



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2024 – 11:34 pm BST

PDB ID : 6ZS9
EMDB ID : EMD-11390
Title : Human mitochondrial ribosome in complex with ribosome recycling factor
Authors : Aibara, S.; Singh, V.; Modelska, A.; Amunts, A.
Deposited on : 2020-07-15
Resolution : 4.00 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

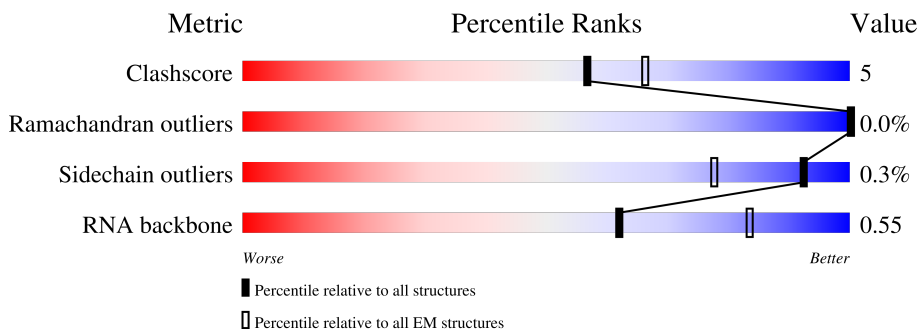
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

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 4.00 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.






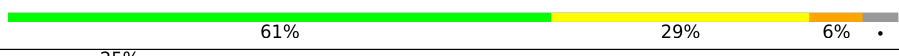
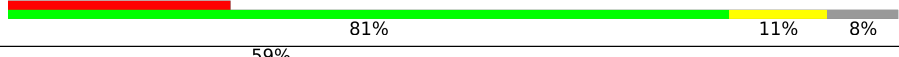



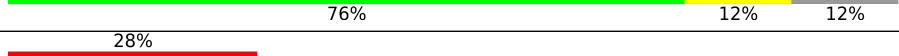
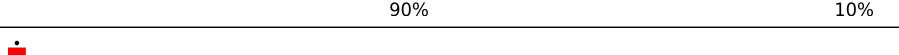
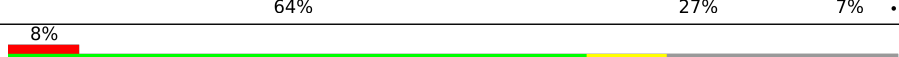
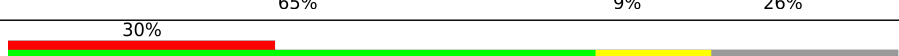

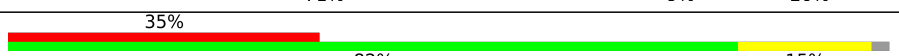

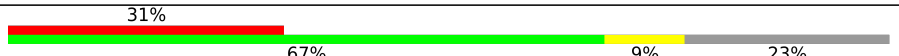
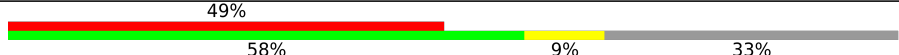




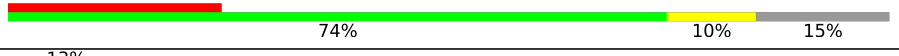

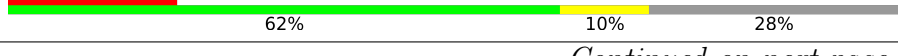

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	0	188	
2	1	65	
3	2	92	
4	3	188	
5	4	103	
6	5	423	
7	6	380	

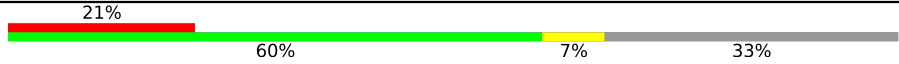
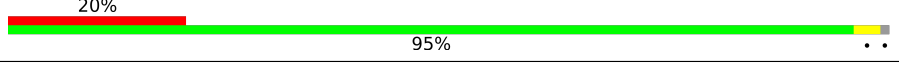
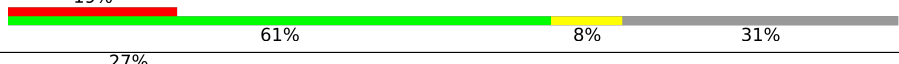



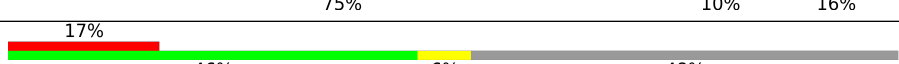
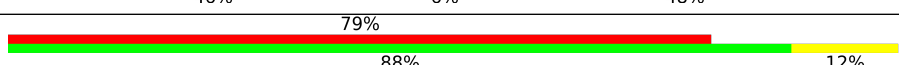

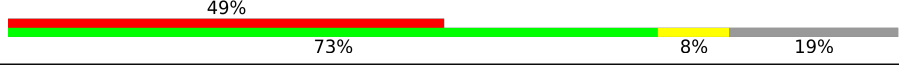

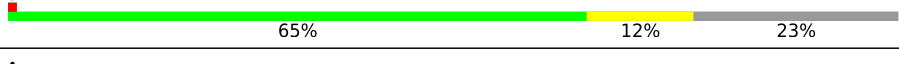
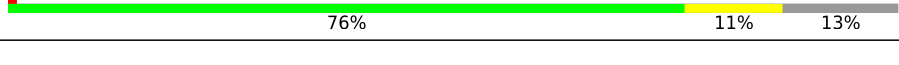

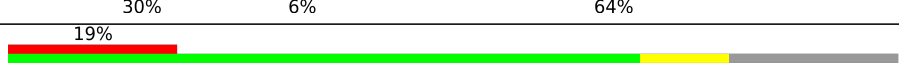

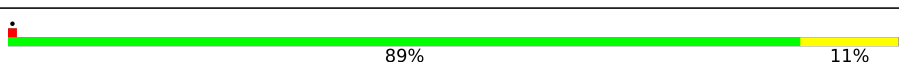








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Mol	Chain	Length	Quality of chain
8	7	338	
9	8	206	
10	9	137	
11	XA	1559	
12	A0	218	
13	A1	323	
14	A2	118	
15	A3	199	
16	A4	634	
17	A5	192	
18	AA	951	
19	AB	296	
20	AC	167	
21	AD	430	
22	AE	125	
23	AF	242	
24	AG	396	
25	AH	201	
26	AI	194	
27	AJ	138	
28	AK	128	
29	AL	257	
30	AM	137	
31	AN	130	
32	AO	258	


























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Mol	Chain	Length	Quality of chain
33	AP	142	
34	AQ	86	
35	AR	360	
36	AS	190	
37	AT	173	
38	AU	205	
39	AV	414	
40	AW	187	
41	AX	348	
42	AY	395	
43	AZ	106	
44	XB	73	
45	XD	305	
46	XE	348	
47	XF	311	
48	XH	267	
49	XI	261	
50	XJ	192	
51	XK	178	
52	XL	145	
53	XM	296	
54	XN	251	
55	XO	175	
56	XP	179	
57	XQ	292	




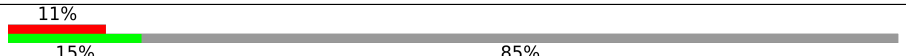
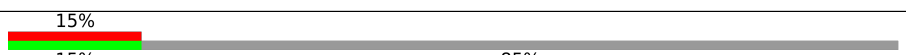
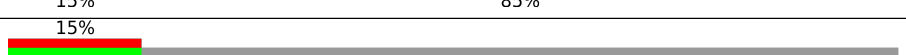
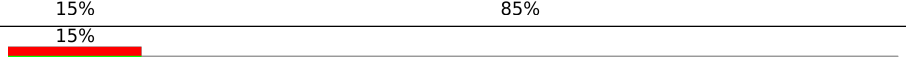


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Mol	Chain	Length	Quality of chain
58	XR	149	 77% 17% 6%
59	XS	205	 66% 12% 22%
60	XT	212	 71% 7% 22%
61	XU	153	 78% 14% 8%
62	XV	216	 78% 15% 6%
63	XW	148	 64% 11% 25%
64	XX	256	 85% 10% 5%
65	XY	250	 58% 13% 29%
66	XZ	161	 69% 6% 25%
67	a	142	 68% 32%
68	b	215	 69% 31%
69	c	332	 83% 17%
70	d	306	 71% 29%
71	e	279	 11% 76% 22%
72	f	212	 8% 67% 33%
73	g	166	 80% 20%
74	h	158	 68% 32%
75	i	128	 76% 24%
76	j	123	 70% 30%
77	k	112	 85% 15%
78	l	138	 58% 42%
79	m	128	 8% 47% 53%
80	o	102	 92% 8%
81	p	206	 62% 38%
82	q	198	 19% 83% 17%

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Mol	Chain	Length	Quality of chain
83	r	196	 78% 22%
84	s	439	 84% 16%
85	t1	198	 17% 23% 77%
85	t2	198	 11% 15% 85%
85	t3	198	 15% 15% 85%
85	t4	198	 15% 15% 85%
85	t5	198	 15% 15% 85%
85	t6	198	 14% 14% 86%
86	A	8	 38% 25% 38%

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 313805 atoms, of which 144698 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	
			Total	C	H	N	O			S
1	0	108	1782	545	902	172	157	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	1	53	919	281	480	84	72	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	2	46	782	233	406	83	59	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
4	3	95	1714	539	883	162	127	3	0	0

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	4	38	702	217	361	72	48	4	0	0

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	5	393	6405	2070	3201	559	564	11	0	0

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
7	6	354	5786	1881	2839	525	532	9	0	0

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
8	7	291	4738	1514	2373	401	432	18	0	0

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	8	135	2311	727	1171	202	209	2	0	0

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	9	124	1983	644	987	170	180	2	0	0

- Molecule 11 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
11	XA	1501	48058	14303	16183	5764	10307	1501	0	0

- Molecule 12 is a protein called 28S ribosomal protein S34, mitochondrial.

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

- Molecule 13 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
13	A1	275	4491	1414	2261	380	425	11	0	0

- Molecule 14 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
14	A2	116	1889	574	964	181	162	8	0	0

- Molecule 15 is a protein called Aurora kinase A-interacting protein.

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

- Molecule 16 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
16	A4	558	9067	2903	4546	764	826	28	0	0

- Molecule 17 is a protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
17	A5	192	3066	923	1577	267	291	8	0	0

- Molecule 18 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
18	AA	927	29687	8828	9997	3550	6385	927	0	0

- Molecule 19 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
19	AB	218	3545	1135	1769	322	309	10	0	0

- Molecule 20 is a protein called 28S ribosomal protein S24, mitochondrial.

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

- Molecule 21 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	AD	343	5501	1706	2785	515	482	13	0	0

- Molecule 22 is a protein called 28S ribosomal protein S6, mitochondrial.

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

- Molecule 23 is a protein called 28S ribosomal protein S7, mitochondrial.

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

- Molecule 24 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	AG	304	4997	1593	2492	444	454	14	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	AH	135	2241	712	1136	187	203	3	0	0

- Molecule 26 is a protein called 28S ribosomal protein S11, mitochondrial.

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

- Molecule 27 is a protein called 28S ribosomal protein S12, mitochondrial.

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

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

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

- Molecule 29 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	AL	164	2855	883	1473	257	235	7	0	0

- Molecule 30 is a protein called 28S ribosomal protein S16, mitochondrial.

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

- Molecule 31 is a protein called 28S ribosomal protein S17, mitochondrial.

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

- Molecule 32 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	AO	185	3018	970	1490	285	267	6	0	0

- Molecule 33 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
33	AP	95	1561	493	796	132	132	8	0	0

- Molecule 34 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
34	AQ	85	1483	455	749	149	123	7	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	50	ARG	CYS	conflict	UNP P82921

- Molecule 35 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
35	AR	250	4134	1314	2074	353	385	8	0	0

- Molecule 36 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
36	AS	133	2203	709	1103	196	194	1	0	0

- Molecule 37 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
37	AT	162	2673	850	1343	231	238	11	0	0

- Molecule 38 is a protein called 28S ribosomal protein S26, mitochondrial.

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

- Molecule 39 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
39	AV	349	5729	1841	2862	478	536	12	0	0

- Molecule 40 is a protein called 28S ribosomal protein S28, mitochondrial.

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

- Molecule 41 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	AX	348	5616	1802	2802	491	510	11	0	0

- Molecule 42 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
42	AY	113	1868	621	912	157	176	2	0	0

- Molecule 43 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
43	AZ	86	1465	467	734	131	129	4	0	0

- Molecule 44 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
44	XB	59	1890	563	635	227	406	59	0	0

- Molecule 45 is a protein called 39S ribosomal protein L2, mitochondrial.

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

- Molecule 46 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
46	XE	304	4798	1539	2402	416	430	11	0	0

- Molecule 47 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 48 is a protein called 39S ribosomal protein L9, mitochondrial.

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

- Molecule 49 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
49	XI	211	Total	C	H	N	O	S	0	0
			3474	1086	1783	303	291	11		

- Molecule 50 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
50	XJ	170	Total	C	H	N	O	S	0	0
			2658	825	1367	230	234	2		

- Molecule 51 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 52 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 53 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 54 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
54	XN	221	Total	C	H	N	O	S	0	0
			3586	1138	1808	325	305	10		

- Molecule 55 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 56 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
56	XP	143	2326	729	1162	223	207	5	0	0

- Molecule 57 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
57	XQ	238	4000	1268	2022	352	349	9	0	0

- Molecule 58 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 59 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
59	XS	160	2638	829	1354	226	225	4	0	0

- Molecule 60 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 61 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
61	XU	141	2335	743	1164	222	203	3	0	0

- Molecule 62 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
62	XV	202	3304	1051	1656	294	295	8	0	0

- Molecule 63 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 64 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
64	XX	243	4089	1317	2054	351	362	5	0	0

- Molecule 65 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
65	XY	178	3109	981	1575	295	254	4	0	0

- Molecule 66 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 67 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
67	a	97	1590	512	777	145	151	5	0	0

- Molecule 68 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 69 is a protein called 39S ribosomal protein L44, mitochondrial.

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

- Molecule 70 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
70	d	217	3510	1128	1747	306	316	13	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	62	PHE	GLU	conflict	UNP Q9BRJ2
d	63	ALA	PHE	conflict	UNP Q9BRJ2

- Molecule 71 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 72 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
72	f	142	2291	731	1152	185	219	4	0	0

- Molecule 73 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
73	g	132	2183	710	1086	191	194	2	0	0

- Molecule 74 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
74	h	108	1749	560	867	154	165	3	0	0

- Molecule 75 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 76 is a protein called cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
76	j	86	1367	426	678	134	127	2	0	0

- Molecule 77 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
77	k	95	1477	456	745	139	132	5	0	0

- Molecule 78 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
78	l	80	1327	427	654	118	125	3	0	0

- Molecule 79 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
79	m	60	1025	309	525	104	85	2	0	0

- Molecule 80 is a protein called Ribosomal protein 63, mitochondrial.

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

- Molecule 81 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 82 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
82	q	164	2738	858	1359	267	249	5	0	0

- Molecule 83 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
83	r	152	2514	792	1267	239	208	8	0	0

- Molecule 84 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
84	s	370	6059	1946	3023	542	534	14	0	0

- Molecule 85 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
85	t1	46	733	228	379	56	70	2	0
85	t2	30	506	154	268	38	46	0	0
85	t3	30	506	154	268	38	46	0	0
85	t4	29	484	148	255	36	45	0	0
85	t5	29	484	148	255	36	45	0	0
85	t6	27	450	137	236	34	43	0	0

- Molecule 86 is a protein called Quinupristin.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
86	A	8	140	53	67	9	10	1	0	0

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

Mol	Chain	Residues	Atoms		AltConf
87	0	1	Total	Zn	0
			1	1	

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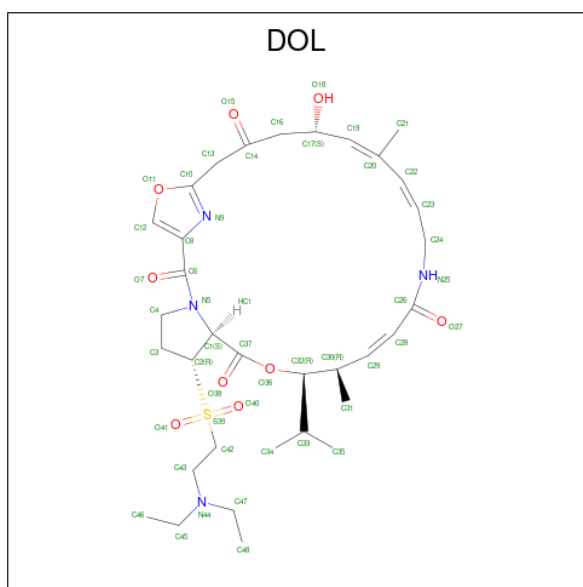
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Mol	Chain	Residues	Atoms		AltConf
87	4	1	Total 1	Zn 1	0
87	AB	1	Total 1	Zn 1	0
87	AO	1	Total 1	Zn 1	0
87	AP	1	Total 1	Zn 1	0
87	AT	1	Total 1	Zn 1	0
87	r	1	Total 1	Zn 1	0

- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

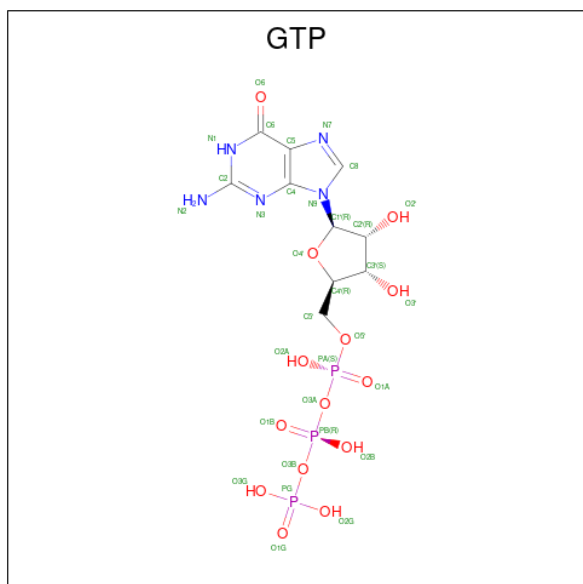
Mol	Chain	Residues	Atoms		AltConf
88	2	1	Total 1	Mg 1	0
88	9	1	Total 1	Mg 1	0
88	XA	140	Total 140	Mg 140	0
88	AA	45	Total 45	Mg 45	0
88	AH	1	Total 1	Mg 1	0
88	XD	1	Total 1	Mg 1	0
88	XI	1	Total 1	Mg 1	0
88	XM	2	Total 2	Mg 2	0
88	XW	1	Total 1	Mg 1	0
88	g	1	Total 1	Mg 1	0
88	o	1	Total 1	Mg 1	0

