



Full wwPDB EM Validation Report ⓘ

Apr 1, 2025 – 10:59 PM EDT

PDB ID : 8QU5 / pdb_00008qu5
EMDB ID : EMD-18461
Title : mt-LSU assembly intermediate in GTPBP8 knock-out cells, state 2
Authors : Valentin Gese, G.; Cipullo, M.; Rorbach, J.; Hallberg, B.M.
Deposited on : 2023-10-13
Resolution : 2.42 Å(reported)

This is a Full wwPDB EM Validation 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:

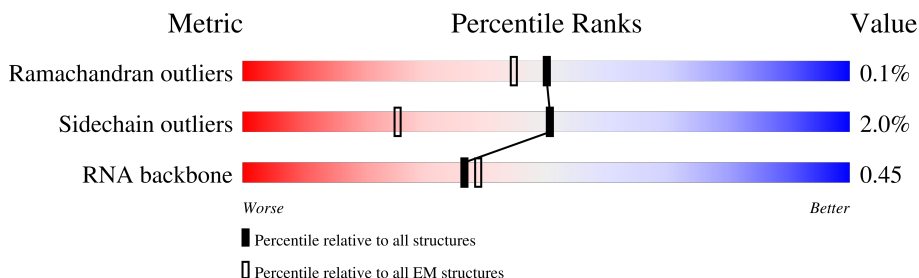
EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

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 2.42 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	<div> <div>47%</div> <div>56%</div> <div>43%</div> </div>
2	1	65	<div> <div>66%</div> <div>72%</div> <div>8%</div> <div>20%</div> </div>
3	2	92	<div> <div>29%</div> <div>45%</div> <div>53%</div> </div>
4	3	188	<div> <div>41%</div> <div>48%</div> <div>49%</div> </div>
5	7	338	<div> <div>70%</div> <div>83%</div> <div>15%</div> </div>
6	8	206	<div> <div>47%</div> <div>48%</div> <div>52%</div> </div>
7	F	311	<div> <div>59%</div> <div>78%</div> <div>20%</div> </div>
8	H	267	<div> <div>33%</div> <div>35%</div> <div>64%</div> </div>

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Mol	Chain	Length	Quality of chain
9	J	192	73%
10	K	178	81% 98%
11	L	145	74% 78% 21%
12	M	296	79% 93%
13	N	251	72% 80% 18%
14	O	175	74% 84% 13%
15	P	180	66% 77% 22%
16	Q	292	66% 73% 26%
17	R	149	78% 89% 6%
18	S	205	62% 76% 24%
19	W	148	59% 72% 26%
20	X	256	77% 92% 5%
21	Y	250	53% 69% 30%
22	Z	161	59% 73% 25%
23	b	215	52% 67% 31%
24	g	166	60% 73% 22%
25	i	128	65% 73% 24%
26	j	123	54% 69% 31%
27	l	138	17% 17% 83%
28	m	128	35% 34% 65%
29	o	102	59% 77% 23%
30	q	222	52% 56% 42%
31	t	28	100% 100%
32	u	234	46% 47% 53%
33	v	70	97% 97%

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Mol	Chain	Length	Quality of chain
34	w	156	
35	5	423	
36	6	380	
37	9	137	
38	A	1559	
39	B	69	
40	D	305	
41	E	348	
42	I	261	
43	T	206	
44	U	153	
45	V	216	
46	a	142	
47	c	332	
48	d	306	
49	e	279	
50	f	212	
51	h	158	
52	k	112	
53	p	206	
54	r	196	
55	s	439	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 89817 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	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	43	Total	C	N	O	S	0	0
			351	218	76	56	1		

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 5 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 6 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 7 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 8 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	95	Total	C	N	O	S	0	0
			784	498	152	134			

- Molecule 9 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 10 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 11 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 12 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 13 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	205	Total	C	N	O	S	0	0
			1654	1056	308	280	10		

- Molecule 14 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 15 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 16 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 17 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 18 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 19 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	109	Total	C	N	O	S	0	0
			859	552	162	142	3		

- Molecule 20 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 21 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 22 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 23 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 24 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 25 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 26 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 27 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	l	23	Total	C	N	O	0	0
			221	137	52	32		

- Molecule 28 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	m	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

- Molecule 29 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	o	79	Total	C	N	O	S	0	0
			665	420	130	112	3		

- Molecule 30 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	q	128	Total	C	N	O	S	0	0
			1076	671	208	192	5		

- Molecule 31 is a protein called Unknown protein or protein extension.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	t	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 32 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	u	111	Total	C	N	O	S	0	0
			927	595	155	167	10		

- Molecule 33 is a protein called MIEF1 upstream open reading frame protein.

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

- Molecule 34 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	5	387	Total	C	N	O	S	0	0
			3156	2039	548	558	11		

- Molecule 36 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	6	324	Total	C	N	O	S	0	0
			2640	1694	470	468	8		

- Molecule 37 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	9	117	Total	C	N	O	S	0	0
			947	614	163	168	2		

- Molecule 38 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A	1049	Total	C	N	O	P	0	0
			22263	9996	4029	7189	1049		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3107	U	UNK	variant	GB 1025814679

- Molecule 39 is a RNA chain called mitochondrial tRNA^{Val}.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 40 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	D	220	Total	C	N	O	S	0	0
			1706	1059	339	299	9		

- Molecule 41 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	E	285	Total	C	N	O	S	0	0
			2258	1457	384	406	11		

- Molecule 42 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	I	158	Total	C	N	O	S	0	0
			1283	828	235	210	10		

- Molecule 43 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	T	159	Total	C	N	O	S	0	0
			1305	835	239	224	7		

- Molecule 44 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	U	139	Total	C	N	O	S	0	0
			1154	734	220	197	3		

- Molecule 45 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V	192	Total	C	N	O	S	0	0
			1575	1003	281	283	8		

- Molecule 46 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	a	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 47 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 48 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	d	211	Total	C	N	O	S	0	0
			1741	1123	299	309	10		

- Molecule 49 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 50 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	f	116	Total	C	N	O	S	0	0
			915	585	152	175	3		

- Molecule 51 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	h	100	Total	C	N	O	S	0	0
			827	524	146	155	2		

- Molecule 52 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

- Molecule 53 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	p	127	Total	C	N	O	S	0	0
			1058	661	201	192	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	r	146	Total	C	N	O	S	0	0
			1203	764	232	199	8		

- Molecule 55 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	s	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

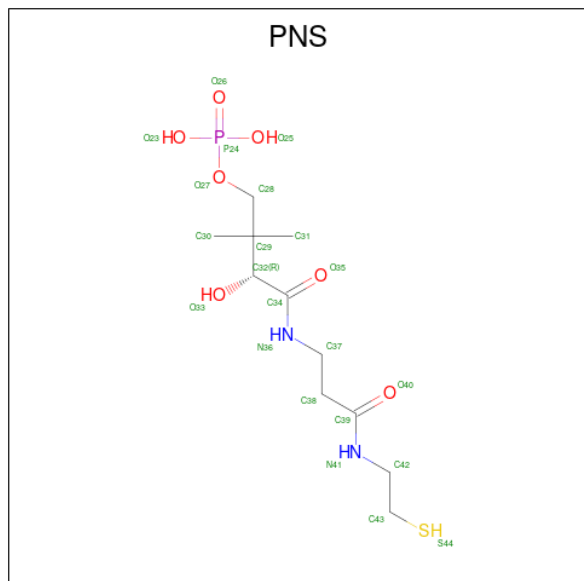
- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	0	1	Total	Zn	0
			1	1	
56	r	1	Total	Zn	0
			1	1	

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	g	1	Total	Mg	0
			1	1	
57	A	47	Total	Mg	0
			47	47	

- Molecule 58 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: C₁₁H₂₃N₂O₇PS).

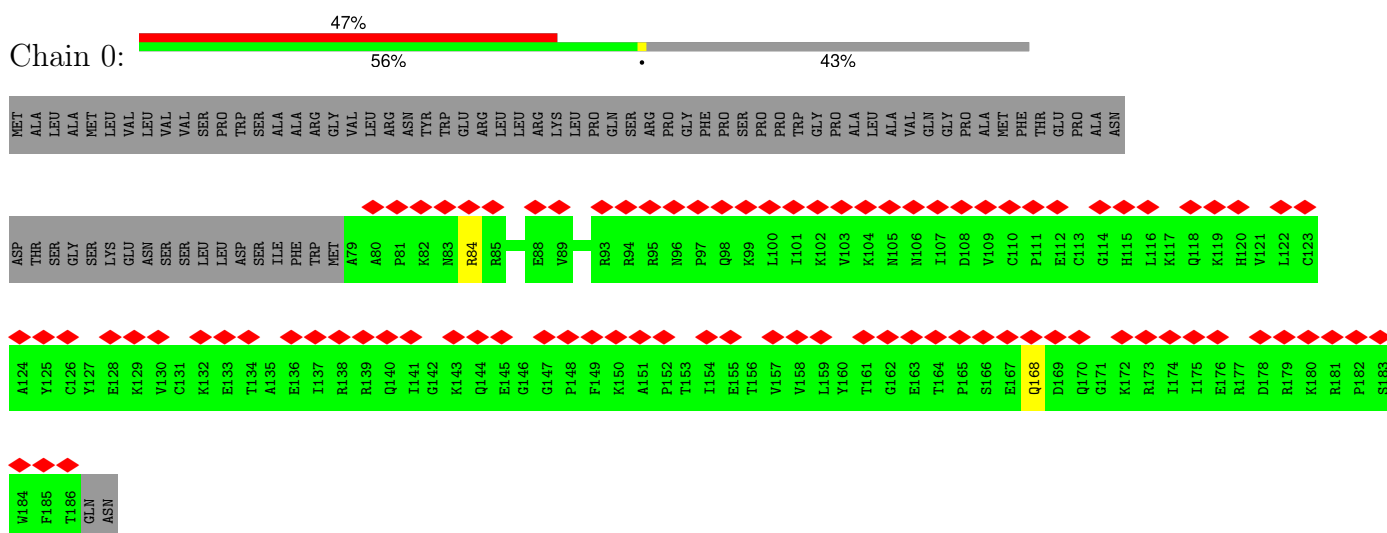


Mol	Chain	Residues	Atoms						AltConf
58	v	1	Total	C	N	O	P	S	0
			21	11	2	6	1	1	

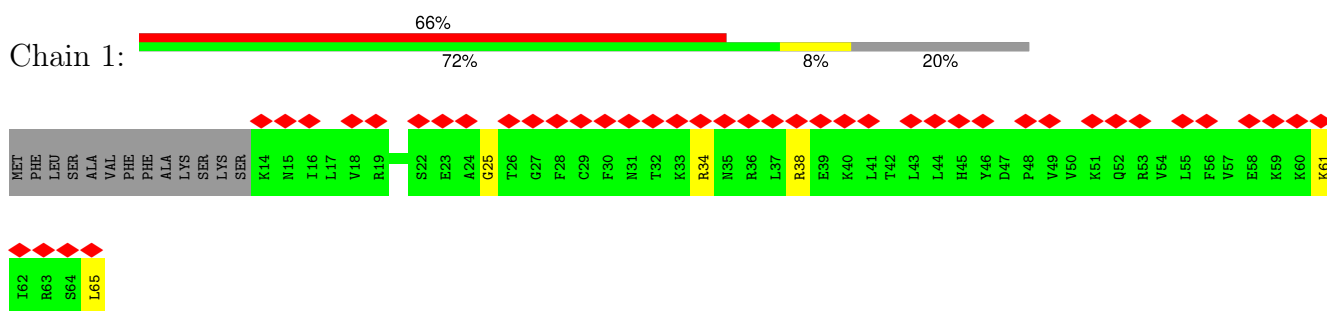
3 Residue-property plots [i](#)

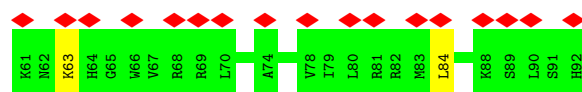
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 39S ribosomal protein L32, mitochondrial



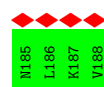
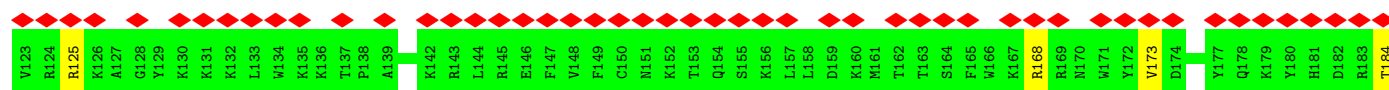
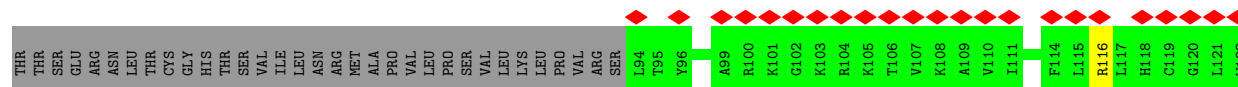
- Molecule 2: 39S ribosomal protein L33, mitochondrial





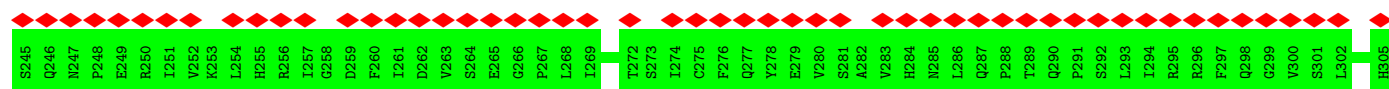
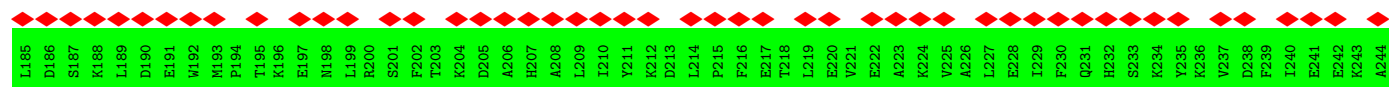
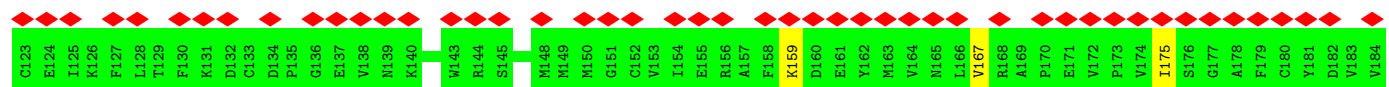
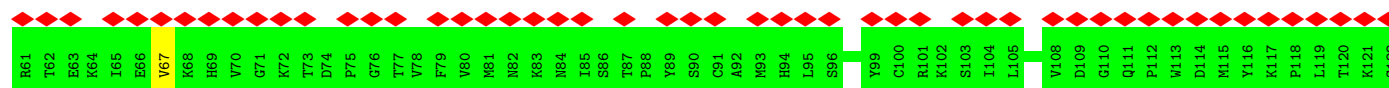
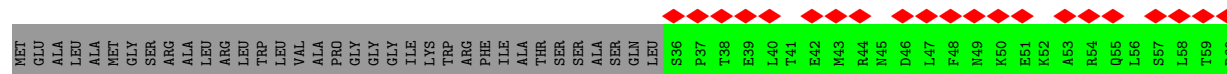
- Molecule 4: 39S ribosomal protein L35, mitochondrial

Chain 3:



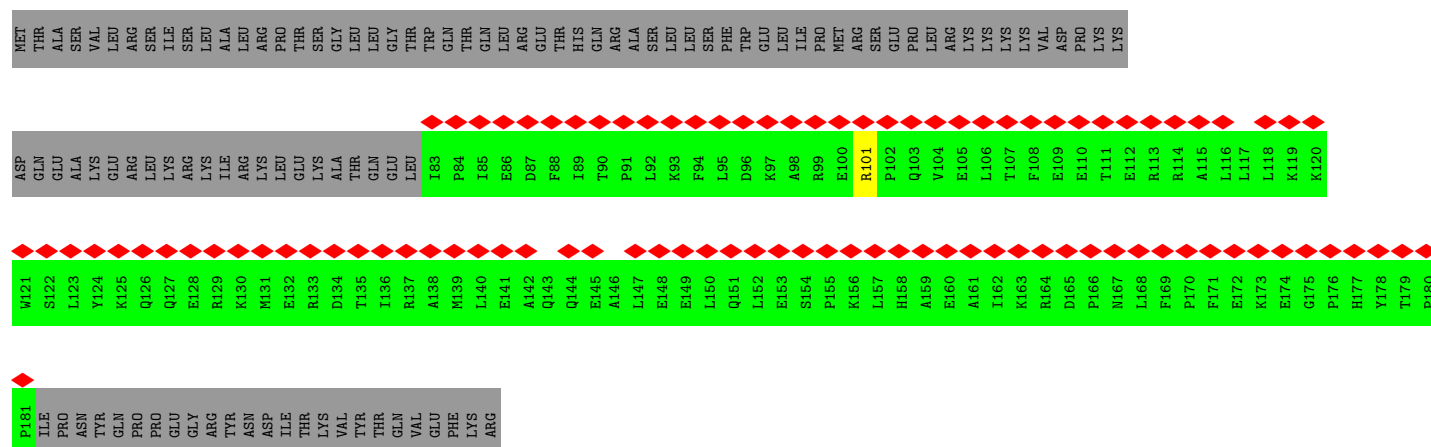
- Molecule 5: 39S ribosomal protein L39, mitochondrial

Chain 7:

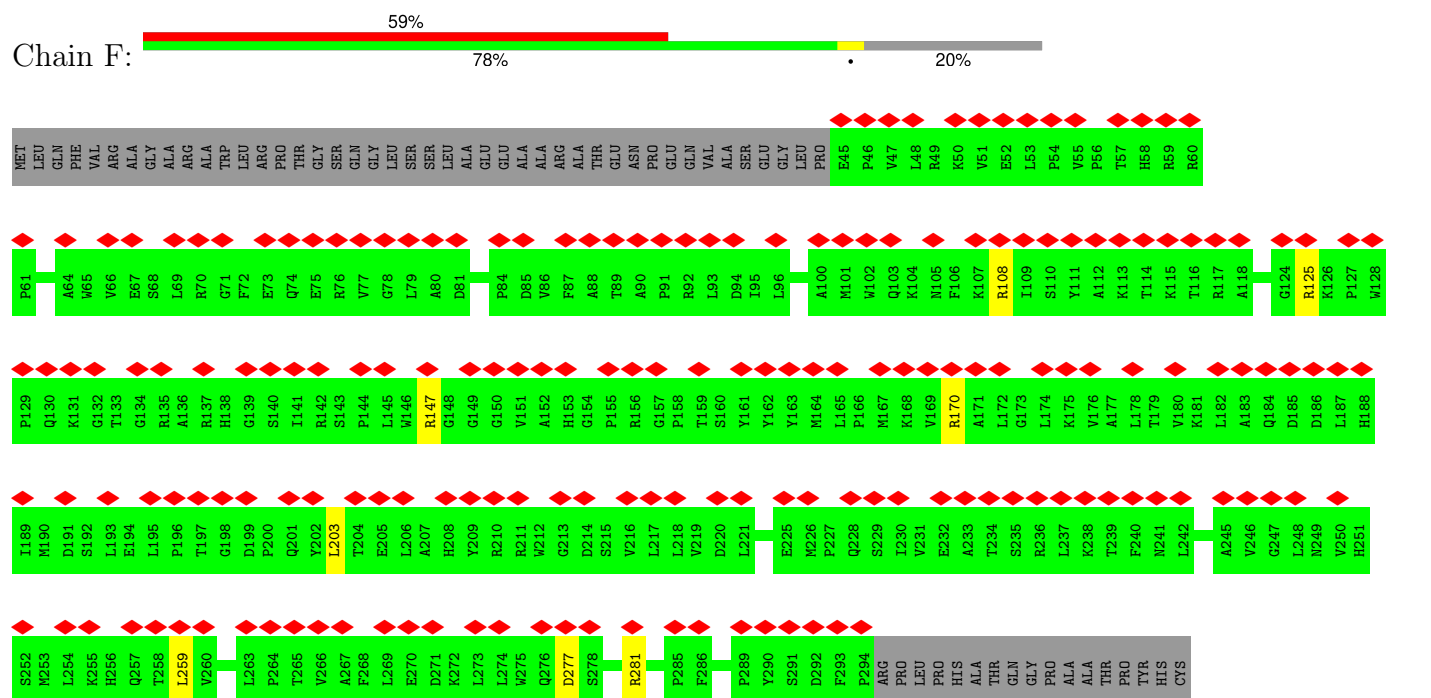


- Molecule 6: 39S ribosomal protein L40, mitochondrial

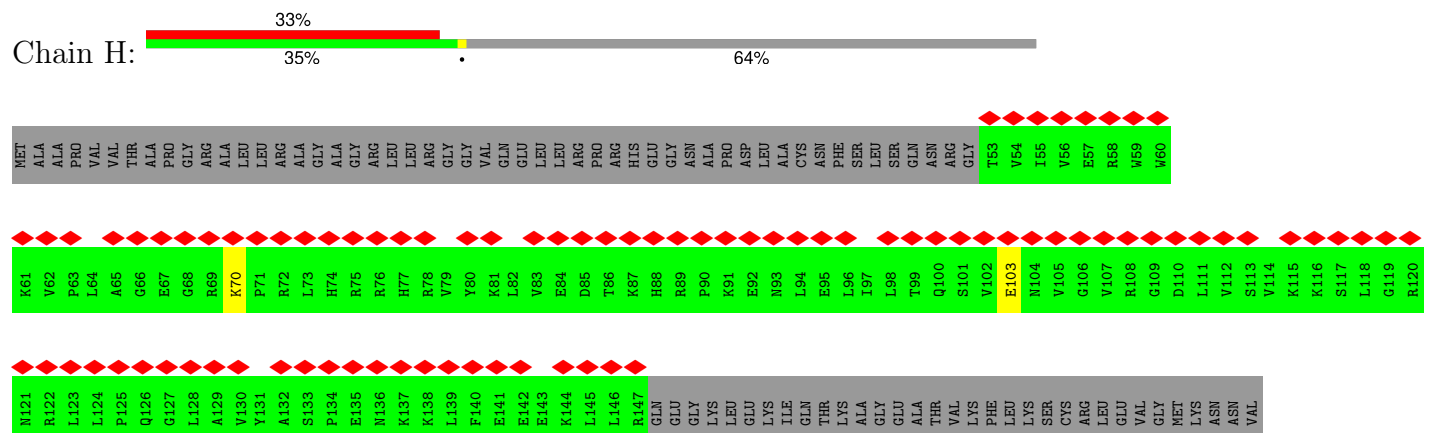
Chain 8:



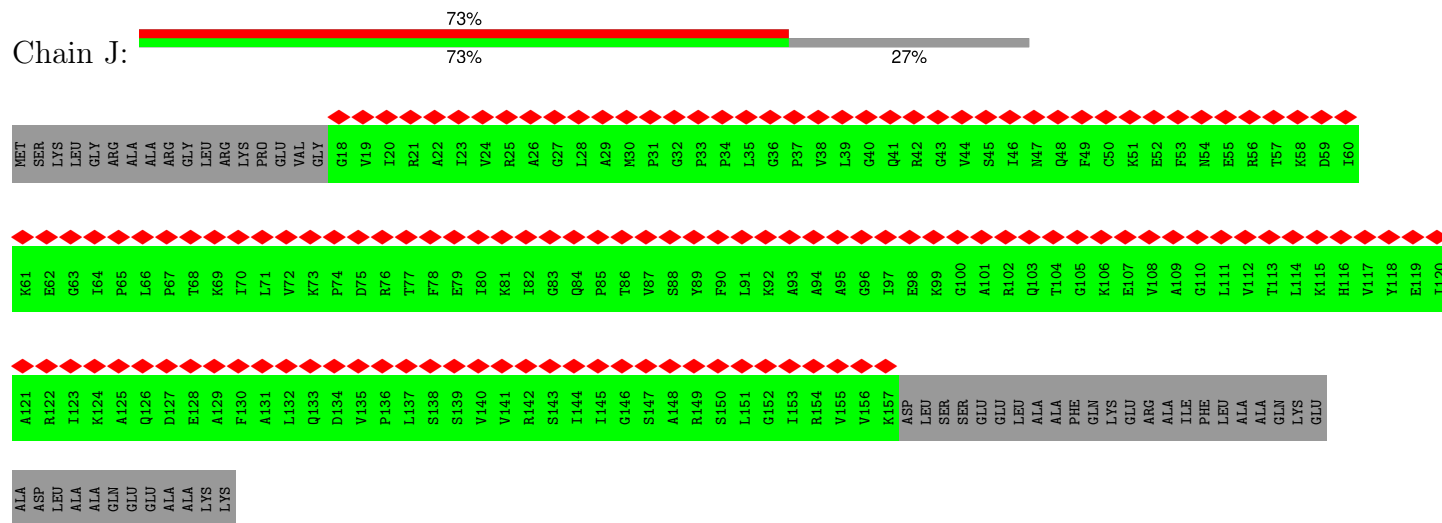
• Molecule 7: 39S ribosomal protein L4, mitochondrial



