wwPDB EM Validation Summary Report (i)

Oct 3, 2026 – 10:31 AM EDT

PDB ID	:	9ZFT / pdb_00009zft
EMDB ID	:	EMD-74153
Title	:	Mitochondrial ATP synthase monomer from Acanthamoeba castellanii
Authors	:	Fry, M.Y.; Luce, B.E.; Stefely, J.A.; Samuelson, J.; Mootha, V.K.; Chao, L.H.
Deposited on	:	2025-12-02
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 (i) 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 (i)) were used in the production of this report:

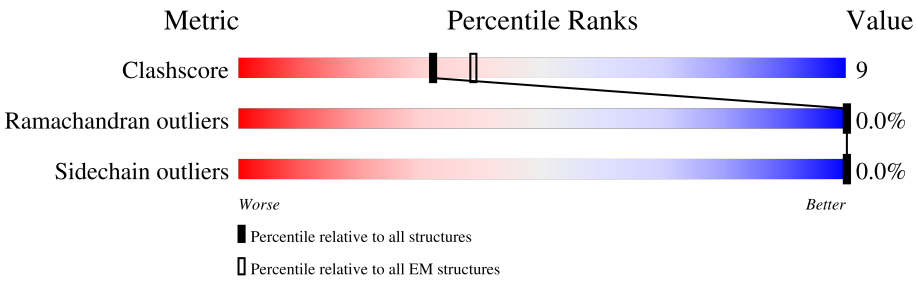
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.51

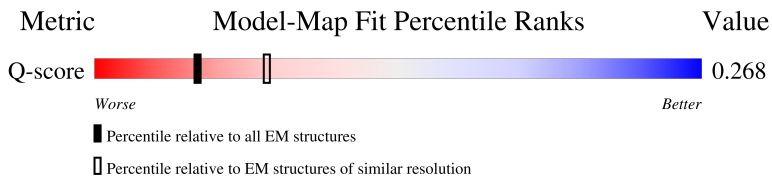
1 Overall quality at a glance (i)

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 <=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	6	208	83%; 75%; 25%
2	8	142	75%; 53%; 36%; 11%
3	A	326	48%; 69%; 17%; 13%
4	B	124	73%; 66%; 31%; •

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Mol	Chain	Length	Quality of chain
5	C	191	73% 70% 11% 19%
6	D	499	21% 18% 8% 74%
7	E	137	17% 18% 80%
8	G	431	28% 39% 7% 55%
9	H	45	91% 82% 18%
10	I	454	83% 74% 10% 16%
10	L	454	84% 75% 12% 12%
11	J	92	33% 29% 66%
12	K	94	43% 41% 6% 52%
13	M	92	26% 17% 10% 73%
14	P	79	89% 77% 23%
14	Q	79	85% 81% 19%
14	R	79	86% 67% 33%
14	S	79	91% 84% 16%
14	T	79	87% 78% 22%
14	U	79	85% 76% 23%
14	V	79	84% 84% 16%
14	W	79	89% 80% 20%
14	X	79	90% 78% 22%
15	Z	142	97% 73% 27%
16	a	522	8% 80% 12% 7%
16	b	522	5% 80% 13% 6%
16	c	522	8% 79% 15% 7%
17	d	687	15% 71% 9% 20%
17	e	687	13% 71% 12% 17%

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Mol	Chain	Length	Quality of chain
17	f	687	11% 70% 15% 15%
18	1	71	96% 97%
19	2	132	81% 92% 8%
20	3	9	100% 100%
21	5	19	100% 100%

2 Entry composition (i)

There are 24 unique types of molecules in this entry. The entry contains 99152 atoms, of which 50017 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 a.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	6	208	3516	1199	1791	248	275	3	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	?	-	PHE	deletion	UNP Q37385
6	?	-	ASN	deletion	UNP Q37385
6	?	-	LEU	deletion	UNP Q37385
6	?	-	PHE	deletion	UNP Q37385
6	?	-	VAL	deletion	UNP Q37385
6	?	-	PRO	deletion	UNP Q37385
6	?	-	SER	deletion	UNP Q37385
6	?	-	GLY	deletion	UNP Q37385
6	?	-	VAL	deletion	UNP Q37385
6	?	-	PRO	deletion	UNP Q37385
6	?	-	LYS	deletion	UNP Q37385

- Molecule 2 is a protein called ORFB.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	8	126	2207	750	1109	167	180	1	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	A	282	4377	1377	2192	378	425	5	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	LEU	-	insertion	UNP L8GG83
A	22	ARG	-	insertion	UNP L8GG83
A	23	LEU	CYS	conflict	UNP L8GG83
A	24	ARG	LYS	conflict	UNP L8GG83

- Molecule 4 is a protein called ORF25.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	B	121	2051	675	1059	147	169	1	0	0

- Molecule 5 is a protein called ATP synthase, Delta/Epsilon chain, betasandwich domain containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	C	154	2308	729	1153	192	229	5	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	D	129	2075	674	998	179	221	3	0	0

- Molecule 7 is a protein called ATP synthase inhibitory factor 1 (IF1).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
7	E	27	463	137	238	47	41	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	G	196	3202	1022	1619	272	284	5	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	H	45	707	216	357	67	66	1	0	0

- Molecule 10 is a protein called malate dehydrogenase.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	I	382	5828	1824	2924	514	552	14	0	0
			Total	C	H	N	O	S		
10	L	398	6050	1891	3035	534	576	14	0	0

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	217	VAL	SER	conflict	UNP L8HFT9
I	218	GLN	ARG	conflict	UNP L8HFT9
I	219	GLY	ALA	conflict	UNP L8HFT9
I	220	LYS	-	insertion	UNP L8HFT9
I	221	ALA	-	insertion	UNP L8HFT9
I	222	LEU	-	insertion	UNP L8HFT9
I	223	ASN	-	insertion	UNP L8HFT9
I	224	LYS	-	insertion	UNP L8HFT9
I	225	VAL	-	insertion	UNP L8HFT9
I	226	ALA	-	insertion	UNP L8HFT9
I	227	ASN	-	insertion	UNP L8HFT9
I	228	ARG	-	insertion	UNP L8HFT9
I	229	ASP	-	insertion	UNP L8HFT9
I	230	THR	-	insertion	UNP L8HFT9
I	231	LEU	-	insertion	UNP L8HFT9
I	232	ARG	-	insertion	UNP L8HFT9
I	233	VAL	-	insertion	UNP L8HFT9
I	234	CYS	-	insertion	UNP L8HFT9
I	235	VAL	-	insertion	UNP L8HFT9
I	236	VAL	-	insertion	UNP L8HFT9
I	237	GLY	-	insertion	UNP L8HFT9
I	238	ASN	-	insertion	UNP L8HFT9
I	239	PRO	-	insertion	UNP L8HFT9
I	240	ALA	-	insertion	UNP L8HFT9
I	241	ASN	-	insertion	UNP L8HFT9
I	242	THR	-	insertion	UNP L8HFT9
I	243	ASN	-	insertion	UNP L8HFT9
I	244	ALA	-	insertion	UNP L8HFT9
I	245	LEU	-	insertion	UNP L8HFT9
I	246	ILE	-	insertion	UNP L8HFT9
I	247	ALA	-	insertion	UNP L8HFT9
I	248	SER	-	insertion	UNP L8HFT9
I	249	ALA	-	insertion	UNP L8HFT9
I	250	ASN	-	insertion	UNP L8HFT9

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Chain	Residue	Modelled	Actual	Comment	Reference
I	251	ALA	-	insertion	UNP L8HFT9
I	252	PRO	-	insertion	UNP L8HFT9
I	253	ASN	-	insertion	UNP L8HFT9
I	254	ILE	-	insertion	UNP L8HFT9
I	255	HIS	-	insertion	UNP L8HFT9
I	256	PRO	-	insertion	UNP L8HFT9
I	257	ARG	-	insertion	UNP L8HFT9
L	217	VAL	SER	conflict	UNP L8HFT9
L	218	GLN	ARG	conflict	UNP L8HFT9
L	219	GLY	ALA	conflict	UNP L8HFT9
L	220	LYS	-	insertion	UNP L8HFT9
L	221	ALA	-	insertion	UNP L8HFT9
L	222	LEU	-	insertion	UNP L8HFT9
L	223	ASN	-	insertion	UNP L8HFT9
L	224	LYS	-	insertion	UNP L8HFT9
L	225	VAL	-	insertion	UNP L8HFT9
L	226	ALA	-	insertion	UNP L8HFT9
L	227	ASN	-	insertion	UNP L8HFT9
L	228	ARG	-	insertion	UNP L8HFT9
L	229	ASP	-	insertion	UNP L8HFT9
L	230	THR	-	insertion	UNP L8HFT9
L	231	LEU	-	insertion	UNP L8HFT9
L	232	ARG	-	insertion	UNP L8HFT9
L	233	VAL	-	insertion	UNP L8HFT9
L	234	CYS	-	insertion	UNP L8HFT9
L	235	VAL	-	insertion	UNP L8HFT9
L	236	VAL	-	insertion	UNP L8HFT9
L	237	GLY	-	insertion	UNP L8HFT9
L	238	ASN	-	insertion	UNP L8HFT9
L	239	PRO	-	insertion	UNP L8HFT9
L	240	ALA	-	insertion	UNP L8HFT9
L	241	ASN	-	insertion	UNP L8HFT9
L	242	THR	-	insertion	UNP L8HFT9
L	243	ASN	-	insertion	UNP L8HFT9
L	244	ALA	-	insertion	UNP L8HFT9
L	245	LEU	-	insertion	UNP L8HFT9
L	246	ILE	-	insertion	UNP L8HFT9
L	247	ALA	-	insertion	UNP L8HFT9
L	248	SER	-	insertion	UNP L8HFT9
L	249	ALA	-	insertion	UNP L8HFT9
L	250	ASN	-	insertion	UNP L8HFT9
L	251	ALA	-	insertion	UNP L8HFT9

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Chain	Residue	Modelled	Actual	Comment	Reference
L	252	PRO	-	insertion	UNP L8HFT9
L	253	ASN	-	insertion	UNP L8HFT9
L	254	ILE	-	insertion	UNP L8HFT9
L	255	HIS	-	insertion	UNP L8HFT9
L	256	PRO	-	insertion	UNP L8HFT9
L	257	ARG	-	insertion	UNP L8HFT9

- Molecule 11 is a protein called ATP synthase subunit i/j, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
11	J	31	517	172	265	42	37	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
12	K	45	756	255	372	71	58	0	0

- Molecule 13 is a protein called ACANB14707.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
13	M	25	391	121	195	35	40	0	0

- Molecule 14 is a protein called ATP synthase subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	P	79	1208	385	629	90	100	4	0	0
14	Q	79	1208	385	629	90	100	4	0	0
14	R	79	1208	385	629	90	100	4	0	0
14	S	79	1208	385	629	90	100	4	0	0
14	T	79	1208	385	629	90	100	4	0	0
14	U	79	1195	385	616	90	100	4	0	0
14	V	79	1208	385	629	90	100	4	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	W	79	1208	385	629	90	100	4	0	0
14	X	79	1208	385	629	90	100	4	0	0

- Molecule 15 is a protein called ACANB04460.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
15	Z	142	2188	683	1096	187	220	2	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	a	483	7539	2373	3807	637	711	11	0	0
16	b	490	7648	2405	3865	645	722	11	0	0
16	c	488	7622	2397	3855	642	717	11	0	0

- Molecule 17 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
17	d	549	8495	2679	4271	718	816	11	0	0
17	e	571	8840	2792	4435	745	858	10	0	0
17	f	581	8993	2836	4518	760	868	11	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-10	SER	ALA	conflict	UNP L8GXZ0
d	201	GLU	-	insertion	UNP L8GXZ0
d	202	ARG	-	insertion	UNP L8GXZ0
d	203	THR	-	insertion	UNP L8GXZ0
d	204	ARG	-	insertion	UNP L8GXZ0
d	205	GLU	-	insertion	UNP L8GXZ0
d	206	GLY	-	insertion	UNP L8GXZ0
e	-10	SER	ALA	conflict	UNP L8GXZ0

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Chain	Residue	Modelled	Actual	Comment	Reference
e	201	GLU	-	insertion	UNP L8GXZ0
e	202	ARG	-	insertion	UNP L8GXZ0
e	203	THR	-	insertion	UNP L8GXZ0
e	204	ARG	-	insertion	UNP L8GXZ0
e	205	GLU	-	insertion	UNP L8GXZ0
e	206	GLY	-	insertion	UNP L8GXZ0
f	-10	SER	ALA	conflict	UNP L8GXZ0
f	201	GLU	-	insertion	UNP L8GXZ0
f	202	ARG	-	insertion	UNP L8GXZ0
f	203	THR	-	insertion	UNP L8GXZ0
f	204	ARG	-	insertion	UNP L8GXZ0
f	205	GLU	-	insertion	UNP L8GXZ0
f	206	GLY	-	insertion	UNP L8GXZ0

- Molecule 18 is a protein called unknown protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
18	1	71	710	213	355	71	71	0	0

- Molecule 19 is a protein called unknown protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
19	2	132	1320	396	660	132	132	0	0

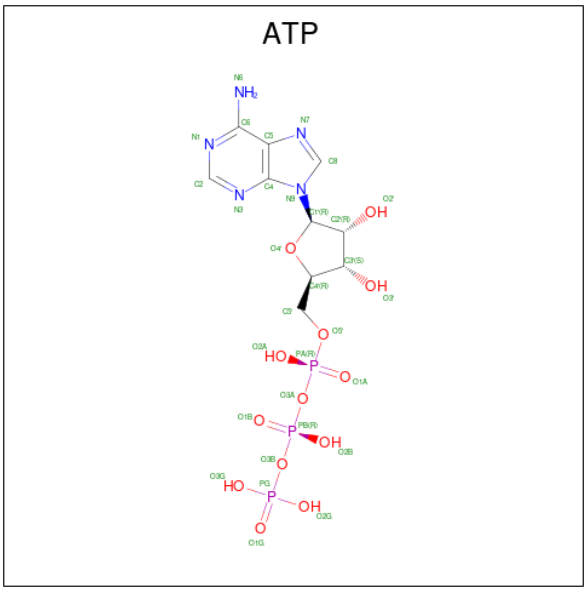
- Molecule 20 is a protein called unknown protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
20	3	9	90	27	45	9	9	0	0

- Molecule 21 is a protein called unknown protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
21	5	19	190	57	95	19	19	0	0

- Molecule 22 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

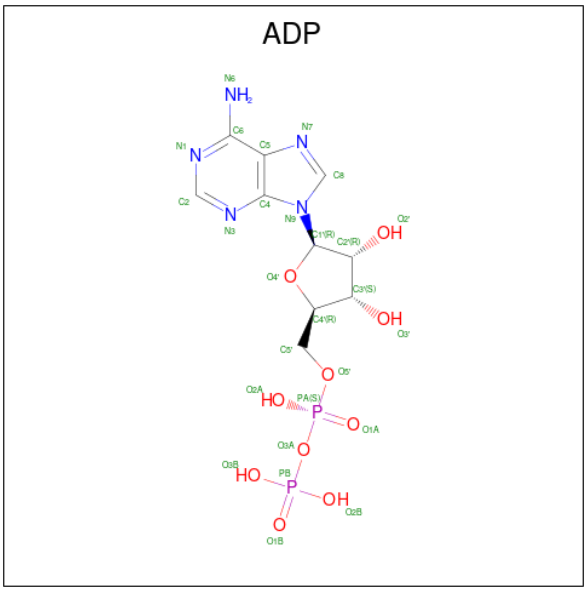


Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
22	a	1	43	10	12	5	13	3	0
22	b	1	43	10	12	5	13	3	0
22	c	1	43	10	12	5	13	3	0

- Molecule 23 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
23	b	1	1	1	0
23	c	1	1	1	0
23	f	1	1	1	0

- Molecule 24 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



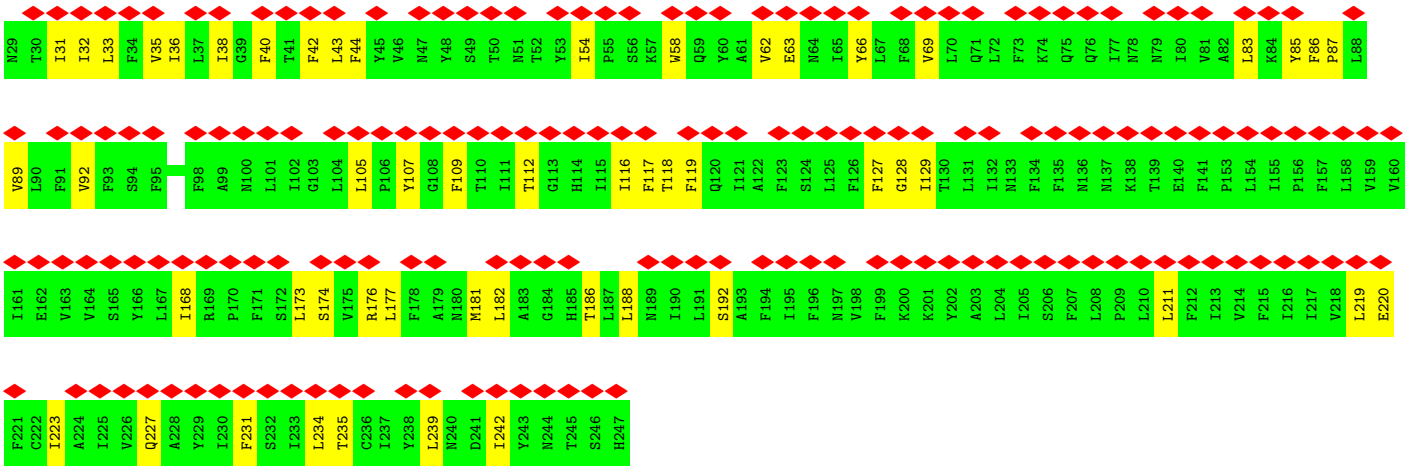
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
24	d	1	39	10	12	5	10	2	0
			Total	C	H	N	O	P	
24	f	1	39	10	12	5	10	2	0

