



wwPDB EM Validation Summary Report ⓘ

Apr 2, 2025 – 03:29 am BST

PDB ID : 7AJE / pdb_00007aje
EMDB ID : EMD-11431
Title : bovine ATP synthase dimer state2:state1
Authors : Spikes, T.E.; Montgomery, M.G.; Walker, J.E.
Deposited on : 2020-09-29
Resolution : 9.40 Å(reported)
Based on initial models : 6ZQM, 6ZPO

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:

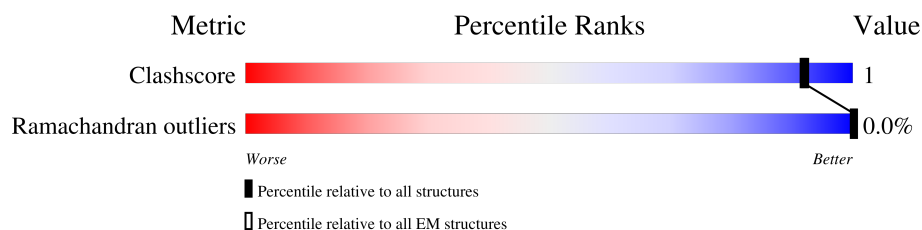
EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

1 Overall quality at a glance

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



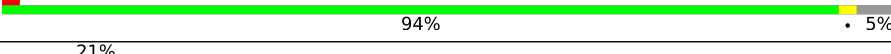
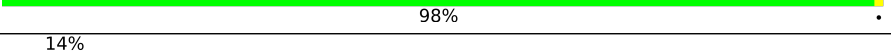
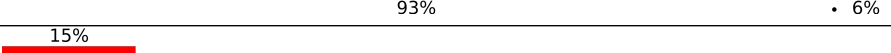
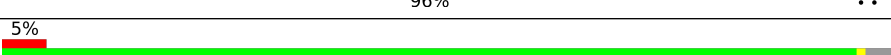
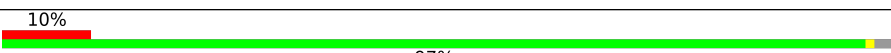
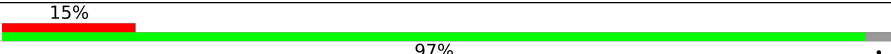

The reported resolution of this entry is 9.40 Å.

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

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	8	66	 55% 42%
1	A8	66	 62% 38%
2	A	510	 94% 5%
2	AA	510	 21% 98%
2	AB	510	 14% 93% 6%
2	AC	510	 15% 96%
2	B	510	 5% 96%
2	C	510	 10% 97%
3	AD	482	 15% 97%

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Mol	Chain	Length	Quality of chain
3	AE	482	16% 96% .
3	AF	482	13% 97% .
3	D	482	7% 97% .
3	E	482	6% 96% ..
3	F	482	5% 96% .
4	AG	273	8% 99% .
4	G	273	. 99% .
5	AH	146	6% 90% 10%
5	H	146	. 89% 10%
6	AI	50	24% 94% 6%
6	I	50	. 94% 6%
7	AJ	66	23% 71% 29%
7	J	66	8% 71% 29%
8	AK	75	21% 91% 8% .
8	AL	75	32% 92% 7% .
8	AM	75	24% 93% 7%
8	AN	75	9% 100%
8	AO	75	44% 100%
8	AP	75	25% 99% .
8	AQ	75	28% 97% .
8	AR	75	17% 93% 7%
8	K	75	. 73% 25% .
8	L	75	15% 88% 12%
8	M	75	9% 91% 8% .
8	N	75	5% 95% ..

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Mol	Chain	Length	Quality of chain
8	O	75	<div> <div>9%</div> <div>95%</div> <div>5%</div> </div>
8	P	75	<div> <div>9%</div> <div>92%</div> <div>7%</div> </div>
8	Q	75	<div> <div>7%</div> <div>93%</div> <div>5%</div> </div>
8	R	75	<div> <div>11%</div> <div>88%</div> <div>11%</div> </div>
9	AS	190	<div> <div>14%</div> <div>99%</div> <div>0%</div> </div>
9	S	190	<div> <div>6%</div> <div>99%</div> <div>0%</div> </div>
10	Aa	226	<div> <div>7%</div> <div>100%</div> <div>0%</div> </div>
10	a	226	<div> <div>7%</div> <div>100%</div> <div>0%</div> </div>
11	Ab	214	<div> <div>13%</div> <div>98%</div> <div>0%</div> </div>
11	b	214	<div> <div>6%</div> <div>98%</div> <div>0%</div> </div>
12	Ad	160	<div> <div>21%</div> <div>98%</div> <div>0%</div> </div>
12	d	160	<div> <div>9%</div> <div>96%</div> <div>0%</div> </div>
13	Ae	70	<div> <div>11%</div> <div>80%</div> <div>20%</div> </div>
13	e	70	<div> <div>0%</div> <div>80%</div> <div>20%</div> </div>
14	Af	87	<div> <div>13%</div> <div>95%</div> <div>5%</div> </div>
14	f	87	<div> <div>8%</div> <div>95%</div> <div>5%</div> </div>
15	Ag	102	<div> <div>6%</div> <div>77%</div> <div>23%</div> </div>
15	g	102	<div> <div>0%</div> <div>77%</div> <div>23%</div> </div>
16	Ah	76	<div> <div>33%</div> <div>82%</div> <div>18%</div> </div>
16	h	76	<div> <div>5%</div> <div>82%</div> <div>18%</div> </div>
17	Aj	60	<div> <div>5%</div> <div>80%</div> <div>20%</div> </div>
17	j	60	<div> <div>5%</div> <div>80%</div> <div>20%</div> </div>
18	Ak	57	<div> <div>14%</div> <div>63%</div> <div>37%</div> </div>
18	k	57	<div> <div>11%</div> <div>63%</div> <div>37%</div> </div>

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 51374 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 ATP synthase protein 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	8	38	Total	C	N	O	0	0
			190	114	38	38		
1	A8	41	Total	C	N	O	0	0
			205	123	41	41		

- Molecule 2 is a protein called ATP synthase subunit alpha, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A	486	Total	C	N	O	0	0
			2383	1411	486	486		
2	B	495	Total	C	N	O	0	0
			2428	1438	495	495		
2	C	501	Total	C	N	O	0	0
			2457	1455	501	501		
2	AA	508	Total	C	N	O	0	0
			2491	1475	508	508		
2	AB	477	Total	C	N	O	0	0
			2339	1385	477	477		
2	AC	498	Total	C	N	O	0	0
			2443	1447	498	498		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLU	GLN	variant	UNP P19483
A	481	GLY	SER	microheterogeneity	UNP P19483
B	1	GLU	GLN	variant	UNP P19483
B	481	GLY	SER	microheterogeneity	UNP P19483
C	1	GLU	GLN	variant	UNP P19483
C	481	GLY	SER	microheterogeneity	UNP P19483
AA	1	GLU	GLN	variant	UNP P19483
AA	481	GLY	SER	microheterogeneity	UNP P19483
AB	1	GLU	GLN	variant	UNP P19483

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Chain	Residue	Modelled	Actual	Comment	Reference
AB	481	GLY	SER	microheterogeneity	UNP P19483
AC	1	GLU	GLN	variant	UNP P19483
AC	481	GLY	SER	microheterogeneity	UNP P19483

- Molecule 3 is a protein called ATP synthase subunit beta, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	469	Total	C	N	O	0	0
			2300	1362	469	469		
3	E	467	Total	C	N	O	0	0
			2290	1356	467	467		
3	F	467	Total	C	N	O	0	0
			2290	1356	467	467		
3	AD	469	Total	C	N	O	0	0
			2300	1362	469	469		
3	AE	467	Total	C	N	O	0	0
			2290	1356	467	467		
3	AF	467	Total	C	N	O	0	0
			2290	1356	467	467		

- Molecule 4 is a protein called ATP synthase subunit gamma, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	272	Total	C	N	O	0	0
			1347	803	272	272		
4	AG	272	Total	C	N	O	0	0
			1347	803	272	272		

- Molecule 5 is a protein called ATP synthase subunit delta, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	132	Total	C	N	O	0	0
			653	389	132	132		
5	AH	132	Total	C	N	O	0	0
			653	389	132	132		

- Molecule 6 is a protein called ATP synthase subunit epsilon, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	47	Total	C	N	O	0	0
			233	139	47	47		

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	AI	47	Total	C	N	O	0	0
			233	139	47	47		

- Molecule 7 is a protein called ATPase inhibitor, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	J	47	Total	C	N	O	0	0
			231	137	47	47		
7	AJ	47	Total	C	N	O	0	0
			231	137	47	47		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	61	HIS	-	expression tag	UNP P01096
J	62	HIS	-	expression tag	UNP P01096
J	63	HIS	-	expression tag	UNP P01096
J	64	HIS	-	expression tag	UNP P01096
J	65	HIS	-	expression tag	UNP P01096
J	66	HIS	-	expression tag	UNP P01096
AJ	61	HIS	-	expression tag	UNP P01096
AJ	62	HIS	-	expression tag	UNP P01096
AJ	63	HIS	-	expression tag	UNP P01096
AJ	64	HIS	-	expression tag	UNP P01096
AJ	65	HIS	-	expression tag	UNP P01096
AJ	66	HIS	-	expression tag	UNP P01096

- Molecule 8 is a protein called ATP synthase F(0) complex subunit C2, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	K	74	Total	C	N	O	0	0
			359	211	74	74		
8	L	75	Total	C	N	O	0	0
			364	214	75	75		
8	M	74	Total	C	N	O	0	0
			359	211	74	74		
8	N	74	Total	C	N	O	0	0
			359	211	74	74		
8	O	74	Total	C	N	O	0	0
			359	211	74	74		
8	P	74	Total	C	N	O	0	0
			359	211	74	74		

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Mol	Chain	Residues	Atoms				AltConf	Trace
8	Q	74	Total	C	N	O	0	0
			359	211	74	74		
8	R	74	Total	C	N	O	0	0
			359	211	74	74		
8	AK	74	Total	C	N	O	0	0
			359	211	74	74		
8	AL	74	Total	C	N	O	0	0
			359	211	74	74		
8	AM	75	Total	C	N	O	0	0
			364	214	75	75		
8	AN	75	Total	C	N	O	0	0
			364	214	75	75		
8	AO	75	Total	C	N	O	0	0
			364	214	75	75		
8	AP	74	Total	C	N	O	0	0
			359	211	74	74		
8	AQ	75	Total	C	N	O	0	0
			364	214	75	75		
8	AR	75	Total	C	N	O	0	0
			364	214	75	75		

- Molecule 9 is a protein called ATP synthase subunit O, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	S	188	Total	C	N	O	0	0
			931	555	188	188		
9	AS	188	Total	C	N	O	0	0
			931	555	188	188		

- Molecule 10 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	a	226	Total	C	N	O	0	0
			1119	667	226	226		
10	Aa	226	Total	C	N	O	0	0
			1119	667	226	226		

- Molecule 11 is a protein called ATP synthase F(0) complex subunit B1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	b	209	Total	C	N	O	0	0
			1035	617	209	209		

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Mol	Chain	Residues	Atoms				AltConf	Trace
11	Ab	209	Total	C	N	O	0	0
			1035	617	209	209		

- Molecule 12 is a protein called ATP synthase subunit d, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	d	154	Total	C	N	O	0	0
			768	460	154	154		
12	Ad	156	Total	C	N	O	0	0
			778	466	156	156		

- Molecule 13 is a protein called ATP synthase subunit e, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	e	56	Total	C	N	O	0	0
			277	165	56	56		
13	Ae	56	Total	C	N	O	0	0
			277	165	56	56		

- Molecule 14 is a protein called ATP synthase subunit f, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	f	83	Total	C	N	O	0	0
			409	243	83	83		
14	Af	83	Total	C	N	O	0	0
			409	243	83	83		

- Molecule 15 is a protein called ATP synthase subunit g, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	g	79	Total	C	N	O	0	0
			390	232	79	79		
15	Ag	79	Total	C	N	O	0	0
			390	232	79	79		

- Molecule 16 is a protein called ATP synthase-coupling factor 6, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	h	62	Total	C	N	O	0	0
			306	182	62	62		
16	Ah	62	Total	C	N	O	0	0
			306	182	62	62		

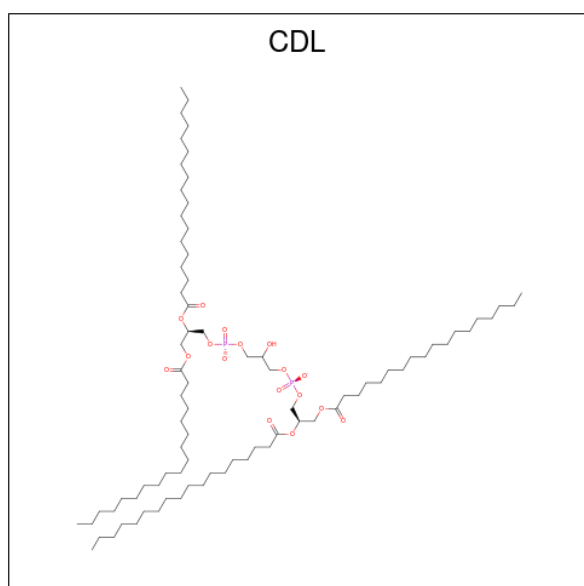
- Molecule 17 is a protein called ATP synthase subunit ATP5MPL, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	j	48	Total	C	N	O	0	0
			238	142	48	48		
17	Aj	48	Total	C	N	O	0	0
			238	142	48	48		

- Molecule 18 is a protein called ATP synthase membrane subunit DAPIT, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	36	Total	C	N	O	0	0
			177	105	36	36		
18	Ak	36	Total	C	N	O	0	0
			177	105	36	36		

- Molecule 19 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



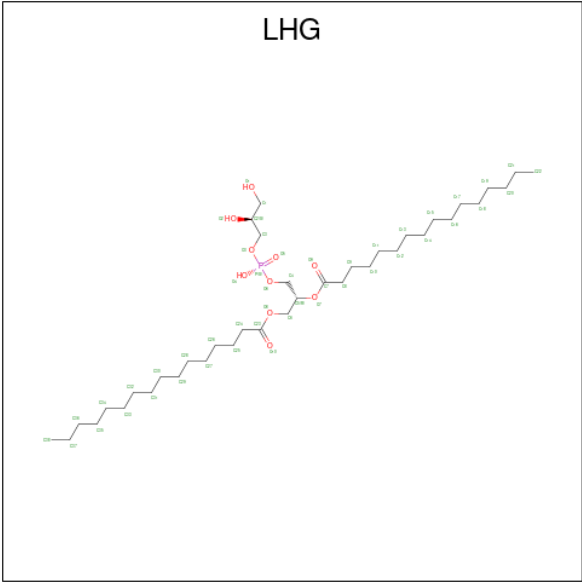
Mol	Chain	Residues	Atoms				AltConf
19	a	1	Total	C	O	P	0
			84	65	17	2	
19	f	1	Total	C	O	P	0
			83	64	17	2	
19	f	1	Total	C	O	P	0
			78	59	17	2	
19	Aa	1	Total	C	O	P	0
			84	65	17	2	
19	Ab	1	Total	C	O	P	0
			83	64	17	2	

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Mol	Chain	Residues	Atoms				AltConf
19	Af	1	Total	C	O	P	0
			78	59	17	2	

- Molecule 20 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: C₃₈H₇₅O₁₀P).

