



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 09:20 PM UTC

PDB ID : 7AJF / pdb_00007ajf
EMDB ID : EMD-11432
Title : bovine ATP synthase dimer state2:state2
Authors : Spikes, T.E.; Montgomery, M.G.; Walker, J.E.
Deposited on : 2020-09-29
Resolution : 8.45 Å(reported)
Based on initial model : 6ZQM

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

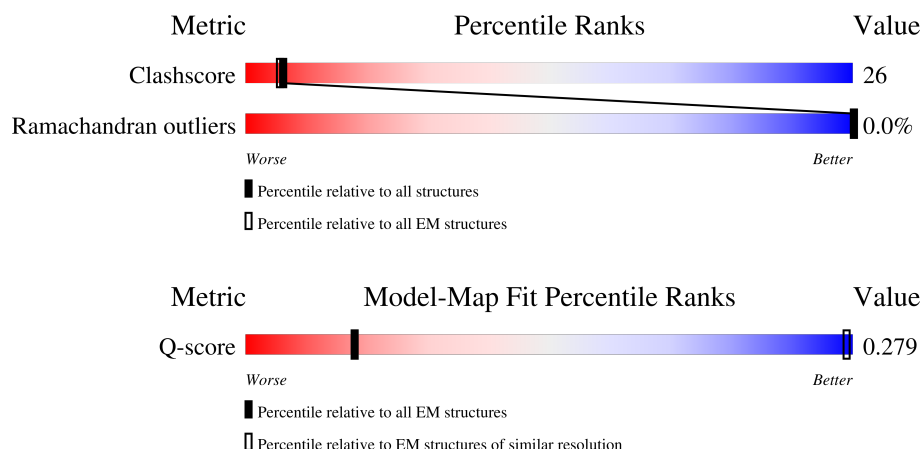
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.45 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.



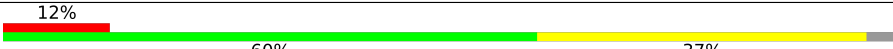
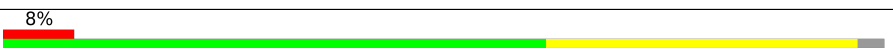
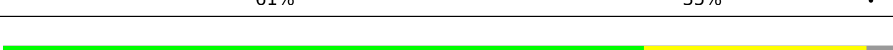
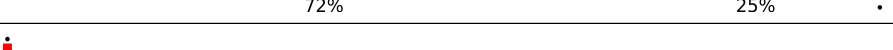
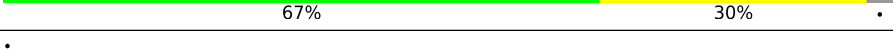
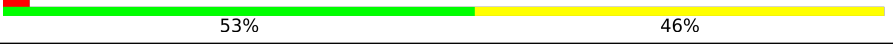
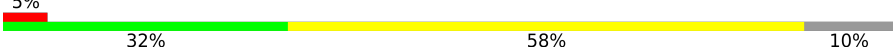
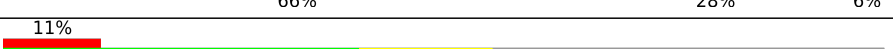
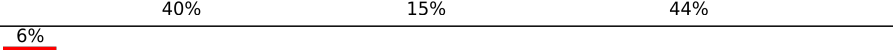
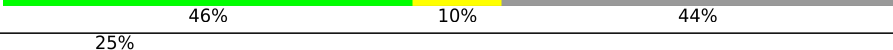
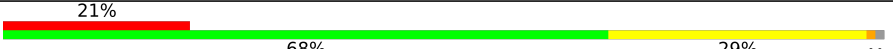
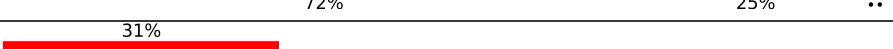
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	328 (8.00 - 9.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	510	7% 68% 27% 5%
1	AA	510	11% 57% 38% 5%
1	AB	510	10% 58% 39% 5%
1	AC	510	10% 61% 37% 5%
1	B	510	71% 26% 5%

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Mol	Chain	Length	Quality of chain
1	C	510	
2	AD	482	
2	AE	482	
2	AF	482	
2	D	482	
2	E	482	
2	F	482	
3	AG	273	
3	G	273	
4	AH	146	
4	H	146	
5	AI	50	
5	I	50	
6	AJ	84	
6	J	84	
7	AK	75	
7	AL	75	
7	AM	75	
7	AN	75	
7	AO	75	
7	AP	75	
7	AQ	75	
7	AR	75	
7	K	75	
7	L	75	

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Mol	Chain	Length	Quality of chain
7	M	75	
7	N	75	
7	O	75	
7	P	75	
7	Q	75	
7	R	75	
8	AS	190	
8	S	190	
9	Aa	226	
9	a	226	
10	Ab	214	
10	b	214	
11	Ad	160	
11	d	160	
12	Ae	70	
12	e	70	
13	Af	87	
13	f	87	
14	Ag	102	
14	g	102	
15	Ah	76	
15	h	76	
16	Aj	60	
16	j	60	
17	Ak	57	

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Mol	Chain	Length	Quality of chain
17	k	57	12% 47% 16% 37%
18	8	66	53% 9% 38%
18	A8	66	5% 59% 38%

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 51354 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 subunit alpha, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	486	Total	C	N	O	0	0
			2383	1411	486	486		
1	B	495	Total	C	N	O	0	0
			2428	1438	495	495		
1	C	501	Total	C	N	O	0	0
			2457	1455	501	501		
1	AA	486	Total	C	N	O	0	0
			2383	1411	486	486		
1	AB	495	Total	C	N	O	0	0
			2428	1438	495	495		
1	AC	501	Total	C	N	O	0	0
			2457	1455	501	501		

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
AB	481	GLY	SER	microheterogeneity	UNP P19483
AC	1	GLU	GLN	variant	UNP P19483
AC	481	GLY	SER	microheterogeneity	UNP P19483

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

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

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

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

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

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

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

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

- Molecule 6 is a protein called ATPase inhibitor, mitochondrial.

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

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

- Molecule 7 is a protein called ATP synthase F(0) complex subunit C2, mitochondrial.

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

- Molecule 8 is a protein called ATP synthase subunit O, mitochondrial.

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

- Molecule 9 is a protein called ATP synthase subunit a.

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

- Molecule 10 is a protein called ATP synthase F(0) complex subunit B1, mitochondrial.

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

- Molecule 11 is a protein called ATP synthase subunit d, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	d	154	Total	C	N	O	0	0
			768	460	154	154		
11	Ad	154	Total	C	N	O	0	0
			768	460	154	154		

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

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

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

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

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

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

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

- Molecule 15 is a protein called ATP synthase-coupling factor 6, mitochondrial.

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

- Molecule 16 is a protein called ATP synthase subunit ATP5MPL, mitochondrial.

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

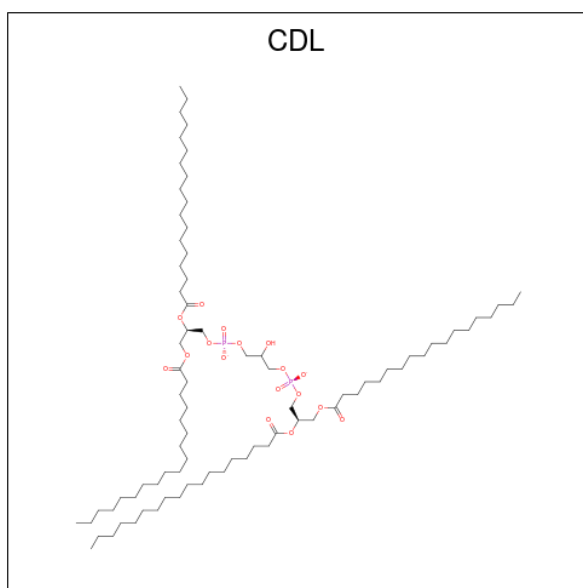
- Molecule 17 is a protein called ATP synthase membrane subunit DAPIT, mitochondrial.

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

- Molecule 18 is a protein called ATP synthase protein 8.

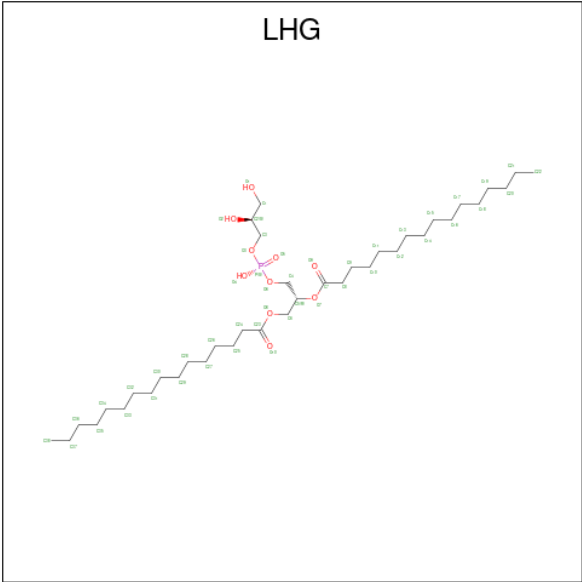
Mol	Chain	Residues	Atoms				AltConf	Trace
18	A8	41	Total	C	N	O	0	0
			205	123	41	41		
18	8	41	Total	C	N	O	0	0
			205	123	41	41		

- 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	b	1	Total	C	O	P	0
			83	64	17	2	
19	b	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	
19	Ab	1	Total	C	O	P	0
			78	59	17	2	

- Molecule 20 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: $C_{38}H_{75}O_{10}P$).

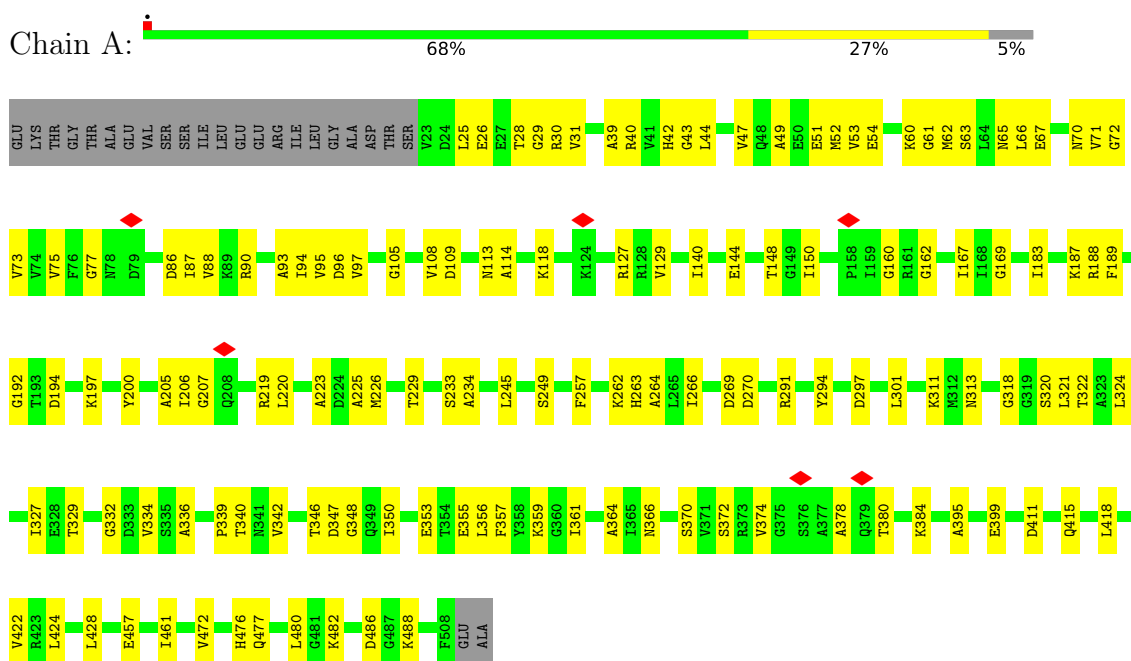


Mol	Chain	Residues	Atoms				AltConf
20	b	1	Total	C	O	P	0
			49	38	10	1	
20	f	1	Total	C	O	P	0
			39	28	10	1	
20	Af	1	Total	C	O	P	0
			49	38	10	1	
20	Af	1	Total	C	O	P	0
			39	28	10	1	

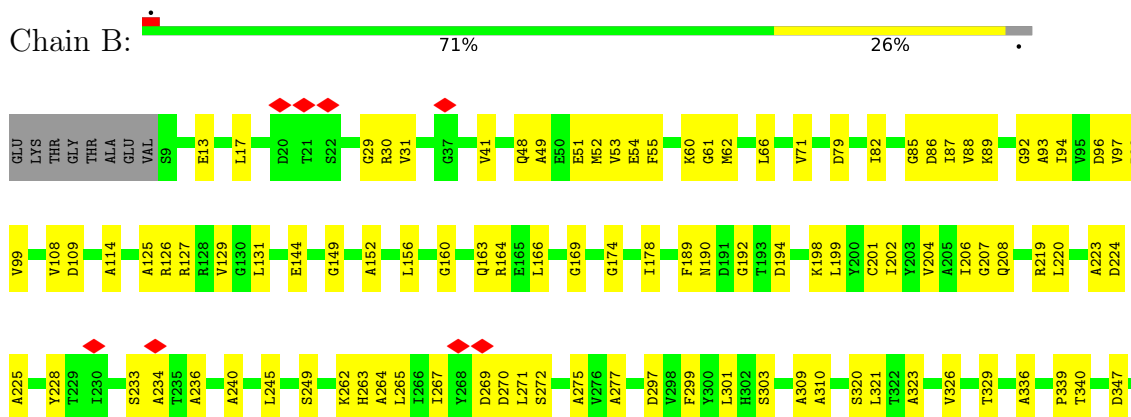
3 Residue-property plots

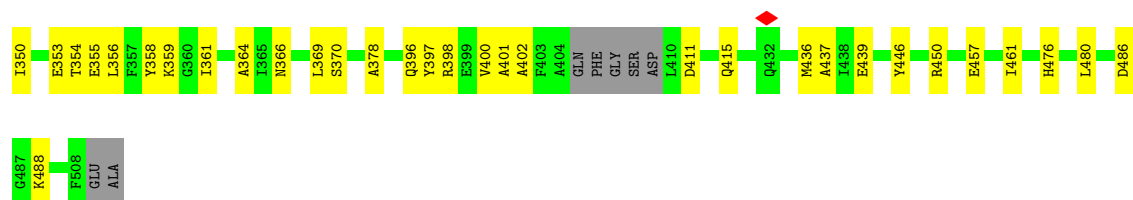
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: ATP synthase subunit alpha, mitochondrial