- Molecule 89 is 5-(2-DIETHYLAMINO-ETHANESULFONYL)-21-HYDROXY-10-ISOPROPYL-11,19-DIMETHYL-9,26-DIOXA-3,15,28-TRIAZA-TRICYCLO[23.2.1.00,255]OCTACOSA-1(27),12,17,19,25(28)-PENTAENE-2,8,14,23-TETRAONE (three-letter code: DOL) (formula: C₃₄H₅₀N₄O₉S).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		S
89	XA	1	98	34	50	4	9	1	0

- Molecule 90 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



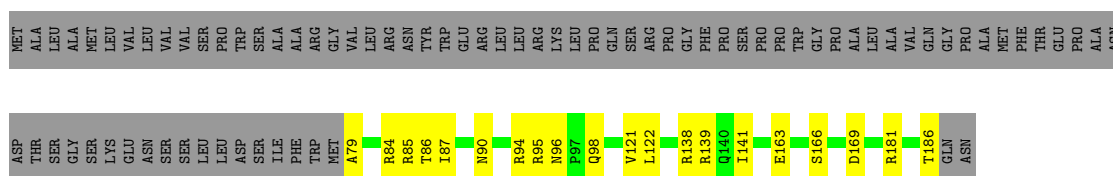
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
90	AX	1	42	10	10	5	14	3	0

3 Residue-property plots [i](#)

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

- Molecule 1: 39S ribosomal protein L32, mitochondrial

Chain 0:  47% 11% 43%




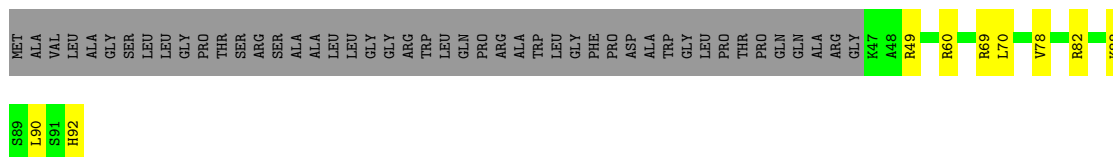
- Molecule 2: 39S ribosomal protein L33, mitochondrial

Chain 1:  74% 8% 18%




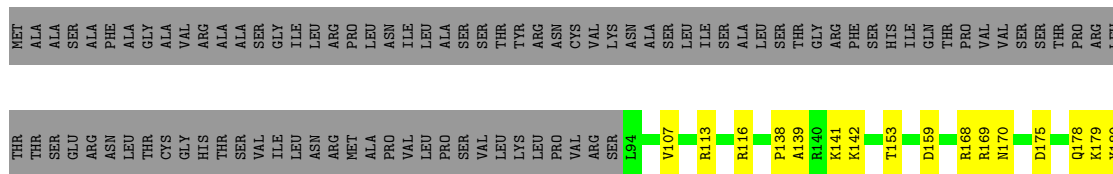
- Molecule 3: 39S ribosomal protein L34, mitochondrial

Chain 2:  40% 10% 50%



- Molecule 4: 39S ribosomal protein L35, mitochondrial

Chain 3:  40% 10% 49%





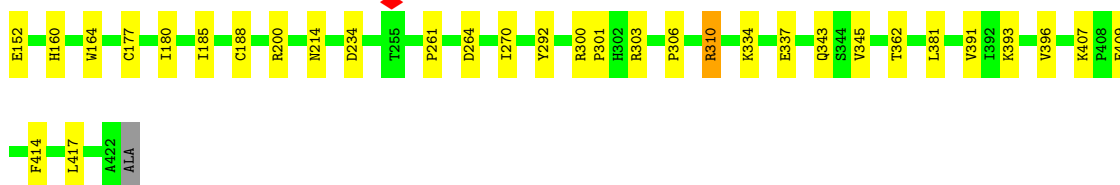
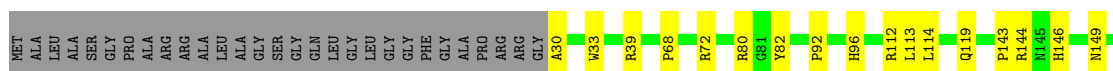
- Molecule 5: 39S ribosomal protein L36, mitochondrial

Chain 4: 33% 63%



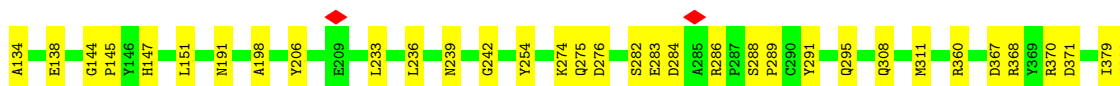
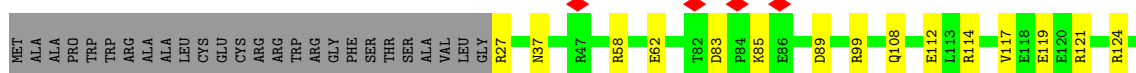
- Molecule 6: 39S ribosomal protein L37, mitochondrial

Chain 5: 81% 11% 7%



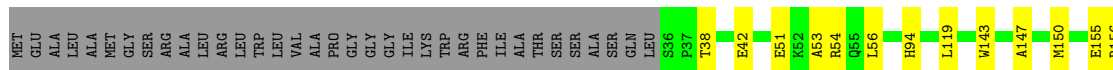
- Molecule 7: 39S ribosomal protein L38, mitochondrial

Chain 6: 80% 13% 7%

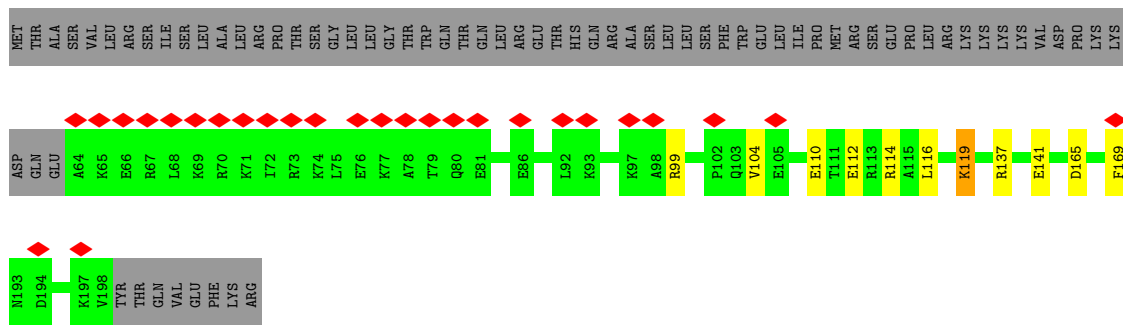


- Molecule 8: 39S ribosomal protein L39, mitochondrial

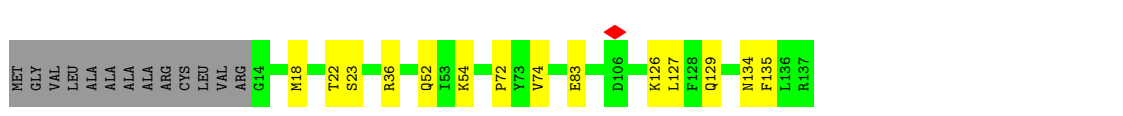
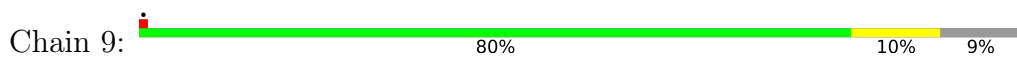
Chain 7: 75% 11% 14%



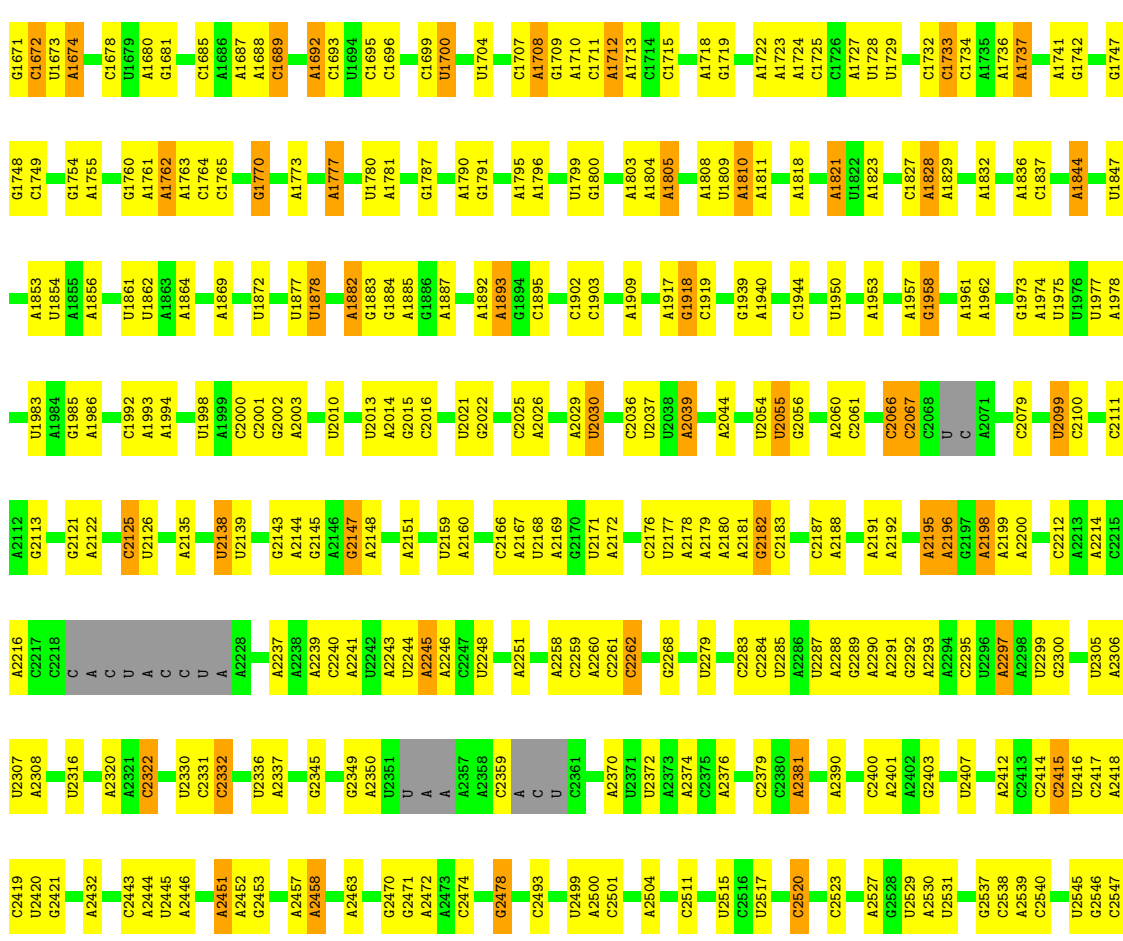
- Molecule 9: 39S ribosomal protein L40, mitochondrial

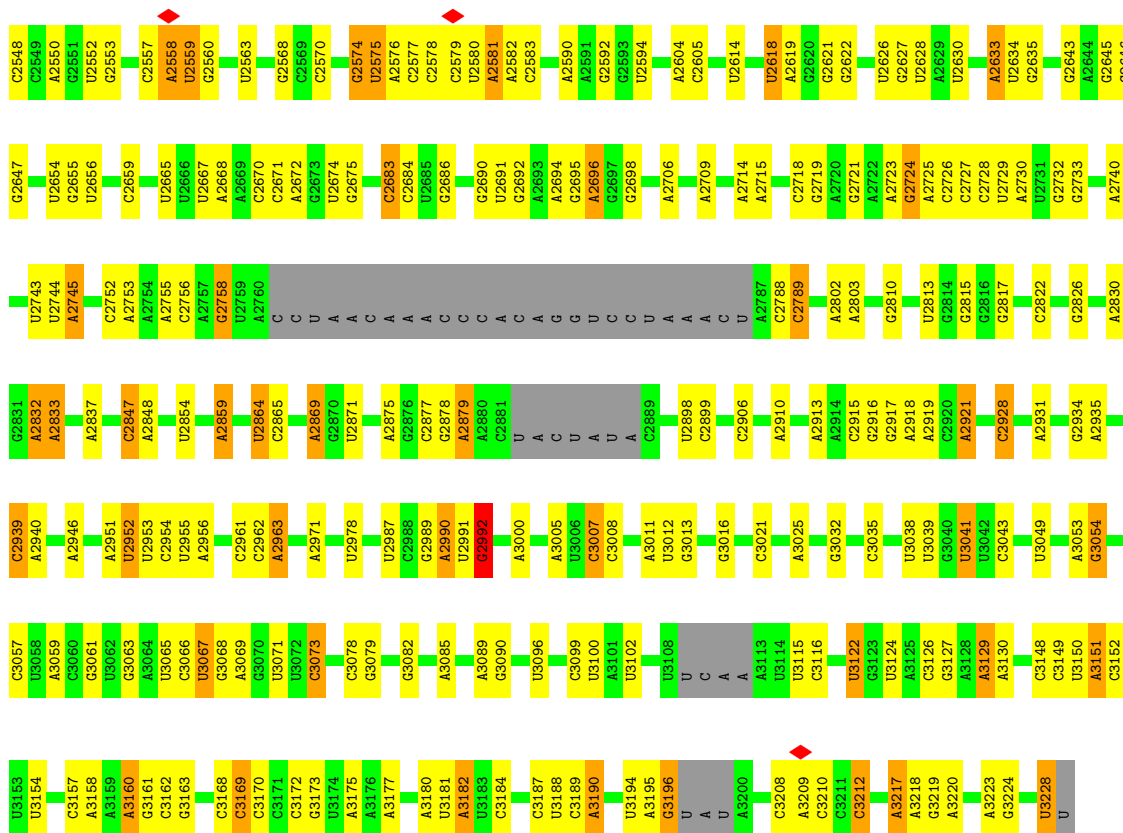


- Molecule 10: 39S ribosomal protein L41, mitochondrial

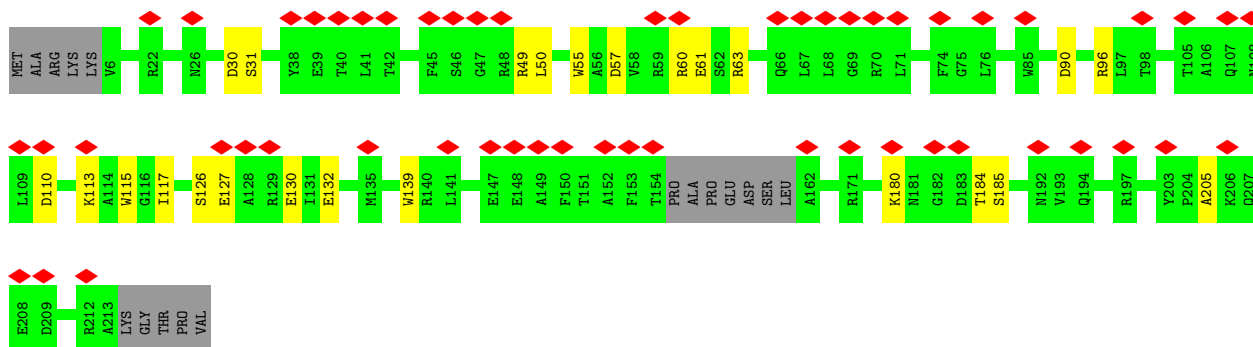
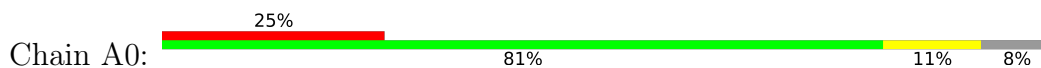


- Molecule 11: 16S rRNA

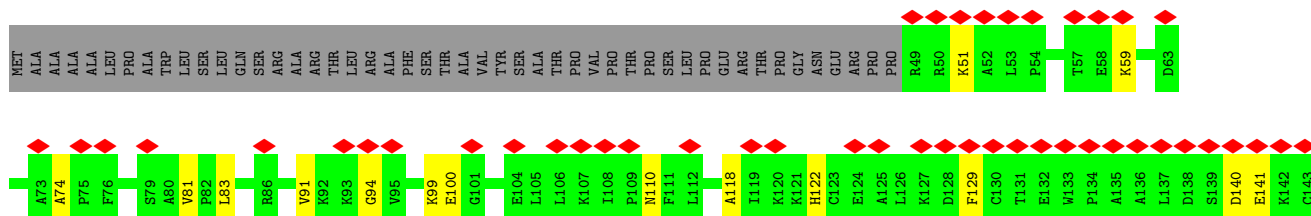
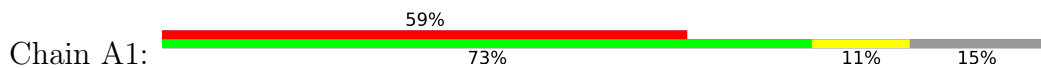