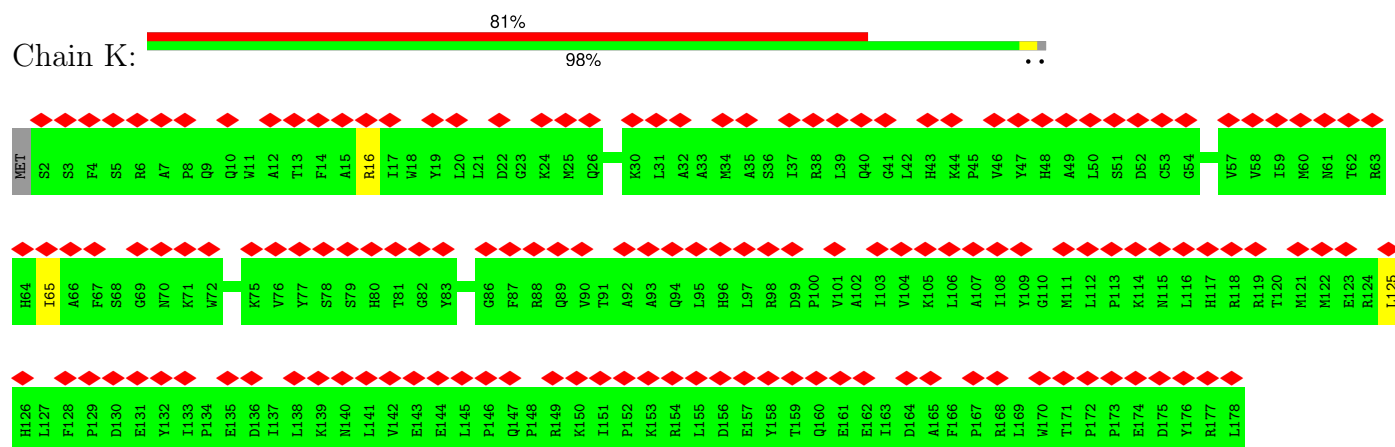
• Molecule 8: 39S ribosomal protein L9, mitochondrial



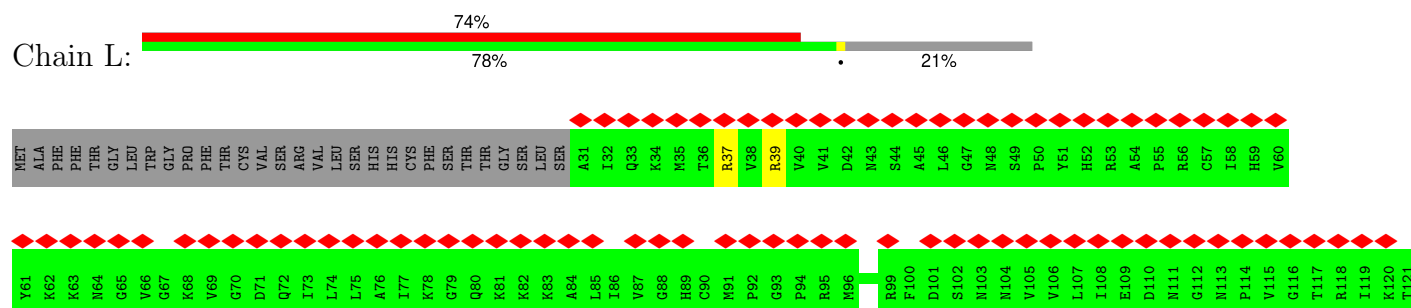
- Molecule 9: 39S ribosomal protein L11, mitochondrial

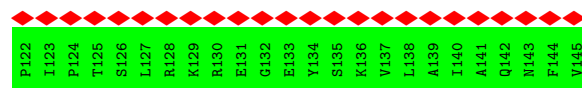


- Molecule 10: 39S ribosomal protein L13, mitochondrial



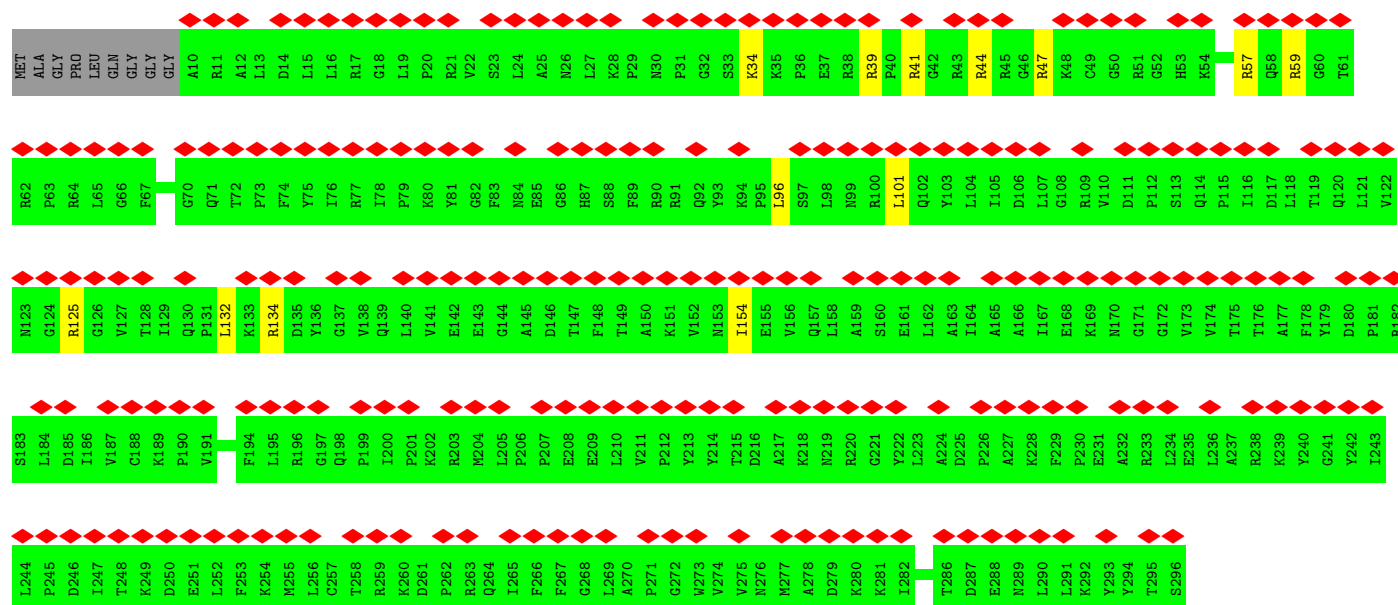
- Molecule 11: 39S ribosomal protein L14, mitochondrial





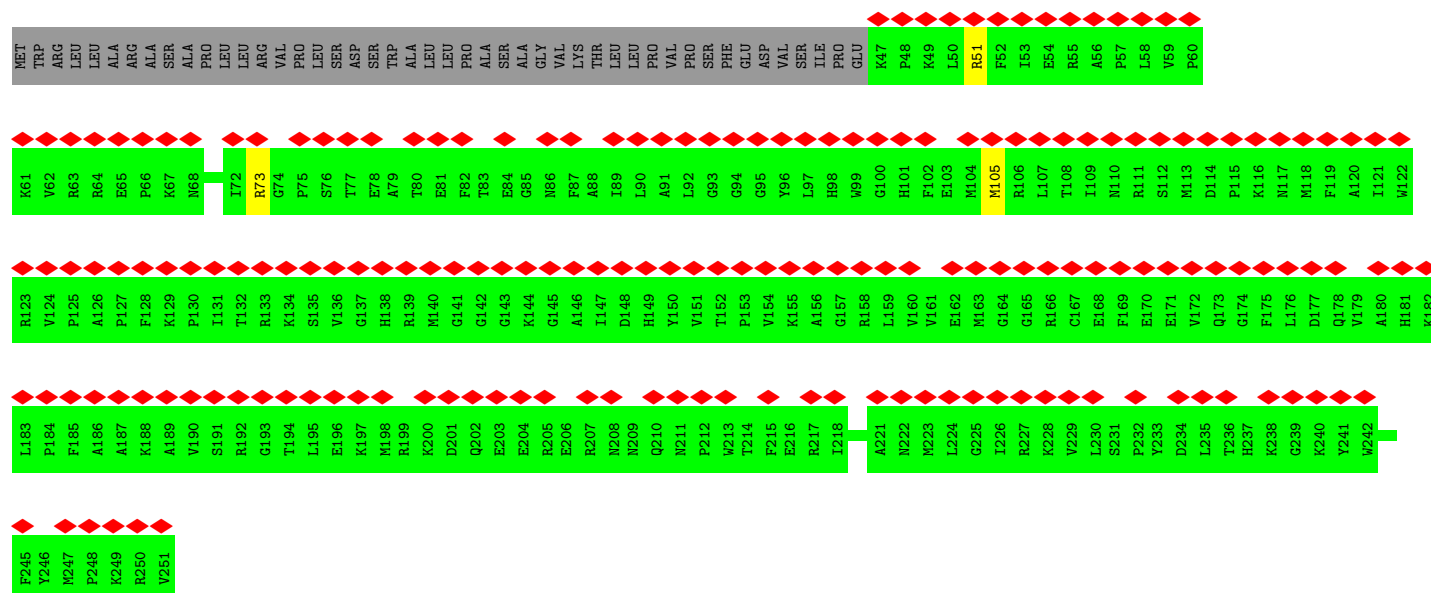
- Molecule 12: 39S ribosomal protein L15, mitochondrial

Chain M: 79% 93%

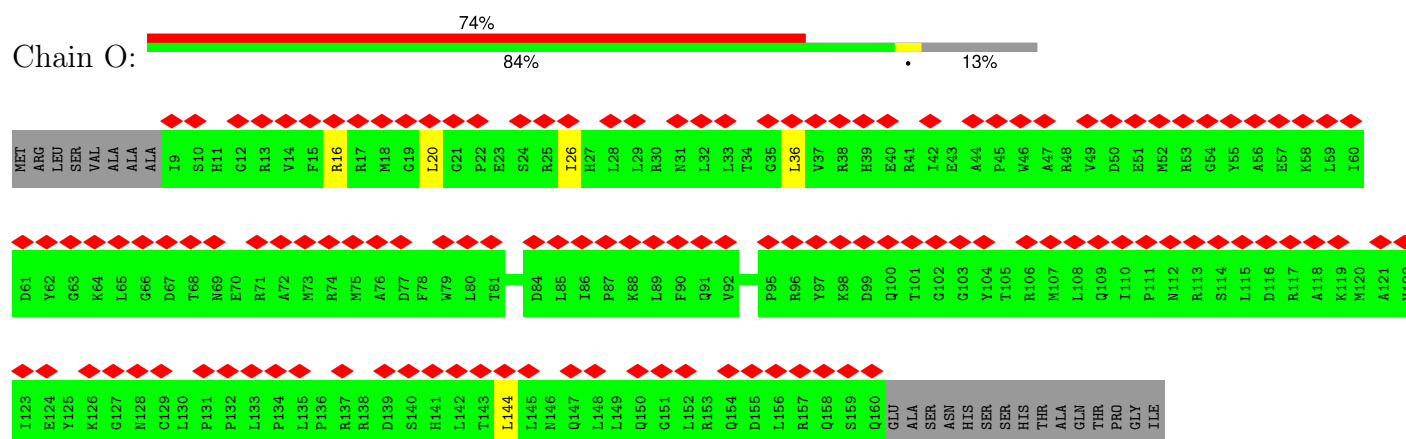


- Molecule 13: 39S ribosomal protein L16, mitochondrial

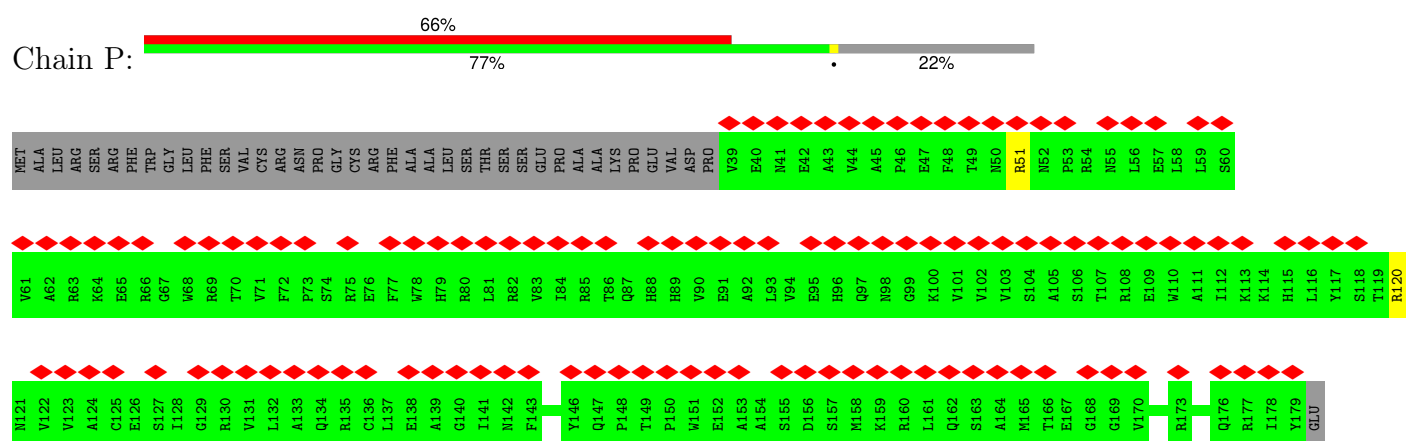
Chain N: 72% 80% 18%



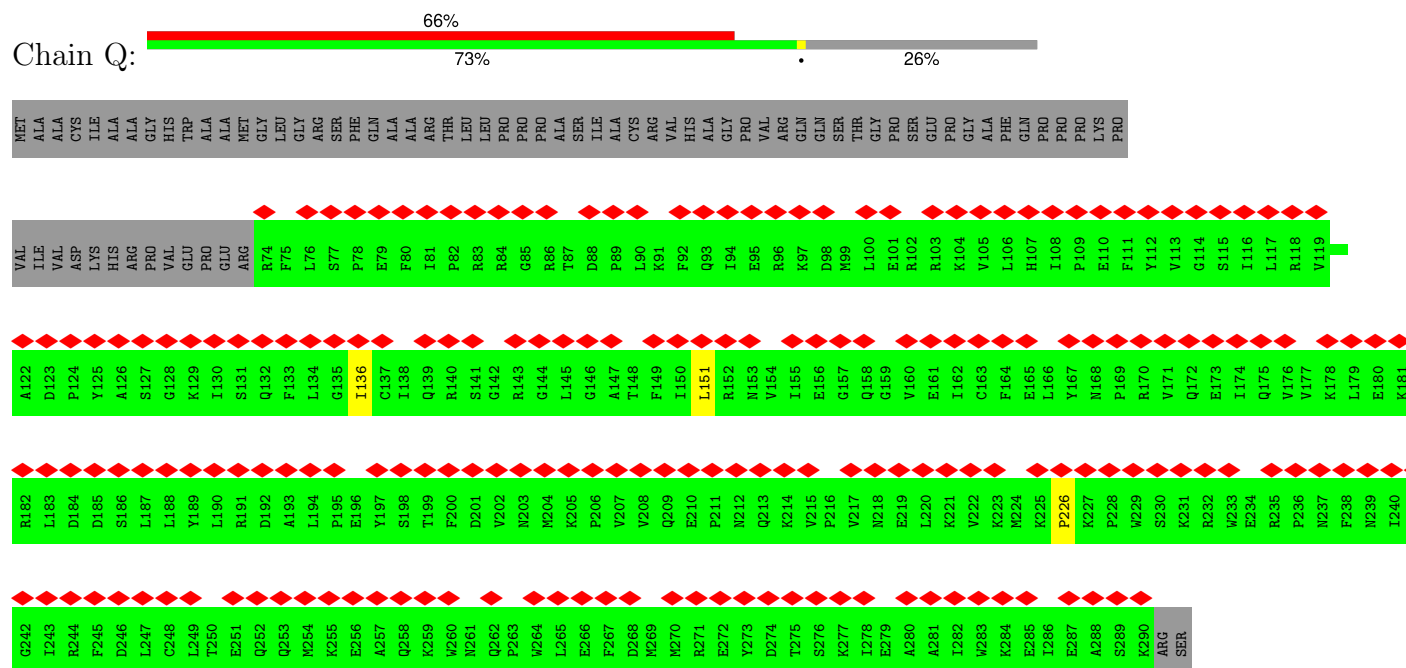
- Molecule 14: 39S ribosomal protein L17, mitochondrial



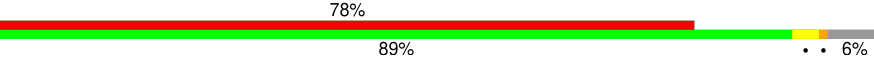
- Molecule 15: 39S ribosomal protein L18, mitochondrial

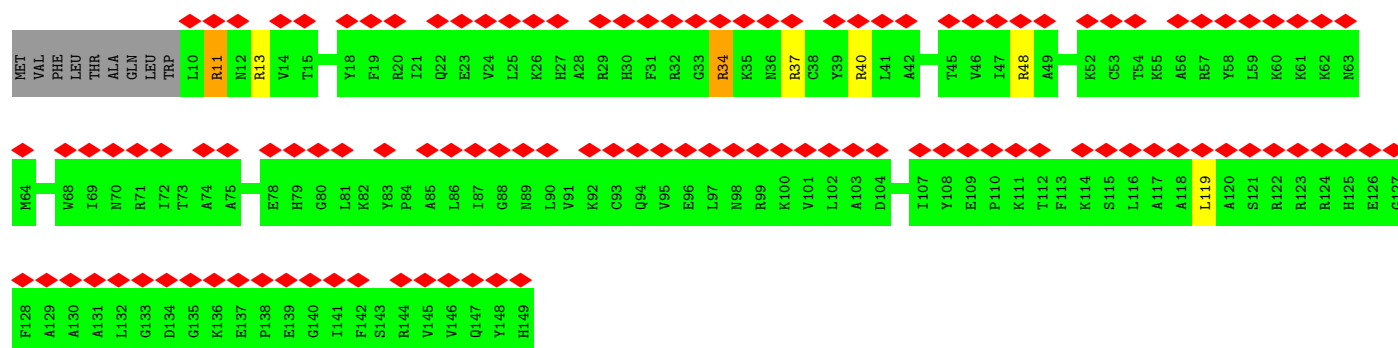


- Molecule 16: 39S ribosomal protein L19, mitochondrial




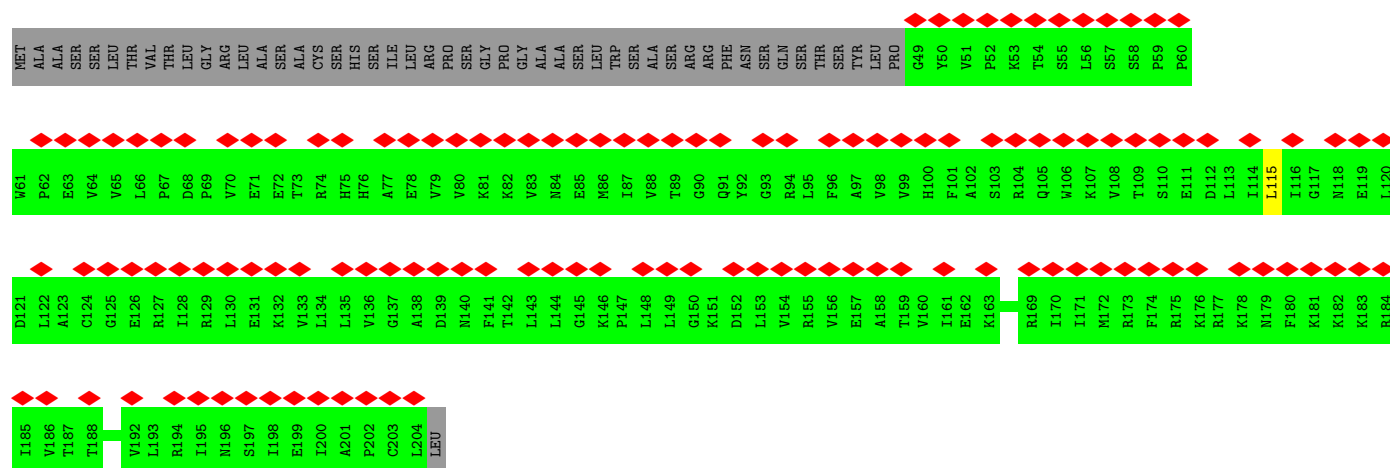
- Molecule 17: 39S ribosomal protein L20, mitochondrial

Chain R: 



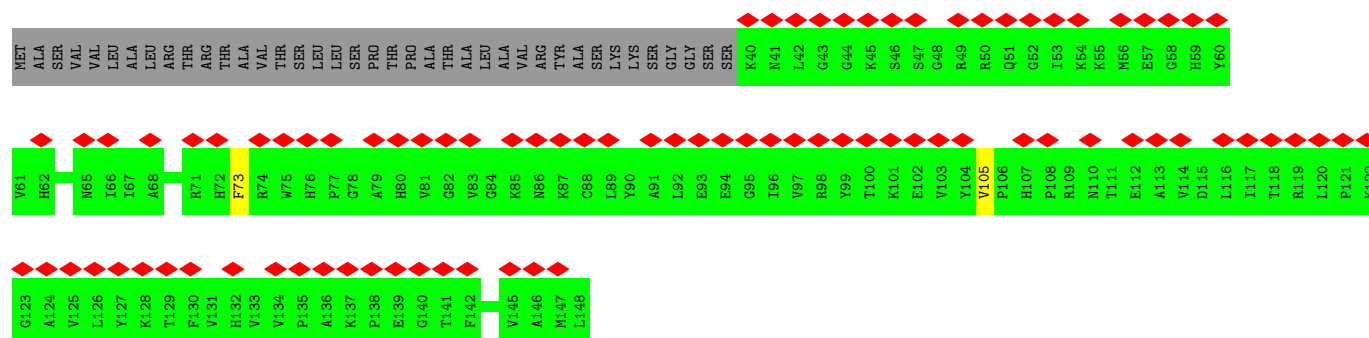
- Molecule 18: 39S ribosomal protein L21, mitochondrial

Chain S: 

