



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 02:41 AM UTC

PDB ID : 8APF / pdb_00008apf
EMDB ID : EMD-15568
Title : rotational state 2a of the Trypanosoma brucei mitochondrial ATP synthase dimer
Authors : Muehleip, A.; Gahura, O.; Zikova, A.; Amunts, A.
Deposited on : 2022-08-09
Resolution : 4.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

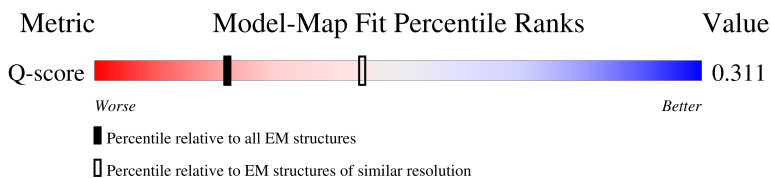
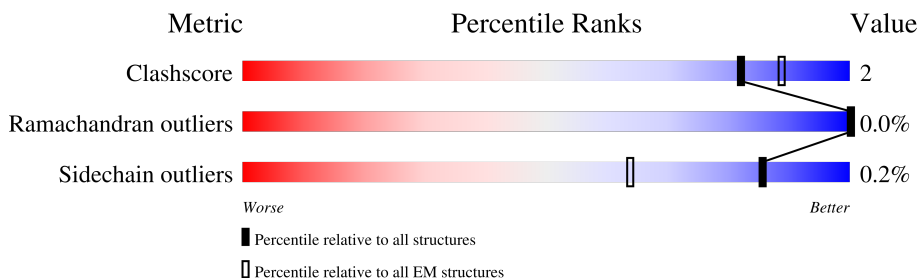
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	H1	182	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">28%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">81%</div> <div style="text-align: center;">7%</div> <div style="text-align: center;">12%</div> </div>
2	I1	75	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">35%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">79%</div> <div style="text-align: center;">8%</div> <div style="text-align: center;">13%</div> </div>
3	J1	188	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">16%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">80%</div> <div style="text-align: center;">8%</div> <div style="text-align: center;">12%</div> </div>
3	K1	188	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">8%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">81%</div> <div style="text-align: center;">7%</div> <div style="text-align: center;">12%</div> </div>

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Mol	Chain	Length	Quality of chain
3	L1	188	15% 85% 12%
4	L	92	15% 65% 5% 29%
4	l	92	30% 64% 7% 29%
5	M	144	33% 84% 6% 10%
5	m	144	15% 83% 7% 10%
6	M1	255	13% 87% 8%
7	O1	118	23% 58% 8% 34%
7	P1	118	29% 60% 6% 34%
7	Q1	118	29% 61% 5% 34%
7	R1	118	12% 65% 34%
7	S1	118	8% 62% 34%
7	T1	118	8% 62% 34%
7	U1	118	16% 61% 34%
7	V1	118	19% 64% 34%
7	W1	118	21% 64% 34%
7	X1	118	21% 59% 7% 34%
8	a	231	95% 5%
9	c	114	65% 11% 25%
10	d	370	10% 84% 6% 10%
11	e	396	90% 7%
12	f	145	86% 7% 7%
13	g	269	44% 88% 11%
14	h	157	22% 83% 13%
15	i	104	90% 9%
16	j	169	93% 6%

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Mol	Chain	Length	Quality of chain
17	k	124	82% 15%
18	n	156	85% 11%
19	o	101	90% 5% 5%
20	p	105	72% 24%
21	q	98	78% 9% 13%
22	r	62	94% 6%
23	G1	305	27% 92% 7%
24	A1	584	8% 85% 5% 10%
24	B1	584	9% 84% 7% 9%
24	C1	584	8% 85% 5% 10%
25	D1	519	8% 87% 7% 6%
25	E1	519	11% 87% 6% 6%
25	F1	519	13% 90% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
29	Q7G	e	407	X	-	-	-
29	Q7G	n	201	X	-	-	-

2 Entry composition [i](#)

There are 34 unique types of molecules in this entry. The entry contains 129563 atoms, of which 65460 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, epsilon chain, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	H1	161	2483	788	1232	211	248	4	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	I1	65	1046	332	513	97	102	2	0	0

- Molecule 3 is a protein called ATP synthase subunit p18, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	J1	166	2591	822	1276	221	258	14	0	0
3	K1	166	2591	822	1276	221	258	14	0	0
3	L1	165	2581	819	1271	220	257	14	0	0

- Molecule 4 is a protein called subunit-e.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	L	65	1082	340	545	104	92	1	0	0
4	l	65	1082	340	545	104	92	1	0	0

- Molecule 5 is a protein called subunit-g.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	M	129	2069	662	1042	177	186	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace	
5	m	129	Total	C	H	N	O	S	0	0
			2069	662	1042	177	186	2		

- Molecule 6 is a protein called OSCP.

Mol	Chain	Residues	Atoms					AltConf	Trace	
6	M1	234	Total	C	H	N	O	S	0	0
			3750	1212	1873	302	360	3		

- Molecule 7 is a protein called ATPase subunit 9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace	
7	O1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		
7	P1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		
7	Q1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		
7	R1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		
7	S1	78	Total	C	H	N	O	S	0	0
			1166	376	601	89	96	4		
7	T1	78	Total	C	H	N	O	S	0	0
			1166	376	601	89	96	4		
7	U1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		
7	V1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		
7	W1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		
7	X1	78	Total	C	H	N	O	S	0	0
			1165	376	600	89	96	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
8	a	231	Total	C	H	N	O	S	0	0
			4076	1459	2044	261	284	28		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	23	TRP	-	insertion	UNP P24499
a	180	TRP	-	insertion	UNP P24499

- Molecule 9 is a protein called subunit-8.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	c	86	1460	494	715	116	130	5	0	0

- Molecule 10 is a protein called subunit-d.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	d	332	5499	1710	2762	505	514	8	0	0

- Molecule 11 is a protein called ATPTB1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
11	e	383	6270	2060	3050	558	585	17	0	0

- Molecule 12 is a protein called subunit-f.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
12	f	135	2256	744	1111	201	195	5	0	0

- Molecule 13 is a protein called ATPTB3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
13	g	268	3953	1211	2020	343	378	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	176	ALA	VAL	conflict	UNP A0A3L6KRX7

- Molecule 14 is a protein called ATPTB4.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	h	137	2158	680	1088	184	203	3	0	0

- Molecule 15 is a protein called subunit-i/j.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
15	i	103	1740	574	857	152	151	6	0	0

- Molecule 16 is a protein called ATPTB6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	j	168	2835	919	1411	249	249	7	0	0

- Molecule 17 is a protein called subunit-k.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
17	k	105	1749	577	876	149	141	6	0	0

- Molecule 18 is a protein called ATPTB11.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
18	n	139	2210	730	1082	183	208	7	0	0

- Molecule 19 is a protein called ATPTB12.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
19	o	96	1556	506	767	140	140	3	0	0

- Molecule 20 is a protein called subunit-b.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
20	p	80	1335	448	651	108	125	3	0	0

- Molecule 21 is a protein called ATPEG3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
21	q	85	1486	499	720	142	125	0	0

- Molecule 22 is a protein called ATPEG4.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
22	r	62	1040	358	498	94	85	5	0	0

- Molecule 23 is a protein called ATP synthase gamma subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
23	G1	300	4774	1507	2387	423	448	9	0	0

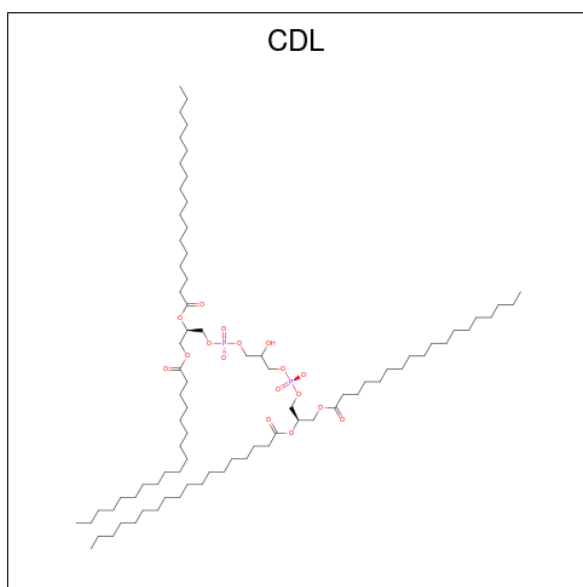
- Molecule 24 is a protein called ATP synthase subunit alpha, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
24	A1	523	8193	2587	4154	701	731	20	0	0
24	B1	529	8260	2603	4187	709	741	20	0	0
24	C1	524	8219	2594	4170	703	732	20	0	0

- Molecule 25 is a protein called ATP synthase subunit beta, mitochondrial.

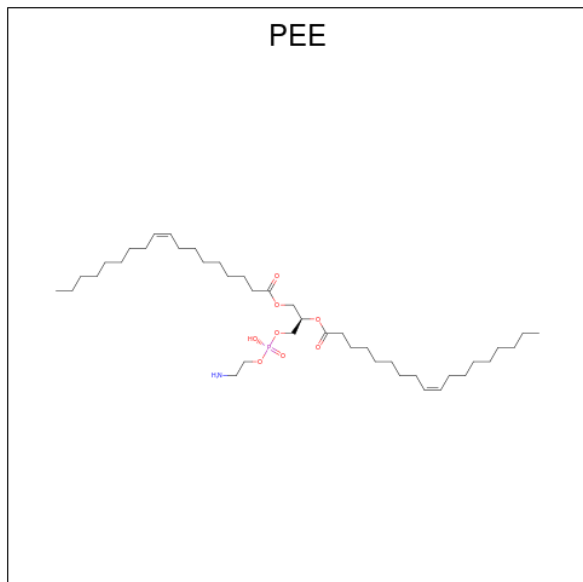
Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
25	D1	488	7446	2334	3750	632	711	19	0	0
25	E1	486	7414	2324	3732	630	709	19	0	0
25	F1	488	7446	2334	3750	632	711	19	0	0

- Molecule 26 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂) (labeled as "Ligand of Interest" by depositor).



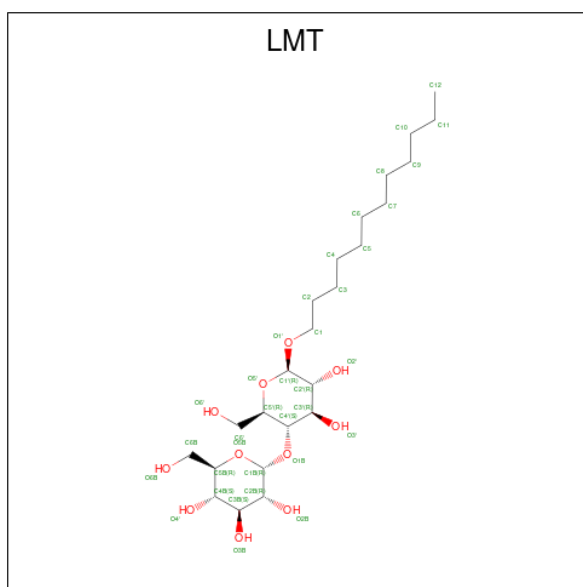
Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	O	P	
26	L	1	256	81	156	17	2	0
26	M	1	256	81	156	17	2	0
26	c	1	256	81	156	17	2	0
26	e	1	256	81	156	17	2	0
26	e	1	256	81	156	17	2	0
26	e	1	256	81	156	17	2	0
26	e	1	256	81	156	17	2	0
26	e	1	256	81	156	17	2	0
26	f	1	256	81	156	17	2	0
26	j	1	256	81	156	17	2	0
26	l	1	256	81	156	17	2	0
26	m	1	256	81	156	17	2	0
26	q	1	256	81	156	17	2	0
26	q	1	256	81	156	17	2	0

- Molecule 27 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$) (labeled as "Ligand of Interest" by depositor).



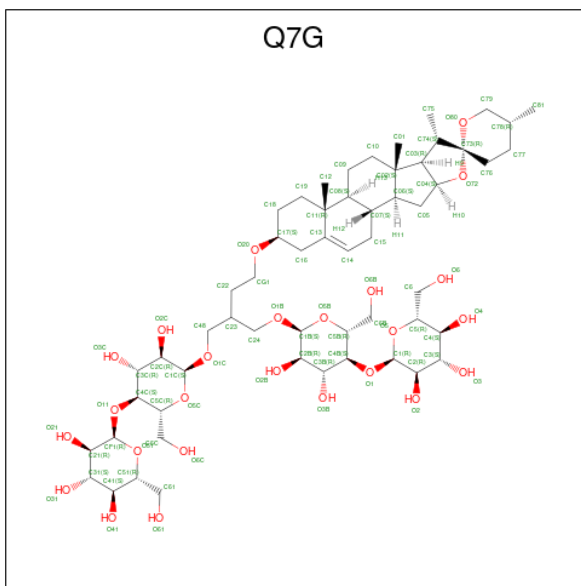
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
27	M	1	Total 133	C 41	H 82	N 1	O 8	P 1	0
27	f	1	Total 133	C 41	H 82	N 1	O 8	P 1	0
27	m	1	Total 133	C 41	H 82	N 1	O 8	P 1	0

- Molecule 28 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: $C_{24}H_{46}O_{11}$).



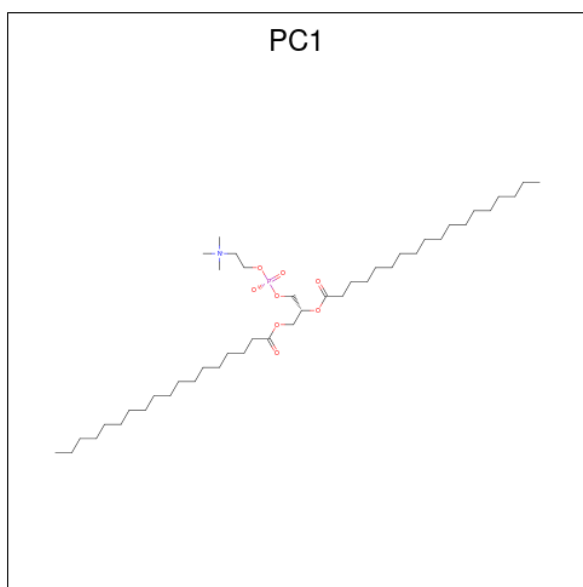
Mol	Chain	Residues	Atoms				AltConf
28	e	1	Total	C	H	O	0
			74	24	39	11	
28	j	1	Total	C	H	O	0
			74	24	39	11	

- Molecule 29 is 2-[[[4-O-alpha-D-glucopyranosyl-alpha-D-glucopyranosyl]oxy]methyl]-4-[[[(3 beta,9beta,14beta,17beta,25R)-spirost-5-en-3-yl]oxy]butyl 4-O-alpha-D-glucopyranosyl-alpha-D-glucopyranoside (CCD ID: Q7G) (formula: C₅₆H₉₂O₂₅).



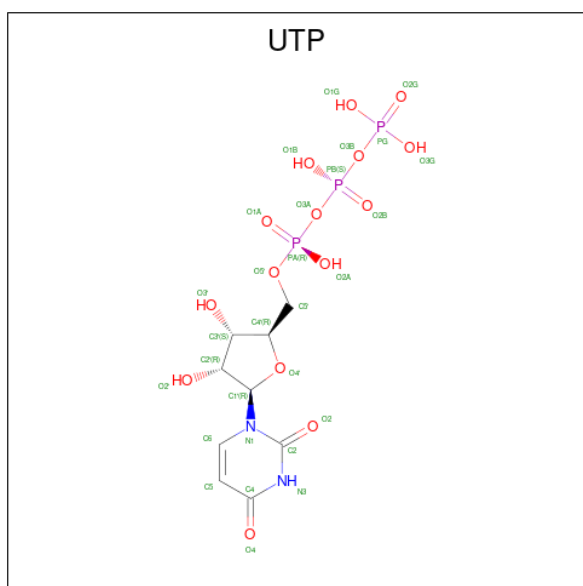
Mol	Chain	Residues	Atoms				AltConf
29	e	1	Total	C	H	O	0
			108	38	60	10	
29	n	1	Total	C	H	O	0
			129	44	70	15	

- Molecule 30 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P) (labeled as "Ligand of Interest" by depositor).



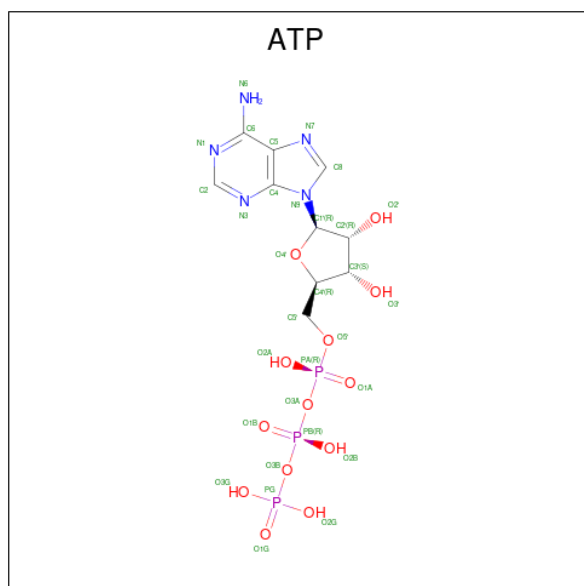
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
30	f	1	Total	C	H	N	O	P	0
			142	44	88	1	8	1	
30	i	1	Total	C	H	N	O	P	0
			142	44	88	1	8	1	
30	j	1	Total	C	H	N	O	P	0
			142	44	88	1	8	1	
30	p	1	Total	C	H	N	O	P	0
			142	44	88	1	8	1	

- Molecule 31 is URIDINE 5'-TRIPHOSPHATE (CCD ID: UTP) (formula: $C_9H_{15}N_2O_{15}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
31	G1	1	40	9	11	2	15	3	0

- Molecule 32 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
32	A1	1	43	10	12	5	13	3	0
32	B1	1	43	10	12	5	13	3	0
32	C1	1	43	10	12	5	13	3	0
32	D1	1	43	10	12	5	13	3	0

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

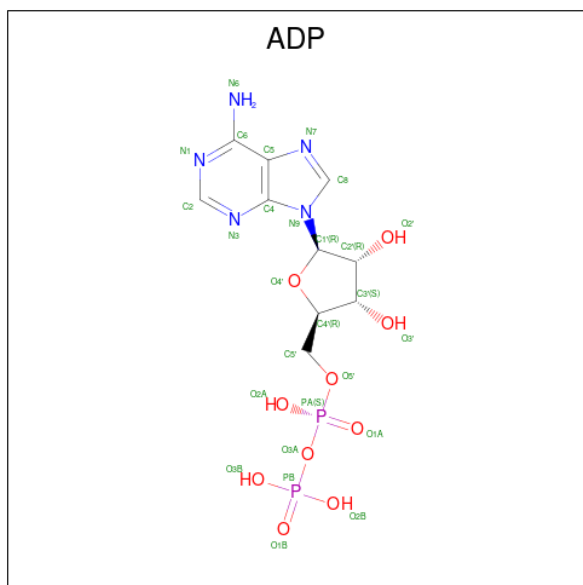
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
33	A1	1	1	1	0
33	B1	1	1	1	0
33	C1	1	1	1	0
33	D1	1	1	1	0

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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
33	E1	1	1	1	0

- Molecule 34 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

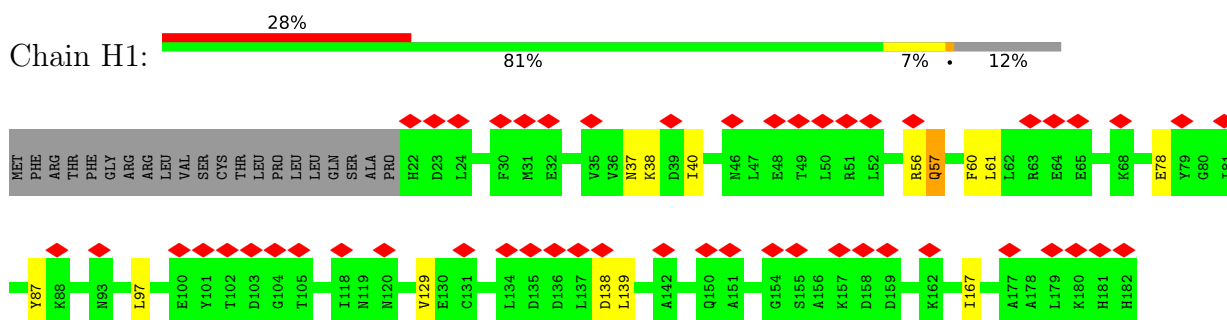


Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
34	E1	1	39	10	12	5	10	2	0

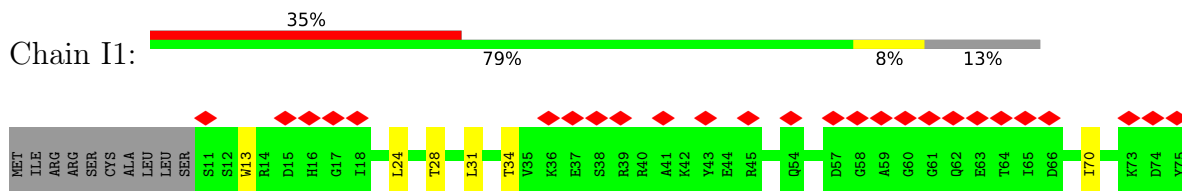
3 Residue-property plots [i](#)

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.