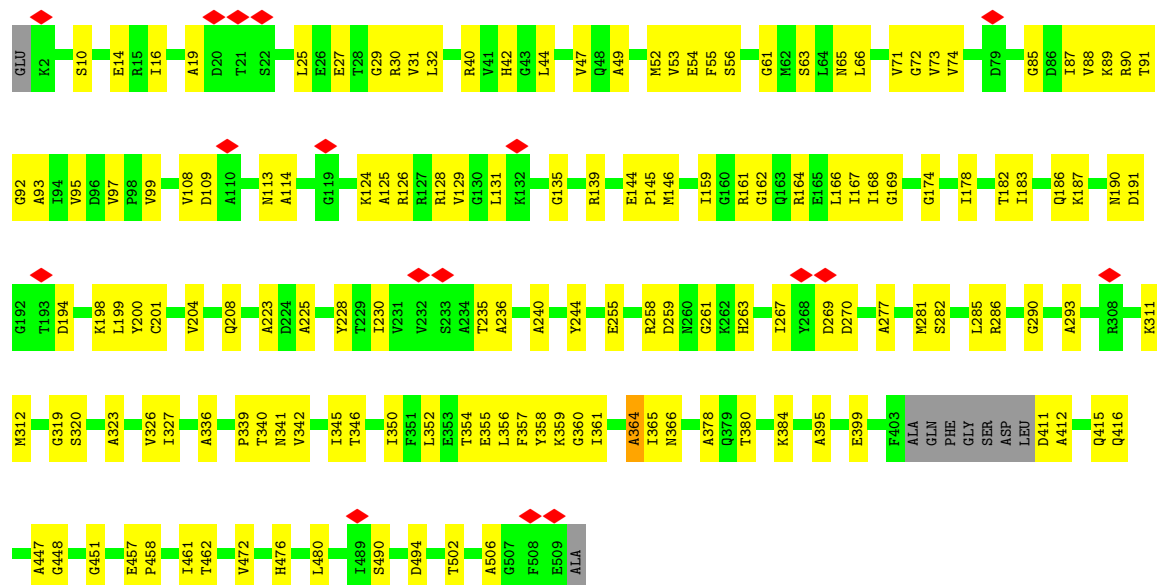


- Molecule 1: ATP synthase subunit alpha, mitochondrial

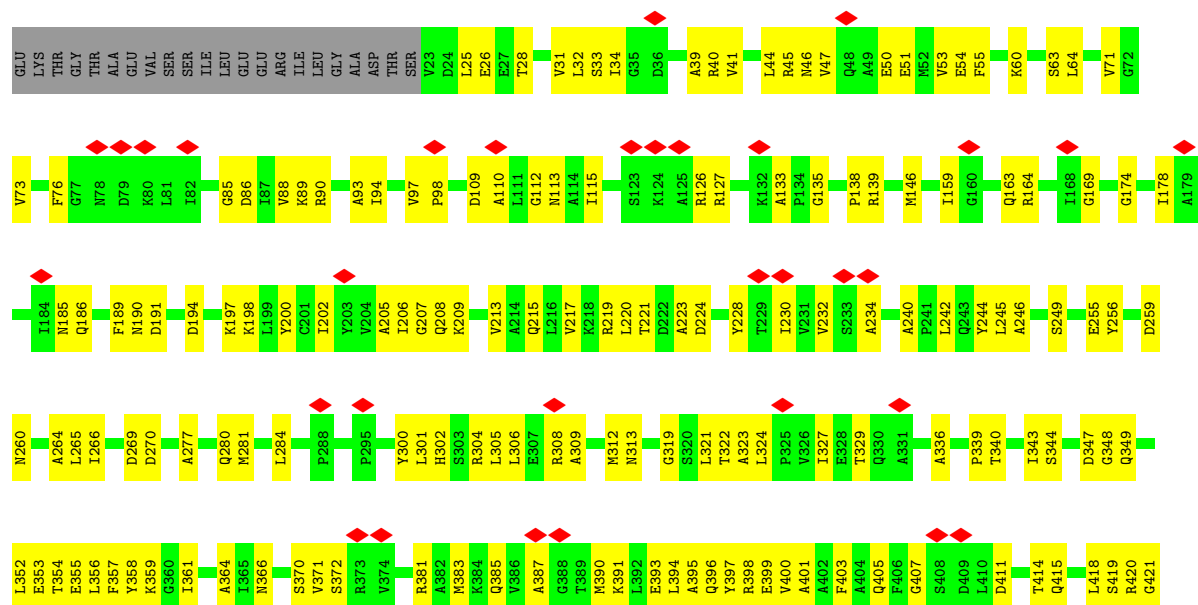




- Molecule 1: ATP synthase subunit alpha, mitochondrial



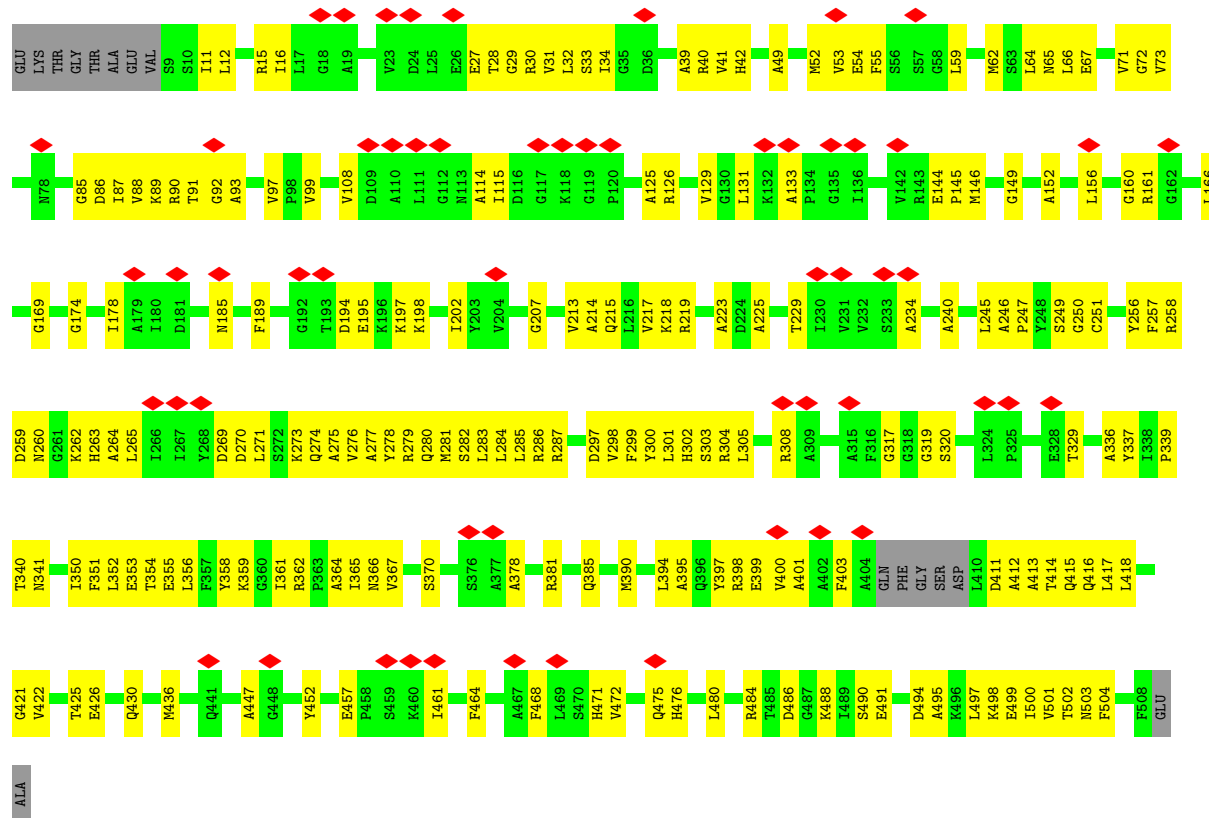
- Molecule 1: ATP synthase subunit alpha, mitochondrial





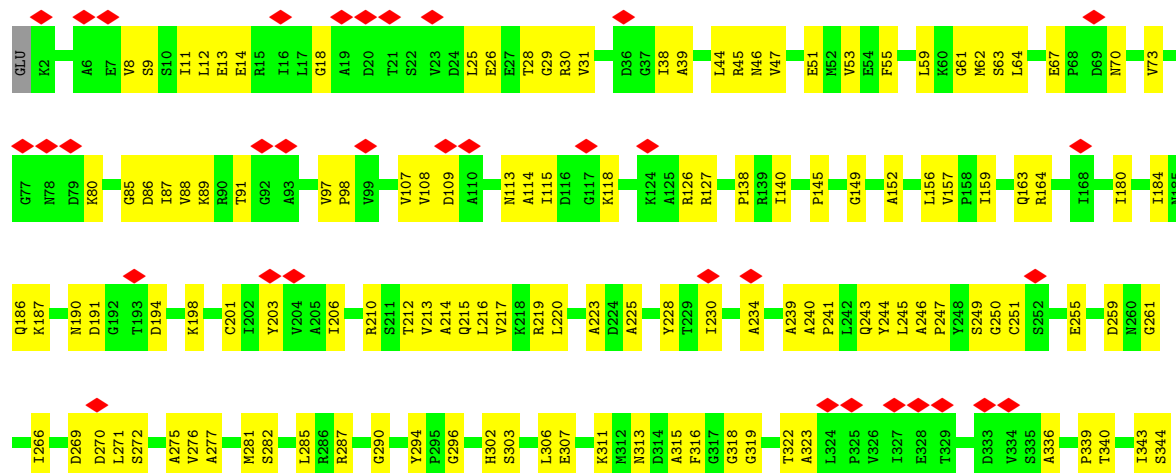
• Molecule 1: ATP synthase subunit alpha, mitochondrial

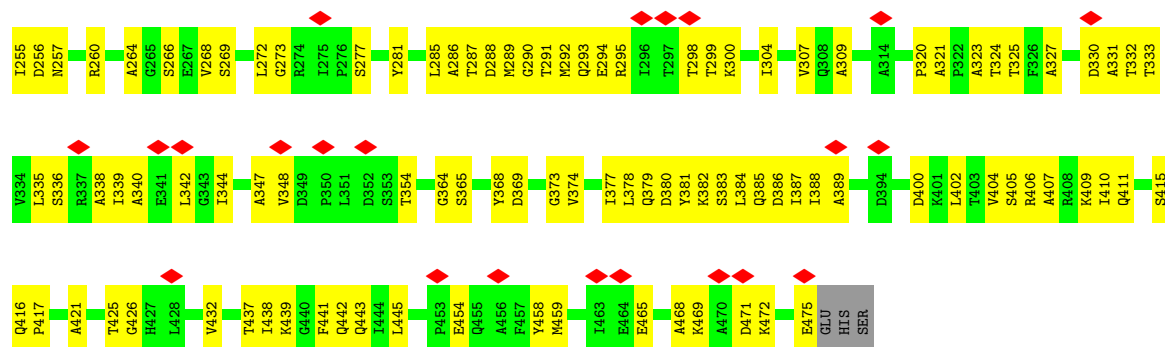
Chain AB: 11% 58% 39%



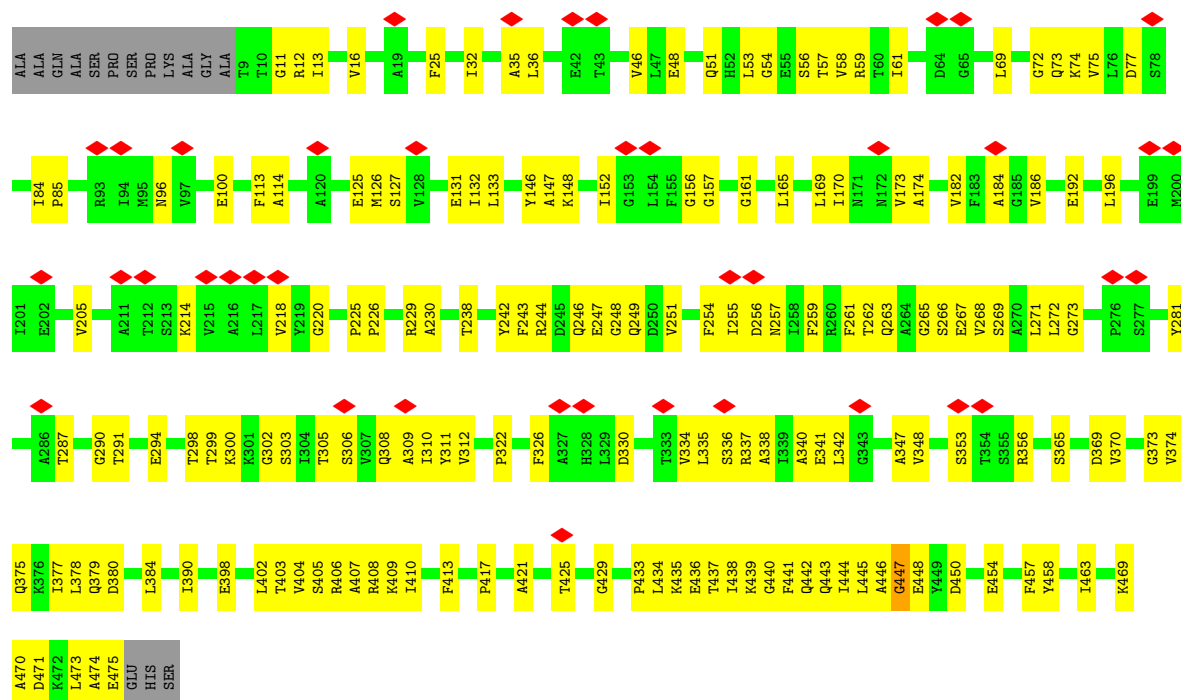
• Molecule 1: ATP synthase subunit alpha, mitochondrial

Chain AC: 10% 61% 37%

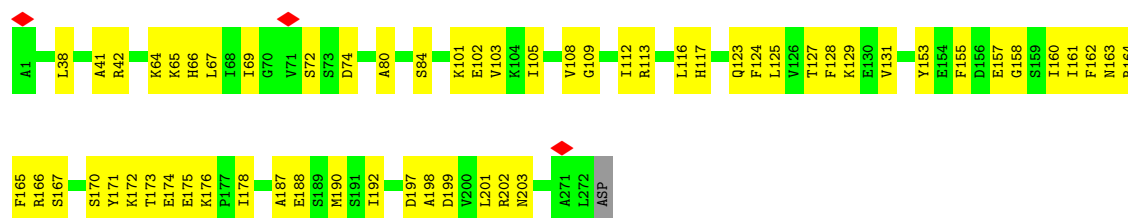
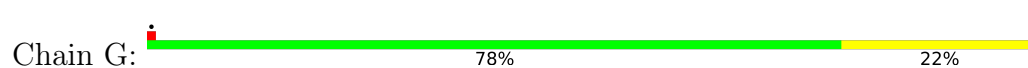




• Molecule 2: ATP synthase subunit beta, mitochondrial

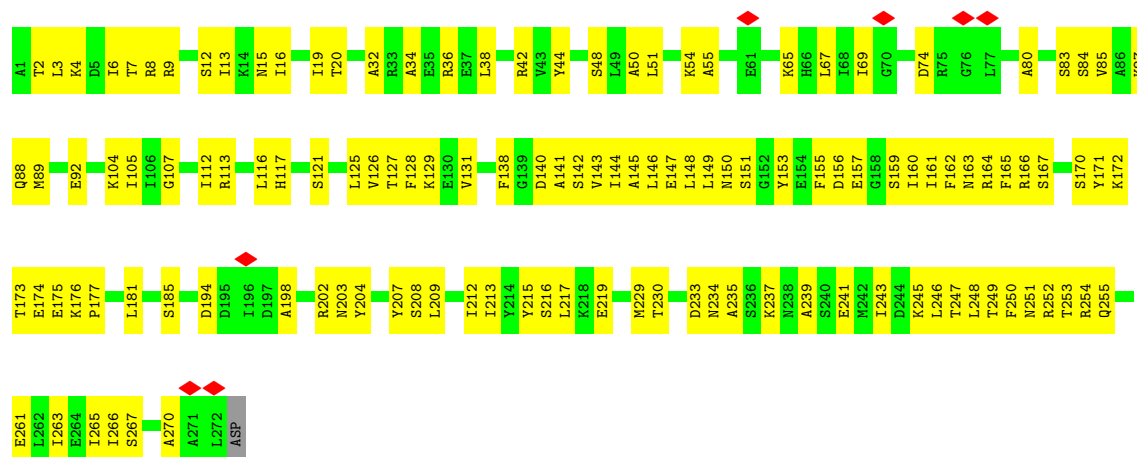


• Molecule 3: ATP synthase subunit gamma, mitochondrial



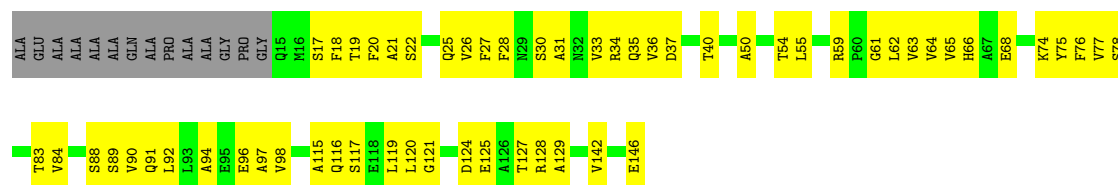
• Molecule 3: ATP synthase subunit gamma, mitochondrial





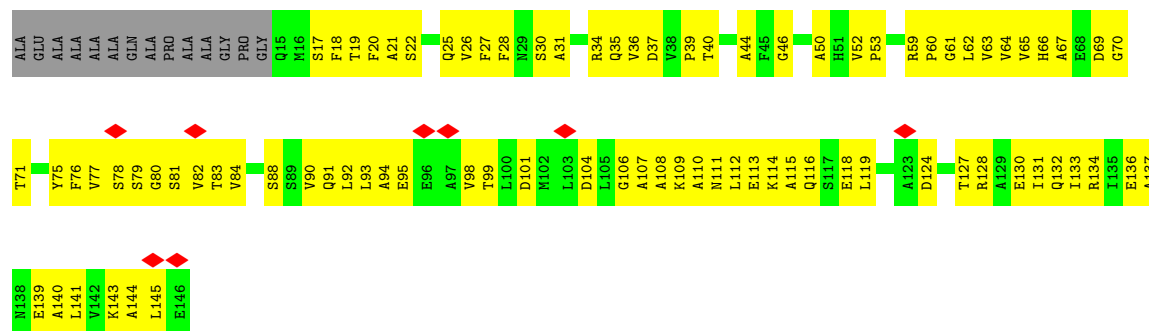
- Molecule 4: ATP synthase subunit delta, mitochondrial

Chain H: 51% 40% 10%



- Molecule 4: ATP synthase subunit delta, mitochondrial

Chain AH: 5% 32% 58% 10%



- Molecule 5: ATP synthase subunit epsilon, mitochondrial

Chain I: 6% 66% 28% 6%



- Molecule 5: ATP synthase subunit epsilon, mitochondrial

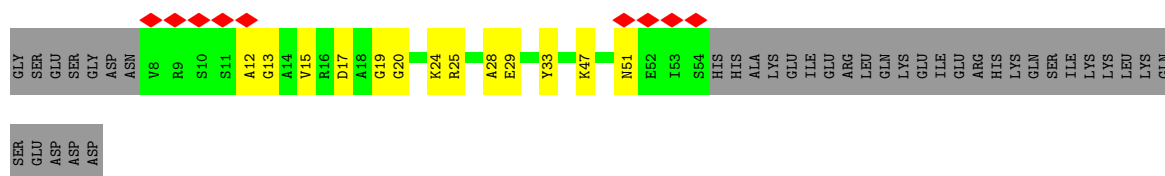
Chain AI: 10% 60% 34% 6%



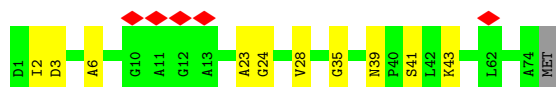
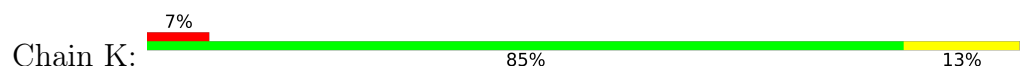
- Molecule 6: ATPase inhibitor, mitochondrial



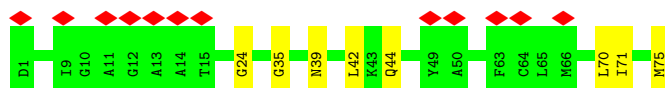
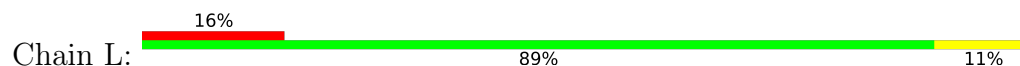
- Molecule 6: ATPase inhibitor, mitochondrial



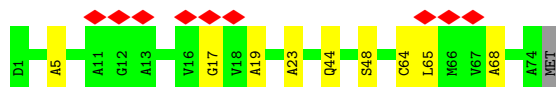
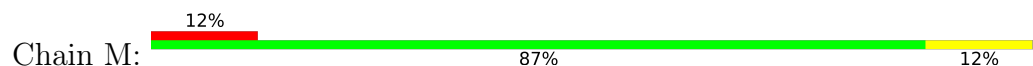
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



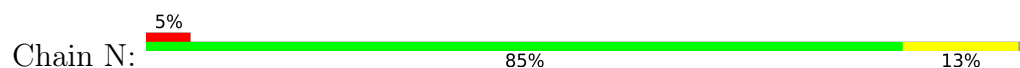
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial