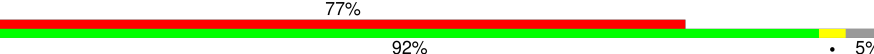


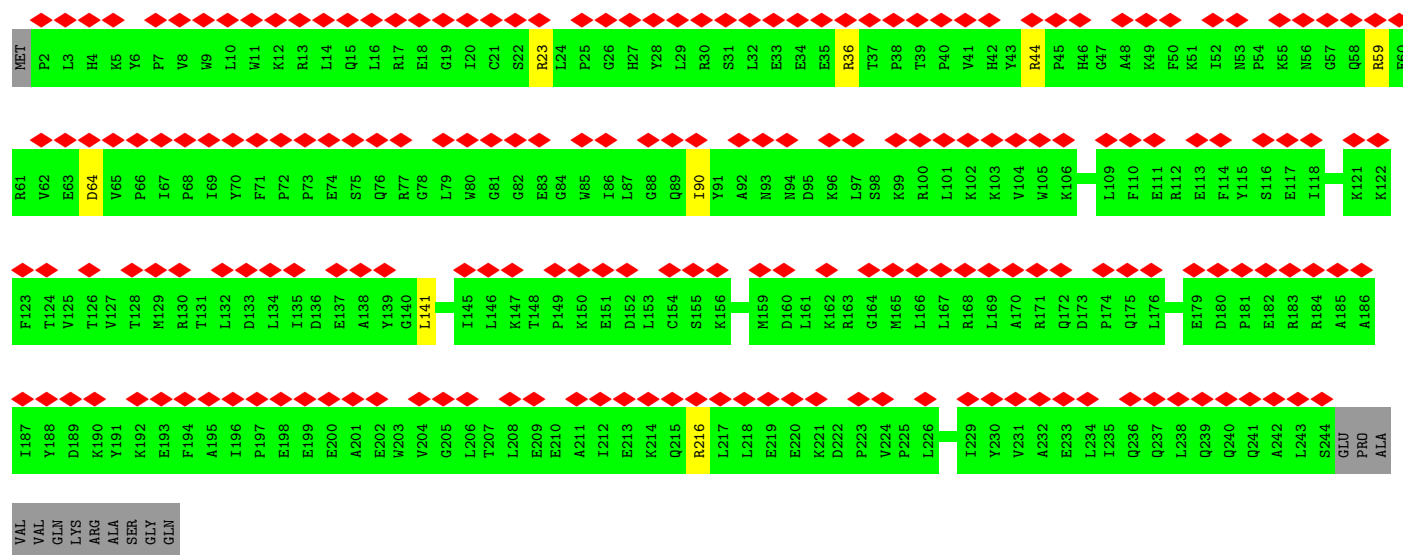
- Molecule 19: 39S ribosomal protein L27, mitochondrial

Chain W: 

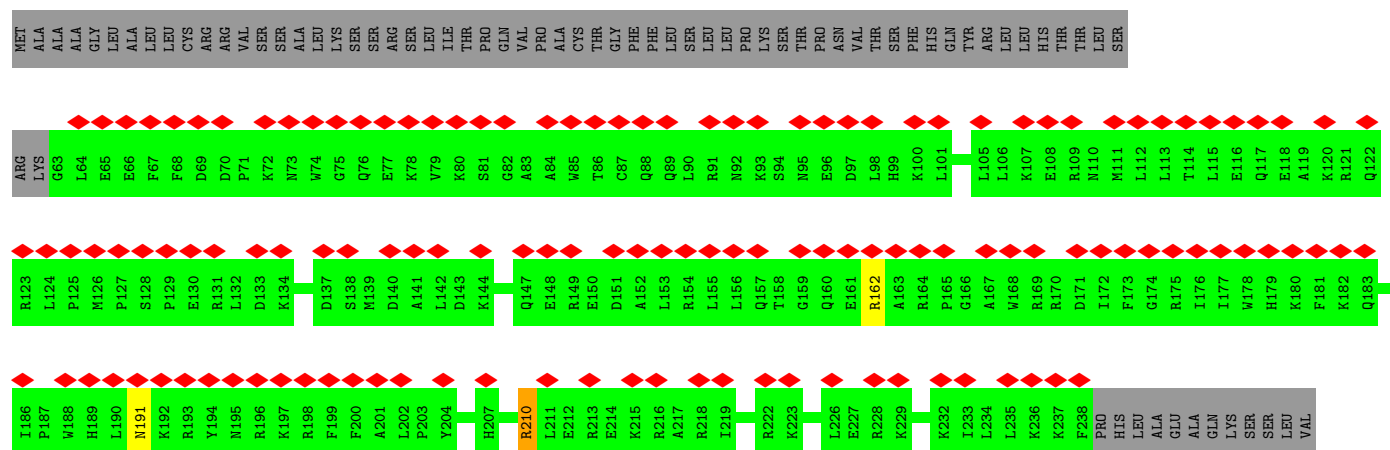


- Molecule 20: 39S ribosomal protein L28, mitochondrial

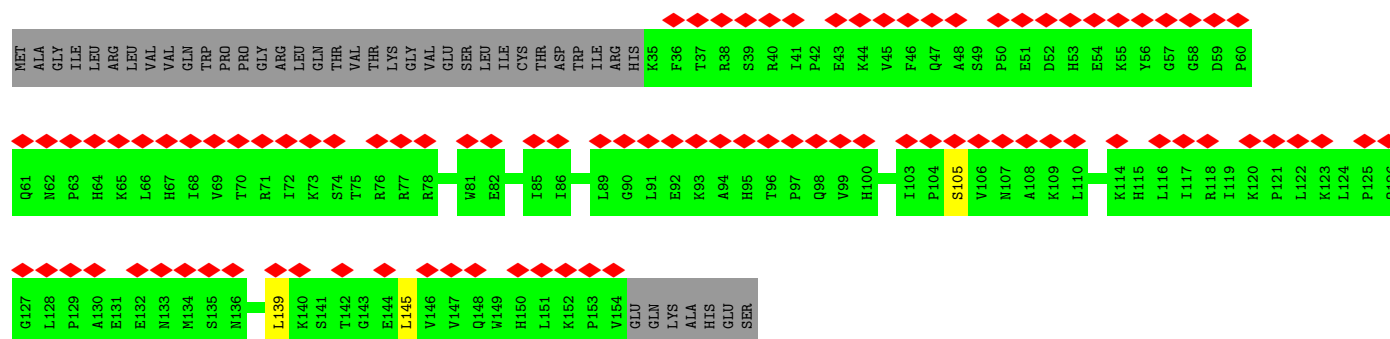
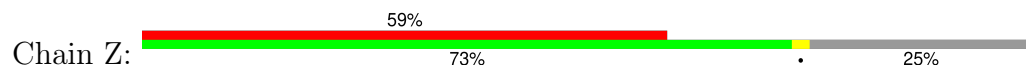
Chain X: 



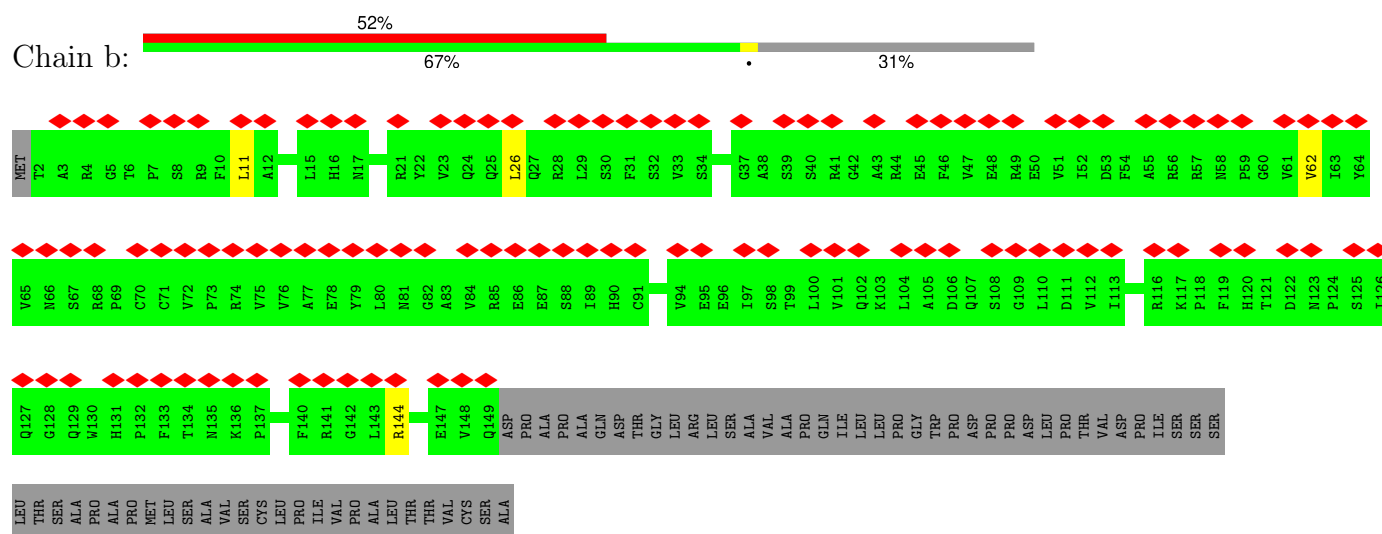
- Molecule 21: 39S ribosomal protein L47, mitochondrial



- Molecule 22: 39S ribosomal protein L30, mitochondrial



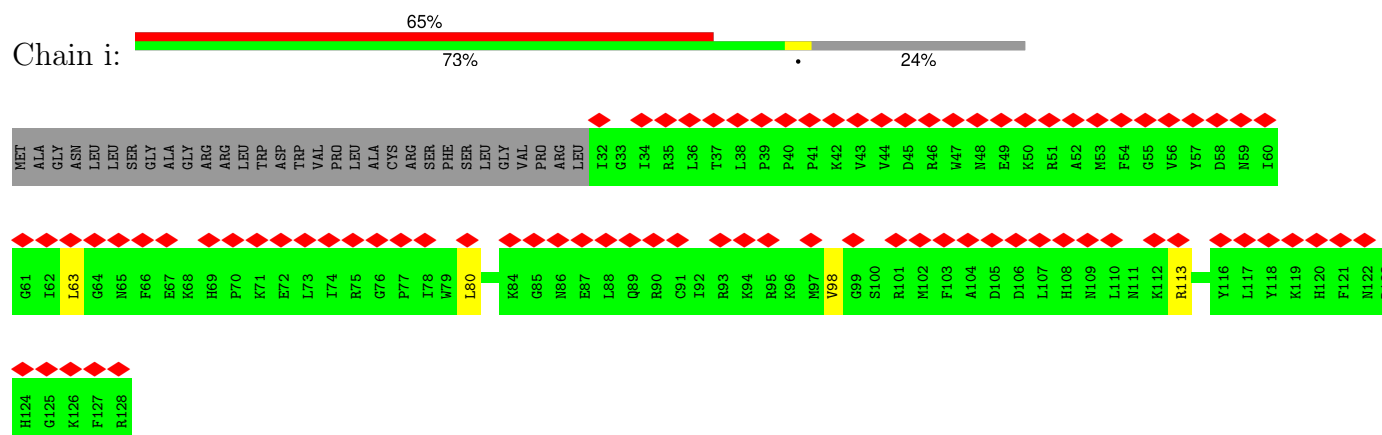
- Molecule 23: 39S ribosomal protein L43, mitochondrial



- Molecule 24: 39S ribosomal protein L49, mitochondrial



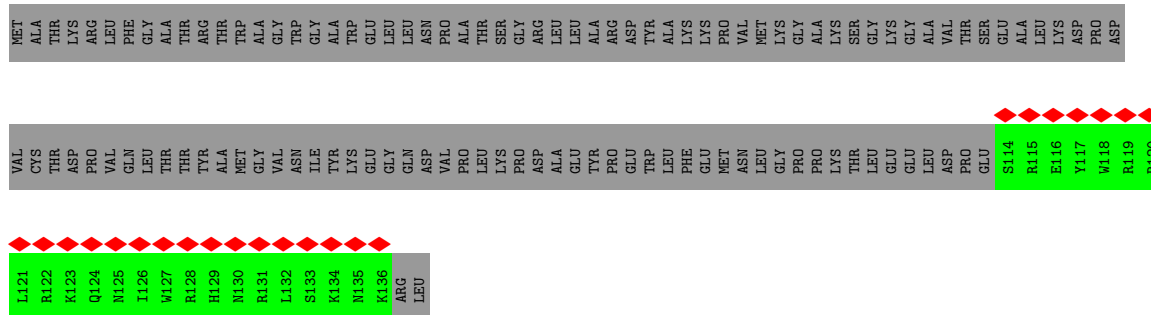
- Molecule 25: 39S ribosomal protein L51, mitochondrial



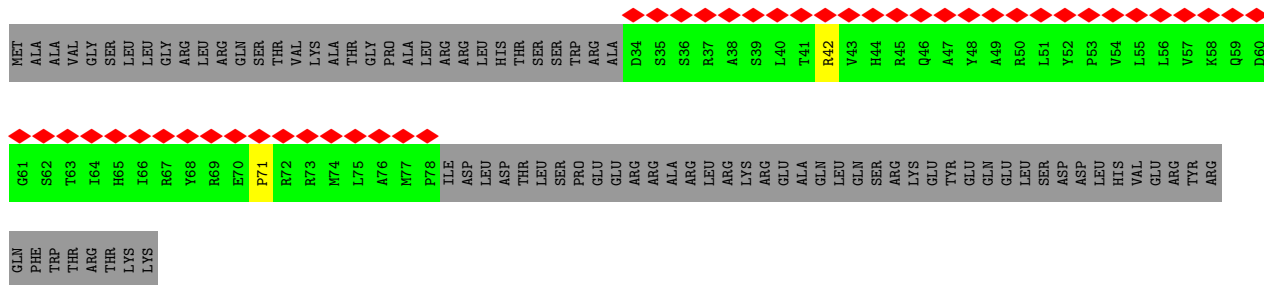
- Molecule 26: 39S ribosomal protein L52, mitochondrial



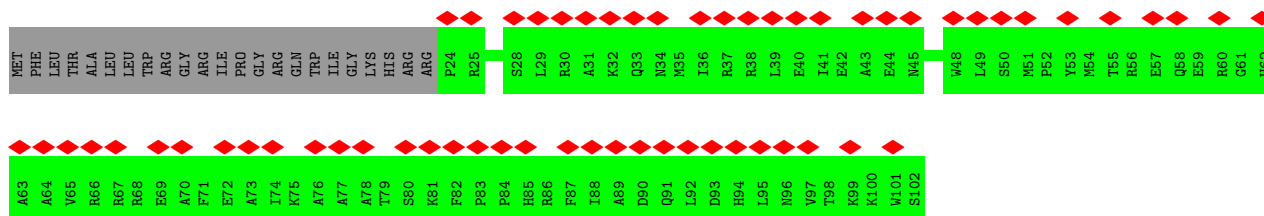
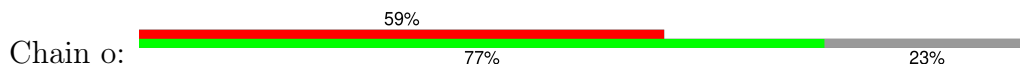
- Molecule 27: 39S ribosomal protein L54, mitochondrial



- Molecule 28: 39S ribosomal protein L55, mitochondrial

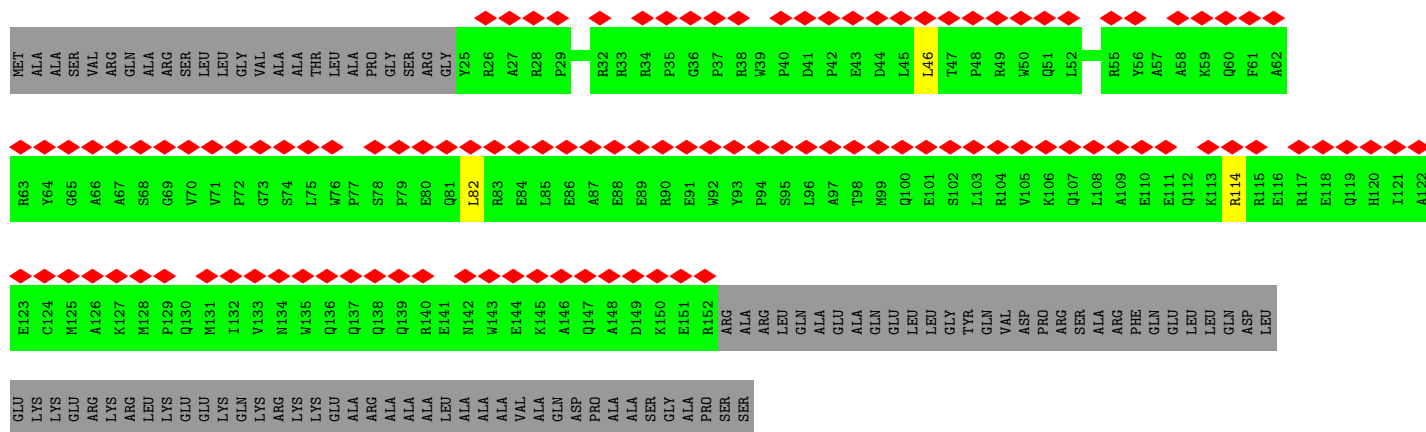


- Molecule 29: Ribosomal protein 63, mitochondrial

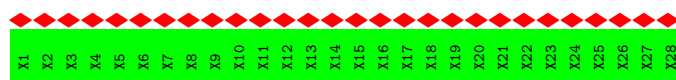


- Molecule 30: Growth arrest and DNA damage-inducible proteins-interacting protein 1

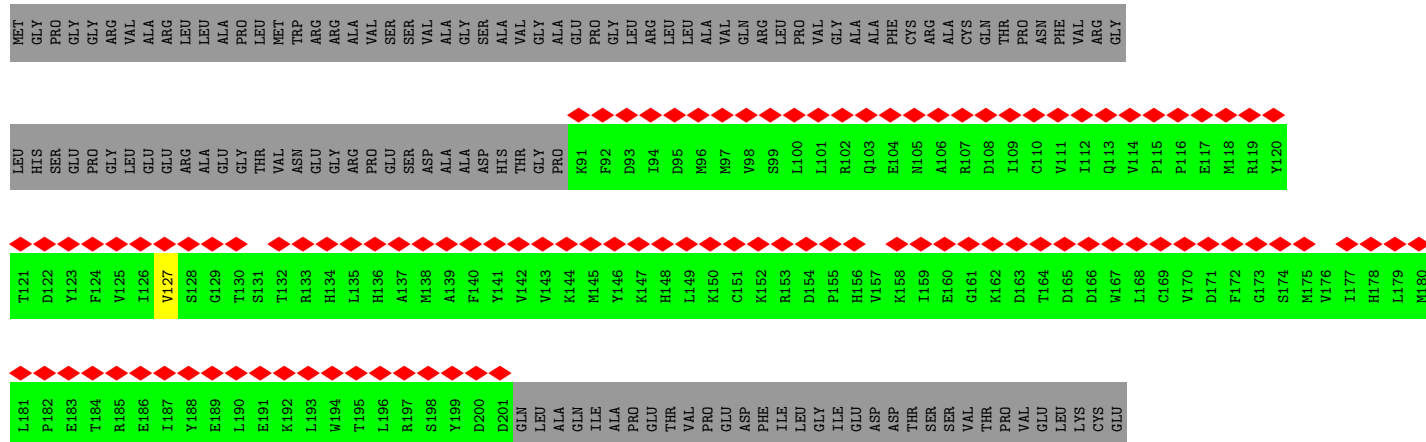




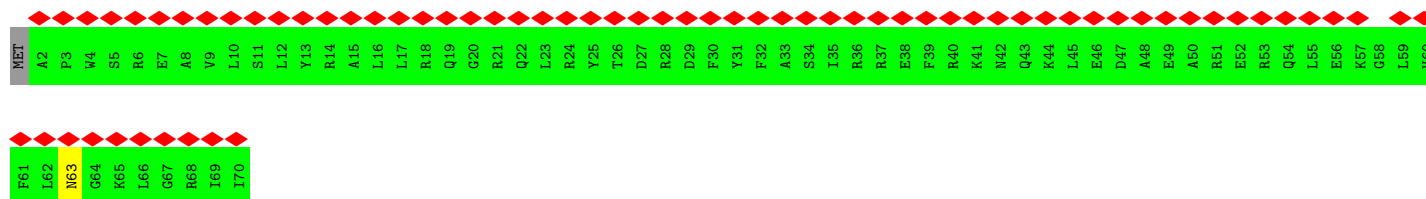
- Molecule 31: Unknown protein or protein extension



- Molecule 32: Mitochondrial assembly of ribosomal large subunit protein 1



- Molecule 33: MIEF1 upstream open reading frame protein

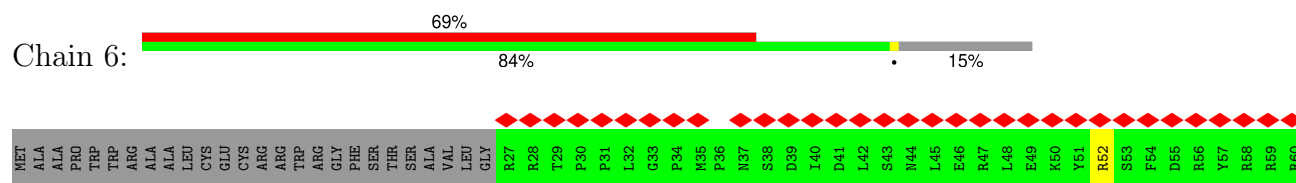


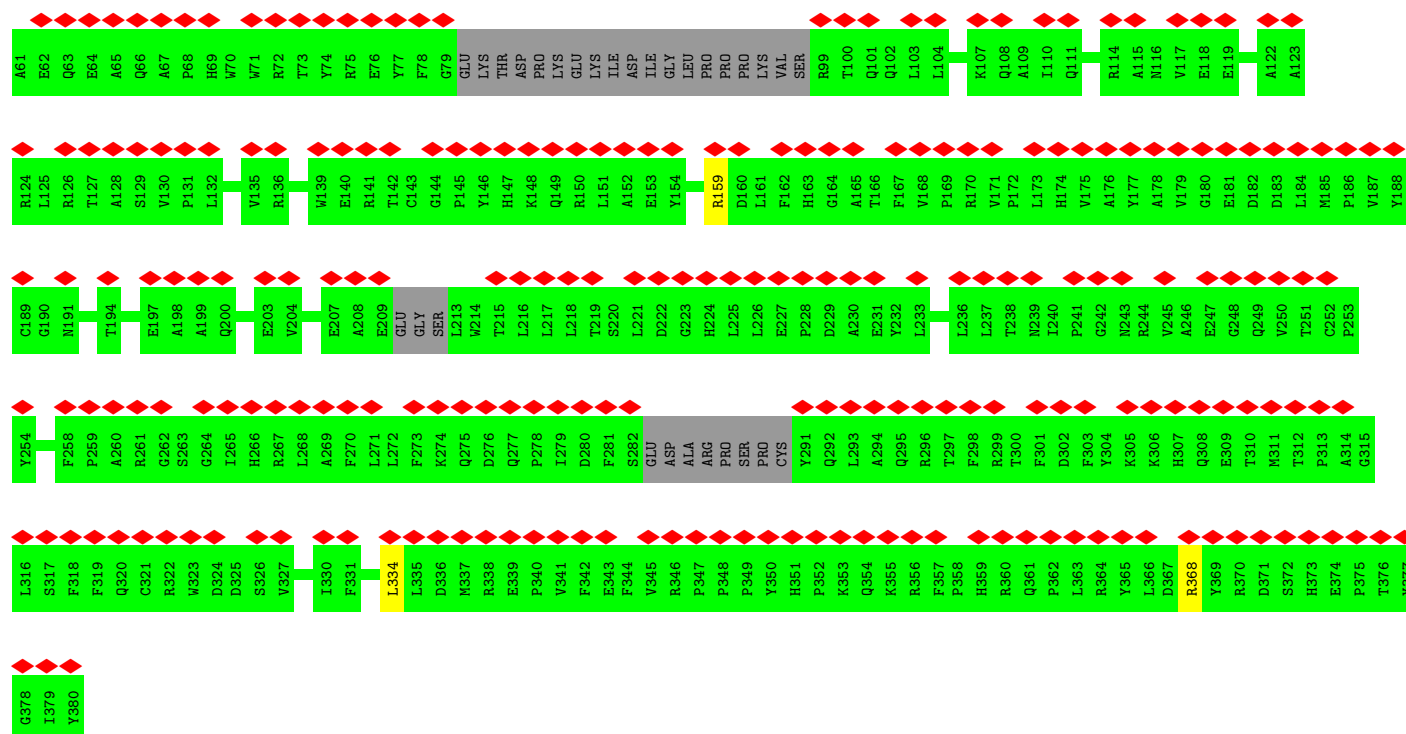
- Molecule 34: Acyl carrier protein, mitochondrial

