



## wwPDB EM Validation Summary Report ⓘ

Nov 7, 2022 – 01:31 AM EST

PDB ID : 6NU3  
EMDB ID : EMD-0515  
Title : Structural insights into unique features of the human mitochondrial ribosome recycling  
Authors : Sharma, M.R.; Koripella, R.K.; Agrawal, R.K.  
Deposited on : 2019-01-30  
Resolution : 4.40 Å (reported)  
Based on initial model : 3J9M

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

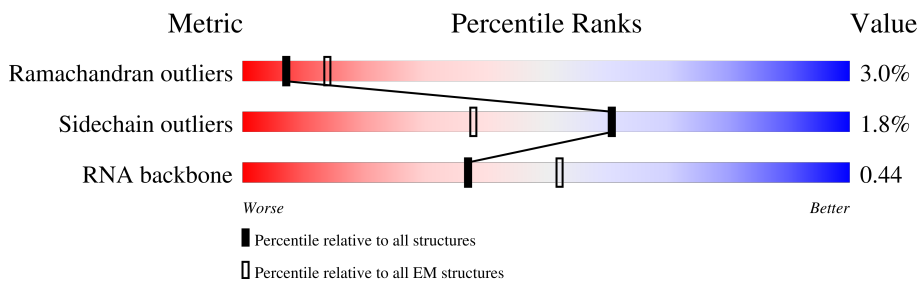
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.40 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.




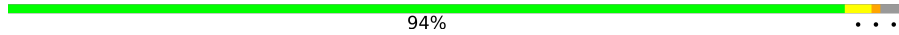



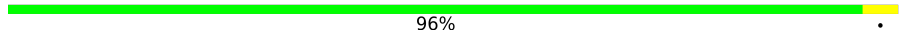
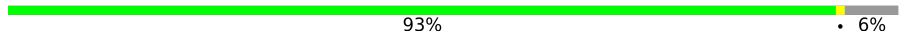





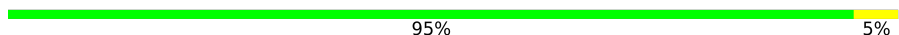












Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	1472	
2	B	56	
3	D	305	
4	E	348	
5	F	311	
6	H	267	
7	I	261	
8	J	192	
9	K	178	









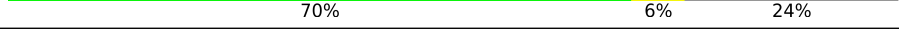

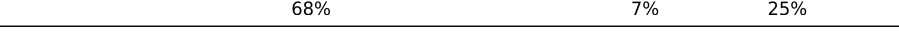
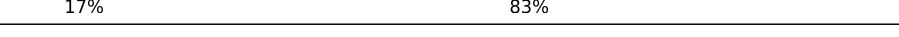

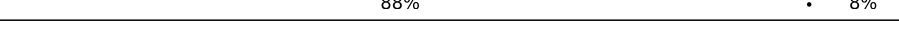


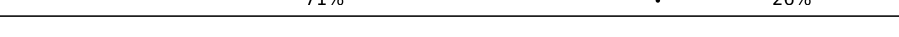

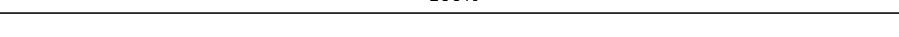






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Mol	Chain	Length	Quality of chain
10	L	145	 77% 21%
11	M	296	 94%
12	N	251	 78% 18%
13	O	175	 85% 13%
14	P	180	 70% 26%
15	Q	219	 96%
16	R	149	 93% 6%
17	S	205	 73% 24%
18	T	206	 78% 19%
19	U	153	 69% 27%
20	V	216	 83% 5% 12%
21	W	148	 73% 25%
22	X	243	 95% 5%
23	Y	250	 69% 30%
24	Z	161	 71% 25%
25	0	188	 55% 43%
26	1	65	 72% 8% 20%
27	2	92	 49% 50%
28	3	188	 49% 49%
29	4	103	 35% 65%
30	5	394	 90% 5% 5%
31	6	380	 81% 5% 14%
32	7	338	 77% 21%
33	8	206	 48% 52%
34	9	137	 76% 20%

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Mol	Chain	Length	Quality of chain
35	a	142	 56% 42%
36	b	215	 67% 31%
37	c	332	 80% 17%
38	d	306	 51% 47%
39	e	279	 76% 22%
40	f	212	 60% 38%
41	g	166	 73% 22%
42	h	158	 59% 37%
43	i	128	 70% 6% 24%
44	j	123	 67% 31%
45	k	112	 68% 7% 25%
46	l	138	 17% 83%
47	m	128	 34% 65%
48	o	102	 88% 8%
49	p	206	 60% 38%
50	q	222	 57% 42%
51	r	196	 71% 26%
52	s	439	 82% 16%
53	t	28	 100%
54	u	2	 100%
55	AA	923	 58% 42%
56	AB	296	 71% 27%
57	AC	167	 75% 21%
58	AD	430	 70% 5% 25%
59	AE	125	 90% 6% ..


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Mol	Chain	Length	Quality of chain
60	AF	242	80% 17%
61	AG	396	72% 23%
62	AH	201	58% 39%
63	AI	194	68% 30%
64	AJ	138	75% 22%
65	AK	128	73% 5% 21%
66	AL	257	60% 36%
67	AM	137	80% 15%
68	AN	130	78% 5% 18%
69	AO	185	92% 8%
70	AP	142	65% 32%
71	AQ	86	94% 6%
72	AR	360	62% 6% 33%
73	AS	190	59% 7% 34%
74	AT	173	87% 6% 6%
75	AU	205	80% 16%
76	AV	414	76% 21%
77	AW	187	48% 48%
78	AX	398	76% 21%
79	AY	395	26% 73%
80	AZ	106	79% 18%
81	A0	225	80% 9% 11%
82	A1	323	74% 6% 21%
83	A2	118	92% 7%
84	A3	199	34% 65%

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Mol	Chain	Length	Quality of chain
85	A4	474	 86% 13%

## 2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 291640 atoms, of which 133281 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	A	1472	47126	14025	15865	5642	10122	1472	0	0

- Molecule 2 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	B	56	1794	534	603	214	387	56	0	0

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	D	236	3738	1145	1896	373	315	9	0	0

- Molecule 4 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	E	300	4743	1523	2378	410	422	10	0	0

- Molecule 5 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	F	250	4058	1294	2045	365	348	6	0	0

- Molecule 6 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
6	H	95	1616	498	832	152	134	0	0

- Molecule 7 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	I	158	2652	828	1369	235	210	10	0	0

- Molecule 8 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	J	140	2202	680	1141	192	187	2	0	0

- Molecule 9 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	K	177	2899	934	1448	259	251	7	0	0

- Molecule 10 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	L	115	1830	559	941	171	154	5	0	0

- Molecule 11 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
11	M	287	4683	1472	2378	425	402	6	0	0

- Molecule 12 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
12	N	205	3335	1056	1681	308	280	10	0	0

- Molecule 13 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
13	O	152	2528	784	1283	239	215	7	0	0

- Molecule 14 is a protein called 39S ribosomal protein L18, mitochondrial.



Mol	Chain	Residues	Atoms					AltConf	Trace	
14	P	133	Total	C	H	N	O	S	0	0
			2161	677	1081	209	189	5		

- Molecule 15 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
15	Q	219	Total	C	H	N	O	S	0	0
			3681	1168	1859	322	323	9		

- Molecule 16 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
16	R	140	Total	C	H	N	O	S	0	0
			2367	732	1214	231	186	4		

- Molecule 17 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
17	S	156	Total	C	H	N	O	S	0	0
			2573	806	1322	222	219	4		

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
18	T	166	Total	C	H	N	O	S	0	0
			2778	875	1410	254	232	7		

- Molecule 19 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
19	U	111	Total	C	H	N	O	S	0	0
			1857	591	935	176	153	2		

- Molecule 20 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
20	V	189	Total	C	H	N	O	S	0	0
			3109	987	1558	278	278	8		

- Molecule 21 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	W	111	1769	558	898	164	146	3	0	0

- Molecule 22 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
22	X	243	4062	1317	2027	351	362	5	0	0

- Molecule 23 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
23	Y	176	3078	970	1561	291	252	4	0	0

- Molecule 24 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	Z	120	2008	626	1030	183	166	3	0	0

- Molecule 25 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	0	108	1784	545	904	172	157	6	0	0

- Molecule 26 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	1	52	908	278	475	83	70	2	0	0

- Molecule 27 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	2	46	782	233	406	83	59	1	0	0

- Molecule 28 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	3	95	1714	539	883	162	127	3	0	0

- Molecule 29 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	4	36	667	203	345	70	46	3	0	0

- Molecule 30 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	5	376	6123	1987	3059	529	538	10	0	0

- Molecule 31 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	6	325	5086	1692	2450	465	470	9	0	0

- Molecule 32 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	7	266	4331	1383	2173	371	388	16	0	0

- Molecule 33 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
33	8	99	1680	535	844	144	155	2	0	0

- Molecule 34 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
34	9	109	1751	565	878	152	154	2	0	0

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
35	a	82	1344	434	658	124	123	5	0	0

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
36	b	148	2358	733	1180	229	213	3	0	0

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
37	c	275	4437	1415	2220	383	410	9	0	0

- Molecule 38 is a protein called cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
38	d	162	2690	870	1343	234	235	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
39	e	217	3529	1124	1767	310	323	5	0	0