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 subunit a

Chain 6:

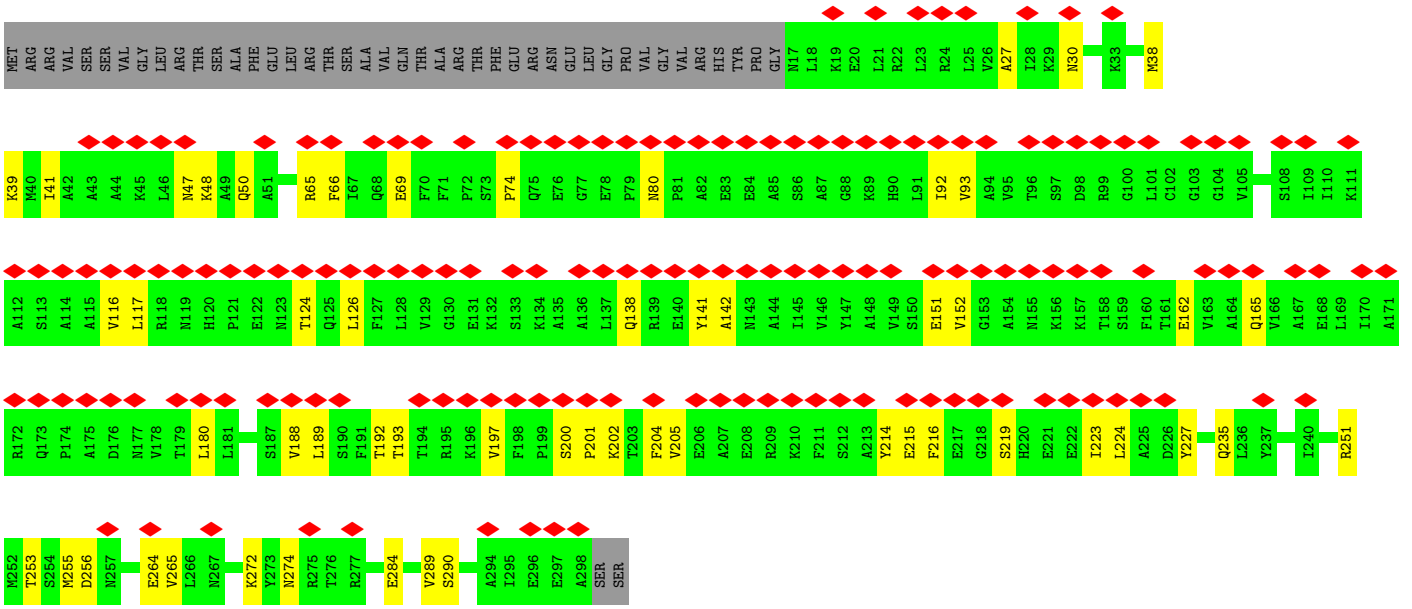


- Molecule 2: ORFB

Chain 8:

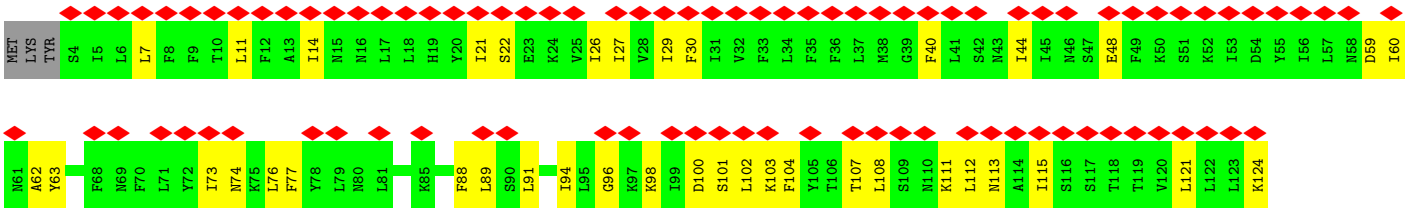
- Molecule 3: F-ATPase gamma subunit,ATP synthase gamma subunit, mitochondrial

Chain A:



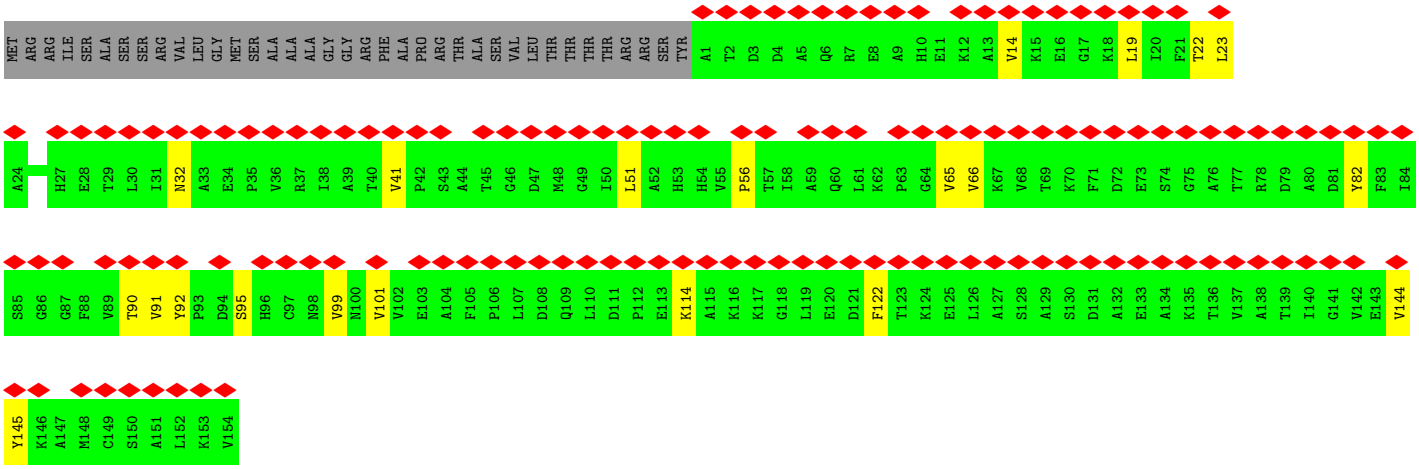
- Molecule 4: ORF25

Chain B:



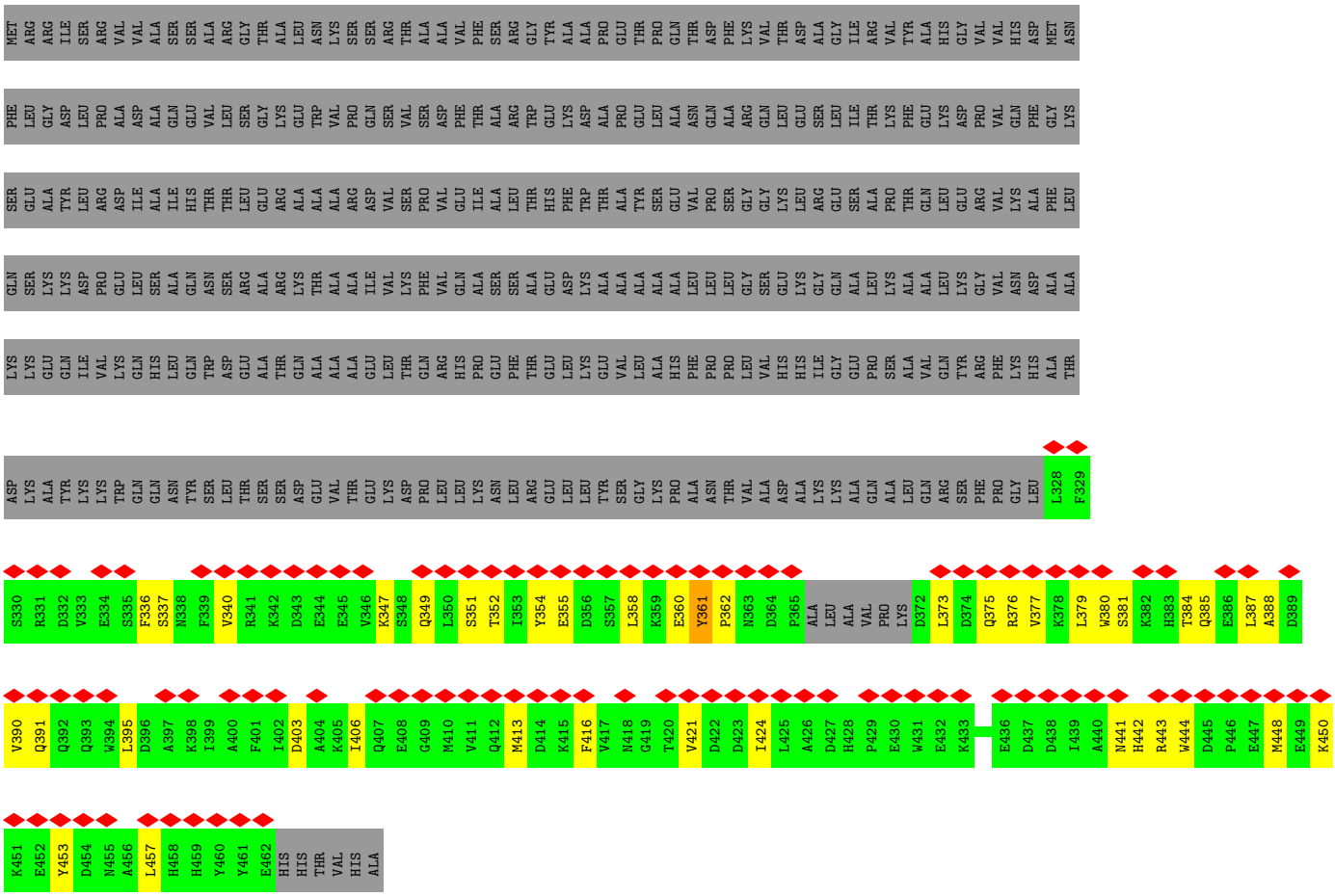
- Molecule 5: ATP synthase, Delta/Epsilon chain, betasandwich domain containing protein

Chain C:



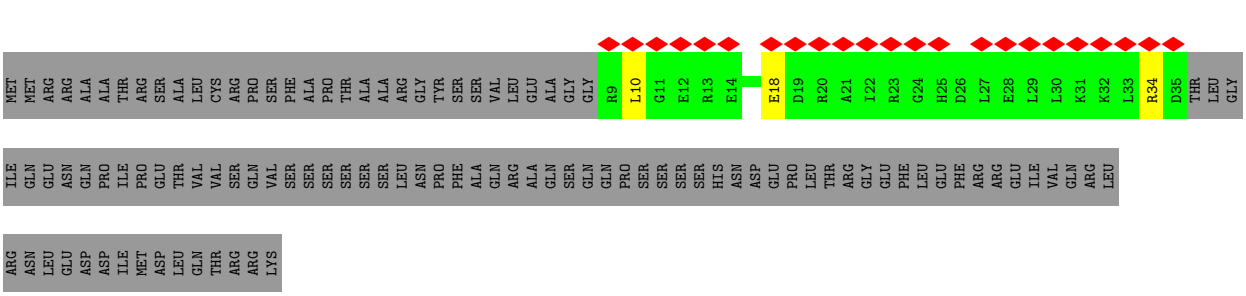
- Molecule 6: ATP synthase subunit d, mitochondrial

Chain D:



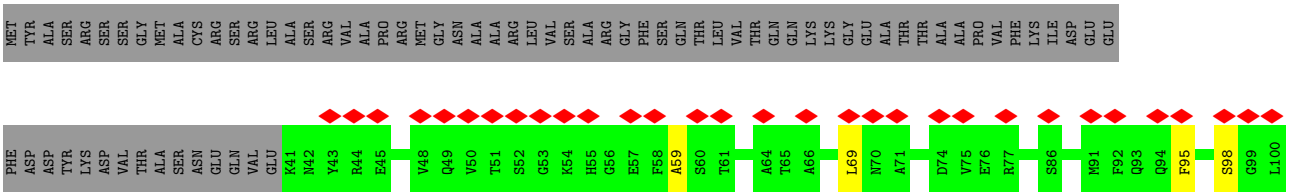
• Molecule 7: ATP synthase inhibitory factor 1 (IF1)

Chain E:



• Molecule 8: ATP synthase OSCP, mitochondrial

Chain G:



P101 D102 K103 K104 V105 M106 R107 K108 L109 K115 G116 A117 D118 F119 H120 R121 L122 F126 L127 V128 T129 E130 L131 L132 E133 A134 L137 K138 L139 V140 P141 D142 I143 A144 Y147 A148 Q149 R155 K156 E157 V158 P159 V160 V161 F162 T163 F164 A165 S166 L167 P168 D169 K170 D171 F172

L173 T174 R175 Q176 I177 V180 K181 K182 Y183 R184 L185 E186 A187 D188 A189 T190 P191 M192 W193 E194 F195 K196 I197 N198 P199 A200 L201 I202 G203 G204 F205 T206 V207 GLU VAL GLY SER ASN Y213 K214 G215 N216 F217 A218 L219 S220 S221 Q222 F223 D224 L225 M226 R227 Q228 Q229 L230 K231 Q232 A233

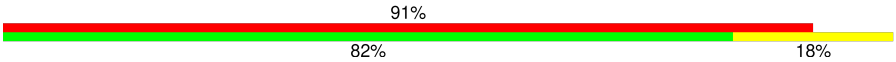
E234 D235 K236 W237 E238 R239 V240 R241 PRO LYS GLU LEU HIS ILE ASN SER PHE ASP THR SER SER LEU PHE ALA PRO LEU SER GLY VAL LYS ILE THR ALA ALA ASP LEU ASP LYS THR LEU ALA ASP VAL LEU GLY SER LYS LYS GLU ALA PHE GLN ALA ALA ASP LEU ASP ARG THR LEU

LYS GLN ALA LEU GLU ASP ALA GLN ARG ASP ALA GLY PHE SER GLY ASP TYR GLU LYS ASN VAL LEU GLU GLN THR ARG ASN LEU ASP PHE GLU LYS LEU LYS THR VAL LYS GLN LEU ASP LEU ALA GLN HIS GLU LYS HIS LEU MET GLN LYS HIS ASN ILE ALA ASP ASN ASP ALA GLU

GLY LYS ARG LYS VAL LYS ALA LYS ILE GLU GLU LEU LYS ARG PHE LYS GLU LEU ASP THR SER PHE ILE GLY GLU VAL LEU LYS LYS HIS GLN PRO GLU THR TYR LYS LYS TYR GLN SER VAL PHE GLN

- Molecule 9: ATP synthase subunit epsilon, mitochondrial, putative

Chain H:



L1 K2 E3 P4 F5 R6 A7 A10 E11 R12 D13 S14 V15 N16 M17 K18 V19 E20 Q21 W22 I23 L24 G25 K26 G27 Q28 D29 K30 V31 D32 V33 K34 R35 A36 N37 E38 I39 A40 G41 S42 A43 G44 H45

- Molecule 10: malate dehydrogenase

Chain I:

MET ARG ARG GLY LEU SER THR VAL SER ARG SER ALA THR VAL PHE GLY LYS GLN ALA CYS LEU ALA SER SER THR LEU ARG VAL ASP ARG ARG ALA TYR ALA THR S36 P37 E38 D39 A40 A41 L42 E43 A44 Q45 I46 E47 K48 V49 L50 D51 L52 V53 K54 K55 Q56 G57 N58 L59 G60

