wwPDB EM Validation Summary Report

Aug 23, 2026 – 05:49 pm BST

PDB ID	:	9H51 / pdb_00009h51
EMDB ID	:	EMD-51873
Title	:	Assembly intermediate of human mitochondrial ribosome small subunit in complex with PUS1, METTL15 and RBFA(IN conformation) (state M1)
Authors	:	Singh, V.; Shiriaev, D.; Khawaja, A.; Rorbach, J.
Deposited on	:	2024-10-22
Resolution	:	3.10 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:

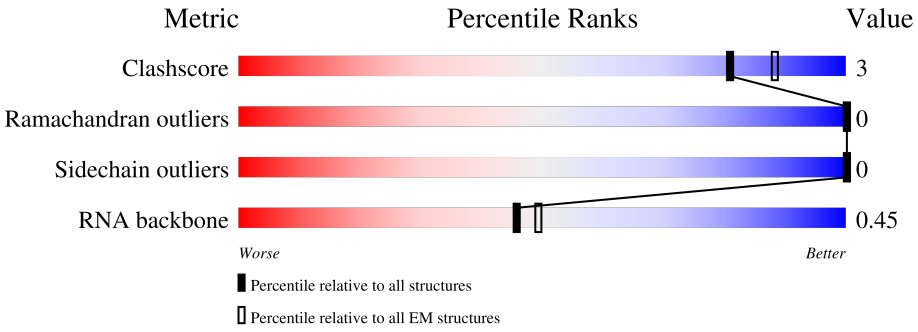
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.50

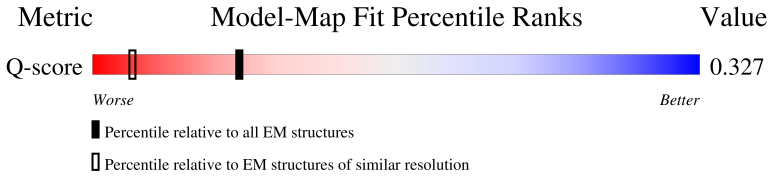
1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	c	384	74% 7% 19%
2	A	959	69% 24%
3	B	296	73% 24%

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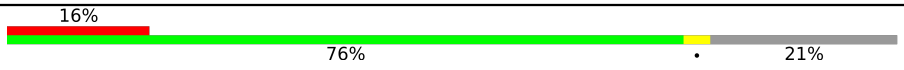
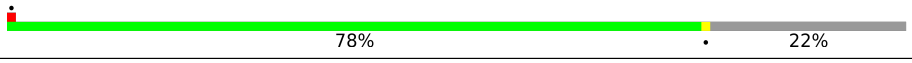
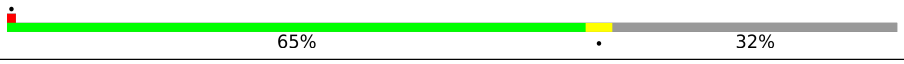
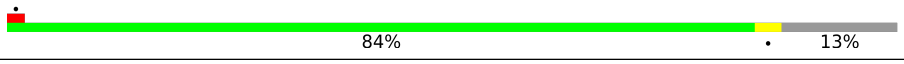
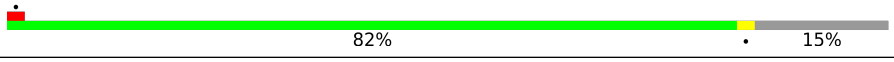
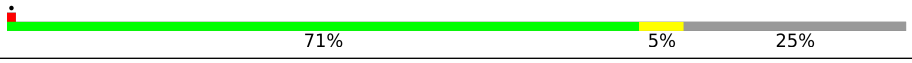
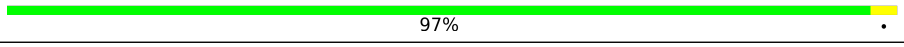
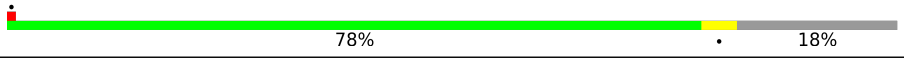
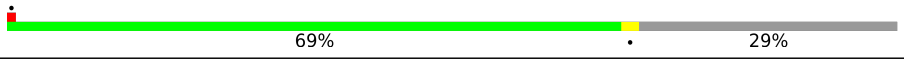
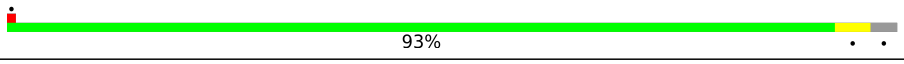
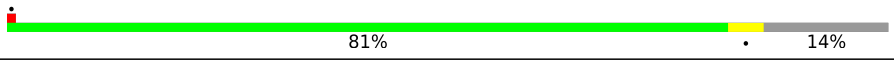
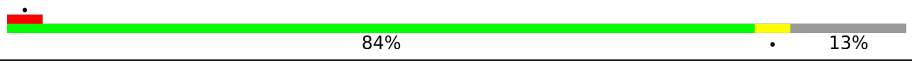
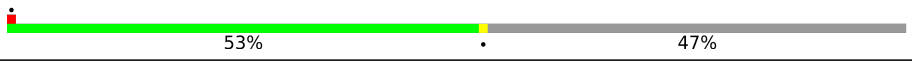
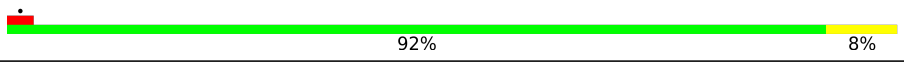
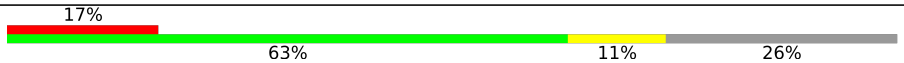
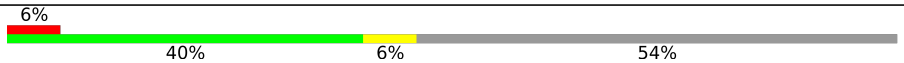
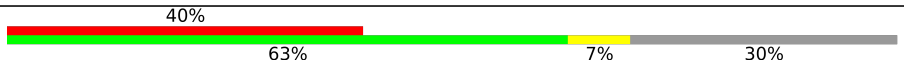
Mol	Chain	Length	Quality of chain
4	D	430	
5	E	125	
6	I	194	
7	J	138	
8	L	257	
9	M	137	
10	N	130	
11	O	258	
12	P	142	
13	Q	87	
14	R	360	
15	S	190	
16	T	173	
17	U	205	
18	V	414	
19	W	187	
20	0	215	
21	3	199	
22	b	407	
23	a	343	
24	4	689	
25	H	201	
26	1	323	
27	Z	106	
28	X	398	

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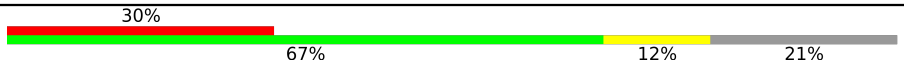
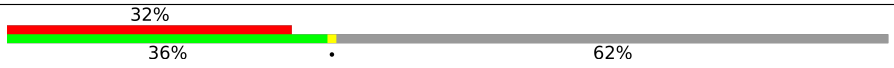
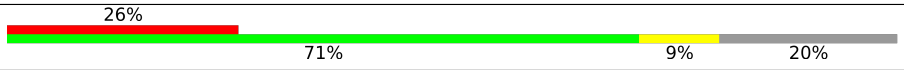
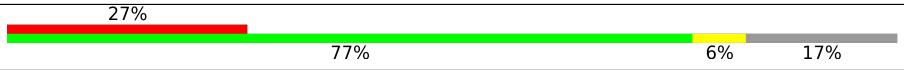
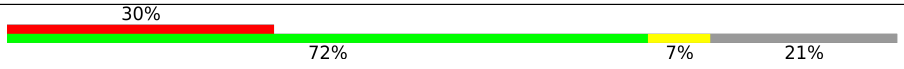
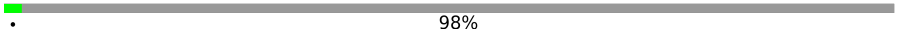
Mol	Chain	Length	Quality of chain
29	K	128	
30	Y	395	
31	G	396	
32	F	242	
33	C	167	
34	9	698	

2 Entry composition (i)

There are 44 unique types of molecules in this entry. The entry contains 134104 atoms, of which 62548 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 Pseudouridylate synthase 1 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	c	311	4988	1580	2493	448	451	16	0	0

- Molecule 2 is a RNA chain called RNA (969-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	A	925	29598	8810	9952	3535	6376	925	0	0

- Molecule 3 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	B	225	3653	1164	1825	331	323	10	0	0

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	341	5511	1704	2794	515	485	13	0	0

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	113	1806	563	914	162	163	4	0	0

- Molecule 6 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	I	137	2077	642	1057	192	182	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	184	5F0	ASN	variant	UNP P82912

- Molecule 7 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	J	108	Total	C	H	N	O	S	0	0
			1730	521	891	169	143	6		

- Molecule 8 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	L	174	Total	C	H	N	O	S	0	0
			2997	925	1544	270	251	7		

- Molecule 9 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	M	119	Total	C	H	N	O	S	0	0
			1913	594	971	185	157	6		

- Molecule 10 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	N	110	Total	C	H	N	O	S	0	0
			1800	562	932	156	147	3		

- Molecule 11 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	O	194	Total	C	H	N	O	S	0	0
			3173	1019	1574	295	278	7		

- Molecule 12 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	P	97	Total	C	H	N	O	S	0	0
			1589	501	808	134	138	8		

- Molecule 13 is a protein called Small ribosomal subunit protein bS21m.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	Q	87	Total	C	H	N	O	S	0	0
			1504	460	760	150	126	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	1	ACE	-	acetylation	UNP P82921
Q	50	ARG	CYS	variant	UNP P82921

- Molecule 14 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	R	295	Total	C	H	N	O	S	0	0
			4844	1533	2435	413	455	8		

- Molecule 15 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	S	135	Total	C	H	N	O	S	0	0
			2227	716	1116	198	196	1		

- Molecule 16 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	T	168	Total	C	H	N	O	S	0	0
			2767	877	1396	239	244	11		

- Molecule 17 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	U	176	Total	C	H	N	O	S	0	0
			2992	916	1504	301	267	4		

- Molecule 18 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	V	362	Total	C	H	N	O	S	0	0
			5939	1904	2970	495	558	12		

- Molecule 19 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	W	100	Total	C	H	N	O	S	0	0
			1594	498	805	141	146	4		

- Molecule 20 is a protein called Small ribosomal subunit protein mS34.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	0	215	Total	C	H	N	O	S	0	0
			3588	1130	1801	339	313	5		

- Molecule 21 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	3	70	Total	C	H	N	O	S	0	0
			1326	401	701	134	89	1		

- Molecule 22 is a protein called 12S rRNA N4-methylcytidine (m4C) methyltransferase.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	b	303	Total	C	H	N	O	S	0	0
			4796	1498	2433	421	431	13		

- Molecule 23 is a protein called Putative ribosome-binding factor A, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	a	157	Total	C	H	N	O	S	0	0
			2500	776	1252	224	242	6		

- Molecule 24 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	4	588	Total	C	H	N	O	S	0	0
			9550	3053	4782	808	879	28		

- Molecule 25 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	H	140	Total	C	H	N	O	S	0	0
			2342	745	1190	194	210	3		

- Molecule 26 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	1	276	Total	C	H	N	O	S	0	0
			4512	1419	2274	381	427	11		

- Molecule 27 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	Z	93	Total	C	H	N	O	S	0	0
			1593	504	805	141	139	4		

- Molecule 28 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	X	352	Total	C	H	N	O	S	0	0
			5707	1822	2858	499	517	11		

- Molecule 29 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	K	101	Total	C	H	N	O	S	0	0
			1750	537	888	179	141	5		

- Molecule 30 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Y	149	Total	C	H	N	O	S	0	0
			2448	801	1202	207	234	4		

- Molecule 31 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	G	316	Total	C	H	N	O	S	0	0
			5202	1652	2599	463	474	14		

- Molecule 32 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	F	202	Total	C	H	N	O	S	0	0
			3397	1066	1726	303	291	11		

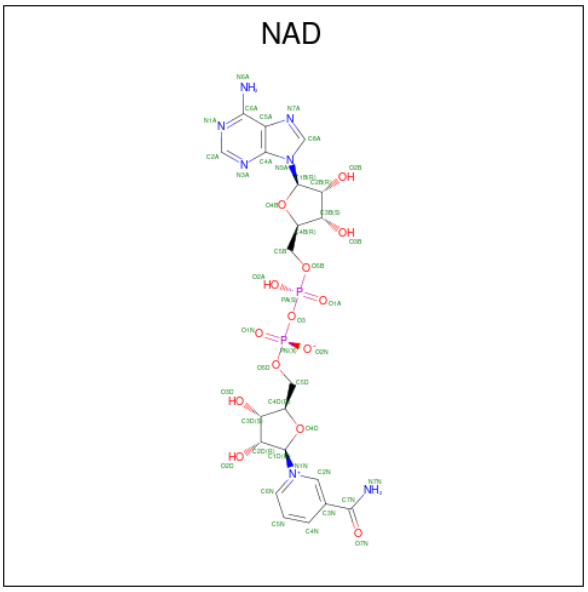
- Molecule 33 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	C	132	Total	C	H	N	O	S	0	0
			2178	699	1095	195	185	4		

- Molecule 34 is a protein called Nitric oxide-associated protein 1.

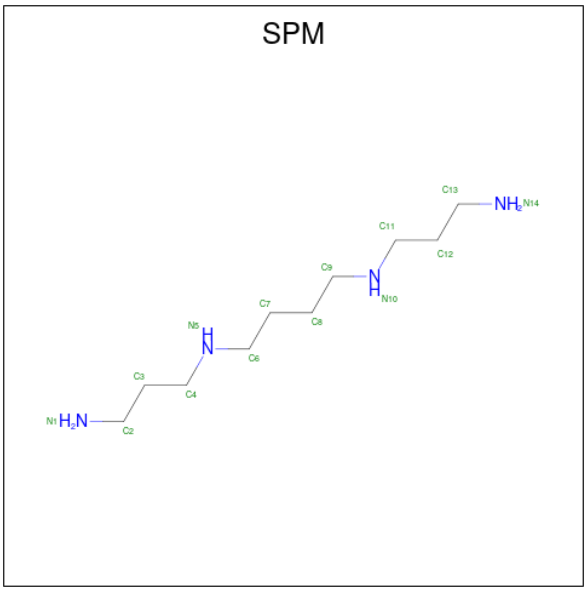
Mol	Chain	Residues	Atoms						AltConf	Trace
34	9	12	Total	C	H	N	O	S	0	0
			219	76	108	16	18	1		

- Molecule 35 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms						AltConf
35	A	1	Total	C	H	N	O	P	0
			70	21	26	7	14	2	

- Molecule 36 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms				AltConf
36	A	1	Total	C	H	N	0
			40	10	26	4	

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	A	38	Total	Mg	0
			38	38	
37	B	1	Total	Mg	0
			1	1	
37	3	1	Total	Mg	0
			1	1	

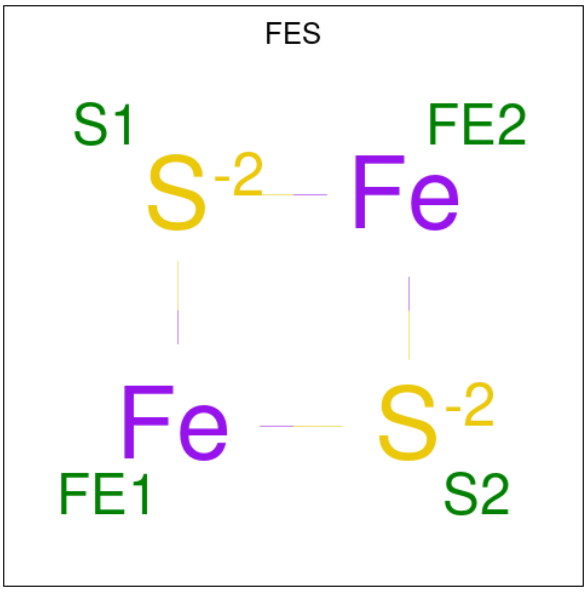
- Molecule 38 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
38	A	6	Total	K	0
			6	6	

- Molecule 39 is ZINC ION (CCD ID: ZN) (formula: Zn).

