



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 11:42 PM UTC

PDB ID : 8IBC / pdb_00008ibc
EMDB ID : EMD-35339
Title : Respiratory complex CIII2, focus-refined of type IB, Wild type mouse under cold temperature
Authors : Shin, Y.-C.; Liao, M.
Deposited on : 2023-02-10
Resolution : 3.60 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.dev132
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) : 2.49

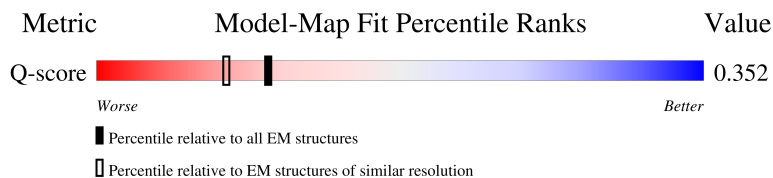
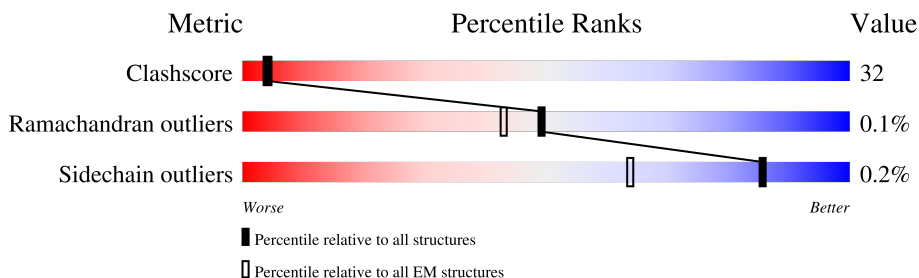
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	

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Mol	Chain	Length	Quality of chain
3	AC	381	
3	Ac	381	
4	AD	325	
4	Ad	325	
5	AE	274	
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 31431 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	399	Total	C	N	O	S	0	0
			3117	1943	554	604	16		
1	Aa	401	Total	C	N	O	S	0	0
			3131	1955	555	605	16		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	414	Total	C	N	O	S	0	0
			3107	1954	546	598	9		
2	Ab	413	Total	C	N	O	S	0	0
			3101	1948	543	601	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	373	Total	C	N	O	S	0	0
			2988	2018	461	489	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	238	Total	C	N	O	S	0	0
			1895	1211	325	345	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	185	Total	C	N	O	S	0	0
			1427	902	250	268	7		
5	AI	51	Total	C	N	O		0	0
			347	221	65	61			
5	Ae	188	Total	C	N	O	S	0	0
			1451	916	254	274	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	98	Total	C	N	O	S	0	0
			864	552	154	155	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	76	Total	C	N	O	S	0	0
			643	418	116	108	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	66	Total	C	N	O	S	0	0
			544	333	101	105	5		

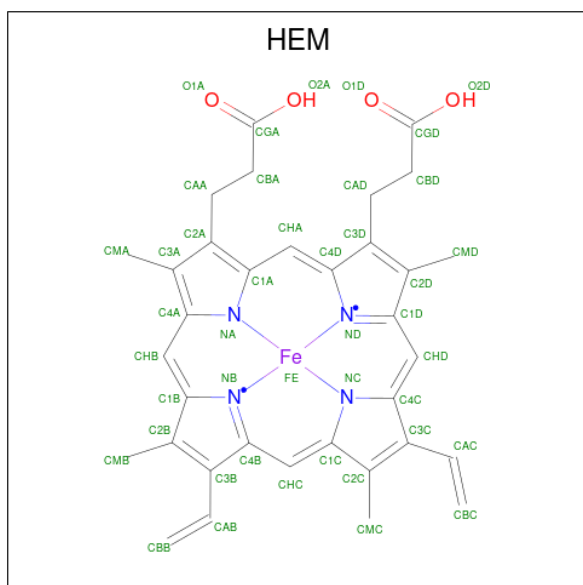
- Molecule 9 is a protein called Cytochrome b-c1 complex subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AJ	38	Total	C	N	O	0	0
			307	201	51	55		
9	Aj	48	Total	C	N	O	0	0
			392	257	67	68		

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

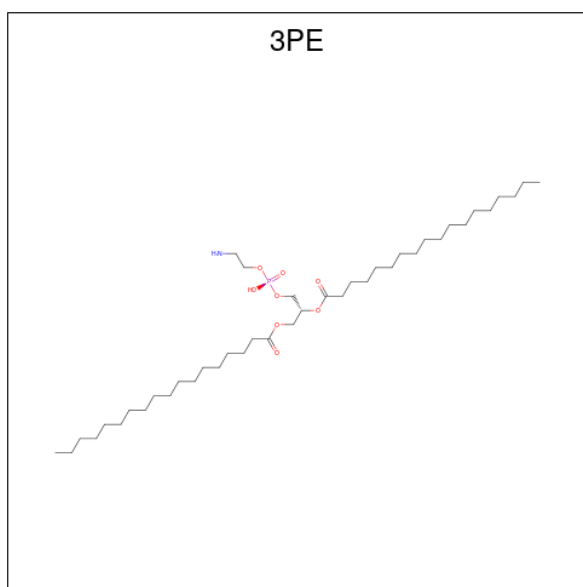
Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	34	Total	C	N	O	S	0	0
			278	183	51	43	1		
10	AK	44	Total	C	N	O	S	0	0
			357	236	63	57	1		

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



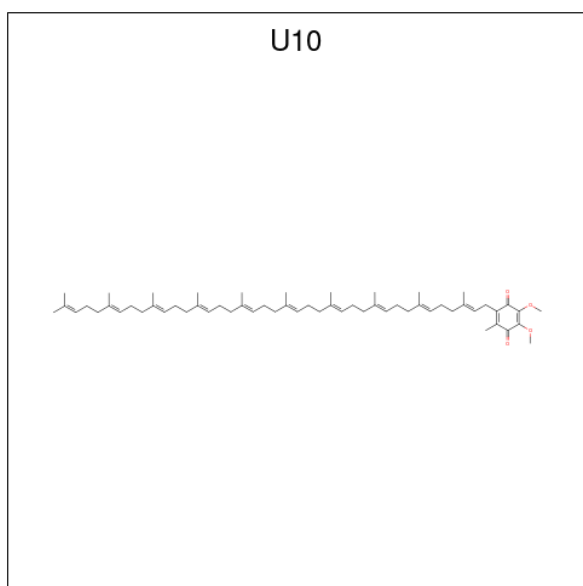
Mol	Chain	Residues	Atoms					AltConf
11	AC	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
11	AC	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
11	Ac	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
11	Ac	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 12 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
12	AC	1	Total	C	N	O	P	0
			25	15	1	8	1	
12	Ac	1	Total	C	N	O	P	0
			35	25	1	8	1	

- Molecule 13 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).



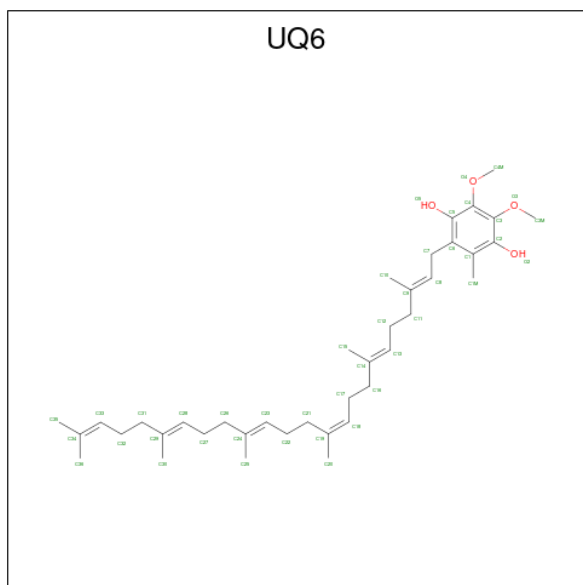
Mol	Chain	Residues	Atoms			AltConf
13	AC	1	Total	C	O	0
			23	19	4	

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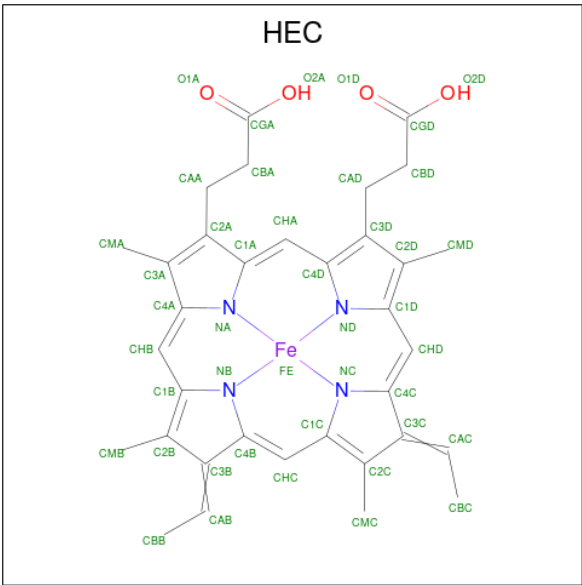
Mol	Chain	Residues	Atoms			AltConf
13	Ac	1	Total	C	O	0
			23	19	4	

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



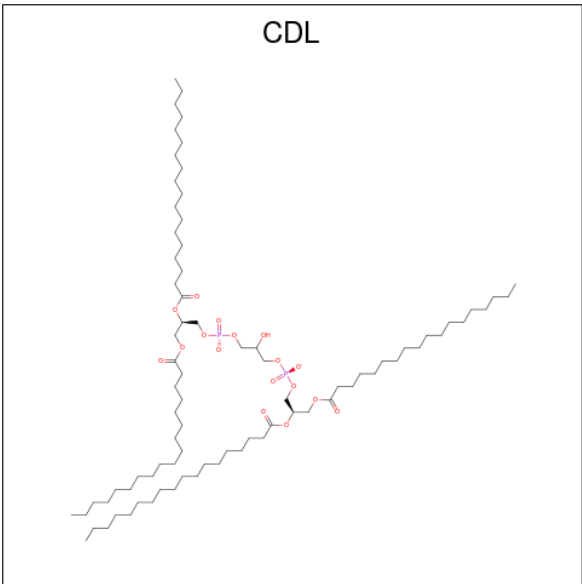
Mol	Chain	Residues	Atoms			AltConf
14	AC	1	Total	C	O	0
			28	24	4	
14	Ac	1	Total	C	O	0
			28	24	4	

- Molecule 15 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 16 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).



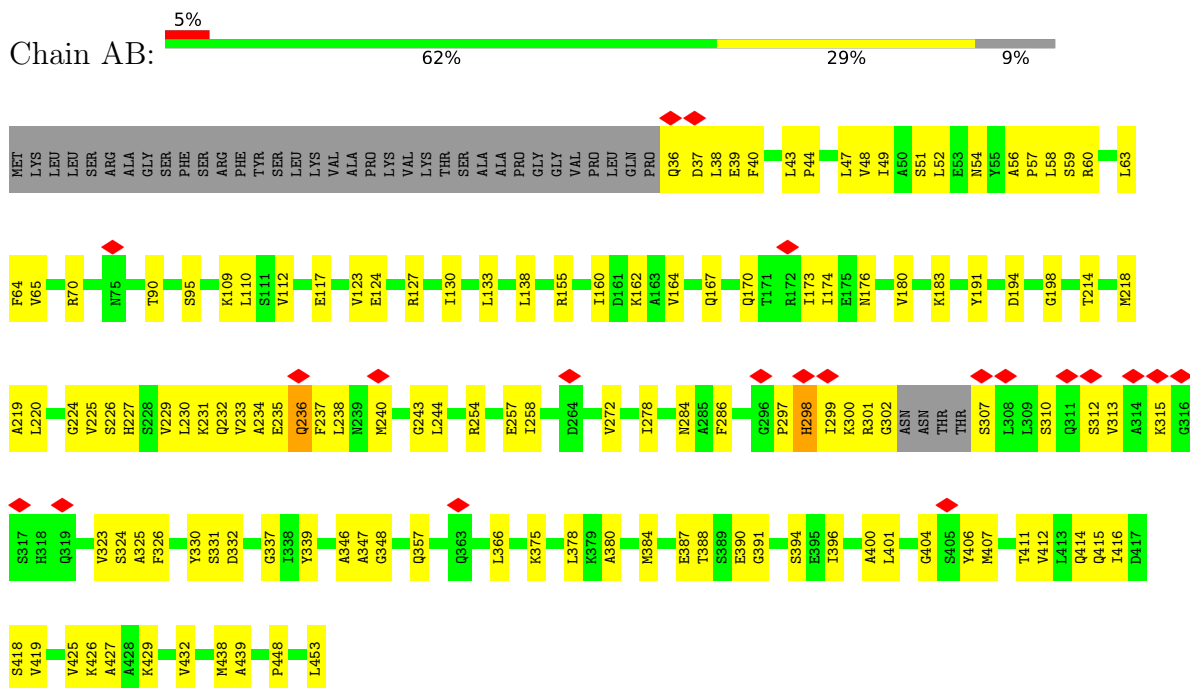
Mol	Chain	Residues	Atoms				AltConf
16	Aa	1	Total	C	O	P	0
			46	27	17	2	

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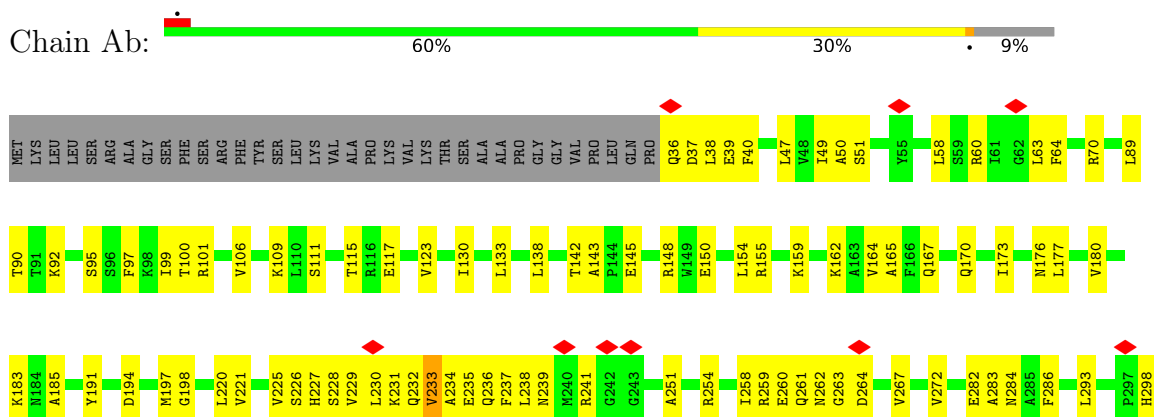
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Mol	Chain	Residues	Atoms				AltConf
16	Ac	1	Total	C	O	P	0
			42	23	17	2	
16	Ag	1	Total	C	O	P	0
			56	37	17	2	