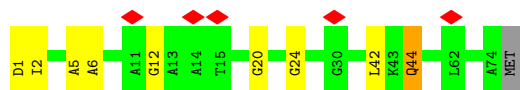
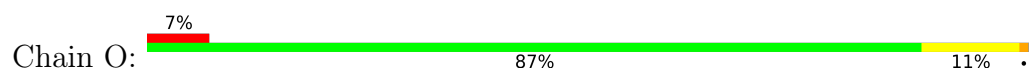


- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial

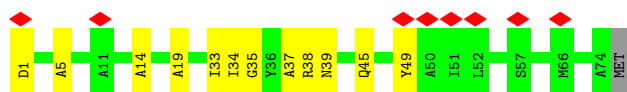
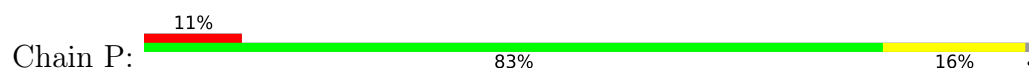




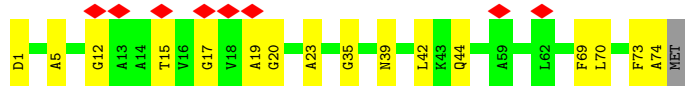
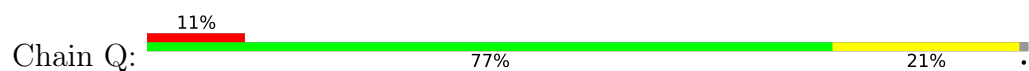
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



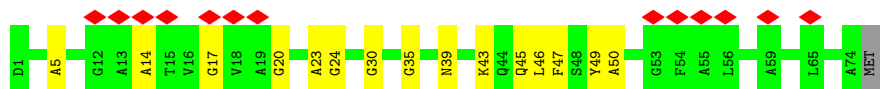
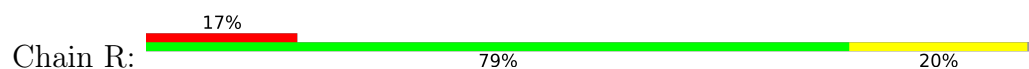
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



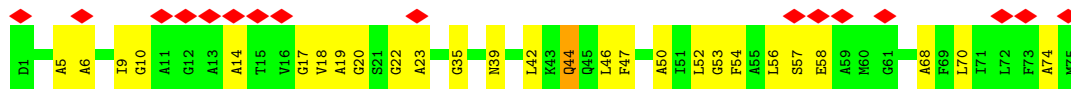
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



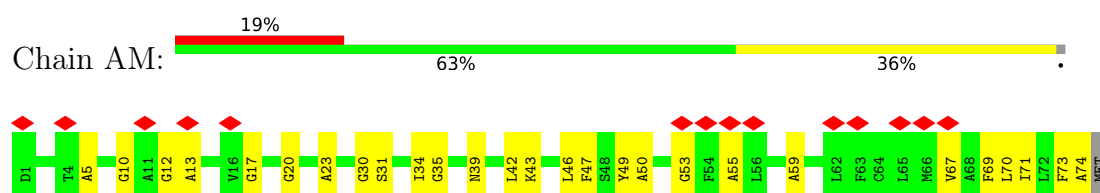
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



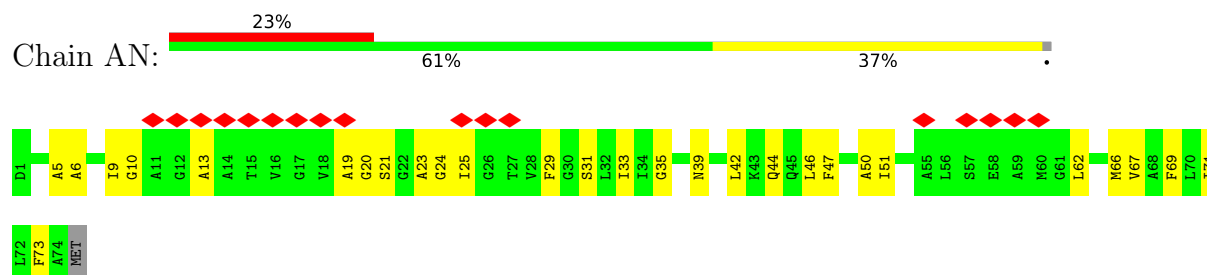
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



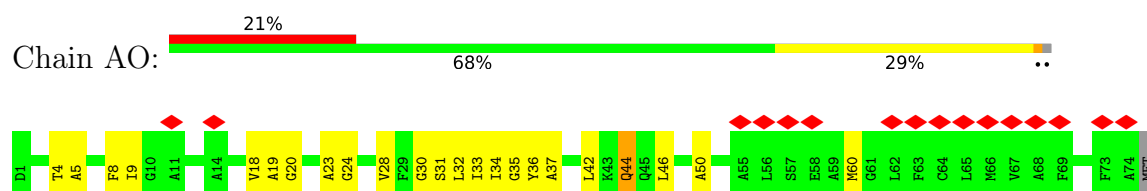
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



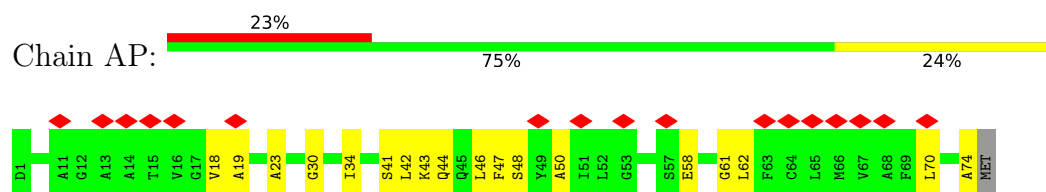
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



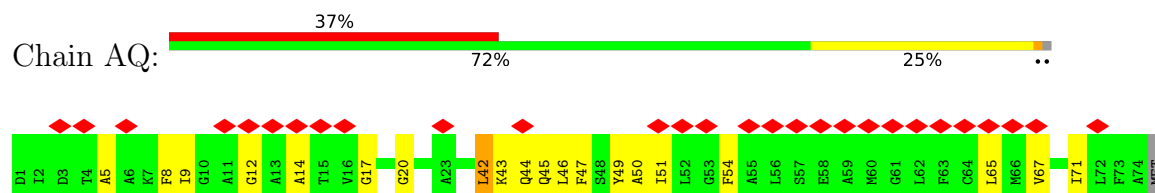
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



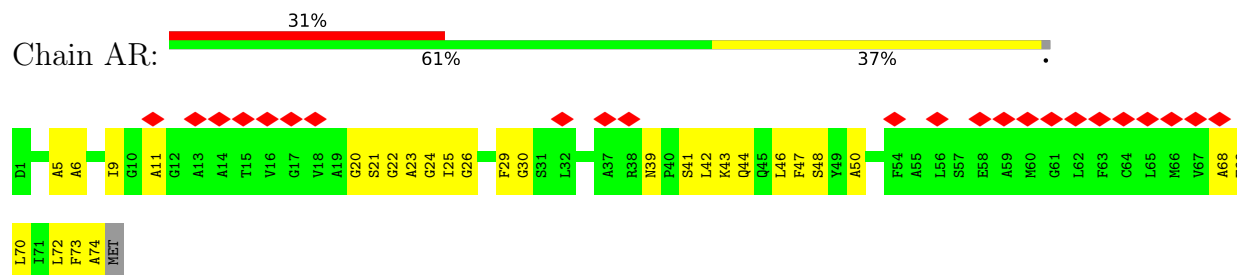
- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial

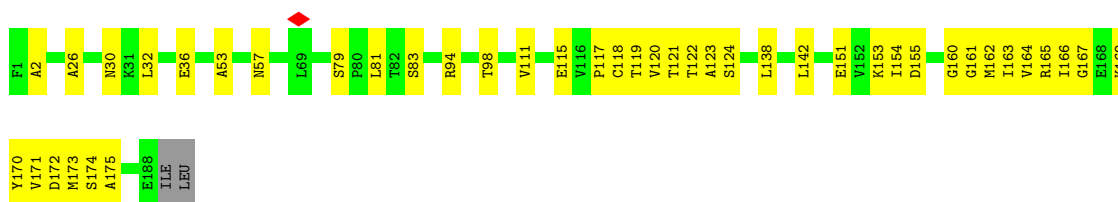


- Molecule 7: ATP synthase F(0) complex subunit C2, mitochondrial



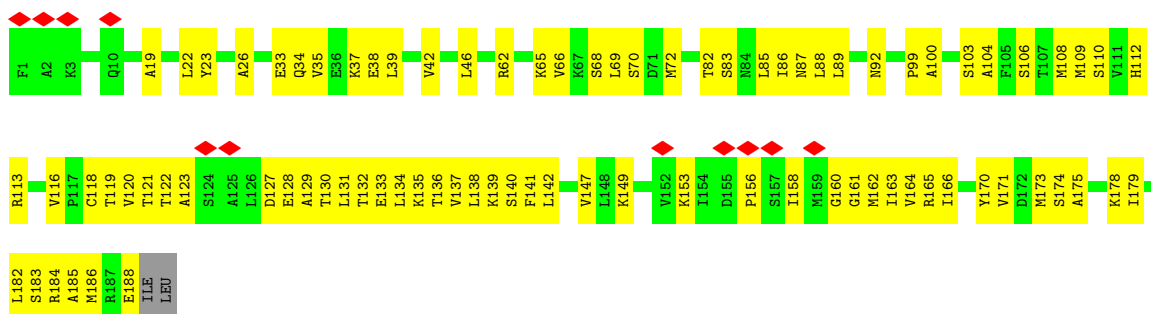
- Molecule 8: ATP synthase subunit O, mitochondrial

Chain S: 

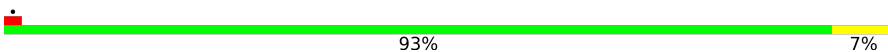


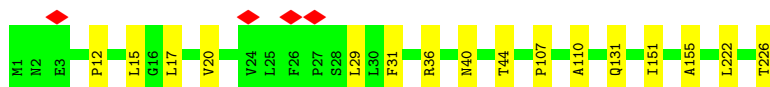
- Molecule 8: ATP synthase subunit O, mitochondrial

Chain AS: 



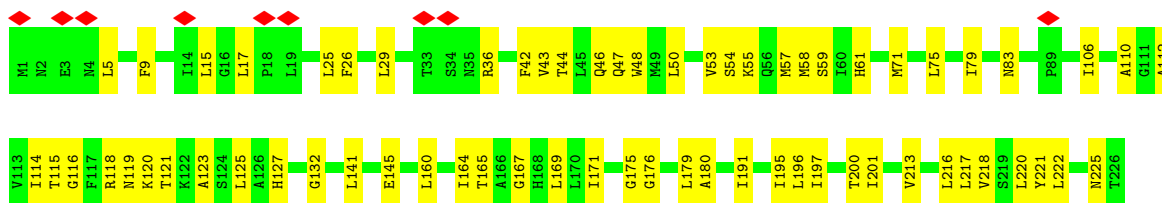
- Molecule 9: ATP synthase subunit a

Chain a: 

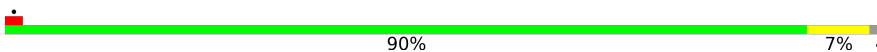


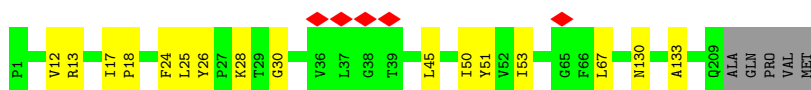
- Molecule 9: ATP synthase subunit a

Chain Aa: 



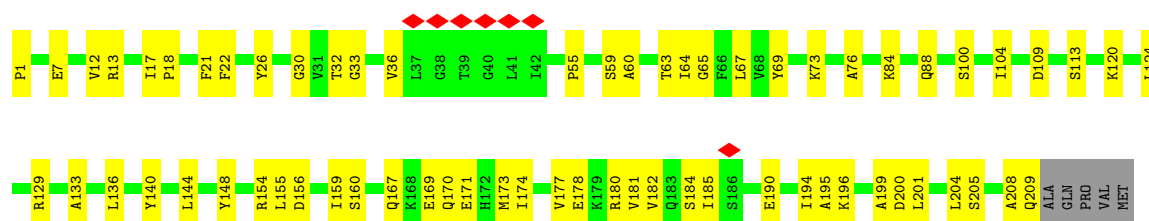
- Molecule 10: ATP synthase F(0) complex subunit B1, mitochondrial

Chain b: 



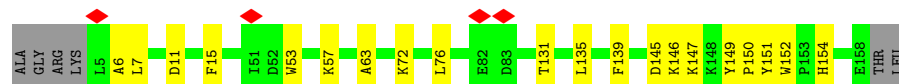
- Molecule 10: ATP synthase F(0) complex subunit B1, mitochondrial

Chain Ab:  67% 31%



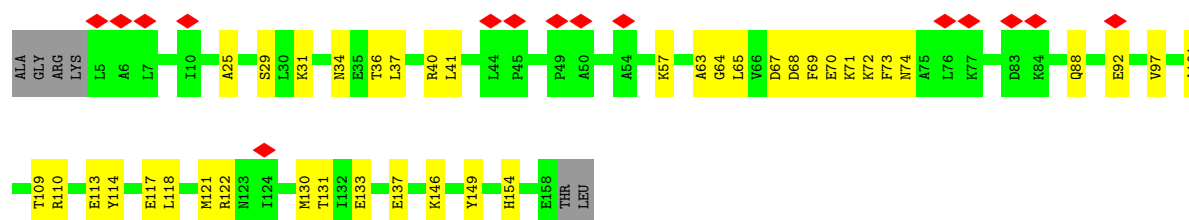
- Molecule 11: ATP synthase subunit d, mitochondrial

Chain d:  84% 12%



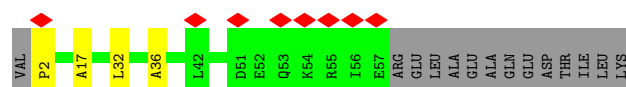
- Molecule 11: ATP synthase subunit d, mitochondrial

Chain Ad:  9% 72% 24%



- Molecule 12: ATP synthase subunit e, mitochondrial

Chain e:  11% 74% 6% 20%



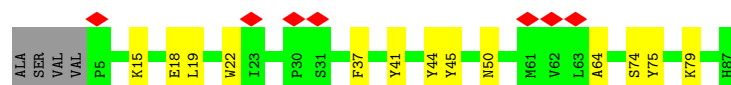
- Molecule 12: ATP synthase subunit e, mitochondrial

Chain Ae:  6% 64% 16% 20%

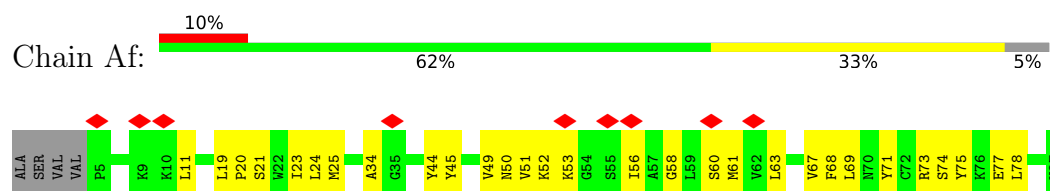


- Molecule 13: ATP synthase subunit f, mitochondrial

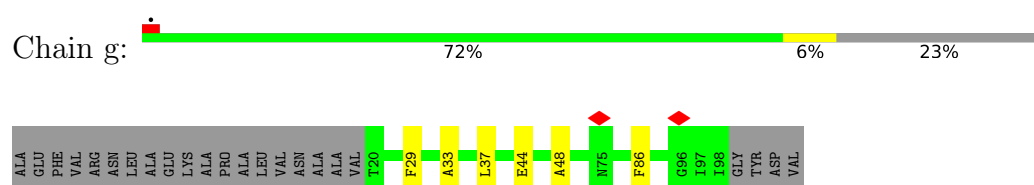
Chain f:  8% 80% 15% 5%



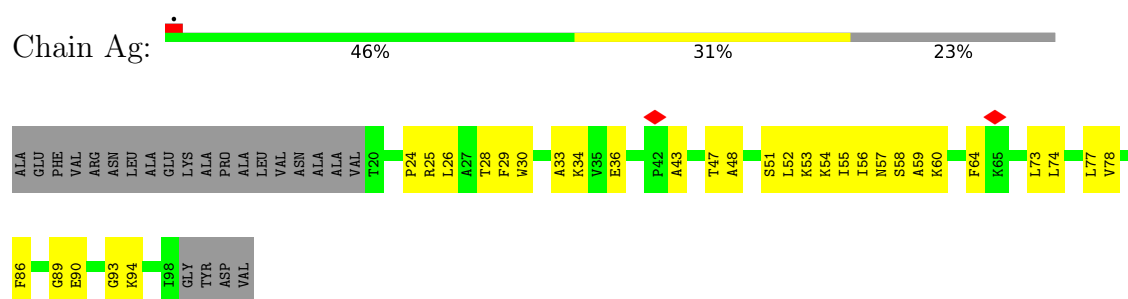
- Molecule 13: ATP synthase subunit f, mitochondrial



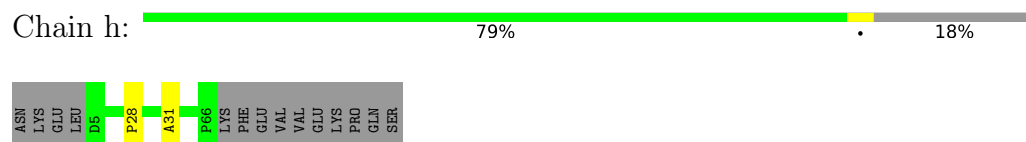
- Molecule 14: ATP synthase subunit g, mitochondrial



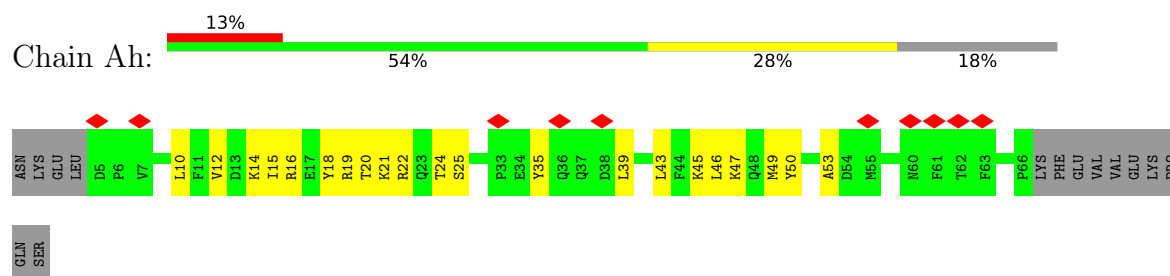
- Molecule 14: ATP synthase subunit g, mitochondrial