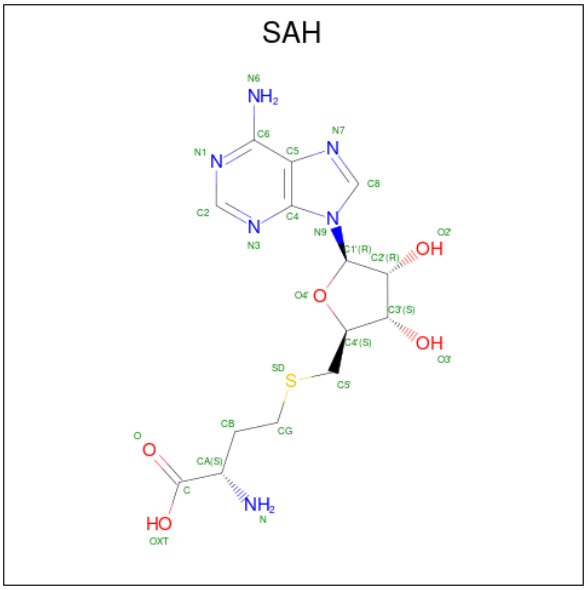
Mol	Chain	Residues	Atoms		AltConf
39	O	1	Total	Zn	0
			1	1	

- Molecule 40 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



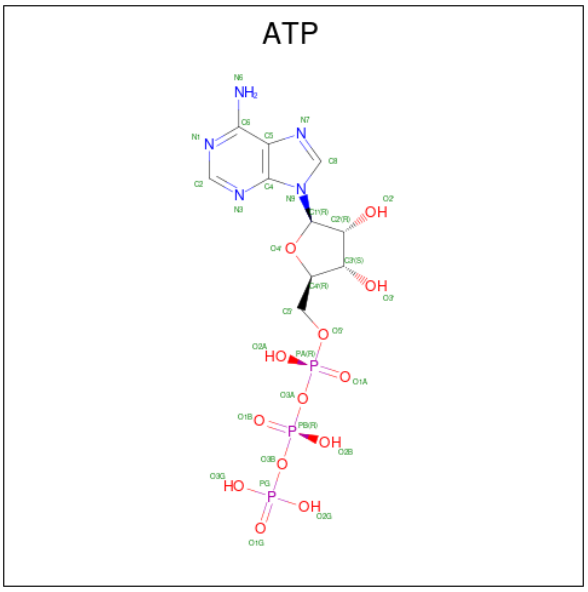
Mol	Chain	Residues	Atoms			AltConf
40	P	1	Total	Fe	S	0
			4	2	2	
40	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 41 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



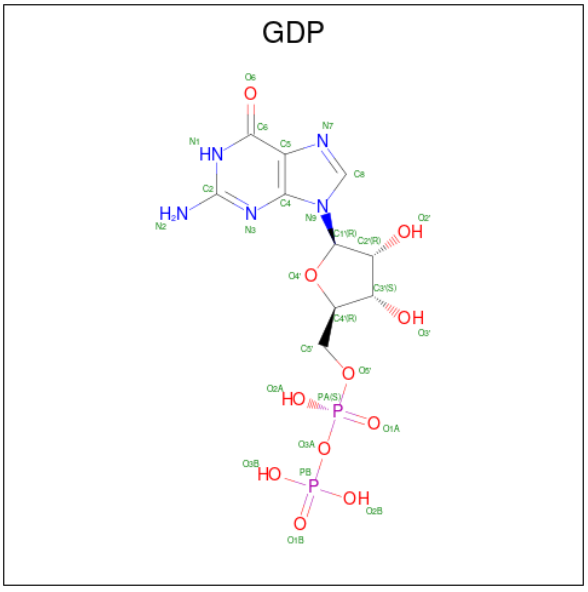
Mol	Chain	Residues	Atoms						AltConf
41	b	1	Total	C	H	N	O	S	0
			45	14	19	6	5	1	

- Molecule 42 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
42	X	1	43	10	12	5	13	3	0

- Molecule 43 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
43	X	1	38	10	10	5	11	2	0

- Molecule 44 is water.

Mol	Chain	Residues	Atoms	AltConf
44	A	1	Total O 1 1	0
44	I	1	Total O 1 1	0
44	0	1	Total O 1 1	0

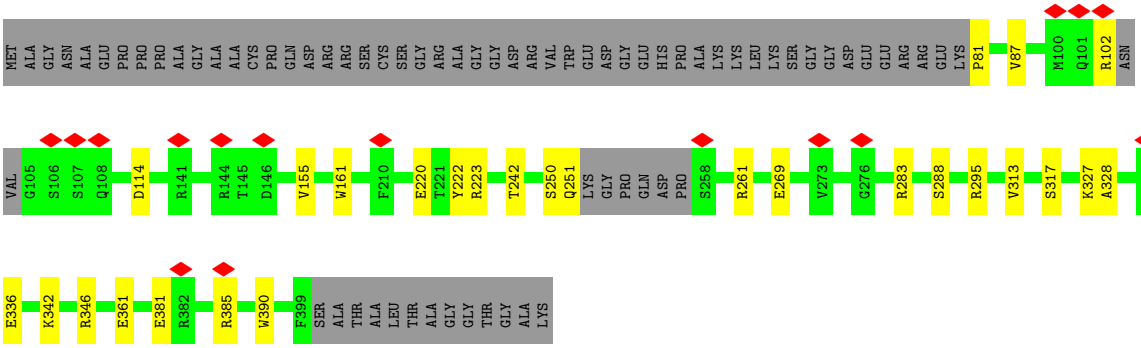
3 Residue-property plots (i)

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: Pseudouridylate synthase 1 homolog

Chain c:

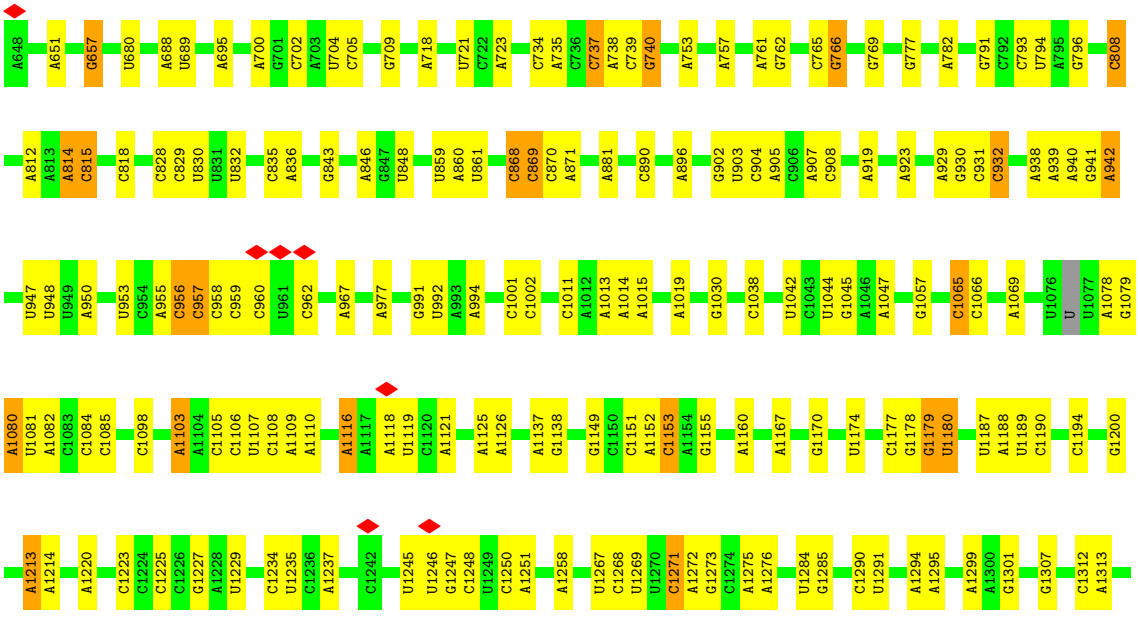


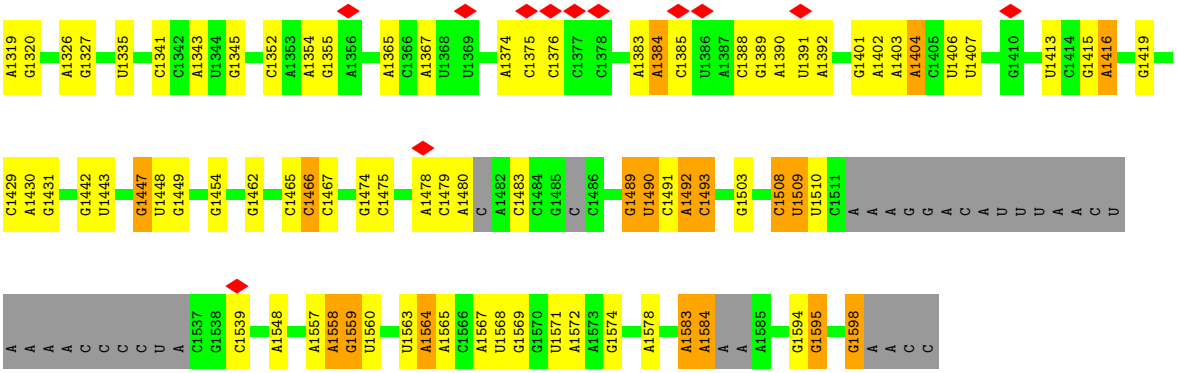


- Molecule 2: RNA (969-MER)

Chain A:



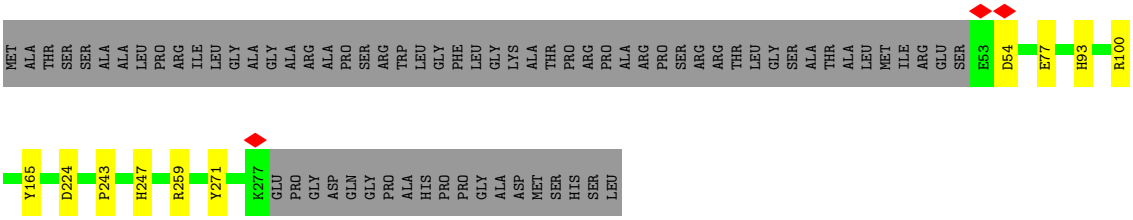




• Molecule 3: 28S ribosomal protein S2, mitochondrial

Chain B:

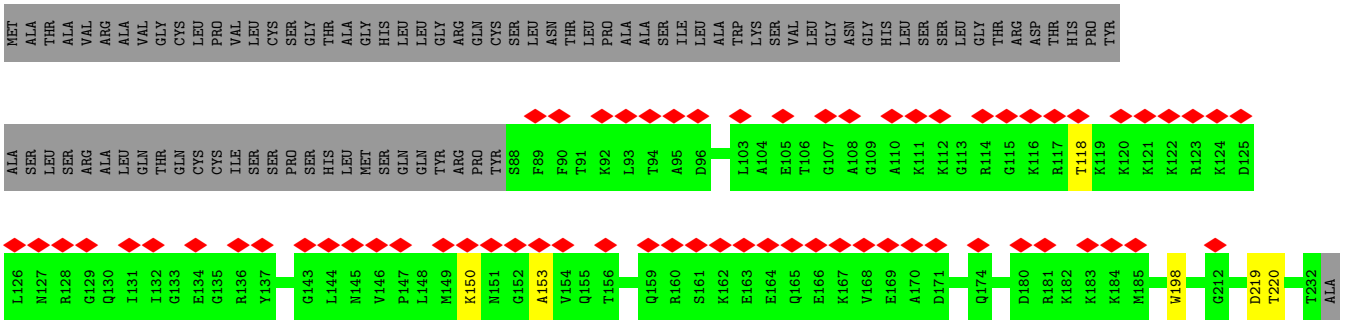




• Molecule 4: 28S ribosomal protein S5, mitochondrial

Chain D:

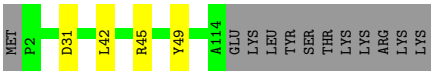




• Molecule 5: 28S ribosomal protein S6, mitochondrial

Chain E:

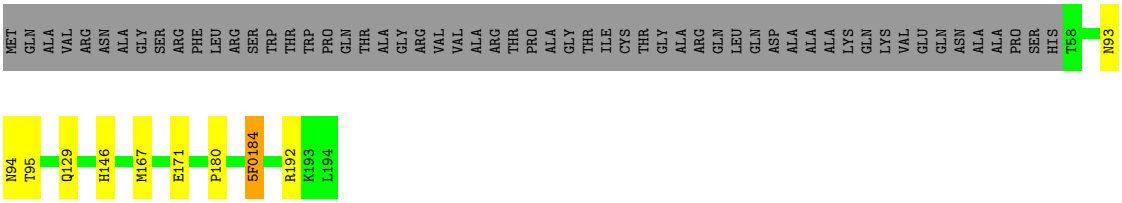




• Molecule 6: 28S ribosomal protein S11, mitochondrial

Chain I:

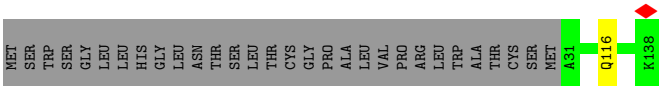




• Molecule 7: 28S ribosomal protein S12, mitochondrial

Chain J:

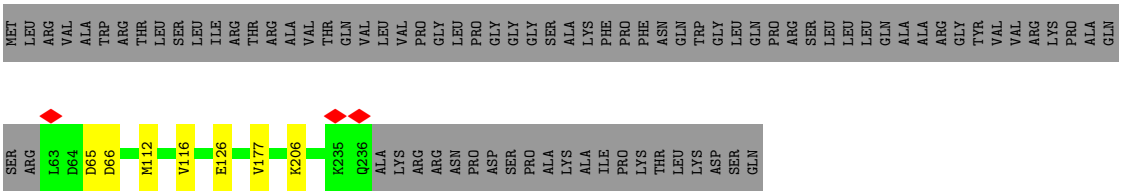




• Molecule 8: 28S ribosomal protein S15, mitochondrial

Chain L:

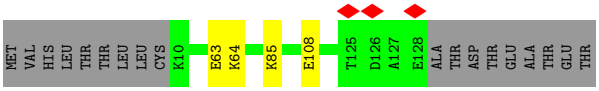




• Molecule 9: 28S ribosomal protein S16, mitochondrial

Chain M:





• Molecule 10: 28S ribosomal protein S17, mitochondrial

Chain N:

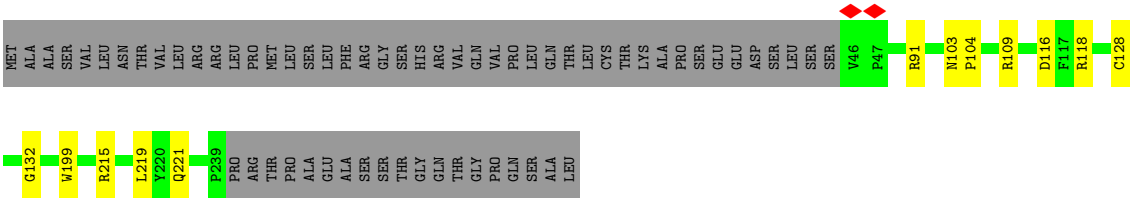




• Molecule 11: 28S ribosomal protein S18b, mitochondrial

Chain O:





• Molecule 12: 28S ribosomal protein S18c, mitochondrial

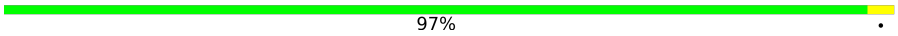
Chain P:

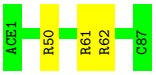




• Molecule 13: Small ribosomal subunit protein bS21m

Chain Q:

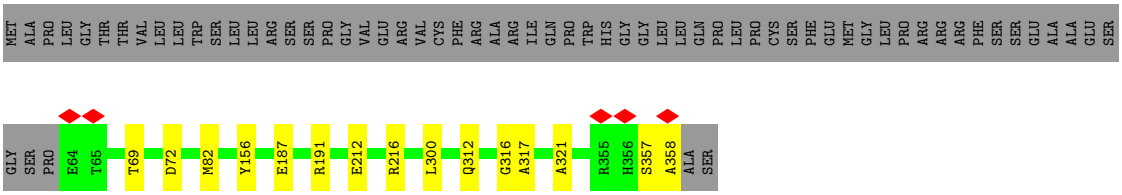




• Molecule 14: 28S ribosomal protein S22, mitochondrial

Chain R:

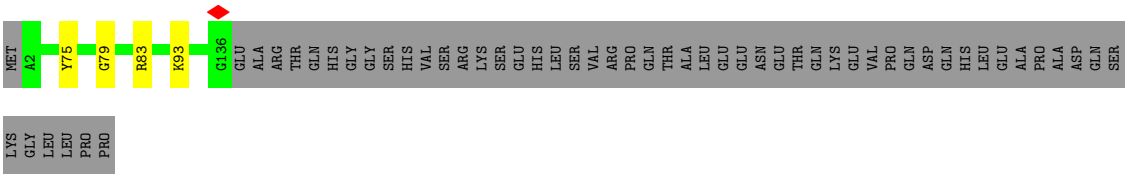




• Molecule 15: 28S ribosomal protein S23, mitochondrial

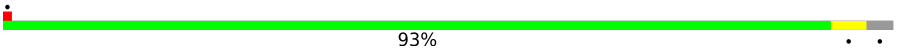
Chain S:

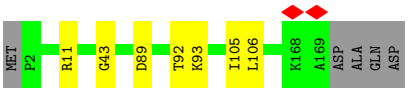




• Molecule 16: 28S ribosomal protein S25, mitochondrial

Chain T:

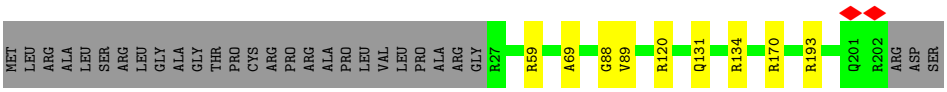




• Molecule 17: 28S ribosomal protein S26, mitochondrial

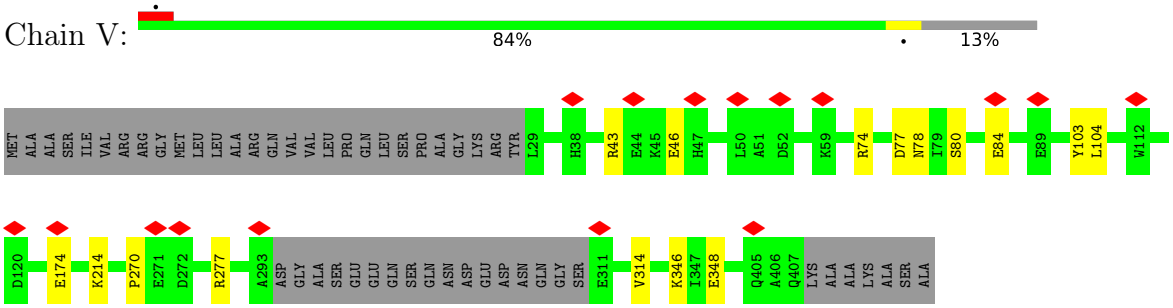
Chain U:





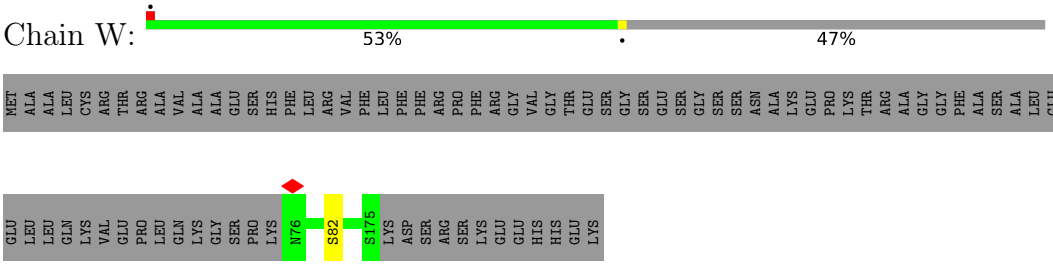
• Molecule 18: 28S ribosomal protein S27, mitochondrial

Chain V:



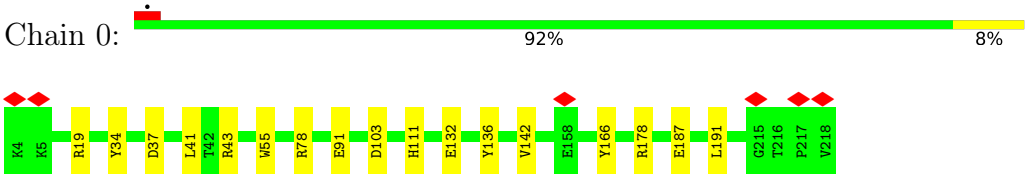
• Molecule 19: 28S ribosomal protein S28, mitochondrial

Chain W:



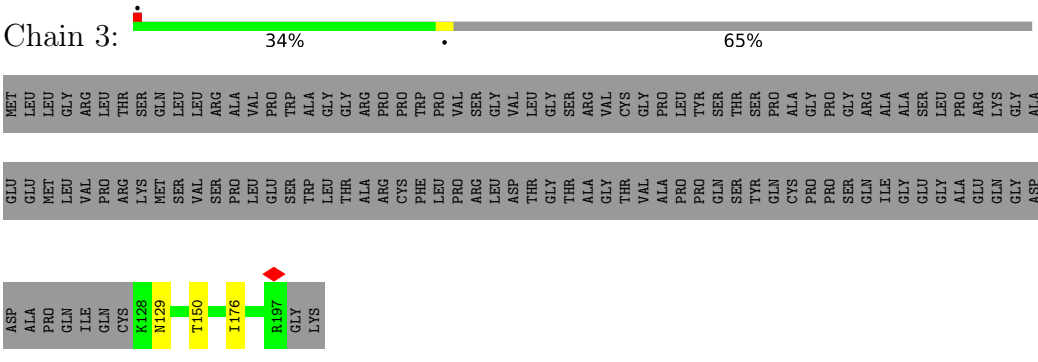
• Molecule 20: Small ribosomal subunit protein mS34

Chain 0:



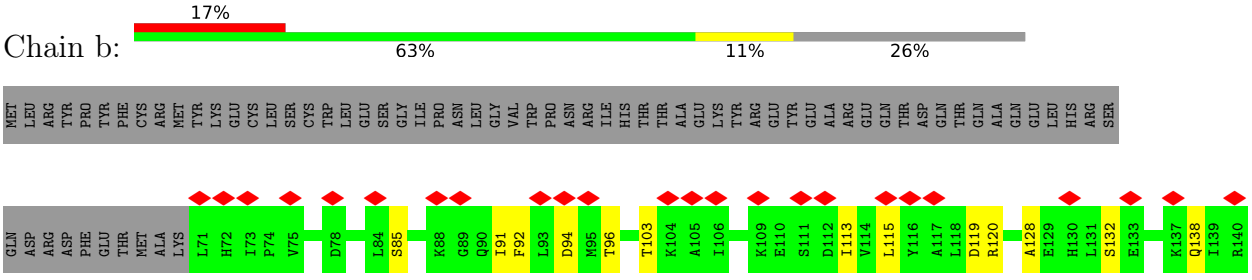
• Molecule 21: Aurora kinase A-interacting protein

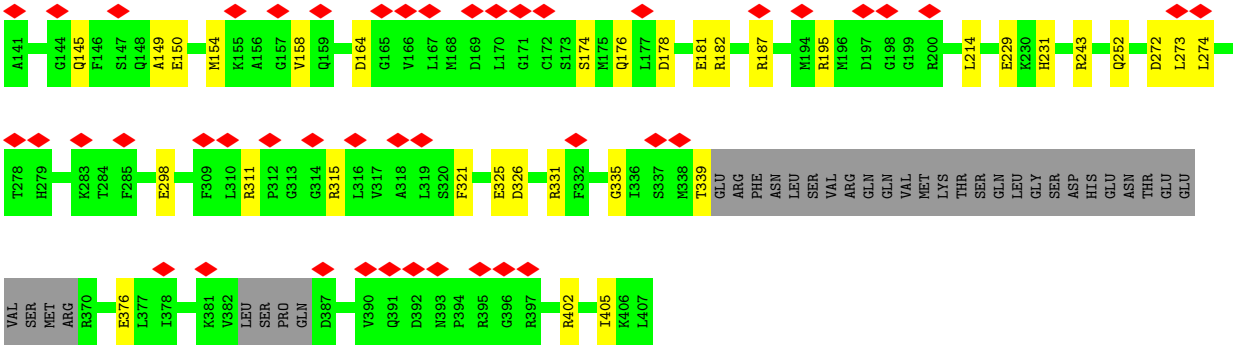
Chain 3:



• Molecule 22: 12S rRNA N4-methylcytidine (m4C) methyltransferase

Chain b:

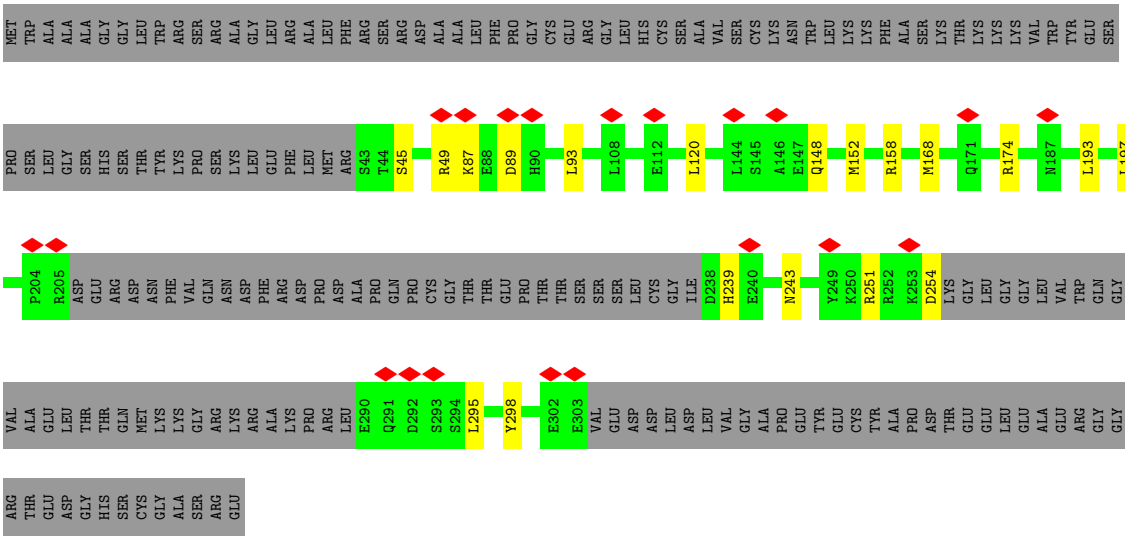




• Molecule 23: Putative ribosome-binding factor A, mitochondrial

Chain a:

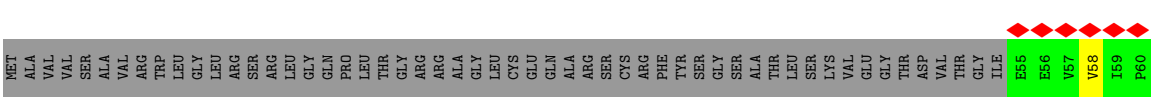


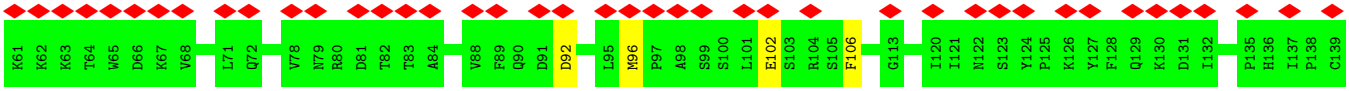


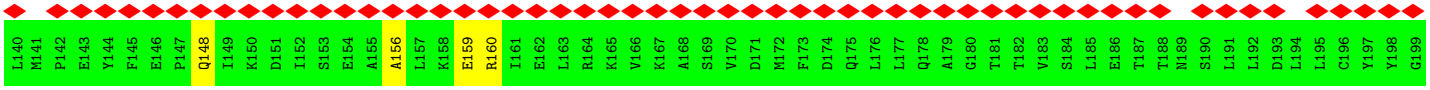
• Molecule 24: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

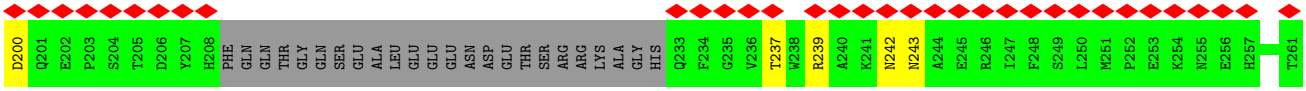
Chain 4:

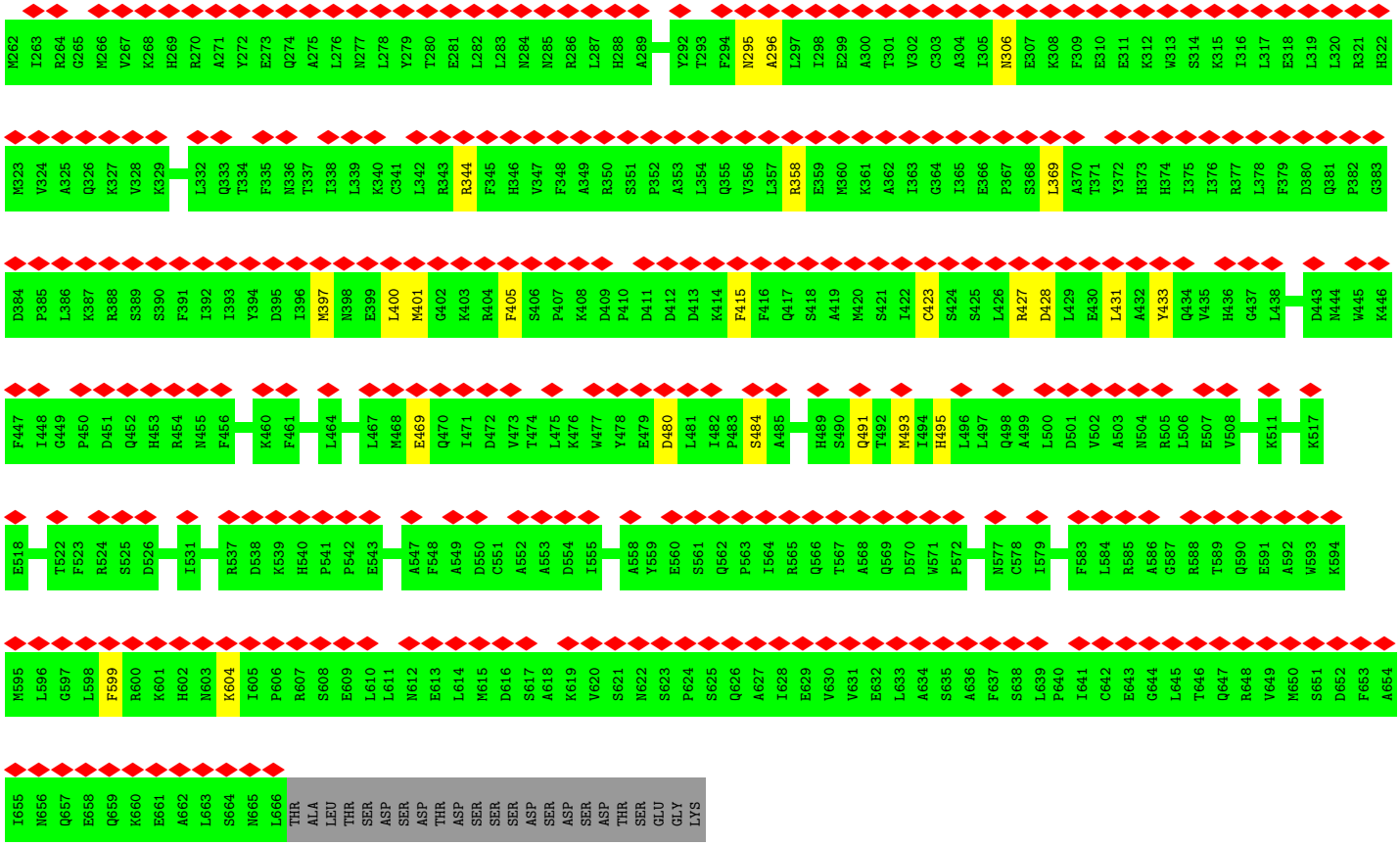








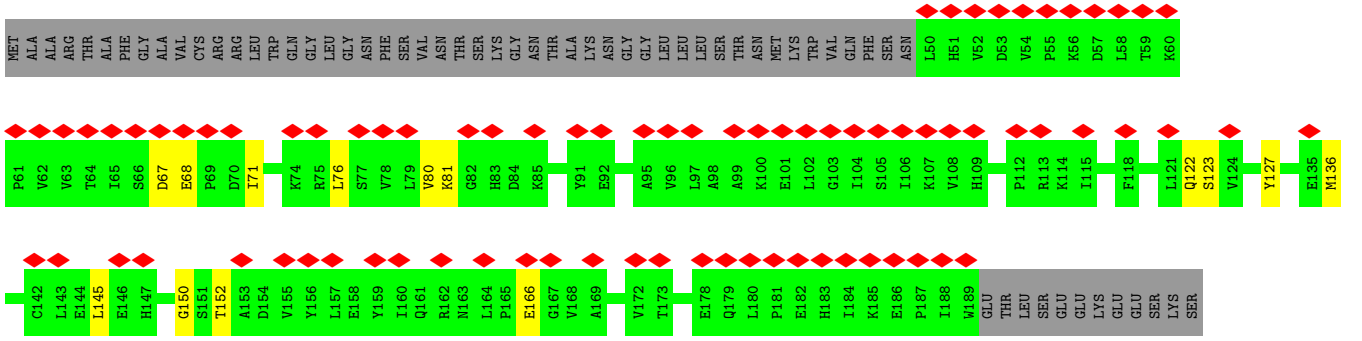




• Molecule 25: 28S ribosomal protein S10, mitochondrial

Chain H:

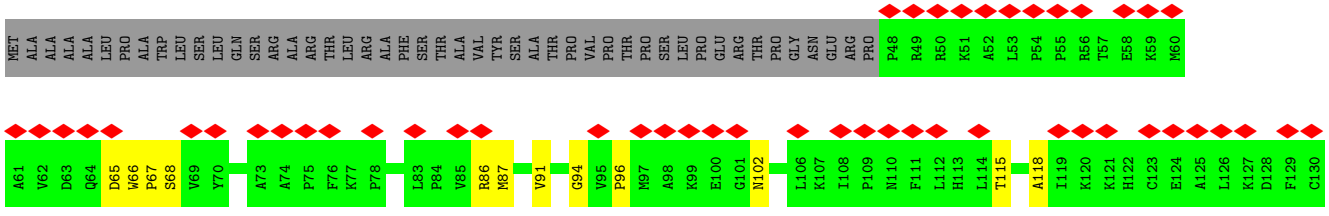


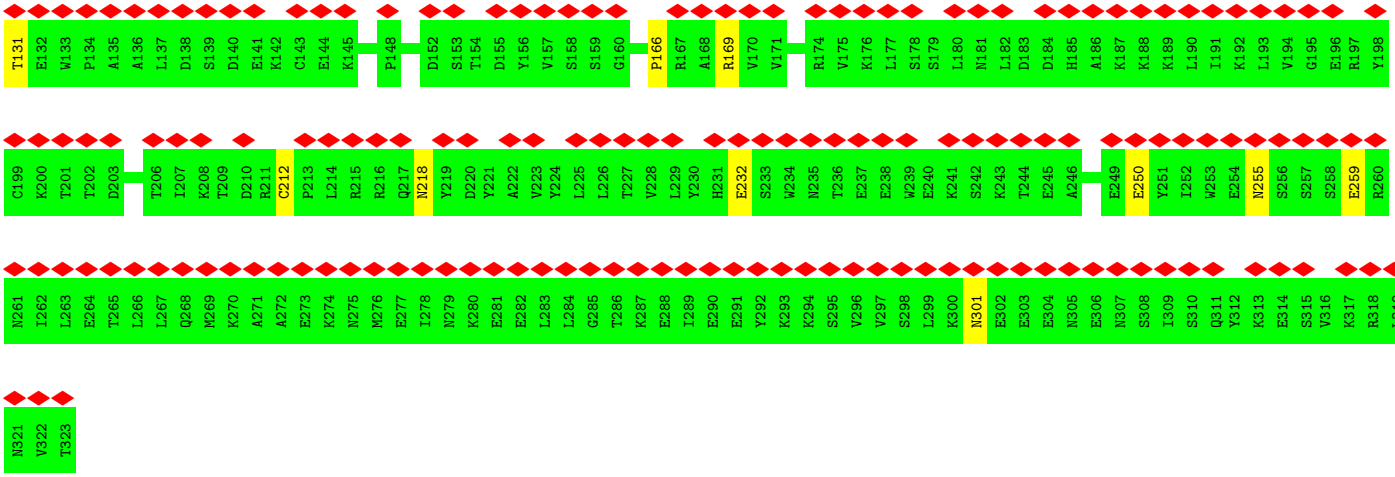


• Molecule 26: 28S ribosomal protein S35, mitochondrial

Chain 1:



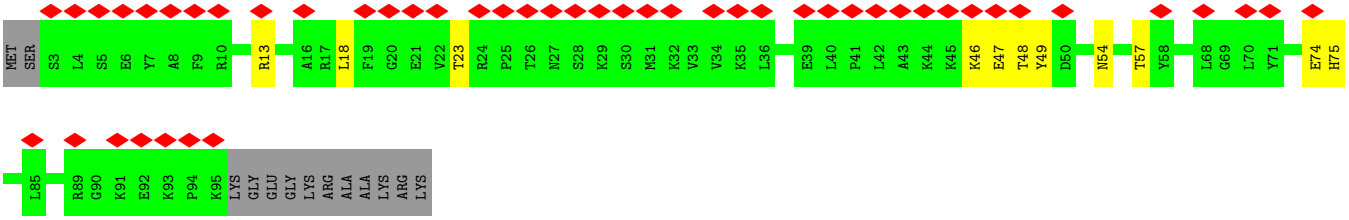




• Molecule 27: 28S ribosomal protein S33, mitochondrial

Chain Z:

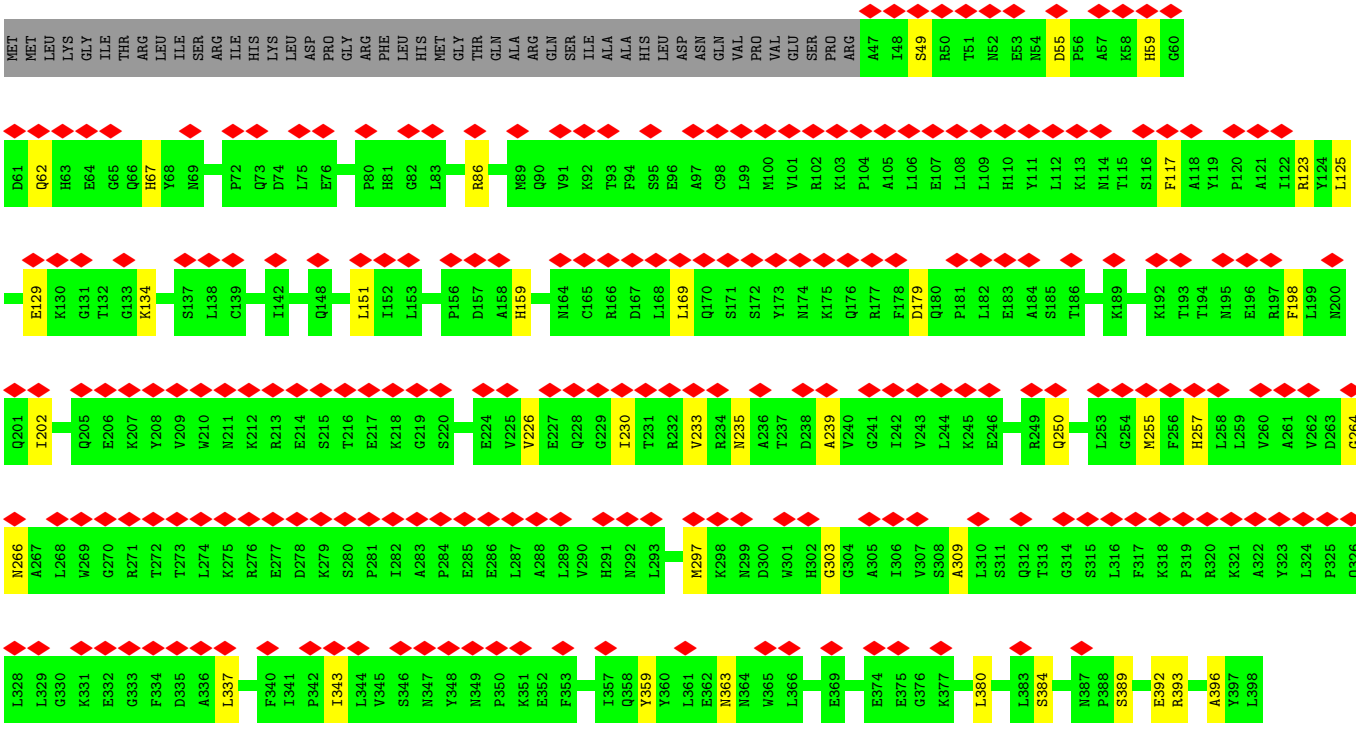




• Molecule 28: 28S ribosomal protein S29, mitochondrial

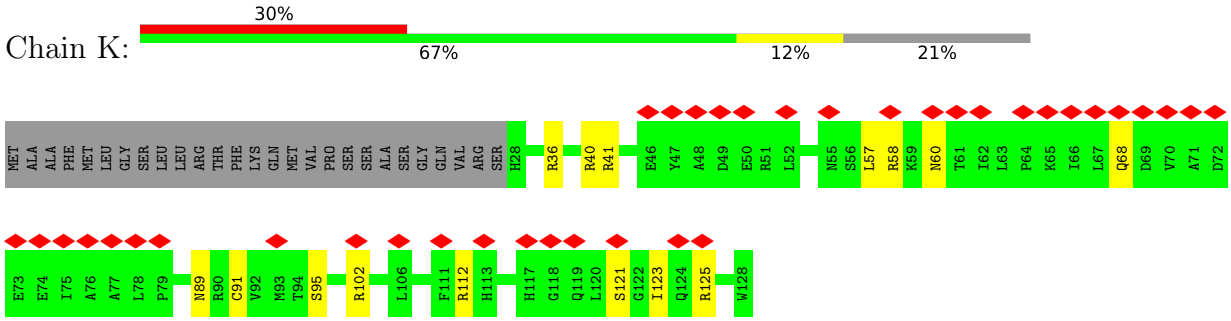
Chain X:





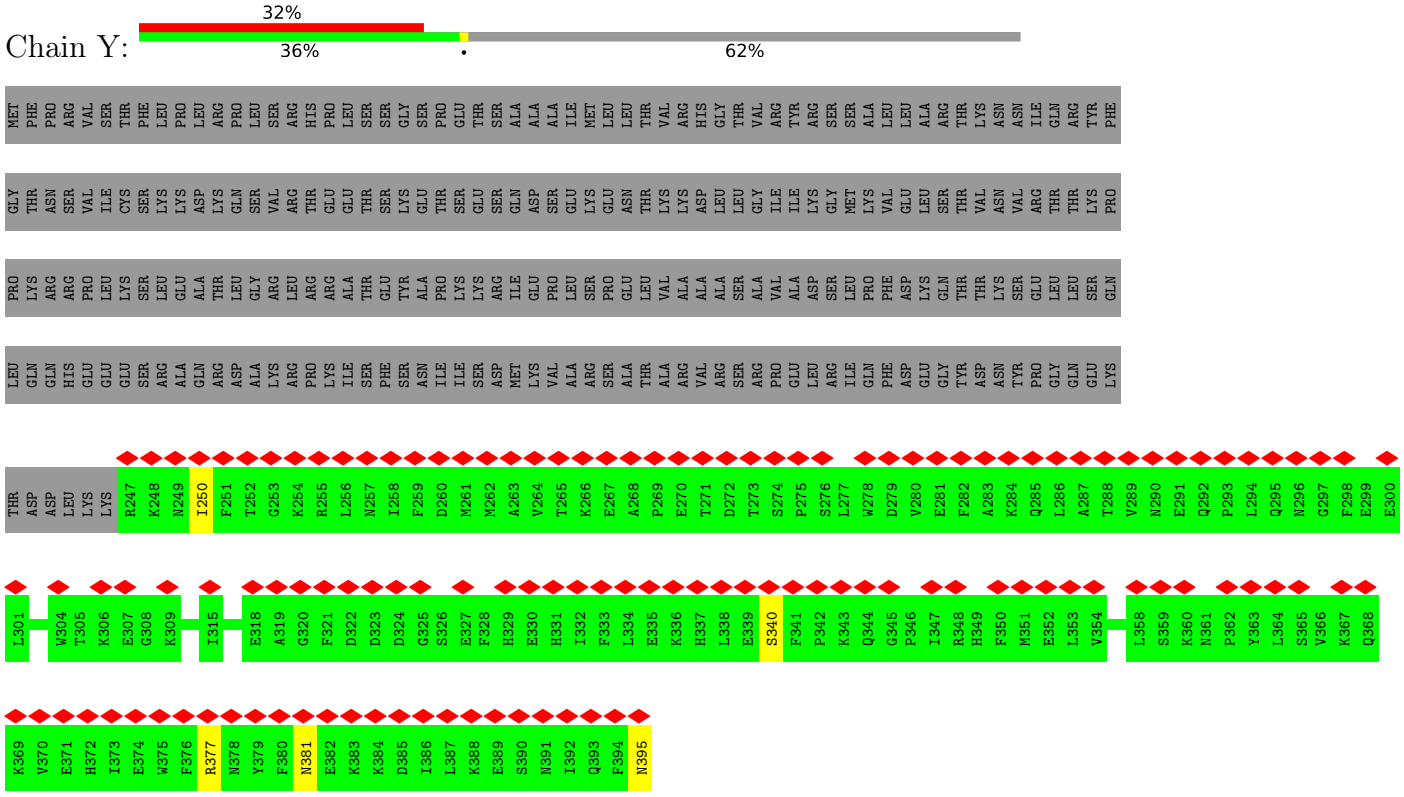
• Molecule 29: 28S ribosomal protein S14, mitochondrial

Chain K:



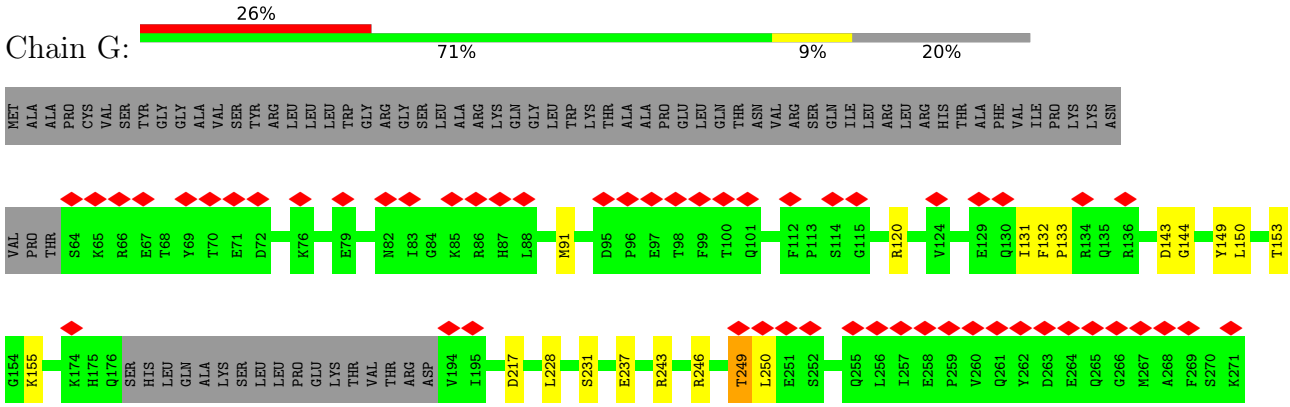
• Molecule 30: 28S ribosomal protein S31, mitochondrial

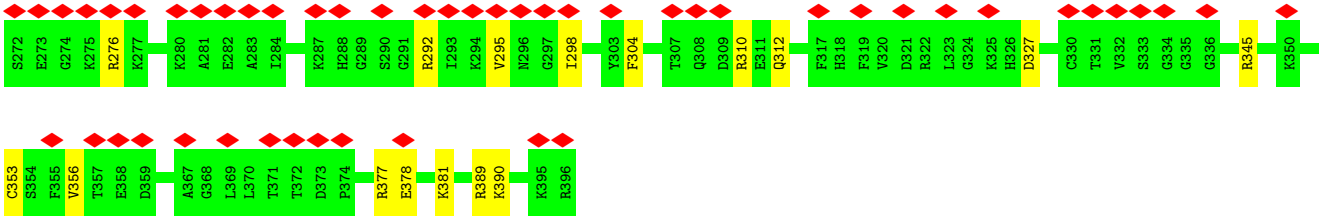
Chain Y:



• Molecule 31: 28S ribosomal protein S9, mitochondrial

Chain G:

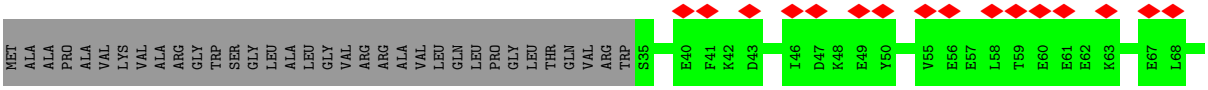


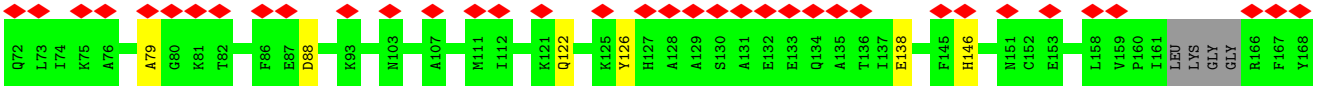


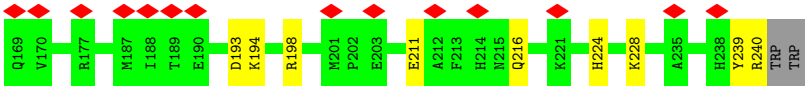
• Molecule 32: 28S ribosomal protein S7, mitochondrial

Chain F:





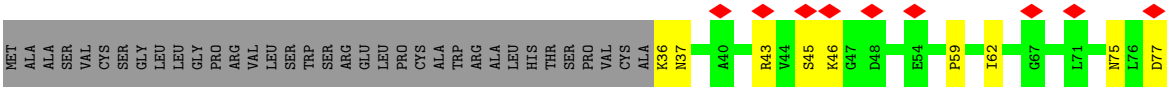


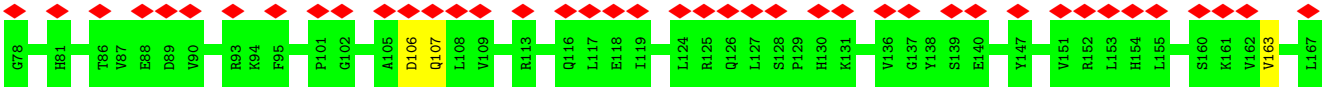


• Molecule 33: 28S ribosomal protein S24, mitochondrial

Chain C:

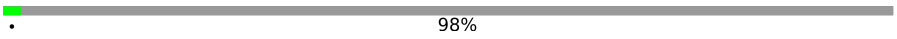


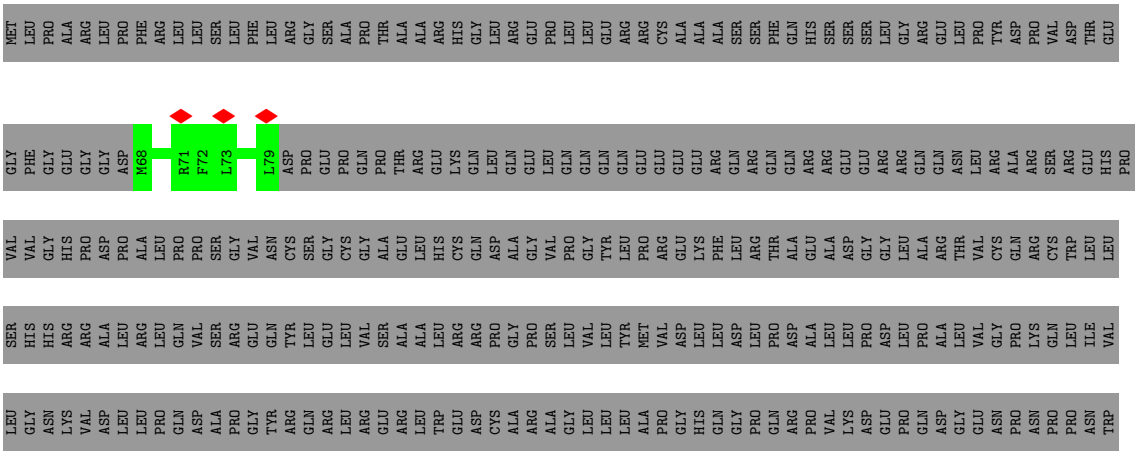




• Molecule 34: Nitric oxide-associated protein 1

Chain 9:





SER ARG THR VAL VAL ARG ASP VAL ARG LEU ILE SER ALA LYS THR GLY TYR GLY VAL GLU GLU LEU ILE SER ALA LEU GLN ARG SER TRP ARG TYR ARG GLY ASP VAL TYR LEU VAL GLY ALA THR ASN ALA GLY LYS SER THR LEU PHE ASN THR LEU LEU GLU SER ASP TYR CYS THR

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

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

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

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

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

ILE LYS GLY GLN ARG ILE LYS LYS SER VAL ALA TYR LYS THR LYS LYS PRO PRO SER LEU MET TYR ASN VAL ARG LYS LYS LYS GLY LYS ILE ASN VAL

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16442	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	45	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.523	Depositor
Minimum map value	-0.582	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.24	Depositor
Map size (Å)	609.12, 609.12, 609.12	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0152, 1.0152, 1.0152	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, SPM, SAH, 5F0, K, ZN, ATP, MG, 5MU, NAD, MA6, FES, ACE

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	c	0.09	0/2549	0.23	0/3431
2	A	0.19	0/21895	0.25	0/34084
3	B	0.16	0/1871	0.26	0/2531
4	D	0.15	0/2768	0.24	0/3703
5	E	0.14	0/908	0.24	0/1229
6	I	0.12	0/1030	0.23	0/1386
7	J	0.16	0/855	0.29	0/1148
8	L	0.16	0/1477	0.27	0/1974
9	M	0.18	0/963	0.29	0/1295
10	N	0.17	0/886	0.30	0/1199
11	O	0.15	0/1655	0.25	0/2254
12	P	0.16	0/798	0.27	0/1070
13	Q	0.18	0/754	0.28	0/1003
14	R	0.14	0/2456	0.25	0/3317
15	S	0.13	0/1138	0.22	0/1533
16	T	0.16	0/1402	0.27	0/1883
17	U	0.12	0/1510	0.22	0/2025
18	V	0.08	0/3030	0.21	0/4093
19	W	0.13	0/801	0.23	0/1079
20	0	0.11	0/1834	0.27	0/2484
21	3	0.14	0/636	0.26	0/839
22	b	0.08	0/2404	0.24	0/3241
23	a	0.10	0/1264	0.24	0/1700
24	4	0.08	0/4877	0.22	0/6598
25	H	0.08	0/1178	0.25	0/1598
26	1	0.08	0/2285	0.22	0/3090
27	Z	0.07	0/806	0.20	0/1076
28	X	0.08	0/2921	0.24	0/3954
29	K	0.07	0/880	0.19	0/1182
30	Y	0.07	0/1280	0.20	0/1725
31	G	0.10	0/2658	0.28	2/3560 (0.1%)
32	F	0.08	0/1708	0.22	0/2292

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	C	0.07	0/1113	0.22	0/1505
34	9	0.09	0/114	0.28	0/152
All	All	0.14	0/74704	0.24	2/105233 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	I	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
31	G	249	THR	CA-C-N	5.57	131.73	121.70
31	G	249	THR	C-N-CA	5.57	131.73	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	I	184	5F0	Mainchain

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	c	2495	2493	2481	20	0
2	A	19646	9952	9985	88	0
3	B	1828	1825	1815	6	0
4	D	2717	2794	2785	8	0
5	E	892	914	910	3	0
6	I	1020	1057	1053	7	0
7	J	839	891	887	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	L	1453	1544	1540	6	0
9	M	942	971	965	4	0
10	N	868	932	928	2	0
11	O	1599	1574	1565	7	0
12	P	781	808	806	3	0
13	Q	744	760	758	3	0
14	R	2409	2435	2428	9	0
15	S	1111	1116	1115	2	0
16	T	1371	1396	1393	5	0
17	U	1488	1504	1499	8	0
18	V	2969	2970	2961	9	0
19	W	789	805	802	1	0
20	0	1787	1801	1796	13	0
21	3	625	701	699	4	0
22	b	2363	2433	2425	30	0
23	a	1248	1252	1247	13	0
24	4	4768	4782	4766	22	0
25	H	1152	1190	1183	10	0
26	1	2238	2274	2269	13	0
27	Z	788	805	802	8	0
28	X	2849	2858	2844	23	0
29	K	862	888	885	14	0
30	Y	1246	1202	1197	3	0
31	G	2603	2599	2591	22	0
32	F	1671	1726	1718	9	0
33	C	1083	1095	1088	9	0
34	9	111	108	108	0	0
35	A	44	26	26	0	0
36	A	14	26	26	0	0
37	3	1	0	0	0	0
37	A	38	0	0	0	0
37	B	1	0	0	0	0
38	A	6	0	0	0	0
39	O	1	0	0	0	0
40	P	4	0	0	0	0
40	T	4	0	0	0	0
41	b	26	19	19	3	0
42	X	31	12	12	0	0
43	X	28	10	12	0	0
44	0	1	0	0	1	0
44	A	1	0	0	0	0
44	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	71556	62548	62389	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 3.

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)
2:A:942:A:N6	2:A:1047:A:OP2	2.11	0.82
9:M:63:GLU:OE2	14:R:191:ARG:NH2	2.14	0.80
2:A:1085:C:OP1	6:I:192:ARG:NH1	2.17	0.77
27:Z:47:GLU:OE1	29:K:102:ARG:NH2	2.19	0.75
22:b:298:GLU:OE1	41:b:501:SAH:N6	2.21	0.74

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	c	305/384 (79%)	297 (97%)	8 (3%)	0	100	100
3	B	223/296 (75%)	221 (99%)	2 (1%)	0	100	100
4	D	337/430 (78%)	335 (99%)	2 (1%)	0	100	100
5	E	111/125 (89%)	108 (97%)	3 (3%)	0	100	100
6	I	134/194 (69%)	132 (98%)	2 (2%)	0	100	100
7	J	106/138 (77%)	100 (94%)	6 (6%)	0	100	100
8	L	172/257 (67%)	171 (99%)	1 (1%)	0	100	100
9	M	117/137 (85%)	114 (97%)	3 (3%)	0	100	100
10	N	108/130 (83%)	106 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	O	192/258 (74%)	188 (98%)	4 (2%)	0	100	100
12	P	95/142 (67%)	94 (99%)	1 (1%)	0	100	100
13	Q	85/87 (98%)	82 (96%)	3 (4%)	0	100	100
14	R	293/360 (81%)	290 (99%)	3 (1%)	0	100	100
15	S	133/190 (70%)	130 (98%)	3 (2%)	0	100	100
16	T	166/173 (96%)	165 (99%)	1 (1%)	0	100	100
17	U	174/205 (85%)	173 (99%)	1 (1%)	0	100	100
18	V	358/414 (86%)	356 (99%)	2 (1%)	0	100	100
19	W	98/187 (52%)	97 (99%)	1 (1%)	0	100	100
20	0	213/215 (99%)	207 (97%)	6 (3%)	0	100	100
21	3	68/199 (34%)	68 (100%)	0	0	100	100
22	b	297/407 (73%)	289 (97%)	8 (3%)	0	100	100
23	a	149/343 (43%)	146 (98%)	3 (2%)	0	100	100
24	4	584/689 (85%)	573 (98%)	11 (2%)	0	100	100
25	H	138/201 (69%)	135 (98%)	3 (2%)	0	100	100
26	1	274/323 (85%)	268 (98%)	6 (2%)	0	100	100
27	Z	91/106 (86%)	89 (98%)	2 (2%)	0	100	100
28	X	350/398 (88%)	345 (99%)	5 (1%)	0	100	100
29	K	99/128 (77%)	99 (100%)	0	0	100	100
30	Y	147/395 (37%)	147 (100%)	0	0	100	100
31	G	312/396 (79%)	304 (97%)	8 (3%)	0	100	100
32	F	198/242 (82%)	196 (99%)	2 (1%)	0	100	100
33	C	130/167 (78%)	130 (100%)	0	0	100	100
34	9	10/698 (1%)	10 (100%)	0	0	100	100
All	All	6267/9014 (70%)	6165 (98%)	102 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	c	269/319 (84%)	269 (100%)	0	100	100
3	B	198/249 (80%)	198 (100%)	0	100	100
4	D	285/357 (80%)	285 (100%)	0	100	100
5	E	95/107 (89%)	95 (100%)	0	100	100
6	I	104/146 (71%)	104 (100%)	0	100	100
7	J	93/118 (79%)	93 (100%)	0	100	100
8	L	158/226 (70%)	158 (100%)	0	100	100
9	M	97/113 (86%)	97 (100%)	0	100	100
10	N	96/115 (84%)	96 (100%)	0	100	100
11	O	175/230 (76%)	175 (100%)	0	100	100
12	P	88/123 (72%)	88 (100%)	0	100	100
13	Q	78/78 (100%)	78 (100%)	0	100	100
14	R	264/318 (83%)	264 (100%)	0	100	100
15	S	116/164 (71%)	116 (100%)	0	100	100
16	T	153/157 (98%)	153 (100%)	0	100	100
17	U	152/174 (87%)	152 (100%)	0	100	100
18	V	325/364 (89%)	325 (100%)	0	100	100
19	W	87/158 (55%)	87 (100%)	0	100	100
20	0	188/188 (100%)	188 (100%)	0	100	100
21	3	65/166 (39%)	65 (100%)	0	100	100
22	b	253/350 (72%)	253 (100%)	0	100	100
23	a	137/288 (48%)	137 (100%)	0	100	100
24	4	526/609 (86%)	526 (100%)	0	100	100
25	H	130/180 (72%)	130 (100%)	0	100	100
26	1	254/291 (87%)	254 (100%)	0	100	100
27	Z	86/95 (90%)	86 (100%)	0	100	100
28	X	311/351 (89%)	311 (100%)	0	100	100
29	K	91/113 (80%)	91 (100%)	0	100	100
30	Y	137/357 (38%)	137 (100%)	0	100	100
31	G	275/342 (80%)	275 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	F	181/209 (87%)	181 (100%)	0	100	100
33	C	115/143 (80%)	115 (100%)	0	100	100
34	9	12/600 (2%)	12 (100%)	0	100	100
All	All	5594/7798 (72%)	5594 (100%)	0	100	100

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

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

Mol	Chain	Res	Type
20	0	145	HIS
24	4	577	ASN
21	3	140	HIS
24	4	122	ASN
26	1	279	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	922/959 (96%)	194 (21%)	2 (0%)

5 of 194 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	651	A
2	A	657	G
2	A	680	U
2	A	688	A
2	A	689	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	1492	A
2	A	1508	C

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	MA6	A	1584	2	23,26,27	1.46	4 (17%)	34,38,41	3.43	12 (35%)
6	5F0	I	184	6	8,8,9	0.56	0	7,9,11	1.17	1 (14%)
2	MA6	A	1583	2	23,26,27	1.46	4 (17%)	34,38,41	3.49	12 (35%)
2	5MU	A	1076	2	19,22,23	0.32	0	28,32,35	0.35	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
2	MA6	A	1584	2	-	0/11/29/30	0/3/3/3
6	5F0	I	184	6	-	0/9/9/10	-
2	MA6	A	1583	2	-	2/11/29/30	0/3/3/3
2	5MU	A	1076	2	-	0/7/25/26	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1584	MA6	C6-N6	4.61	1.50	1.36
2	A	1583	MA6	C6-N6	4.57	1.50	1.36
2	A	1583	MA6	C5-C4	-2.77	1.33	1.39
2	A	1584	MA6	C5-C4	-2.64	1.34	1.39
2	A	1584	MA6	C5-N7	-2.27	1.34	1.39

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1583	MA6	N1-C6-N6	-14.27	101.48	117.08
2	A	1584	MA6	N1-C6-N6	-13.74	102.06	117.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1583	MA6	C5-C6-N6	7.54	138.44	125.30
2	A	1584	MA6	C5-C6-N6	7.37	138.13	125.30
2	A	1583	MA6	N1-C2-N3	-5.55	119.92	128.60

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1583	MA6	O4'-C4'-C5'-O5'
2	A	1583	MA6	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1584	MA6	4	0
2	A	1583	MA6	3	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 54 ligands modelled in this entry, 47 are monoatomic - leaving 7 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	$\#\|Z\| > 2$
42	ATP	X	501	-	29,33,33	0.48	0	44,52,52	0.51	0
36	SPM	A	1702	-	13,13,13	0.28	0	12,12,12	0.95	0
35	NAD	A	1701	37	45,48,48	0.41	0	63,73,73	0.44	0
41	SAH	b	501	-	27,28,28	1.07	4 (14%)	38,40,40	1.96	9 (23%)
40	FES	P	201	12,5	0,4,4	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
40	FES	T	201	9,16	0,4,4	-	-	-		
43	GDP	X	502	-	28,30,30	0.43	0	44,47,47	0.48	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
42	ATP	X	501	-	-	6/22/38/38	0/3/3/3
36	SPM	A	1702	-	-	2/11/11/11	-
35	NAD	A	1701	37	-	2/30/62/62	0/5/5/5
41	SAH	b	501	-	-	4/15/31/31	0/3/3/3
40	FES	P	201	12,5	-	-	0/1/1/1
40	FES	T	201	9,16	-	-	0/1/1/1
43	GDP	X	502	-	-	2/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	b	501	SAH	C2-N3	2.45	1.38	1.33
41	b	501	SAH	C2-N1	2.45	1.38	1.33
41	b	501	SAH	OXT-C	-2.12	1.23	1.30
41	b	501	SAH	C8-N7	2.02	1.35	1.31

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
41	b	501	SAH	N3-C2-N1	-5.39	120.17	128.60
41	b	501	SAH	C5-C4-N3	-4.90	120.35	126.75
41	b	501	SAH	N9-C8-N7	-3.99	108.46	113.91
41	b	501	SAH	C5-N7-C8	3.73	108.81	103.51
41	b	501	SAH	C2-N3-C4	3.58	120.21	111.75

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	A	1702	SPM	C7-C8-C9-N10
42	X	501	ATP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
42	X	501	ATP	PB-O3B-PG-O1G
41	b	501	SAH	C2'-C1'-N9-C8
42	X	501	ATP	C3'-C4'-C5'-O5'

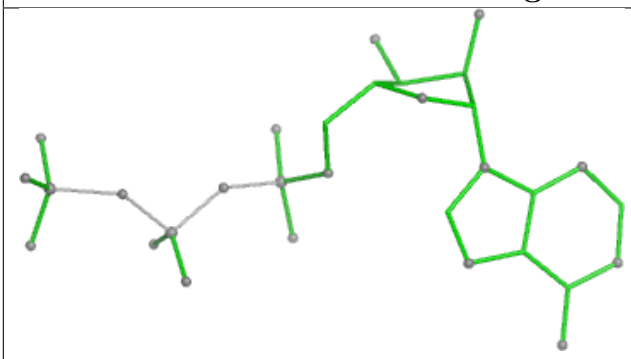
There are no ring outliers.