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

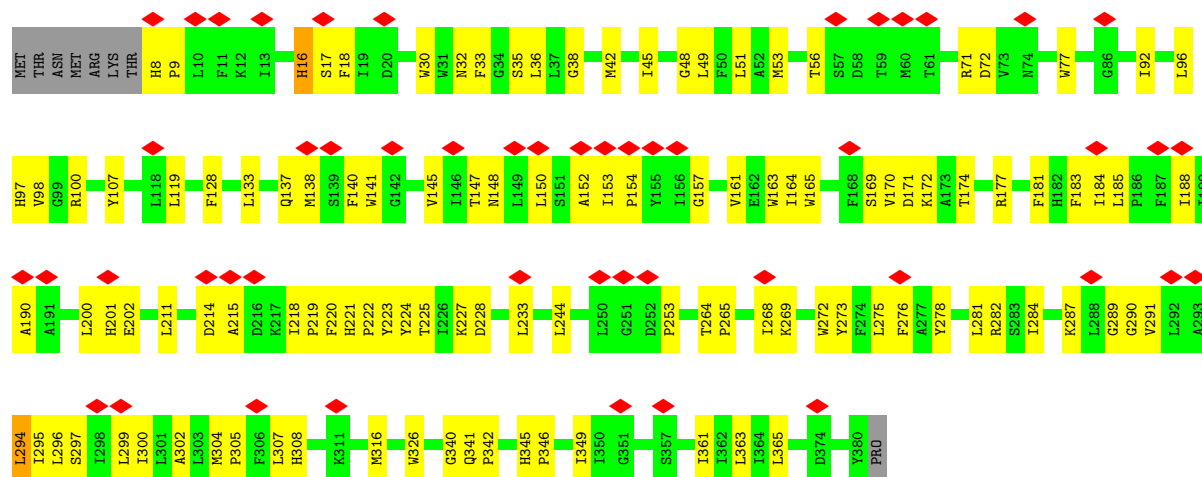


- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial

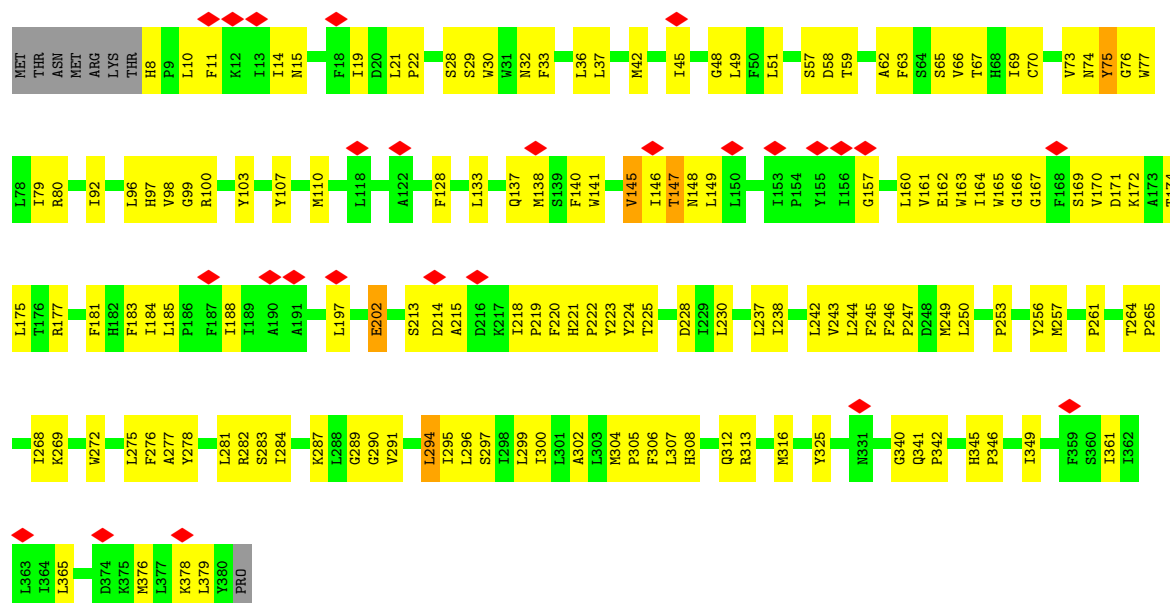




• Molecule 3: Cytochrome b

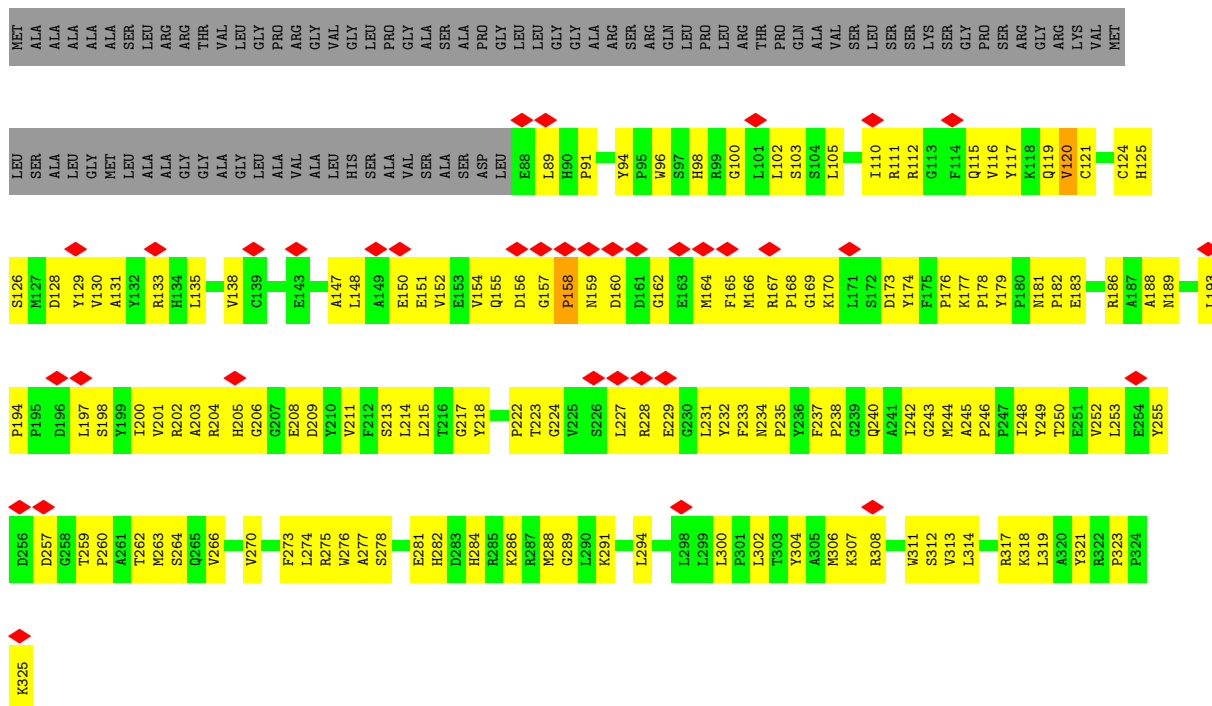


• Molecule 3: Cytochrome b

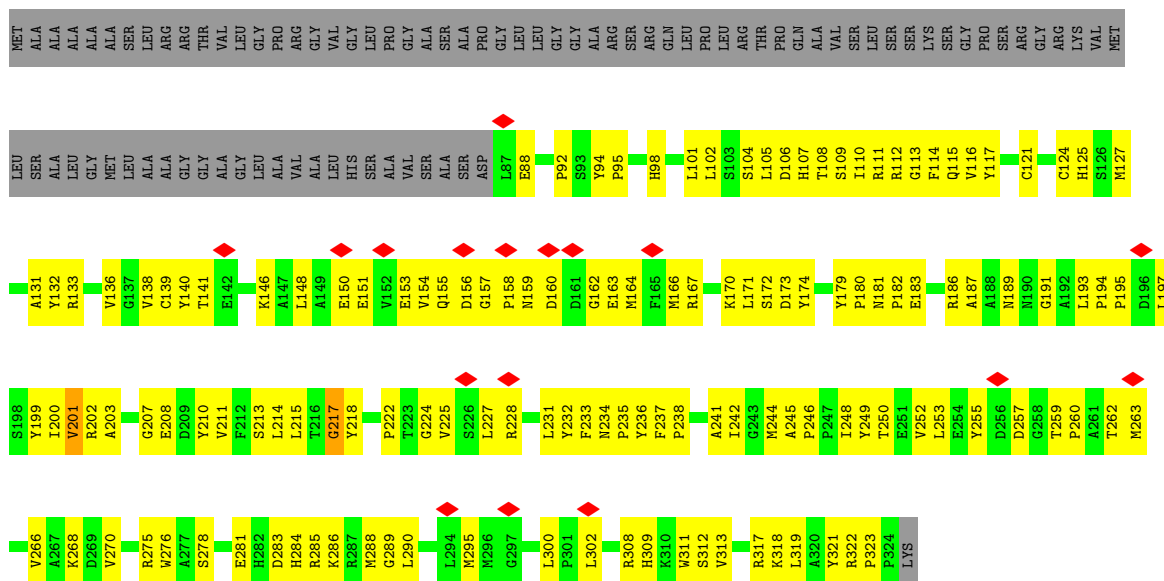


• Molecule 4: Cytochrome c1, heme protein, mitochondrial

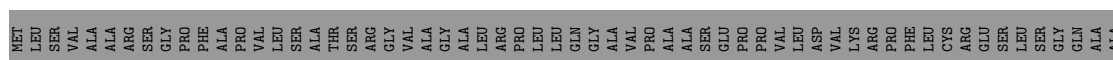
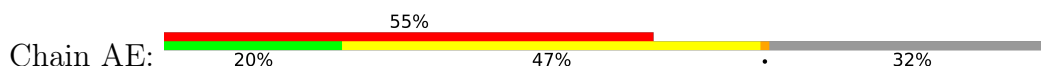


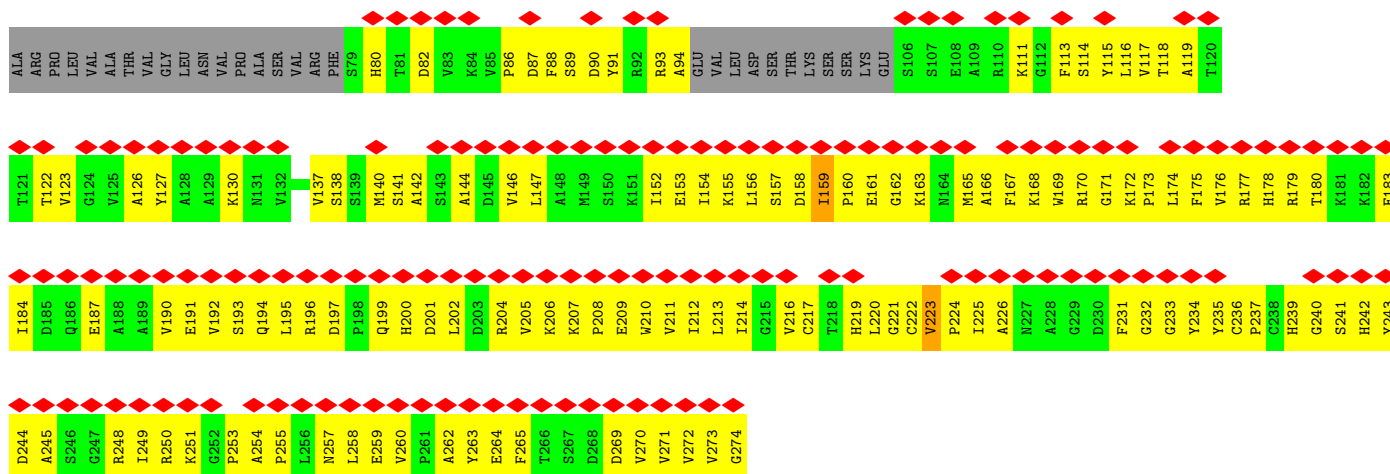


- Molecule 4: Cytochrome c1, heme protein, mitochondrial

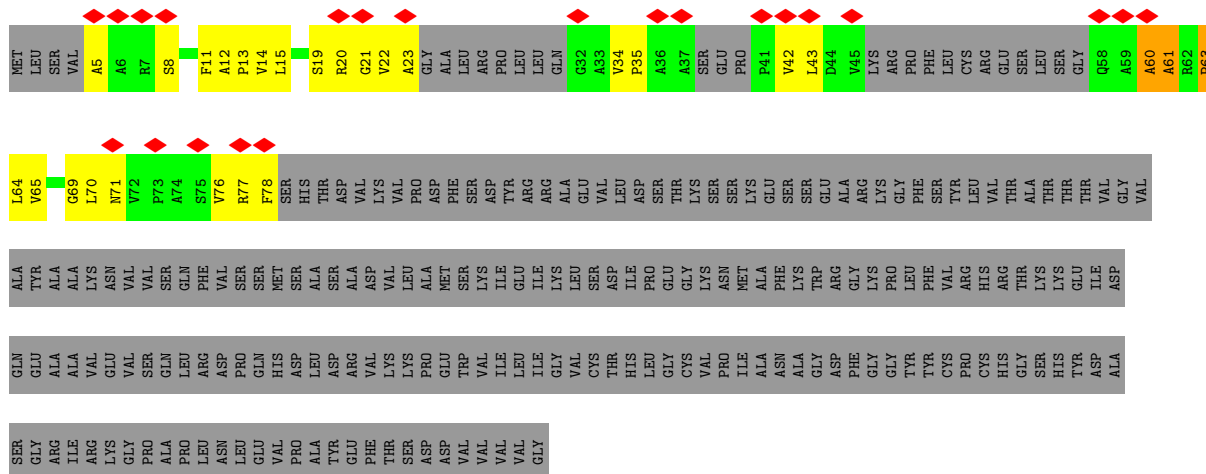


- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial

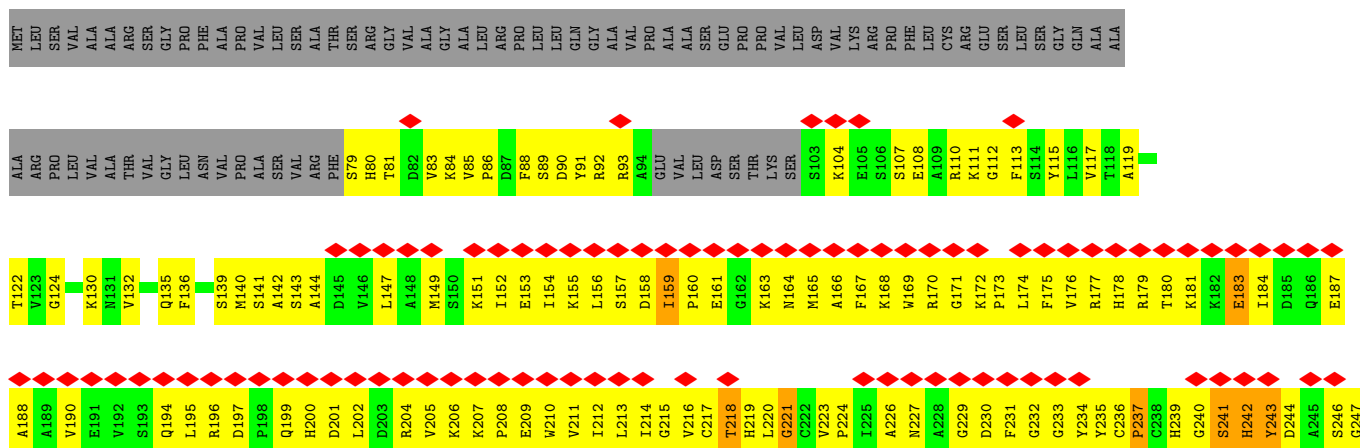
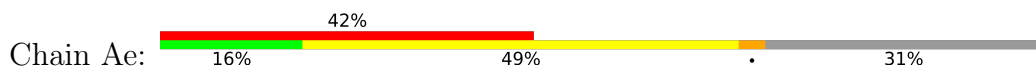




- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial

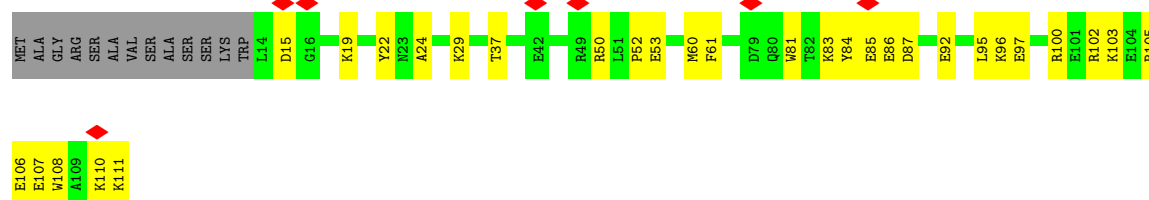


- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial

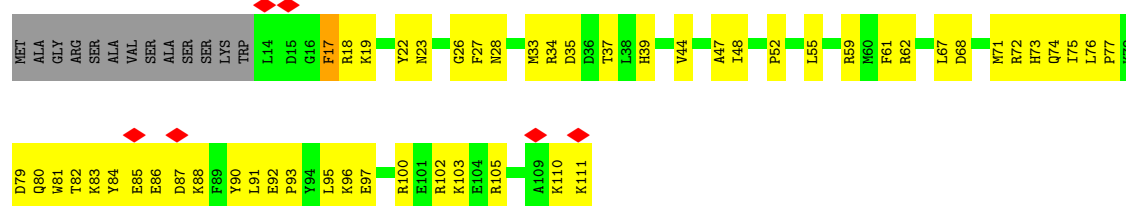




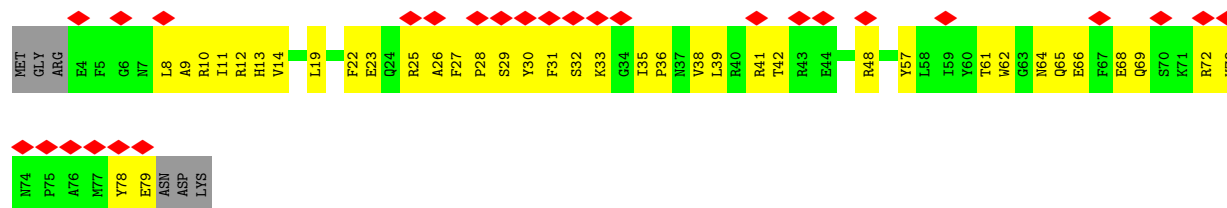
• Molecule 6: Cytochrome b-c1 complex subunit 7



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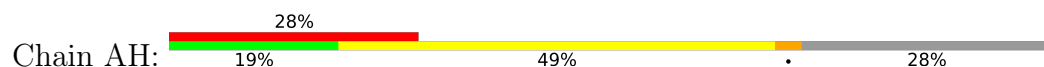
• Molecule 7: Cytochrome b-c1 complex subunit 8

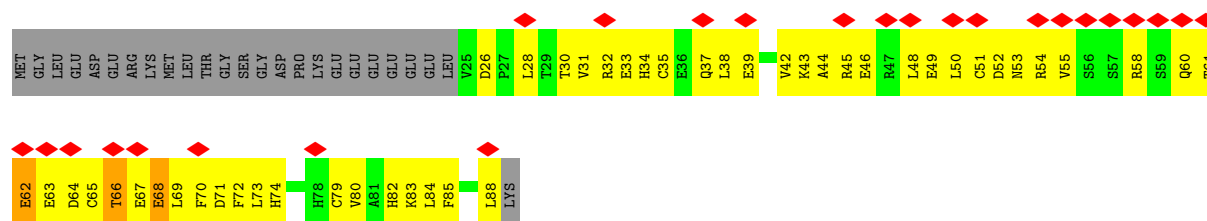


• Molecule 7: Cytochrome b-c1 complex subunit 8

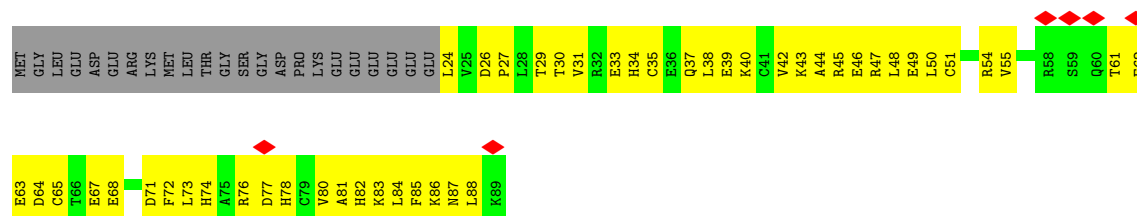


• Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial

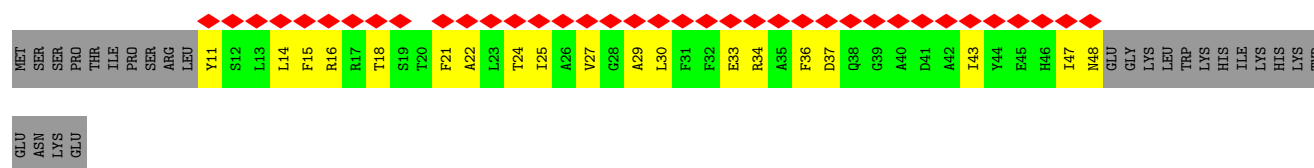
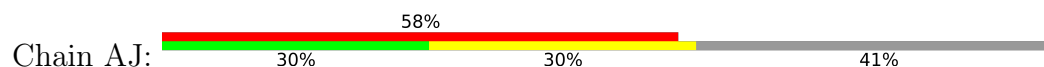




