



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 10:28 AM UTC

PDB ID : 8PK0 / pdb_00008pk0
EMDB ID : EMD-17719
Title : human mitoribosomal large subunit assembly intermediate 1 with GTPBP10-GTPBP7
Authors : Kummer, E.; Nguyen, T.G.; Ritter, C.
Deposited on : 2023-06-23
Resolution : 3.03 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

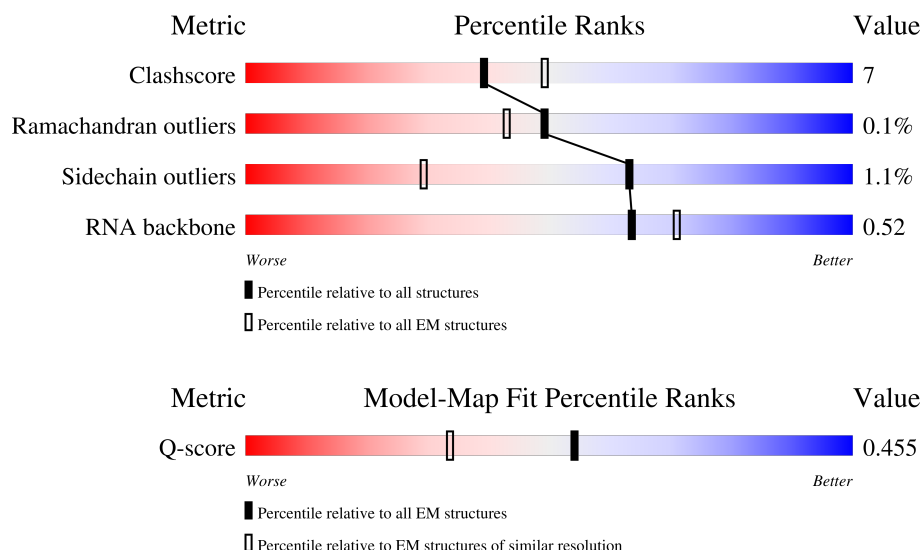
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.03 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	13929 (2.53 - 3.53)

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

Mol	Chain	Length	Quality of chain
1	0	188	
2	T	206	
3	u	234	

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Mol	Chain	Length	Quality of chain
4	1	65	
5	U	153	
6	v	70	
7	2	92	
8	V	216	
9	w	156	
10	3	188	
11	W	148	
12	x	384	
13	5	423	
14	X	256	
15	y	381	
16	6	380	
17	Y	250	
18	z	334	
19	7	338	
20	Z	161	
21	8	206	
22	a	142	
23	9	137	
24	b	215	
25	A	1589	
26	c	332	
27	B	72	
28	d	306	

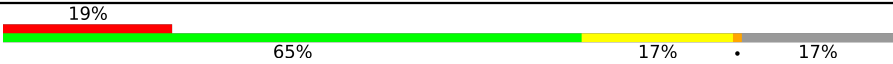
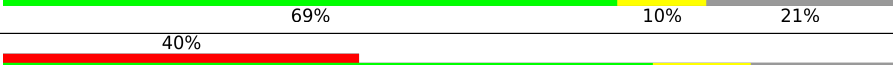
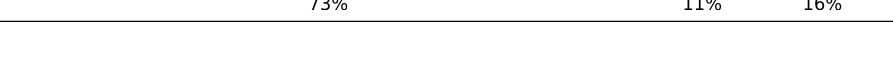
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Mol	Chain	Length	Quality of chain
29	D	305	
30	e	279	
31	E	348	
32	f	212	
33	F	311	
34	g	166	
35	H	267	
36	h	158	
37	I	261	
38	i	128	
39	J	192	
40	j	123	
41	K	178	
42	k	112	
43	L	145	
44	l	138	
45	M	296	
46	m	128	
47	N	251	
48	o	102	
49	O	175	
50	p	206	
51	P	180	
52	q	222	
53	Q	292	

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Mol	Chain	Length	Quality of chain
54	r	196	
55	R	149	
56	s	439	
57	S	205	
58	t	387	

2 Entry composition [i](#)

There are 64 unique types of molecules in this entry. The entry contains 108702 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	110	Total	C	N	O	S	0	0
			898	554	176	162	6		

- Molecule 2 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	T	166	Total	C	N	O	S	0	0
			1369	875	254	233	7		

- Molecule 3 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	u	126	Total	C	N	O	S	0	0
			1044	671	172	191	10		

- Molecule 4 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1	55	Total	C	N	O	S	0	0
			455	290	87	76	2		

- Molecule 5 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	U	152	Total	C	N	O	S	0	0
			1251	788	234	226	3		

- Molecule 6 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	v	69	Total	C	N	O	0	0
			588	372	116	100		

- Molecule 7 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	2	46	Total	C	N	O	S	0	0
			377	233	83	60	1		

- Molecule 8 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	205	Total	C	N	O	S	0	0
			1676	1068	298	302	8		

- Molecule 9 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	w	79	Total	C	N	O	S	0	0
			638	410	95	128	5		

- Molecule 10 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	3	95	Total	C	N	O	S	0	0
			832	539	162	128	3		

- Molecule 11 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	W	106	Total	C	N	O	S	0	0
			835	536	157	139	3		

- Molecule 12 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	x	338	Total	C	N	O	S	0	0
			2676	1703	467	489	17		

- Molecule 13 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	5	394	Total	C	N	O	S	0	0
			3210	2073	560	566	11		

- Molecule 14 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	X	244	Total	C	N	O	S	0	0
			2044	1322	352	365	5		

- Molecule 15 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	y	244	Total	C	N	O	S	0	0
			1980	1264	342	362	12		

- Molecule 16 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 17 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	181	Total	C	N	O	S	0	0
			1556	995	298	259	4		

- Molecule 18 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	z	311	Total	C	N	O	S	0	0
			2443	1549	445	433	16		

- Molecule 19 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	7	294	Total	C	N	O	S	0	0
			2390	1529	405	438	18		

- Molecule 20 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	122	Total	C	N	O	S	0	0
			996	636	186	171	3		

- Molecule 21 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	8	102	Total	C	N	O	S	0	0
			860	543	152	163	2		

- Molecule 22 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	100	Total	C	N	O	S	0	0
			840	529	152	154	5		

- Molecule 23 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 24 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	150	Total	C	N	O	S	0	0
			1189	739	230	217	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	2	ACE	-	acetylation	UNP Q8N983

- Molecule 25 is a RNA chain called 16S rRNA + pre-H68-71 segment.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	1423	Total	C	N	O	P	0	0
			30199	13555	5442	9779	1423		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2737	A	G	conflict	GB 1858624182
A	3138	U	-	insertion	GB 1858624182

- Molecule 26 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	286	Total	C	N	O	S	0	0
			2299	1470	397	423	9		

- Molecule 27 is a RNA chain called CP tRNA-Val.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B	72	Total	C	N	O	P	0	0
			1522	683	269	498	72		

- Molecule 28 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	255	Total	C	N	O	S	0	0
			2088	1335	360	379	14		

- Molecule 29 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	D	240	Total	C	N	O	S	0	0
			1872	1165	378	320	9		

- Molecule 30 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	228	Total	C	N	O	S	0	0
			1848	1174	326	342	6		

- Molecule 31 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	E	305	Total	C	N	O	S	0	0
			2406	1545	418	432	11		

- Molecule 32 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	150	Total	C	N	O	S	0	0
			1196	764	197	231	4		

- Molecule 33 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	F	252	Total	C	N	O	S	0	0
			2031	1305	370	350	6		

- Molecule 34 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	134	Total	C	N	O	S	0	0
			1113	719	193	199	2		

- Molecule 35 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	H	97	Total	C	N	O	S	0	0
			802	508	155	139			

- Molecule 36 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	110	Total	C	N	O	S	0	0
			895	568	156	168	3		

- Molecule 37 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	I	158	Total	C	N	O	S	0	0
			871	533	169	166	3		

- Molecule 38 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	97	Total	C	N	O	S	0	0
			828	532	165	127	4		

- Molecule 39 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	J	162	Total	C	N	O	S	0	0
			798	474	162	162			

- Molecule 40 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	90	Total	C	N	O	S	0	0
			722	449	140	131	2		

- Molecule 41 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	177	Total	C	N	O	S	0	0
			1455	936	259	253	7		

- Molecule 42 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	k	101	Total	C	N	O	0	0
			502	299	101	102		

- Molecule 43 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L	115	Total	C	N	O	S	0	0
			890	559	171	155	5		

- Molecule 44 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	l	72	Total	C	N	O	0	0
			353	209	72	72		

- Molecule 45 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	M	291	Total	C	N	O	S	0	0
			2327	1483	430	408	6		

- Molecule 46 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	51	Total	C	N	O	S	0	0
			419	262	82	73	2		

- Molecule 47 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	N	144	Total	C	N	O	S	0	0
			799	485	157	156	1		

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	80	Total	C	N	O	S	0	0
			677	426	134	114	3		

- Molecule 49 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	O	154	Total	C	N	O	S	0	0
			1259	792	241	219	7		

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	147	Total	C	N	O	S	0	0
			1205	748	228	225	4		

- Molecule 51 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	P	144	Total	C	N	O	S	0	0
			1173	733	224	211	5		

- Molecule 52 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	q	141	Total	C	N	O	S	0	0
			1177	732	229	211	5		

- Molecule 53 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Q	221	Total	C	N	O	S	0	0
			1843	1179	327	328	9		

- Molecule 54 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	r	162	Total	C	N	O	S	0	0
			1251	791	243	209	8		

- Molecule 55 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	R	140	Total	C	N	O	S	0	0
			1154	732	231	187	4		

- Molecule 56 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	s	386	Total	C	N	O	S	0	0
			3155	2023	559	559	14		

- Molecule 57 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S	161	Total	C	N	O	S	0	0
			1293	835	227	227	4		

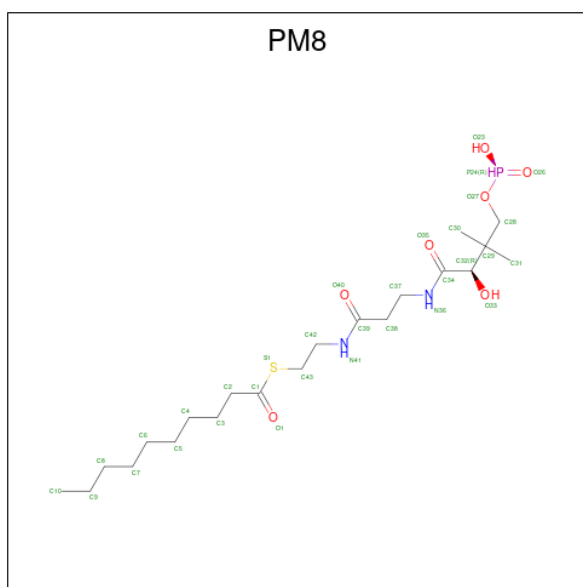
- Molecule 58 is a protein called GTP-binding protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	t	325	Total	C	N	O	S	0	0
			1958	1202	380	372	4		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

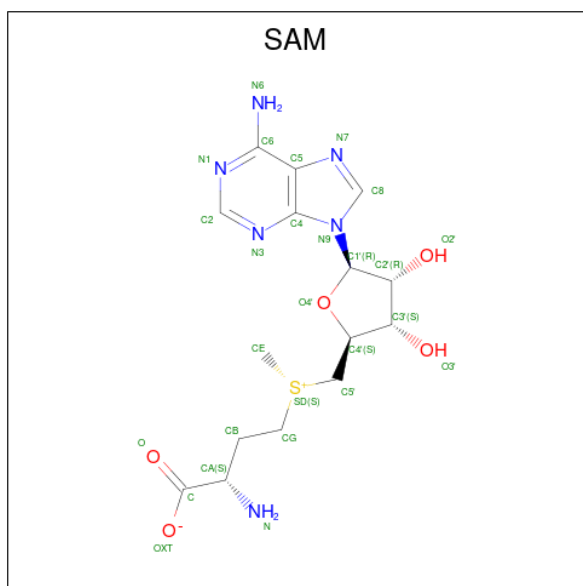
Mol	Chain	Residues	Atoms		AltConf
59	0	1	Total	Zn	0
			1	1	

- Molecule 60 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (CCD ID: PM8) (formula: C₂₁H₄₁N₂O₇PS).



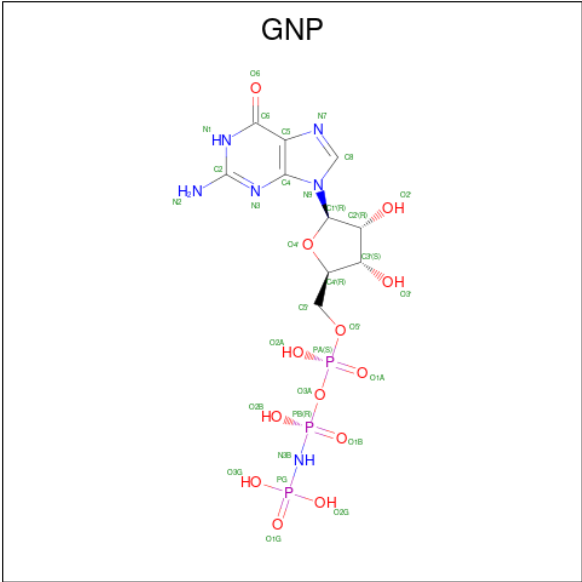
Mol	Chain	Residues	Atoms						AltConf
60	w	1	Total	C	N	O	P	S	0
			32	21	2	7	1	1	

- Molecule 61 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



Mol	Chain	Residues	Atoms					AltConf
61	x	1	Total	C	N	O	S	0
			27	15	6	5	1	

- Molecule 62 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
62	z	1	Total	C	N	O	P	0
			32	10	6	13	3	
62	t	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
63	z	1	Total	Mg	0
			1	1	
63	A	92	Total	Mg	0
			92	92	
63	E	1	Total	Mg	0
			1	1	
63	g	1	Total	Mg	0
			1	1	
63	t	1	Total	Mg	0
			1	1	

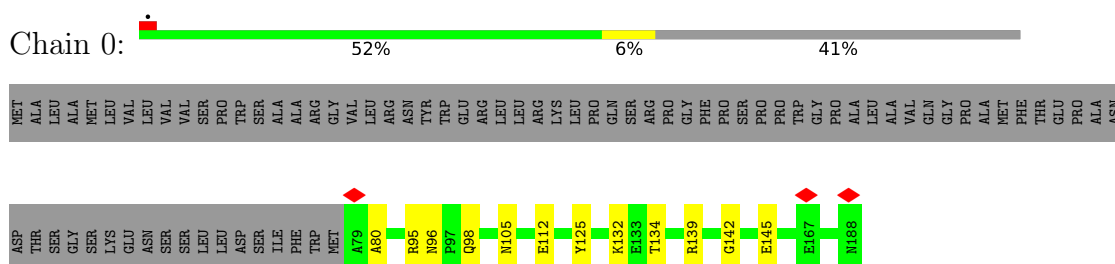
- Molecule 64 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
64	A	10	Total	K	0
			10	10	

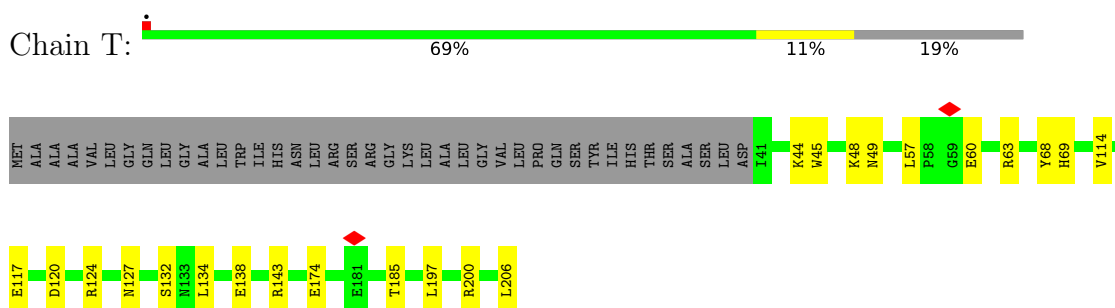
3 Residue-property plots

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

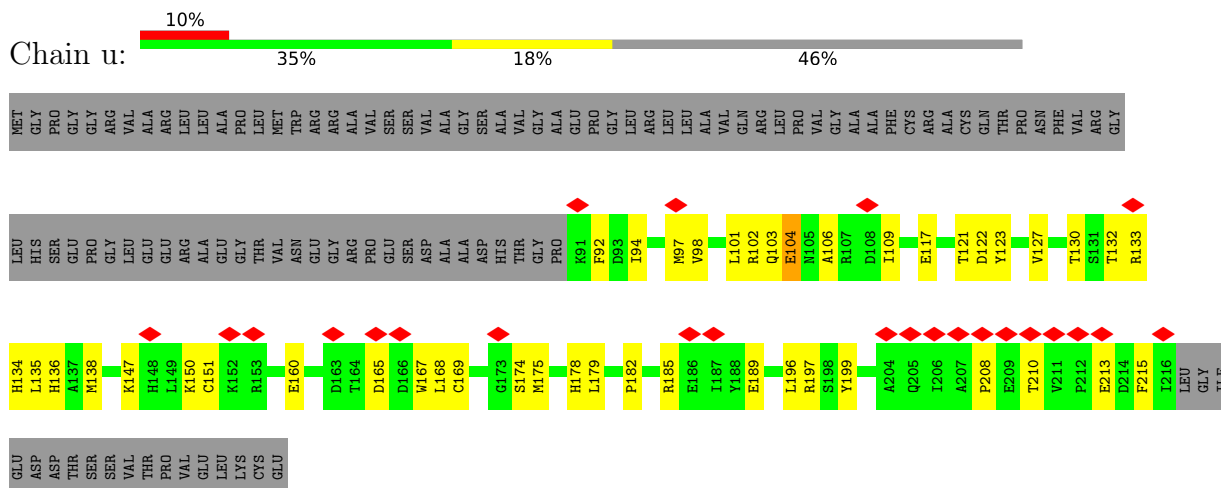
- Molecule 1: 39S ribosomal protein L32, mitochondrial



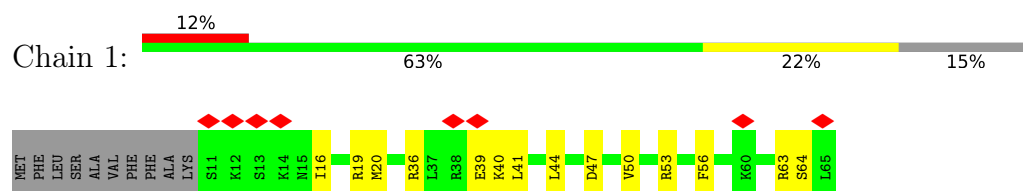
- Molecule 2: 39S ribosomal protein L22, mitochondrial



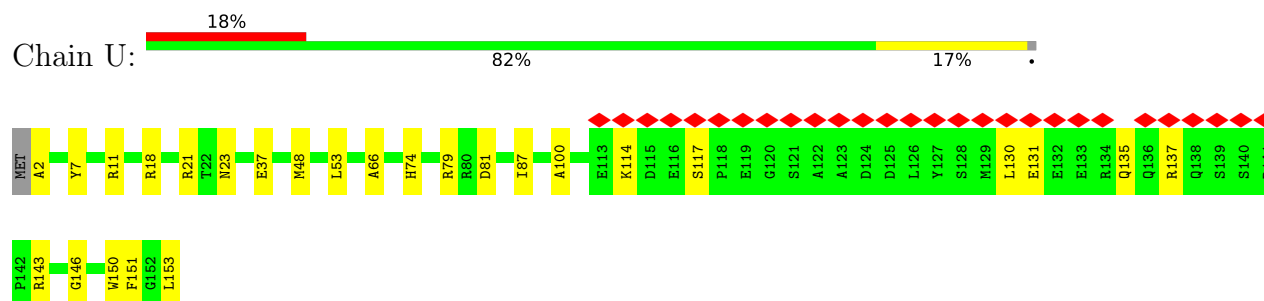
- Molecule 3: Mitochondrial assembly of ribosomal large subunit protein 1



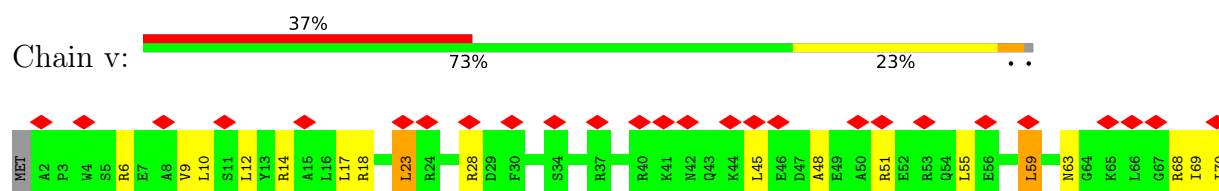
- Molecule 4: 39S ribosomal protein L33, mitochondrial