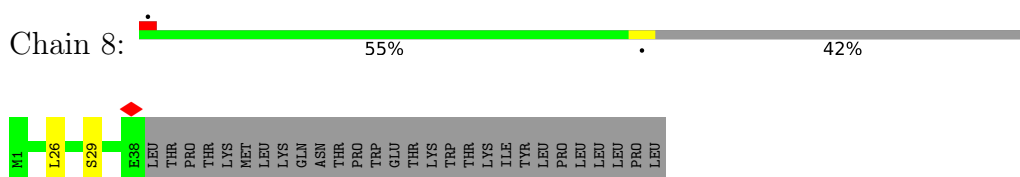


Mol	Chain	Residues	Atoms				AltConf
20	f	1	Total	C	O	P	0
			49	38	10	1	
20	f	1	Total	C	O	P	0
			39	28	10	1	
20	Af	1	Total	C	O	P	0
			39	28	10	1	
20	Af	1	Total	C	O	P	0
			49	38	10	1	

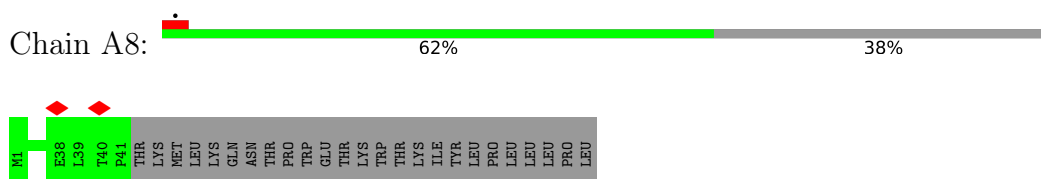
3 Residue-property plots [i](#)

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

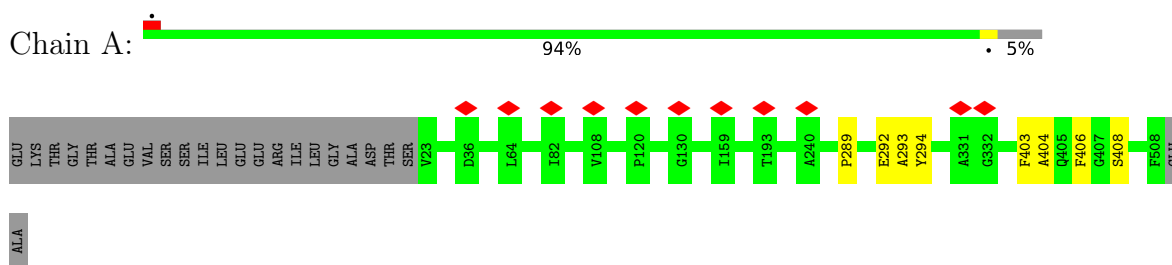
- Molecule 1: ATP synthase protein 8



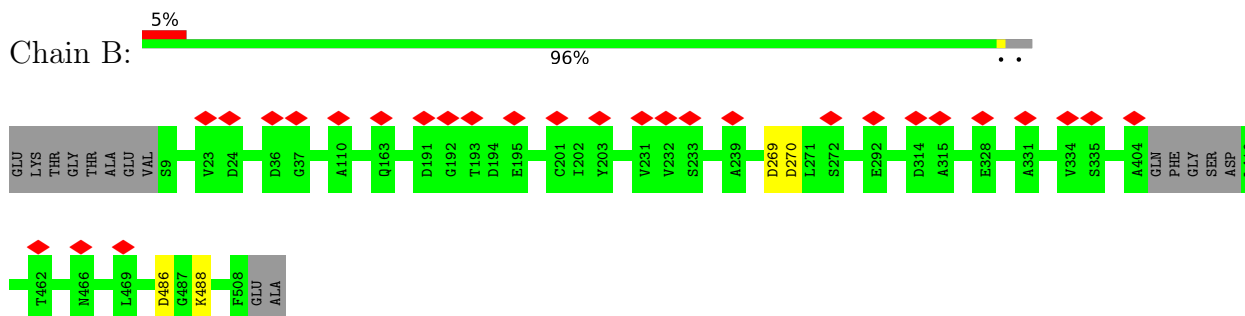
- Molecule 1: ATP synthase protein 8



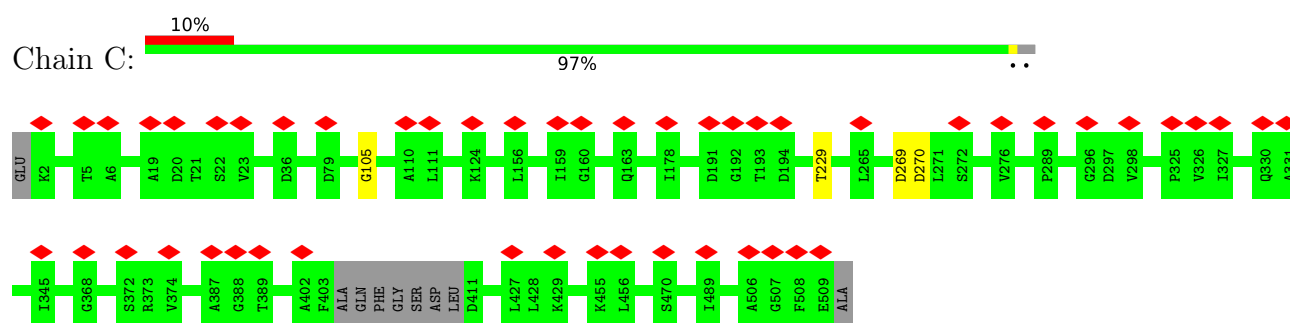
- Molecule 2: ATP synthase subunit alpha, mitochondrial



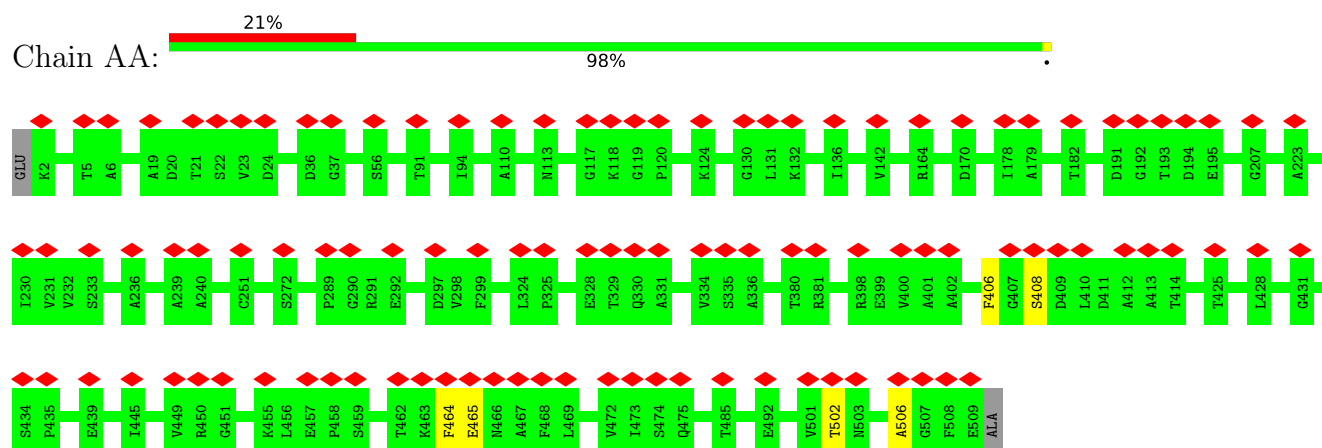
- Molecule 2: ATP synthase subunit alpha, mitochondrial



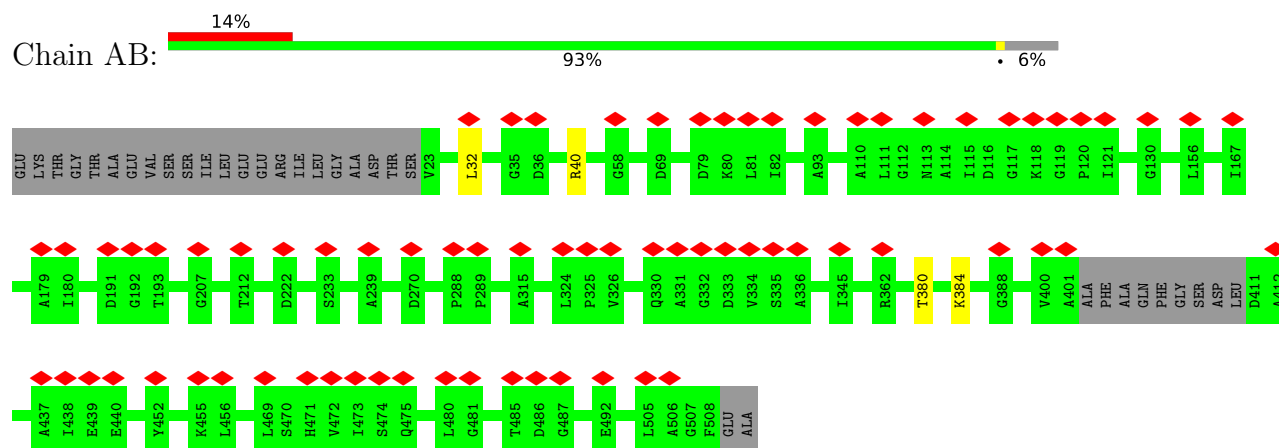
- Molecule 2: ATP synthase subunit alpha, mitochondrial



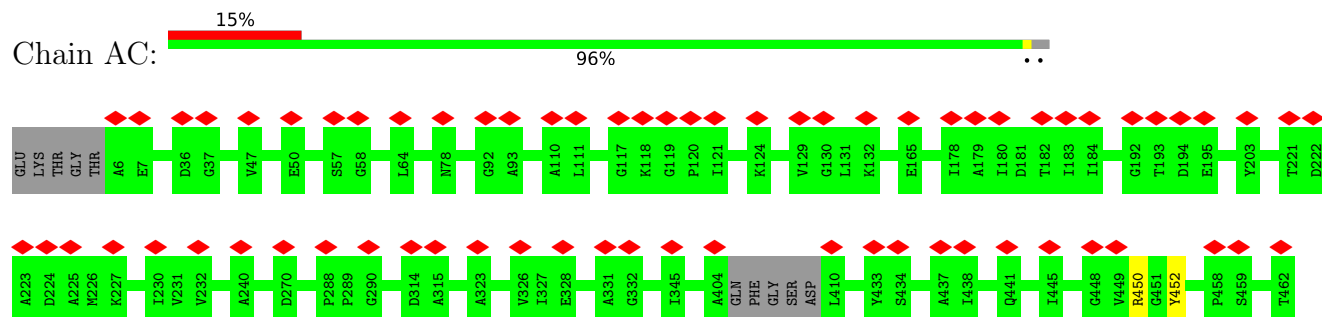
- Molecule 2: ATP synthase subunit alpha, mitochondrial

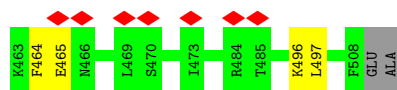


- Molecule 2: ATP synthase subunit alpha, mitochondrial



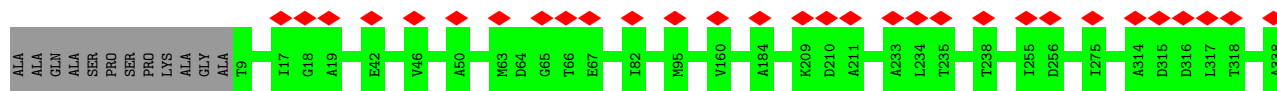
- Molecule 2: ATP synthase subunit alpha, mitochondrial





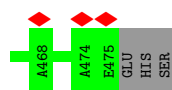
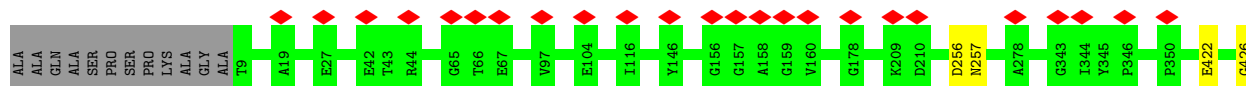
- Molecule 3: ATP synthase subunit beta, mitochondrial

Chain D: 7% 97%



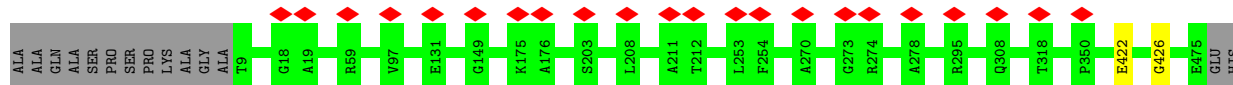
- Molecule 3: ATP synthase subunit beta, mitochondrial

Chain E: 6% 96%



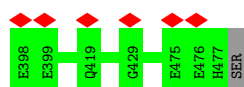
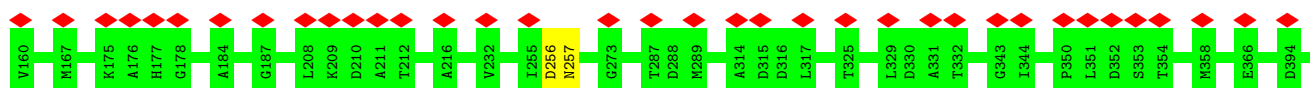
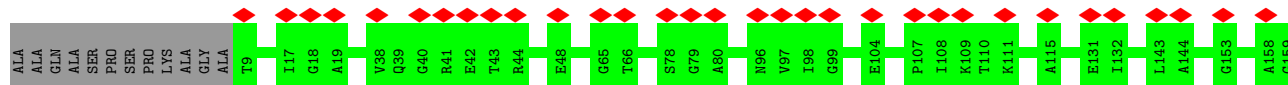
- Molecule 3: ATP synthase subunit beta, mitochondrial

Chain F: 5% 96%

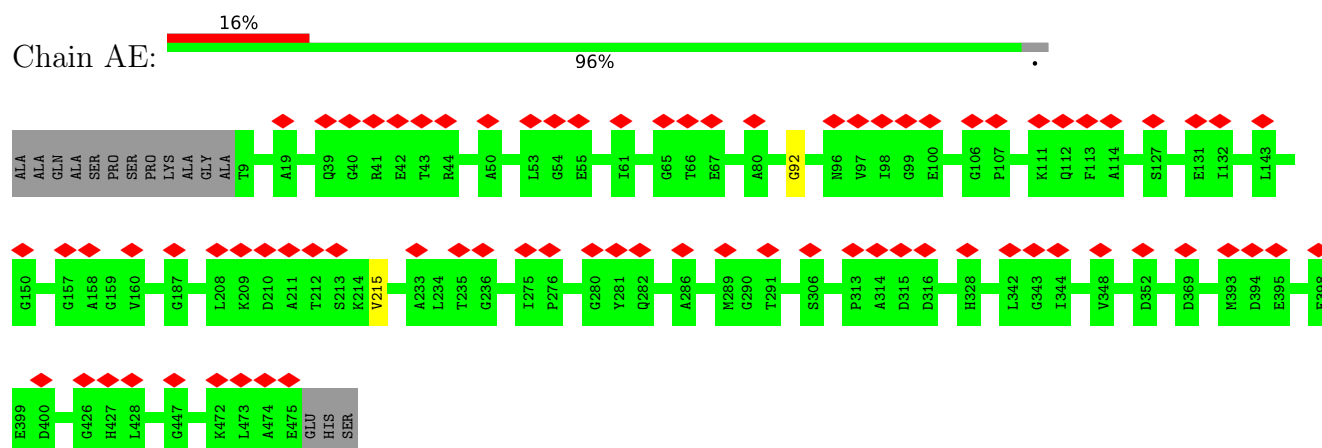


- Molecule 3: ATP synthase subunit beta, mitochondrial

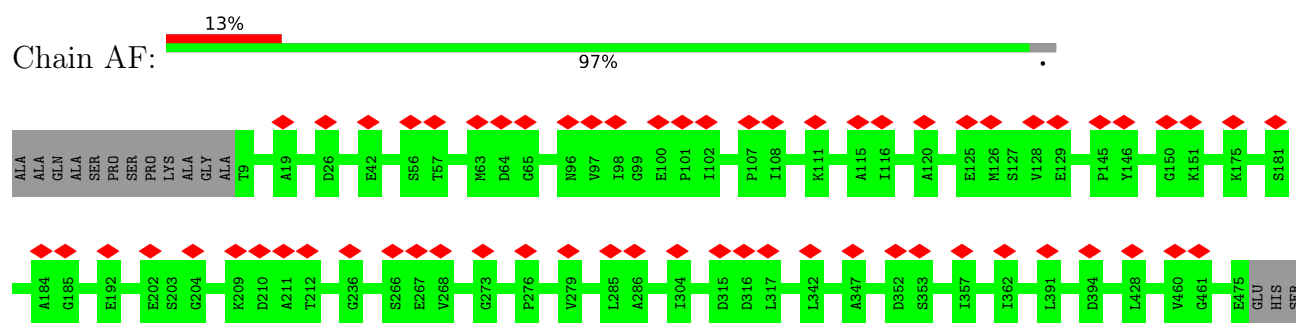
Chain AD: 15% 97%



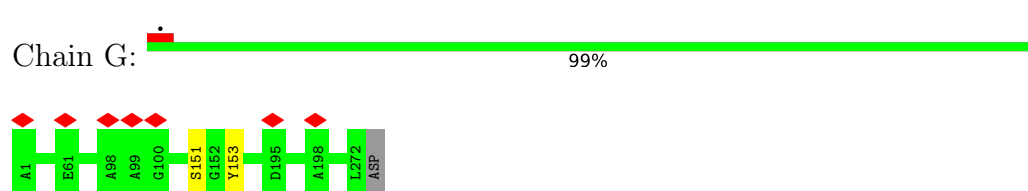
- Molecule 3: ATP synthase subunit beta, mitochondrial



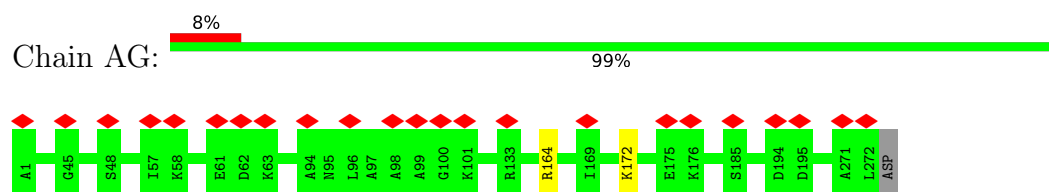
- Molecule 3: ATP synthase subunit beta, mitochondrial



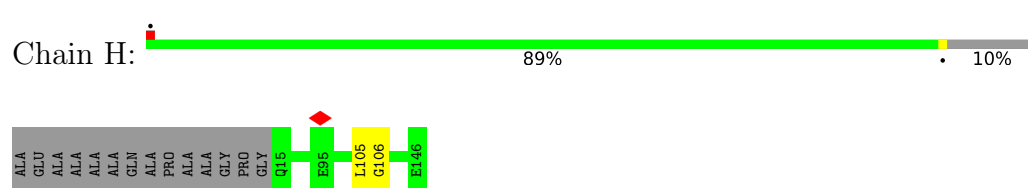
- Molecule 4: ATP synthase subunit gamma, mitochondrial



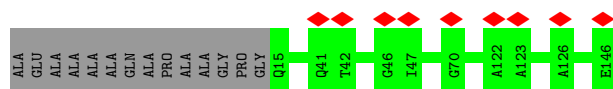
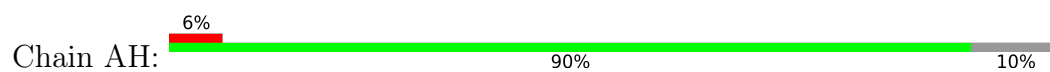
- Molecule 4: ATP synthase subunit gamma, mitochondrial



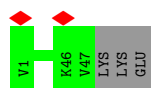
- Molecule 5: ATP synthase subunit delta, mitochondrial



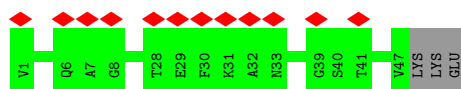
- Molecule 5: ATP synthase subunit delta, mitochondrial



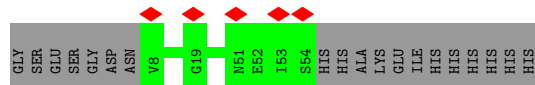
- Molecule 6: ATP synthase subunit epsilon, mitochondrial