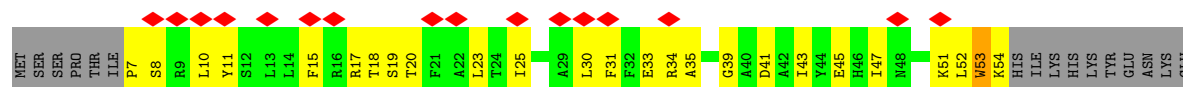
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial



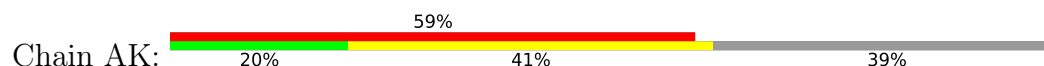
- Molecule 9: Cytochrome b-c1 complex subunit 9



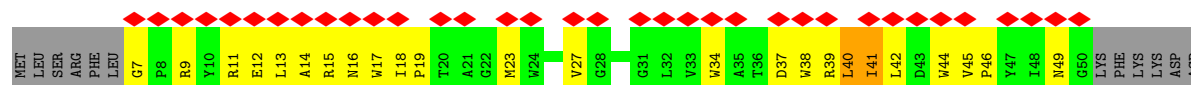
- Molecule 9: Cytochrome b-c1 complex subunit 9



- 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	147426	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.1, 45.9	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.469	Depositor
Minimum map value	-1.236	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.055	Depositor
Recommended contour level	0.35	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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: U10, CDL, HEC, 3PE, 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	0.57	1/3176 (0.0%)	0.85	7/4305 (0.2%)
1	Aa	0.45	0/3190	0.78	9/4325 (0.2%)
2	AB	0.44	1/3156 (0.0%)	0.62	3/4263 (0.1%)
2	Ab	0.44	0/3149	0.69	5/4255 (0.1%)
3	AC	0.41	0/3089	0.72	6/4221 (0.1%)
3	Ac	0.48	0/3089	0.79	5/4221 (0.1%)
4	AD	0.54	0/1955	0.81	1/2655 (0.0%)
4	Ad	0.65	2/1954 (0.1%)	0.86	4/2655 (0.2%)
5	AE	0.50	0/1459	0.94	4/1976 (0.2%)
5	AI	0.96	1/351 (0.3%)	1.34	5/478 (1.0%)
5	Ae	0.56	0/1483	1.04	8/2007 (0.4%)
6	AF	0.38	0/884	0.52	0/1184
6	Af	0.72	1/884 (0.1%)	0.82	0/1184
7	AG	0.50	0/662	0.87	1/895 (0.1%)
7	Ag	0.54	0/662	0.94	2/895 (0.2%)
8	AH	0.54	0/534	0.95	4/717 (0.6%)
8	Ah	0.65	0/551	0.82	0/739
9	AJ	0.46	0/314	0.60	0/424
9	Aj	0.62	0/402	0.80	1/541 (0.2%)
10	AK	0.49	0/287	0.84	1/393 (0.3%)
10	Ak	0.53	0/371	0.82	2/511 (0.4%)
All	All	0.52	6/31602 (0.0%)	0.80	68/42844 (0.2%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AI	63	PRO	N-CD	-13.53	1.28	1.47
4	Ad	182	PRO	N-CD	-11.67	1.31	1.47
2	AB	240	MET	C-N	8.57	1.45	1.33
4	Ad	217	GLY	C-O	-5.62	1.16	1.23
6	Af	17	PHE	C-N	-5.30	1.27	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Ae	242	HIS	N-CA-C	11.44	125.36	109.11
5	AI	63	PRO	N-CA-CB	-10.69	93.84	103.25
1	AA	187	LEU	N-CA-C	-9.83	100.39	112.38
1	Aa	385	GLU	N-CA-C	9.71	121.95	111.36
5	AI	63	PRO	CA-N-CD	9.15	124.81	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	AA	3117	0	3032	188	0
1	Aa	3131	0	3055	155	0
2	AB	3107	0	3116	148	0
2	Ab	3101	0	3098	134	0
3	AC	2988	0	3045	144	0
3	Ac	2988	0	3045	187	0
4	AD	1896	0	1846	188	0
4	Ad	1895	0	1844	173	0
5	AE	1427	0	1407	230	0
5	AI	347	0	363	46	0
5	Ae	1451	0	1433	250	0
6	AF	864	0	854	27	0
6	Af	864	0	854	56	0
7	AG	643	0	643	64	0
7	Ag	643	0	643	55	0
8	AH	527	0	507	73	0
8	Ah	544	0	529	56	0
9	AJ	307	0	295	34	0
9	Aj	392	0	388	30	0
10	AK	278	0	278	37	0
10	Ak	357	0	347	25	0
11	AC	86	0	60	8	0
11	Ac	86	0	60	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	AC	25	0	24	4	0
12	Ac	35	0	44	4	0
13	AC	23	0	23	9	0
13	Ac	23	0	23	12	0
14	AC	28	0	31	7	0
14	Ac	28	0	31	8	0
15	AD	43	0	32	5	0
15	Ad	43	0	32	18	0
16	Aa	46	0	36	3	0
16	Ac	42	0	28	5	0
16	Ag	56	0	56	6	0
All	All	31431	0	31102	2006	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 32.

The worst 5 of 2006 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)
5:AE:88:PHE:CB	7:AG:19:LEU:HD11	1.71	1.19
2:AB:167:GLN:HE21	5:AI:35:PRO:HD3	1.08	1.12
3:Ac:98:VAL:HG22	11:Ac:402:HEM:HBC2	1.25	1.12
5:Ae:239:HIS:CD2	5:Ae:253:PRO:HD2	1.83	1.12
9:Aj:31:PHE:O	9:Aj:34:ARG:HG2	1.47	1.11

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	AA	393/480 (82%)	378 (96%)	15 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aa	395/480 (82%)	384 (97%)	11 (3%)	0	100	100
2	AB	410/453 (90%)	400 (98%)	10 (2%)	0	100	100
2	Ab	407/453 (90%)	397 (98%)	10 (2%)	0	100	100
3	AC	371/381 (97%)	367 (99%)	4 (1%)	0	100	100
3	Ac	371/381 (97%)	362 (98%)	8 (2%)	1 (0%)	36	65
4	AD	236/325 (73%)	229 (97%)	6 (2%)	1 (0%)	30	61
4	Ad	236/325 (73%)	224 (95%)	12 (5%)	0	100	100
5	AE	181/274 (66%)	168 (93%)	13 (7%)	0	100	100
5	AI	43/274 (16%)	41 (95%)	2 (5%)	0	100	100
5	Ae	184/274 (67%)	171 (93%)	12 (6%)	1 (0%)	24	57
6	AF	96/111 (86%)	96 (100%)	0	0	100	100
6	Af	96/111 (86%)	96 (100%)	0	0	100	100
7	AG	74/82 (90%)	74 (100%)	0	0	100	100
7	Ag	74/82 (90%)	73 (99%)	1 (1%)	0	100	100
8	AH	62/89 (70%)	62 (100%)	0	0	100	100
8	Ah	64/89 (72%)	63 (98%)	1 (2%)	0	100	100
9	AJ	36/64 (56%)	36 (100%)	0	0	100	100
9	Aj	46/64 (72%)	45 (98%)	1 (2%)	0	100	100
10	AK	32/56 (57%)	31 (97%)	1 (3%)	0	100	100
10	Ak	42/56 (75%)	41 (98%)	1 (2%)	0	100	100
All	All	3849/4904 (78%)	3738 (97%)	108 (3%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	Ac	75	TYR
4	AD	158	PRO
5	Ae	237	PRO

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	337/398 (85%)	337 (100%)	0	100	100
1	Aa	339/398 (85%)	338 (100%)	1 (0%)	86	83
2	AB	324/356 (91%)	324 (100%)	0	100	100
2	Ab	325/356 (91%)	324 (100%)	1 (0%)	86	83
3	AC	325/333 (98%)	324 (100%)	1 (0%)	86	83
3	Ac	325/333 (98%)	324 (100%)	1 (0%)	86	83
4	AD	203/260 (78%)	203 (100%)	0	100	100
4	Ad	203/260 (78%)	202 (100%)	1 (0%)	81	80
5	AE	155/224 (69%)	154 (99%)	1 (1%)	78	79
5	AI	34/224 (15%)	34 (100%)	0	100	100
5	Ae	158/224 (70%)	158 (100%)	0	100	100
6	AF	90/99 (91%)	90 (100%)	0	100	100
6	Af	90/99 (91%)	90 (100%)	0	100	100
7	AG	69/74 (93%)	69 (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	63/83 (76%)	63 (100%)	0	100	100
9	AJ	30/55 (54%)	30 (100%)	0	100	100
9	Aj	39/55 (71%)	39 (100%)	0	100	100
10	AK	26/46 (56%)	26 (100%)	0	100	100
10	Ak	34/46 (74%)	34 (100%)	0	100	100
All	All	3299/4080 (81%)	3293 (100%)	6 (0%)	85	85

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Ab	260	GLU
3	Ac	294	LEU
4	Ad	201	VAL
5	AE	223	VAL
3	AC	294	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58

such sidechains are listed below:

Mol	Chain	Res	Type
1	Aa	160	GLN
7	Ag	24	GLN
2	Ab	227	HIS
6	Af	80	GLN
4	Ad	107	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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$
14	UQ6	Ac	405	-	28,28,43	0.83	2 (7%)	36,37,55	0.81	1 (2%)
14	UQ6	AC	405	-	28,28,43	2.49	6 (21%)	36,37,55	1.61	8 (22%)
13	U10	Ac	404	-	23,23,63	1.28	4 (17%)	30,31,79	2.06	7 (23%)
11	HEM	AC	401	3	50,50,50	1.61	8 (16%)	67,82,82	1.80	13 (19%)
11	HEM	AC	402	3	50,50,50	1.60	9 (18%)	67,82,82	1.80	13 (19%)
16	CDL	Ac	406	16	41,41,99	1.39	4 (9%)	47,53,111	1.42	7 (14%)
12	3PE	AC	403	-	24,24,50	1.31	2 (8%)	27,29,55	1.19	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	U10	AC	404	-	23,23,63	1.81	2 (8%)	30,31,79	1.74	8 (26%)
15	HEC	AD	401	4	46,50,50	2.55	25 (54%)	58,82,82	2.08	21 (36%)
11	HEM	Ac	402	3	50,50,50	1.56	8 (16%)	67,82,82	1.78	14 (20%)
16	CDL	Aa	501	-	45,45,99	1.35	4 (8%)	51,57,111	1.28	6 (11%)
16	CDL	Ag	101	16	55,55,99	1.21	4 (7%)	61,67,111	1.22	6 (9%)
15	HEC	Ad	401	4	46,50,50	2.51	23 (50%)	58,82,82	2.18	20 (34%)
12	3PE	Ac	403	-	34,34,50	1.10	2 (5%)	37,39,55	1.22	3 (8%)
11	HEM	Ac	401	3	50,50,50	1.60	10 (20%)	67,82,82	1.71	14 (20%)

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
14	UQ6	Ac	405	-	-	13/21/21/39	0/1/1/1
14	UQ6	AC	405	-	-	2/21/21/39	0/1/1/1
13	U10	Ac	404	-	-	6/15/39/87	0/1/1/1
11	HEM	AC	401	3	-	8/14/54/54	-
11	HEM	AC	402	3	-	9/14/54/54	-
16	CDL	Ac	406	16	-	18/52/52/110	-
12	3PE	AC	403	-	-	7/28/28/54	-
13	U10	AC	404	-	-	3/15/39/87	0/1/1/1
15	HEC	AD	401	4	-	3/14/54/54	-
11	HEM	Ac	402	3	-	8/14/54/54	-
16	CDL	Aa	501	-	-	11/56/56/110	-
16	CDL	Ag	101	16	-	22/66/66/110	-
15	HEC	Ad	401	4	-	4/14/54/54	-
12	3PE	Ac	403	-	-	2/38/38/54	-
11	HEM	Ac	401	3	-	9/14/54/54	-

The worst 5 of 113 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	AC	404	U10	C6-C1	7.50	1.48	1.35
14	AC	405	UQ6	C5-C6	6.01	1.48	1.40
14	AC	405	UQ6	C2-C3	5.92	1.49	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	AC	405	UQ6	C5-C4	5.86	1.48	1.39
11	Ac	401	HEM	FE-NB	5.24	2.11	1.94

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	Ac	404	U10	C6-C1-C2	7.88	125.39	119.17
11	AC	401	HEM	CHC-C4B-NB	6.09	130.98	124.42
11	AC	402	HEM	CHC-C4B-NB	5.81	130.67	124.42
11	Ac	402	HEM	CHC-C4B-NB	5.42	130.26	124.42
11	Ac	401	HEM	CHC-C4B-NB	5.25	130.07	124.42

There are no chirality outliers.

5 of 125 torsion outliers are listed below:

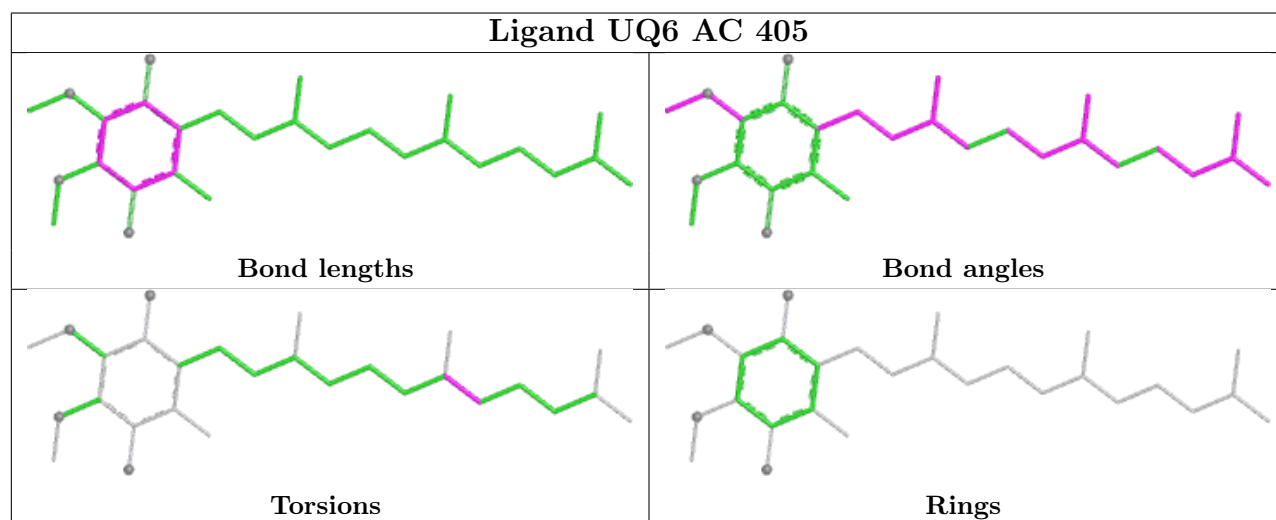
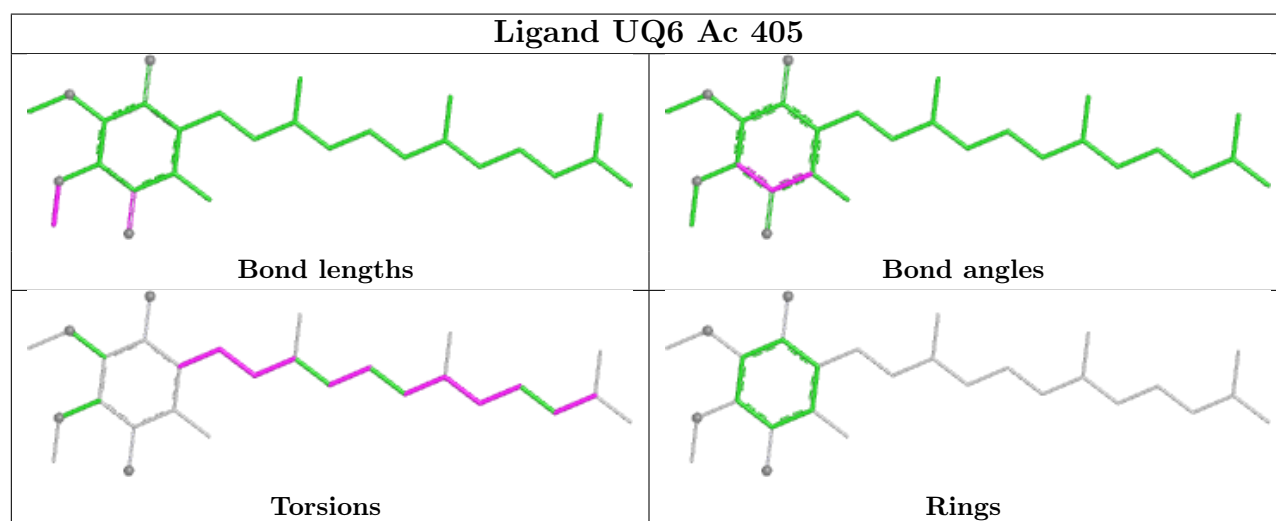
Mol	Chain	Res	Type	Atoms
11	AC	401	HEM	C2C-C3C-CAC-CBC
11	AC	402	HEM	C2B-C3B-CAB-CBB
11	AC	402	HEM	C4B-C3B-CAB-CBB
11	AC	402	HEM	C2C-C3C-CAC-CBC
11	Ac	401	HEM	C2C-C3C-CAC-CBC