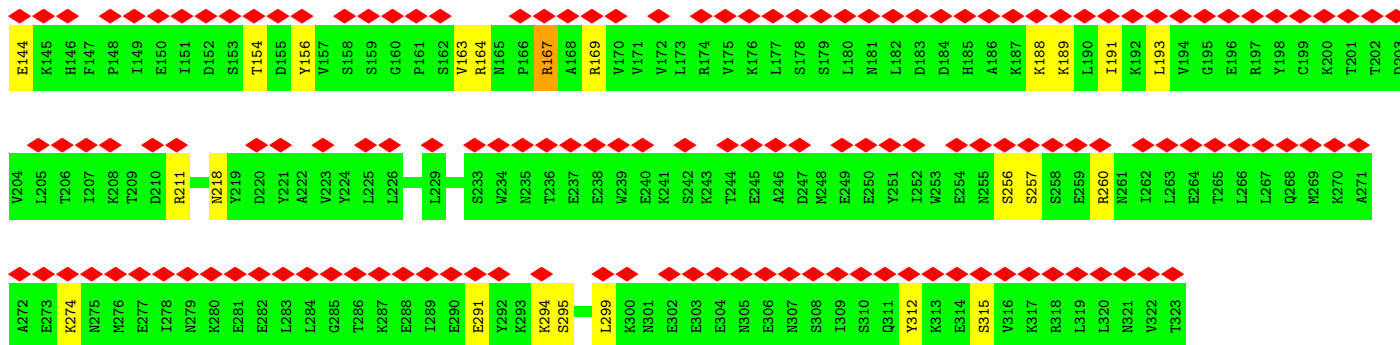


● Molecule 12: 28S ribosomal protein S34, mitochondrial

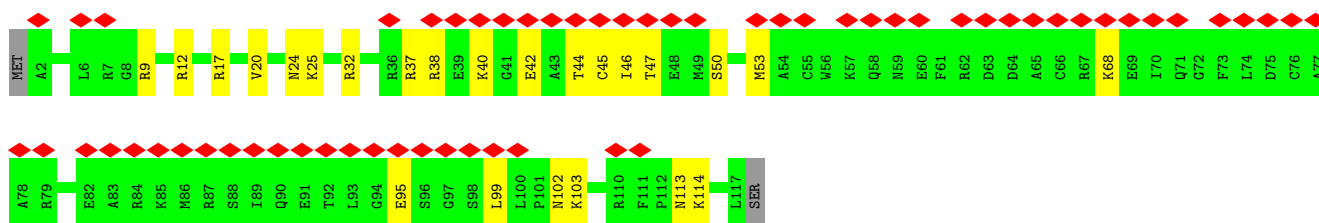


● Molecule 13: 28S ribosomal protein S35, mitochondrial

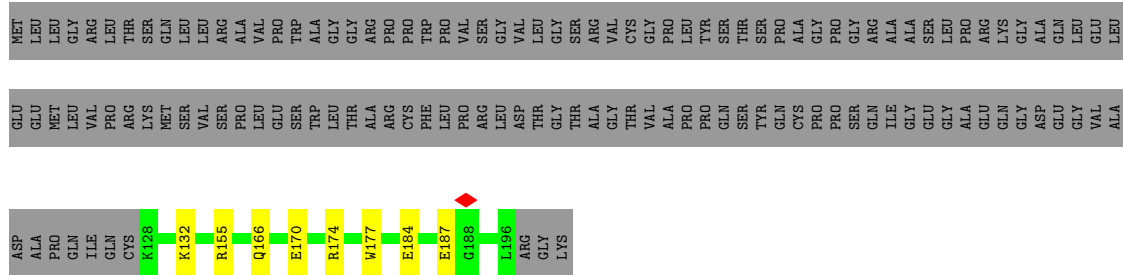




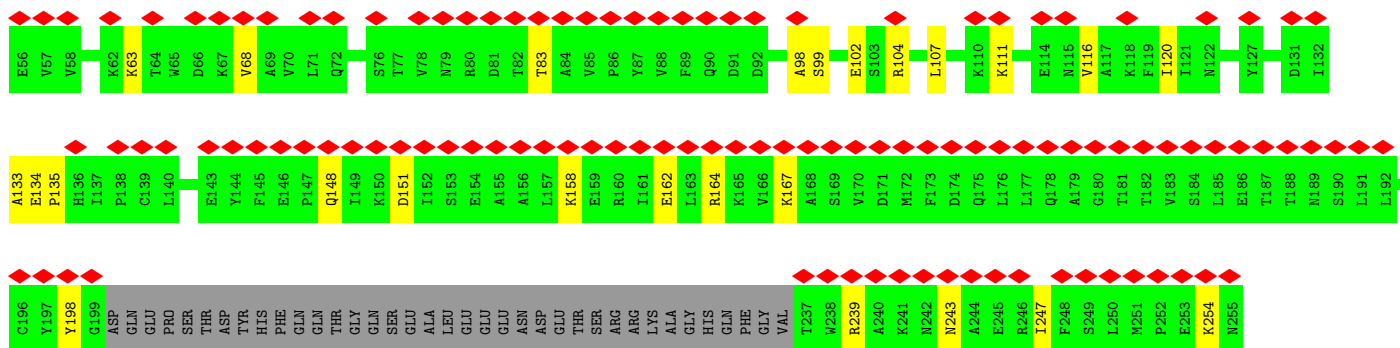
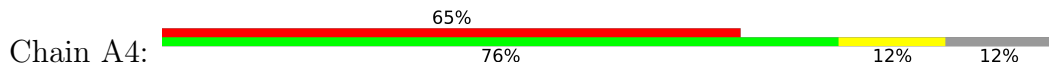
• Molecule 14: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

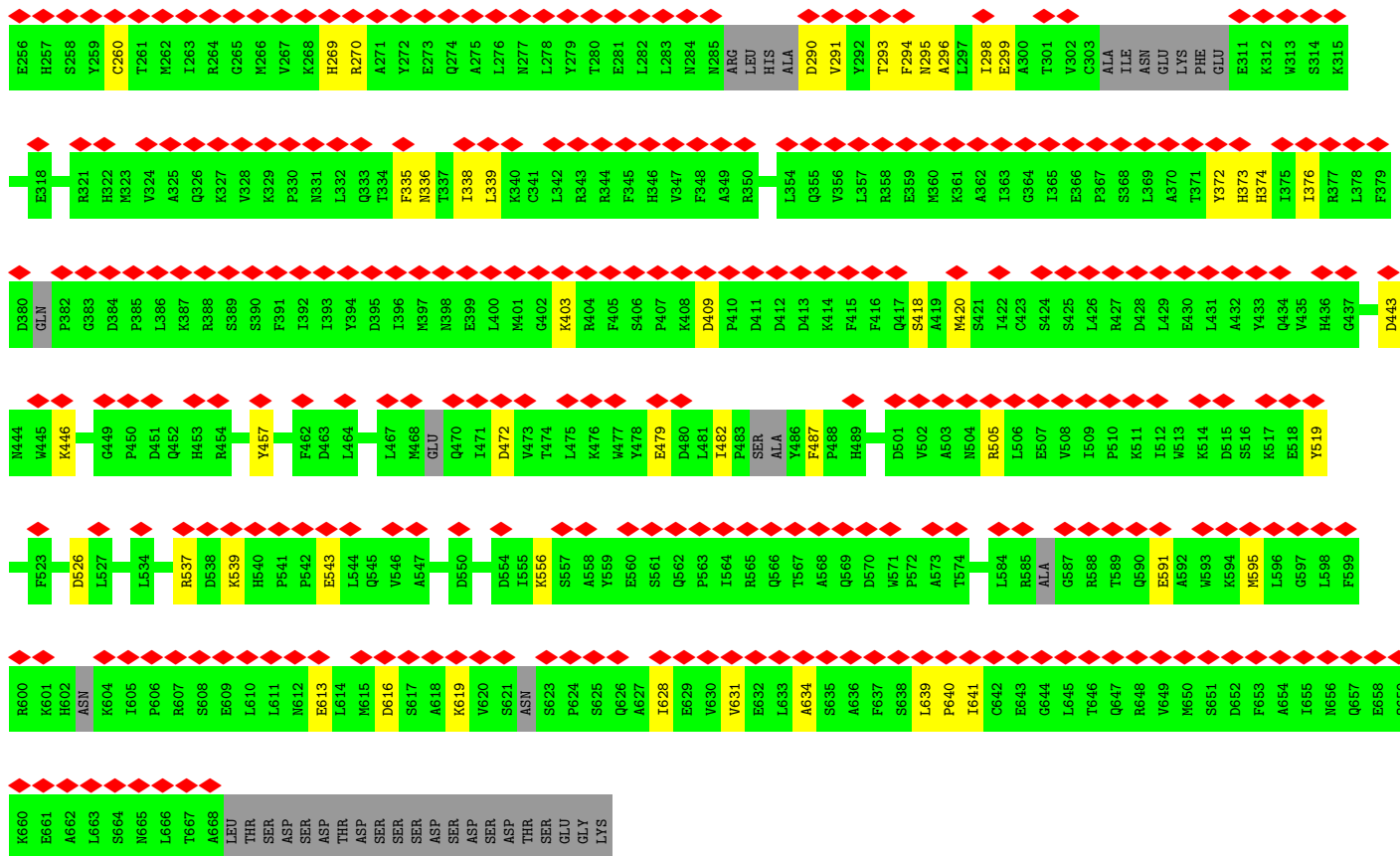


• Molecule 15: Aurora kinase A-interacting protein

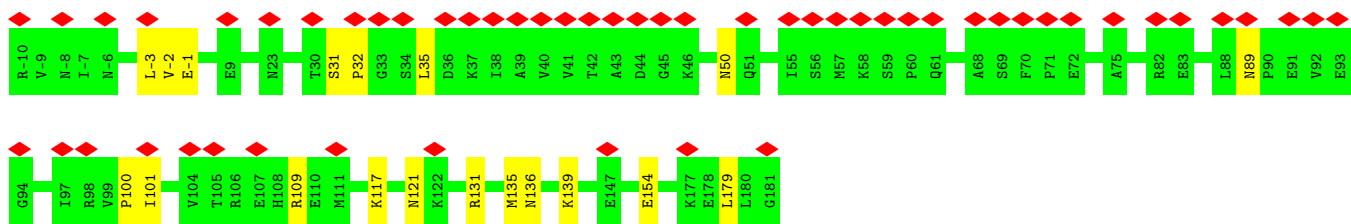
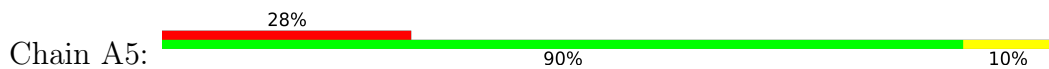


• Molecule 16: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

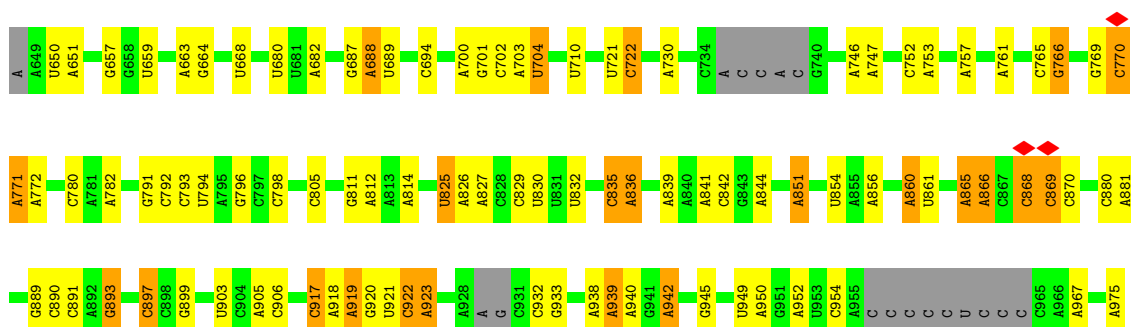




• Molecule 17: Ribosome-recycling factor, mitochondrial

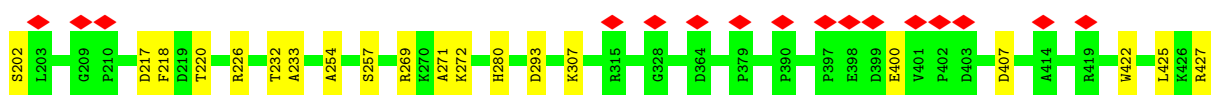
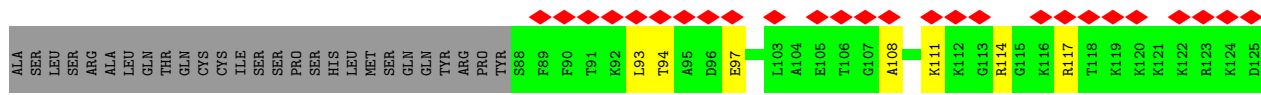
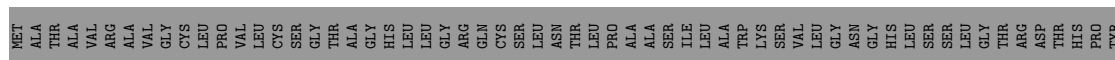
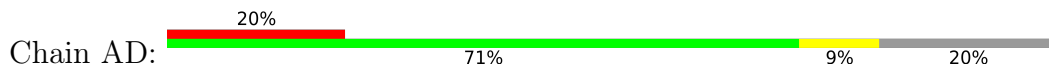


• Molecule 18: 12S rRNA

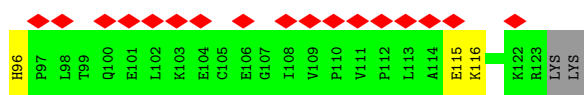
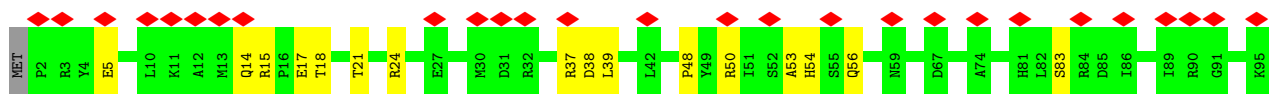
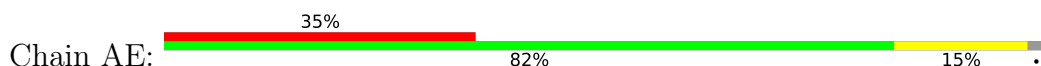




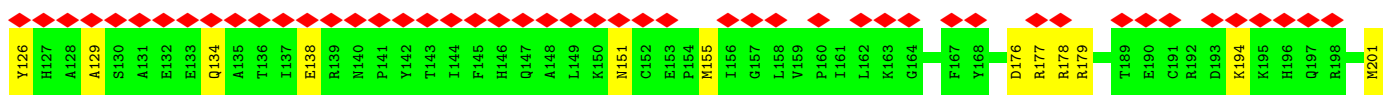
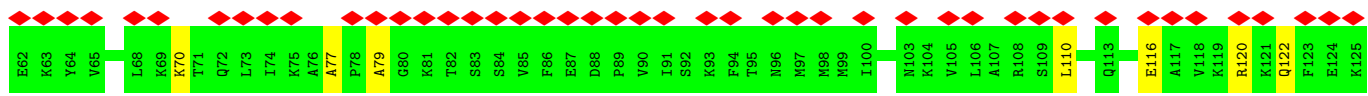
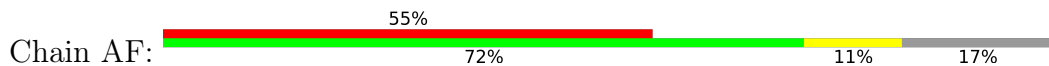
• Molecule 21: 28S ribosomal protein S5, mitochondrial