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
40	f	131	2083	663	1044	169	203	4	0	0

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	g	129	2123	690	1056	185	190	2	0	0

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
42	h	100	1633	524	806	146	155	2	0	0

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
43	i	97	1684	532	857	165	126	4	0	0

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
44	j	85	1357	423	673	133	126	2	0	0

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
45	k	84	1311	407	656	122	121	5	0	0

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	H	N			O
46	l	23	448	137	227	52	32	0	0

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
47	m	45	759	232	387	76	62	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
48	o	94	1601	501	804	165	128	3	0	0

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
49	p	127	2141	661	1083	201	192	4	0	0

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
50	q	128	2125	671	1049	208	192	5	0	0

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
51	r	146	2424	764	1221	232	199	8	0	0

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
52	s	370	6058	1946	3022	542	534	14	0	0

- Molecule 53 is a protein called Unknown protein/protein extension.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
53	t	28	170	84	30	28	28	0	0

- Molecule 54 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
54	u	2	65	19	23	8	13	2	0	0

- Molecule 55 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
55	AA	923	29558	8790	9952	3535	6358	923	0	0

- Molecule 56 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
56	AB	217	3534	1131	1766	321	306	10	0	0

- Molecule 57 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
57	AC	132	2170	699	1088	195	184	4	0	0

- Molecule 58 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
58	AD	322	5153	1611	2596	476	457	13	0	0

- Molecule 59 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
59	AE	122	1973	614	1001	177	177	4	0	0

- Molecule 60 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
60	AF	201	3384	1069	1716	305	283	11	0	0

- Molecule 61 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
61	AG	305	5019	1599	2503	448	455	14	0	0

- Molecule 62 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
62	AH	122	2023	643	1024	168	185	3	0	0

- Molecule 63 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
63	AI	136	2063	637	1052	192	178	4	0	0

- Molecule 64 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
64	AJ	108	1725	521	887	169	142	6	0	0

- Molecule 65 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
65	AK	101	1746	537	885	179	140	5	0	0

- Molecule 66 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
66	AL	164	2854	883	1472	257	235	7	0	0

- Molecule 67 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
67	AM	116	1871	582	951	182	150	6	0	0

- Molecule 68 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
68	AN	107	1754	549	908	153	141	3	0	0

- Molecule 69 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
69	AO	185	3016	970	1488	285	267	6	0	0

- Molecule 70 is a protein called 28S ribosomal protein S18c, mitochondrial.



Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
70	AP	96	1578	498	804	133	135	8	0	0

- Molecule 71 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
71	AQ	86	1476	455	741	147	124	9	0	0

- Molecule 72 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
72	AR	242	4039	1285	2031	343	372	8	0	0

- Molecule 73 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
73	AS	126	2079	673	1037	183	185	1	0	0

- Molecule 74 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
74	AT	162	2674	850	1344	231	238	11	0	0

- Molecule 75 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
75	AU	173	2932	900	1471	294	263	4	0	0

- Molecule 76 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
76	AV	328	5392	1737	2690	452	502	11	0	0

- Molecule 77 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
77	AW	97	1551	486	785	137	139	4	0	0

- Molecule 78 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
78	AX	316	5051	1625	2520	440	455	11	0	0

- Molecule 79 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
79	AY	108	1773	593	859	150	169	2	0	0

- Molecule 80 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
80	AZ	87	1487	473	747	133	130	4	0	0

- Molecule 81 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
81	A0	201	3369	1065	1685	322	292	5	0	0

- Molecule 82 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
82	A1	256	4173	1321	2097	350	395	10	0	0

- Molecule 83 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
83	A2	116	1887	574	962	181	162	8	0	0

- Molecule 84 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
84	A3	69	1292	393	682	130	86	1	0	0

- Molecule 85 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial,mS39.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
85	A4	414	5097	1805	2259	490	529	14	0	0

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A	97	Total	Mg	0
			97	97	
86	M	1	Total	Mg	0
			1	1	
86	g	1	Total	Mg	0
			1	1	
86	AA	28	Total	Mg	0
			28	28	

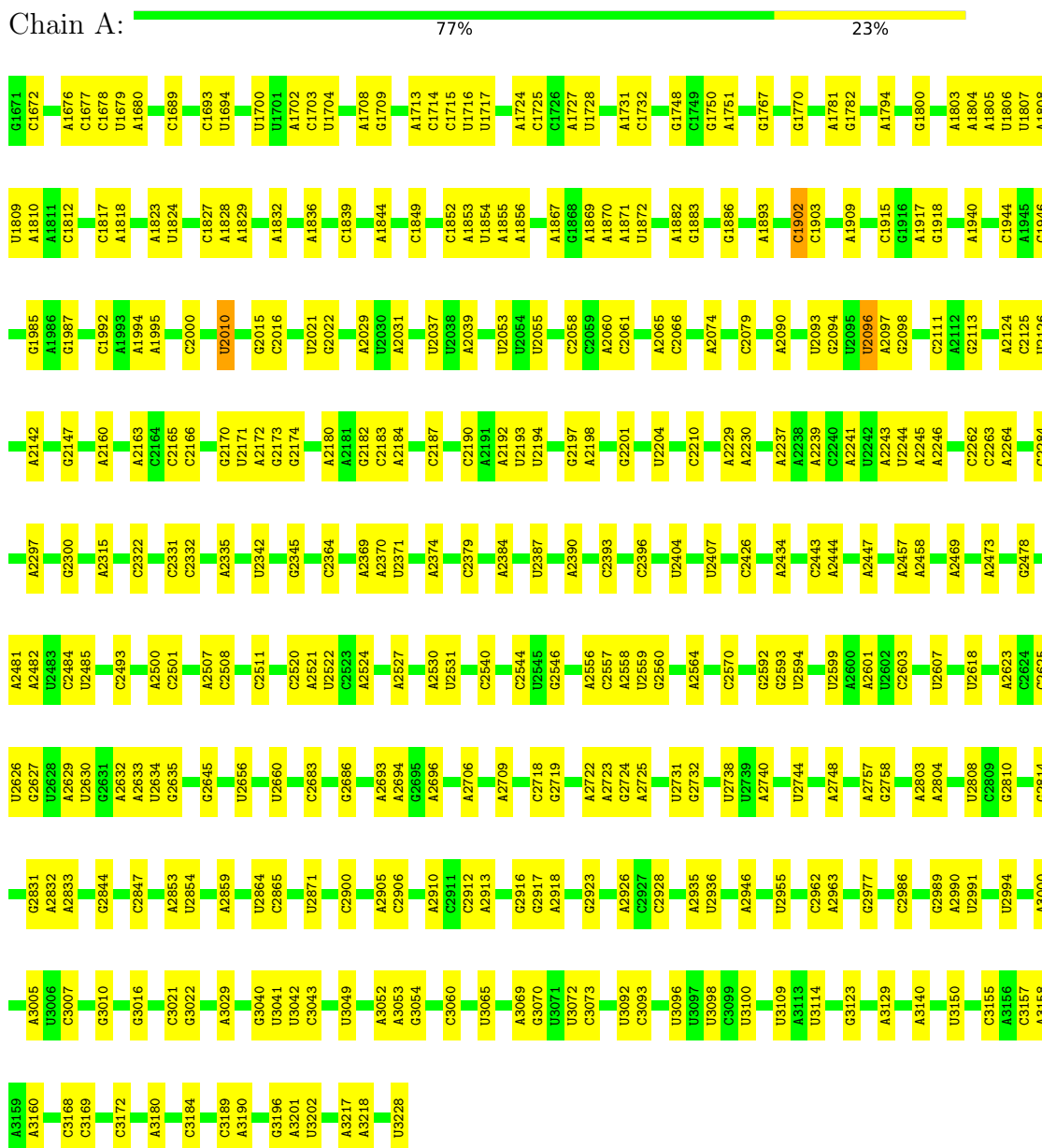
- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	0	1	Total	Zn	0
			1	1	
87	4	1	Total	Zn	0
			1	1	
87	r	1	Total	Zn	0
			1	1	
87	AB	1	Total	Zn	0
			1	1	
87	AO	1	Total	Zn	0
			1	1	
87	AP	1	Total	Zn	0
			1	1	
87	AT	1	Total	Zn	0
			1	1	

### 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. 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. 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: 16S rRNA

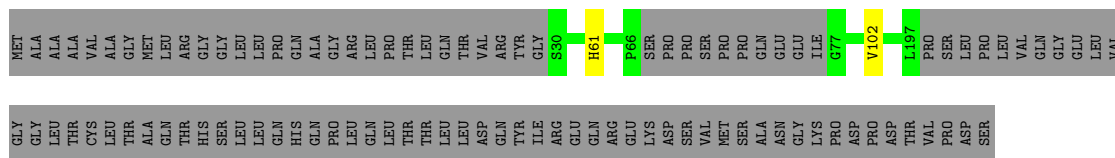


- Molecule 2: mt-tRNAVal



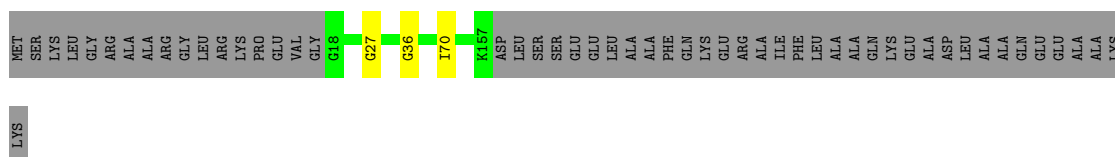
- Molecule 7: 39S ribosomal protein L10, mitochondrial