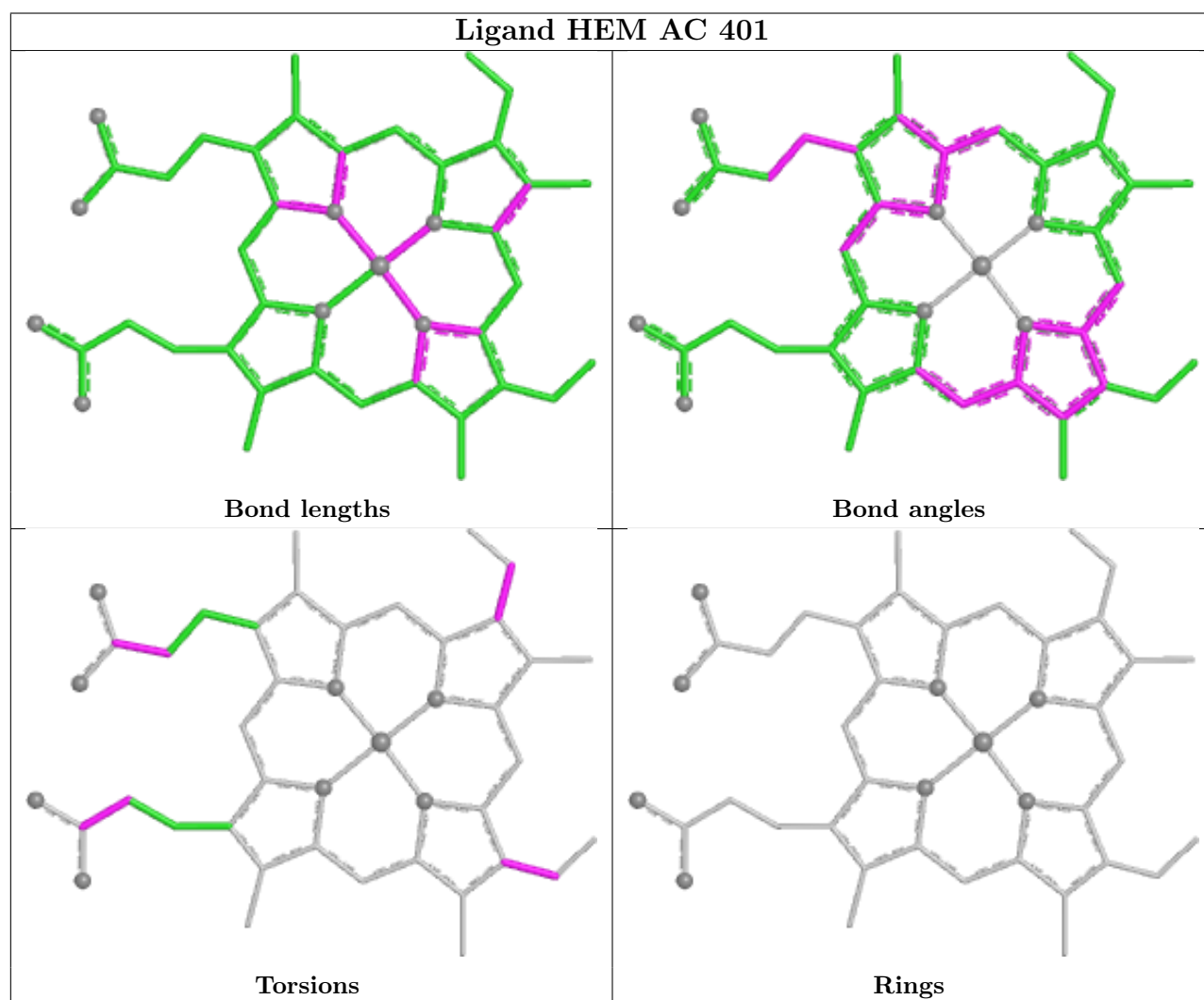
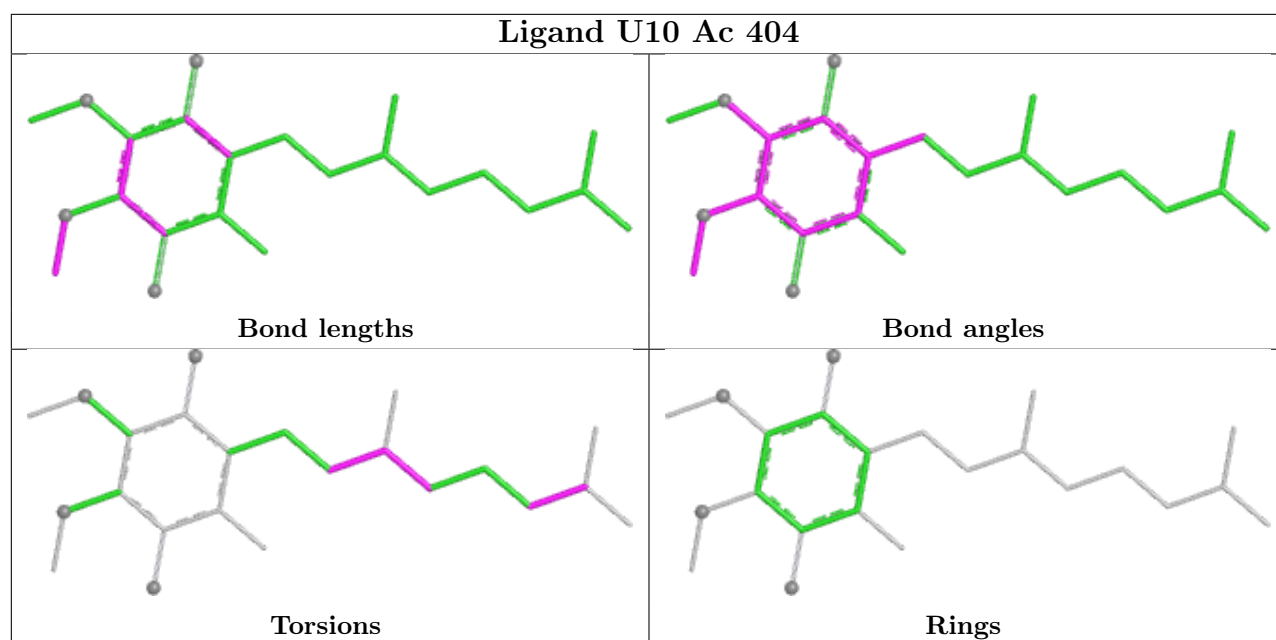
There are no ring outliers.

15 monomers are involved in 95 short contacts:

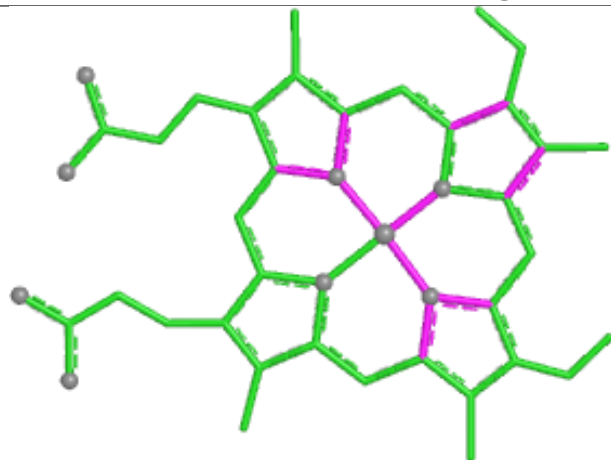
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	Ac	405	UQ6	8	0
14	AC	405	UQ6	7	0
13	Ac	404	U10	12	0
11	AC	401	HEM	3	0
11	AC	402	HEM	5	0
16	Ac	406	CDL	5	0
12	AC	403	3PE	4	0
13	AC	404	U10	9	0
15	AD	401	HEC	5	0
11	Ac	402	HEM	3	0
16	Aa	501	CDL	3	0
16	Ag	101	CDL	6	0
15	Ad	401	HEC	18	0
12	Ac	403	3PE	4	0
11	Ac	401	HEM	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.

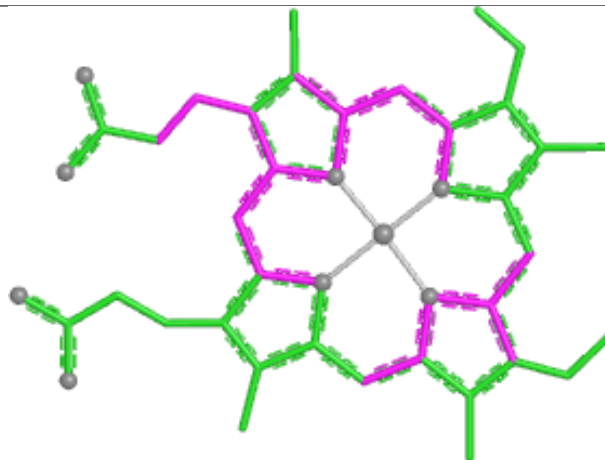




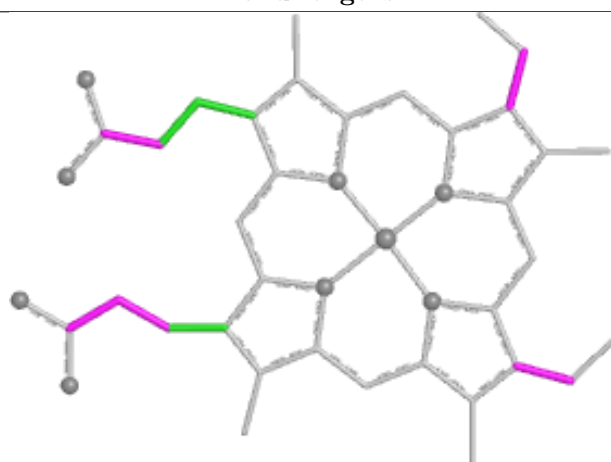
Ligand HEM AC 402



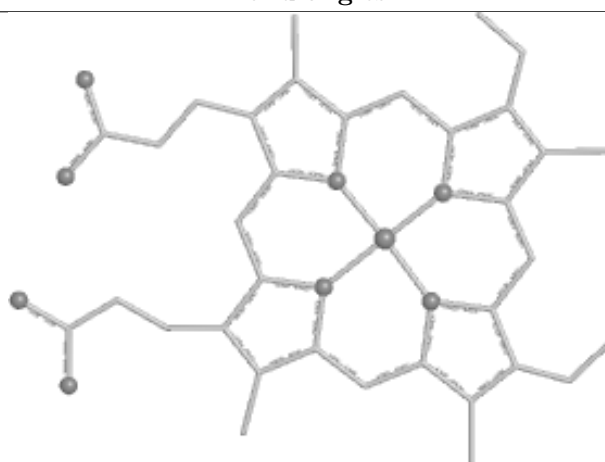
Bond lengths



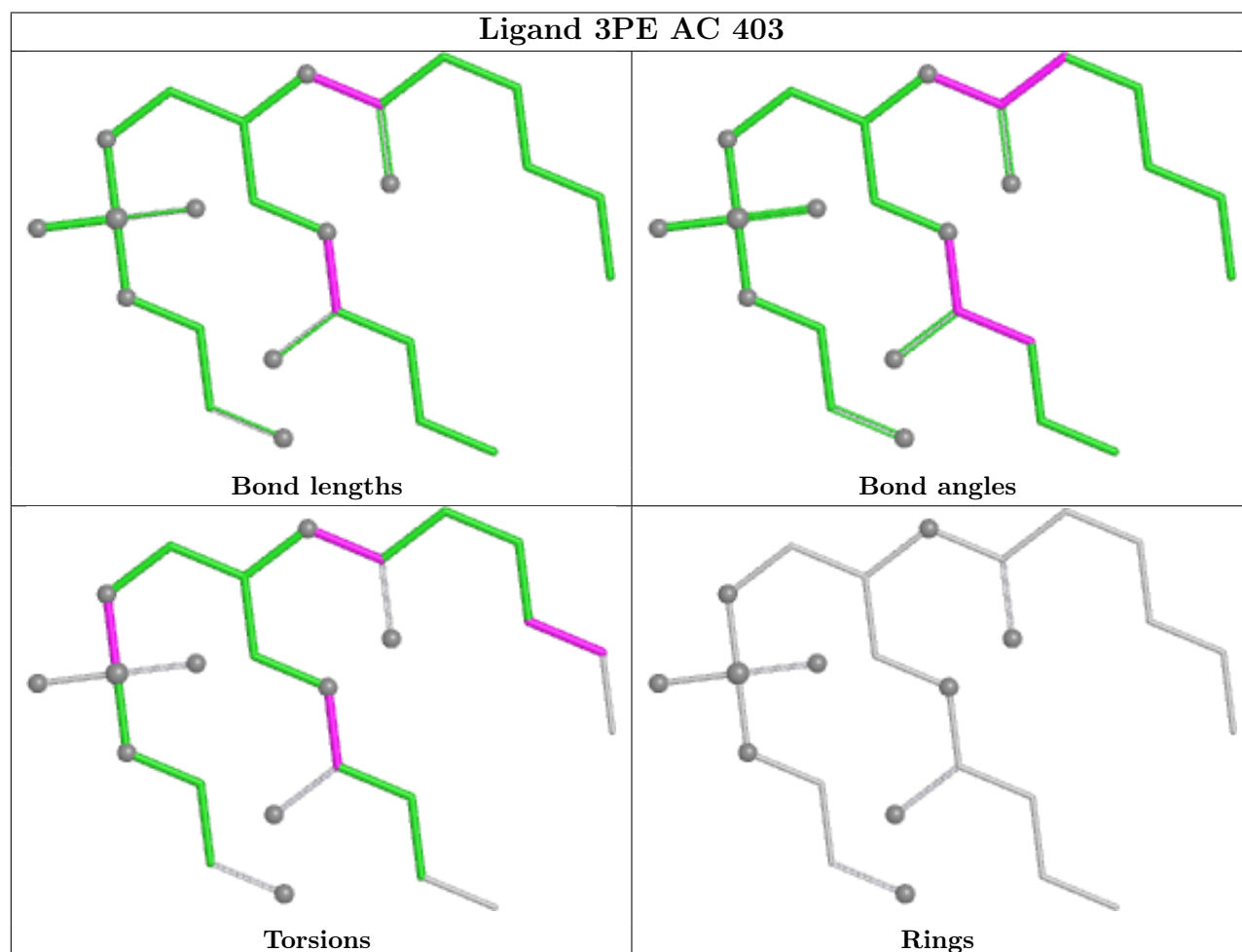
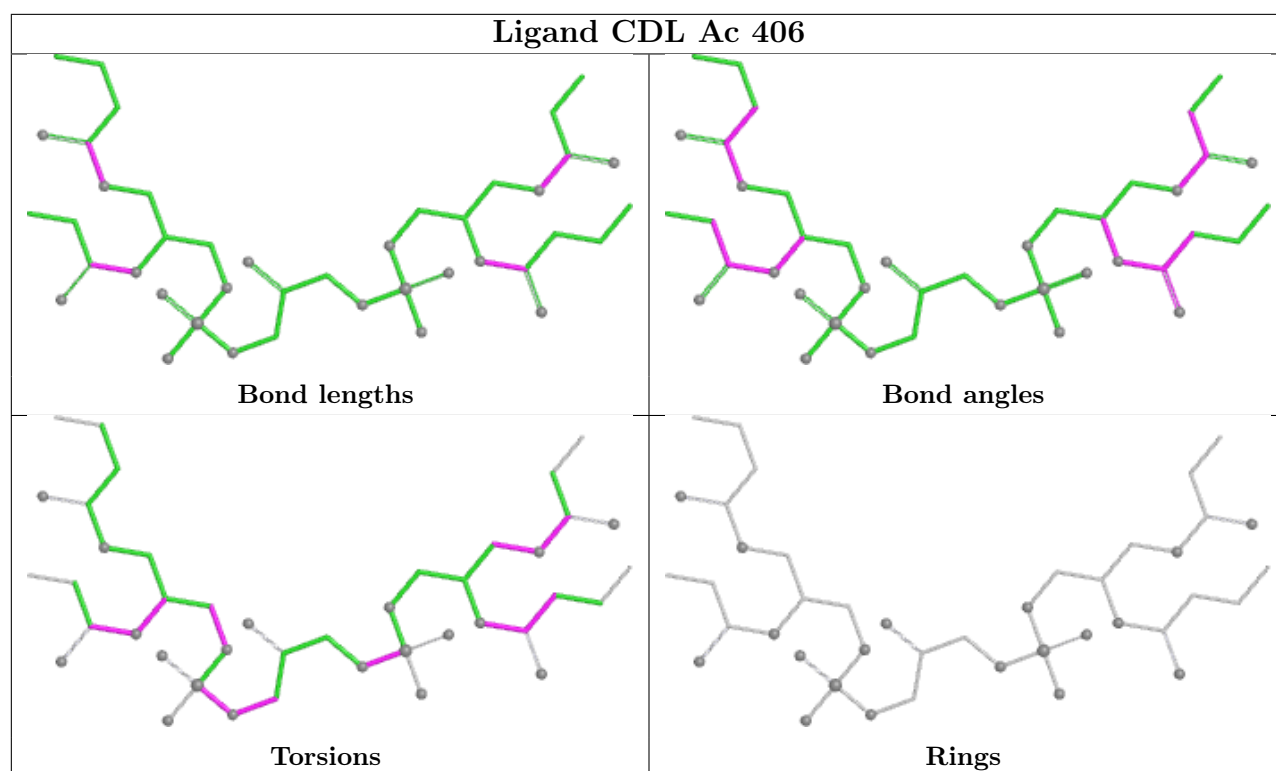
Bond angles

