,22-HEXAENYL)-2,3-DIMETHOXY-6-METHYL-BENZENE-1,4-DIOL (three-letter code: UQ6) (formula: $C_{39}H_{60}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
12	AC	1	Total	C	O	0
			28	24	4	
12	Ac	1	Total	C	O	0
			23	19	4	

- Molecule 13 is HEME C (three-letter code: HEC) (formula: C₃₄H₃₄FeN₄O₄) (labeled as "Ligand of Interest" by depositor).



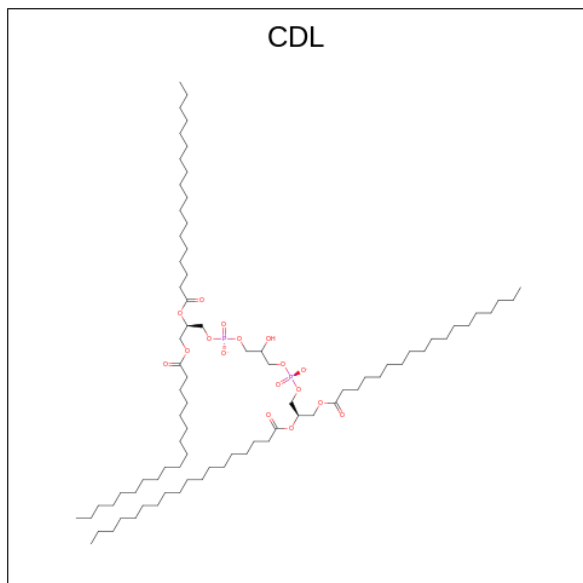
Mol	Chain	Residues	Atoms					AltConf
13	AD	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

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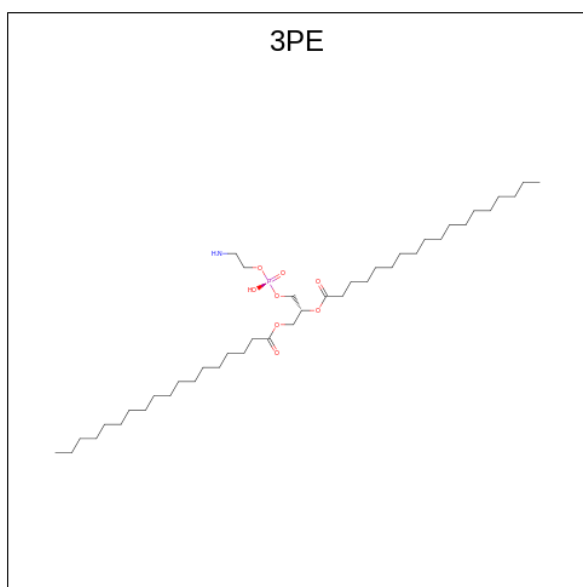
Mol	Chain	Residues	Atoms					AltConf
13	Ad	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 14 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).



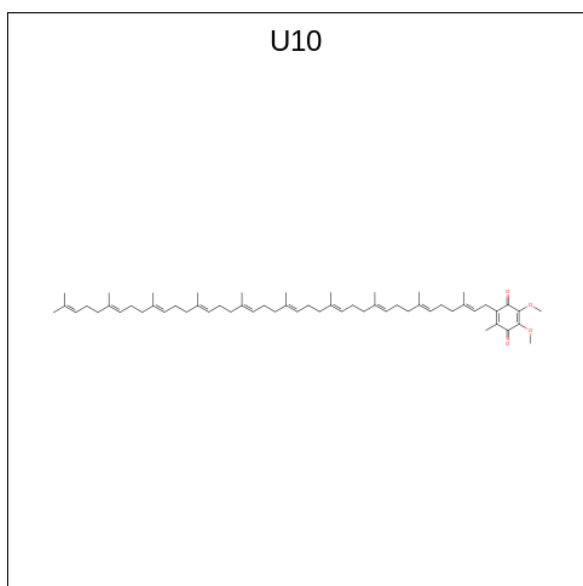
Mol	Chain	Residues	Atoms				AltConf
14	Aa	1	Total	C	O	P	0
			46	27	17	2	
14	Ag	1	Total	C	O	P	0
			42	23	17	2	
14	Ag	1	Total	C	O	P	0
			56	37	17	2	

- Molecule 15 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: $C_{41}H_{82}NO_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
15	Ac	1	Total	C	N	O	P	0
			23	13	1	8	1	
15	Ac	1	Total	C	N	O	P	0
			35	25	1	8	1	
15	Ag	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 16 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).

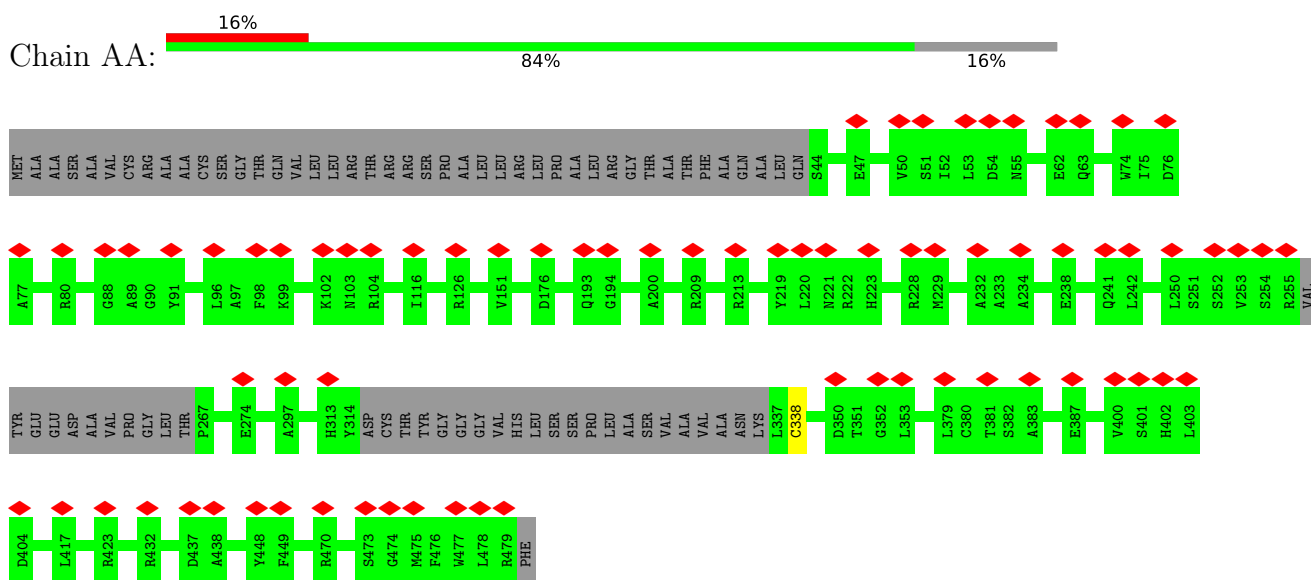


Mol	Chain	Residues	Atoms			AltConf
16	Ac	1	Total	C	O	0
			23	19	4	

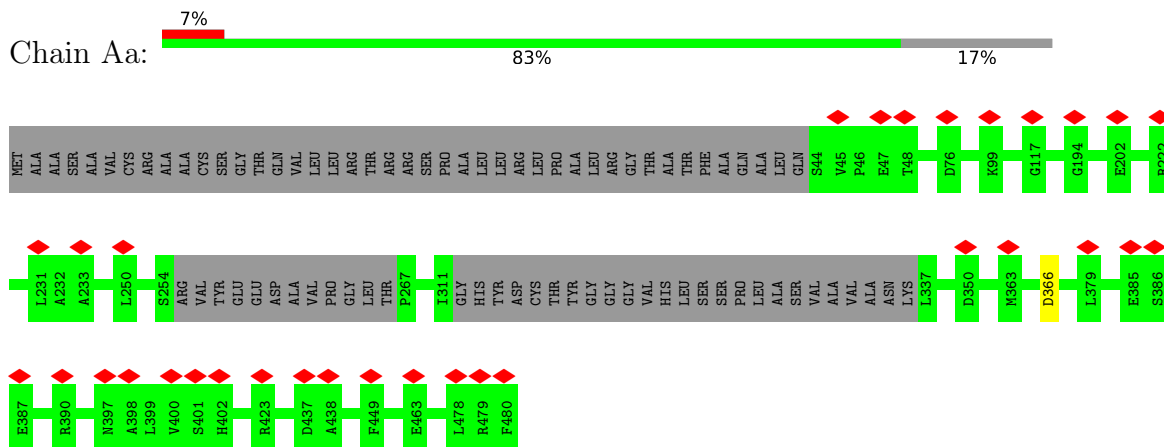
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial

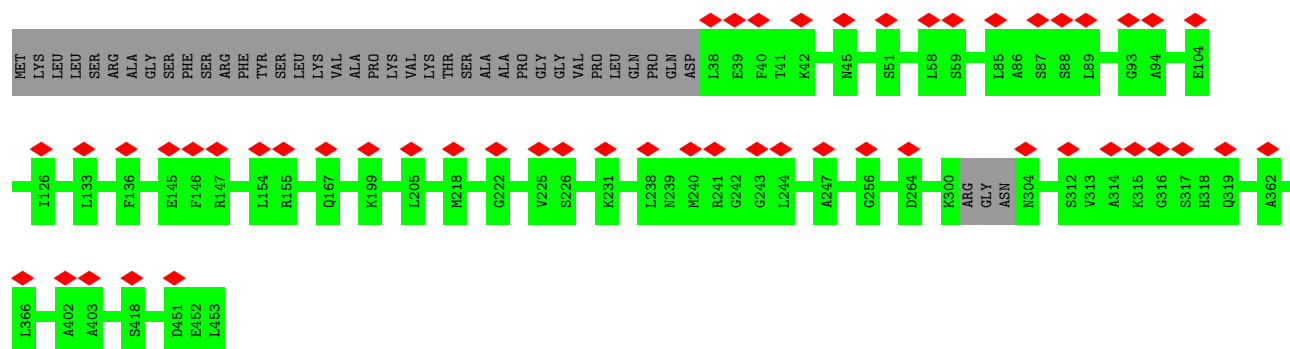


- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial



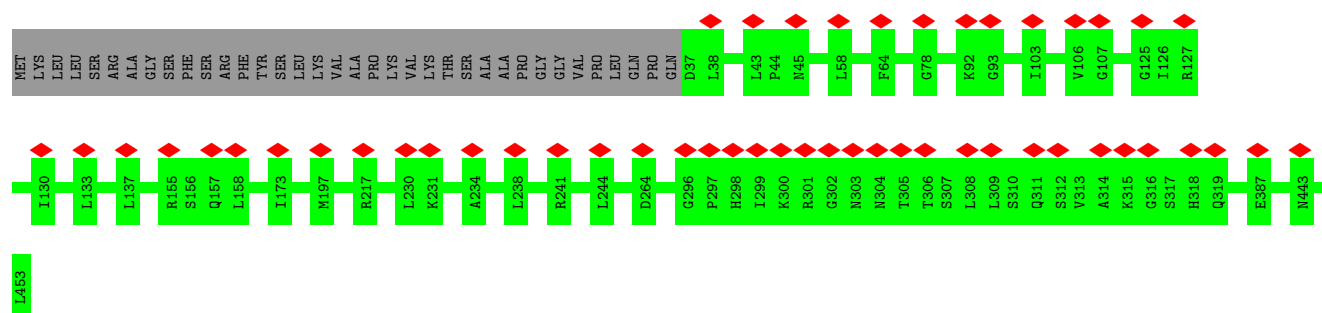
- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial





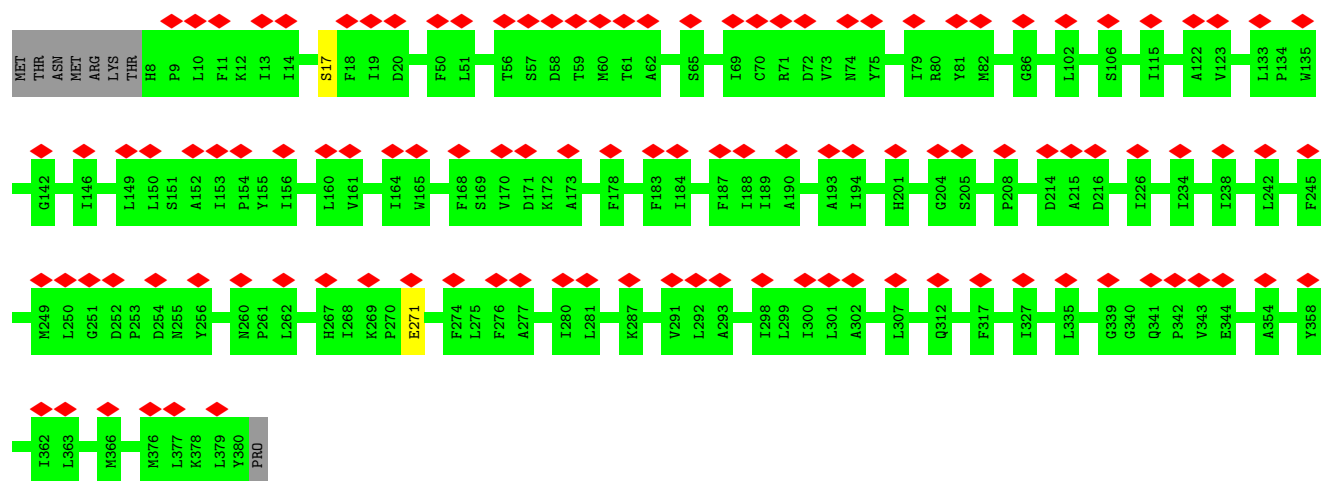
• Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial

Chain Ab: 11% 92% 8%



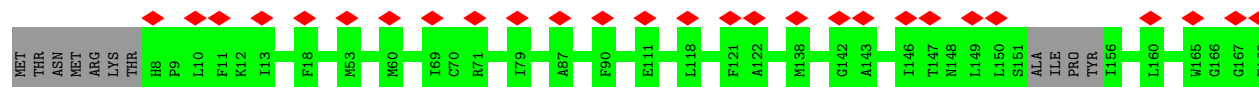
• Molecule 3: Cytochrome b

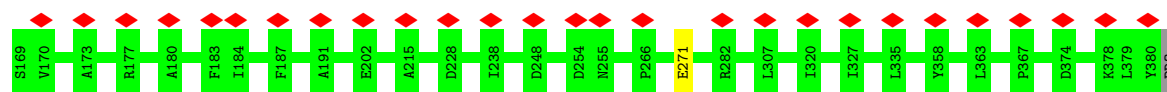
Chain AC: 30% 97% 2%



• Molecule 3: Cytochrome b

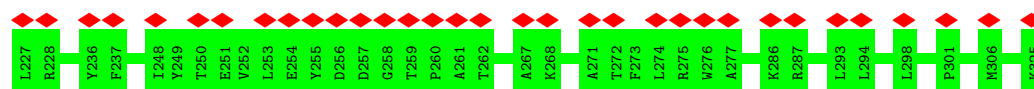
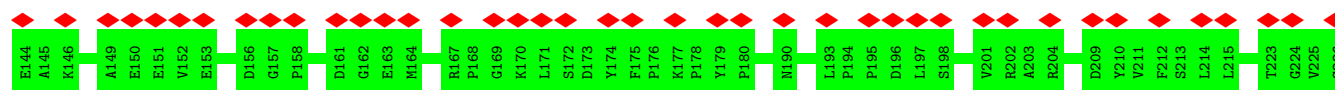
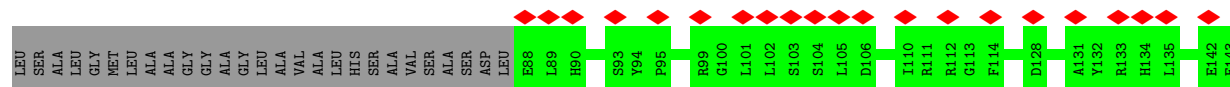
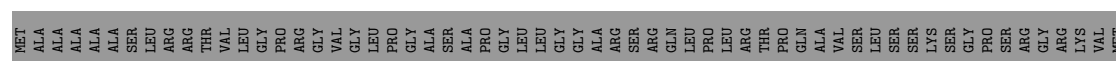
Chain AC: 14% 97% 1%