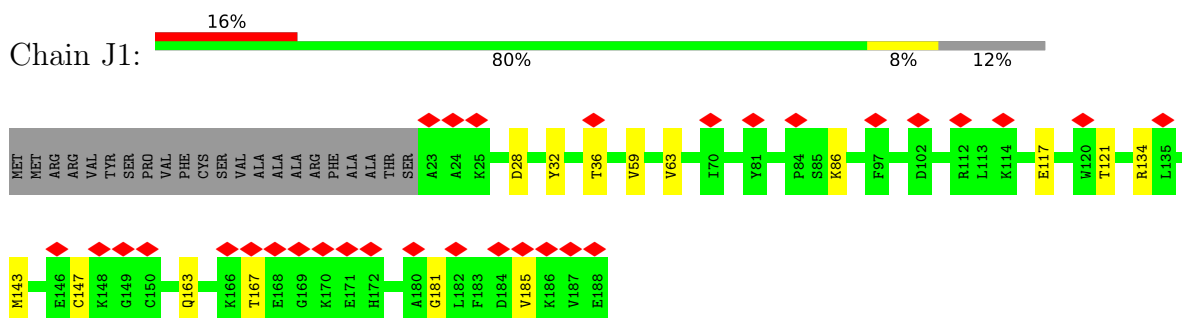
- Molecule 1: ATP synthase, epsilon chain, putative



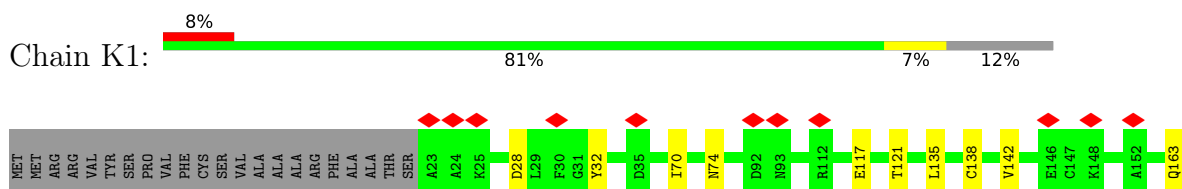
- Molecule 2: ATP synthase subunit epsilon, mitochondrial

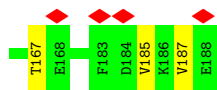


- Molecule 3: ATP synthase subunit p18, mitochondrial

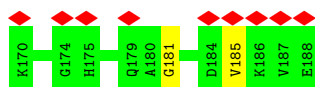
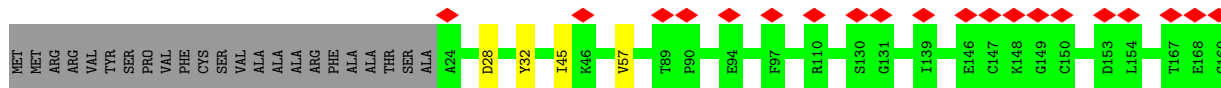
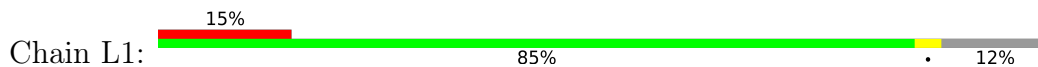


- Molecule 3: ATP synthase subunit p18, mitochondrial

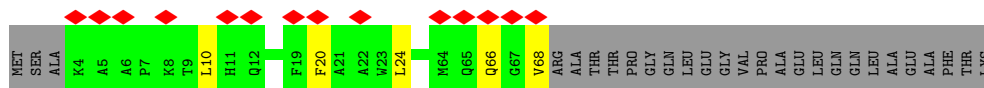




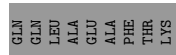
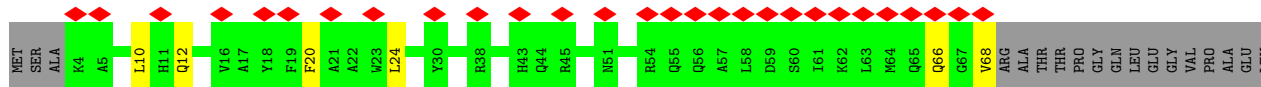
• Molecule 3: ATP synthase subunit p18, mitochondrial



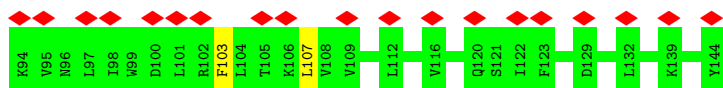
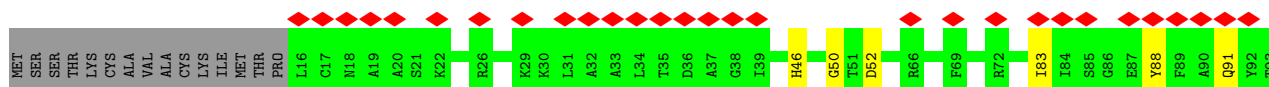
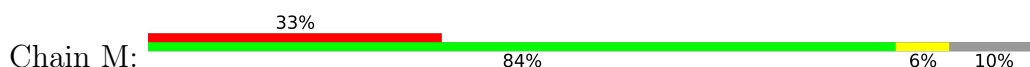
• Molecule 4: subunit-e



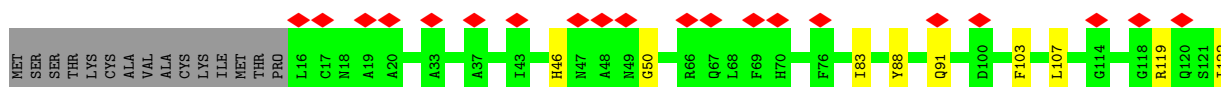
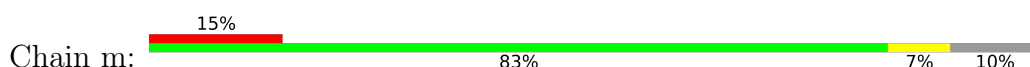
• Molecule 4: subunit-e

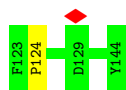


• Molecule 5: subunit-g

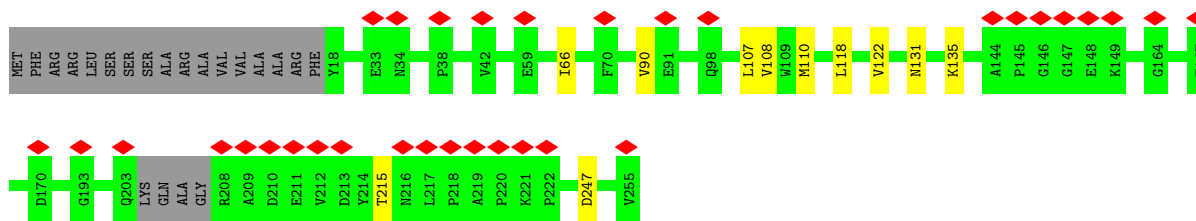
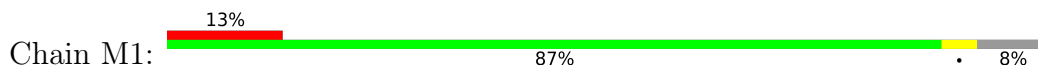


• Molecule 5: subunit-g

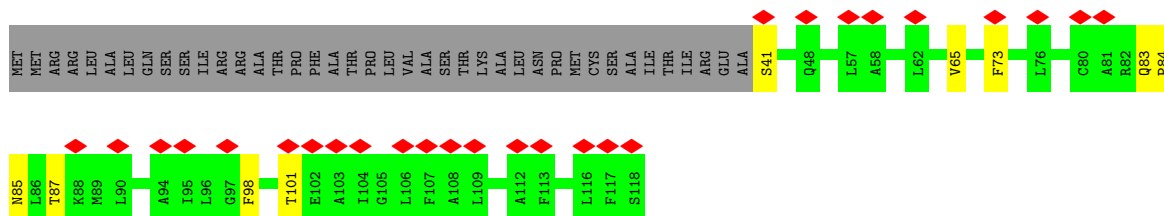




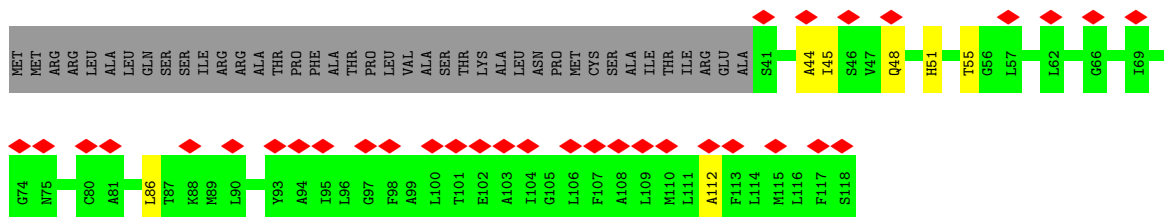
• Molecule 6: OSCP



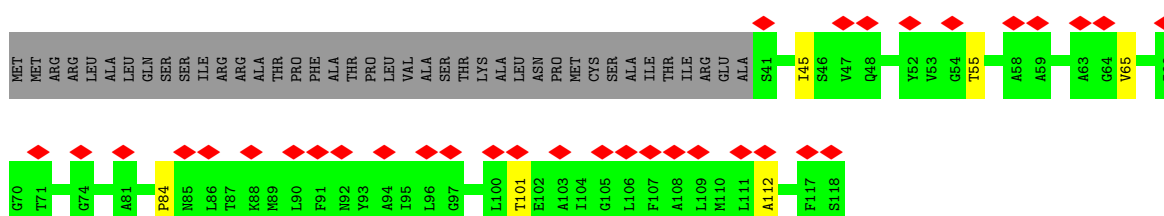
• Molecule 7: ATPase subunit 9, putative



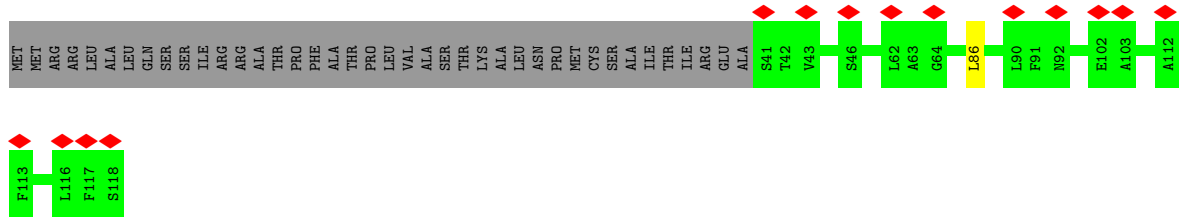
• Molecule 7: ATPase subunit 9, putative



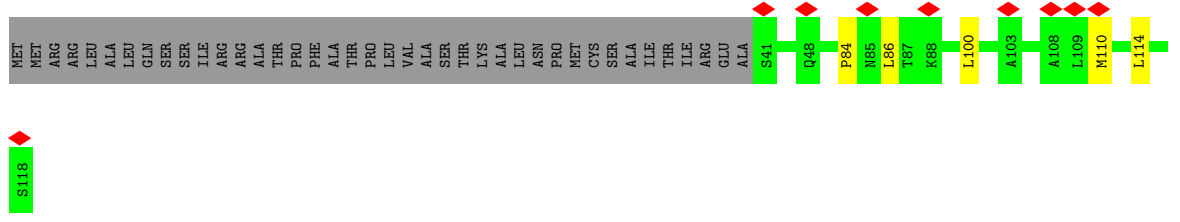
• Molecule 7: ATPase subunit 9, putative



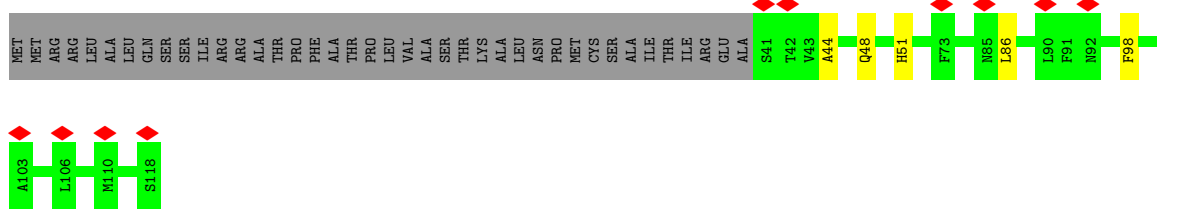
• Molecule 7: ATPase subunit 9, putative



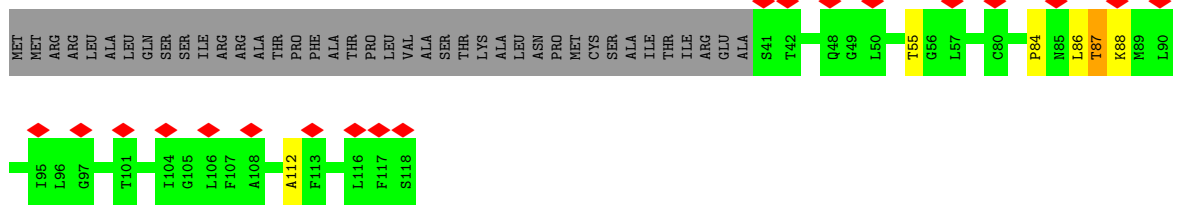
• Molecule 7: ATPase subunit 9, putative



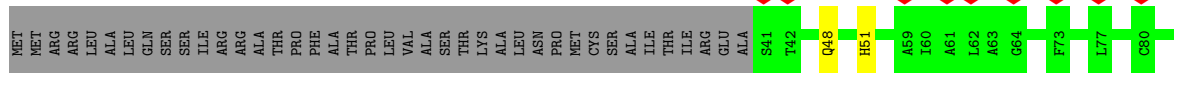
• Molecule 7: ATPase subunit 9, putative

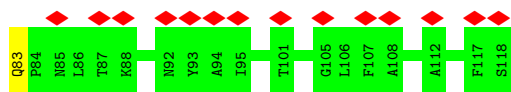


• Molecule 7: ATPase subunit 9, putative

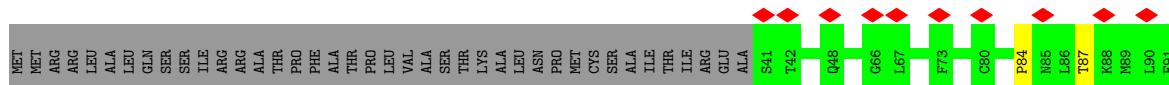


• Molecule 7: ATPase subunit 9, putative

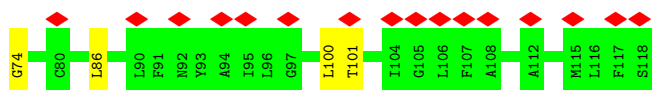
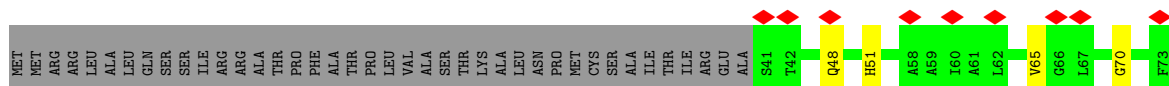




• Molecule 7: ATPase subunit 9, putative



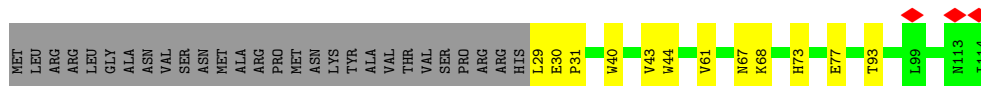
• Molecule 7: ATPase subunit 9, putative



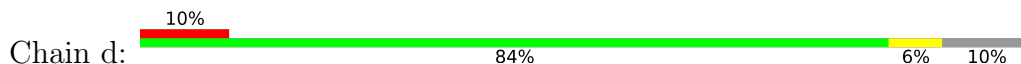
• Molecule 8: ATP synthase subunit a

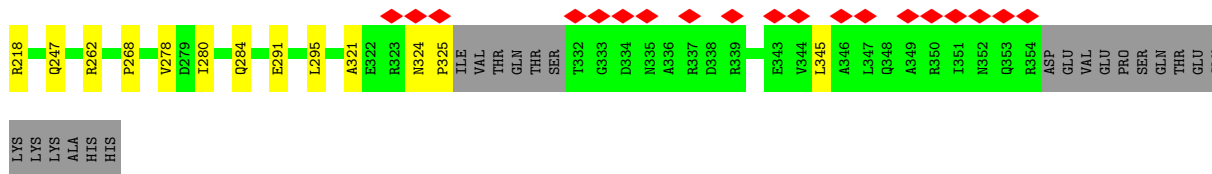


• Molecule 9: subunit-8

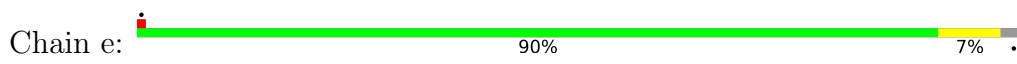


• Molecule 10: subunit-d

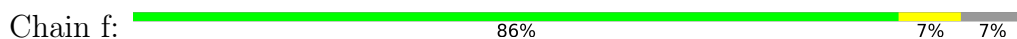




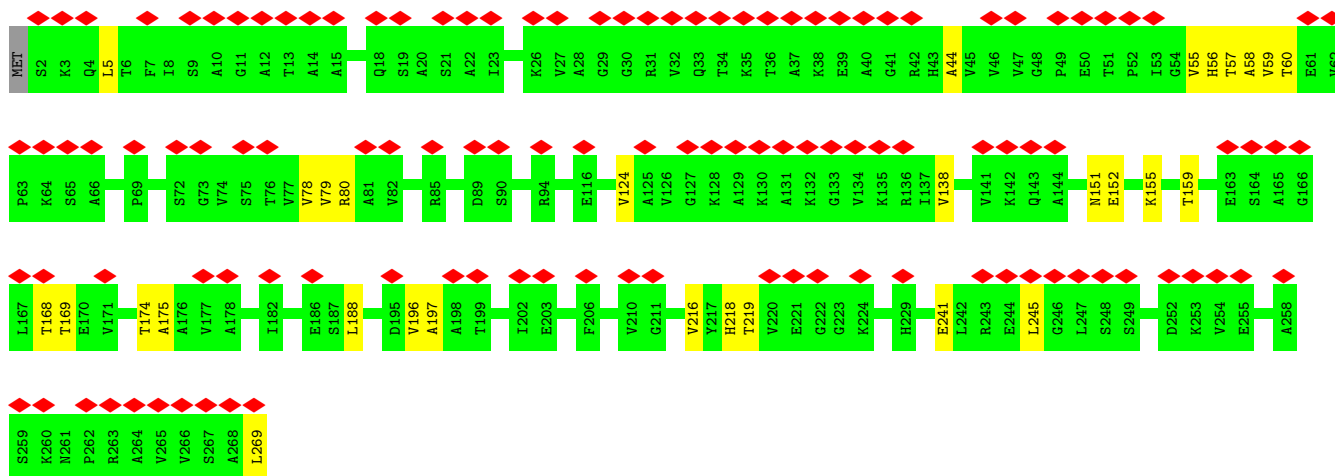
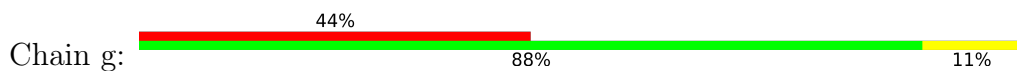
• Molecule 11: ATPTB1



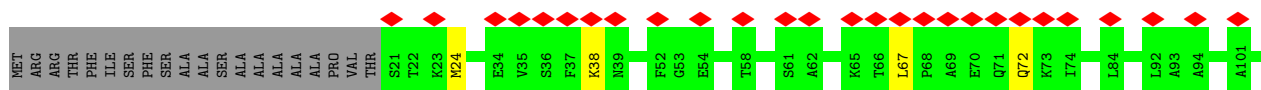
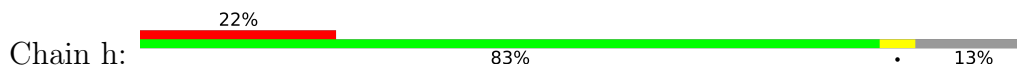
• Molecule 12: subunit-f

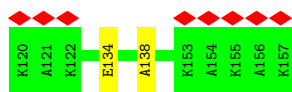


• Molecule 13: ATPTB3



• Molecule 14: ATPTB4





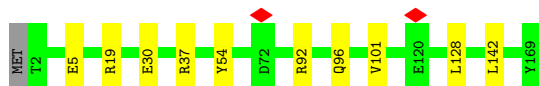
- Molecule 15: subunit-i/j

Chain i: 90% 9%



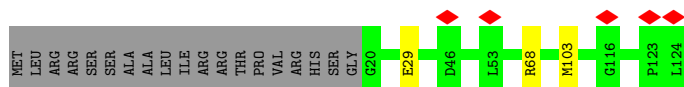
- Molecule 16: ATPTB6

Chain j: 93% 6%



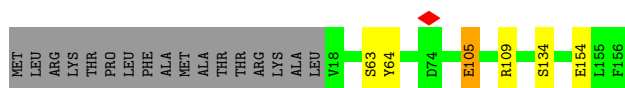
- Molecule 17: subunit-k

Chain k: 82% 15%



- Molecule 18: ATPTB11

Chain n: 85% 11%



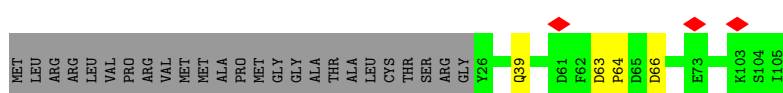
- Molecule 19: ATPTB12

Chain o: 90% 5% 5%



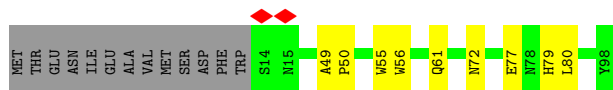
- Molecule 20: subunit-b

Chain p: 72% 24%

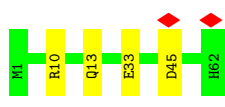
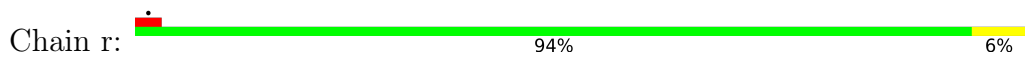


- Molecule 21: ATPEG3

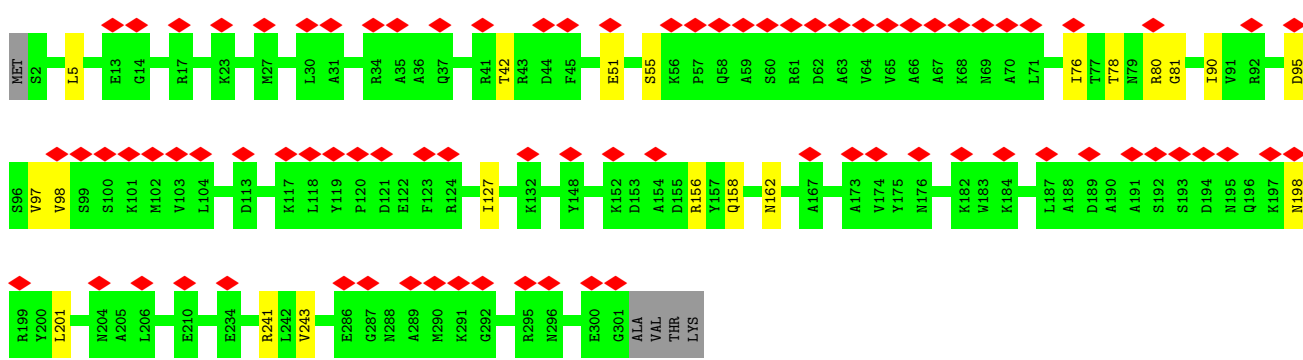
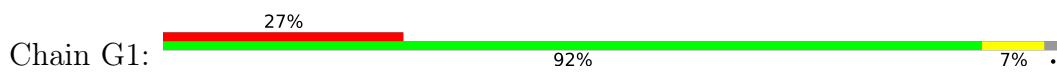
Chain q: 78% 9% 13%