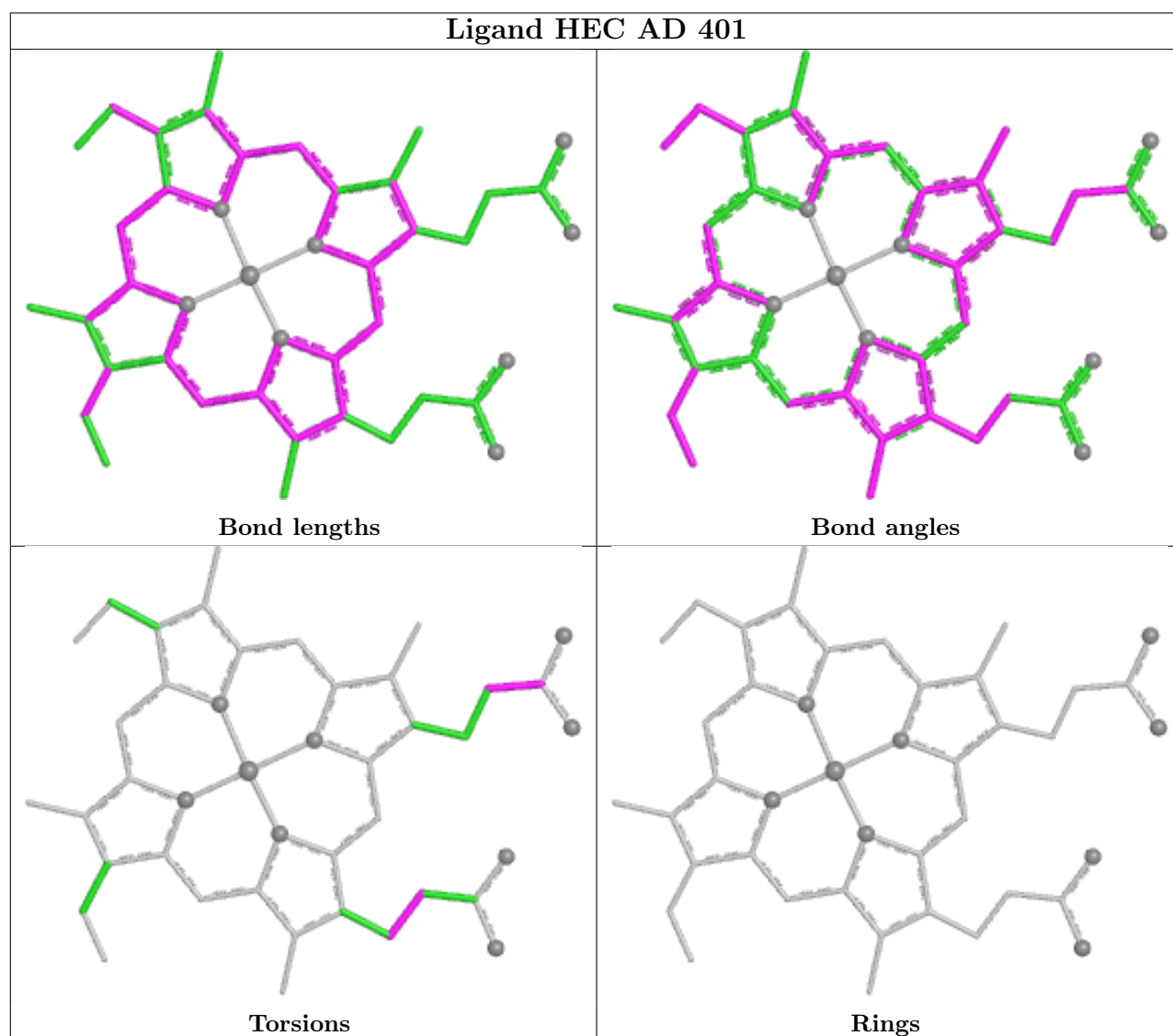
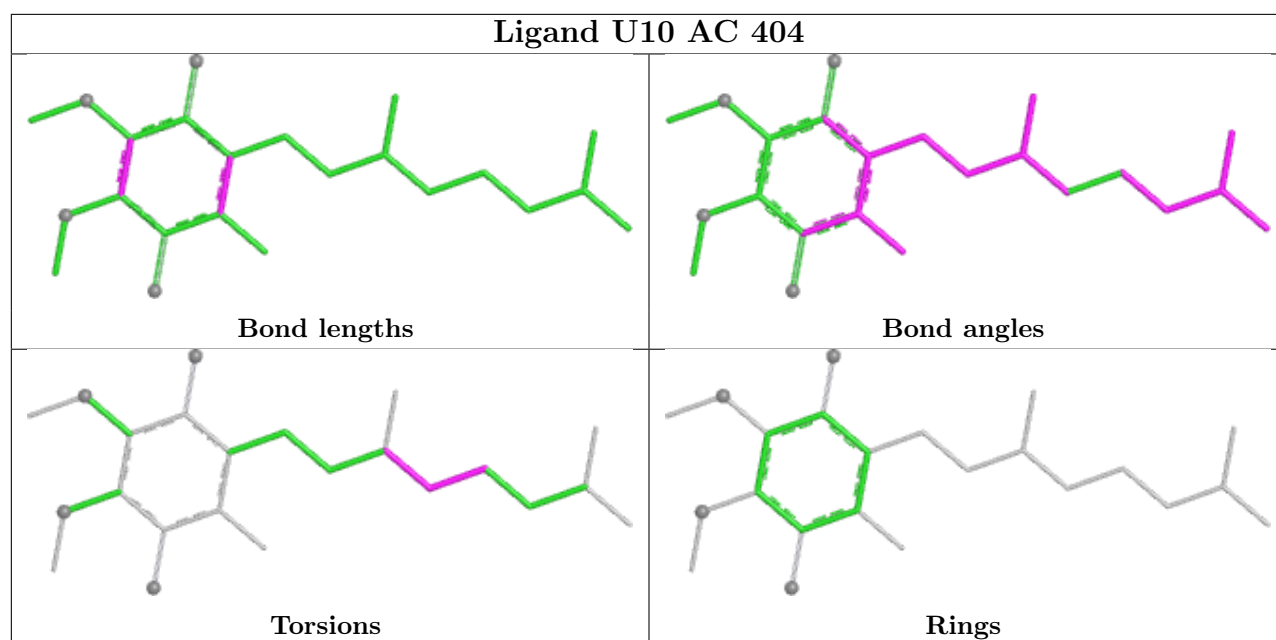


Torsions

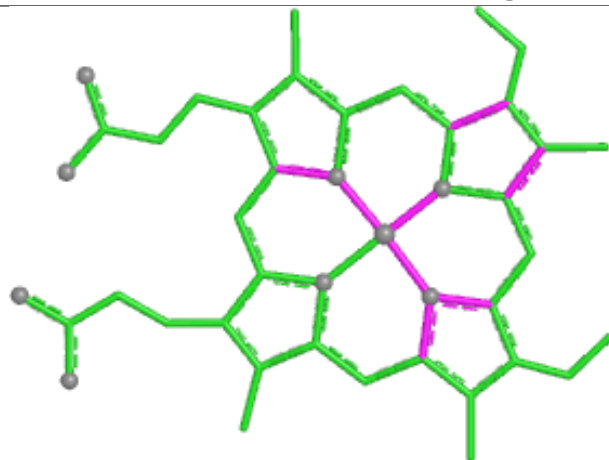


Rings

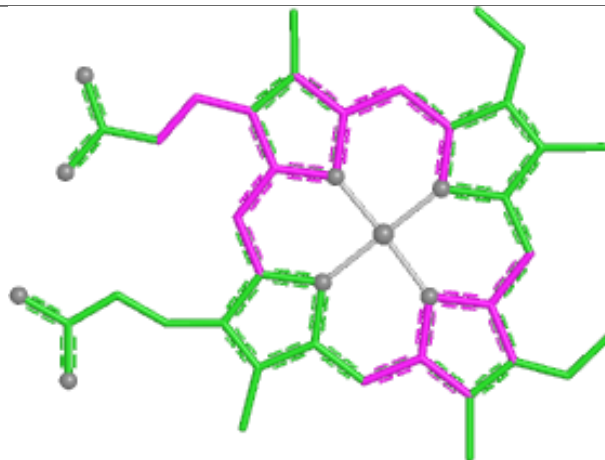




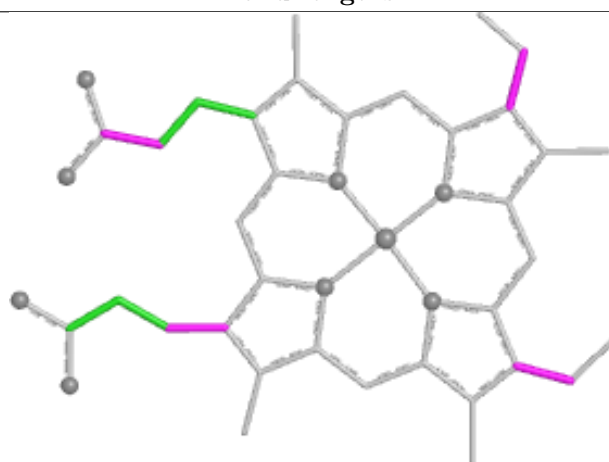
Ligand HEM Ac 402



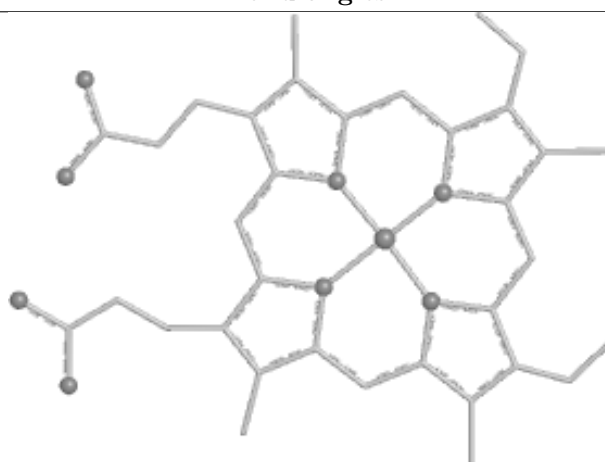
Bond lengths



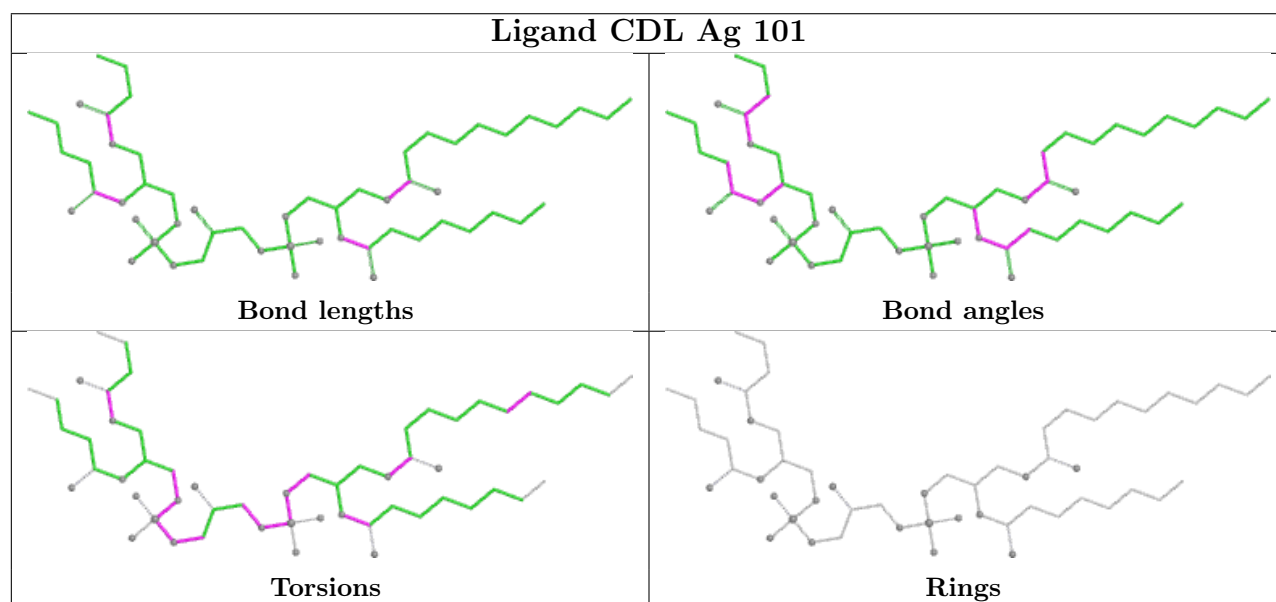
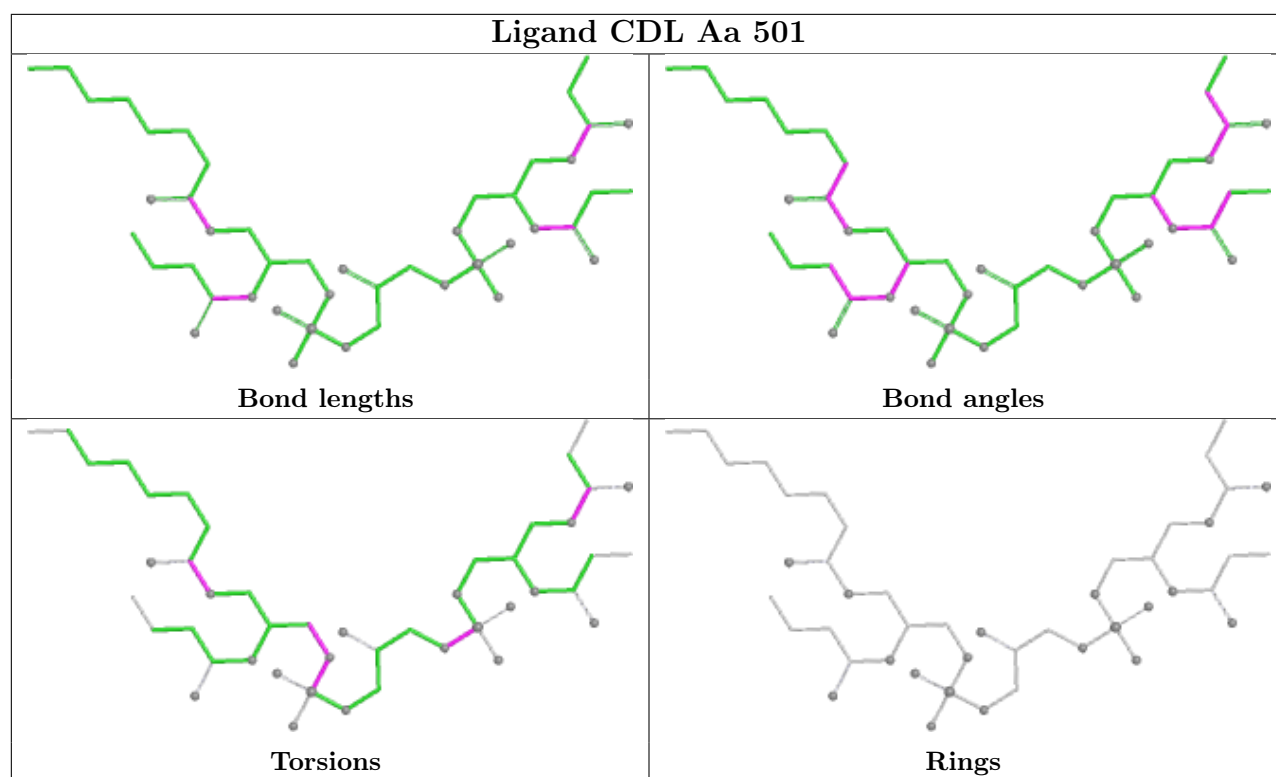
Bond angles