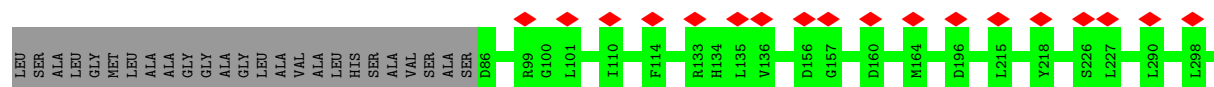
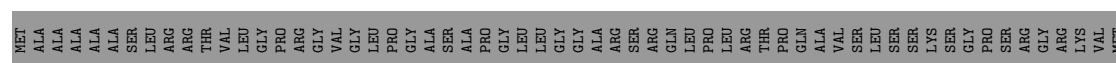
- Molecule 4: Cytochrome c1, heme protein, mitochondrial

Chain AD:



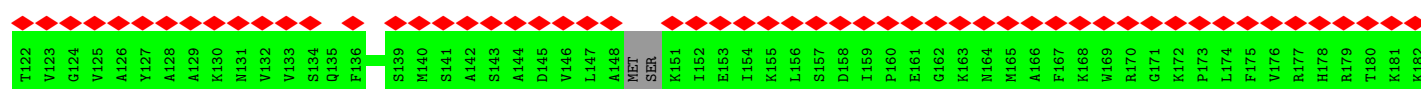
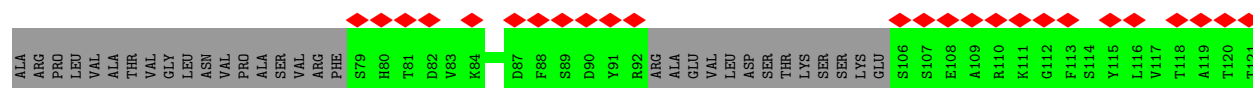
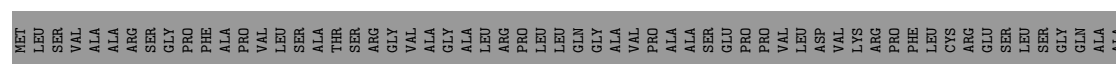
- Molecule 4: Cytochrome c1, heme protein, mitochondrial

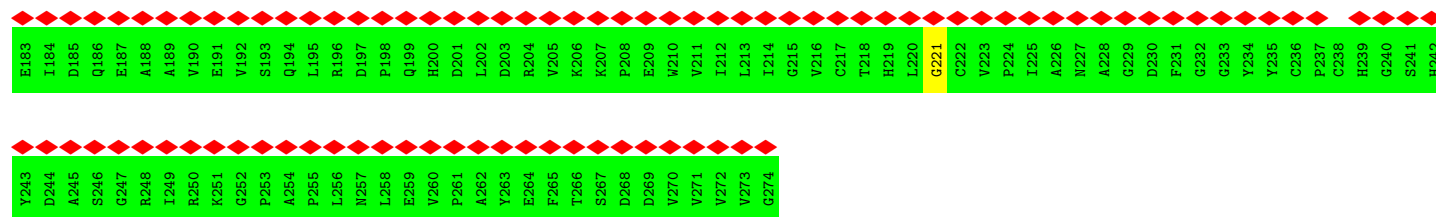
Chain Ad:



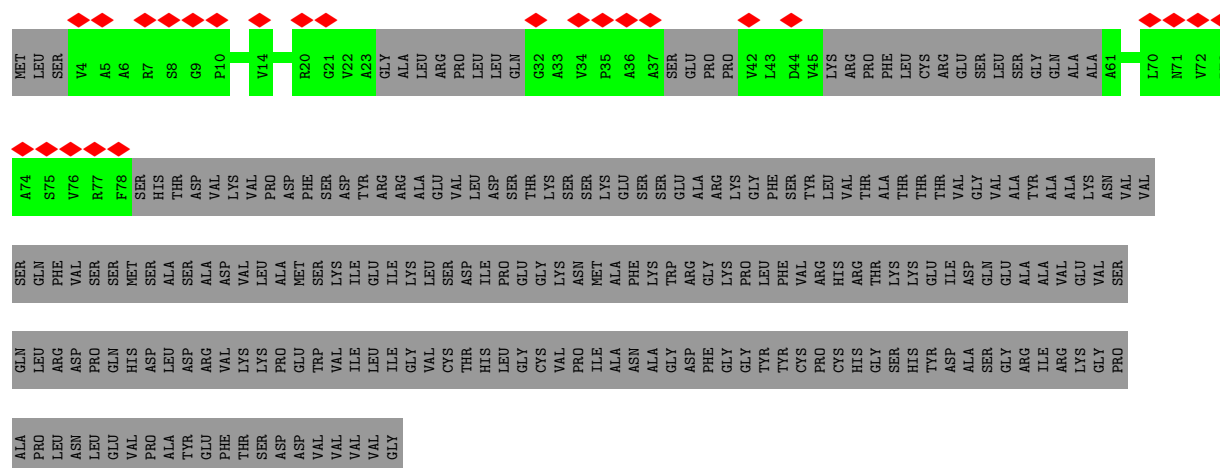
- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial

Chain AE:

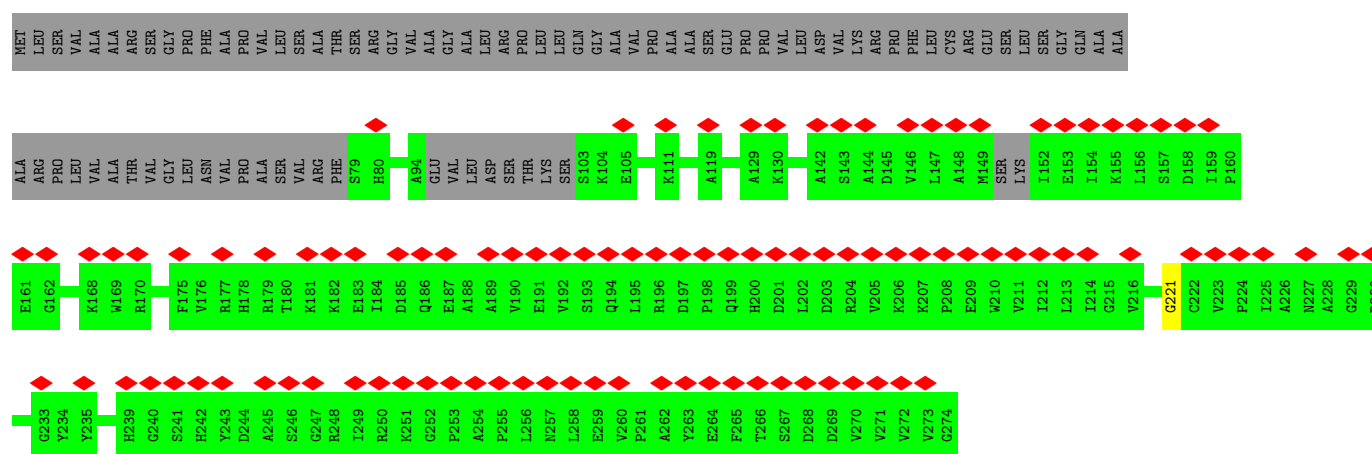
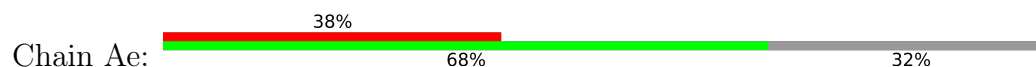




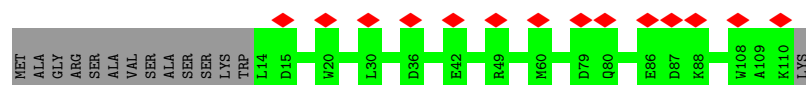
• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



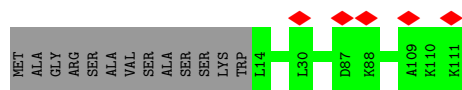
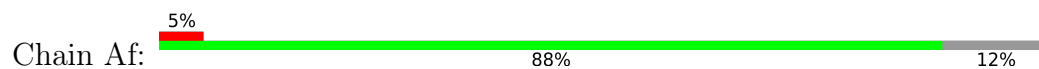
• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



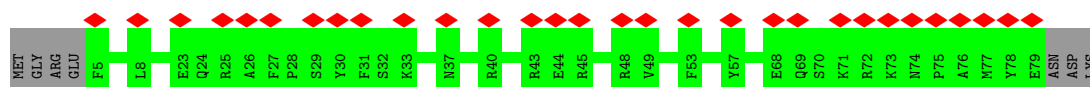
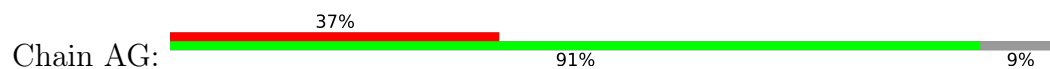
• Molecule 6: Cytochrome b-c1 complex subunit 7



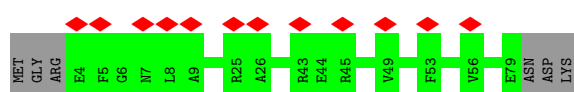
- Molecule 6: Cytochrome b-c1 complex subunit 7



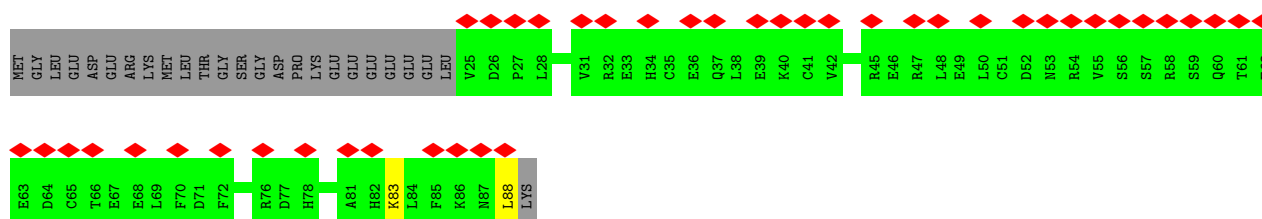
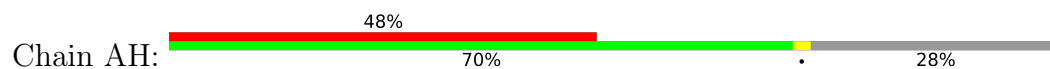
- Molecule 7: Cytochrome b-c1 complex subunit 8



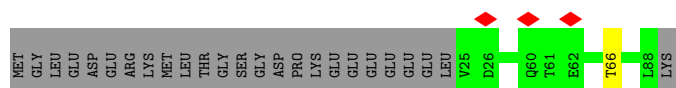
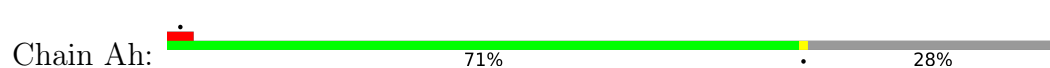
- Molecule 7: Cytochrome b-c1 complex subunit 8



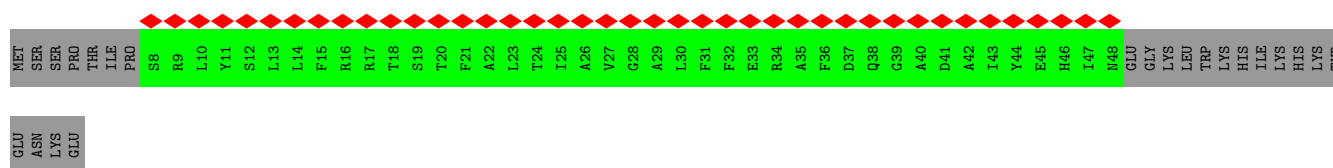
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial



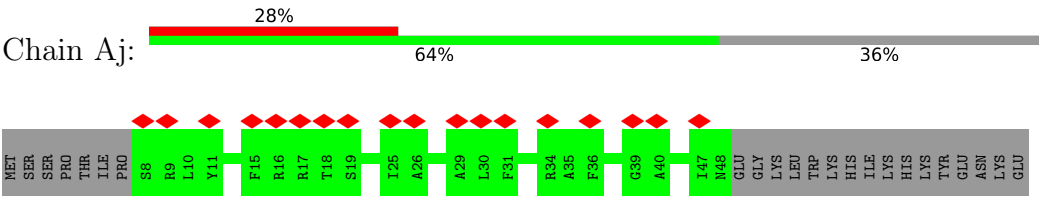
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial



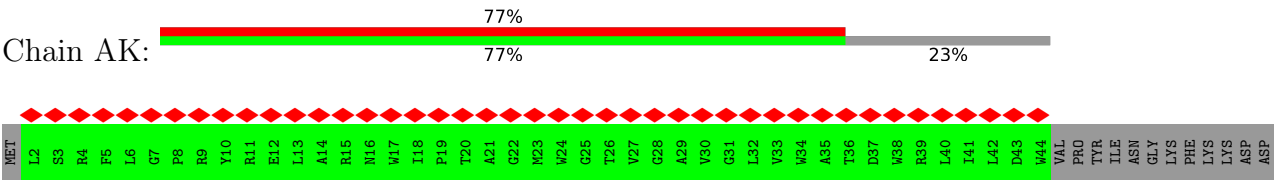
- Molecule 9: Cytochrome b-c1 complex subunit 9



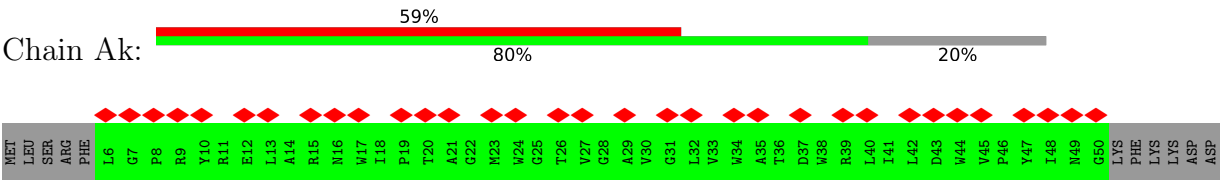
• Molecule 9: Cytochrome b-c1 complex subunit 9



• Molecule 10: Cytochrome b-c1 complex subunit 10



• Molecule 10: Cytochrome b-c1 complex subunit 10



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45095	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.2	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.191	Depositor
Minimum map value	-0.591	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.3	Depositor
Map size (\AA)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CDL, HEC, 3PE, U10, HEM, UQ6

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	AA	0.35	0/3218	0.58	1/4362 (0.0%)
1	Aa	0.33	0/3191	0.60	1/4326 (0.0%)
2	AB	0.33	0/3146	0.56	0/4252
2	Ab	0.32	0/3178	0.55	0/4296
3	AC	0.36	1/3089 (0.0%)	0.55	1/4221 (0.0%)
3	Ac	0.37	1/3054 (0.0%)	0.54	0/4170
4	AD	0.33	0/1955	0.54	0/2655
4	Ad	0.33	0/1971	0.50	0/2677
5	AE	0.45	0/1428	0.60	1/1934 (0.1%)
5	AI	0.34	0/331	0.53	0/451
5	Ae	0.45	0/1467	0.59	1/1985 (0.1%)
6	AF	0.32	0/875	0.52	0/1173
6	Af	0.32	0/884	0.43	0/1184
7	AG	0.37	0/653	0.56	0/883
7	Ag	0.36	0/662	0.56	0/895
8	AH	0.31	0/534	0.68	2/717 (0.3%)
8	Ah	0.36	0/534	0.58	1/717 (0.1%)
9	AJ	0.35	0/339	0.48	0/457
9	Aj	0.35	0/339	0.48	0/457
10	AK	0.32	0/368	0.46	0/504
10	Ak	0.28	0/379	0.42	0/522
All	All	0.35	2/31595 (0.0%)	0.56	8/42838 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AC	271	GLU	C-N	7.82	1.52	1.34
3	Ac	271	GLU	C-N	7.76	1.51	1.34