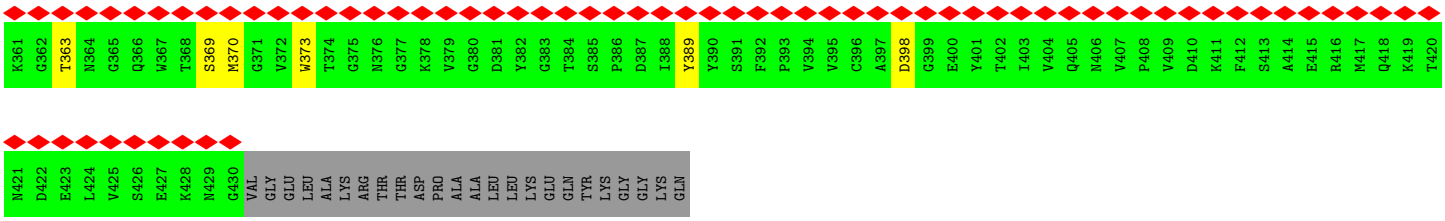
SER GLU K63 L64 T65 V66 R67 K68 L69 T70 E71 L72 R73 Q74 T75 V76 P77 E78 I79 D80 R81 A82 L83 S84 S85 V86 G87 D88 S89 A90 V91 K92 Y93 M94 A95 E96 L97 E98 K99 P100 G101 ALA GLY PRO LEU S106 A107 V108 P109 P110 V111 R112 V113 T114 V115 T116 G117 A118 A119 G120

A121 I122 G123 Y124 A125 M126 L127 F128 R129 I130 A131 S132 G133 E134 M135 L136 G137 K138 H139 Q140 P141 V142 I143 L144 Q145 L146 L147 E148 L149 E150 P151 A152 M153 K154 A155 L156 E157 G158 V159 I160 M161 E162 L163 K164 D165 C166 A167 F168 P169 L170 L171 H172 G173 V174 T175 A176 S177 S178 D179 V180

N181 K182 A183 F184 E185 G186 A187 D188 F189 A190 M191 L192 V193 G194 A195 K196 P197 R198 T199 LYS GLY MET GLU R204 G205 D206 L207 L208 K209 E210 N211 A212 N213 I214 F215 S216 V217 Q218 G219 K220 A221 L222 N223 K224 V225 A226 N227 R228 D229 T230 L231 R232 V233 C234 V235 V236 G237 N238 P239 A240

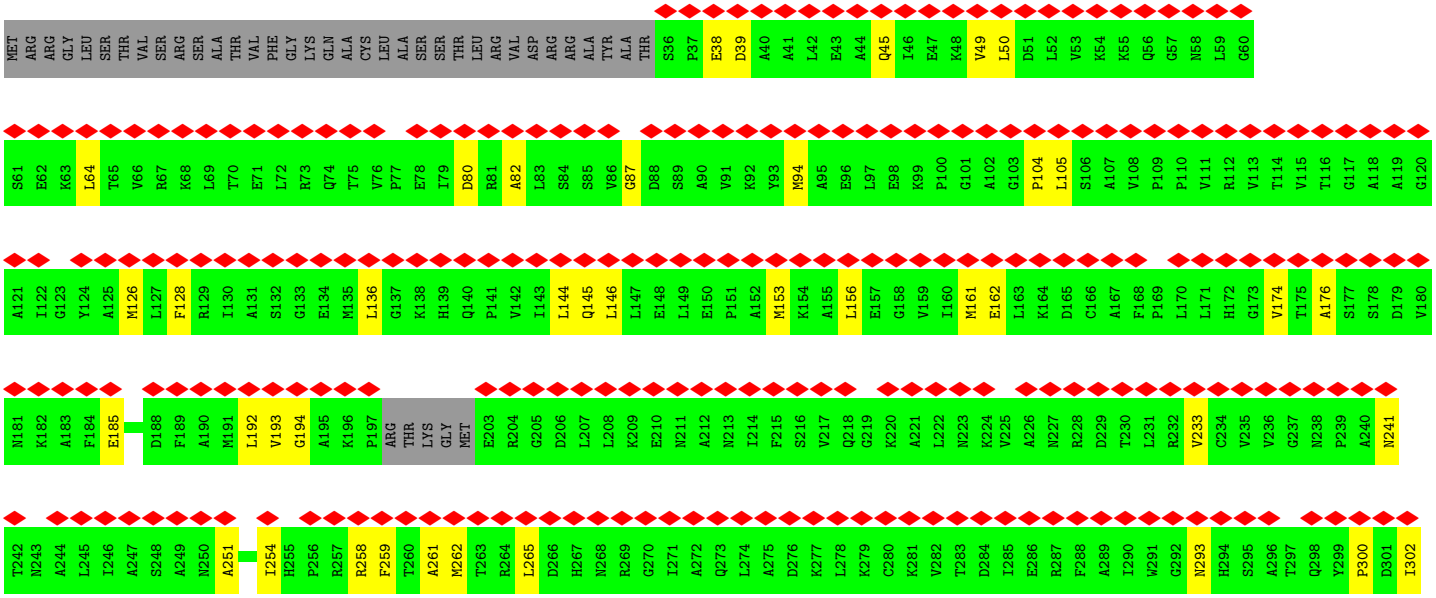
N241 T242 N243 A244 L245 I246 A247 S248 A249 N250 A251 P252 N253 I254 H255 P256 R257 R258 F259 T260 A261 M262 T263 R264 L265 D266 H267 N268 R269 G270 I271 A272 Q273 L274 A275 D276 K277 L278 K279 C280 K281 V282 T283 D284 I285 E286 R287 F288 A289 I290 W291 G292 N293 H294 S295 A296 T297 Q298 Y299 P300

D301 I302 S303 H304 T305 Q306 I307 N308 G309 K310 W311 A312 K313 D314 L315 V316 D317 E318 K319 W320 V321 K322 D323 T324 F325 I326 P327 D328 V329 Q330 Q331 R332 G333 A334 A335 I336 I337 A338 A339 ARG GLY SER S343 S344 A345 A346 S347 A348 A349 N350 A351 A352 I353 E354 H355 M356 R357 D358 W359 V360



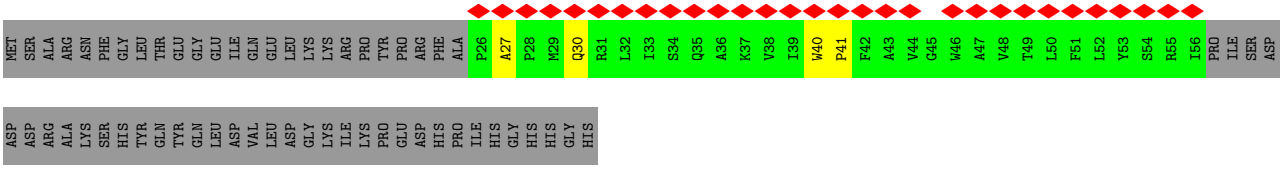
• Molecule 10: malate dehydrogenase

Chain L:



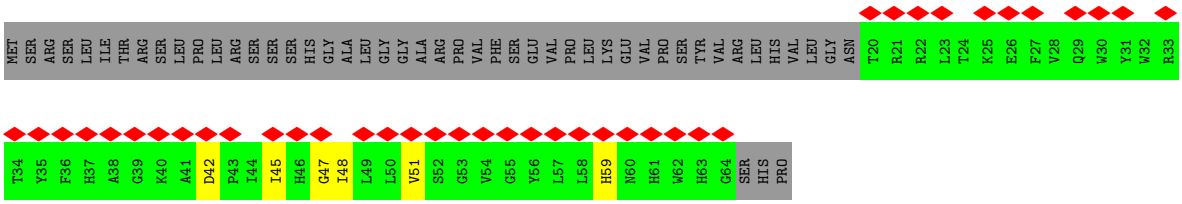
• Molecule 11: ATP synthase subunit i/j, mitochondrial

Chain J:



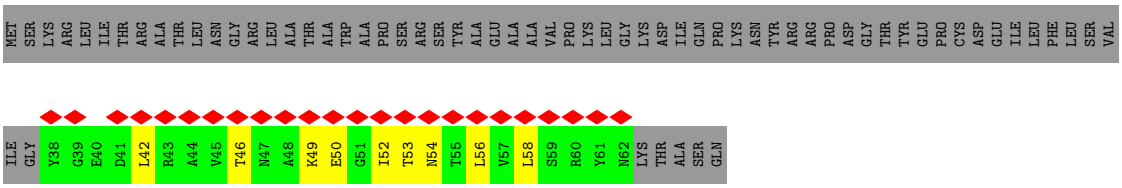
- Molecule 12: ATP synthase subunit f, mitochondrial

Chain K:



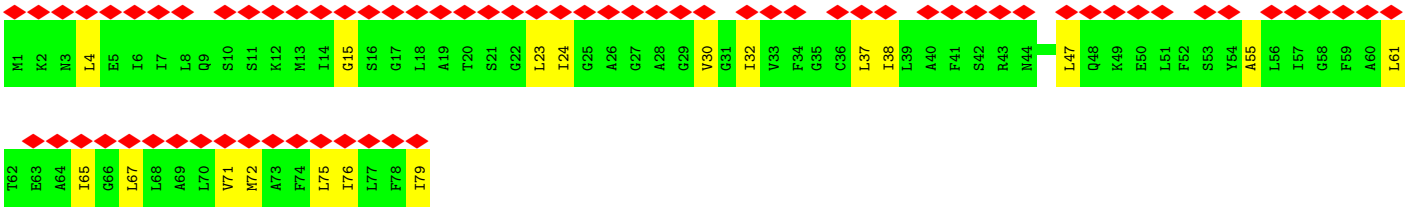
- Molecule 13: ACANB14707

Chain M:



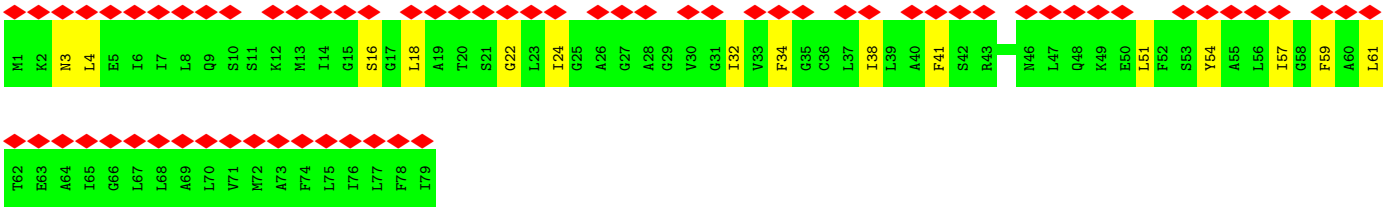
- Molecule 14: ATP synthase subunit 9, mitochondrial

Chain P:



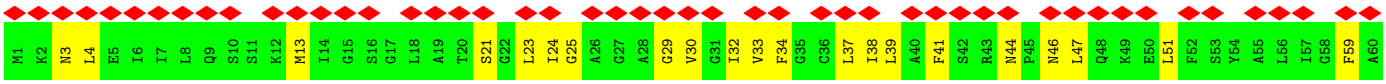
- Molecule 14: ATP synthase subunit 9, mitochondrial

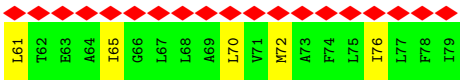
Chain Q:



- Molecule 14: ATP synthase subunit 9, mitochondrial

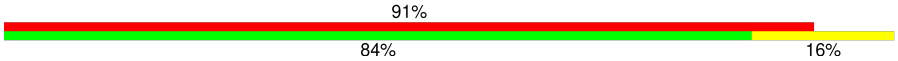
Chain R:

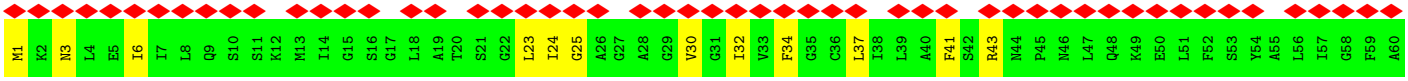


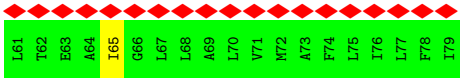


• Molecule 14: ATP synthase subunit 9, mitochondrial

Chain S:

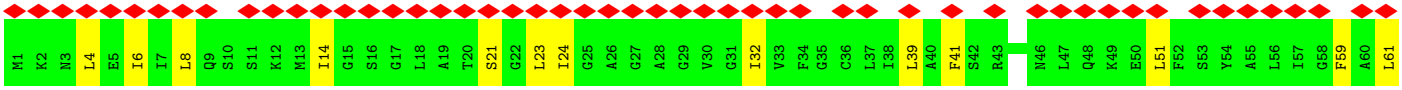


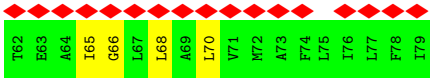




• Molecule 14: ATP synthase subunit 9, mitochondrial

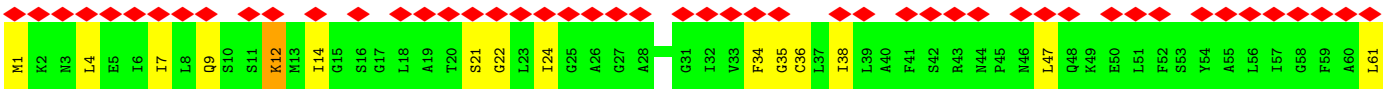
Chain T:

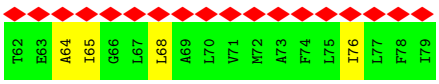




• Molecule 14: ATP synthase subunit 9, mitochondrial

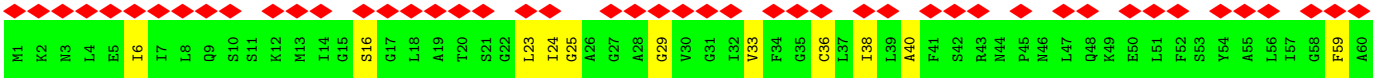
Chain U:

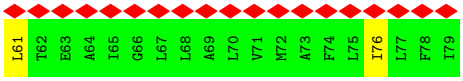




• Molecule 14: ATP synthase subunit 9, mitochondrial

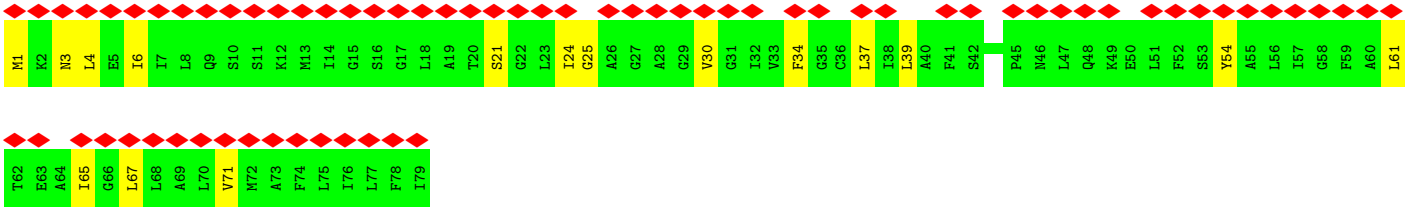
Chain V:





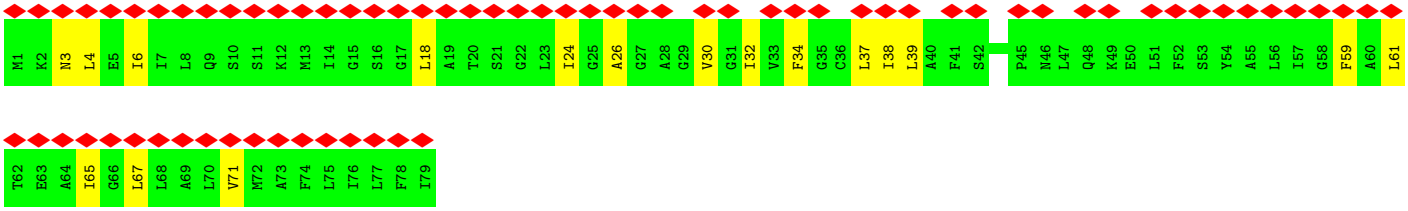
• Molecule 14: ATP synthase subunit 9, mitochondrial

Chain W:



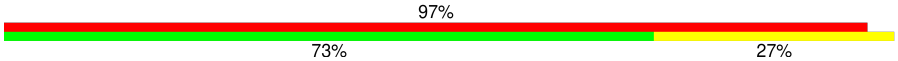
- Molecule 14: ATP synthase subunit 9, mitochondrial

Chain X:



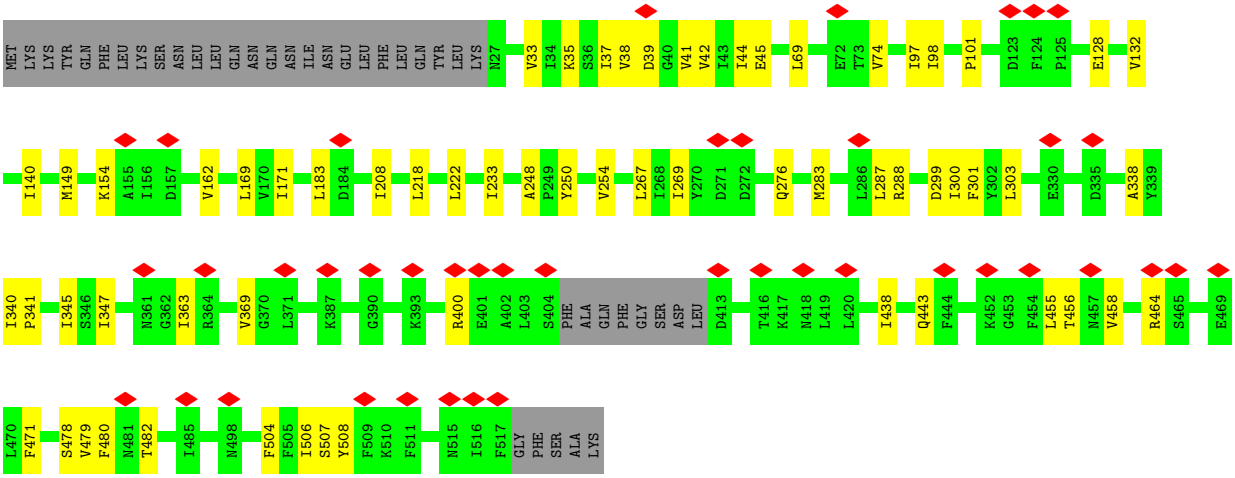
- Molecule 15: ACANB04460

Chain Z:



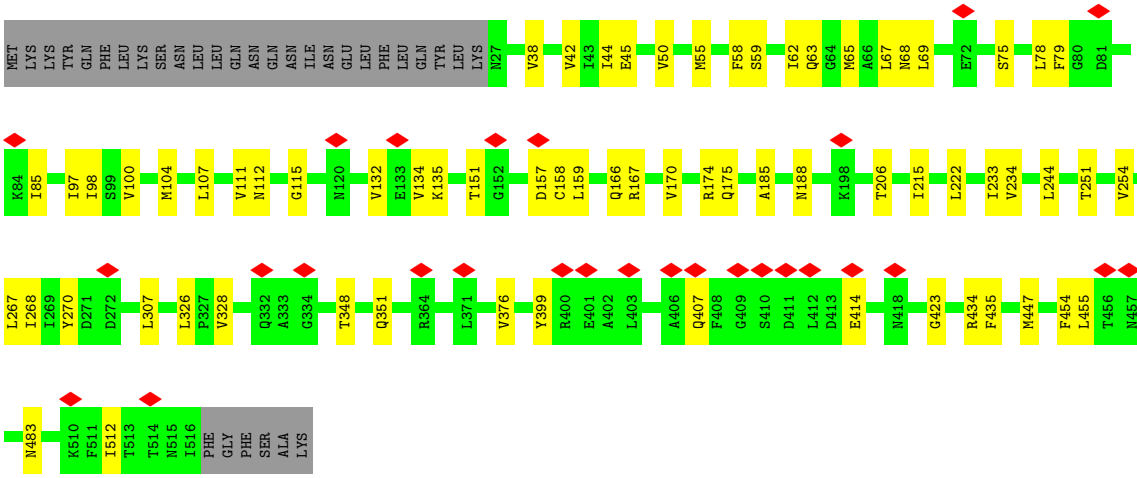
- Molecule 16: ATP synthase subunit alpha, mitochondrial

Chain a:



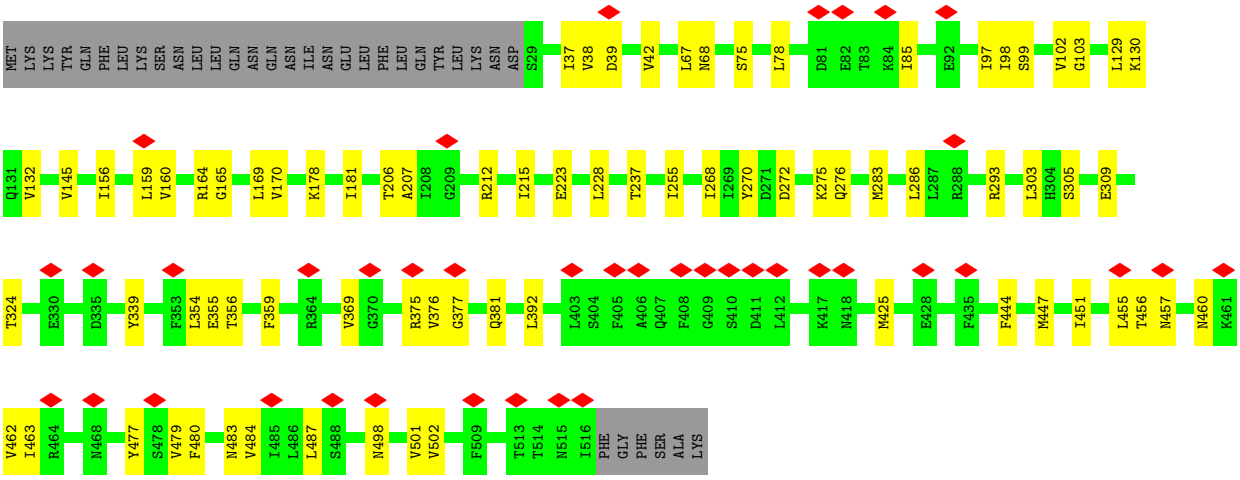
• Molecule 16: ATP synthase subunit alpha, mitochondrial

Chain b:



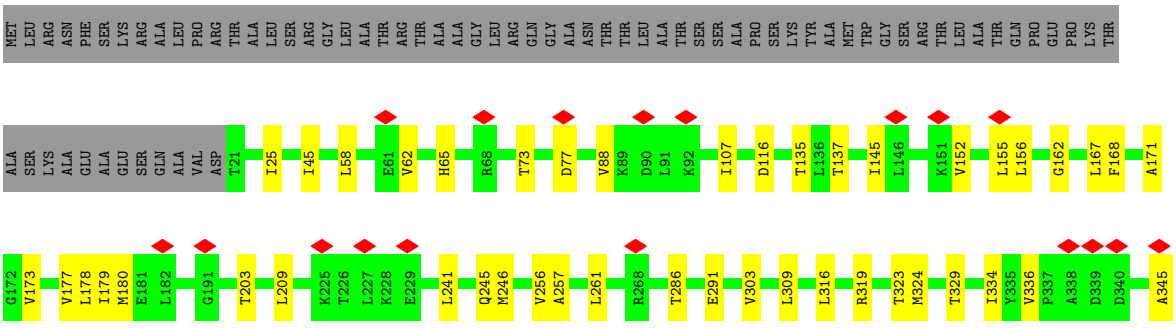
• Molecule 16: ATP synthase subunit alpha, mitochondrial

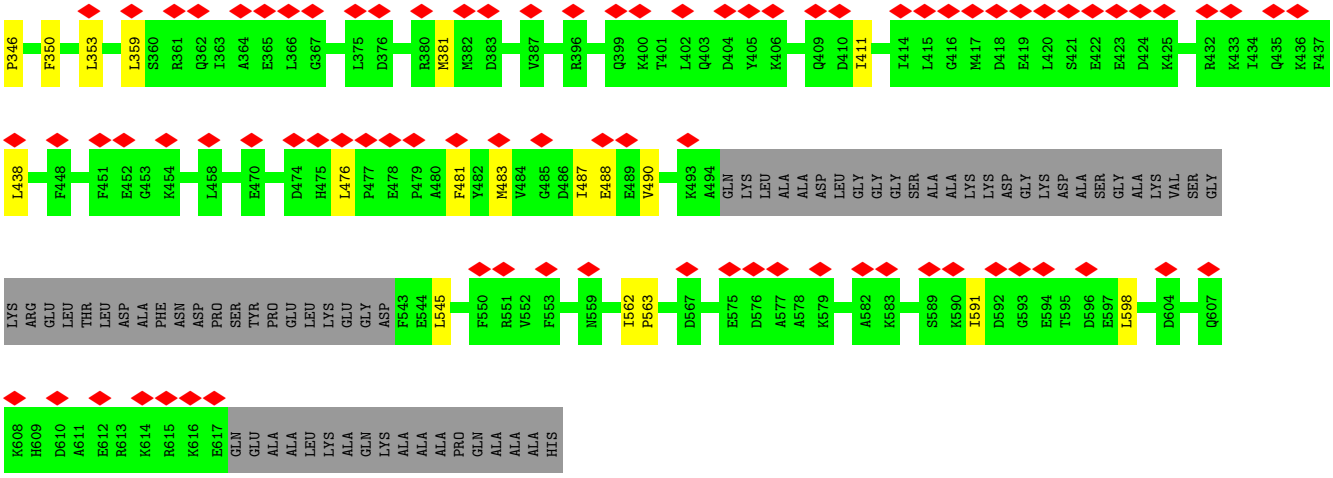
Chain c:



• Molecule 17: ATP synthase subunit beta

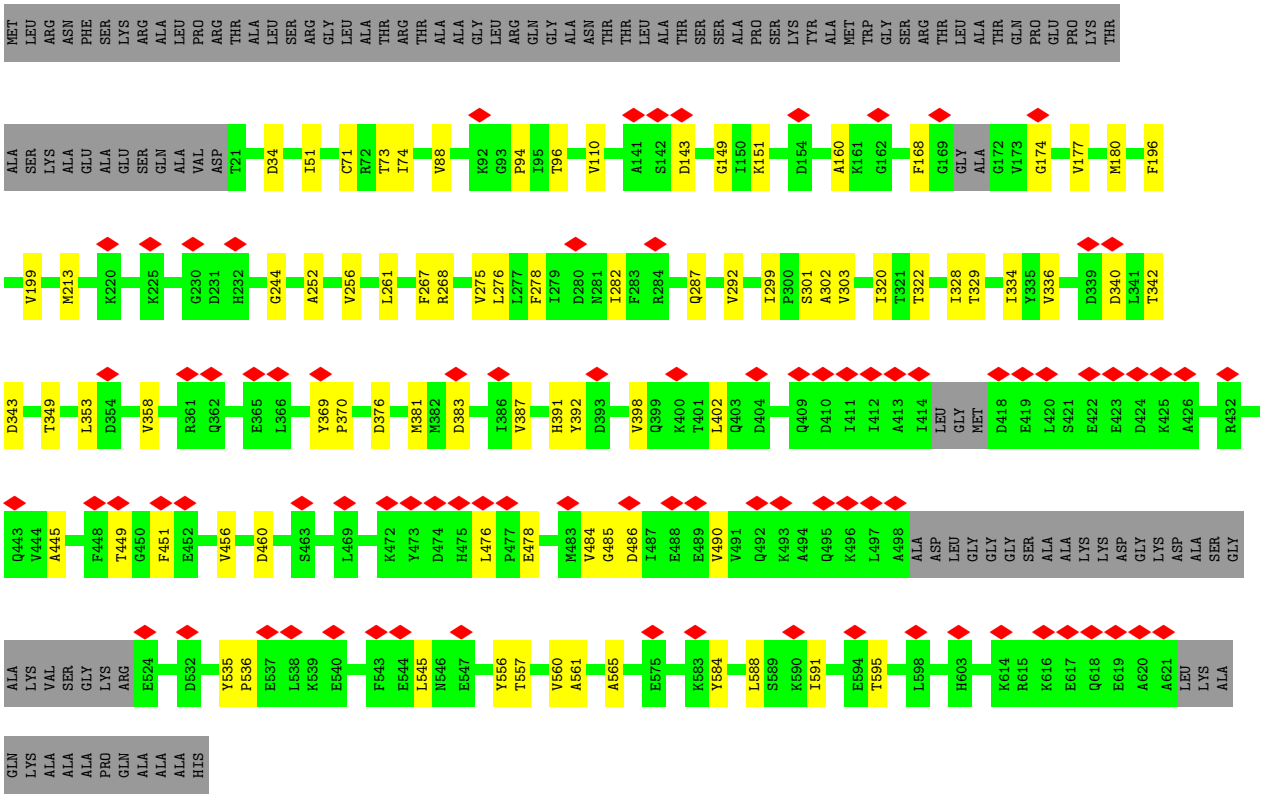
Chain d:





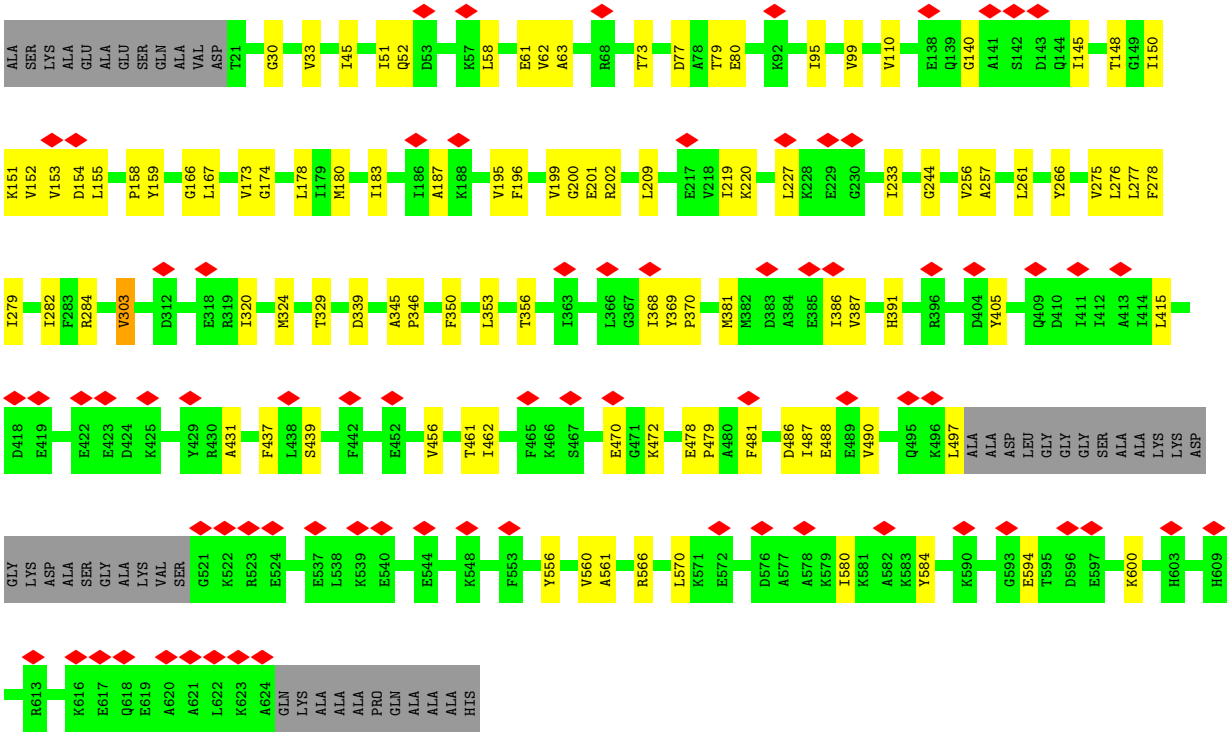
- Molecule 17: ATP synthase subunit beta

Chain e:



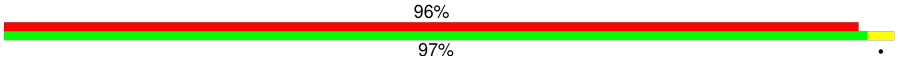
- Molecule 17: ATP synthase subunit beta

Chain f:



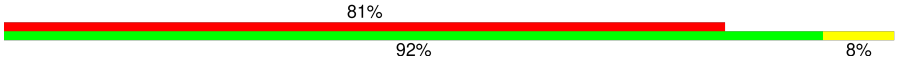
- Molecule 18: unknown protein

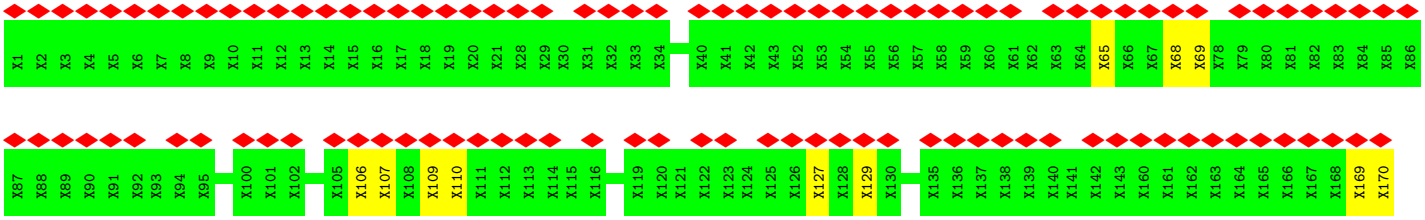
Chain 1:



- Molecule 19: unknown protein

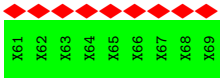
Chain 2:





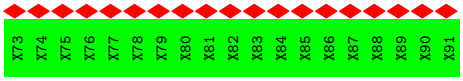
- Molecule 20: unknown protein

Chain 3:



- Molecule 21: unknown protein

Chain 5:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10863	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	0.99	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.407	Depositor
Minimum map value	-0.175	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.111	Depositor
Map size (Å)	361.68002, 361.68002, 361.68002	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, ATP, MG