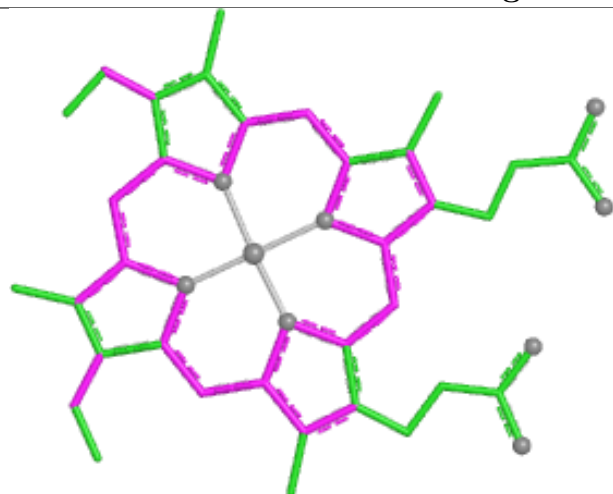
Torsions



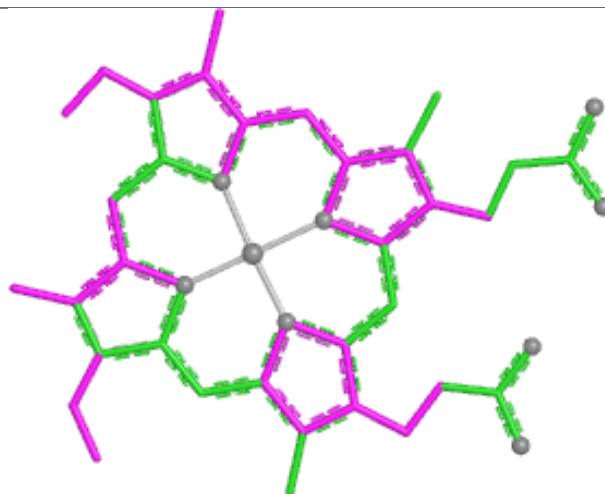
Rings



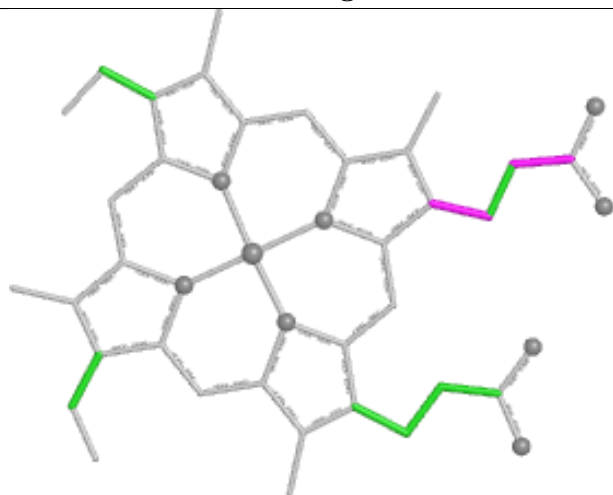
Ligand HEC Ad 401



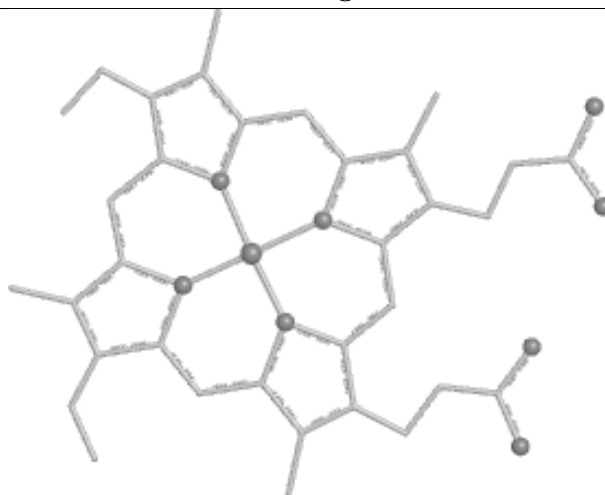
Bond lengths



Bond angles

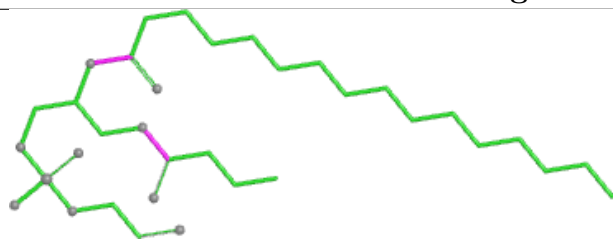


Torsions

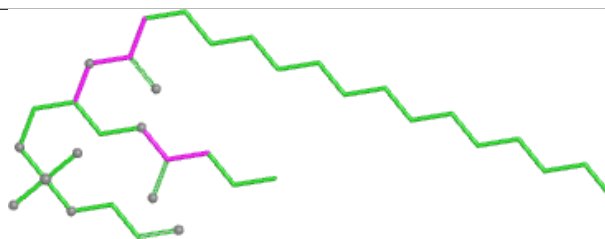


Rings

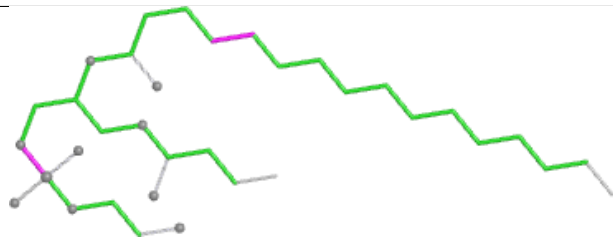
Ligand 3PE Ac 403



Bond lengths



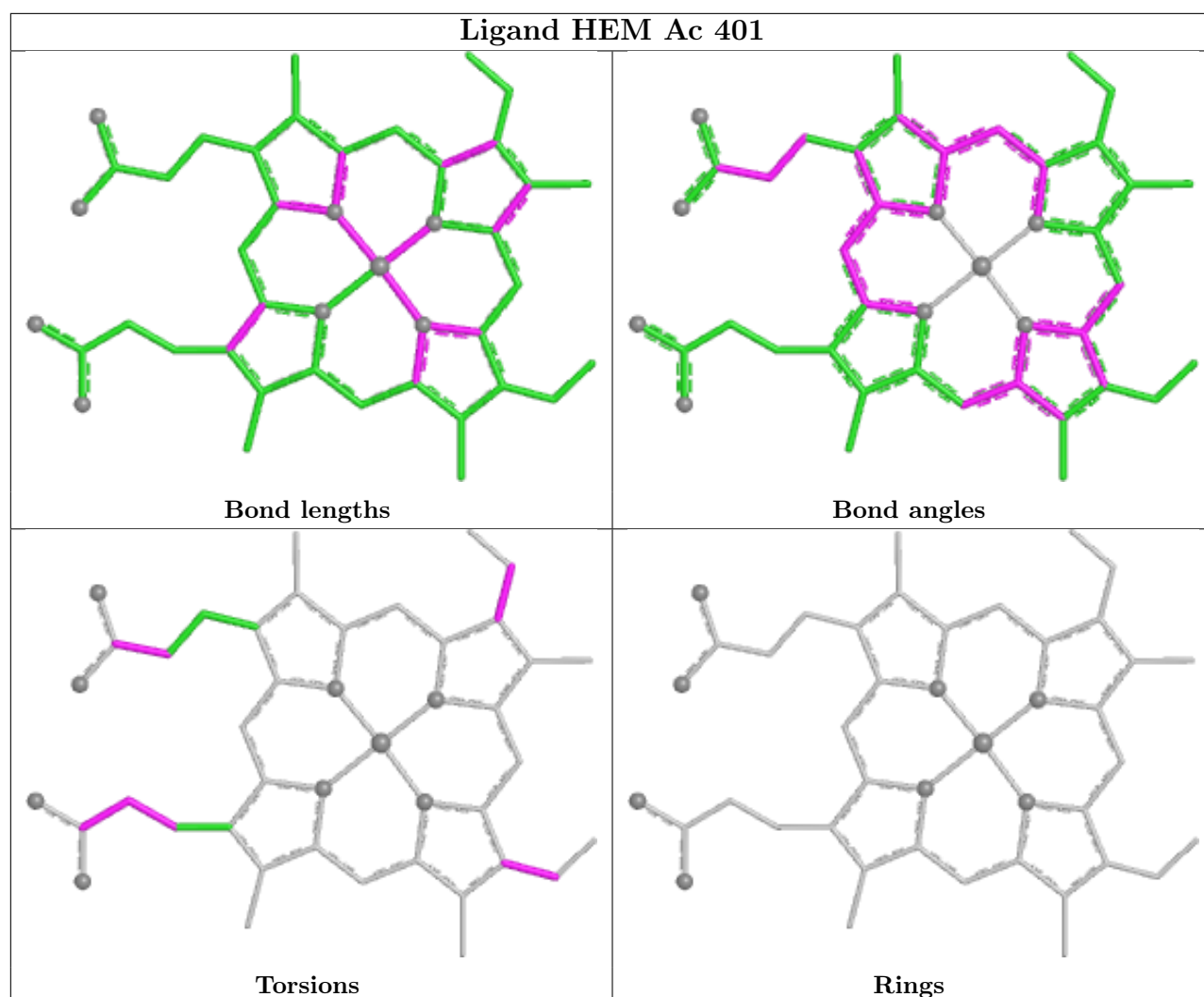
Bond angles



Torsions



Rings



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.

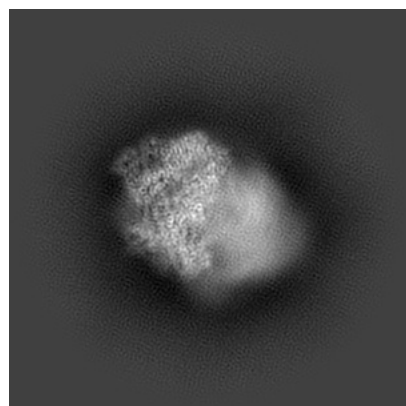
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35339. These allow visual inspection of the internal detail of the map and identification of artifacts.

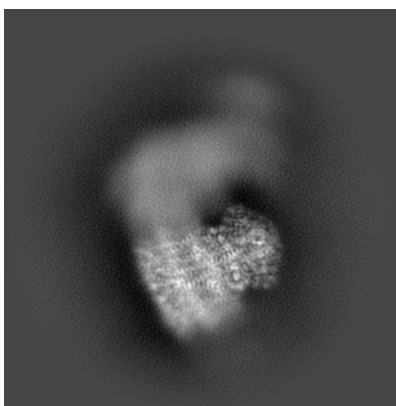
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

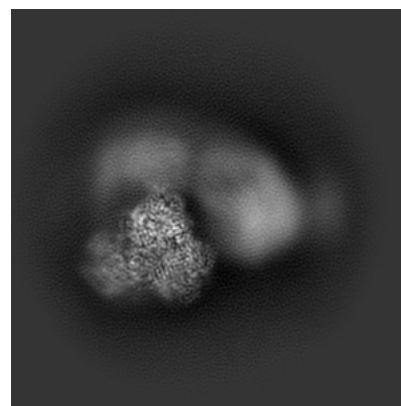
6.1.1 Primary map



X

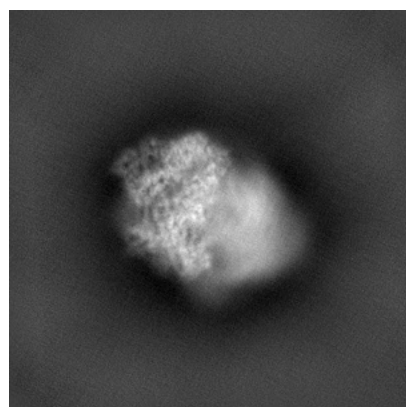


Y

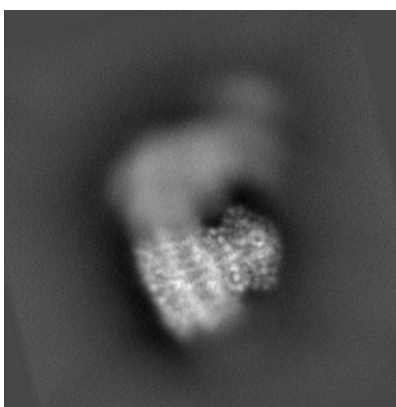


Z

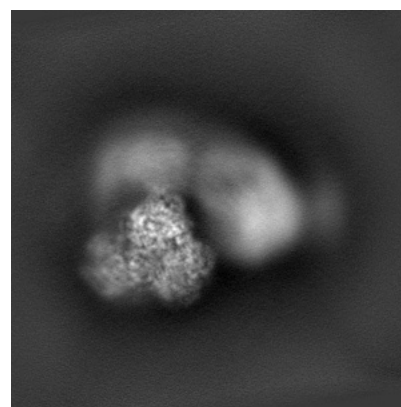
6.1.2 Raw map



X



Y

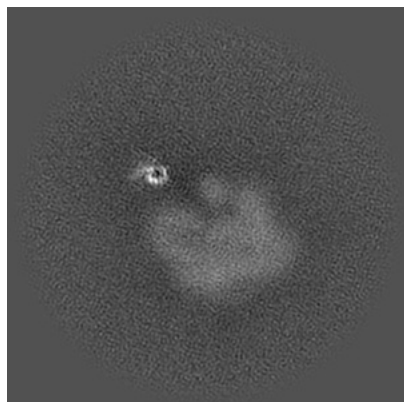


Z

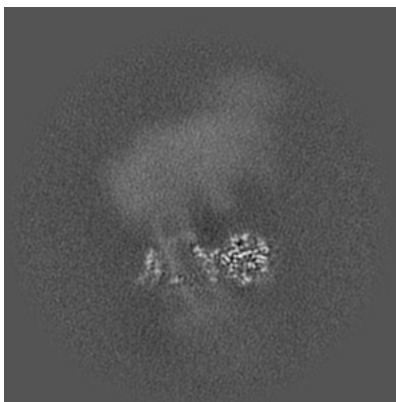
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

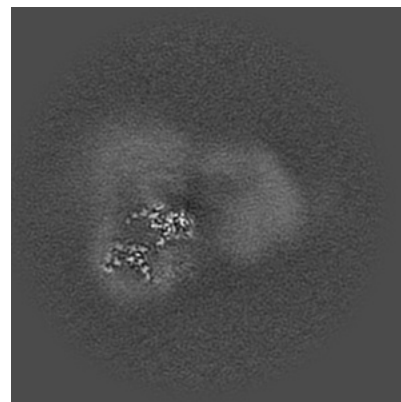
6.2.1 Primary map



X Index: 192

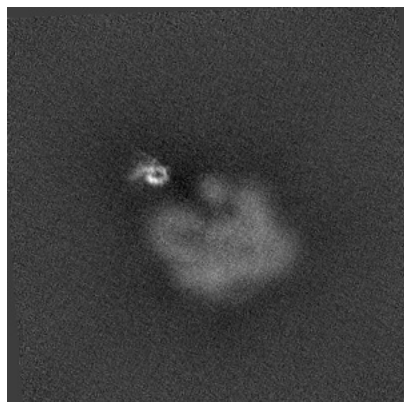


Y Index: 192

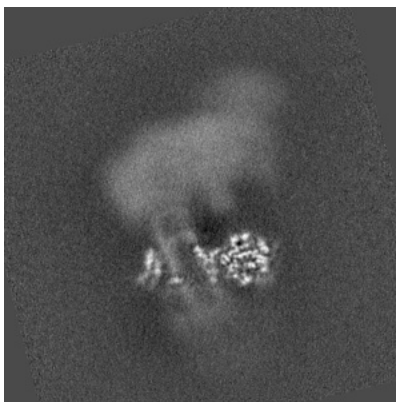


Z Index: 192

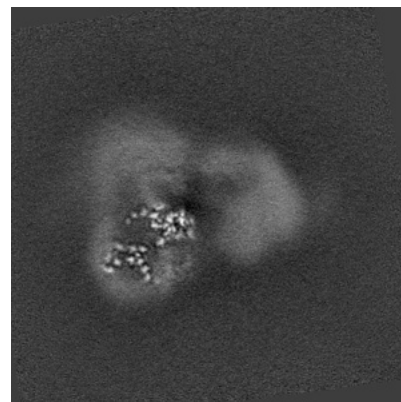
6.2.2 Raw map



X Index: 192



Y Index: 192

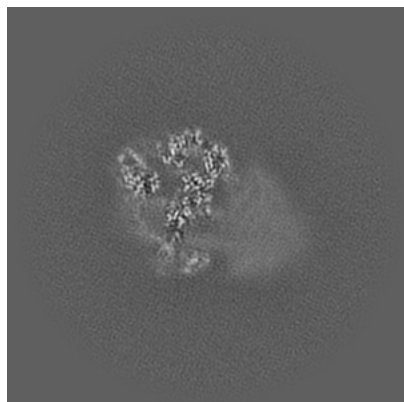


Z Index: 192

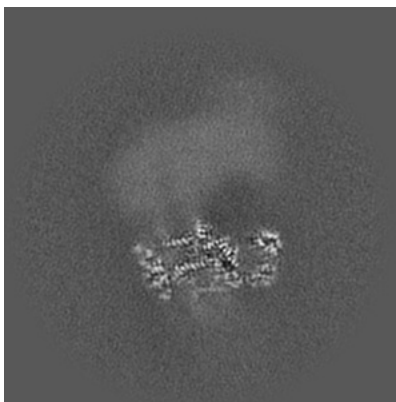
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

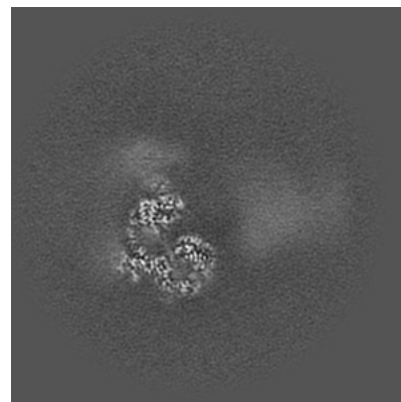
6.3.1 Primary map



X Index: 146

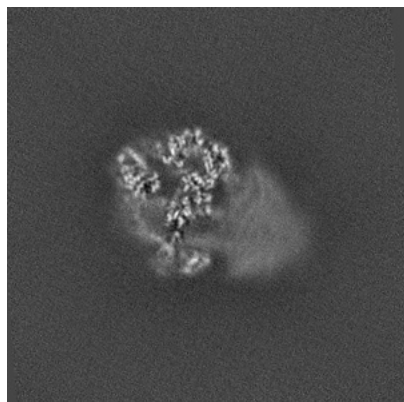


Y Index: 177

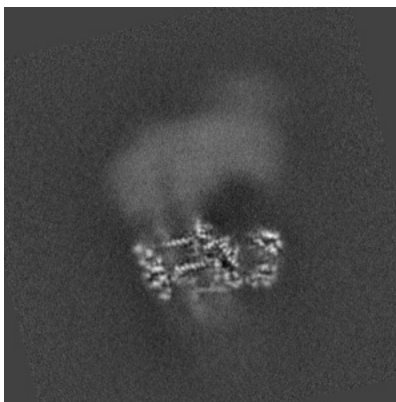


Z Index: 222

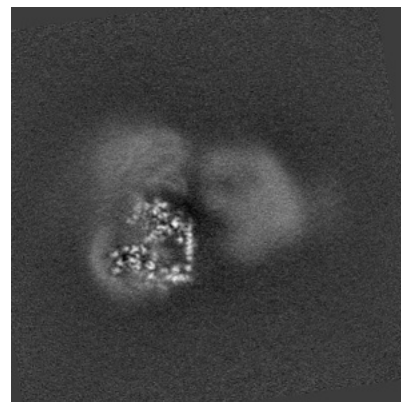
6.3.2 Raw map



X Index: 146



Y Index: 177

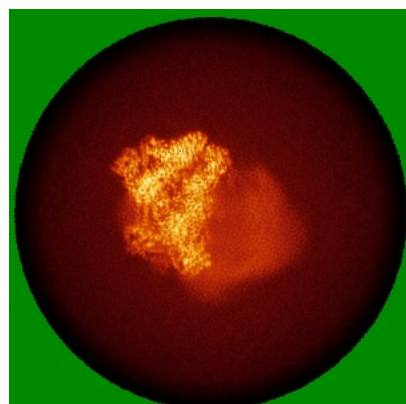


Z Index: 200

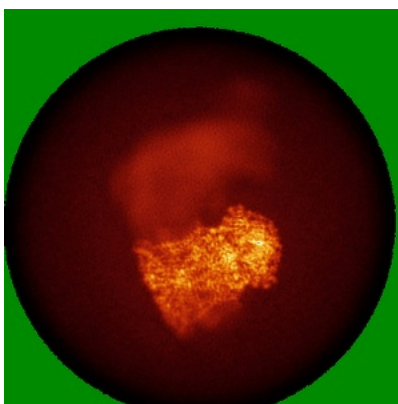
The images above show the largest variance slices of the map in three orthogonal directions.