1 monomer is involved in 3 short contacts:

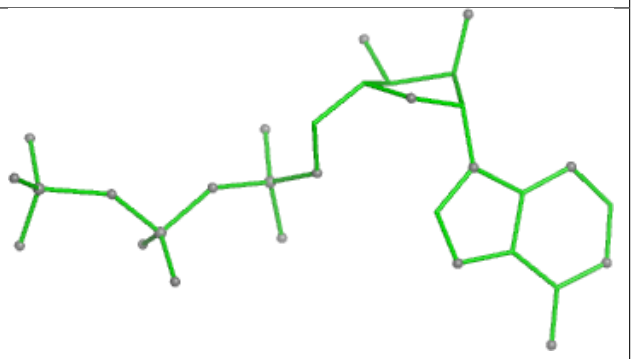
Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	b	501	SAH	3	0

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

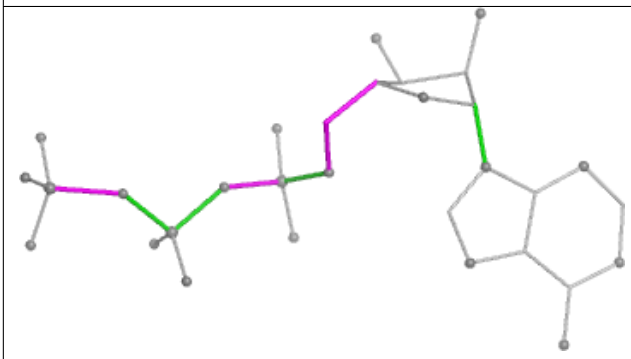
Ligand ATP X 501



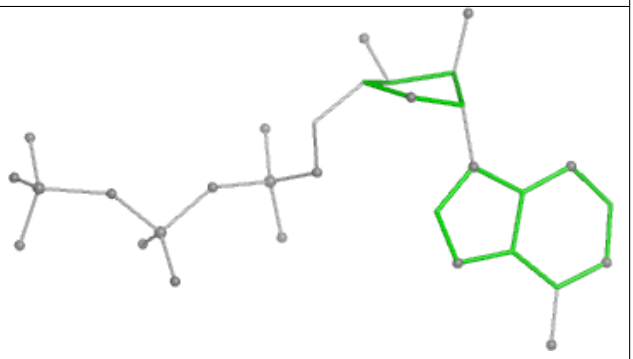
Bond lengths



Bond angles

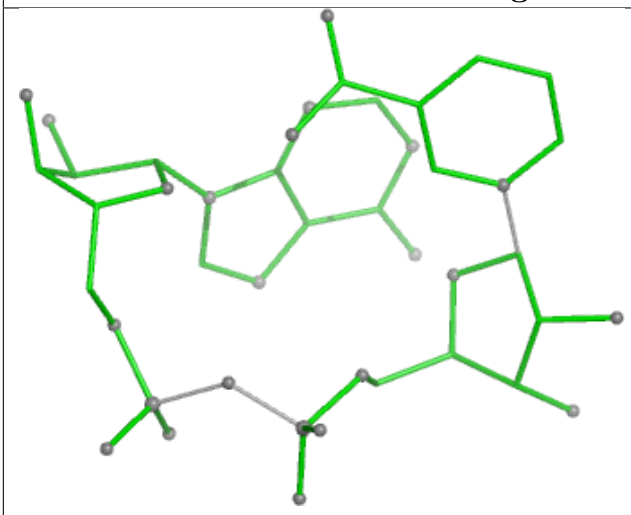


Torsions

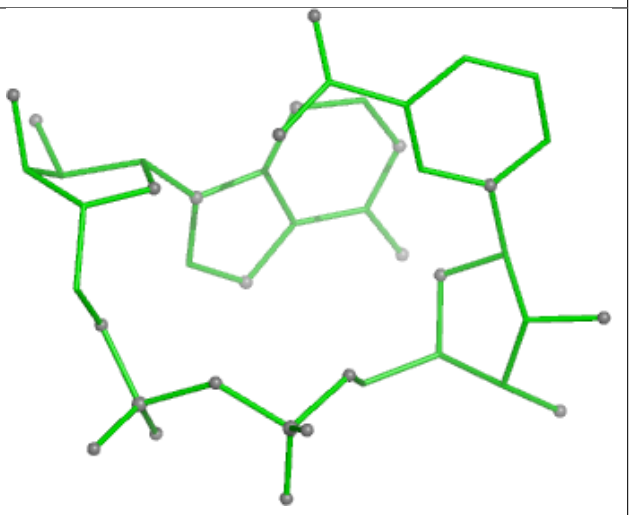


Rings

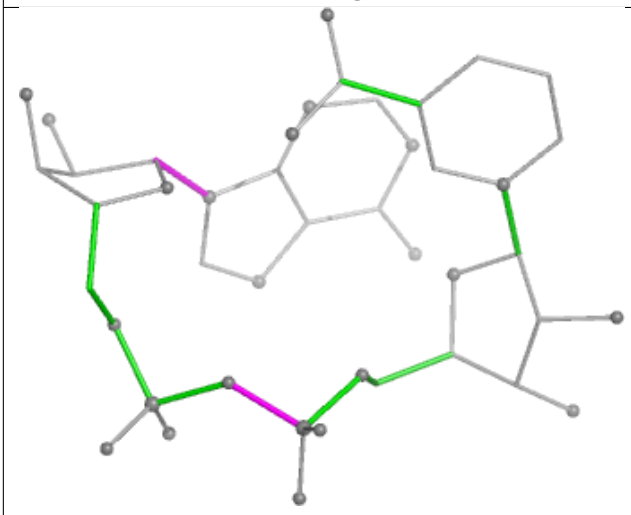
Ligand NAD A 1701



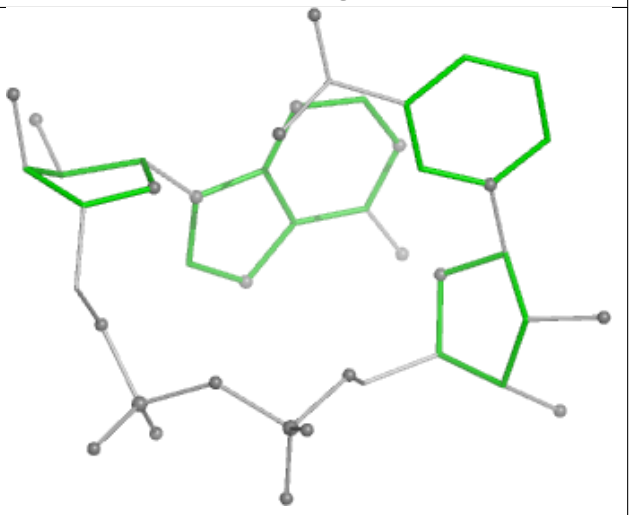
Bond lengths



Bond angles

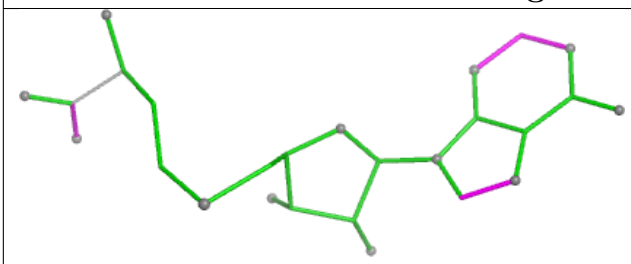


Torsions

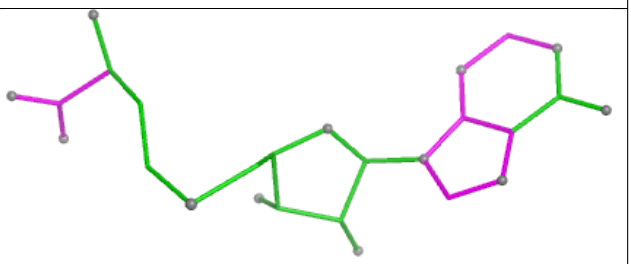


Rings

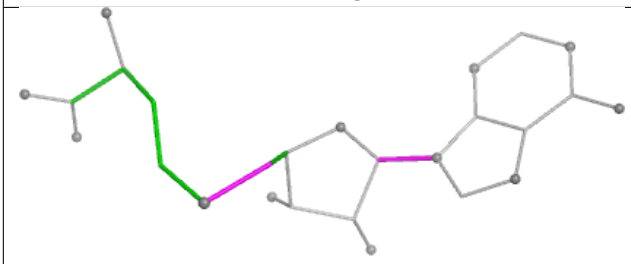
Ligand SAH b 501



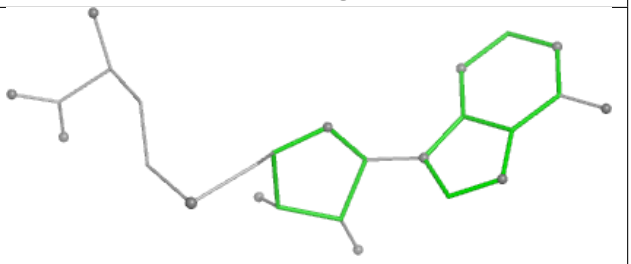
Bond lengths



Bond angles

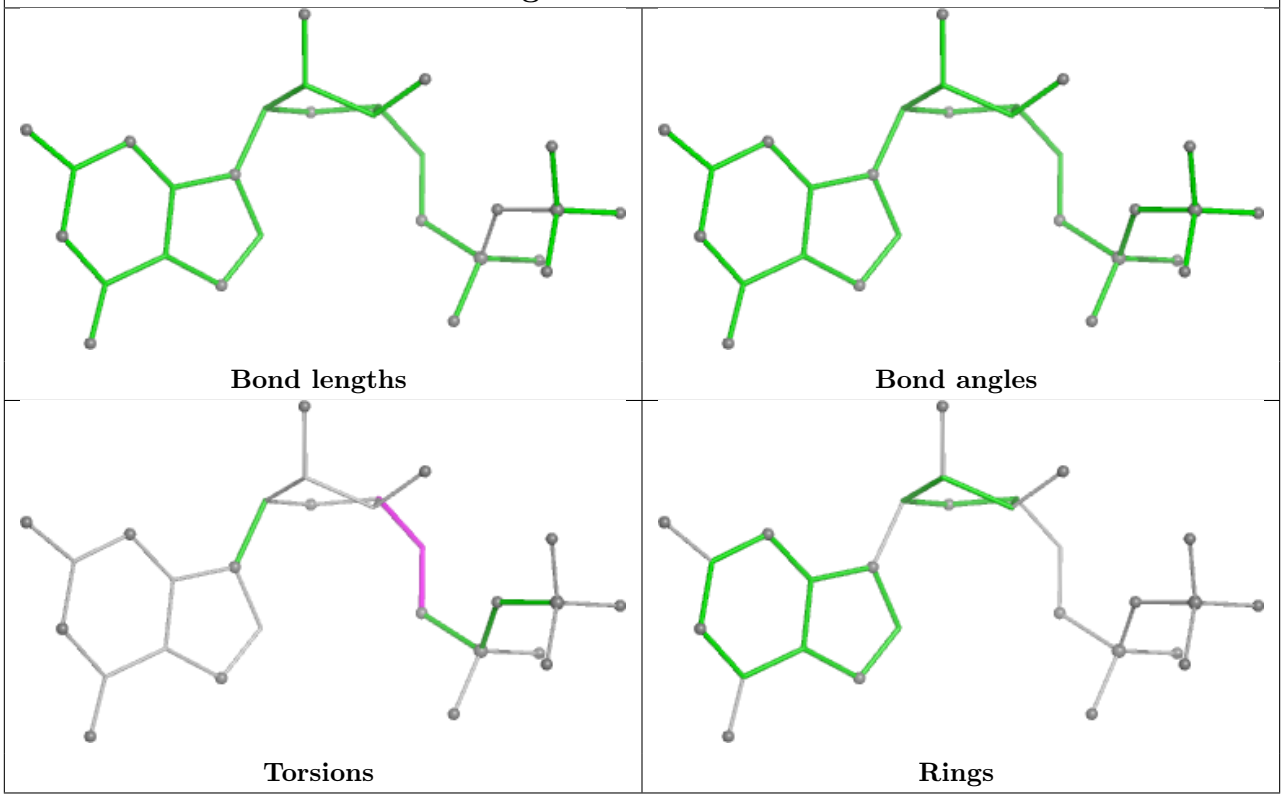


Torsions



Rings

Ligand GDP X 502



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
23	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	49:ARG	C	87:LYS	N	39.97

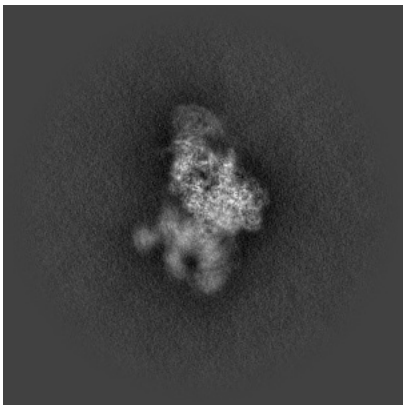
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-51873. These allow visual inspection of the internal detail of the map and identification of artifacts.

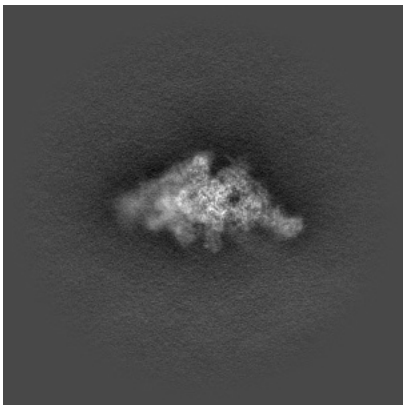
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

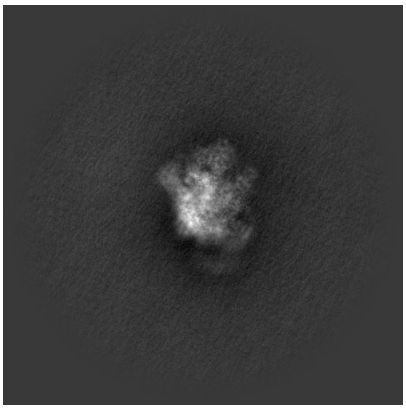
6.1.1 Primary map



X

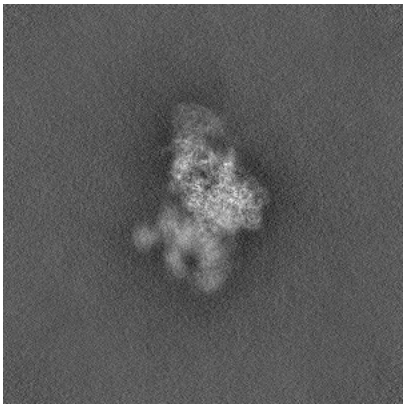


Y

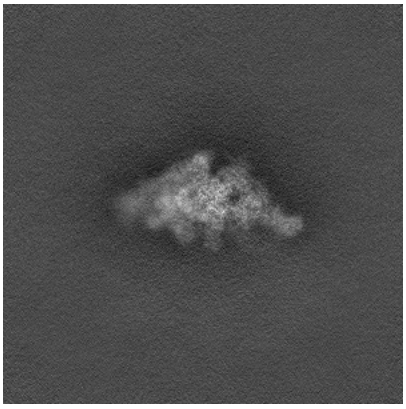


Z

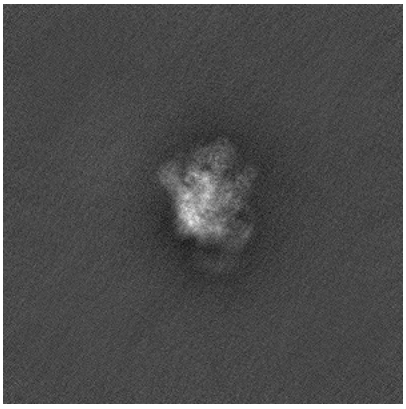
6.1.2 Raw map



X



Y

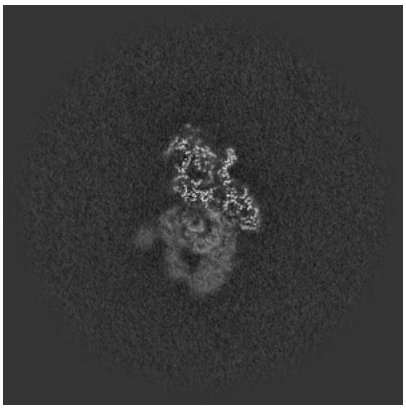


Z

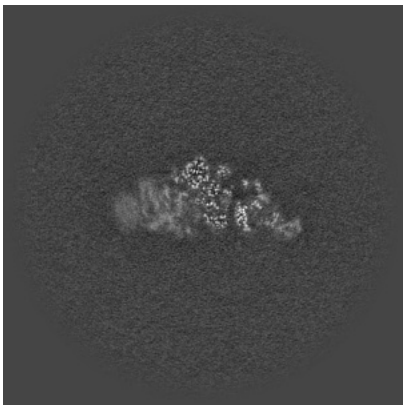
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