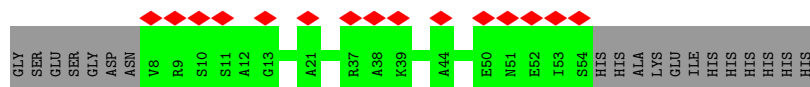
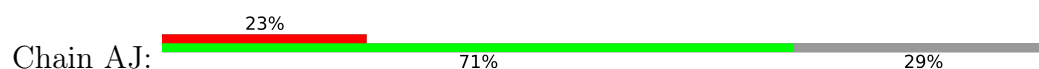
- Molecule 6: ATP synthase subunit epsilon, mitochondrial



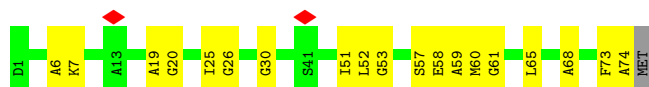
- Molecule 7: ATPase inhibitor, mitochondrial



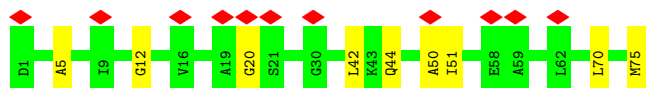
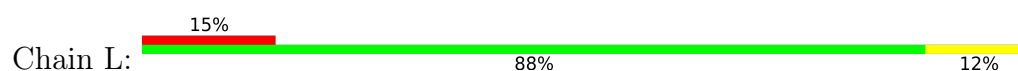
- Molecule 7: ATPase inhibitor, mitochondrial



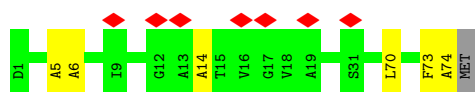
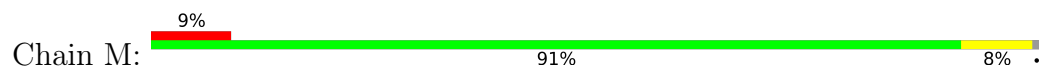
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



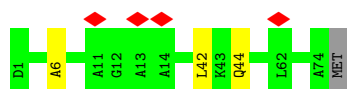
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



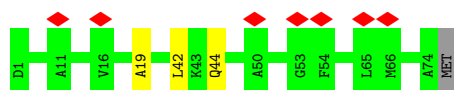
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



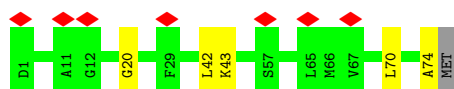
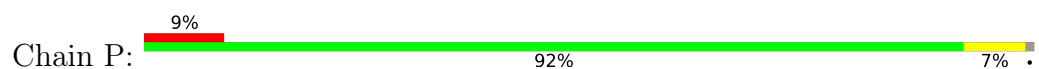
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



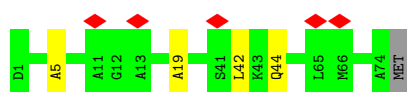
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



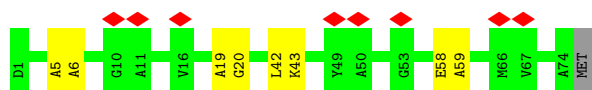
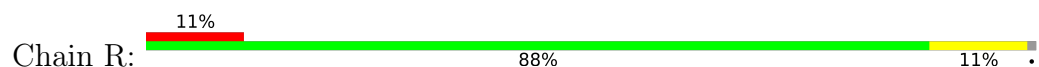
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial

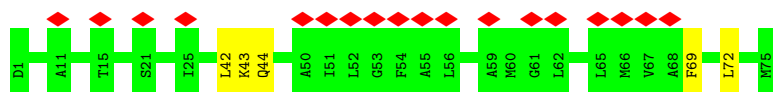




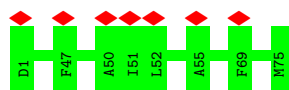
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



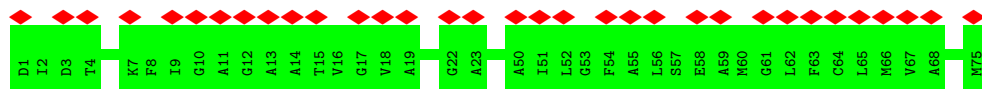
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



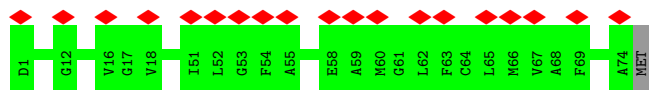
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



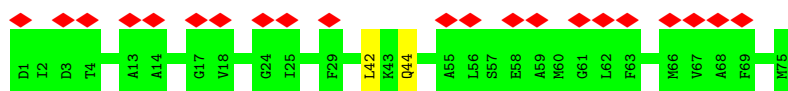
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



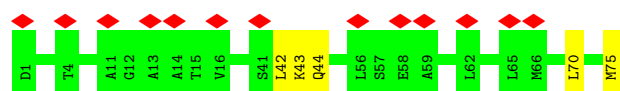
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



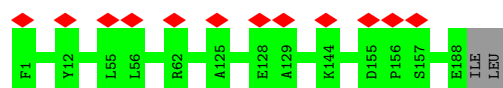
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



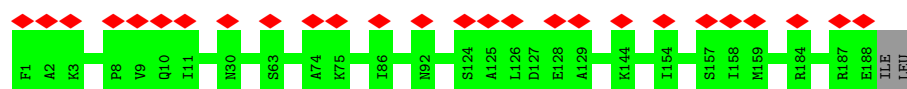
- Molecule 8: ATP synthase F(0) complex subunit C2, mitochondrial



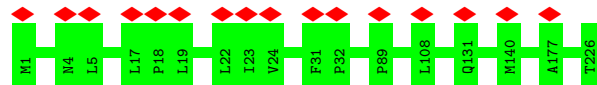
- Molecule 9: ATP synthase subunit O, mitochondrial



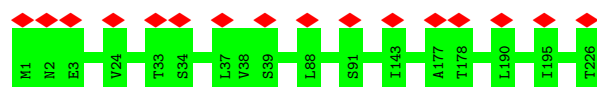
- Molecule 9: ATP synthase subunit O, mitochondrial



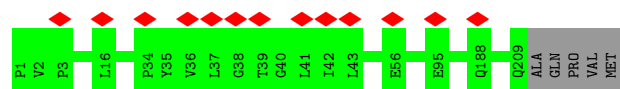
- Molecule 10: ATP synthase subunit a



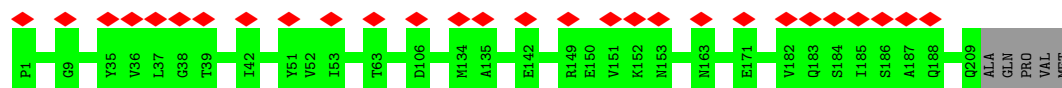
- Molecule 10: ATP synthase subunit a



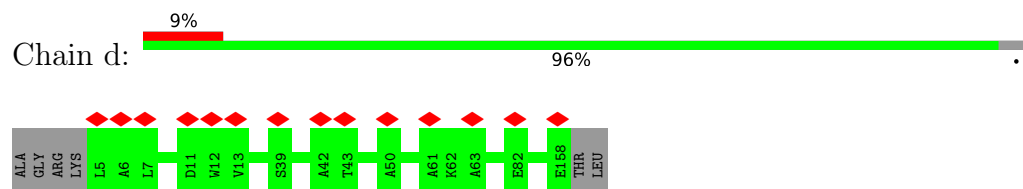
- Molecule 11: ATP synthase F(0) complex subunit B1, mitochondrial



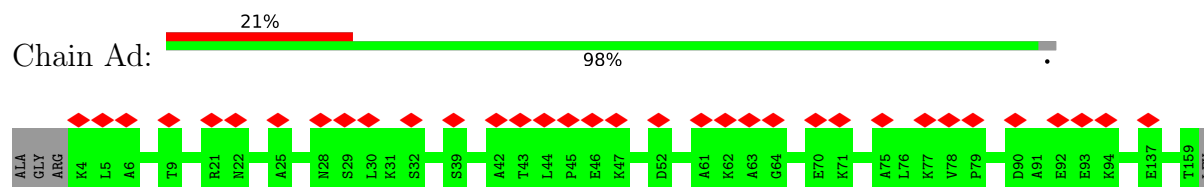
- Molecule 11: ATP synthase F(0) complex subunit B1, mitochondrial



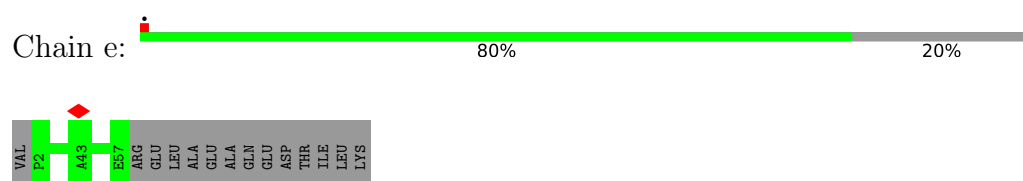
- Molecule 12: ATP synthase subunit d, mitochondrial



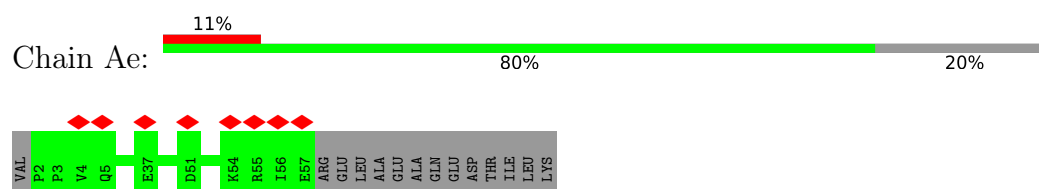
- Molecule 12: ATP synthase subunit d, mitochondrial



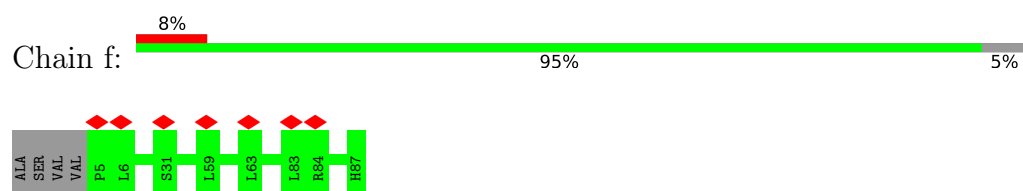
- Molecule 13: ATP synthase subunit e, mitochondrial



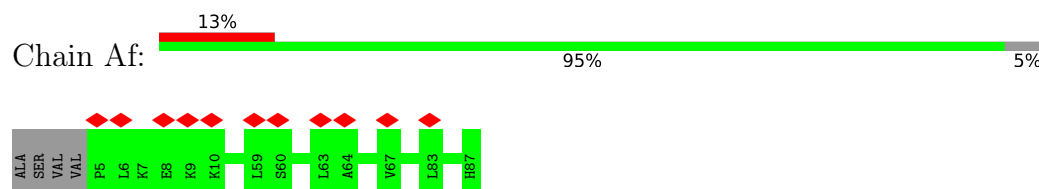
- Molecule 13: ATP synthase subunit e, mitochondrial



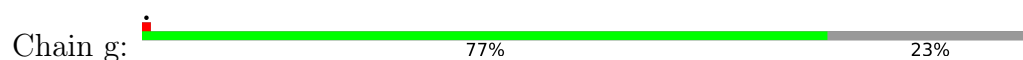
- Molecule 14: ATP synthase subunit f, mitochondrial

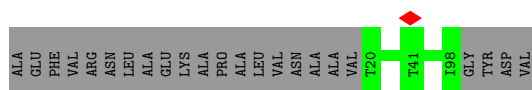


- Molecule 14: ATP synthase subunit f, mitochondrial

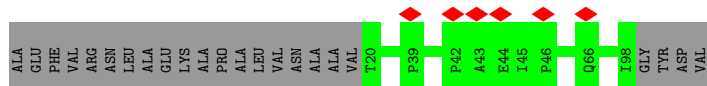
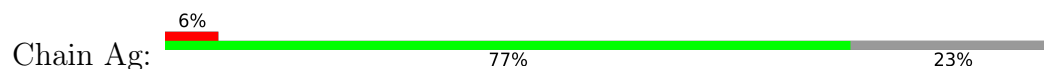


- Molecule 15: ATP synthase subunit g, mitochondrial

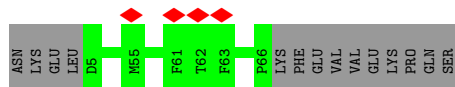
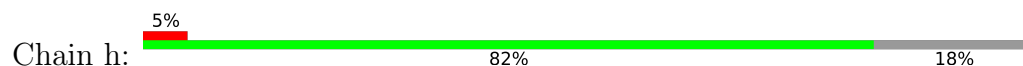




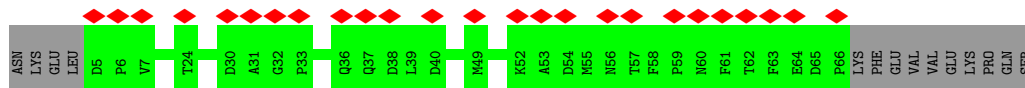
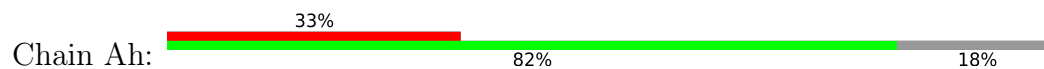
- Molecule 15: ATP synthase subunit g, mitochondrial



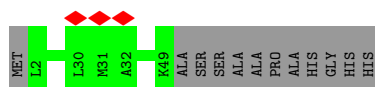
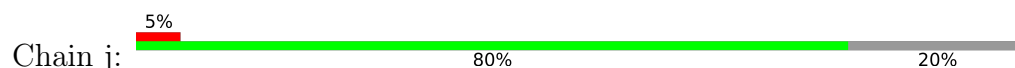
- Molecule 16: ATP synthase-coupling factor 6, mitochondrial



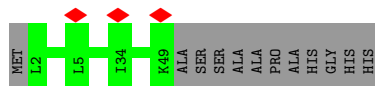
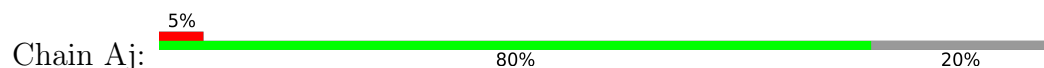
- Molecule 16: ATP synthase-coupling factor 6, mitochondrial



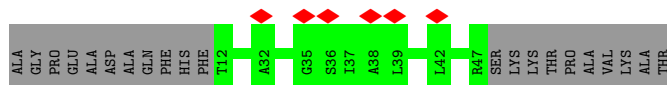
- Molecule 17: ATP synthase subunit ATP5MPL, mitochondrial



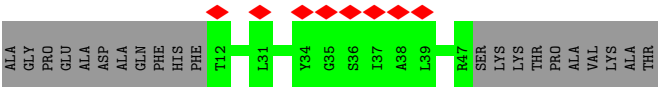
- Molecule 17: ATP synthase subunit ATP5MPL, mitochondrial



- Molecule 18: ATP synthase membrane subunit DAPIT, mitochondrial



- Molecule 18: ATP synthase membrane subunit DAPIT, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10353	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 ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.041	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0118	Depositor
Map size (Å)	524.0, 524.0, 524.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.048, 1.048, 1.048	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LHG, M3L, CDL

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	8	0.36	0/189	0.49	0/263
1	A8	0.32	0/204	0.48	0/284
2	A	0.34	0/2382	0.49	0/3305
2	AA	0.28	0/2490	0.47	0/3455
2	AB	0.28	0/2337	0.47	0/3241
2	AC	0.28	0/2441	0.47	0/3386
2	B	0.34	0/2426	0.49	0/3365
2	C	0.34	0/2455	0.48	0/3405
3	AD	0.28	0/2299	0.47	0/3190
3	AE	0.28	0/2289	0.47	0/3176
3	AF	0.28	0/2289	0.46	0/3176
3	D	0.34	0/2299	0.49	0/3190
3	E	0.33	0/2289	0.49	0/3176
3	F	0.34	0/2289	0.50	0/3176
4	AG	0.28	0/1346	0.45	0/1875
4	G	0.31	0/1346	0.47	0/1875
5	AH	0.30	0/652	0.50	0/907
5	H	0.34	0/652	0.50	0/907
6	AI	0.28	0/232	0.44	0/322
6	I	0.33	0/232	0.49	0/322
7	AJ	0.26	0/230	0.42	0/318
7	J	0.30	0/230	0.48	0/318
8	AK	0.29	0/353	0.48	0/486
8	AL	0.30	0/353	0.48	0/486
8	AM	0.28	0/358	0.48	0/493
8	AN	0.28	0/358	0.50	0/493
8	AO	0.28	0/358	0.47	0/493
8	AP	0.27	0/353	0.47	0/486
8	AQ	0.28	0/358	0.51	0/493
8	AR	0.27	0/358	0.48	0/493
8	K	0.35	0/353	0.54	0/486
8	L	0.32	0/358	0.53	0/493

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	M	0.33	0/353	0.50	0/486
8	N	0.35	0/353	0.52	0/486
8	O	0.31	0/353	0.55	0/486
8	P	0.34	0/353	0.52	0/486
8	Q	0.34	0/353	0.55	0/486
8	R	0.33	0/353	0.52	0/486
9	AS	0.26	0/930	0.43	0/1295
9	S	0.28	0/930	0.45	0/1295
10	Aa	0.29	0/1118	0.47	0/1557
10	a	0.33	0/1118	0.48	0/1557
11	Ab	0.28	0/1034	0.45	0/1440
11	b	0.31	0/1034	0.48	0/1440
12	Ad	0.26	0/777	0.44	0/1085
12	d	0.30	0/767	0.48	0/1071
13	Ae	0.27	0/276	0.44	0/383
13	e	0.29	0/276	0.48	0/383
14	Af	0.27	0/408	0.48	0/566
14	f	0.31	0/408	0.49	0/566
15	Ag	0.28	0/389	0.48	0/540
15	g	0.29	0/389	0.47	0/540
16	Ah	0.24	0/305	0.44	0/423
16	h	0.27	0/305	0.48	0/423
17	Aj	0.24	0/237	0.43	0/329
17	j	0.30	0/237	0.42	0/329
18	Ak	0.23	0/176	0.39	0/243
18	k	0.24	0/176	0.38	0/243
All	All	0.30	0/50566	0.48	0/70158