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

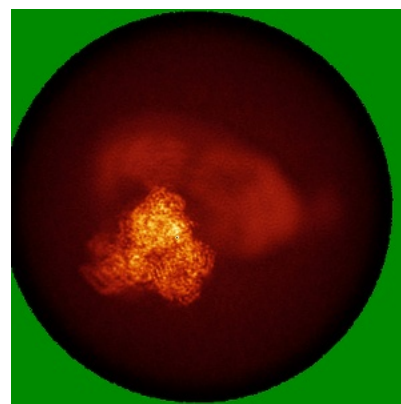
6.4.1 Primary map



X

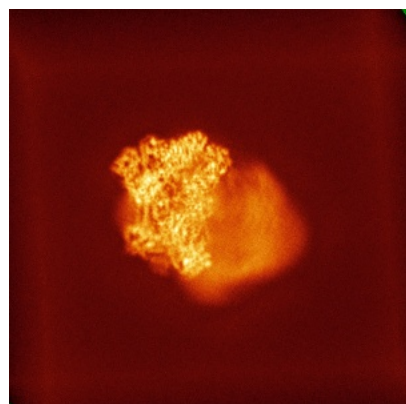


Y

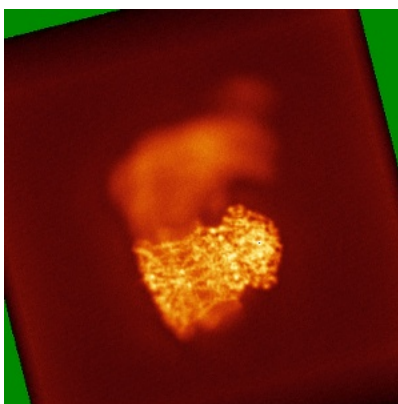


Z

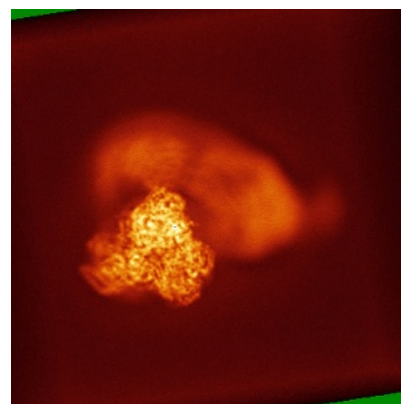
6.4.2 Raw map



X



Y

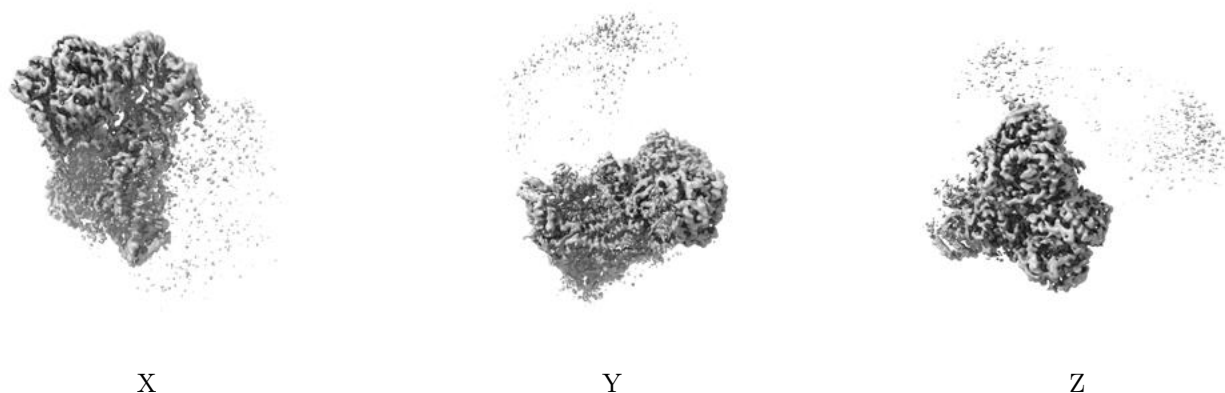


Z

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.

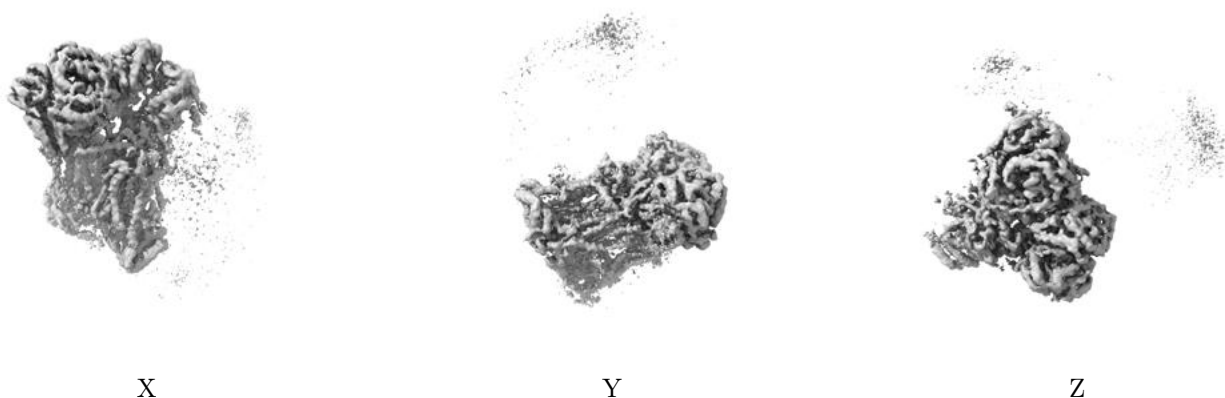
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. 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.

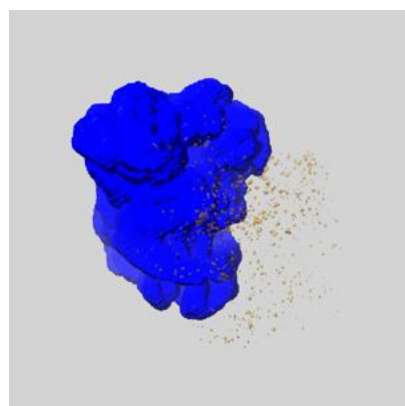
6.6 Mask visualisation [i](#)

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

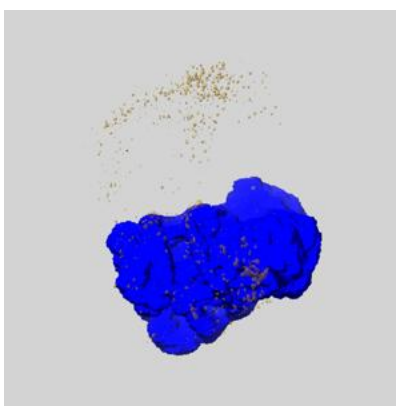
A mask typically either:

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

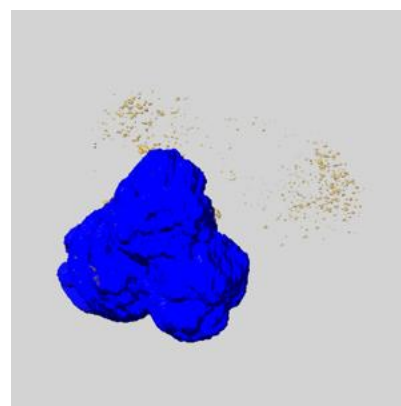
6.6.1 emd_35339_msk_1.map [i](#)



X



Y

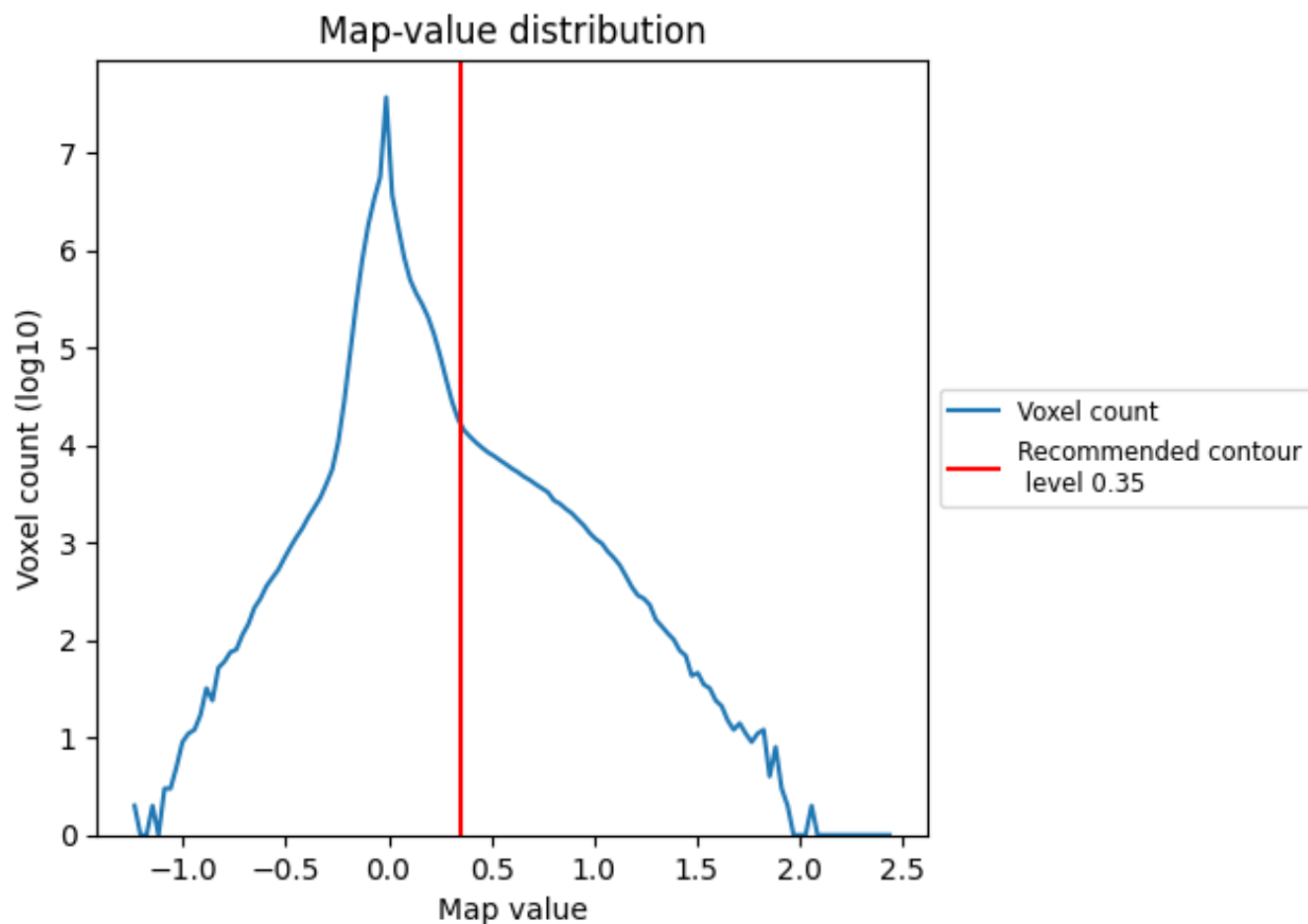


Z

7 Map analysis [i](#)

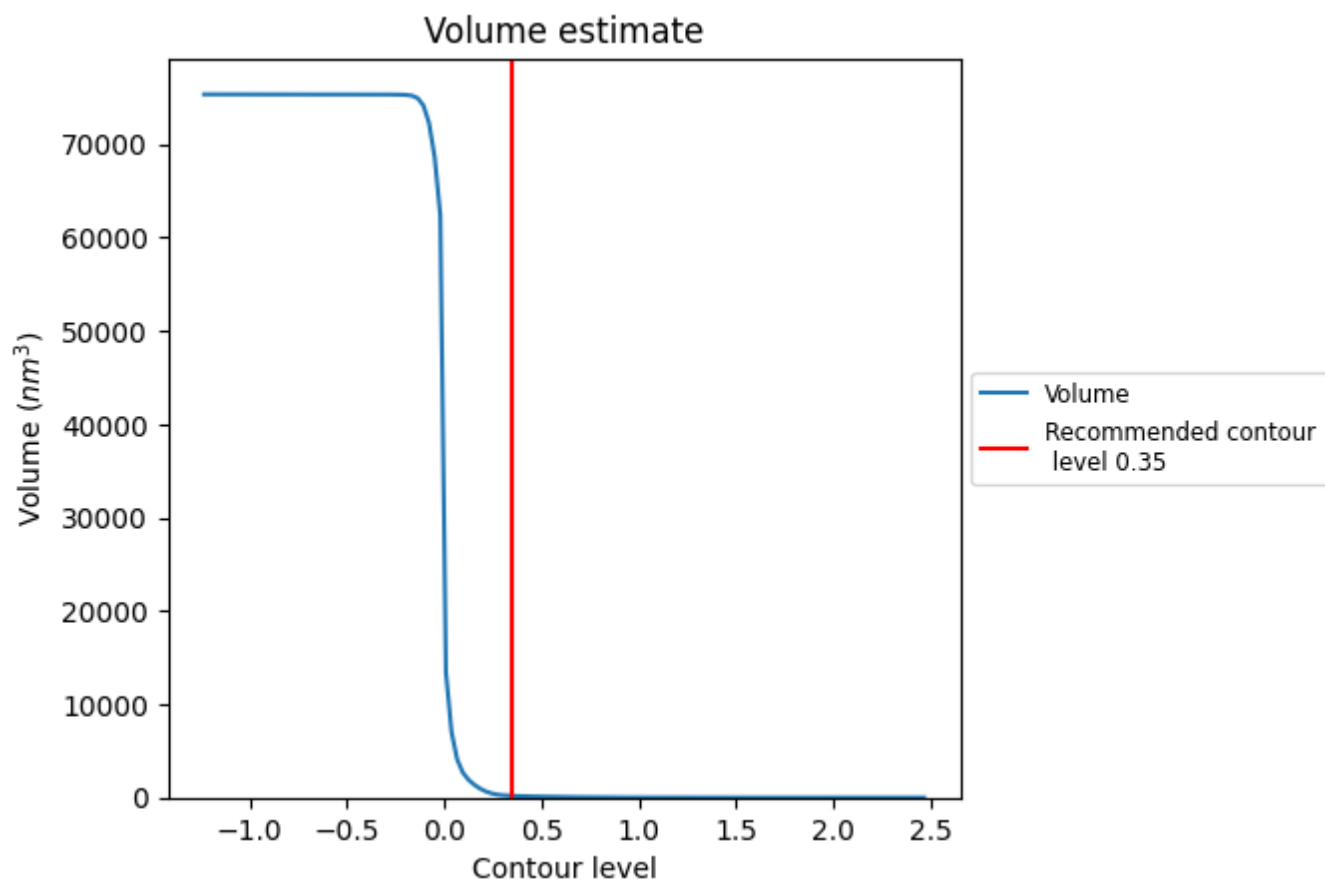
This section contains the results of statistical analysis of the map.

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.