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Aa	366	ASP	CB-CG-OD1	9.43	126.79	118.30
1	AA	338	CYS	CA-CB-SG	-6.98	101.44	114.00
8	AH	83	LYS	N-CA-CB	5.88	121.19	110.60
3	AC	17	SER	N-CA-CB	-5.63	102.05	110.50
5	AE	221	GLY	N-CA-C	5.50	126.85	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	AA	397/480 (83%)	385 (97%)	12 (3%)	0	100	100
1	Aa	394/480 (82%)	385 (98%)	9 (2%)	0	100	100
2	AB	409/453 (90%)	397 (97%)	12 (3%)	0	100	100
2	Ab	415/453 (92%)	406 (98%)	9 (2%)	0	100	100
3	AC	371/381 (97%)	365 (98%)	6 (2%)	0	100	100
3	Ac	365/381 (96%)	361 (99%)	4 (1%)	0	100	100
4	AD	236/325 (73%)	230 (98%)	6 (2%)	0	100	100
4	Ad	238/325 (73%)	229 (96%)	9 (4%)	0	100	100
5	AE	175/274 (64%)	164 (94%)	11 (6%)	0	100	100
5	AI	40/274 (15%)	38 (95%)	2 (5%)	0	100	100
5	Ae	180/274 (66%)	167 (93%)	13 (7%)	0	100	100
6	AF	95/111 (86%)	95 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	Af	96/111 (86%)	96 (100%)	0	0	100	100
7	AG	73/82 (89%)	73 (100%)	0	0	100	100
7	Ag	74/82 (90%)	74 (100%)	0	0	100	100
8	AH	62/89 (70%)	60 (97%)	2 (3%)	0	100	100
8	Ah	62/89 (70%)	60 (97%)	2 (3%)	0	100	100
9	AJ	39/64 (61%)	39 (100%)	0	0	100	100
9	Aj	39/64 (61%)	39 (100%)	0	0	100	100
10	AK	41/56 (73%)	39 (95%)	2 (5%)	0	100	100
10	Ak	43/56 (77%)	40 (93%)	3 (7%)	0	100	100
All	All	3844/4904 (78%)	3742 (97%)	102 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	AA	341/398 (86%)	341 (100%)	0	100	100
1	Aa	339/398 (85%)	339 (100%)	0	100	100
2	AB	324/356 (91%)	324 (100%)	0	100	100
2	Ab	327/356 (92%)	327 (100%)	0	100	100
3	AC	325/333 (98%)	325 (100%)	0	100	100
3	Ac	322/333 (97%)	322 (100%)	0	100	100
4	AD	203/260 (78%)	203 (100%)	0	100	100
4	Ad	205/260 (79%)	205 (100%)	0	100	100
5	AE	152/224 (68%)	152 (100%)	0	100	100
5	AI	33/224 (15%)	33 (100%)	0	100	100
5	Ae	156/224 (70%)	156 (100%)	0	100	100
6	AF	89/99 (90%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Af	90/99 (91%)	90 (100%)	0	100	100
7	AG	68/74 (92%)	68 (100%)	0	100	100
7	Ag	69/74 (93%)	69 (100%)	0	100	100
8	AH	61/83 (74%)	61 (100%)	0	100	100
8	Ah	61/83 (74%)	61 (100%)	0	100	100
9	AJ	33/55 (60%)	33 (100%)	0	100	100
9	Aj	33/55 (60%)	33 (100%)	0	100	100
10	AK	34/46 (74%)	34 (100%)	0	100	100
10	Ak	35/46 (76%)	35 (100%)	0	100	100
All	All	3300/4080 (81%)	3300 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
3	Ac	312	GLN
7	Ag	13	HIS
3	Ac	341	GLN
5	Ae	242	HIS
8	Ah	78	HIS

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

15 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
15	3PE	Ac	404	-	34,34,50	0.32	0	37,39,55	0.41	0
15	3PE	Ac	401	-	22,22,50	0.47	0	25,27,55	0.74	1 (4%)
11	HEM	Ac	403	3	41,50,50	1.26	3 (7%)	45,82,82	1.69	9 (20%)
13	HEC	AD	401	4	32,50,50	2.17	3 (9%)	24,82,82	1.64	5 (20%)
14	CDL	Ag	101	-	41,41,99	0.45	0	47,53,111	0.36	0
12	UQ6	Ac	406	-	23,23,43	2.77	6 (26%)	27,31,55	1.96	5 (18%)
16	U10	Ac	405	-	23,23,63	1.24	3 (13%)	28,31,79	2.08	7 (25%)
11	HEM	AC	402	3	41,50,50	1.35	4 (9%)	45,82,82	1.96	9 (20%)
11	HEM	AC	401	3	41,50,50	1.24	4 (9%)	45,82,82	1.68	8 (17%)
13	HEC	Ad	401	4	32,50,50	2.15	3 (9%)	24,82,82	1.64	4 (16%)
12	UQ6	AC	403	-	28,28,43	2.42	6 (21%)	33,37,55	2.03	9 (27%)
14	CDL	Ag	102	-	55,55,99	0.39	0	61,67,111	0.33	0
14	CDL	Aa	501	-	45,45,99	0.43	0	51,57,111	0.36	0
11	HEM	Ac	402	3	41,50,50	1.22	4 (9%)	45,82,82	1.69	8 (17%)
15	3PE	Ag	103	-	50,50,50	0.31	0	53,55,55	0.29	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
15	3PE	Ac	404	-	-	13/38/38/54	-
15	3PE	Ac	401	-	-	7/26/26/54	-
11	HEM	Ac	403	3	-	6/12/54/54	-
13	HEC	AD	401	4	-	0/10/54/54	-
14	CDL	Ag	101	-	-	14/52/52/110	-
12	UQ6	Ac	406	-	-	2/15/15/39	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	U10	Ac	405	-	-	6/15/39/87	0/1/1/1
11	HEM	AC	402	3	-	7/12/54/54	-
11	HEM	AC	401	3	-	7/12/54/54	-
13	HEC	Ad	401	4	-	0/10/54/54	-
12	UQ6	AC	403	-	-	4/21/21/39	0/1/1/1
14	CDL	Ag	102	-	-	13/66/66/110	-
14	CDL	Aa	501	-	-	17/56/56/110	-
11	HEM	Ac	402	3	-	7/12/54/54	-
15	3PE	Ag	103	-	-	10/54/54/54	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	AC	403	UQ6	C5-C4	8.00	1.52	1.39
13	Ad	401	HEC	C3C-C2C	-6.41	1.34	1.40
13	AD	401	HEC	C3C-C2C	-6.40	1.34	1.40
13	AD	401	HEC	C2B-C3B	-6.15	1.34	1.40
13	Ad	401	HEC	C2B-C3B	-6.01	1.34	1.40

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Ac	405	U10	C6-C1-C2	7.72	125.28	119.18
12	Ac	406	UQ6	C4M-O4-C4	5.92	131.00	114.78
12	AC	403	UQ6	C7-C8-C9	-5.78	118.27	127.24
11	AC	402	HEM	CHC-C4B-NB	5.38	130.28	124.43
11	AC	402	HEM	CHD-C1D-ND	4.85	129.70	124.43

There are no chirality outliers.

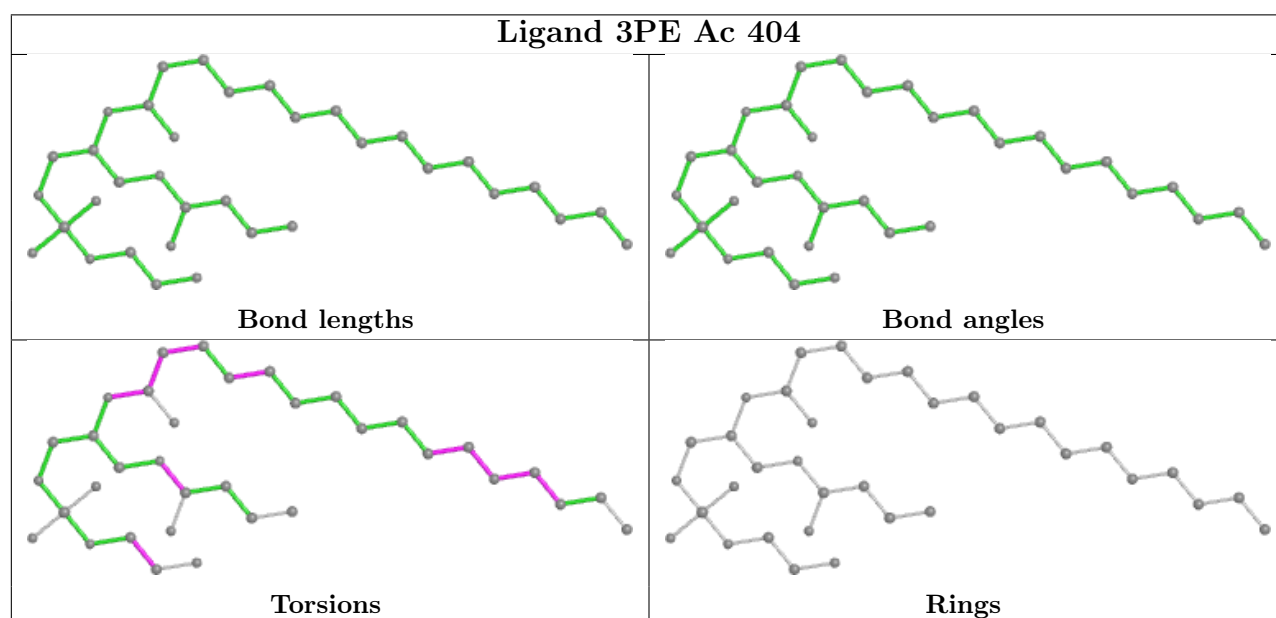
5 of 113 torsion outliers are listed below:

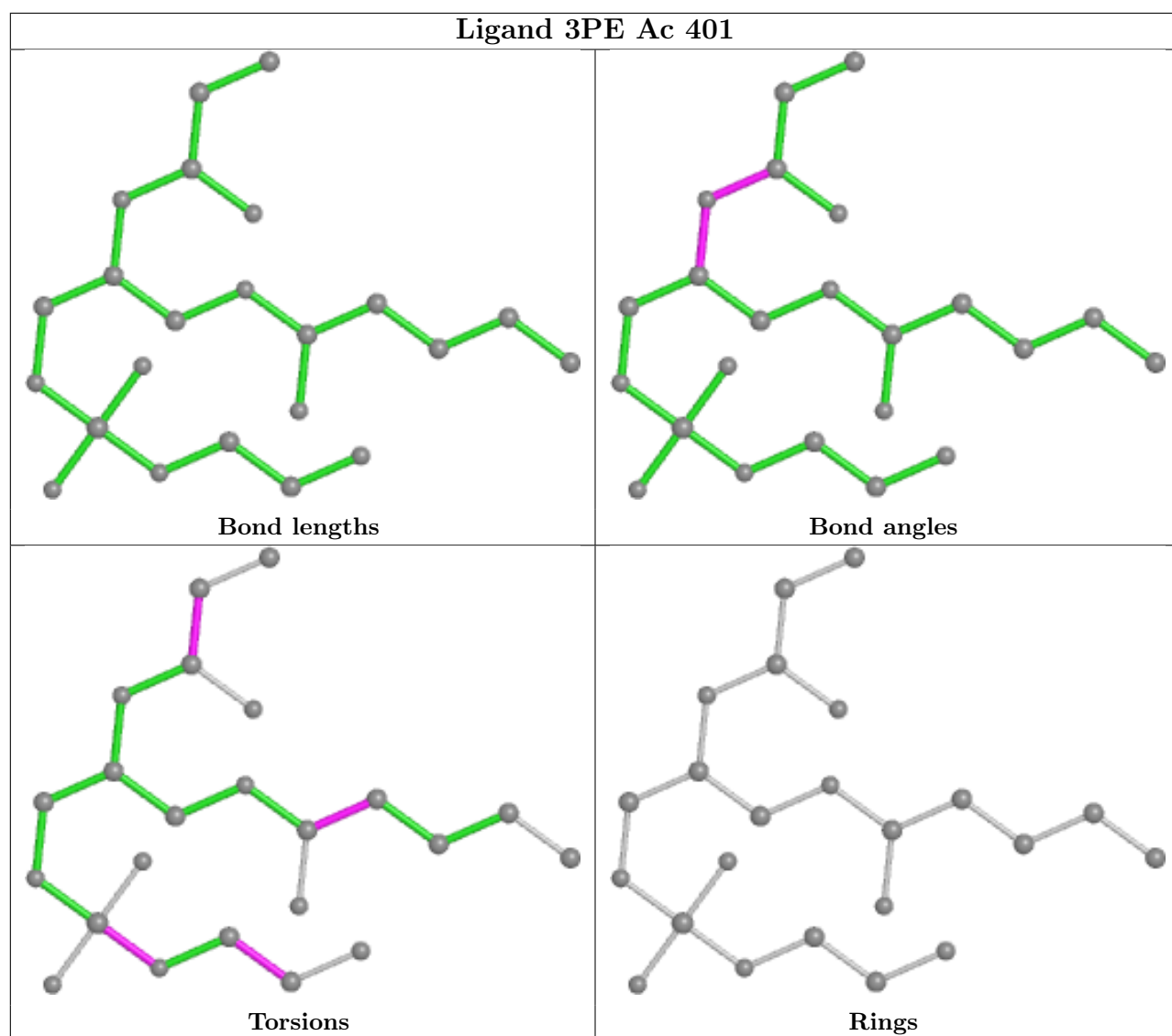
Mol	Chain	Res	Type	Atoms
11	AC	401	HEM	C2B-C3B-CAB-CBB
11	AC	402	HEM	C2B-C3B-CAB-CBB
11	AC	402	HEM	C4B-C3B-CAB-CBB
11	Ac	402	HEM	C2B-C3B-CAB-CBB
11	Ac	403	HEM	C2B-C3B-CAB-CBB

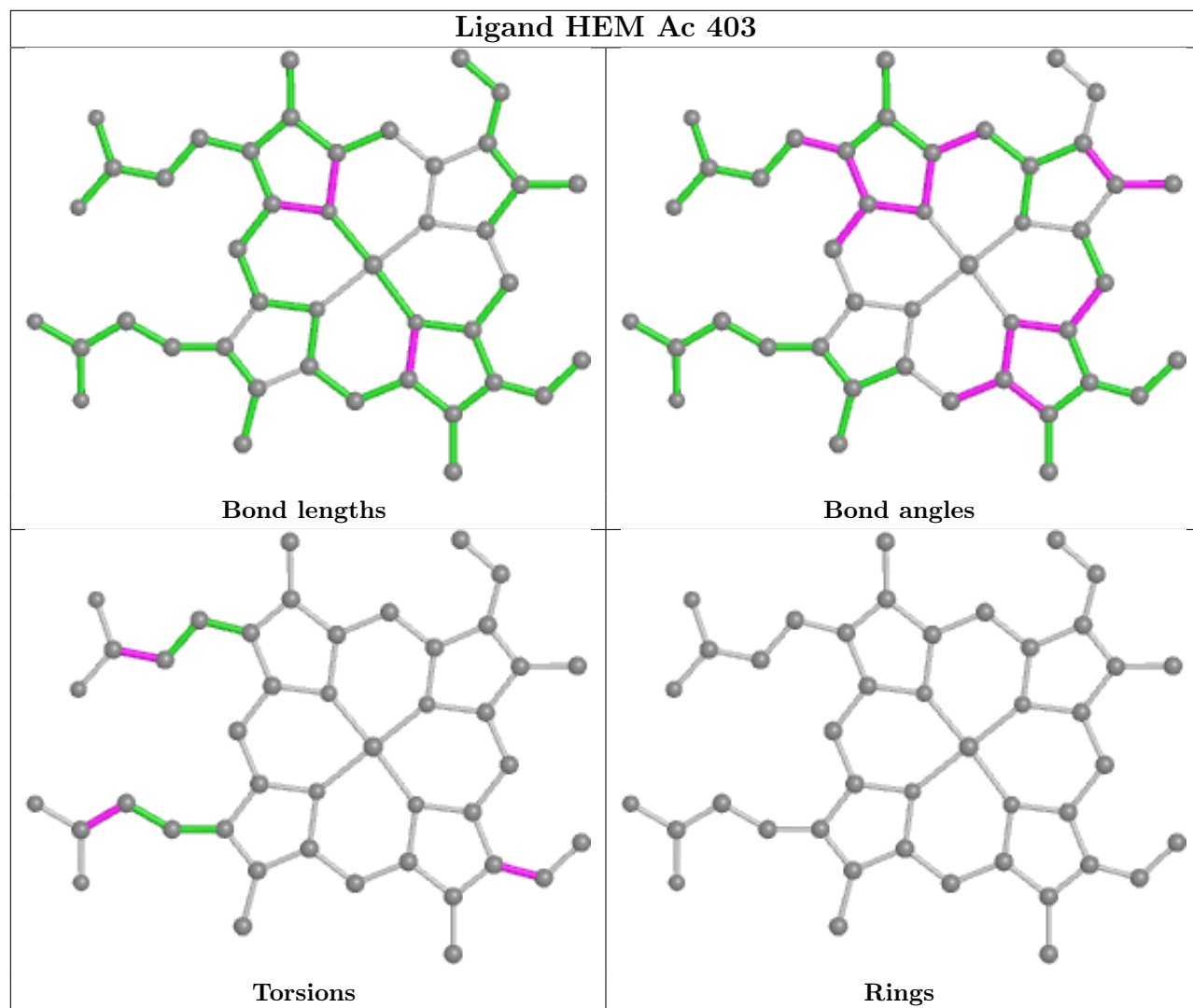
There are no ring outliers.