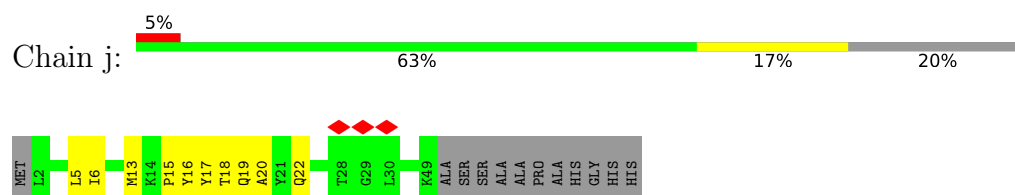
- Molecule 15: ATP synthase-coupling factor 6, mitochondrial



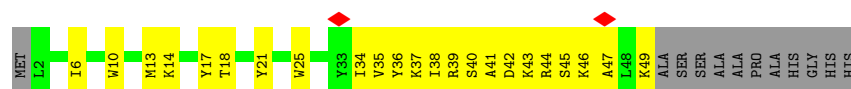
- Molecule 15: ATP synthase-coupling factor 6, mitochondrial



- Molecule 16: ATP synthase subunit ATP5MPL, mitochondrial



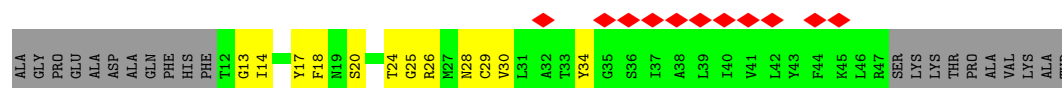
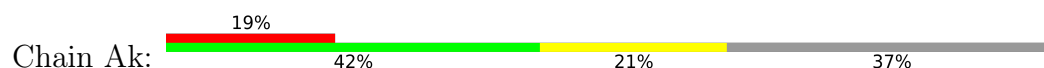
- Molecule 16: ATP synthase subunit ATP5MPL, mitochondrial



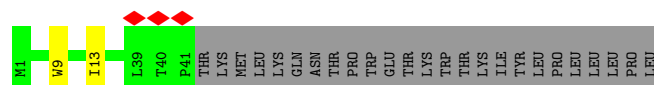
- Molecule 17: ATP synthase membrane subunit DAPIT, mitochondrial



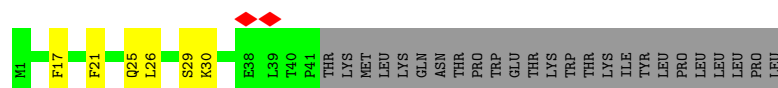
- Molecule 17: ATP synthase membrane subunit DAPIT, mitochondrial



- Molecule 18: ATP synthase protein 8



- Molecule 18: ATP synthase protein 8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15370	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	0.044	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0146	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: M3L, CDL, LHG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.30	0/2382	0.59	0/3305
1	AA	0.25	0/2382	0.58	1/3305 (0.0%)
1	AB	0.26	0/2426	0.60	1/3365 (0.0%)
1	AC	0.25	0/2455	0.54	0/3405
1	B	0.32	0/2426	0.60	0/3365
1	C	0.28	0/2455	0.58	1/3405 (0.0%)
2	AD	0.24	0/2299	0.58	1/3190 (0.0%)
2	AE	0.27	0/2289	0.58	1/3176 (0.0%)
2	AF	0.26	0/2289	0.57	2/3176 (0.1%)
2	D	0.29	0/2299	0.61	3/3190 (0.1%)
2	E	0.32	0/2289	0.61	0/3176
2	F	0.31	0/2289	0.59	1/3176 (0.0%)
3	AG	0.30	0/1346	0.54	0/1875
3	G	0.41	0/1346	0.53	0/1875
4	AH	0.32	0/652	0.59	0/907
4	H	0.39	0/652	0.57	0/907
5	AI	0.31	0/232	0.59	0/322
5	I	0.34	0/232	0.57	0/322
6	AJ	0.22	0/230	0.45	0/318
6	J	0.30	0/230	0.46	0/318
7	AK	0.24	0/353	0.57	0/486
7	AL	0.20	0/358	0.48	0/493
7	AM	0.19	0/353	0.48	0/486
7	AN	0.22	0/353	0.62	0/486
7	AO	0.21	0/353	0.57	0/486
7	AP	0.19	0/353	0.49	0/486
7	AQ	0.24	0/353	0.52	0/486
7	AR	0.31	0/353	0.64	0/486
7	K	0.30	0/353	0.59	0/486
7	L	0.26	0/358	0.49	0/493
7	M	0.23	0/353	0.42	0/486
7	N	0.27	0/353	0.48	0/486

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	O	0.25	0/353	0.49	0/486
7	P	0.29	0/353	0.45	0/486
7	Q	0.26	0/353	0.47	0/486
7	R	0.30	0/353	0.58	0/486
8	AS	0.24	0/930	0.46	0/1295
8	S	0.28	0/930	0.51	0/1295
9	Aa	0.28	0/1118	0.54	0/1557
9	a	0.33	0/1118	0.56	0/1557
10	Ab	0.22	0/1034	0.49	0/1440
10	b	0.26	0/1034	0.44	0/1440
11	Ad	0.27	0/767	0.55	0/1071
11	d	0.30	0/767	0.54	0/1071
12	Ae	0.17	0/276	0.38	0/383
12	e	0.22	0/276	0.35	0/383
13	Af	0.24	0/408	0.58	0/566
13	f	0.31	0/408	0.56	0/566
14	Ag	0.19	0/389	0.56	0/540
14	g	0.20	0/389	0.52	0/540
15	Ah	0.21	0/305	0.63	0/423
15	h	0.26	0/305	0.55	0/423
16	Aj	0.29	0/237	0.60	0/329
16	j	0.28	0/237	0.58	0/329
17	Ak	0.18	0/176	0.44	0/243
17	k	0.17	0/176	0.36	0/243
18	8	0.29	0/204	0.49	0/284
18	A8	0.25	0/204	0.63	0/284
All	All	0.28	0/50546	0.56	11/70130 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AE	0	1
2	E	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	161	GLY	N-CA-C	-7.14	105.86	115.36
2	AF	390	ILE	N-CA-C	-6.86	106.36	112.12
1	C	364	ALA	CA-C-O	-6.77	114.93	121.02
2	AF	447	GLY	N-CA-C	-5.84	105.28	114.10
1	AA	115	ILE	N-CA-C	-5.51	108.13	113.53

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AE	187	GLY	Peptide
2	E	25	PHE	Peptide

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	A	2383	0	1139	99	0
1	AA	2383	0	1139	120	0
1	AB	2428	0	1159	127	0
1	AC	2457	0	1172	118	0
1	B	2428	0	1159	92	0
1	C	2457	0	1172	99	0
2	AD	2300	0	1094	89	0
2	AE	2290	0	1090	111	0
2	AF	2290	0	1090	105	0
2	D	2300	0	1094	80	0
2	E	2290	0	1090	95	0
2	F	2290	0	1090	74	0
3	AG	1347	0	641	78	0
3	G	1347	0	641	44	0
4	AH	653	0	326	63	0
4	H	653	0	326	38	0
5	AI	233	0	119	11	0
5	I	233	0	119	14	0
6	AJ	231	0	124	7	0
6	J	231	0	124	6	0
7	AK	359	0	199	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	AL	364	0	201	17	0
7	AM	359	0	199	20	0
7	AN	359	0	199	19	0
7	AO	359	0	199	13	0
7	AP	359	0	199	11	0
7	AQ	359	0	198	16	0
7	AR	359	0	198	20	0
7	K	359	0	199	10	0
7	L	364	0	201	6	0
7	M	359	0	198	6	0
7	N	359	0	199	8	0
7	O	359	0	199	7	0
7	P	359	0	198	8	0
7	Q	359	0	198	13	0
7	R	359	0	199	17	0
8	AS	931	0	427	50	0
8	S	931	0	427	34	0
9	Aa	1119	0	498	40	0
9	a	1119	0	498	11	0
10	Ab	1035	0	459	40	0
10	b	1035	0	459	14	0
11	Ad	768	0	340	23	0
11	d	768	0	340	14	0
12	Ae	277	0	129	8	0
12	e	277	0	129	4	0
13	Af	409	0	184	21	0
13	f	409	0	184	15	0
14	Ag	390	0	178	21	0
14	g	390	0	178	6	0
15	Ah	306	0	128	12	0
15	h	306	0	128	1	0
16	Aj	238	0	107	18	0
16	j	238	0	107	7	0
17	Ak	177	0	80	7	0
17	k	177	0	80	5	0
18	8	205	0	81	3	0
18	A8	205	0	81	1	0
19	Aa	84	0	115	9	0
19	Ab	161	0	216	19	0
19	a	84	0	115	11	0
19	b	161	0	216	21	0
20	Af	88	0	122	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	b	49	0	74	4	0
20	f	39	0	48	1	0
All	All	51354	0	25219	1981	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 26.

The worst 5 of 1981 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:AS:118:CYS:HA	8:AS:166:ILE:HA	1.53	0.91
2:F:161:GLY:O	2:F:165:LEU:N	2.06	0.89
7:AK:9:ILE:HA	7:AL:10:GLY:HA3	1.54	0.89
5:I:2:ALA:O	5:I:6:GLN:N	2.05	0.89
1:C:53:VAL:HA	1:C:90:ARG:HA	1.56	0.87

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	A	484/510 (95%)	413 (85%)	71 (15%)	0	100	100
1	AA	484/510 (95%)	436 (90%)	48 (10%)	0	100	100
1	AB	491/510 (96%)	427 (87%)	64 (13%)	0	100	100
1	AC	497/510 (98%)	433 (87%)	64 (13%)	0	100	100
1	B	491/510 (96%)	430 (88%)	61 (12%)	0	100	100
1	C	497/510 (98%)	431 (87%)	66 (13%)	0	100	100
2	AD	467/482 (97%)	407 (87%)	60 (13%)	0	100	100
2	AE	465/482 (96%)	402 (86%)	63 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AF	465/482 (96%)	410 (88%)	55 (12%)	0	100	100
2	D	467/482 (97%)	394 (84%)	73 (16%)	0	100	100
2	E	465/482 (96%)	406 (87%)	59 (13%)	0	100	100
2	F	465/482 (96%)	398 (86%)	67 (14%)	0	100	100
3	AG	270/273 (99%)	236 (87%)	34 (13%)	0	100	100
3	G	270/273 (99%)	236 (87%)	34 (13%)	0	100	100
4	AH	130/146 (89%)	110 (85%)	20 (15%)	0	100	100
4	H	130/146 (89%)	116 (89%)	14 (11%)	0	100	100
5	AI	45/50 (90%)	40 (89%)	5 (11%)	0	100	100
5	I	45/50 (90%)	41 (91%)	4 (9%)	0	100	100
6	AJ	45/84 (54%)	42 (93%)	3 (7%)	0	100	100
6	J	45/84 (54%)	44 (98%)	1 (2%)	0	100	100
7	AK	71/75 (95%)	59 (83%)	12 (17%)	0	100	100
7	AL	72/75 (96%)	67 (93%)	4 (6%)	1 (1%)	9	40
7	AM	71/75 (95%)	65 (92%)	6 (8%)	0	100	100
7	AN	71/75 (95%)	67 (94%)	4 (6%)	0	100	100
7	AO	71/75 (95%)	68 (96%)	2 (3%)	1 (1%)	9	40
7	AP	71/75 (95%)	68 (96%)	3 (4%)	0	100	100
7	AQ	71/75 (95%)	66 (93%)	4 (6%)	1 (1%)	9	40
7	AR	71/75 (95%)	68 (96%)	2 (3%)	1 (1%)	9	40
7	K	71/75 (95%)	68 (96%)	3 (4%)	0	100	100
7	L	72/75 (96%)	69 (96%)	3 (4%)	0	100	100
7	M	71/75 (95%)	68 (96%)	3 (4%)	0	100	100
7	N	71/75 (95%)	67 (94%)	4 (6%)	0	100	100
7	O	71/75 (95%)	66 (93%)	4 (6%)	1 (1%)	9	40
7	P	71/75 (95%)	70 (99%)	1 (1%)	0	100	100
7	Q	71/75 (95%)	66 (93%)	5 (7%)	0	100	100
7	R	71/75 (95%)	67 (94%)	4 (6%)	0	100	100
8	AS	186/190 (98%)	171 (92%)	15 (8%)	0	100	100
8	S	186/190 (98%)	165 (89%)	21 (11%)	0	100	100
9	Aa	224/226 (99%)	201 (90%)	23 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	a	224/226 (99%)	198 (88%)	26 (12%)	0	100	100
10	Ab	207/214 (97%)	195 (94%)	12 (6%)	0	100	100
10	b	207/214 (97%)	194 (94%)	13 (6%)	0	100	100
11	Ad	152/160 (95%)	139 (91%)	13 (9%)	0	100	100
11	d	152/160 (95%)	133 (88%)	19 (12%)	0	100	100
12	Ae	54/70 (77%)	51 (94%)	3 (6%)	0	100	100
12	e	54/70 (77%)	51 (94%)	3 (6%)	0	100	100
13	Af	81/87 (93%)	71 (88%)	10 (12%)	0	100	100
13	f	81/87 (93%)	71 (88%)	10 (12%)	0	100	100
14	Ag	77/102 (76%)	72 (94%)	5 (6%)	0	100	100
14	g	77/102 (76%)	71 (92%)	6 (8%)	0	100	100
15	Ah	60/76 (79%)	51 (85%)	9 (15%)	0	100	100
15	h	60/76 (79%)	51 (85%)	9 (15%)	0	100	100
16	Aj	46/60 (77%)	43 (94%)	3 (6%)	0	100	100
16	j	46/60 (77%)	41 (89%)	5 (11%)	0	100	100
17	Ak	34/57 (60%)	33 (97%)	1 (3%)	0	100	100
17	k	34/57 (60%)	33 (97%)	1 (3%)	0	100	100
18	8	39/66 (59%)	34 (87%)	5 (13%)	0	100	100
18	A8	39/66 (59%)	34 (87%)	5 (13%)	0	100	100
All	All	10176/10874 (94%)	9024 (89%)	1147 (11%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	AQ	42	LEU
7	AL	44	GLN
7	AO	44	GLN
7	O	44	GLN
7	AR	42	LEU

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	$\# Z > 2$
7	M3L	AR	43	7	3,4,12	0.85	0	2,4,16	0.04	0
7	M3L	AM	43	7	3,4,12	0.85	0	2,4,16	0.47	0
7	M3L	K	43	7	3,4,12	0.87	0	2,4,16	0.20	0
7	M3L	L	43	7	3,4,12	0.76	0	2,4,16	0.36	0
7	M3L	AP	43	7	3,4,12	0.83	0	2,4,16	0.24	0
7	M3L	P	43	7	3,4,12	0.97	0	2,4,16	0.48	0
7	M3L	Q	43	7	3,4,12	0.90	0	2,4,16	0.45	0
7	M3L	R	43	7	3,4,12	0.80	0	2,4,16	0.13	0
7	M3L	AO	43	7	3,4,12	0.93	0	2,4,16	0.44	0
7	M3L	AN	43	7	3,4,12	0.93	0	2,4,16	0.67	0
7	M3L	M	43	7	3,4,12	0.89	0	2,4,16	0.62	0
7	M3L	AQ	43	7	3,4,12	0.88	0	2,4,16	0.46	0
7	M3L	AL	43	7	3,4,12	0.94	0	2,4,16	0.53	0
7	M3L	O	43	7	3,4,12	0.87	0	2,4,16	0.48	0
7	M3L	AK	43	7	3,4,12	0.93	0	2,4,16	0.28	0
7	M3L	N	43	7	3,4,12	0.95	0	2,4,16	0.33	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
7	M3L	AR	43	7	-	1/1/2/12	-
7	M3L	AM	43	7	-	0/1/2/12	-
7	M3L	K	43	7	-	0/1/2/12	-
7	M3L	L	43	7	-	0/1/2/12	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	M3L	AP	43	7	-	0/1/2/12	-
7	M3L	P	43	7	-	1/1/2/12	-
7	M3L	Q	43	7	-	0/1/2/12	-
7	M3L	R	43	7	-	0/1/2/12	-
7	M3L	AO	43	7	-	0/1/2/12	-
7	M3L	AN	43	7	-	0/1/2/12	-
7	M3L	M	43	7	-	0/1/2/12	-
7	M3L	AQ	43	7	-	0/1/2/12	-
7	M3L	AL	43	7	-	0/1/2/12	-
7	M3L	O	43	7	-	0/1/2/12	-
7	M3L	AK	43	7	-	0/1/2/12	-
7	M3L	N	43	7	-	0/1/2/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	P	43	M3L	O-C-CA-CB
7	AR	43	M3L	O-C-CA-CB

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	AR	43	M3L	1	0
7	AM	43	M3L	1	0
7	K	43	M3L	1	0
7	AP	43	M3L	2	0
7	R	43	M3L	1	0
7	AQ	43	M3L	4	0
7	AK	43	M3L	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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$
20	LHG	Af	102	-	38,38,48	0.72	0	41,44,54	1.32	5 (12%)
19	CDL	Aa	301	-	83,83,99	1.00	7 (8%)	89,95,111	1.10	4 (4%)
19	CDL	Ab	302	-	77,77,99	1.02	6 (7%)	83,89,111	1.20	5 (6%)
19	CDL	b	302	-	77,77,99	1.01	6 (7%)	83,89,111	1.22	7 (8%)
20	LHG	Af	101	-	48,48,48	0.66	1 (2%)	51,54,54	1.30	7 (13%)
19	CDL	a	301	-	83,83,99	1.01	7 (8%)	89,95,111	1.11	6 (6%)
19	CDL	b	301	-	82,82,99	1.01	7 (8%)	88,94,111	1.12	4 (4%)
19	CDL	Ab	301	-	82,82,99	1.00	6 (7%)	88,94,111	1.10	6 (6%)
20	LHG	b	303	-	48,48,48	0.67	1 (2%)	51,54,54	1.30	6 (11%)
20	LHG	f	101	-	38,38,48	0.70	1 (2%)	41,44,54	1.31	5 (12%)

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
20	LHG	Af	102	-	-	21/43/43/53	-
19	CDL	Aa	301	-	-	50/94/94/110	-
19	CDL	Ab	302	-	-	51/88/88/110	-
19	CDL	b	302	-	-	59/88/88/110	-
20	LHG	Af	101	-	-	25/53/53/53	-
19	CDL	a	301	-	-	51/94/94/110	-
19	CDL	b	301	-	-	51/93/93/110	-
19	CDL	Ab	301	-	-	59/93/93/110	-
20	LHG	b	303	-	-	22/53/53/53	-
20	LHG	f	101	-	-	25/43/43/53	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	b	302	CDL	OB6-CB4	-3.04	1.39	1.46
19	Ab	302	CDL	OA6-CA4	-2.94	1.39	1.46
19	Ab	301	CDL	OA6-CA4	-2.92	1.39	1.46
19	Aa	301	CDL	OB8-CB7	2.84	1.41	1.33
19	a	301	CDL	OA6-CA4	-2.83	1.40	1.46

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	b	302	CDL	OA6-CA5-C11	5.08	122.46	111.48
19	b	301	CDL	OA6-CA5-C11	4.52	121.25	111.48
20	f	101	LHG	O4-P-O5	4.47	133.23	112.44
20	b	303	LHG	O4-P-O5	4.44	133.08	112.44
20	Af	101	LHG	O4-P-O5	4.44	133.08	112.44

There are no chirality outliers.