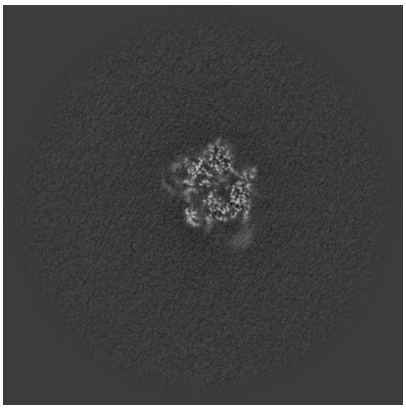
6.2.1 Primary map



X Index: 300

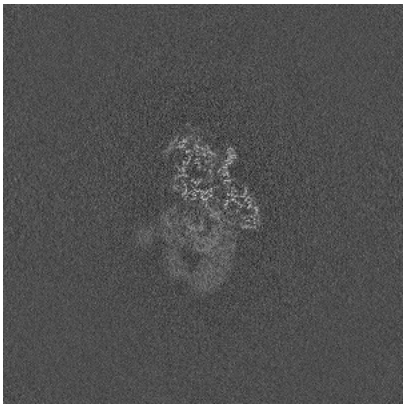


Y Index: 300

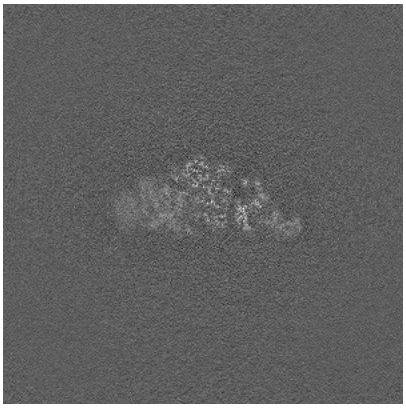


Z Index: 300

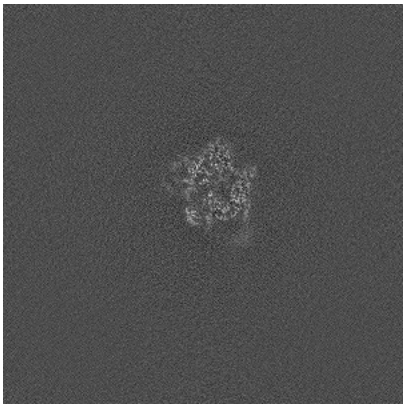
6.2.2 Raw map



X Index: 300



Y Index: 300

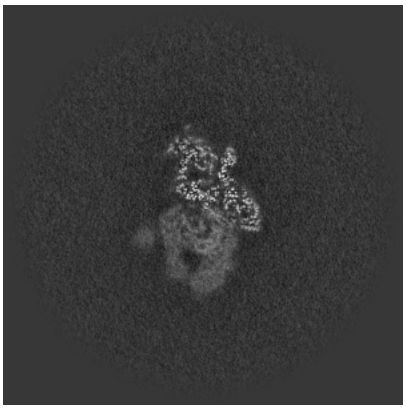


Z Index: 300

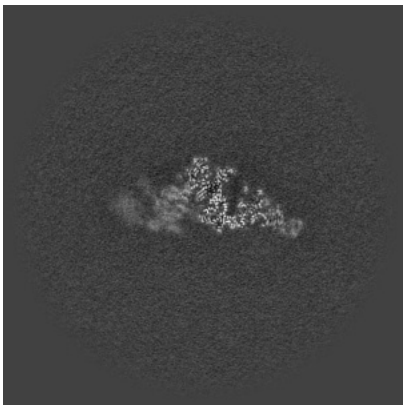
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

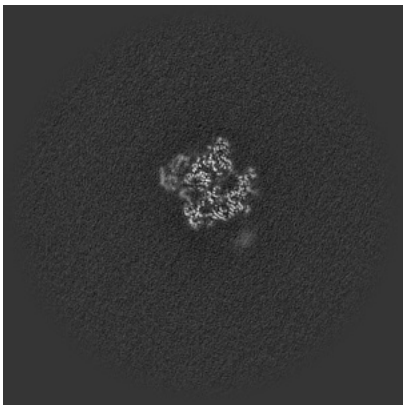
6.3.1 Primary map



X Index: 302

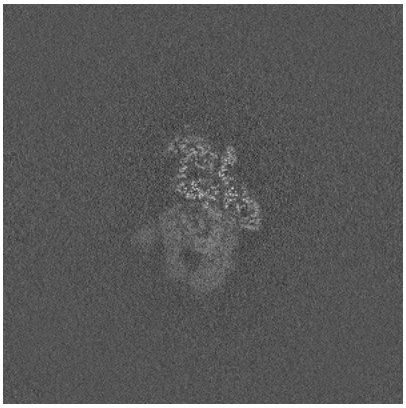


Y Index: 293

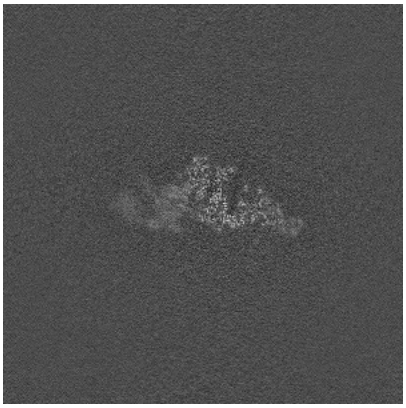


Z Index: 305

6.3.2 Raw map



X Index: 302



Y Index: 293

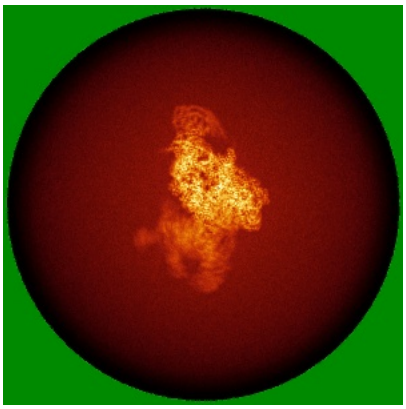


Z Index: 314

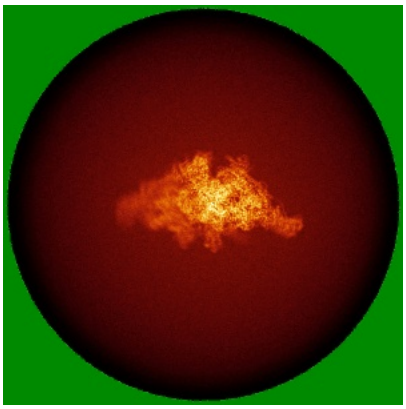
The images above show the largest variance slices of the map in three orthogonal directions.

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

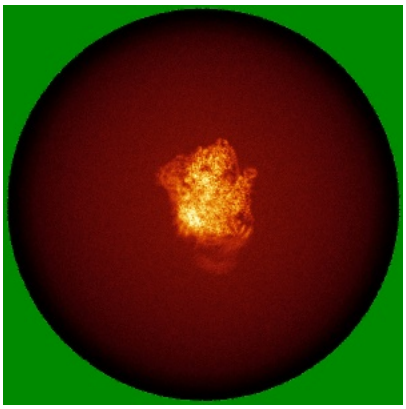
6.4.1 Primary map



X

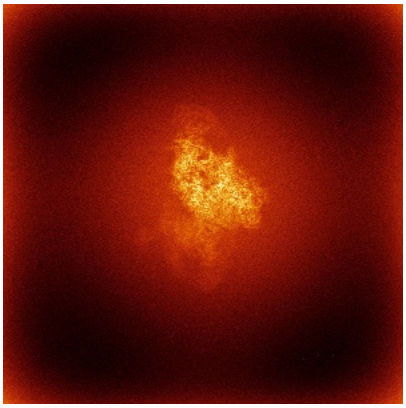


Y

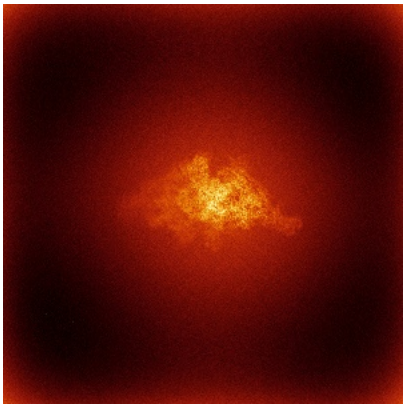


Z

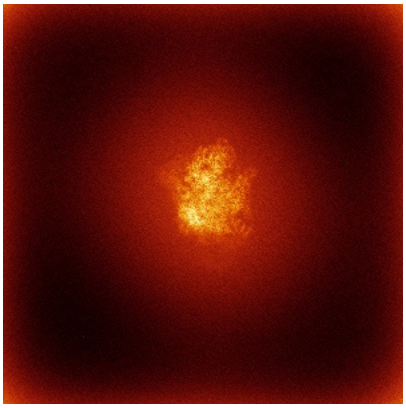
6.4.2 Raw map



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)

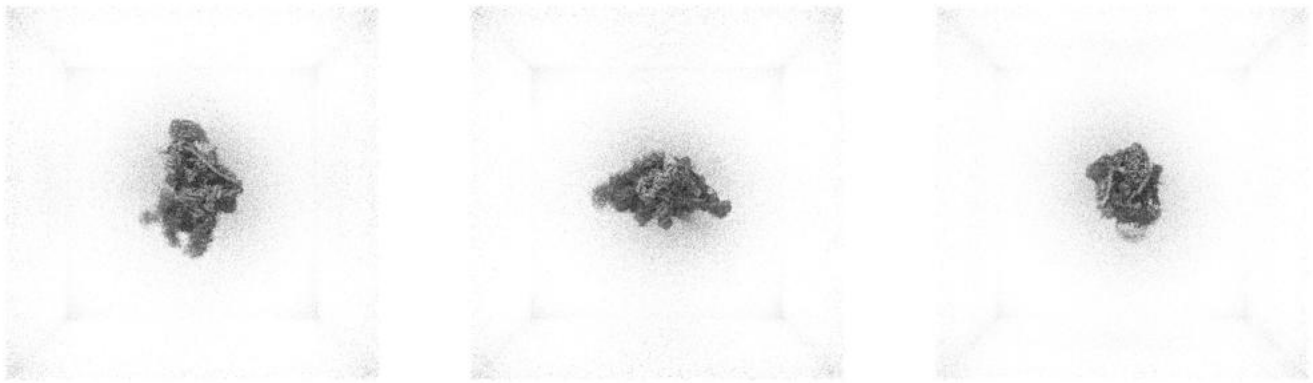
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.24. 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.

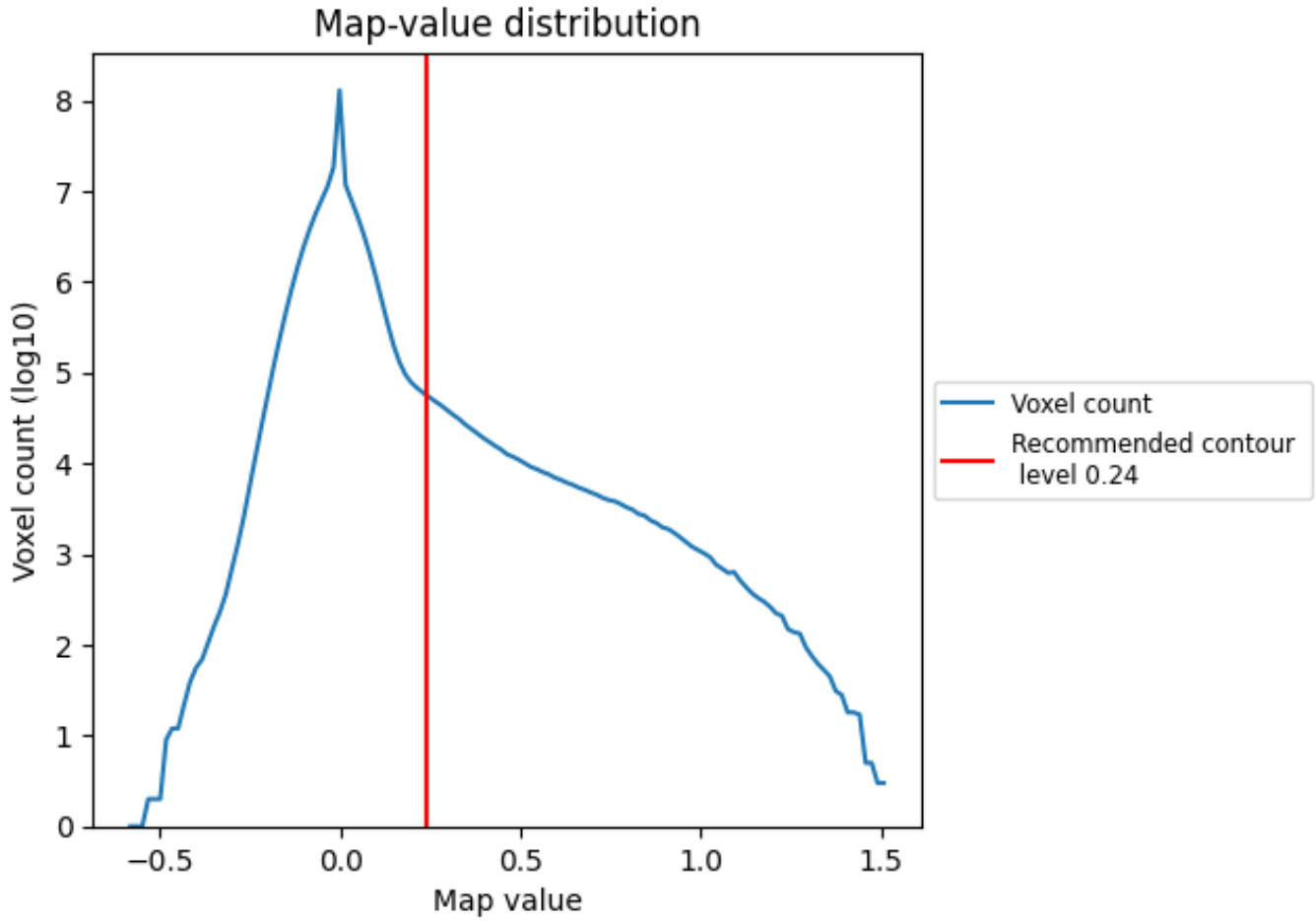
6.6 Mask visualisation (i)

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

7 Map analysis

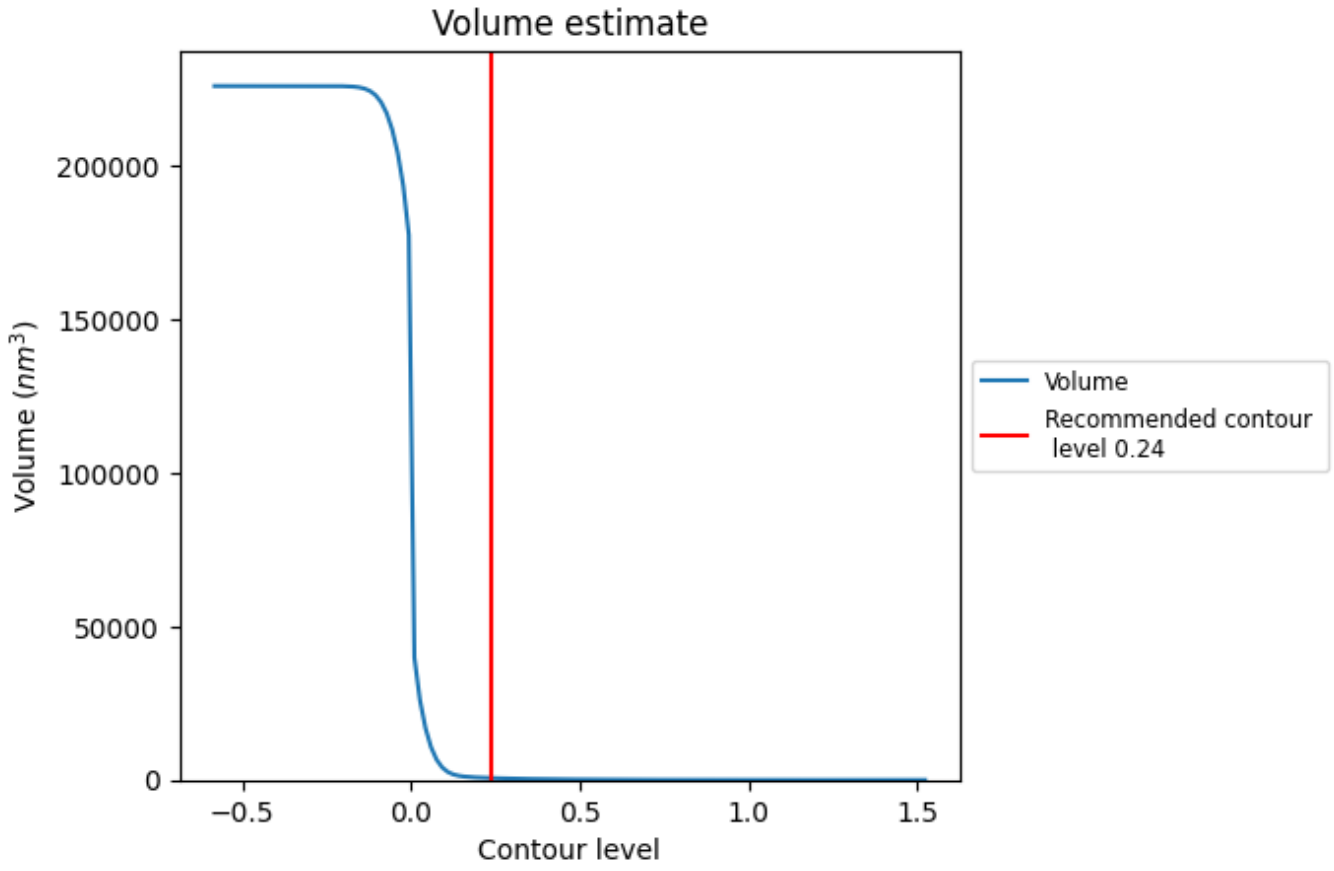
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