No monomer is involved in short contacts.

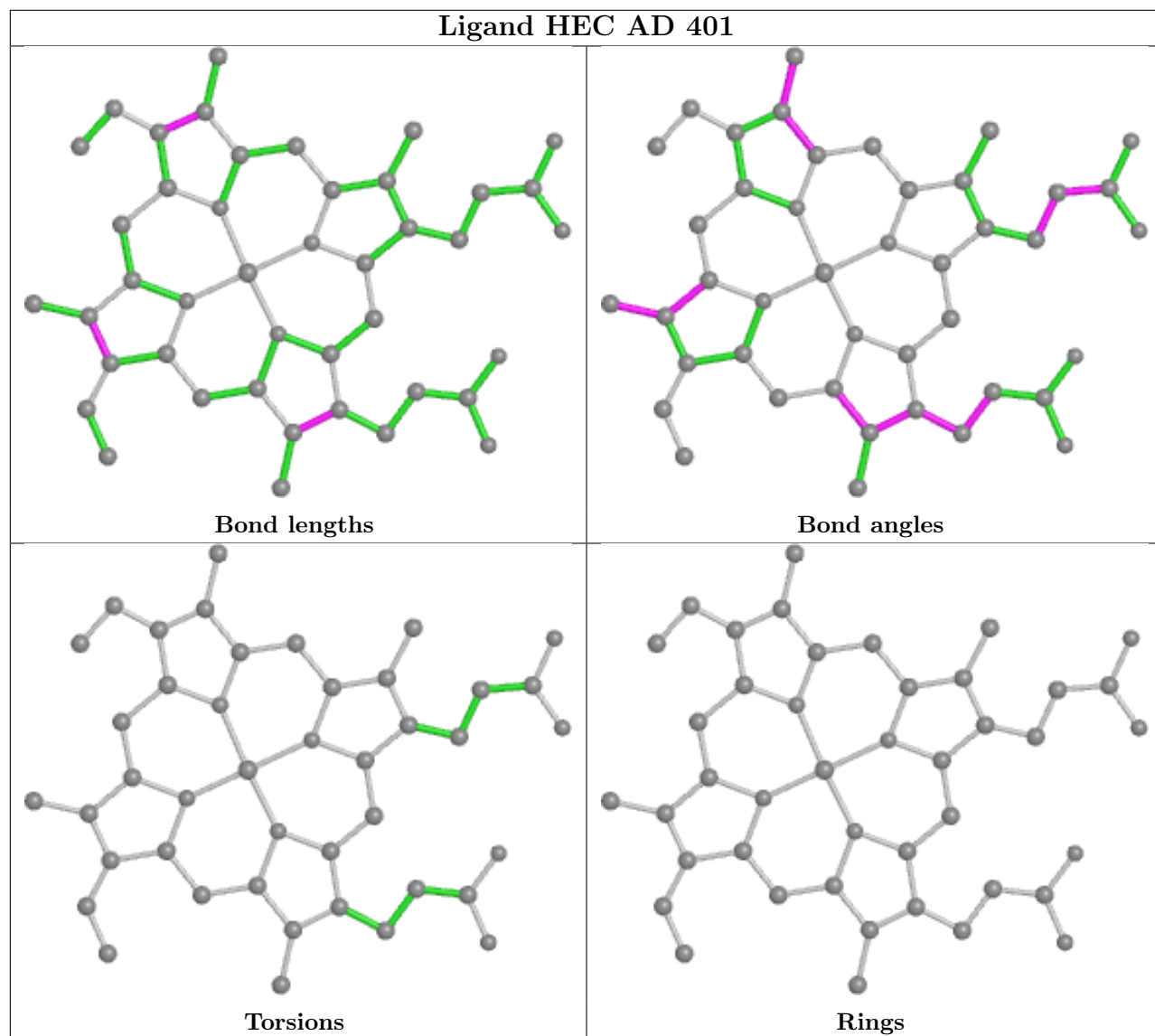
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

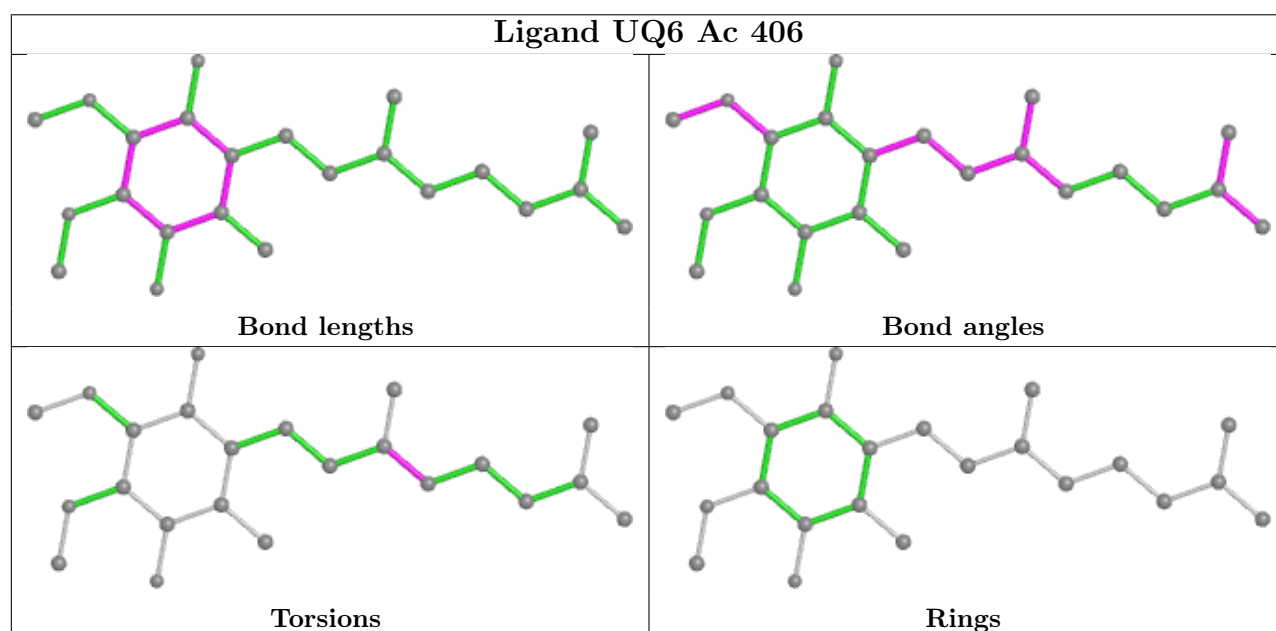
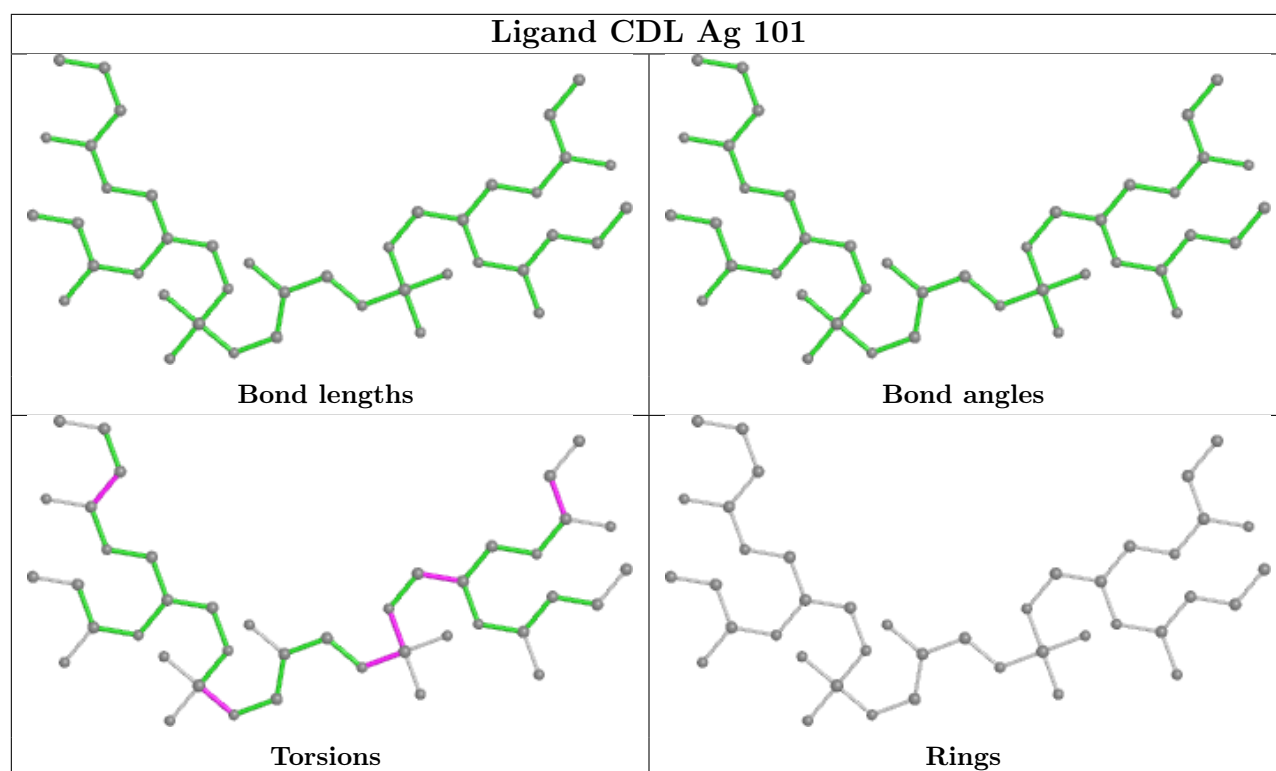


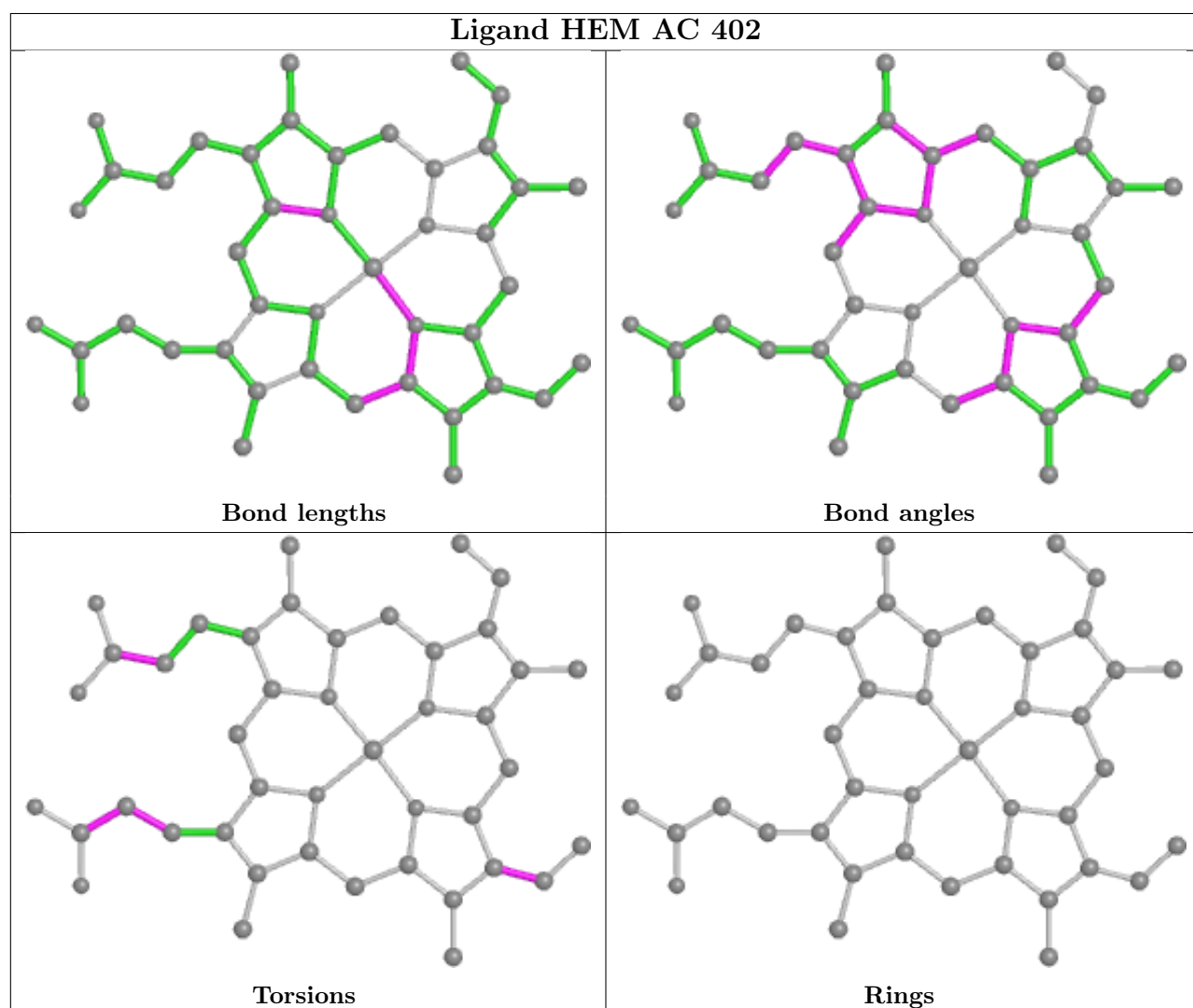
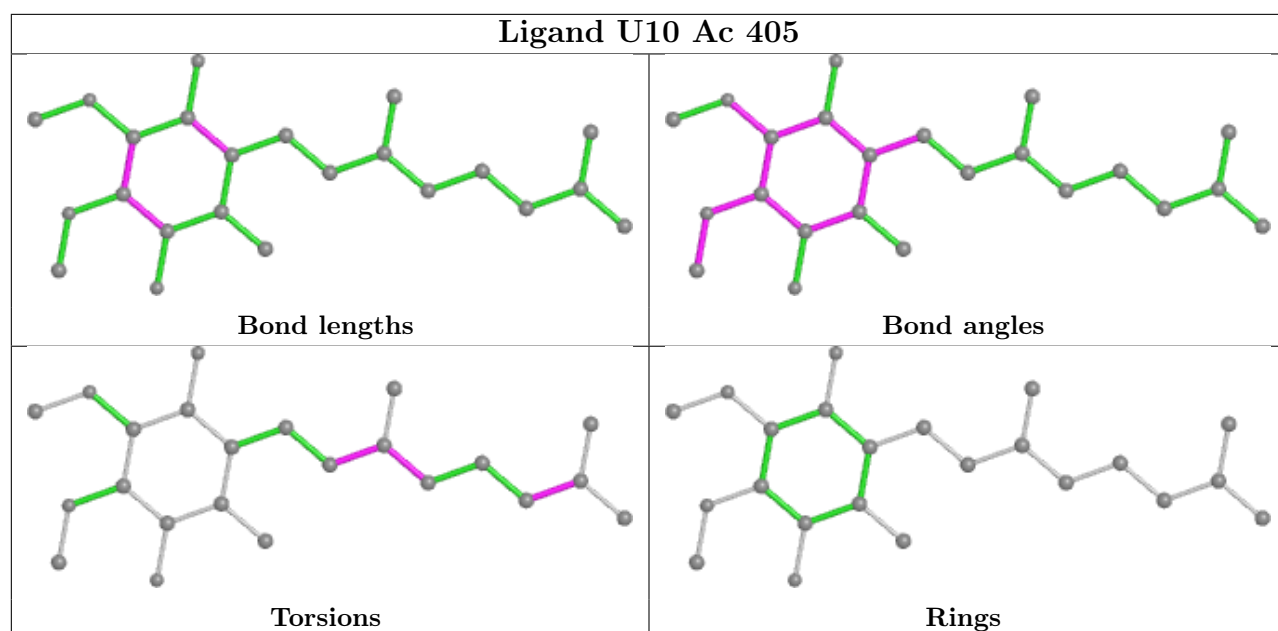