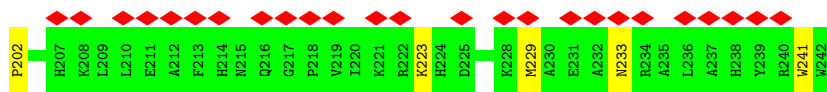


• Molecule 22: 28S ribosomal protein S6, mitochondrial

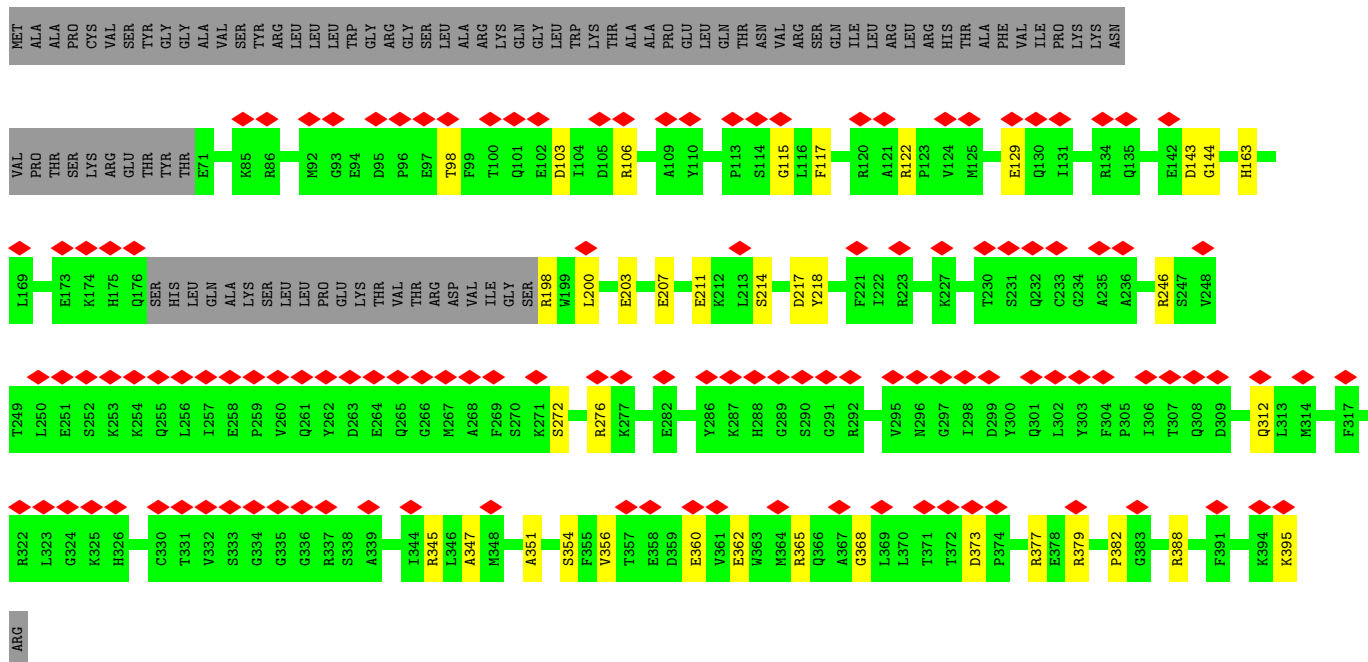


• Molecule 23: 28S ribosomal protein S7, mitochondrial

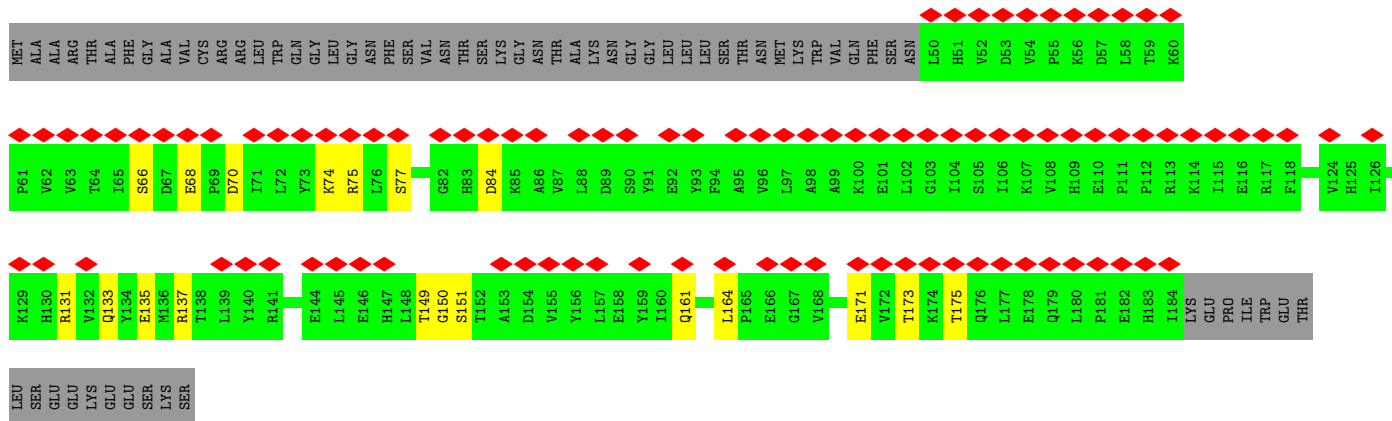




• Molecule 24: 28S ribosomal protein S9, mitochondrial

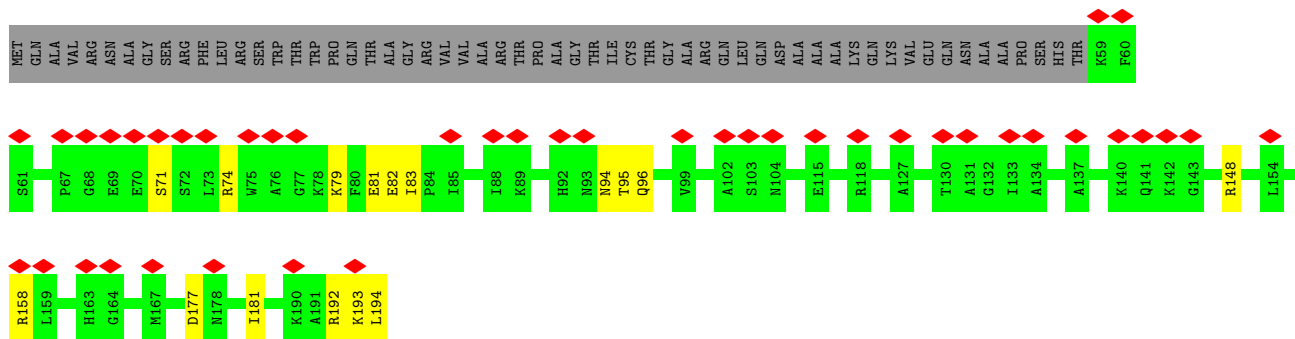


• Molecule 25: 28S ribosomal protein S10, mitochondrial

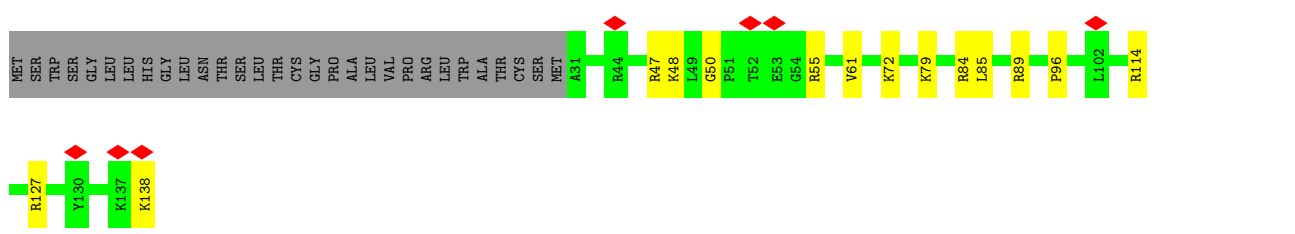


• Molecule 26: 28S ribosomal protein S11, mitochondrial

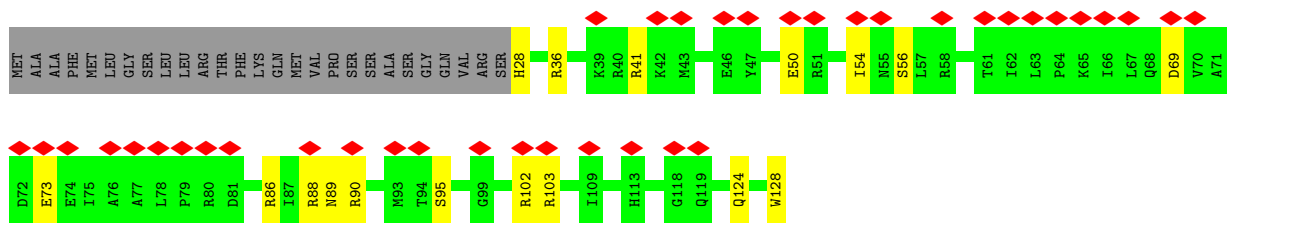




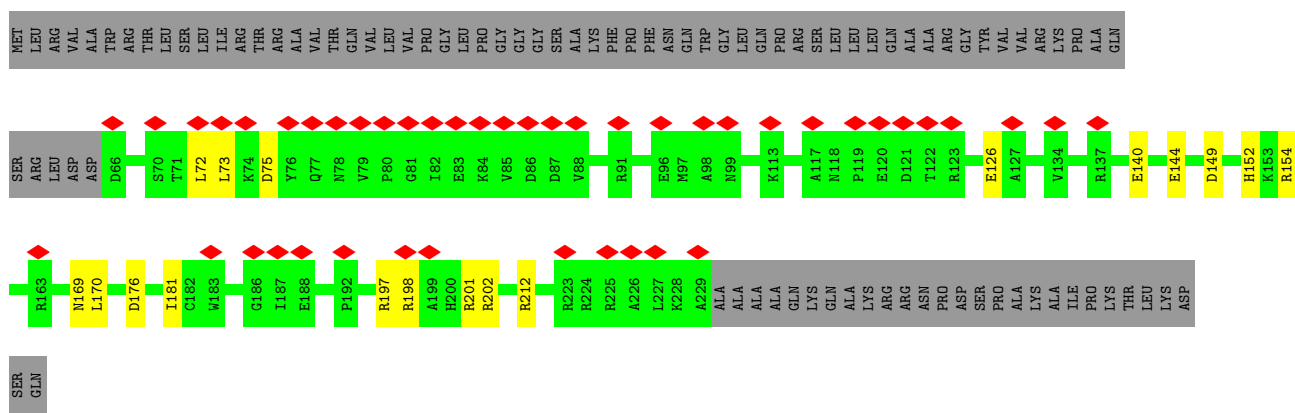
• Molecule 27: 28S ribosomal protein S12, mitochondrial



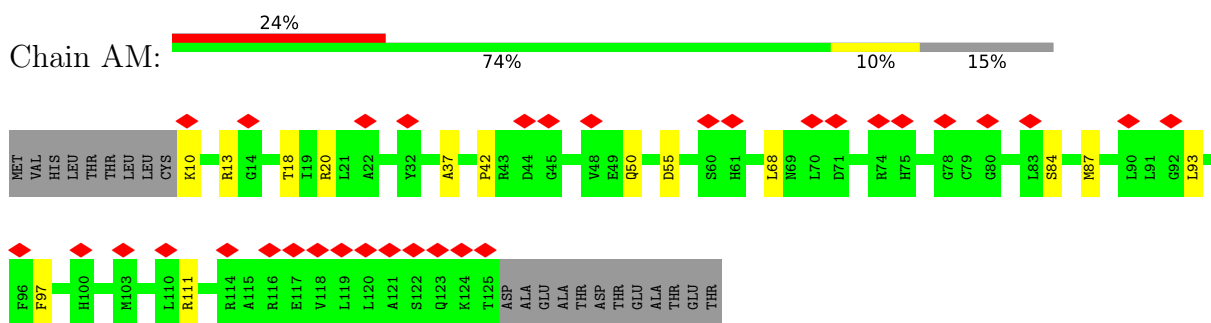
• Molecule 28: 28S ribosomal protein S14, mitochondrial



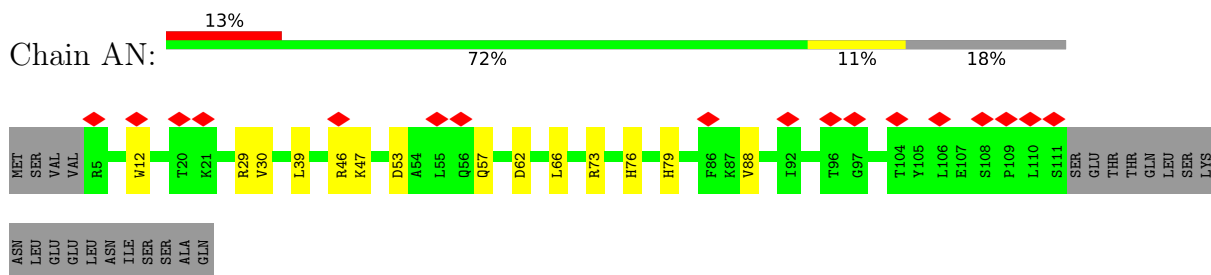
• Molecule 29: 28S ribosomal protein S15, mitochondrial



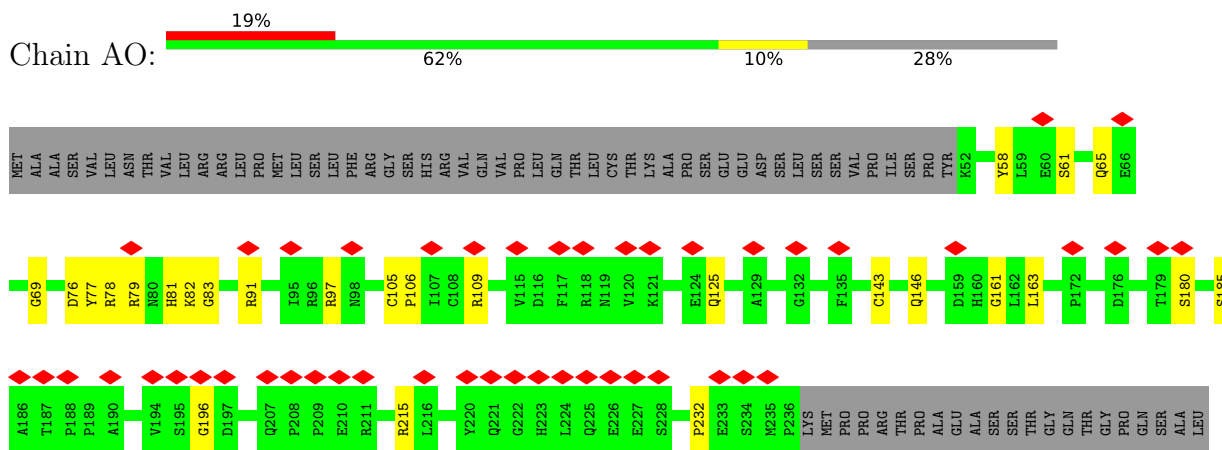
• Molecule 30: 28S ribosomal protein S16, mitochondrial



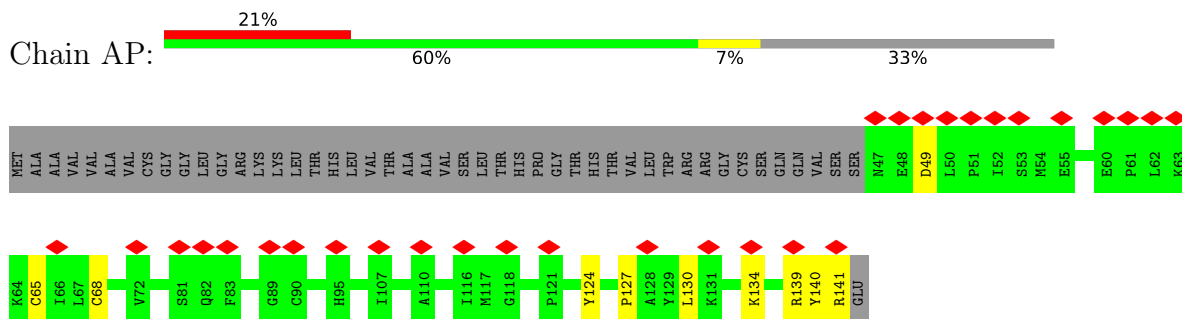
- Molecule 31: 28S ribosomal protein S17, mitochondrial



- Molecule 32: 28S ribosomal protein S18b, mitochondrial

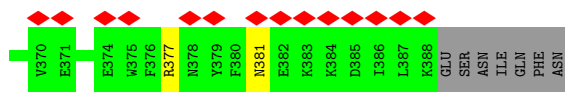


- Molecule 33: 28S ribosomal protein S18c, mitochondrial

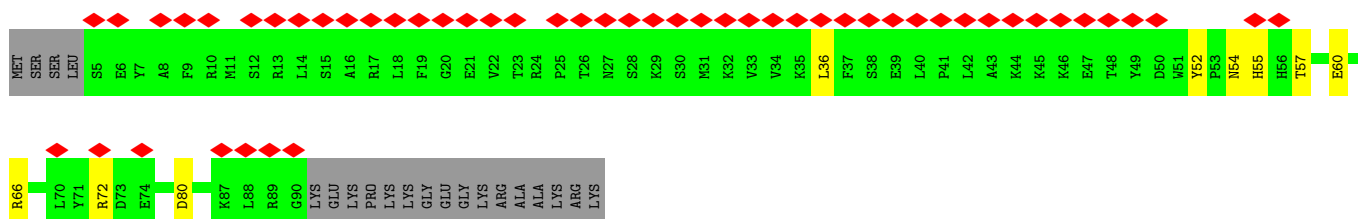
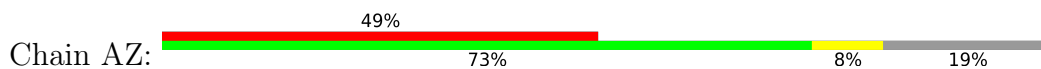


- Molecule 34: 28S ribosomal protein S21, mitochondrial





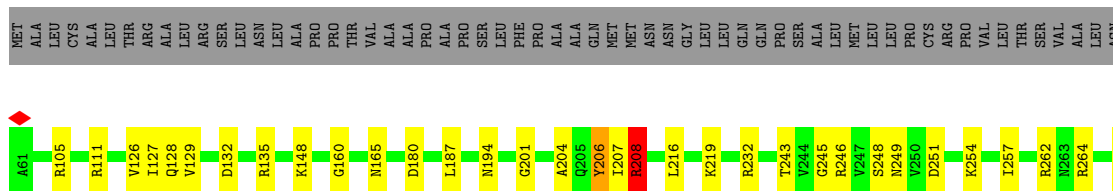
- Molecule 43: 28S ribosomal protein S33, mitochondrial



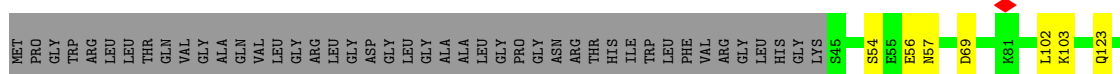
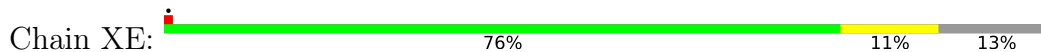
- Molecule 44: mt-tRNAVal



- Molecule 45: 39S ribosomal protein L2, mitochondrial




- Molecule 46: 39S ribosomal protein L3, mitochondrial



- Molecule 47: 39S ribosomal protein L4, mitochondrial



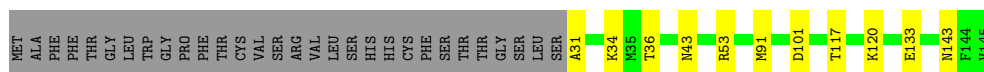
- Molecule 51: 39S ribosomal protein L13, mitochondrial

Chain XK:  89% 11%




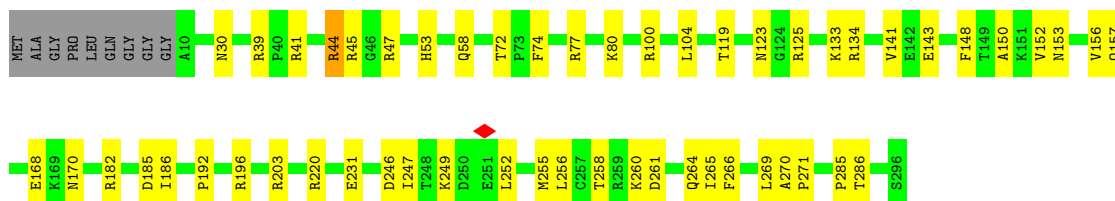
- Molecule 52: 39S ribosomal protein L14, mitochondrial

Chain XL:  72% 8% 21%




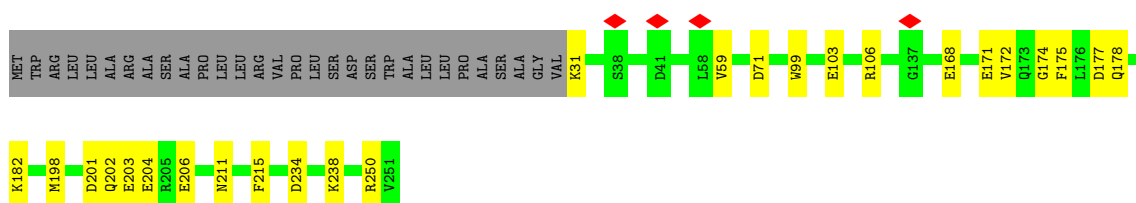
- Molecule 53: 39S ribosomal protein L15, mitochondrial

Chain XM:  79% 18%



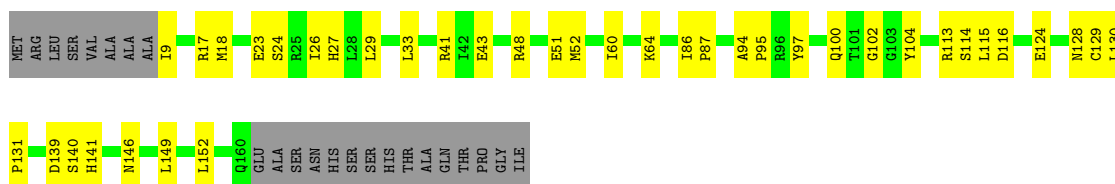
- Molecule 54: 39S ribosomal protein L16, mitochondrial

Chain XN:  78% 10% 12%



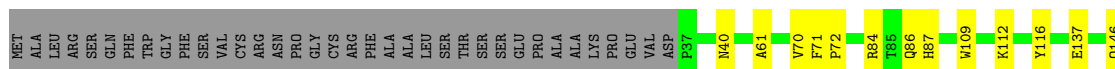
- Molecule 55: 39S ribosomal protein L17, mitochondrial

Chain XO:  65% 22% 13%

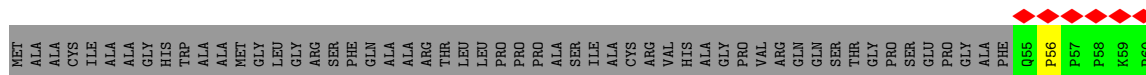


- Molecule 56: Mitochondrial ribosomal protein L18, isoform CRA_b

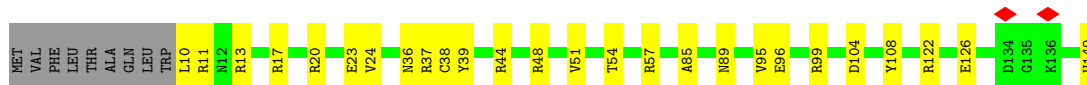
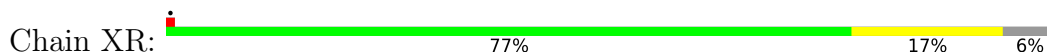
Chain XP:  72% 8% 20%