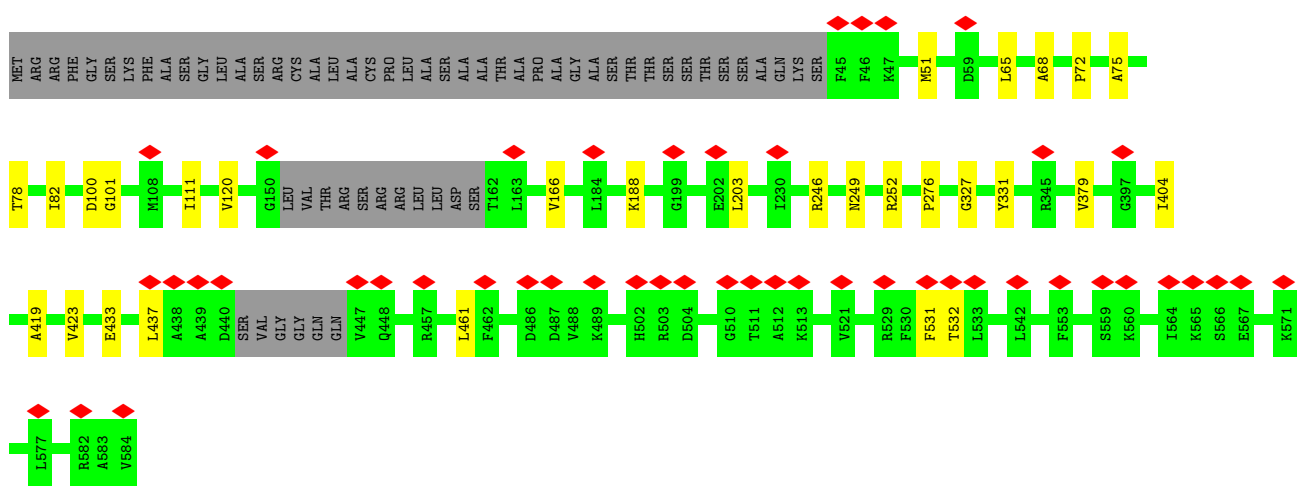
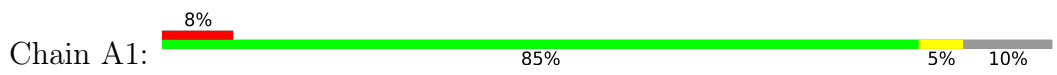
• Molecule 22: ATPEG4



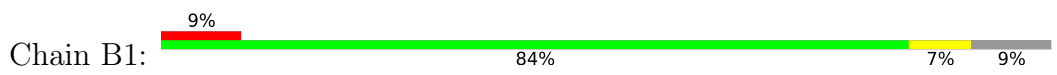
• Molecule 23: ATP synthase gamma subunit

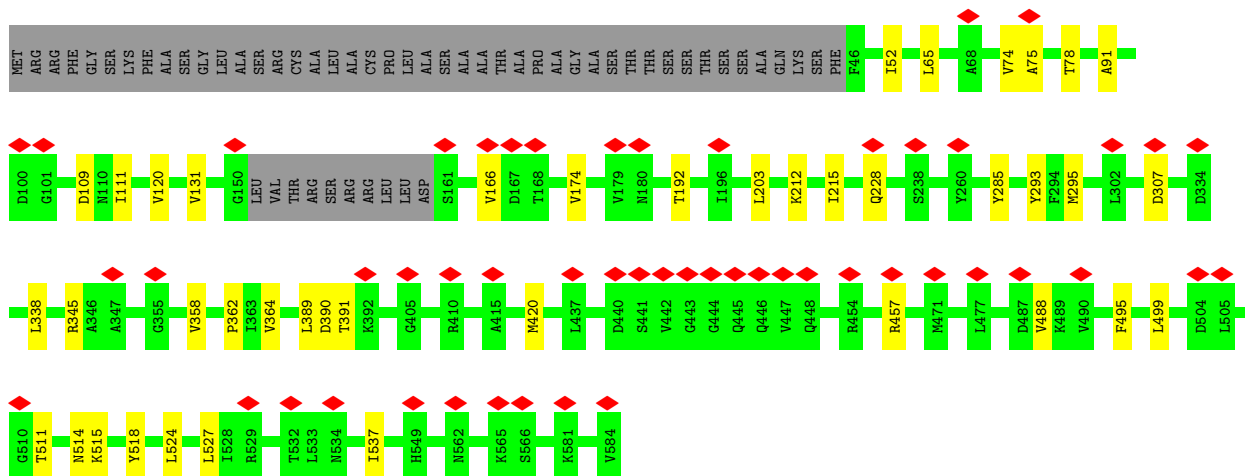


• Molecule 24: ATP synthase subunit alpha, mitochondrial

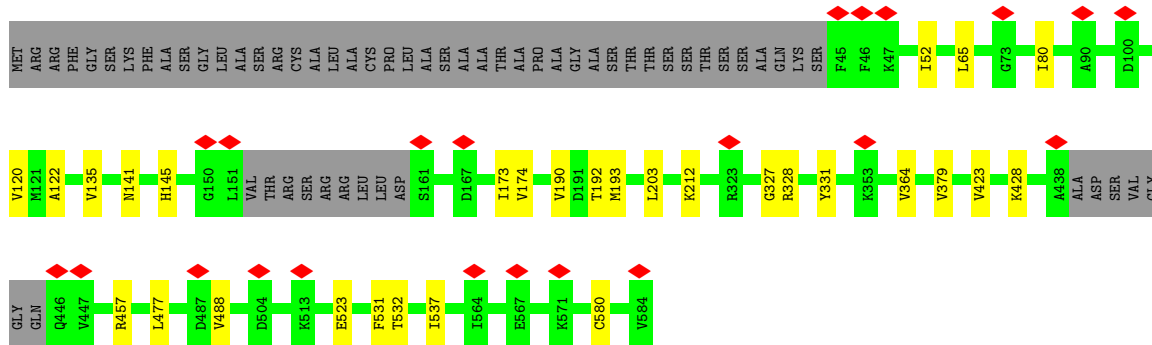
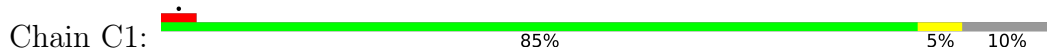


• Molecule 24: ATP synthase subunit alpha, mitochondrial

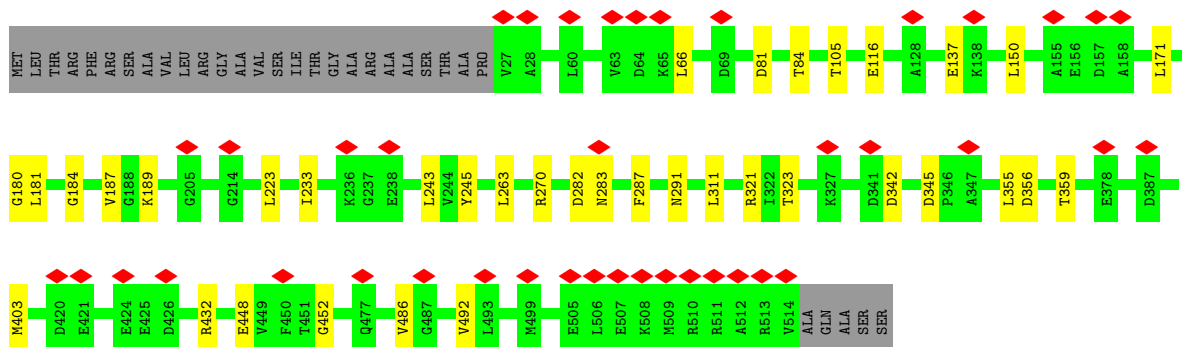
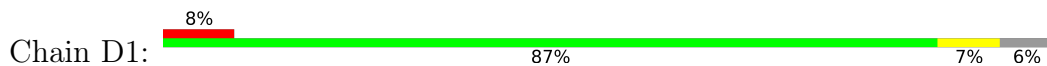




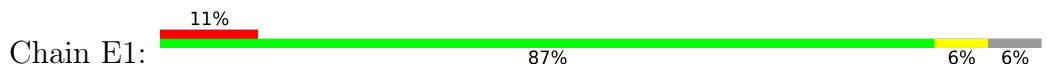
• Molecule 24: ATP synthase subunit alpha, mitochondrial

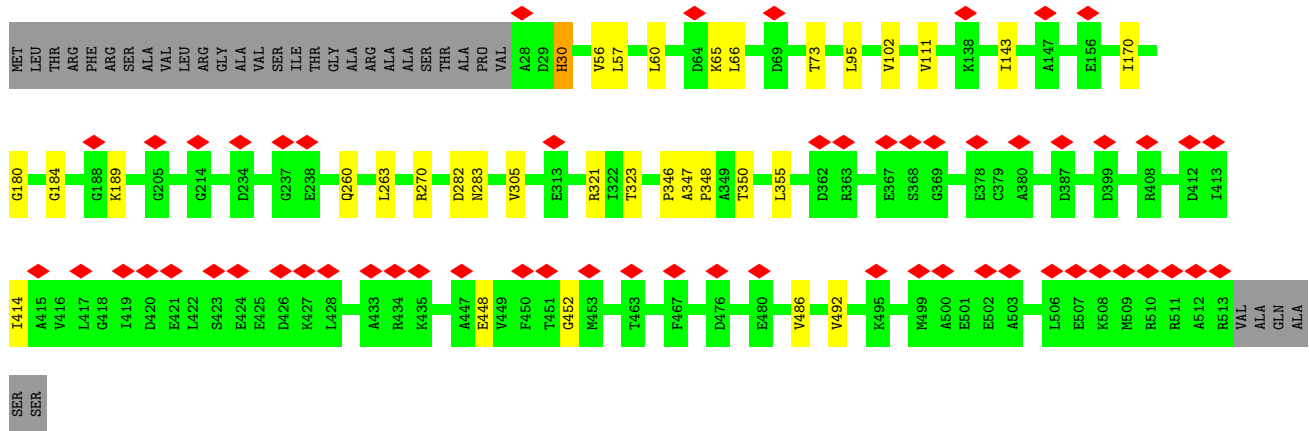


• Molecule 25: ATP synthase subunit beta, mitochondrial

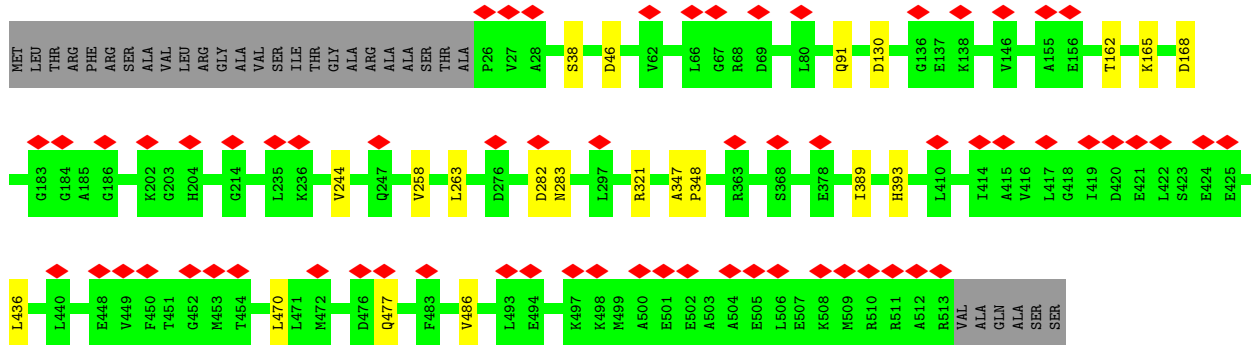
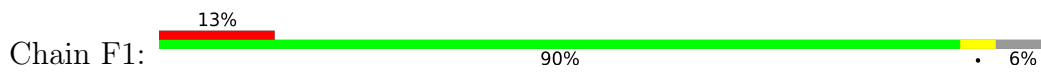


• Molecule 25: ATP synthase subunit beta, mitochondrial





• Molecule 25: ATP synthase subunit beta, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12173	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 ($e^-/\text{\AA}^2$)	33	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.105	Depositor
Minimum map value	-0.063	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	464.8, 464.8, 464.8	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, PEE, PC1, UTP, CDL, Q7G, MG, LMT, ATP, AME

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	H1	0.13	0/1274	0.21	0/1728
2	I1	0.07	0/547	0.20	0/738
3	J1	0.07	0/1342	0.21	0/1810
3	K1	0.07	0/1342	0.20	0/1810
3	L1	0.06	0/1337	0.21	0/1803
4	L	0.05	0/547	0.14	0/735
4	l	0.07	0/547	0.17	0/735
5	M	0.06	0/1049	0.16	0/1423
5	m	0.08	0/1049	0.20	0/1423
6	M1	0.07	0/1916	0.20	0/2591
7	O1	0.06	0/574	0.16	0/777
7	P1	0.06	0/574	0.16	0/777
7	Q1	0.06	0/574	0.15	0/777
7	R1	0.08	0/574	0.18	0/777
7	S1	0.08	0/574	0.20	0/777
7	T1	0.08	0/574	0.18	0/777
7	U1	0.09	0/574	0.22	0/777
7	V1	0.06	0/574	0.15	0/777
7	W1	0.06	0/574	0.16	0/777
7	X1	0.06	0/574	0.15	0/777
8	a	0.15	0/2111	0.26	0/2861
9	c	0.14	0/772	0.27	0/1054
10	d	0.08	0/2786	0.20	0/3760
11	e	0.11	0/3305	0.22	0/4482
12	f	0.11	0/1183	0.26	0/1601
13	g	0.06	0/1953	0.18	0/2650
14	h	0.06	0/1088	0.16	0/1466
15	i	0.12	0/913	0.22	0/1240
16	j	0.09	0/1462	0.19	0/1973
17	k	0.08	0/904	0.21	0/1228
18	n	0.11	0/1166	0.23	0/1581
19	o	0.08	0/814	0.18	0/1100

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	p	0.08	0/707	0.22	0/957
21	q	0.10	0/799	0.24	0/1091
22	r	0.10	0/567	0.24	0/767
23	G1	0.08	0/2427	0.22	0/3268
24	A1	0.08	0/4113	0.22	0/5569
24	B1	0.08	0/4147	0.24	0/5616
24	C1	0.09	0/4123	0.25	0/5582
25	D1	0.08	0/3752	0.25	0/5087
25	E1	0.09	0/3738	0.24	0/5067
25	F1	0.08	0/3753	0.22	0/5088
All	All	0.09	0/63273	0.22	0/85654

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 [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	H1	1251	1232	1231	14	0
2	I1	533	513	513	6	0
3	J1	1315	1276	1276	9	0
3	K1	1315	1276	1276	10	0
3	L1	1310	1271	1271	3	0
4	L	537	545	545	3	0
4	l	537	545	545	4	0
5	M	1027	1042	1042	6	0
5	m	1027	1042	1042	7	0
6	M1	1877	1873	1873	8	0
7	O1	565	600	599	7	0
7	P1	565	600	599	5	0
7	Q1	565	600	599	4	0
7	R1	565	600	599	1	0
7	S1	565	601	599	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	T1	565	601	599	4	0
7	U1	565	600	599	3	0
7	V1	565	600	599	2	0
7	W1	565	600	599	1	0
7	X1	565	600	599	6	0
8	a	2032	2044	2044	9	0
9	c	745	715	715	9	0
10	d	2737	2762	2763	17	0
11	e	3220	3050	3061	18	0
12	f	1145	1111	1111	9	0
13	g	1933	2020	2020	17	0
14	h	1070	1088	1088	4	0
15	i	883	857	857	6	0
16	j	1424	1411	1411	8	0
17	k	873	876	876	3	0
18	n	1128	1082	1082	4	0
19	o	789	767	767	4	0
20	p	684	651	651	5	0
21	q	766	720	720	7	0
22	r	542	498	498	5	0
23	G1	2387	2387	2387	15	0
24	A1	4039	4154	4154	20	0
24	B1	4073	4187	4187	26	0
24	C1	4049	4170	4170	24	0
25	D1	3696	3750	3750	26	0
25	E1	3682	3732	3732	21	0
25	F1	3696	3750	3750	13	0
26	L	100	156	156	0	0
26	M	100	156	156	1	0
26	c	100	156	156	1	0
26	e	500	780	780	4	0
26	f	100	156	156	0	0
26	j	100	156	156	1	0
26	l	100	156	156	0	0
26	m	100	156	156	0	0
26	q	200	312	312	2	0
27	M	51	82	82	1	0
27	f	51	82	82	0	0
27	m	51	82	82	0	0
28	e	35	39	46	0	0
28	j	35	39	46	0	0
29	e	48	60	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	n	59	70	0	0	0
30	f	54	88	88	1	0
30	i	54	88	88	0	0
30	j	54	88	88	0	0
30	p	54	88	88	0	0
31	G1	29	11	11	0	0
32	A1	31	12	12	0	0
32	B1	31	12	12	1	0
32	C1	31	12	12	1	0
32	D1	31	12	12	1	0
33	A1	1	0	0	0	0
33	B1	1	0	0	0	0
33	C1	1	0	0	0	0
33	D1	1	0	0	0	0
33	E1	1	0	0	0	0
34	E1	27	12	12	0	0
All	All	64103	65460	65343	323	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 2.

The worst 5 of 323 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)
16:j:19:ARG:NH2	21:q:77:GLU:O	2.15	0.79
25:E1:260:GLN:N	25:E1:260:GLN:OE1	2.22	0.73
9:c:93:THR:HG21	10:d:136:ASP:OD2	1.89	0.73
12:f:16:GLU:OE1	12:f:16:GLU:N	2.22	0.72
25:E1:184:GLY:O	25:E1:189:LYS:NZ	2.23	0.71

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	H1	159/182 (87%)	156 (98%)	3 (2%)	0	100	100
2	I1	63/75 (84%)	61 (97%)	2 (3%)	0	100	100
3	J1	164/188 (87%)	161 (98%)	3 (2%)	0	100	100
3	K1	164/188 (87%)	163 (99%)	1 (1%)	0	100	100
3	L1	163/188 (87%)	162 (99%)	1 (1%)	0	100	100
4	L	63/92 (68%)	63 (100%)	0	0	100	100
4	l	63/92 (68%)	63 (100%)	0	0	100	100
5	M	127/144 (88%)	127 (100%)	0	0	100	100
5	m	127/144 (88%)	127 (100%)	0	0	100	100
6	M1	230/255 (90%)	226 (98%)	4 (2%)	0	100	100
7	O1	76/118 (64%)	75 (99%)	1 (1%)	0	100	100
7	P1	76/118 (64%)	76 (100%)	0	0	100	100
7	Q1	76/118 (64%)	76 (100%)	0	0	100	100
7	R1	76/118 (64%)	76 (100%)	0	0	100	100
7	S1	76/118 (64%)	76 (100%)	0	0	100	100
7	T1	76/118 (64%)	75 (99%)	1 (1%)	0	100	100
7	U1	76/118 (64%)	74 (97%)	1 (1%)	1 (1%)	9	41
7	V1	76/118 (64%)	76 (100%)	0	0	100	100
7	W1	76/118 (64%)	76 (100%)	0	0	100	100
7	X1	76/118 (64%)	75 (99%)	1 (1%)	0	100	100
8	a	229/231 (99%)	224 (98%)	5 (2%)	0	100	100
9	c	84/114 (74%)	83 (99%)	1 (1%)	0	100	100
10	d	328/370 (89%)	323 (98%)	5 (2%)	0	100	100
11	e	381/396 (96%)	377 (99%)	4 (1%)	0	100	100
12	f	133/145 (92%)	130 (98%)	3 (2%)	0	100	100
13	g	266/269 (99%)	264 (99%)	2 (1%)	0	100	100
14	h	135/157 (86%)	133 (98%)	2 (2%)	0	100	100
15	i	101/104 (97%)	100 (99%)	1 (1%)	0	100	100
16	j	166/169 (98%)	161 (97%)	5 (3%)	0	100	100
17	k	103/124 (83%)	99 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	n	137/156 (88%)	130 (95%)	7 (5%)	0	100	100
19	o	94/101 (93%)	93 (99%)	1 (1%)	0	100	100
20	p	78/105 (74%)	77 (99%)	1 (1%)	0	100	100
21	q	83/98 (85%)	81 (98%)	2 (2%)	0	100	100
22	r	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
23	G1	298/305 (98%)	292 (98%)	6 (2%)	0	100	100
24	A1	517/584 (88%)	509 (98%)	8 (2%)	0	100	100
24	B1	525/584 (90%)	515 (98%)	10 (2%)	0	100	100
24	C1	518/584 (89%)	507 (98%)	11 (2%)	0	100	100
25	D1	486/519 (94%)	476 (98%)	10 (2%)	0	100	100
25	E1	484/519 (93%)	474 (98%)	10 (2%)	0	100	100
25	F1	486/519 (94%)	473 (97%)	13 (3%)	0	100	100
All	All	7775/8943 (87%)	7644 (98%)	130 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	U1	87	THR

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H1	137/156 (88%)	136 (99%)	1 (1%)	76	79
2	I1	58/67 (87%)	58 (100%)	0	100	100
3	J1	145/162 (90%)	145 (100%)	0	100	100
3	K1	145/162 (90%)	145 (100%)	0	100	100
3	L1	145/162 (90%)	145 (100%)	0	100	100
4	L	55/75 (73%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	l	55/75 (73%)	55 (100%)	0	100	100
5	M	111/124 (90%)	111 (100%)	0	100	100
5	m	111/124 (90%)	111 (100%)	0	100	100
6	M1	200/215 (93%)	199 (100%)	1 (0%)	81	81
7	O1	56/89 (63%)	56 (100%)	0	100	100
7	P1	56/89 (63%)	56 (100%)	0	100	100
7	Q1	56/89 (63%)	56 (100%)	0	100	100
7	R1	56/89 (63%)	56 (100%)	0	100	100
7	S1	56/89 (63%)	56 (100%)	0	100	100
7	T1	56/89 (63%)	56 (100%)	0	100	100
7	U1	56/89 (63%)	55 (98%)	1 (2%)	51	67
7	V1	56/89 (63%)	56 (100%)	0	100	100
7	W1	56/89 (63%)	56 (100%)	0	100	100
7	X1	56/89 (63%)	56 (100%)	0	100	100
8	a	225/225 (100%)	224 (100%)	1 (0%)	84	82
9	c	80/104 (77%)	80 (100%)	0	100	100
10	d	297/334 (89%)	296 (100%)	1 (0%)	86	84
11	e	334/341 (98%)	334 (100%)	0	100	100
12	f	119/124 (96%)	118 (99%)	1 (1%)	73	77
13	g	205/206 (100%)	205 (100%)	0	100	100
14	h	110/123 (89%)	110 (100%)	0	100	100
15	i	95/96 (99%)	95 (100%)	0	100	100
16	j	149/150 (99%)	149 (100%)	0	100	100
17	k	91/107 (85%)	91 (100%)	0	100	100
18	n	123/137 (90%)	122 (99%)	1 (1%)	73	77
19	o	82/86 (95%)	82 (100%)	0	100	100
20	p	75/94 (80%)	75 (100%)	0	100	100
21	q	80/92 (87%)	80 (100%)	0	100	100
22	r	56/56 (100%)	56 (100%)	0	100	100
23	G1	253/257 (98%)	253 (100%)	0	100	100
24	A1	434/479 (91%)	434 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	B1	438/479 (91%)	436 (100%)	2 (0%)	81	81
24	C1	436/479 (91%)	436 (100%)	0	100	100
25	D1	399/420 (95%)	397 (100%)	2 (0%)	81	81
25	E1	397/420 (94%)	396 (100%)	1 (0%)	86	84
25	F1	399/420 (95%)	399 (100%)	0	100	100
All	All	6599/7441 (89%)	6587 (100%)	12 (0%)	85	85

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	B1	74	VAL
24	B1	111	ILE
25	E1	30	HIS
25	D1	66	LEU
8	a	144	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
24	B1	296	ASN
24	C1	245	GLN
24	B1	339	HIS
24	B1	463	ASN
25	D1	39	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
11	AME	e	1	11	9,10,11	0.26	0	9,11,13	0.45	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
11	AME	e	1	11	-	3/9/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	e	1	AME	N-CA-CB-CG
11	e	1	AME	C-CA-N-CT1
11	e	1	AME	CB-CA-N-CT1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	e	1	AME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 5 are monoatomic - leaving 31 for Mogul analysis.