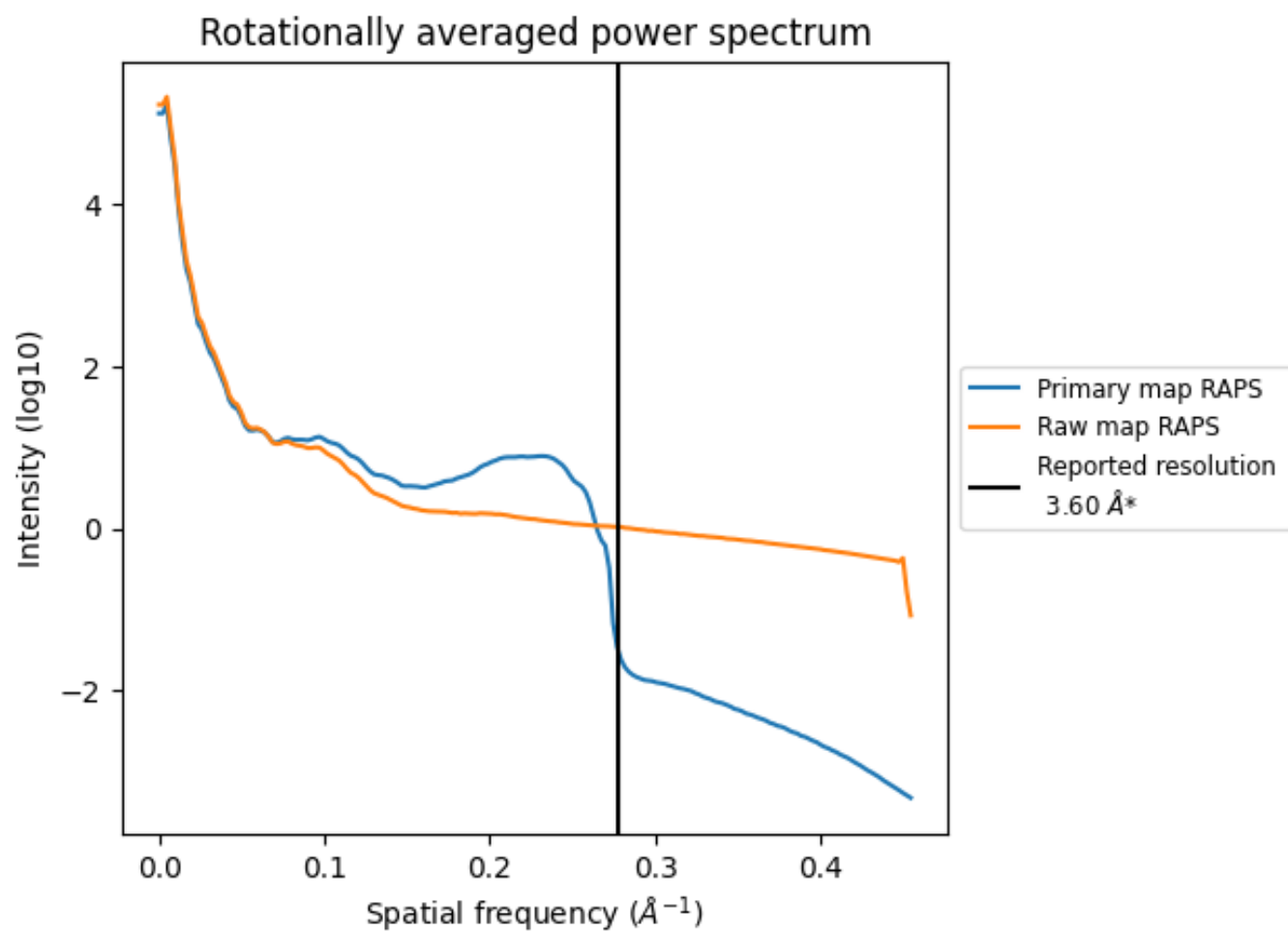
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 184 nm³; this corresponds to an approximate mass of 166 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 ⓘ

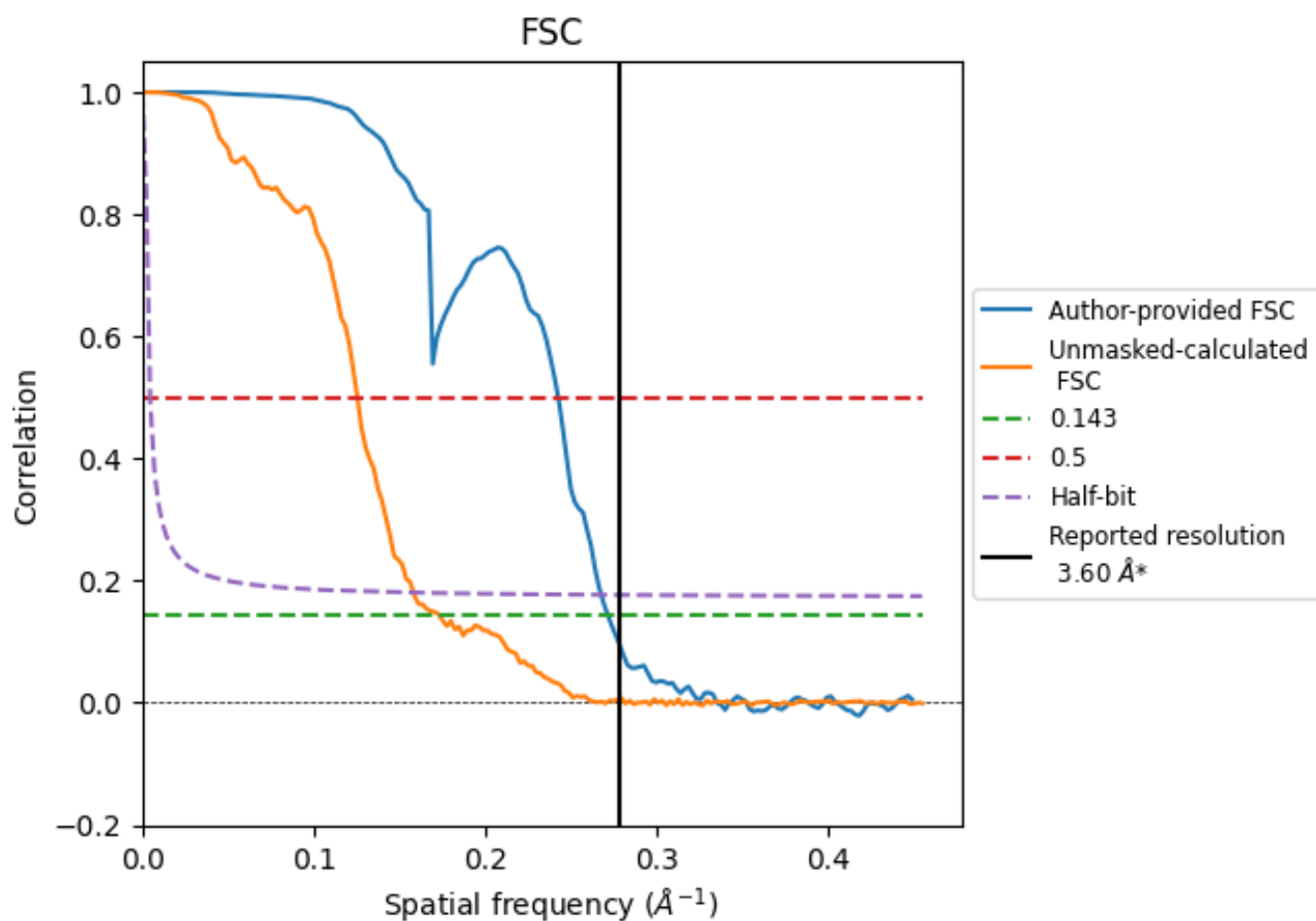


*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

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 $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

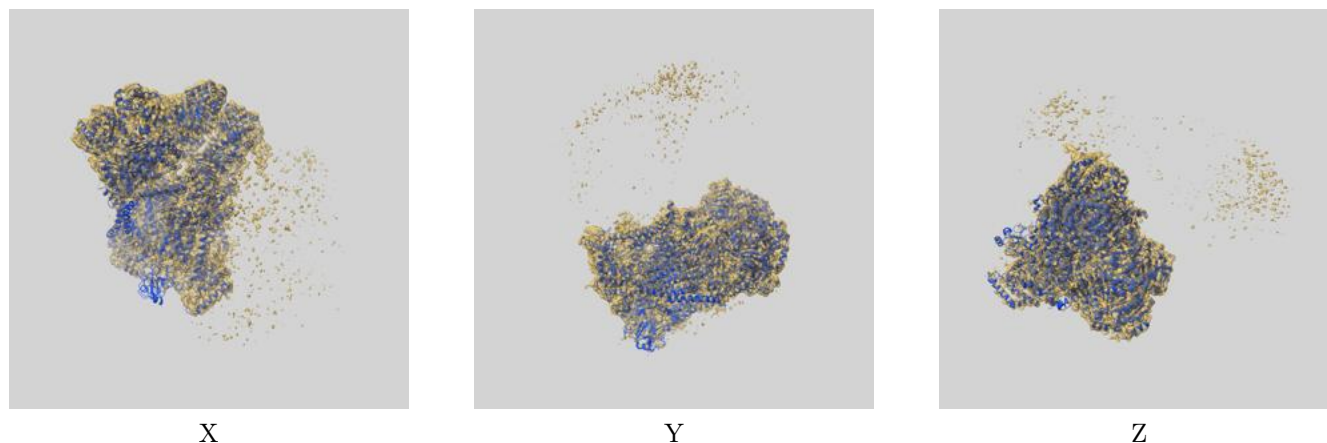
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.68	4.13	3.74
Unmasked-calculated*	5.77	7.97	6.33

*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 5.77 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

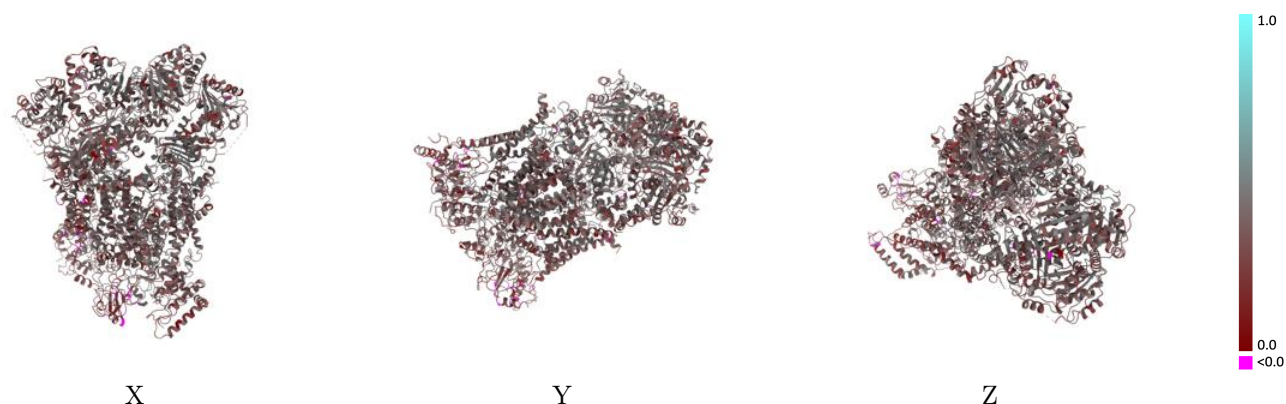
This section contains information regarding the fit between EMDB map EMD-35339 and PDB model 8IBC. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



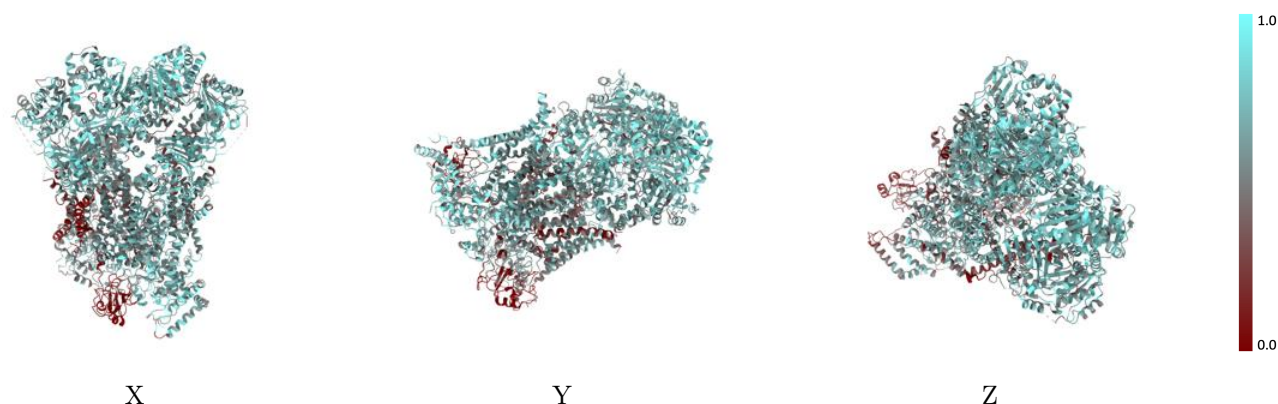
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



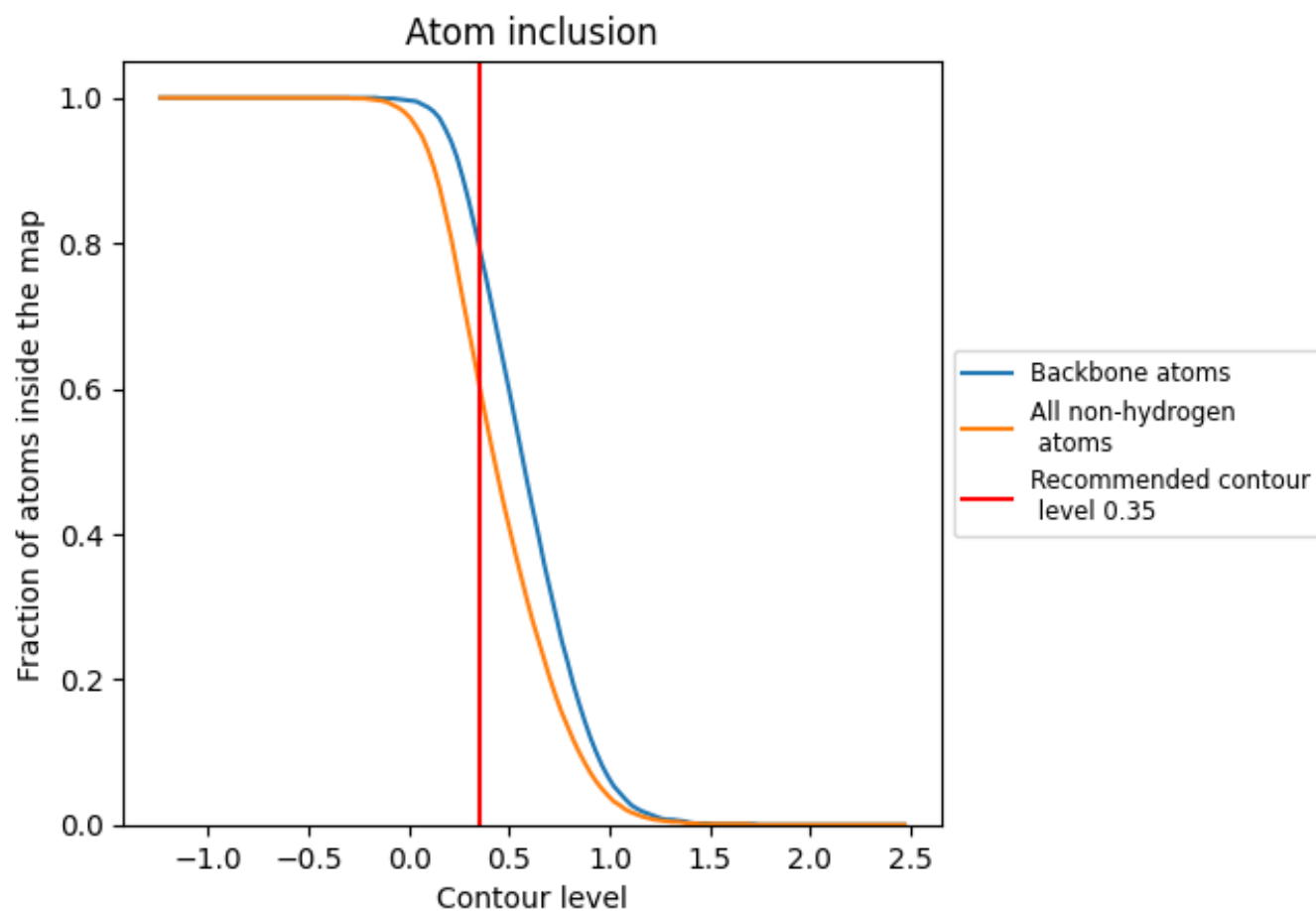
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 61% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6070	 0.3520
AA	 0.6840	 0.3640
AB	 0.6980	 0.3750
AC	 0.6010	 0.3510
AD	 0.6050	 0.3210
AE	 0.1820	 0.2700
AF	 0.6630	 0.3670
AG	 0.4890	 0.2910
AH	 0.4760	 0.2710
AI	 0.4430	 0.3720
AJ	 0.1100	 0.2680
AK	 0.0790	 0.2310
Aa	 0.7000	 0.3710
Ab	 0.7250	 0.3760
Ac	 0.6580	 0.3840
Ad	 0.7040	 0.3580
Ae	 0.3000	 0.2900
Af	 0.7040	 0.4130
Ag	 0.6610	 0.3730
Ah	 0.6540	 0.2950
Aj	 0.4930	 0.3430
Ak	 0.2600	 0.3220