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	6	0.19	0/1778	0.34	0/2423
2	8	0.24	0/1131	0.45	0/1530
3	A	0.16	0/2220	0.34	0/3004
4	B	0.24	0/1012	0.41	0/1366
5	C	0.14	0/1176	0.34	0/1596
6	D	0.26	0/1100	0.41	0/1487
7	E	0.13	0/225	0.21	0/296
8	G	0.16	0/1616	0.29	0/2179
9	H	0.13	0/354	0.30	0/470
10	I	0.14	0/2952	0.26	0/3995
10	L	0.17	0/3067	0.28	0/4154
11	J	0.13	0/261	0.29	0/356
12	K	0.15	0/400	0.27	0/544
13	M	0.23	0/197	0.45	0/266
14	P	0.15	0/586	0.28	0/787
14	Q	0.13	0/586	0.33	0/787
14	R	0.15	0/586	0.30	0/787
14	S	0.11	0/586	0.25	0/787
14	T	0.13	0/586	0.33	0/787
14	U	0.25	0/586	0.39	0/787
14	V	0.12	0/586	0.31	0/787
14	W	0.11	0/586	0.23	0/787
14	X	0.14	0/586	0.29	0/787
15	Z	0.18	0/1103	0.39	0/1491
16	a	0.22	0/3788	0.29	0/5127
16	b	0.23	0/3841	0.28	0/5200
16	c	0.23	0/3825	0.31	0/5178
17	d	0.19	0/4296	0.27	0/5810
17	e	0.18	0/4479	0.29	0/6057
17	f	0.21	0/4551	0.32	0/6153
All	All	0.19	0/48646	0.31	0/65765

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	6	1725	1791	1788	58	0
2	8	1098	1109	1108	56	0
3	A	2185	2192	2206	47	0
4	B	992	1059	1058	37	0
5	C	1155	1153	1155	19	0
6	D	1077	998	996	53	0
7	E	225	238	237	3	0
8	G	1583	1619	1617	21	0
9	H	350	357	357	15	0
10	I	2904	2924	2919	34	0
10	L	3015	3035	3033	45	0
11	J	252	265	265	2	0
12	K	384	372	371	7	0
13	M	196	195	194	8	0
14	P	579	629	629	29	0
14	Q	579	629	629	27	0
14	R	579	629	629	46	0
14	S	579	629	629	19	0
14	T	579	629	629	19	0
14	U	579	616	629	23	0
14	V	579	629	629	15	0
14	W	579	629	629	20	0
14	X	579	629	629	23	0
15	Z	1092	1096	1106	38	0
16	a	3732	3807	3818	49	0
16	b	3783	3865	3864	58	0
16	c	3767	3855	3854	58	0
17	d	4224	4271	4269	53	0
17	e	4405	4435	4431	55	0
17	f	4475	4518	4516	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	1	355	355	86	1	0
19	2	660	660	143	7	0
20	3	45	45	11	0	0
21	5	95	95	21	0	0
22	a	31	12	12	0	0
22	b	31	12	12	0	0
22	c	31	12	12	0	0
23	b	1	0	0	0	0
23	c	1	0	0	0	0
23	f	1	0	0	0	0
24	d	27	12	12	1	0
24	f	27	12	12	1	0
All	All	49135	50017	49144	845	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 9.

The worst 5 of 845 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)
3:A:117:LEU:HD11	3:A:126:LEU:HD11	1.53	0.90
17:f:151:LYS:HA	17:f:155:LEU:HD12	1.61	0.81
1:6:118:THR:HG23	1:6:177:LEU:HD23	1.61	0.81
14:P:61:LEU:HD11	14:R:59:PHE:CD1	2.17	0.80
14:P:23:LEU:HD21	14:S:65:ILE:HG22	1.66	0.78

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	6	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
2	8	124/142 (87%)	120 (97%)	4 (3%)	0	100	100
3	A	280/326 (86%)	272 (97%)	8 (3%)	0	100	100
4	B	119/124 (96%)	115 (97%)	4 (3%)	0	100	100
5	C	152/191 (80%)	143 (94%)	9 (6%)	0	100	100
6	D	125/499 (25%)	120 (96%)	4 (3%)	1 (1%)	16	52
7	E	25/137 (18%)	25 (100%)	0	0	100	100
8	G	192/431 (44%)	178 (93%)	14 (7%)	0	100	100
9	H	43/45 (96%)	41 (95%)	2 (5%)	0	100	100
10	I	372/454 (82%)	361 (97%)	11 (3%)	0	100	100
10	L	394/454 (87%)	384 (98%)	10 (2%)	0	100	100
11	J	29/92 (32%)	29 (100%)	0	0	100	100
12	K	43/94 (46%)	41 (95%)	2 (5%)	0	100	100
13	M	23/92 (25%)	20 (87%)	3 (13%)	0	100	100
14	P	77/79 (98%)	76 (99%)	1 (1%)	0	100	100
14	Q	77/79 (98%)	76 (99%)	1 (1%)	0	100	100
14	R	77/79 (98%)	74 (96%)	3 (4%)	0	100	100
14	S	77/79 (98%)	76 (99%)	1 (1%)	0	100	100
14	T	77/79 (98%)	76 (99%)	1 (1%)	0	100	100
14	U	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
14	V	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
14	W	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
14	X	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
15	Z	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
16	a	479/522 (92%)	454 (95%)	25 (5%)	0	100	100
16	b	488/522 (94%)	459 (94%)	29 (6%)	0	100	100
16	c	486/522 (93%)	461 (95%)	25 (5%)	0	100	100
17	d	545/687 (79%)	512 (94%)	33 (6%)	0	100	100
17	e	563/687 (82%)	534 (95%)	29 (5%)	0	100	100
17	f	577/687 (84%)	537 (93%)	39 (7%)	1 (0%)	43	77
All	All	6096/7769 (78%)	5809 (95%)	285 (5%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	361	TYR
17	f	303	VAL

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	6	192/192 (100%)	192 (100%)	0	100	100
2	8	123/140 (88%)	123 (100%)	0	100	100
3	A	235/272 (86%)	235 (100%)	0	100	100
4	B	115/118 (98%)	115 (100%)	0	100	100
5	C	124/152 (82%)	124 (100%)	0	100	100
6	D	118/419 (28%)	118 (100%)	0	100	100
7	E	23/119 (19%)	23 (100%)	0	100	100
8	G	170/369 (46%)	170 (100%)	0	100	100
9	H	35/35 (100%)	35 (100%)	0	100	100
10	I	307/362 (85%)	307 (100%)	0	100	100
10	L	318/362 (88%)	318 (100%)	0	100	100
11	J	26/79 (33%)	26 (100%)	0	100	100
12	K	38/81 (47%)	38 (100%)	0	100	100
13	M	21/76 (28%)	21 (100%)	0	100	100
14	P	60/60 (100%)	60 (100%)	0	100	100
14	Q	60/60 (100%)	60 (100%)	0	100	100
14	R	60/60 (100%)	60 (100%)	0	100	100
14	S	60/60 (100%)	60 (100%)	0	100	100
14	T	60/60 (100%)	60 (100%)	0	100	100
14	U	60/60 (100%)	59 (98%)	1 (2%)	53	67
14	V	60/60 (100%)	60 (100%)	0	100	100
14	W	60/60 (100%)	60 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	X	60/60 (100%)	60 (100%)	0	100	100
15	Z	118/118 (100%)	118 (100%)	0	100	100
16	a	413/448 (92%)	413 (100%)	0	100	100
16	b	418/448 (93%)	418 (100%)	0	100	100
16	c	416/448 (93%)	416 (100%)	0	100	100
17	d	450/547 (82%)	450 (100%)	0	100	100
17	e	470/547 (86%)	470 (100%)	0	100	100
17	f	476/547 (87%)	476 (100%)	0	100	100
All	All	5146/6419 (80%)	5145 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	U	12	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
17	d	54	HIS
17	f	443	GLN
17	d	435	GLN
17	f	83	GLN
8	G	229	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)

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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	$\#\|Z\| > 2$
22	ATP	c	601	23	32,33,33	0.58	0	48,52,52	0.75	1 (2%)
22	ATP	b	602	23	32,33,33	0.79	2 (6%)	48,52,52	0.77	2 (4%)
22	ATP	a	601	-	32,33,33	0.59	0	48,52,52	0.76	2 (4%)
24	ADP	d	701	-	28,29,29	1.36	5 (17%)	43,45,45	1.87	11 (25%)
24	ADP	f	702	23	28,29,29	1.37	5 (17%)	43,45,45	1.85	10 (23%)

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
22	ATP	c	601	23	-	0/22/38/38	0/3/3/3
22	ATP	b	602	23	-	2/22/38/38	0/3/3/3
22	ATP	a	601	-	-	3/22/38/38	0/3/3/3
24	ADP	d	701	-	-	2/16/32/32	0/3/3/3
24	ADP	f	702	23	-	2/16/32/32	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	f	702	ADP	C5-C4	4.44	1.47	1.39
24	d	701	ADP	C5-C4	4.33	1.46	1.39
22	b	602	ATP	PB-O3B	-3.21	1.56	1.59
24	f	702	ADP	C5-C6	2.58	1.48	1.41
24	d	701	ADP	C5-N7	-2.54	1.34	1.39

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	f	702	ADP	C5-C4-N3	-5.54	119.09	126.72
24	d	701	ADP	C5-C4-N3	-5.46	119.20	126.72
24	d	701	ADP	N3-C4-N9	4.41	134.67	127.17
24	f	702	ADP	N3-C4-N9	4.41	134.67	127.17
24	d	701	ADP	N3-C2-N1	-3.87	122.73	128.58

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	a	601	ATP	PB-O3B-PG-O2G
22	b	602	ATP	O4'-C4'-C5'-O5'
24	f	702	ADP	C5'-O5'-PA-O3A
24	d	701	ADP	C3'-C4'-C5'-O5'
22	b	602	ATP	C3'-C4'-C5'-O5'

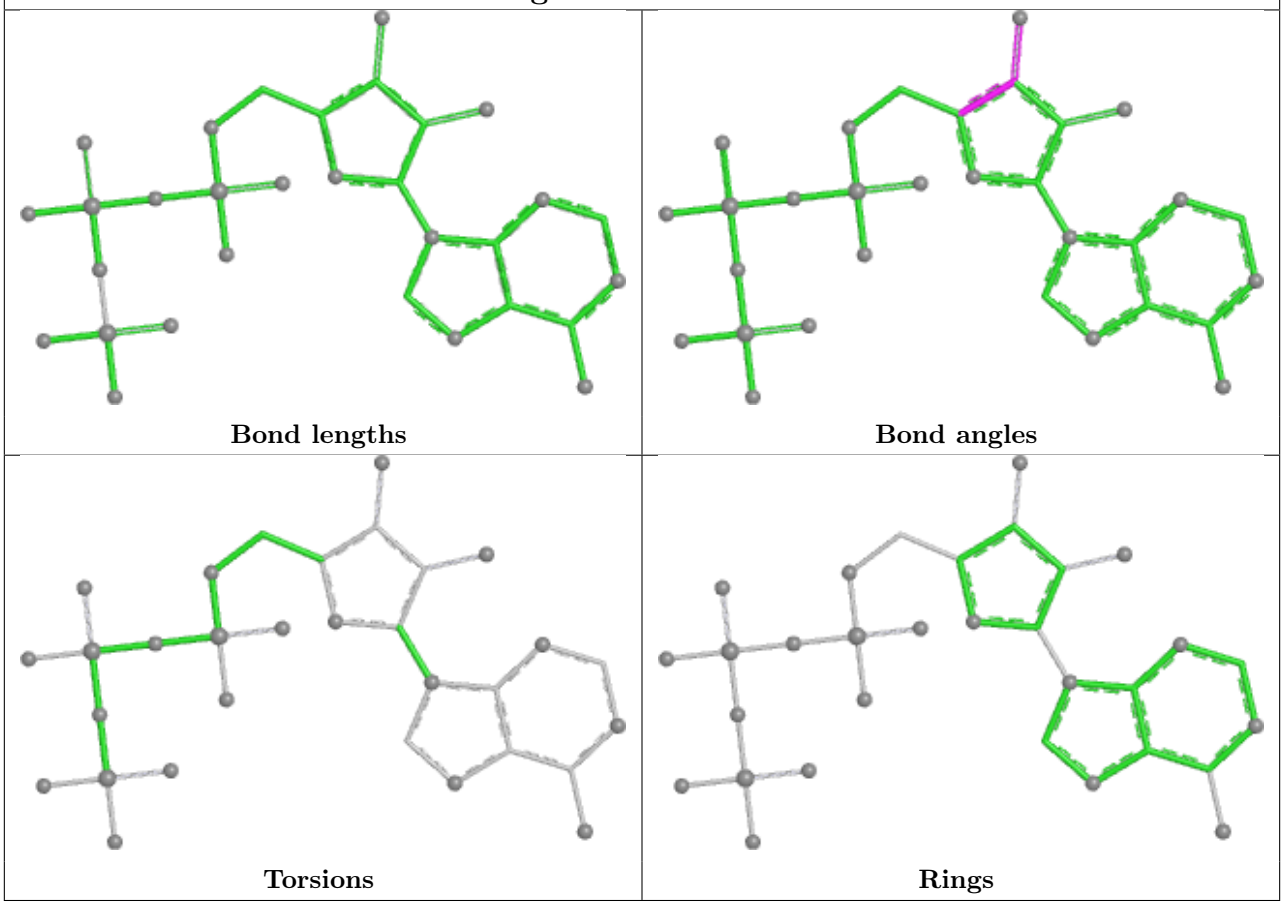
There are no ring outliers.

2 monomers are involved in 2 short contacts:

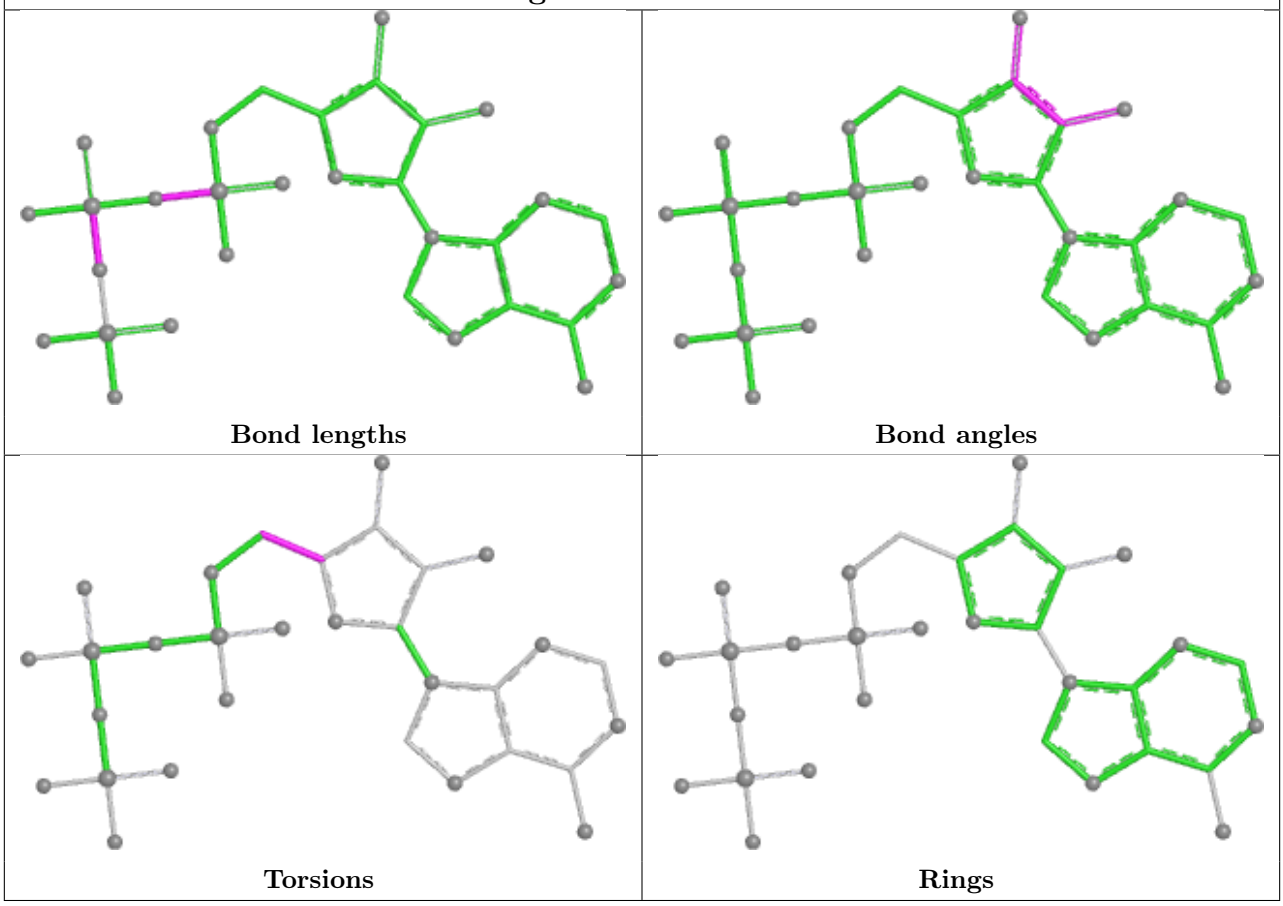
Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	d	701	ADP	1	0
24	f	702	ADP	1	0