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
28	LMT	e	406	-	36,36,36	0.10	0	47,47,47	0.16	0
26	CDL	l	101	-	99,99,99	0.29	0	105,111,111	0.25	0
26	CDL	e	405	-	99,99,99	0.29	0	105,111,111	0.25	0
26	CDL	f	201	-	99,99,99	0.29	0	105,111,111	0.27	0
29	Q7G	e	407	-	54,54,90	0.13	0	80,84,138	0.25	0
32	ATP	C1	601	33	32,33,33	0.28	0	48,52,52	0.29	0
26	CDL	e	402	-	99,99,99	0.29	0	105,111,111	0.26	0
30	PC1	f	203	-	53,53,53	0.27	0	59,61,61	0.30	0
34	ADP	E1	601	33	28,29,29	0.41	0	43,45,45	0.49	0
26	CDL	q	101	-	99,99,99	0.29	0	105,111,111	0.25	0
26	CDL	q	102	-	99,99,99	0.29	0	105,111,111	0.28	0
30	PC1	p	201	-	53,53,53	0.28	0	59,61,61	0.29	0
26	CDL	e	404	-	99,99,99	0.29	0	105,111,111	0.26	0
32	ATP	A1	601	33	32,33,33	0.28	0	48,52,52	0.29	0
31	UTP	G1	401	-	29,30,30	0.29	0	43,47,47	0.30	0
26	CDL	e	401	-	99,99,99	0.29	0	105,111,111	0.26	0
26	CDL	e	403	-	99,99,99	0.29	0	105,111,111	0.26	0
26	CDL	c	201	-	99,99,99	0.29	0	105,111,111	0.26	0
26	CDL	m	202	-	99,99,99	0.29	0	105,111,111	0.25	0
27	PEE	M	202	-	50,50,50	0.76	2 (4%)	53,55,55	0.49	0
26	CDL	j	201	-	99,99,99	0.29	0	105,111,111	0.25	0
29	Q7G	n	201	-	66,66,90	0.13	0	98,102,138	0.29	0
27	PEE	m	201	-	50,50,50	0.77	2 (4%)	53,55,55	0.48	0
28	LMT	j	203	-	36,36,36	0.11	0	47,47,47	0.18	0
30	PC1	j	202	-	53,53,53	0.28	0	59,61,61	0.27	0
26	CDL	M	201	-	99,99,99	0.29	0	105,111,111	0.34	1 (0%)
32	ATP	B1	601	33	32,33,33	0.28	0	48,52,52	0.28	0
26	CDL	L	101	-	99,99,99	0.29	0	105,111,111	0.25	0
30	PC1	i	201	-	53,53,53	0.29	0	59,61,61	0.28	0
27	PEE	f	202	-	50,50,50	0.78	2 (4%)	53,55,55	0.47	0
32	ATP	D1	601	33	32,33,33	0.28	0	48,52,52	0.28	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	LMT	e	406	-	-	1/21/61/61	0/2/2/2
26	CDL	l	101	-	-	19/110/110/110	-
26	CDL	e	405	-	-	32/110/110/110	-
29	Q7G	e	407	-	1/1/19/34	5/15/123/200	0/7/7/10
26	CDL	f	201	-	-	21/110/110/110	-
32	ATP	C1	601	33	-	8/22/38/38	0/3/3/3
26	CDL	e	402	-	-	22/110/110/110	-
30	PC1	f	203	-	-	12/57/57/57	-
34	ADP	E1	601	33	-	1/16/32/32	0/3/3/3
26	CDL	q	101	-	-	30/110/110/110	-
26	CDL	q	102	-	-	24/110/110/110	-
30	PC1	p	201	-	-	10/57/57/57	-
26	CDL	e	404	-	-	19/110/110/110	-
32	ATP	A1	601	33	-	6/22/38/38	0/3/3/3
31	UTP	G1	401	-	-	0/22/38/38	0/2/2/2
26	CDL	e	401	-	-	24/110/110/110	-
26	CDL	e	403	-	-	25/110/110/110	-
26	CDL	c	201	-	-	25/110/110/110	-
26	CDL	m	202	-	-	28/110/110/110	-
27	PEE	M	202	-	-	25/54/54/54	-
29	Q7G	n	201	-	2/2/24/34	6/20/148/200	0/8/8/10
26	CDL	j	201	-	-	24/110/110/110	-
27	PEE	m	201	-	-	23/54/54/54	-
28	LMT	j	203	-	-	5/21/61/61	0/2/2/2
30	PC1	j	202	-	-	15/57/57/57	-
26	CDL	M	201	-	-	27/110/110/110	-
32	ATP	B1	601	33	-	6/22/38/38	0/3/3/3
26	CDL	L	101	-	-	17/110/110/110	-
30	PC1	i	201	-	-	9/57/57/57	-
27	PEE	f	202	-	-	17/54/54/54	-
32	ATP	D1	601	33	-	3/22/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	f	202	PEE	C39-C38	3.66	1.52	1.31
27	m	201	PEE	C18-C19	3.66	1.52	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	M	202	PEE	C18-C19	3.64	1.52	1.31
27	f	202	PEE	C18-C19	3.63	1.52	1.31
27	m	201	PEE	C39-C38	3.58	1.52	1.31

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	M	201	CDL	C27-C26-C25	2.38	129.44	113.36

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
29	e	407	Q7G	C1B
29	n	201	Q7G	C1C
29	n	201	Q7G	C1B

5 of 489 torsion outliers are listed below:

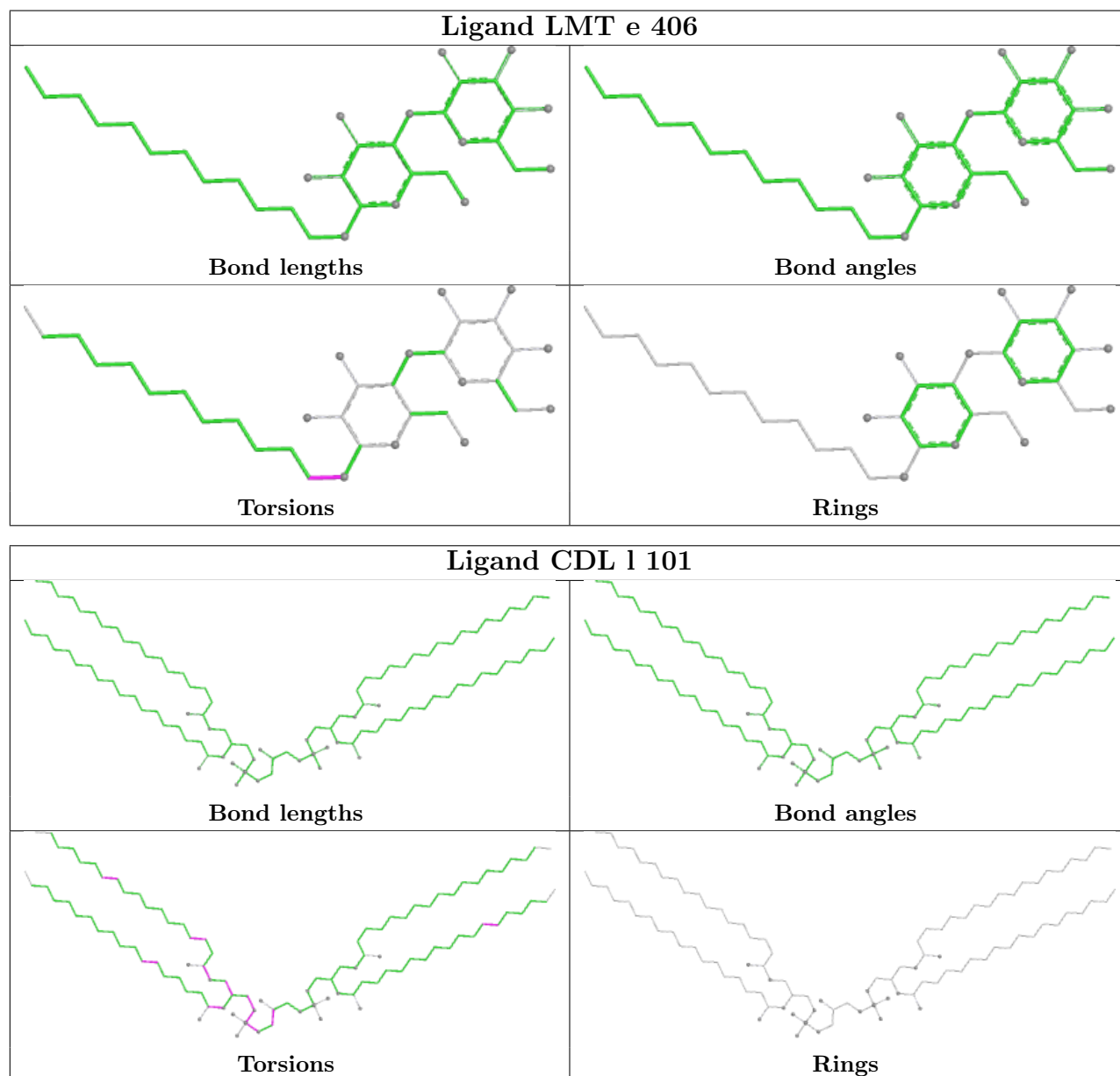
Mol	Chain	Res	Type	Atoms
26	L	101	CDL	CA2-OA2-PA1-OA3
26	L	101	CDL	CA2-OA2-PA1-OA4
26	L	101	CDL	CA2-OA2-PA1-OA5
26	L	101	CDL	CA3-OA5-PA1-OA2
26	M	201	CDL	CA2-C1-CB2-OB2

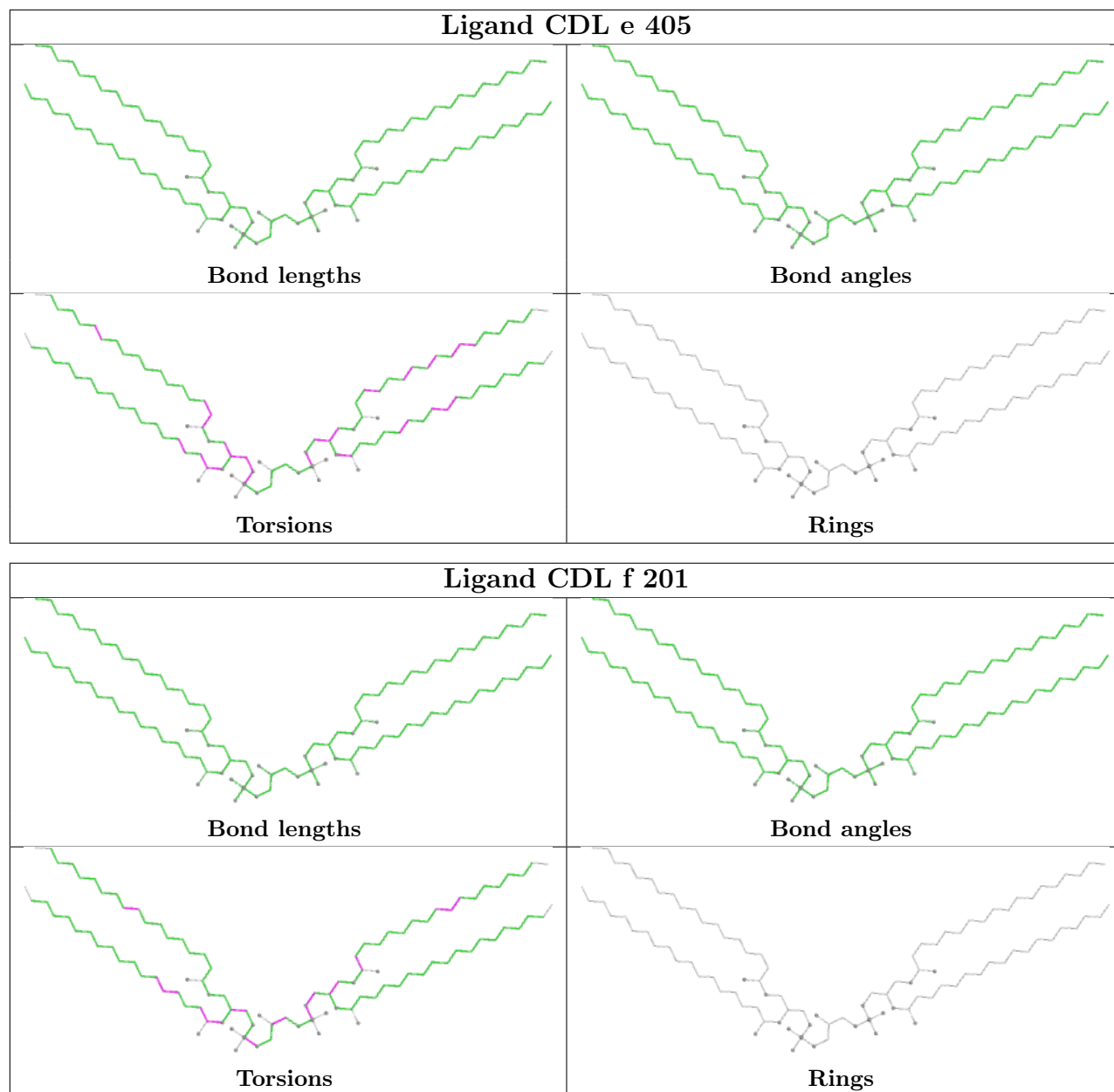
There are no ring outliers.

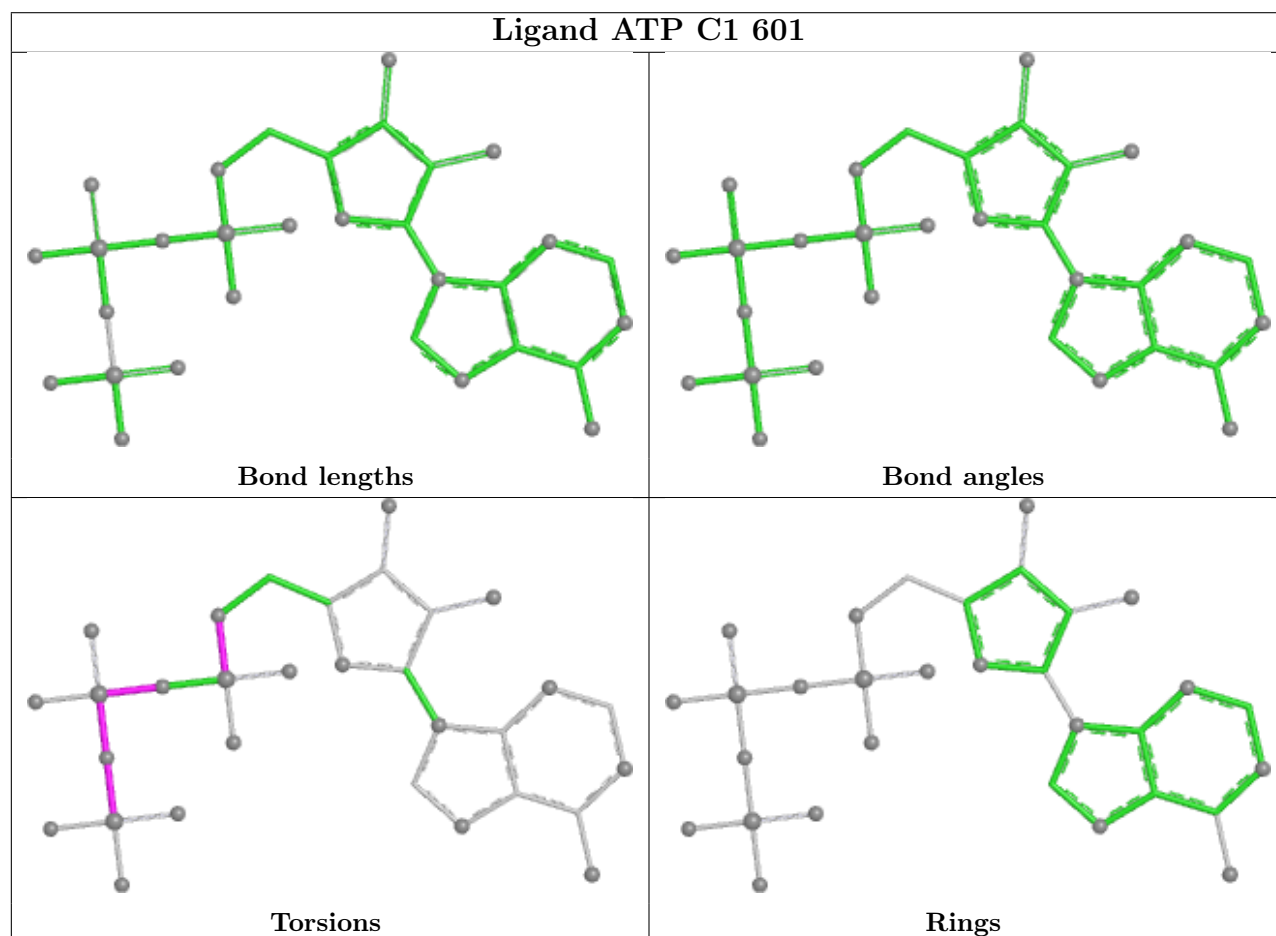
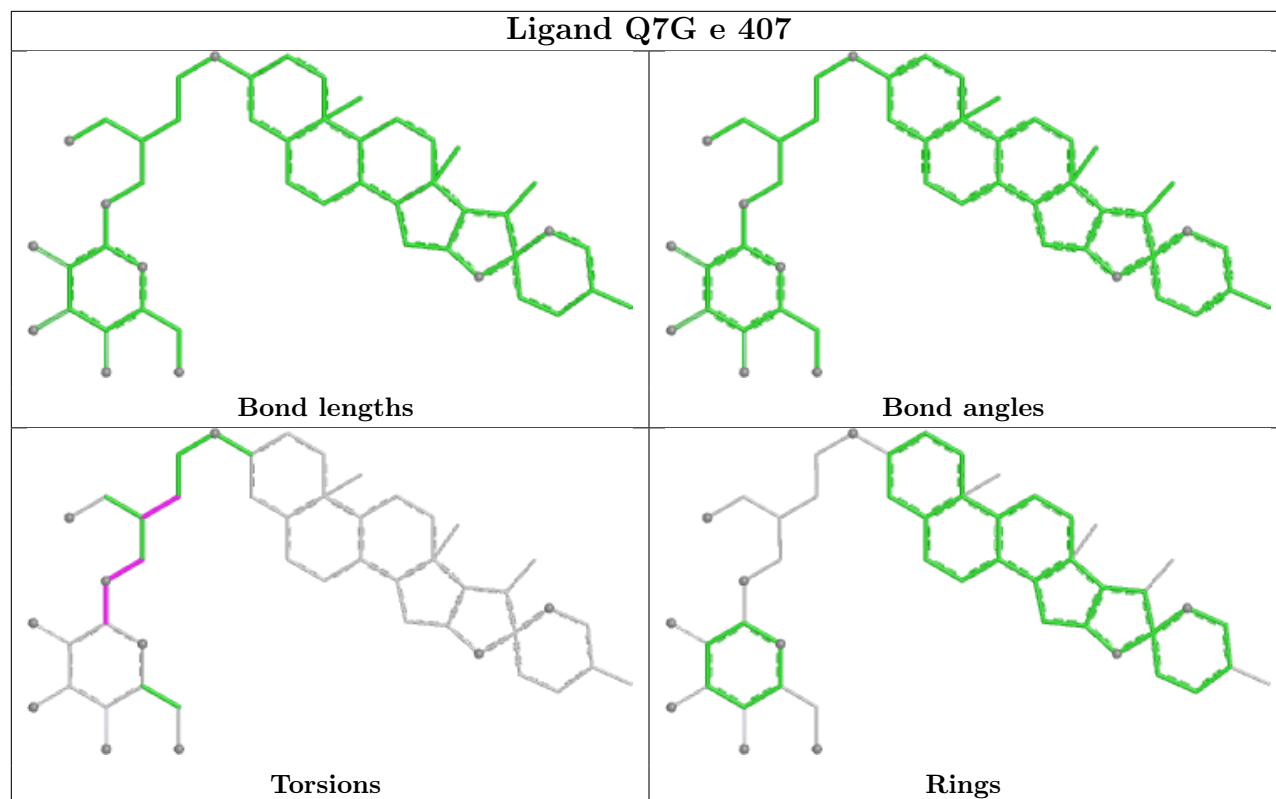
12 monomers are involved in 13 short contacts:

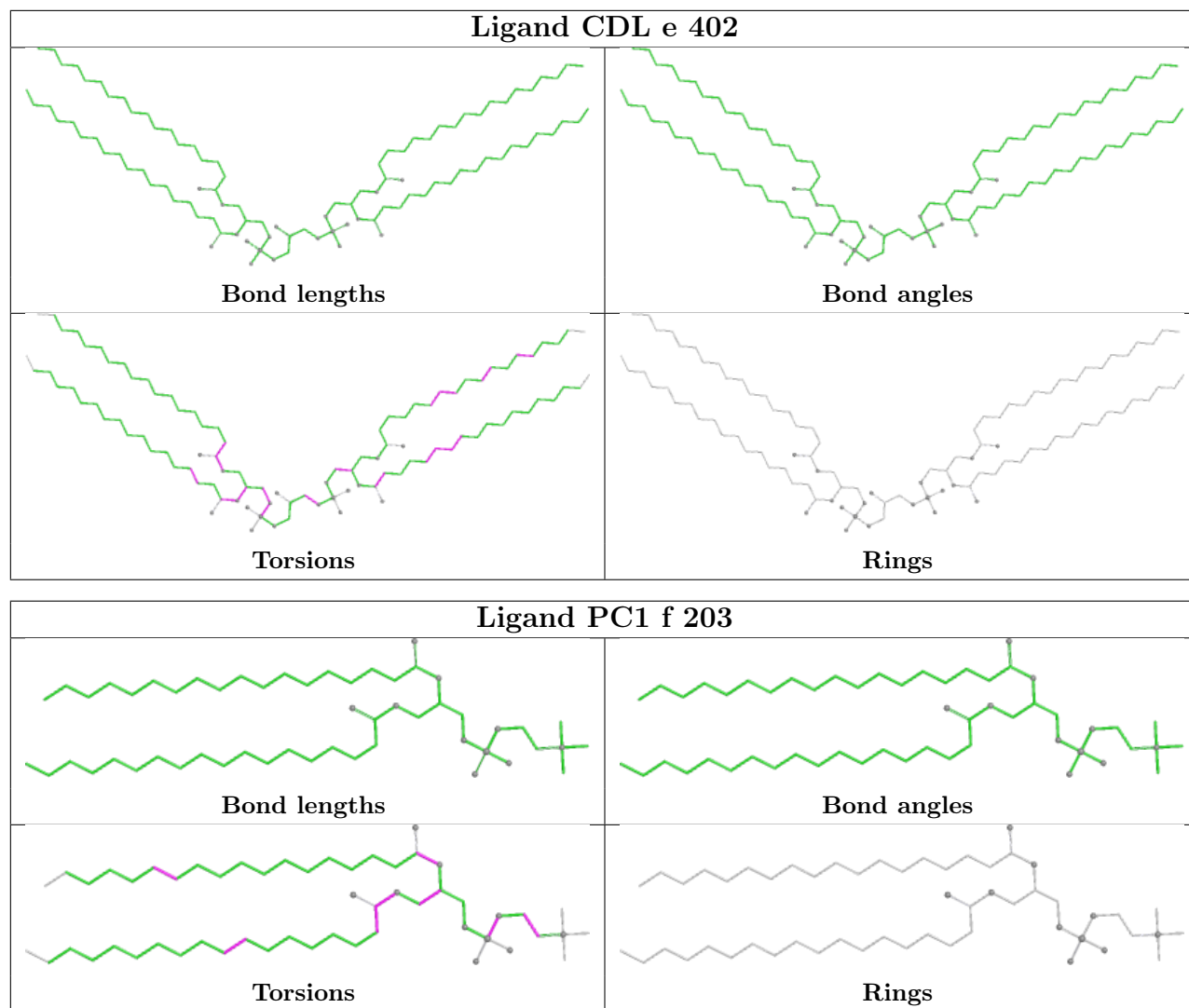
Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	C1	601	ATP	1	0
26	e	402	CDL	3	0
30	f	203	PC1	1	0
26	q	101	CDL	1	0
26	q	102	CDL	1	0
26	e	403	CDL	2	0
26	c	201	CDL	1	0
27	M	202	PEE	1	0
26	j	201	CDL	1	0
26	M	201	CDL	1	0
32	B1	601	ATP	1	0
32	D1	601	ATP	1	0

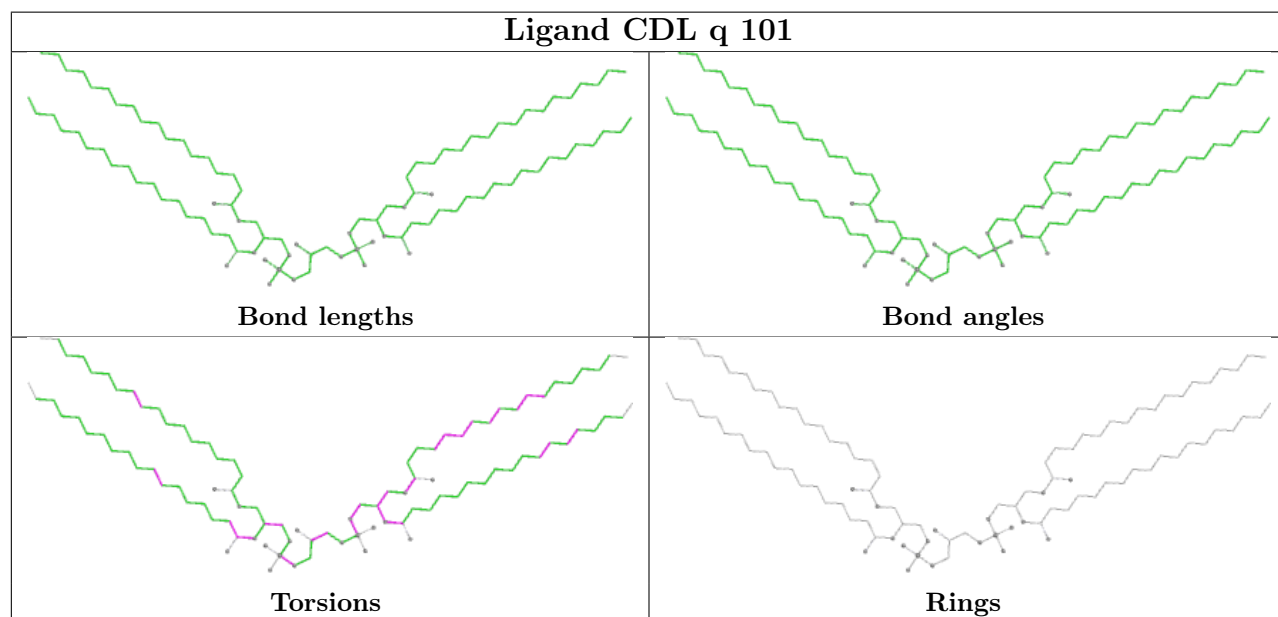
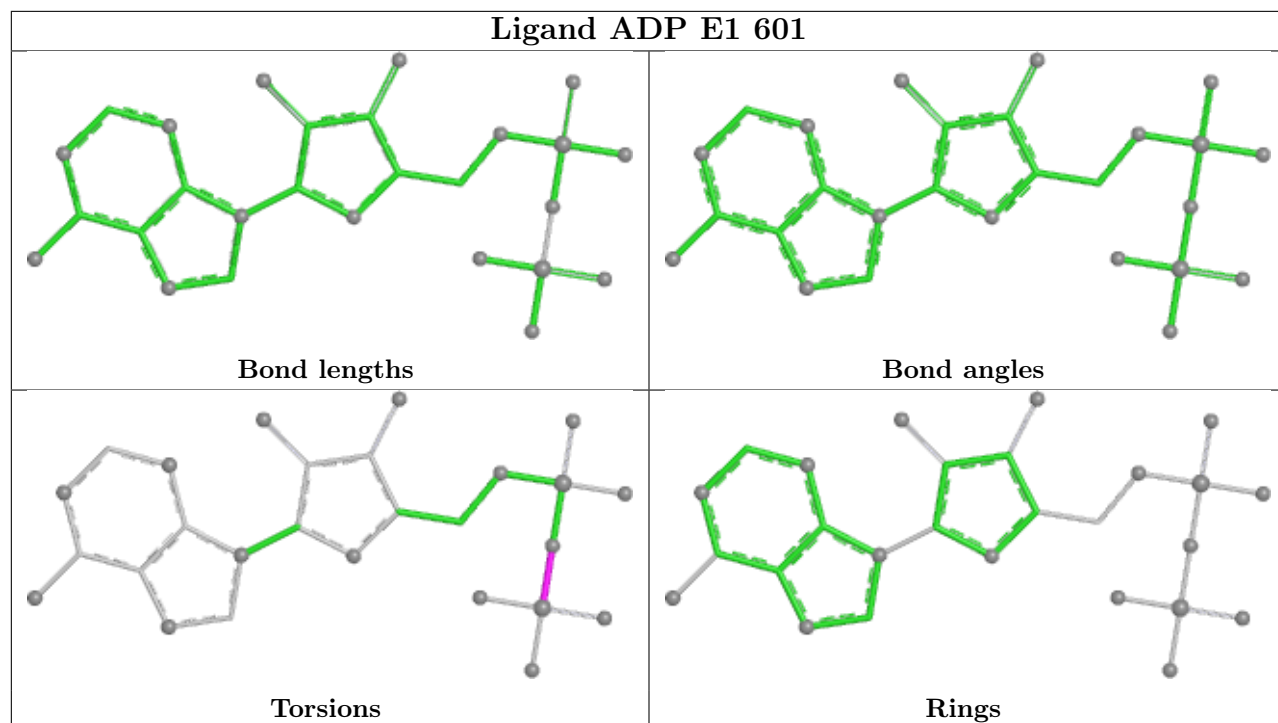
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