Chain I:  60% 39%



- Molecule 8: 39S ribosomal protein L11, mitochondrial

Chain J:  71% 27%




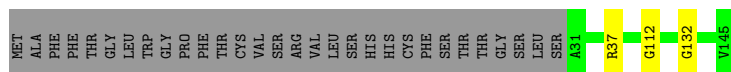
- Molecule 9: 39S ribosomal protein L13, mitochondrial

Chain K:  96%



- Molecule 10: 39S ribosomal protein L14, mitochondrial

Chain L:  77% 21%




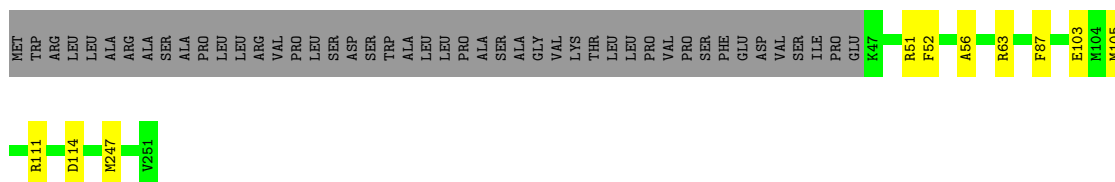
- Molecule 11: 39S ribosomal protein L15, mitochondrial

Chain M:  94%




- Molecule 12: 39S ribosomal protein L16, mitochondrial

Chain N:  78% 18%



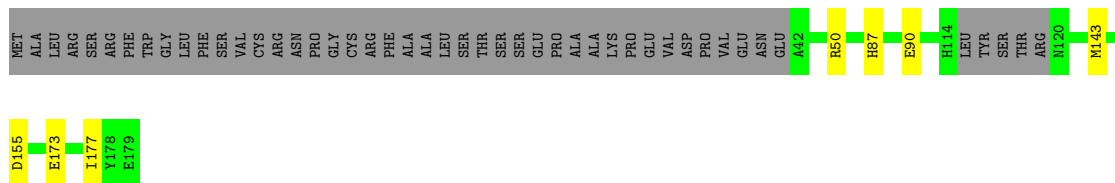
- Molecule 13: 39S ribosomal protein L17, mitochondrial

Chain O:  85% 13%



- Molecule 14: 39S ribosomal protein L18, mitochondrial

Chain P:  70% 26%



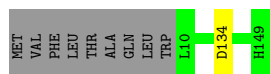
- Molecule 15: 39S ribosomal protein L19, mitochondrial

Chain Q:  96%



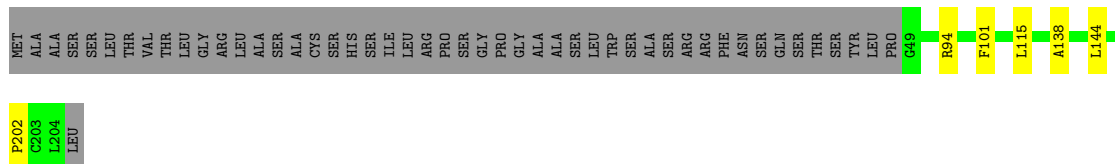
- Molecule 16: 39S ribosomal protein L20, mitochondrial

Chain R:  93% 6%




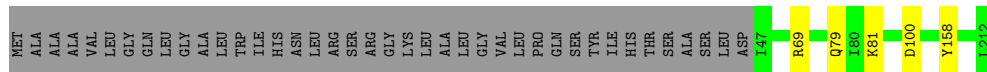
- Molecule 17: 39S ribosomal protein L21, mitochondrial

Chain S:  73% 24%



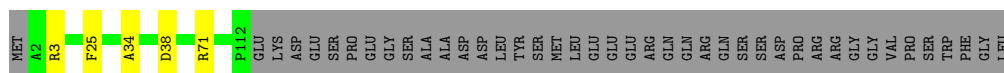
- Molecule 18: 39S ribosomal protein L22, mitochondrial

Chain T:  78% 19%




- Molecule 19: 39S ribosomal protein L23, mitochondrial

Chain U:  69% 27%



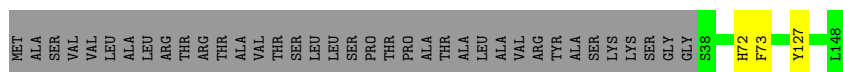
- Molecule 20: 39S ribosomal protein L24, mitochondrial

Chain V:  83% 5% 12%



- Molecule 21: 39S ribosomal protein L27, mitochondrial

Chain W:  73% 25%



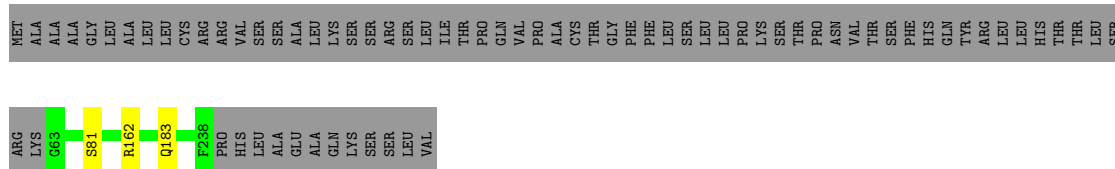
- Molecule 22: 39S ribosomal protein L28, mitochondrial

Chain X:  95% 5%



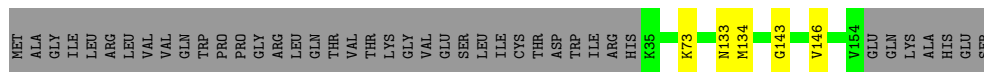
- Molecule 23: 39S ribosomal protein L47, mitochondrial

Chain Y:  69% 30%



- Molecule 24: 39S ribosomal protein L30, mitochondrial

Chain Z:  71% 25%

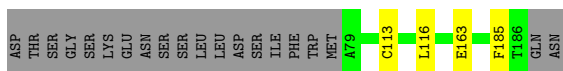


- Molecule 25: 39S ribosomal protein L32, mitochondrial

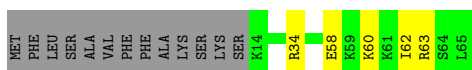
Chain 0:  55% 43%



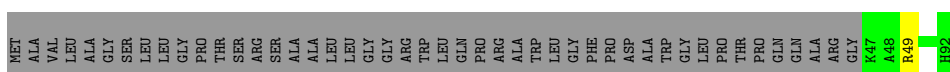




• Molecule 26: 39S ribosomal protein L33, mitochondrial



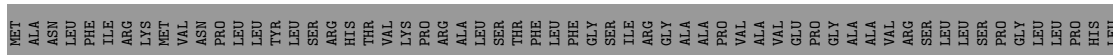
• Molecule 27: 39S ribosomal protein L34, mitochondrial



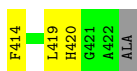
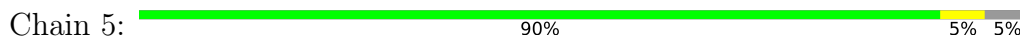
• Molecule 28: 39S ribosomal protein L35, mitochondrial



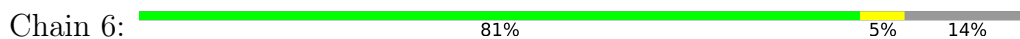
• Molecule 29: 39S ribosomal protein L36, mitochondrial

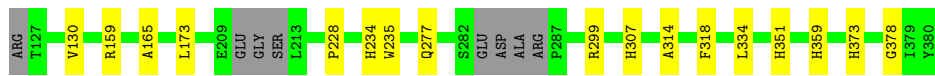


• Molecule 30: 39S ribosomal protein L37, mitochondrial

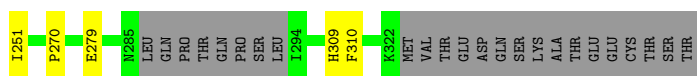
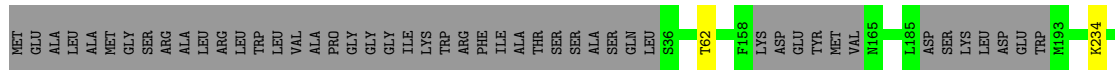
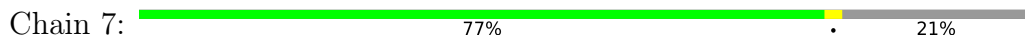


• Molecule 31: 39S ribosomal protein L38, mitochondrial

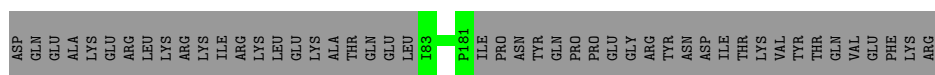
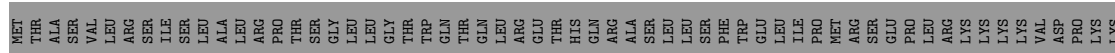




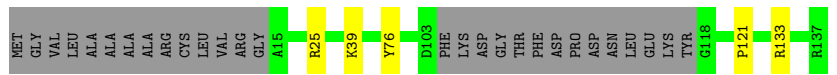
• Molecule 32: 39S ribosomal protein L39, mitochondrial



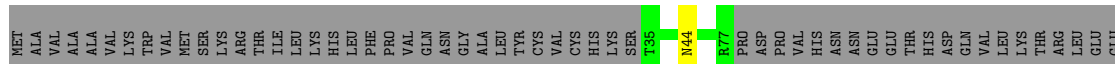
• Molecule 33: 39S ribosomal protein L40, mitochondrial