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	8	190	0	76	1	0
1	A8	205	0	81	0	0
2	A	2383	0	1139	5	0
2	AA	2491	0	1191	3	0
2	AB	2339	0	1113	2	0
2	AC	2443	0	1168	3	0
2	B	2428	0	1159	2	0
2	C	2457	0	1172	2	0
3	AD	2300	0	1094	1	0
3	AE	2290	0	1090	1	0
3	AF	2290	0	1090	0	0
3	D	2300	0	1094	1	0
3	E	2290	0	1090	2	0
3	F	2290	0	1090	1	0
4	AG	1347	0	641	1	0
4	G	1347	0	641	1	0
5	AH	653	0	326	0	0
5	H	653	0	326	1	0
6	AI	233	0	119	0	0
6	I	233	0	119	0	0
7	AJ	231	0	124	0	0
7	J	231	0	124	0	0
8	AK	359	0	199	3	0
8	AL	359	0	198	2	0
8	AM	364	0	200	3	0
8	AN	364	0	201	0	0
8	AO	364	0	201	0	0
8	AP	359	0	199	0	0
8	AQ	364	0	201	1	0
8	AR	364	0	200	3	0
8	K	359	0	199	13	0
8	L	364	0	201	6	0
8	M	359	0	199	6	0
8	N	359	0	199	4	0
8	O	359	0	199	2	0
8	P	359	0	198	3	0
8	Q	359	0	198	3	0
8	R	359	0	199	6	0
9	AS	931	0	427	0	0
9	S	931	0	427	0	0
10	Aa	1119	0	498	0	0
10	a	1119	0	498	0	0
11	Ab	1035	0	459	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	b	1035	0	459	0	0
12	Ad	778	0	344	0	0
12	d	768	0	340	0	0
13	Ae	277	0	129	0	0
13	e	277	0	129	0	0
14	Af	409	0	184	0	0
14	f	409	0	184	0	0
15	Ag	390	0	178	0	0
15	g	390	0	178	0	0
16	Ah	306	0	128	0	0
16	h	306	0	128	0	0
17	Aj	238	0	107	0	0
17	j	238	0	107	0	0
18	Ak	177	0	80	0	0
18	k	177	0	80	0	0
19	Aa	84	0	115	0	0
19	Ab	83	0	113	0	0
19	Af	78	0	103	0	0
19	a	84	0	115	0	0
19	f	161	0	216	0	0
20	Af	88	0	122	0	0
20	f	88	0	122	0	0
All	All	51374	0	25228	72	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 1.

The worst 5 of 72 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)
8:AM:42:LEU:O	8:AM:44:GLN:N	2.13	0.80
8:AR:42:LEU:O	8:AR:44:GLN:N	2.17	0.78
8:N:42:LEU:O	8:N:44:GLN:N	2.19	0.76
8:L:42:LEU:O	8:L:44:GLN:N	2.27	0.68
8:AQ:42:LEU:O	8:AQ:44:GLN:N	2.27	0.65

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	8	36/66 (54%)	29 (81%)	7 (19%)	0	100	100
1	A8	39/66 (59%)	29 (74%)	10 (26%)	0	100	100
2	A	484/510 (95%)	444 (92%)	40 (8%)	0	100	100
2	AA	506/510 (99%)	475 (94%)	31 (6%)	0	100	100
2	AB	473/510 (93%)	450 (95%)	23 (5%)	0	100	100
2	AC	494/510 (97%)	462 (94%)	32 (6%)	0	100	100
2	B	491/510 (96%)	451 (92%)	40 (8%)	0	100	100
2	C	497/510 (98%)	461 (93%)	36 (7%)	0	100	100
3	AD	467/482 (97%)	440 (94%)	27 (6%)	0	100	100
3	AE	465/482 (96%)	434 (93%)	31 (7%)	0	100	100
3	AF	465/482 (96%)	431 (93%)	34 (7%)	0	100	100
3	D	467/482 (97%)	419 (90%)	48 (10%)	0	100	100
3	E	465/482 (96%)	433 (93%)	32 (7%)	0	100	100
3	F	465/482 (96%)	422 (91%)	43 (9%)	0	100	100
4	AG	270/273 (99%)	259 (96%)	11 (4%)	0	100	100
4	G	270/273 (99%)	256 (95%)	14 (5%)	0	100	100
5	AH	130/146 (89%)	119 (92%)	11 (8%)	0	100	100
5	H	130/146 (89%)	115 (88%)	15 (12%)	0	100	100
6	AI	45/50 (90%)	43 (96%)	2 (4%)	0	100	100
6	I	45/50 (90%)	41 (91%)	4 (9%)	0	100	100
7	AJ	45/66 (68%)	44 (98%)	1 (2%)	0	100	100
7	J	45/66 (68%)	42 (93%)	3 (7%)	0	100	100
8	AK	71/75 (95%)	68 (96%)	3 (4%)	0	100	100
8	AL	71/75 (95%)	66 (93%)	4 (6%)	1 (1%)	9	41
8	AM	72/75 (96%)	71 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AN	72/75 (96%)	71 (99%)	1 (1%)	0	100	100
8	AO	72/75 (96%)	70 (97%)	2 (3%)	0	100	100
8	AP	71/75 (95%)	70 (99%)	1 (1%)	0	100	100
8	AQ	72/75 (96%)	69 (96%)	3 (4%)	0	100	100
8	AR	72/75 (96%)	67 (93%)	5 (7%)	0	100	100
8	K	71/75 (95%)	60 (84%)	11 (16%)	0	100	100
8	L	72/75 (96%)	67 (93%)	5 (7%)	0	100	100
8	M	71/75 (95%)	67 (94%)	4 (6%)	0	100	100
8	N	71/75 (95%)	68 (96%)	3 (4%)	0	100	100
8	O	71/75 (95%)	70 (99%)	1 (1%)	0	100	100
8	P	71/75 (95%)	67 (94%)	4 (6%)	0	100	100
8	Q	71/75 (95%)	65 (92%)	6 (8%)	0	100	100
8	R	71/75 (95%)	66 (93%)	5 (7%)	0	100	100
9	AS	186/190 (98%)	177 (95%)	9 (5%)	0	100	100
9	S	186/190 (98%)	175 (94%)	11 (6%)	0	100	100
10	Aa	224/226 (99%)	207 (92%)	17 (8%)	0	100	100
10	a	224/226 (99%)	201 (90%)	23 (10%)	0	100	100
11	Ab	207/214 (97%)	201 (97%)	6 (3%)	0	100	100
11	b	207/214 (97%)	200 (97%)	7 (3%)	0	100	100
12	Ad	154/160 (96%)	141 (92%)	13 (8%)	0	100	100
12	d	152/160 (95%)	133 (88%)	19 (12%)	0	100	100
13	Ae	54/70 (77%)	53 (98%)	1 (2%)	0	100	100
13	e	54/70 (77%)	53 (98%)	1 (2%)	0	100	100
14	Af	81/87 (93%)	79 (98%)	2 (2%)	0	100	100
14	f	81/87 (93%)	73 (90%)	8 (10%)	0	100	100
15	Ag	77/102 (76%)	70 (91%)	7 (9%)	0	100	100
15	g	77/102 (76%)	68 (88%)	9 (12%)	0	100	100
16	Ah	60/76 (79%)	48 (80%)	12 (20%)	0	100	100
16	h	60/76 (79%)	49 (82%)	11 (18%)	0	100	100
17	Aj	46/60 (77%)	44 (96%)	2 (4%)	0	100	100
17	j	46/60 (77%)	43 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	Ak	34/57 (60%)	32 (94%)	2 (6%)	0	100	100
18	k	34/57 (60%)	33 (97%)	1 (3%)	0	100	100
All	All	10180/10838 (94%)	9461 (93%)	718 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	AL	42	LEU

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

16 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
8	M3L	AP	43	8	3,4,12	0.87	0	2,4,16	0.74	0
8	M3L	AQ	43	8	3,4,12	0.76	0	2,4,16	0.87	0
8	M3L	AL	43	8	3,4,12	0.87	0	2,4,16	0.52	0
8	M3L	AN	43	8	3,4,12	0.90	0	2,4,16	0.20	0
8	M3L	R	43	8	3,4,12	0.90	0	2,4,16	0.25	0
8	M3L	AM	43	8	3,4,12	0.73	0	2,4,16	0.57	0
8	M3L	N	43	8	3,4,12	0.79	0	2,4,16	0.60	0
8	M3L	AK	43	8	3,4,12	1.02	0	2,4,16	0.14	0
8	M3L	M	43	8	3,4,12	1.02	0	2,4,16	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	M3L	O	43	8	3,4,12	0.77	0	2,4,16	0.73	0
8	M3L	AO	43	8	3,4,12	0.85	0	2,4,16	0.23	0
8	M3L	K	43	8	3,4,12	0.88	0	2,4,16	0.34	0
8	M3L	Q	43	8	3,4,12	0.85	0	2,4,16	0.41	0
8	M3L	AR	43	8	3,4,12	0.72	0	2,4,16	0.28	0
8	M3L	P	43	8	3,4,12	0.79	0	2,4,16	0.38	0
8	M3L	L	43	8	3,4,12	0.73	0	2,4,16	0.52	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
8	M3L	AP	43	8	-	0/0/2/12	-
8	M3L	AQ	43	8	-	0/0/2/12	-
8	M3L	AL	43	8	-	0/0/2/12	-
8	M3L	AN	43	8	-	0/0/2/12	-
8	M3L	R	43	8	-	0/0/2/12	-
8	M3L	AM	43	8	-	0/0/2/12	-
8	M3L	N	43	8	-	0/0/2/12	-
8	M3L	AK	43	8	-	0/0/2/12	-
8	M3L	M	43	8	-	0/0/2/12	-
8	M3L	O	43	8	-	0/0/2/12	-
8	M3L	AO	43	8	-	0/0/2/12	-
8	M3L	K	43	8	-	0/0/2/12	-
8	M3L	Q	43	8	-	0/0/2/12	-
8	M3L	AR	43	8	-	0/0/2/12	-
8	M3L	P	43	8	-	0/0/2/12	-
8	M3L	L	43	8	-	0/0/2/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	R	43	M3L	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	AM	43	M3L	1	0
8	AR	43	M3L	1	0
8	P	43	M3L	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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$
19	CDL	f	101	-	82,82,99	0.98	6 (7%)	88,94,111	1.15	5 (5%)
19	CDL	Aa	301	-	83,83,99	0.98	7 (8%)	89,95,111	1.10	4 (4%)
20	LHG	f	104	-	38,38,48	0.73	1 (2%)	41,44,54	1.27	4 (9%)
19	CDL	Af	101	-	77,77,99	1.00	6 (7%)	83,89,111	1.10	5 (6%)
20	LHG	Af	102	-	38,38,48	0.52	0	41,44,54	0.58	1 (2%)
19	CDL	f	102	-	77,77,99	1.01	7 (9%)	83,89,111	1.14	5 (6%)
19	CDL	Ab	301	-	82,82,99	0.98	6 (7%)	88,94,111	1.12	4 (4%)
19	CDL	a	301	-	83,83,99	0.98	7 (8%)	89,95,111	1.07	4 (4%)
20	LHG	Af	103	-	48,48,48	0.61	0	51,54,54	1.22	4 (7%)
20	LHG	f	103	-	48,48,48	0.63	1 (2%)	51,54,54	1.24	6 (11%)

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
19	CDL	f	101	-	-	38/93/93/110	-
19	CDL	Aa	301	-	-	28/94/94/110	-
20	LHG	f	104	-	-	22/43/43/53	-
19	CDL	Af	101	-	-	29/88/88/110	-
20	LHG	Af	102	-	-	17/43/43/53	-
19	CDL	f	102	-	-	36/88/88/110	-
19	CDL	Ab	301	-	-	32/93/93/110	-
19	CDL	a	301	-	-	32/94/94/110	-
20	LHG	Af	103	-	-	12/53/53/53	-
20	LHG	f	103	-	-	17/53/53/53	-

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	f	101	CDL	OA6-CA4	-2.88	1.39	1.46
19	Aa	301	CDL	OB8-CB7	2.77	1.41	1.33
19	f	102	CDL	OB8-CB7	2.75	1.41	1.33
19	Af	101	CDL	OA6-CA4	-2.74	1.39	1.46
19	f	101	CDL	OB8-CB7	2.73	1.41	1.33

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	Ab	301	CDL	OA6-CA5-C11	4.54	121.28	111.50
19	f	101	CDL	OB6-CB5-C51	4.31	120.80	111.50
20	f	103	LHG	O4-P-O5	4.25	133.28	112.24
20	Af	103	LHG	O4-P-O5	4.19	132.94	112.24
19	f	102	CDL	OA6-CA5-C11	4.19	120.52	111.50

There are no chirality outliers.

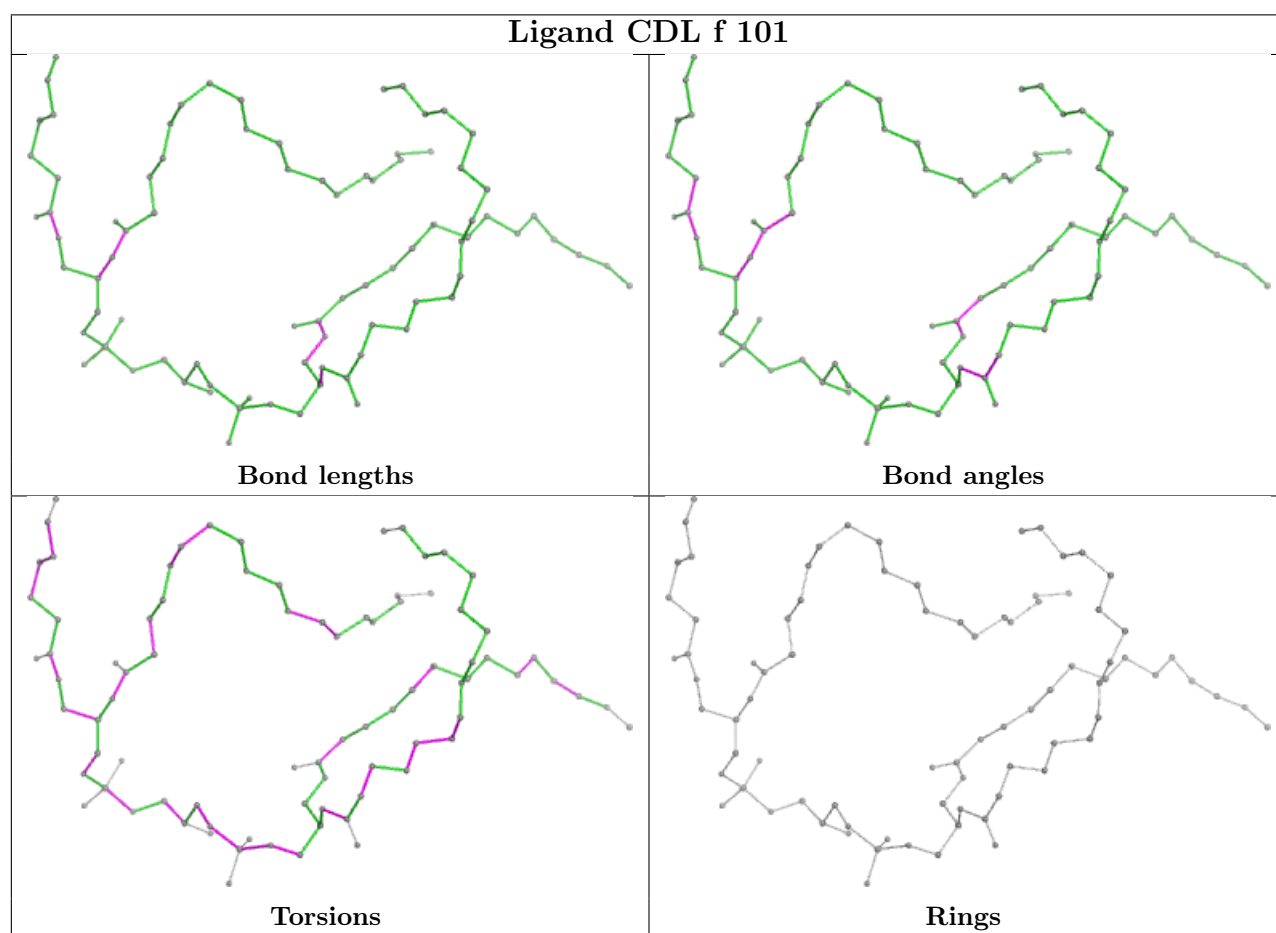
5 of 263 torsion outliers are listed below:

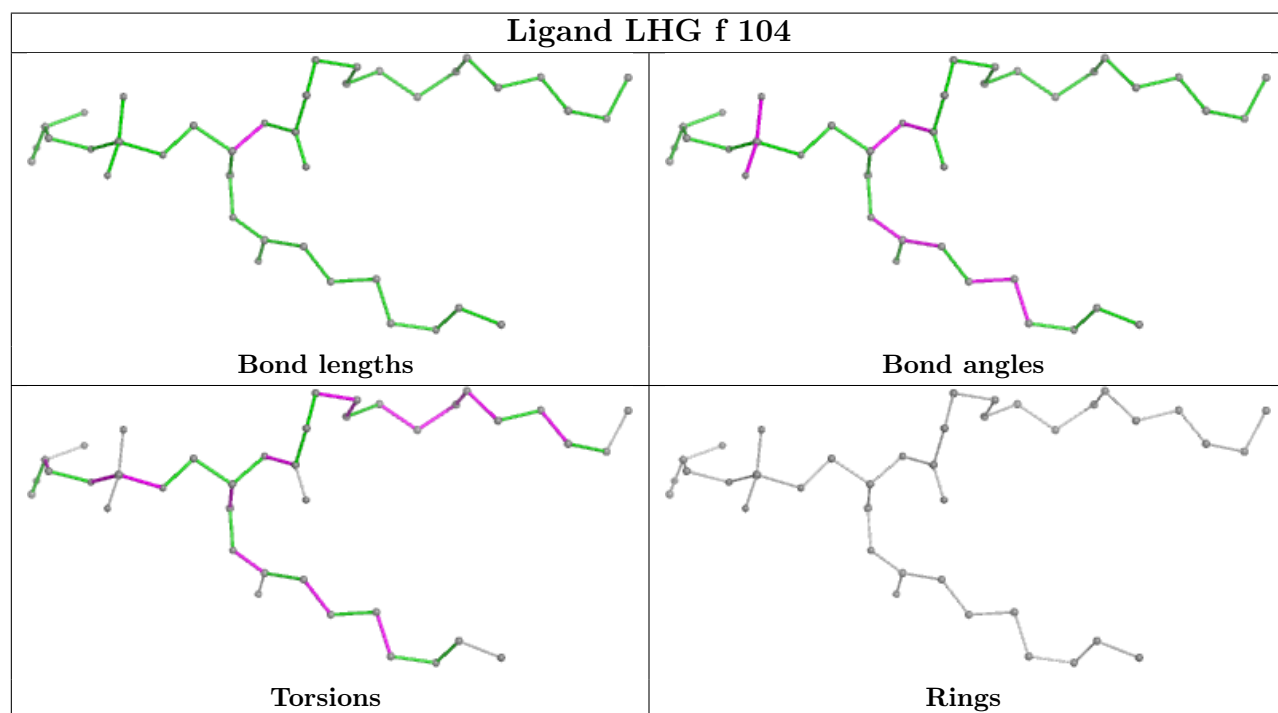
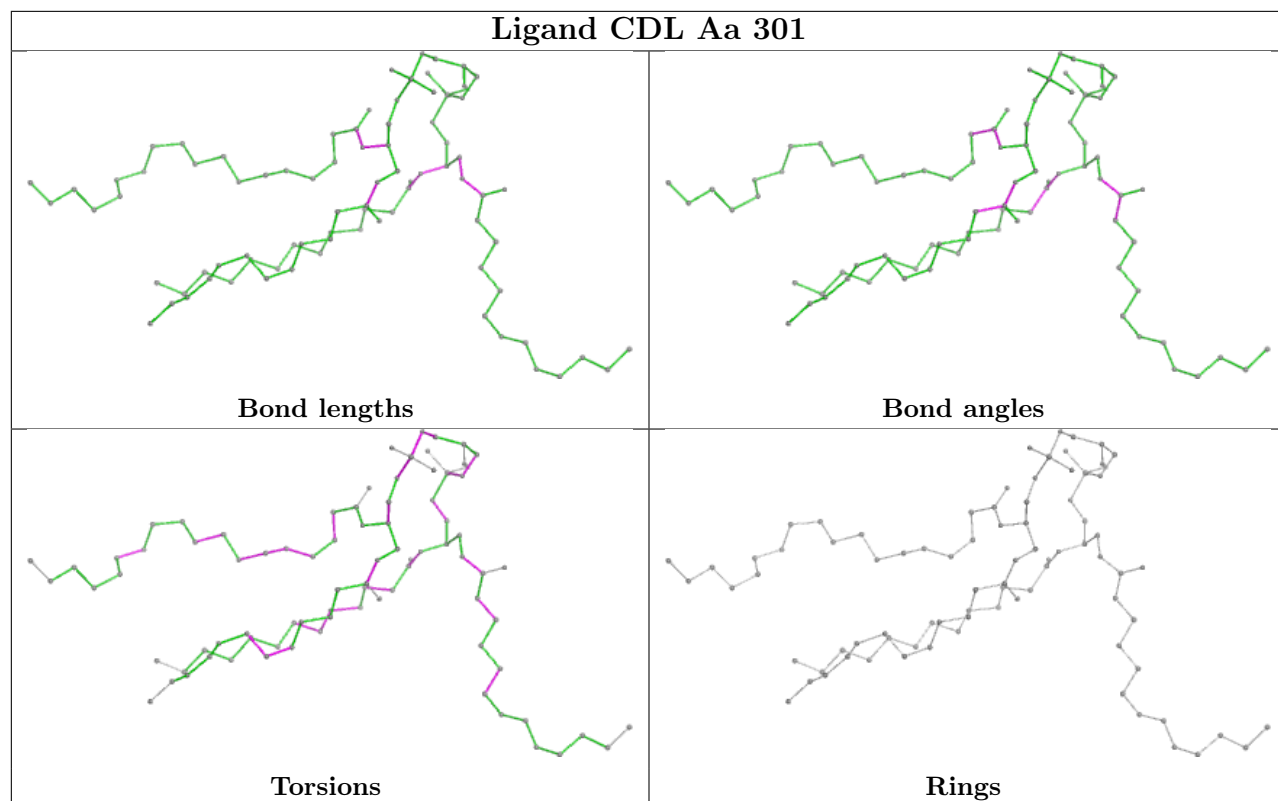
Mol	Chain	Res	Type	Atoms
19	f	101	CDL	C1-CA2-OA2-PA1
19	f	101	CDL	CA2-OA2-PA1-OA3
19	f	101	CDL	CA2-OA2-PA1-OA4
19	f	101	CDL	CA2-OA2-PA1-OA5
19	f	101	CDL	CA3-OA5-PA1-OA2

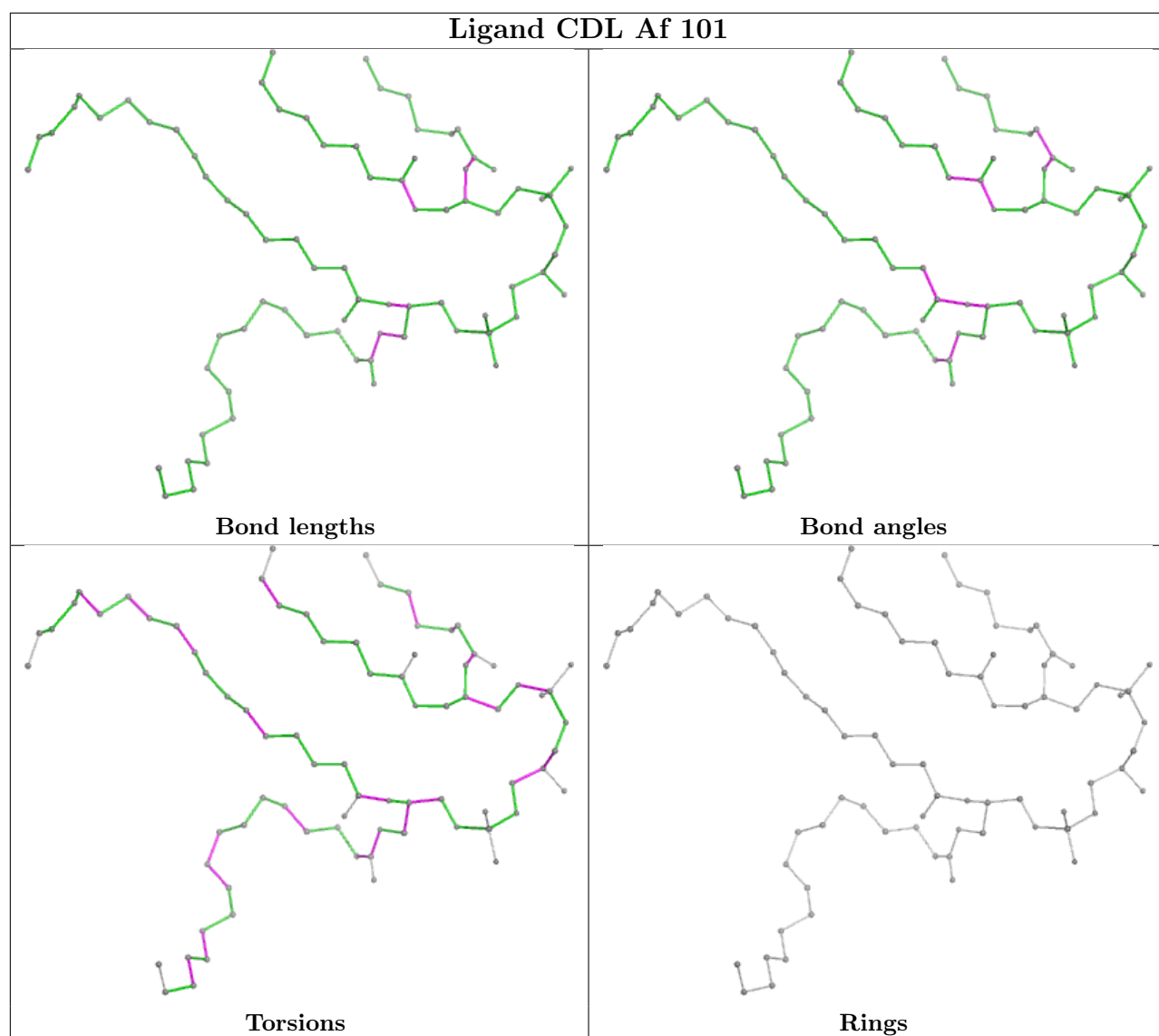
There are no ring outliers.

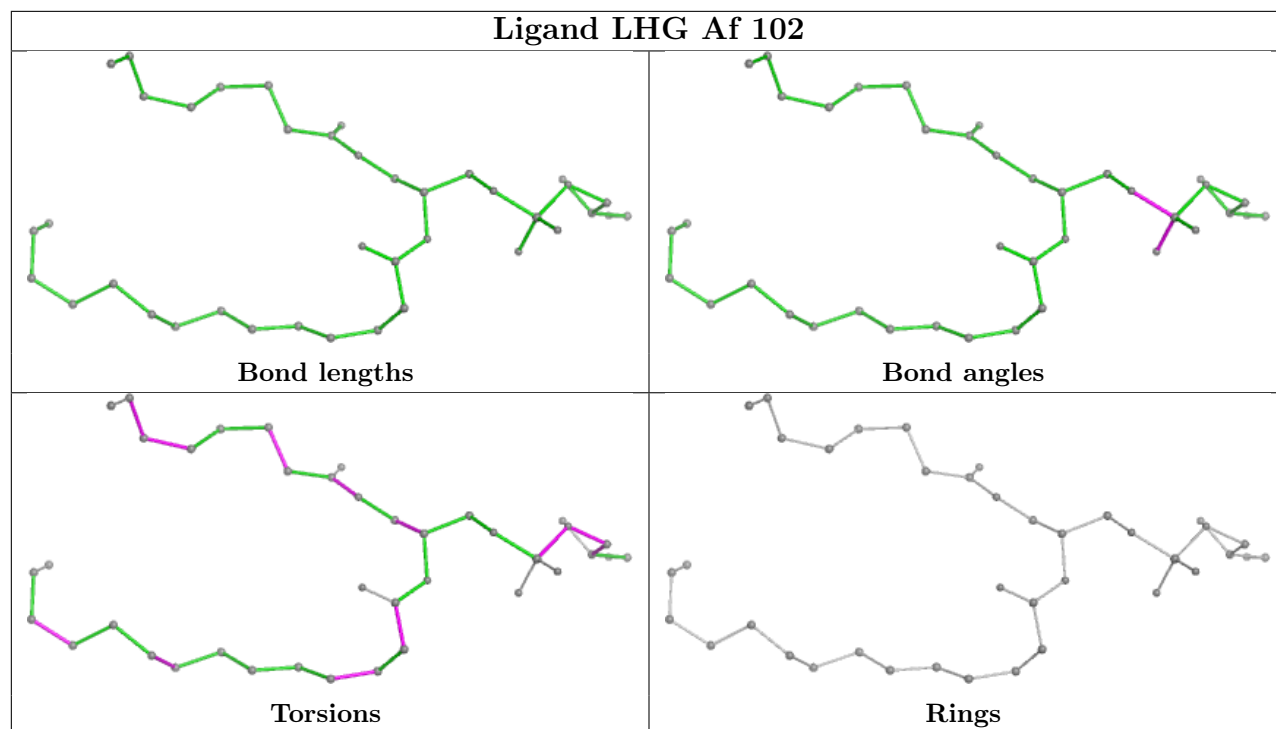
No monomer is involved in short contacts.

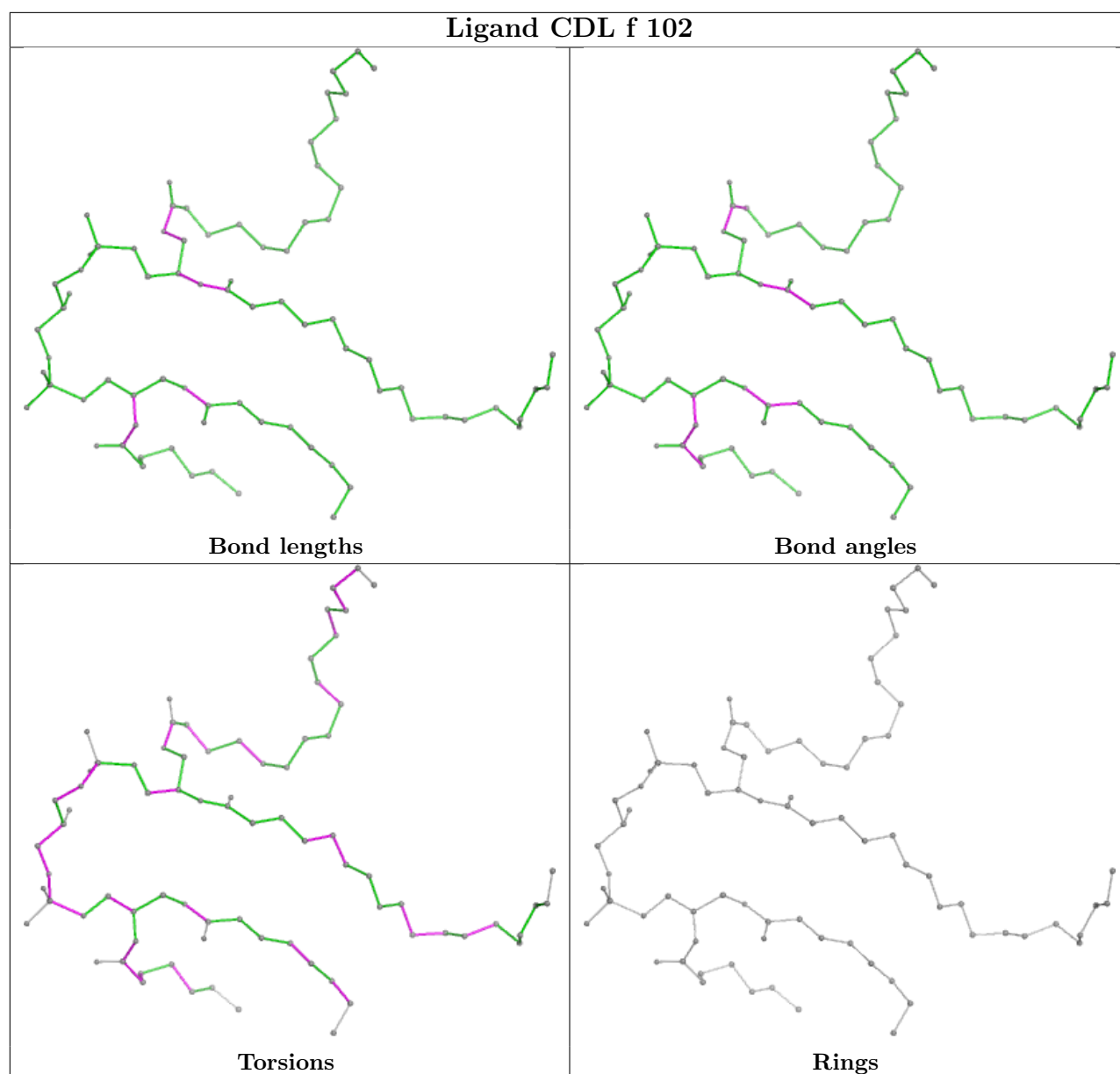
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