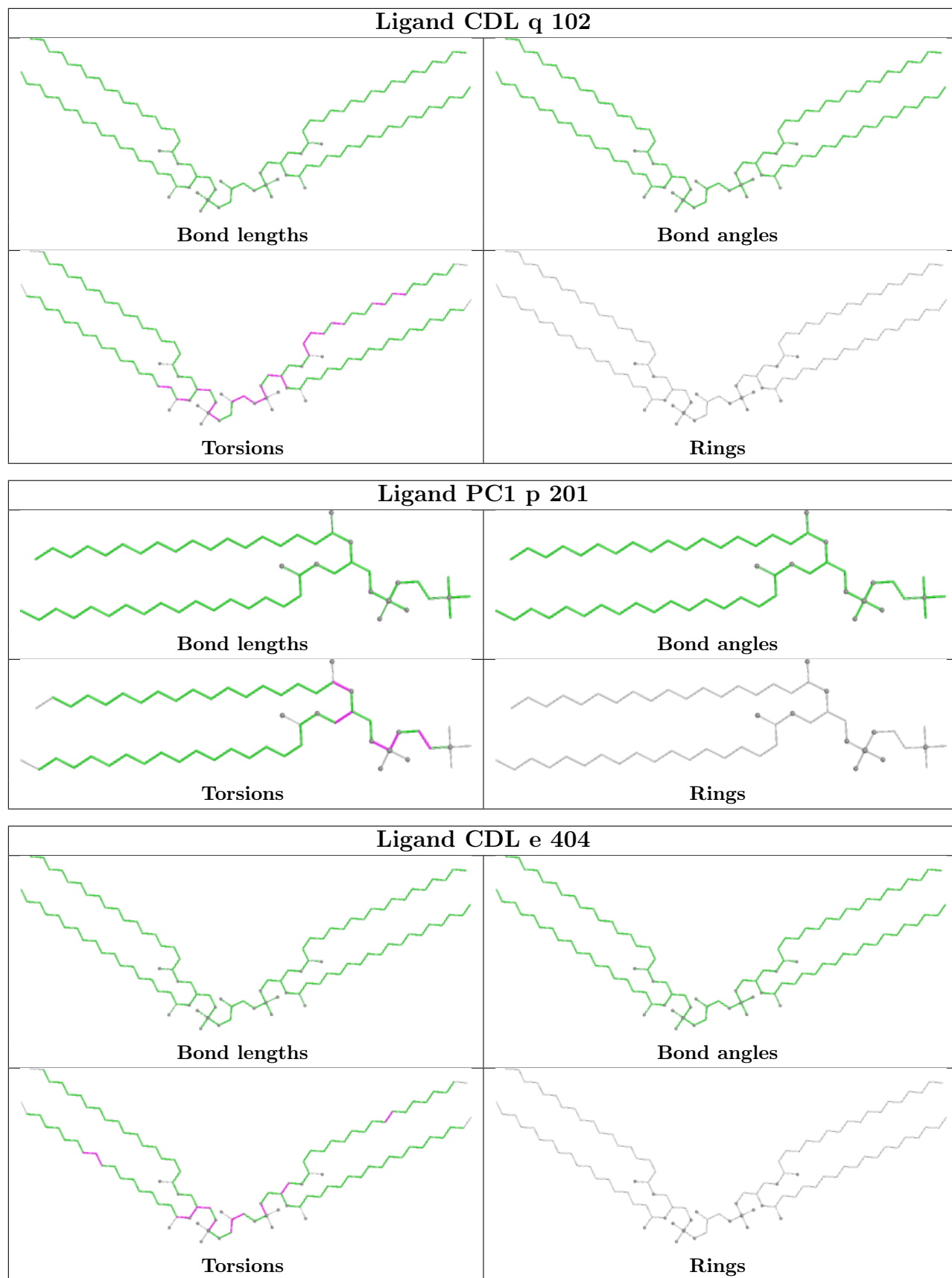


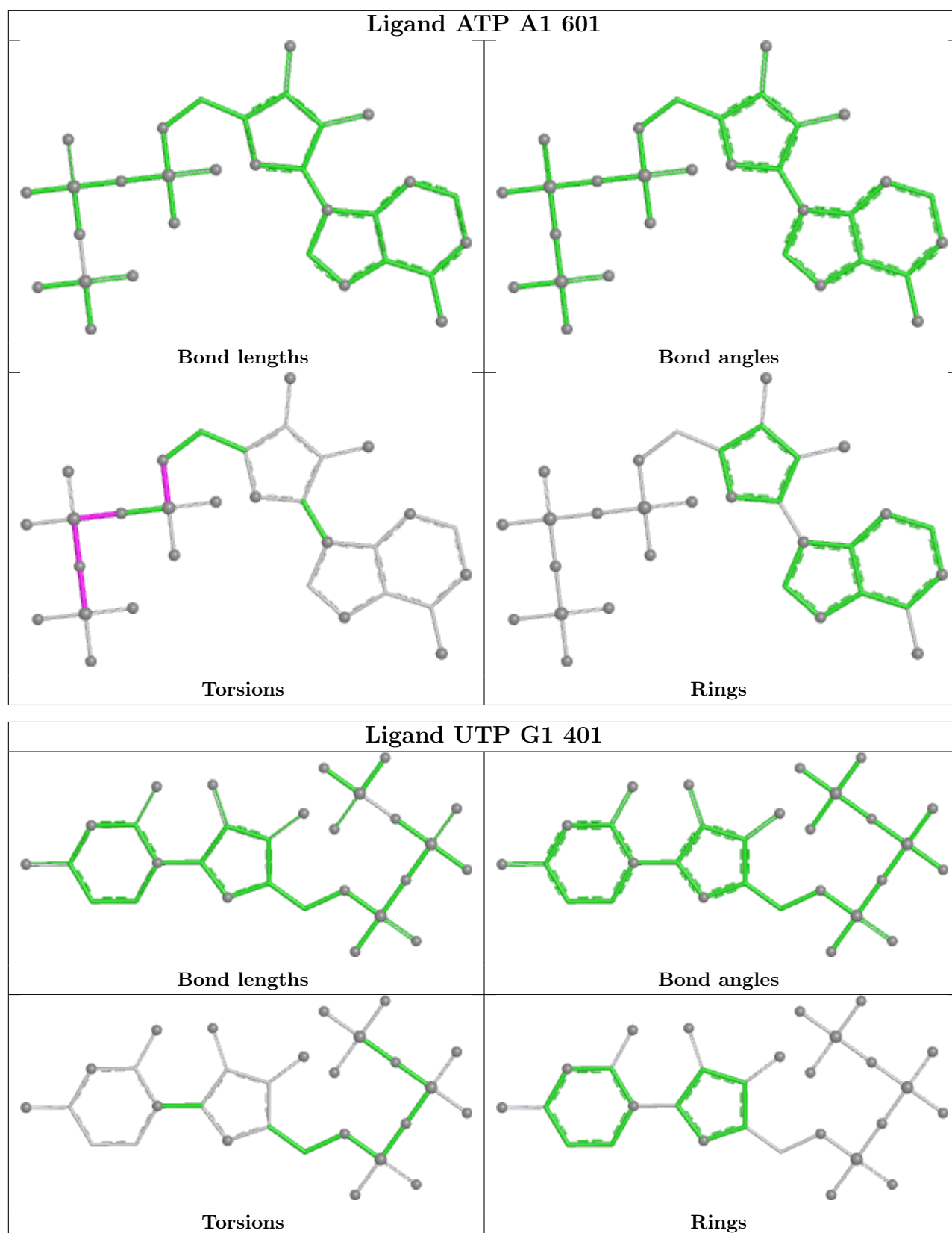


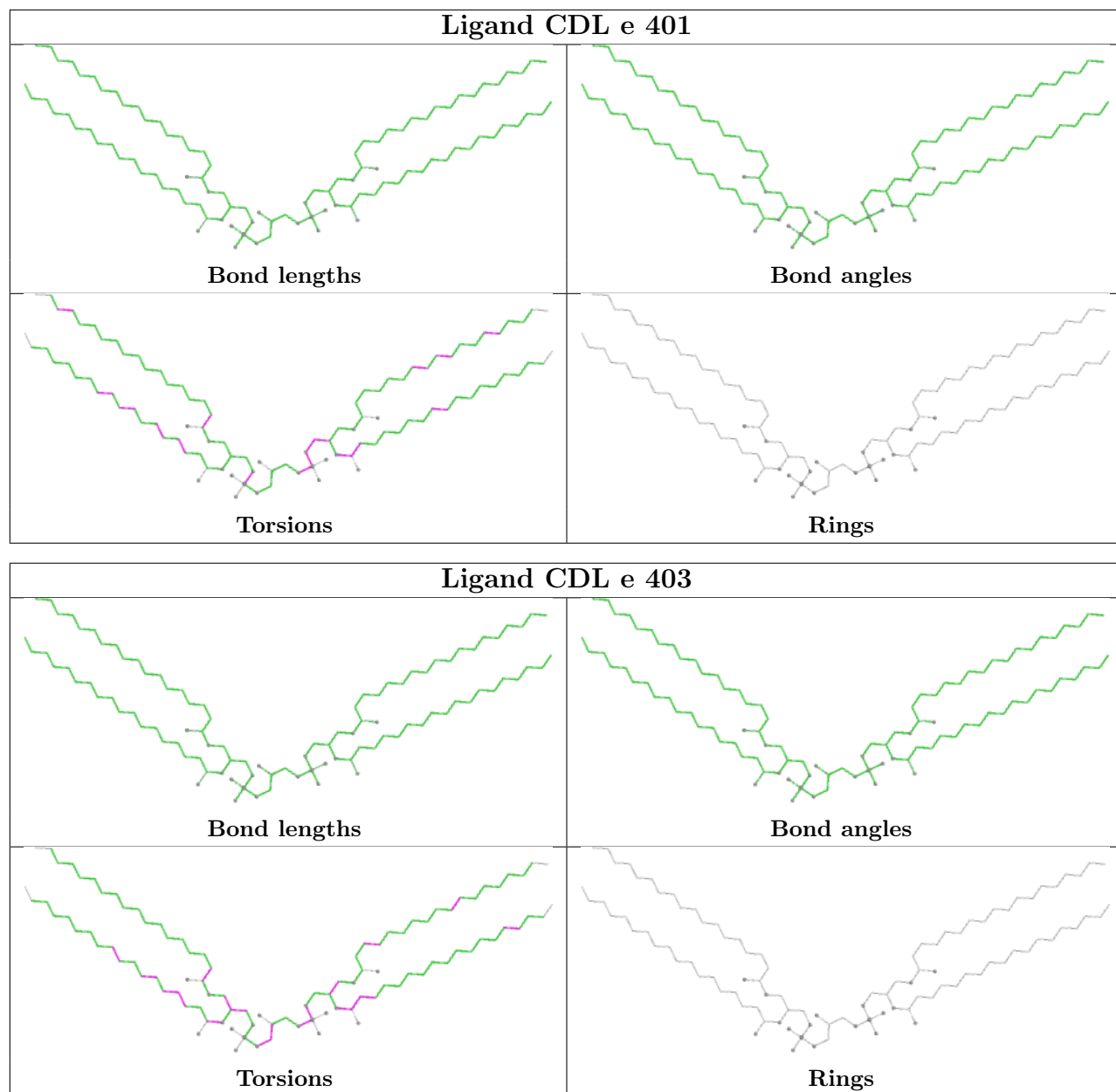


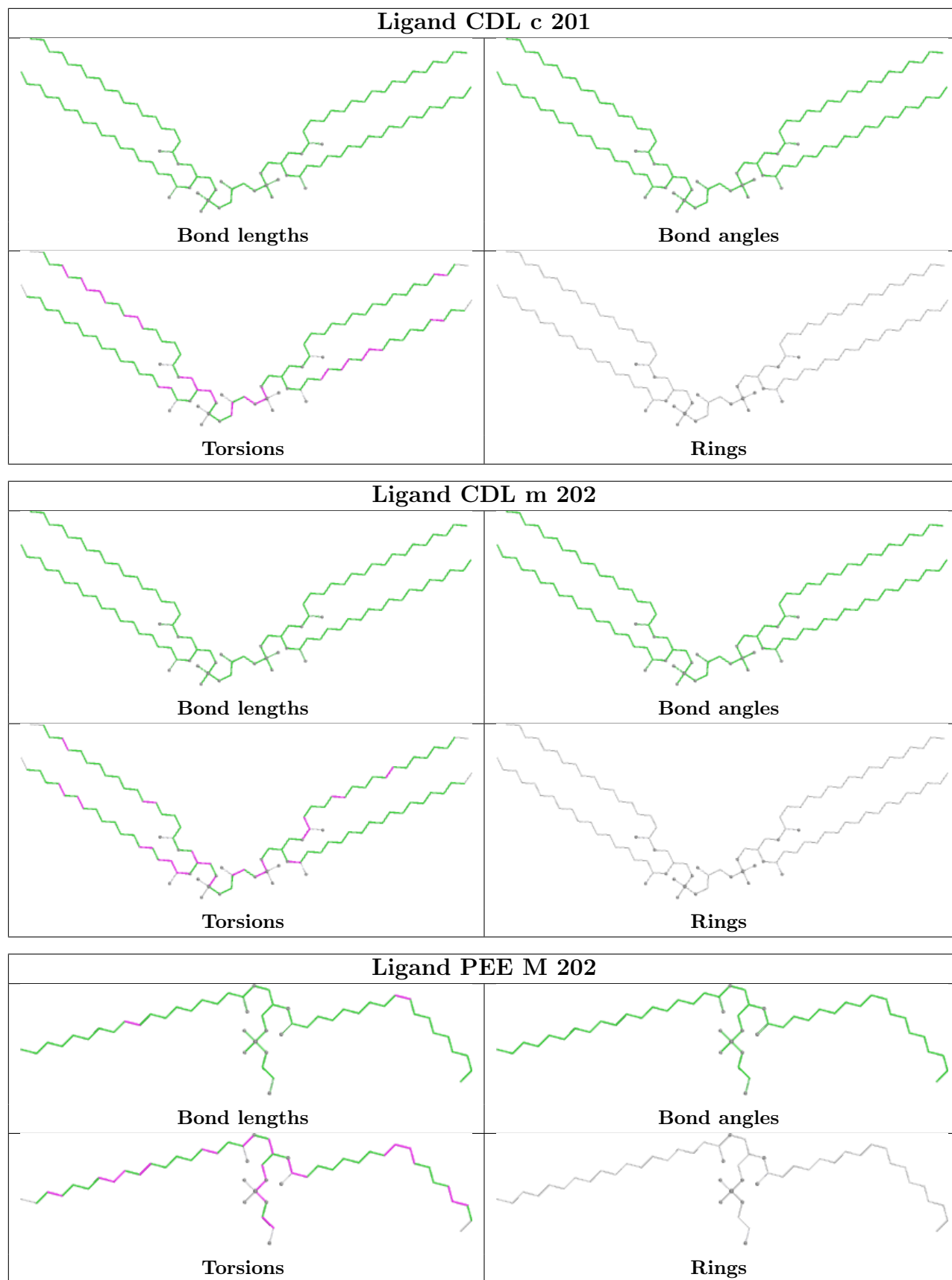


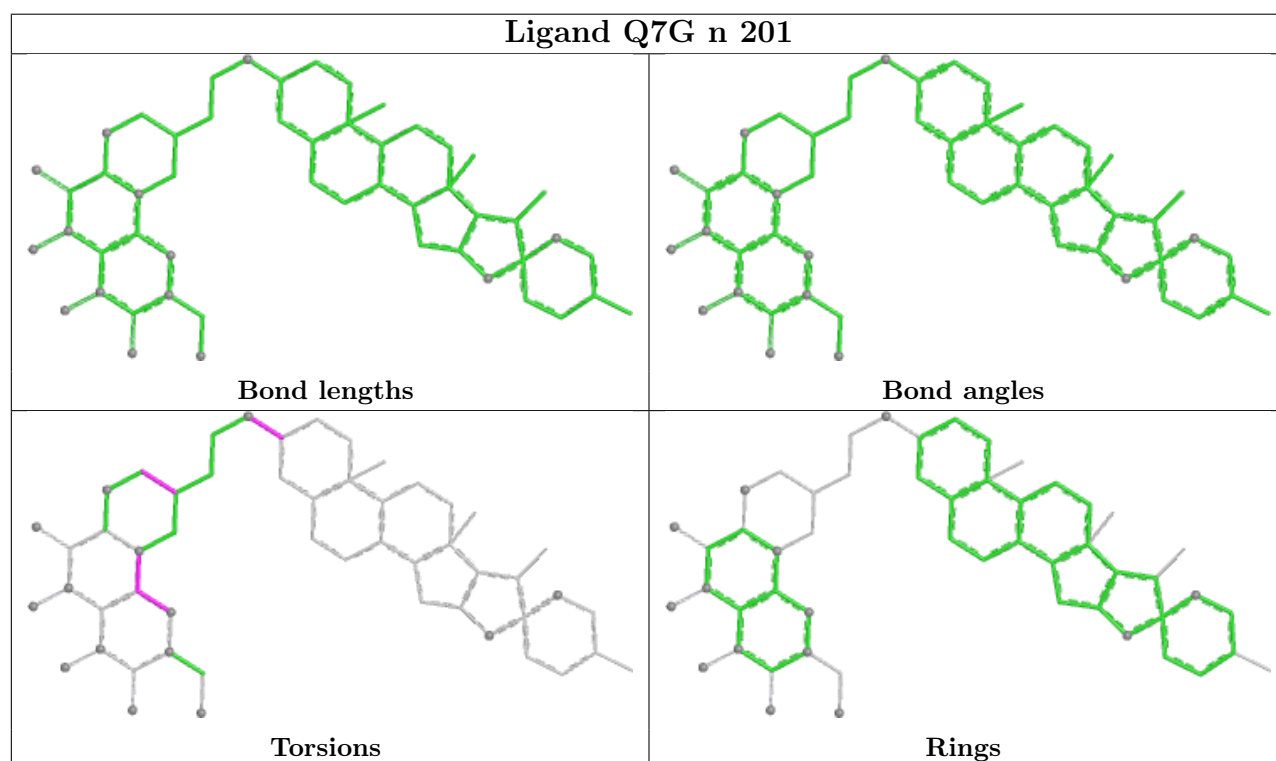
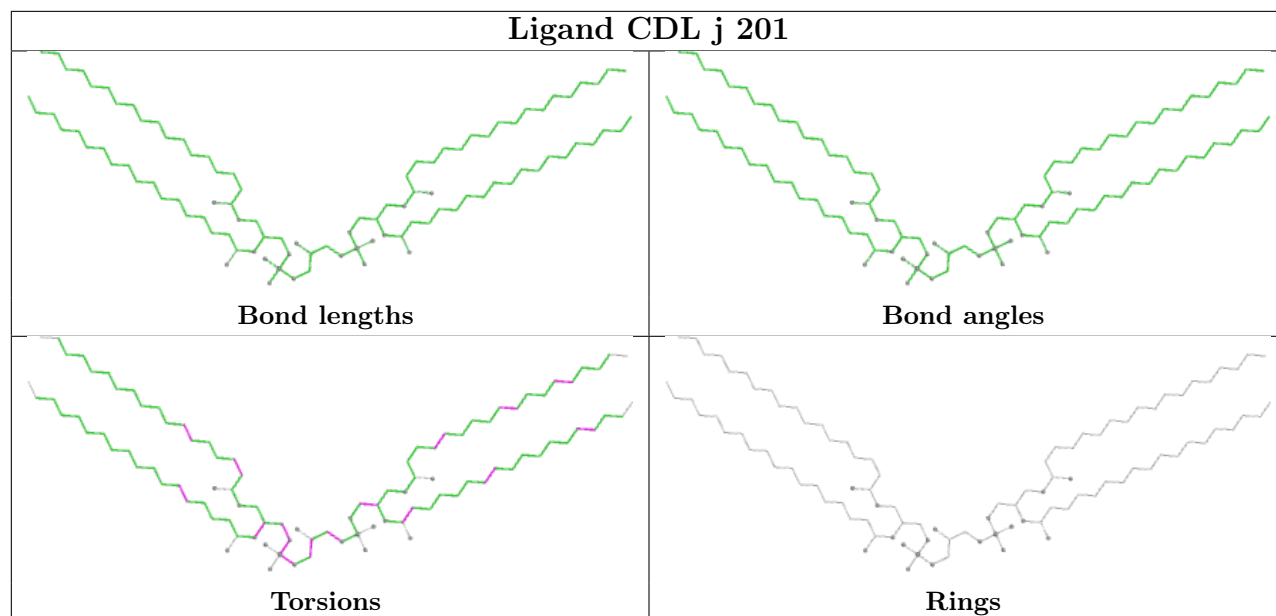


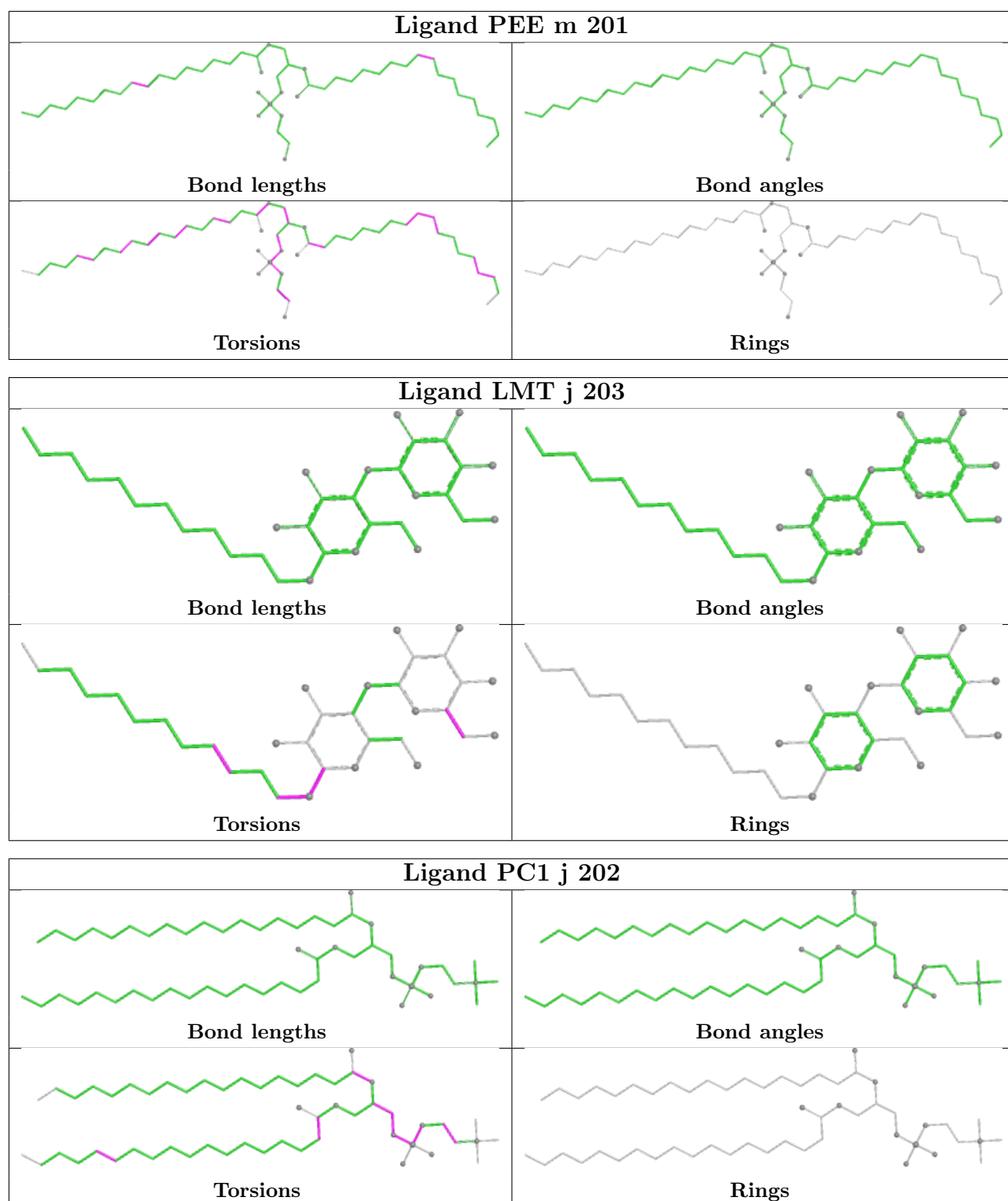


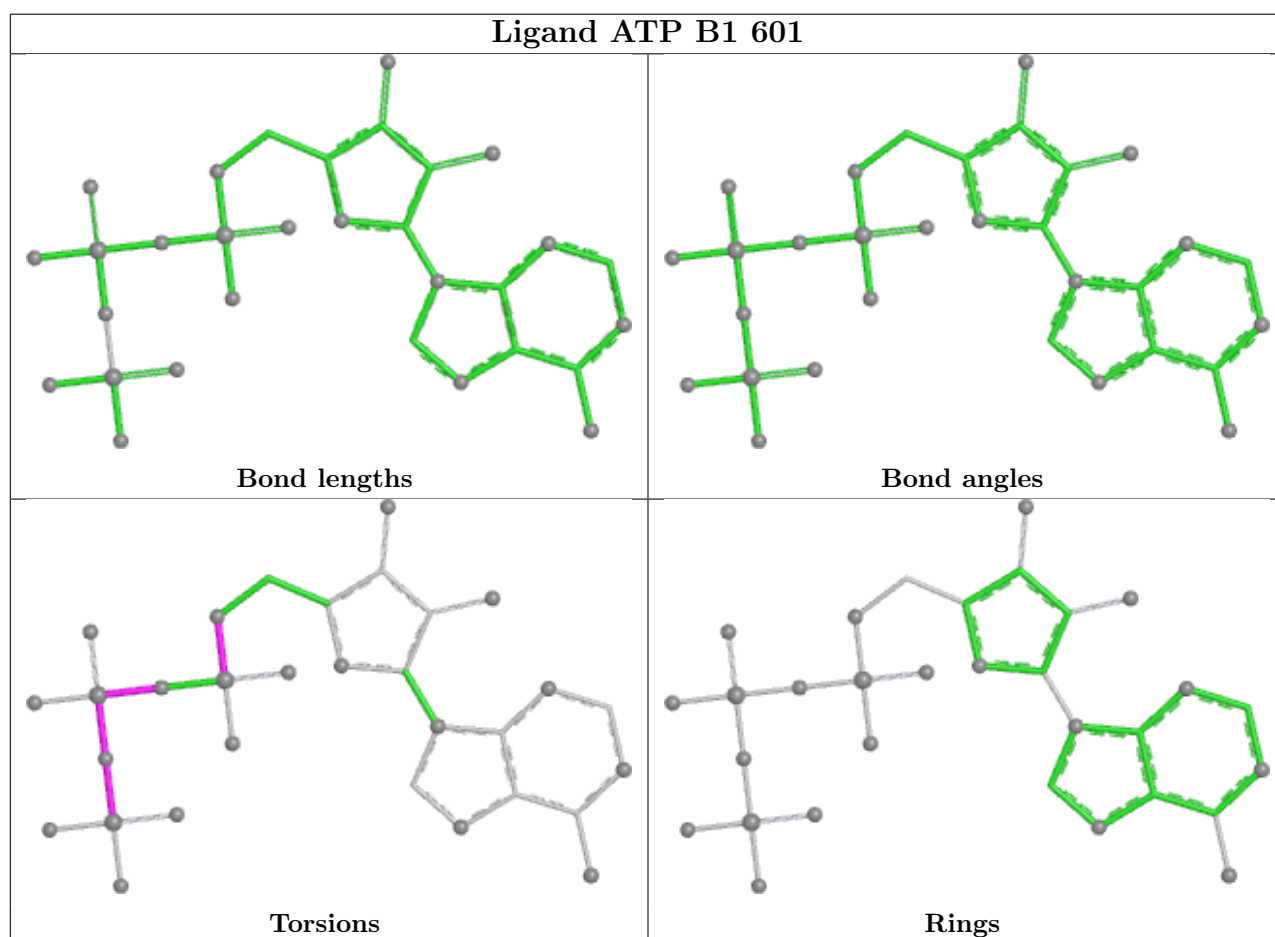
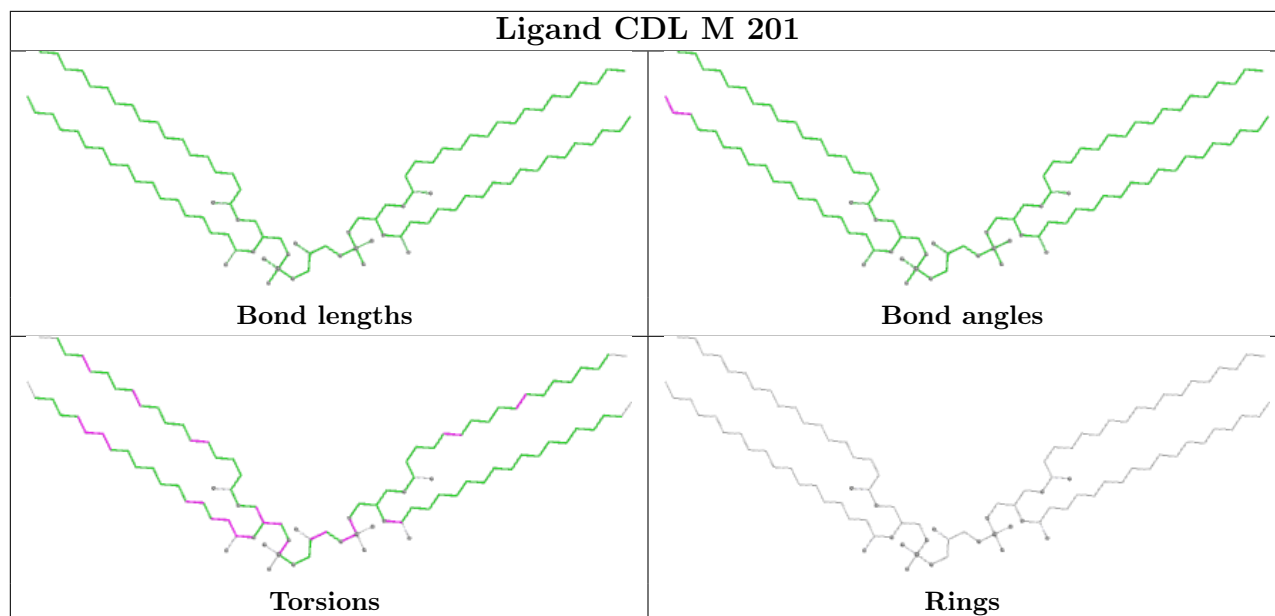


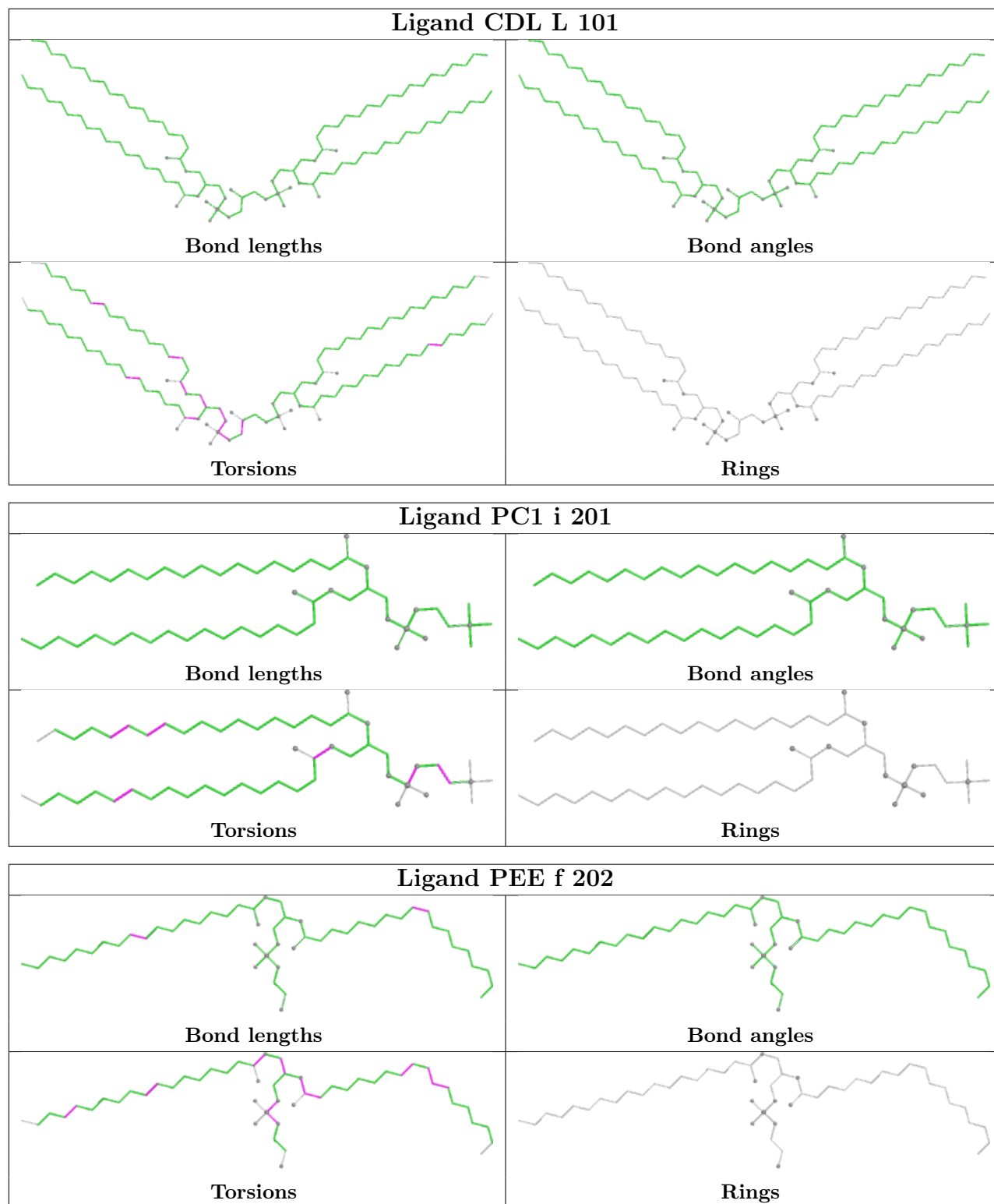


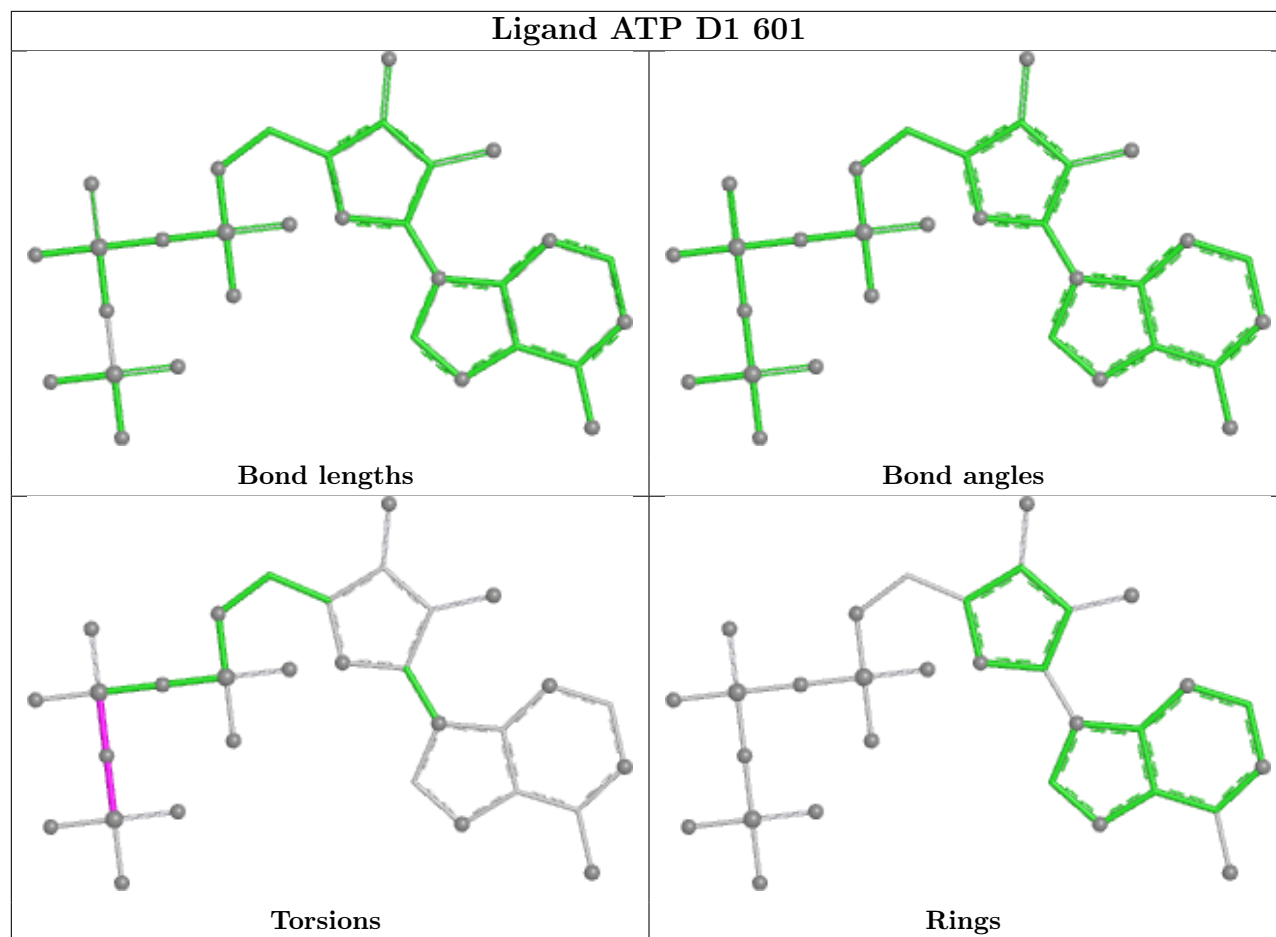












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

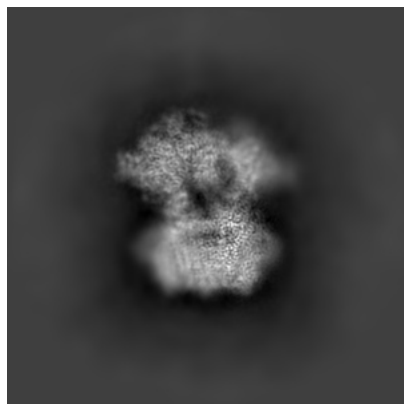
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15568. These allow visual inspection of the internal detail of the map and identification of artifacts.