- Molecule 35: 39S ribosomal protein L37, mitochondrial

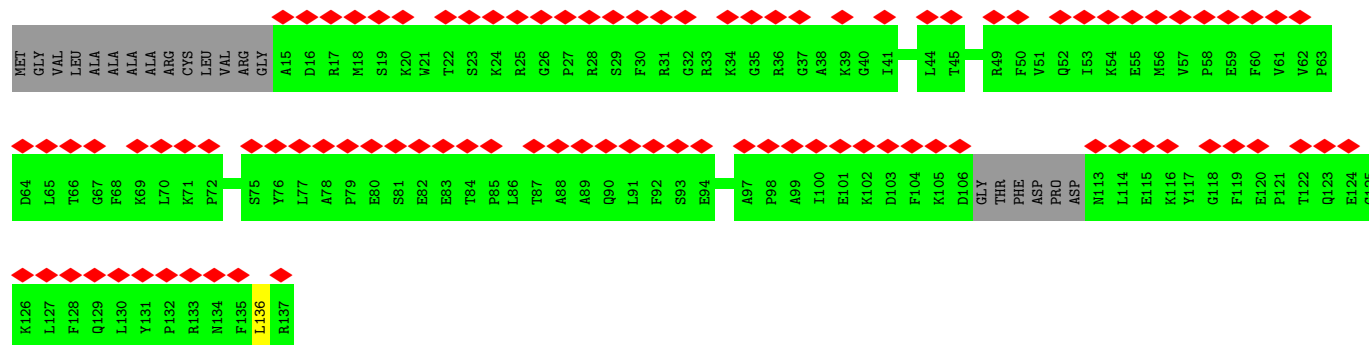
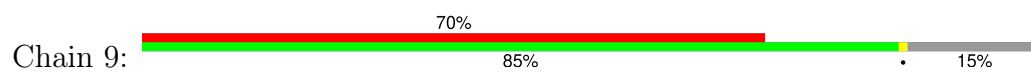


- Molecule 36: 39S ribosomal protein L38, mitochondrial

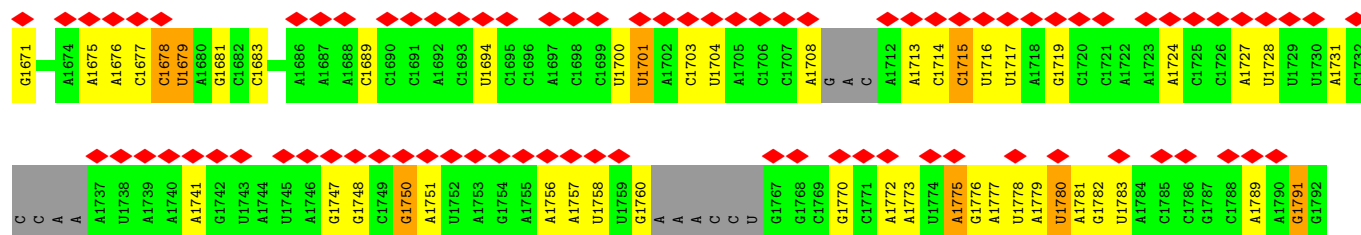




• Molecule 37: 39S ribosomal protein L41, mitochondrial

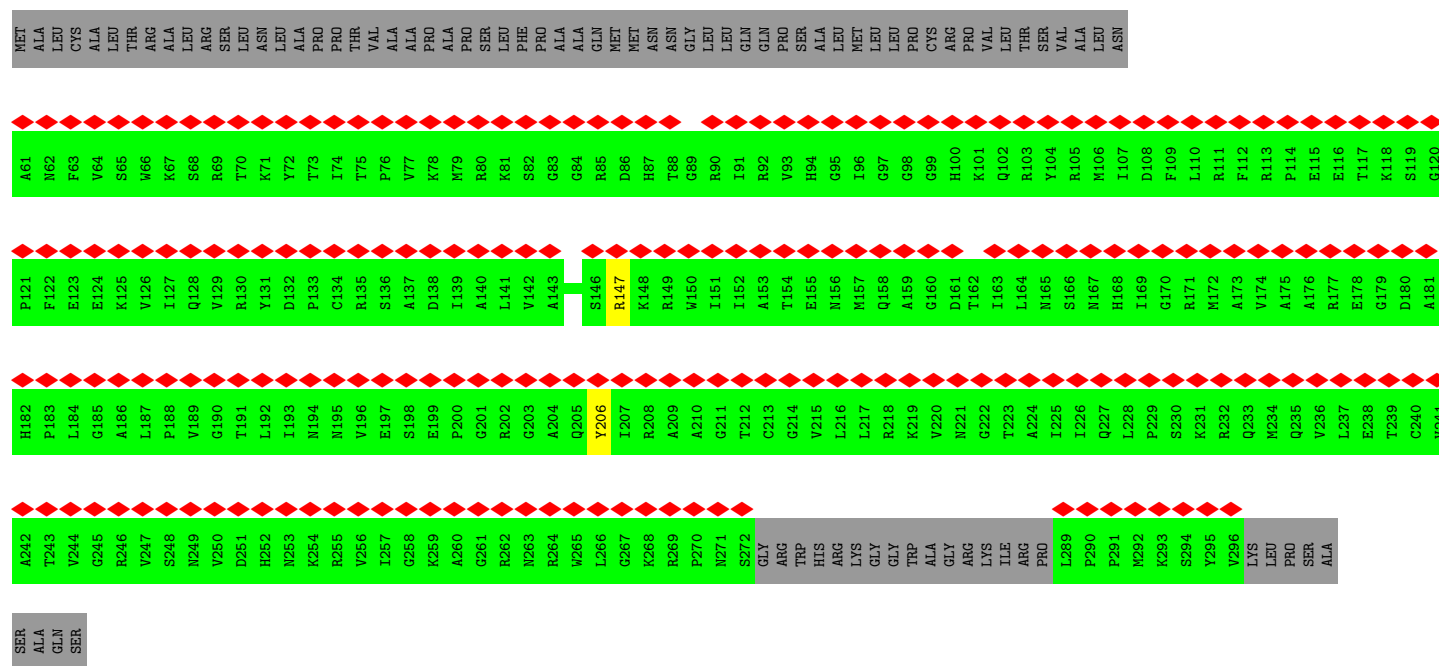


• Molecule 38: 16S ribosomal RNA



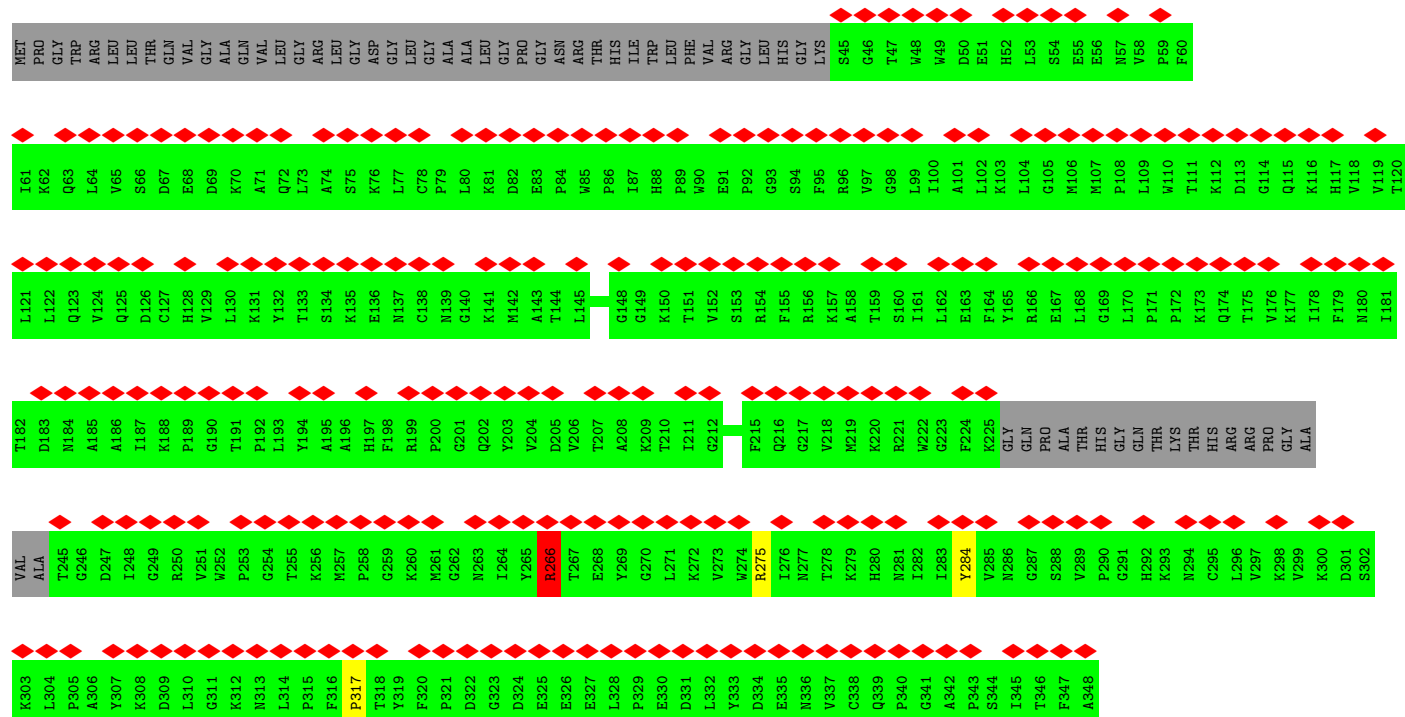






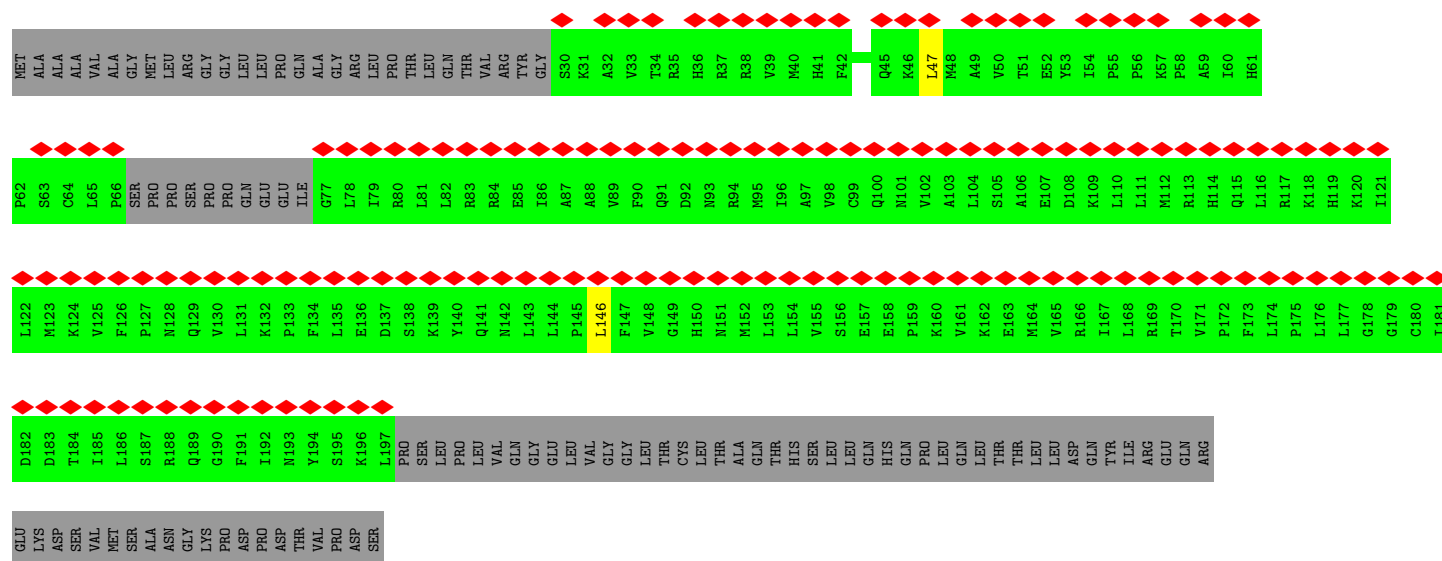
- Molecule 41: 39S ribosomal protein L3, mitochondrial

Chain E: 68% 81% 18%

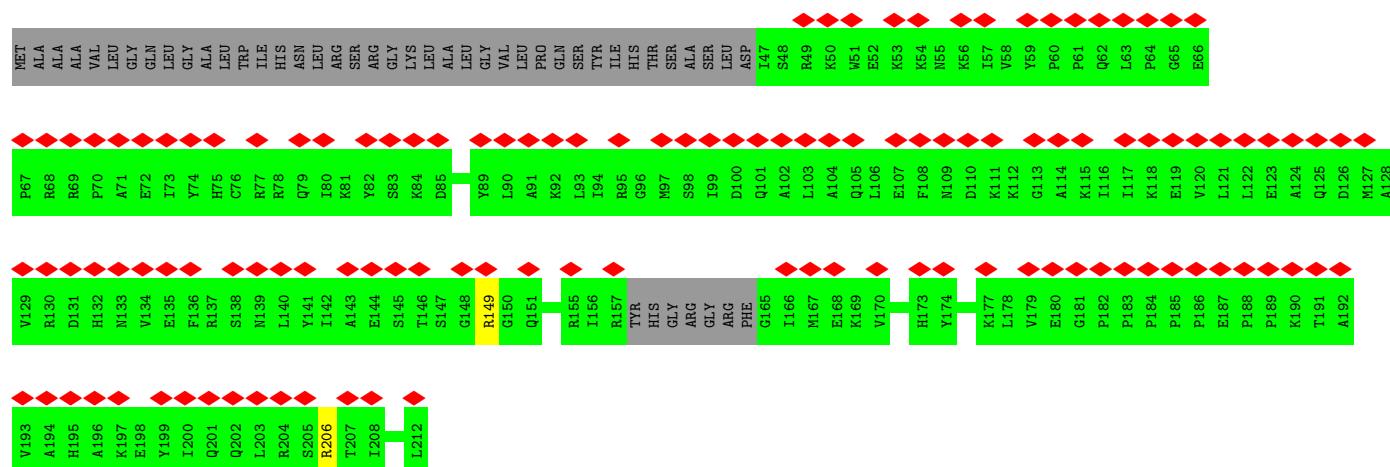
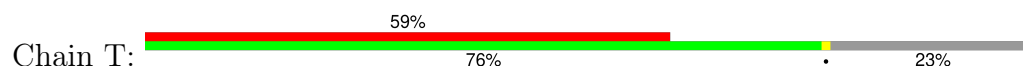


- Molecule 42: 39S ribosomal protein L10, mitochondrial

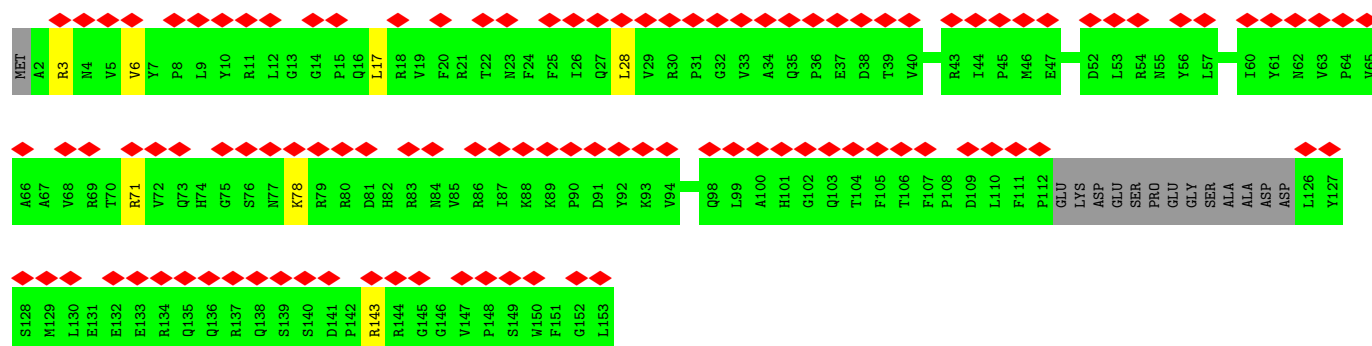
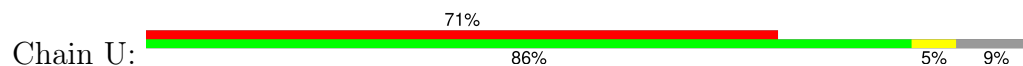
Chain I: 57% 60% 39%



• Molecule 43: 39S ribosomal protein L22, mitochondrial



• Molecule 44: 39S ribosomal protein L23, mitochondrial



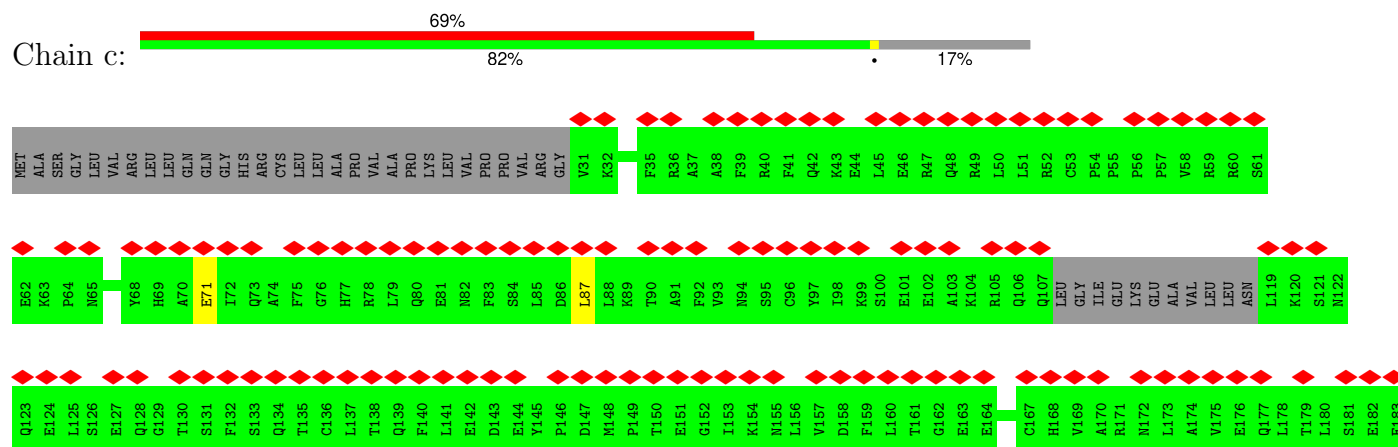
- Chain V:

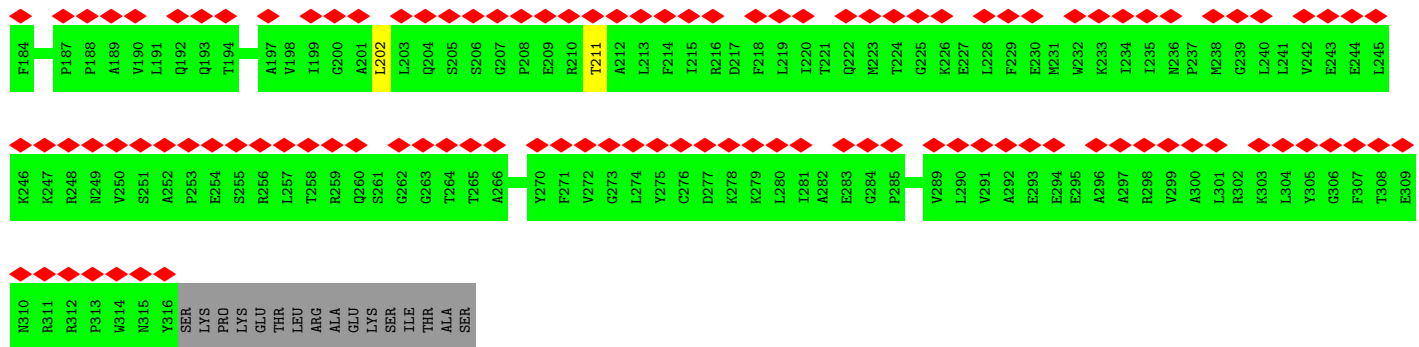


Chain a:

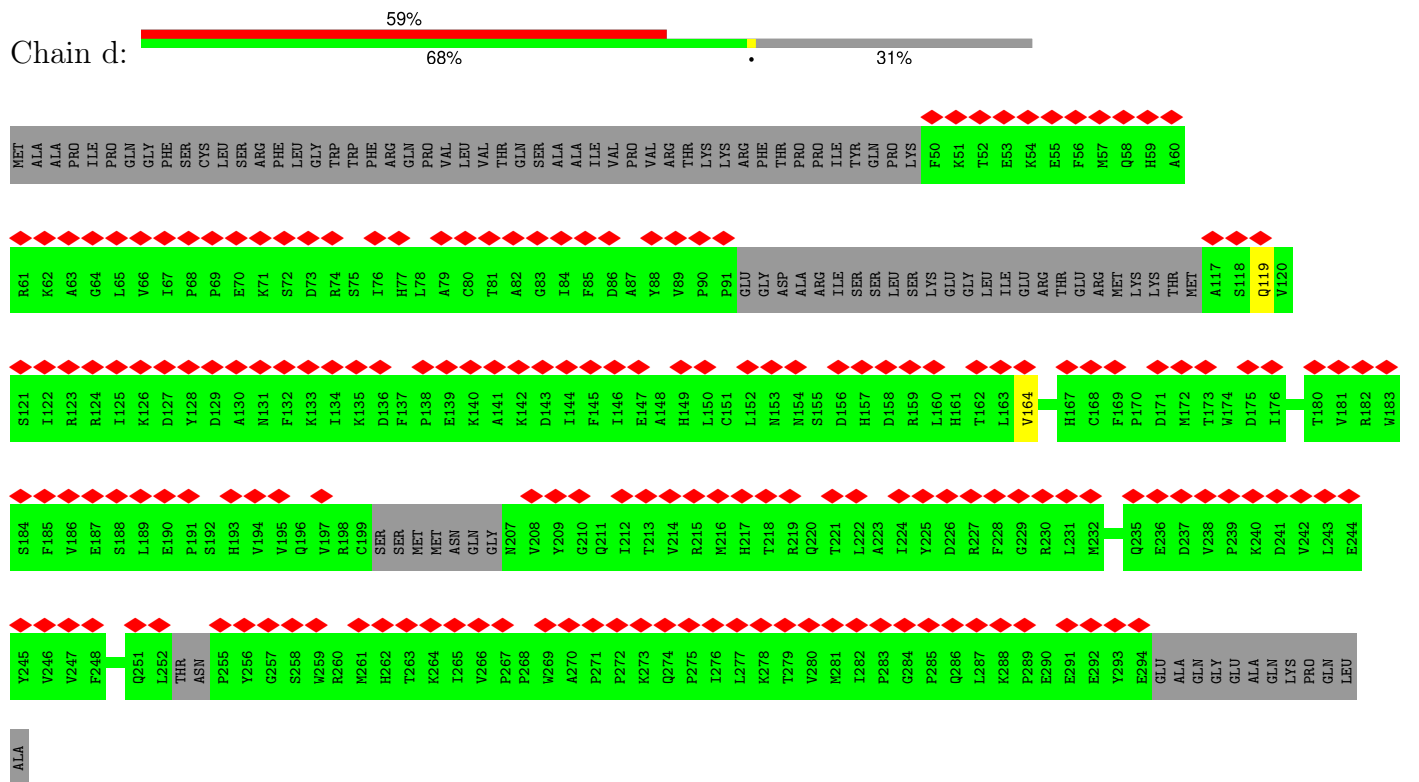


Chain c:

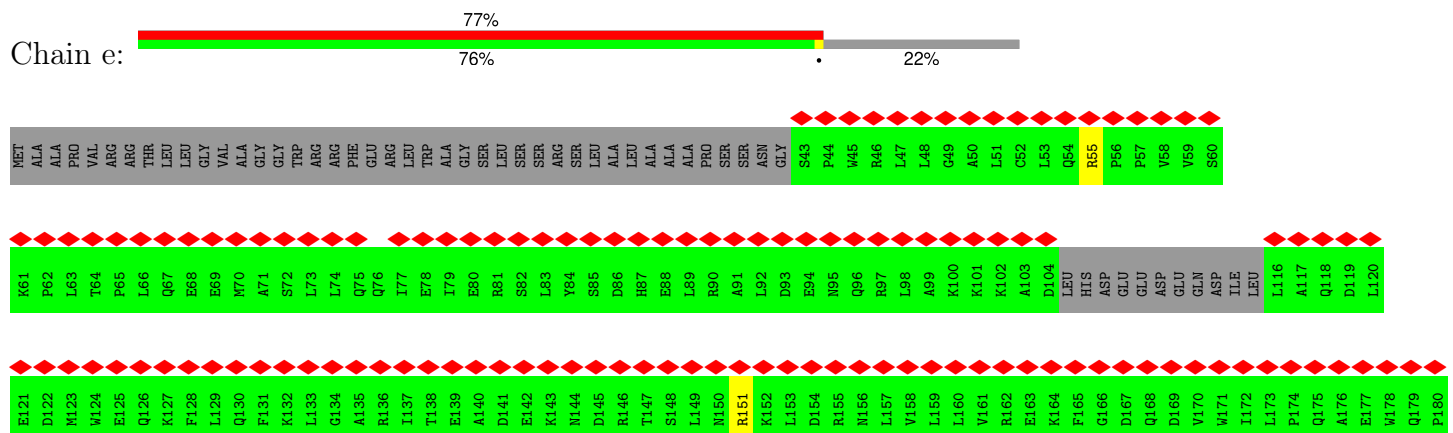


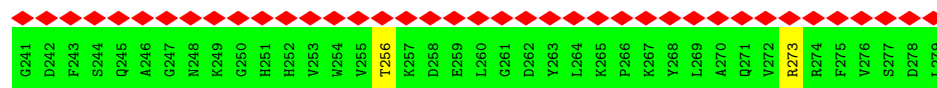
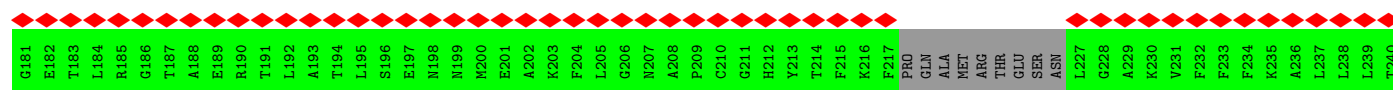


- Molecule 48: 39S ribosomal protein L45, mitochondrial

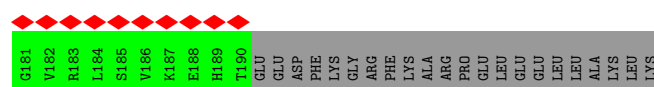
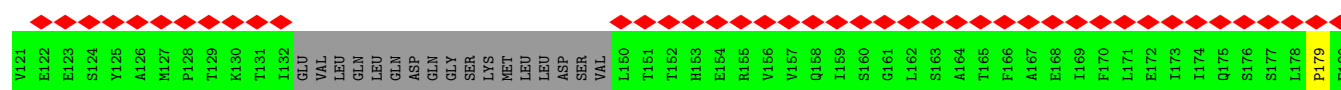
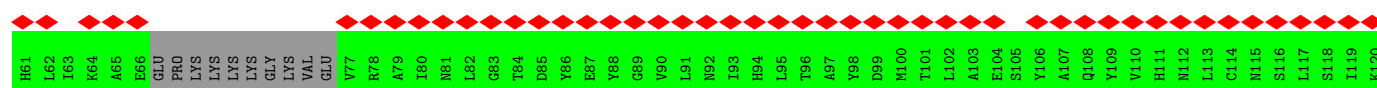
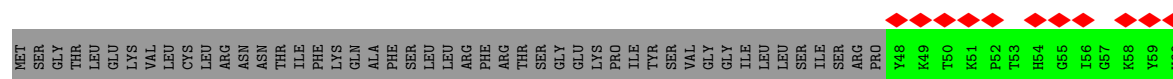


- Molecule 49: 39S ribosomal protein L46, mitochondrial

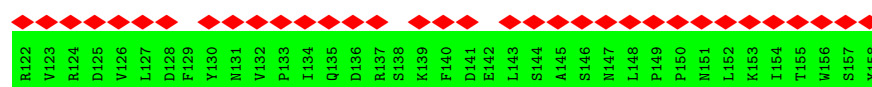
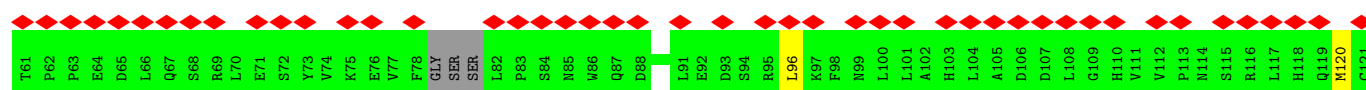




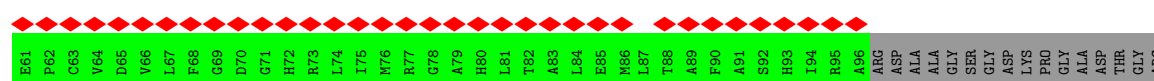
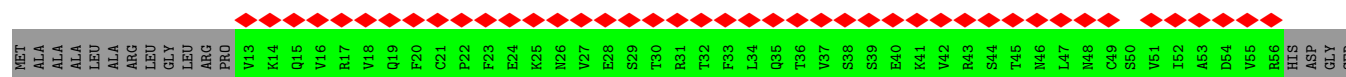
• Molecule 50: 39S ribosomal protein L48, mitochondrial



• Molecule 51: 39S ribosomal protein L50, mitochondrial

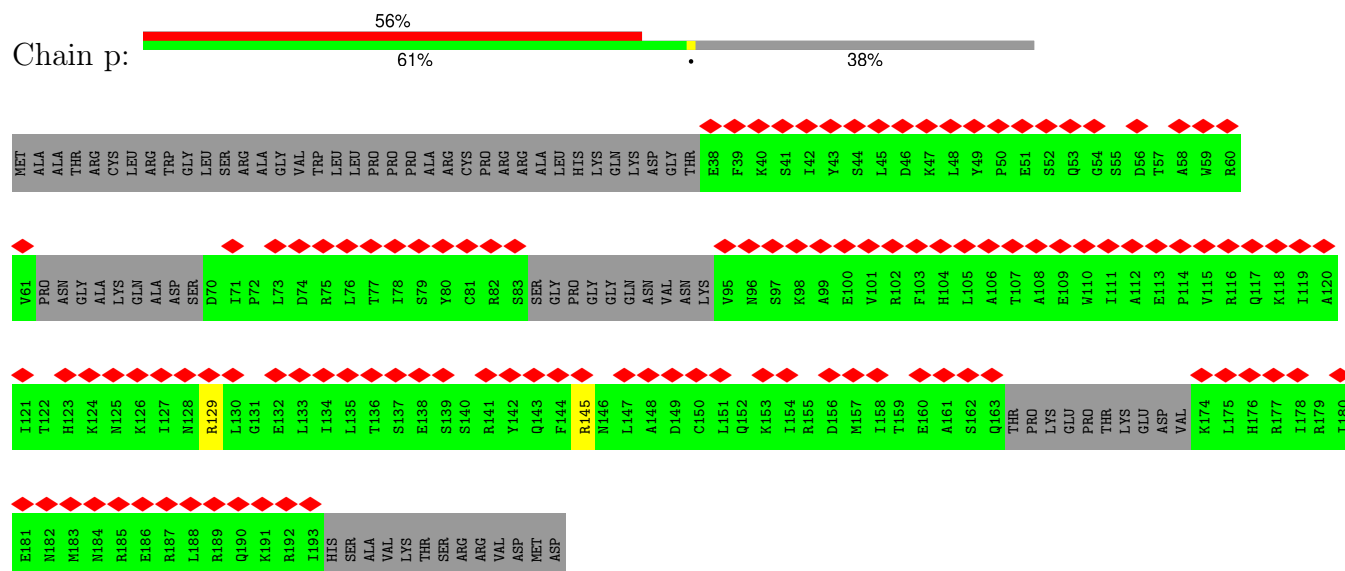


• Molecule 52: 39S ribosomal protein L53, mitochondrial



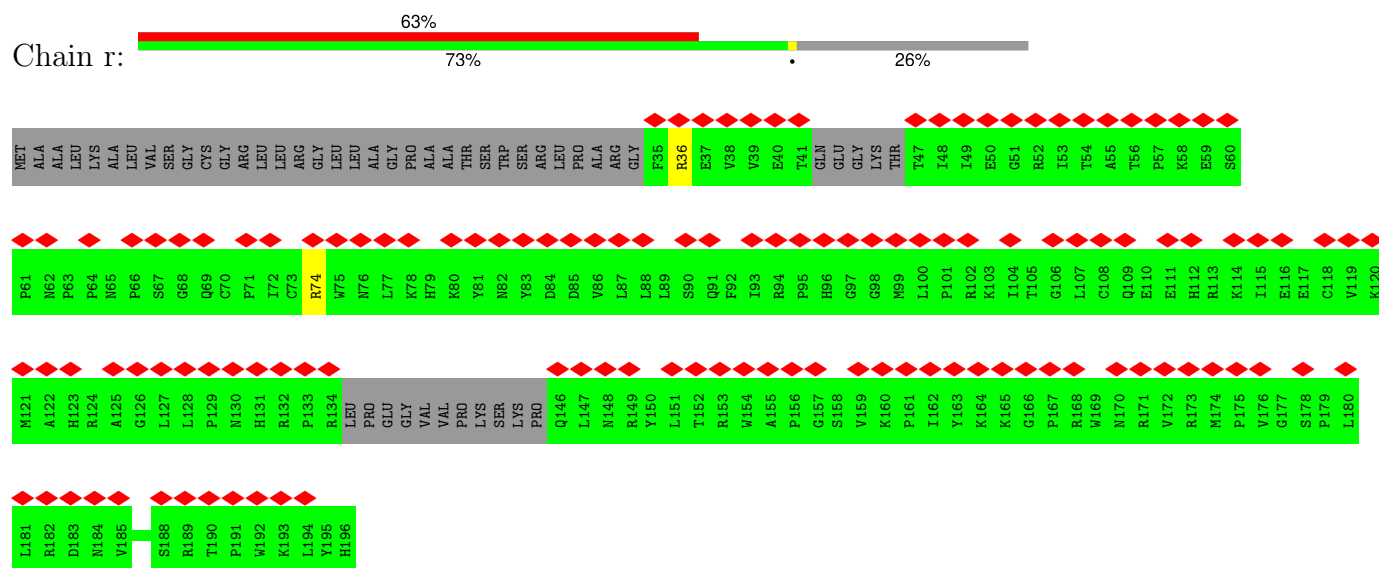
- Molecule 53: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:



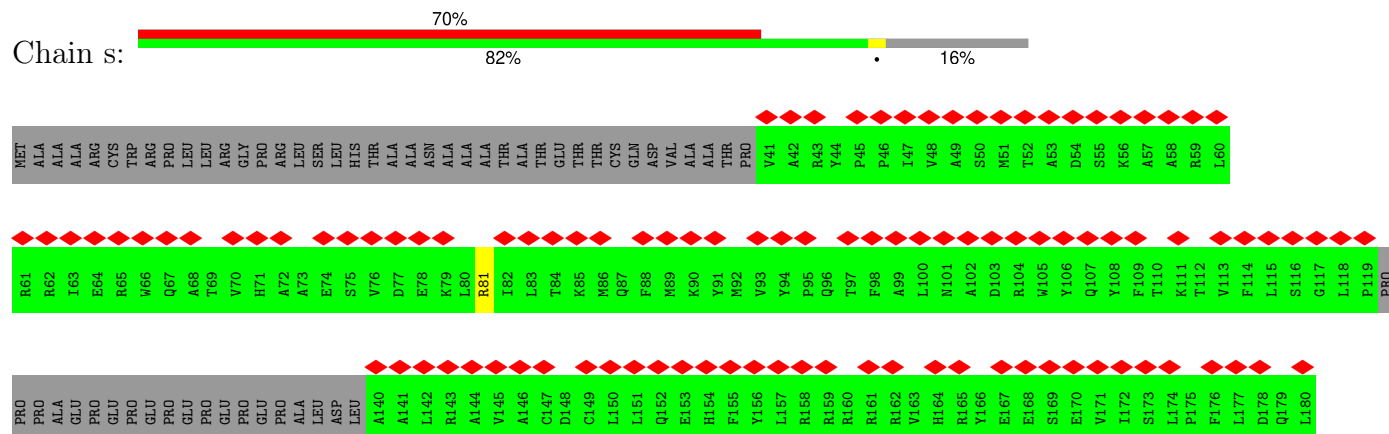
- Molecule 54: 39S ribosomal protein S18a, mitochondrial

Chain r:



- Molecule 55: 39S ribosomal protein S30, mitochondrial

Chain s:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76796	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.129	Depositor
Minimum map value	-1.129	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	606.0, 606.0, 606.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PNS, 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	0.38	0/895	0.72	0/1201
2	1	0.33	0/438	0.69	0/583
3	2	0.49	0/357	0.73	0/475
4	3	0.45	0/852	0.80	1/1136 (0.1%)
5	7	0.35	0/2391	0.57	0/3234
6	8	0.27	0/855	0.44	0/1152
7	F	0.43	0/2071	0.72	0/2817
8	H	0.32	0/798	0.64	0/1073
9	J	0.26	0/1077	0.50	0/1452
10	K	0.40	0/1495	0.66	0/2029
11	L	0.29	0/904	0.55	0/1218
12	M	0.40	0/2359	0.71	0/3185
13	N	0.31	0/1697	0.55	0/2281
14	O	0.39	0/1269	0.74	1/1708 (0.1%)
15	P	0.37	0/1173	0.61	0/1588
16	Q	0.32	0/1846	0.60	0/2487
17	R	0.46	0/1174	0.81	3/1572 (0.2%)
18	S	0.42	0/1276	0.73	0/1729
19	W	0.42	0/881	0.64	0/1188
20	X	0.34	0/2090	0.60	0/2825
21	Y	0.37	0/1552	0.63	0/2079
22	Z	0.39	0/1003	0.67	0/1354
23	b	0.45	0/1202	0.73	0/1626
24	g	0.43	0/1102	0.76	2/1503 (0.1%)
25	i	0.43	0/849	0.76	0/1135
26	j	0.40	0/698	0.60	0/940
27	l	0.27	0/226	0.42	0/299
28	m	0.29	0/379	0.59	0/510
29	o	0.41	0/682	0.64	0/916
30	q	0.32	0/1107	0.56	0/1498
32	u	0.27	0/949	0.50	0/1281
33	v	0.27	0/597	0.46	0/796

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	w	0.26	0/647	0.47	0/871
35	5	0.31	0/3250	0.59	0/4429
36	6	0.34	0/2726	0.60	0/3715
37	9	0.37	0/972	0.60	0/1306
38	A	0.68	3/24893 (0.0%)	1.26	117/38695 (0.3%)
39	B	0.48	0/1328	0.94	2/2056 (0.1%)
40	D	0.32	0/1736	0.56	0/2335
41	E	0.35	0/2322	0.64	2/3148 (0.1%)
42	I	0.27	0/1308	0.54	0/1761
43	T	0.46	0/1335	0.69	1/1796 (0.1%)
44	U	0.36	0/1183	0.69	0/1600
45	V	0.35	0/1616	0.59	0/2189
46	a	0.39	0/709	0.62	0/963
47	c	0.38	0/2264	0.63	0/3059
48	d	0.32	0/1790	0.56	0/2423
49	e	0.26	0/1797	0.50	0/2422
50	f	0.32	0/931	0.49	0/1259
51	h	0.35	0/847	0.58	0/1150
52	k	0.28	0/635	0.53	0/855
53	p	0.34	0/1071	0.54	0/1433
54	r	0.36	0/1238	0.64	0/1676
55	s	0.36	0/3114	0.65	0/4225
All	All	0.47	3/93956 (0.0%)	0.86	129/132236 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1	0	1
4	3	0	1
5	7	0	1
12	M	0	3
13	N	0	1
16	Q	0	1
17	R	0	5
21	Y	0	1
24	g	0	2
35	5	0	4
36	6	0	1
41	E	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
43	T	0	1
53	p	0	1
55	s	0	1
All	All	0	25

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A	2875	A	P-O5'	8.27	1.68	1.59
38	A	2317	G	P-O5'	5.15	1.65	1.59
38	A	1789	A	N9-C4	-5.08	1.34	1.37

All (129) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A	1778	U	O5'-P-OP1	-53.08	47.00	110.70
38	A	2317	G	O5'-P-OP1	38.53	156.94	110.70
38	A	2691	U	O5'-P-OP1	-33.14	70.93	110.70
38	A	2691	U	O5'-P-OP2	29.73	146.37	110.70
38	A	1779	A	O5'-P-OP1	27.20	143.34	110.70
38	A	2317	G	OP1-P-OP2	-26.39	80.01	119.60
38	A	2452	A	OP1-P-OP2	-25.62	81.17	119.60
38	A	2451	A	OP1-P-O3'	23.07	155.95	105.20
38	A	1778	U	O5'-P-OP2	19.38	133.95	110.70
38	A	1779	A	O5'-P-OP2	-19.34	87.49	110.70
38	A	1776	G	OP1-P-OP2	-17.61	93.18	119.60
38	A	2691	U	OP1-P-OP2	-17.58	93.23	119.60
38	A	2690	G	OP1-P-O3'	17.48	143.65	105.20
38	A	2453	G	O5'-P-OP2	-16.03	91.27	105.70
38	A	2015	G	O5'-P-OP1	-15.74	91.53	105.70
38	A	2875	A	O5'-P-OP1	15.46	129.25	110.70
38	A	1776	G	O5'-P-OP1	14.85	128.52	110.70
38	A	2468	A	O5'-P-OP1	-14.82	92.36	105.70
38	A	1795	A	O5'-P-OP1	14.79	128.45	110.70
38	A	1777	A	OP1-P-O3'	14.39	136.85	105.20
38	A	1795	A	O5'-P-OP2	-11.02	95.78	105.70
38	A	1778	U	OP1-P-OP2	-10.80	103.40	119.60
38	A	2469	A	O5'-P-OP2	-10.54	96.21	105.70
38	A	1757	A	O5'-P-OP1	-10.42	96.32	105.70
41	E	266	ARG	NE-CZ-NH1	-10.37	115.11	120.30
38	A	2469	A	O5'-P-OP1	10.03	122.73	110.70
38	A	2469	A	OP1-P-OP2	-10.03	104.56	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A	2875	A	O5'-P-OP2	-9.86	96.83	105.70
38	A	2863	U	OP1-P-O3'	9.54	126.18	105.20
38	A	1758	U	O5'-P-OP1	9.51	122.12	110.70
38	A	2316	U	OP2-P-O3'	9.45	125.98	105.20
38	A	1791	G	O5'-P-OP2	-9.43	97.21	105.70
38	A	2690	G	OP2-P-O3'	-9.33	84.67	105.20
38	A	2875	A	OP1-P-OP2	-9.27	105.69	119.60
38	A	2451	A	OP2-P-O3'	-8.82	85.80	105.20
38	A	2014	A	OP1-P-O3'	-8.44	86.64	105.20
41	E	266	ARG	NE-CZ-NH2	8.41	124.50	120.30
38	A	2875	A	P-O5'-C5'	-8.37	107.51	120.90
38	A	2015	G	OP1-P-OP2	8.15	131.82	119.60
38	A	2733	G	O5'-P-OP1	8.11	120.44	110.70
38	A	2421	G	OP1-P-O3'	8.09	122.99	105.20
38	A	2467	A	OP1-P-O3'	8.06	122.93	105.20
38	A	1823	A	C2'-C3'-O3'	8.01	127.12	109.50
38	A	2317	G	O5'-P-OP2	-7.81	98.67	105.70
38	A	1780	U	P-O3'-C3'	7.68	128.92	119.70
38	A	2864	U	OP1-P-OP2	-7.67	108.10	119.60
38	A	2451	A	O3'-P-O5'	-7.66	89.44	104.00
38	A	1779	A	OP1-P-OP2	-7.52	108.32	119.60
38	A	2322	C	C2-N1-C1'	7.51	127.06	118.80
38	A	1823	A	P-O3'-C3'	7.49	128.69	119.70
38	A	2015	G	O5'-P-OP2	7.27	119.43	110.70
38	A	2468	A	OP1-P-O3'	7.15	120.94	105.20
38	A	2423	C	O5'-P-OP1	6.99	119.08	110.70
38	A	2309	A	O5'-P-OP2	-6.93	99.46	105.70
38	A	1795	A	OP1-P-OP2	-6.89	109.27	119.60
38	A	3212	C	C2-N1-C1'	6.84	126.33	118.80
38	A	1758	U	O5'-P-OP2	-6.82	99.56	105.70
38	A	1750	G	O4'-C1'-N9	6.80	113.64	108.20
38	A	2690	G	O3'-P-O5'	-6.77	91.13	104.00
38	A	2690	G	P-O3'-C3'	6.66	127.69	119.70
17	R	34	ARG	CB-CG-CD	-6.65	94.30	111.60
38	A	1777	A	O3'-P-O5'	-6.65	91.37	104.00
38	A	2030	U	P-O3'-C3'	6.64	127.67	119.70
38	A	1777	A	P-O3'-C3'	6.59	127.61	119.70
38	A	2014	A	O3'-P-O5'	6.54	116.44	104.00
38	A	2318	A	O5'-P-OP1	-6.54	99.81	105.70
38	A	1783	U	O5'-P-OP2	-6.51	99.84	105.70
38	A	1833	C	O5'-P-OP1	-6.51	99.84	105.70
38	A	1782	G	O4'-C1'-N9	6.43	113.35	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	A	2898	U	O4'-C1'-N1	6.35	113.28	108.20
38	A	3201	A	P-O3'-C3'	6.22	127.17	119.70
38	A	1750	G	C4'-C3'-C2'	-6.22	96.38	102.60
38	A	1679	U	C3'-C2'-C1'	-6.16	96.58	101.50
38	A	3212	C	O4'-C1'-N1	6.11	113.09	108.20
38	A	2684	C	C2-N1-C1'	6.09	125.50	118.80
38	A	1775	A	OP2-P-O3'	6.08	118.57	105.20
38	A	2317	G	P-O5'-C5'	-5.97	111.35	120.90
38	A	2457	A	P-O3'-C3'	5.94	126.83	119.70
17	R	11	ARG	CG-CD-NE	-5.88	99.45	111.80
38	A	1906	G	OP1-P-O3'	5.82	118.01	105.20
38	A	2684	C	N1-C2-O2	5.82	122.39	118.90
38	A	2864	U	O5'-P-OP2	-5.82	100.47	105.70
38	A	2322	C	N1-C2-O2	5.73	122.34	118.90
38	A	2165	C	C2'-C3'-O3'	5.67	122.77	113.70
38	A	2309	A	O5'-P-OP1	5.64	117.47	110.70
38	A	2251	A	OP1-P-O3'	5.64	117.60	105.20
4	3	116	ARG	CG-CD-NE	-5.61	100.02	111.80
38	A	2066	C	C2-N1-C1'	5.60	124.96	118.80
38	A	1715	C	C2-N1-C1'	5.57	124.92	118.80
38	A	2852	C	C2-N1-C1'	5.53	124.88	118.80
38	A	2379	C	C2-N1-C1'	5.52	124.87	118.80
38	A	2322	C	C6-N1-C1'	-5.52	114.18	120.80
38	A	1671	G	O4'-C1'-N9	5.51	112.61	108.20
17	R	13	ARG	CB-CG-CD	-5.46	97.39	111.60
38	A	2731	U	O5'-P-OP2	-5.46	100.78	105.70
38	A	2243	A	P-O3'-C3'	5.45	126.24	119.70
38	A	1776	G	O5'-P-OP2	-5.42	100.83	105.70
38	A	1683	C	O5'-P-OP2	-5.38	100.86	105.70
38	A	2846	G	O4'-C1'-N9	5.33	112.47	108.20
38	A	2165	C	P-O3'-C3'	5.33	126.10	119.70
24	g	90	ARG	CB-CA-C	-5.26	99.87	110.40
38	A	2665	U	O5'-P-OP2	-5.26	100.97	105.70
38	A	2744	U	O4'-C1'-N1	5.26	112.41	108.20
38	A	1805	A	C2'-C3'-O3'	5.25	122.11	113.70
38	A	2684	C	C6-N1-C1'	-5.25	114.50	120.80
38	A	1879	G	C6-C5-N7	-5.24	127.25	130.40
14	O	16	ARG	NE-CZ-NH1	-5.24	117.68	120.30
38	A	1747	G	N9-C4-C5	5.24	107.50	105.40
38	A	2297	A	OP1-P-O3'	5.22	116.70	105.20
38	A	1701	U	N1-C2-O2	5.21	126.44	122.80
38	A	1679	U	O3'-P-O5'	-5.20	94.11	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	g	105	ARG	CG-CD-NE	-5.19	100.90	111.80
38	A	1715	C	O4'-C1'-N1	5.18	112.34	108.20
38	A	1775	A	P-O3'-C3'	-5.17	113.50	119.70
39	B	1607	U	P-O3'-C3'	5.14	125.87	119.70
38	A	1870	A	OP2-P-O3'	5.13	116.49	105.20
38	A	2507	A	P-O3'-C3'	5.10	125.82	119.70
38	A	1775	A	OP1-P-O3'	5.09	116.40	105.20
38	A	2135	A	O4'-C1'-N9	5.08	112.27	108.20
38	A	2451	A	C2'-C3'-O3'	5.08	121.83	113.70
38	A	1678	C	P-O5'-C5'	-5.08	112.78	120.90
39	B	1607	U	C2'-C3'-O3'	5.07	121.81	113.70
38	A	2243	A	OP2-P-O3'	5.04	116.30	105.20
38	A	2317	G	C4'-C3'-C2'	-5.03	97.57	102.60
38	A	2245	A	C3'-C2'-C1'	-5.03	97.48	101.50
43	T	206	ARG	CG-CD-NE	-5.03	101.24	111.80
38	A	1756	A	OP1-P-O3'	5.02	116.24	105.20
38	A	2186	C	P-O3'-C3'	5.01	125.72	119.70
38	A	2457	A	C2'-C3'-O3'	5.01	121.72	113.70

There are no chirality outliers.