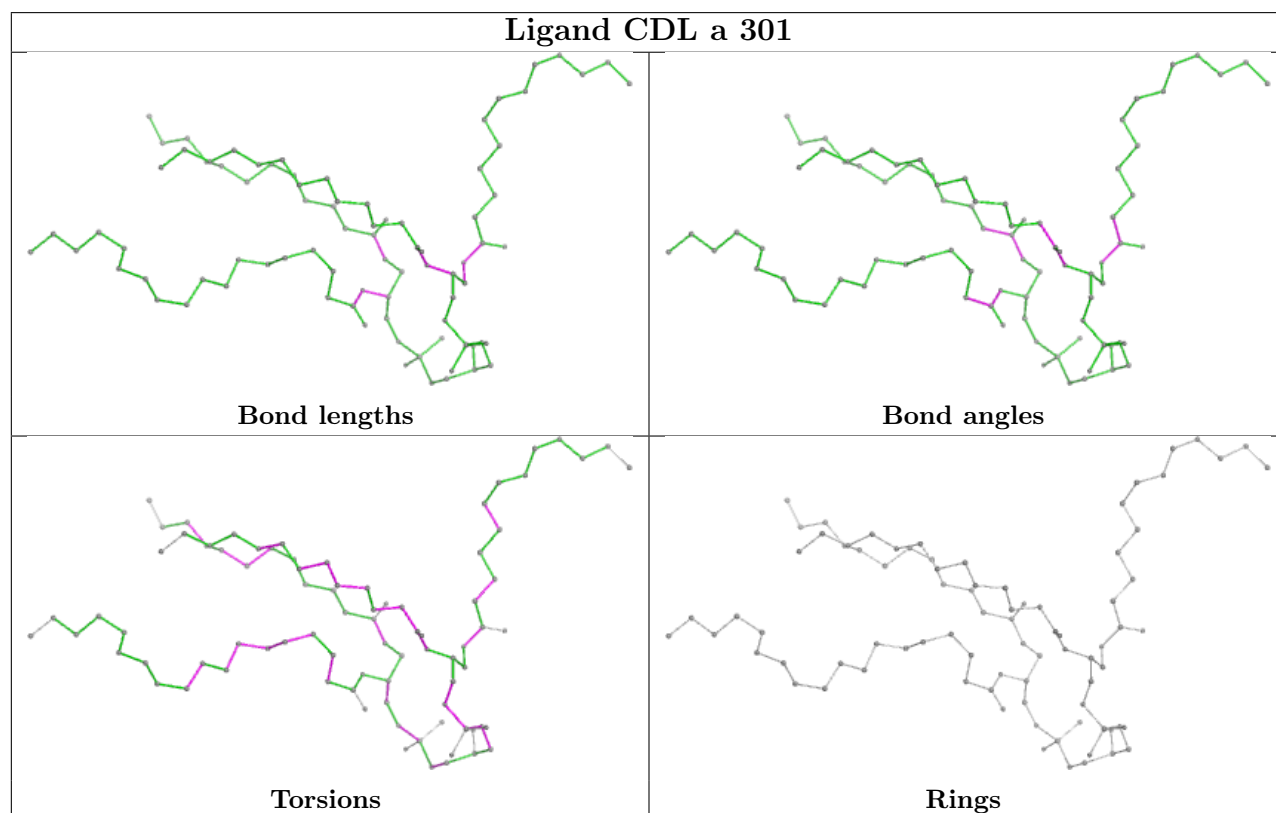
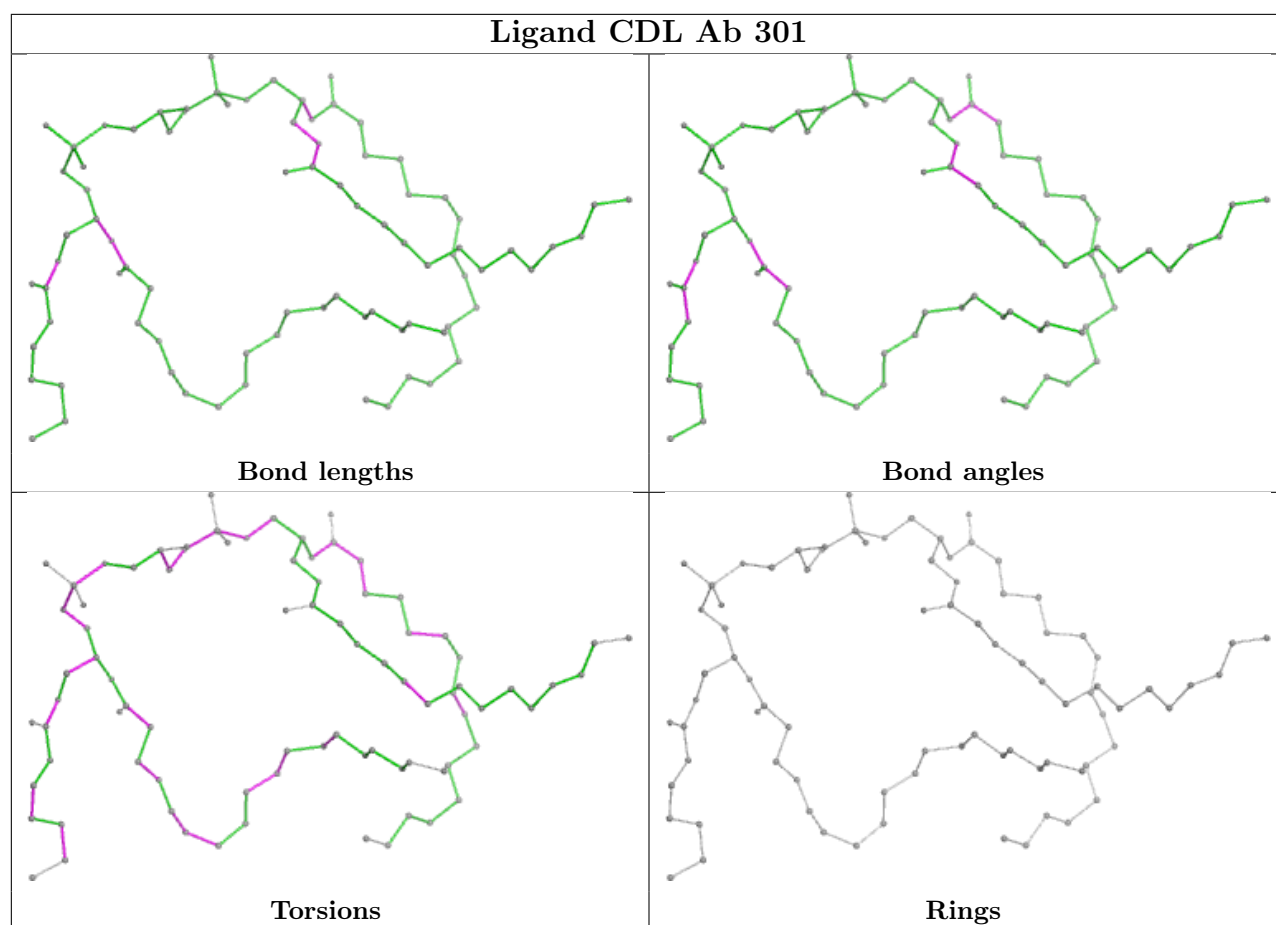


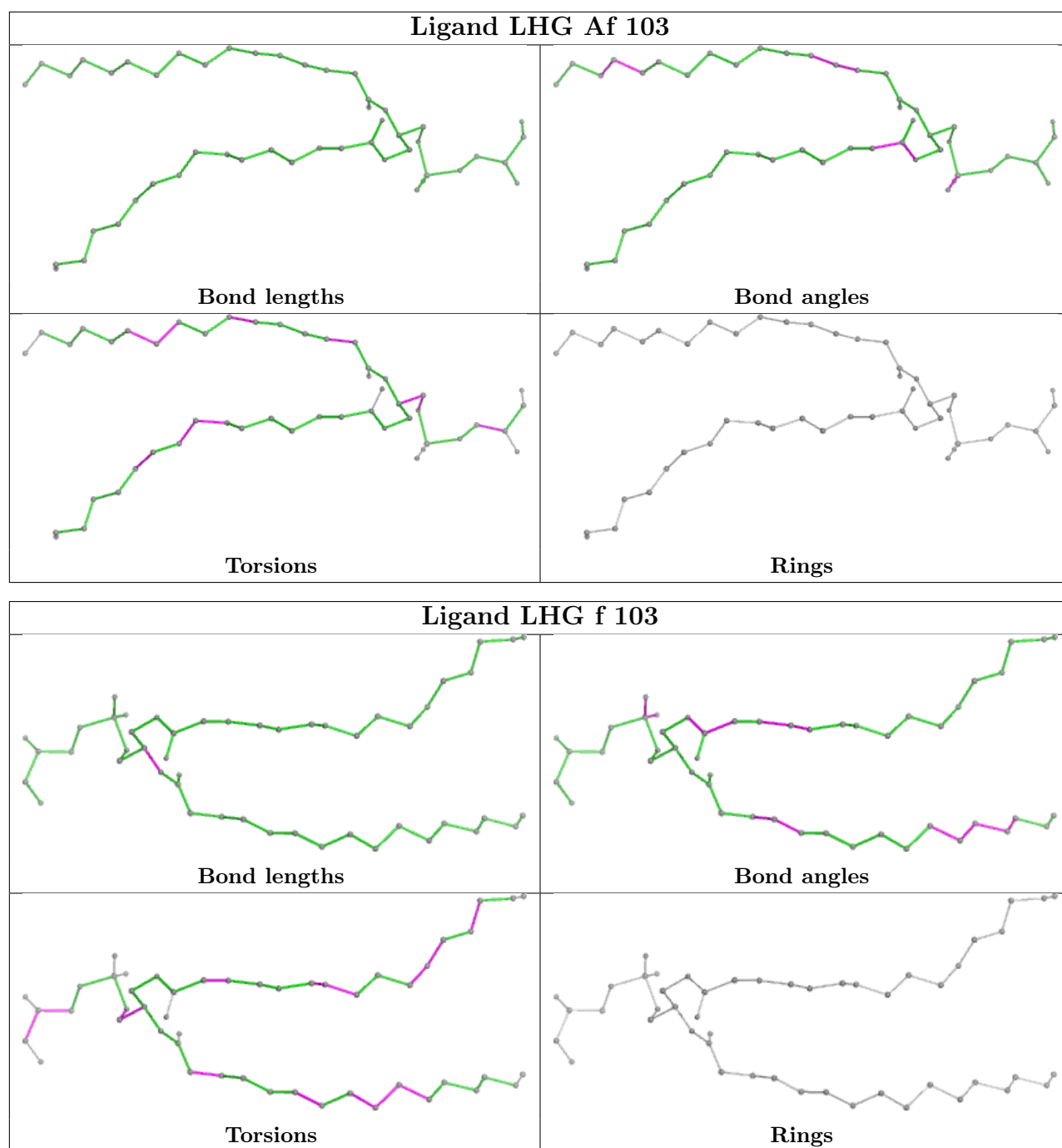












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

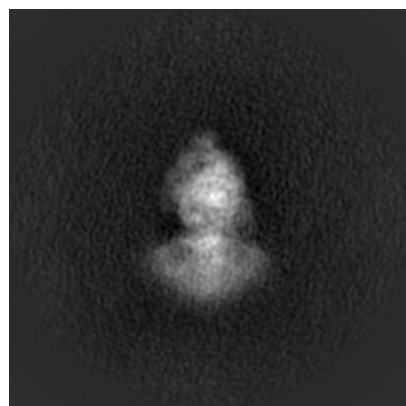
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11431. These allow visual inspection of the internal detail of the map and identification of artifacts.

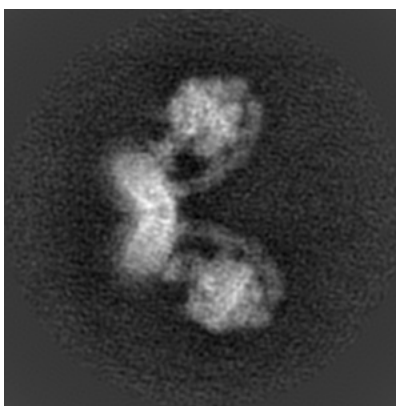
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

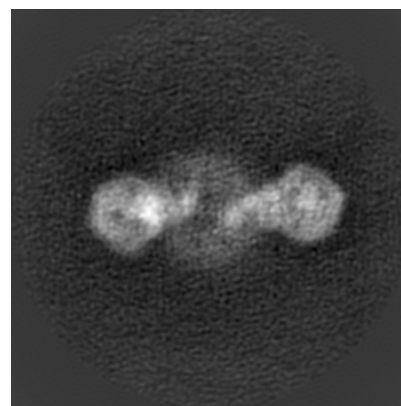
6.1.1 Primary map



X

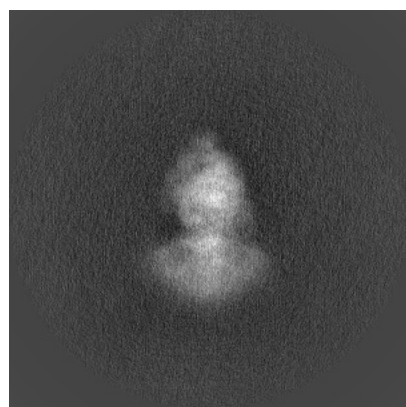


Y

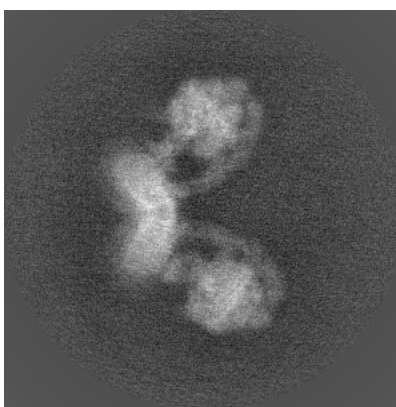


Z

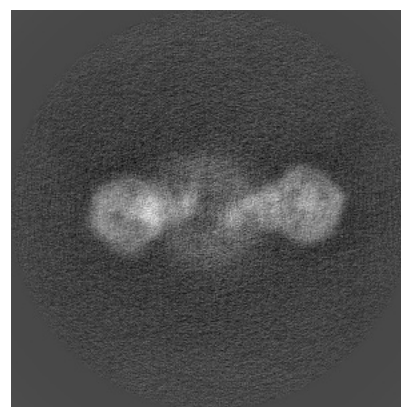
6.1.2 Raw map



X



Y

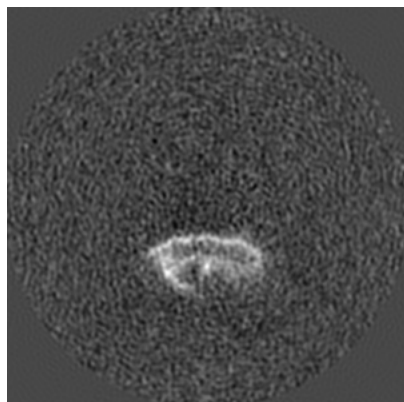


Z

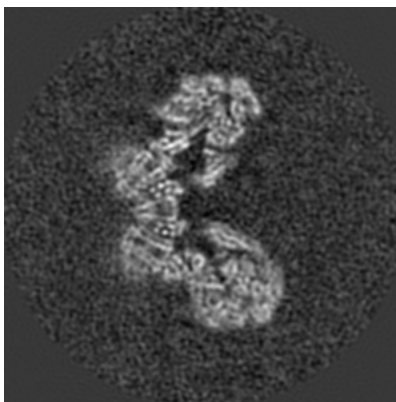
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

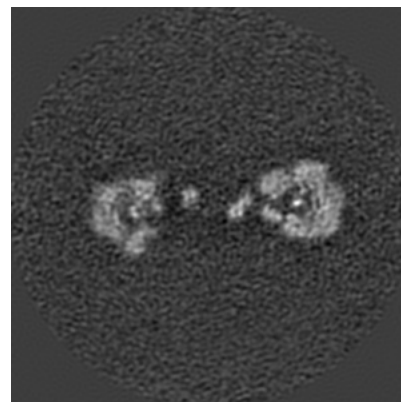
6.2.1 Primary map



X Index: 250

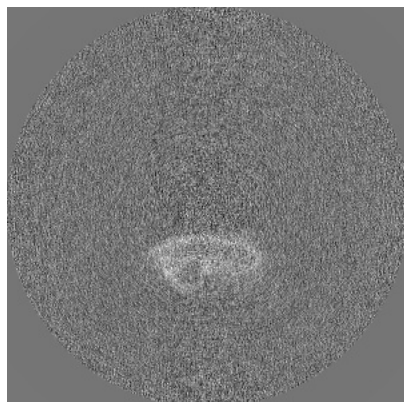


Y Index: 250

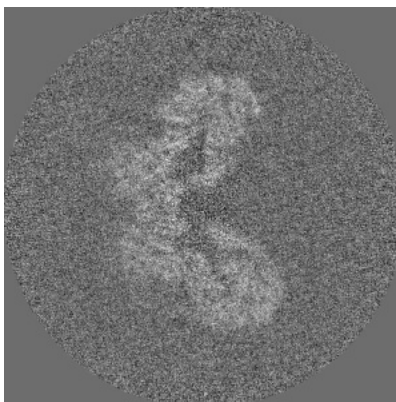


Z Index: 250

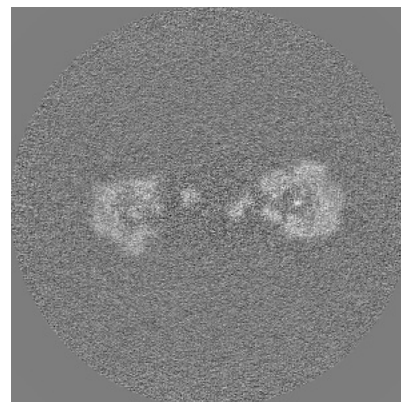
6.2.2 Raw map



X Index: 250



Y Index: 250

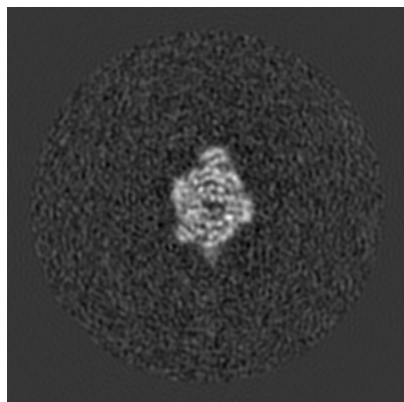


Z Index: 250

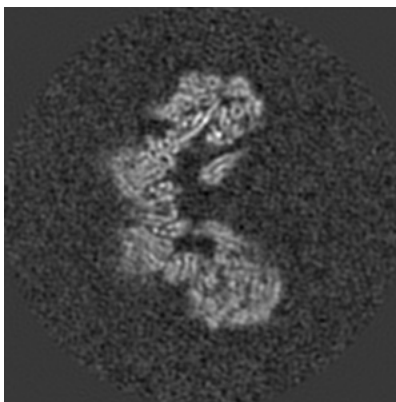
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