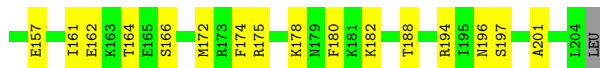
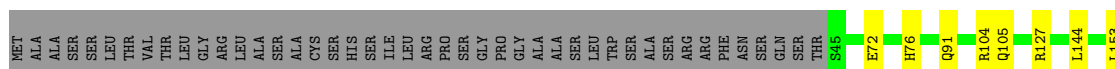
- Molecule 57: 39S ribosomal protein L19, mitochondrial



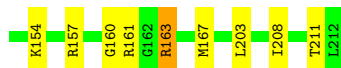
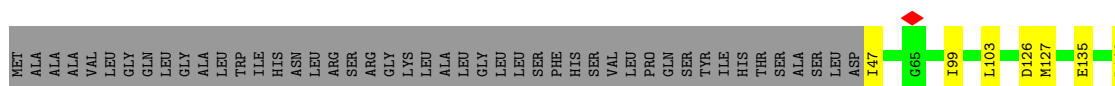
- Molecule 58: 39S ribosomal protein L20, mitochondrial



- Molecule 59: 39S ribosomal protein L21, mitochondrial

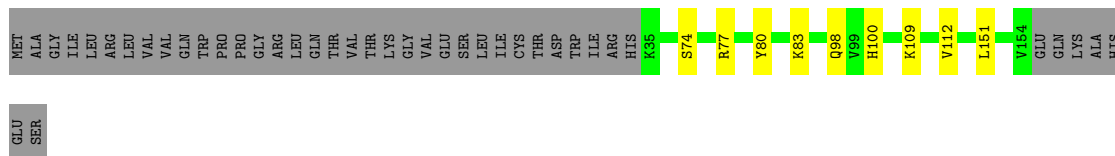


- Molecule 60: 39S ribosomal protein L22, mitochondrial



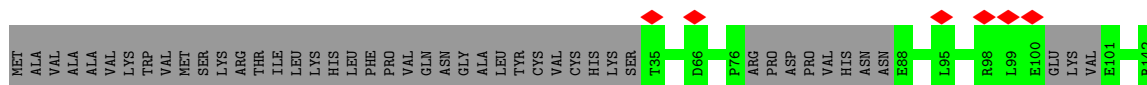
- Molecule 61: 39S ribosomal protein L23, mitochondrial

Chain XZ:  69% 6% 25%



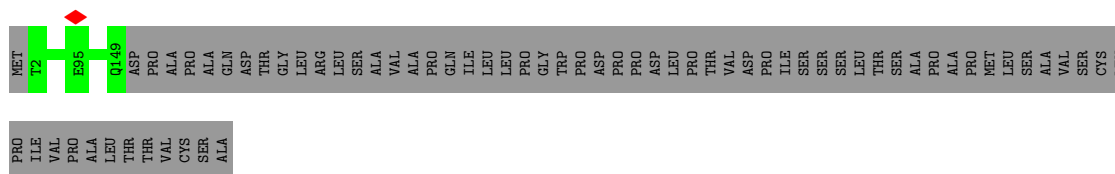
- Molecule 67: 39S ribosomal protein L42, mitochondrial

Chain a:  68% 32%




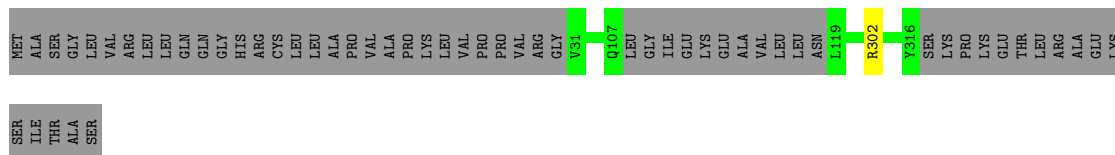
- Molecule 68: 39S ribosomal protein L43, mitochondrial

Chain b:  69% 31%



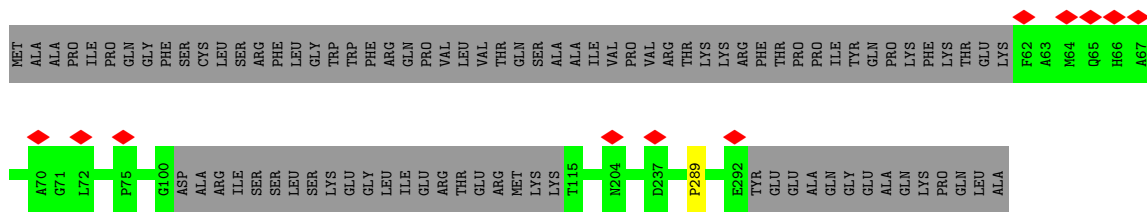
- Molecule 69: 39S ribosomal protein L44, mitochondrial

Chain c:  83% 17%




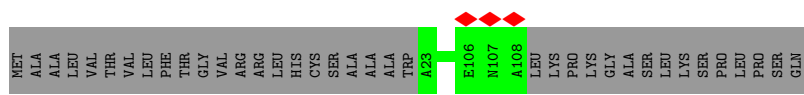
- Molecule 70: 39S ribosomal protein L45, mitochondrial

Chain d:  71% 29%

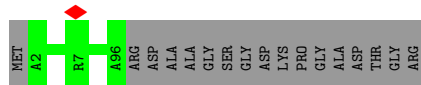
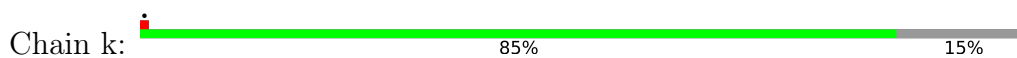


- Molecule 71: 39S ribosomal protein L46, mitochondrial

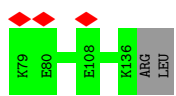
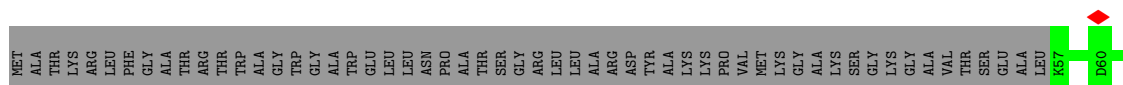
Chain e:  11% 76% 22%



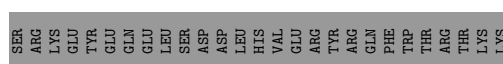
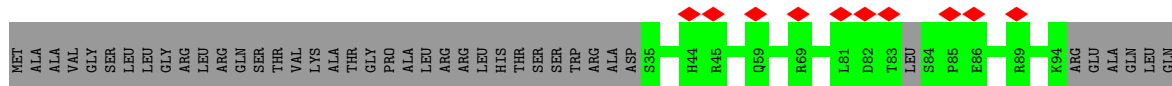
• Molecule 77: 39S ribosomal protein L53, mitochondrial



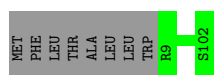
• Molecule 78: 39S ribosomal protein L54, mitochondrial



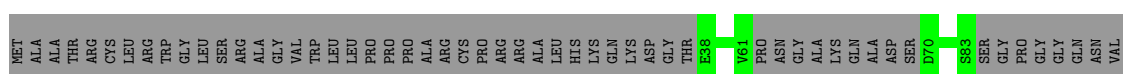
• Molecule 79: 39S ribosomal protein L55, mitochondrial



• Molecule 80: Ribosomal protein 63, mitochondrial



• Molecule 81: Peptidyl-tRNA hydrolase ICT1, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14502	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.287	Depositor
Minimum map value	-0.154	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	546.0, 546.0, 546.0	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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: MHT, DBB, ZN, GTP, DOL, MHV, MG, MHU, 004, MHW

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	0.31	0/895	0.46	0/1201
2	1	0.26	0/444	0.46	0/591
3	2	0.36	0/382	0.46	0/507
4	3	0.35	0/852	0.45	0/1136
5	4	0.32	0/349	0.46	0/461
6	5	0.27	0/3299	0.43	0/4495
7	6	0.28	0/3040	0.43	0/4134
8	7	0.26	0/2420	0.42	0/3270
9	8	1.83	1/1164 (0.1%)	0.46	2/1566 (0.1%)
10	9	0.29	0/1024	0.42	0/1379
11	XA	0.40	0/35662	0.80	13/55502 (0.0%)
12	A0	0.23	0/1727	0.42	0/2338
13	A1	0.24	0/2276	0.40	0/3079
14	A2	0.24	0/939	0.41	0/1256
15	A3	0.26	0/621	0.43	0/820
16	A4	0.24	0/4615	0.41	0/6228
17	A5	0.24	0/1497	0.40	0/2013
18	AA	0.21	0/22022	0.76	11/34275 (0.0%)
19	AB	0.24	0/1819	0.41	0/2462
20	AC	0.24	0/1112	0.41	0/1505
21	AD	0.24	0/2768	0.42	0/3707
22	AE	0.24	0/989	0.44	0/1335
23	AF	0.24	0/1708	0.39	0/2291
24	AG	0.25	0/2559	0.40	0/3429
25	AH	0.23	0/1128	0.42	0/1529
26	AI	0.25	0/1031	0.42	0/1390
27	AJ	0.25	0/854	0.46	0/1148
28	AK	0.22	0/879	0.40	0/1182
29	AL	0.25	0/1406	0.39	0/1878
30	AM	0.25	0/941	0.42	0/1265
31	AN	0.25	0/864	0.44	0/1169
32	AO	0.24	0/1580	0.39	0/2150

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AP	0.25	0/782	0.38	0/1050
34	AQ	0.23	0/746	0.42	0/993
35	AR	0.24	0/2103	0.40	0/2842
36	AS	0.25	0/1127	0.40	0/1518
37	AT	0.25	0/1361	0.41	0/1829
38	AU	0.23	0/1482	0.39	0/1987
39	AV	0.24	0/2925	0.42	0/3948
40	AW	0.25	0/778	0.43	0/1048
41	AX	0.24	0/2884	0.43	0/3903
42	AY	0.24	0/985	0.37	0/1329
43	AZ	0.24	0/748	0.38	0/1000
44	XB	0.21	0/1400	0.73	0/2168
45	XD	0.29	0/1879	0.46	0/2527
46	XE	0.32	0/2465	0.45	0/3344
47	XF	0.34	0/2071	0.47	0/2817
48	XH	0.26	0/798	0.44	0/1073
49	XI	0.26	0/1727	0.43	0/2340
50	XJ	0.24	0/1309	0.40	0/1764
51	XK	0.31	0/1495	0.44	0/2029
52	XL	0.29	0/904	0.44	0/1218
53	XM	0.31	0/2359	0.44	0/3185
54	XN	0.30	0/1825	0.45	0/2458
55	XO	0.29	0/1269	0.45	0/1708
56	XP	0.26	0/1190	0.44	0/1611
57	XQ	0.27	0/2026	0.44	0/2734
58	XR	0.36	0/1174	0.49	0/1572
59	XS	0.32	0/1311	0.47	0/1778
60	XT	0.33	0/1402	0.44	0/1886
61	XU	0.31	0/1200	0.43	0/1623
62	XV	0.28	0/1693	0.44	0/2297
63	XW	0.33	0/893	0.46	0/1204
64	XX	0.28	0/2090	0.41	0/2825
65	XY	0.28	0/1571	0.41	0/2106
66	XZ	0.32	0/1003	0.44	0/1354
67	a	0.29	0/838	0.45	0/1138
68	b	0.30	0/1202	0.48	0/1626
69	c	0.28	0/2264	0.43	0/3059
70	d	0.26	0/1811	0.43	0/2454
71	e	1.43	6/1797 (0.3%)	0.42	0/2422
72	f	0.27	0/1159	0.42	0/1565
73	g	0.30	0/1134	0.45	0/1547
74	h	0.26	0/905	0.43	0/1233
75	i	0.35	0/849	0.45	0/1135

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	j	0.28	0/703	0.42	0/947
77	k	0.24	0/743	0.44	0/1003
78	l	0.24	0/692	0.37	0/939
79	m	0.23	0/508	0.44	0/682
80	o	0.31	0/818	0.45	0/1097
81	p	0.24	0/1071	0.42	0/1433
82	q	0.26	0/1413	0.39	0/1906
83	r	0.30	0/1282	0.42	0/1734
84	s	0.29	0/3114	0.44	0/4225
85	t1	0.25	0/366	0.38	0/497
85	t2	0.22	0/238	0.38	0/319
85	t3	0.22	0/238	0.37	0/319
85	t4	0.23	0/229	0.37	0/308
85	t5	0.22	0/229	0.38	0/308
85	t6	0.22	0/213	0.38	0/286
86	A	4.68	2/13 (15.4%)	3.06	2/15 (13.3%)
All	All	0.36	9/177670 (0.0%)	0.58	28/251956 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
45	XD	0	1
49	XI	0	1
62	XV	0	1
71	e	0	1
72	f	0	1
74	h	0	1
86	A	1	0
All	All	1	6

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	8	99	ARG	CG-CD	61.78	3.06	1.51
71	e	84	TYR	CD2-CE2	31.82	1.87	1.39
71	e	84	TYR	CD1-CE1	31.25	1.86	1.39
71	e	84	TYR	CE2-CZ	21.80	1.66	1.38
71	e	84	TYR	CE1-CZ	21.25	1.66	1.38

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	XA	2758	G	N3-C4-N9	-9.29	120.43	126.00
11	XA	2758	G	C5-C6-O6	7.38	133.03	128.60
11	XA	2789	C	C5-C4-N4	7.27	125.29	120.20
86	A	4	PRO	N-CA-CB	7.05	111.77	103.30
11	XA	2758	G	N3-C4-C5	6.88	132.04	128.60

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
86	A	2	THR	CB

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
45	XD	206	TYR	Peptide
49	XI	197	LEU	Peptide
62	XV	148	THR	Peptide
71	e	265	LYS	Peptide
72	f	138	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	880	902	902	16	0
2	1	439	480	480	4	0
3	2	376	406	406	8	0
4	3	831	883	883	15	0
5	4	341	361	361	3	0
6	5	3204	3201	3201	32	0
7	6	2947	2839	2839	38	0
8	7	2365	2373	2372	22	0
9	8	1140	1171	1171	8	0
10	9	996	987	987	12	0
11	XA	31875	16183	16192	283	0
12	A0	1684	1685	1685	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	A1	2230	2261	2261	24	0
14	A2	925	964	964	16	0
15	A3	610	682	682	6	0
16	A4	4521	4546	4545	46	0
17	A5	1489	1577	1577	11	0
18	AA	19690	9997	10003	163	0
19	AB	1776	1769	1769	19	0
20	AC	1082	1088	1088	17	0
21	AD	2716	2785	2785	25	0
22	AE	972	1001	1001	14	0
23	AF	1668	1716	1716	21	0
24	AG	2505	2492	2490	27	0
25	AH	1105	1136	1136	14	0
26	AI	1011	1052	1052	11	0
27	AJ	838	887	887	10	0
28	AK	861	885	885	12	0
29	AL	1382	1473	1472	13	0
30	AM	920	951	951	12	0
31	AN	846	908	908	11	0
32	AO	1528	1490	1490	20	0
33	AP	765	796	796	7	0
34	AQ	734	749	749	2	0
35	AR	2060	2074	2074	19	0
36	AS	1100	1103	1103	12	0
37	AT	1330	1343	1343	18	0
38	AU	1461	1471	1471	19	0
39	AV	2867	2862	2862	24	0
40	AW	766	785	785	9	0
41	AX	2814	2802	2802	23	0
42	AY	956	912	911	9	0
43	AZ	731	734	734	6	0
44	XB	1255	635	640	9	0
45	XD	1842	1896	1896	29	0
46	XE	2396	2402	2402	25	0
47	XF	2013	2045	2044	31	0
48	XH	784	832	832	10	0
49	XI	1691	1783	1783	16	0
50	XJ	1291	1367	1364	12	0
51	XK	1451	1448	1448	12	0
52	XL	889	941	941	8	0
53	XM	2305	2378	2378	37	0
54	XN	1778	1808	1808	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	XO	1245	1283	1283	25	0
56	XP	1164	1162	1162	14	0
57	XQ	1978	2022	2022	29	0
58	XR	1153	1214	1214	24	0
59	XS	1284	1354	1354	19	0
60	XT	1368	1410	1410	14	0
61	XU	1171	1164	1164	16	0
62	XV	1648	1656	1654	21	0
63	XW	871	898	898	10	0
64	XX	2035	2054	2054	20	0
65	XY	1534	1575	1575	26	0
66	XZ	978	1030	1030	7	0
67	a	813	777	777	0	0
68	b	1178	1180	1180	0	0
69	c	2217	2220	2220	0	0
70	d	1763	1747	1746	0	0
71	e	1762	1767	1767	0	0
72	f	1139	1152	1152	0	0
73	g	1097	1086	1085	0	0
74	h	882	867	867	0	0
75	i	827	857	857	0	0
76	j	689	678	678	0	0
77	k	732	745	745	0	0
78	l	673	654	653	0	0
79	m	500	525	525	0	0
80	o	797	804	804	0	0
81	p	1058	1083	1083	0	0
82	q	1379	1359	1359	0	0
83	r	1247	1267	1267	0	0
84	s	3036	3023	3022	0	0
85	t1	354	379	374	0	0
85	t2	238	268	270	0	0
85	t3	238	268	270	0	0
85	t4	229	255	257	0	0
85	t5	229	255	257	0	0
85	t6	214	236	236	0	0
86	A	73	67	64	2	0
87	0	1	0	0	0	0
87	4	1	0	0	0	0
87	AB	1	0	0	0	0
87	AO	1	0	0	0	0
87	AP	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	AT	1	0	0	0	0
87	r	1	0	0	0	0
88	2	1	0	0	0	0
88	9	1	0	0	0	0
88	AA	45	0	0	0	0
88	AH	1	0	0	0	0
88	XA	140	0	0	0	0
88	XD	1	0	0	0	0
88	XI	1	0	0	0	0
88	XM	2	0	0	0	0
88	XW	1	0	0	0	0
88	g	1	0	0	0	0
88	o	1	0	0	0	0
89	XA	48	50	50	4	0
90	AX	32	10	12	1	0
All	All	169107	144698	144704	1255	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1255 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:XA:2721:G:O6	11:XA:2990:A:C6	1.84	1.30
11:XA:2724:G:OP1	47:XF:131:LYS:NZ	1.91	1.03
11:XA:3063:G:O2'	11:XA:3066:C:OP2	1.86	0.94
11:XA:2864:U:O5'	63:XW:50:ARG:NH1	2.04	0.91
11:XA:1777:A:N6	11:XA:1780:U:OP2	2.03	0.91