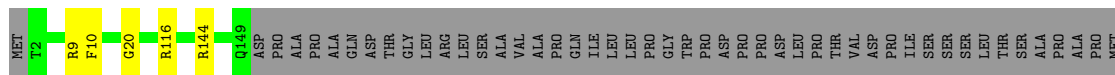
• Molecule 34: 39S ribosomal protein L41, mitochondrial



• Molecule 35: 39S ribosomal protein L42, mitochondrial



• Molecule 36: 39S ribosomal protein L43, mitochondrial



LEU  
SER  
ALA  
VAL  
SER  
CYS  
LEU  
PRO  
ILE  
VAL  
PRO  
ALA  
LEU  
THR  
THR  
CYS  
SER  
SER  
ALA

- Molecule 37: 39S ribosomal protein L44, mitochondrial

Chain c: 80% 17%

MET  
ALA  
SER  
GLY  
LEU  
VAL  
PRO  
ARG  
LEU  
LEU  
GLN  
VAL  
PRO  
GLN  
CYS  
GLY  
THR  
ALA  
HIS  
ARG  
CYS  
LEU  
LEU  
LEU  
LEU  
PRO  
ALA  
VAL  
VAL  
PRO  
PRO  
VAL  
VAL  
ARG  
GLY  
V81  
P64  
M65  
Q107  
LEU  
GLY  
ILE  
GLU  
GLU  
LYS  
GLU  
GLU  
ALA  
VAL  
LEU  
LEU  
ASN  
LI19  
Q123  
D147  
G162  
E183  
R210  
R311

W314  
N315  
Y316  
SER  
PRO  
LYS  
THR  
ARG  
ALA  
GLU  
SER  
SER  
ILE  
THR  
ALA  
SER

- Molecule 38: cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial

Chain d: 51% 47%

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

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

E187  
C199  
SER  
SER  
MET  
MET  
ASN  
GLN  
GLY  
N207  
V208  
Y233  
L252  
THR  
ASN  
P255  
W269  
P272  
L287  
LYS  
PRO  
GLU  
GLU  
GLY  
TYR  
GLU  
ALA  
ALA  
GLY  
GLY  
ALA  
GLN  
LYS  
PRO  
LEU  
LEU  
ALA

- Molecule 39: 39S ribosomal protein L46, mitochondrial

Chain e: 76% 22%

MET  
ALA  
ALA  
PRO  
VAL  
ARG  
ARG  
THR  
LEU  
LEU  
GLY  
LEU  
VAL  
VAL  
ALA  
GLY  
GLY  
TRP  
ARG  
ARG  
PHE  
GLU  
ARG  
TRP  
LEU  
LEU  
GLY  
SER  
LEU  
SER  
SER  
SER  
SER  
LEU  
ALA  
LEU  
ALA  
ALA  
ALA  
PRO  
SER  
SER  
ASN  
ASN  
GLY  
S43  
R55  
Y84  
D104  
LEU  
HIS  
ASP  
GLU  
GLU  
GLY  
ASP  
GLY  
GLN  
ASP  
ILE  
LEU

L116  
A117  
D145  
P174  
F217  
PRO  
GLN  
ALA  
ALA  
MET  
ARG  
ARG  
THR  
GLU  
SER  
ASN  
L227  
D242  
L279

- Molecule 40: 39S ribosomal protein L48, mitochondrial

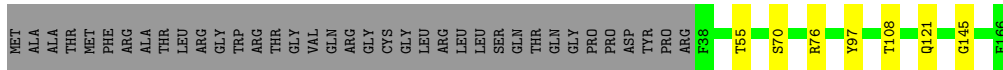
Chain f: 60% 38%

MET  
SER  
GLY  
THR  
LEU  
LEU  
LYS  
VAL  
LEU  
LEU  
CYS  
LEU  
LEU  
ARG  
ASN  
ASN  
THR  
ILE  
PHE  
LYS  
GLN  
ALA  
PHE  
SER  
SER  
LEU  
LEU  
LEU  
ARG  
PHE  
ARG  
THR  
SER  
SER  
GLY  
GLY  
LYS  
PRO  
ALA  
ILE  
TYR  
SER  
VAL  
GLY  
GLY  
ILE  
LEU  
LEU  
SER  
SER  
SER  
ARG  
PRO  
Y48  
E66  
GLU  
PRO  
ASP  
LYS  
LYS  
LYS  
LYS  
GLY  
LYS  
VAL  
LEU

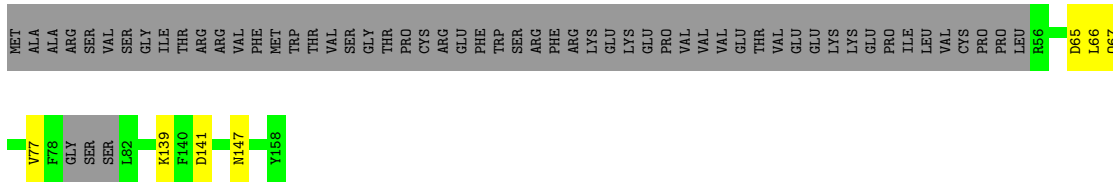
V77  
V90  
Q138  
ASP  
GLN  
GLY  
SER  
M144  
E154  
T190  
D193  
PHE  
LYS  
GLY  
ARG  
PHE  
SER  
LYS  
LYS  
ALA  
ALA  
PRO  
PRO  
GLU  
LEU  
LEU  
LEU  
LEU  
LEU  
LEU  
LEU  
LYS

- Molecule 41: 39S ribosomal protein L49, mitochondrial

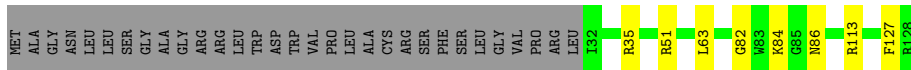
Chain g: 73% 22%



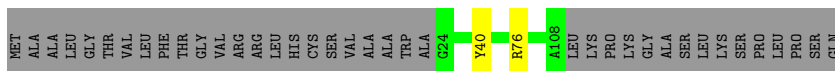
- Molecule 42: 39S ribosomal protein L50, mitochondrial



- Molecule 43: 39S ribosomal protein L51, mitochondrial



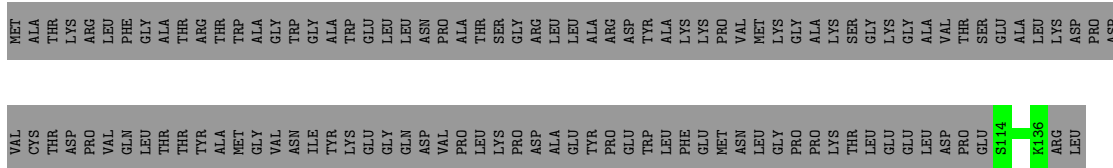
- Molecule 44: 39S ribosomal protein L52, mitochondrial



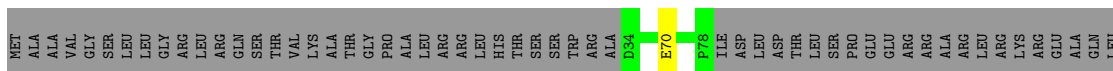
- Molecule 45: 39S ribosomal protein L53, mitochondrial



- Molecule 46: 39S ribosomal protein L54, mitochondrial




- Molecule 47: 39S ribosomal protein L55, mitochondrial



GLN  
SER  
ARG  
LYS  
GLU  
TYR  
GLU  
GLN  
LEU  
SER  
SER  
ASP  
ASP  
LEU  
HIS  
VAL  
GLU  
ARG  
TYR  
ARG  
GLN  
PHE  
TRP  
THR  
THR  
ARG  
THR  
LYS  
LYS

- Molecule 48: Ribosomal protein 63, mitochondrial

Chain o:  88% 8%

MET  
PHE  
LEU  
THR  
LEU  
ALA  
LEU  
TRP  
R9  
P13  
G61  
K81  
W101  
S102

- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:  60% 38%

MET  
ALA  
THR  
VAL  
CYS  
LEU  
ARG  
TRP  
GLY  
SER  
SER  
ARG  
ALA  
GLY  
VAL  
TRP  
LEU  
LEU  
PRO  
PRO  
ALA  
ALA  
ARG  
CYS  
PRO  
ARG  
VAL  
ALA  
LYS  
THR  
SER  
HIS  
LYS  
GLN  
ASP  
GLY  
THR  
E38  
D86  
V61  
PRO  
ASN  
GLY  
ALA  
LYS  
GLN  
ALA  
ASP  
SER  
D70  
S83  
SER  
GLY  
PRO  
GLY  
GLN

ASN  
VAL  
ASN  
LYS  
V95  
R129  
L135  
Q163  
THR  
PRO  
LYS  
GLU  
ALA  
PRO  
THR  
LYS  
LEU  
ASP  
VAL  
K174  
I193  
HIS  
SER  
ALA  
VAL  
LYS  
THR  
SER  
ARG  
ARG  
VAL  
ASP  
MET  
ASP

- Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q:  57% 42%

MET  
ALA  
SER  
VAL  
ARG  
GLN  
ARG  
ALA  
SER  
SER  
LEU  
LEU  
GLY  
VAL  
ALA  
THR  
LYS  
LEU  
ALA  
PRO  
GLY  
SER  
SER  
ARG  
GLY  
ALA  
ALA  
GLY  
Y295  
F61  
R114  
R152  
ARG  
PRO  
ALA  
ALA  
LEU  
LEU  
GLN  
ALA  
GLY  
TYR  
GLY  
GLN  
VAL  
VAL  
PRO  
ASP  
ARG  
SER  
ALA  
ALA  
PHE  
GLN  
GLY  
LEU  
LEU  
GLN  
ASP

LEU  
GLU  
LYS  
GLU  
ARG  
LYS  
ARG  
LYS  
GLU  
GLY  
GLN  
ARG  
LYS  
LEU  
ALA  
ALA  
ALA  
ALA  
LEU  
ALA  
ALA  
ALA  
ALA  
ALA  
SER  
SER  
SER


- Molecule 51: 39S ribosomal protein S18a, mitochondrial

Chain r:  71% 26%

MET  
ALA  
LEU  
LYS  
LYS  
VAL  
LEU  
ALA  
CYS  
GLY  
ARG  
LEU  
LEU  
ARG  
GLY  
PRO  
ALA  
ALA  
ALA  
THR  
SER  
SER  
THR  
SER  
SER  
ARG  
ARG  
PRO  
ALA  
ALA  
GLY  
F35  
R36  
T41  
GLN  
GLU  
GLY  
LYS  
THR  
T47  
A55  
P61  
P64  
R134  
LEU  
PRO  
GLY  
VAL  
VAL  
PRO  
LYS

SER  
LYS  
PRO  
Q146  
S158  
V185  
C186  
Y187  
H196

- Molecule 52: 39S ribosomal protein S30, mitochondrial

Chain s:  82% 16%

MET  
ALA  
ALA  
ALA  
ARG  
CYS  
TRP  
ARG  
PRO  
SER  
LEU  
LEU  
GLY  
PRO  
ARG  
LEU  
SER  
HIS  
THR  
ALA  
ASN  
ALA  
ALA  
ALA  
ALA  
THR  
THR  
THR  
THR  
CYS  
ARG  
GLN  
ASP  
VAL  
ALA  
ALA  
PRO  
V41  
P119  
PRO  
PRO  
ALA  
GLU  
PRO  
GLU  
PRO  
GLU  
PRO  
GLU  
GLU  
ALA

LEU  
ASP  
LEU  
A140  
D148  
Q152  
F176  
R203  
F250  
D254  
I264  
P272  
N386  
D407  
K430  
GLU  
GLU  
LYS  
SER  
GLN  
LEU  
LEU  
GLU  
ASN

- Molecule 53: Unknown protein/protein extension

Chain t:  100%

There are no outlier residues recorded for this chain.

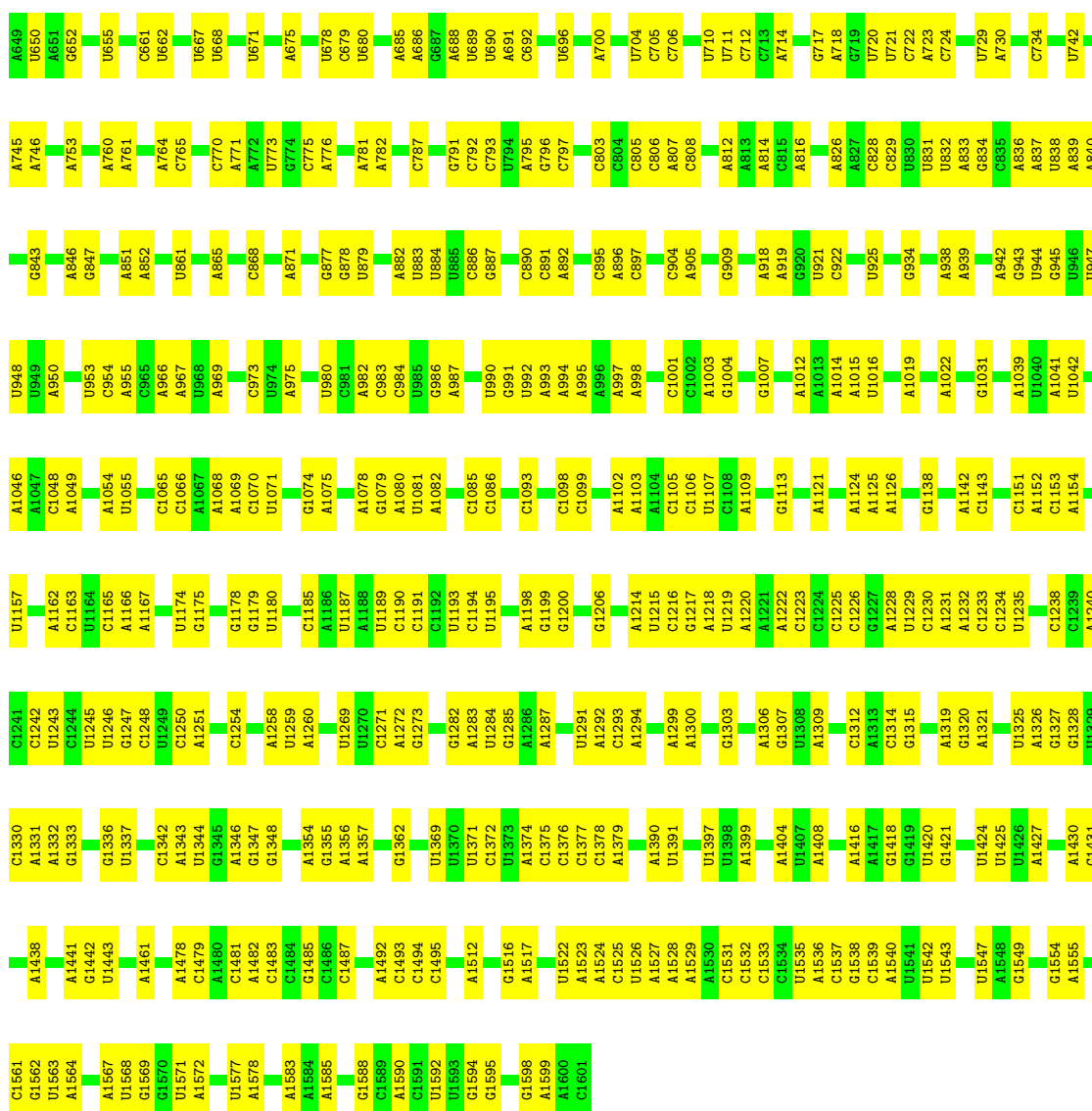
- Molecule 54: E-site tRNA

Chain u:  100%

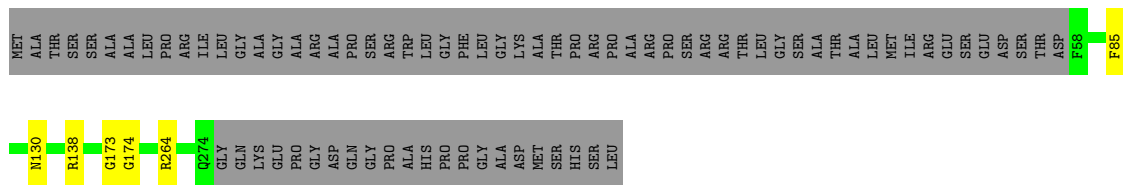
There are no outlier residues recorded for this chain.

- Molecule 55: 12S rRNA

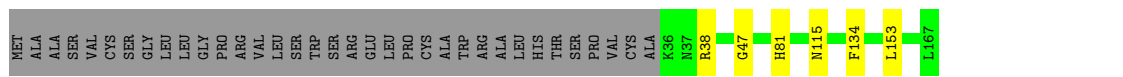
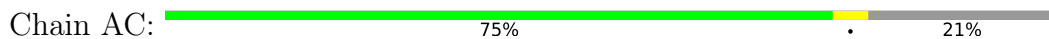
Chain AA:  58%



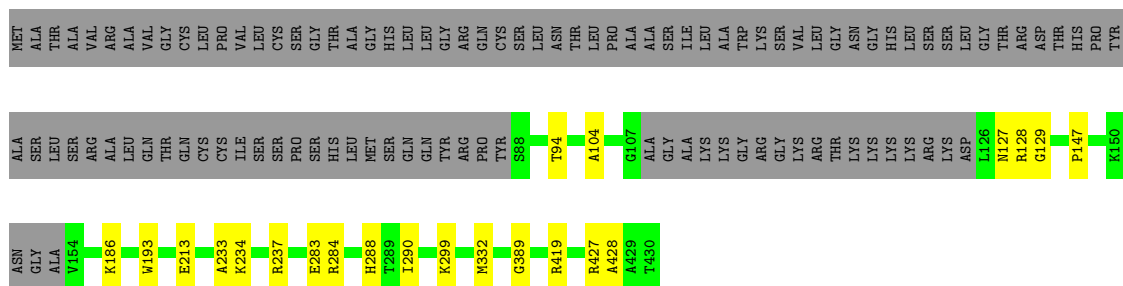
- Molecule 56: 28S ribosomal protein S2, mitochondrial



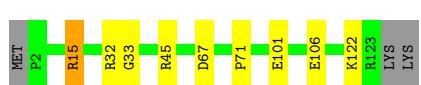
• Molecule 57: 28S ribosomal protein S24, mitochondrial