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

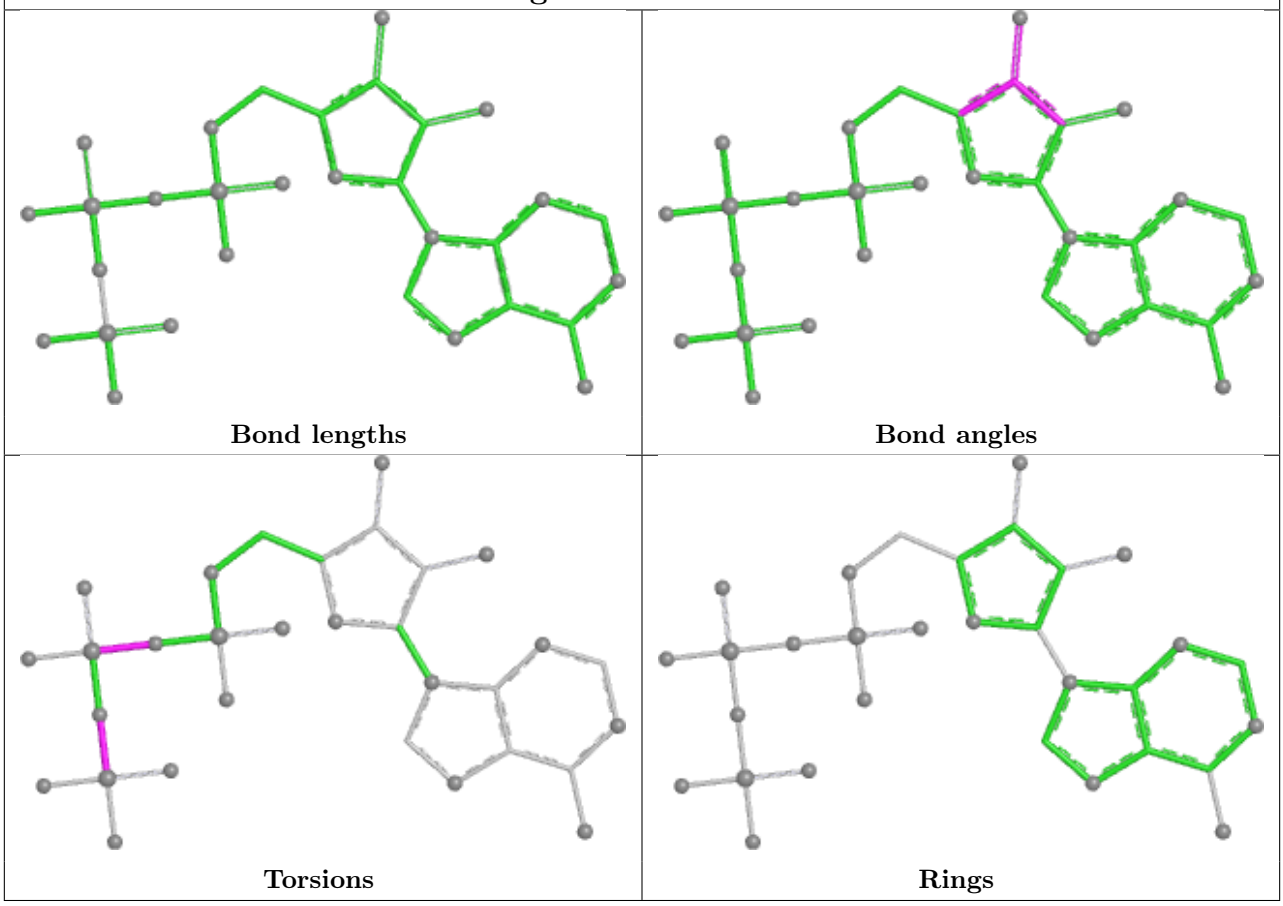
Ligand ATP c 601



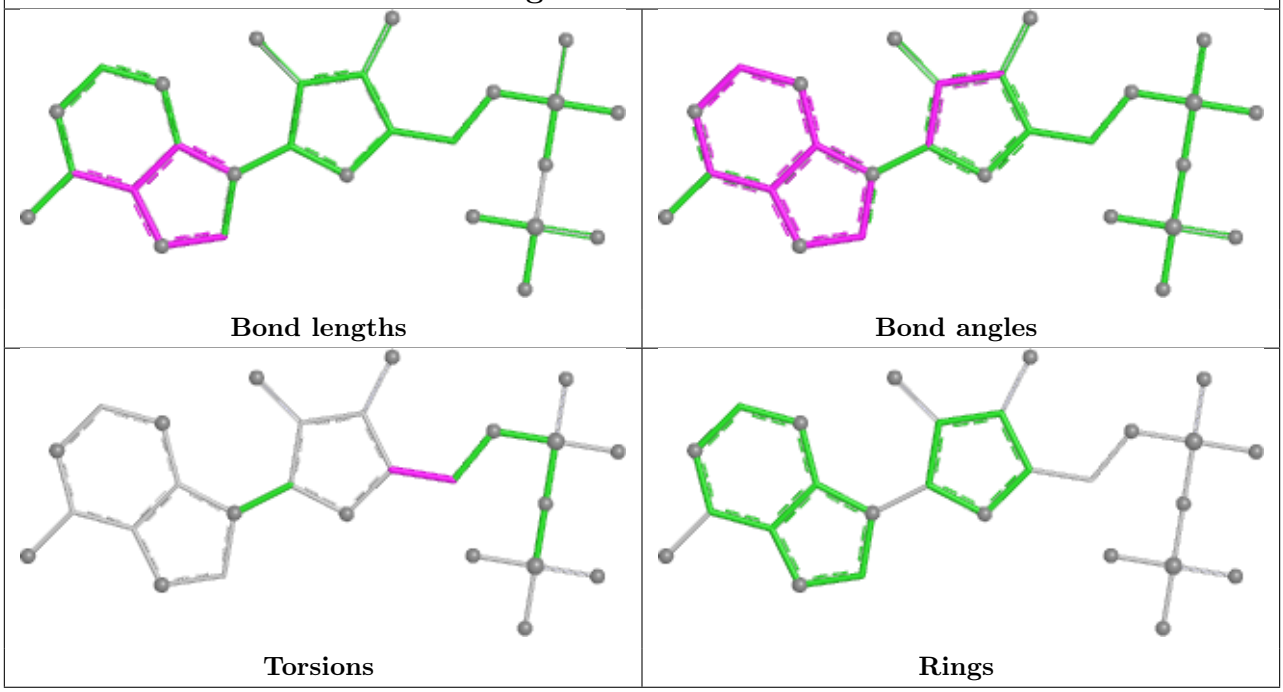
Ligand ATP b 602

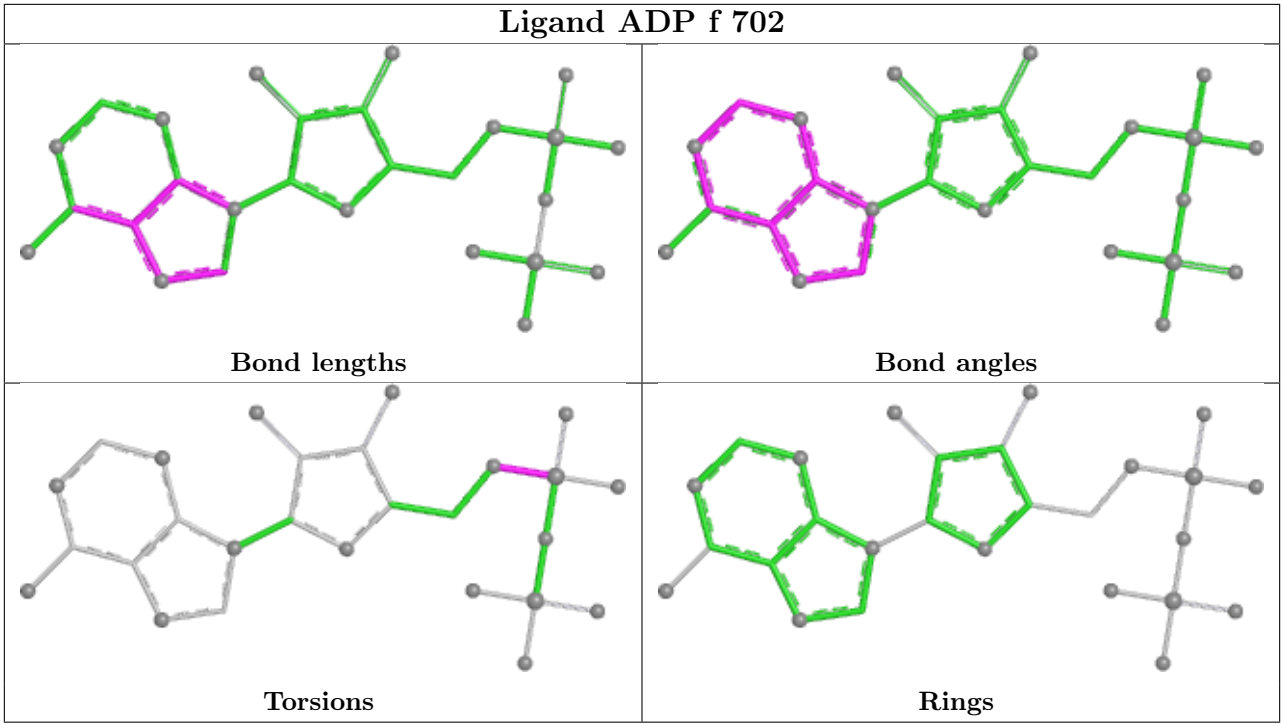


Ligand ATP a 601



Ligand ADP d 701





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
18	1	5
19	2	4
1	6	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	143:UNK	C	160:UNK	N	71.74
1	1	69:UNK	C	81:UNK	N	49.61
1	2	43:UNK	C	52:UNK	N	27.68
1	1	89:UNK	C	117:UNK	N	19.10
1	1	125:UNK	C	135:UNK	N	16.94

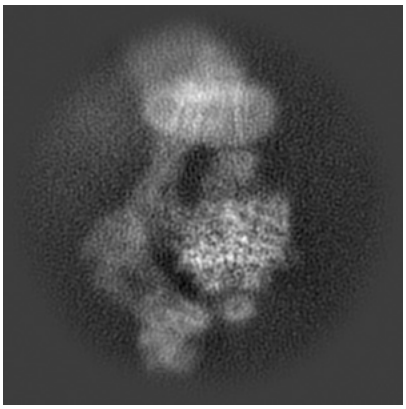
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-74153. These allow visual inspection of the internal detail of the map and identification of artifacts.

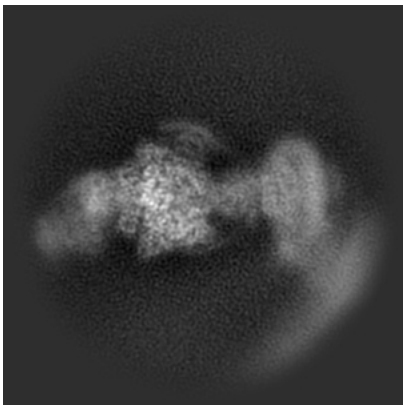
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

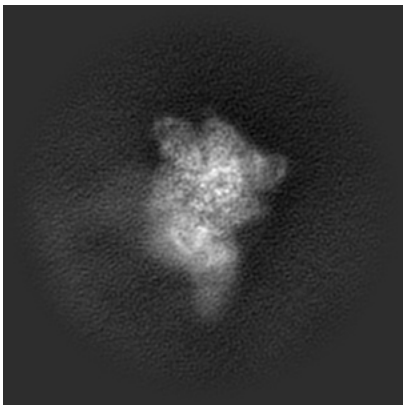
6.1.1 Primary map



X

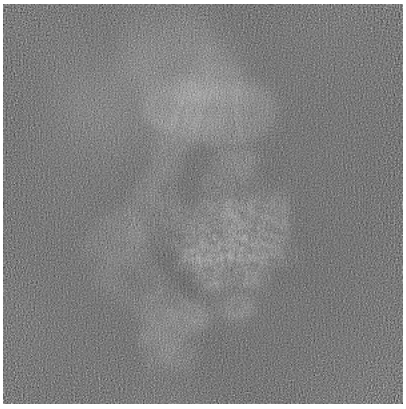


Y

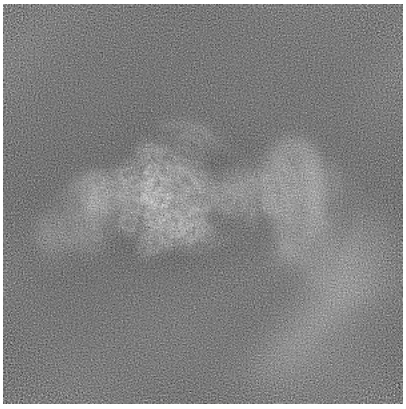


Z

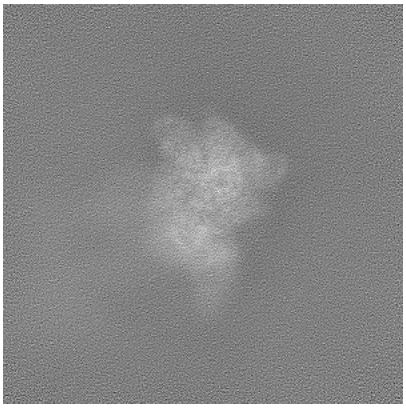
6.1.2 Raw map



X



Y

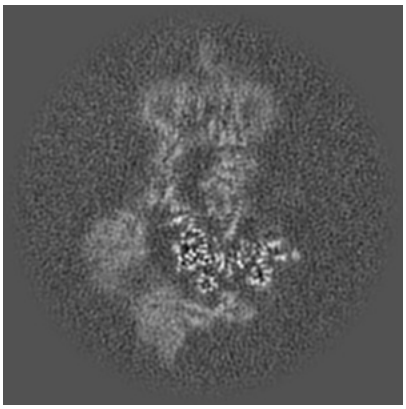


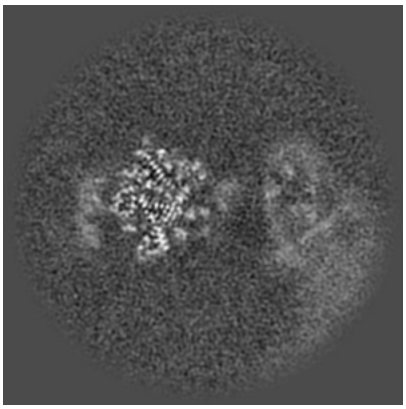
Z

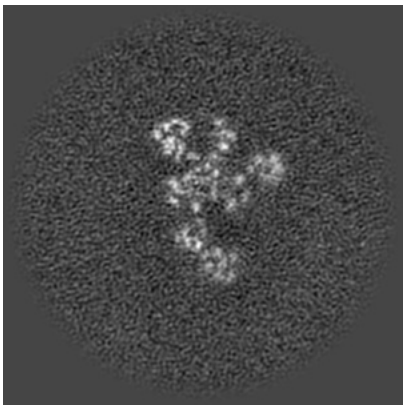
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

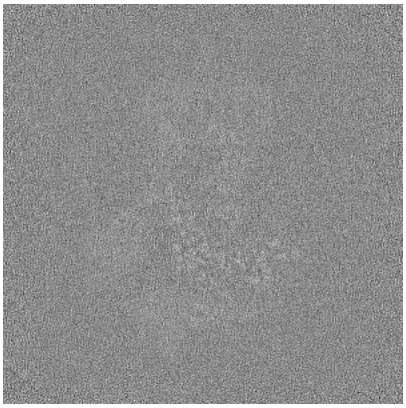
6.2.1 Primary map


X Index: 220


Y Index: 220


Z Index: 220

6.2.2 Raw map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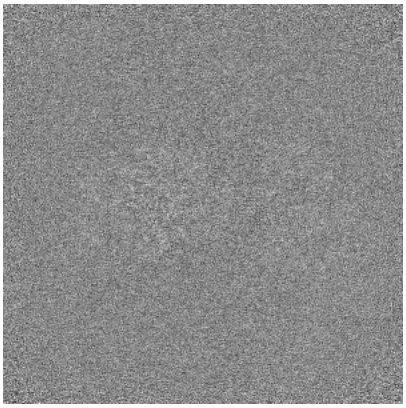
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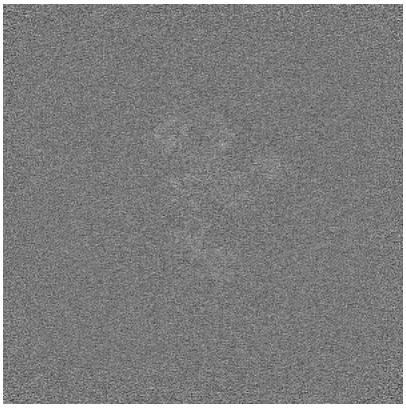
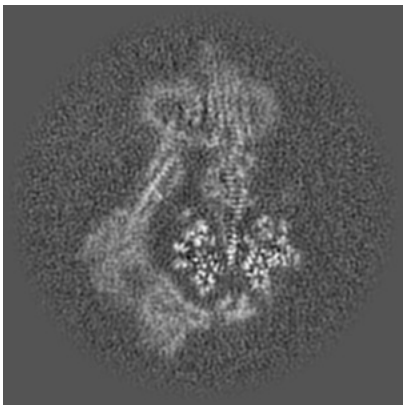