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	106/188 (56%)	103 (97%)	3 (3%)	0	100	100
2	1	51/65 (78%)	47 (92%)	4 (8%)	0	100	100
3	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
4	3	93/188 (50%)	92 (99%)	1 (1%)	0	100	100
5	4	36/103 (35%)	35 (97%)	1 (3%)	0	100	100
6	5	391/423 (92%)	367 (94%)	24 (6%)	0	100	100
7	6	348/380 (92%)	325 (93%)	23 (7%)	0	100	100
8	7	285/338 (84%)	265 (93%)	20 (7%)	0	100	100
9	8	133/206 (65%)	126 (95%)	7 (5%)	0	100	100
10	9	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
12	A0	197/218 (90%)	190 (96%)	7 (4%)	0	100	100
13	A1	273/323 (84%)	260 (95%)	13 (5%)	0	100	100
14	A2	114/118 (97%)	108 (95%)	6 (5%)	0	100	100
15	A3	67/199 (34%)	66 (98%)	1 (2%)	0	100	100
16	A4	536/634 (84%)	503 (94%)	33 (6%)	0	100	100
17	A5	188/192 (98%)	179 (95%)	9 (5%)	0	100	100
19	AB	216/296 (73%)	209 (97%)	7 (3%)	0	100	100
20	AC	130/167 (78%)	128 (98%)	2 (2%)	0	100	100
21	AD	341/430 (79%)	328 (96%)	13 (4%)	0	100	100
22	AE	120/125 (96%)	115 (96%)	5 (4%)	0	100	100
23	AF	197/242 (81%)	192 (98%)	5 (2%)	0	100	100
24	AG	300/396 (76%)	292 (97%)	8 (3%)	0	100	100
25	AH	133/201 (66%)	125 (94%)	8 (6%)	0	100	100
26	AI	134/194 (69%)	133 (99%)	1 (1%)	0	100	100
27	AJ	106/138 (77%)	95 (90%)	11 (10%)	0	100	100
28	AK	99/128 (77%)	98 (99%)	1 (1%)	0	100	100
29	AL	162/257 (63%)	156 (96%)	6 (4%)	0	100	100
30	AM	114/137 (83%)	113 (99%)	1 (1%)	0	100	100
31	AN	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
32	AO	183/258 (71%)	178 (97%)	5 (3%)	0	100	100
33	AP	93/142 (66%)	85 (91%)	8 (9%)	0	100	100
34	AQ	83/86 (96%)	78 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	AR	248/360 (69%)	237 (96%)	11 (4%)	0	100	100
36	AS	131/190 (69%)	124 (95%)	7 (5%)	0	100	100
37	AT	160/173 (92%)	149 (93%)	11 (7%)	0	100	100
38	AU	171/205 (83%)	167 (98%)	4 (2%)	0	100	100
39	AV	341/414 (82%)	322 (94%)	19 (6%)	0	100	100
40	AW	95/187 (51%)	92 (97%)	3 (3%)	0	100	100
41	AX	342/348 (98%)	324 (95%)	18 (5%)	0	100	100
42	AY	111/395 (28%)	104 (94%)	7 (6%)	0	100	100
43	AZ	84/106 (79%)	83 (99%)	1 (1%)	0	100	100
45	XD	234/305 (77%)	223 (95%)	9 (4%)	2 (1%)	17	55
46	XE	302/348 (87%)	290 (96%)	12 (4%)	0	100	100
47	XF	248/311 (80%)	238 (96%)	10 (4%)	0	100	100
48	XH	93/267 (35%)	87 (94%)	6 (6%)	0	100	100
49	XI	209/261 (80%)	194 (93%)	15 (7%)	0	100	100
50	XJ	168/192 (88%)	156 (93%)	12 (7%)	0	100	100
51	XK	175/178 (98%)	168 (96%)	7 (4%)	0	100	100
52	XL	113/145 (78%)	107 (95%)	6 (5%)	0	100	100
53	XM	285/296 (96%)	271 (95%)	14 (5%)	0	100	100
54	XN	219/251 (87%)	206 (94%)	13 (6%)	0	100	100
55	XO	150/175 (86%)	142 (95%)	8 (5%)	0	100	100
56	XP	141/179 (79%)	131 (93%)	10 (7%)	0	100	100
57	XQ	236/292 (81%)	222 (94%)	14 (6%)	0	100	100
58	XR	138/149 (93%)	133 (96%)	5 (4%)	0	100	100
59	XS	158/205 (77%)	152 (96%)	6 (4%)	0	100	100
60	XT	164/212 (77%)	160 (98%)	4 (2%)	0	100	100
61	XU	137/153 (90%)	130 (95%)	7 (5%)	0	100	100
62	XV	200/216 (93%)	191 (96%)	9 (4%)	0	100	100
63	XW	109/148 (74%)	105 (96%)	4 (4%)	0	100	100
64	XX	241/256 (94%)	230 (95%)	11 (5%)	0	100	100
65	XY	176/250 (70%)	169 (96%)	7 (4%)	0	100	100
66	XZ	118/161 (73%)	116 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	a	93/142 (66%)	83 (89%)	10 (11%)	0	100	100
68	b	146/215 (68%)	135 (92%)	11 (8%)	0	100	100
69	c	271/332 (82%)	259 (96%)	12 (4%)	0	100	100
70	d	211/306 (69%)	201 (95%)	9 (4%)	1 (0%)	29	67
71	e	211/279 (76%)	206 (98%)	5 (2%)	0	100	100
72	f	138/212 (65%)	131 (95%)	7 (5%)	0	100	100
73	g	130/166 (78%)	122 (94%)	8 (6%)	0	100	100
74	h	106/158 (67%)	101 (95%)	5 (5%)	0	100	100
75	i	95/128 (74%)	92 (97%)	3 (3%)	0	100	100
76	j	84/123 (68%)	83 (99%)	1 (1%)	0	100	100
77	k	93/112 (83%)	87 (94%)	6 (6%)	0	100	100
78	l	78/138 (56%)	72 (92%)	6 (8%)	0	100	100
79	m	58/128 (45%)	53 (91%)	5 (9%)	0	100	100
80	o	92/102 (90%)	87 (95%)	5 (5%)	0	100	100
81	p	119/206 (58%)	114 (96%)	5 (4%)	0	100	100
82	q	162/198 (82%)	159 (98%)	3 (2%)	0	100	100
83	r	144/196 (74%)	136 (94%)	8 (6%)	0	100	100
84	s	366/439 (83%)	352 (96%)	14 (4%)	0	100	100
85	t1	45/198 (23%)	42 (93%)	3 (7%)	0	100	100
85	t2	28/198 (14%)	28 (100%)	0	0	100	100
85	t3	28/198 (14%)	28 (100%)	0	0	100	100
85	t4	27/198 (14%)	25 (93%)	2 (7%)	0	100	100
85	t5	27/198 (14%)	26 (96%)	1 (4%)	0	100	100
85	t6	25/198 (13%)	25 (100%)	0	0	100	100
86	A	2/8 (25%)	0	0	2 (100%)	0	0
All	All	13976/19235 (73%)	13324 (95%)	647 (5%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
86	A	2	THR
86	A	4	PRO
45	XD	207	ILE

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Mol	Chain	Res	Type
45	XD	208	ARG
70	d	289	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	97/164 (59%)	97 (100%)	0	100	100
2	1	50/60 (83%)	50 (100%)	0	100	100
3	2	40/72 (56%)	40 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	37/89 (42%)	37 (100%)	0	100	100
6	5	353/368 (96%)	351 (99%)	2 (1%)	86	92
7	6	313/332 (94%)	312 (100%)	1 (0%)	92	95
8	7	267/303 (88%)	267 (100%)	0	100	100
9	8	124/190 (65%)	123 (99%)	1 (1%)	81	89
10	9	104/112 (93%)	104 (100%)	0	100	100
12	A0	176/190 (93%)	175 (99%)	1 (1%)	86	92
13	A1	253/291 (87%)	250 (99%)	3 (1%)	71	84
14	A2	99/101 (98%)	96 (97%)	3 (3%)	41	64
15	A3	63/166 (38%)	63 (100%)	0	100	100
16	A4	500/566 (88%)	498 (100%)	2 (0%)	91	94
17	A5	171/171 (100%)	171 (100%)	0	100	100
19	AB	192/249 (77%)	192 (100%)	0	100	100
20	AC	115/143 (80%)	115 (100%)	0	100	100
21	AD	283/357 (79%)	281 (99%)	2 (1%)	84	90
22	AE	104/107 (97%)	104 (100%)	0	100	100
23	AF	178/209 (85%)	178 (100%)	0	100	100
24	AG	264/342 (77%)	264 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	AH	125/180 (69%)	125 (100%)	0	100	100
26	AI	104/147 (71%)	104 (100%)	0	100	100
27	AJ	93/118 (79%)	92 (99%)	1 (1%)	73	85
28	AK	91/113 (80%)	91 (100%)	0	100	100
29	AL	152/226 (67%)	152 (100%)	0	100	100
30	AM	95/113 (84%)	95 (100%)	0	100	100
31	AN	93/115 (81%)	93 (100%)	0	100	100
32	AO	166/230 (72%)	166 (100%)	0	100	100
33	AP	86/123 (70%)	85 (99%)	1 (1%)	71	84
34	AQ	77/78 (99%)	77 (100%)	0	100	100
35	AR	229/318 (72%)	227 (99%)	2 (1%)	78	88
36	AS	115/164 (70%)	114 (99%)	1 (1%)	78	88
37	AT	150/157 (96%)	150 (100%)	0	100	100
38	AU	149/174 (86%)	148 (99%)	1 (1%)	84	90
39	AV	315/364 (86%)	314 (100%)	1 (0%)	92	95
40	AW	84/158 (53%)	84 (100%)	0	100	100
41	AX	307/308 (100%)	304 (99%)	3 (1%)	76	86
42	AY	104/357 (29%)	104 (100%)	0	100	100
43	AZ	79/95 (83%)	79 (100%)	0	100	100
45	XD	190/245 (78%)	189 (100%)	1 (0%)	88	93
46	XE	259/290 (89%)	259 (100%)	0	100	100
47	XF	217/262 (83%)	217 (100%)	0	100	100
48	XH	86/228 (38%)	86 (100%)	0	100	100
49	XI	194/232 (84%)	194 (100%)	0	100	100
50	XJ	133/150 (89%)	132 (99%)	1 (1%)	81	89
51	XK	155/156 (99%)	155 (100%)	0	100	100
52	XL	98/124 (79%)	98 (100%)	0	100	100
53	XM	245/249 (98%)	244 (100%)	1 (0%)	91	94
54	XN	188/211 (89%)	188 (100%)	0	100	100
55	XO	133/150 (89%)	133 (100%)	0	100	100
56	XP	125/154 (81%)	125 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	XQ	220/256 (86%)	220 (100%)	0	100	100
58	XR	118/126 (94%)	117 (99%)	1 (1%)	81	89
59	XS	145/180 (81%)	145 (100%)	0	100	100
60	XT	146/182 (80%)	144 (99%)	2 (1%)	67	81
61	XU	126/135 (93%)	126 (100%)	0	100	100
62	XV	179/191 (94%)	177 (99%)	2 (1%)	73	85
63	XW	91/119 (76%)	89 (98%)	2 (2%)	52	71
64	XX	219/229 (96%)	219 (100%)	0	100	100
65	XY	161/223 (72%)	161 (100%)	0	100	100
66	XZ	111/147 (76%)	111 (100%)	0	100	100
67	a	93/133 (70%)	93 (100%)	0	100	100
68	b	130/186 (70%)	130 (100%)	0	100	100
69	c	241/288 (84%)	240 (100%)	1 (0%)	91	94
70	d	196/273 (72%)	196 (100%)	0	100	100
71	e	188/236 (80%)	185 (98%)	3 (2%)	62	79
72	f	127/188 (68%)	127 (100%)	0	100	100
73	g	122/148 (82%)	122 (100%)	0	100	100
74	h	103/148 (70%)	103 (100%)	0	100	100
75	i	86/110 (78%)	86 (100%)	0	100	100
76	j	68/97 (70%)	68 (100%)	0	100	100
77	k	80/90 (89%)	80 (100%)	0	100	100
78	l	74/116 (64%)	74 (100%)	0	100	100
79	m	54/113 (48%)	54 (100%)	0	100	100
80	o	80/87 (92%)	80 (100%)	0	100	100
81	p	117/181 (65%)	117 (100%)	0	100	100
82	q	141/163 (86%)	141 (100%)	0	100	100
83	r	138/169 (82%)	138 (100%)	0	100	100
84	s	326/381 (86%)	325 (100%)	1 (0%)	92	95
85	t1	41/158 (26%)	40 (98%)	1 (2%)	49	69
85	t2	29/158 (18%)	29 (100%)	0	100	100
85	t3	29/158 (18%)	29 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
85	t4	28/158 (18%)	28 (100%)	0	100	100
85	t5	28/158 (18%)	28 (100%)	0	100	100
85	t6	26/158 (16%)	26 (100%)	0	100	100
86	A	2/2 (100%)	2 (100%)	0	100	100
All	All	12571/16582 (76%)	12530 (100%)	41 (0%)	92	95

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	XR	44	ARG
69	c	302	ARG
60	XT	154	LYS
62	XV	212	LYS
71	e	249	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
60	XT	210	HIS
78	l	135	ASN
85	t5	4	GLN
82	q	147	GLN
23	AF	72	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	XA	1492/1559 (95%)	261 (17%)	7 (0%)
18	AA	920/951 (96%)	164 (17%)	3 (0%)
44	XB	54/73 (73%)	9 (16%)	0
All	All	2466/2583 (95%)	434 (17%)	10 (0%)

5 of 434 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	XA	1672	C
11	XA	1674	A
11	XA	1681	G

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Mol	Chain	Res	Type
11	XA	1685	C
11	XA	1689	C

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	AA	770	C
18	AA	1048	C
18	AA	1234	C
11	XA	2558	A
11	XA	2574	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
86	004	A	7	86	9,10,11	1.03	0	9,12,14	0.90	0
86	MHW	A	1	86	9,9,10	2.62	3 (33%)	10,11,13	2.58	2 (20%)
86	DBB	A	3	86	4,5,6	0.81	0	1,5,7	0.81	0
86	MHU	A	5	86	14,15,16	2.19	4 (28%)	18,19,21	1.49	3 (16%)
86	MHV	A	6	86	7,9,10	6.01	1 (14%)	7,11,13	6.05	5 (71%)

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
86	004	A	7	86	-	2/4/6/8	0/1/1/1
86	MHW	A	1	86	-	2/2/2/4	0/1/1/1
86	DBB	A	3	86	-	3/3/4/6	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	MHU	A	5	86	-	0/9/12/14	0/1/1/1
86	MHV	A	6	86	-	0/1/12/14	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	A	6	MHV	OD1-CG	15.69	1.48	1.21
86	A	5	MHU	CZ-NZ	6.19	1.52	1.37
86	A	1	MHW	CA-C	5.81	1.54	1.48
86	A	1	MHW	OG1-CB	4.21	1.45	1.36
86	A	1	MHW	CB-CA	-2.39	1.36	1.40

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	A	6	MHV	OD1-CG-CB	-12.24	106.43	121.96
86	A	6	MHV	OD1-CG-CD2	-8.64	107.29	122.05
86	A	1	MHW	O-C-CA	-7.21	117.39	124.22
86	A	5	MHU	CM-N-CA	3.50	124.52	113.64
86	A	6	MHV	CB-CA-N	-3.45	105.36	112.50

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	A	1	MHW	O-C-CA-N
86	A	1	MHW	O-C-CA-CB
86	A	3	DBB	O-C-CA-CB
86	A	3	DBB	C-CA-CB-CG
86	A	3	DBB	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	A	1	MHW	2	0

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 204 ligands modelled in this entry, 202 are monoatomic - leaving 2 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
90	GTP	AX	500	-	26,34,34	1.11	2 (7%)	32,54,54	1.49	6 (18%)
89	DOL	XA	5141	-	43,50,50	3.48	14 (32%)	51,70,70	2.75	13 (25%)

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
90	GTP	AX	500	-	-	8/18/38/38	0/3/3/3
89	DOL	XA	5141	-	-	16/58/77/77	0/2/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	XA	5141	DOL	C28-C29	10.18	1.56	1.32
89	XA	5141	DOL	C22-C23	9.53	1.56	1.32
89	XA	5141	DOL	C19-C20	7.15	1.56	1.34
89	XA	5141	DOL	C26-N25	6.58	1.48	1.34
89	XA	5141	DOL	C6-N5	6.42	1.49	1.34

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	XA	5141	DOL	O40-S39-O41	-14.72	101.41	118.19
89	XA	5141	DOL	C24-N25-C26	-6.43	111.63	122.03
89	XA	5141	DOL	C4-N5-C1	-3.69	107.91	112.45
90	AX	500	GTP	PA-O3A-PB	-3.65	120.31	132.83
89	XA	5141	DOL	C32-O36-C37	-3.61	111.58	117.78