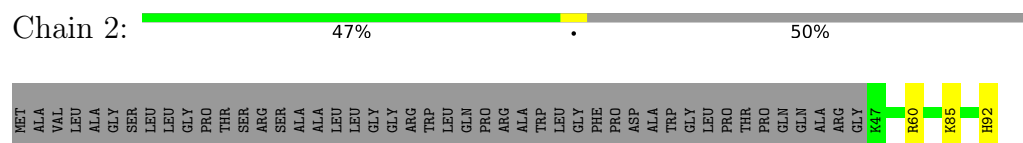
- Molecule 5: 39S ribosomal protein L23, mitochondrial



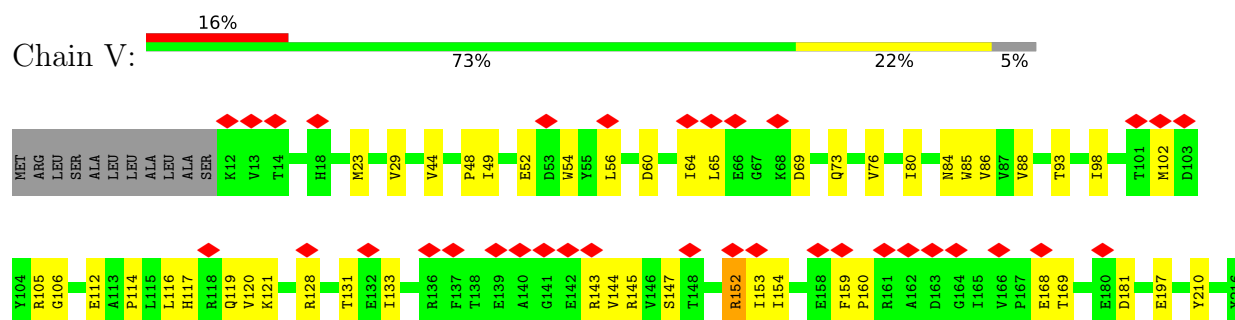
- Molecule 6: MIEF1 upstream open reading frame protein



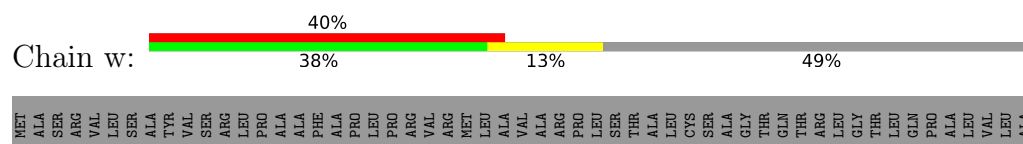
- Molecule 7: 39S ribosomal protein L34, mitochondrial



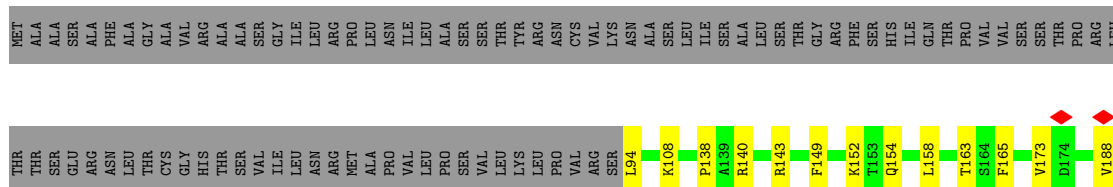
- Molecule 8: 39S ribosomal protein L24, mitochondrial



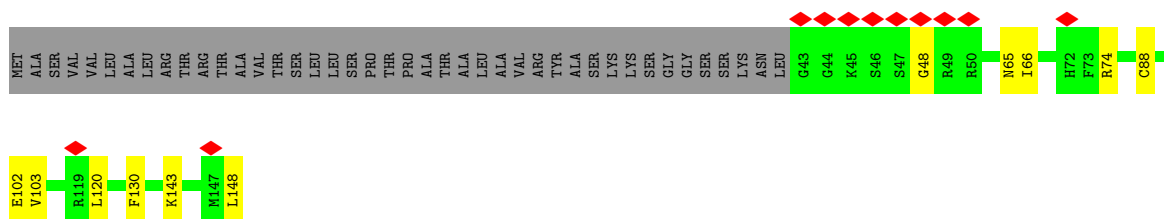
- Molecule 9: Acyl carrier protein, mitochondrial



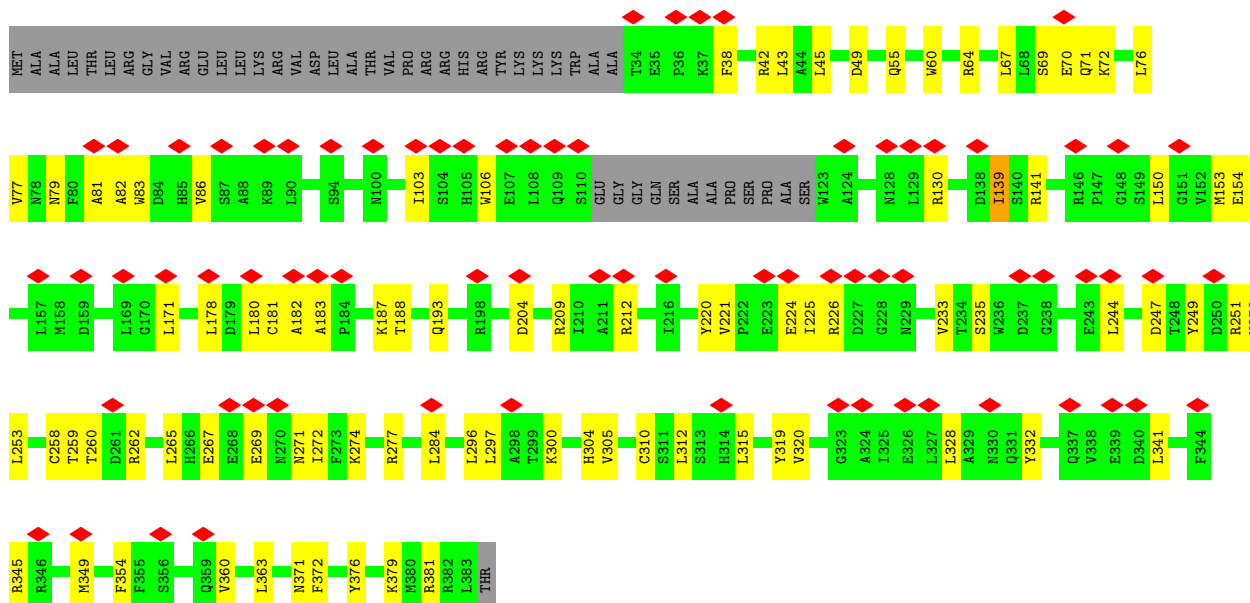
- Molecule 10: 39S ribosomal protein L35, mitochondrial

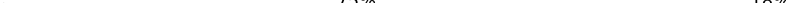


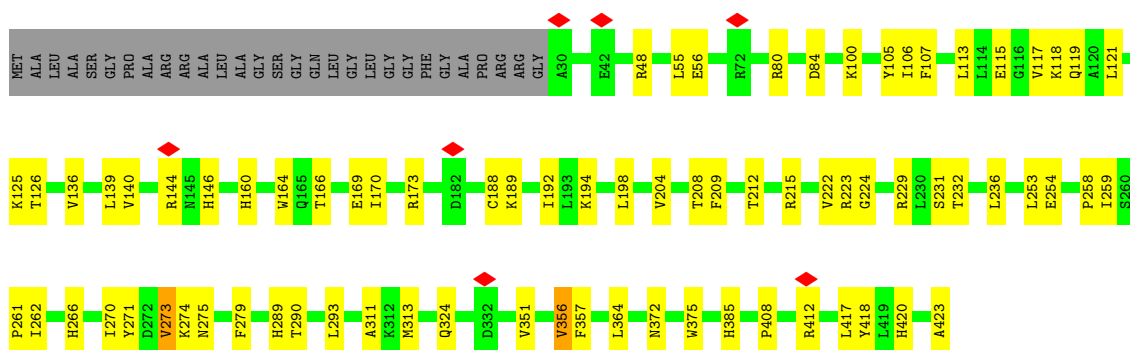
- Molecule 11: 39S ribosomal protein L27, mitochondrial



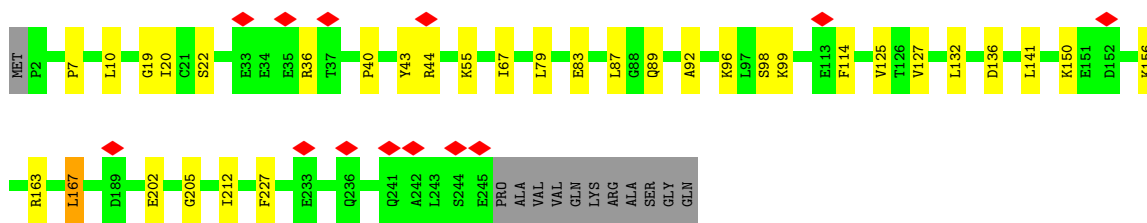
- Molecule 12: 5-methylcytosine rRNA methyltransferase NSUN4

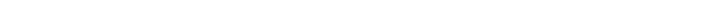


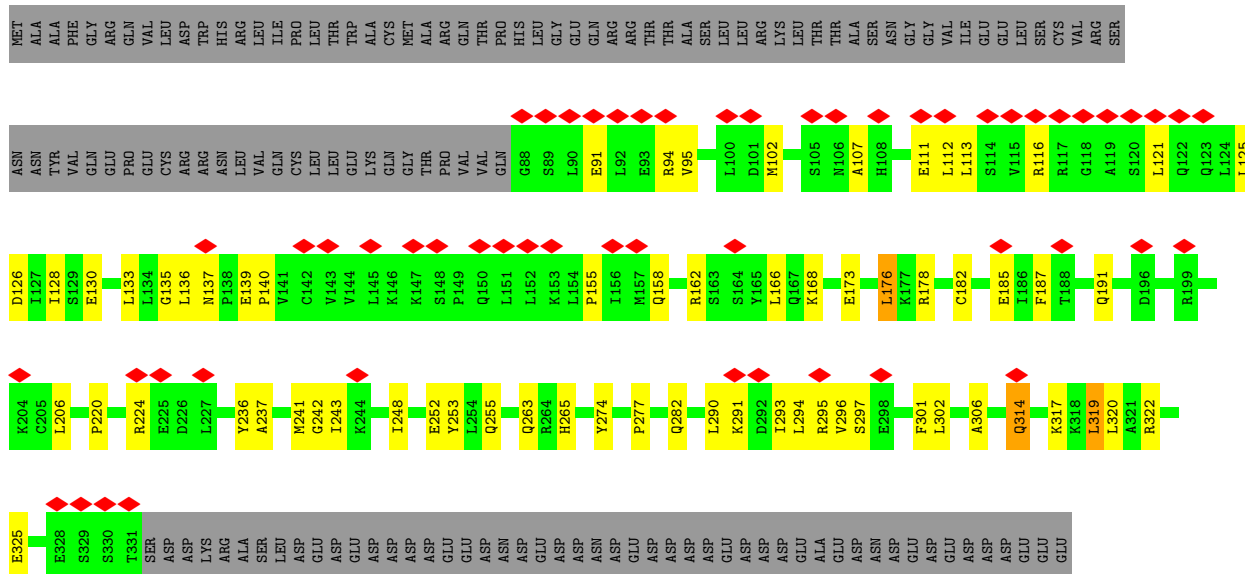
- Chain 5:  75% 18% 7%

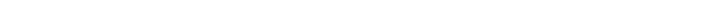


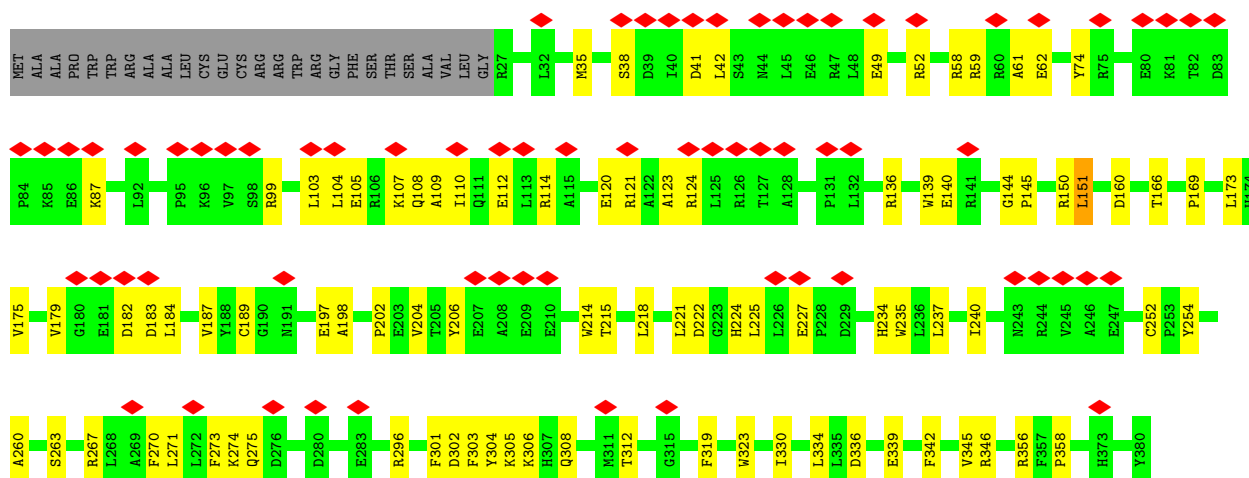
- Chain X: 



- Chain v: 

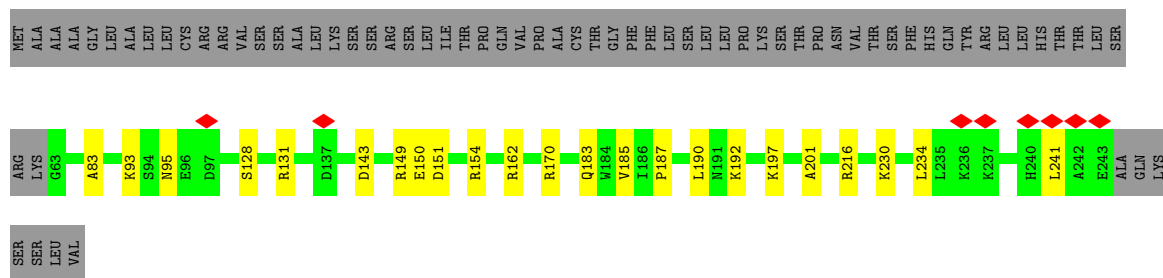


- Chain 6:  18% 69% 24% 7%



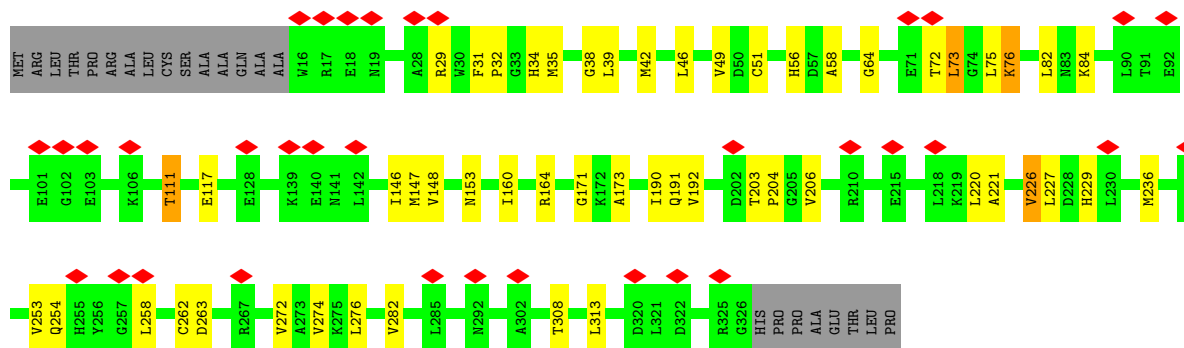
- Molecule 17: 39S ribosomal protein L47, mitochondrial

Chain Y: 63% 9% 28%



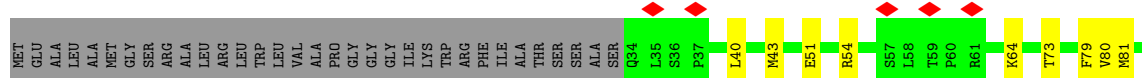
- Molecule 18: Mitochondrial ribosome-associated GTPase 1

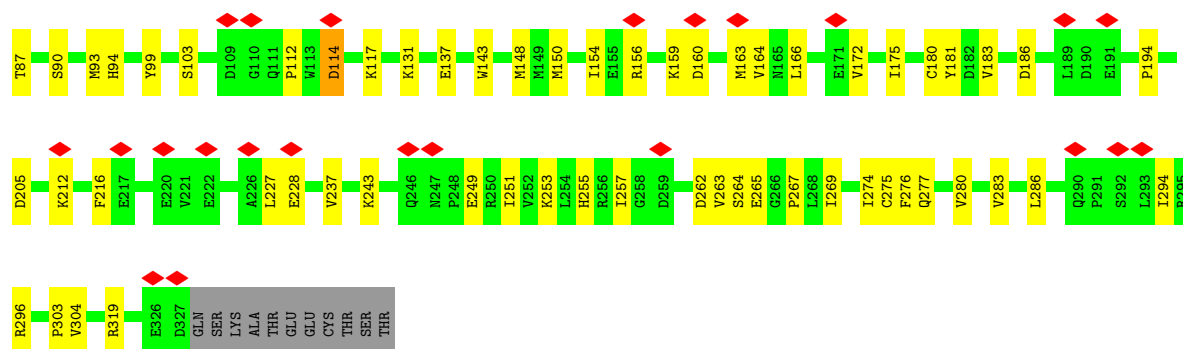
Chain z: 10% 77% 15% 7%



- Molecule 19: 39S ribosomal protein L39, mitochondrial

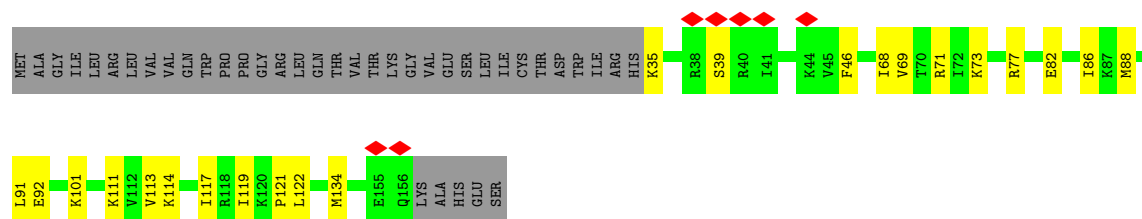
Chain 7: 8% 67% 20% 13%





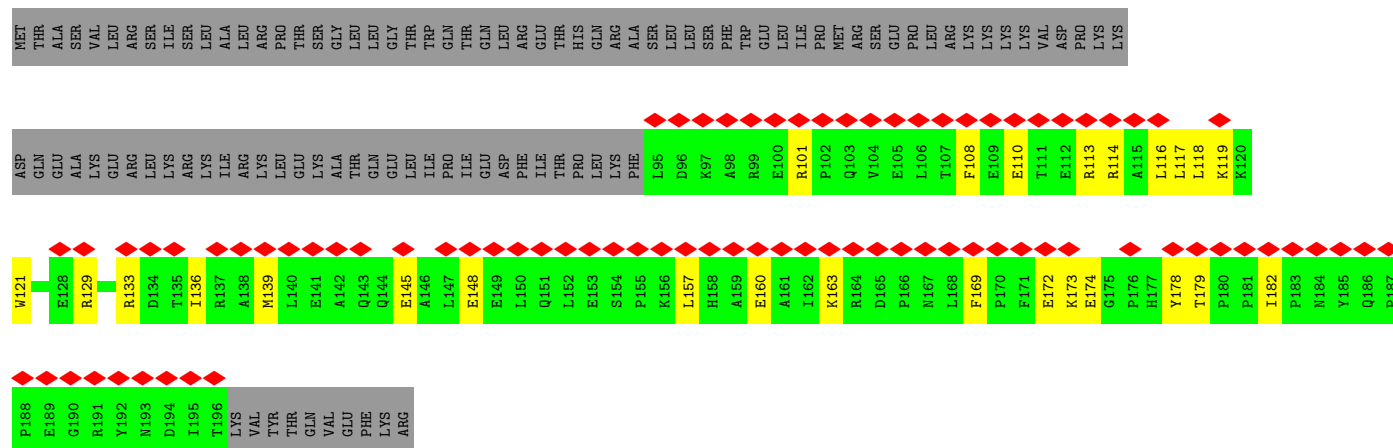
- Molecule 20: 39S ribosomal protein L30, mitochondrial