All (25) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	25	GLY	Peptide
4	3	184	THR	Peptide
35	5	173	ARG	Sidechain
35	5	300	ARG	Sidechain
35	5	303	ARG	Sidechain
35	5	350	ARG	Sidechain
36	6	368	ARG	Sidechain
5	7	159	LYS	Peptide
41	E	266	ARG	Sidechain
12	M	125	ARG	Sidechain
12	M	41	ARG	Sidechain
12	M	59	ARG	Sidechain
13	N	73	ARG	Sidechain
16	Q	226	PRO	Peptide
17	R	11	ARG	Sidechain
17	R	34	ARG	Sidechain
17	R	37	ARG	Sidechain
17	R	40	ARG	Sidechain
17	R	48	ARG	Sidechain

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Mol	Chain	Res	Type	Group
43	T	149	ARG	Sidechain
21	Y	210	ARG	Sidechain
24	g	105	ARG	Sidechain
24	g	90	ARG	Sidechain
53	p	145	ARG	Sidechain
55	s	357	SER	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	106/188 (56%)	102 (96%)	4 (4%)	0	100	100
2	1	50/65 (77%)	50 (100%)	0	0	100	100
3	2	41/92 (45%)	40 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
5	7	285/338 (84%)	259 (91%)	26 (9%)	0	100	100
6	8	97/206 (47%)	90 (93%)	7 (7%)	0	100	100
7	F	248/311 (80%)	232 (94%)	16 (6%)	0	100	100
8	H	93/267 (35%)	84 (90%)	8 (9%)	1 (1%)	12	17
9	J	138/192 (72%)	122 (88%)	16 (12%)	0	100	100
10	K	175/178 (98%)	166 (95%)	9 (5%)	0	100	100
11	L	113/145 (78%)	104 (92%)	9 (8%)	0	100	100
12	M	285/296 (96%)	274 (96%)	11 (4%)	0	100	100
13	N	203/251 (81%)	191 (94%)	12 (6%)	0	100	100
14	O	150/175 (86%)	144 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	P	139/180 (77%)	131 (94%)	8 (6%)	0	100	100
16	Q	215/292 (74%)	201 (94%)	14 (6%)	0	100	100
17	R	138/149 (93%)	132 (96%)	6 (4%)	0	100	100
18	S	154/205 (75%)	147 (96%)	7 (4%)	0	100	100
19	W	107/148 (72%)	103 (96%)	3 (3%)	1 (1%)	14	21
20	X	241/256 (94%)	236 (98%)	5 (2%)	0	100	100
21	Y	174/250 (70%)	169 (97%)	5 (3%)	0	100	100
22	Z	118/161 (73%)	111 (94%)	7 (6%)	0	100	100
23	b	146/215 (68%)	131 (90%)	15 (10%)	0	100	100
24	g	127/166 (76%)	115 (91%)	12 (9%)	0	100	100
25	i	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
26	j	83/123 (68%)	82 (99%)	1 (1%)	0	100	100
27	l	21/138 (15%)	21 (100%)	0	0	100	100
28	m	43/128 (34%)	38 (88%)	4 (9%)	1 (2%)	5	5
29	o	77/102 (76%)	77 (100%)	0	0	100	100
30	q	126/222 (57%)	124 (98%)	2 (2%)	0	100	100
32	u	109/234 (47%)	100 (92%)	9 (8%)	0	100	100
33	v	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
34	w	77/156 (49%)	69 (90%)	8 (10%)	0	100	100
35	5	383/423 (90%)	359 (94%)	24 (6%)	0	100	100
36	6	316/380 (83%)	300 (95%)	16 (5%)	0	100	100
37	9	113/137 (82%)	108 (96%)	5 (4%)	0	100	100
40	D	216/305 (71%)	203 (94%)	13 (6%)	0	100	100
41	E	281/348 (81%)	269 (96%)	11 (4%)	1 (0%)	30	42
42	I	154/261 (59%)	142 (92%)	12 (8%)	0	100	100
43	T	155/206 (75%)	153 (99%)	2 (1%)	0	100	100
44	U	135/153 (88%)	128 (95%)	7 (5%)	0	100	100
45	V	188/216 (87%)	182 (97%)	6 (3%)	0	100	100
46	a	78/142 (55%)	74 (95%)	4 (5%)	0	100	100
47	c	271/332 (82%)	264 (97%)	7 (3%)	0	100	100
48	d	203/306 (66%)	192 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	e	211/279 (76%)	181 (86%)	29 (14%)	1 (0%)	25	36
50	f	110/212 (52%)	99 (90%)	10 (9%)	1 (1%)	14	21
51	h	96/158 (61%)	91 (95%)	5 (5%)	0	100	100
52	k	76/112 (68%)	69 (91%)	7 (9%)	0	100	100
53	p	119/206 (58%)	115 (97%)	4 (3%)	0	100	100
54	r	140/196 (71%)	133 (95%)	7 (5%)	0	100	100
55	s	366/439 (83%)	350 (96%)	15 (4%)	1 (0%)	37	50
All	All	7945/11026 (72%)	7503 (94%)	435 (6%)	7 (0%)	50	64

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	m	71	PRO
8	H	103	GLU
55	s	272	PRO
49	e	256	THR
50	f	179	PRO
19	W	73	PHE
41	E	317	PRO

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	97/164 (59%)	95 (98%)	2 (2%)	48	67
2	1	49/60 (82%)	45 (92%)	4 (8%)	9	14
3	2	38/72 (53%)	36 (95%)	2 (5%)	19	31
4	3	88/166 (53%)	85 (97%)	3 (3%)	32	50
5	7	263/303 (87%)	259 (98%)	4 (2%)	60	77
6	8	91/190 (48%)	90 (99%)	1 (1%)	70	84
7	F	217/262 (83%)	209 (96%)	8 (4%)	29	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	86/228 (38%)	85 (99%)	1 (1%)	67	82
9	J	113/150 (75%)	113 (100%)	0	100	100
10	K	155/156 (99%)	152 (98%)	3 (2%)	52	70
11	L	98/124 (79%)	96 (98%)	2 (2%)	50	68
12	M	245/249 (98%)	235 (96%)	10 (4%)	26	42
13	N	172/211 (82%)	170 (99%)	2 (1%)	67	82
14	O	133/150 (89%)	129 (97%)	4 (3%)	36	55
15	P	123/155 (79%)	121 (98%)	2 (2%)	58	75
16	Q	199/256 (78%)	197 (99%)	2 (1%)	73	85
17	R	118/126 (94%)	117 (99%)	1 (1%)	79	89
18	S	141/180 (78%)	140 (99%)	1 (1%)	81	91
19	W	89/119 (75%)	88 (99%)	1 (1%)	70	84
20	X	219/229 (96%)	211 (96%)	8 (4%)	29	46
21	Y	159/223 (71%)	156 (98%)	3 (2%)	52	70
22	Z	111/147 (76%)	108 (97%)	3 (3%)	40	58
23	b	130/186 (70%)	126 (97%)	4 (3%)	35	54
24	g	119/148 (80%)	113 (95%)	6 (5%)	20	34
25	i	86/110 (78%)	82 (95%)	4 (5%)	22	36
26	j	68/97 (70%)	68 (100%)	0	100	100
27	l	23/116 (20%)	23 (100%)	0	100	100
28	m	40/113 (35%)	39 (98%)	1 (2%)	42	61
29	o	68/87 (78%)	68 (100%)	0	100	100
30	q	110/178 (62%)	107 (97%)	3 (3%)	40	58
32	u	105/200 (52%)	104 (99%)	1 (1%)	73	85
33	v	59/60 (98%)	58 (98%)	1 (2%)	56	73
34	w	73/136 (54%)	72 (99%)	1 (1%)	62	79
35	5	348/368 (95%)	339 (97%)	9 (3%)	41	60
36	6	265/332 (80%)	262 (99%)	3 (1%)	70	84
37	9	99/112 (88%)	98 (99%)	1 (1%)	73	85
40	D	179/245 (73%)	177 (99%)	2 (1%)	70	84
41	E	246/290 (85%)	243 (99%)	3 (1%)	67	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	I	145/232 (62%)	143 (99%)	2 (1%)	62	79
43	T	141/176 (80%)	141 (100%)	0	100	100
44	U	124/135 (92%)	117 (94%)	7 (6%)	17	28
45	V	172/191 (90%)	168 (98%)	4 (2%)	45	64
46	a	78/133 (59%)	76 (97%)	2 (3%)	41	60
47	c	241/288 (84%)	237 (98%)	4 (2%)	56	73
48	d	193/274 (70%)	191 (99%)	2 (1%)	73	85
49	e	188/236 (80%)	185 (98%)	3 (2%)	58	75
50	f	101/188 (54%)	101 (100%)	0	100	100
51	h	95/148 (64%)	93 (98%)	2 (2%)	48	67
52	k	71/90 (79%)	71 (100%)	0	100	100
53	p	117/181 (65%)	116 (99%)	1 (1%)	75	87
54	r	133/169 (79%)	131 (98%)	2 (2%)	60	77
55	s	326/381 (86%)	320 (98%)	6 (2%)	54	72
All	All	7147/9520 (75%)	7006 (98%)	141 (2%)	50	68

All (141) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	84	ARG
1	0	168	GLN
2	1	34	ARG
2	1	38	ARG
2	1	61	LYS
2	1	65	LEU
3	2	63	LYS
3	2	84	LEU
4	3	125	ARG
4	3	168	ARG
4	3	173	VAL
5	7	67	VAL
5	7	167	VAL
5	7	175	ILE
5	7	319	ARG
6	8	101	ARG
7	F	108	ARG
7	F	125	ARG

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Mol	Chain	Res	Type
7	F	147	ARG
7	F	170	ARG
7	F	203	LEU
7	F	259	LEU
7	F	277	ASP
7	F	281	ARG
8	H	70	LYS
10	K	16	ARG
10	K	65	ILE
10	K	125	LEU
11	L	37	ARG
11	L	39	ARG
12	M	34	LYS
12	M	39	ARG
12	M	44	ARG
12	M	47	ARG
12	M	57	ARG
12	M	96	LEU
12	M	101	LEU
12	M	132	LEU
12	M	134	ARG
12	M	154	ILE
13	N	51	ARG
13	N	105	MET
14	O	20	LEU
14	O	26	ILE
14	O	36	LEU
14	O	144	LEU
15	P	51	ARG
15	P	120	ARG
16	Q	136	ILE
16	Q	151	LEU
17	R	119	LEU
18	S	115	LEU
19	W	105	VAL
20	X	23	ARG
20	X	36	ARG
20	X	44	ARG
20	X	59	ARG
20	X	64	ASP
20	X	90	ILE
20	X	141	LEU

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Mol	Chain	Res	Type
20	X	216	ARG
21	Y	162	ARG
21	Y	191	ASN
21	Y	210	ARG
22	Z	105	SER
22	Z	139	LEU
22	Z	145	LEU
23	b	11	LEU
23	b	26	LEU
23	b	62	VAL
23	b	144	ARG
24	g	68	THR
24	g	100	ILE
24	g	108	THR
24	g	137	VAL
24	g	140	VAL
24	g	147	LEU
25	i	63	LEU
25	i	80	LEU
25	i	98	VAL
25	i	113	ARG
28	m	42	ARG
30	q	46	LEU
30	q	82	LEU
30	q	114	ARG
32	u	127	VAL
33	v	63	ASN
34	w	106	LYS
35	5	36	ARG
35	5	98	LEU
35	5	102	GLN
35	5	106	ILE
35	5	155	LEU
35	5	218	LEU
35	5	229	ARG
35	5	262	ILE
35	5	350	ARG
36	6	52	ARG
36	6	159	ARG
36	6	334	LEU
37	9	136	LEU
40	D	147	ARG

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Mol	Chain	Res	Type
40	D	206	TYR
41	E	266	ARG
41	E	275	ARG
41	E	284	TYR
42	I	47	LEU
42	I	146	LEU
44	U	3	ARG
44	U	6	VAL
44	U	17	LEU
44	U	28	LEU
44	U	71	ARG
44	U	78	LYS
44	U	143	ARG
45	V	92	ASN
45	V	138	THR
45	V	143	ARG
45	V	208	ARG
46	a	111	GLN
46	a	122	ARG
47	c	71	GLU
47	c	87	LEU
47	c	202	LEU
47	c	211	THR
48	d	119	GLN
48	d	164	VAL
49	e	55	ARG
49	e	151	ARG
49	e	273	ARG
51	h	96	LEU
51	h	120	MET
53	p	129	ARG
54	r	36	ARG
54	r	74	ARG
55	s	81	ARG
55	s	230	ARG
55	s	238	ASN
55	s	251	VAL
55	s	360	VAL
55	s	361	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	96	ASN
1	0	118	GLN
11	L	142	GLN
14	O	147	GLN
15	P	79	HIS
15	P	87	GLN
17	R	30	HIS
17	R	89	ASN
17	R	125	HIS
18	S	118	ASN
18	S	140	ASN
19	W	76	HIS
20	X	46	HIS
21	Y	191	ASN
21	Y	195	ASN
22	Z	107	ASN
23	b	27	GLN
25	i	108	HIS
25	i	120	HIS
33	v	63	ASN
35	5	302	HIS
35	5	305	GLN
35	5	308	GLN
36	6	359	HIS
40	D	205	GLN
40	D	227	GLN
41	E	184	ASN
43	T	75	HIS
44	U	35	GLN
44	U	74	HIS
44	U	82	HIS
45	V	92	ASN
48	d	251	GLN
49	e	212	HIS
50	f	112	ASN
51	h	67	GLN
52	k	15	GLN
52	k	26	ASN
54	r	112	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
38	A	1028/1559 (65%)	289 (28%)	25 (2%)
39	B	51/69 (73%)	15 (29%)	1 (1%)
All	All	1079/1628 (66%)	304 (28%)	26 (2%)

All (304) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
38	A	1675	A
38	A	1676	A
38	A	1677	C
38	A	1678	C
38	A	1679	U
38	A	1681	G
38	A	1689	C
38	A	1694	U
38	A	1700	U
38	A	1701	U
38	A	1703	C
38	A	1704	U
38	A	1708	A
38	A	1713	A
38	A	1714	C
38	A	1715	C
38	A	1716	U
38	A	1717	U
38	A	1719	G
38	A	1724	A
38	A	1727	A
38	A	1728	U
38	A	1731	A
38	A	1741	A
38	A	1748	G
38	A	1750	G
38	A	1751	A
38	A	1760	G
38	A	1770	G
38	A	1773	A
38	A	1775	A
38	A	1780	U
38	A	1781	A
38	A	1791	G
38	A	1794	A
38	A	1803	A

Continued on next page...

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Mol	Chain	Res	Type
38	A	1804	A
38	A	1805	A
38	A	1806	U
38	A	1812	C
38	A	1817	C
38	A	1820	A
38	A	1823	A
38	A	1824	U
38	A	1827	C
38	A	1828	A
38	A	1829	A
38	A	1832	A
38	A	1836	A
38	A	1844	A
38	A	1849	C
38	A	1867	A
38	A	1869	A
38	A	1870	A
38	A	1871	A
38	A	1872	U
38	A	1874	A
38	A	1875	C
38	A	1878	U
38	A	1882	A
38	A	1883	G
38	A	1887	A
38	A	1888	G
38	A	1890	C
38	A	1892	A
38	A	1893	A
38	A	1901	C
38	A	1903	C
38	A	1914	A
38	A	1918	G
38	A	2012	A
38	A	2015	G
38	A	2020	U
38	A	2021	U
38	A	2022	G
38	A	2027	A
38	A	2028	G
38	A	2029	A

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Mol	Chain	Res	Type
38	A	2030	U
38	A	2031	A
38	A	2032	G
38	A	2036	C
38	A	2037	U
38	A	2039	A
38	A	2041	U
38	A	2053	U
38	A	2055	U
38	A	2060	A
38	A	2065	A
38	A	2074	A
38	A	2079	C
38	A	2083	U
38	A	2085	A
38	A	2095	U
38	A	2105	G
38	A	2113	G
38	A	2124	A
38	A	2125	C
38	A	2126	U
38	A	2132	A
38	A	2134	A
38	A	2141	U
38	A	2142	A
38	A	2147	G
38	A	2154	A
38	A	2156	A
38	A	2157	U
38	A	2158	U
38	A	2159	U
38	A	2161	A
38	A	2163	A
38	A	2166	C
38	A	2168	U
38	A	2171	U
38	A	2172	A
38	A	2173	G
38	A	2174	G
38	A	2180	A
38	A	2181	A
38	A	2182	G

Continued on next page...

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Mol	Chain	Res	Type
38	A	2183	C
38	A	2187	C
38	A	2190	C
38	A	2193	U
38	A	2194	U
38	A	2195	A
38	A	2197	G
38	A	2198	A
38	A	2200	A
38	A	2204	U
38	A	2207	A
38	A	2210	C
38	A	2216	A
38	A	2237	A
38	A	2239	A
38	A	2241	A
38	A	2243	A
38	A	2244	U
38	A	2245	A
38	A	2257	C
38	A	2259	C
38	A	2261	C
38	A	2262	C
38	A	2263	C
38	A	2264	A
38	A	2283	C
38	A	2284	C
38	A	2285	U
38	A	2290	A
38	A	2297	A
38	A	2299	U
38	A	2300	G
38	A	2321	A
38	A	2324	U
38	A	2332	C
38	A	2335	A
38	A	2342	U
38	A	2345	G
38	A	2371	U
38	A	2374	A
38	A	2375	C
38	A	2381	A

Continued on next page...