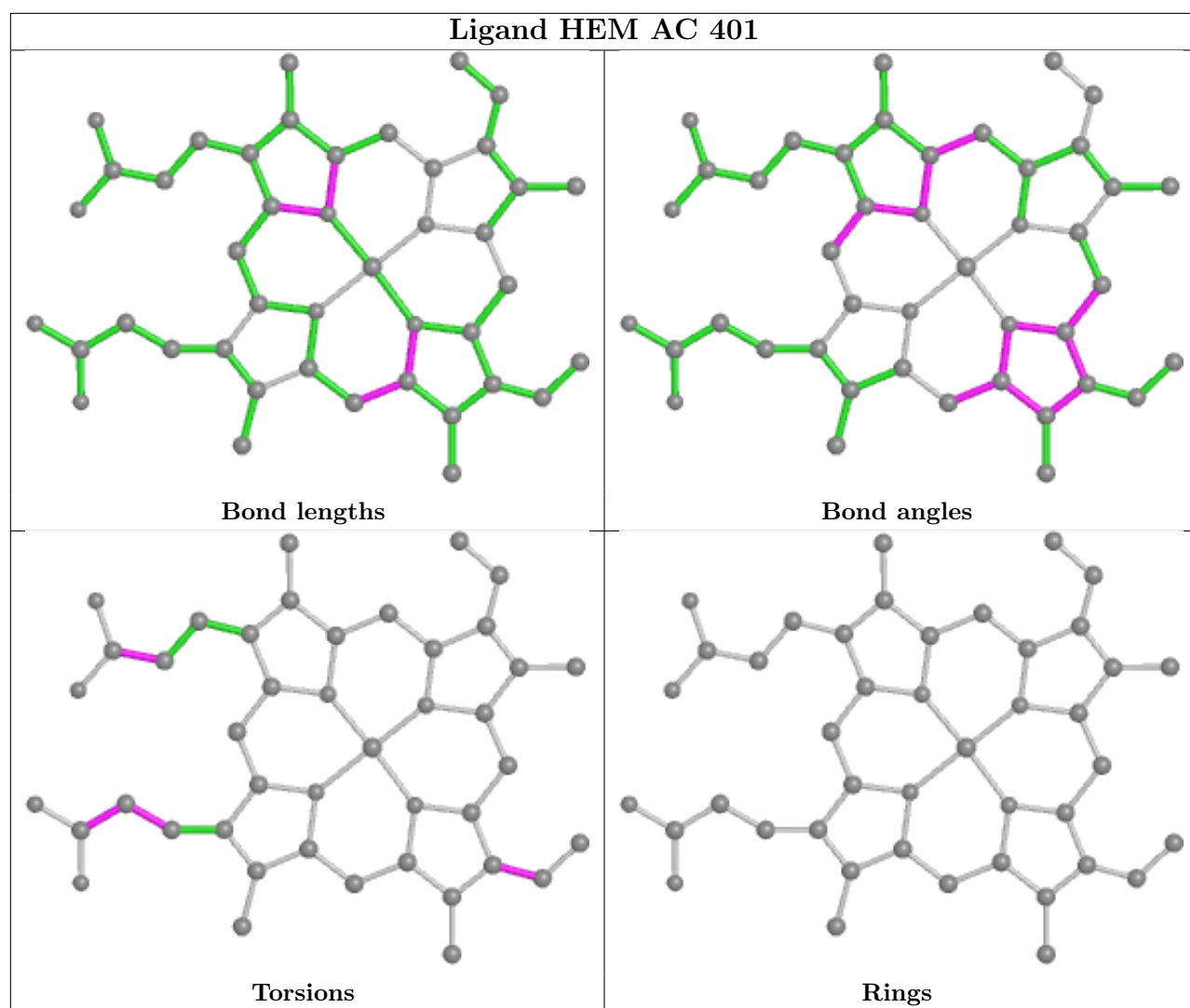


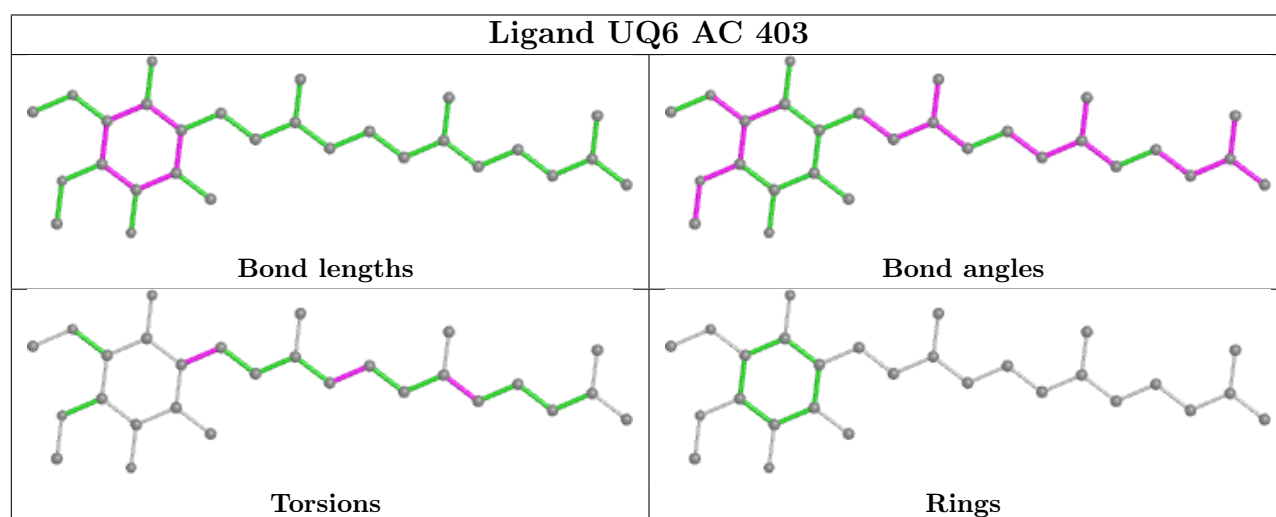
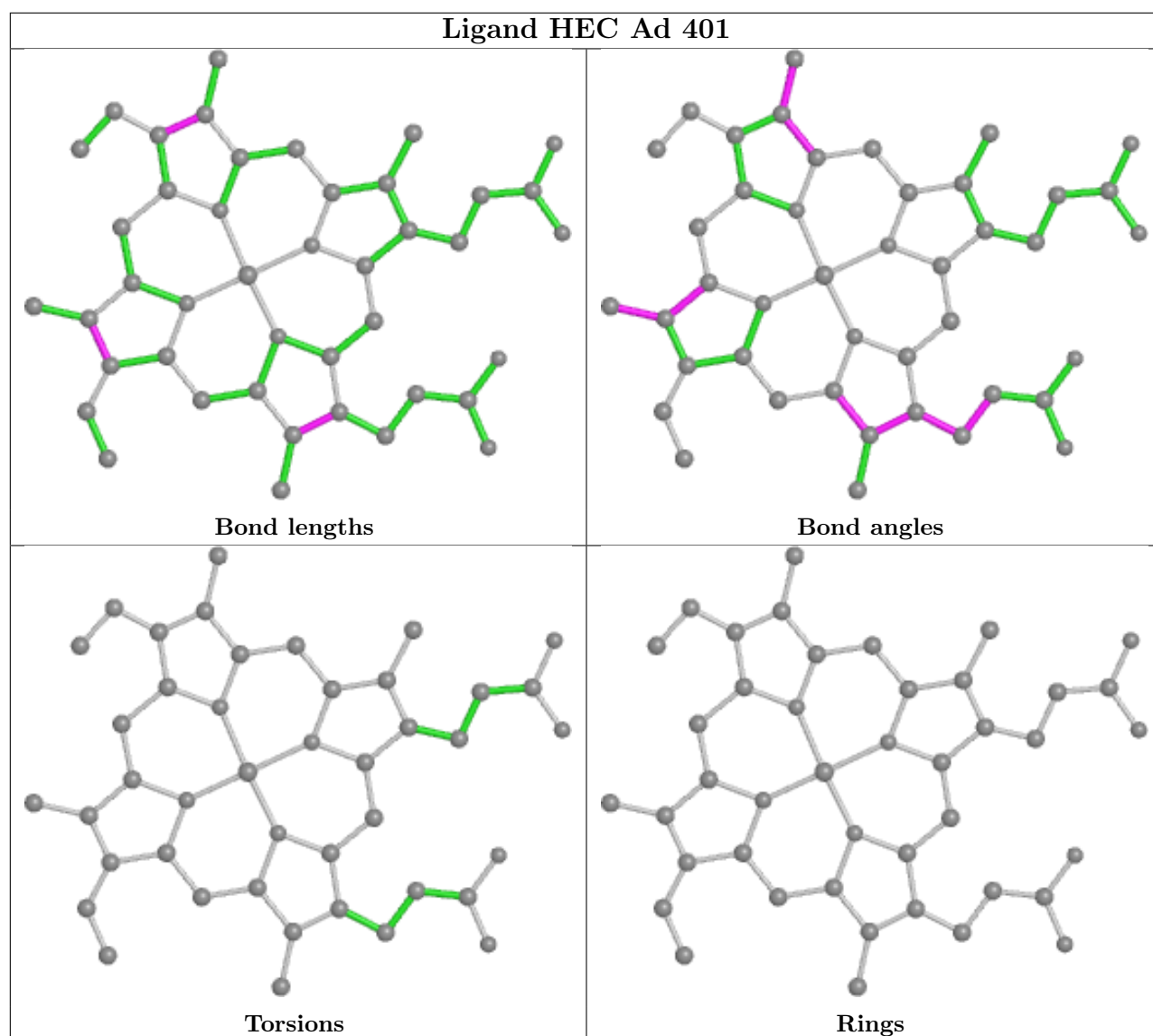
Ligand HEC AD 401

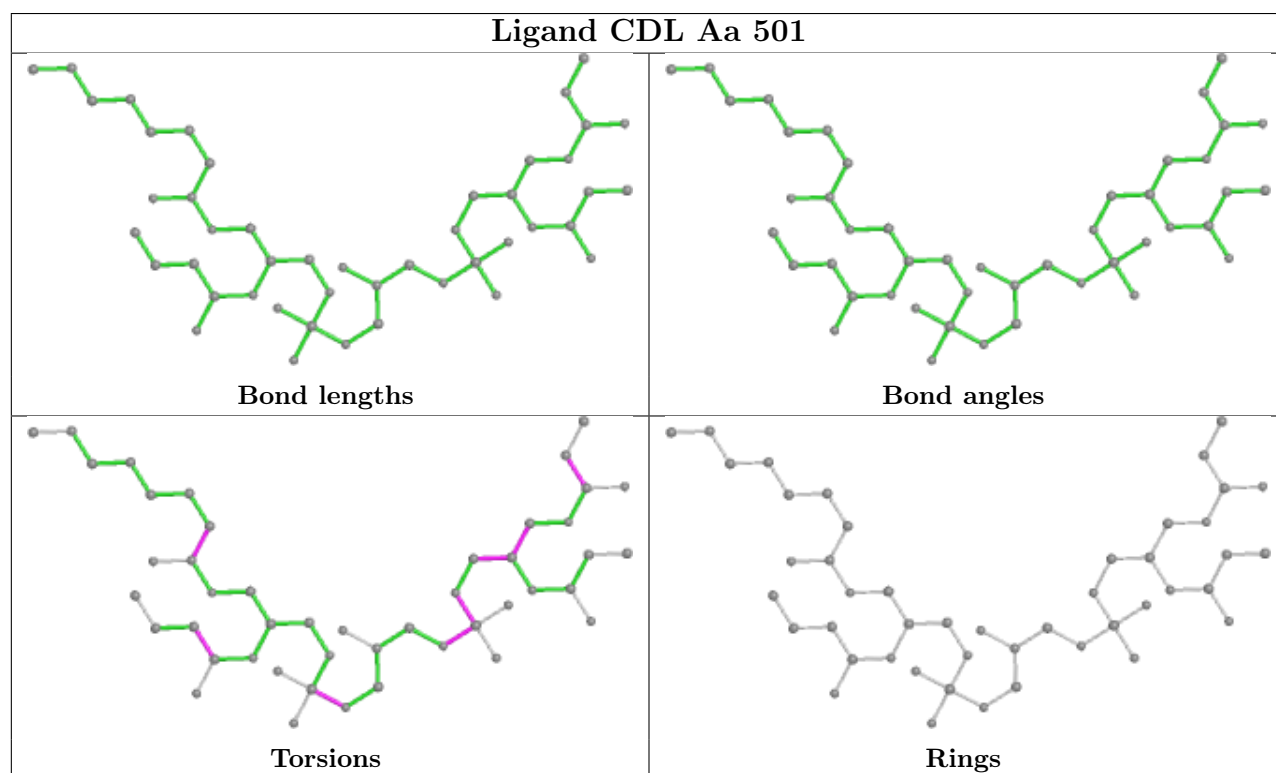
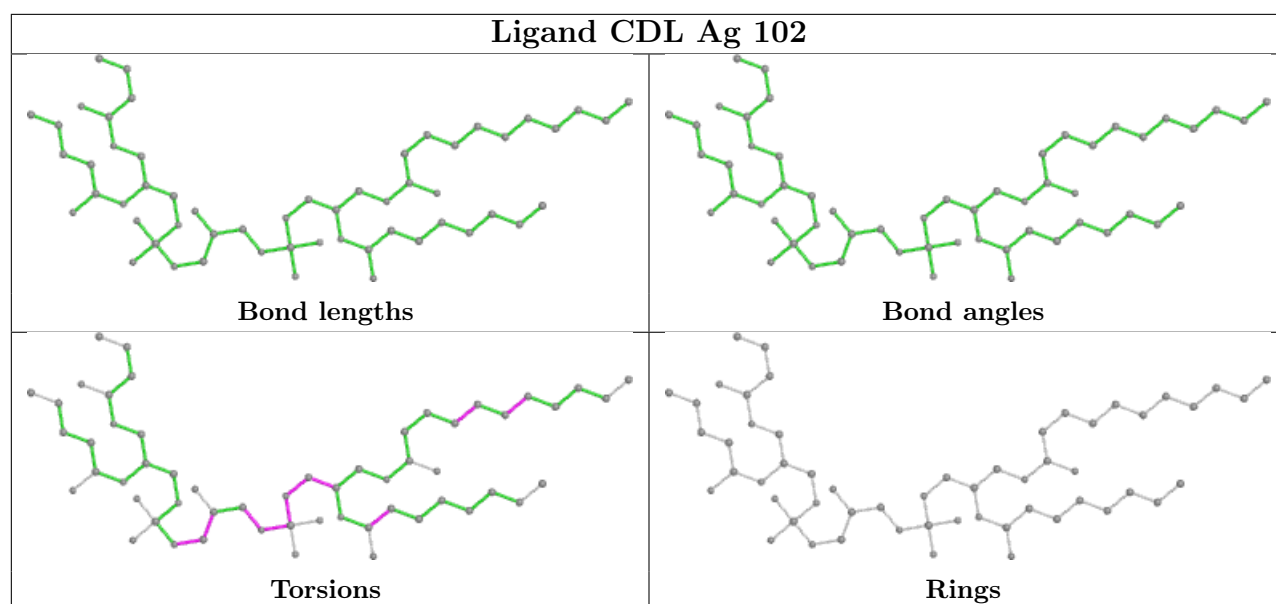