Chain Z: 62% 14% 24%



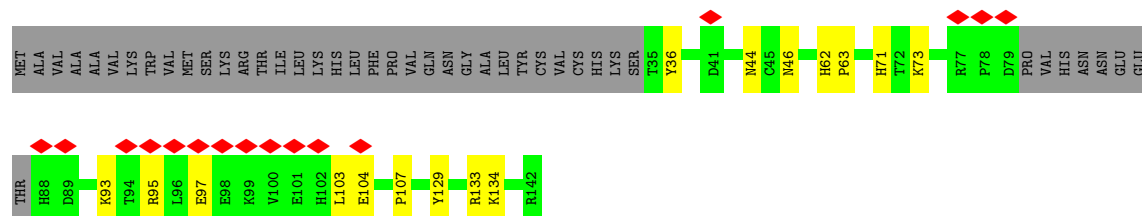
- Molecule 21: 39S ribosomal protein L40, mitochondrial

Chain 8: 40% 37% 13% 50%

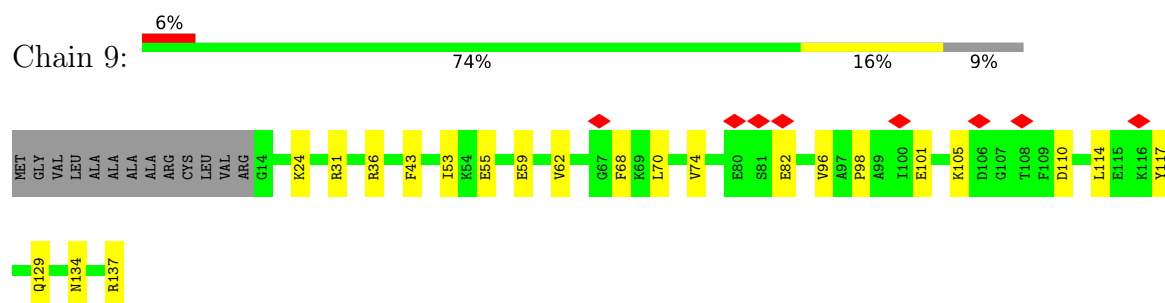


- Molecule 22: 39S ribosomal protein L42, mitochondrial

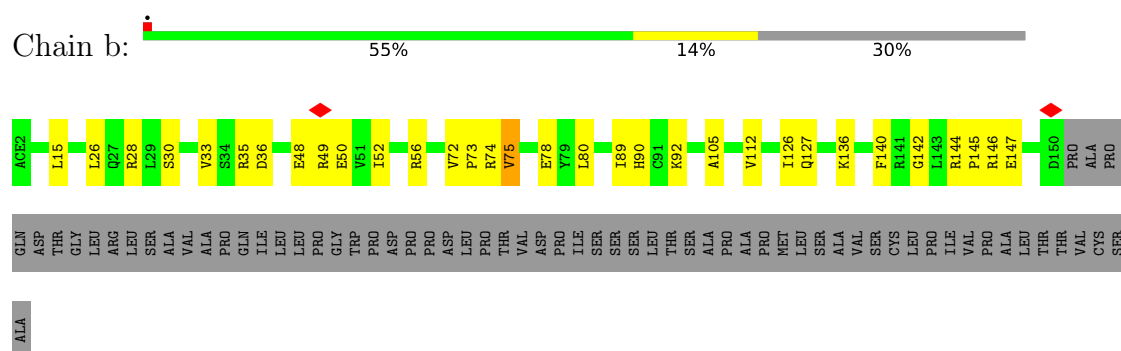
Chain a: 11% 59% 11% 30%



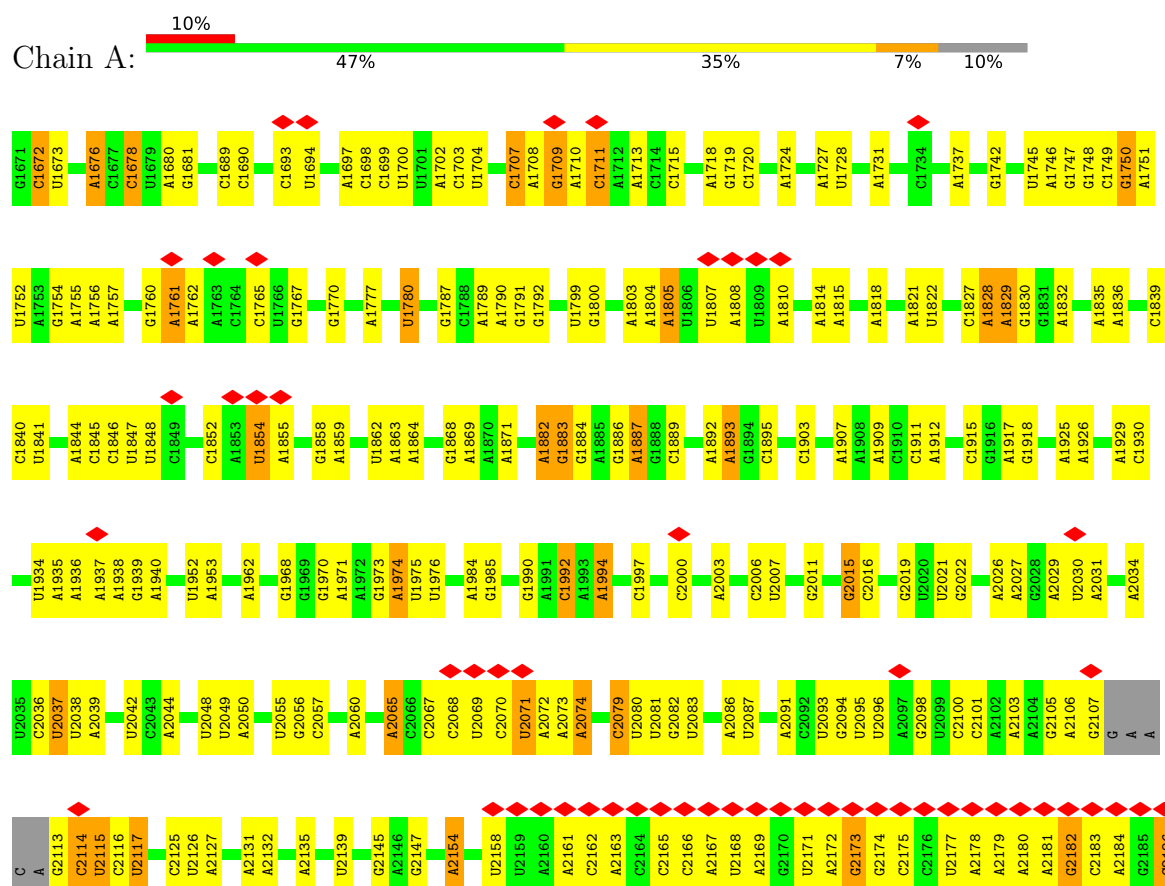
- Molecule 23: 39S ribosomal protein L41, mitochondrial



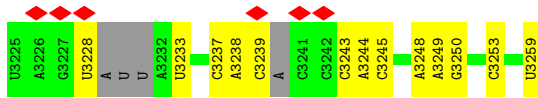
- Molecule 24: Large ribosomal subunit protein mL43



- Molecule 25: 16S rRNA + pre-H68-71 segment

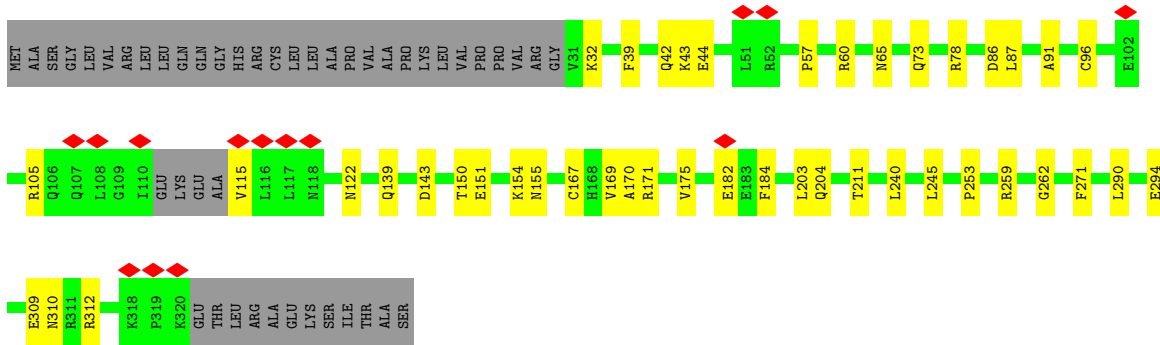






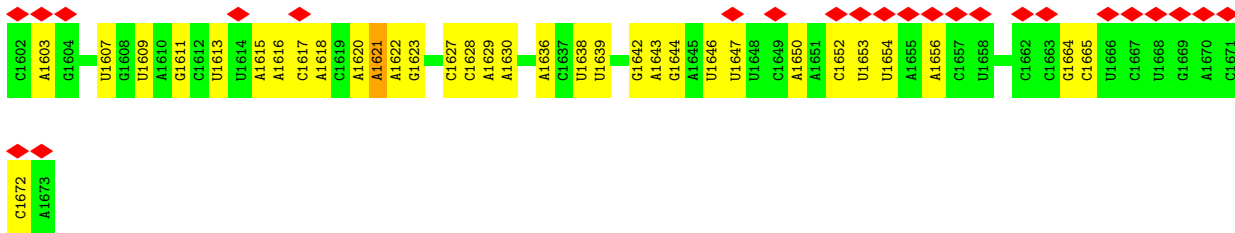
- Molecule 26: 39S ribosomal protein L44, mitochondrial

Chain c: 73% 13% 14%



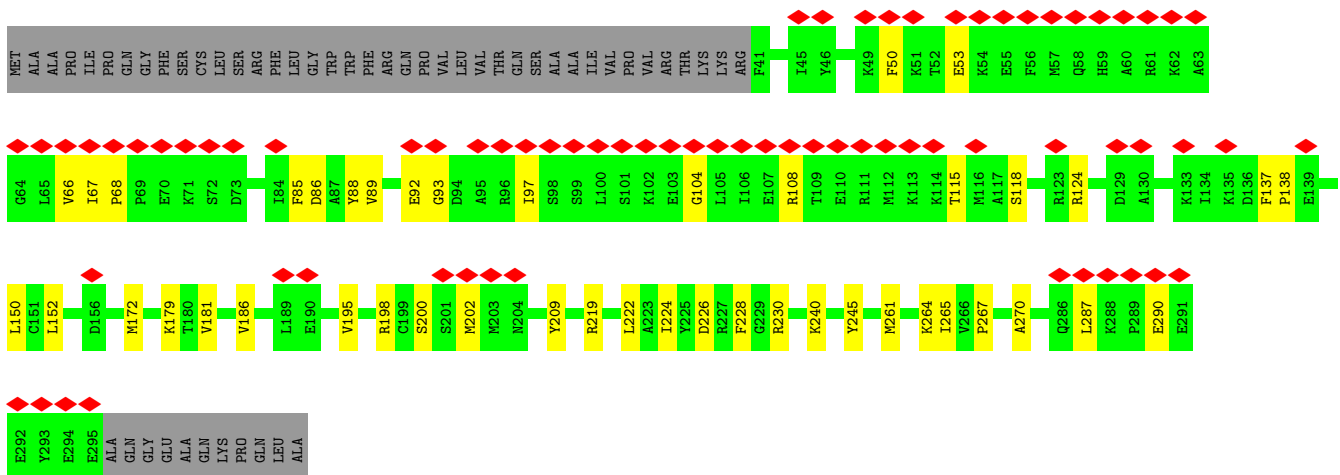
- Molecule 27: CP tRNA-Val

Chain B: 33% 54% 44%



- Molecule 28: 39S ribosomal protein L45, mitochondrial

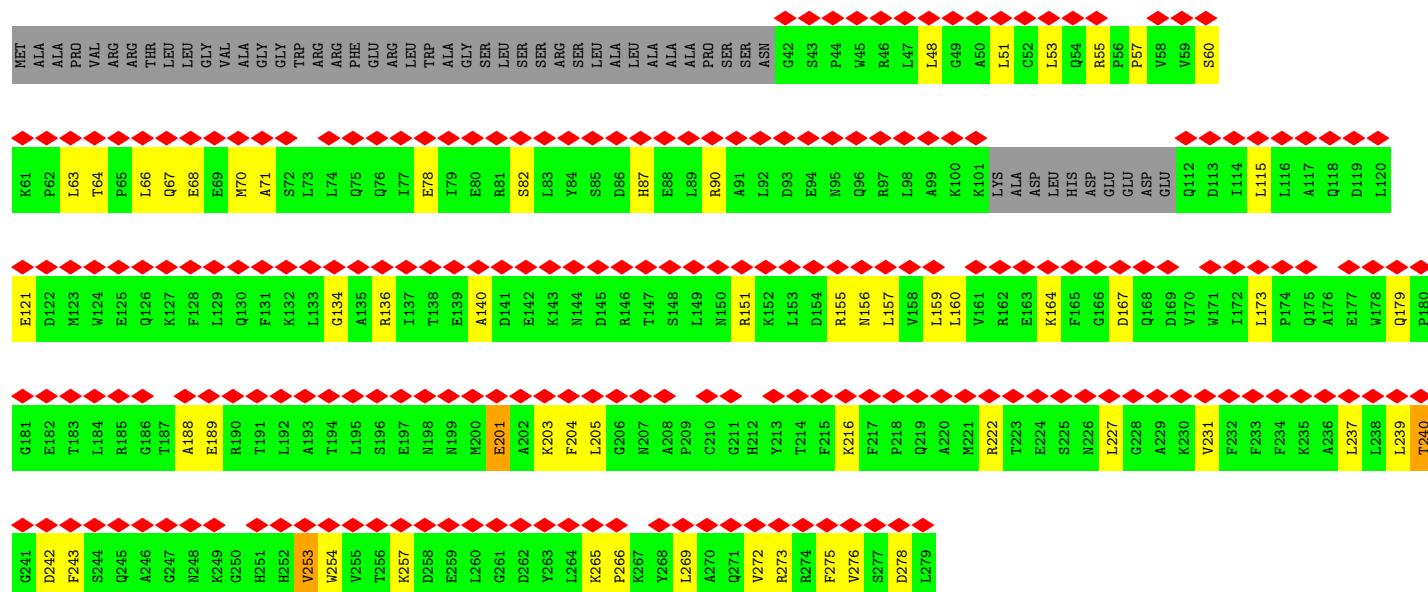
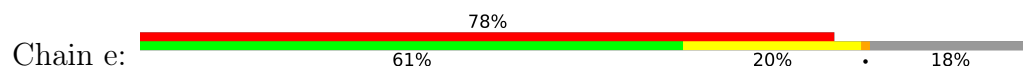
Chain d: 24% 69% 15% 17%



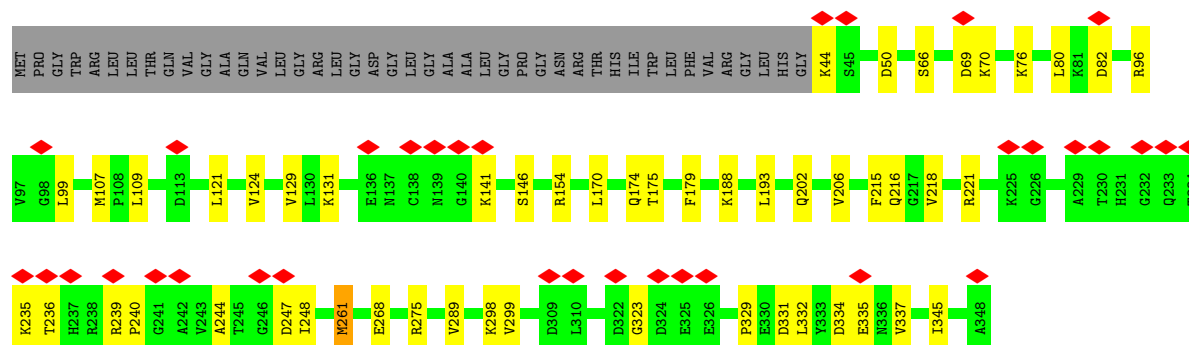
- Molecule 29: 39S ribosomal protein L2, mitochondrial



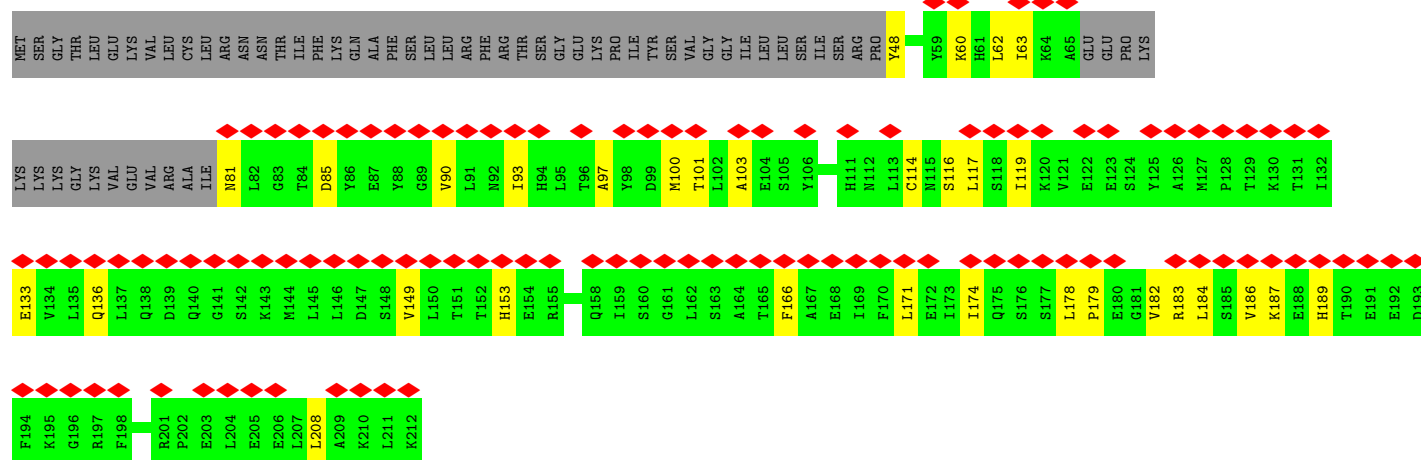
• Molecule 30: 39S ribosomal protein L46, mitochondrial



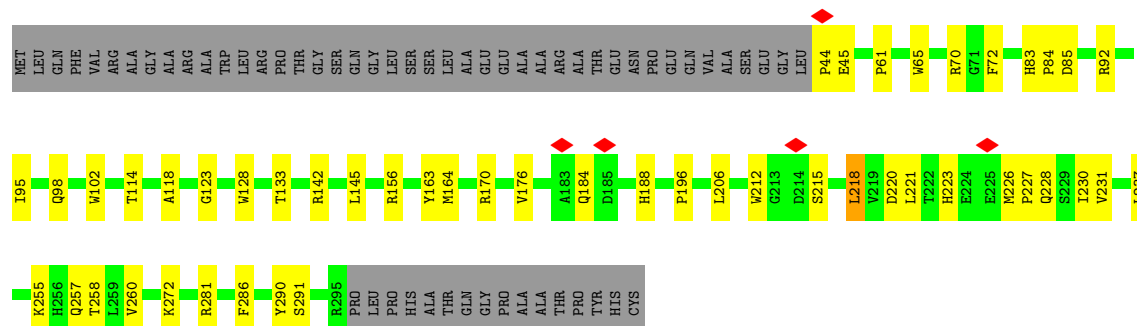
• Molecule 31: 39S ribosomal protein L3, mitochondrial



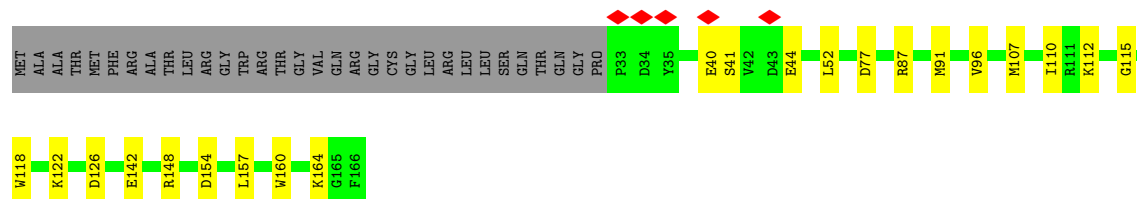
• Molecule 32: 39S ribosomal protein L48, mitochondrial



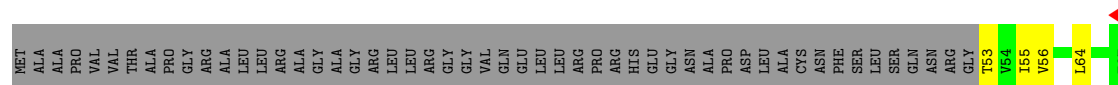
• Molecule 33: 39S ribosomal protein L4, mitochondrial