Z Index: 220

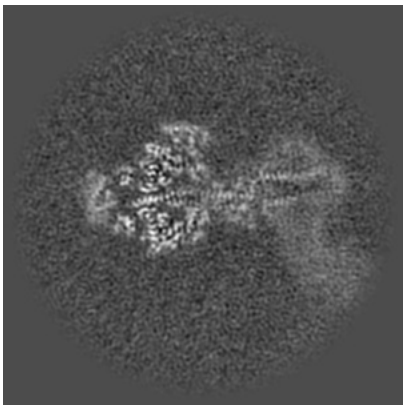
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

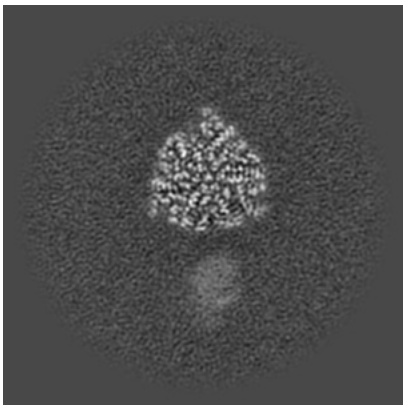
6.3.1 Primary map



X Index: 227

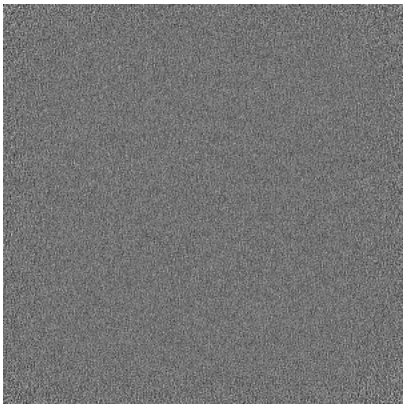


Y Index: 250

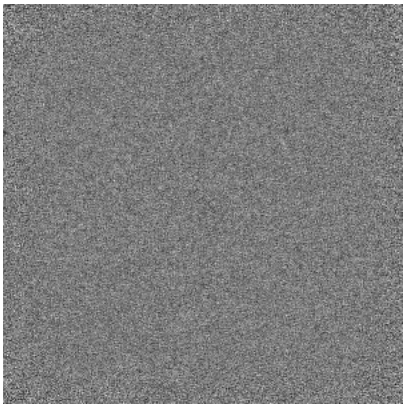


Z Index: 162

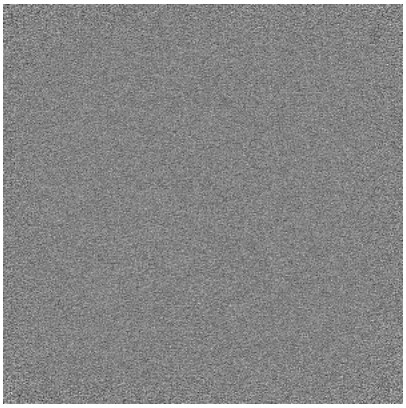
6.3.2 Raw map



X Index: 0



Y Index: 0

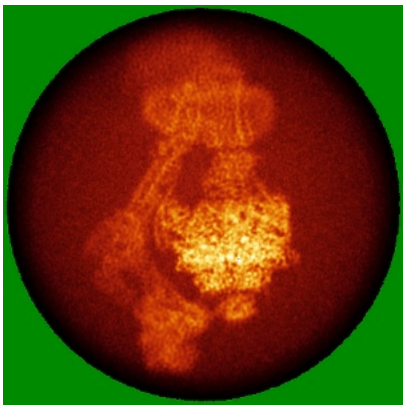


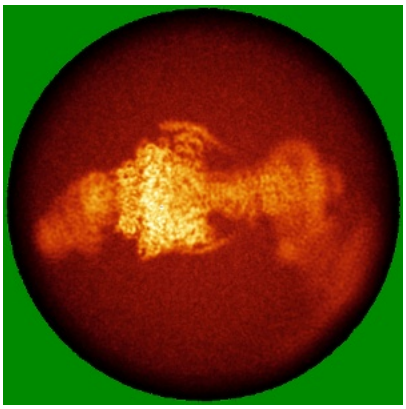
Z Index: 0

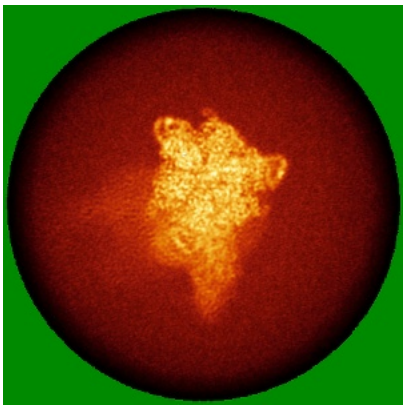
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

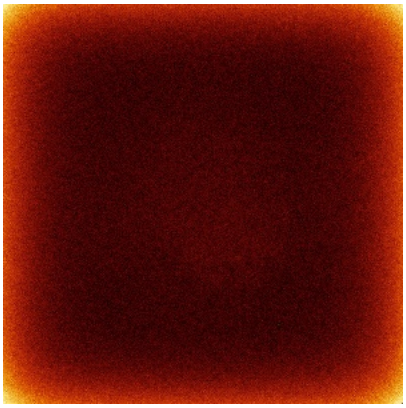
6.4.1 Primary map

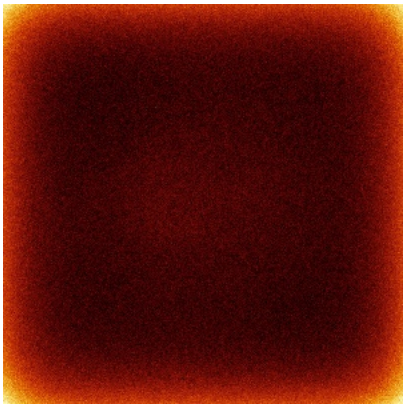

X

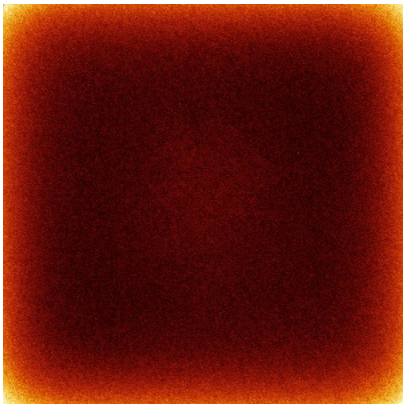

Y


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.

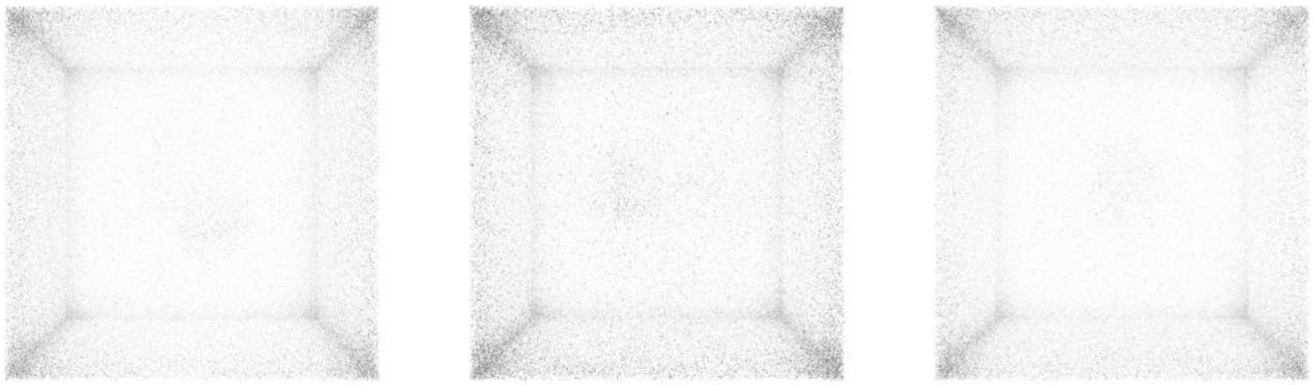
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.111. 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.

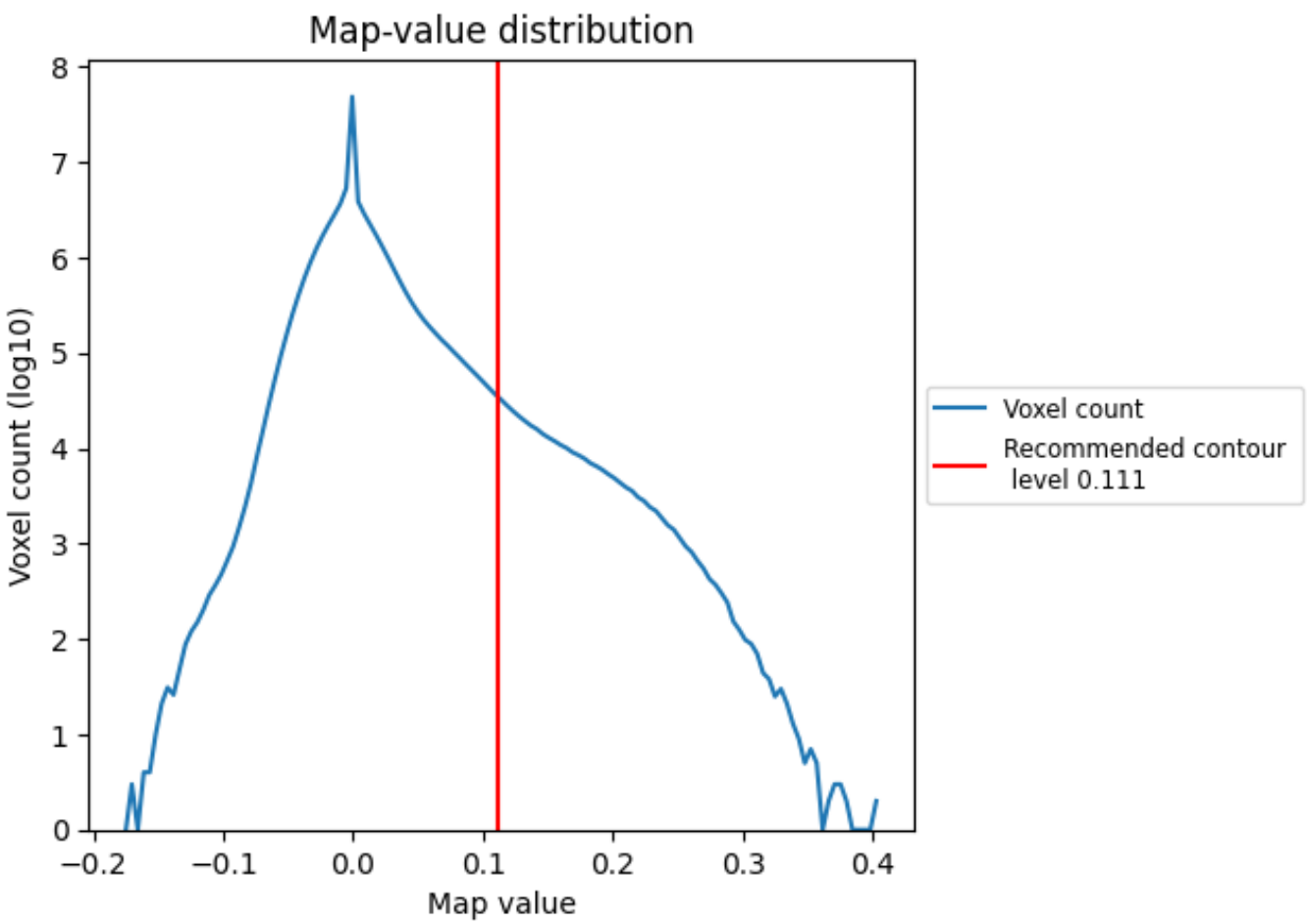
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

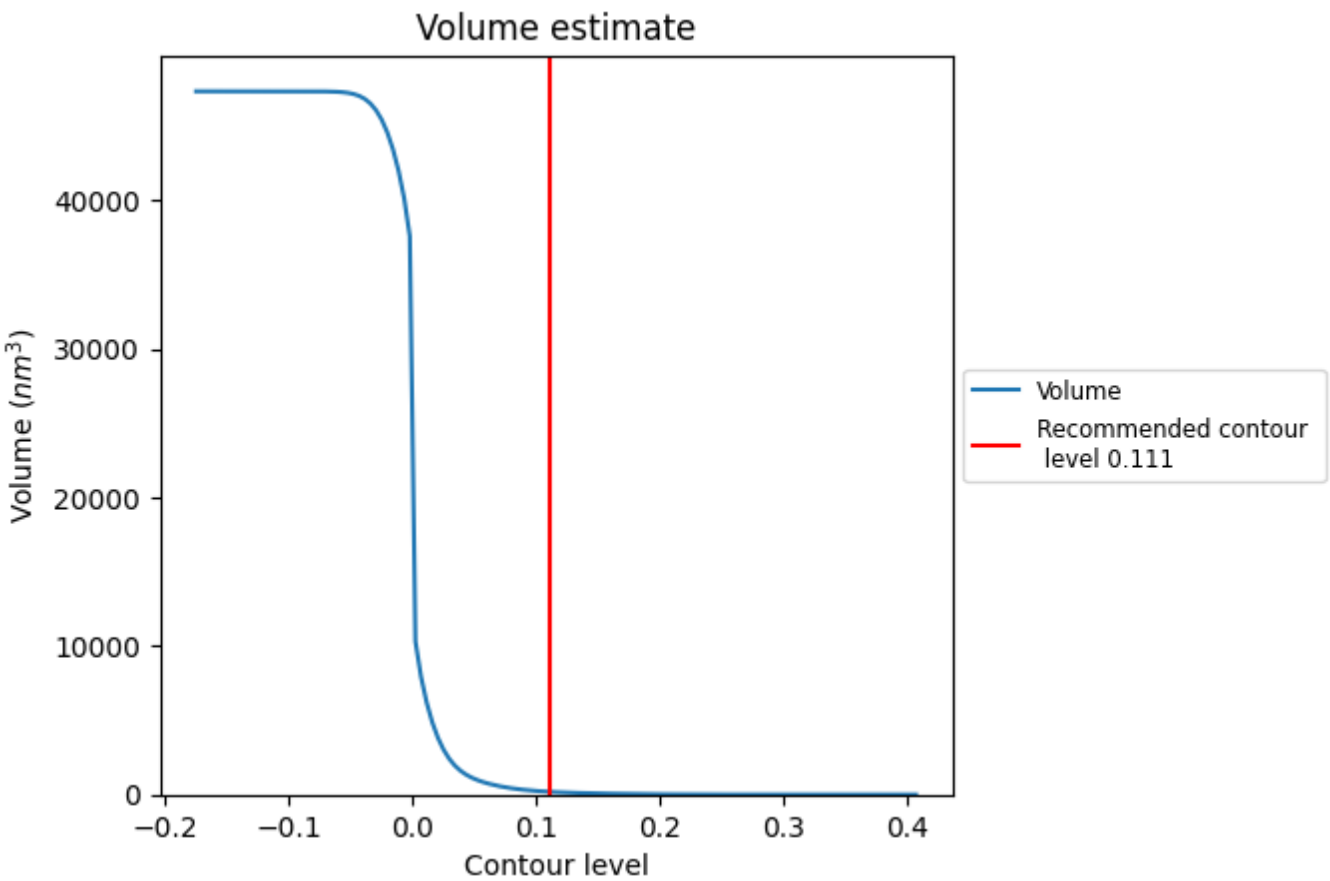
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