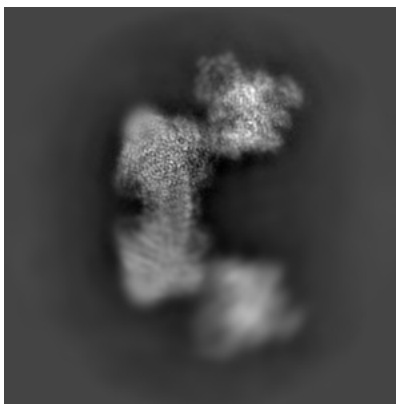
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

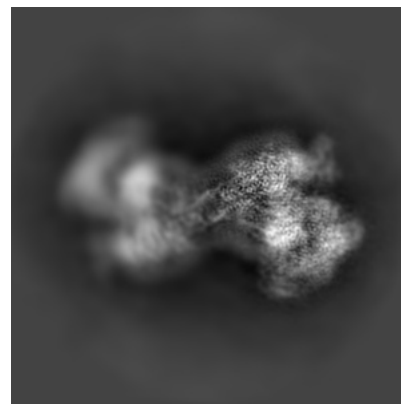
6.1.1 Primary map



X

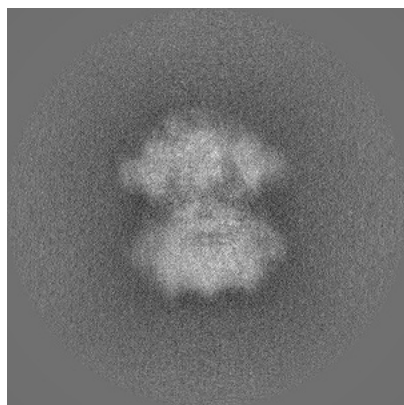


Y

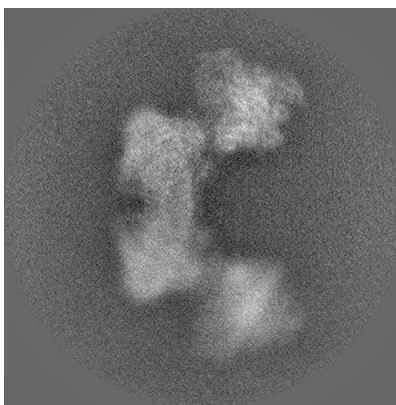


Z

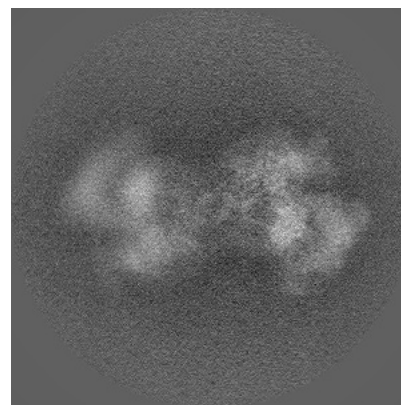
6.1.2 Raw map



X



Y

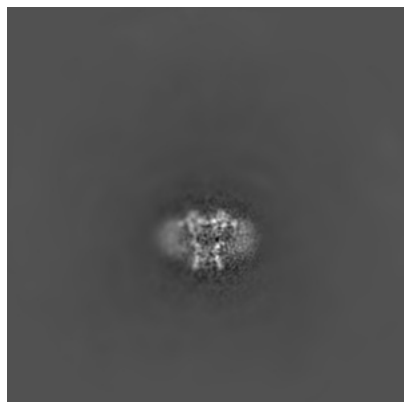


Z

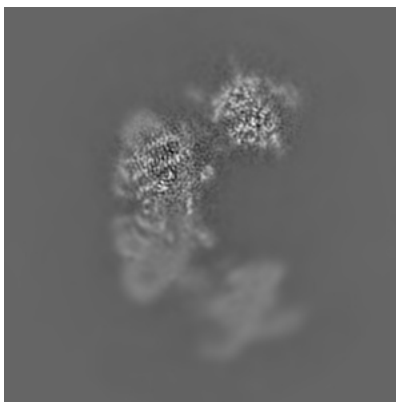
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

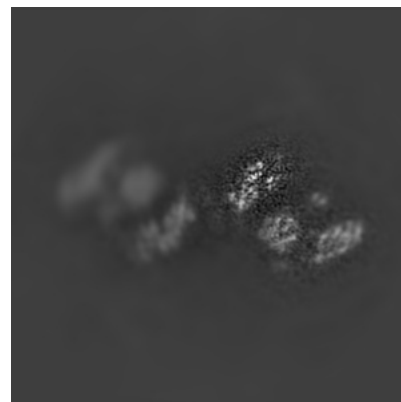
6.2.1 Primary map



X Index: 280

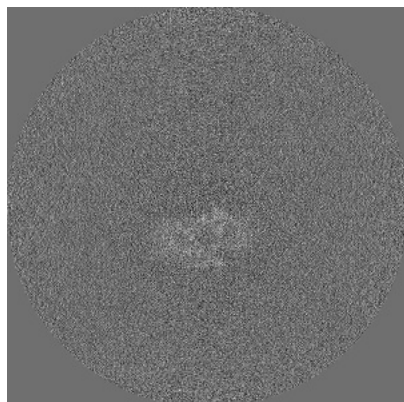


Y Index: 280

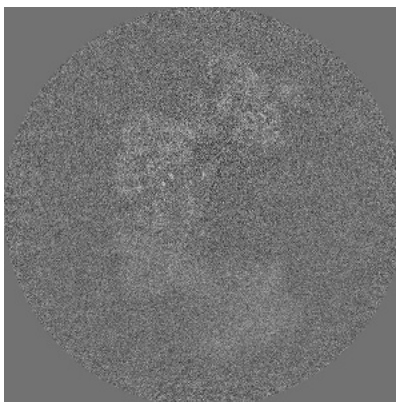


Z Index: 280

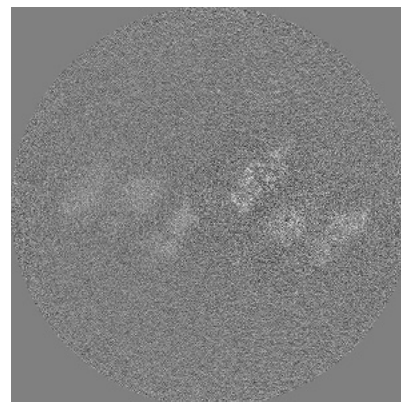
6.2.2 Raw map



X Index: 280



Y Index: 280

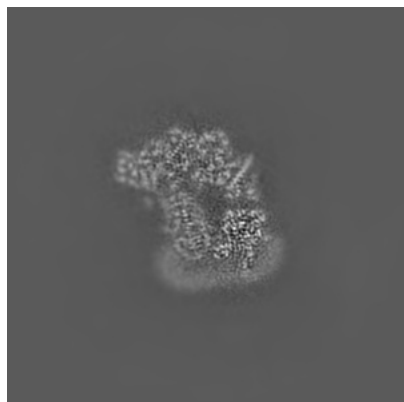


Z Index: 280

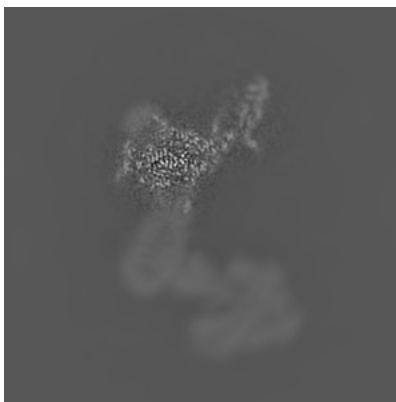
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

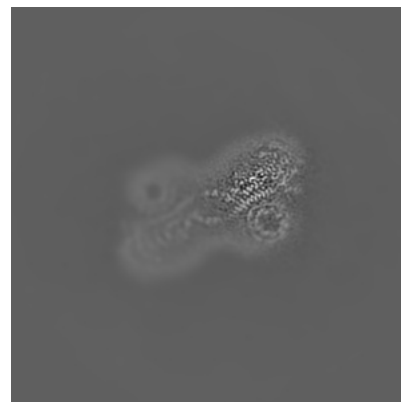
6.3.1 Primary map



X Index: 378

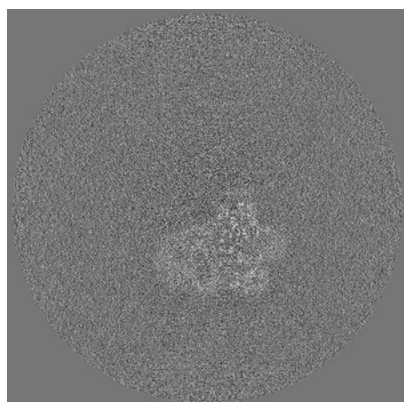


Y Index: 319

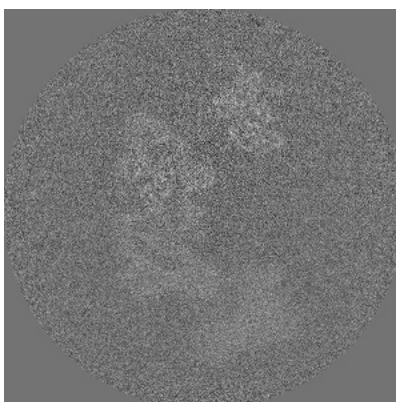


Z Index: 233

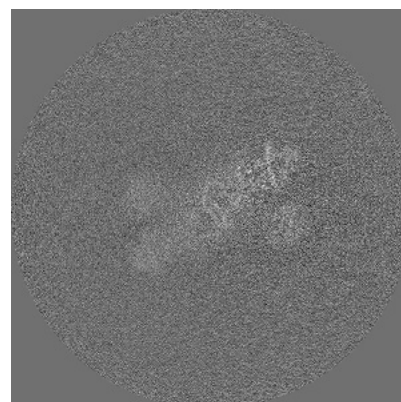
6.3.2 Raw map



X Index: 347



Y Index: 288

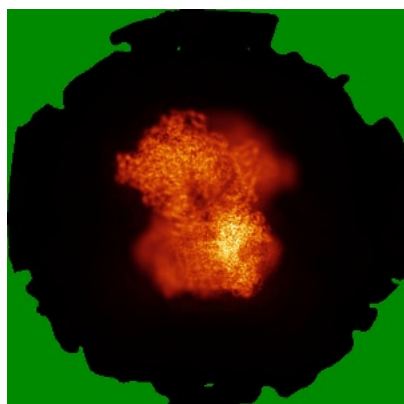


Z Index: 259

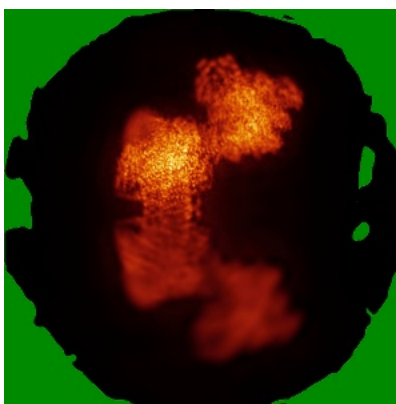
The images above show the largest variance slices of the map in three orthogonal directions.

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

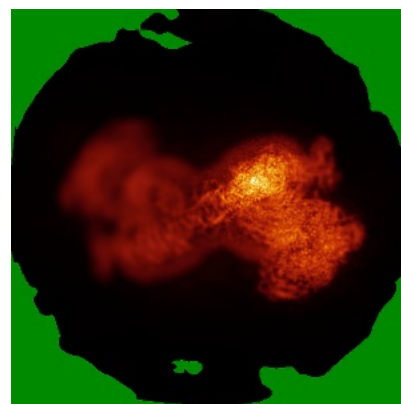
6.4.1 Primary map



X

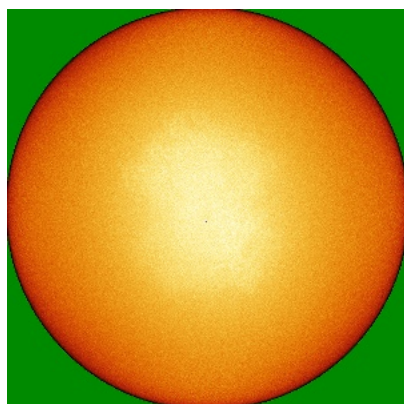


Y

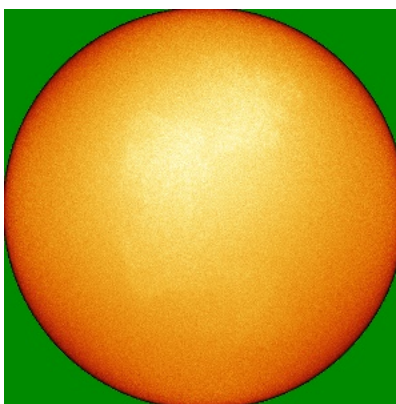


Z

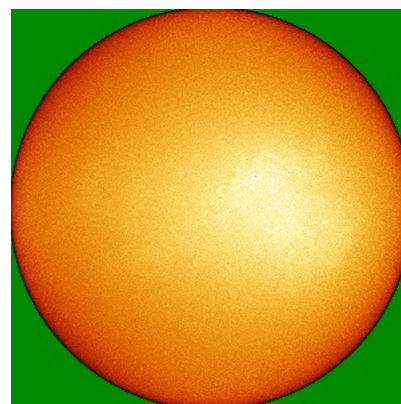
6.4.2 Raw map



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](#)

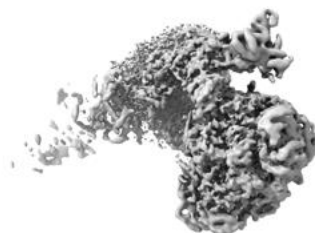
6.5.1 Primary map



X



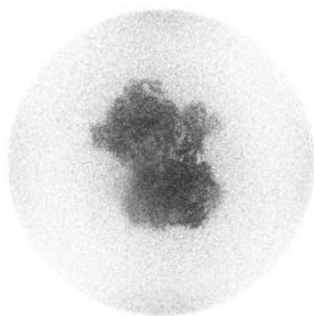
Y



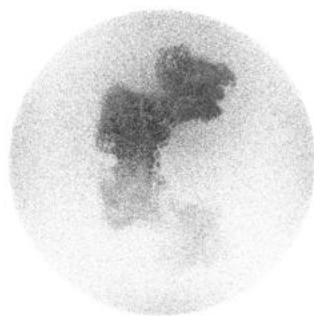
Z

The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

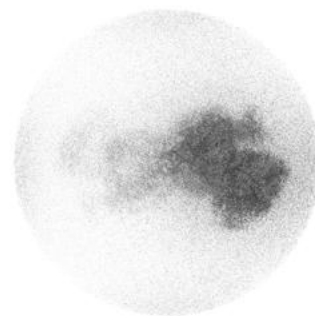
6.5.2 Raw map



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.

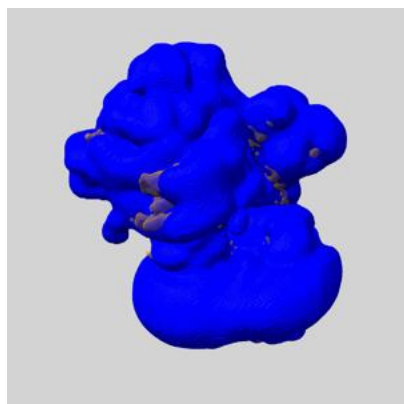
6.6 Mask visualisation [i](#)

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

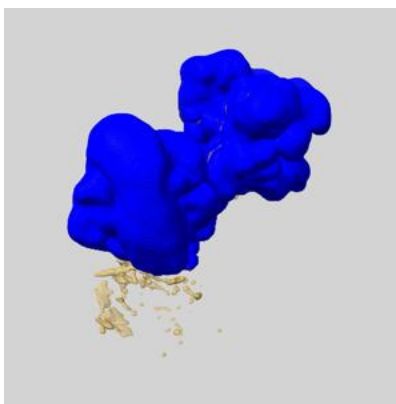
A mask typically either:

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

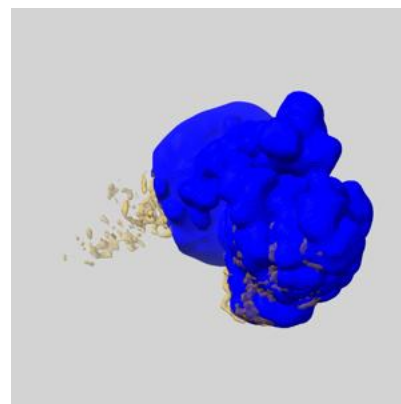
6.6.1 emd_15568_msk_1.map [i](#)