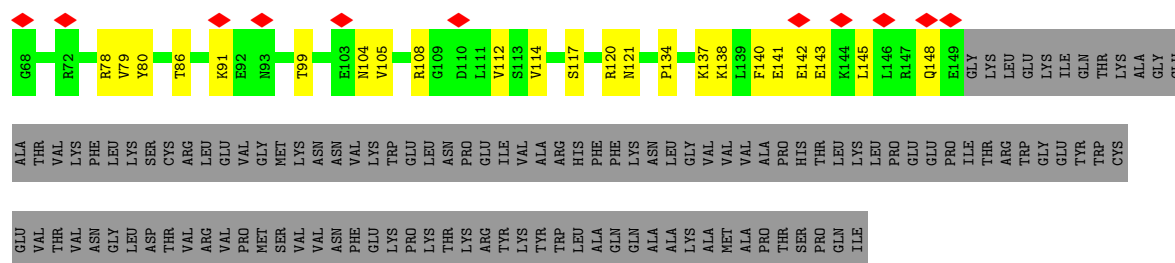


• Molecule 34: 39S ribosomal protein L49, mitochondrial

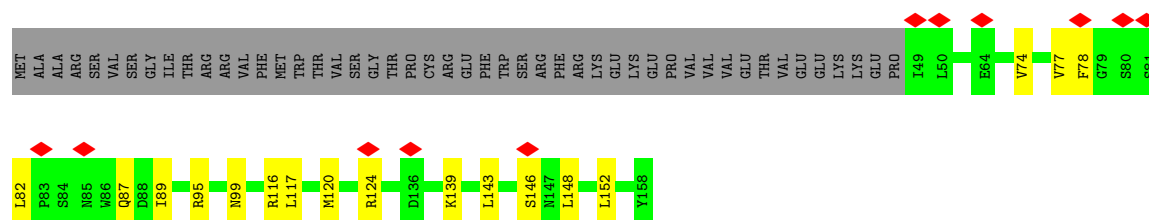


• Molecule 35: 39S ribosomal protein L9, mitochondrial

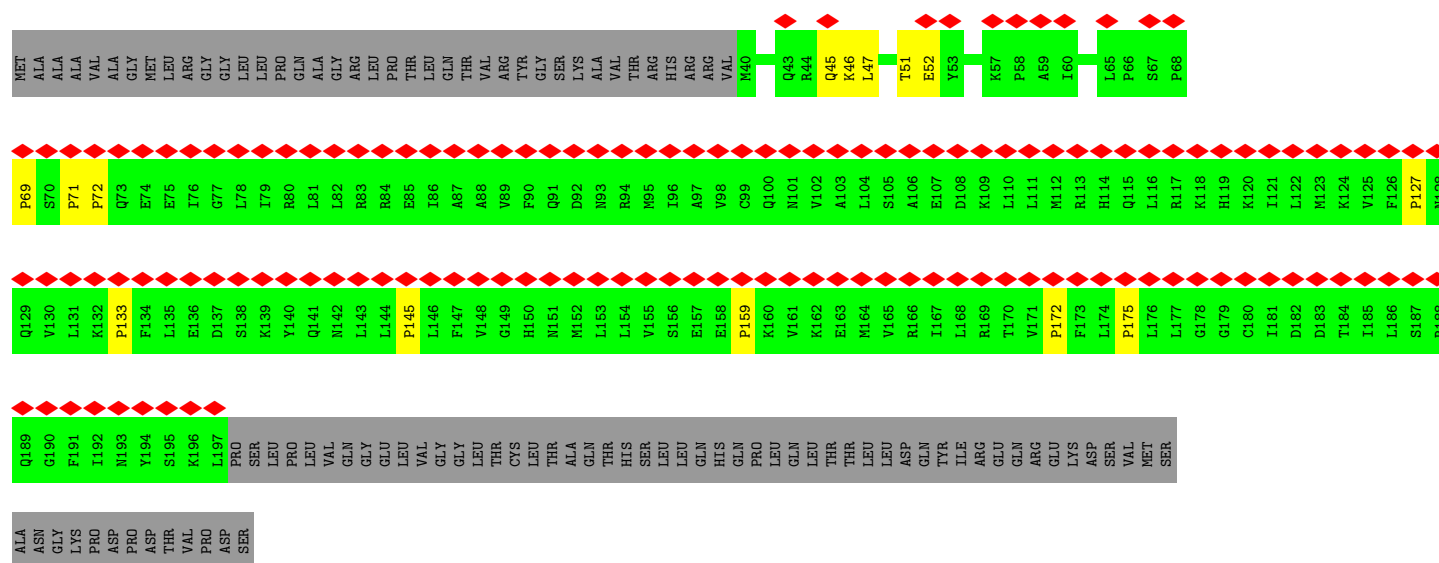




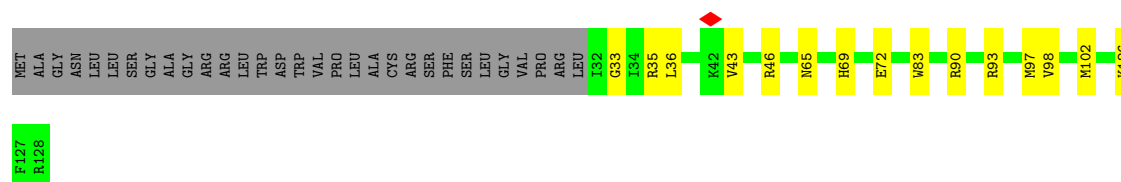
- Molecule 36: 39S ribosomal protein L50, mitochondrial



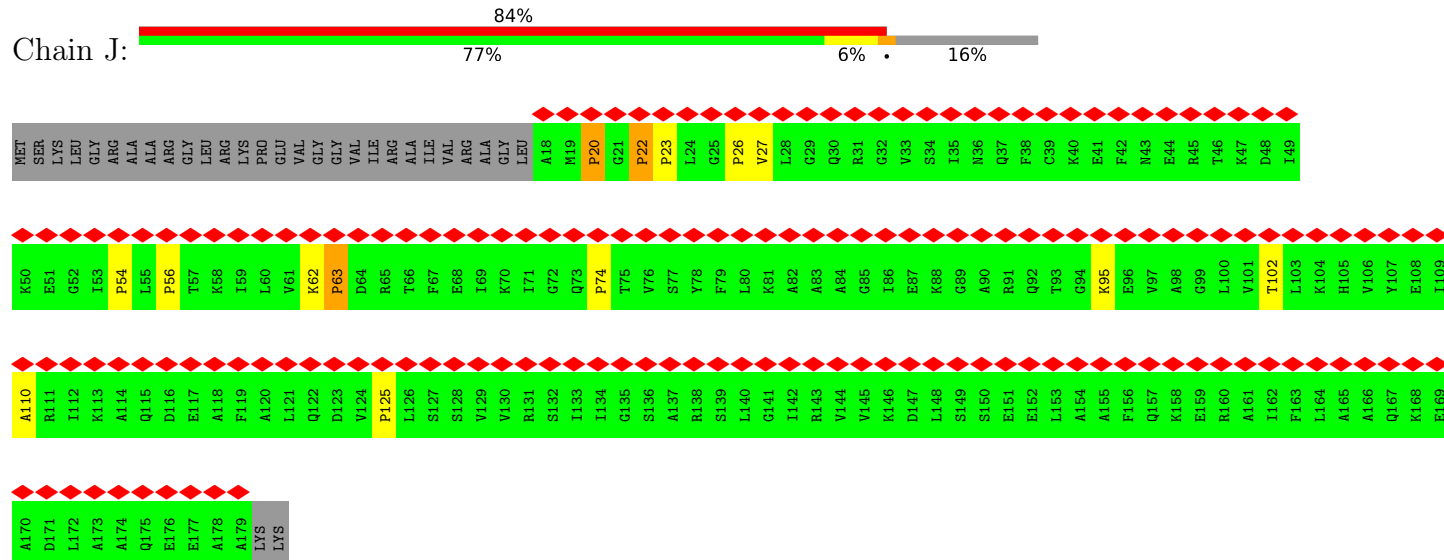
- Molecule 37: 39S ribosomal protein L10, mitochondrial



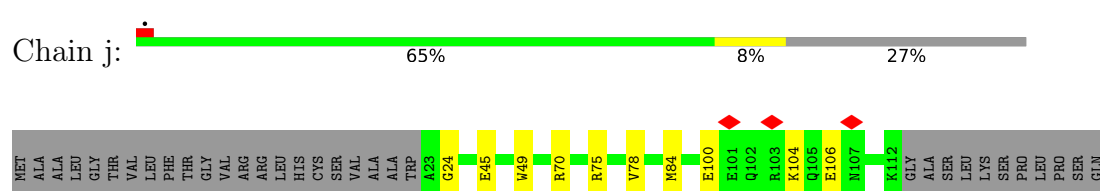
- Molecule 38: 39S ribosomal protein L51, mitochondrial



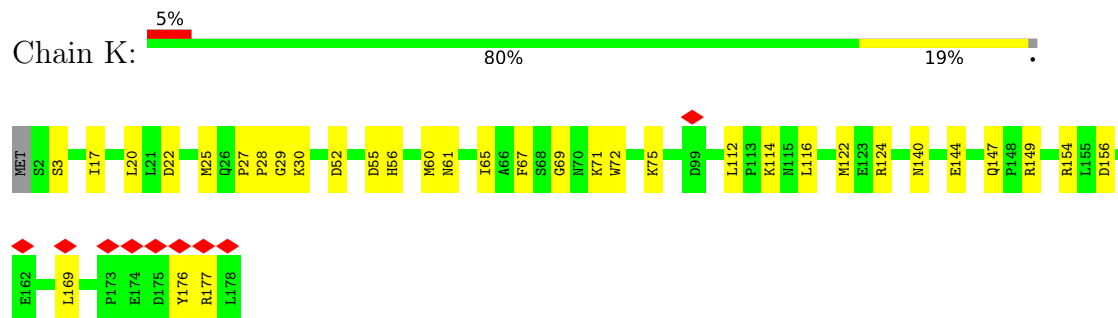
- Molecule 39: 39S ribosomal protein L11, mitochondrial



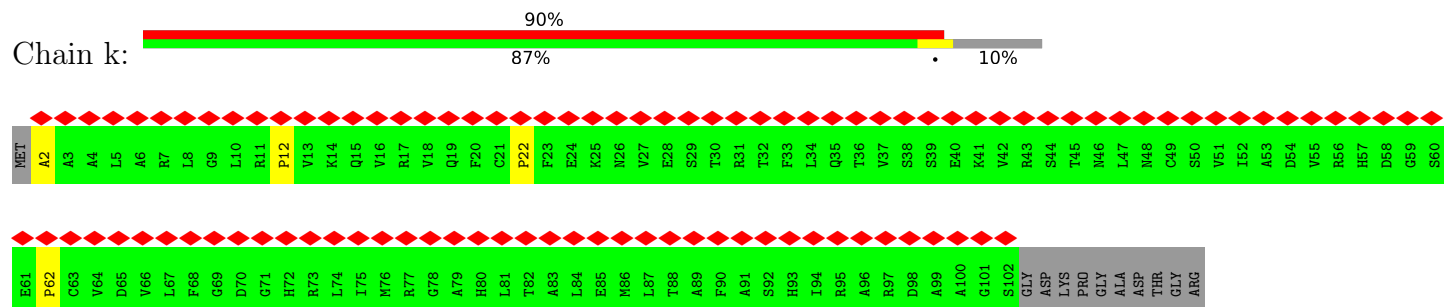
- Molecule 40: 39S ribosomal protein L52, mitochondrial



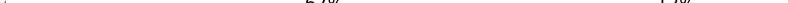
- Molecule 41: 39S ribosomal protein L13, mitochondrial

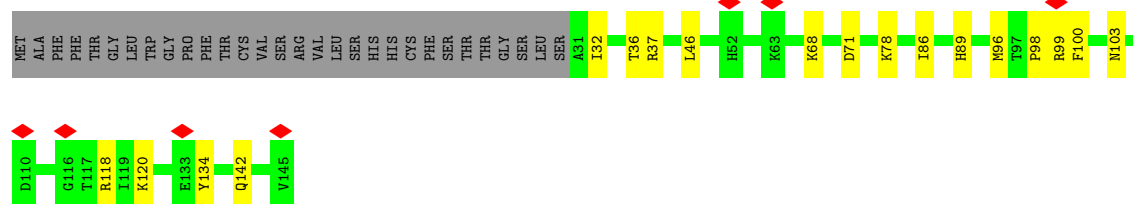


- Molecule 42: 39S ribosomal protein L53, mitochondrial

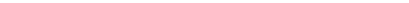


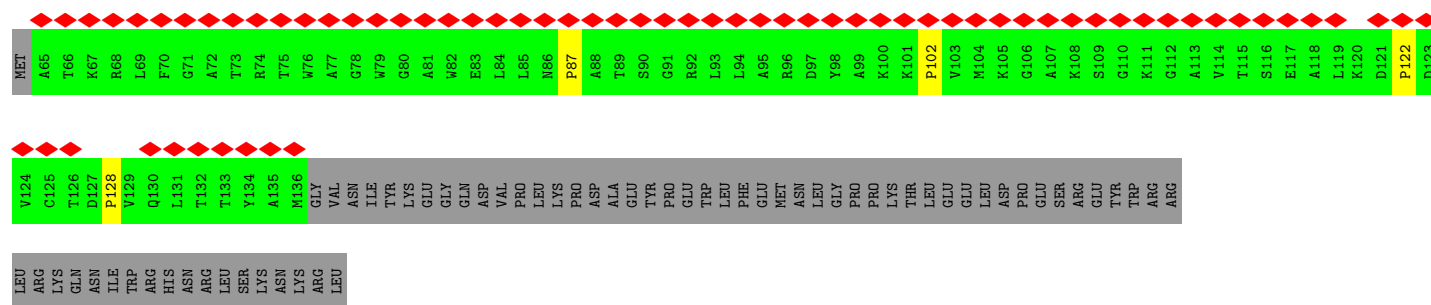
- Molecule 43: 39S ribosomal protein L14, mitochondrial

Chain L:  5% 67% 12% 21%

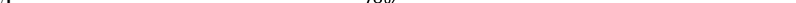


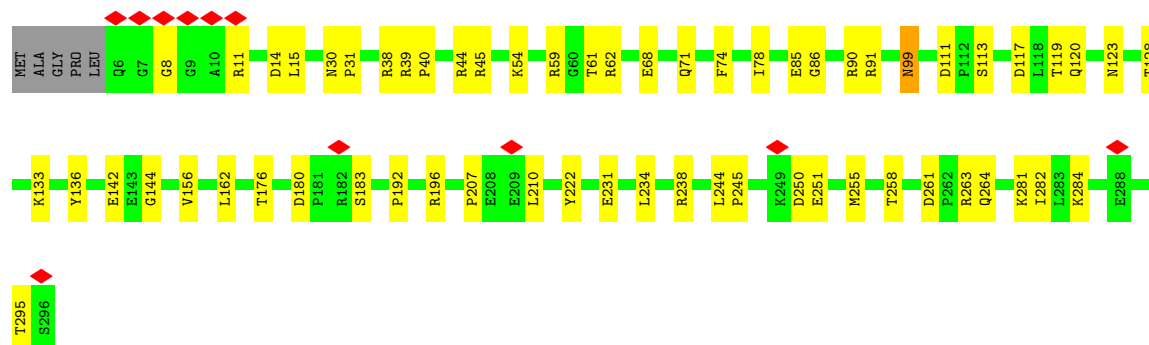
- Molecule 44: 39S ribosomal protein L54, mitochondrial

Chain 1:  49% 49% . 48%

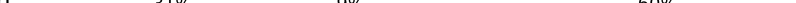


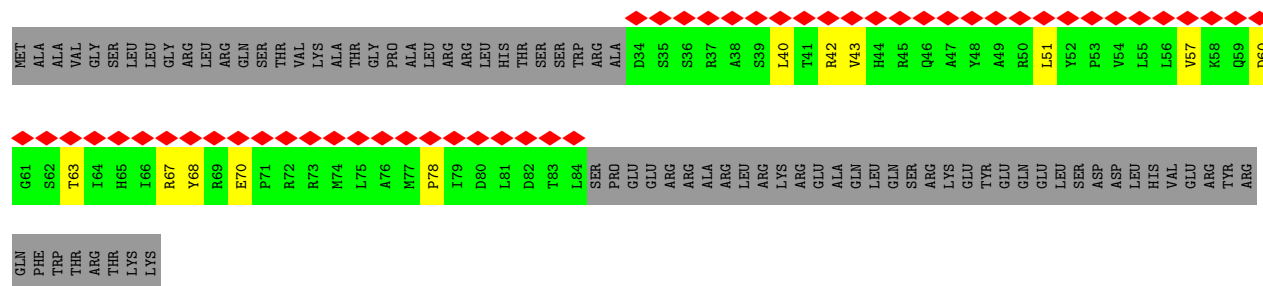
- Molecule 45: 39S ribosomal protein L15, mitochondrial

Chain M:  78% 20%

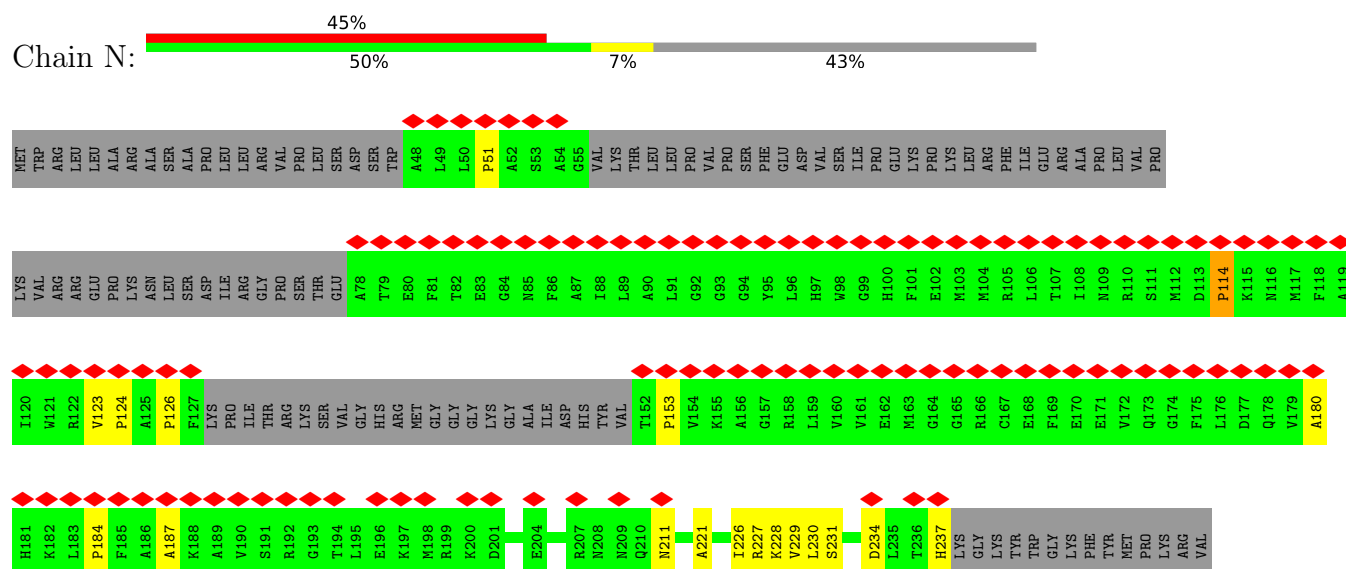


- Molecule 46: 39S ribosomal protein L55, mitochondrial

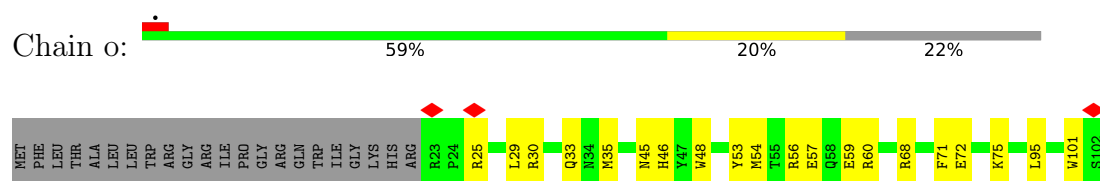
Chain m: 



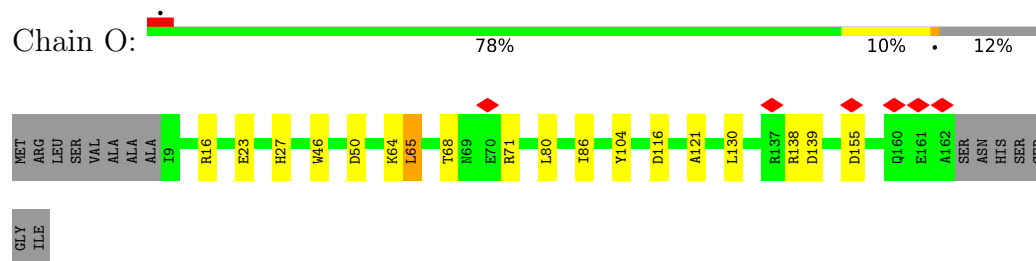
- Molecule 47: 39S ribosomal protein L16, mitochondrial