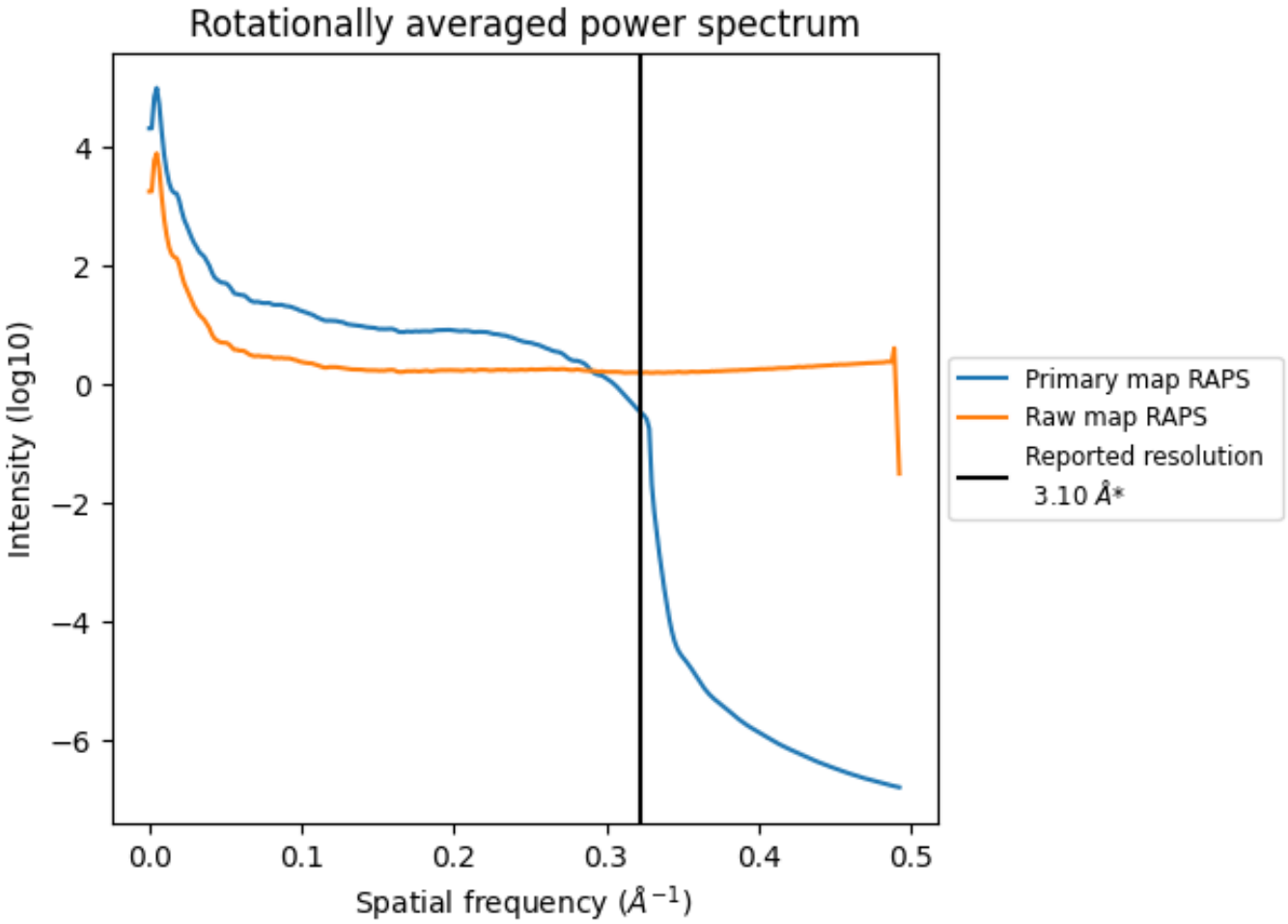
7.2 Volume estimate (i)



The volume at the recommended contour level is 613 nm^3; this corresponds to an approximate mass of 554 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)

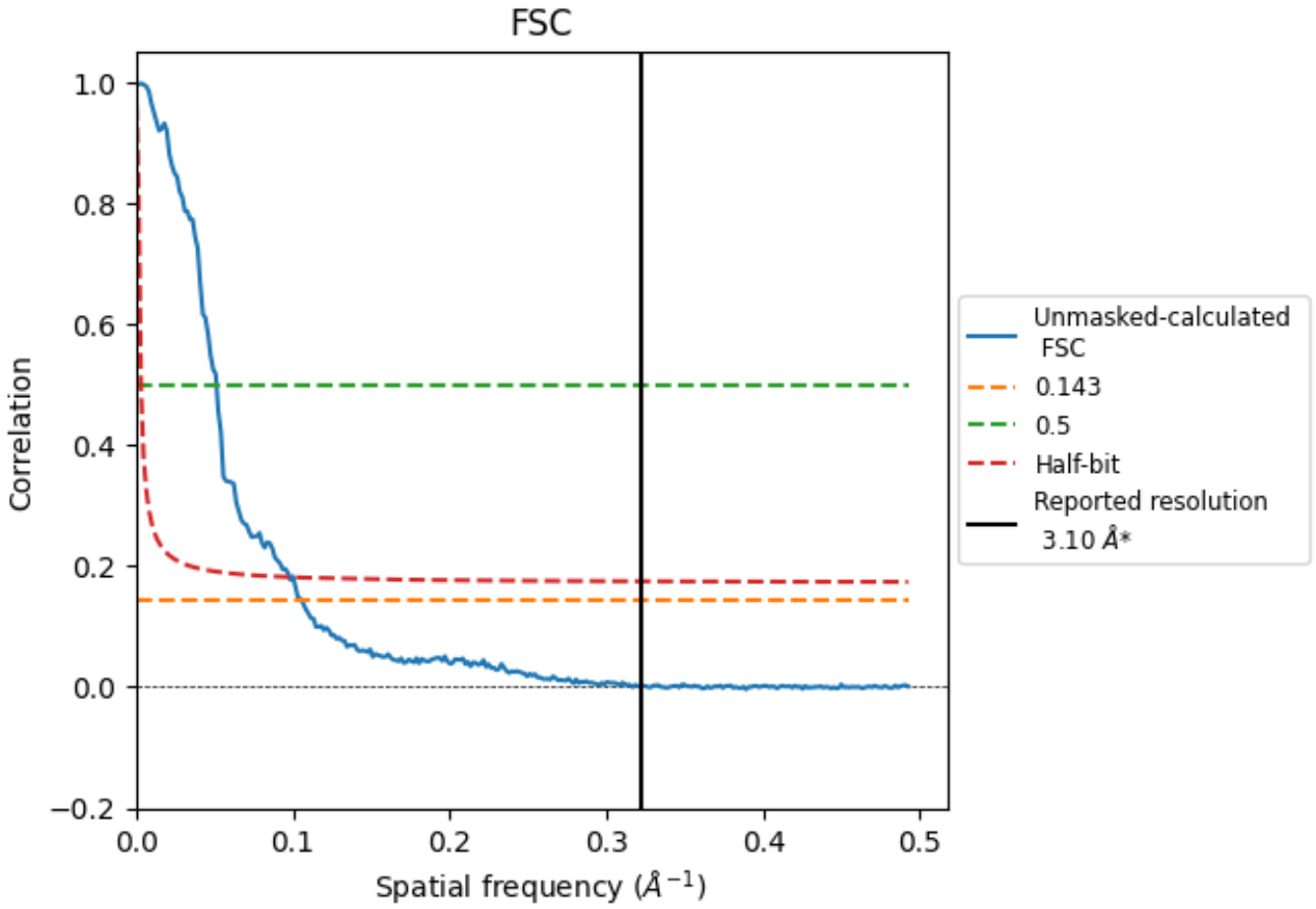


*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8.2 Resolution estimates (i)

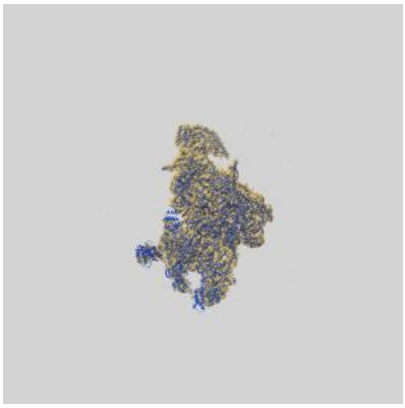
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.47	19.46	10.21

*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 9.47 differs from the reported value 3.1 by more than 10 %

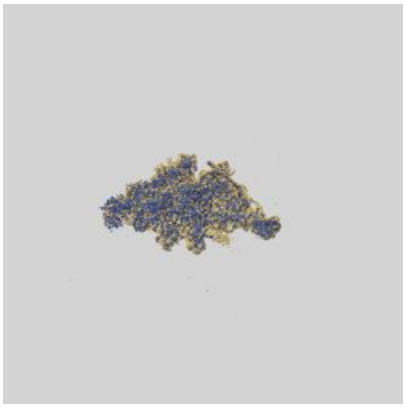
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-51873 and PDB model 9H51. Per-residue inclusion information can be found in section 3 on page 15.

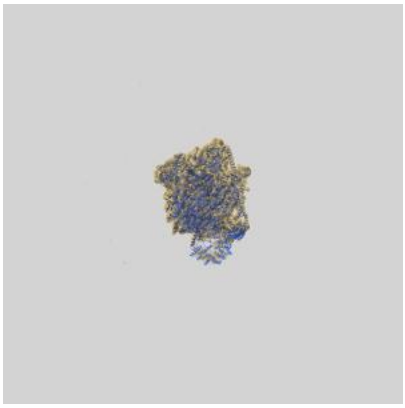
9.1 Map-model overlay



X



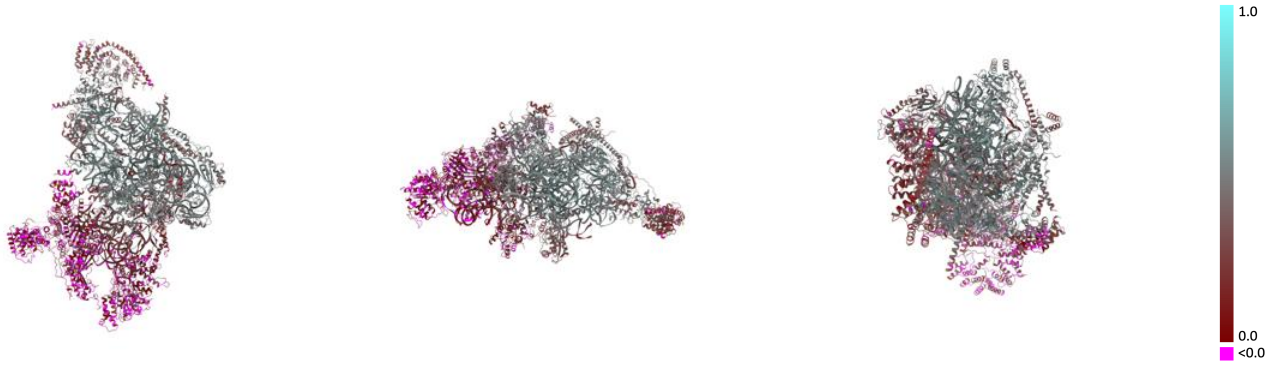
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.24 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.

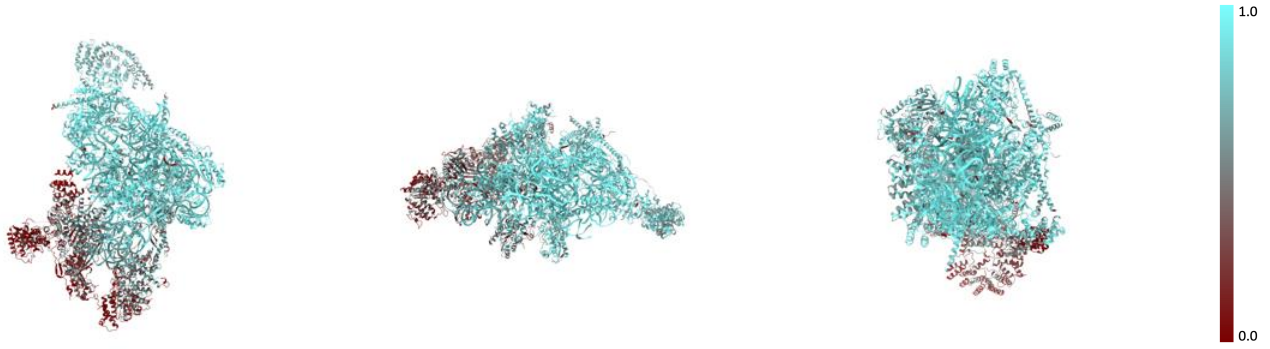
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

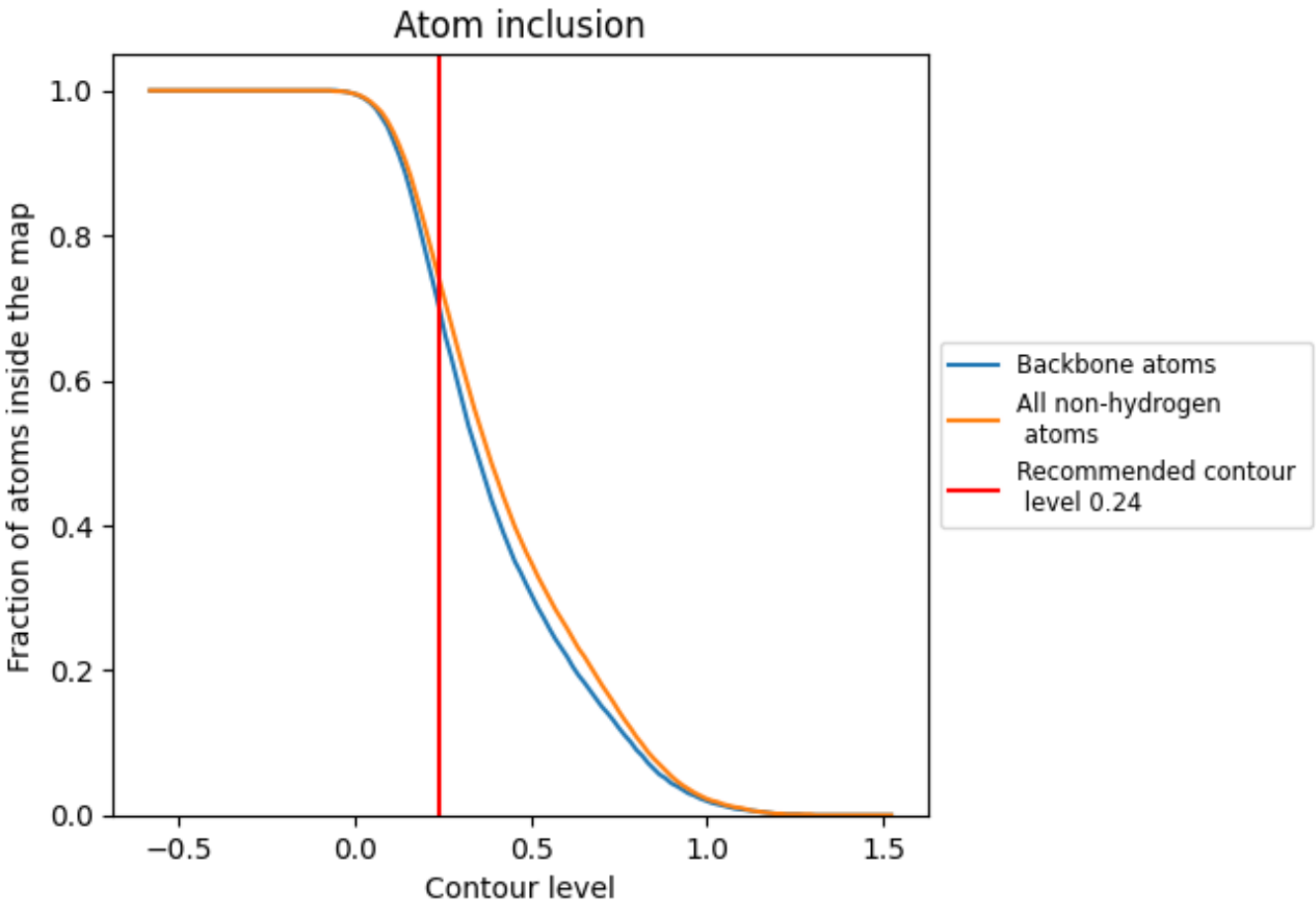
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.24).

9.4 Atom inclusion (i)



At the recommended contour level, 70% of all backbone atoms, 74% 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 (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7380	0.3270
0	0.8390	0.4300
1	0.2230	0.0510
3	0.8440	0.4810
4	0.2070	0.0580
9	0.6300	0.1870
A	0.9290	0.4070
B	0.9000	0.4950
C	0.5170	0.1890
D	0.7180	0.4100
E	0.8660	0.4900
F	0.5440	0.1410
G	0.5520	0.2000
H	0.3550	0.0940
I	0.8950	0.4780
J	0.9010	0.5150
K	0.5450	0.1400
L	0.8690	0.4840
M	0.9080	0.5140
N	0.9120	0.5300
O	0.9130	0.4980
P	0.8990	0.4980
Q	0.8900	0.5030
R	0.8700	0.4600
S	0.8530	0.4230
T	0.8890	0.5040
U	0.8520	0.4370
V	0.7180	0.2560
W	0.8560	0.4670
X	0.3260	0.0470
Y	0.1530	0.0600
Z	0.4120	0.1080
a	0.6260	0.3160
b	0.5980	0.1910
c	0.7550	0.3740