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Mol	Chain	Res	Type
38	A	2387	U
38	A	2389	C
38	A	2390	A
38	A	2393	C
38	A	2394	A
38	A	2396	C
38	A	2397	C
38	A	2401	A
38	A	2405	C
38	A	2406	A
38	A	2407	U
38	A	2414	C
38	A	2415	C
38	A	2417	C
38	A	2418	A
38	A	2426	C
38	A	2427	C
38	A	2431	C
38	A	2435	G
38	A	2443	C
38	A	2444	A
38	A	2445	U
38	A	2446	A
38	A	2449	G
38	A	2457	A
38	A	2458	A
38	A	2468	A
38	A	2508	C
38	A	2511	C
38	A	2512	A
38	A	2520	C
38	A	2521	A
38	A	2522	U
38	A	2523	C
38	A	2524	A
38	A	2526	C
38	A	2527	A
38	A	2655	G
38	A	2656	U
38	A	2659	C
38	A	2660	U
38	A	2683	C

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Mol	Chain	Res	Type
38	A	2684	C
38	A	2686	G
38	A	2698	G
38	A	2699	C
38	A	2706	A
38	A	2707	A
38	A	2708	C
38	A	2709	A
38	A	2725	A
38	A	2732	G
38	A	2739	U
38	A	2740	A
38	A	2744	U
38	A	2750	U
38	A	2752	C
38	A	2803	A
38	A	2804	A
38	A	2810	G
38	A	2813	U
38	A	2814	G
38	A	2815	G
38	A	2831	G
38	A	2832	A
38	A	2833	A
38	A	2844	G
38	A	2846	G
38	A	2847	C
38	A	2852	C
38	A	2854	U
38	A	2859	A
38	A	2861	A
38	A	2864	U
38	A	2865	C
38	A	2870	G
38	A	2871	U
38	A	2879	A
38	A	2893	A
38	A	2895	U
38	A	2896	G
38	A	2901	A
38	A	2906	C
38	A	2910	A

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Mol	Chain	Res	Type
38	A	2912	C
38	A	2913	A
38	A	2914	A
38	A	2917	G
38	A	2918	A
38	A	2919	A
38	A	2922	A
38	A	2926	A
38	A	2928	C
38	A	3102	U
38	A	3108	U
38	A	3109	U
38	A	3114	U
38	A	3123	G
38	A	3124	U
38	A	3128	A
38	A	3129	A
38	A	3131	G
38	A	3134	C
38	A	3137	G
38	A	3138	A
38	A	3139	G
38	A	3141	A
38	A	3150	U
38	A	3155	C
38	A	3157	C
38	A	3158	A
38	A	3160	A
38	A	3162	C
38	A	3168	C
38	A	3177	A
38	A	3180	A
38	A	3183	U
38	A	3184	C
38	A	3185	A
38	A	3189	C
38	A	3190	A
38	A	3192	C
38	A	3202	U
38	A	3204	C
38	A	3207	A
38	A	3217	A

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Mol	Chain	Res	Type
38	A	3218	A
39	B	1607	U
39	B	1608	G
39	B	1609	U
39	B	1611	G
39	B	1614	U
39	B	1615	A
39	B	1625	A
39	B	1631	C
39	B	1632	U
39	B	1640	A
39	B	1641	G
39	B	1644	G
39	B	1645	A
39	B	1649	C
39	B	1651	A

All (26) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A	1678	C
38	A	1703	C
38	A	1713	A
38	A	1727	A
38	A	1772	A
38	A	1780	U
38	A	1805	A
38	A	1823	A
38	A	2030	U
38	A	2036	C
38	A	2125	C
38	A	2141	U
38	A	2165	C
38	A	2172	A
38	A	2186	C
38	A	2243	A
38	A	2321	A
38	A	2373	A
38	A	2444	A
38	A	2457	A
38	A	2507	A
38	A	2744	U

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Mol	Chain	Res	Type
38	A	2905	A
38	A	3108	U
38	A	3201	A
39	B	1607	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 51 ligands modelled in this entry, 50 are monoatomic - leaving 1 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	$\# Z > 2$
58	PNS	v	101	-	14,20,21	0.20	0	18,26,29	0.94	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
58	PNS	v	101	-	-	7/24/26/27	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

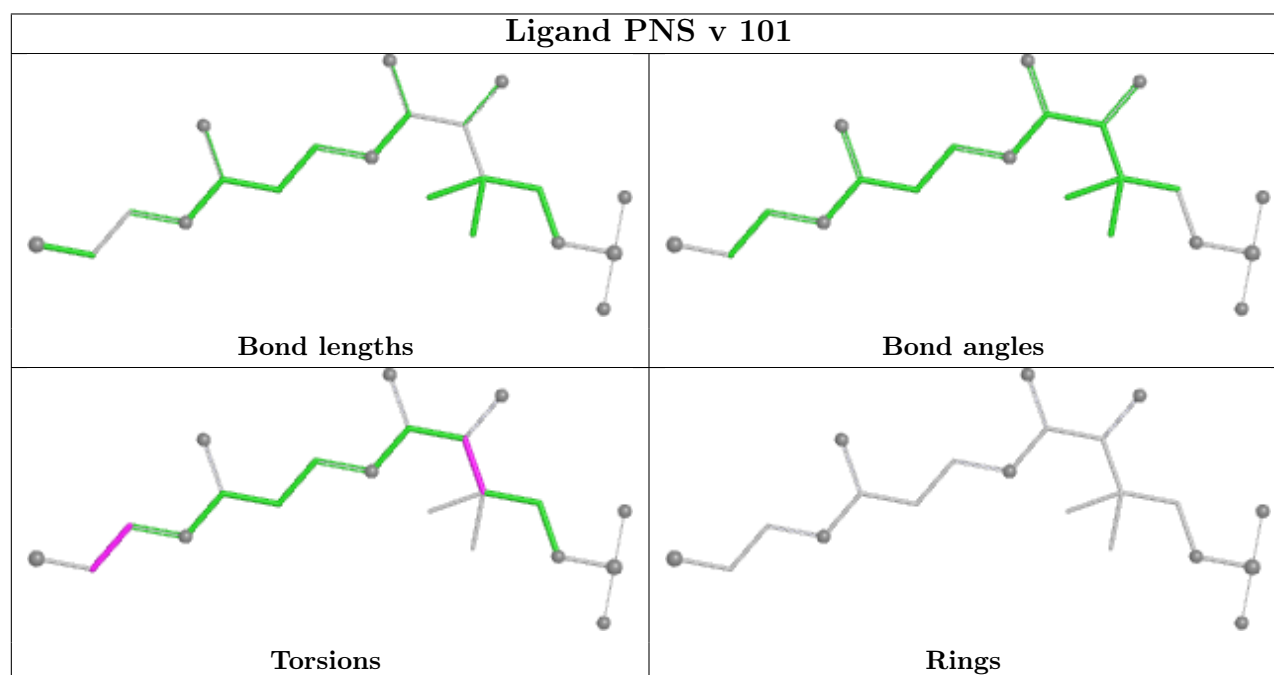
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	v	101	PNS	C28-C29-C32-O33
58	v	101	PNS	C28-C29-C32-C34
58	v	101	PNS	C31-C29-C32-O33
58	v	101	PNS	C31-C29-C32-C34
58	v	101	PNS	N41-C42-C43-S44
58	v	101	PNS	C30-C29-C32-O33
58	v	101	PNS	C30-C29-C32-C34

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

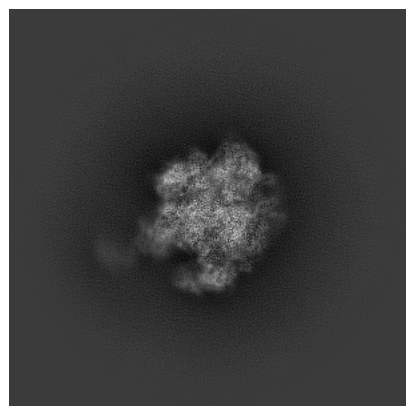
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18461. These allow visual inspection of the internal detail of the map and identification of artifacts.

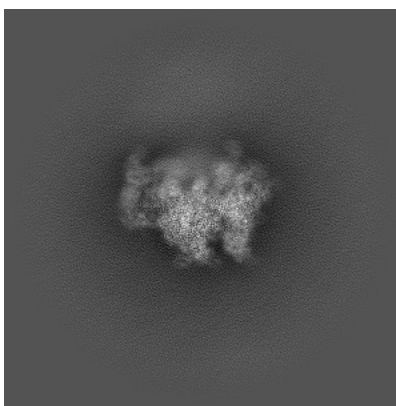
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

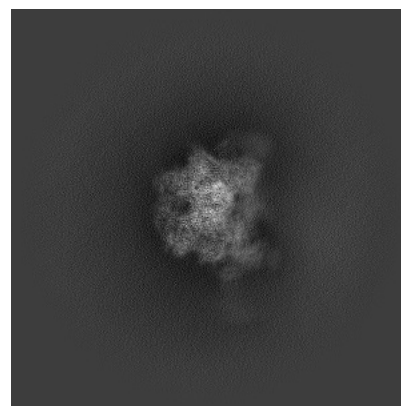
6.1.1 Primary map



X

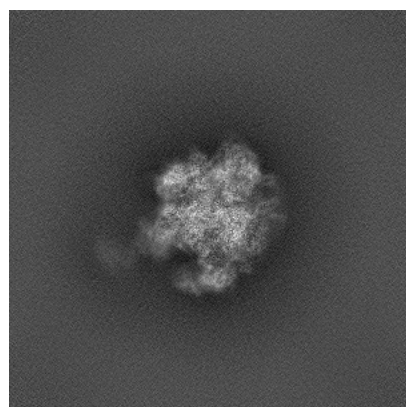


Y

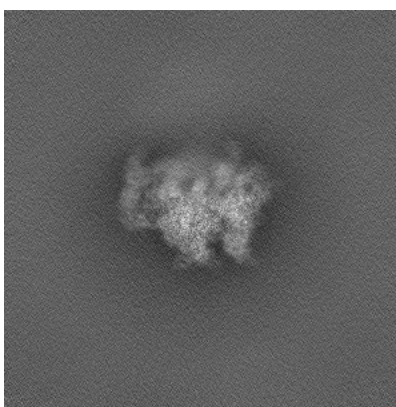


Z

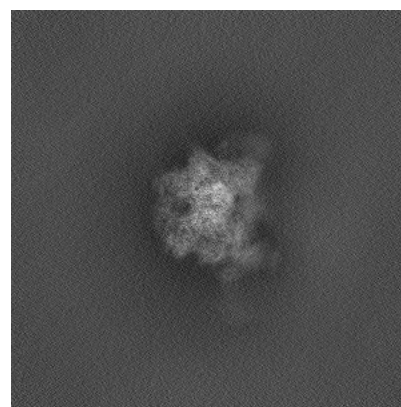
6.1.2 Raw map



X



Y

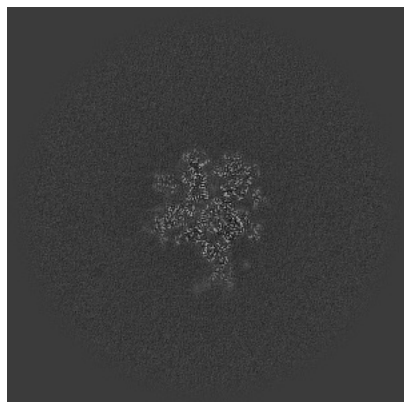


Z

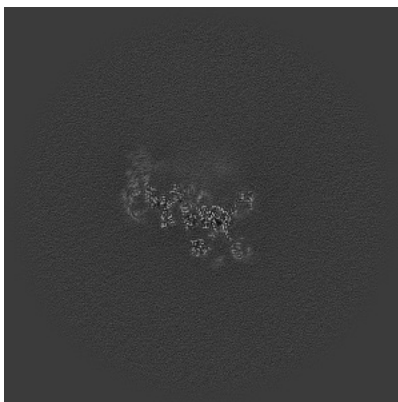
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

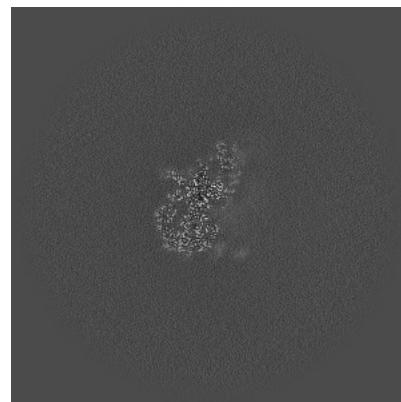
6.2.1 Primary map



X Index: 300

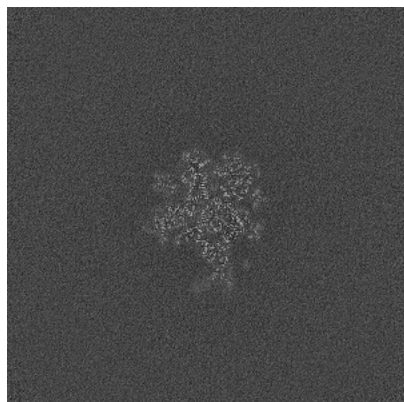


Y Index: 300

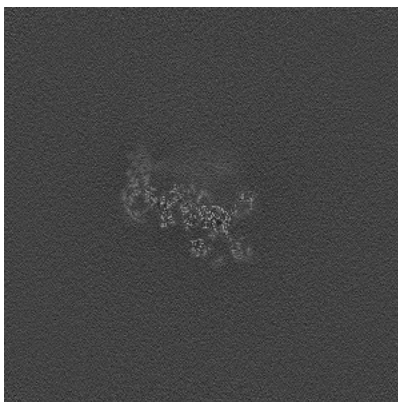


Z Index: 300

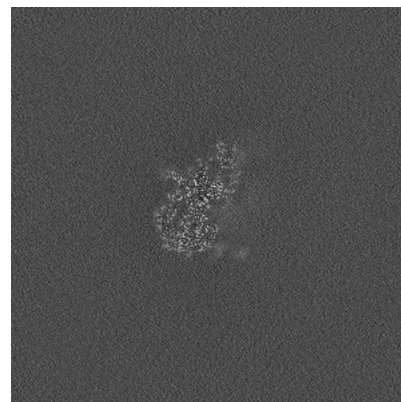
6.2.2 Raw map



X Index: 300



Y Index: 300

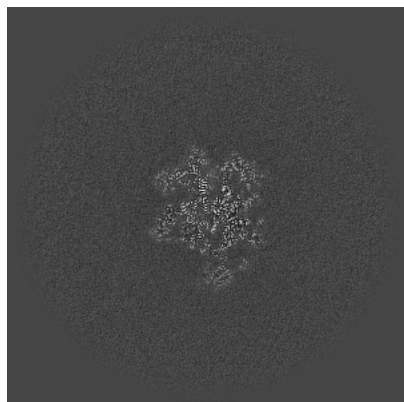


Z Index: 300

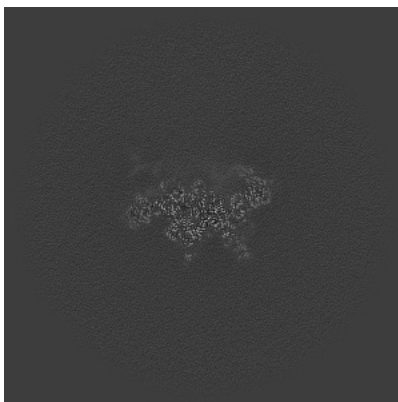
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

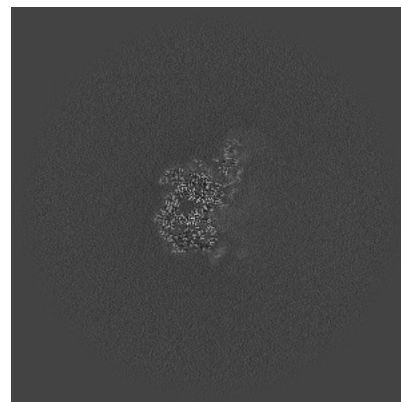
6.3.1 Primary map



X Index: 293

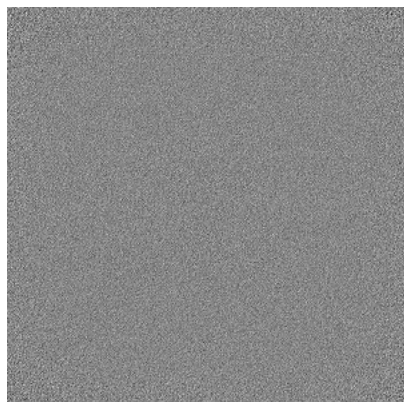


Y Index: 326

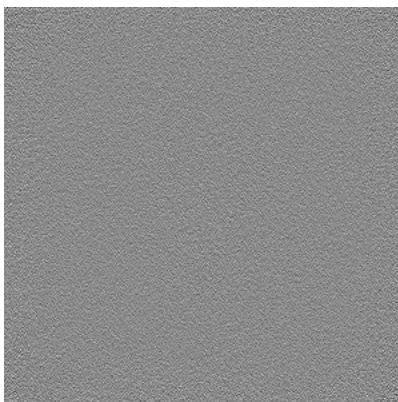


Z Index: 294

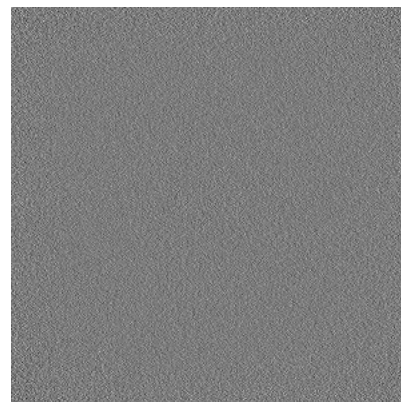
6.3.2 Raw map



X Index: 0



Y Index: 0

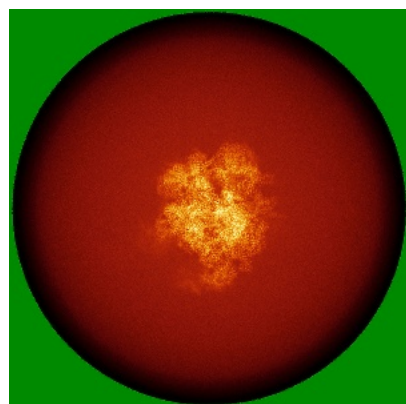


Z Index: 0

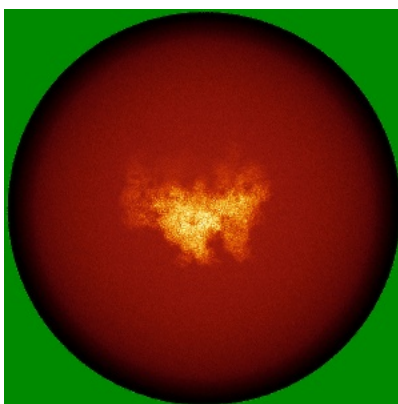
The images above show the largest variance slices of the map in three orthogonal directions.

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

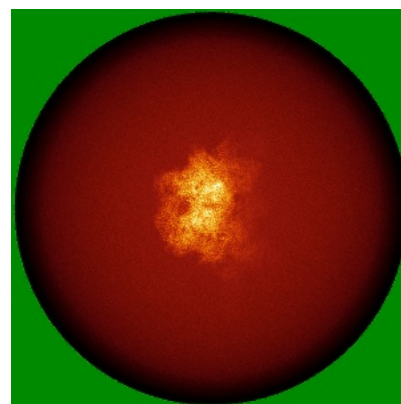
6.4.1 Primary map



X

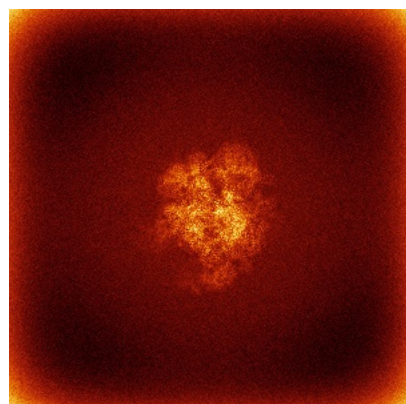


Y

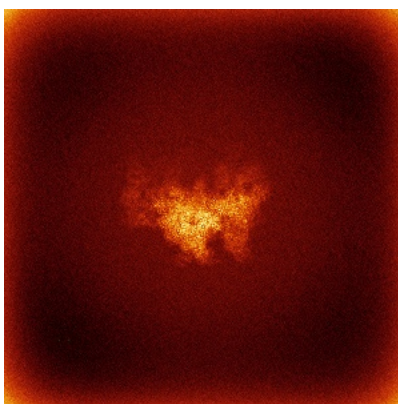


Z

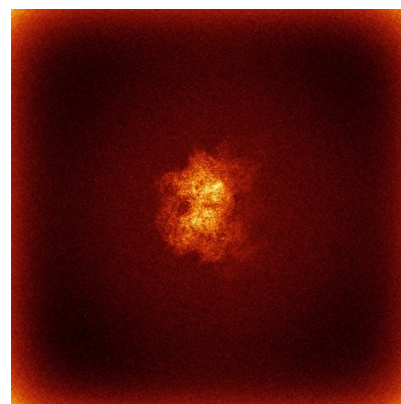
6.4.2 Raw map



X



Y

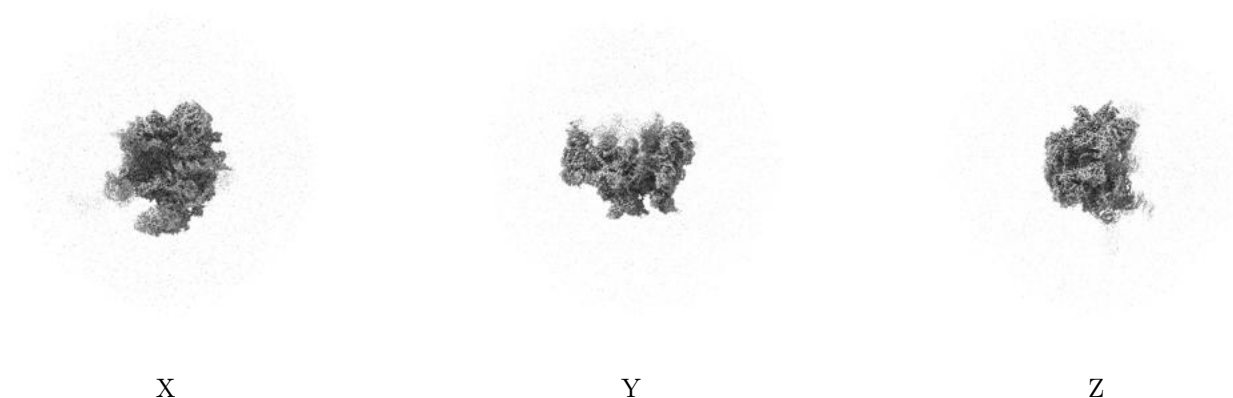


Z

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

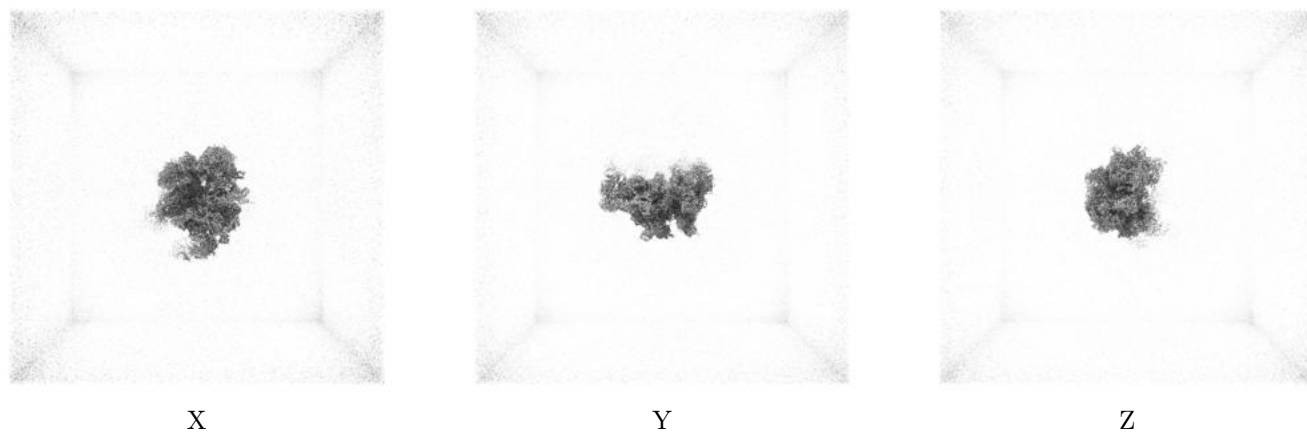
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. 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.