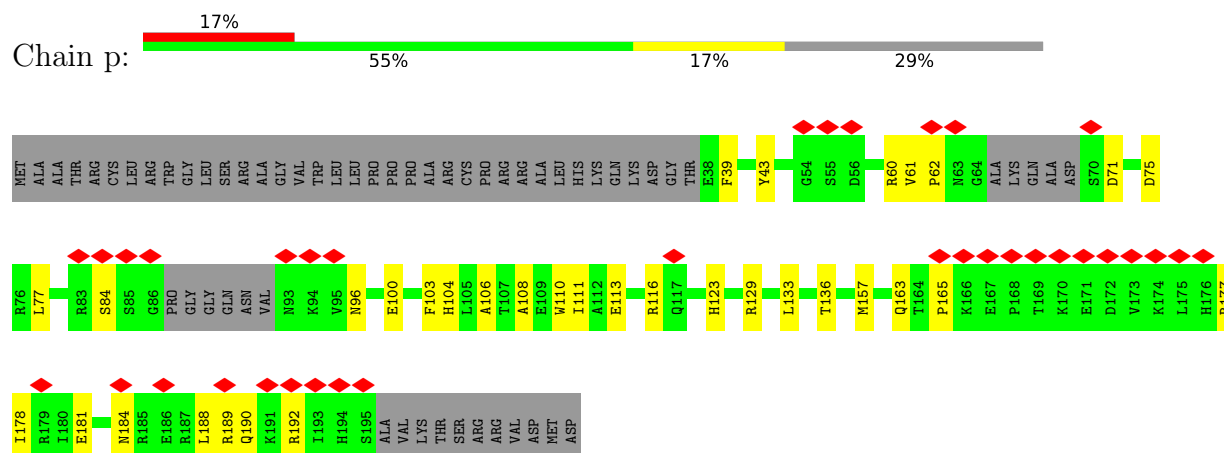
- Molecule 48: Ribosomal protein 63, mitochondrial

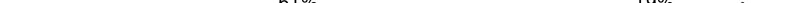


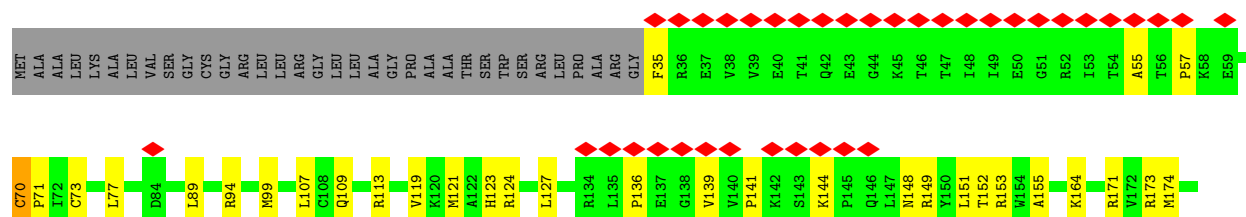
- Molecule 49: 39S ribosomal protein L17, mitochondrial

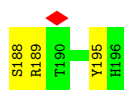


- Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial



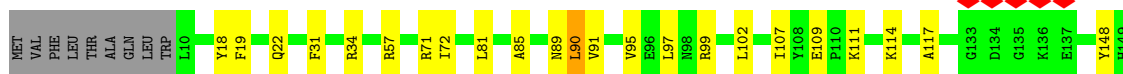
- Chain P: 





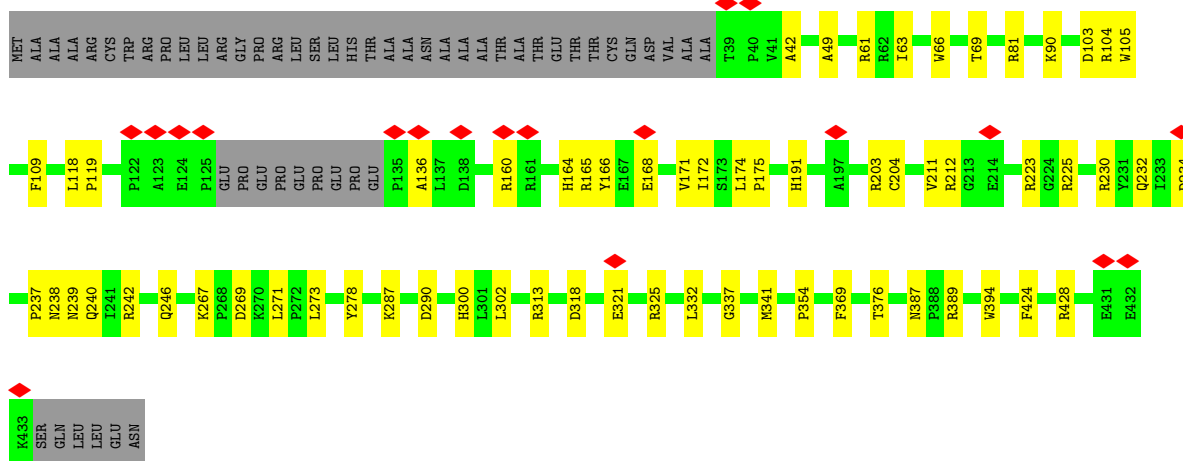
- Molecule 55: 39S ribosomal protein L20, mitochondrial

Chain R: 79% 15% 6%



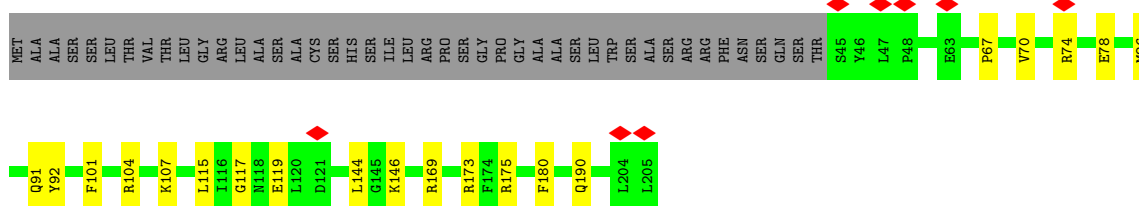
- Molecule 56: 39S ribosomal protein S30, mitochondrial

Chain s: 73% 15% 12%



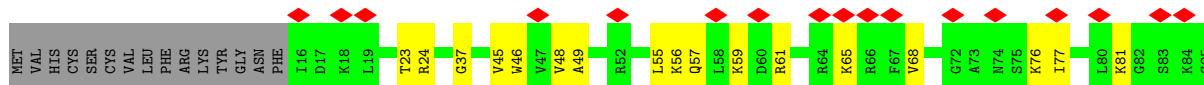
- Molecule 57: 39S ribosomal protein L21, mitochondrial

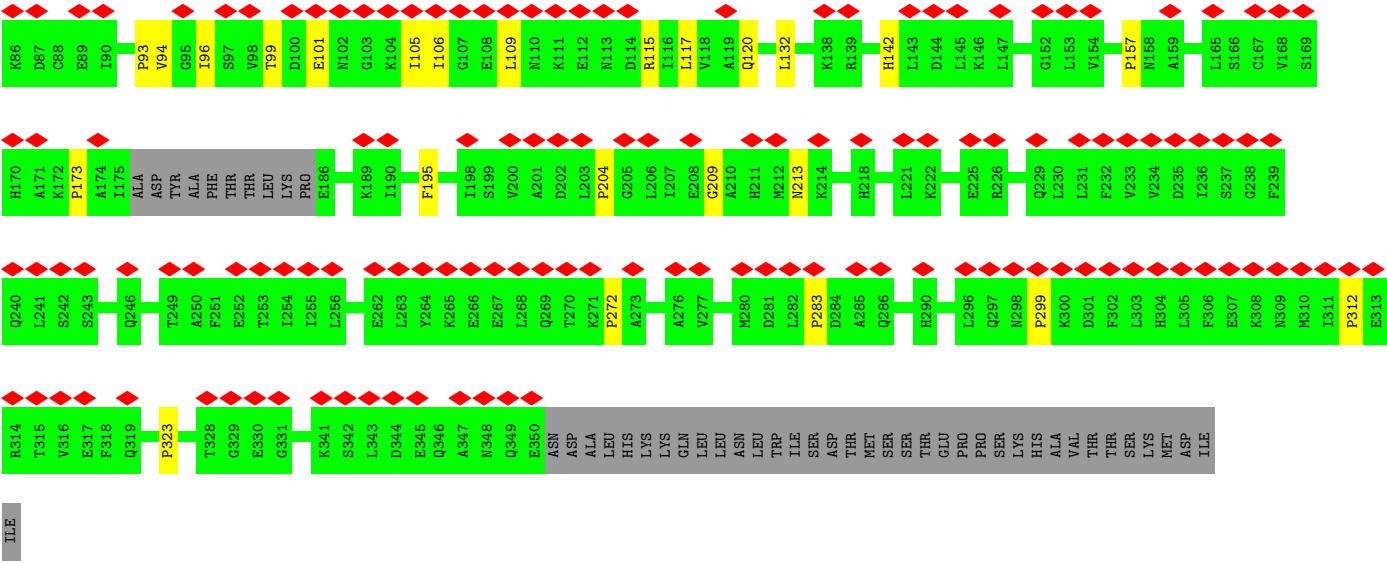
Chain S: 69% 10% 21%



- Molecule 58: GTP-binding protein 10

Chain t: 40% 73% 11% 16%





ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31656	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	4.028	Depositor
Minimum map value	-2.106	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.160	Depositor
Recommended contour level	0.747	Depositor
Map size ($\text{\AA}$)	518.4, 518.4, 518.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	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: AYA, ACE, SAC, PM8, K, ZN, SAM, GNP, 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	0	0.11	0/913	0.22	0/1224
2	T	0.11	0/1403	0.24	0/1886
3	u	0.12	0/1069	0.30	0/1447
4	1	0.10	0/460	0.23	0/610
5	U	0.11	0/1274	0.24	0/1723
6	v	0.14	0/597	0.34	0/796
7	2	0.11	0/383	0.22	0/507
8	V	0.09	0/1721	0.22	0/2333
9	w	0.12	0/647	0.37	0/871
10	3	0.11	0/853	0.23	0/1136
11	W	0.11	0/857	0.22	0/1155
12	x	0.11	0/2737	0.26	0/3714
13	5	0.11	0/3305	0.25	0/4502
14	X	0.10	0/2099	0.22	0/2837
15	y	0.11	0/2011	0.25	0/2702
16	6	0.10	0/3043	0.26	0/4140
17	Y	0.11	0/1593	0.21	0/2136
18	z	0.11	0/2484	0.26	0/3349
19	7	0.10	0/2447	0.23	0/3310
20	Z	0.10	0/1021	0.24	0/1378
21	8	0.10	0/880	0.31	0/1188
22	a	0.11	0/866	0.25	0/1174
23	9	0.11	0/1025	0.24	0/1379
24	b	0.14	0/1211	0.26	0/1639
25	A	0.12	0/33779	0.25	0/52552
26	c	0.10	0/2347	0.23	0/3171
27	B	0.08	0/1700	0.17	0/2641
28	d	0.09	0/2145	0.23	0/2903
29	D	0.11	0/1910	0.25	0/2569
30	e	0.08	0/1885	0.25	0/2542
31	E	0.10	0/2475	0.24	0/3355
32	f	0.09	0/1216	0.24	0/1638

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	F	0.12	0/2090	0.27	0/2842
34	g	0.11	0/1151	0.25	0/1569
35	H	0.10	0/816	0.23	0/1097
36	h	0.09	0/918	0.21	0/1249
37	I	0.22	0/880	0.75	9/1220 (0.7%)
38	i	0.12	0/850	0.23	0/1135
39	J	0.26	0/797	0.90	11/1107 (1.0%)
40	j	0.10	0/737	0.19	0/992
41	K	0.11	0/1490	0.24	0/2021
42	k	0.25	0/493	0.70	3/685 (0.4%)
43	L	0.11	0/905	0.26	0/1218
44	l	0.22	0/352	0.77	4/487 (0.8%)
45	M	0.11	0/2381	0.24	0/3212
46	m	0.07	0/426	0.19	0/575
47	N	0.22	0/803	0.75	6/1105 (0.5%)
48	o	0.11	0/694	0.24	0/931
49	O	0.11	0/1283	0.24	0/1727
50	p	0.09	0/1223	0.22	0/1641
51	P	0.10	0/1199	0.24	0/1623
52	q	0.10	0/1208	0.21	0/1633
53	Q	0.10	0/1884	0.22	0/2535
54	r	0.13	0/1289	0.31	1/1752 (0.1%)
55	R	0.12	0/1175	0.23	0/1572
56	s	0.12	0/3239	0.25	0/4400
57	S	0.12	0/1320	0.27	0/1789
58	t	0.19	0/1971	0.56	8/2684 (0.3%)
All	All	0.12	0/113930	0.28	42/161308 (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
21	8	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	t	173	PRO	N-CA-CB	10.84	110.49	103.23
42	k	62	PRO	N-CA-CB	10.45	110.23	103.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	J	63	PRO	N-CA-CB	9.72	113.45	103.25
58	t	157	PRO	N-CA-CB	8.61	110.97	103.31
47	N	153	PRO	N-CA-CB	8.50	110.41	103.36

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	8	169	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	898	0	916	14	0
2	T	1369	0	1410	16	0
3	u	1044	0	1035	31	0
4	1	455	0	498	10	0
5	U	1251	0	1232	23	0
6	v	588	0	604	12	0
7	2	377	0	406	2	0
8	V	1676	0	1687	29	0
9	w	638	0	636	15	0
10	3	832	0	883	9	0
11	W	835	0	858	10	0
12	x	2676	0	2652	58	0
13	5	3210	0	3206	49	0
14	X	2044	0	2060	28	0
15	y	1980	0	2066	51	0
16	6	2948	0	2841	70	0
17	Y	1556	0	1597	22	0
18	z	2443	0	2545	40	0
19	7	2390	0	2397	46	0
20	Z	996	0	1044	18	0
21	8	860	0	852	26	0
22	a	840	0	810	14	0
23	9	997	0	987	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	b	1189	0	1188	24	0
25	A	30199	0	15338	427	0
26	c	2299	0	2320	30	0
27	B	1522	0	776	21	0
28	d	2088	0	2079	32	0
29	D	1872	0	1932	39	0
30	e	1848	0	1849	40	0
31	E	2406	0	2415	33	0
32	f	1196	0	1212	27	0
33	F	2031	0	2065	31	0
34	g	1113	0	1097	17	0
35	H	802	0	846	22	0
36	h	895	0	881	10	0
37	I	871	0	506	5	0
38	i	828	0	857	12	0
39	J	798	0	389	2	0
40	j	722	0	722	7	0
41	K	1455	0	1452	28	0
42	k	502	0	244	0	0
43	L	890	0	941	14	0
44	l	353	0	179	0	0
45	M	2327	0	2395	43	0
46	m	419	0	435	8	0
47	N	799	0	503	9	0
48	o	677	0	676	18	0
49	O	1259	0	1294	14	0
50	p	1205	0	1223	25	0
51	P	1173	0	1165	25	0
52	q	1177	0	1154	14	0
53	Q	1843	0	1878	27	0
54	r	1251	0	1204	28	0
55	R	1154	0	1214	18	0
56	s	3155	0	3139	44	0
57	S	1293	0	1365	15	0
58	t	1958	0	1486	24	0
59	0	1	0	0	0	0
60	w	32	0	39	2	0
61	x	27	0	22	4	0
62	t	32	0	13	0	0
62	z	32	0	13	2	0
63	A	92	0	0	0	0
63	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	g	1	0	0	0	0
63	t	1	0	0	0	0
63	z	1	0	0	0	0
64	A	10	0	0	0	0
All	All	108702	0	91728	1425	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 7.

The worst 5 of 1425 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)
25:A:2354:A:N6	25:A:2361:G:H1	1.42	1.18
27:B:1607:U:H3	27:B:1664:G:H1	1.05	1.02
25:A:2351:U:H3	25:A:2362:A:H62	1.11	0.91
25:A:2351:U:H3	25:A:2362:A:N6	1.75	0.85
13:5:126:THR:HG22	13:5:372:ASN:HB2	1.62	0.80

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	0	108/188 (57%)	108 (100%)	0	0	100	100
2	T	164/206 (80%)	162 (99%)	2 (1%)	0	100	100
3	u	124/234 (53%)	117 (94%)	7 (6%)	0	100	100
4	1	53/65 (82%)	53 (100%)	0	0	100	100
5	U	150/153 (98%)	148 (99%)	2 (1%)	0	100	100
6	v	67/70 (96%)	64 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	2	44/92 (48%)	44 (100%)	0	0	100	100
8	V	203/216 (94%)	201 (99%)	2 (1%)	0	100	100
9	w	77/156 (49%)	70 (91%)	7 (9%)	0	100	100
10	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
11	W	104/148 (70%)	102 (98%)	2 (2%)	0	100	100
12	x	334/384 (87%)	324 (97%)	10 (3%)	0	100	100
13	5	392/423 (93%)	385 (98%)	7 (2%)	0	100	100
14	X	242/256 (94%)	239 (99%)	3 (1%)	0	100	100
15	y	242/381 (64%)	238 (98%)	4 (2%)	0	100	100
16	6	352/380 (93%)	340 (97%)	12 (3%)	0	100	100
17	Y	179/250 (72%)	178 (99%)	1 (1%)	0	100	100
18	z	309/334 (92%)	302 (98%)	7 (2%)	0	100	100
19	7	292/338 (86%)	281 (96%)	11 (4%)	0	100	100
20	Z	120/161 (74%)	118 (98%)	2 (2%)	0	100	100
21	8	100/206 (48%)	98 (98%)	2 (2%)	0	100	100
22	a	96/142 (68%)	95 (99%)	1 (1%)	0	100	100
23	9	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
24	b	148/215 (69%)	143 (97%)	5 (3%)	0	100	100
26	c	282/332 (85%)	276 (98%)	6 (2%)	0	100	100
28	d	253/306 (83%)	251 (99%)	2 (1%)	0	100	100
29	D	238/305 (78%)	227 (95%)	11 (5%)	0	100	100
30	e	224/279 (80%)	221 (99%)	3 (1%)	0	100	100
31	E	303/348 (87%)	296 (98%)	7 (2%)	0	100	100
32	f	146/212 (69%)	142 (97%)	4 (3%)	0	100	100
33	F	250/311 (80%)	248 (99%)	2 (1%)	0	100	100
34	g	132/166 (80%)	129 (98%)	3 (2%)	0	100	100
35	H	95/267 (36%)	95 (100%)	0	0	100	100
36	h	108/158 (68%)	104 (96%)	4 (4%)	0	100	100
37	I	156/261 (60%)	153 (98%)	3 (2%)	0	100	100
38	i	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
39	J	160/192 (83%)	149 (93%)	7 (4%)	4 (2%)	4	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	j	88/123 (72%)	87 (99%)	1 (1%)	0	100	100
41	K	175/178 (98%)	171 (98%)	4 (2%)	0	100	100
42	k	99/112 (88%)	97 (98%)	2 (2%)	0	100	100
43	L	113/145 (78%)	110 (97%)	3 (3%)	0	100	100
44	l	70/138 (51%)	67 (96%)	3 (4%)	0	100	100
45	M	289/296 (98%)	288 (100%)	1 (0%)	0	100	100
46	m	49/128 (38%)	48 (98%)	1 (2%)	0	100	100
47	N	138/251 (55%)	132 (96%)	4 (3%)	2 (1%)	9	33
48	o	78/102 (76%)	78 (100%)	0	0	100	100
49	O	152/175 (87%)	148 (97%)	4 (3%)	0	100	100
50	p	141/206 (68%)	136 (96%)	5 (4%)	0	100	100
51	P	142/180 (79%)	141 (99%)	1 (1%)	0	100	100
52	q	139/222 (63%)	139 (100%)	0	0	100	100
53	Q	219/292 (75%)	217 (99%)	2 (1%)	0	100	100
54	r	160/196 (82%)	159 (99%)	1 (1%)	0	100	100
55	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
56	s	382/439 (87%)	374 (98%)	8 (2%)	0	100	100
57	S	159/205 (78%)	158 (99%)	1 (1%)	0	100	100
58	t	321/387 (83%)	307 (96%)	14 (4%)	0	100	100
All	All	9609/12512 (77%)	9399 (98%)	204 (2%)	6 (0%)	49	78

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	J	22	PRO
39	J	63	PRO
47	N	114	PRO
39	J	20	PRO
39	J	27	VAL