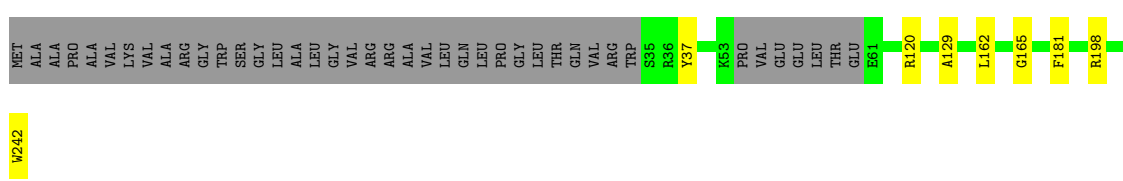
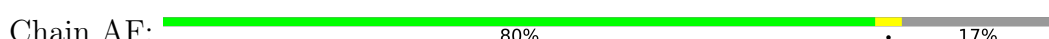
• Molecule 58: 28S ribosomal protein S5, mitochondrial



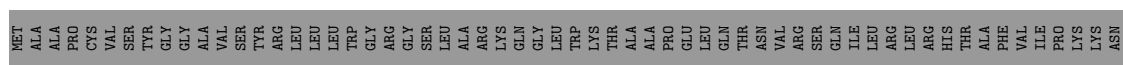
• Molecule 59: 28S ribosomal protein S6, mitochondrial

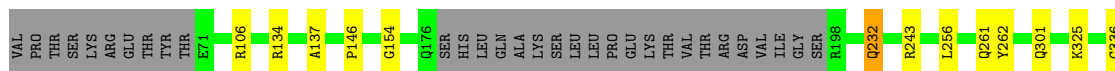


• Molecule 60: 28S ribosomal protein S7, mitochondrial

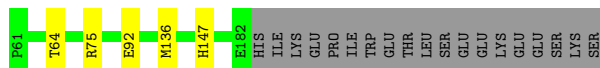


• Molecule 61: 28S ribosomal protein S9, mitochondrial

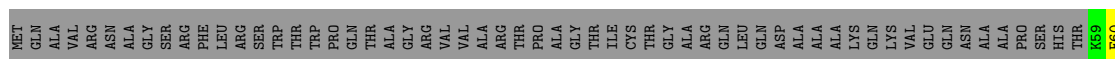




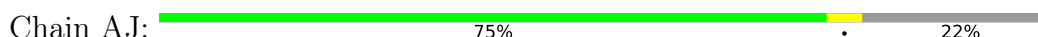
- Molecule 62: 28S ribosomal protein S10, mitochondrial



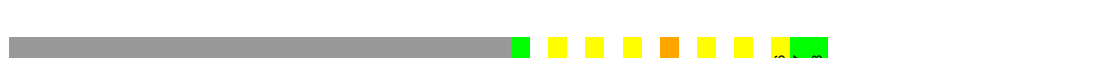
- Molecule 63: 28S ribosomal protein S11, mitochondrial



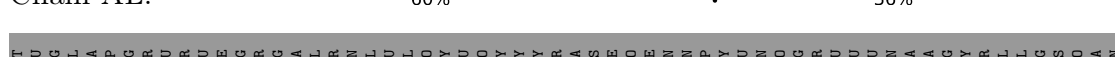
- Molecule 64: 28S ribosomal protein S12, mitochondrial



- Molecule 65: 28S ribosomal protein S14, mitochondrial



- Molecule 66: 28S ribosomal protein S15, mitochondrial

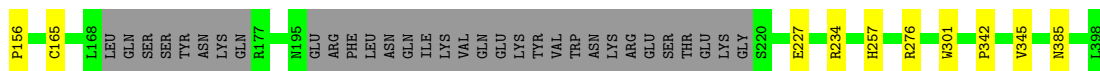


- Molecule 67: 28S ribosomal protein S16, mitochondrial





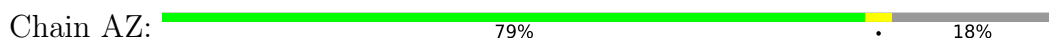




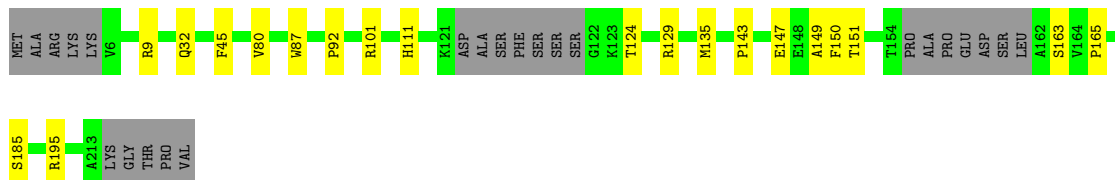
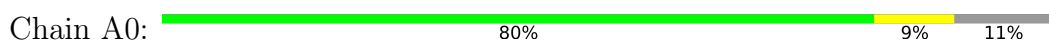
• Molecule 79: 28S ribosomal protein S31, mitochondrial



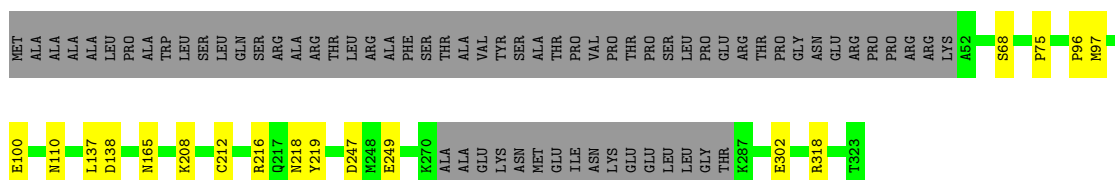
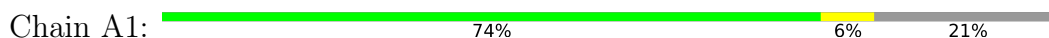
• Molecule 80: 28S ribosomal protein S33, mitochondrial



• Molecule 81: 28S ribosomal protein S34, mitochondrial

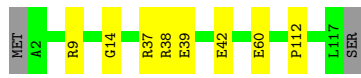


• Molecule 82: 28S ribosomal protein S35, mitochondrial



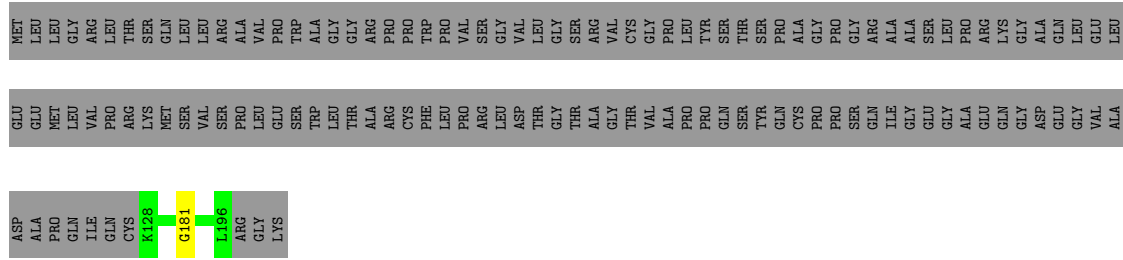
- Molecule 83: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

Chain A2:  92% 7%




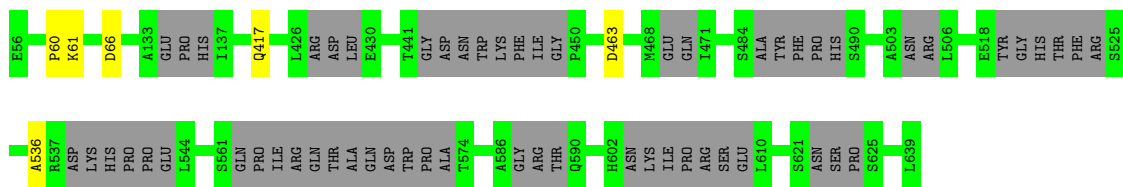
- Molecule 84: Aurora kinase A-interacting protein

Chain A3:  34% 65%



- Molecule 85: Pentatricopeptide repeat domain-containing protein 3, mitochondrial,mS39

Chain A4:  86% 13%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26195	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	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: ZN, 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	A	0.14	0/34967	0.72	7/54407 (0.0%)
2	B	0.13	0/1328	0.70	0/2056
3	D	0.23	0/1879	0.41	0/2527
4	E	0.23	0/2433	0.39	0/3299
5	F	0.23	0/2071	0.37	0/2817
6	H	0.22	0/798	0.40	0/1073
7	I	0.23	0/1308	0.37	0/1761
8	J	0.24	0/1077	0.39	0/1452
9	K	0.23	0/1495	0.36	0/2029
10	L	0.23	0/904	0.41	0/1218
11	M	0.24	0/2359	0.37	0/3185
12	N	0.24	0/1697	0.39	0/2281
13	O	0.23	0/1269	0.36	0/1708
14	P	0.23	0/1103	0.39	0/1491
15	Q	0.23	0/1863	0.37	0/2509
16	R	0.23	0/1174	0.35	0/1572
17	S	0.23	0/1276	0.41	0/1729
18	T	0.23	0/1402	0.36	0/1886
19	U	0.24	0/946	0.39	0/1283
20	V	0.22	0/1590	0.39	0/2151
21	W	0.23	0/893	0.39	0/1204
22	X	0.23	0/2090	0.35	0/2825
23	Y	0.23	0/1552	0.34	0/2079
24	Z	0.23	0/1003	0.38	0/1354
25	0	0.23	0/895	0.38	0/1201
26	1	0.23	0/438	0.40	0/583
27	2	0.23	0/382	0.36	0/507
28	3	0.23	0/852	0.38	0/1136
29	4	0.21	0/329	0.39	0/435
30	5	0.23	0/3154	0.38	0/4295
31	6	0.23	0/2722	0.36	0/3709
32	7	0.23	0/2207	0.36	0/2978