5 of 414 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	a	301	CDL	CA2-OA2-PA1-OA3
19	a	301	CDL	CA2-OA2-PA1-OA5
19	a	301	CDL	CA3-OA5-PA1-OA2
19	a	301	CDL	CA3-OA5-PA1-OA3
19	a	301	CDL	CA3-OA5-PA1-OA4

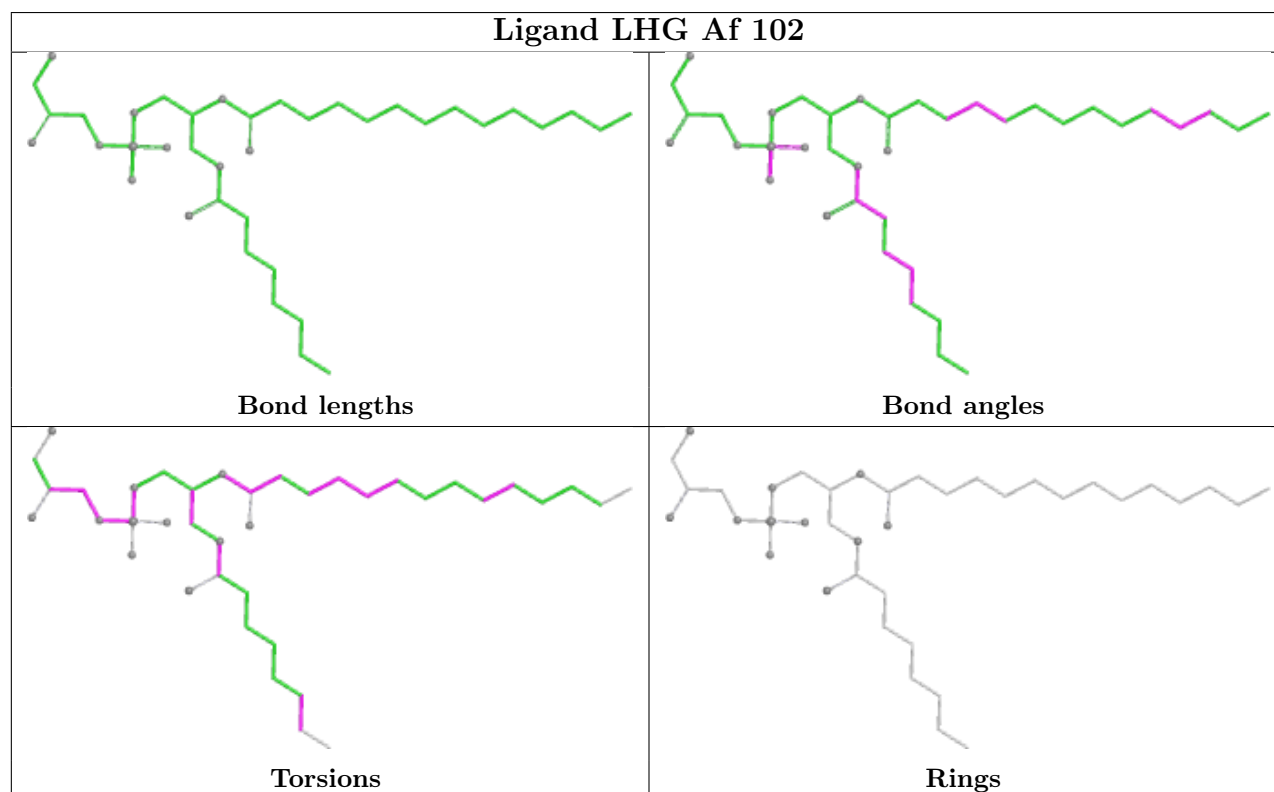
There are no ring outliers.

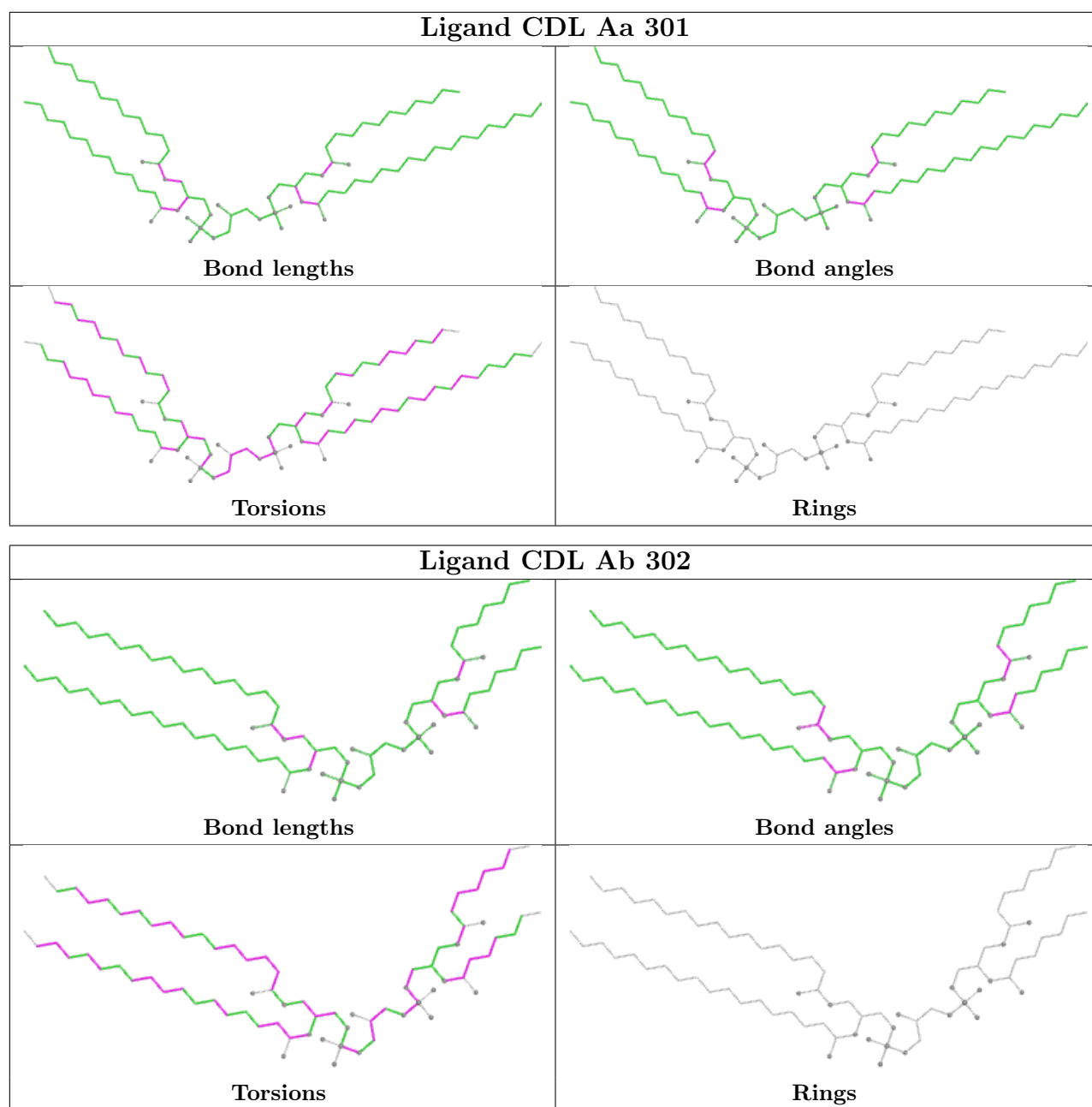
10 monomers are involved in 71 short contacts:

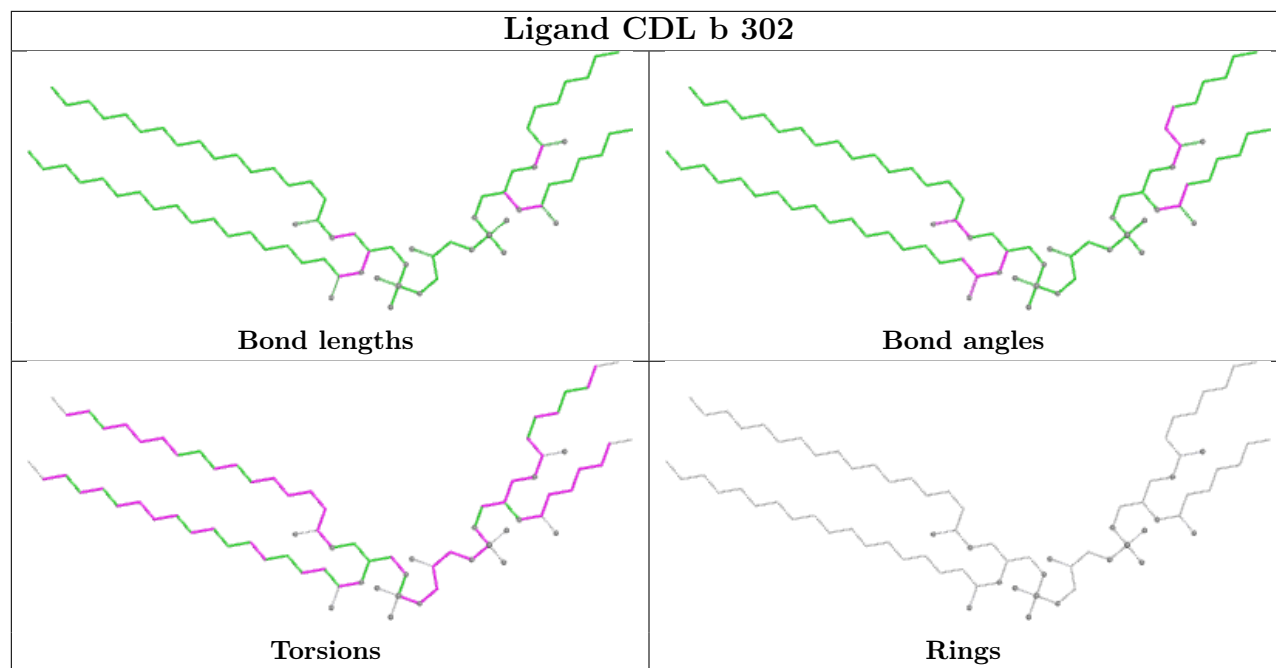
Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	Af	102	LHG	4	0
19	Aa	301	CDL	9	0
19	Ab	302	CDL	9	0
19	b	302	CDL	17	0
20	Af	101	LHG	4	0
19	a	301	CDL	11	0
19	b	301	CDL	4	0
19	Ab	301	CDL	10	0
20	b	303	LHG	4	0
20	f	101	LHG	1	0

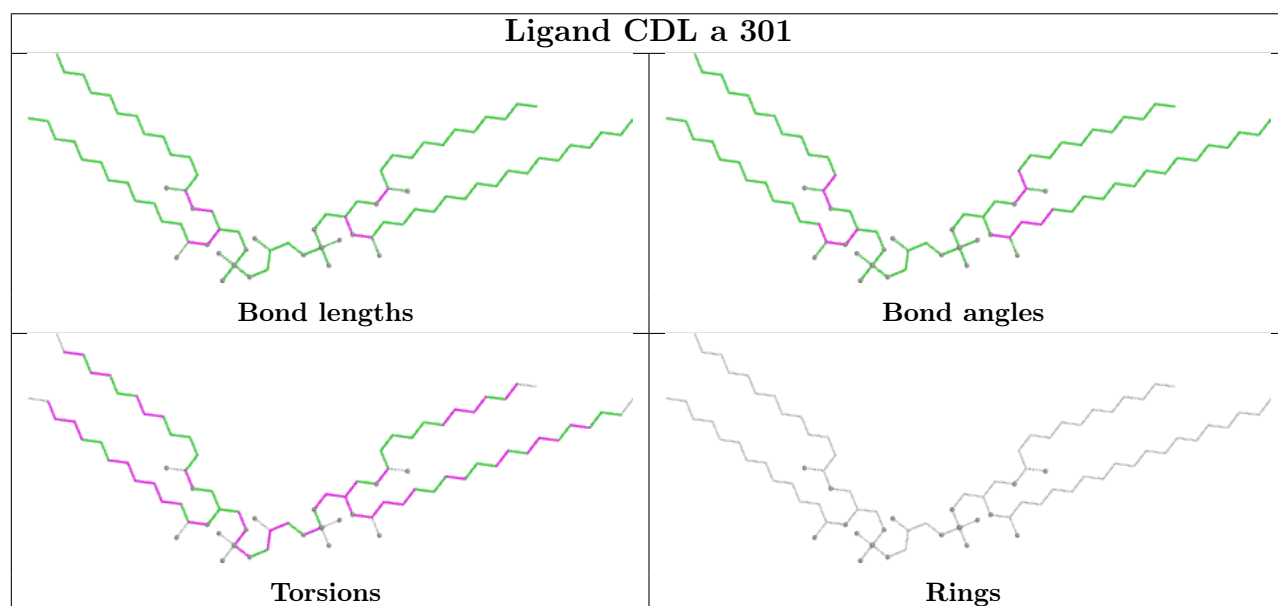
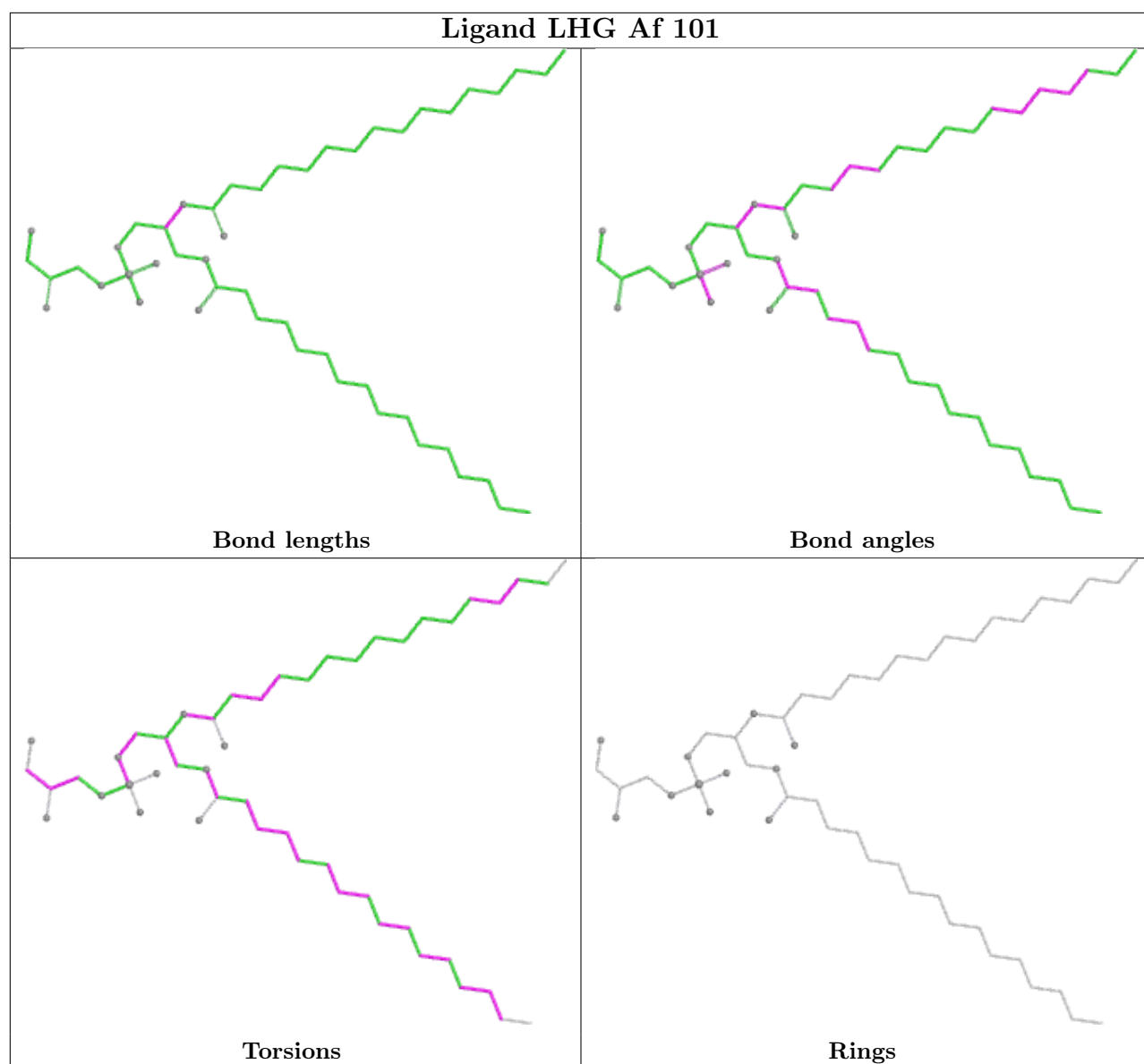
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