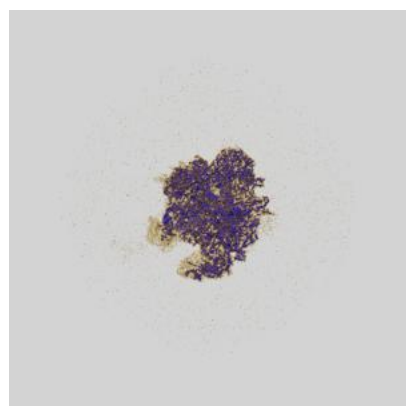
6.6 Mask visualisation [i](#)

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

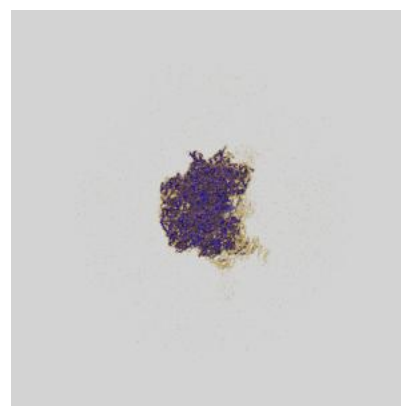
6.6.1 emd_18461_msk_1.map [i](#)



X



Y

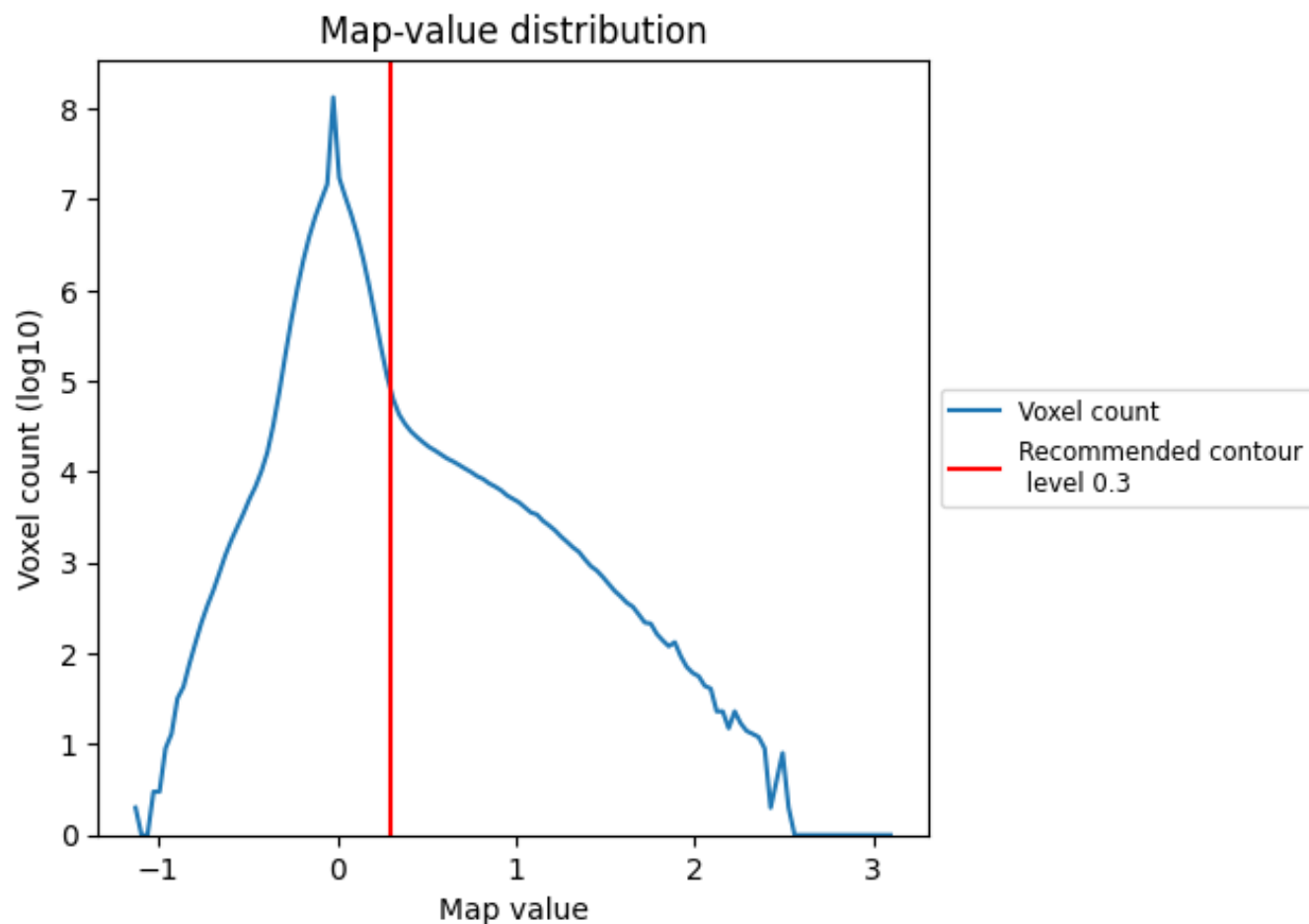


Z

7 Map analysis [i](#)

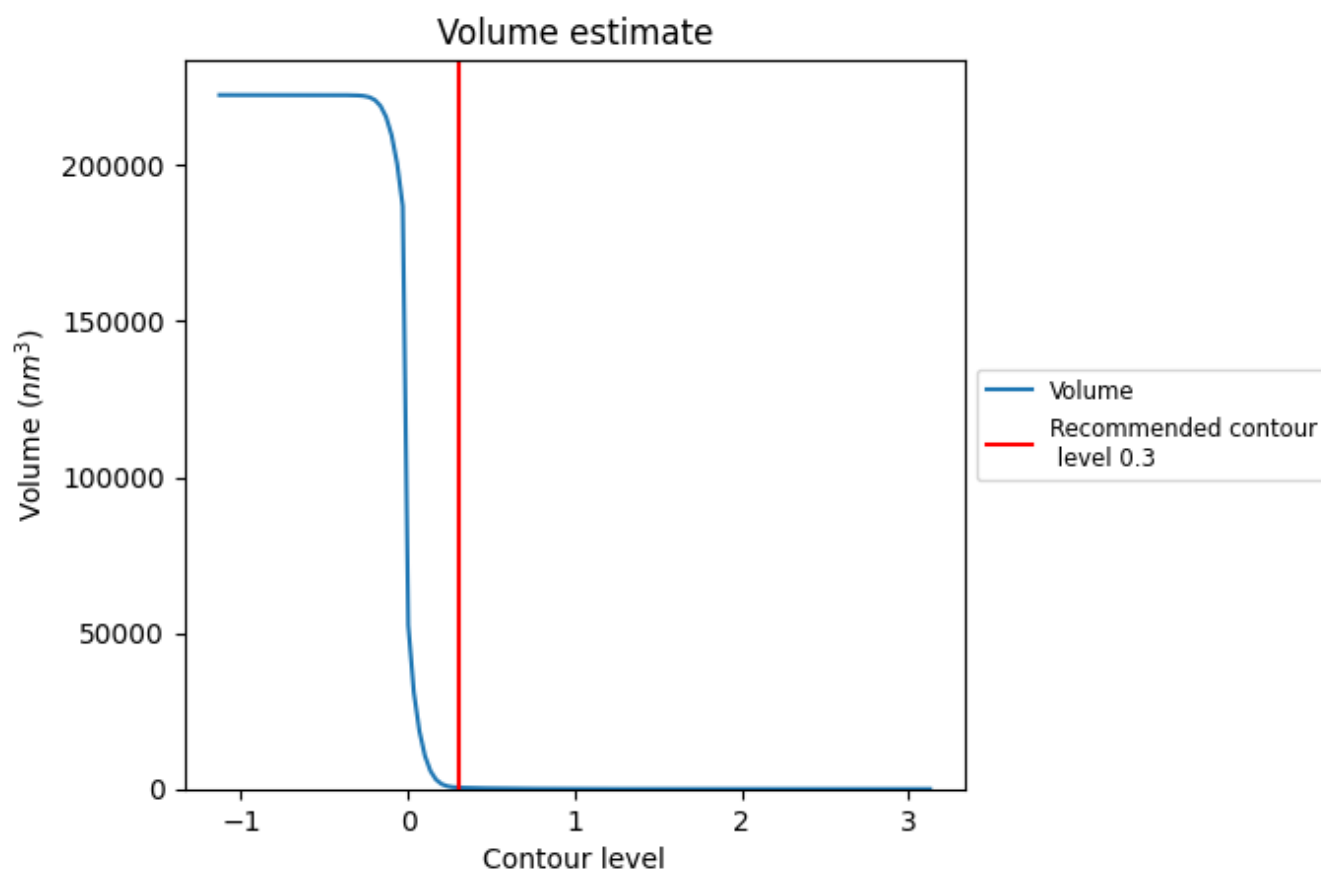
This section contains the results of statistical analysis of the map.

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.

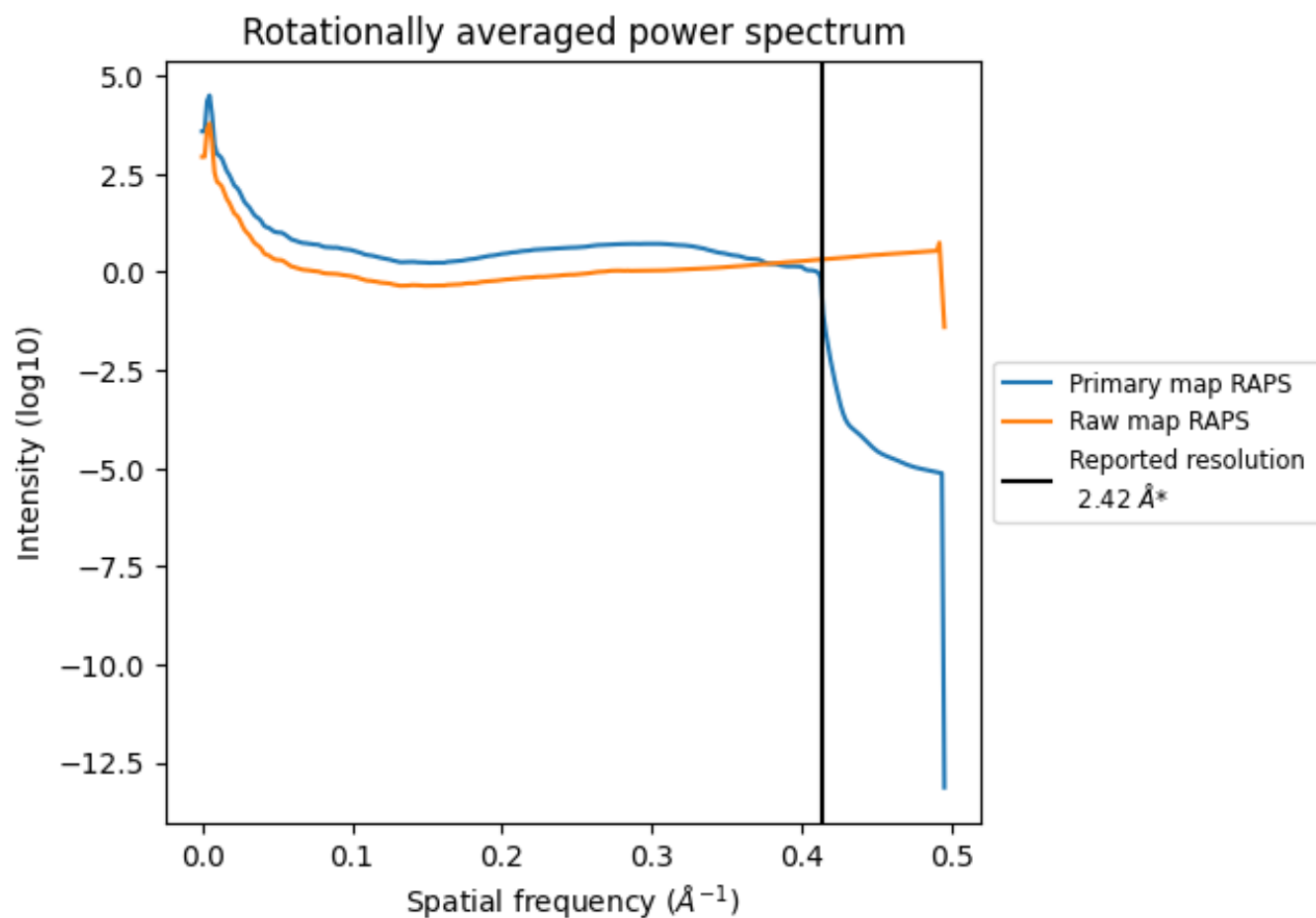
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 458 nm^3 ; this corresponds to an approximate mass of 414 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 ⓘ

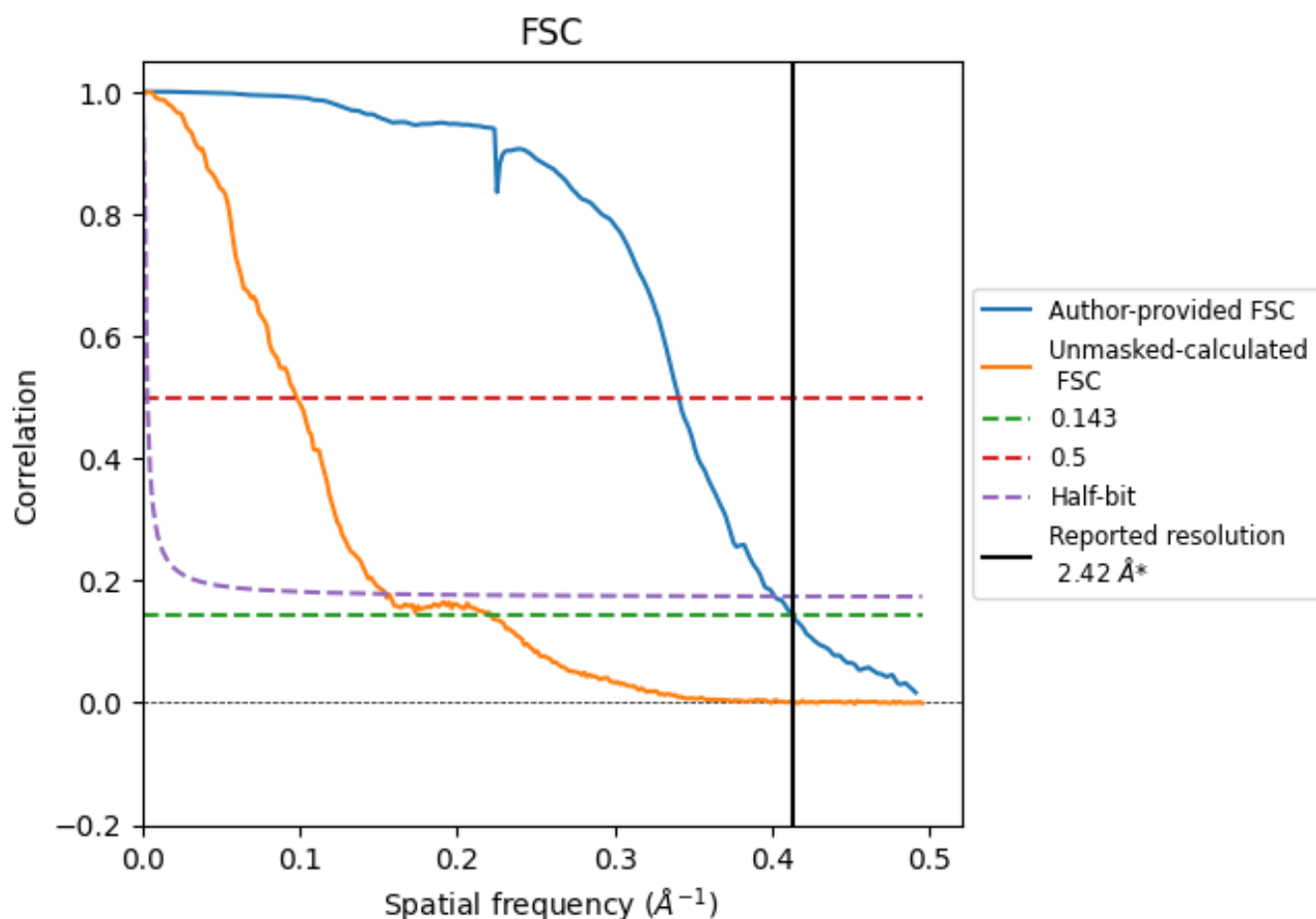


*Reported resolution corresponds to spatial frequency of 0.413 \AA^{-1}

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 0.413 Å⁻¹

8.2 Resolution estimates [i](#)

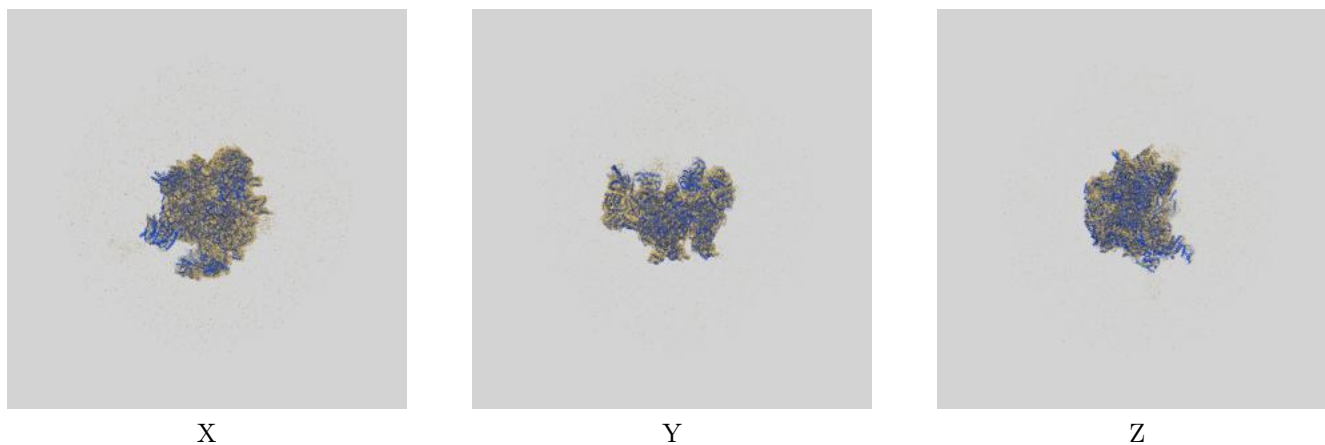
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.42	-	-
Author-provided FSC curve	2.42	2.94	2.49
Unmasked-calculated*	4.51	10.21	6.49

*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 4.51 differs from the reported value 2.42 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18461 and PDB model 8QU5. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



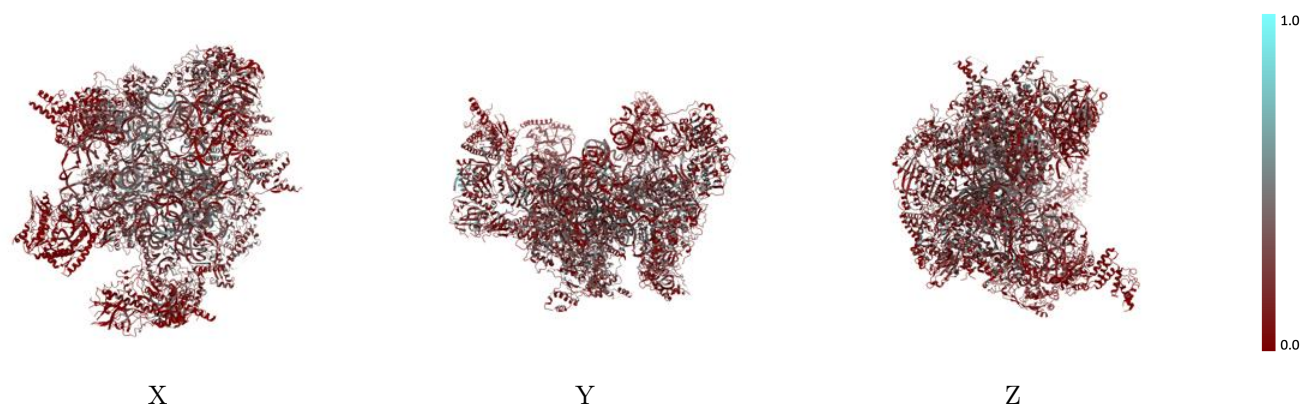
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



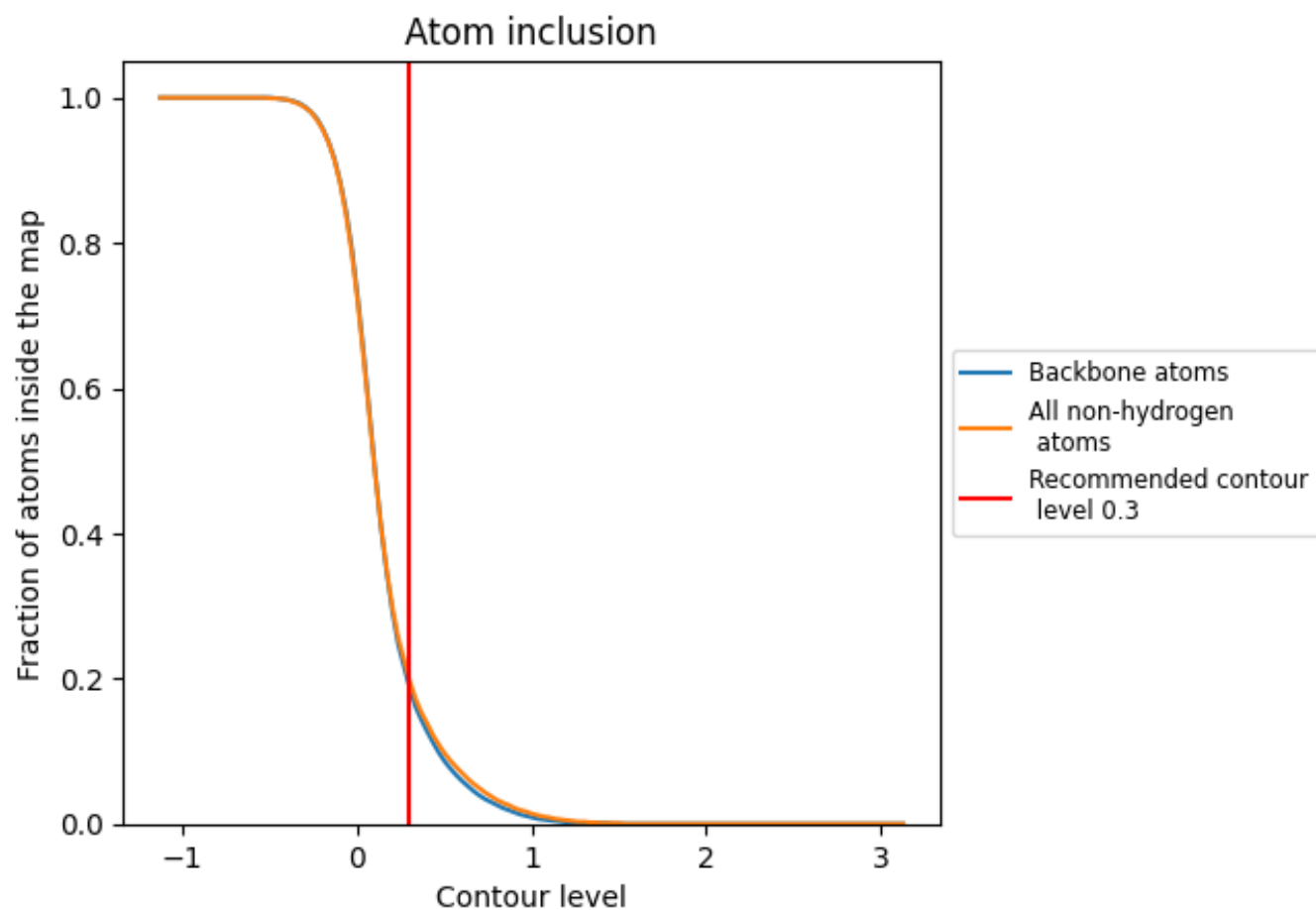
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 19% of all backbone atoms, 20% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.1970	 0.0060
0	 0.1960	 -0.0140
1	 0.2020	 -0.0110
2	 0.2820	 0.0440
3	 0.2320	 0.0000
5	 0.1690	 0.0150
6	 0.2110	 0.0060
7	 0.1930	 0.0130
8	 0.0730	 0.0040
9	 0.1970	 0.0150
A	 0.2580	 0.0320
B	 0.2290	 0.0200
D	 0.0220	 0.0070
E	 0.1980	 -0.0250
F	 0.2600	 -0.0090
H	 0.1460	 -0.0190
I	 0.0560	 0.0040
J	 0.0070	 0.0030
K	 0.2150	 -0.0060
L	 0.1020	 -0.0640
M	 0.2250	 -0.0310
N	 0.1640	 -0.0080
O	 0.2070	 -0.0520
P	 0.1900	 -0.0150
Q	 0.1660	 -0.0370
R	 0.2270	 -0.0420
S	 0.2050	 -0.0190
T	 0.2510	 -0.0010
U	 0.2230	 0.0390
V	 0.1770	 0.0240
W	 0.2290	 -0.0200
X	 0.1950	 -0.0000
Y	 0.2480	 0.0210
Z	 0.2190	 0.0210
a	 0.1970	 0.0260



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Chain	Atom inclusion	Q-score
b	 0.2510	 -0.0080
c	 0.2040	 0.0070
d	 0.1610	 0.0150
e	 0.0390	 0.0270
f	 0.0920	 0.0030
g	 0.2280	 0.0070
h	 0.1590	 -0.0190
i	 0.2210	 -0.0350
j	 0.2090	 -0.0090
k	 0.0700	 0.0420
l	 0.0580	 0.0410
m	 0.0110	 0.0130
o	 0.2200	 0.0320
p	 0.1640	 -0.0030
q	 0.1510	 -0.0160
r	 0.1930	 -0.0190
s	 0.2120	 -0.0100
t	 0.0000	 0.0050
u	 0.0810	 -0.0080
v	 0.0400	 -0.0020
w	 0.0170	 0.0150