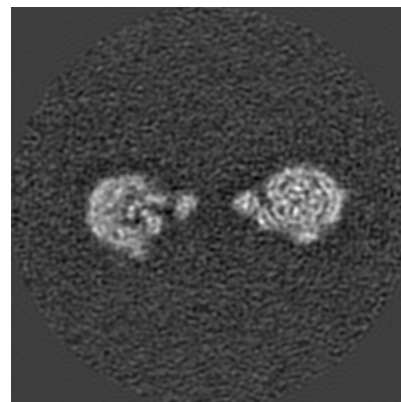
6.3.1 Primary map



X Index: 373

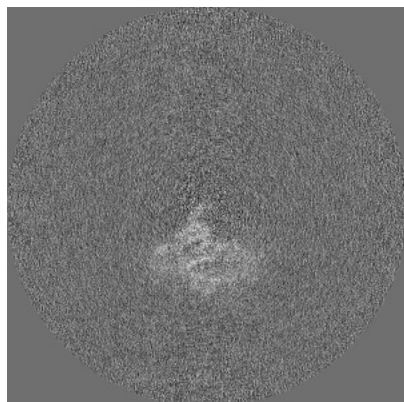


Y Index: 255

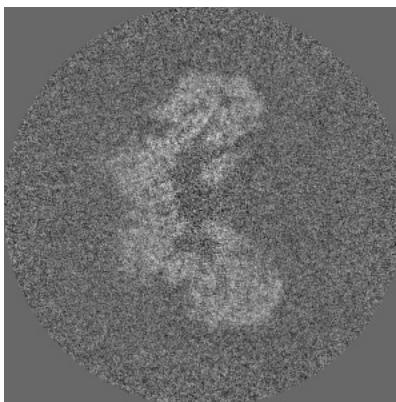


Z Index: 264

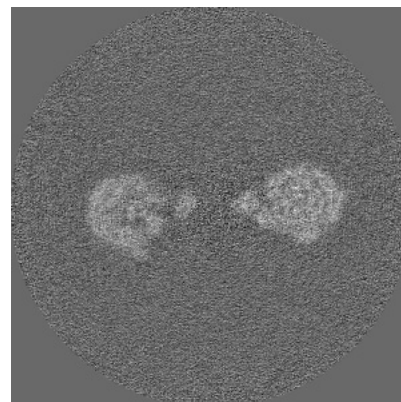
6.3.2 Raw map



X Index: 271



Y Index: 255

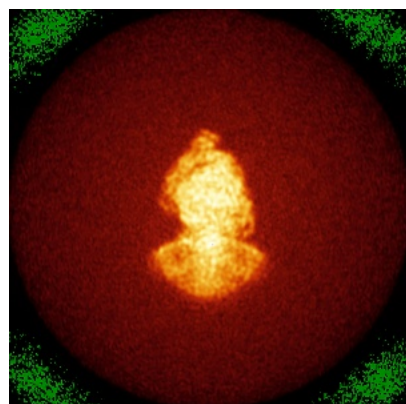


Z Index: 263

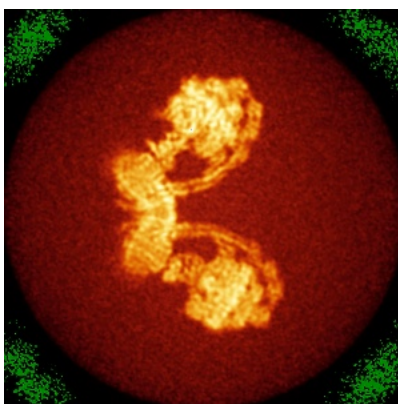
The images above show the largest variance slices of the map in three orthogonal directions.

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

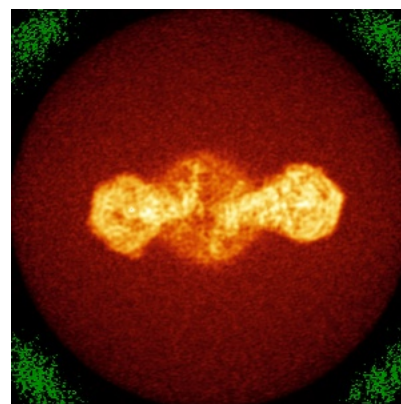
6.4.1 Primary map



X

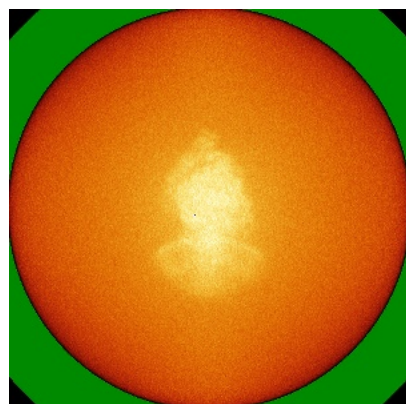


Y

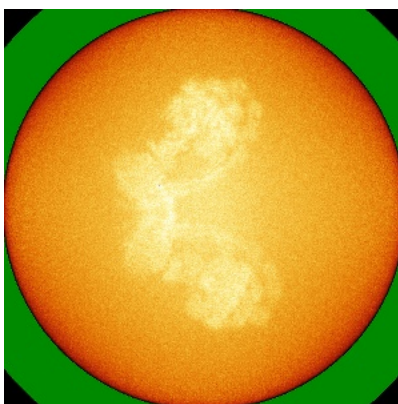


Z

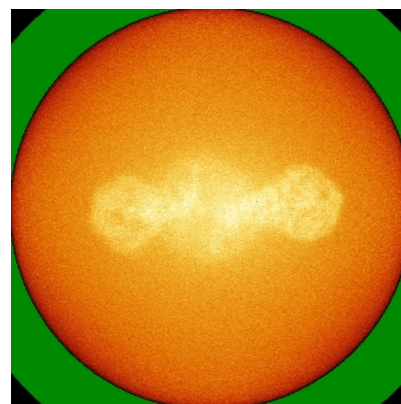
6.4.2 Raw map



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.

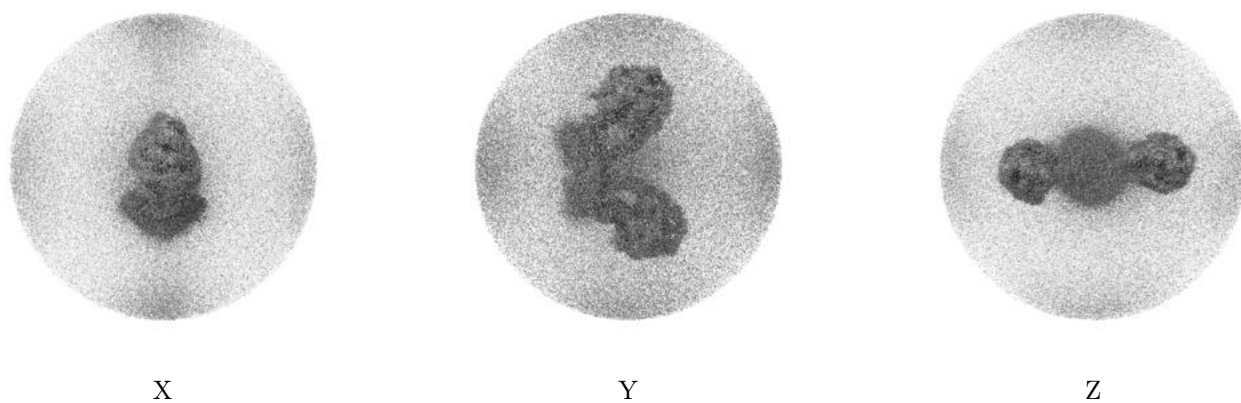
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0118. 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.

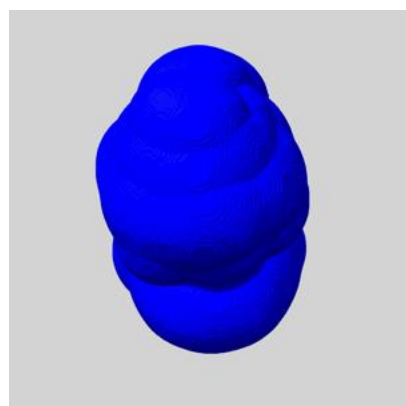
6.6 Mask visualisation [i](#)

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

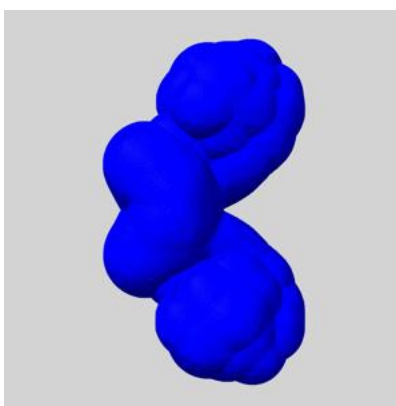
A mask typically either:

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

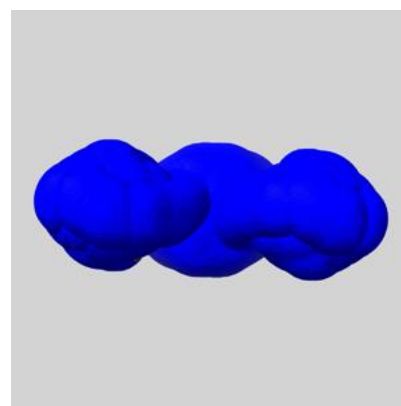
6.6.1 emd_11431_msk_1.map [i](#)



X



Y

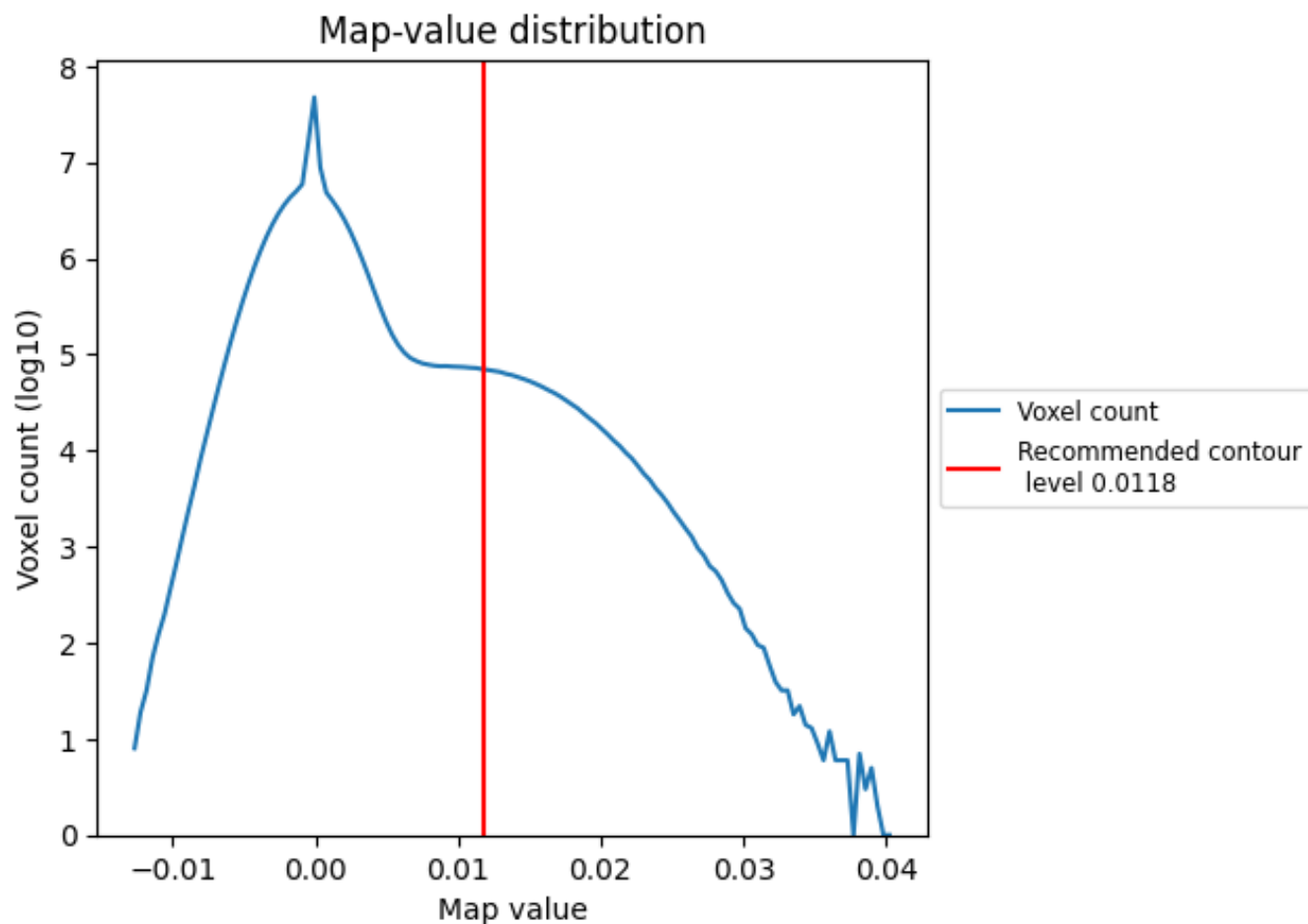


Z

7 Map analysis [i](#)

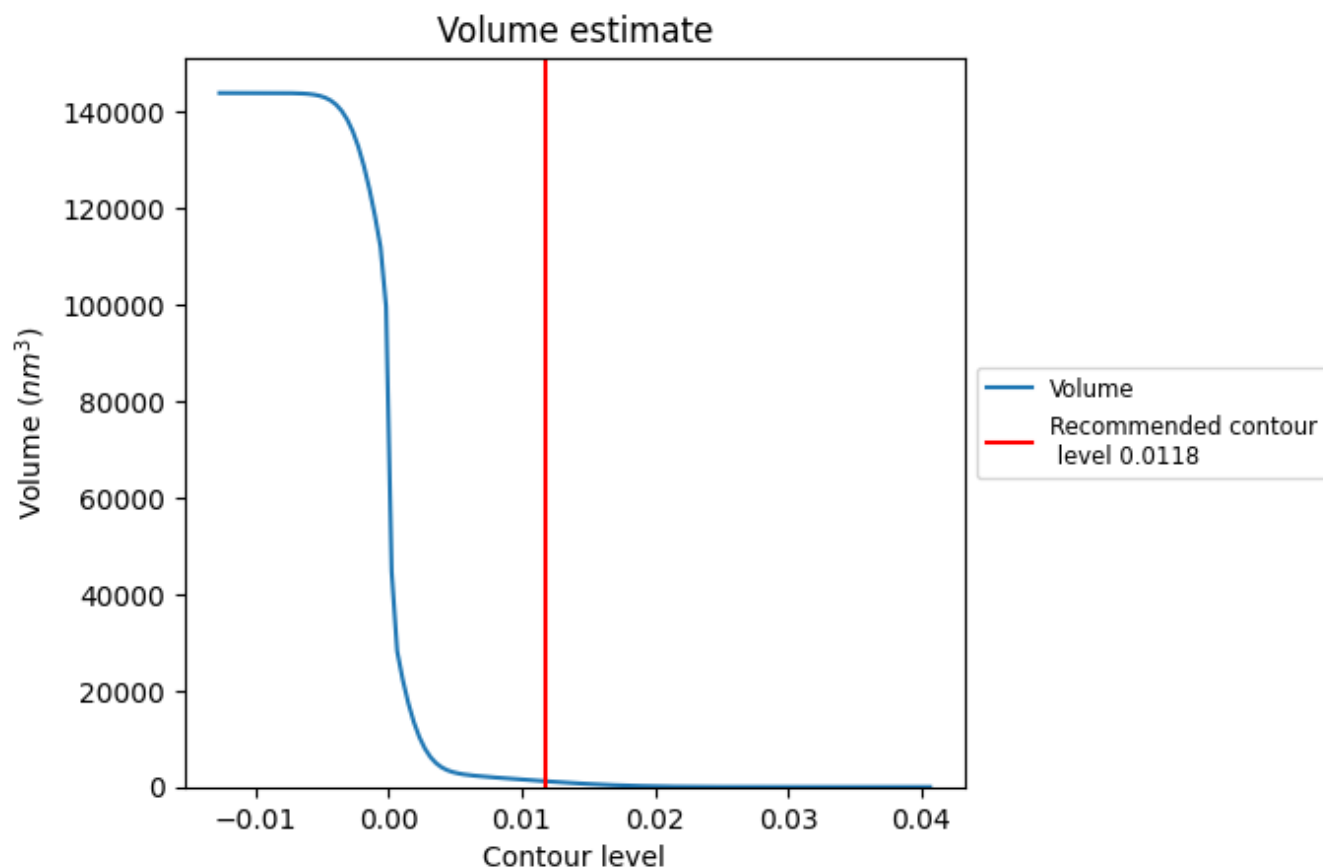
This section contains the results of statistical analysis of the map.

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.