5.3.2 Protein sidechains ⓘ

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	0	99/164 (60%)	99 (100%)	0	100	100
2	T	146/176 (83%)	144 (99%)	2 (1%)	59	78
3	u	118/200 (59%)	114 (97%)	4 (3%)	32	63
4	1	52/60 (87%)	52 (100%)	0	100	100
5	U	134/135 (99%)	134 (100%)	0	100	100
6	v	59/60 (98%)	55 (93%)	4 (7%)	14	42
7	2	40/72 (56%)	40 (100%)	0	100	100
8	V	183/191 (96%)	178 (97%)	5 (3%)	39	68
9	w	73/136 (54%)	72 (99%)	1 (1%)	59	78
10	3	88/166 (53%)	87 (99%)	1 (1%)	65	80
11	W	86/119 (72%)	86 (100%)	0	100	100
12	x	293/328 (89%)	287 (98%)	6 (2%)	48	73
13	5	353/368 (96%)	348 (99%)	5 (1%)	59	78
14	X	220/229 (96%)	219 (100%)	1 (0%)	81	86
15	y	226/350 (65%)	222 (98%)	4 (2%)	51	74
16	6	313/332 (94%)	311 (99%)	2 (1%)	78	85
17	Y	163/223 (73%)	163 (100%)	0	100	100
18	z	270/287 (94%)	261 (97%)	9 (3%)	33	64
19	7	270/303 (89%)	268 (99%)	2 (1%)	76	84
20	Z	113/147 (77%)	113 (100%)	0	100	100
21	8	93/190 (49%)	93 (100%)	0	100	100
22	a	96/133 (72%)	96 (100%)	0	100	100
23	9	104/112 (93%)	102 (98%)	2 (2%)	50	73
24	b	131/185 (71%)	128 (98%)	3 (2%)	44	70
26	c	251/288 (87%)	249 (99%)	2 (1%)	73	83
28	d	233/274 (85%)	231 (99%)	2 (1%)	70	82
29	D	194/245 (79%)	194 (100%)	0	100	100
30	e	198/236 (84%)	193 (98%)	5 (2%)	42	69
31	E	260/290 (90%)	258 (99%)	2 (1%)	73	83
32	f	133/188 (71%)	133 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	F	219/262 (84%)	217 (99%)	2 (1%)	70	82
34	g	124/148 (84%)	124 (100%)	0	100	100
35	H	88/228 (39%)	88 (100%)	0	100	100
36	h	104/148 (70%)	104 (100%)	0	100	100
37	I	27/232 (12%)	27 (100%)	0	100	100
38	i	86/110 (78%)	85 (99%)	1 (1%)	63	79
40	j	72/97 (74%)	71 (99%)	1 (1%)	59	78
41	K	154/155 (99%)	153 (99%)	1 (1%)	78	85
43	L	98/124 (79%)	98 (100%)	0	100	100
45	M	246/249 (99%)	243 (99%)	3 (1%)	63	79
46	m	46/113 (41%)	46 (100%)	0	100	100
47	N	25/211 (12%)	24 (96%)	1 (4%)	28	59
48	o	69/87 (79%)	69 (100%)	0	100	100
49	O	134/150 (89%)	133 (99%)	1 (1%)	76	84
50	p	135/181 (75%)	135 (100%)	0	100	100
51	P	126/155 (81%)	125 (99%)	1 (1%)	73	83
52	q	119/178 (67%)	118 (99%)	1 (1%)	73	83
53	Q	203/256 (79%)	201 (99%)	2 (1%)	68	81
54	r	126/169 (75%)	125 (99%)	1 (1%)	73	83
55	R	118/126 (94%)	117 (99%)	1 (1%)	73	83
56	s	340/381 (89%)	340 (100%)	0	100	100
57	S	146/180 (81%)	145 (99%)	1 (1%)	76	84
58	t	106/331 (32%)	102 (96%)	4 (4%)	29	60
All	All	7903/10458 (76%)	7820 (99%)	83 (1%)	63	80

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	e	201	GLU
49	O	65	LEU
30	e	253	VAL
40	j	106	GLU
53	Q	275	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
53	Q	209	GLN
55	R	89	ASN
56	s	387	ASN
18	z	290	ASN
18	z	153	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	A	1409/1589 (88%)	295 (20%)	11 (0%)
27	B	71/72 (98%)	12 (16%)	0
All	All	1480/1661 (89%)	307 (20%)	11 (0%)

5 of 307 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	A	1672	C
25	A	1676	A
25	A	1678	C
25	A	1681	G
25	A	1689	C

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	2994	A
25	A	2995	U
25	A	3073	U
25	A	3071	G
25	A	2530	A

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

3 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	$\# Z > 2$
5	AYA	U	2	5	6,7,8	1.33	1 (16%)	6,8,10	1.01	1 (16%)
42	AYA	k	2	42	6,7,8	1.24	1 (16%)	6,8,10	1.09	1 (16%)
41	SAC	K	2	41	7,8,9	1.02	0	7,9,11	0.97	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
5	AYA	U	2	5	-	2/5/6/8	-
42	AYA	k	2	42	-	0/5/6/8	-
41	SAC	K	2	41	-	3/7/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	U	2	AYA	CA-N	-2.60	1.43	1.46
42	k	2	AYA	CA-N	-2.19	1.44	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	k	2	AYA	CB-CA-N	2.48	112.48	109.68
5	U	2	AYA	CB-CA-N	2.33	112.31	109.68

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	U	2	AYA	O-C-CA-CB
41	K	2	SAC	O-C-CA-CB
41	K	2	SAC	N-CA-CB-OG
41	K	2	SAC	C-CA-CB-OG
5	U	2	AYA	C-CA-N-CT

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 111 ligands modelled in this entry, 107 are monoatomic - leaving 4 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	$\# Z > 2$
60	PM8	w	200	9	26,31,31	1.81	6 (23%)	30,38,38	1.83	9 (30%)
62	GNP	z	401	63	34,34,34	1.27	5 (14%)	47,54,54	0.65	0
61	SAM	x	401	-	27,29,29	1.10	4 (14%)	34,42,42	2.00	9 (26%)
62	GNP	t	1000	63	34,34,34	1.32	5 (14%)	47,54,54	0.62	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
60	PM8	w	200	9	-	17/36/38/38	-
62	GNP	z	401	63	-	6/18/38/38	0/3/3/3
61	SAM	x	401	-	-	8/17/33/33	0/3/3/3
62	GNP	t	1000	63	-	3/18/38/38	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	w	200	PM8	C34-N36	5.66	1.46	1.33
60	w	200	PM8	C39-N41	5.01	1.45	1.33
62	t	1000	GNP	PB-O3A	4.61	1.64	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	z	401	GNP	PB-O3A	4.32	1.64	1.59
62	t	1000	GNP	PB-O1B	3.29	1.51	1.46

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	w	200	PM8	C2-C1-S1	5.66	120.14	113.40
61	x	401	SAM	N3-C2-N1	-5.46	120.31	128.58
61	x	401	SAM	C5-C4-N3	-4.61	120.37	126.72
61	x	401	SAM	N9-C8-N7	-3.75	108.62	113.94
61	x	401	SAM	C2-N3-C4	3.41	120.16	111.83

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

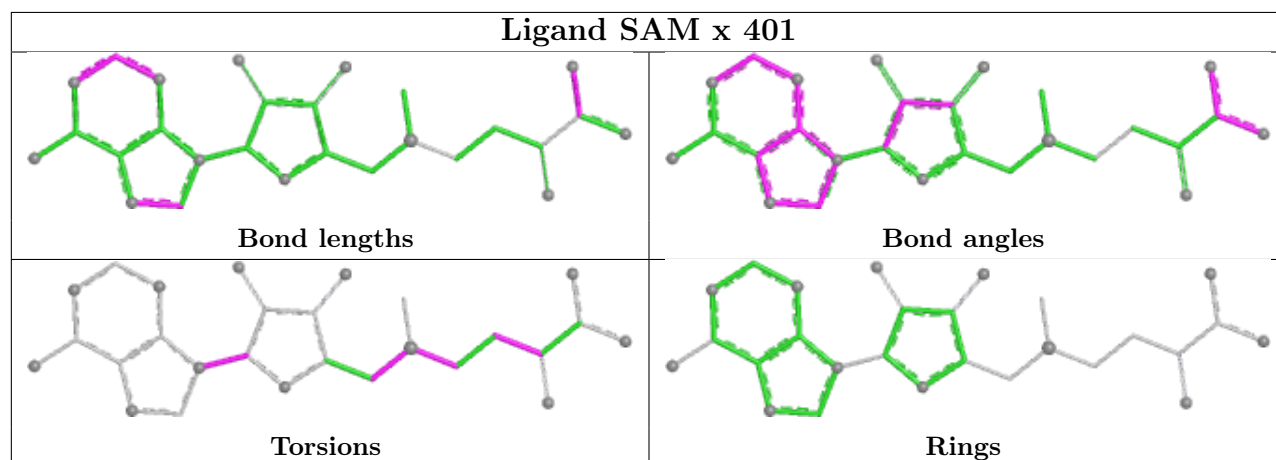
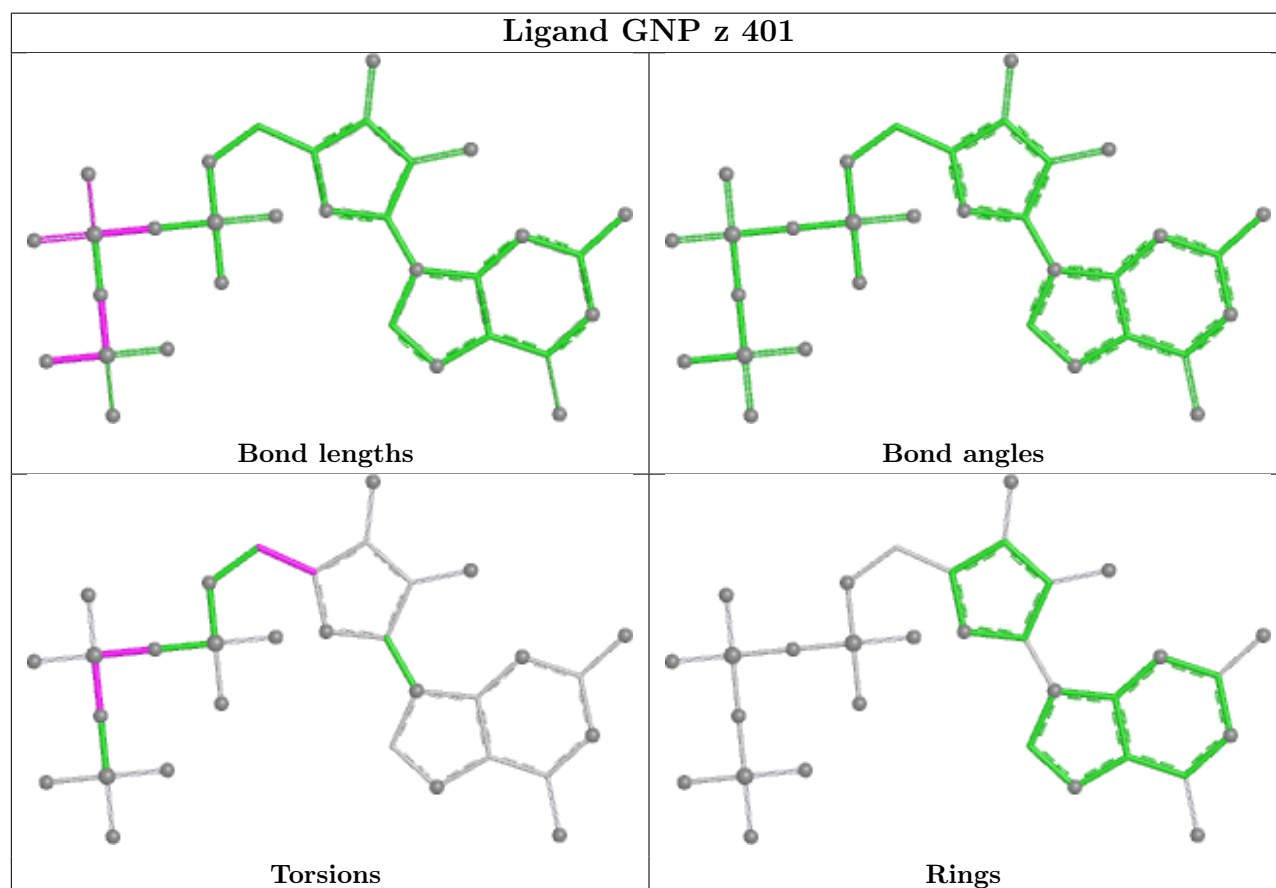
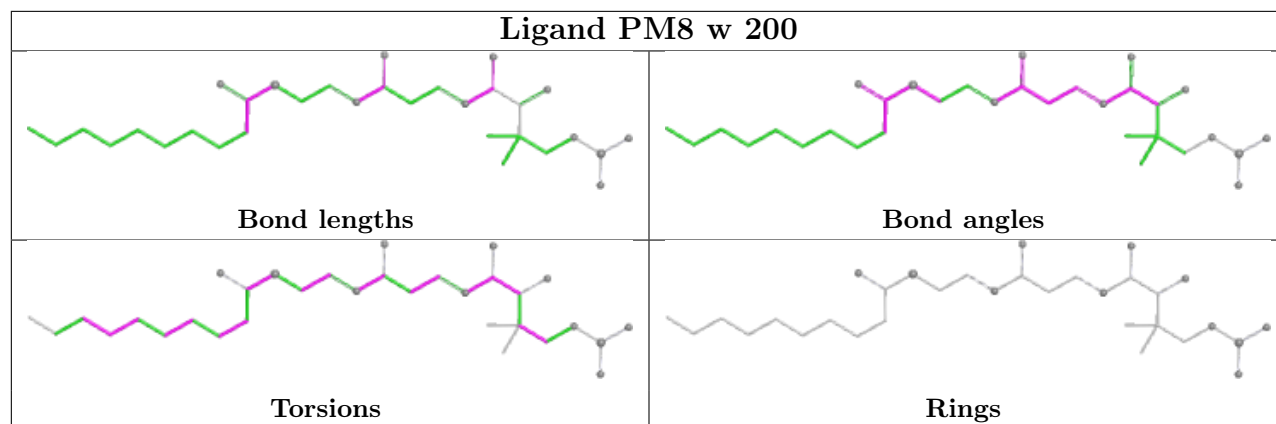
Mol	Chain	Res	Type	Atoms
60	w	200	PM8	O27-C28-C29-C30
60	w	200	PM8	O27-C28-C29-C31
60	w	200	PM8	O27-C28-C29-C32
60	w	200	PM8	C32-C34-N36-C37
60	w	200	PM8	N36-C37-C38-C39

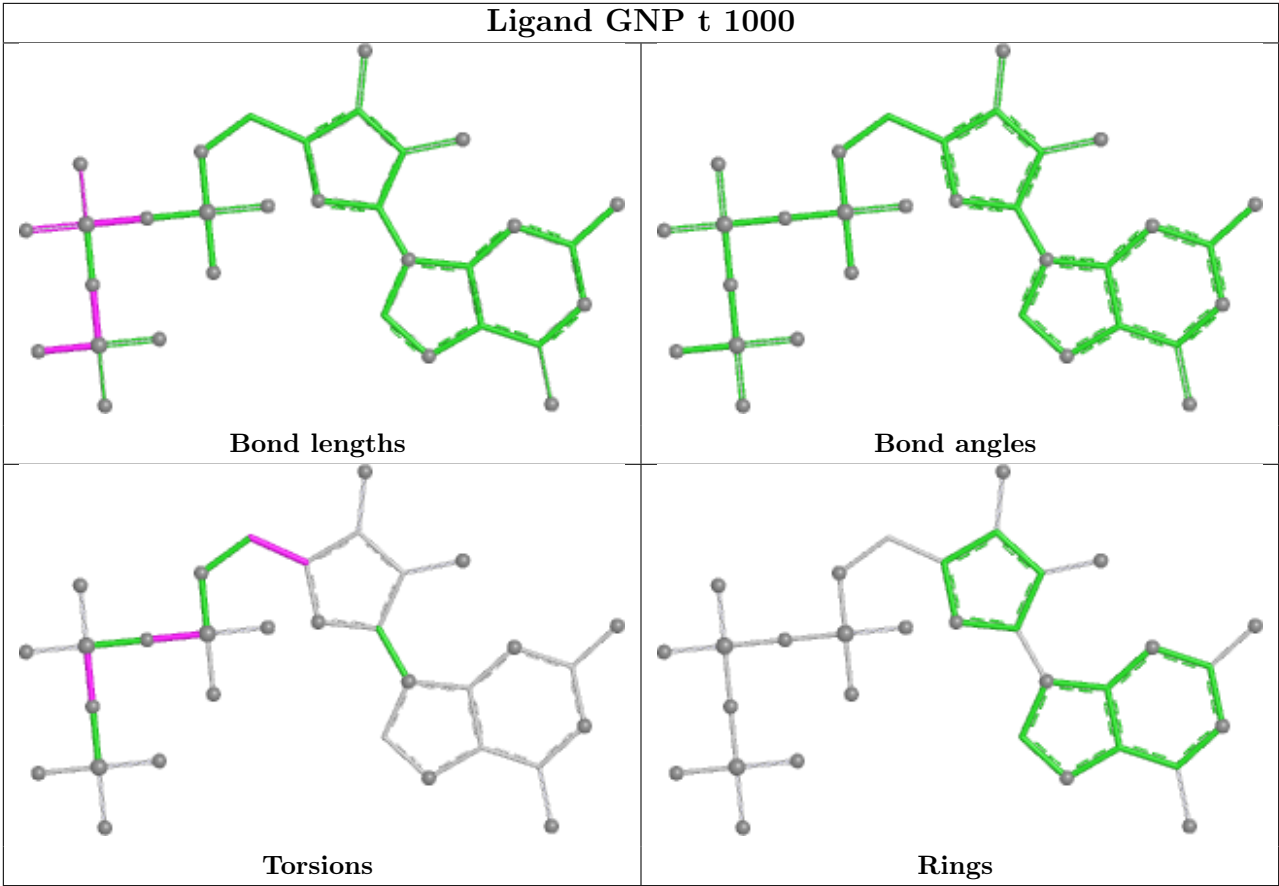
There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	w	200	PM8	2	0
62	z	401	GNP	2	0
61	x	401	SAM	4	0

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





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2554:U	O3'	2555:A	P	17.72
1	A	2570:U	O3'	2571:A	P	17.44
1	A	2547:C	O3'	2548:U	P	12.62

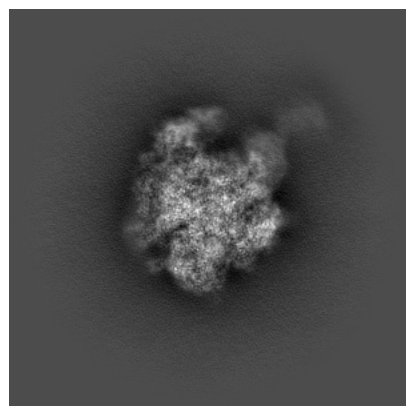
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17719. These allow visual inspection of the internal detail of the map and identification of artifacts.