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	8	0.23	0/855	0.33	0/1152
34	9	0.25	0/896	0.37	0/1205
35	a	0.22	0/709	0.39	0/963
36	b	0.23	0/1202	0.39	0/1626
37	c	0.24	0/2264	0.36	0/3059
38	d	0.22	0/1385	0.38	0/1877
39	e	0.23	0/1797	0.36	0/2422
40	f	0.23	0/1055	0.40	0/1427
41	g	0.24	0/1102	0.37	0/1503
42	h	0.22	0/847	0.37	0/1150
43	i	0.23	0/849	0.34	0/1135
44	j	0.23	0/698	0.35	0/940
45	k	0.23	0/665	0.37	0/897
46	l	0.20	0/226	0.30	0/299
47	m	0.22	0/379	0.39	0/510
48	o	0.22	0/818	0.35	0/1097
49	p	0.22	0/1071	0.37	0/1433
50	q	0.23	0/1107	0.33	0/1498
51	r	0.22	0/1238	0.36	0/1676
52	s	0.23	0/3114	0.38	0/4225
54	u	0.06	0/46	0.61	0/69
55	AA	0.16	0/21926	0.75	5/34121 (0.0%)
56	AB	0.24	0/1811	0.38	0/2451
57	AC	0.23	0/1112	0.36	0/1505
58	AD	0.23	0/2607	0.39	0/3498
59	AE	0.23	0/989	0.41	0/1335
60	AF	0.23	0/1708	0.37	0/2291
61	AG	0.23	0/2570	0.36	0/3443
62	AH	0.23	0/1019	0.39	0/1379
63	AI	0.24	0/1031	0.40	0/1390
64	AJ	0.23	0/854	0.39	0/1148
65	AK	0.21	0/879	0.38	0/1182
66	AL	0.23	0/1406	0.35	0/1878
67	AM	0.23	0/941	0.38	0/1265
68	AN	0.22	0/864	0.39	0/1169
69	AO	0.24	0/1580	0.40	1/2150 (0.0%)
70	AP	0.23	0/791	0.36	0/1062
71	AQ	0.23	0/747	0.38	0/995
72	AR	0.23	0/2050	0.36	0/2770
73	AS	0.24	0/1069	0.36	0/1441
74	AT	0.24	0/1361	0.38	0/1829
75	AU	0.22	0/1482	0.36	0/1987
76	AV	0.23	0/2758	0.34	0/3724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
77	AW	0.24	0/778	0.39	0/1048
78	AX	0.23	0/2596	0.37	0/3519
79	AY	0.24	0/943	0.32	0/1274
80	AZ	0.23	0/757	0.34	0/1011
81	A0	0.22	0/1727	0.38	0/2338
82	A1	0.23	0/2121	0.37	0/2873
83	A2	0.23	0/939	0.39	0/1256
84	A3	0.22	0/621	0.36	0/820
85	A4	0.23	0/2137	0.32	0/2872
All	All	0.21	0/165953	0.54	13/235927 (0.0%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2010	U	C5-C4-O4	9.58	131.65	125.90
1	A	2010	U	N3-C4-O4	-8.86	113.20	119.40
1	A	1693	C	C2-N1-C1'	6.97	126.46	118.80
1	A	1902	C	C2-N1-C1'	6.15	125.56	118.80
1	A	1693	C	N1-C2-O2	5.83	122.40	118.90

There are no chirality outliers.

There are no planarity outliers.

## 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	
3	D	234/305 (77%)	197 (84%)	35 (15%)	2 (1%)	17	56
4	E	296/348 (85%)	253 (86%)	34 (12%)	9 (3%)	4	31
5	F	248/311 (80%)	209 (84%)	30 (12%)	9 (4%)	3	28
6	H	93/267 (35%)	85 (91%)	7 (8%)	1 (1%)	14	52
7	I	154/261 (59%)	140 (91%)	12 (8%)	2 (1%)	12	48
8	J	138/192 (72%)	119 (86%)	16 (12%)	3 (2%)	6	38
9	K	175/178 (98%)	152 (87%)	18 (10%)	5 (3%)	4	32
10	L	113/145 (78%)	93 (82%)	17 (15%)	3 (3%)	5	34
11	M	285/296 (96%)	240 (84%)	36 (13%)	9 (3%)	4	30
12	N	203/251 (81%)	181 (89%)	20 (10%)	2 (1%)	15	54
13	O	150/175 (86%)	132 (88%)	15 (10%)	3 (2%)	7	40
14	P	129/180 (72%)	114 (88%)	12 (9%)	3 (2%)	6	37
15	Q	217/219 (99%)	180 (83%)	29 (13%)	8 (4%)	3	28
16	R	138/149 (93%)	125 (91%)	12 (9%)	1 (1%)	22	62
17	S	154/205 (75%)	132 (86%)	19 (12%)	3 (2%)	8	41
18	T	164/206 (80%)	148 (90%)	12 (7%)	4 (2%)	6	36
19	U	109/153 (71%)	92 (84%)	15 (14%)	2 (2%)	8	42
20	V	183/216 (85%)	151 (82%)	24 (13%)	8 (4%)	2	25
21	W	109/148 (74%)	94 (86%)	12 (11%)	3 (3%)	5	33
22	X	241/243 (99%)	201 (83%)	32 (13%)	8 (3%)	4	30
23	Y	174/250 (70%)	157 (90%)	14 (8%)	3 (2%)	9	43
24	Z	118/161 (73%)	100 (85%)	14 (12%)	4 (3%)	3	29
25	0	106/188 (56%)	89 (84%)	14 (13%)	3 (3%)	5	33
26	1	50/65 (77%)	43 (86%)	4 (8%)	3 (6%)	1	19
27	2	44/92 (48%)	40 (91%)	4 (9%)	0	100	100
28	3	93/188 (50%)	86 (92%)	7 (8%)	0	100	100
29	4	34/103 (33%)	33 (97%)	1 (3%)	0	100	100
30	5	368/394 (93%)	308 (84%)	47 (13%)	13 (4%)	3	29
31	6	313/380 (82%)	258 (82%)	45 (14%)	10 (3%)	4	30
32	7	258/338 (76%)	217 (84%)	36 (14%)	5 (2%)	8	41
33	8	97/206 (47%)	88 (91%)	9 (9%)	0	100	100
34	9	105/137 (77%)	90 (86%)	12 (11%)	3 (3%)	4	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	a	78/142 (55%)	72 (92%)	5 (6%)	1 (1%)	12	48
36	b	146/215 (68%)	128 (88%)	16 (11%)	2 (1%)	11	47
37	c	271/332 (82%)	233 (86%)	31 (11%)	7 (3%)	5	35
38	d	156/306 (51%)	132 (85%)	20 (13%)	4 (3%)	5	35
39	e	211/279 (76%)	188 (89%)	20 (10%)	3 (1%)	11	47
40	f	125/212 (59%)	106 (85%)	17 (14%)	2 (2%)	9	45
41	g	127/166 (76%)	106 (84%)	18 (14%)	3 (2%)	6	36
42	h	96/158 (61%)	80 (83%)	11 (12%)	5 (5%)	2	22
43	i	95/128 (74%)	76 (80%)	16 (17%)	3 (3%)	4	30
44	j	83/123 (68%)	77 (93%)	5 (6%)	1 (1%)	13	50
45	k	82/112 (73%)	62 (76%)	12 (15%)	8 (10%)	0	10
46	l	21/138 (15%)	21 (100%)	0	0	100	100
47	m	43/128 (34%)	38 (88%)	5 (12%)	0	100	100
48	o	92/102 (90%)	80 (87%)	8 (9%)	4 (4%)	2	25
49	p	119/206 (58%)	109 (92%)	10 (8%)	0	100	100
50	q	126/222 (57%)	118 (94%)	8 (6%)	0	100	100
51	r	140/196 (71%)	121 (86%)	13 (9%)	6 (4%)	2	25
52	s	366/439 (83%)	315 (86%)	44 (12%)	7 (2%)	8	41
56	AB	215/296 (73%)	186 (86%)	27 (13%)	2 (1%)	17	56
57	AC	130/167 (78%)	97 (75%)	31 (24%)	2 (2%)	10	46
58	AD	316/430 (74%)	255 (81%)	46 (15%)	15 (5%)	2	24
59	AE	120/125 (96%)	87 (72%)	25 (21%)	8 (7%)	1	18
60	AF	197/242 (81%)	168 (85%)	25 (13%)	4 (2%)	7	40
61	AG	301/396 (76%)	245 (81%)	45 (15%)	11 (4%)	3	28
62	AH	120/201 (60%)	93 (78%)	24 (20%)	3 (2%)	5	35
63	AI	134/194 (69%)	106 (79%)	24 (18%)	4 (3%)	4	31
64	AJ	106/138 (77%)	83 (78%)	20 (19%)	3 (3%)	5	33
65	AK	99/128 (77%)	86 (87%)	7 (7%)	6 (6%)	1	19
66	AL	162/257 (63%)	137 (85%)	19 (12%)	6 (4%)	3	28
67	AM	114/137 (83%)	93 (82%)	17 (15%)	4 (4%)	3	29
68	AN	105/130 (81%)	82 (78%)	19 (18%)	4 (4%)	3	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AO	183/185 (99%)	141 (77%)	33 (18%)	9 (5%)	2	23
70	AP	94/142 (66%)	73 (78%)	18 (19%)	3 (3%)	4	30
71	AQ	84/86 (98%)	77 (92%)	6 (7%)	1 (1%)	13	50
72	AR	240/360 (67%)	171 (71%)	55 (23%)	14 (6%)	1	20
73	AS	124/190 (65%)	102 (82%)	14 (11%)	8 (6%)	1	19
74	AT	160/173 (92%)	130 (81%)	21 (13%)	9 (6%)	2	21
75	AU	171/205 (83%)	152 (89%)	13 (8%)	6 (4%)	3	29
76	AV	320/414 (77%)	267 (83%)	43 (13%)	10 (3%)	4	31
77	AW	95/187 (51%)	65 (68%)	23 (24%)	7 (7%)	1	16
78	AX	310/398 (78%)	253 (82%)	46 (15%)	11 (4%)	3	29
79	AY	106/395 (27%)	86 (81%)	14 (13%)	6 (6%)	1	20
80	AZ	85/106 (80%)	74 (87%)	9 (11%)	2 (2%)	6	36
81	A0	197/225 (88%)	152 (77%)	29 (15%)	16 (8%)	1	14
82	A1	252/323 (78%)	198 (79%)	45 (18%)	9 (4%)	3	28
83	A2	114/118 (97%)	89 (78%)	20 (18%)	5 (4%)	2	25
84	A3	67/199 (34%)	58 (87%)	8 (12%)	1 (2%)	10	46
85	A4	237/474 (50%)	222 (94%)	12 (5%)	3 (1%)	12	48
All	All	12628/17575 (72%)	10637 (84%)	1611 (13%)	380 (3%)	7	31