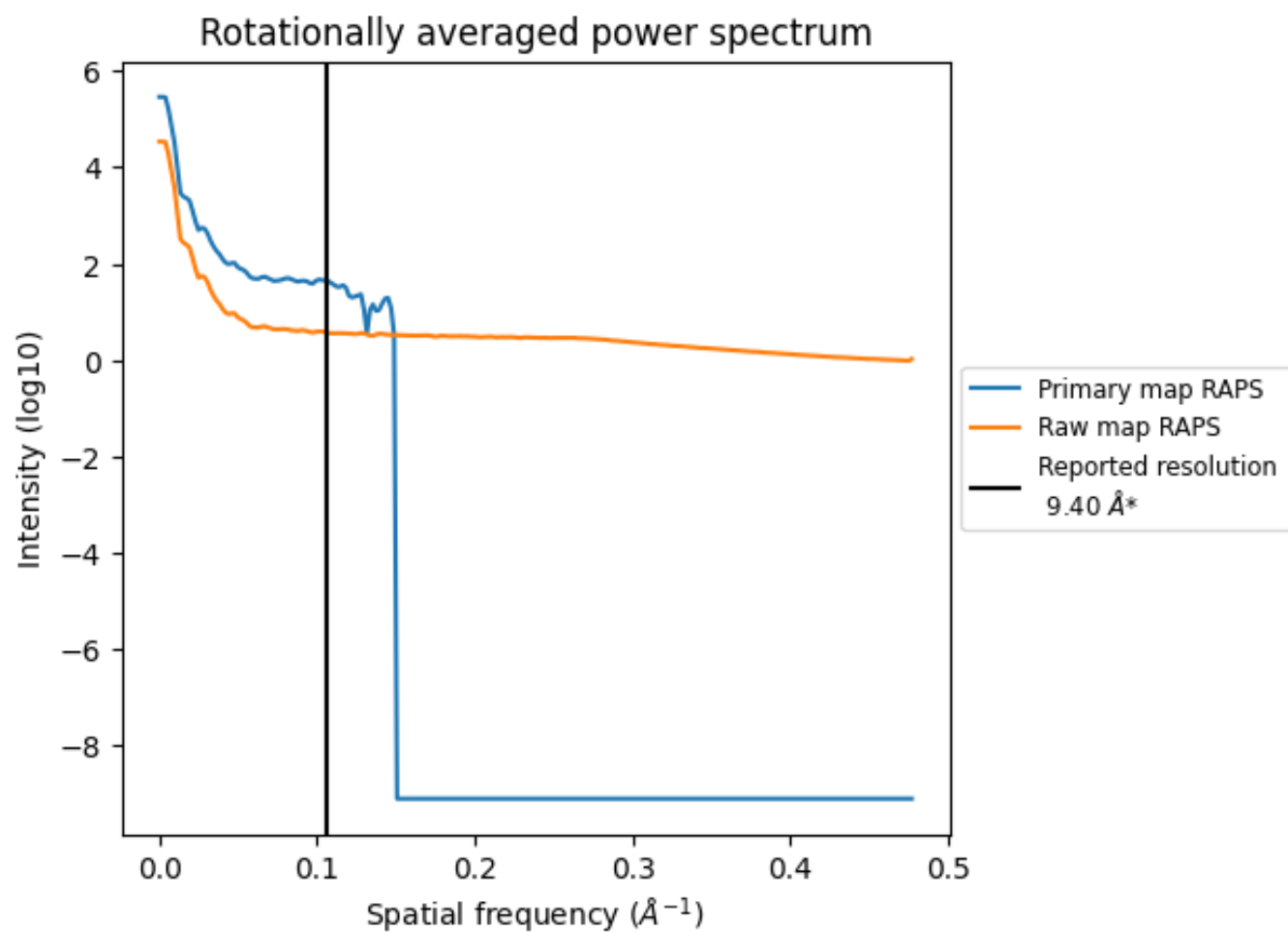
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1185 nm³; this corresponds to an approximate mass of 1070 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 ⓘ

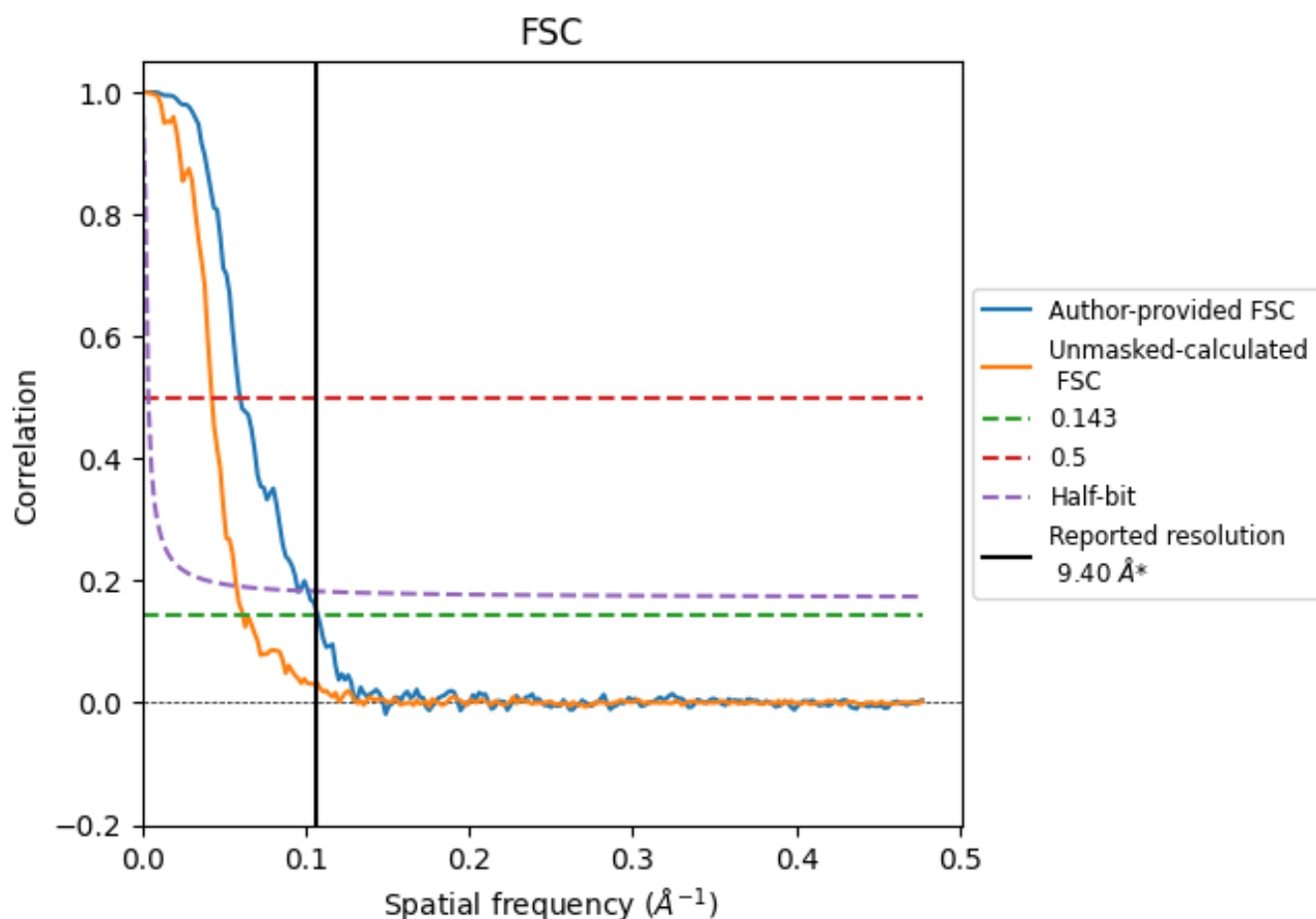


*Reported resolution corresponds to spatial frequency of 0.106 \AA^{-1}

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 0.106 Å⁻¹

8.2 Resolution estimates [i](#)

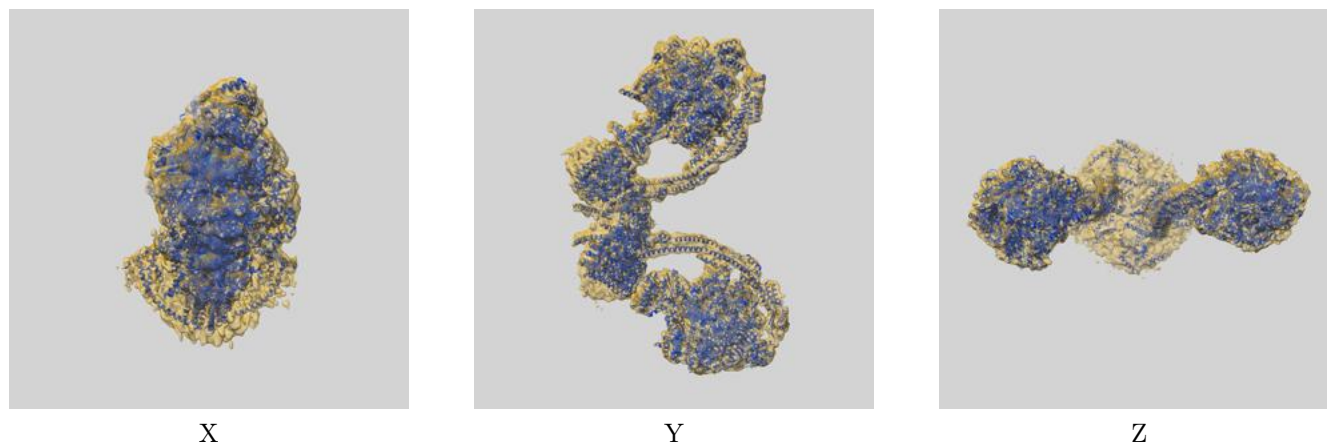
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.40	-	-
Author-provided FSC curve	9.32	16.72	10.49
Unmasked-calculated*	16.23	23.47	17.39

*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 16.23 differs from the reported value 9.4 by more than 10 %

9 Map-model fit [i](#)

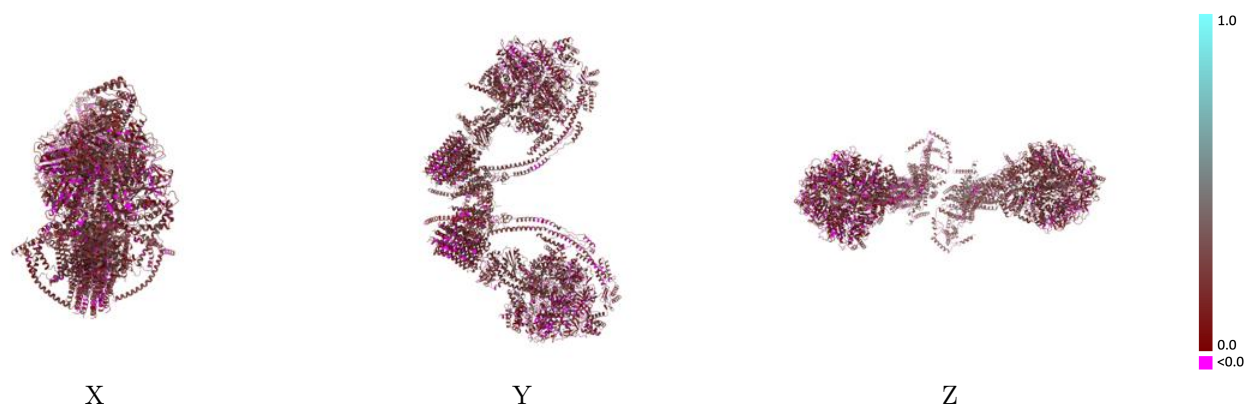
This section contains information regarding the fit between EMDB map EMD-11431 and PDB model 7AJE. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



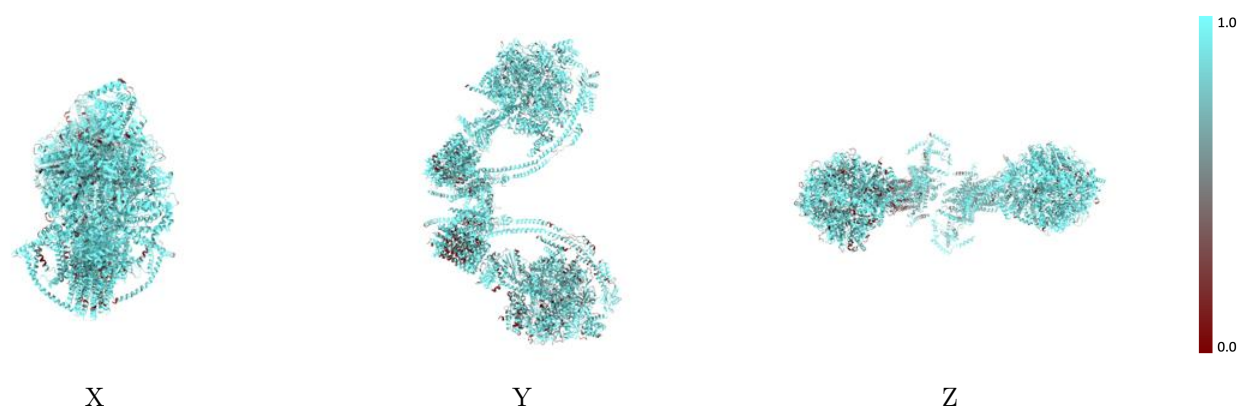
The images above show the 3D surface view of the map at the recommended contour level 0.0118 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



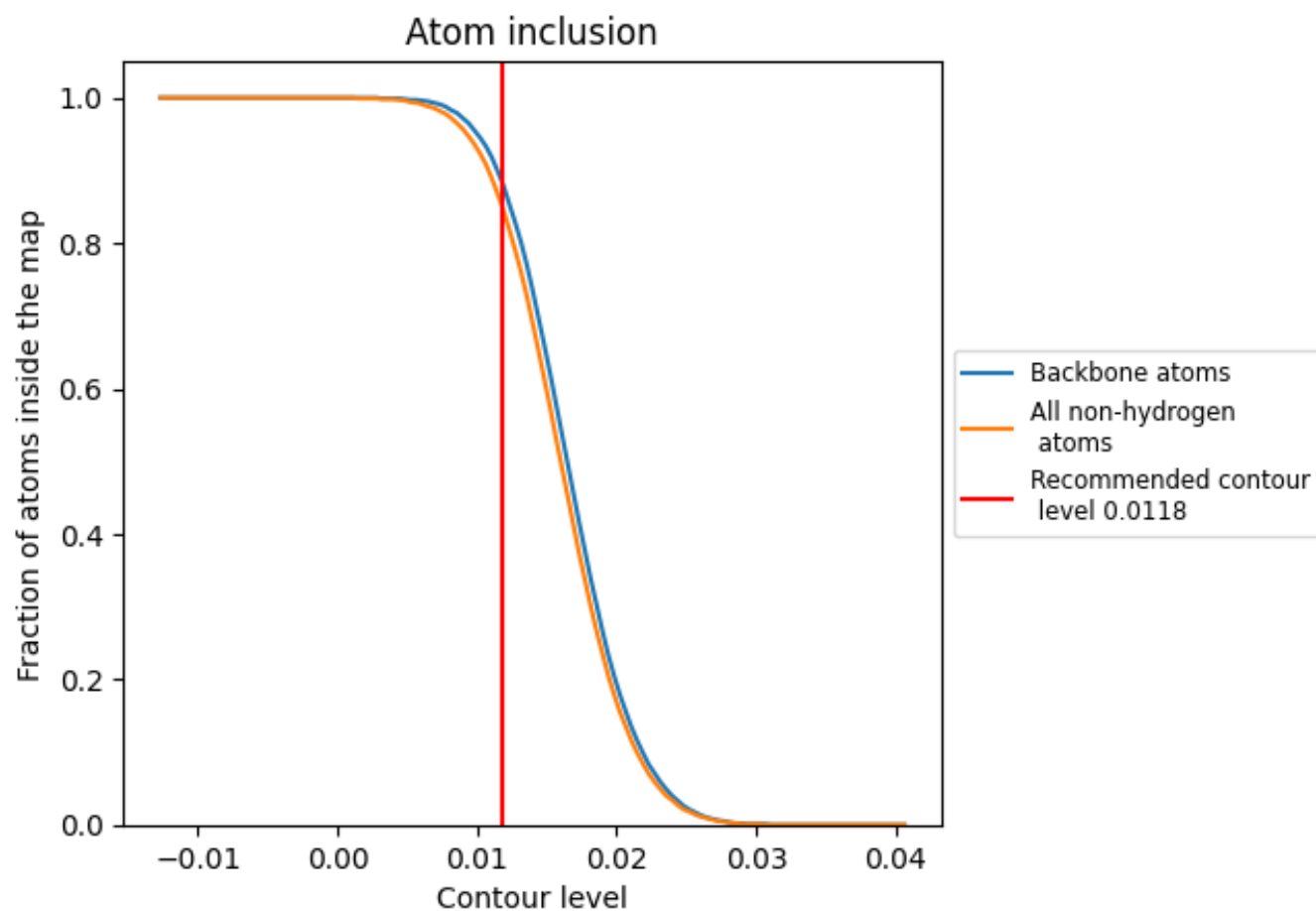
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0118).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.0118) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8520	 0.1770
8	 0.9160	 0.2090
A	 0.9340	 0.1910
A8	 0.9020	 0.2460
AA	 0.7820	 0.1380
AB	 0.8150	 0.1400
AC	 0.8210	 0.1690
AD	 0.8170	 0.1400
AE	 0.7980	 0.1390
AF	 0.8360	 0.1720
AG	 0.8760	 0.2280
AH	 0.9050	 0.1860
AI	 0.7550	 0.2040
AJ	 0.6540	 0.1590
AK	 0.7600	 0.1490
AL	 0.6180	 0.1020
AM	 0.7090	 0.1910
AN	 0.8380	 0.1900
AO	 0.6180	 0.1060
AP	 0.7580	 0.1300
AQ	 0.7280	 0.0870
AR	 0.8160	 0.1320
AS	 0.8400	 0.1710
Aa	 0.8330	 0.2040
Ab	 0.8100	 0.1640
Ad	 0.7490	 0.1700
Ae	 0.8200	 0.1670
Af	 0.6660	 0.1120
Ag	 0.9180	 0.1800
Ah	 0.6080	 0.1920
Aj	 0.8740	 0.2070
Ak	 0.7740	 0.1740
B	 0.9110	 0.2110
C	 0.8740	 0.1510
D	 0.9070	 0.1740



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Chain	Atom inclusion	Q-score
E	 0.9040	 0.1970
F	 0.9240	 0.1760
G	 0.9510	 0.2420
H	 0.9430	 0.2400
I	 0.9360	 0.2460
J	 0.8660	 0.2170
K	 0.9050	 0.2140
L	 0.8210	 0.1780
M	 0.8860	 0.1980
N	 0.9190	 0.1830
O	 0.8910	 0.1930
P	 0.8550	 0.1490
Q	 0.9000	 0.2040
R	 0.8520	 0.1770
S	 0.9150	 0.2020
a	 0.8440	 0.2180
b	 0.9160	 0.2190
d	 0.8970	 0.2070
e	 0.9420	 0.2180
f	 0.7010	 0.1240
g	 0.9460	 0.1880
h	 0.8950	 0.1760
j	 0.9030	 0.2490
k	 0.8310	 0.2010