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

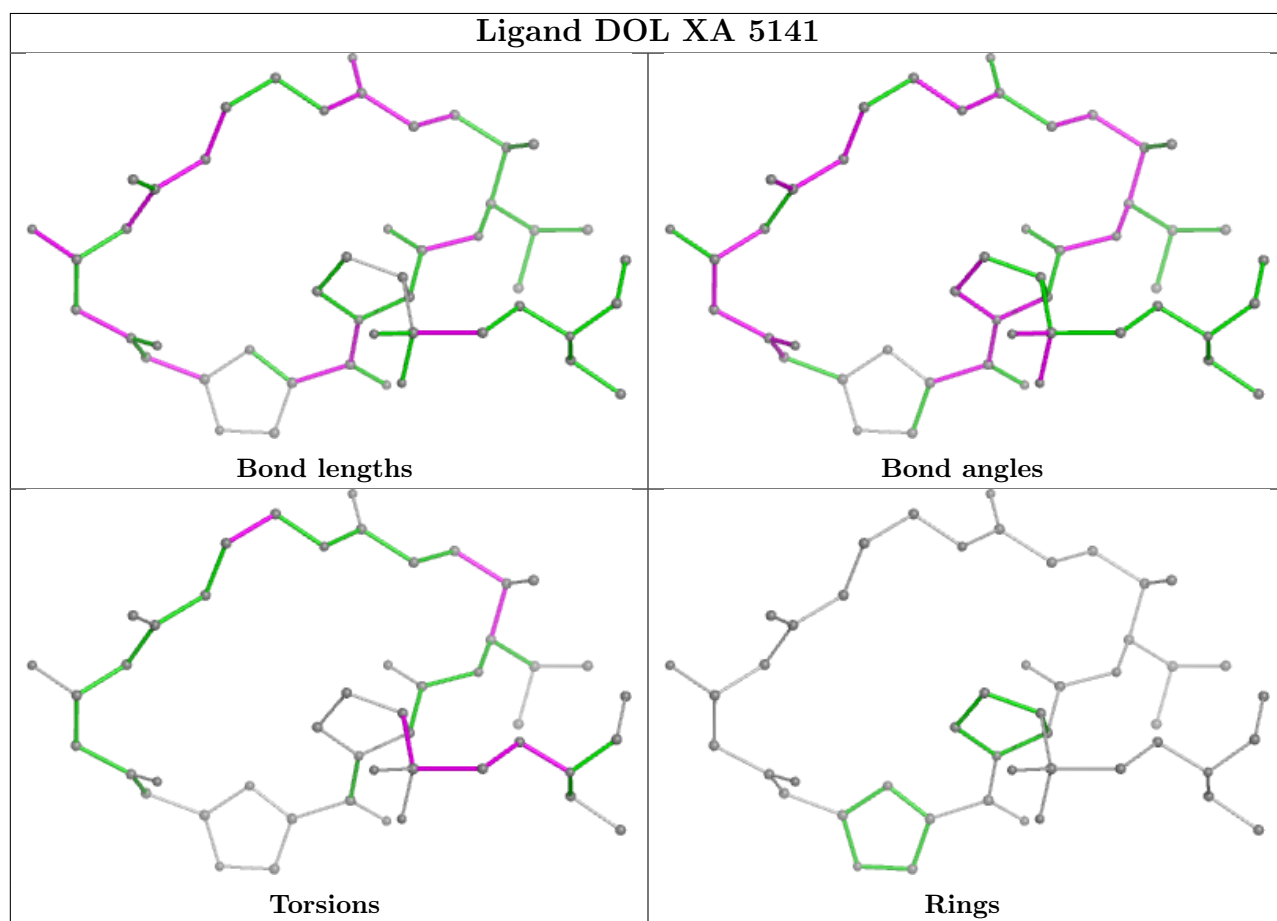
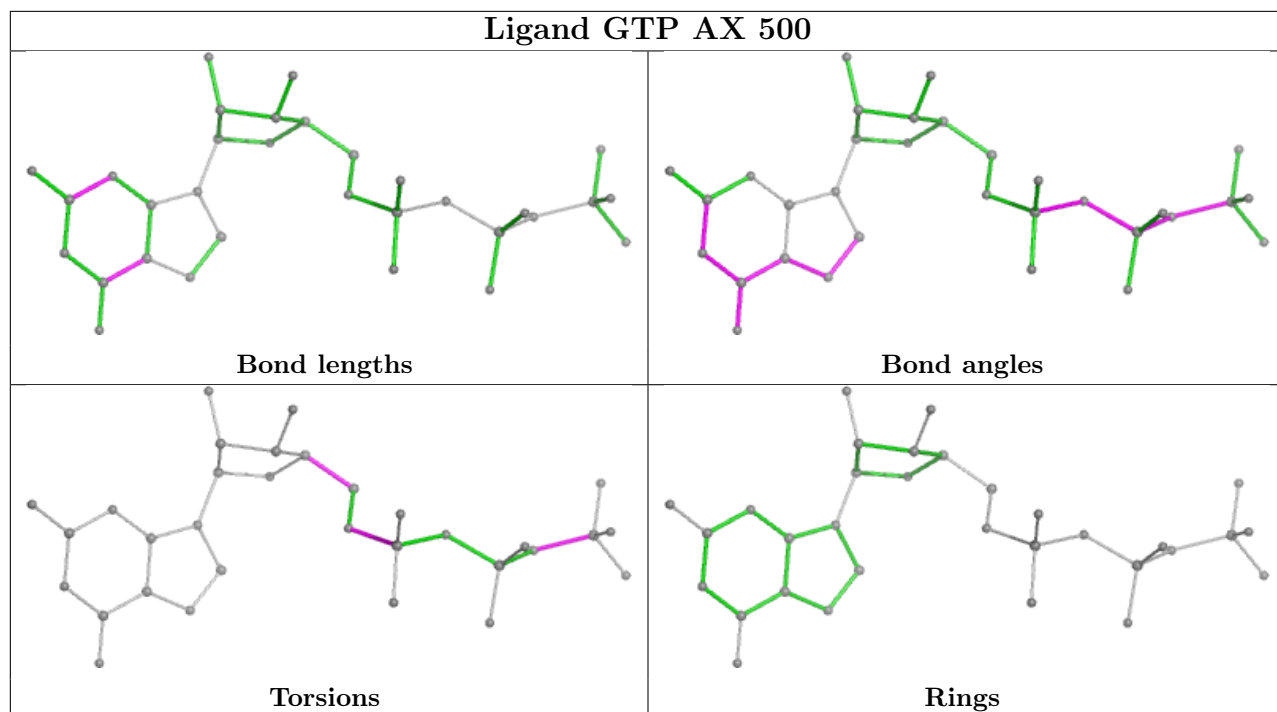
Mol	Chain	Res	Type	Atoms
89	XA	5141	DOL	C1-C2-S39-O41
89	XA	5141	DOL	C1-C2-S39-O40
89	XA	5141	DOL	C43-C42-S39-C2
89	XA	5141	DOL	C43-C42-S39-O41
89	XA	5141	DOL	C29-C30-C32-C33

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
90	AX	500	GTP	1	0
89	XA	5141	DOL	4	0

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



5.7 Other polymers [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
8	7	2
41	AX	2
7	6	2
18	AA	1
16	A4	1
83	r	1
39	AV	1
17	A5	1
70	d	1
86	A	1

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	1383:A	O3'	1388:C	P	8.11
1	A4	537:ARG	C	538:ASP	N	6.58
1	7	285:ASN	C	286:LEU	N	5.98
1	r	134:ARG	C	135:LEU	N	5.36
1	AV	269:SER	C	270:PRO	N	5.00

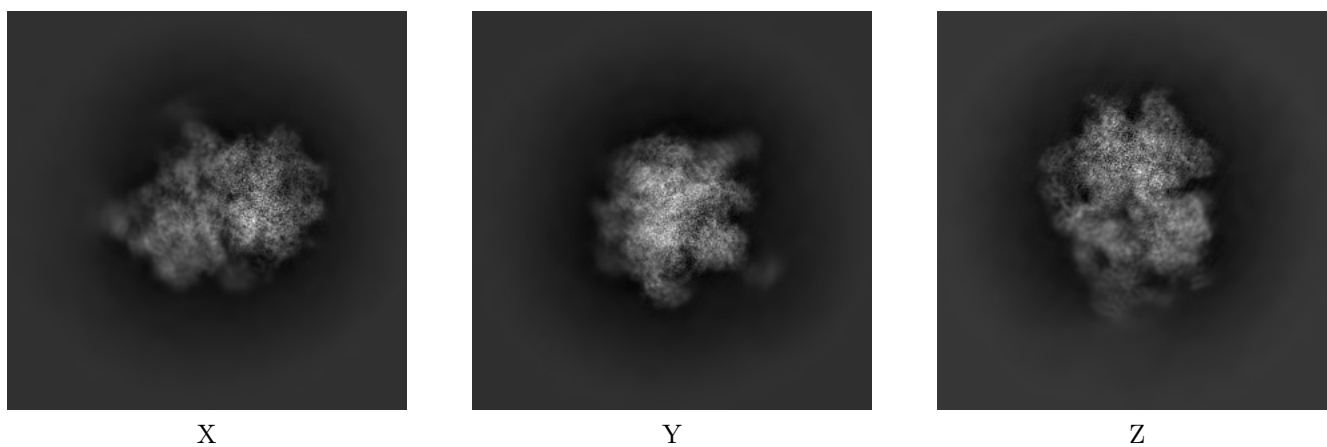
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11390. 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 [i](#)

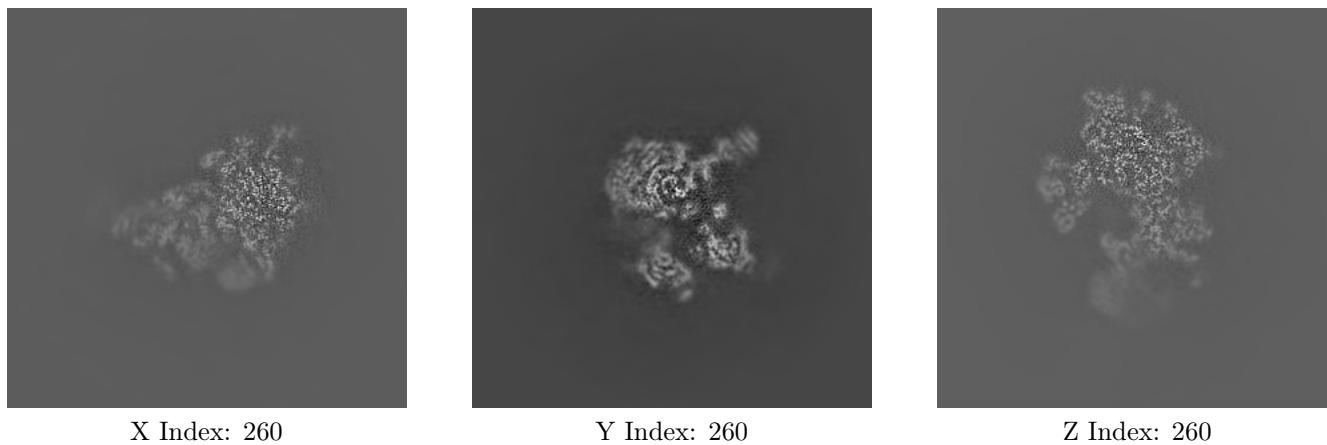
6.1.1 Primary map



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

6.2 Central slices [i](#)

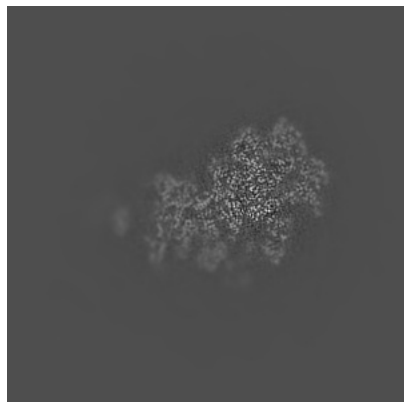
6.2.1 Primary map



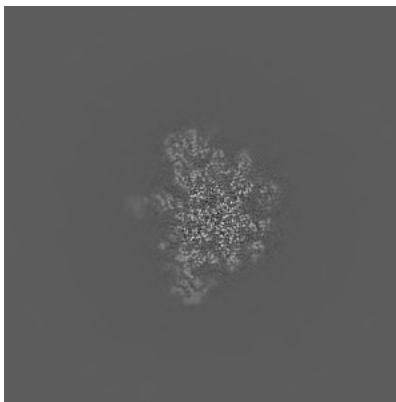
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

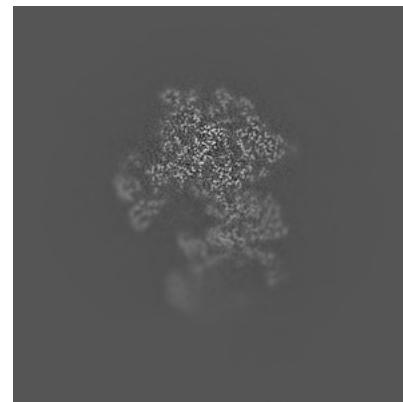
6.3.1 Primary map



X Index: 278



Y Index: 321

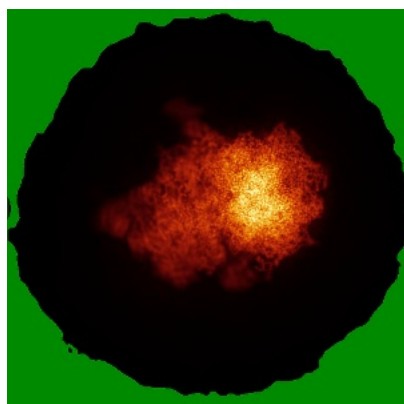


Z Index: 264

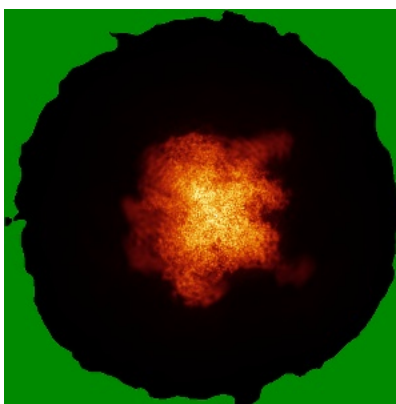
The images above show the largest variance slices of the map in three orthogonal directions.

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

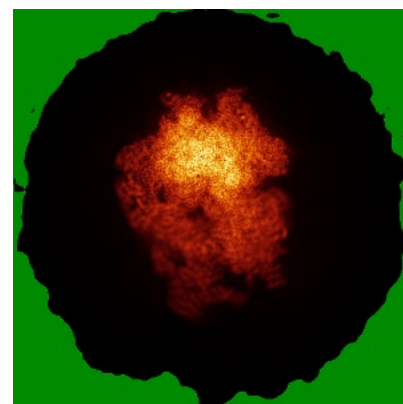
6.4.1 Primary map



X



Y

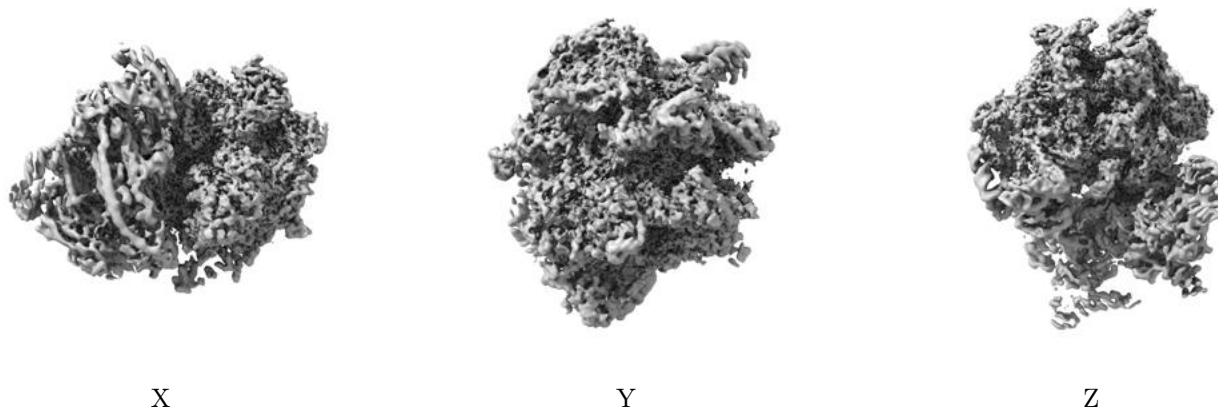


Z

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 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

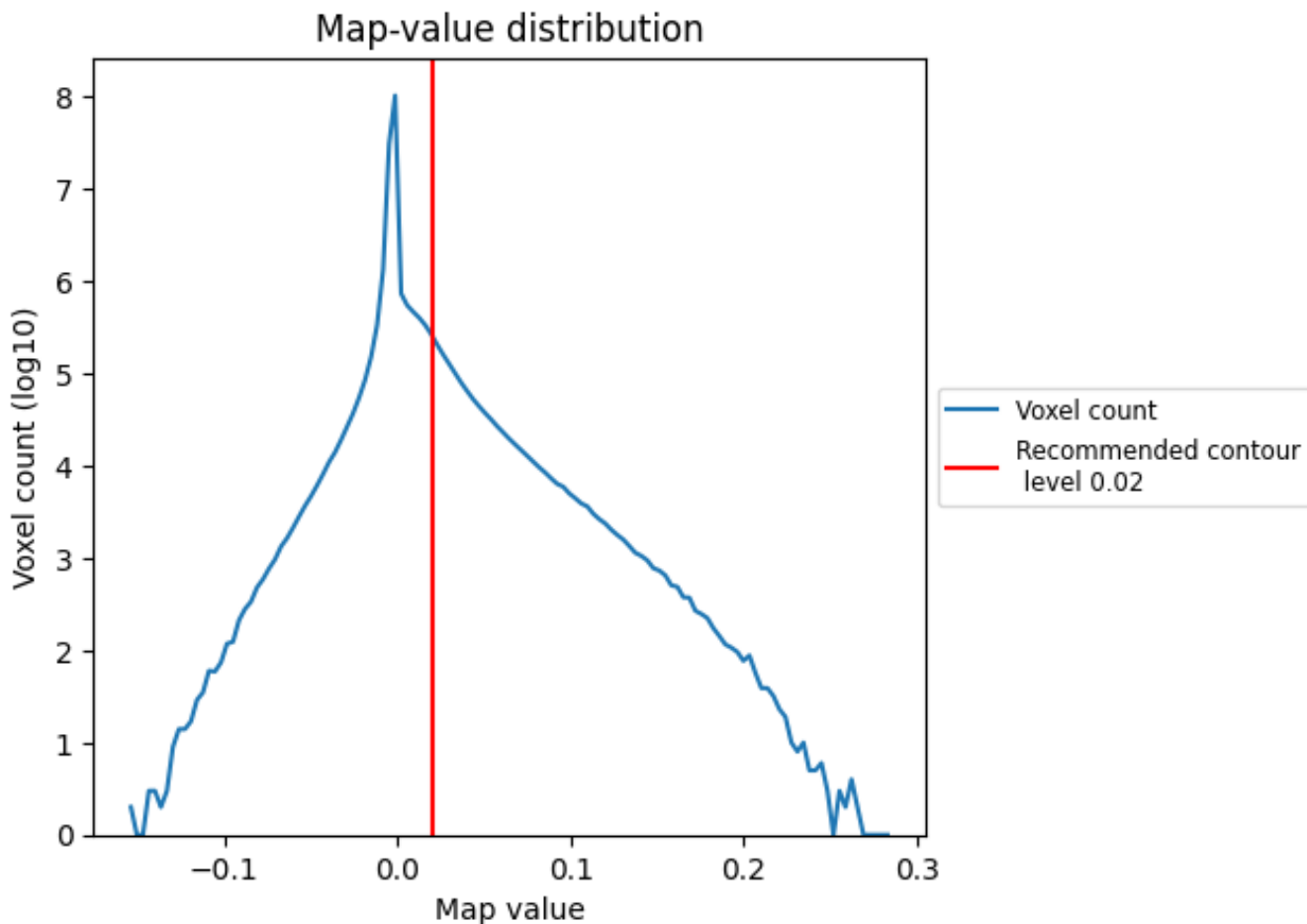
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