5 of 380 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	W	73	PHE
22	X	69	ILE
22	X	149	PRO
30	5	263	ILE
30	5	296	LYS

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	190/245 (78%)	184 (97%)	6 (3%)	39	62
4	E	255/290 (88%)	255 (100%)	0	100	100
5	F	217/262 (83%)	213 (98%)	4 (2%)	59	77
6	H	86/228 (38%)	83 (96%)	3 (4%)	36	60
7	I	145/232 (62%)	145 (100%)	0	100	100
8	J	113/150 (75%)	113 (100%)	0	100	100
9	K	155/156 (99%)	154 (99%)	1 (1%)	86	92
10	L	98/124 (79%)	98 (100%)	0	100	100
11	M	245/249 (98%)	242 (99%)	3 (1%)	71	84
12	N	172/211 (82%)	164 (95%)	8 (5%)	26	53
13	O	133/150 (89%)	132 (99%)	1 (1%)	81	89
14	P	115/155 (74%)	111 (96%)	4 (4%)	36	60
15	Q	201/201 (100%)	200 (100%)	1 (0%)	88	93
16	R	118/126 (94%)	118 (100%)	0	100	100
17	S	141/180 (78%)	138 (98%)	3 (2%)	53	72
18	T	146/176 (83%)	145 (99%)	1 (1%)	84	90
19	U	99/135 (73%)	96 (97%)	3 (3%)	41	63
20	V	169/191 (88%)	167 (99%)	2 (1%)	71	84
21	W	91/119 (76%)	91 (100%)	0	100	100
22	X	219/219 (100%)	216 (99%)	3 (1%)	67	81
23	Y	159/223 (71%)	159 (100%)	0	100	100
24	Z	111/147 (76%)	110 (99%)	1 (1%)	78	88
25	0	97/164 (59%)	96 (99%)	1 (1%)	76	86
26	1	49/60 (82%)	47 (96%)	2 (4%)	30	56
27	2	40/72 (56%)	39 (98%)	1 (2%)	47	68
28	3	88/166 (53%)	85 (97%)	3 (3%)	37	61
29	4	35/89 (39%)	35 (100%)	0	100	100
30	5	337/353 (96%)	328 (97%)	9 (3%)	44	66
31	6	266/332 (80%)	257 (97%)	9 (3%)	37	61
32	7	242/303 (80%)	240 (99%)	2 (1%)	81	89
33	8	91/190 (48%)	91 (100%)	0	100	100
34	9	91/112 (81%)	89 (98%)	2 (2%)	52	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	a	78/133 (59%)	76 (97%)	2 (3%)	46	67
36	b	130/186 (70%)	127 (98%)	3 (2%)	50	70
37	c	241/288 (84%)	239 (99%)	2 (1%)	81	89
38	d	151/274 (55%)	149 (99%)	2 (1%)	69	82
39	e	188/236 (80%)	185 (98%)	3 (2%)	62	79
40	f	117/188 (62%)	116 (99%)	1 (1%)	78	88
41	g	119/148 (80%)	115 (97%)	4 (3%)	37	61
42	h	95/148 (64%)	93 (98%)	2 (2%)	53	72
43	i	86/110 (78%)	81 (94%)	5 (6%)	20	47
44	j	68/97 (70%)	67 (98%)	1 (2%)	65	80
45	k	74/90 (82%)	74 (100%)	0	100	100
46	l	23/116 (20%)	23 (100%)	0	100	100
47	m	40/113 (35%)	39 (98%)	1 (2%)	47	68
48	o	80/87 (92%)	80 (100%)	0	100	100
49	p	117/181 (65%)	113 (97%)	4 (3%)	37	61
50	q	110/178 (62%)	108 (98%)	2 (2%)	59	77
51	r	133/169 (79%)	132 (99%)	1 (1%)	81	89
52	s	326/381 (86%)	323 (99%)	3 (1%)	78	88
56	AB	191/249 (77%)	187 (98%)	4 (2%)	53	72
57	AC	115/143 (80%)	111 (96%)	4 (4%)	36	60
58	AD	269/357 (75%)	262 (97%)	7 (3%)	46	67
59	AE	104/107 (97%)	102 (98%)	2 (2%)	57	75
60	AF	178/209 (85%)	174 (98%)	4 (2%)	52	71
61	AG	265/342 (78%)	257 (97%)	8 (3%)	41	63
62	AH	112/180 (62%)	110 (98%)	2 (2%)	59	77
63	AI	104/147 (71%)	104 (100%)	0	100	100
64	AJ	93/118 (79%)	91 (98%)	2 (2%)	52	71
65	AK	91/113 (80%)	89 (98%)	2 (2%)	52	71
66	AL	152/226 (67%)	149 (98%)	3 (2%)	55	73
67	AM	95/113 (84%)	93 (98%)	2 (2%)	53	72
68	AN	93/115 (81%)	91 (98%)	2 (2%)	52	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	AO	166/166 (100%)	160 (96%)	6 (4%)	35	60
70	AP	87/123 (71%)	87 (100%)	0	100	100
71	AQ	78/78 (100%)	74 (95%)	4 (5%)	24	50
72	AR	224/318 (70%)	218 (97%)	6 (3%)	44	66
73	AS	109/164 (66%)	104 (95%)	5 (5%)	27	53
74	AT	150/157 (96%)	148 (99%)	2 (1%)	69	82
75	AU	149/174 (86%)	147 (99%)	2 (1%)	69	82
76	AV	295/364 (81%)	290 (98%)	5 (2%)	60	78
77	AW	84/158 (53%)	83 (99%)	1 (1%)	71	84
78	AX	275/351 (78%)	272 (99%)	3 (1%)	73	85
79	AY	99/357 (28%)	99 (100%)	0	100	100
80	AZ	80/95 (84%)	79 (99%)	1 (1%)	69	82
81	A0	176/196 (90%)	172 (98%)	4 (2%)	50	70
82	A1	237/291 (81%)	228 (96%)	9 (4%)	33	58
83	A2	99/101 (98%)	96 (97%)	3 (3%)	41	63
84	A3	63/166 (38%)	63 (100%)	0	100	100
85	A4	226/291 (78%)	223 (99%)	3 (1%)	69	82
All	All	11349/15102 (75%)	11144 (98%)	205 (2%)	61	77

5 of 205 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	AC	134	PHE
65	AK	63	LEU
83	A2	9	ARG
58	AD	237	ARG
61	AG	106	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
52	s	96	GLN
83	A2	90	GLN
58	AD	424	ASN
78	AX	66	GLN

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Mol	Chain	Res	Type
58	AD	165	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1458/1472 (99%)	332 (22%)	23 (1%)
2	B	51/56 (91%)	9 (17%)	1 (1%)
54	u	1/2 (50%)	0	0
55	AA	914/923 (99%)	366 (40%)	24 (2%)
All	All	2424/2453 (98%)	707 (29%)	48 (1%)

5 of 707 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1676	A
1	A	1677	C
1	A	1678	C
1	A	1679	U

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	AA	833	A
55	AA	982	A
55	AA	878	G
55	AA	943	G
55	AA	1102	A

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 134 ligands modelled in this entry, 134 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	14
85	A4	13
55	AA	8
2	B	4

The worst 5 of 39 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2218:C	O3'	2228:A	P	41.52
1	A4	399:UNK	C	414:LYS	N	32.07
1	A	2760:A	O3'	2792:A	P	25.98
1	A	1760:G	O3'	1766:U	P	24.98
1	AA	955:A	O3'	965:C	P	24.64



## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0515. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal surface views

This section was not generated.

### 6.5 Mask visualisation

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

## 7 Map analysis

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

### 7.1 Map-value distribution

This section was not generated.

### 7.2 Volume estimate versus contour level

This section was not generated.

### 7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit

This section was not generated.