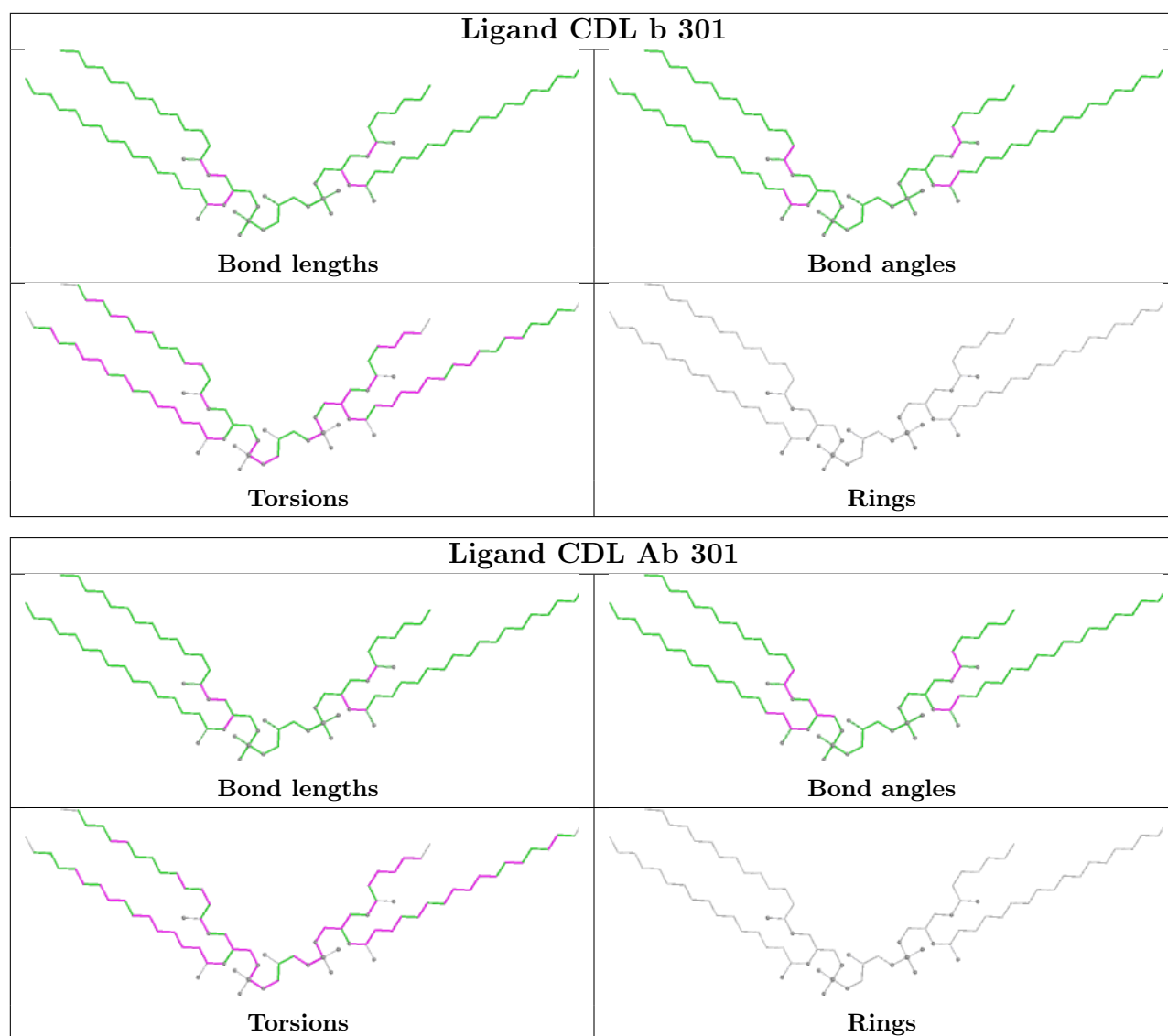
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within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

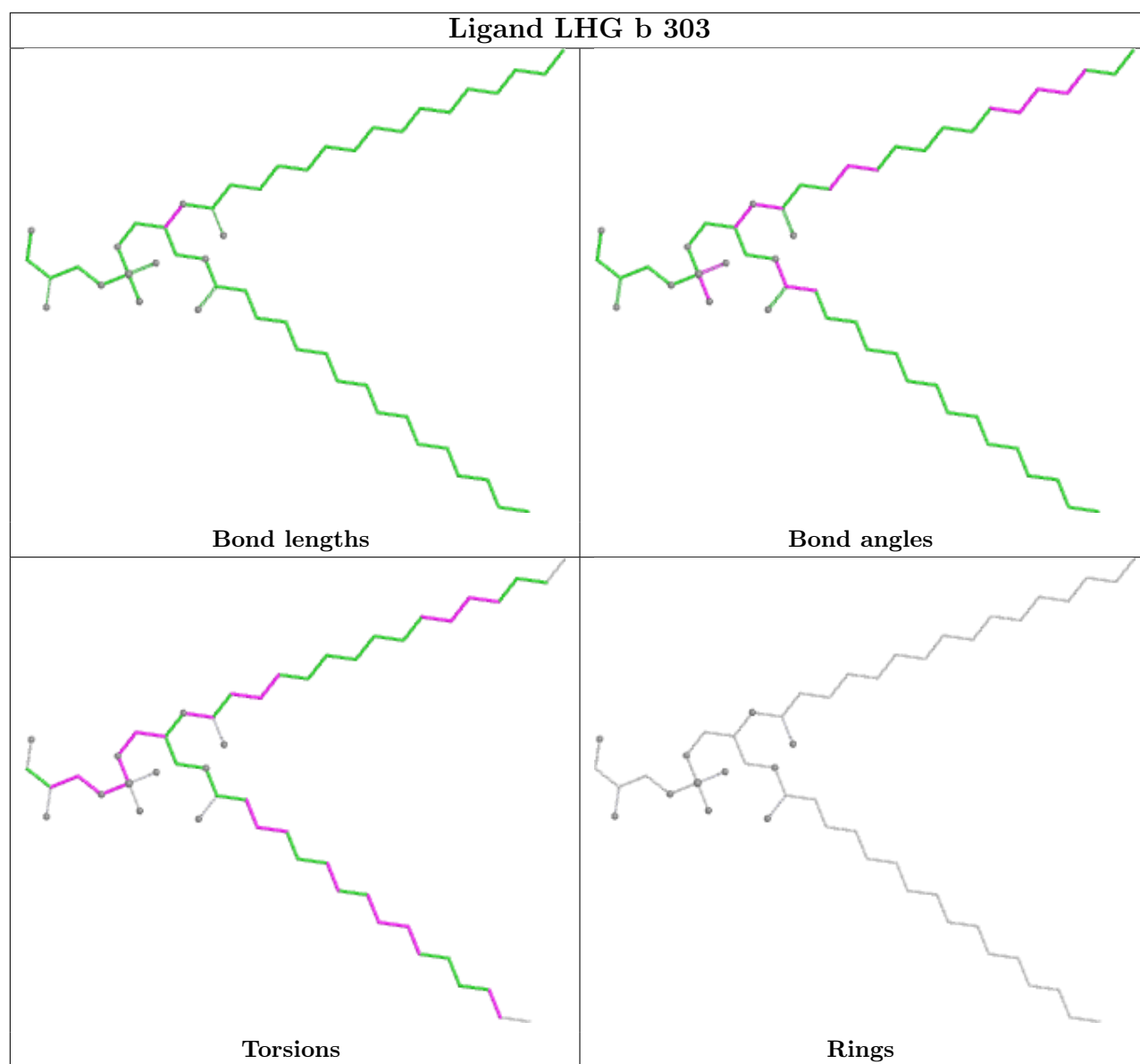


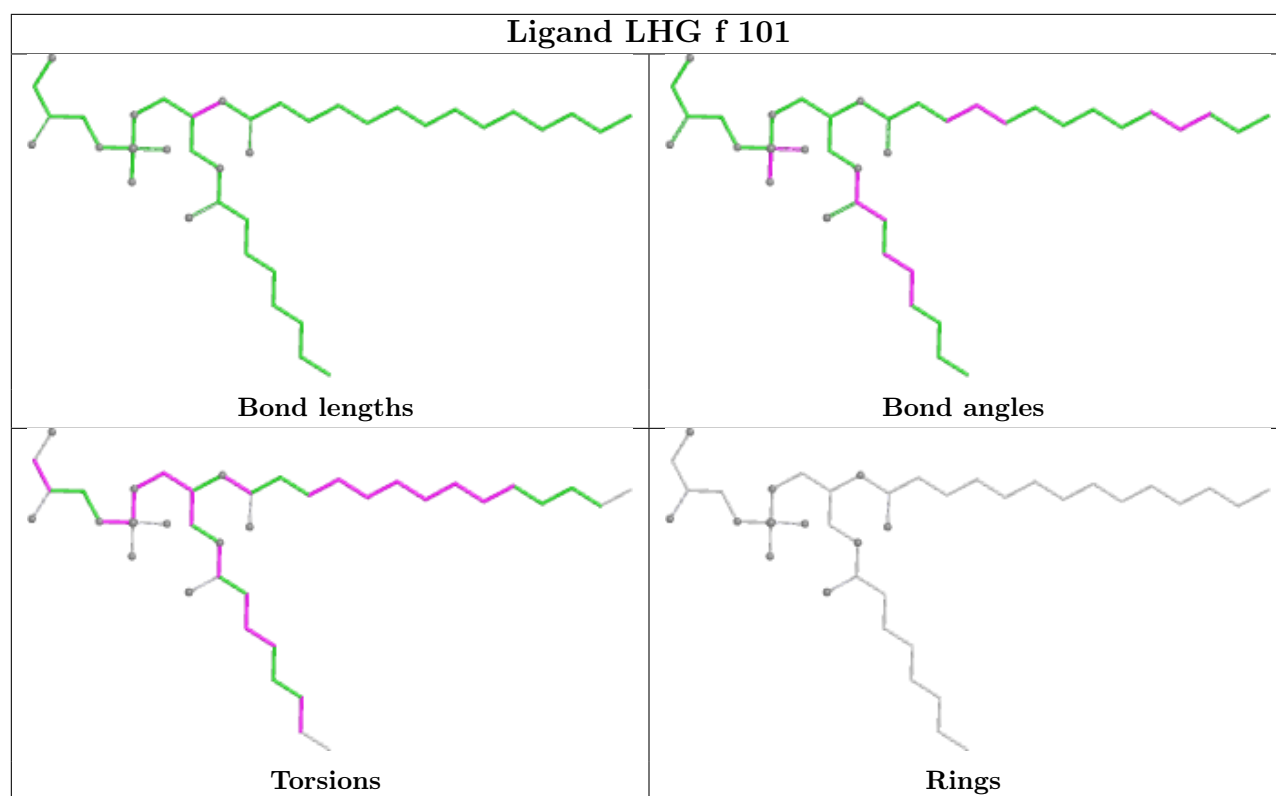












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

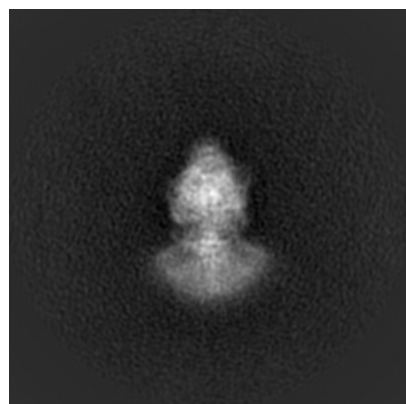
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11432. These allow visual inspection of the internal detail of the map and identification of artifacts.

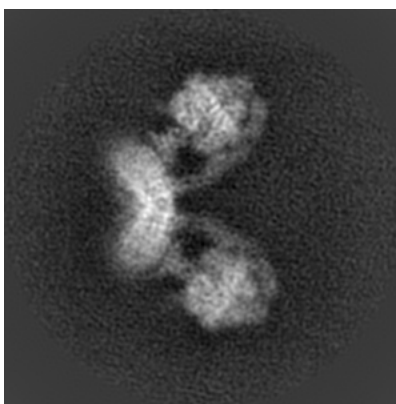
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

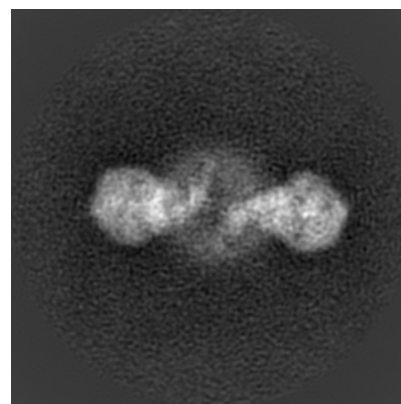
6.1.1 Primary map



X

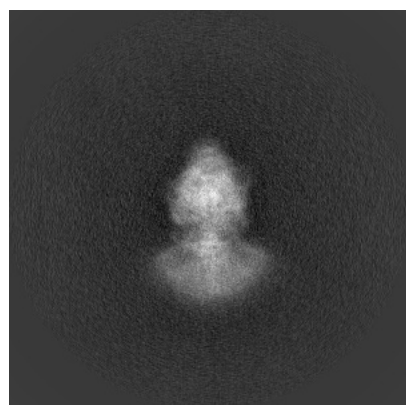


Y

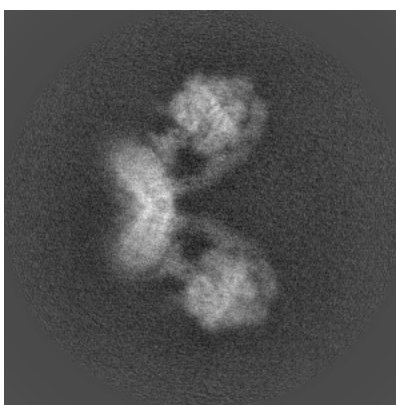


Z

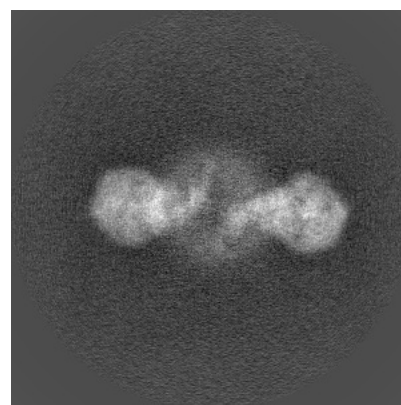
6.1.2 Raw map



X



Y

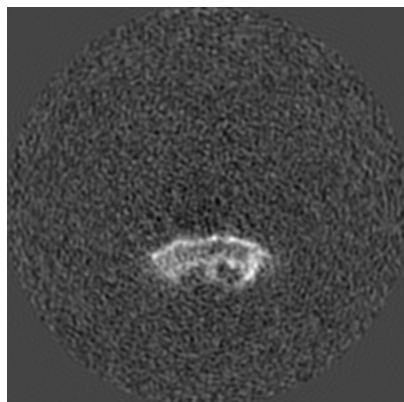


Z

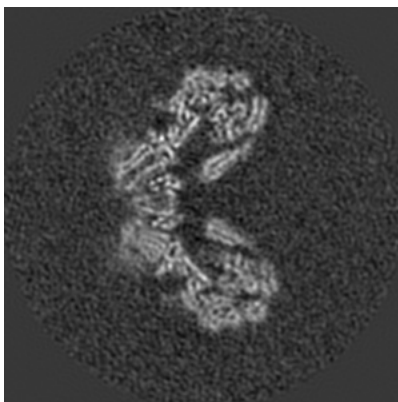
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

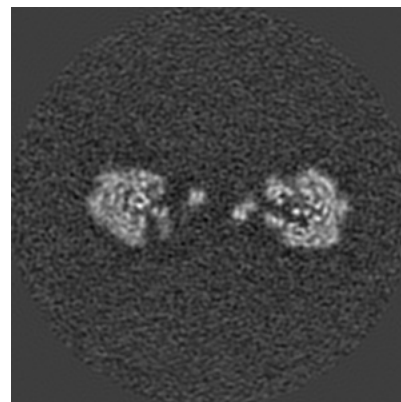
6.2.1 Primary map



X Index: 250

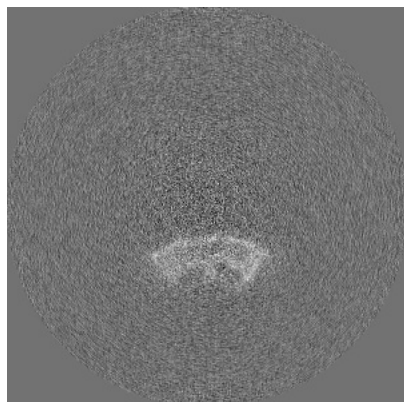


Y Index: 250

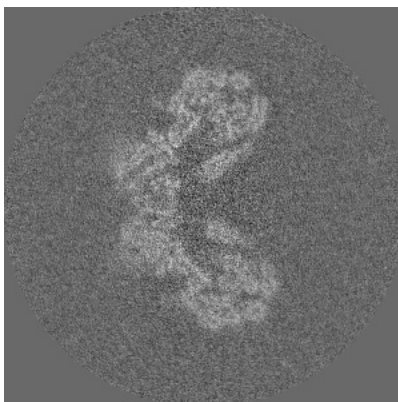


Z Index: 250

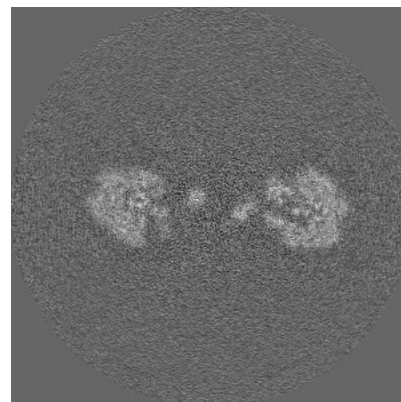
6.2.2 Raw map



X Index: 250



Y Index: 250

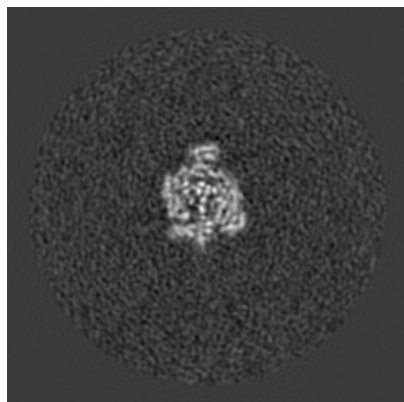


Z Index: 250

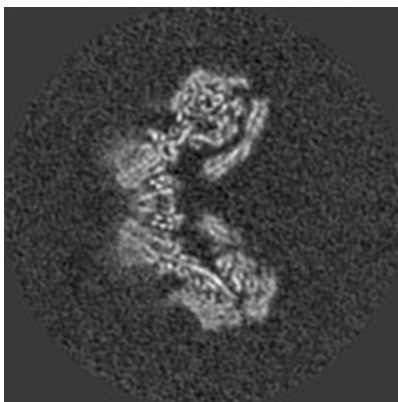
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