X



Y

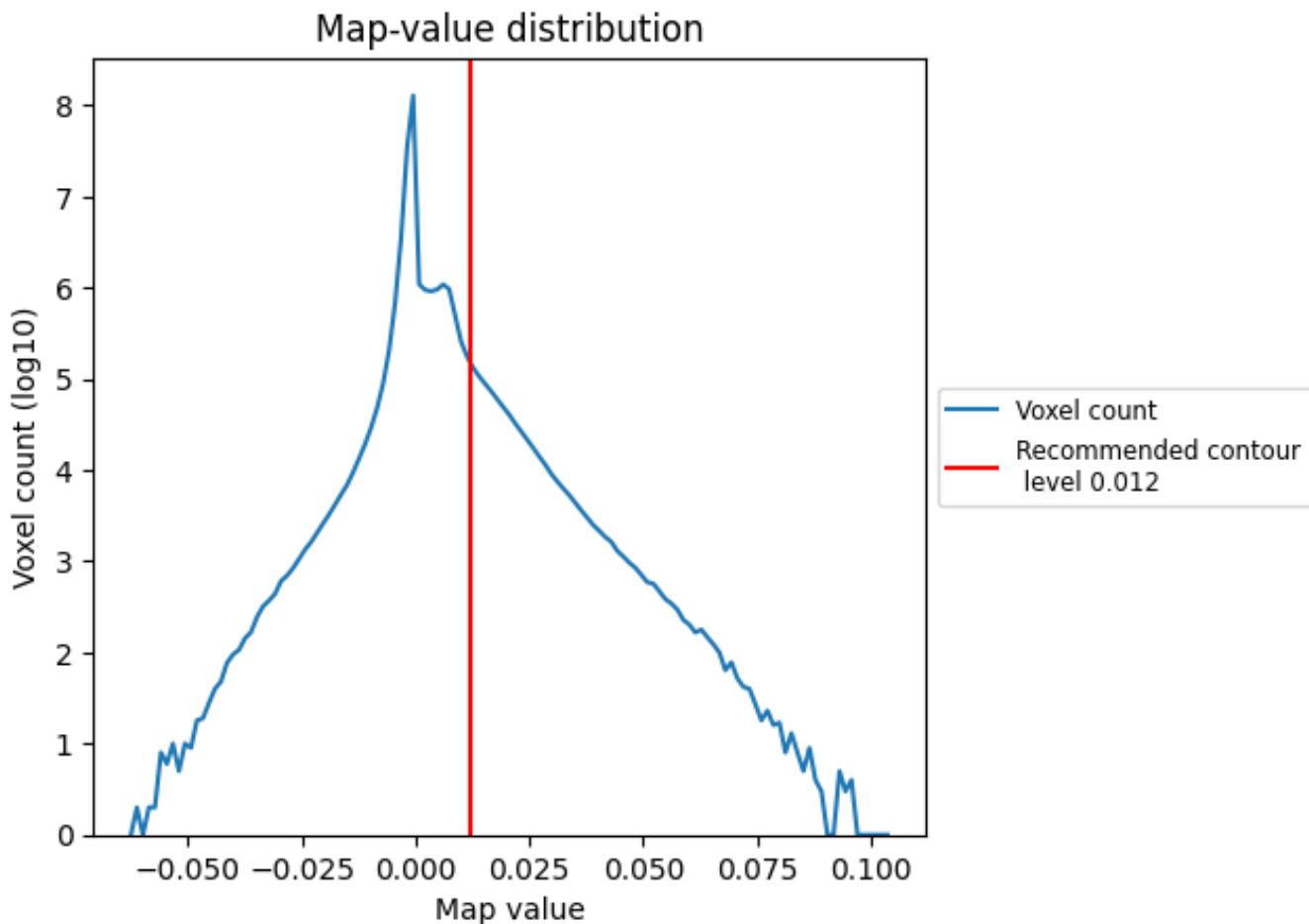


Z

7 Map analysis [i](#)

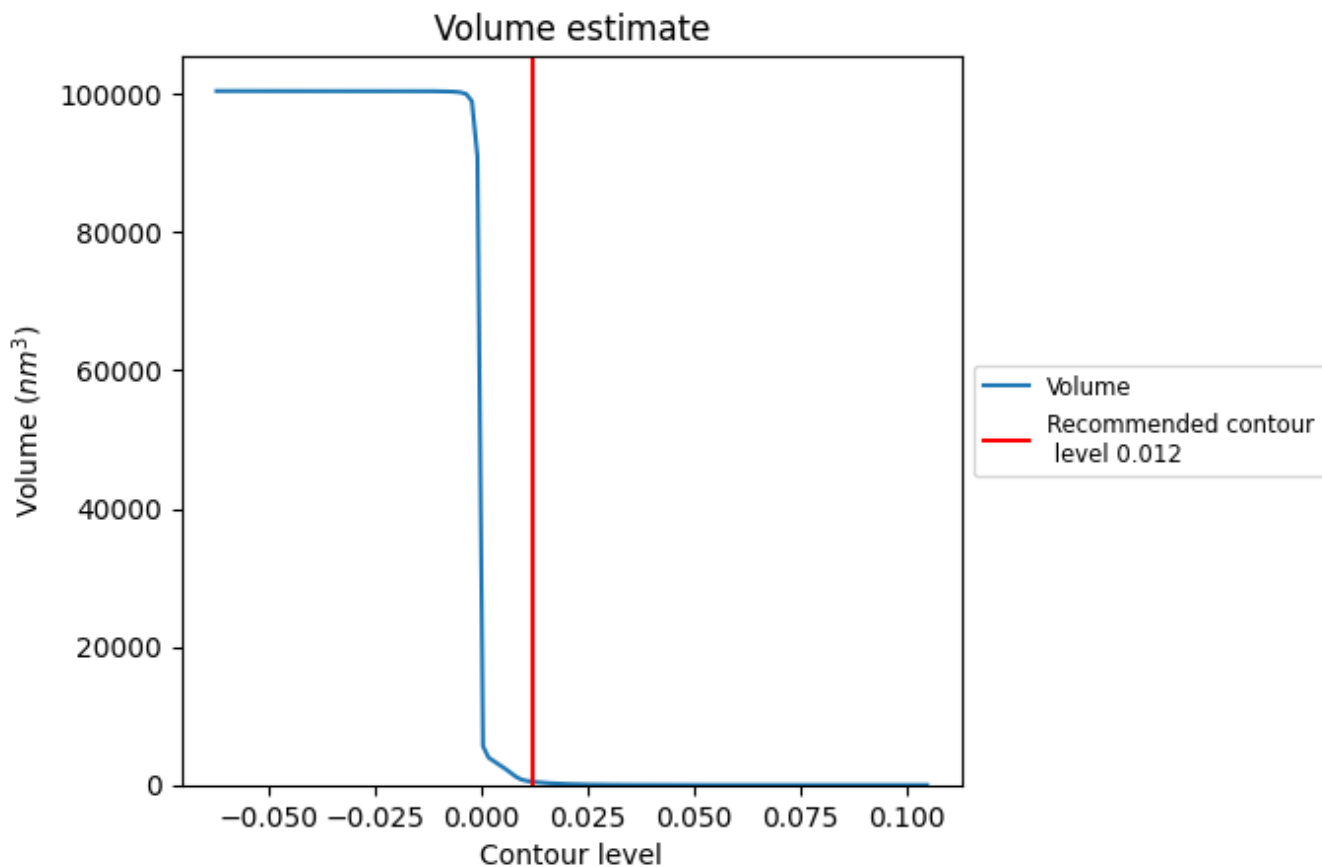
This section contains the results of statistical analysis of the map.

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.

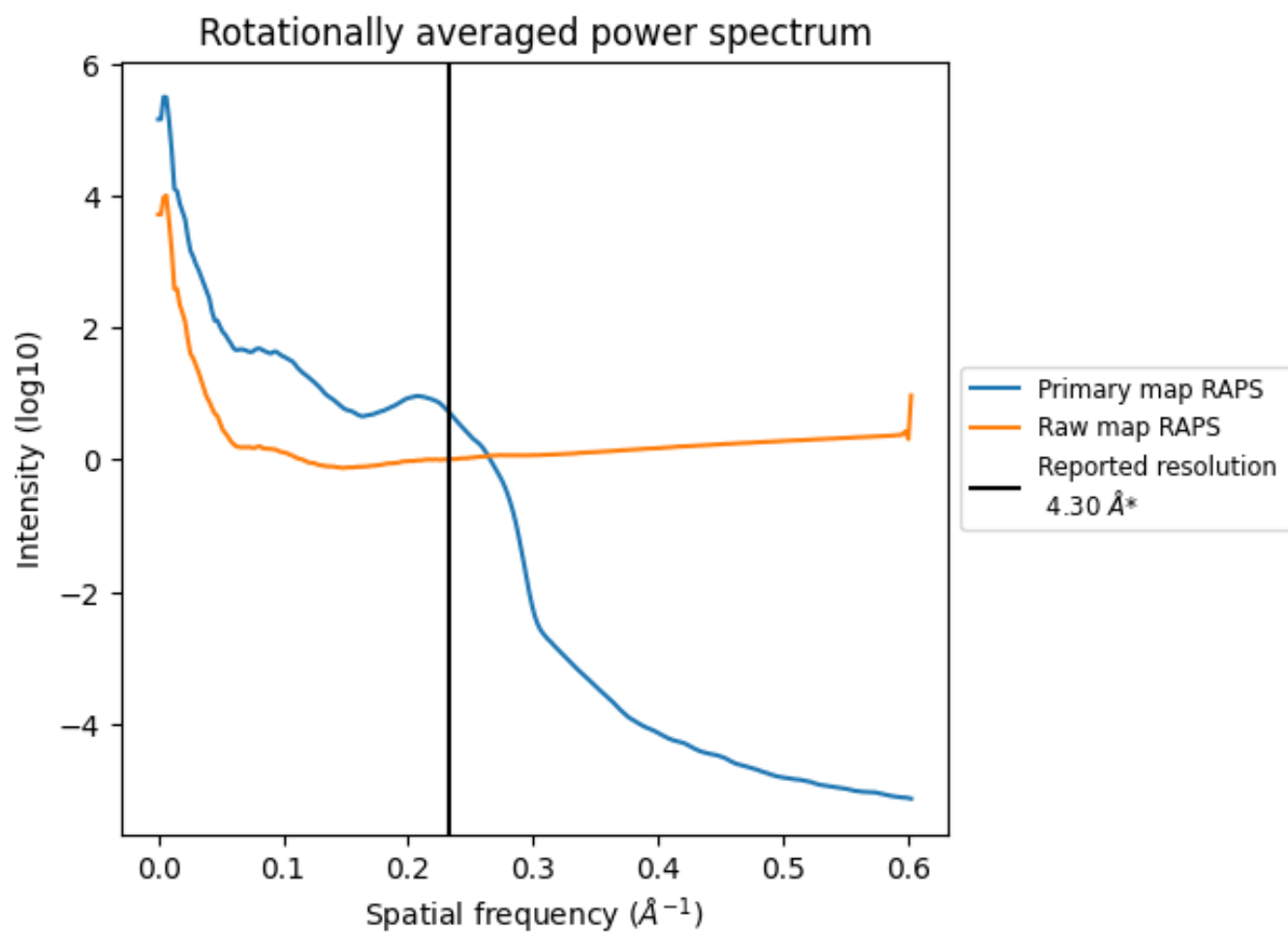
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 465 nm³; this corresponds to an approximate mass of 420 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 i

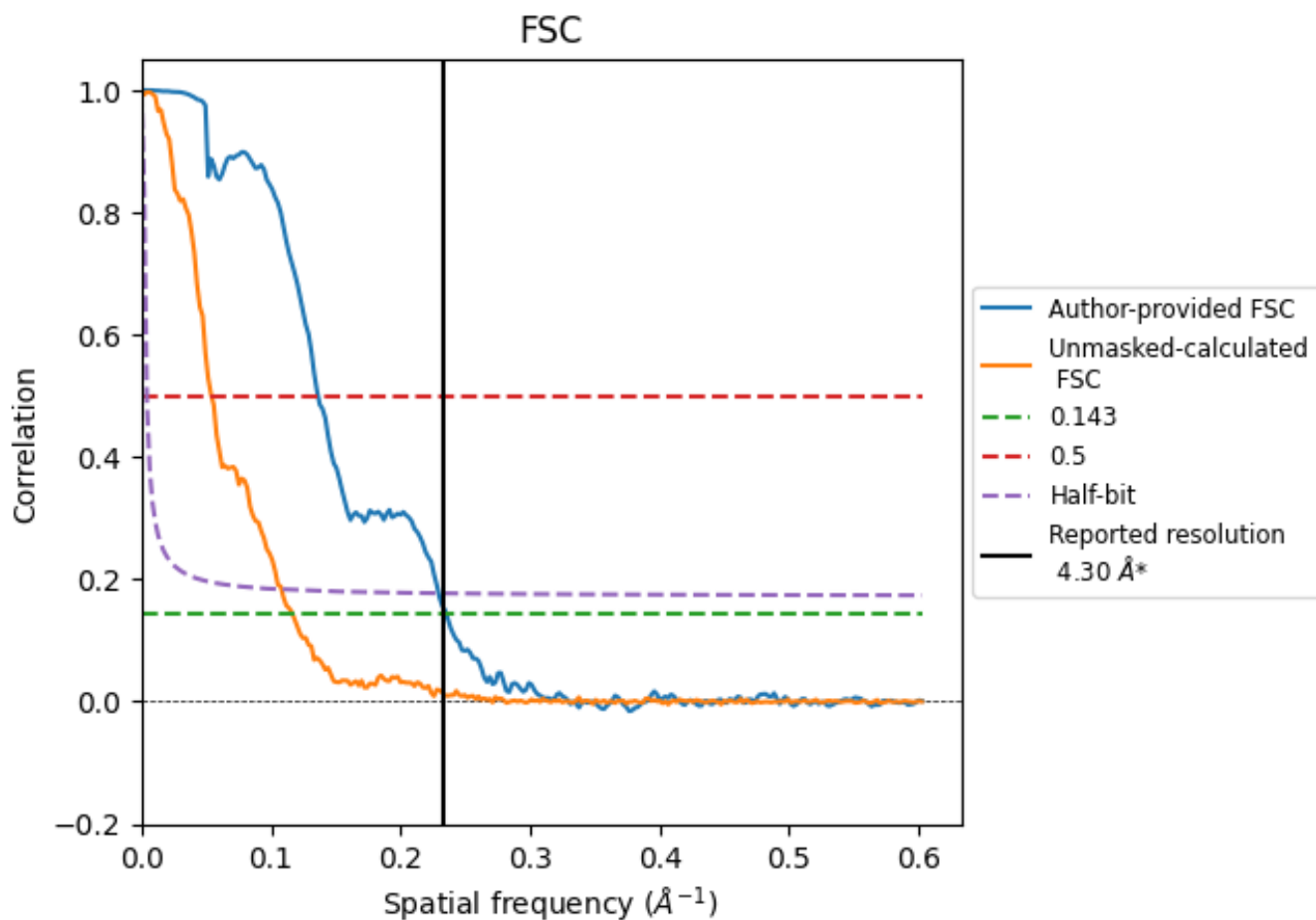


*Reported resolution corresponds to spatial frequency of 0.233 \AA^{-1}

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 0.233 Å⁻¹

8.2 Resolution estimates [i](#)

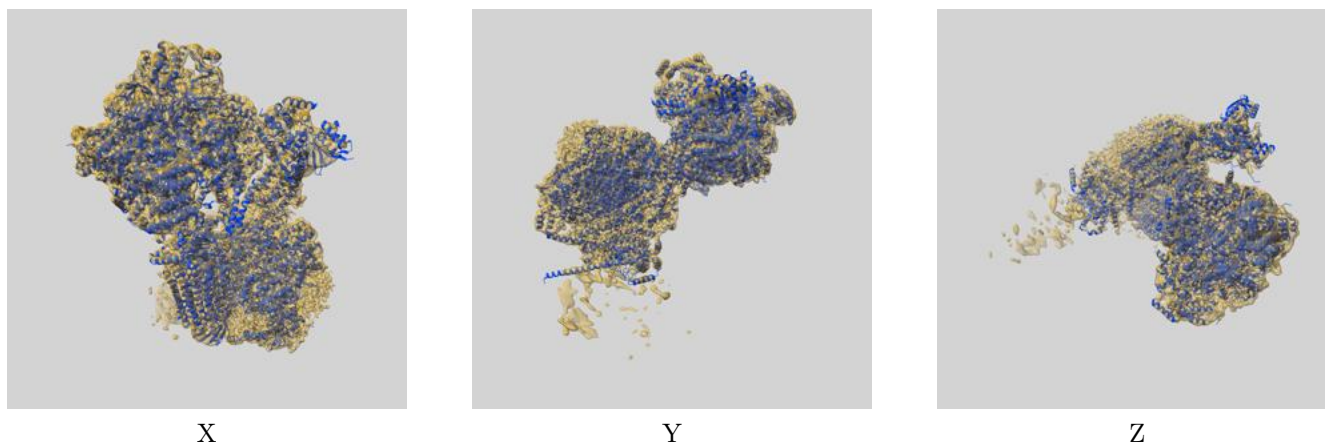
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.25	7.33	4.36
Unmasked-calculated*	8.57	18.48	9.24

*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 8.57 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

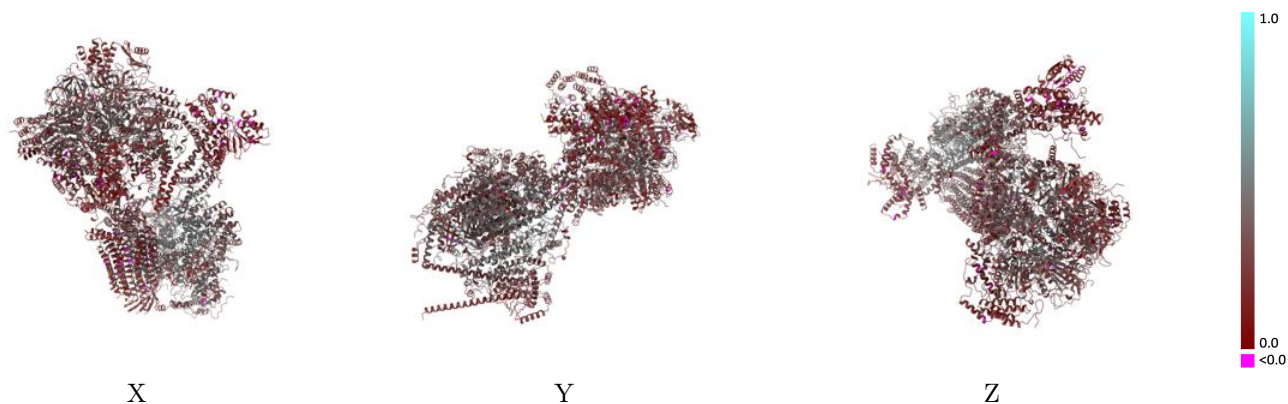
This section contains information regarding the fit between EMDB map EMD-15568 and PDB model 8APF. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



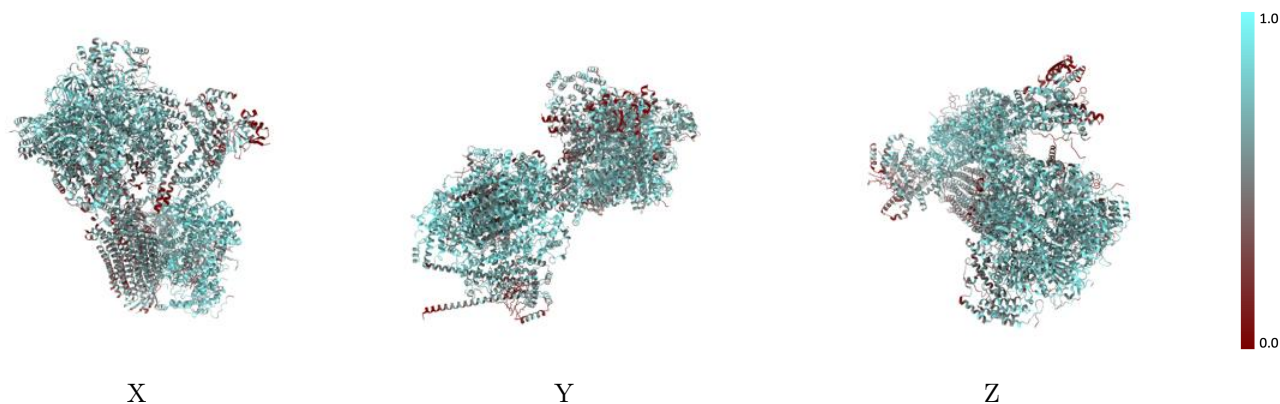
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



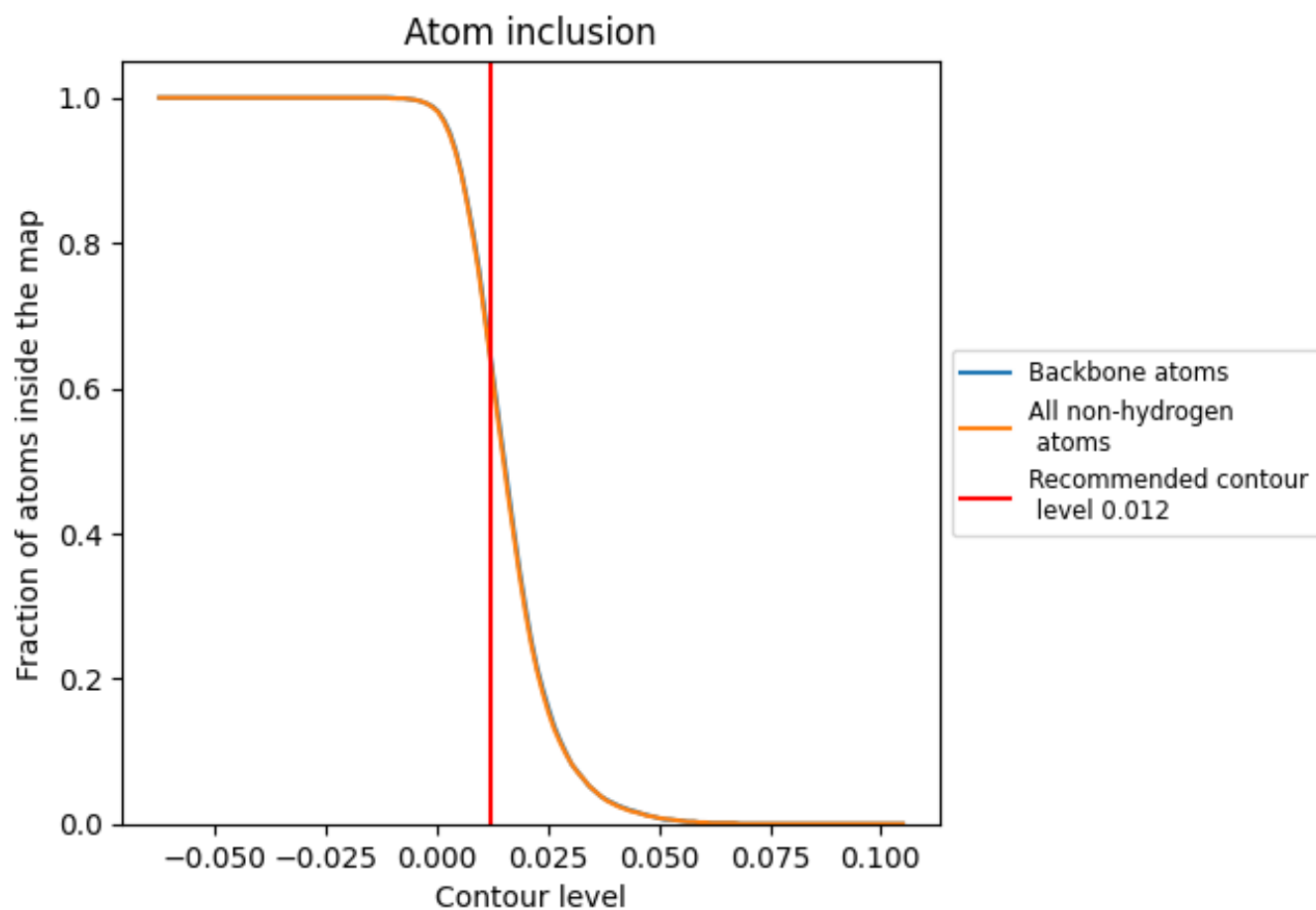
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 64% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6410	 0.3110
A1	 0.6600	 0.3130
B1	 0.6630	 0.2880
C1	 0.7210	 0.3610
D1	 0.6690	 0.3330
E1	 0.6620	 0.3110
F1	 0.6360	 0.3040
G1	 0.5510	 0.2790
H1	 0.5040	 0.2720
I1	 0.4840	 0.2510
J1	 0.5820	 0.1870
K1	 0.6450	 0.2780
L	 0.4560	 0.2210
L1	 0.5800	 0.2050
M	 0.4150	 0.2180
M1	 0.5820	 0.2460
O1	 0.5100	 0.2250
P1	 0.4530	 0.2220
Q1	 0.4690	 0.2350
R1	 0.5760	 0.2820
S1	 0.6240	 0.2880
T1	 0.6100	 0.2720
U1	 0.5360	 0.2300
V1	 0.5170	 0.2320
W1	 0.4900	 0.2460
X1	 0.5200	 0.2330
a	 0.7970	 0.4560
c	 0.7590	 0.4300
d	 0.6780	 0.3120
e	 0.7640	 0.3970
f	 0.7730	 0.4300
g	 0.4380	 0.1670
h	 0.5430	 0.1680
i	 0.8280	 0.4400
j	 0.7500	 0.3590



Continued on next page...

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Chain	Atom inclusion	Q-score
k	 0.7530	 0.3780
l	 0.3980	 0.2110
m	 0.5280	 0.2420
n	 0.8240	 0.4540
o	 0.7820	 0.3610
p	 0.7000	 0.3800
q	 0.7500	 0.4110
r	 0.7660	 0.3940