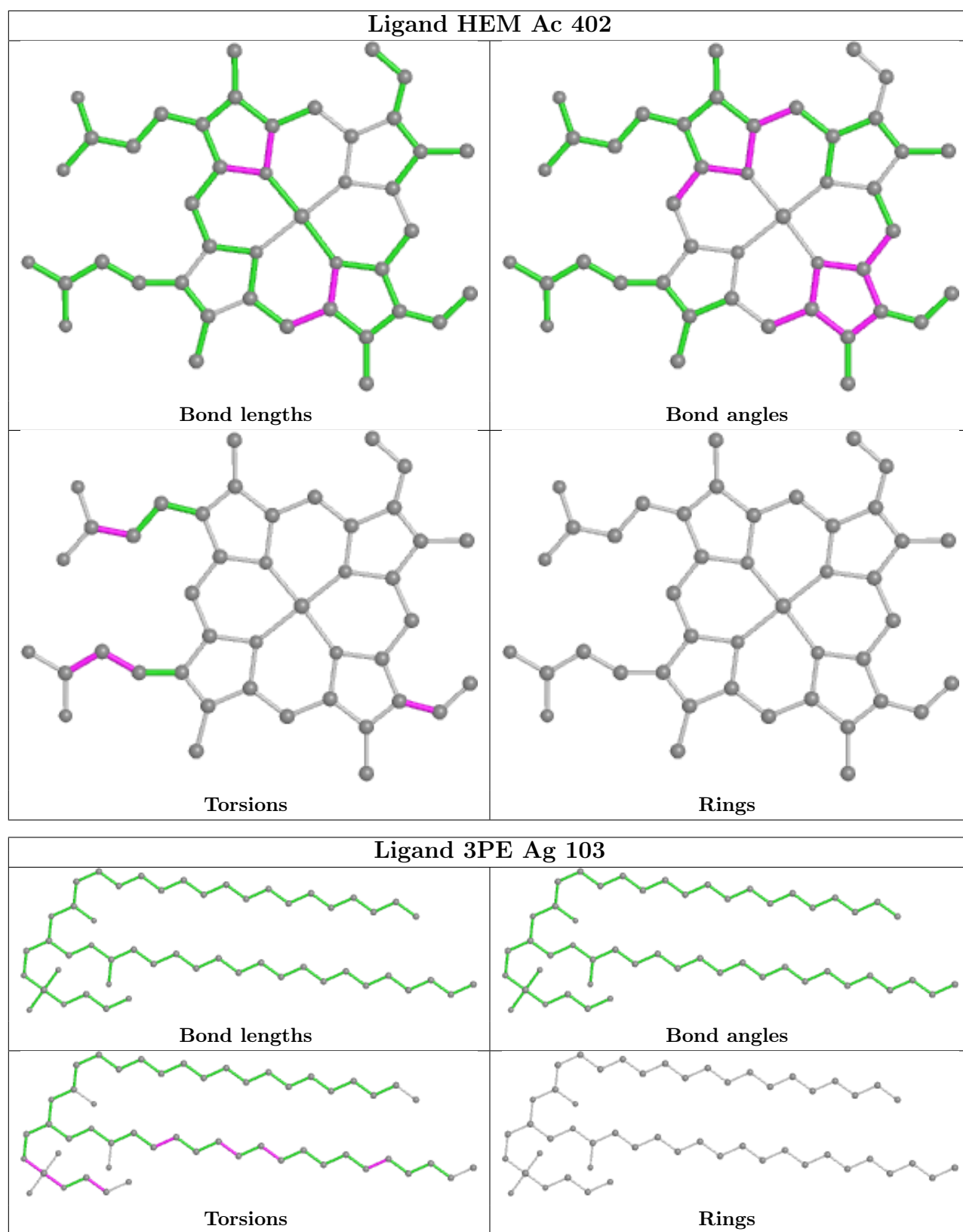












5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

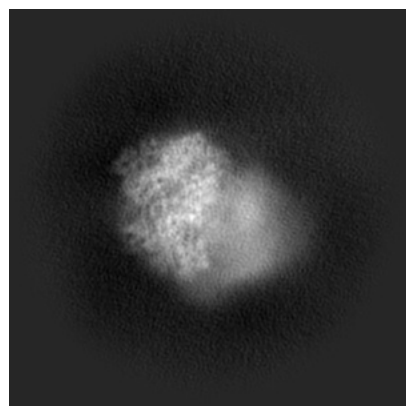
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35355. These allow visual inspection of the internal detail of the map and identification of artifacts.

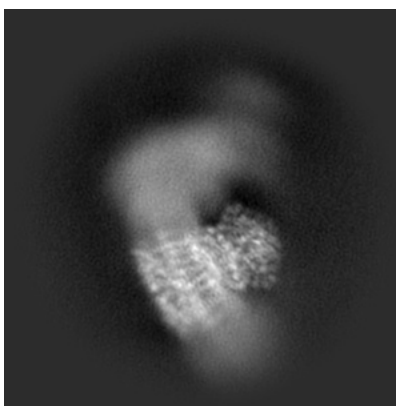
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

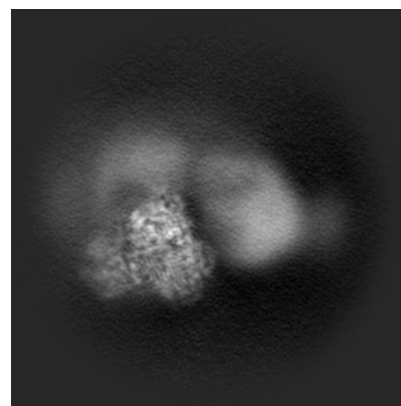
6.1.1 Primary map



X

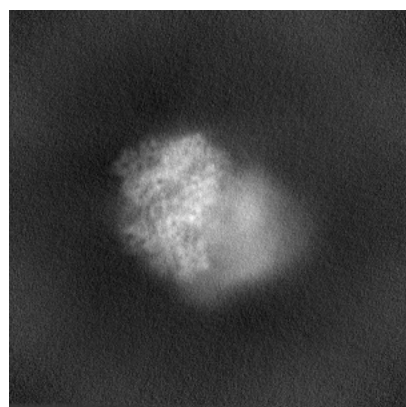


Y

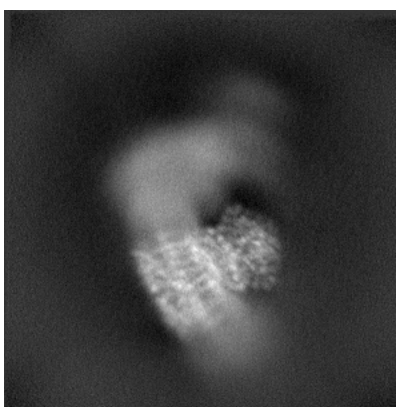


Z

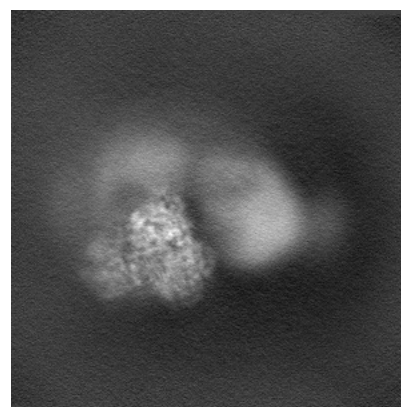
6.1.2 Raw map



X



Y

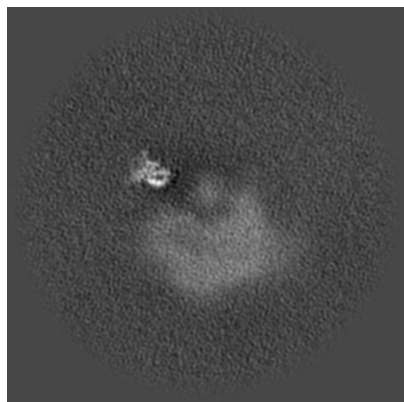


Z

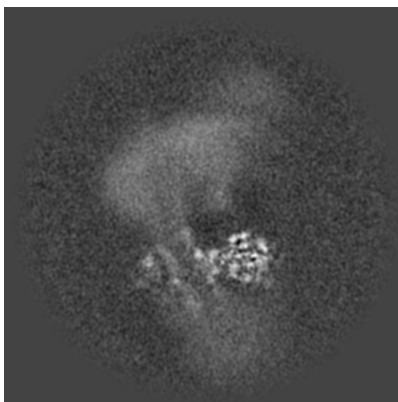
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

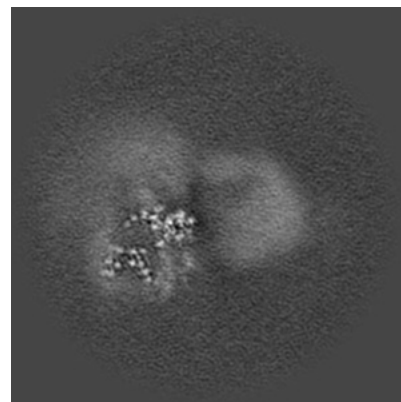
6.2.1 Primary map



X Index: 256

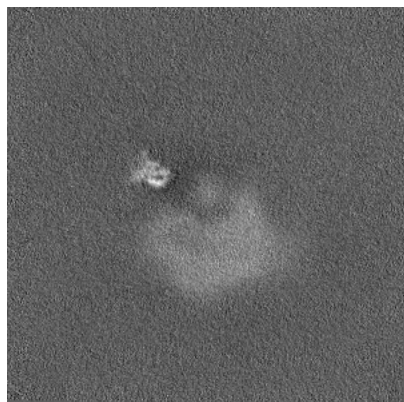


Y Index: 256



Z Index: 256

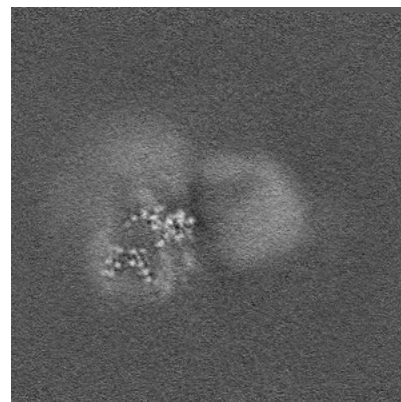
6.2.2 Raw map



X Index: 256



Y Index: 256

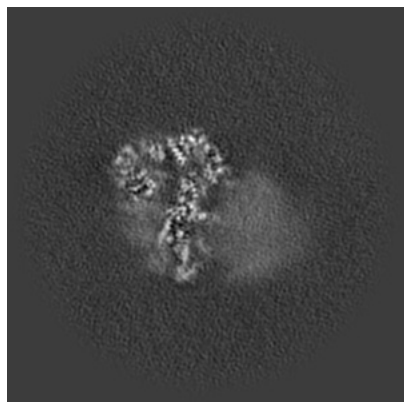


Z Index: 256

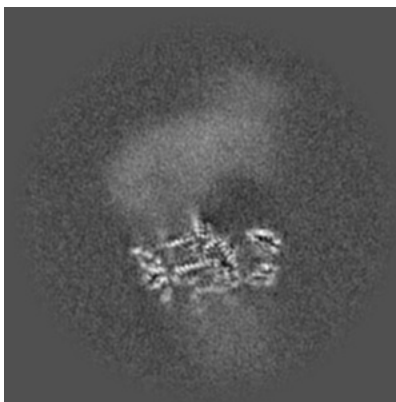
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

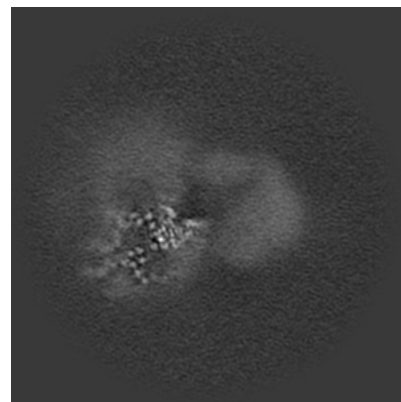
6.3.1 Primary map



X Index: 203

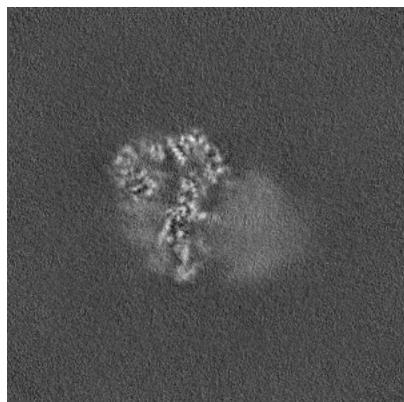


Y Index: 233



Z Index: 245

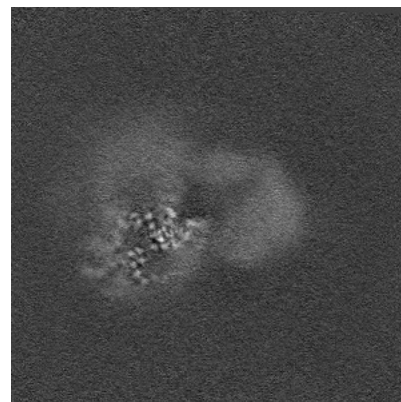
6.3.2 Raw map



X Index: 203



Y Index: 233

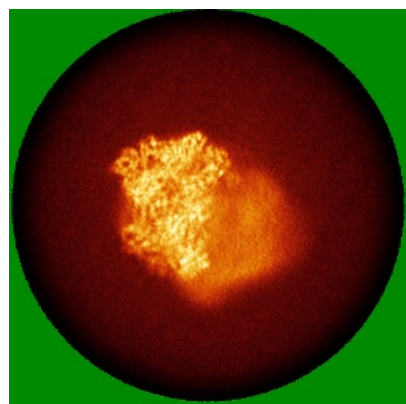


Z Index: 244

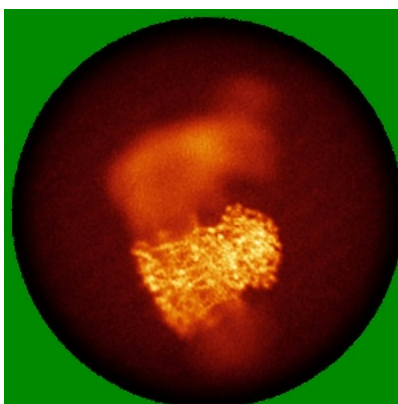
The images above show the largest variance slices of the map in three orthogonal directions.