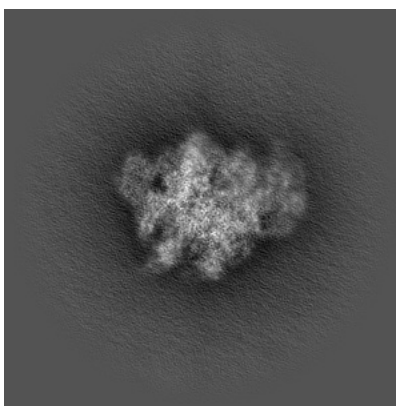
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

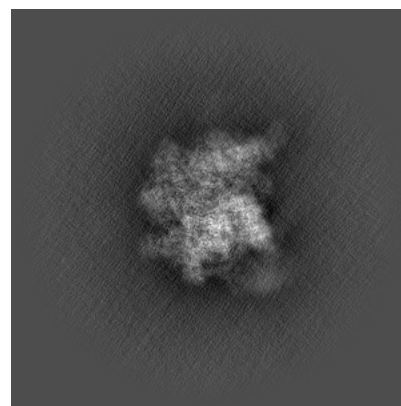
6.1.1 Primary map



X

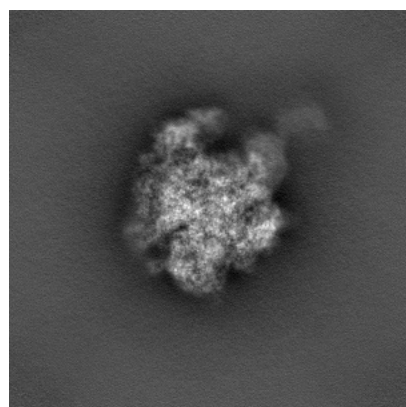


Y

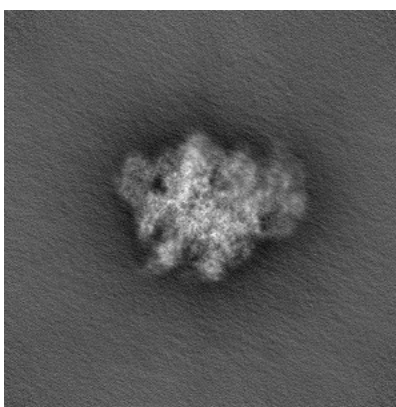


Z

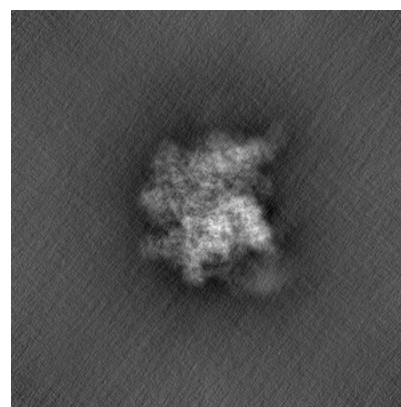
6.1.2 Raw map



X



Y

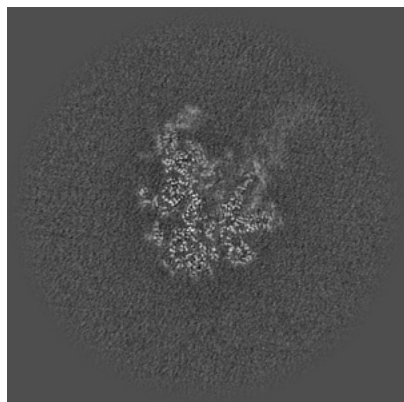


Z

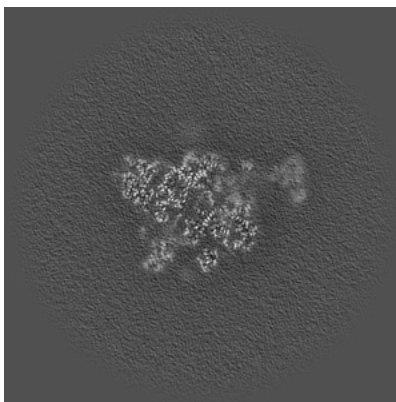
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

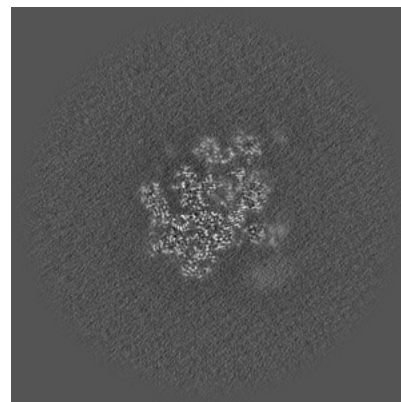
6.2.1 Primary map



X Index: 240

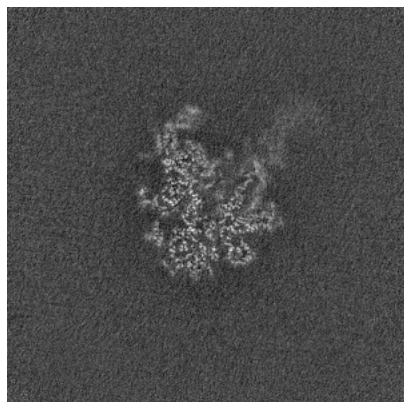


Y Index: 240

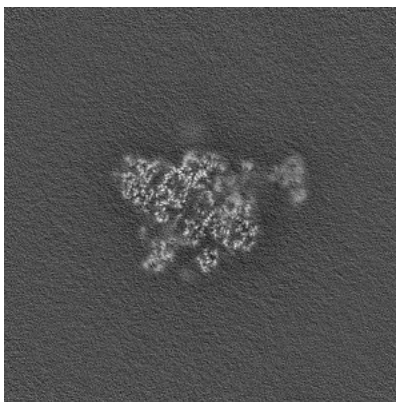


Z Index: 240

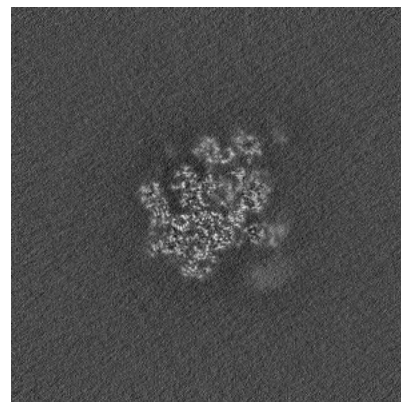
6.2.2 Raw map



X Index: 240



Y Index: 240

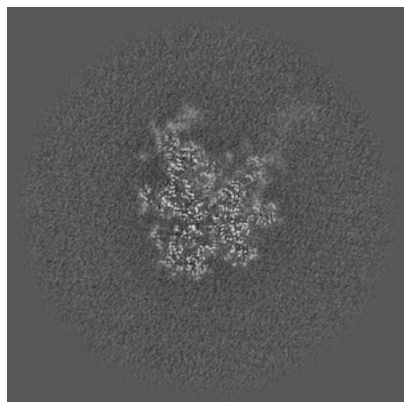


Z Index: 240

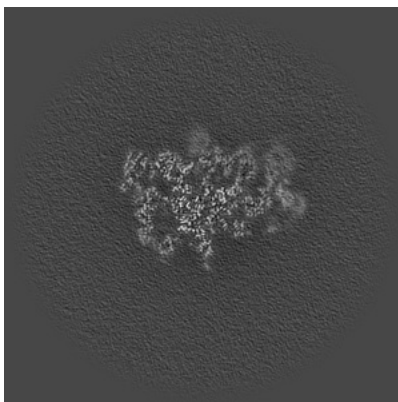
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

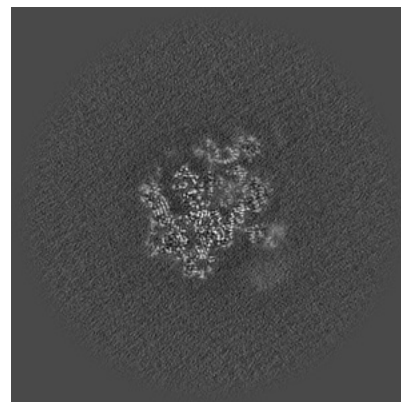
6.3.1 Primary map



X Index: 237

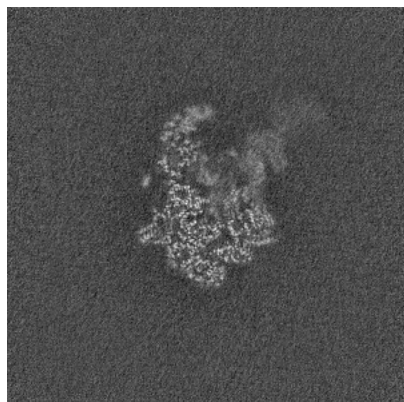


Y Index: 217

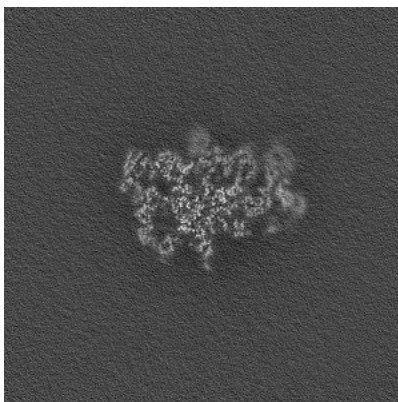


Z Index: 242

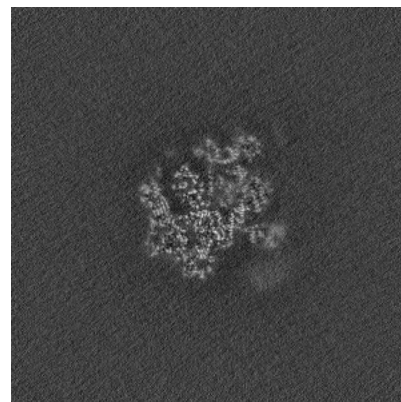
6.3.2 Raw map



X Index: 250



Y Index: 217

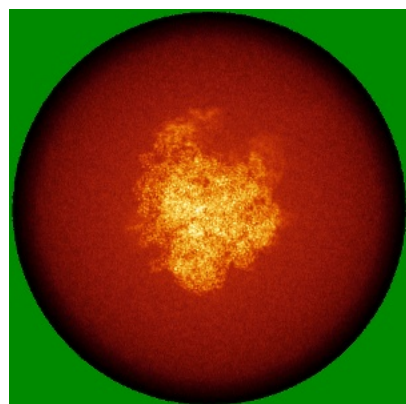


Z Index: 242

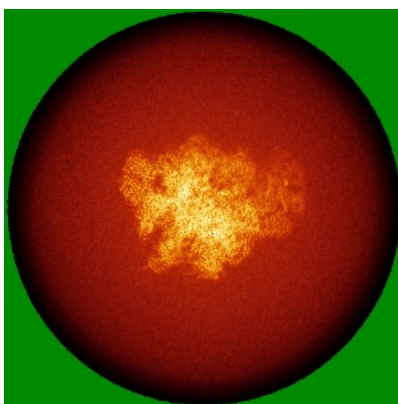
The images above show the largest variance slices of the map in three orthogonal directions.

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

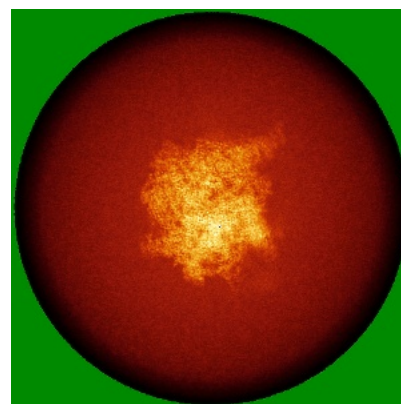
6.4.1 Primary map



X

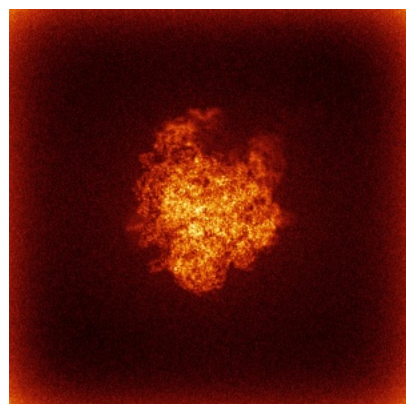


Y

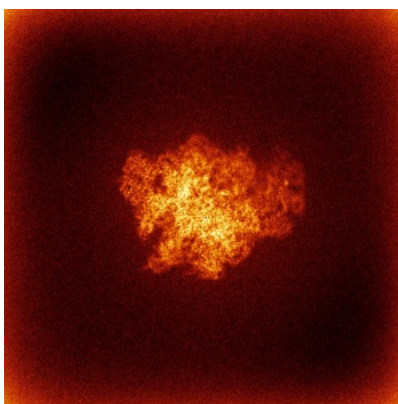


Z

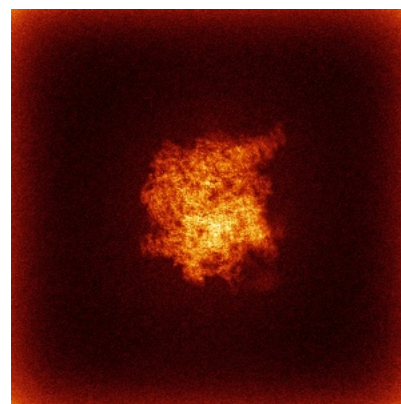
6.4.2 Raw map



X



Y

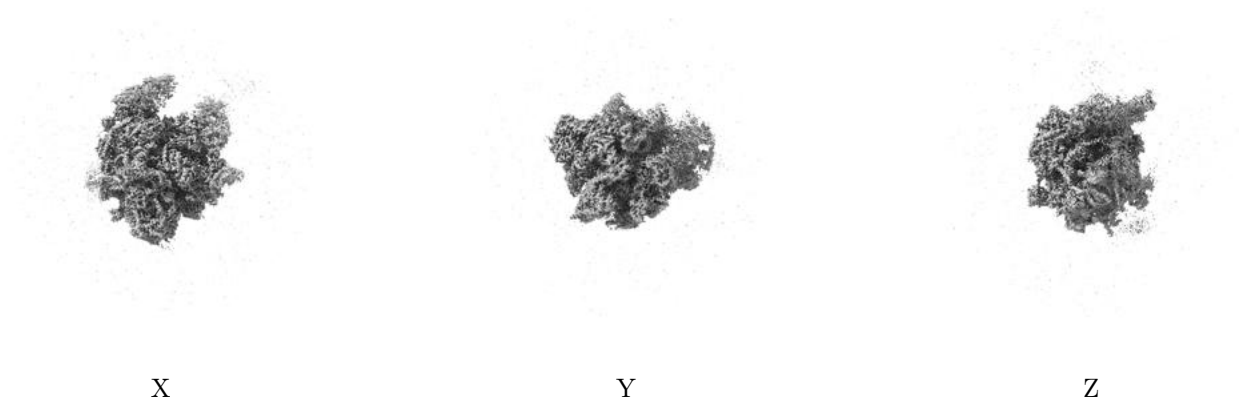


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

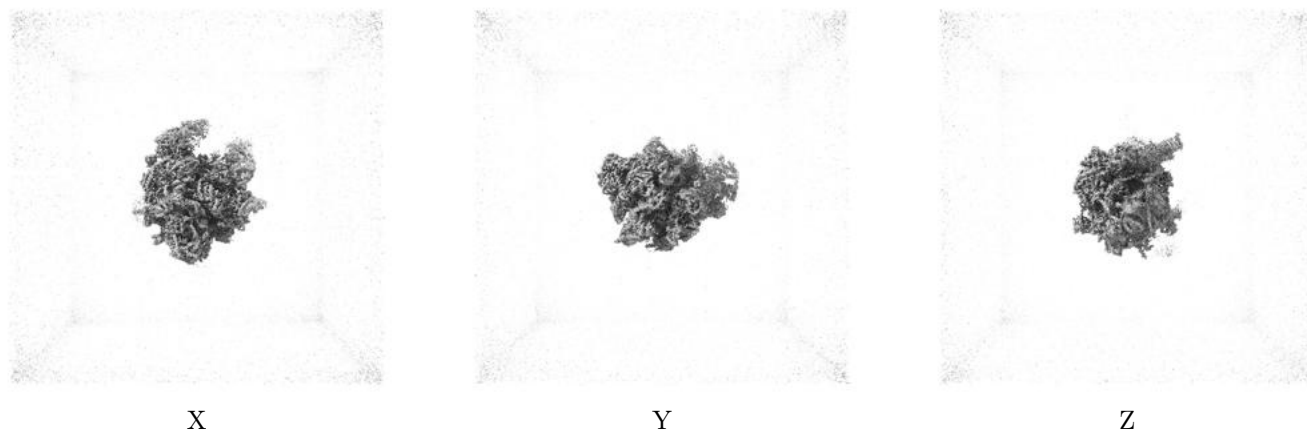
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.747. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

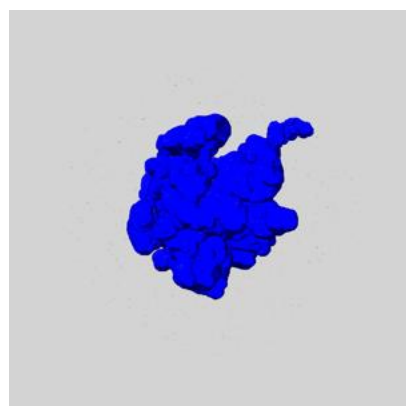
6.6 Mask visualisation [i](#)

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

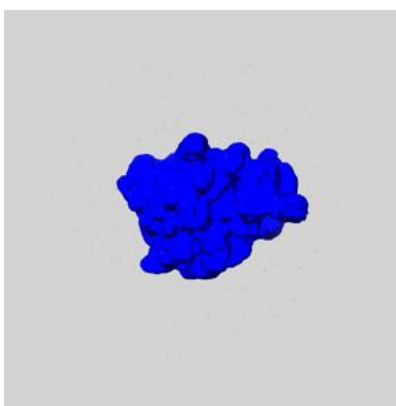
A mask typically either:

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

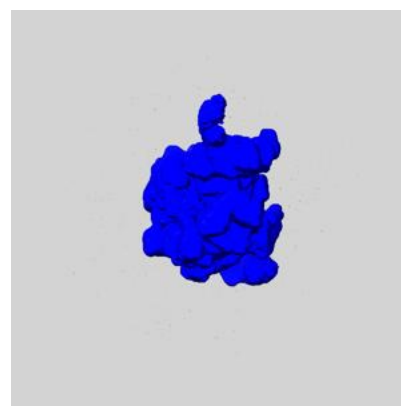
6.6.1 emd_17719_msk_1.map [i](#)



X



Y

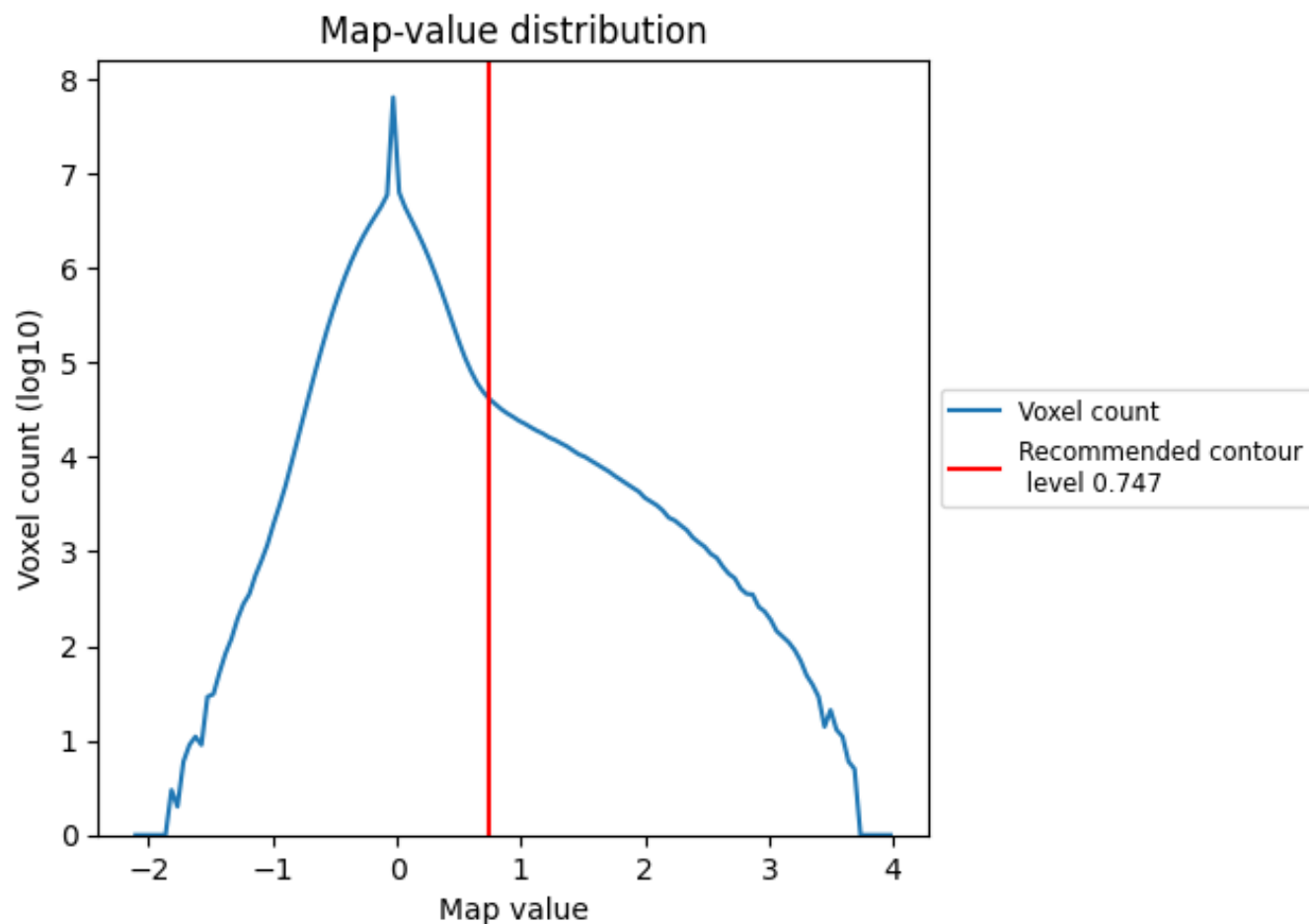


Z

7 Map analysis [i](#)

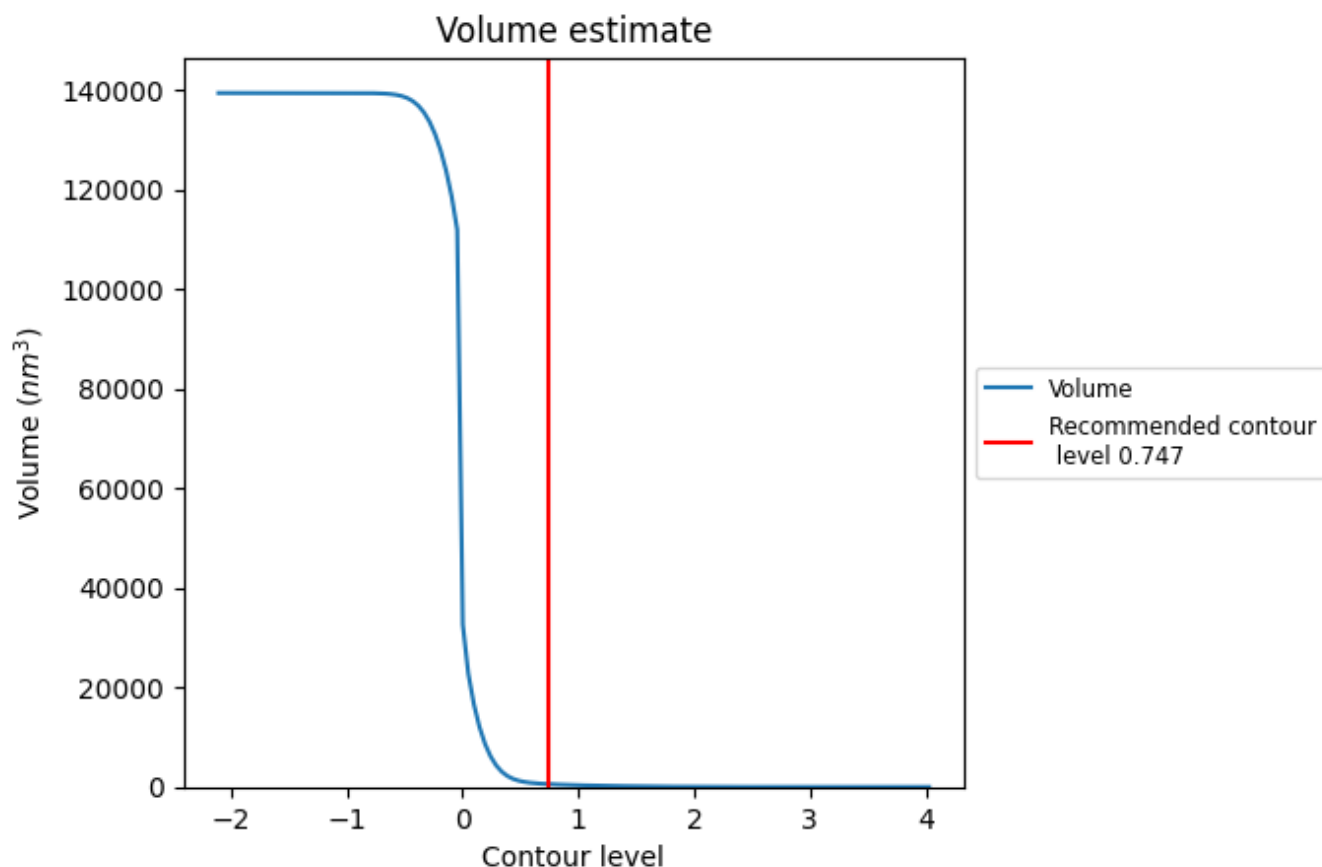
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