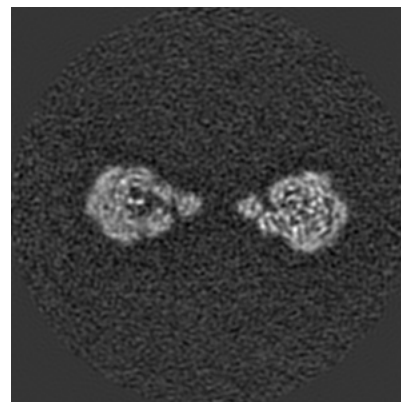
6.3.1 Primary map



X Index: 368

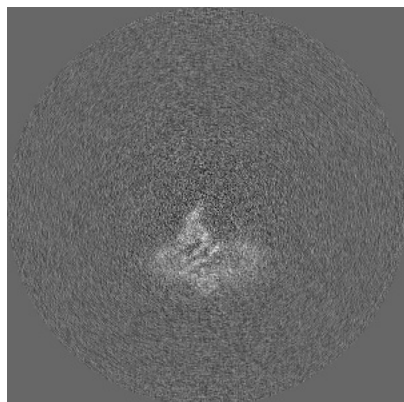


Y Index: 255

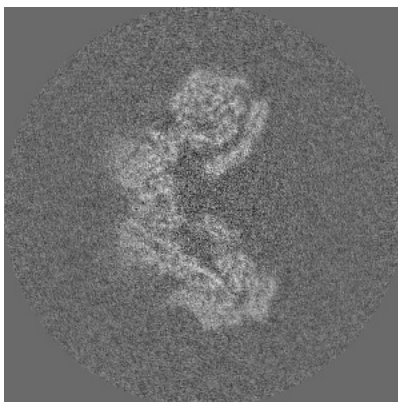


Z Index: 263

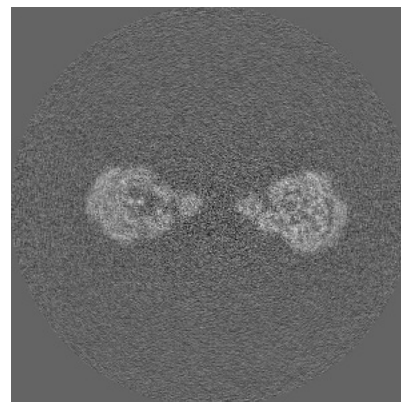
6.3.2 Raw map



X Index: 277



Y Index: 256

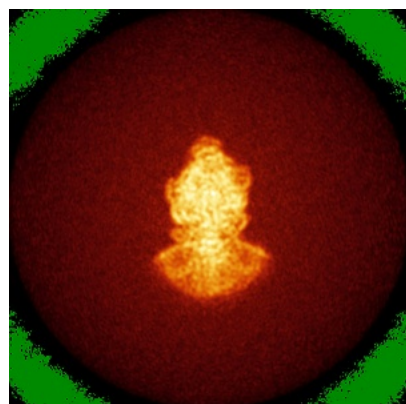


Z Index: 262

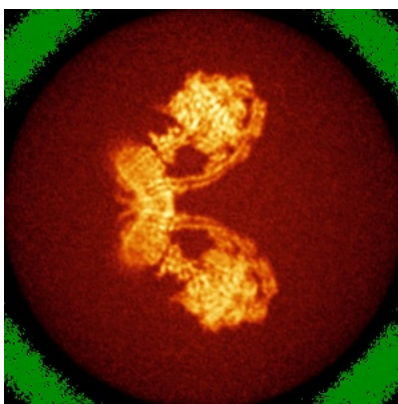
The images above show the largest variance slices of the map in three orthogonal directions.

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

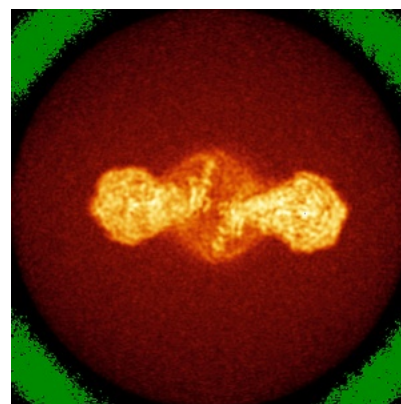
6.4.1 Primary map



X

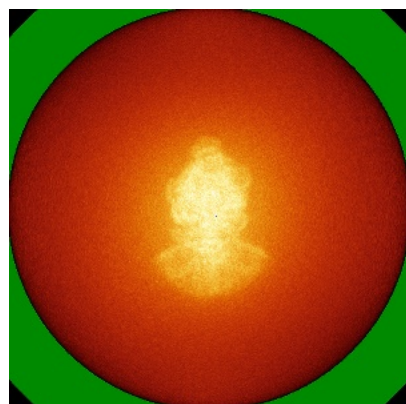


Y

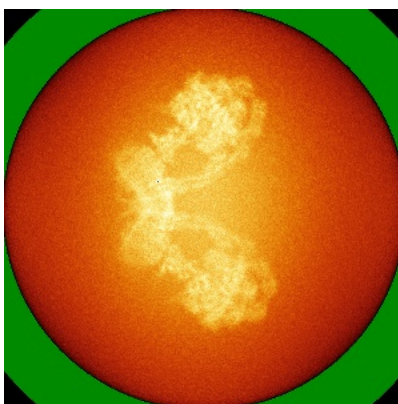


Z

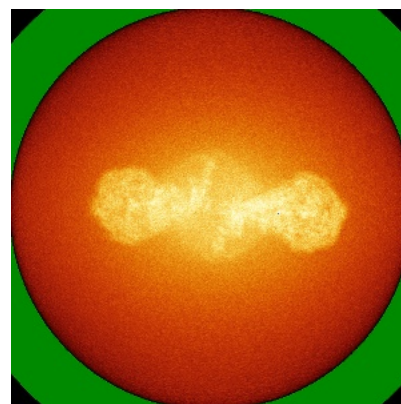
6.4.2 Raw map



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](#)

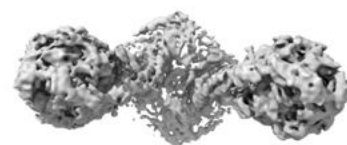
6.5.1 Primary map



X



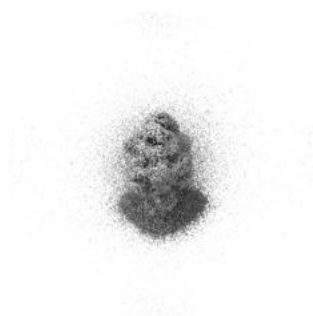
Y



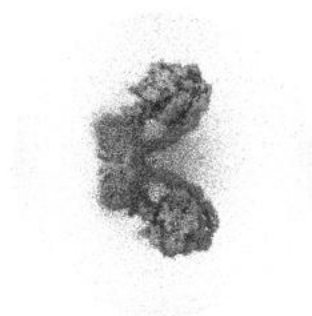
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0146. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

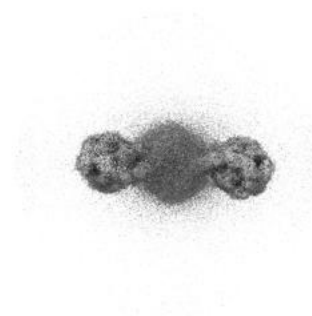
6.5.2 Raw map



X



Y



Z

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.

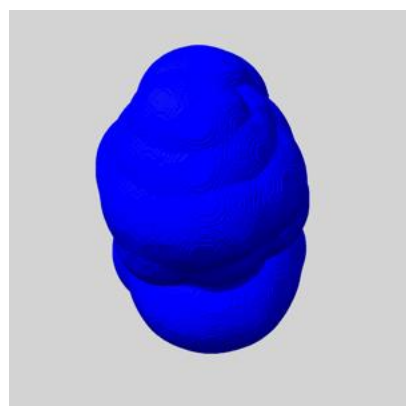
6.6 Mask visualisation [i](#)

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

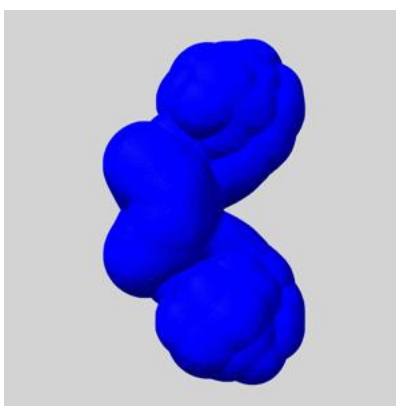
A mask typically either:

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

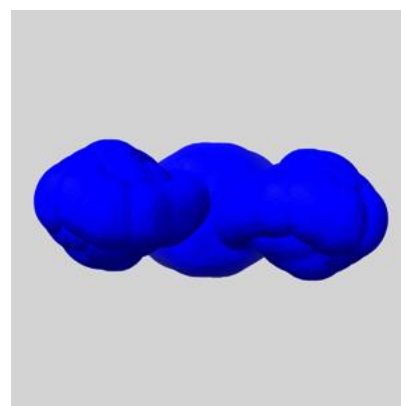
6.6.1 emd_11432_msk_1.map [i](#)



X



Y

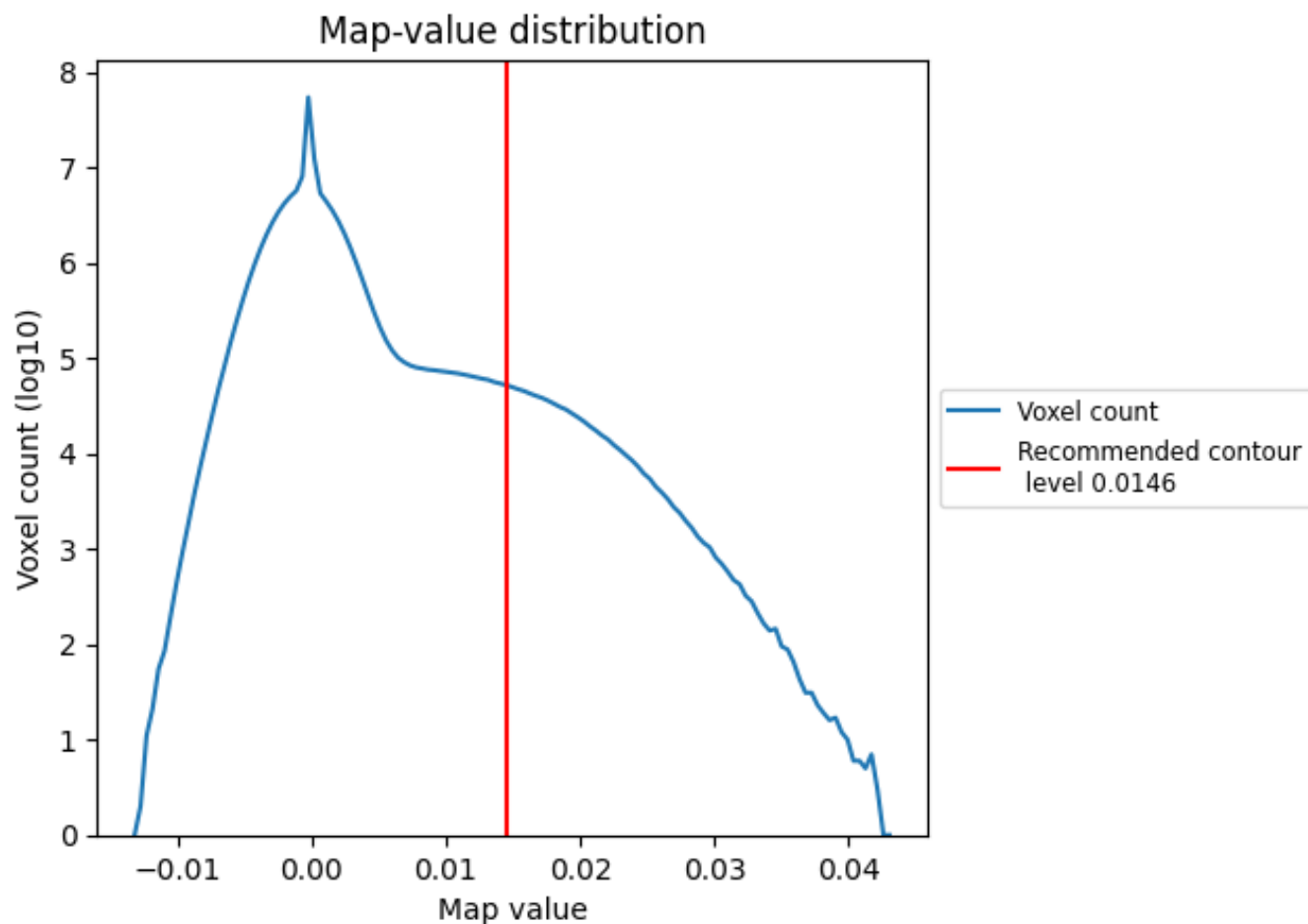


Z

7 Map analysis [i](#)

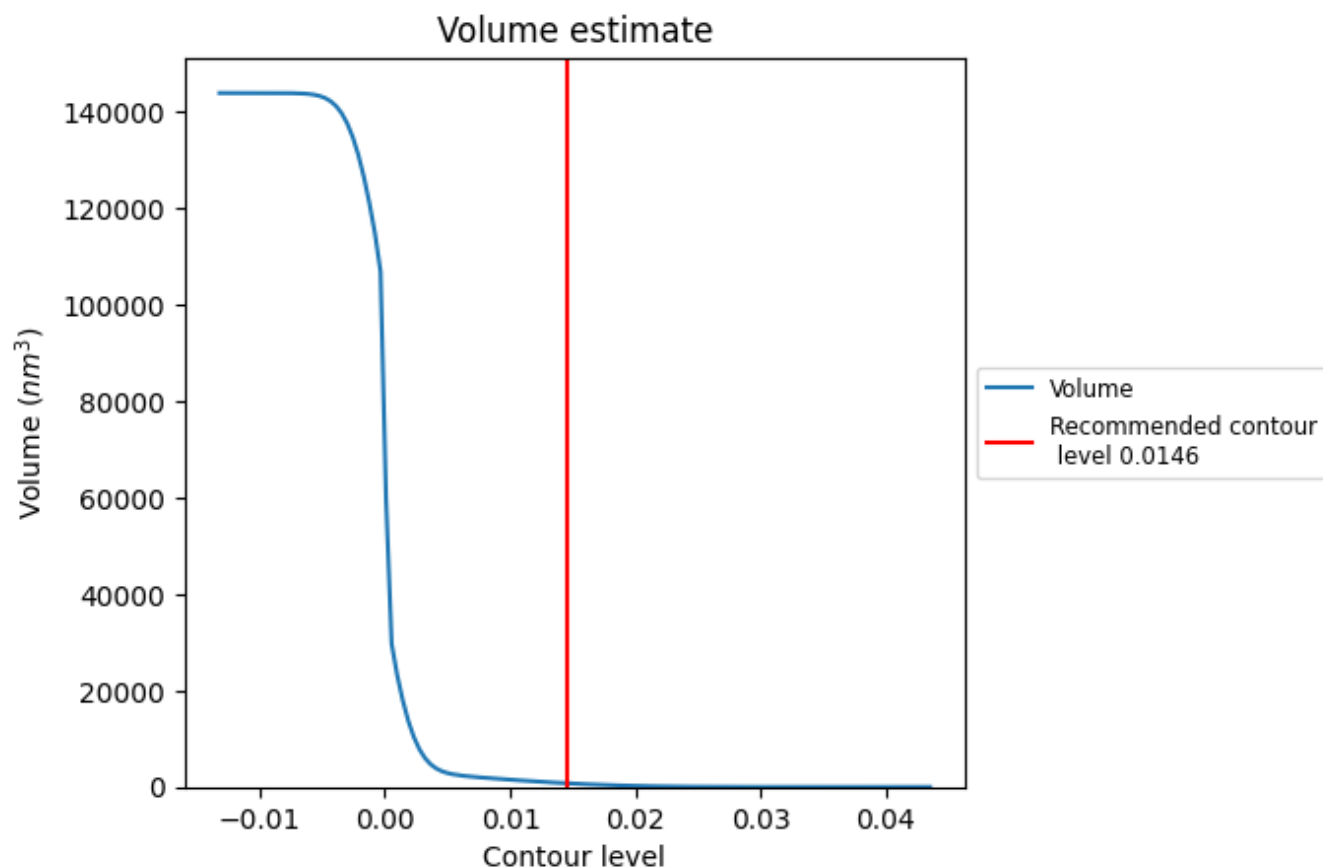
This section contains the results of statistical analysis of the map.

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.