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

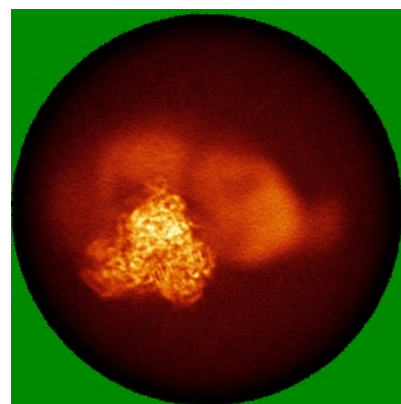
6.4.1 Primary map



X

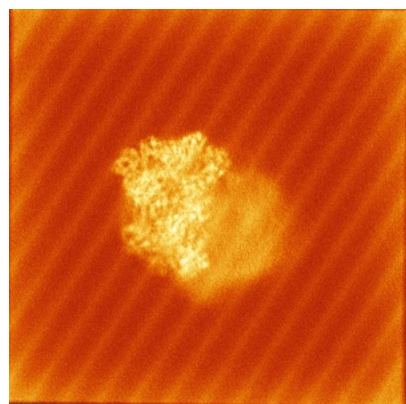


Y

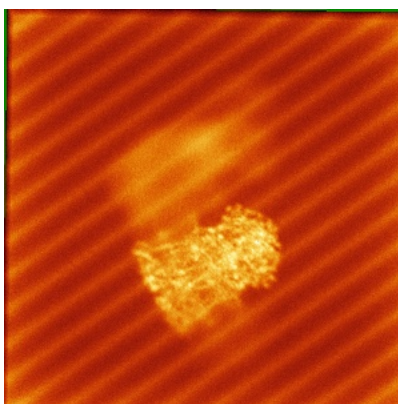


Z

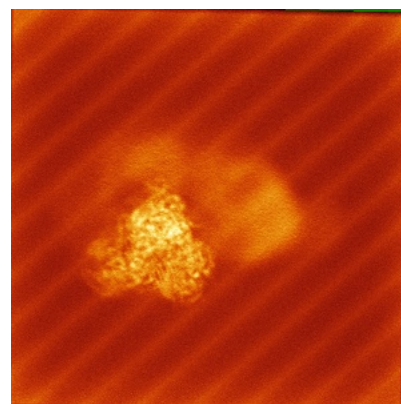
6.4.2 Raw map



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.

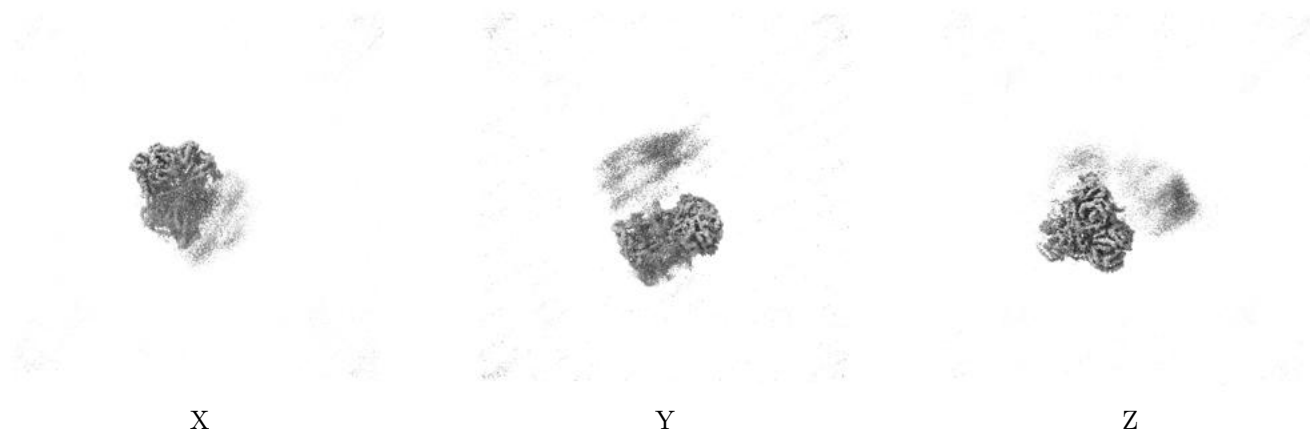
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. 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.

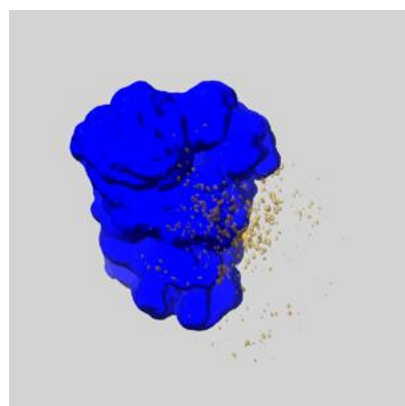
6.6 Mask visualisation [i](#)

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

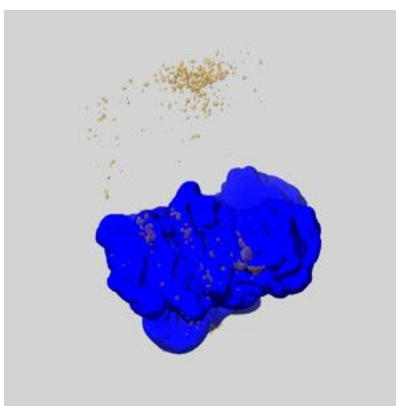
A mask typically either:

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

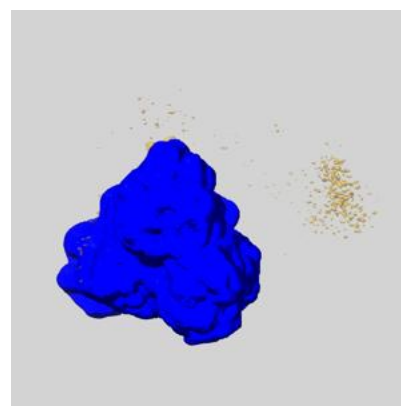
6.6.1 emd_35355_msk_1.map [i](#)



X



Y

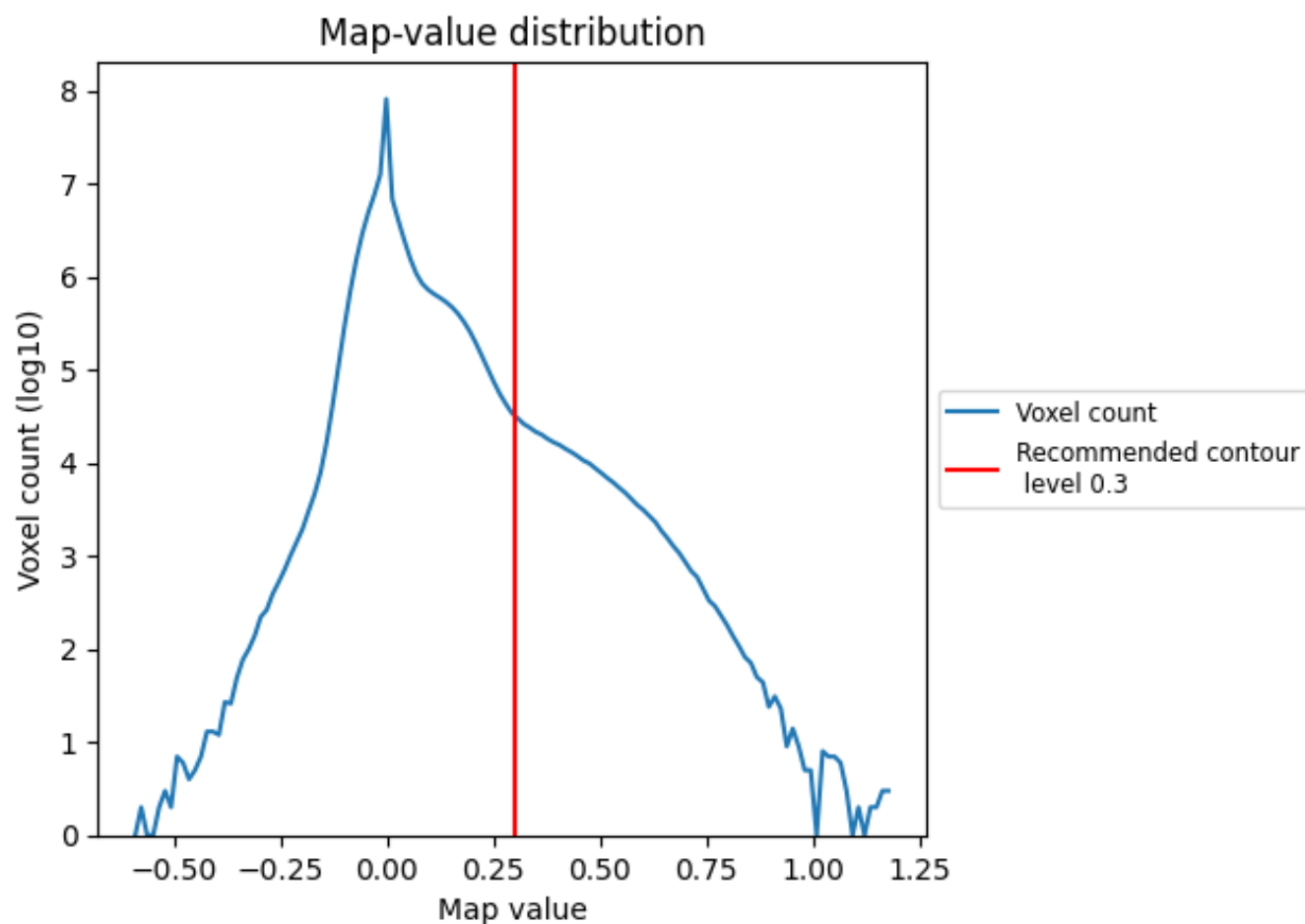


Z

7 Map analysis [i](#)

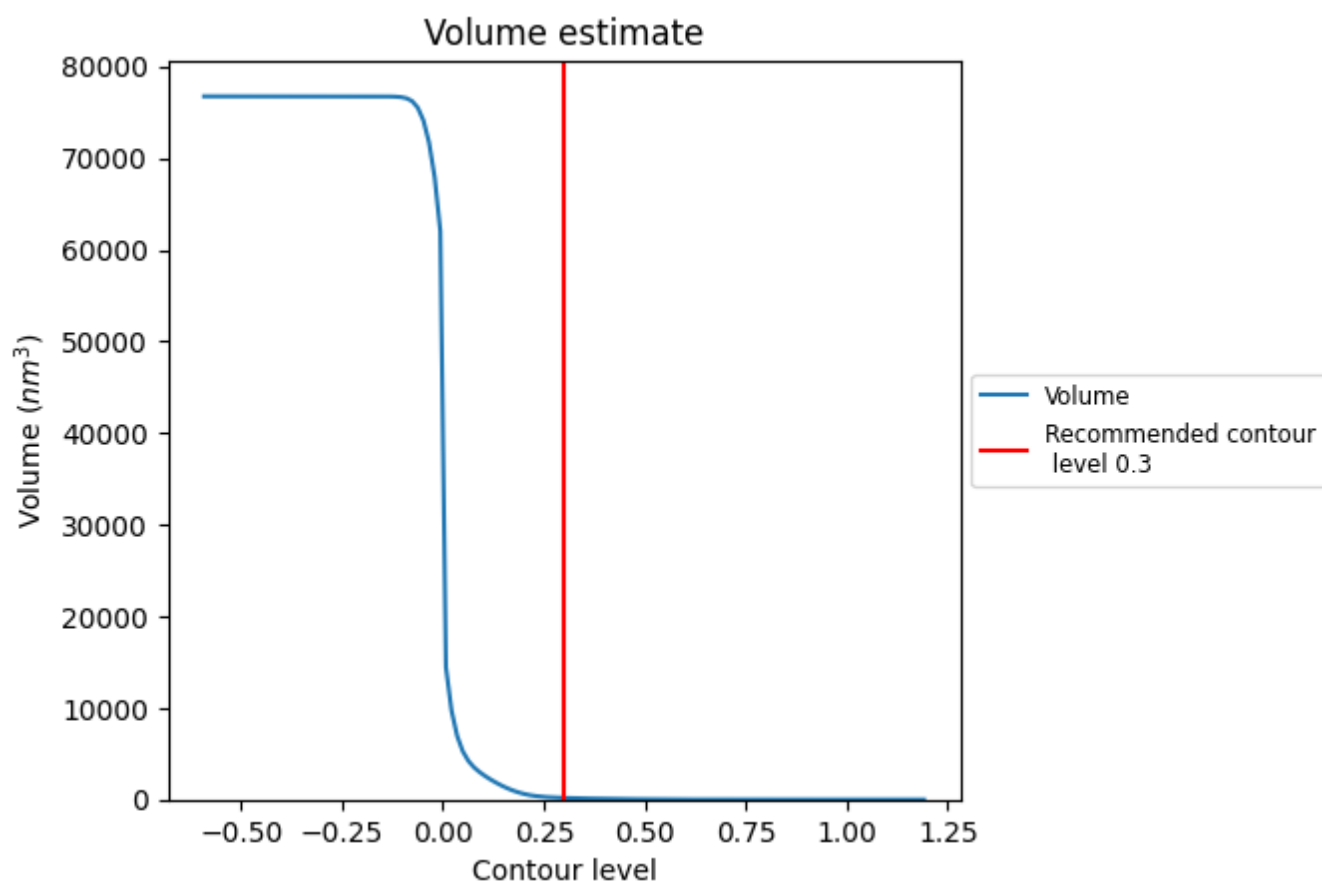
This section contains the results of statistical analysis of the map.

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.