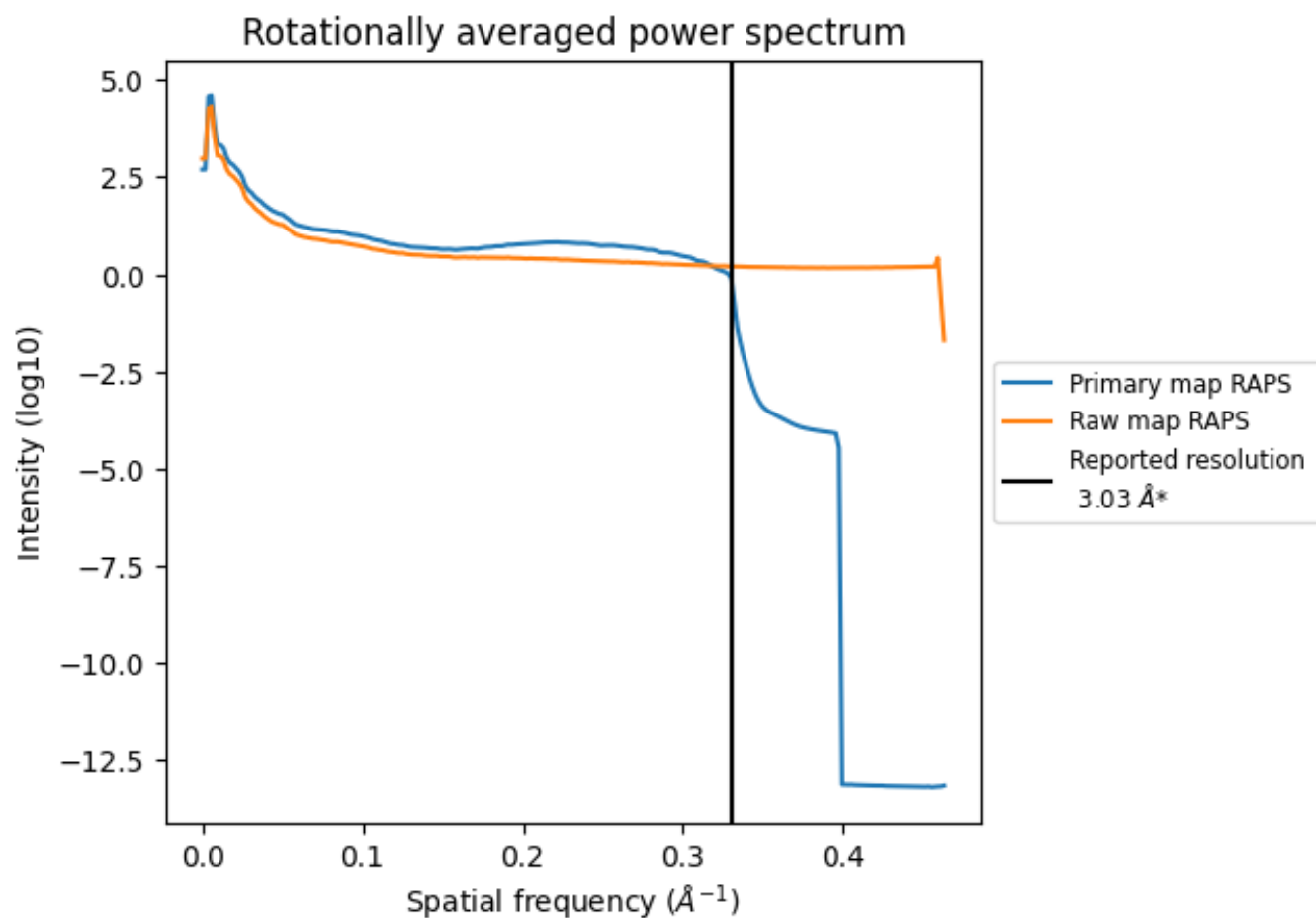
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 564 nm³; this corresponds to an approximate mass of 510 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

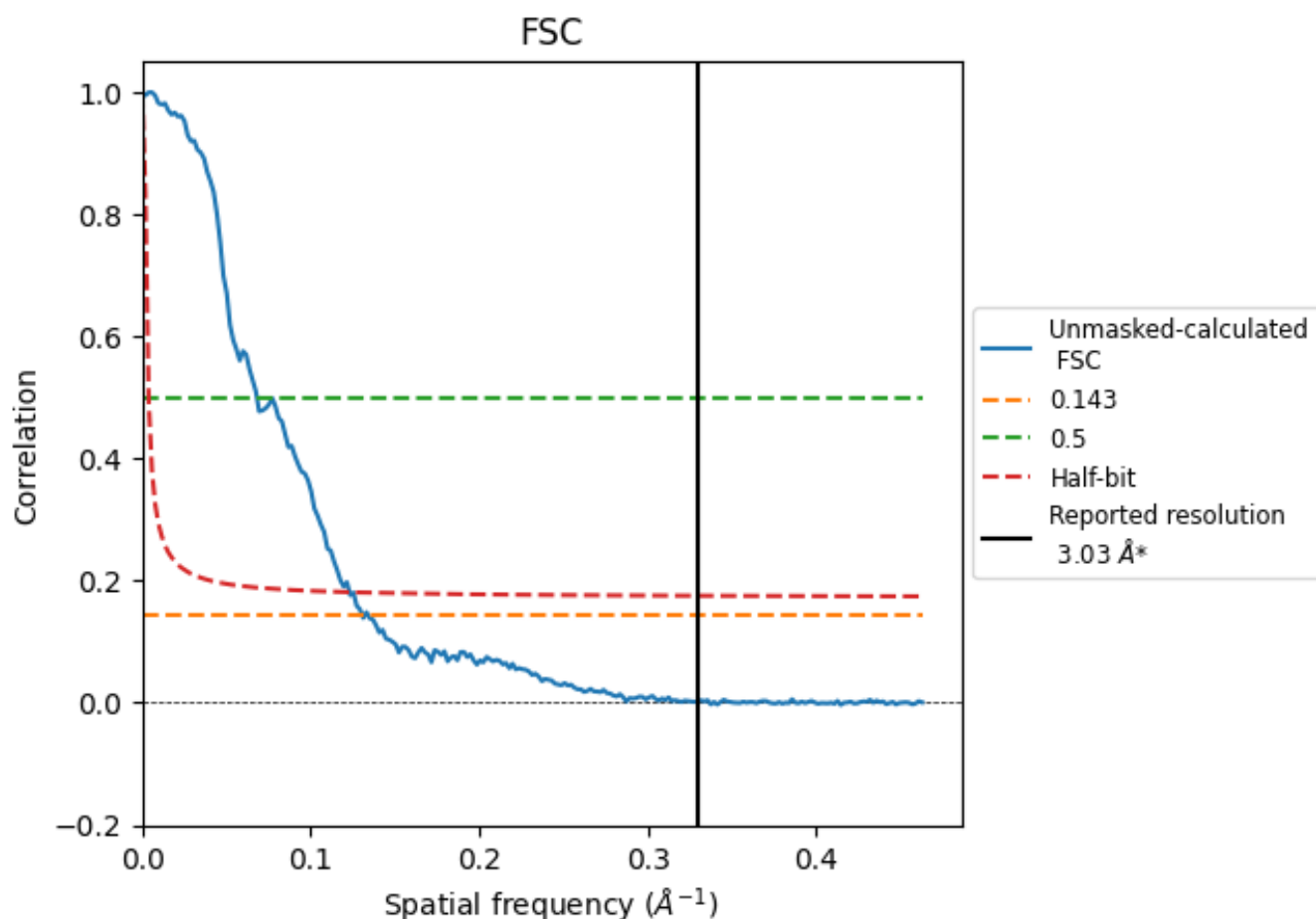


*Reported resolution corresponds to spatial frequency of 0.330 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.330 Å⁻¹

8.2 Resolution estimates [i](#)

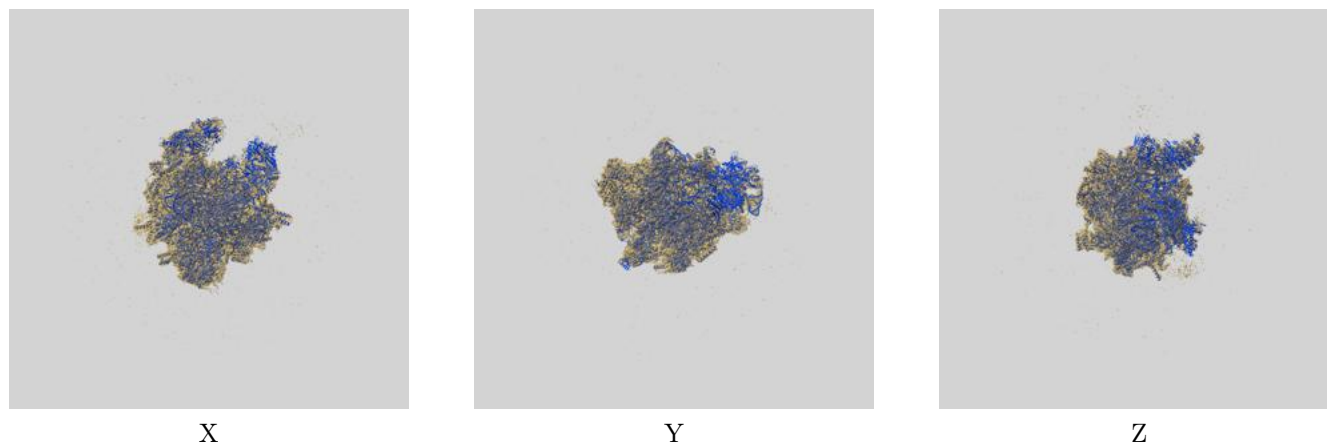
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.03	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.66	14.68	8.13

*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 7.66 differs from the reported value 3.03 by more than 10 %

9 Map-model fit [i](#)

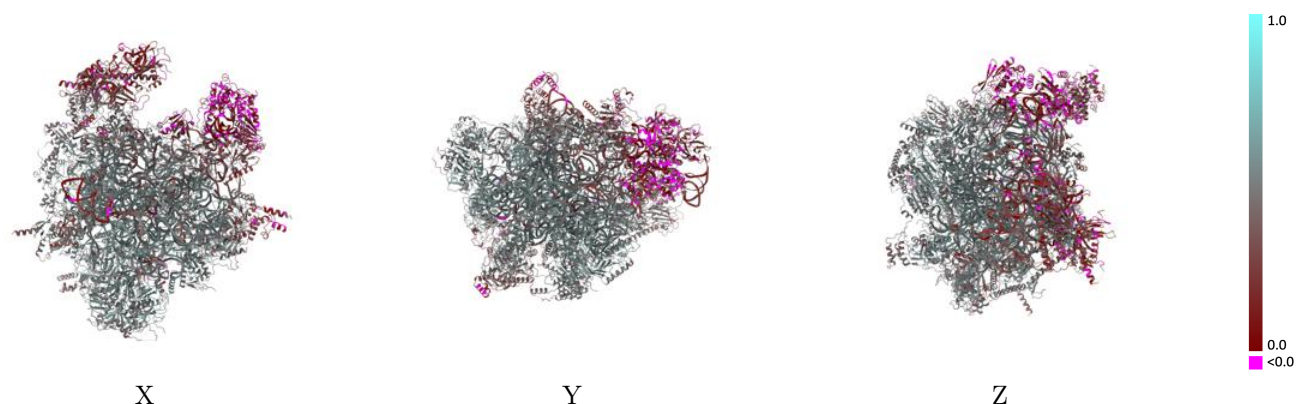
This section contains information regarding the fit between EMDB map EMD-17719 and PDB model 8PK0. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



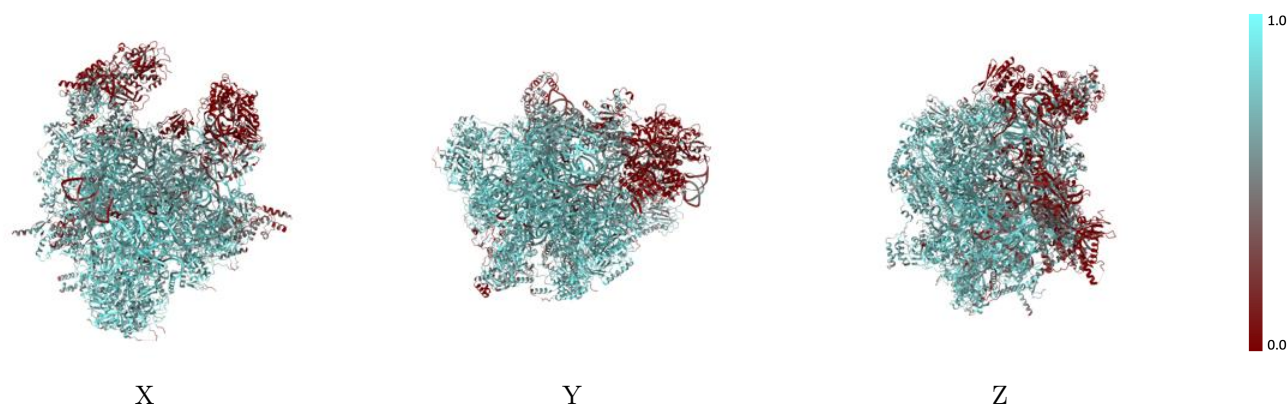
The images above show the 3D surface view of the map at the recommended contour level 0.747 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



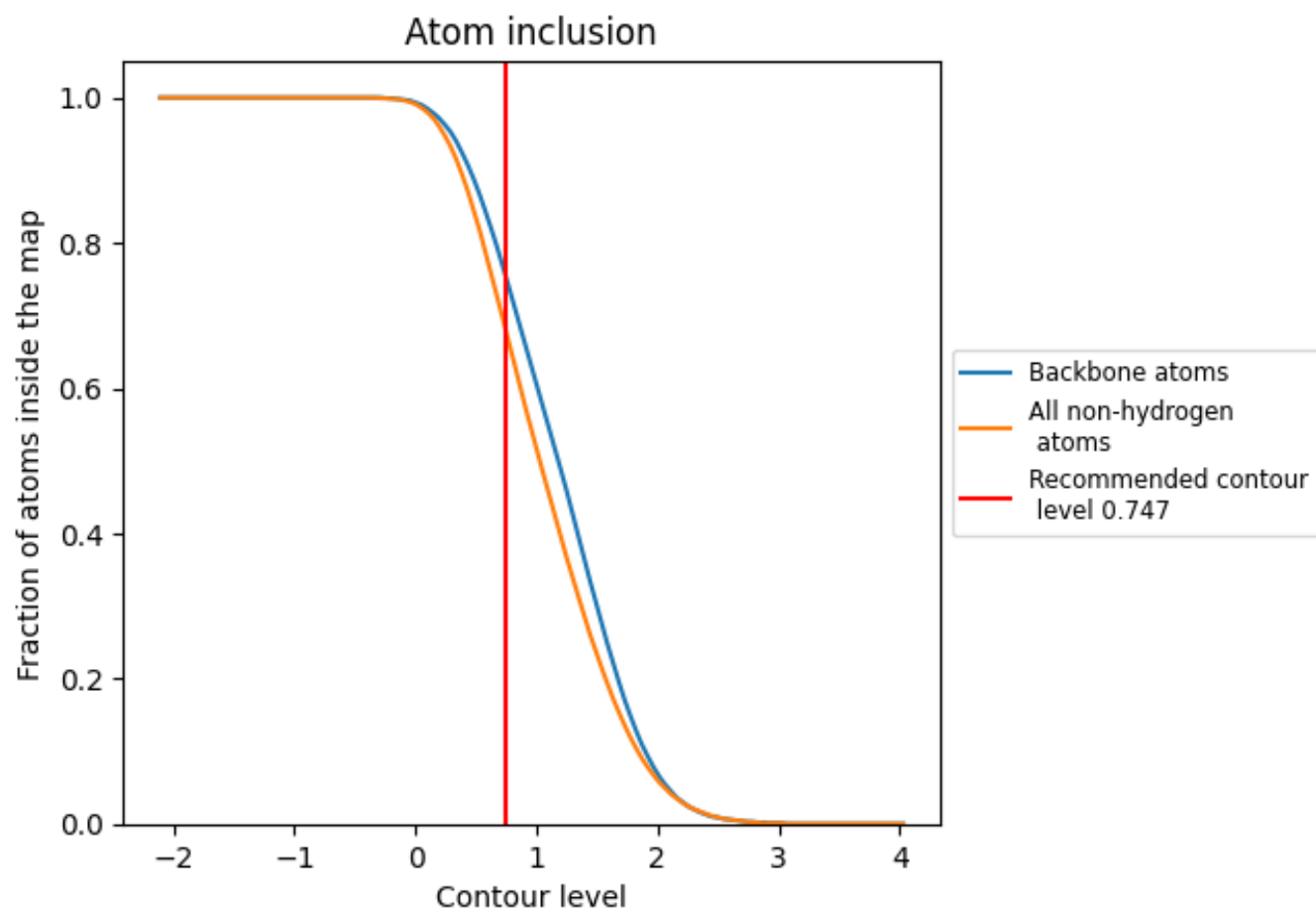
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.747).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 68% 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 (0.747) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.4550
0	 0.7520	 0.5190
1	 0.6810	 0.4910
2	 0.8310	 0.5780
3	 0.8300	 0.5760
5	 0.7690	 0.5100
6	 0.6210	 0.4180
7	 0.6830	 0.4410
8	 0.2150	 0.2230
9	 0.7520	 0.4980
A	 0.7870	 0.4750
B	 0.5510	 0.2720
D	 0.7420	 0.5150
E	 0.7180	 0.5090
F	 0.8000	 0.5360
H	 0.6490	 0.4750
I	 0.1430	 0.1430
J	 0.0260	 0.0530
K	 0.7580	 0.5220
L	 0.6800	 0.5140
M	 0.7890	 0.5310
N	 0.2550	 0.2650
O	 0.7900	 0.5300
P	 0.6860	 0.4740
Q	 0.7310	 0.4990
R	 0.7900	 0.5420
S	 0.7460	 0.5270
T	 0.7920	 0.5460
U	 0.7050	 0.4860
V	 0.6440	 0.4490
W	 0.7180	 0.5200
X	 0.7470	 0.5140
Y	 0.7580	 0.5170
Z	 0.7330	 0.5180
a	 0.6920	 0.4900



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Chain	Atom inclusion	Q-score
b	 0.8000	 0.5300
c	 0.7260	 0.4860
d	 0.5370	 0.3870
e	 0.1180	 0.1790
f	 0.2380	 0.2840
g	 0.7950	 0.5290
h	 0.6800	 0.4390
i	 0.8130	 0.5580
j	 0.7450	 0.4930
k	 0.0380	 0.1050
l	 0.0960	 0.1110
m	 0.0750	 0.1910
o	 0.7440	 0.5120
p	 0.5680	 0.4360
q	 0.6560	 0.4470
r	 0.6340	 0.4350
s	 0.7750	 0.5270
t	 0.4460	 0.3430
u	 0.5710	 0.4150
v	 0.4910	 0.3380
w	 0.2540	 0.2030
x	 0.5790	 0.4350
y	 0.5700	 0.4320
z	 0.6520	 0.4700