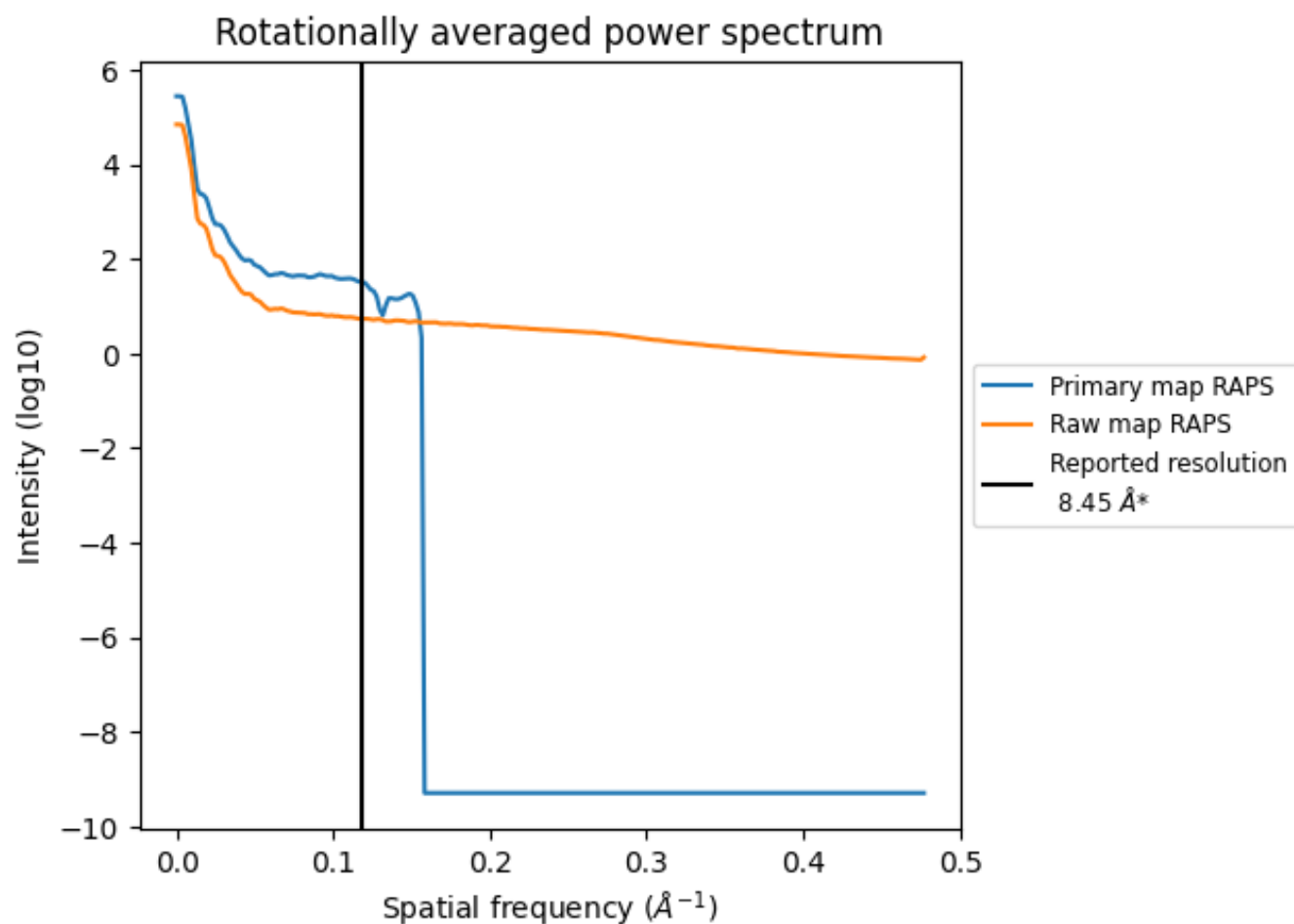
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 756 nm³; this corresponds to an approximate mass of 683 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 ⓘ

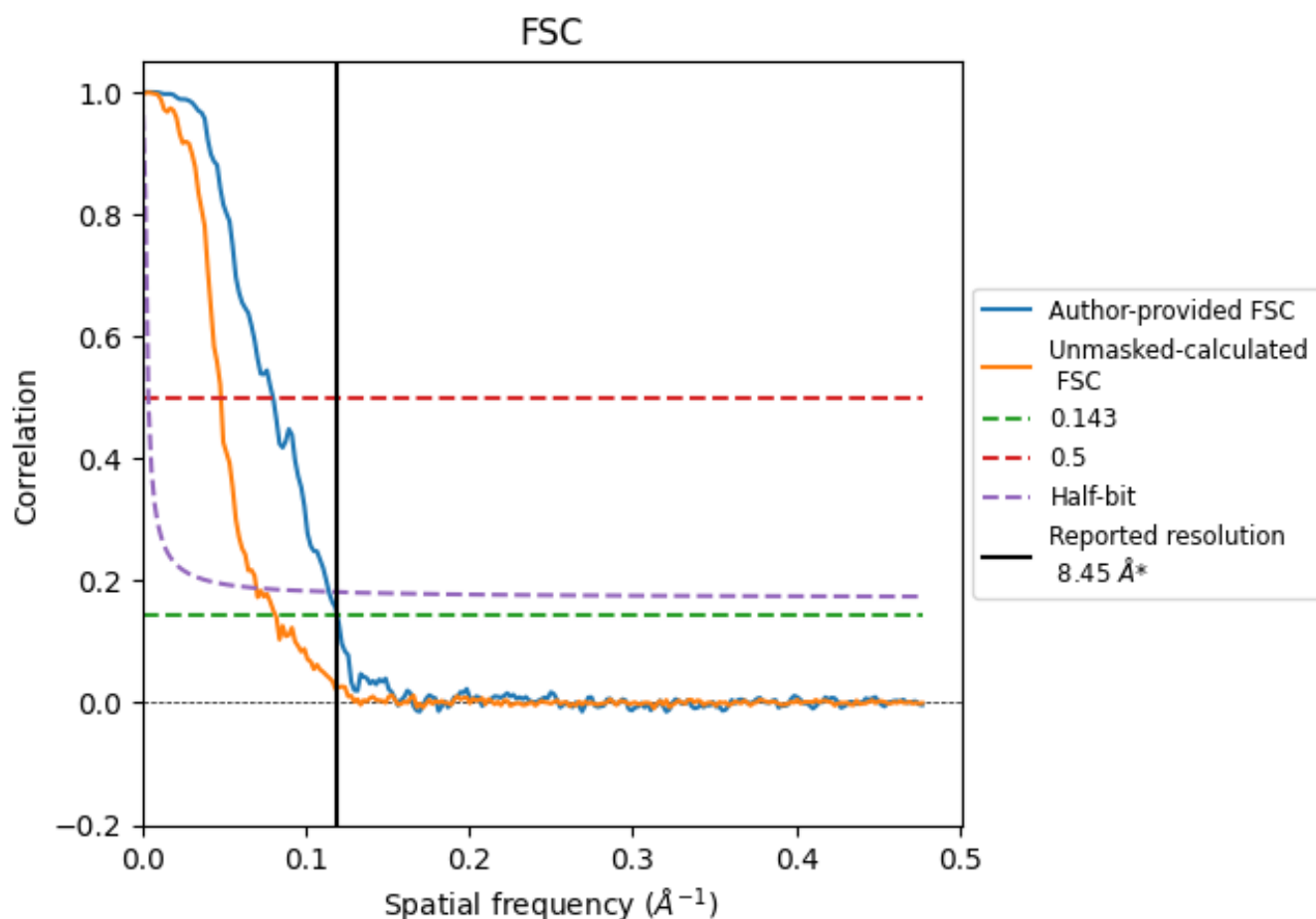


*Reported resolution corresponds to spatial frequency of 0.118 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.118 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

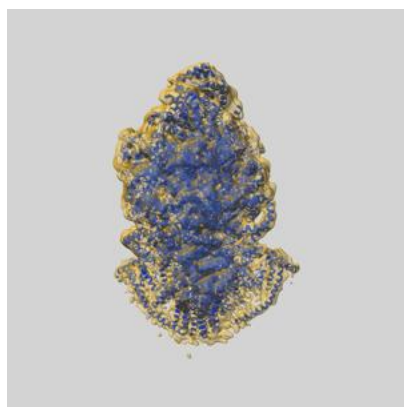
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.45	-	-
Author-provided FSC curve	8.38	12.52	8.76
Unmasked-calculated*	12.27	20.79	14.33

*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 12.27 differs from the reported value 8.45 by more than 10 %

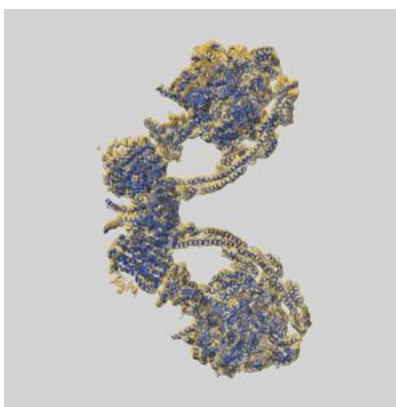
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11432 and PDB model 7AJF. Per-residue inclusion information can be found in section [3](#) on page [13](#).

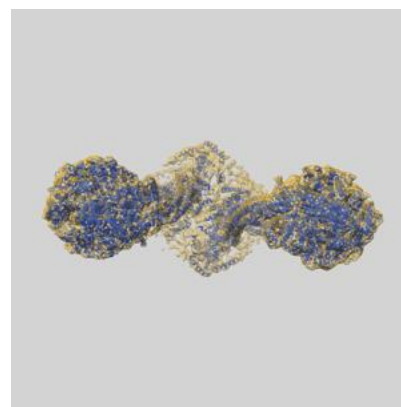
9.1 Map-model overlay [i](#)



X



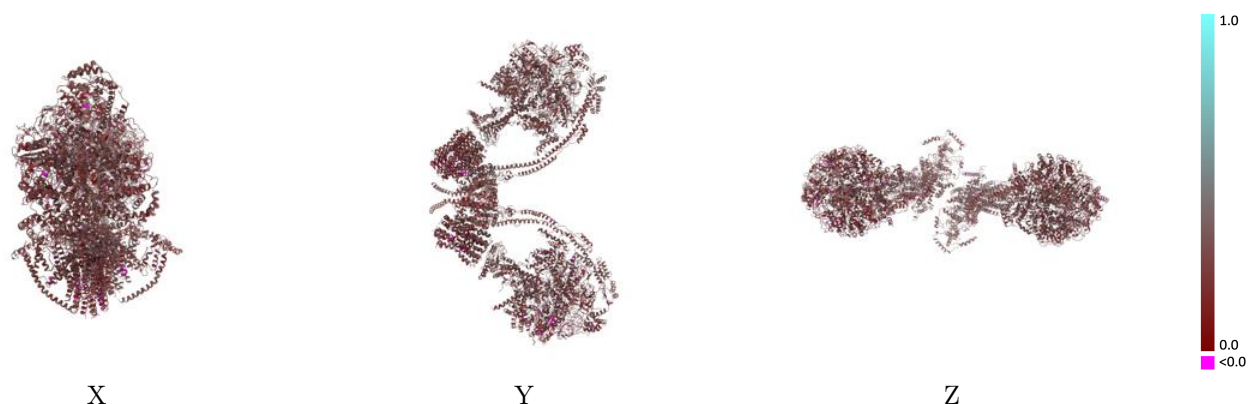
Y



Z

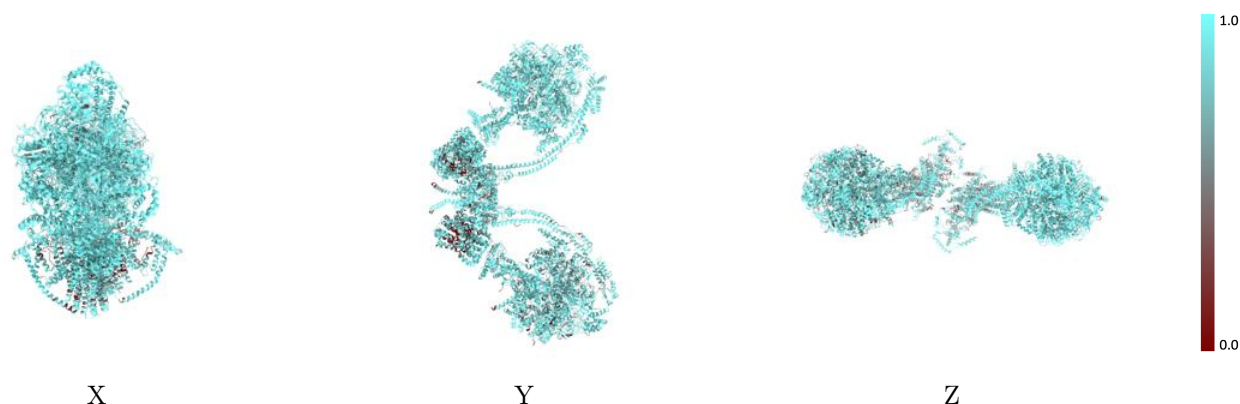
The images above show the 3D surface view of the map at the recommended contour level 0.0146 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



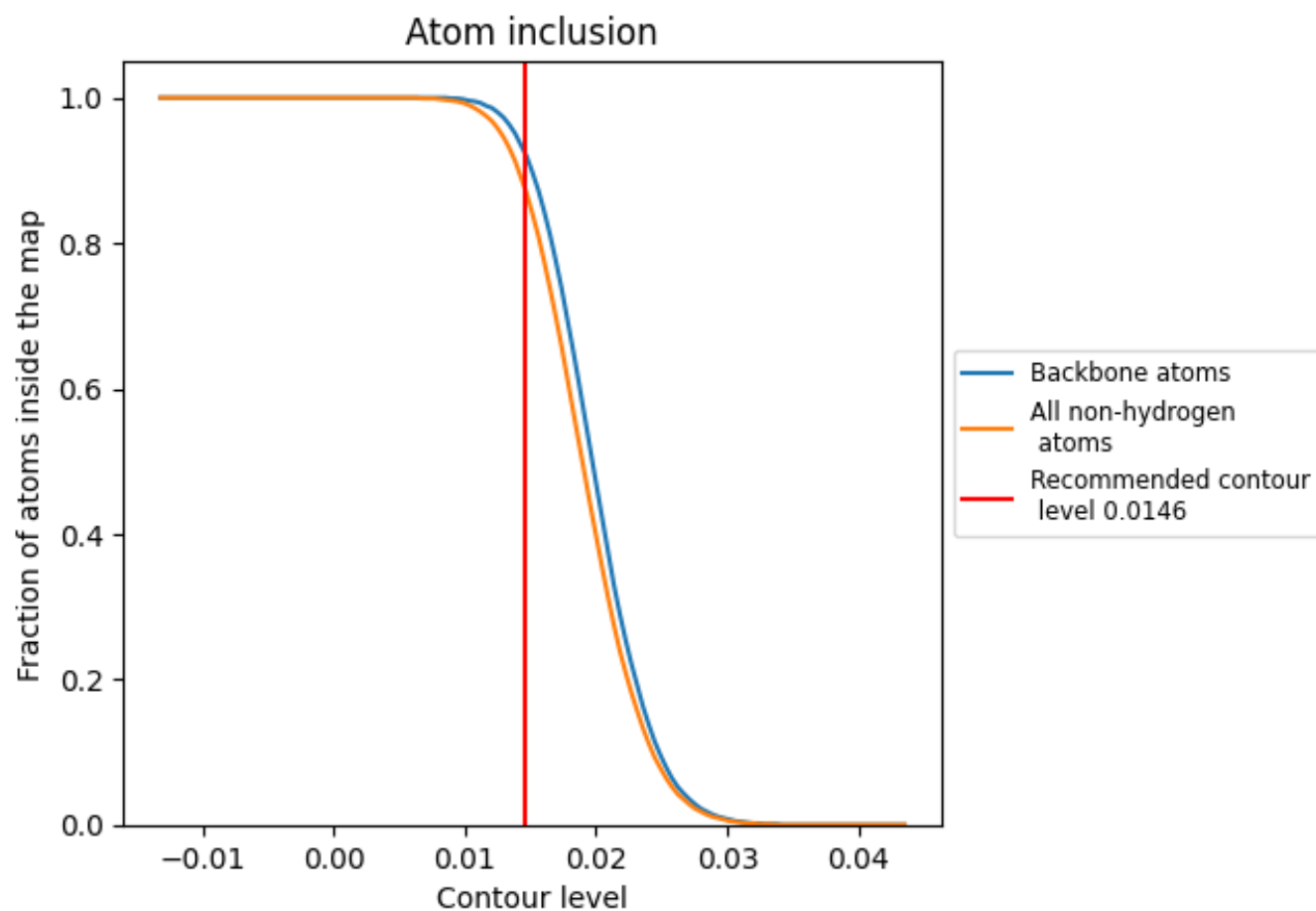
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0146).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 88% 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 (0.0146) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.2790
8	 0.9170	 0.3130
A	 0.9560	 0.2900
A8	 0.8340	 0.2760
AA	 0.8720	 0.2640
AB	 0.8220	 0.2800
AC	 0.8450	 0.2510
AD	 0.8110	 0.2600
AE	 0.8250	 0.2710
AF	 0.8580	 0.2740
AG	 0.9220	 0.3070
AH	 0.8970	 0.2920
AI	 0.8710	 0.2960
AJ	 0.7710	 0.3020
AK	 0.7300	 0.2840
AL	 0.7250	 0.2540
AM	 0.7550	 0.2670
AN	 0.6990	 0.2650
AO	 0.7350	 0.2430
AP	 0.7100	 0.2420
AQ	 0.5740	 0.2330
AR	 0.6460	 0.2590
AS	 0.8860	 0.2800
Aa	 0.8200	 0.2980
Ab	 0.8730	 0.2660
Ad	 0.8520	 0.2700
Ae	 0.8990	 0.2640
Af	 0.7730	 0.2750
Ag	 0.9150	 0.2770
Ah	 0.8040	 0.2600
Aj	 0.9080	 0.3010
Ak	 0.6840	 0.2580
B	 0.9470	 0.3050
C	 0.9360	 0.2800
D	 0.9500	 0.2890



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Continued from previous page...

Chain	Atom inclusion	Q-score
E	 0.9400	 0.2940
F	 0.9400	 0.2940
G	 0.9610	 0.3080
H	 0.9800	 0.3240
I	 0.9140	 0.3160
J	 0.8570	 0.2890
K	 0.8470	 0.2770
L	 0.7800	 0.2510
M	 0.8160	 0.2480
N	 0.8690	 0.2550
O	 0.8750	 0.2620
P	 0.8330	 0.2410
Q	 0.8220	 0.2590
R	 0.7600	 0.2330
S	 0.9560	 0.3000
a	 0.8540	 0.2820
b	 0.8750	 0.2620
d	 0.9450	 0.2680
e	 0.8200	 0.2530
f	 0.8640	 0.2660
g	 0.9330	 0.2830
h	 0.9710	 0.3050
j	 0.8610	 0.2830
k	 0.7570	 0.2240