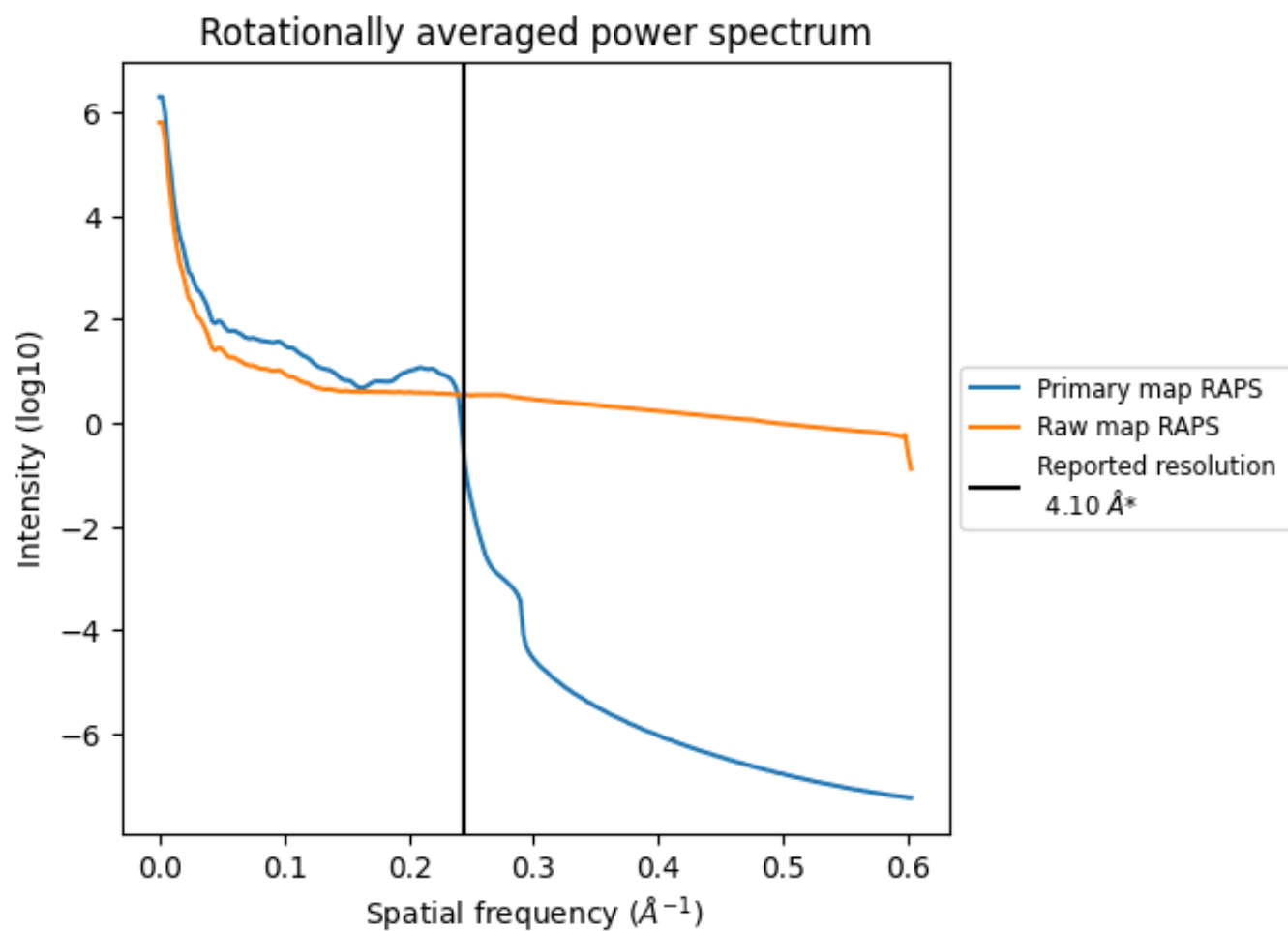
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm³; this corresponds to an approximate mass of 162 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 ⓘ

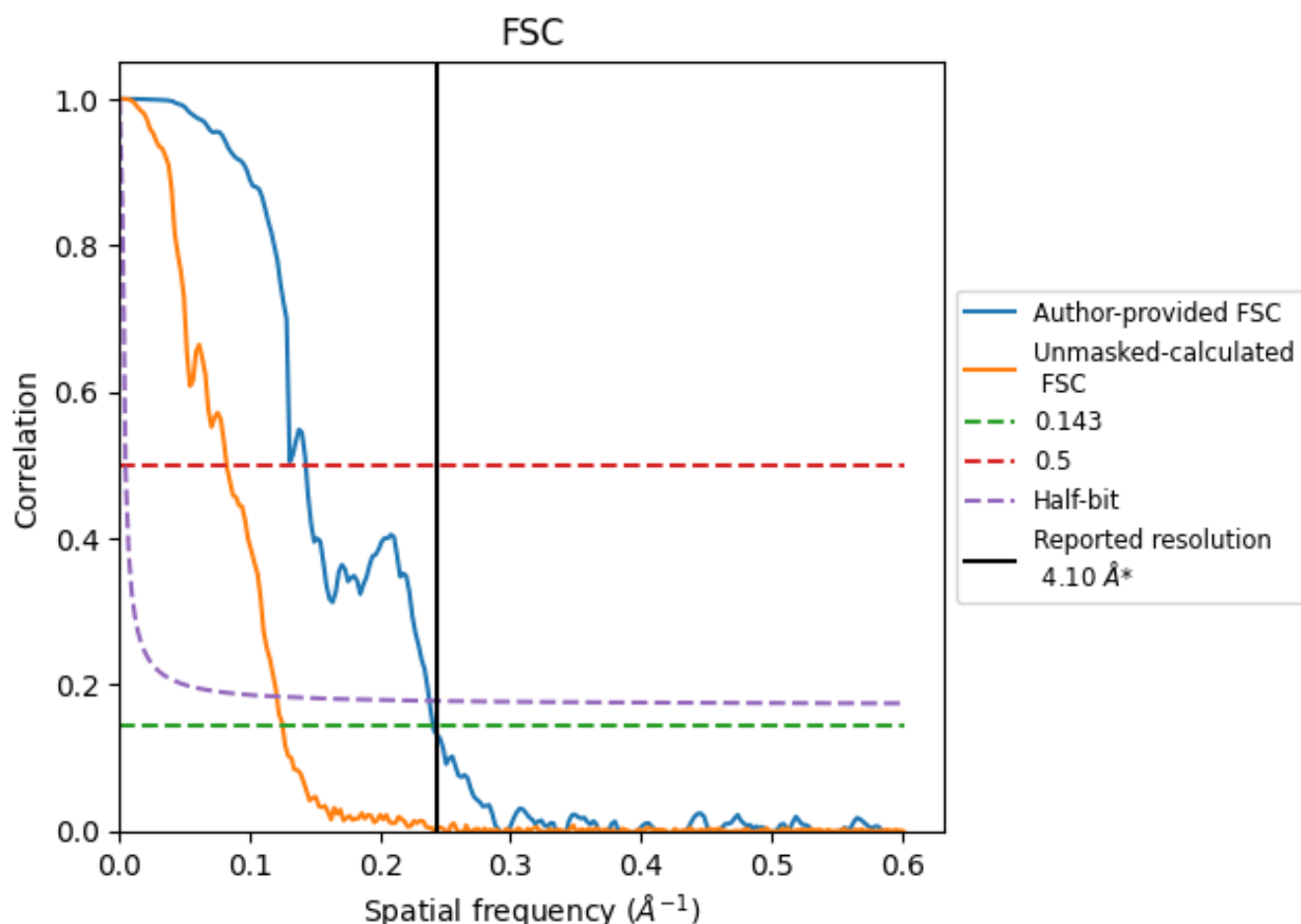


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

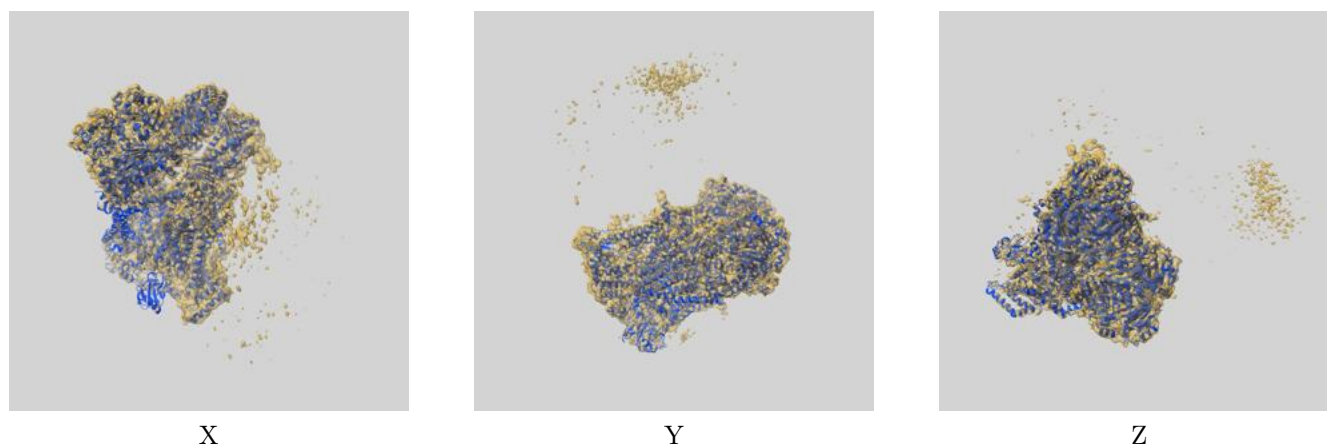
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.15	7.00	4.21
Unmasked-calculated*	7.99	12.18	8.29

*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 7.99 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

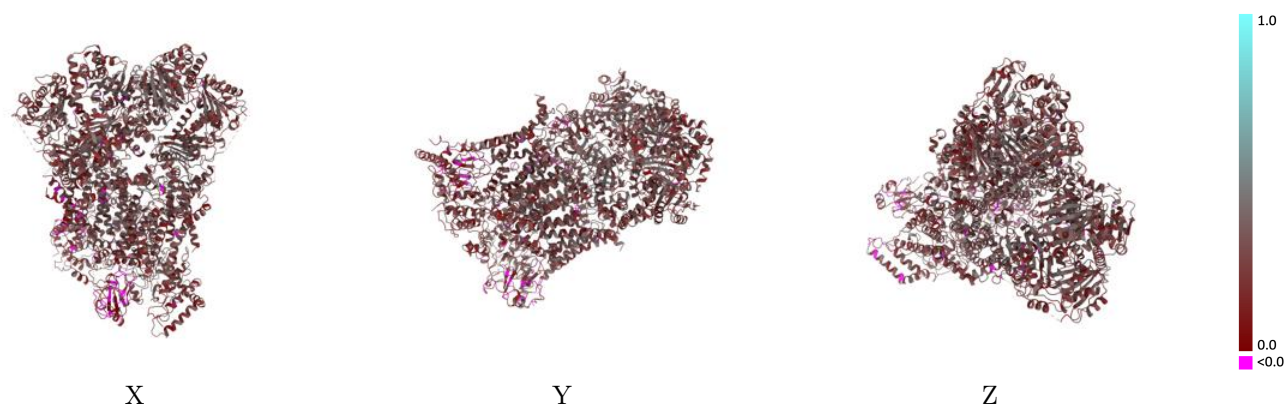
This section contains information regarding the fit between EMDB map EMD-35355 and PDB model 8IC5. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



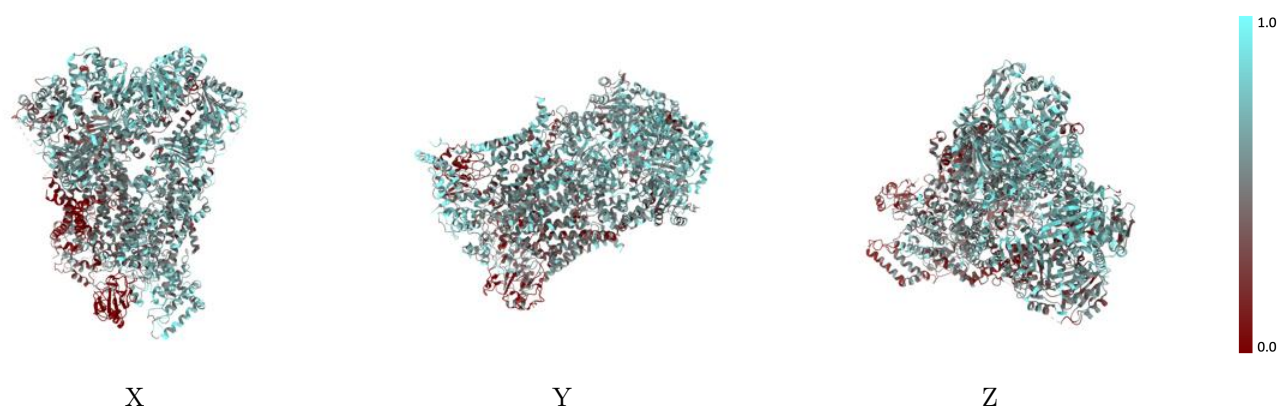
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



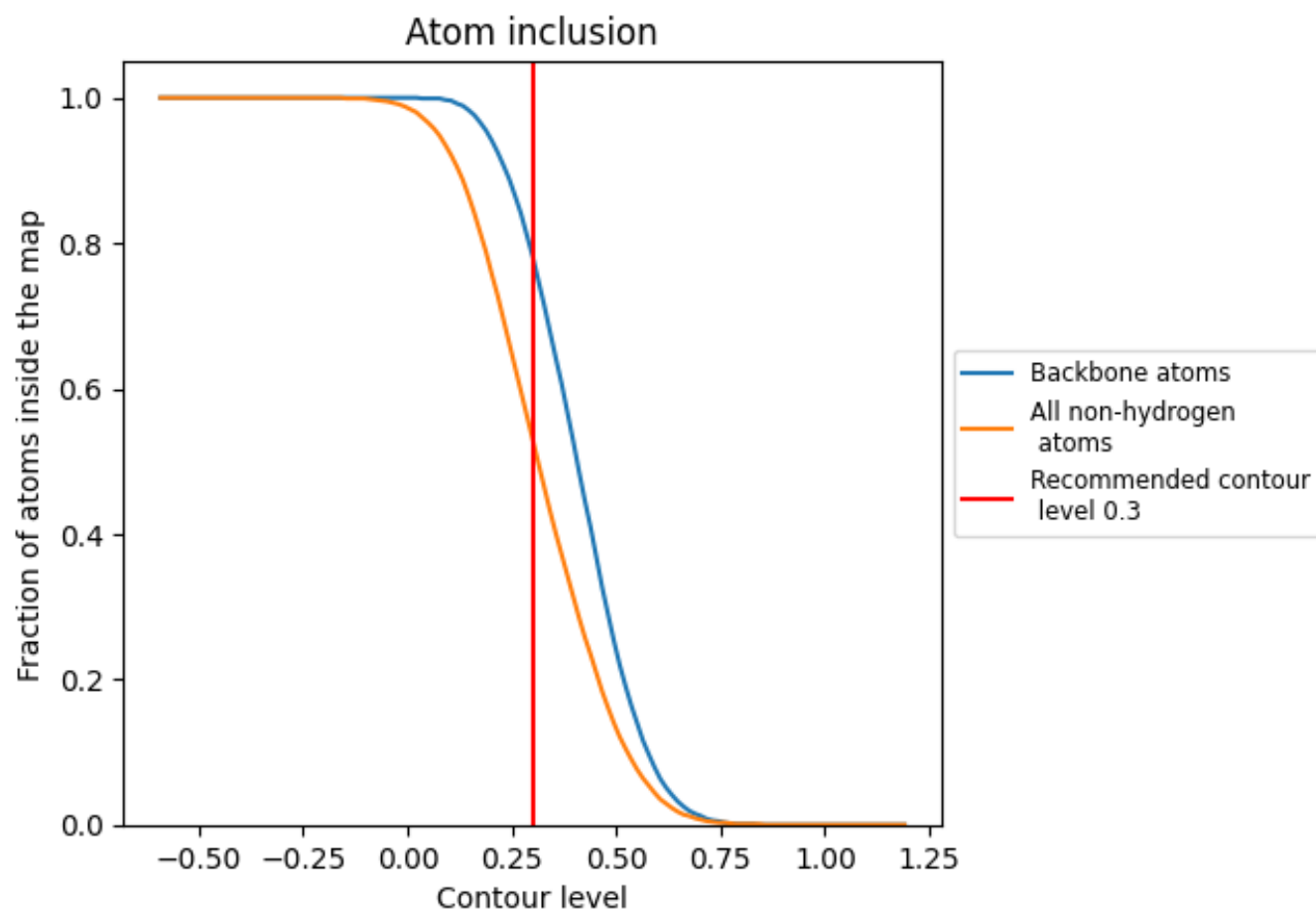
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).













































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 53% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5300	 0.2720
AA	 0.5740	 0.2830
AB	 0.6290	 0.3020
AC	 0.5010	 0.2810
AD	 0.4650	 0.2470
AE	 0.0740	 0.1570
AF	 0.5930	 0.3040
AG	 0.4530	 0.2850
AH	 0.2780	 0.1890
AI	 0.3810	 0.3150
AJ	 0.0620	 0.1310
AK	 0.0380	 0.1600
Aa	 0.6250	 0.2910
Ab	 0.6410	 0.3000
Ac	 0.5800	 0.2910
Ad	 0.6560	 0.2800
Ae	 0.3540	 0.2260
Af	 0.6420	 0.3000
Ag	 0.5630	 0.2790
Ah	 0.6970	 0.2290
Aj	 0.4500	 0.2220
Ak	 0.2860	 0.2410