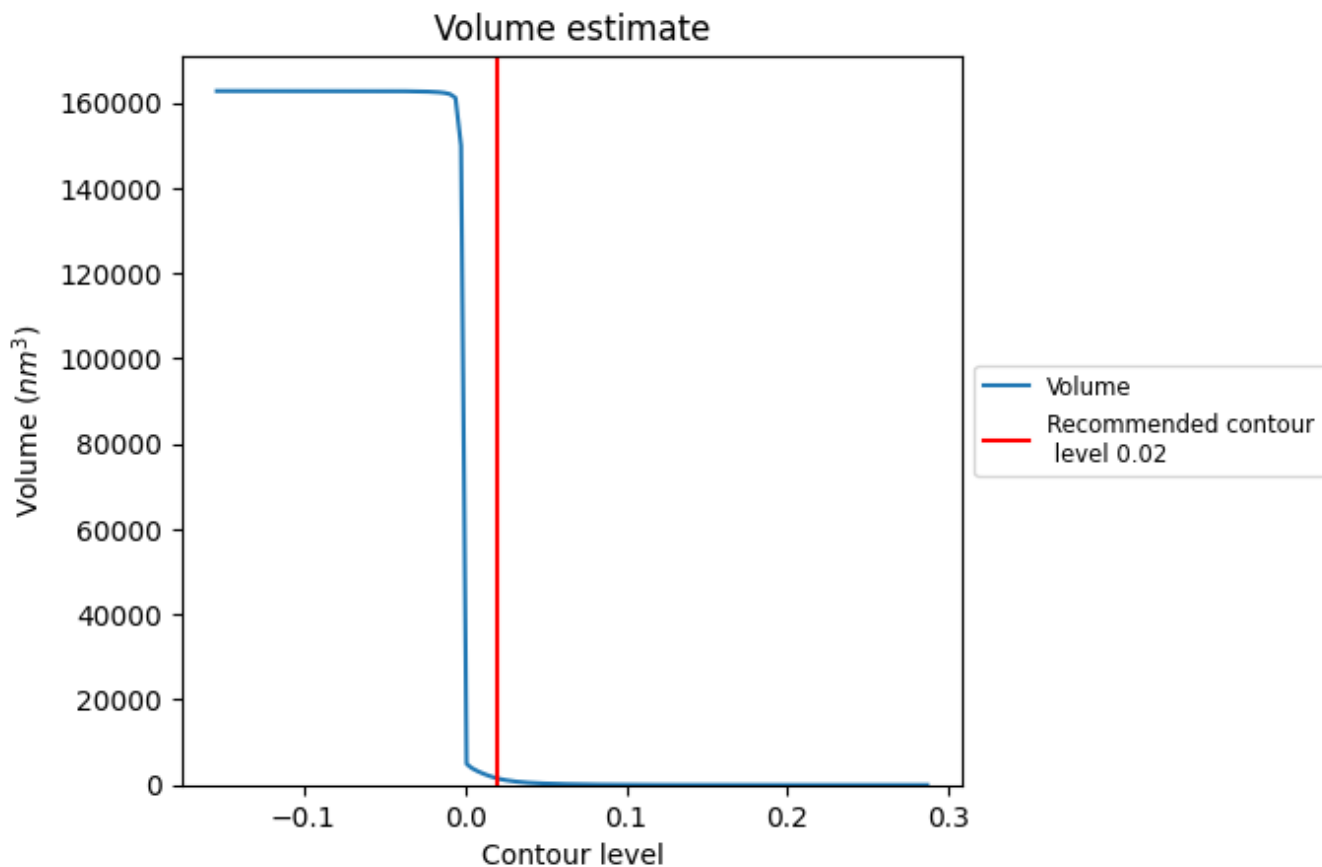
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

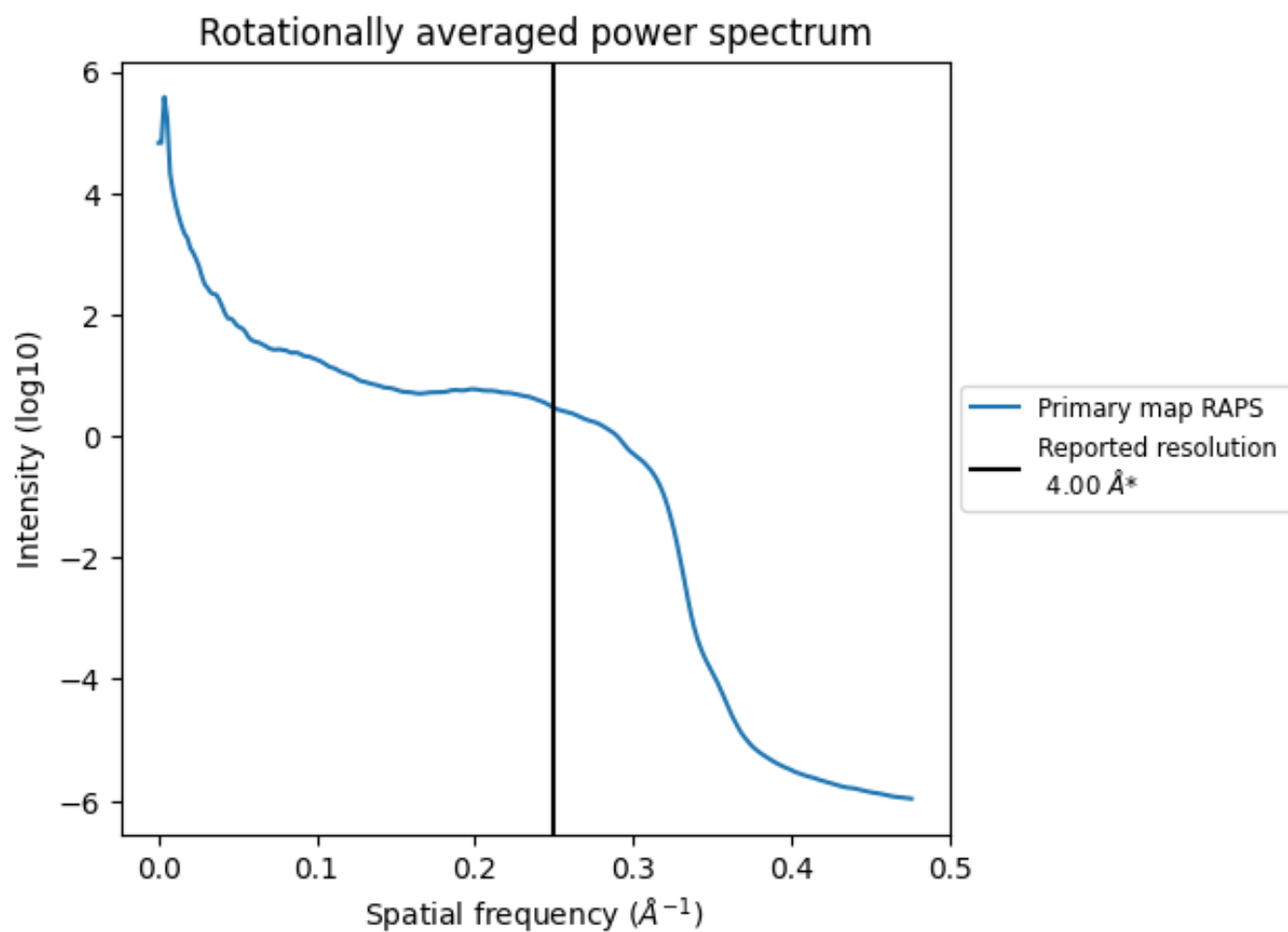
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1563 nm^3 ; this corresponds to an approximate mass of 1412 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.250\AA^{-1}

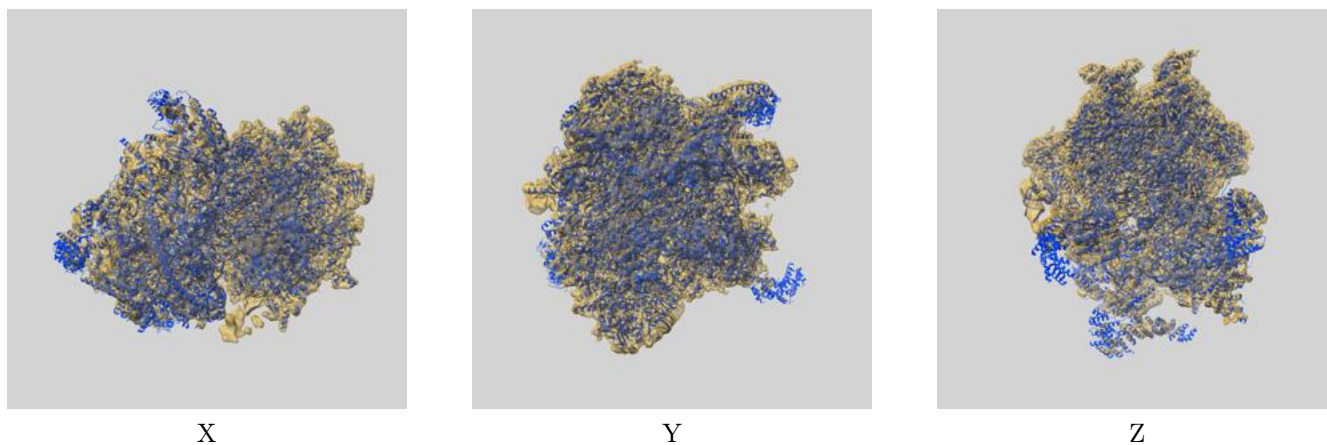
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

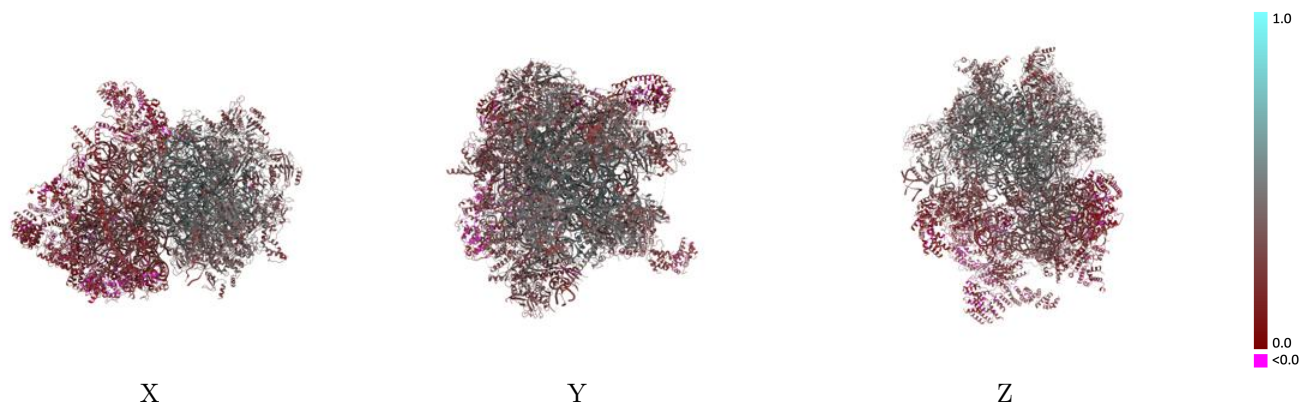
This section contains information regarding the fit between EMDB map EMD-11390 and PDB model 6ZS9. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



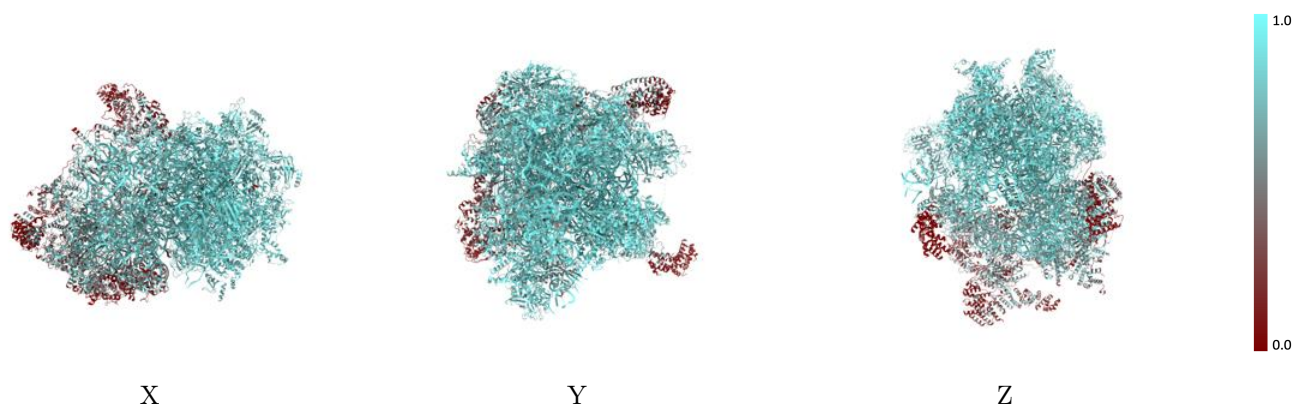
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



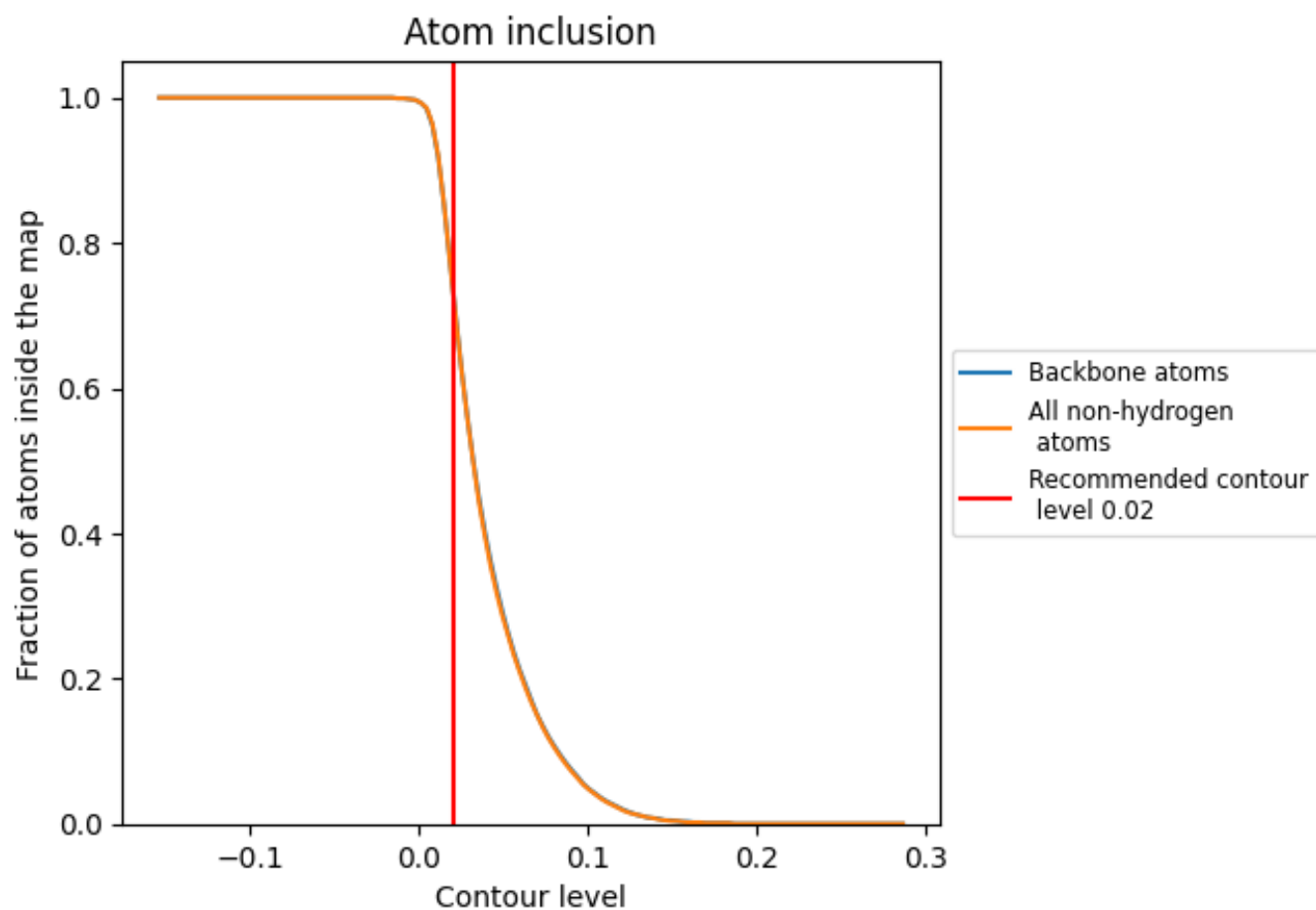
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 73% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7340	 0.3220
0	 0.8690	 0.4080
1	 0.8380	 0.3940
2	 0.9170	 0.5100
3	 0.8950	 0.4860
4	 0.9110	 0.4660
5	 0.8290	 0.3750
6	 0.8140	 0.3390
7	 0.7920	 0.3450
8	 0.5980	 0.2100
9	 0.8230	 0.3920
A	 0.8900	 0.4820
A0	 0.5810	 0.1780
A1	 0.2490	 0.1060
A2	 0.3720	 0.1990
A3	 0.7870	 0.3580
A4	 0.2210	 0.1310
A5	 0.5650	 0.2350
AA	 0.8810	 0.2660
AB	 0.6390	 0.1850
AC	 0.4620	 0.1490
AD	 0.5750	 0.2260
AE	 0.4920	 0.1860
AF	 0.3010	 0.1090
AG	 0.4580	 0.1420
AH	 0.2400	 0.1200
AI	 0.5450	 0.1730
AJ	 0.7230	 0.3000
AK	 0.4830	 0.0970
AL	 0.5550	 0.1820
AM	 0.5870	 0.1950
AN	 0.6480	 0.2110
AO	 0.6160	 0.2230
AP	 0.5320	 0.1890
AQ	 0.6700	 0.2480

































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Chain	Atom inclusion	Q-score
AR	0.5380	0.1660
AS	0.5060	0.1830
AT	0.6470	0.2290
AU	0.5110	0.1810
AV	0.3200	0.1320
AW	0.5490	0.1580
AX	0.1840	0.0640
AY	0.2640	0.1160
AZ	0.3230	0.1370
XA	0.9540	0.4670
XB	0.9580	0.3160
XD	0.8580	0.4280
XE	0.8690	0.4320
XF	0.8810	0.4510
XH	0.7950	0.3670
XI	0.5960	0.2500
XJ	0.6560	0.2080
XK	0.8680	0.4460
XL	0.8720	0.4420
XM	0.8690	0.4280
XN	0.8540	0.4310
XO	0.8580	0.4160
XP	0.8330	0.3680
XQ	0.7620	0.3760
XR	0.8660	0.4470
XS	0.8630	0.4440
XT	0.8720	0.4470
XU	0.8650	0.4200
XV	0.8210	0.3660
XW	0.8930	0.4700
XX	0.8300	0.3870
XY	0.8700	0.4200
XZ	0.8870	0.4600
a	0.8320	0.3980
b	0.8870	0.4390
c	0.8410	0.3820
d	0.7640	0.3340
e	0.6470	0.1870
f	0.6570	0.2440
g	0.8480	0.4110
h	0.8000	0.3470
i	0.8690	0.4730

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Chain	Atom inclusion	Q-score
j	 0.8500	 0.4030
k	 0.7660	 0.2760
l	 0.7220	 0.2560
m	 0.6570	 0.2000
o	 0.9070	 0.4700
p	 0.7970	 0.3320
q	 0.6440	 0.3000
r	 0.8670	 0.4100
s	 0.8610	 0.4140
t1	 0.2520	 0.2020
t2	 0.2020	 0.1940
t3	 0.0000	 0.1650
t4	 0.0000	 0.1480
t5	 0.0000	 0.1500
t6	 0.0000	 0.1200