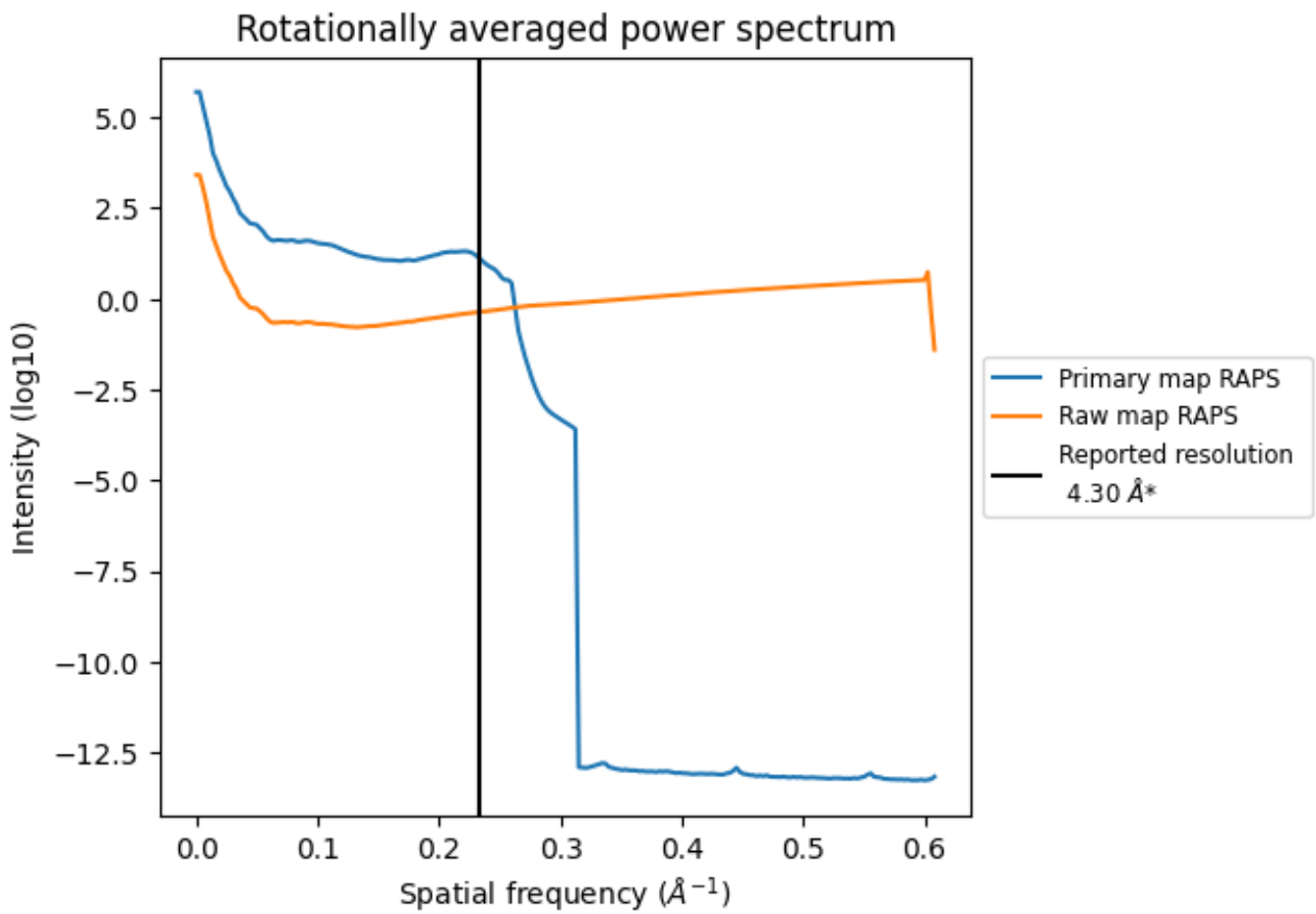
7.2 Volume estimate (i)



The volume at the recommended contour level is 184 nm^3; this corresponds to an approximate mass of 166 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

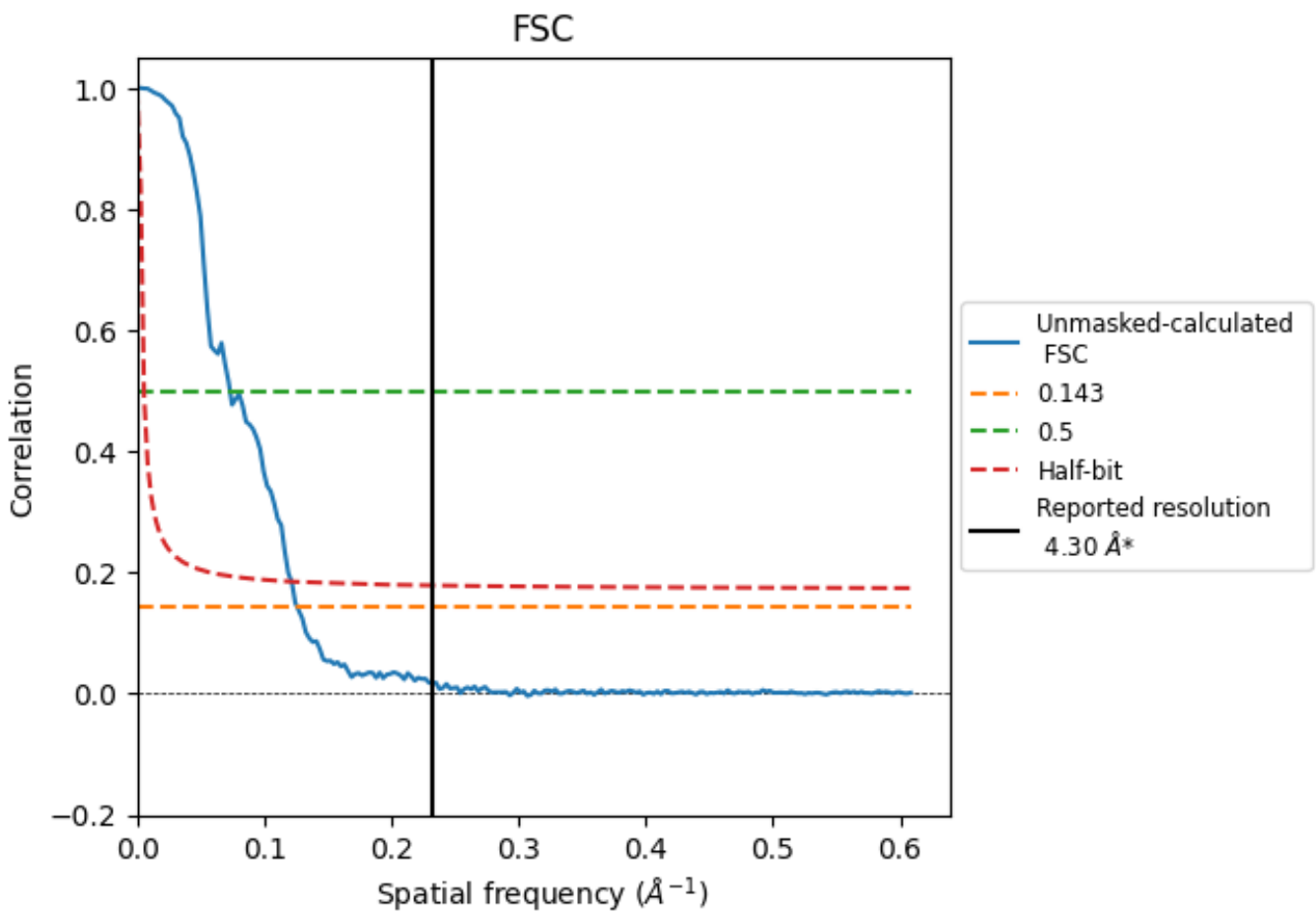


*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

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 0.233 Å^{-1}

8.2 Resolution estimates (i)

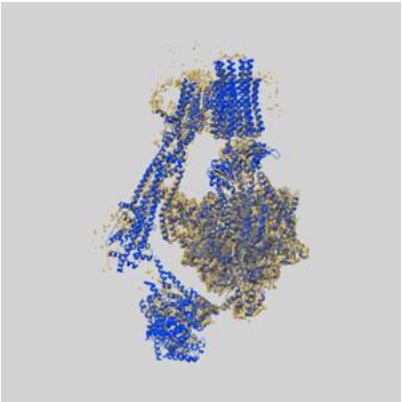
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.94	13.70	8.24

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

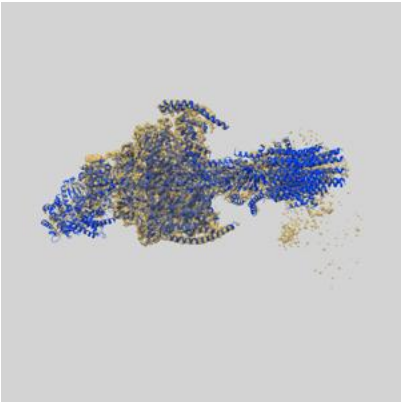
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-74153 and PDB model 9ZFT. Per-residue inclusion information can be found in section 3 on page 14.

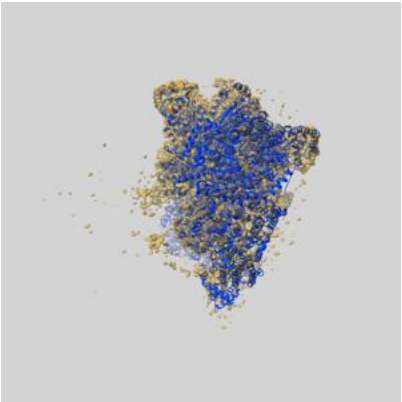
9.1 Map-model overlay (i)



X



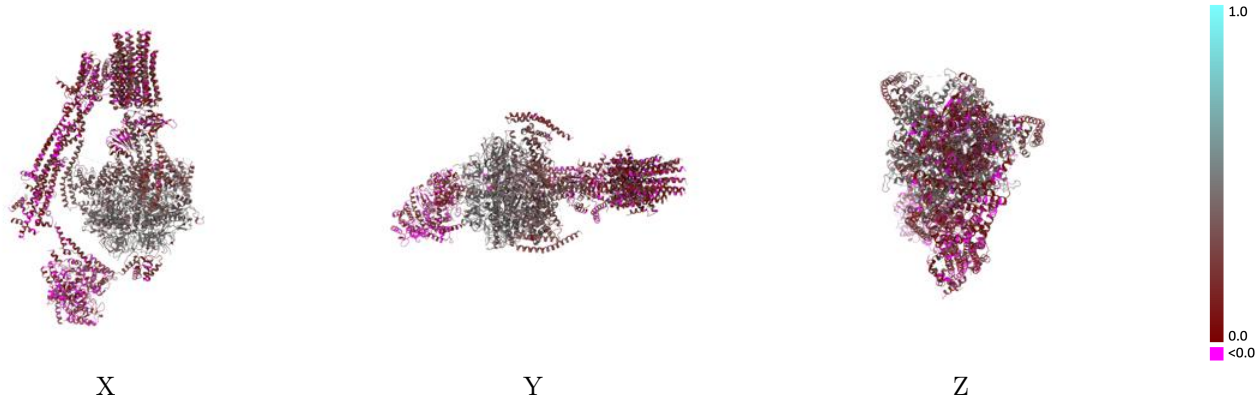
Y



Z

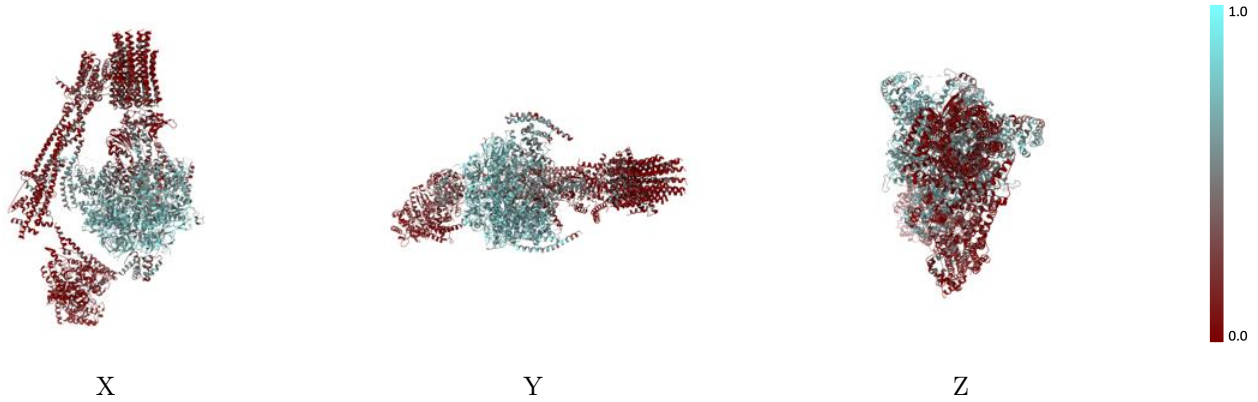
The images above show the 3D surface view of the map at the recommended contour level 0.111 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



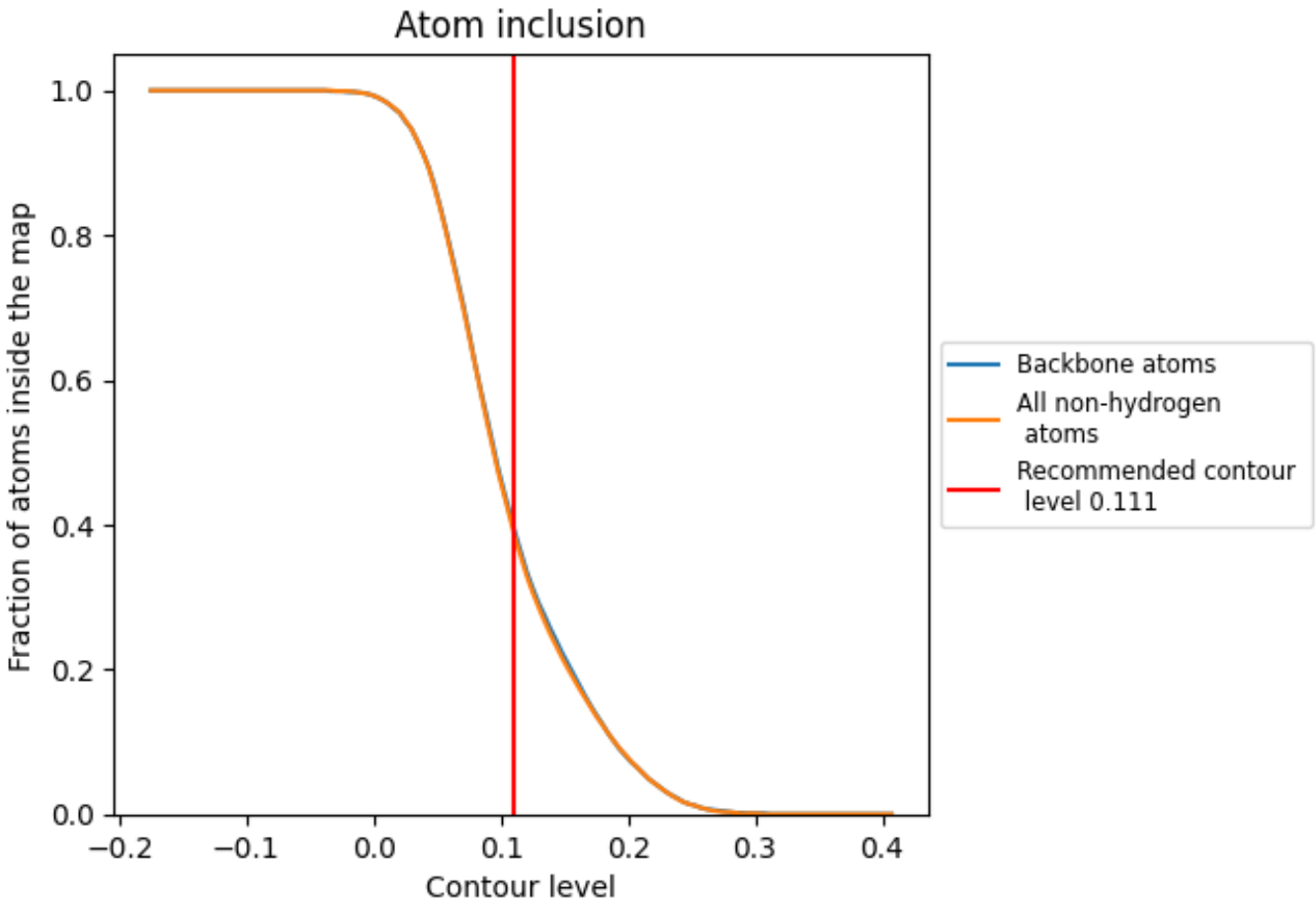
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.111).

9.4 Atom inclusion (i)



At the recommended contour level, 39% of all backbone atoms, 38% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.111) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3850	0.2680
1	0.0850	0.1440
2	0.2230	0.1850
3	0.0000	0.0490
5	0.0530	0.0970
6	0.1870	0.1500
8	0.1940	0.1280
A	0.3380	0.2500
B	0.2270	0.1450
C	0.1040	0.1310
D	0.1880	0.1130
E	0.1670	0.3070
G	0.3290	0.1730
H	0.1370	0.1530
I	0.0360	0.0480
J	0.1470	0.1280
K	0.1850	0.1310
L	0.0640	0.0720
M	0.0890	0.0780
P	0.1490	0.2150
Q	0.1630	0.1660
R	0.1490	0.1940
S	0.1340	0.1820
T	0.1750	0.2030
U	0.2220	0.2250
V	0.1720	0.1880
W	0.1290	0.1970
X	0.1270	0.1840
Z	0.0700	0.1160
a	0.6280	0.3940
b	0.6730	0.4210
c	0.6410	0.4030
d	0.5680	0.3750
e	0.6000	0.3780
f	0.6150	0.3900